

Galactose Oxidase Oxidation and Glycosidase Digestion for GlycoRNA Analysis

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Contents

Experiments and Data Analysis	3
Comprehensive Workflow for Small RNA Sequences	3
Raw RNA-seq Data Processing	3
Small RNA Identification	3
Supplementary Tables	4
Table S1. The list of identified glycosylated miRNAs from colon tissue.	4
Table S2. The list o	8
Table S3. The list of identified glycosylated snoRNA in paracancerous tissue (PCA) and cancer tissue (CA).	79

Experiments and Data Analysis

Comprehensive Workflow for Small RNA Sequences. Sequence small RNAs using the Illumina HiSeq or MGISEQ-2000 platform with paired-end reads of 150 base pairs (PE150) to generate Illumina NGS data. Analyze GlycoRNA data on Ubuntu 20.04.6 by following this detailed workflow to examine the raw data (Pass Filter Data).

Raw RNA-seq Data Processing. Initially, raw sequencing data undergoes quality control and preprocessing using Trimmomatic software (version 0.30). This step eliminates adapter sequences and low-quality reads, resulting in clean data suitable for further analysis. The output is a high-quality dataset devoid of adapter contamination and low-quality sequences, ensuring reliable and accurate downstream analysis.

Small RNA Identification. Next, the Rfam database (version 14), containing a comprehensive collection of non-coding RNA family sequences, is downloaded, along with the Homo_sapiens.GRCh38.ncrna.fa file containing human genomic non-coding RNA data. These resources are combined to create a non-coding RNA database. BLASTN (V2.2.28+) is then used to align the Clean Data with this database, identifying the most optimal matches to classify non-coding miRNAs, tRNAs, and snoRNAs.

Supplementary Tables

Table S1. The list of identified glycosylated miRNAs from colon tissue. The N-glycoRNAs are enriched by SPCgRNA. NT

= Nucleotide Length, TPM = Transcripts Per Million, PCA = Paracancerous Tissue, CA = Cancer Tissue.

Gene	NT	PCA-TPM				CA-TPM			
		#1	#2	#3	#4	#1	#2	#3	#4
let-7a-3p	21	0	6.66	40.68	0	0	102.97	259.78	0
let-7b-5p	22	0	492.74	399.61	0	0	289.59	116.32	0
let-7c-5p	22	0	0	31.11	0	0	0	0	42.18
let-7e-5p	22	0	43.28	0	0	0	0	0	87.37
let-7i-5p	22	0	0	1275.4	346.39	0	0	639.76	2009.53
miR-106a-5p	23	0	0	23.93	22.71	0	83.66	0	0
miR-106b-3p	22	0	0	703.5	0	0	0	4424.02	3136.31
miR-10b-5p	23	8899.05	18990.36	82996.74	0	9103.41	7020.95	19502.93	0
miR-1185-1-3p	22	0	0	0	0	0	64.35	42.65	0
miR-125a-5p	24	335.33	542.68	0	0	221.93	250.98	0	0
miR-125b-5p	22	388.28	635.9	0	0	413.4	360.38	0	0
miR-1260b	19	0	0	445.07	0	0	1962.78	2958.4	1021.34
miR-127-5p	22	892.26	1201.88	0	0	857.25	572.75	0	0
miR-1296-5p	22	213.75	236.38	0	119.25	130.55	0	0	34.65
miR-133a-3p	22	145.11	289.65	0	0	87.03	96.53	0	0
miR-135b-3p	22	0	0	0	0	0	0	263.66	149.13
miR-135b-5p	23	0	0	0	0	356.83	257.41	0	0
miR-139-5p	23	27.45	53.27	0	0	0	0	0	0
miR-1-3p	22	0	429.48	1634.33	0	0	180.19	434.26	0
miR-142-3p	23	0	342.92	0	0	0	0	0	213.91
miR-143-3p	21	0	152152.56	0	64656.45	0	86265.7	0	404361.31
miR-143-5p	22	2910.13	2586.87	971.51	0	1740.61	1242.02	5905.16	0
miR-145-3p	22	302	712.47	0	0	161.01	173.75	0	0

miR-146a-5p	22	0	0	983.47	0	0	0	407.12	735.12
miR-146b-5p	23	0	0	1579.29	164.68	1005.2	0	922.8	1465.72
miR-148a-5p	22	878.53	0	390.04	306.64	983.45	0	131.83	108.46
miR-149-5p	23	33.34	0	21.54	0	0	0	0	0
miR-15a-5p	22	0	0	0	0	82.68	0	54.28	0
miR-16-5p	22	115.7	143.16	1689.37	56.79	1527.39	965.3	814.24	513.68
miR-17-5p	23	402.01	506.05	799.22	289.61	5474.23	3616.66	434.26	171.73
miR-181a-3p	22	0	0	23.93	28.39	0	0	531.19	341.95
miR-181c-3p	22	0	0	7.18	0	0	0	158.97	106.95
miR-181d-5p	23	0	0	0	0	91.38	64.35	0	0
miR-182-5p	24	145.11	0	2002.83	130.61	1257.59	0	65.91	63.27
miR-183-5p	22	80.4	0	478.57	0	822.44	0	0	0
miR-185-3p	22	41.18	0	14.36	0	21.76	0	189.99	0
miR-186-5p	22	5930.09	6888.33	3929.09	1993.19	6749.23	4080	2694.74	1256.33
miR-188-5p	21	0	0	0	0	43.52	51.48	0	0
miR-18a-5p	23	21.57	39.95	0	22.71	361.18	212.37	0	0
miR-192-3p	22	0	0	131.61	28.39	0	0	11.63	9.04
miR-192-5p	21	70861	154453.11	146175.71	36791.6	78832.4	76895.85	2113.14	2359.01
miR-194-5p	22	0	0	14048.55	3997.73	0	0	205.5	147.63
miR-196b-3p	22	0	0	4.79	0	0	0	209.38	170.22
miR-196b-5p	22	0	0	399.61	0	0	0	108.57	138.59
miR-19a-3p	23	94.13	83.23	105.29	34.07	0	0	0	0
miR-200a-3p	22	0	0	10487.95	4968.77	0	0	5672.52	4347.45
miR-200a-5p	22	0	0	1067.22	982.4	0	0	73.67	79.84
miR-200b-5p	22	0	0	201	68.14	0	0	38.77	12.05
miR-20a-3p	22	0	0	4.79	0	0	0	143.46	66.28
miR-20a-5p	23	1543.31	1621.37	2433.55	897.22	19003.15	10599	1178.71	445.89
miR-210-3p	22	531.43	945.52	0	0	522.18	527.7	0	0
miR-21-3p	21	0	569.31	473.79	0	0	3623.1	4776.86	0
miR-214-3p	22	0	0	71.79	0	221.93	0	348.96	0
miR-215-5p	21	0	23168.63	39278.98	6763.2	0	10895.03	488.54	497.11
miR-21-5p	22	33870.52	47366.02	0	23503.69	357796.21	301328.25	0	225249.57

miR-217-5p	23	0	0	0	0	0	0	65.91	54.23
miR-218-5p	21	0	39.95	0	0	0	0	0	78.33
miR-221-5p	22	0	0	74.18	0	174.06	0	0	0
miR-223-3p	22	19.61	0	0	0	461.26	315.33	0	0
miR-224-5p	25	0	0	0	0	369.88	373.25	0	0
miR-23b-3p	23	0	592.62	1445.29	0	0	0	0	0
miR-26a-5p	22	484.37	496.07	5587.35	0	3768.43	2844.42	3078.59	0
miR-26b-5p	21	15.69	33.29	220.14	0	178.41	186.62	108.57	0
miR-27a-3p	21	1682.54	702.48	3196.88	0	14625.51	12130.61	25291.77	0
miR-28-3p	22	6351.7	12082.05	0	0	4978.16	5682.4	0	0
miR-30c-2-3p	22	25.49	63.26	0	0	0	12.87	0	0
miR-3158-3p	22	15.69	26.63	0	0	0	0	0	0
miR-320a-3p	22	0	1524.82	0	0	0	727.19	0	772.78
miR-335-3p	22	41.18	19.98	0	0	718	405.43	0	0
miR-362-5p	24	0	0	45.46	28.39	0	0	0	0
miR-374a-3p	22	86.28	116.53	0	221.47	918.17	559.87	0	1840.81
miR-374a-5p	22	154.92	119.85	0	0	1932.08	778.68	0	0
miR-374b-5p	22	84.32	73.24	0	0	818.09	398.99	0	0
miR-375-3p	22	3086.63	12348.39	4031.99	0	1993	3719.63	1407.47	0
miR-378a-3p	22	87457	142154.66	48391.03	63912.55	35055.96	35722.56	17219.18	13018.26
miR-378a-5p	22	158.84	196.43	71.79	51.11	121.84	64.35	34.9	21.09
miR-378d	20	3374.89	5163.75	2299.55	0	0	0	0	0
miR-378i	21	1537.43	2363.81	574.29	0	0	0	0	0
miR-381-3p	22	4614.25	0	0	3781.94	4912.88	0	0	3178.49
miR-382-3p	21	0	0	21.54	0	0	77.22	178.36	0
miR-3913-5p	22	0	53.27	31.11	0	0	0	0	0
miR-3934-5p	22	17.65	29.96	0	0	0	0	0	0
miR-409-5p	23	0	0	0	0	34.81	70.79	0	0
miR-424-5p	22	0	0	0	0	43.52	0	31.02	0
miR-4454	20	180.41	0	0	0	0	0	616.49	224.45
miR-452-5p	22	0	0	67	0	0	141.58	0	46.7
miR-454-3p	23	0	0	16.75	0	39.16	0	0	0

miR-486-5p	22	125.5	0	244.07	0	108.79	0	104.69	0
miR-490-3p	22	45.1	123.18	52.64	0	0	0	767.71	0
miR-503-5p	23	0	0	7.18	0	108.79	96.53	143.46	76.83
miR-542-3p	22	11.77	0	0	28.39	282.85	0	0	593.52
miR-548e-3p	22	0	26.63	43.07	0	0	0	0	0
miR-552-3p	21	0	0	52.64	141.96	0	0	833.62	861.66
miR-584-5p	22	0	0	0	0	73.98	70.79	0	0
miR-652-3p	21	327.49	639.23	0	0	313.31	218.8	0	0
miR-654-3p	22	0	0	11.96	0	78.33	0	96.93	0
miR-6715b-3p	22	17.65	46.61	0	0	0	0	0	0
miR-708-3p	22	0	109.87	28.71	0	0	0	926.68	637.2
miR-708-5p	23	25.49	49.94	19.14	0	239.33	0	286.92	159.68
miR-769-5p	22	2290.46	3608.97	0	0	1670.99	1969.21	0	0
miR-889-3p	21	17.65	36.62	0	0	178.41	212.37	0	0
miR-92a-3p	22	0	1408.3	0	494.04	0	5663.1	0	5264.85
miR-93-5p	23	0	0	1328.04	533.79	0	0	763.83	441.37
miR-9983-3p	22	15.69	36.62	0	0	0	0	0	0
miR-99a-5p	22	119.62	169.79	0	0	108.79	64.35	0	0

Table S2. The list o identified glycosylated tRNA in paracancerous tissue (PCA) and cancer tissue (CA). (a) N-

linked glycosylated tRNAs from PCA, (b) N-linked glycosylated tRNAs from CA

(a)

Qseqid	Sseqid	NT	Evalue	Bitscore	Number	Sequence
ex3_96 6031_x 6622	GL00025 3.2/24775 9-247830	30	#####	60	###	TCCCTGGTGGTCTAGTGGTTAGGATTCGGCGCTCTCACCGCCGCGGCC GGTTTCGATTCCCGGTCAGGGAA
ex3_10 82355_ x5530	AF347001 .1/16015- 15948	20	#####	40.1	###	CAGAGAAUAGUUUAAAUUAGAAUCUUAGCUUUGGGUGCUAAUGGUGGAG UAAAAGACUUUUUCUCUGA
ex3_10 98642_ x5332	AC09268 6.3/29631 -29561	28	#####	56	###	GCAUUGGUGGUUCAGUGGUAGAAUUCUCGCCUGCCACGCGGGAGGCC GGUUCGAUUCGCGCCAAUGCA
ex3_14 20023_ x3131	AF347015 .1/1604- 1672	17	#####	34.2	###	CAGAGUGUAGCUUAAACACAAAGCACCCAACUUACACUUAGGAGAUUUC ACUUAACUUGACCGCUCUGA
ex3_15 74449_ x2459	ENST000 00387421 .1	20	#####	40.1	###	CACTGTAAAGCTAACTTAGCATTAACTTTTAAGTTAAAGATTAAGAGAACC AACACCTC
ex3_16 19497_ x2305	CM00067 8.2/31915 01- 3191573	35	#####	69.9	###	GCCCGGCTAGCTCAGTCGGTAGAGCATGGGACTCTTAATCTCAGGGTCGT GGTTTCGAGCCCCACGTTGGGCG
ex3_17 73623_ x1843	CM00066 3.2/14830 2805- 14830273 4	33	#####	65.9	###	GCCGTGATCGTATAGTGGTTAGTACTCTGCGTTGTGGCCGACGCAACCTC GTTTCGAATCCGAGTCACGGCA
ex3_18 13187_ x1755	AC09331 1.2/14003 6-139968	31	#####	61.9	###	GUUCUUGUAGUUGAAUACAACGAUGGUUUUCAUAUCAUUGGUCGUG GUUGUAGUCCGUGCGAGAAUA
ex3_18 47796_ x1702	CM00067 7.2/26082 305- 26082234	31	#####	61.9	###	TCCCACATGGTCTAGCGGTTAGGATTCCTGGTTTTCCACCCAGGCGGCCCG GTTTCGACTCCCGGTGTGGGAA

ex3_19 61494_ x1449	ENST000 00387449 .1	25	#####	50.1	###	GAGAAAGCTCACAGAAGCTGCTAACTCATGCCCCCATGTCTAACAAACATGG CTTTCTCA
ex3_20 34089_ x1332	ENST000 00387441 .1	22	#####	44.1	###	GTAAATATAGTTTAAACCAAAACATCAGATTGTGAATCTGACAACAGAGGCTT ACGACCCC
ex3_21 07121_ x1219	CM00066 3.2/16145 0677- 16145074 7	28	#####	56	###	GCATGGGTGGTTCAGTGGTAGAATTCTCGCCTGCCACGCGGGAGGCCCG GGTTCGATTCCCGGCCCATGCA
ex3_21 96754_ x1084	CM00066 3.2/14545 9658- 14545972 9	32	#####	63.9	###	GGTTCATGGTGTAATGGTGAGCACTCTGGACTCTGAATCCAGCGATCCG AGTTCGAGTCTCGGTGGAACCT
ex3_23 46903_ x890	AF382005 .1/581- 651	30	#####	60	890	GUUUAUGUAGCUUACCUCCUCAAGCAAUACACUGAAAUGUUUAGACG GGCUCACAUACCCCAUAAACA
ex3_25 13440_ x726	CM00067 5.2/41060 809- 41060738	31	#####	61.9	726	TCCCATATGGTCTAGCGGTTAGGATTCTGGTTTTACCCAGGTGGCCCG GGTTCGACTCCCGGTATGGGAA
ex3_26 77903_ x595	CM00066 8.2/27295 433- 27295504	20	#####	40.1	595	GGTTCATGGTGTAATGGTTAGCACTCTGGACTCTGAATCCGGTAATCCGA GTTCAAATCTCGGTGGAACCT
ex3_27 00757_ x576	AC00844 3.10/4259 0-42518	39	#####	77.8	576	GCCCGGCUAGCUCAGUCGGUAGAGCAUGAGACUCUJAAUCUCAGGGUC GUGGGUUCGAGCCCCACGUUGGCG
ex3_27 03633_ x575	CM00067 6.2/58239 967- 58239895	41	#####	81.8	575	GCCCGGCTAGCTCAGTCGGTAGAGCATGGGACTCTTAATCCAGGGTCGT GGTTCGAGCCCCACGTTGGGCG
ex3_27 24618_ x560	CM00066 4.2/20261 4781- 20261471 3	13	0.008	26.3	560	AAGAGAGTCATAGAAGTTATGGGATTGGCTTGAAACCAATTTCTGGAAGTT CAATTCCTTCTTTCTTG
ex3_28	ENST000	14	0.003	28.2	481	AGTAAGGTCAGCTAAATAAGCTATCGGGCCCATACCCCGAAAATGTTGGTT

59322_	00387377					ATACCCTTC
x481	.1					
ex3_28	J01415.2/	38	#####	75.8	471	GTAATATAGTTTAAACCAAACATCAGATTGTGAATCTGACAACAGAGGCTT
75035_	12138-					ACGACCCCTTATTTACC
x471	12206					
ex3_28	GL00025	25	#####	50.1	466	GGTTCATGGTGTAATGGTTAGCACTCTGGACTCTGAATCCAGCGATCCG
84417_	6.2/25106					AGTTCAAATCTCGGTGGAACCT
x466	6-250995					
ex3_31	CM00066	20	#####	40.1	345	GGGGATGTAGCTCAGTGGTAGAGCGCATGCTTAGCATGCATGAGGTCCC
52091_	8.2/28658					GGTTTCGATCCCCAGCATCTCCA
x345	308-					
	28658237					
ex3_31	AP00044	26	#####	52	341	GCCCGGAUAGCUCAGUCGGUAGAGCAUCAGACUUUUAUCUGAGGGUC
62391_	2.6/2022-					CAGGGUUCAAGUCCUGUUCGGGCG
x341	1950					
ex3_31	CM00066	20	#####	40.1	333	GGTTCATGGTGTAATGGTGAGCACTCTGGACTCTGAATCCAGAATCAGC
77530_	5.2/11064					TTAAATTAACCTATACTGTTACTG
x333	0242-					
	11064031					
	6					
ex3_32	AC00729	38	#####	75.8	320	UCCUCGUUAGUAGUGGUGAGUAUCCCCGCCUGUCACGCGGGAGACC
08848_	8.17/1453					GGGGUUCGAUUCGCCGACGGGGAG
x320	66-					
	145295					
ex3_32	GL00025	13	0.008	26.3	297	GCCTGGATAGCTCAGTTGGTAGAACATCAGACTTTTAATCTGACGGTGCAG
71729_	2.2/13342					GGTTCAAGTCCCTGTTTCAGGCG
x297	-13414					
ex3_34	ENST000	32	#####	63.9	237	GGTAAATGGCTGAGTGAAGCATTGGACTGTAAATCTAAAGACAGGGGTT
63015_	00387409					AGGCCTCTTT
x237	.1					
ex3_35	CM00068	20	#####	40.1	224	GCCCGGATGATCCTCAGTGGTCTGGGGTGCAGGCTTCAAACCTGTAGCTG
04270_	1.2/45478					TCTAGCGACAGAGTGGTTCAATTCCACCTTTCGGGC
x224	687-					
	45478602					
ex3_35	CM00066	23	#####	46.1	220	GCTTCTGTAGTGTAGTGGTTATCACGTTTCGCCTCACACGCGAAAGGTCCC
16903_	8.2/27280					CGGTTTCGAAACCGGGCAGAAGCA
x220	342-					
	27280270					
ex3_35	ENST000	29	#####	58	201	CAGAGAATAGTTTAAATTAGAATCTTAGCTTTGGGTGCTAATGGTGGAGTT
80548_	00387461					AAAGACTTT

x201	.2						
ex3_36 83341_ x175	KI270713. 1/31706- 31635	30	#####	60	175	TCCCTGGTGGTCTAGTGGCTAGGATTCGGCGCTTTCACCGCTGCGGCC GGTTTCGATTCCCGGTCAGGGAA	
ex3_36 95879_ x173	CM00068 5.2/18674 981- 18674909	35	#####	69.9	173	GGTTCATAGTGTAGTGGTTATCACGTCTGCTTTACACGCAGAAGGTCCTG GGTTCGAGCCCCAGTGGAAACA	
ex3_37 07043_ x171	AC00644 9.19/1968 57- 196784	23	#####	46.1	171	GUCUCUGUGGCGCAAUCGGUUAGCGCGUUCGGCUGUUAACCGAAAGGU UGGUGGUUCGAGCCCACCCAGGGACG	
ex3_37 22381_ x167	AC00844 3.10/4300 6-42934	23	#####	46.1	167	GUUUCGUGAGUGUAGUGGUUAUCACGUUCGCCUCACACGCGAAAGGUC CCCGGUUCGAAACCGGGCGGAAACA	
ex3_37 45403_ x160	CM00066 8.2/26311 267- 26311196	21	#####	42.1	160	GGCCCCATGGTGTAAATGGTTAGCACTCTGGACTTTGAATCCAGCGATCCG AGTTCAAATCTCGGTGGGACCT	
ex3_37 71530_ x154	AF346992 .1/15890- 15955	29	#####	58	154	GUCCUUGUAGUAUAAACUAAUACACCAGUCUUGUAAACCGGAGAUGAAA ACCUUUUUCCAAGGACA	
ex3_37 83932_ x152	CM00068 0.2/46089 377- 46089305	30	#####	60	152	GACGAGCTAGCTCAGTCGGTAGAGCATGGGACTCTTAATCCCAGGGTCGT GGTTTTGAGCCCCATGTTGGCA	
ex3_37 91335_ x150	CM00066 4.2/70249 061- 70248991	22	#####	44.1	150	GCGCCGCTGGTGTAGTGGTATCATGCAAGATTCCCATTCTTGCGACCCGG GTTTCGATTCCCGGGCGGCGCA	
ex3_39 72378_ x114	ENST000 00387456 .1	38	#####	75.8	114	ACTTTTAAAGGATAACAGCTATCCATTGGTCTTAGGCCCCAAAATTTTGGT GCAACTCC	
ex3_39 86185_ x112	CM00067 8.2/71426 493- 71426565	22	#####	44.1	112	GCCCTCTTAGCGCAGTGGGCAGCGCGTCAGTCTCATAATCTGAAGGTCCT GAGTTCGAGCCTCAGAGAGGGCA	
ex3_40 08513_ x108	ENST000 00387459 .1	20	#####	40.1	108	GTTCTTGTAGTTGAAATACAACGATGGTTTTTCATATCATTGGTCGTGGTTG TAGTCCGT	

ex3_40 30547_ x104	CM00066 8.2/27777 885- 27777956	23	#####	46.1	104	AGCAGAGTGGCGCAGCGGAAGCGTGCTGGGCCATAACCCAGAGGTCTGA TGGATCTAAACCATCTCTGCTA
ex3_40 84087_ x95	AC00844 3.10/9027 -8955	32	#####	63.9	95	GUUUCCGUAGUGUAGUGGUCAUCACGUUCGCCU AACACGCGAAAGGUC CCCGGUUCGAAACCGGGCGGAAACA
ex3_41 21228_ x90	AF381996 .2/4265- 4333	26	#####	52	90	AGAAUAUGUCUGAUAAAAGAGUUACUUUGAUAGAGUAAAUAUAGGAG CUUAAACCCCUU AUUUCUA
ex3_41 47591_ x86	CM00066 3.2/16146 2447- 16146237 6	29	#####	58	86	GCGTTGGTGGTATAGTGGTGAGCATAGCTGCCTTCCAAGCAGTTGACCCG GGTTCGATTCCCGGCCAACGCA
ex3_42 02547_ x78	AF347005 .1/12268- 12338	33	#####	65.9	78	ACUUUUAAAGGAUAACAGCUAUCCA UUGGUCU UAGGCCCAA AAAUUUU GGUGCAACUCCAAAUAAAAGUA
ex3_42 52029_ x72	CM00066 9.2/13934 0700- 13934077 2	22	#####	36.2	72	GCCCCAGTGGCCTAATGGATAAGGCATTGGCCTCCTAAGCCAGGGATTGT GGTTTCGAGTCCCATCTGGGGTG
ex3_42 90368_ x67	AC00867 0.6/83597 -83665	17	#####	34.2	67	GUAAAUAUAGUUUAACCAAACAUCAGAUUGUGAAUCUGACAACAGAGG CUCACGACCCCUU AUUUUACC
ex3_43 03221_ x66	CM00066 3.2/16144 0242- 16144017 1	21	#####	42.1	66	GCGTTGGTGGTATAGTGGTGAGCATAGTTGCCTTCCAAGCAGTTGACCCG GGCTCGATTCCCGCCAACGCA
ex3_43 04211_ x66	AF347015 .1/5827- 5762	18	#####	36.2	66	AGCUCCGAGGUGAUUUUCAU AUUGAAUUGCAA AUUCGAAGAAGCAGCUU CAAACCUGCCGGGGCUU
ex3_43 15094_ x65	CM00066 7.2/18120 6868- 18120693 9	32	#####	63.9	65	GGGGATGTAGCTCAGTGGTAGAGCGCATGCTTTGCATGTATGAGGCCCCG GGTTCGATCCCGGCATCTCCA
ex3_43	ENST000	27	#####	54	63	GTTAAGATGGCAGAGCCCGTAATCGCATAAACTTAAACTTTACAGTCA

27414_x63	00386347					GAGGTTCAA
ex3_43_37728_x62	CM00067 8.2/87384 094- 87384022	21	#####	42.1	62	GCCTCGTTAGCGCAGTAGGCAGCGCGTCAGTCTCATAATCTGAAGGTCGT GAGTTCGAGCCTCACACGGGGCA
ex3_43_50892_x60	AF346999 .1/4402- 4331	32	#####	63.9	60	UAGGAUGGGGUGUGAUAGGUGGCACGGAGAAUUUUGGAUUCUCAGGGA UGGGUUCGAUUCUCAUAGUCCUAG
ex3_43_55872_x60	AC01863 8.5/4694- 4623	20	#####	40.1	60	GGCUCGUUGGUCUAGGGGUAUGAUUCUCGCUUAGGGUGCGAGAGGUC CCGGGUUCAAAUCCCGGACGAGCCC
ex3_43_62149_x59	ENST000 00387314 .1	20	#####	40.1	59	GTTTATGTAGCTTACCTCCTCAAAGCAATACACTGAAAATGTTTAGACGGG CTCACATCA
ex3_43_64627_x59	CM00067 6.2/20683 273- 20683361	15	0.0005	30.2	59	CCTTCGATAGCTCAGCTGGTAGAGCGGAGGACTGTAGTACTTAATGTGTG GTCATCCTTAGGTGCTGGTTGATTCCGGCTCGAAGGA
ex3_43_82127_x57	CM00066 9.2/13349 7812- 13349774 5	14	0.003	28.2	57	TCCTCATTAGTATAGTGATATCCCTGCCTGTCACGCGGGAGACCAGGGTT CGATTCCCAGACAAGGAG
ex3_43_99368_x55	CM00068 1.2/47240 70- 4724141	29	#####	58	55	GCGTTGGTGGTATAGTGGTTAGCATAGCTGCCTTCCAAGCAGTTGACCCG GGTTCGATTCCCGGCCAACGCA
ex3_44_08352_x54	CM00066 3.2/93847 573- 93847657	34	#####	67.9	54	GGCTCCGTGGCGCAATGGATAGCGCATTGGACTTCTAGAGGCTGAAGGC ATTCAAAGGTTCCGGGTTTCGAGTCCCGGCGGAGTCG
ex3_44_17119_x53	ENST000 00387342 .1	23	#####	46.1	53	CAGAGTGTAGCTTAACACAAAGCACCCAACTTACACTTAGGAGATTTCAAC TTAACTTGA
ex3_44_45071_x51	AC00578 3.1/27398 -27326	32	#####	63.9	51	GUUUCGUAGUGUAGCGGUUAUCACAUUCGCCUCACACGCGAAAGGUC CCCGGUUCGAUCCCGGGCGGAAACA
ex3_45_16301_x51	AC00844 3.10/8240	20	#####	40.1	44	GGUAGCGUGGCCGAGCGGUCUAAGGCGCUGGAUUAAGGCUCCAGUCUC UUCGGGGCGUGGGUUCGAAUCCACCGCUGCCA

x44 -8321

ex3_45 30312_ x42	GL00025 2.2/82908 -82837	20	#####	40.1	42	GGGGGTGTAGCTCAGTGGTAGAGCGCATGCTTTGCATGTATGAGGCCTCG GGTTCGATCCCCGACACCTCCA
ex3_45 33630_ x42	AF347015 .1/5892- 5827	25	#####	50.1	42	GGUAAAAUGGCUGAGUGAAGCAUUGGACUGUAAAUCUAAAGACAGGGGU UAGCCUCUUUUUACCA
ex3_45 38502_ x42	ENST000 00387392 .1	30	#####	60	42	AAGGGCTTAGCTTAATTAAGTGGCTGATTTGCGTTCAGTTGATGCAGAGT GGGGTTTTG
ex3_45 53403_ x40	CM00067 4.2/12493 9966- 12494003 7	35	#####	69.9	40	GGGGATGTAGCTCAGTGGTAGAGCGCATGCTTTGCACGTATGAGGCCCC GGTTCAATCCCCGGCATCTCCA
ex3_46 09993_ x36	CM00067 9.2/68019 969- 68019897	20	#####	40.1	36	GACCCAGTGGCCTAATGGATAAGGCATCAGCCTCCGGAGCTGGGGATTGT GGTTTCGAGTCCCATCTGGGTCCG
ex3_46 29869_ x34	CM00067 9.2/81395 25- 8139452	35	#####	69.9	34	GGCGCCGTGGCTTAGCTGGTTAAAGCGCCTGTCTAGTAAACAGGAGATCC TGGTTTCGAATCCCAGCGGTGCCT
ex3_46 31909_ x34	ENST000 00387365 .1	33	#####	65.9	34	AGAAATATGTCTGATAAAAGAGTTACTTTGATAGAGTAAATAATAGGAGCTT AAACCCCC
ex3_46 41141_ x33	AF382013 .1/10403- 10467	37	#####	73.8	33	UGGUUAUUAUUUAAACAAAACGAAUGAUUUCGACUCAUUAUUUAUGA UAAUCAUUAUUACCAA
ex3_46 48071_ x33	X93334.1/ 6942- 7009	19	#####	38.2	33	AAGGUUUUAGAAAAACCAUUUCAUAACUUUGUCAAGUUUUUUUAUAGGC UAAAUCCUAUAUAUCUUA
ex3_46 53038_ x32	CM00067 9.2/75033 906- 75033978	20	#####	40.1	32	GCCCCAGTGGCCTAATGGATAAGGCACTGGCCTCCTAAGCCAGGGATTGT GGTTTCGAGTCCCACCTGGGGTA
ex3_46 65465_ x31	ENST000 00387372 .1	27	#####	54	31	TAGGATGGGGTGTGATAGGTGGCACGGAGAATTTTGGATTCTCAGGGATG GGTTCGATTC

ex3_46 71231_ x31	AC06784 9.6/4771- 4840	18	#####	36.2	31	CACUGUAAAGCUAACUUAGCAUUAACCUUUUAAGUUAAGAUUAAGAGAA CCAACACCUCUUUACAGUGA
ex3_46 71882_ x31	CM00067 9.2/82229 04- 8222833	21	#####	42.1	31	GGCTCGTTGGTCTAGGGGTATGATTCTCGCTTCGGGTGCGAGAGGTCCC GGTTCAAATCCCGGACGAGCCC
ex3_46 87323_ x30	CM00067 4.2/98503 503- 98503574	35	#####	69.9	30	TCCTCGTTAGTATAGTGGTTAGTATCCCCGCCTGTCACGCGGGAGACCGG GTTCAATCCCGACGGGGAG
ex3_47 01904_ x29	AC00532 9.1/7043- 6971	36	#####	71.9	29	GCCGAAAUAGCUCAGUUGGGAGAGCGUUAGACUGAAGAUCUAAAGGUC CCUGGUUCGAUCCCGGGUUUCGGCA
ex3_47 06302_ x28	KV88076 8.1/90924 7-909328	32	#####	63.9	28	GGTAGCGTGGCCGAGTGGTCTAAGGCGCTGGATTTAGGCTCCAGTCATTT CGATGGCGTGGGTTTGAATCCCACCGCTGCCA
ex3_47 06834_ x28	CM00067 9.2/39153 805- 39153734	26	#####	52	28	GGGGGTATAGCTCAGTGGTAGAGCATTGACTGCAGATCAAGAGGTCCCC GTTCAAATCCGGGTGCCCCCT
ex3_47 36001_ x26	GL00025 6.2/17300 1-172930	21	#####	42.1	26	GGGGGTGTAGCTCAGTGGTAGAGCGCGTGCTTAGCATGCACGAGGCCCC GGTTCAATCCCGGCACCTCCA
ex3_47 38159_ x26	CM00067 3.2/66348 120- 66348201	22	#####	44.1	26	GACGAGGTGGCCGAGTGGTTAAGGCGATGGACTGCTAATCCATTGTGCTT TGCACGCGTGGGTTTGAATCCCATCCTCGTCCG
ex3_47 41773_ x26	ENST000 00387439 .1	22	#####	44.1	26	TGGTATATAGTTTAAACAAAACGAATGATTTGACTCATTAAATTATGATAAT CATATTT
ex3_47 62471_ x25	CM00066 3.2/16546 009- 16545939	35	#####	69.9	25	GCATTGGTGGTTCAGTGGTAGAATTCTCGCCTCCCACGCGGGAGACCCG GTTCAATCCCGGCCAATGCA
ex3_47 80985_ x23	CM00067 9.2/82215 48- 8221619	29	#####	58	23	GCGTTGGTGGTATAGTGGTAAGCATAGCTGCCTTCCAAGCAGTTGACCCG GTTTCGATTCCCGGCCAACGCA

ex3_48 05993_ x22	CM00066 8.2/27547 823- 27547752	21	#####	42.1	22	GGTTCATGGTGTAAATGGTTAGCACTCTGGACTCTGAATCCAGCGATCCG AGTTCAAGTCTCGGTGGAACCT
ex3_48 09315_ x22	CM00066 8.2/26575 570- 26575659	31	#####	61.9	22	CTTTCGATAGCTCAGTTGGTAGAGCGGAGGACTGTAGGTTCACTAACTAA GGCATCCTTAGGTCGCTGGTTCGAATCCGGCTCGAAGGA
ex3_48 15269_ x21	CM00067 6.2/22929 701- 22929773	35	#####	69.9	21	GGGCCAGTGGCGCAATGGATAACCGCTCTGACTACGGATCAGAAGATTCC AGGTTGACTCCTGGCTGGCTCG
ex3_48 32258_ x21	CM00066 8.2/57800 211- 57800284	20	#####	40.1	21	GGCCGGTTAGCTCAGTCGGTTAGAGCGTGGTGCTAATAACGCCAAGGTCCG CGGGTTCGATCCCCGTGCCGGTCA
ex3_48 37996_ x20	AL352978 .6/119697 -119770	17	#####	34.2	20	GGCCGGUUAGCUCAGUUAGGUAAGAGCGUGGUGCUAAUACGCCAAGGU CGCGGGUUCGAUCCCCGUACGGGCCA
ex3_48 69881_ x18	CM00066 4.2/45710 374- 45710302	14	0.003	28.2	18	GGCTGTGTACCTCAGTGGGCAAGGGTATGGACTTTGAAGCCAGACTATTT GGTTCAAATCCCAGCTTGGCCT
ex3_48 75173_ x18	AC10808 1.2/59868 -59786	20	#####	40.1	18	GUCAGGAUGGCCGAGCGGUCUAAGGCGCUGCGUUCAGGUCGCAGUCUC CCUGGAGGCGUGGGUUCGAAUCCCACUUCUGACA
ex3_48 77873_ x18	J01415.2/ 7514- 7446	21	#####	42.1	18	GAAAAAGTCATGGAGGCCATGGGGTTGGCTTGAACCAGCTTTGGGGGGT TCGATTCCTTCTTTTTTG
ex3_48 81275_ x18	CM00067 4.2/98504 252- 98504323	19	#####	38.2	18	GACCTCGTGGCGCAACGGTAGCGCGTCTGACTCCAGATCAGAAGGCTGC GTGTTCAATCACGTCGGGGTCA
ex3_48 89666_ x17	J01415.2/ 3230- 3304	15	0.0005	30.2	17	GTTAAGATGGCAGAGCCCGGTAATCGCATAAACTTAAACTTTACAGTCA GAGGTTCAATTCCTCTTAAACA
ex3_48 90737_ x17	CM00068 1.2/39412 260- 39412168	20	#####	40.1	17	GCTCCAGTGGCGCAATCGGTTAGCGCGGTACTIONTATATGACAGTGCAG CGGAGCAATGCCGAGTTGTGAGTTCGATCCTCACCTGGAGCA

ex3_48 94868_ x17	CM00066 8.2/26705 377- 26705449	14	0.006	28.2	17	GGGGAATTAGCTCAAGCGGTAGAGCGCTTGCTTAGCATGCAAGAGGTAGT GGGATCGATGCCACATTCTCCA
ex3_49 01124_ x17	CM00067 7.2/89335 073- 89335145	22	#####	44.1	17	GGCCGCGTGGCCTAATGGATAAGGCGTCTGACTTCGGATCAGAAGATTGC AGGTTGAGTCCTGCCGCGGTGCG
ex3_49 06003_ x17	ENST000 00387419 .1	20	#####	40.1	17	AAGGTATTAGAAAAACCATTTTCATAACTTTGTCAAAGTTAAATTATAGGCTA AATCCTAT
ex3_49 07890_ x17	CM00067 6.2/20657 557- 20657464	13	0.009	26.3	17	CCTTCGATAGCTCAGCTGGTAGAGCGGAGGACTGTAGATTGTATAGACAT TTGCGGACATCCTTAGGTGCTGGTTCGATTCCAGCTCGAAGGA
ex3_49 10350_ x16	GL00025 1.2/13811 8-138045	35	#####	69.9	16	GGCTCTGTGGCTTAGTTGGCTAAAGCGCCTGTCTCGTAAACAGGAGATCC TGGTTTGAATCCCAGCGGGGCCT
ex3_49 22190_ x16	AL132988 .4/95773- 95841	28	#####	56	16	AAGGGCUUAGCUUAAUUAAAGUGGCUGAUUUUGCGUUCAGUUGAUGCAG AGUGGGGUUUUGCAGUCCUUA
ex3_49 30333_ x15	CM00066 8.2/26553 503- 26553574	31	#####	61.9	15	GGGGATGTAGCTCAGTGGTAGAGCGCATGCTTCGCATGTATGAGGTCCCG GGTTCGATCCCCGGCATCTCCA
ex3_49 33378_ x15	CM00066 8.2/26577 104- 26577192	13	0.01	26.3	15	CCTTCGATAGCTCAGTTGGTAGAGCGGAGGACTGTAGGCTCATTAAGCAA GGTATCCTTAGGTGCTGGTTCGAATCCGGCTCGGAGGA
ex3_49 34413_ x15	CM00066 8.2/27902 564- 27902493	20	#####	40.1	15	AGCAGAGTGGCGCAGCGGAAGCGTGCTGGGCCATAACCCAGAGGTCTGA TGGATCGAAACCATCCTCTGCTA
ex3_49 36363_ x15	CM00066 5.2/45689 071- 45688999	18	#####	36.2	15	GGGCCAGTGGCGCAATGGATAACGCGTCTGACTACGGATCAGAAGATTCT AGGTTGACTCCTGGCTGGCTCG
ex3_49 50328_ x15	CM00066 8.2/27545 689-	41	#####	81.8	15	GTAGTCGTGGCCGAGTGGTTAAGGCGATGGACTTGAAATCCATTGGGGTT TCCCCGCGCAGGTTTGAATCCTGCCGACTACG

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ex3_49 52113_ x14	AC02499 5.8/16571 7-165798	24	#####	48.1	14	GUAGUCGUGGCCGAGUGGUUAAGGCGAUGGACUAGAAAUCCAUUGGGG UCUCCCCGCGCAGGUUCGAAUCCUGCCGACUACG
ex3_49 58749_ x14	CM00067 9.2/19508 181- 19508252	17	#####	34.2	14	GACCTCGTGGCGCAATGGTAGCGCTGACTCCAGATCAGAAGGTTGC GTGTTCAAGTCACGTCGGGGTCA
ex3_49 67443_ x14	CM00067 2.2/69592 941- 69593006	13	0.01	26.3	14	GGTAAATGGCTGAGCAAGCATTGGACTGTAAATCTAAAGACAGATGTTGA GCCATCTTTTGTAGCA
ex3_49 72539_ x14	ENST000 00387400 .1	36	#####	63.9	14	TAGATTGAAGCCAGTTGATTAGGGTGCTTAGCTGTAACTAAGTGTGTTGTG GTTTAAAGT
ex3_49 89358_ x13	AF134583 .1/1816- 1744	19	#####	38.2	13	UAGAUUGAAGCCAGUUGAUUAGGGUGCUUAGCUGUUAACUAAGUGUUU GUGGGUUUAAGUCCCAUUGGUCUAG
ex3_49 99105_ x12	CM00067 3.2/76235 896- 76235825	35	#####	69.9	12	GGCTCGTTGGTCTAGGGGTATGATTCTCGGTTTGGGTCCGAGAGGTCCCG GTTCAAATCCCGGACGAGCCC
ex3_50 01313_ x12	CM00067 7.2/40593 906- 40593825	19	#####	38.2	12	GACGAGGTGGCCGAGTGGTTAAGGCGATGGACTGCTAATCCATTGTGCTC TGCACGCGTGGGTTTCAATCCCATCCTCGTCG
ex3_50 01985_ x12	AF134583 .1/1599- 1666	30	#####	60	12	AGAAUUUAGGUUAAAUACAGACCAAGAGCCUUCAAAGCCCUCAGUAAG UUGCAAUACUAAUUUCUG
ex3_50 21113_ x12	CM00066 8.2/28941 053- 28941157	23	#####	46.1	12	GTCAGGATGGCCGAGTGGTCTAAGGCGCCAGACTCAAGCTTGGCTTCCTC GTGTTGAGGATTCTGGTCTCCAATGGAGGCGTGGGTTTCAATCCCCTTC TGACA
ex3_50 30622_ x11	CM00067 0.2/67585 596- 67585528	13	0.008	26.3	11	GTAGCTGTAGTTTAAGCAAACATTAGATTGTGGATCTAACAATAGAAGCC TTCAATTTCTTATCTACC

ex3_50 34252_ x11	CM00067 7.2/95784 645- 95784717	14	0.003	28.2	11	GCACTGCACAGTCAGTCAGTAGAGCATGGGACTCTTAATCCCAGGGTCGT GGGTTCAAGCCCCACGTTGGGCG
ex3_50 34934_ x11	CM00066 6.2/54883 22- 5488403	14	0.003	28.2	11	GATTTTATGGTGTAAATGGTGAGCACTCTGGACTTGAATCCAGAATTAACA AACAGAACATCCTGCAATTTTATTAAGAGCA
ex3_50 37431_ x11	GL00025 2.2/8616- 8544	35	#####	69.9	11	GGCCGCGTGGCCTAATGGATAAGGCGTCTGATTCCGGATCAGAAGATTGA GGTTTCGAGTCCCTTCGTGGTCCG
ex3_50 41259_ x11	AL163195 .5/3702- 3774	21	#####	42.1	11	GGCUCCAUAGCUCAGGGGUUAGAGCACUGGUCUUGUAAACCAGGGGUC GCGAGUUCAAUCUCGCGUGGGGCCU
ex3_50 44086_ x11	GL00025 1.2/21669 9-216772	22	#####	44.1	11	GGCTCCGTAGCTTAGTTGGTTAAAGCGCCTGTCTAGTAAACAGGAGATCC TGGTTTCGACTCCCAGCGGGGCCT
ex3_50 44691_ x11	CM00066 8.2/26571 936- 26571864	21	#####	42.1	11	GGGAATTAGCTCAAATGGTAGAGCGCTCGCTTAGCATGCGAGAGGTAGC GGATCGATGCCCGCATTCTCCA
ex3_50 46165_ x11	CM00067 9.2/81209 25- 8121012	34	#####	67.9	11	GGCTCTGTGGCGCAATGGATAGCGCATTGGACTTCTAGTGACGAATAGAG CAATTCAAAGGTTGTGGTTTCGAATCCCACCAGAGTCG
ex3_50 46429_ x11	CM00066 8.2/14421 6547- 14421662 9	23	#####	46.1	11	ACCAGGATGGCCGAGTGGTTAAGGCGTTGGACTTAAGATCCAATGGACAT ATGTCCGCGTGGTTTCGAACCCCACTCCTGGTA
ex3_50 46935_ x11	CM00066 8.2/27562 184- 27562270	25	#####	50.1	11	GGCTCTGTGGCGCAATGGATAGCGCATTGGACTTCTAGCCTAAATCAAGA GATTCAAAGGTTGCGGGTTCGAGTCCCTCCAGAGTCG
ex3_50 54868_ x10	CM00066 4.2/15640 0769- 15640084 0	31	#####	61.9	10	GGGGATGTAGCTCAGTGGTAGAGCGCGCGCTTCGCATGTGTGAGGTCCC GGTTCAATCCCCGGCATCTCCA

ex3_50 56248_ x10	CM00066 3.2/24887 3855- 24887396 0	39	#####	77.8	10	GTCAGGATGGCCGAGTGGTCTAAGGCGCCAGACTCAAGGTAAGCACCTT GCCTGCGGGCTTTCTGGTCTCCGGATGGAGGCGTGGGTTCGAATCCCAC TTCTGACA
ex3_50 64778_ x10	CM00066 4.2/20336 4478- 20336440 8	25	#####	50.1	10	GCAATGGTGGTTCAGTGGTAGAATTCTCGCCTTTCACACAGGAGACCCGG GTTCAATTCCTGACCCATGTA
ex3_50 66998_ x10	CM00066 8.2/26319 173- 26319102	35	#####	69.9	10	GACCTCGTGGCGCAACGGTAGCGGTCTGACTCCAGATCAGAAGGTTGC GTGTTCAAATCACGTCGGGGTCA
ex3_50 67238_ x10	CM00067 8.2/31880 94- 3188165	24	#####	48.1	10	GGCTCGTTGGTCTAGGGGTATGATTCTCGCTTTGGGTGCGAGAGGTCCCG GGTTCAAATCCCGGACGAGCCC
ex3_50 72148_ x10	CM00066 8.2/26299 677- 26299749	25	#####	50.1	10	GACCACGTGGCCTAATGGATAAGGCGTCTGACTTCGGATCAGAAGATTGA GGTTCTGAATCCCTTCGTGGTTA
ex3_50 74328_ x10	CM00067 0.2/12315 7302- 12315723 0	35	#####	69.9	10	GCCTCGTTAGCGCAGTAGGTAGCGCGTCAGTCTCATAATCTGAAGGTCGT GAGTTCGATCCTCACACGGGGCA
ex3_50 75628_ x10	ENST000 00387382 .1	22	#####	44.1	10	AGAAATTTAGGTTAAATACAGACCAAGAGCCTTCAAAGCCCTCAGTAAGTT GCAATACTT
ex3_50 79222_ x9	CM00066 7.2/16838 9710- 16838963 9	14	0.003	28.2	9	GCCCAACTGGTTCAGTCGGTAGAGAATGAGACTCTTAATCTCAGGTCATAG ATTCATGTACATGTTGGGTG
ex3_50 88933_ x9	CM00066 8.2/28807 905- 28807833	20	0.0001	32.2	9	GCCGAGATAGCTCAGTTGGGAGAGCGTTAGACTGAAGATCTAAAGGTCCC TGTTCAATCCCGGGTTTCGGCA
ex3_50	ENST000	22	#####	44.1	9	ACTCTTTTAGTATAAATAGTACCGTTAACTTCCAATTAAGTCTTTGACAAC

95665_	00387429					ATTCAAA
x9	.1					
ex3_50	CM00066	29	#####	58	9	GGTCCCATGGTGTAAATGGTTAGCACTCTGGGCTTTGAATCCAGCAATCCG
97987_	8.2/14518					AGTTCGAATCTTGGTGGGACCT
x9	2723-					
	14518279					
	4					
ex3_51	GL00025	22	#####	44.1	8	GGTCCCATGGTGTAAATGGTTAGCACTCTGGACTTTGAATCCAGCAATCCGA
25944_	1.2/79253					GTTTCGAATCTCGGTGGGACCT
x8	-79324					
ex3_51	CM00068	25	#####	50.1	8	ACTTTTAAAGGATTAGAGTTAACCATTGGTCTAAGGAACCAAAAACACTGG
27080_	1.2/56922					TGCAACTCCAAATAAAAGTA
x8	350-					
	56922420					
ex3_51	CM00066	13	0.008	26.3	8	GTAGTTATAGTTTAAATTAACATTAGATTGTGGATCTAATAATAGAAGTCTA
29832_	5.2/10689					CAGCTTCTTACCTACC
x8	4340-					
	10689427					
	3					
ex3_51	ENST000	23	#####	46.1	8	GAAAAAGTCATGGAGGCCATGGGGTTGGCTTGAAACCAGCTTTGGGGGGT
33304_	00387416					TCGATTCCTT
x8	.2					
ex3_51	CM00067	18	#####	36.2	8	GCCTGGATAGCTCAGTTGGTAGAGCATCAGACTTTTAACTCTGAGGGTCCA
37584_	8.2/73478					GGGTTCAAGTCCCTGTTCAGGCA
x8	389-					
	73478317					
ex3_51	CM00067	13	0.008	26.3	7	AAGGAGTTAGCTCAATTAAGTGATTGATTTGCATTCAGTTGATGTAAGATA
42475_	4.2/26572					AGATCTTGCAGTCCTTA
x7	619-					
	26572687					
ex3_51	ENST000	22	#####	44.1	7	GTCCTTGTAGTATAAACTAATACACCAGTCTTGTAACCGGAGATGAAAAC
54179_	00387460					CTTTTTCCA
x7	.2					
ex3_51	CM00067	23	#####	46.1	7	GGGGGATTAGCTCAAATGGTAGAGCGCTCGCTTAGCATGCGAGAGGTAG
62656_	0.2/66114					CGGGATCGATGCCCCGCATCCTCCA
x7	189-					
	66114261					
ex3_51	ENST000	28	#####	56	7	AGCTCCGAGGTGATTTTCATATTGAATTGCAAATTCGAAGAAGCAGCTTCA
76537_	00387405					AACCTGCCG
x7	.1					

ex3_51 76670_ x7	CM00067 1.2/12834 0166- 12834007 6	34	#####	67.9	7	GGCTCTGTGGCGCAATGGATAGCGCATTGGACTTCTAGCTGAGCCTAGTG TGGTCATTCAAAGGTTGTGGGTTCCAGTCCCACCAGAGTCG
ex3_51 88643_ x6	CM00066 3.2/12101 6915- 12101684 5	28	#####	56	6	GCACTGGTGGTTCAGTGGTAGAATTCTCGCCTCCCACGCGGGAGACCCG GGTTC AATTCCCGGTCAAGATA
ex3_52 04327_ x6	CM00067 9.2/40117 373- 40117300	14	0.002	28.2	6	GACCGTGTGGCCTTAATGGATAAGGTGTCTGACTTCAGATCAGAAGATTGA GGGTTTGAGTCCCTTTGTGGTCA
ex3_52 06547_ x6	CM00067 2.2/62110 58- 6210975	17	#####	34.2	6	GGGGATATAGCTCAGGGGTAGAGCATTGACTGCAGAACAAGAGAGGGG CGCACCGGGCACGGTGGCTCACGCCTGTAATCCCA
ex3_52 13603_ x6	CM00067 8.2/14285 893- 14285964	33	#####	65.9	6	GGCGCGGTGGCCAAGTGGTAAGGCGTCGGTCTCGTAAACCGAAGATCAC GGTTTCGAACCCCGTCCGTGCCT
ex3_52 15241_ x6	GL00025 6.2/25397 1-254043	30	#####	60	6	GCCTCCTTAGCGCAGTAGGCAGCGCGTCAGTCTCATAATCTGAAGGTCCT GAGTTCGAACCTCAGAGGGGGCA
ex3_52 16699_ x6	CM00066 8.2/27791 427- 27791356	24	#####	48.1	6	GGCCCCATGGTGTAAATGGTCAGCACTCTGGACTCTGAATCCAGCGATCCG AGTTCAAATCTCGGTGGGACCC
ex3_52 20051_ x5	CM00067 6.2/20613 862- 20613790	34	#####	67.9	5	GGCTCCATAGCTCAGGGGTTAGAGCGCTGGTCTTGTAACCAGGGGTGCG CGAGTTCAATTCTCGCTGGGGCCT
ex3_52 47681_ x5	CM00067 8.2/10721 565- 10721495	17	#####	34.2	5	ACTTTTAAAGGATAAGAGTTATCCATTGGTCTCAGGAACCAAAAACATCGG TGCAACTCCAAATAAAAGTA
ex3_52 48706_ x5	CM00066 8.2/26322 818-	35	#####	69.9	5	GACCACGTGGCCTAATGGATAAGGCGTCTGACTTCGGATCAGAAGATTGA GGTTTCGAATCCCTCCGTGGTTA

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ex3_52 51026_ x5	CM00066 8.2/27618 356- 27618429	17	0.01	26.3	5	GGCCCTGTAGCTCAGCGGTTGGAGCGCTGGTCTCGTAAACCTAGGGGTC GTGAGTTCAAATCTCACCAGGGCCT
ex3_52 54701_ x5	CM00066 4.2/13027 3728- 13027365 6	13	0.009	26.3	5	TAGATTGAAGCCAGTTGATTAGGGTGTTTATCTGTTAATTAATGTTTCGTGG GTTTAAGTCCCATCAATCTAG
ex3_52 57326_ x5	CM00066 8.2/27273 960- 27274033	19	0.0008	30.2	5	GGCTGGTTAGTTCAGTTGGTTAGAGCGTGGTGCTAATAACGCCAAGGTCTG TGGTTTCGATCCCCATATCGGCCA
ex3_52 60746_ x5	GL00025 4.2/1093- 1022	26	#####	52	5	GGGGGTGTAGCTCAGTGGTAGAGCGTATGCTTAACATTCATGAGGCTCTG GTTTCGATCCCCAGCACTTCCA
ex3_52 66835_ x4	CM00066 3.2/14832 8812- 14832888 3	32	#####	63.9	4	GGTTCATGGTGTAATGGTAAGCACTCTGGACTCTGAATCCAGCCATCTGA GTTTCGAGTCTCTGTGGAACCT
ex3_52 70211_ x4	CM00066 8.2/27335 062- 27334990	26	#####	52	4	GCCTGGGTAGCTCAGTCGGTAGAGCATCAGACTTTTAATCTGAGGGTCCA GGTTCAAGTCCCTGTCCAGGCG
ex3_52 74403_ x4	CM00066 8.2/27591 886- 27591814	29	#####	58	4	GCCTGGATAGCTCAGTCGGTAGAGCATCAGACTTTTAATCTGAGGGTCCA GGTTCAAGTCCCTGTTCAGGCG
ex3_52 75459_ x4	CM00067 9.2/38869 363- 38869292	20	0.0001	32.2	4	GGGGGTATAGCTCAGTGGTAGAGCATTGACTGCAGATCAAGAGGTCCCT GTTCAAATCCGGGTGCCCCCT
ex3_52 81515_ x4	CM00067 3.2/59551 294- 59551379	16	0.0001	32.2	4	GGCTCTGTGGCGCAATGGATAGCGCATTGGACTTCTAGATAGTTAGAGAA ATTCAAAGGTTGTGGGTTTCGAGTCCCACCAGAGTCG

ex3_52 82383_ x4	CM00067 4.2/97096 986- 97096913	14	0.004	28.2	4	GGCAATGTAGCATTGTGGCTAAGTGCACAGGCTTTGGAAACTGGCAGGCC TGGTTCAAATCCCAGCTTATTCA
ex3_52 82655_ x4	CM00066 8.2/28474 625- 28474552	26	#####	52	4	GGCTCTATGGCTTAGTTGGTTAAAGCGCCTGTCTTGTAACAGGAGATCCT GGTTTCGAATCCCAGTAGAGCCT
ex3_52 82891_ x4	GL00025 5.2/16191 0-161805	21	#####	42.1	4	GTCAGGATGGCCGAGTGGTCTAAGGCGCCAGACTCAAGCTAAGCTTCCTC CGCGGTGGGATTCTGGTCTCCAATGGAGGCGTGGTTTCGAATCCCCTT CTGACA
ex3_52 86767_ x4	CM00068 5.2/10201 0285- 10201035 5	13	0.009	26.3	4	GTTAGTGTAGCTTAATATGGTAAAGCAAGGCACTGAAAGTGCGTAGATGAG TTCATGTA ACTCCATAAACA
ex3_52 91467_ x4	CM00067 1.2/50964 08- 5096340	13	0.008	26.3	4	AAGGACTTAGCTTAATTAAGTGGTTGATTTGCGTTCAACTGATGCAGAAT AGAGTTTTGCAGTCCTTG
ex3_52 94091_ x4	CM00067 9.2/31550 074- 31550145	32	#####	63.9	4	GGCGCGGTGGCCAAGTGGTAAGGCGTCGGTCTCGTAAACCGAAGATCGC GGTTTCGAACCCCGTCCGTGCCT
ex3_53 05835_ x4	GL00025 4.2/61628 -61557	21	#####	42.1	4	GGGGTATAGCTCAGTGGTAGAGCGCGTGCTTAGCATGCACGAGGTCCT GGTTTCGATCCCCAGTACCTCCA
ex3_53 12343_ x4	CM00066 8.2/27275 284- 27275211	35	#####	69.9	4	GGCTGGTTAGCTCAGTTGGTTAGAGCGTGGTGCTAATAACGCCAAGGTTCG CGGTTTCGATCCCCGTA CTGGCCA
ex3_53 17963_ x4	CM00066 8.2/27297 996- 27298077	28	#####	56	4	GACGAGGTGGCCGAGTGGTTAAGGCGATGGACTGCTAATCCATTGTGCTC TGCACGCGTGGTTTCGAATCCCACCTTCGTCG
ex3_53 19019_ x4	CM00066 3.2/15914 1684- 15914161 1	23	0.0007	30.2	4	GTCTCTGTGGCGCAATGGACGAGCGCGCTGGACTTCTAATCCAGAGGTTCC CGGTTTCGAGTCCC GGCAGAGATG

ex3_53 19677_ x3	CM00066 3.2/16727 285- 16727355	21	#####	42.1	3	GCCTTGGTGGTGCAGTGGTAGAATTCTCGCCTCCCACGTGGGAGACCCG GGTTCAATTCCCGGCCAATGCA
ex3_53 20757_ x3	CM00067 7.2/79744 655- 79744727	30	#####	60	3	GGGGGTATAGCTCAGTGGGTAGAGCATTGACTGCAGATCAAGAGGTCCC CGGTTCAAATCCGGGTGCCCCCT
ex3_53 23958_ x3	CM00067 9.2/19860 862- 19860932	18	#####	36.2	3	GCATTGGTGGTTCAATGGTAGAATTCTCGCCTCCCACGCAGGAGACCCAG GTTCGATTCTGGCCAATGCA
ex3_53 25896_ x3	CM00067 6.2/20681 690- 20681762	26	#####	52	3	GGCCCTATAGCTCAGGGGTTAGAGCACTGGTCTTGTAACCAGGGGTCCG GAGTTCAAATCTCGCTGGGGCCT
ex3_53 30303_ x3	CM00068 3.2/35891 030- 35891100	13	0.008	26.3	3	GAGGATTTAGTTTAATTAATAAATGTTTGATTTGCATTCAATTGATGTAAGATA GAGAGTGTGCAGTCCTTA
ex3_53 32814_ x3	CM00066 3.2/14802 0474- 14802054 4	15	0.001	30.2	3	GCGTTGGCAGTTCAGTGGTAGAATTCTCGCCTCCCACCCGGGAGACCTGG ATTCCATTTCCGGCAAATGCA
ex3_53 32886_ x3	CM00067 2.2/67764 503- 67764584	20	0.0001	32.2	3	GCAGCGATGGCCGAGTGGTTAAGGCGTTGGACTTGAAATCCAATGGGGTC TCCCCGCGCAGGTTCGAACCCCTGCTCGCTGCG
ex3_53 34191_ x3	CM00066 9.2/64110 400- 64110468	13	0.008	26.3	3	AAGGGCTTAGCTTAATTAAGTGATTGATTTGCATTCAATTGATACAGAATA GAGTTTTTTCAGTCCTTA
ex3_53 35100_ x3	CM00066 3.2/14824 6758- 14824683 1	15	0.0006	30.2	3	GTCTCTGTGGCGCAATCGGTCAGAGCGTTCGGCTATTAACCGAACGGTGA GTAGTTCAAGACCACCCAGGGACG
ex3_53 36708_ x3	GL00025 0.2/77722	20	#####	40.1	3	GGGGGTATAGCTCAGCGGTAGAGCGCGTGCTTAGCATGCACGAGGTCTC GGTTCAATCCCAATACCTCCA

x3	-77651						
ex3_53 38001_ x3	CM00067 9.2/60786 232- 60786302	26	#####	36.2	3	GCCCGGATAGTTCAGTTGGTAGAGCATCAGACTTAATCAGAGGGTCCAGG GTTCAAGTCCCTGTTTGGGTG	
ex3_53 39519_ x3	CM00066 3.2/22246 5005- 22246507 7	14	0.005	28.2	3	GGCTCCATAGCTCAGTGGTTAGAGCACTGGTCTTGTAACCAGGGGTCCG GAGTTCGATCCTCGCTGGGGCCT	
ex3_53 40467_ x3	CM00067 3.2/10916 5312- 10916539 3	13	0.01	26.3	3	TGAGTTGTAGCTGAGTGGTTAAGGCAACGAGCTAGAAATTCGTTGGTTTCT CTCTGTGCAGTTTGAATCCTGCTAATTATG	
ex3_53 42909_ x3	CM00066 3.2/14969 8551- 14969847 8	17	0.009	26.3	3	ATCTCCGTGGAGCAATTGGTTAGCGCGTTCGGCTGTTAACCGGAAAGTTG GTGGTTCGAGCCTACCCAGGGACG	
ex3_53 45954_ x3	CM00067 6.2/84172 756- 84172830	15	0.002	30.2	3	GTTAAGATGACAGAGCCTGGCAATTGCGTAAACTTAAACTTTATAATCA GAGGTTCAACTTCTGCTCTTAACA	
ex3_53 46119_ x3	CM00067 1.2/78741 498- 78741570	13	0.009	26.3	3	GAGATTGAGACCAGTTGATTAAGGTGTTTAGCTGTTAACTAAATTTTTGTGG GTTTGAATTCCATCAATCTAG	
ex3_53 49512_ x3	CM00066 4.2/21824 5826- 21824591 8	14	0.004	28.2	3	CCTTCAATAGTTCAGCTGGTAGAGCAGAGGACTATAGCTACTTCCTCAGTA GGAGACGTCCTTAGGTTGCTGGTTCGATTCCAGCTTGAAGGA	
ex3_53 50487_ x3	CM00066 5.2/13222 9171- 13222910 0	32	#####	63.9	3	GGGGGTGTAGCTCAGTGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCT GTTCAAATCCAGGTGCCCCCT	

ex3_53 51606_ x3	CM00068 5.2/24601 905- 24601837	21	#####	42.1	3	GTGGGTATAGCTCAGAGGTAGAGCATTCAACTGCAGATCGAAGTGGCTGT ACCATTTTGCATTCCCACC
ex3_53 51681_ x3	CM00066 3.2/14826 5179- 14826510 8	40	#####	79.8	3	GGTTCCATGGTGTAAATGGTAAGCACTCTGGACTCTGAATCCAGCGATCCG AGTTCGAGTCTCGGTGGAACCT
ex3_53 54642_ x3	CM00067 3.2/10340 5997- 10340606 9	14	0.004	28.2	3	TAGATTGAAGCCAGTTGATTAGGATGTTTAGCTGTAACTAAATTATCCTGG GTTTGAATTCCACCAATCTAG
ex3_53 56982_ x3	CM00068 5.2/11960 3898- 11960396 6	14	0.002	28.2	3	GCAGCTGTGGCTCAGTGGAAGAGCATCAGTCTGGGTATCAGAAGACCTA GGTCCTAGCCCCAGCTGTA
ex3_53 62073_ x3	GL00025 1.2/12401 9-123948	19	0.002	30.2	3	GTGGATGTAGTTTAGTGGTAGAACGCGCGCTTTGCATGTATGAGGTCCCG GTTTCGATCCCTGGCGTTTCCA
ex3_53 62529_ x3	CM00067 2.2/58537 83- 5853711	14	0.005	28.2	3	GGTTCCATAGTGTAGTGGTTATCACATCTGCTTTACACGCAGAAGGTCTG GGTTCAAGCCCCAGTGAACCA
ex3_53 62805_ x3	CM00066 3.2/14441 9267- 14441934 0	26	#####	52	3	GTCTCTGTGGCGCAATCGGTTAGCGCATTCCGGCTGTTAACCGAAAGGTTG GTGGTTCGAGCCCACCCAGGGACG
ex3_53 69090_ x3	CM00067 3.2/63489 530- 63489598	13	0.008	26.3	3	ATTAAGGTAGTATAGTAGAGTAAAATACTTCGAAGCCAAAAGATCTAGGTTT GAATCCTAGCTTTCATG
ex3_53 72444_ x3	CM00066 8.2/26594 874- 26594962	19	#####	38.2	3	CCTTCGATAGCTCAGCTGGTAGAGCGGAGGACTGTAGGGGTTTGAATGTG GTCATCCTTAGGTGCTGGTTCGAATCCGGCTCGGAGGA

ex3_53 73299_ x3	CM00066 8.2/27672 531- 27672450	24	#####	48.1	3	GCTGTGATGGCCGAGTGGTTAAGGTGTTGGACTCGAAATCCAATGGGGGT TCCCCGCGCAGGTTCAAATCCTGCTCACAGCG
ex3_53 74100_ x3	CM00067 0.2/13375 5832- 13375576 7	15	0.0008	30.2	3	GGTAAAATGACTGAATAAGCCTTAGACTGTAAATCTGAAGACAGAGGTCAA GGCCTCTTTTTACCA
ex3_53 75492_ x3	CM00066 3.2/16889 677- 16889750	21	#####	42.1	3	GTCTCTGTGGCGCAATCGGTTAGCGCGTTCGGCTGTTAACCGAAAGATTG GTGGTTCGAGCCCACCCAGGGACG
ex3_53 78639_ x3	CM00067 8.2/31574 77- 3157405	33	#####	65.9	3	GCCCGGCTAGCTCAGTCGGTAGAGCATGAGACCCTTAATCTCAGGGTCGT GGTTCGAGCCCCACGTTGGGCG
ex3_53 79581_ x3	CM00067 6.2/20633 006- 20633077	22	#####	44.1	3	GGCTCGTTGGTCTAGTGGTATGATTCTCGCTTTGGGTGCGAGAGGTCCCG GGTCAAATCCCGGACGAGCCC
ex3_53 79752_ x3	CM00067 4.2/69827 047- 69826978	13	0.008	26.3	3	GAGGGTATAGCTCAGAGGTAGAGCACTGGACTGCAGATCAAGAATATCAG CTTCAGTTCAGCTGCCTTCA
ex3_53 85773_ x3	GL00025 1.2/33067 -32995	35	#####	69.9	3	GACCACGTGGCCTAATGGATAAGGCGTCTGACTTCGGATCAGAAGATTGA GGTTCGAATCCCTTCGTGGTTG
ex3_53 92844_ x3	CM00066 9.2/69333 643- 69333709	13	0.009	26.3	3	GGTAAAATGGCTGAGCAAGCATTAGACTGTAAATCTGAAAACAGAGGTCAA AGGTCTCTTTTTACCA
ex3_53 94950_ x3	CM00066 8.2/27553 494- 27553413	33	#####	65.9	3	GTAGTCGTGGCCGAGTGGTTAAGGTGATGGACTAGAAACCCATTGGGGTC TCCCCGCGCAGGTTCAATCCTGCCGACTACG
ex3_53 95280_ x3	CM00066 3.2/16678 341- 16678271	20	#####	40.1	3	GCGTTGGTGGTTTGTAGTGGTAGAATTCTCGCCTCCCATGCGGGAGACCCGG GTTCAATCCCGGCCACTGCA

ex3_53 95304_ x3	CM00068 5.2/10278 6742- 10278666 9	13	0.008	26.3	3	TAGAATATAGTGTATCAGGTAGCACAAAGATTTTTGAATTCTTAAGAGAGTA GGTTCAATTCCTATAATCCTGT
ex3_53 95505_ x3	CM00067 6.2/20625 370- 20625451	31	#####	61.9	3	GGTAGTGTGGCCGAGCGGTCTAAGGCGCTGGATTTAGGCTCCAGTCTCTT CGGGGGCGTGGGTTTCGAATCCCACCACTGCCA
ex3_53 96711_ x3	CM00067 8.2/31529 00- 3152972	33	#####	65.9	3	GCCCCGGTGGCCTAATGGATAAGGCATTGGCCTCCTAAGCCAGGGATTGT GGTTTCGAGTCCCACCCGGGGTA
ex3_53 98190_ x3	CM00067 8.2/33709 82- 3370908	13	0.008	26.3	3	TTTAAGATGGCAGACCCCGGCAATTACCTAAGACTTAAAACCTTAAAATCA GAGGTTCAACTCCTCTTCTTAACA
ex3_54 00143_ x3	CM00067 4.2/56190 364- 56190445	24	#####	48.1	3	GTCACGGTGGCCGAGTGGTTAAGGCGTTGGACTCGAAATCCAATGGGGTT TCCCCGCACAGGTTTCGAATCCTGTTTCGTGACG
ex3_54 00803_ x3	GL00025 2.2/55434 -55363	32	#####	63.9	3	GGGGGTGTAGCTCAGTGGTAGAGCGCATGCTTTGCATGTATGAGGTCCCG GGTTCGATCCCCGGCACCTCCA
ex3_54 04211_ x3	CM00067 3.2/59551 059- 59550987	29	#####	58	3	GGTTCATAGTGTAGCGGTTATCACGTCTGCTTTACACGCAGAAGGTCCT GGTTCGAGCCCCAGTGGAACCA
ex3_54 07327_ x2	CM00066 4.2/13027 3890- 13027382 6	14	0.002	28.2	2	GGTAAAATGGCTGAGTAAGCATTAGACTGTAATCTAAAAACAGAGATCAAG ACCTCTTTTTACCA
ex3_54 08059_ x2	AC00494 1.2/32735 -32806	18	#####	36.2	2	GGGGGUAGCUCAGGGGUAGAGCAUUUGACUGCAGAUCAAGAGGUCC CUGGUUCAAAUCCAGGUGCCCCCU
ex3_54 11057_ x2	CM00068 1.2/12188 561- 12188634	18	0.003	28.2	2	GGCTCTGTGGCTTTGTGGGTTAAAGTACTTGTCTGGCAAACAGGAGATGC TGGATTTCAATCCCAGCAGGGCCT

ex3_54 11421_ x2	CM00066 3.2/63634 501- 63634429	18	#####	36.2	2	GGTTGTACAGCTTAGAGCTTAAGAGCCTGGACTCTGGAATCAGAGTGTCT GGTTCAAATCCCAGCTCTGCCA
ex3_54 14039_ x2	CM00067 9.2/75034 503- 75034431	33	#####	65.9	2	GCCCCAGTGGCCTAATGGATAAGGCACTGGCCTCCTAAGCCAGGGATTGT GGTTTCGAGTCCCACCTGGGGTG
ex3_54 16025_ x2	CM00066 6.2/75046 18- 7504555	14	0.003	28.2	2	GGCTGGGAAGCCAGCCCTGGGGTCCAGAGCCAGATGGATGTGGGTTCAA ATCCCACCACAGCCA
ex3_54 16085_ x2	CM00066 3.2/14358 4701- 14358477 2	14	0.003	28.2	2	GGTTCATGGTGTAATGGTGAGGGCTTTGGACTCTGACTACAGTGATCAG AGTTCAAGTCTCAGTGGGACCT
ex3_54 19097_ x2	GL00025 6.2/19126 -19197	22	#####	44.1	2	GGGGTGTAGCTCAGTGGTAGAGCGCGTGCTTAGCATGCACGAGGCCCT GGTTCAATCCCCAGCACCTCCA
ex3_54 19179_ x2	CM00067 9.2/81389 62- 8138881	14	0.003	28.2	2	GCTGTGATGGCCGAGTGGTTAAGGCGTTGGACTCGAAATCCAATGGGGTC TCCCCGCGCAGGTTCCAATCCTGCTCACAGCG
ex3_54 20237_ x2	CM00067 2.2/69593 173- 69593241	15	0.001	30.2	2	AAGGGCTTAGCTTAAGTAAAGCAATTGATTTGCATACAATTGATGTAGGAC AGAGTCTTGCAGTCCTTA
ex3_54 20999_ x2	CM00066 3.2/12084 4335- 12084426 2	14	0.003	28.2	2	GTCTCTGTGGCGTAGTCCGTTAGCGCGTTCCGGCTGTTAACCGAAAGGTTG GTGGTTTCGAGCCCACCCAGGAACG
ex3_54 22503_ x2	CM00066 4.2/14022 4222- 14022415 2	14	0.002	28.2	2	GTTAATGTAGCTTAATTATTCAAAGCAAGACACTGAAAATGTCTAGATGGGT CTGCACAACCCCATAAACA
ex3_54 23417_	CM00066 5.2/14333	15	0.001	30.2	2	GGTGGTGAAGACAATGGACTGAGGAGTCTGTTGGACCTGGGTTCGAATCC CAGCTCCACCA

x2	639- 14333699						
ex3_54 23565_ x2	CM00066 8.2/26701 483- 26701555	18	0.003	28.2	2	GCCCTCTTAGCGCAGCTGGCAGCGCGTCAGTCTCATAATCTGAAGGTCCT GAGTTCAAGCCTCAGAGAGGGCA	
ex3_54 23719_ x2	CM00067 9.2/19605 432- 19605367	13	0.008	26.3	2	GGTAAATGGCTGAGTAAGCATGAGACTGTAAATCTAAAGACAGAGGTCAA GACCTCTTTTTACCA	
ex3_54 24303_ x2	CM00067 9.2/82270 64- 8226991	20	#####	40.1	2	GGCCGGTTAGCTCAGTTGGTTAGAGCGTGGTGCTAATAACGCCAAGGTCG CGGGTTCGAACCCCGTACGGGCCA	
ex3_54 25343_ x2	CM00067 1.2/64046 744- 64046678	15	0.0008	30.2	2	GGTAAATGACTGAGTAGGGCATTAGACTGTACATCTAAAAACAGAGGTCA AGGCCTGTTTTTACCA	
ex3_54 27603_ x2	CM00066 7.2/78023 024- 78022952	14	0.002	28.2	2	AGCTGTATATTATAGTGAATAAATGTGGACTTTGAAGTTAGATACACCTG GTTCAAATCCCAGTGCTGTCA	
ex3_54 27833_ x2	CM00067 6.2/73588 891- 73588832	18	#####	36.2	2	ATAGCTCAGTTGATAGAGCATCAGACTTTTAATCTGAGGGTCCAGGGTTCA TGCCCTGT	
ex3_54 28411_ x2	CM00066 9.2/14955 8042- 14955811 4	18	0.003	28.2	2	GGGGGTATAGCTCAGGGCTAGAGCTTTTTGACTGTAGAGCAAGAGGTCCC TGGTTCAAATCCAGGTTCTCCCT	
ex3_54 30567_ x2	CM00067 0.2/98141 234- 98141302	13	0.009	26.3	2	GGTCTTGCTCAGTGGAAGCCTCTGTCTGACCATACAGATGATCCAGGT TCGAATCCTGGCAAGGCCA	
ex3_54 31425_ x2	CM00066 9.2/14961 3136- 14961306	13	0.01	26.3	2	GGGGGTATAGCTCAGGGGTAGAGCATTTGACTGCAAATCAAGAGGTCCCT GATTCAAATCCAGGTGCCCCCT	

ex3_54 31661_ x2	CM00066 5.2/12072 2386- 12072231 8	15	0.001	30.2	2	GAAAAAGTCATAGAGGTTATGAGGTTGGCTTGAAACCAGTTTTAGGGGGTT GGATTCCTTCCTTTTTTCG
ex3_54 36995_ x2	CM00066 3.2/93933 954- 93934017	13	0.008	26.3	2	GGTAAAATGGCTGAGTAAGCTTTAGACTATAAATCTAAAGAGAGATTGAGC TCTCTTTTTACCA
ex3_54 37543_ x2	CM00066 7.2/12376 0805- 12376087 3	14	0.004	28.2	2	GTTTATGTAGCTTAATTATTAAGCAAGACACTGAAAATGTCTAGACGGAC TTATTACCCATAAACA
ex3_54 37809_ x2	CM00066 8.2/27230 637- 27230555	13	0.008	26.3	2	ACCGGGATGGCTGAGTGGTTAAGGCGTTGGACTTAAGATCCAATGGACAG GTGTCCGCGTGGTTTCGAGCCCCACTCCCGGTA
ex3_54 39775_ x2	CM00066 4.2/30054 702- 30054774	13	0.01	26.3	2	GGGCCAGTGGCTCAATGGATAATGCGTCTGACTAAGAATCAGAAGATTCC AGCCTTGACTCCTGGCTGGCTCA
ex3_54 40527_ x2	GL00025 1.2/21999 1-220062	26	#####	52	2	GGGGGTGTAGCTCAGTGGTAGAGCGCGTGCTTCGCATGTACGAGGCCCC GGTTTCGACCCCCGGCTCCTCCA
ex3_54 41541_ x2	CM00066 3.2/16145 6332- 16145641 4	20	#####	40.1	2	GTCAGGATGGCCGAGCGGTCTAAGGCGCTGCGTTCAGGTCGCAGTCTCC CCTGGAGGCGTGGTTTCGAATCCCCTCCTGACA
ex3_54 41675_ x2	CM00068 5.2/14343 4095- 14343402 4	14	0.004	28.2	2	TAGGATATGGTATATTAGGTAGCACAAAGAATTTGAATTCTCAGGGGTAG ATTCAATTCCTATAATTCTAG
ex3_54 41751_ x2	CM00067 7.2/58152 510- 58152578	13	0.008	26.3	2	GTAATATAGTATAACCAAACATTAGATTGTGGATCTAATAACAGAAGTCT GAACTTCTTATCTACT

ex3_54 42567_ x2	CM00067 9.2/19605 267- 19605195	14	0.004	28.2	2	TAGATTGAAGCCAATTGATTAGGGTGTTTAGATGTTAGCTAAATTTTCGTGG GTTTGAATTCCACCAGCCTAG
ex3_54 43119_ x2	CM00068 6.2/83715 87- 8371660	13	0.008	26.3	2	GTTAAGATGGCAGAACCTGGCAGTTTCATAAACTTAAAGTTTATAATCAGA GTTTCAACTCCTCTTCTTAACA
ex3_54 44403_ x2	CM00066 8.2/27020 346- 27020439	31	#####	61.9	2	GCTCCAGTGGCGCAATCGGTTAGCGCGCGGTACTTATATGGCAGTATGTG TGCGAGTGATGCCGAGGTTGTGAGTTCGAGCCTCACCTGGAGCA
ex3_54 45731_ x2	CM00067 9.2/19603 208- 19603276	18	#####	36.2	2	GGAAATATGTCTGACAAAAGAATTACTTTGATAGAGTAAATAATAGAGGTTA AAATCCTCTTATTTCTA
ex3_54 45887_ x2	CM00066 7.2/15186 8584- 15186851 3	13	0.008	26.3	2	GGTAGTGTAGTCTACTGGTTAAACGCTTGGGCTCTGACATTAACGTCCTGG GTTCAAATCCCAGCTTTGTCA
ex3_54 45949_ x2	CM00066 8.2/28607 156- 28607227	14	0.002	28.2	2	GGGGGTGTAGCTCAGTGGTAGAGCGCGTGCTTAGCATGTACGAGGTCCC GGTTCAATCCCCGGCACCTCCA
ex3_54 46901_ x2	CM00067 0.2/67585 468- 67585398	19	0.0005	30.2	2	ACTTTTAAAGGATGAGAGTCATCCGTTGGTCTTAAGAACCAAAAACACTGG TGCAACTCCAAATAAAAGTA
ex3_54 50023_ x2	CM00067 9.2/19603 345- 19603274	13	0.01	26.3	2	TAGGATGTGGTGTAATAGGTGGCATGGAGAATTTTGGATTATCAGGGGTA GTTTCAATTCCTATAGTTCTAG
ex3_54 50047_ x2	CM00066 3.2/16161 2029- 16161194 6	17	0.01	26.3	2	GTCAGGATGGCCGAGCAGTCTTAAGGCGCTGCGTTCAAATCGCACCTCC GCTGGAGGCGTGGGTTTCGAATCCCACCTTTTGACA
ex3_54 50269_	CM00067 4.2/74457	14	0.004	28.2	2	CCATGGTGTAAATGGTAAGCACCTGGACTCTGAATCCAGCAACCAGAGTT CCAGTCTCAGCGTGGA

x2	406- 74457471						
ex3_54 50479_ x2	CM00066 8.2/78958 365- 78958293	20	#####	40.1	2	GCCAAAATAGCTCAGCTGGGAGAGCATTAGACTGAAGATCTAAAGGTCTC TGGTTTGATCCTGGGTTTCAGAA	
ex3_54 50671_ x2	CM00066 9.2/68098 326- 68098258	15	0.0005	30.2	2	GAGAAGGTCATAGAGGTTATGGGATTGGCTTGAAACCAGTTTCTGGAGGT TCCATTCTTTCCTTTTTTCG	
ex3_54 52895_ x2	CM00067 8.2/29276 61- 2927733	14	0.003	28.2	2	CCCCGGCTGGCTCAGTCAGTAGATCATGAGACTCTTAATCTCAGGGTCGT GGTTACAGCCCCACACTGGGCG	
ex3_54 54069_ x2	CM00068 5.2/55180 233- 55180304	13	0.008	26.3	2	TAGGACATGGTGTGATAGGTAGCATGGAGAATTTTGGATTCTCAGGGGTA GTTCAATTCCTACAGTTCTAG	
ex3_54 55487_ x2	CM00066 8.2/18053 386- 18053467	19	#####	38.2	2	GGGCCAGTGGCGCAATGGATAACGCGTCTGACTACGGATCAGAAGATTCT AGAAATAGTAACTAAGGGCAGAATTTGGCCCA	
ex3_54 58237_ x2	CM00067 6.2/61184 426- 61184490	15	0.0007	30.2	2	GACAGTTTGGCTTAGTGGTTAAGAGCTTTGGTACCAGATGGAATGGGTTCA AATCCCAACTCTCT	
ex3_54 58827_ x2	CM00066 9.2/57170 776- 57170844	14	0.002	28.2	2	GTAATATAGTTTTAATCAAACATTAGATTGTGGGTCTAATAATAAAAGTCT GCAACTTCTTATTTACT	
ex3_54 59403_ x2	CM00066 3.2/14700 5272- 14700520 1	15	0.0008	30.2	2	GGTTCCATGGTGTAATGGTGACCACTTTGGACTCTGAATACAGTGATCAGA GTTCAAGTCTCACTGGAACCT	
ex3_54 59869_ x2	CM00068 2.2/57358 446- 57358372	14	0.004	28.2	2	GTAAAGATGGCAGAGCCCAGCGATTGCATAAACTTAACACTTTATAATCA GAGTTCAACTCCTCTTCTTAACA	

ex3_54 64725_ x2	CM00067 2.2/36434 683- 36434615	15	0.001	30.2	2	GTAATATAGTTTAGTCAAAATATTAGATTGTGGATCTGATAATAGAAGTCT GTAACCTTCTTATTACT
ex3_54 65079_ x2	CM00067 6.2/20660 051- 20659958	17	#####	34.2	2	CCTTCGATAGCTCAGCTGGTAGAGCGGAGGACTGTAGACTGCGGAAACGT TTGTGGACATCCTTAGGTTCGCTGGTTCAATCCGGCTCGAAGGA
ex3_54 69309_ x2	CM00066 6.2/84855 315- 84855245	16	0.0003	32.2	2	AATATAGTACTGAGTGATGAAGAGCCTGGCTTGAATCAGATAGATGTAGT TTTAAATTCTGTCTGTATTG
ex3_54 70389_ x2	CM00067 0.2/33015 028- 33015130	13	0.01	26.3	2	GGAAATATGTCTGACAAAATAATTACTTTGATAGAGTAAACAATACAGGTTA AAATCTCTCATTTCTAGAACTACAATAGAGGTTAAAATCCTCTTATTCTA
ex3_54 70511_ x2	CM00067 8.2/70788 694- 70788764	37	#####	73.8	2	GCATTGGTGGTTCAGTGGTAGAATTCTCGCCTGCCATGCGGGCGGCCGG GCTTCGATTCTGGCCAATGCA
ex3_54 71367_ x2	GL00025 3.2/24013 -23942	21	#####	42.1	2	GGGGGTGTAGCTCAGTGGTAGAGCACATGCTTTGCATGTGTGAGGCCCC GGTTTCGATCCCCGGCACCTCCA
ex3_54 71415_ x2	CM00066 8.2/14225 7639- 14225770 9	13	0.008	26.3	2	GCATGGGTGATTCAGTGGTAGAATTTTCACCTGCCATGCAGGAGGTCCAG GTTCAATTCCTGGCCTATGCA
ex3_54 79377_ x2	CM00066 3.2/16148 0566- 16148063 6	27	#####	54	2	GCATAGGTGGTTCAGTGGTAGAATTCTTGCCTGCCACGCAGGAGGCCAG GTTTGATTCTGGCCCATGCA
ex3_54 81289_ x2	CM00066 4.2/20121 3158- 20121308 8	14	0.002	28.2	2	ACTTTTAGAGGATGAGAGTTATCCATTGGTCTTAGGAACCAAAAATATTGG TGCAACTCCAAATAAAAGTA
ex3_54 83565_	CM00067 0.2/79428	13	0.008	26.3	2	GGCACTGTAGTTTGGATTGAGAAACACAGGCTTTAGAGGCAGAAGTTCTG GGTTCAAACCCAGCATTGCCA

x2	812- 79428742						
ex3_54 87481_ x2	CM00067 6.2/20653 192- 20653099	15	0.0008	30.2	2	CCTTCGATAGCTCAGCTGGTAGAGCGGAGGACTGTAGCCTGTAGAAACAT TTGTGGACATCCTTAGGTTCGCTGGTTCGATTCCGGCTCGAAGGA	
ex3_54 91011_ x2	CM00066 3.2/14366 1253- 14366118 2	26	#####	52	2	GCCATGATCGTATAGTGGTTAGTACTCTGCGCTGTGGCCGCAGCAACCTC GATTCGAATCCGAGTCACGGCA	
ex3_54 91347_ x2	CM00066 4.2/15526 3777- 15526384 2	13	0.008	26.3	2	CGTAAATGGCTGAGTAAGGCATTAGACTGTAAATCTAAAGACAGAGGCTA AACCTCTTTTTACCA	
ex3_54 91915_ x2	CM00068 1.2/35575 848- 35575920	13	0.008	26.3	2	GCCCAGCTAGCTCAGTCGGTAGAGCATAAGACTCTTAATCTCAGGGTTGT GGATTCGTGCCCCATGCTGGGTG	
ex3_54 92517_ x2	CM00066 4.2/11551 708- 11551764	13	0.009	26.3	2	TGGTCTAGTGGTTAGGATTCAGCGCTCCCACCGCCGCAGCCCGGGTTTCG ATTCCCGG	
ex3_54 94493_ x2	CM00067 0.2/65697 384- 65697297	15	0.001	30.2	2	TCTTCAATAGCTCAGCTGGTAGAGCGGAGGACTGTAGGTGCACGCCCGTG GCCATTCTTAGGTGCTGGTTTGATTCCGACTTGGAGAG	
ex3_54 94815_ x2	GL00025 1.2/18581 4-185743	13	0.009	26.3	2	GGGGGTGTAGATCAGTGGTAGAGCGCGTGCTTCGCATGTACGAGGTCCC TGTTCAATCCCTGGCACCTCCA	
ex3_54 95949_ x2	CM00067 9.2/75035 113- 75035185	31	#####	61.9	2	GACCGCGTGGCCTAATGGATAAGGCGTCTGACTTCGGATCAGAAGATTGA GGTTCGAGTCCCTTCGTGGTTCG	
ex3_54 95967_ x2	CM00068 2.2/50335 886- 50335805	14	0.003	28.2	2	GGTAGGGTGGCCGAGCGGTCTAAGGCACTGTATTAAGACTCCAGTCTCTT CAGAGGCATGGGTTTGAATCCCACTGCTGCCA	

ex3_54 96939_ x2	CM00066 8.2/27664 766- 27664841	13	0.009	26.3	2	GCCGAAATAGCTCAATTGGGAGAGTGTTAGACTGAAGATCTTCTGCAGGT CTCTGGTTCAATTCCGGGTTTTGACA
ex3_54 97183_ x2	CM00066 8.2/28213 037- 28213118	35	#####	69.9	2	GACGAGGTGGCCGAGTGGTTAAGGCGATGGACTGCTAATCCATTGTGCTC TGCACACGTGGGTTCGAATCCCATCCTCGTCG
ex3_54 99419_ x2	CM00067 3.2/59551 755- 59551837	20	0.0002	32.2	2	ACCAGAATGGCCGAGTGGTTAAGGCGTTGGACTTAAGATCCAATGGATTC ATATCCGCGTGGGTTCCGAACCCCACTTCTGGTA
ex3_55 00023_ x2	CM00067 3.2/50274 779- 50274708	13	0.01	26.3	2	GGGGGTGTAGCTCAGTGGTAGAGCGGATGCTTTGCATGTATGAGACTTTG GGTTGGATCCCCAGCACCTCCA
ex3_55 00501_ x2	CM00067 1.2/11019 8523- 11019859 5	15	0.0005	30.2	2	GGCCGTGTGGCCTAATGGATAAGGCGTCTGACTTCGGATCAAAGATTGC AGGTTTGAGTTCTGCCACGGTCG
ex3_55 01479_ x2	CM00067 8.2/31649 38- 3165010	13	0.008	26.3	2	GCCTGGCTAGCTCAGTCGGCAAAGCATGAGACTCTTAATCTCAGGGTCGT GGGCTCGAGCTCCATGTTGGGCG
ex3_55 01579_ x2	CM00066 5.2/15211 466- 15211541	15	0.0007	30.2	2	GCCTGGATAGCTCCTTCGGTAGAGCATCATCAGACTTTTAATGTGAGGGTC CAGGGTTCAAGTTCCTGTTTGGGCG
ex3_55 03537_ x2	CM00066 3.2/14648 8866- 14648893 6	18	0.003	28.2	2	GCGTCAGTGGTTTAGTGGTGAATTCCTGCCTCCCATGCACGAGATCCGT GTTCAACTCCTGGTTGGTGCA
ex3_55 04643_ x2	GL00025 6.2/1818- 1745	19	#####	38.2	2	GCCTGGGTAGCTCAGTCGGTAGAGCTATCAGACTTTTAGCCTGAGGATTC AGGGTTCAATCCCTTGCTGGGGCG
ex3_55 14431_ x2	CM00066 4.2/22332 1669-	21	#####	34.2	2	GTTGGGGTAACTCAGTTGGTAGAGTAGCAGACTTTTCATCTGAGGGTCCA GGGTTTAAGTCCATGTCCAGGCA

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ex3_55 18805_ x2	CM00068 5.2/25262 043- 25261972	14	0.003	28.2	2	AGTCAAGTGGTTT AGTGAAAGAACATTGGATTGGAAGTCAAGAGGCCTG GATTCTTGCTCCAGCTTCACCA	
ex3_55 19329_ x2	CM00066 4.2/21177 8080- 21177800 8	14	0.004	28.2	2	TAGATTGAAGCCAGTTGATTAGGGGGTTTAACTGTAACTAAATTTTCGTG GTTTTGAATTCCACCAGTCTAG	
ex3_55 24437_ x2	CM00066 9.2/14954 6540- 14954661 1	14	0.003	28.2	2	GGGGGTATAGCTCAGGGGTAGAGCACTTGACTGCAGATCAAGAAGTCCTT GTTCAAATCCAGGTGCCCCCT	
ex3_55 26159_ x2	CM00066 4.2/13138 2569- 13138263 8	15	0.001	30.2	2	GAGAAGGTCATAGAGGTTATGGGATTGGCTTGAAACCAGTCTCTGGGGGG TTCGATTCCCTCCTTTTTCA	
ex3_55 32505_ x2	CM00066 9.2/14941 5209- 14941513 8	13	0.01	26.3	2	GGGGGTATAGCTTAGCGGTAGAGCATTGACTGCAGATCAAGAGGTCCCC GTTCAAATCCGGGTGCCCCCT	
ex3_55 33897_ x2	CM00067 9.2/15505 371- 15505444	18	0.002	28.2	2	GGCAGTGACGCCTACTGGTTTAGAGCACAGATTCTAGATCGAGACATTCC TGGTTCAAATCCCAGCACTGTTG	
ex3_55 38919_ x2	CM00066 8.2/57861 238- 57861166	14	0.003	28.2	2	GGGGAATTAGCGCAAGTGGTAGAGTGCTTGCTTAGCATGCAAGAGGTAGT GGGATCGATGCCACATTCTCCA	
ex3_55 40499_ x2	CM00067 9.2/22528 921- 22528853	14	0.004	28.2	2	GAAAAAGTCATAGGGGTTATGAGGCTGGCTTGAAACCAGCCTTAGGAGGT TCAATTCCTTCTTTTTTG	

ex3_55 41939_ x2	GL00025 4.2/88976 -88903	13	0.008	26.3	2	GCCGAAATAGCTCAGTGGGGAGAGCGTTAGACTGAAGATCTTAAAGGTCC CTGGTTCAATCCCGGGTTTCGGCA
ex3_55 42753_ x2	CM00066 9.2/14969 1252- 14969118 1	22	#####	36.2	2	GGGGATATAGCTCAGGGGTAGAGCATTGACTGCAGATCAAGAGGTCCCC GGTTCAAATCCGGGTGCCCCC
ex3_55 43579_ x2	CM00066 4.2/84858 752- 84858824	14	0.002	28.2	2	GGTTCATAGTGTAACAGTTATCATGTCTGCTTTACACACTGAAGGTCCTG GGTTCAAACCTCAGTGGAACCA
ex3_55 49429_ x2	KI270765. 1/51018- 50945	14	0.005	28.2	2	GTCTCTGTGGCACAATCGGTTAGCGCGTTTGGCTGTTAATCTAAAGTTTGG TGGTTAGAGCCCACTGAGGGACG
ex3_55 52069_ x2	CM00066 9.2/14931 0190- 14931026 1	29	#####	50.1	2	GGGGGCATAGCTCAGTGGTAGAGCATTGACTGCAGATCAAGAGGTCCCT GGTTCAAATCCAGGTGCCCCCT
ex3_55 57829_ x2	CM00066 4.2/14309 6757- 14309668 9	14	0.002	28.2	2	GTAATATAGTTTAAACCAAAACATTAGATTGTGAATCTAATAATAGAAGCCT GTAACCTTCTTATCTACC
ex3_55 59187_ x2	CM00066 3.2/14637 0101- 14637017 4	14	0.003	28.2	2	GTCTCTGTGGCGCAATCGGTTAGCGCGTTCCGGCTGTTAACCGCAAGGTTG GTGGTTCCAGCCCACCCAGGGACG
ex3_55 60247_ x2	CM00066 9.2/67399 631- 67399560	14	0.004	28.2	2	GGCCTCATGGTGCAACAGTAGTGTGTCTGACTCCAGATCAGAAGGTTGTA TGTTCAAATCACGTAGGGGTCA
ex3_55 61195_ x2	CM00066 8.2/27303 860- 27303789	13	0.008	26.3	2	GGCAGAGTGGTGCAGCGGAAGCGTGCTGGGCCCGTAACCCAGAGGTCAA TGGATCGAAGCCATCCTTGGCTA
ex3_55 62965_ x2	CM00068 5.2/55180	13	0.008	26.3	2	GGAAATATGTCTGACAAAAGAACTACTTTGATAGAGTAAACAACAGAGGTT AAAATCCTCTTATTTCTA

x2	370- 55180302						
ex3_55 66731_ x2	CM00067 3.2/39766 947- 39766879	13	0.01	26.3	2	GAGAGAGTCATAGAGGGTATGGGATTGGCTTGAAACCAGTTTCTGGAGGT TTGATTCCTTCCTTTCTCG	
ex3_55 66975_ x2	CM00066 7.2/18109 7555- 18109747	36	#####	71.9	2	GGTAGCGTGGCCGAGCGGTCTAAGGCGCTGGATTAAGGCTCCAGTCTCTT CGGAGGCGTGGTTTCGAATCCCACCGCTGCCA	
ex3_55 68425_ x2	CM00066 9.2/14964 7026- 14964695	16	0.0002	32.2	2	GGGGGTATAGCTTAGGGGTAGAGCATTTGACTGCAGATCAAAGGTCCCT GTTCAAATCCAGGTGCCCTT	
ex3_55 70075_ x2	CM00067 8.2/31806 26- 3180554	15	0.0006	30.2	2	GCCCGGCTAGCTCAGTCGATAGAGCATGAGACTCTTAATCTCAGGGTCGT GGTTTCGAGCCGCACGTTGGGCG	
ex3_55 75289_ x2	KI270713. 1/28828- 28755	14	0.003	28.2	2	GTCTCTGTGGCGCAGTCGGTTAGCGCGTTTCGGCTGTTAACCGGAAGGTTG GTGGTTTCGAGACCACCCAAGGACG	
ex3_55 77181_ x2	CM00067 3.2/92752 43- 9275316	14	0.002	28.2	2	GCCTCCTTAGTGAGTAGGTAGCGCATCAGTCTCAAATCTGAATGGTCCT GAGTTCAAGCCTCAGAGGGGGCA	
ex3_55 78923_ x2	CM00066 4.2/42810 536- 42810628	30	#####	60	2	GCTCCAGTGGCGCAATCGGTTAGCGCGCGGTACTIONTATACAGCAGTACATG CAGAGCAATGCCGAGGTTGTGAGTTTCGAGCCTCACCTGGAGCA	
ex3_55 80905_ x2	CM00067 0.2/18537 373- 18537307	13	0.008	26.3	2	GGTAATATAGCTTAAGAGCCGTGGGTTTTGAACTCAGATTGCCTTGGTTCA AATCCGAGTTTCATTT	
ex3_55 81877_ x2	CM00068 1.2/41242 309- 41242237	13	0.008	26.3	2	GCCAGGATAGTTCAGGTGGTAGAGCATCAGACTTTTAACTGAGGGTTCA GGTTCAAGTCTCTGTTTGGGCG	

ex3_55 88729_ x2	CM00066 5.2/10689 4213- 10689414 3	13	0.008	26.3	2	ACTTTTAAAGGATAGGAGTTATCTATTGATCTTAGGAACCAAAAACATTGGT TCAACTCCAAGTAAAGGTA
ex3_55 89775_ x2	CM00066 8.2/28537 590- 28537683	14	0.004	28.2	2	GCTCCAGTGGCGCAATCGGTTAGCGCGCGGTTACTTATAAGACAGTGCACC TGTGAGCAATGCCGAGGTTGTGAGTTCAAGCCTCACCTGGAGCA
ex3_55 96973_ x2	CM00066 8.2/27505 909- 27505828	19	#####	38.2	2	GTAGTCGTGGCCGAGTGGTTAAGGCGATGGACTTGAAATCCATTGGGGTT TCCCCGCGCAGGTTCAATCCTGTCTGGCTACG
ex3_56 01723_ x2	CM00067 9.2/22525 692- 22525760	14	0.003	28.2	2	AGAAATATGTCTGACAAAAGAGTGACTTTGATAGAGTAAATAATAGAGGTTT GAATCCTCTTATTCTA
ex3_56 01989_ x2	CM00066 5.2/16623 3278- 16623320 8	14	0.004	28.2	2	GTTGATGTGGTTTAAATATGTTAAAACAAGGCATTGAAAATGTCTAGATGAGT TCTCATAGCTCCATAAACA
ex3_56 03859_ x2	CM00067 8.2/31919 89- 3192060	18	#####	36.2	2	GGCTCGTTGGTCTAGGGGTATGATTCTCGCTTAGGATGCGAGAGGTCCCG GGTTCAAATCCCGGACGAGCCC
ex3_56 05025_ x2	CM00066 9.2/14936 3270- 14936320 7	14	0.002	28.2	2	GTGGATATAGTCTGCATTTGACTGCAAATTAAGAAGTCTCTGGTTCAAAT CCAGCTGTCCCCT
ex3_56 08453_ x2	CM00066 3.2/14970 1404- 14970133 3	14	0.005	28.2	2	TGCATGGTTGTCTAGTGGCTAGGATTCGGTGCTGAAAGCGCCACGGCCCG GGTTCGATTCCCGGTCAGGGAA
ex3_56 09899_ x2	CM00066 3.2/20547 4143- 20547421	13	0.008	26.3	2	GCCCGGAGAGCTCAGTGGGTAGAGCATCAGACTTTTAAATCTGAGGGTCCA GGTTCAAGTCTCTCGTTCGGGCA

5

ex3_56 11225_ x2	CM00066 8.2/57813 562- 57813490	13	0.008	26.3	2	GAGGAATTAGCTCAGGCGGTAGAGCGCTCGCTTAGCATGCGAGAGGTAG CGGGATCGACGCCCGCATTCTCCA
ex3_56 14553_ x2	CM00066 4.2/11702 5004- 11702493 3	18	0.004	28.2	2	TAGGACATGGTGTAATAGGTAGAATGGAGAATTTTGAATTCTCAGGGGTAG GTTCAATTCCTATAGTTCTAG
ex3_56 24589_ x2	CM00066 7.2/15260 9036- 15260921 1	14	0.003	28.2	2	GGCTGTATAGCTCAGTGGTAGAGCATTGACTACAGAATCCTATACTCAGG GGAAGGAGAAGTGGGGTTTTCTCAGTGGGTCAAAGGACTTGTAGTGGTAA ATCAAAAGCAACTCTATAAGCTATGTAACAACTTTAAAGTCATATGTAGCT GGTTCAAATCCTGTTTCTGCCA
ex3_56 25569_ x2	CM00066 7.2/53964 07- 5396475	13	0.008	26.3	2	GAAGAAGTCATGGAGGTTATGGGATTGGCTTGAAACCAGTCTTTGGGGGT TCAATTCCTTCTTTTCA
ex3_56 27889_ x2	CM00066 8.2/27668 583- 27668656	20	#####	40.1	2	GGCCGGTTAGCTCAGTCGGCTAGAGCGTGGTGCTAATAACGCCAAGGTC GCGGGTTCGATCCCCGTACGGGCCA
ex3_56 29575_ x2	CM00066 9.2/14180 5039- 14180496 5	13	0.009	26.3	2	GTTAAGATGGCAGAGCCCGGCAATTGCATAAACTTAAACTTTATAACTG GAGGTTCAACTCCTCTTCTTCTTC
ex3_56 33114_ x1	CM00068 6.2/83721 71- 8372101	14	0.003	28.2	1	TAGGACGTGGTGTAATAGGTAGCACAGAGAATTTTGGATTCTCAGGTGCA GGTTCAATTCCTATATTCTAG
ex3_56 33996_ x1	CM00066 9.2/57187 595- 57187527	13	0.008	26.3	1	CATGGCTTAGCTTAATTAAGTGATTGATTTGCATTCAATTGATGCAGAATA CAGTTTTGCAGTCTTTA
ex3_56 36195_ x1	GL00025 5.2/21015 6-210228	22	#####	44.1	1	GCCTCCTTAGCGCAGTAGGCAGCGCTCAGTCTCATAATCTGAAGGTCCT GAGCTCGAACCTCAGAGGGGCCA

ex3_56 37158_ x1	CM00066 7.2/10004 8984- 10004891 6	16	0.0002	32.2	1	GTAAATATAGTTTAAACCAAAACATCAGATTGTGAATCTGATAACAGAGGCTC ACAGCCCCTTATTTACC
ex3_56 37778_ x1	CM00066 8.2/57808 645- 57808718	14	0.005	28.2	1	GTCTTCTTAGCGCAGTGAGCAGCGGTCAGTCTCATAATCTGAAGGTCCT GATGTTTCGAGCCTGAGAAAAGGCA
ex3_56 38421_ x1	CM00066 3.2/12047 6923- 12047685 2	18	0.002	28.2	1	GGTTCATGGTGTAATGGTGAGCACTTTGGACTCTGAATACAGTGATCAGA GTTCAAGTCTCACTGGGACCT
ex3_56 39977_ x1	CM00067 9.2/22524 659- 22524733	13	0.009	26.3	1	GTTAAGATGGCAGACCCCAGCAATTGCATAAAATTTAAACTTTACAACCA GAGGTTCAACCCCTCTTCTTAACA
ex3_56 40248_ x1	CM00066 3.2/14371 7365- 14371729 2	13	0.009	26.3	1	GTCTCTGTGGCACAATCGGTTAGAGCGTTCGGCTGTTAATCTAAAGGTTG GTGGCTAGAACCCACTGAGGGACG
ex3_56 40817_ x1	CM00068 5.2/55178 989- 55179057	13	0.009	26.3	1	AAGGGCTTAGCTTAATTAAGGTGGTTGATTTGCATTCAATTGATGCAGAAT AGAGTCTTGCAGTCCTCA
ex3_56 42340_ x1	CM00066 4.2/82819 272- 82819338	13	0.01	26.3	1	GCCCTTGTAGTATAATTCAATACTCTGGTCTTGTAACCAGAAATGGAGGA TCTCCTCCCCAGGACA
ex3_56 42649_ x1	CM00068 4.2/36179 392- 36179460	13	0.01	26.3	1	GGAAATATGTCTGATAAGAGAGTTACTTTGACAGAGTAAATTACAGAGGTT TAAATCTTCCTATTTCTA
ex3_56 42870_ x1	CM00066 3.2/14963 9453- 14963952 6	14	0.003	28.2	1	GTCTCTGTGGTGCAATCGGTTAGCGCGTTTGACTGTTAACTGAAAGGTTG GTGGTGCAAGCCCATCCAGGGATG

ex3_56 44466_ x1	CM00066 4.2/27050 782- 27050870	14	0.005	28.2	1	CCTTCGATAGCTCAGTTGGTAGAGCGGAGGACTGTAGTGGATAGGGCGTG GCAATCCTTAGGTTCGCTGGTTCGATTCCGGCTCGAAGGA
ex3_56 47425_ x1	CM00066 4.2/13138 4079- 13138414 3	19	0.0008	30.2	1	GGTAAAATGGCTGAGTAAGCATTAGACTGTAATCTGAAAACAGAGGTCAAG ACCTCTTTTTACCA
ex3_56 47648_ x1	CM00068 6.2/11133 337- 11133271	17	0.009	26.3	1	GGTAAAATGACTAAGTAGGGCATTAGACTGTACATCTAAAAACAGAGGTCA AGGCCTGTTTTACCA
ex3_56 47796_ x1	CM00067 4.2/41699 391- 41699323	18	#####	36.2	1	AGAAATATGTCTGATAAAAGAGTTACTCTGATAGAGTAAATAATAGAGGTTT AAACCCTCTTATTCTA
ex3_56 48031_ x1	CM00067 3.2/59556 429- 59556501	14	0.003	28.2	1	GCCCGGATAGCTCAGTCGGTAGAGCATCAGACTTTTAATCTGAGGGTCCG GGTTCAAGTCCCTGTTCCGGCG
ex3_56 48187_ x1	CM00067 3.2/20200 305- 20200250	14	0.003	28.2	1	GAAGGTATAGCTCAGGGGTAGAGCATTTGACTGCAGATCAAGAAAATACT CCTTTG
ex3_56 48333_ x1	CM00066 7.2/14239 4494- 14239442 3	27	#####	54	1	TCCTCATCAGTATAGTGGTGAGTATCCCCGCCTGTCACGCGGGAGACTGG GGTTCGATTCCCTGAGGAGGAG
ex3_56 50116_ x1	CM00067 9.2/38833 793- 38833722	14	0.003	28.2	1	GGGGGTAGGGCTCAGGGATAGAGCATTTGACTGCAGATCAAGAGGTCCC CGTTTCGAATCTAGGTGCCCCCT
ex3_56 51239_ x1	CM00067 0.2/88133 080- 88133007	13	0.009	26.3	1	GGTACAGTGTTAAAGGGGAGAAAATTGCTGACTTTGAATACAGTAGACCT AGGTTTGAATCCTGGCTTTACCA
ex3_56 52066_ x1	CM00066 8.2/27091	36	#####	71.9	1	GGCTCGTTGGTCTAGGGGTATGATTCTCGCTTCGGGTGTGAGAGGTCCCG GGTCAAATCCCGACGAGCCC

x1	742- 27091813					
ex3_56 52929_ x1	CM00066 8.2/94447 329- 94447261	13	0.008	26.3	1	AGAAATATGTCTGACAAAAGAGTTACTTTGATATAATAAATTATAGAGG TTC AAACCCTCTTATTTCTA
ex3_56 57489_ x1	CM00066 4.2/14021 7252- 14021731 7	13	0.008	26.3	1	GGTAAAATGACTGAGTAAACATTAGACTGTAAATCTAAATACAGAGGCCAA GGCCTCTTTTTACCA
ex3_56 60539_ x1	CM00067 9.2/81203 95- 8120314	31	#####	61.9	1	GGTAGCGTGGCCGAGCGGTCTAAGGCGCTGGATTTAGGCTCCAGTCTCTT CGGAGGCGTGGGTTTGAATCCCACCGCTGCCA
ex3_56 70254_ x1	CM00066 8.2/27602 675- 27602569	34	#####	67.9	1	GTCAGGATGGCCGAGTGGTCTAAGGCGCCAGACTCAAGTTGCTACTTCCC AGGTTTGGGGCTTCTGGTCTCCGCATGGAGGCGTGGGTTTGAATCCCCT TCTGACA
ex3_56 71376_ x1	CM00067 2.2/47633 857- 47633927	14	0.004	28.2	1	GTTAATGTAGCTTAATTATTTAAAGCAAGGCACTGAAAATGCCTAGATGGG TCCGCACAACCCGGTAAACA
ex3_56 72492_ x1	CM00067 9.2/38861 755- 38861684	23	#####	38.2	1	GGGGGTATAGCTCAGGGGTAGAGCATTGACTGCAGATCAAGAAGTCCCC GGTTCAAATCCGGGTGCCCCCT
ex3_56 72608_ x1	CM00066 8.2/27721 201- 27721119	13	0.01	26.3	1	ACCGGGATGGCCGAGTGGTTAAGGCGTTGGACTTAAGATCCAATGGGCTG GTGCCC GCGTGGGTTTGAACCCCACTCTCGGTA
ex3_56 72673_ x1	CM00068 1.2/49534 748- 49534676	13	0.01	26.3	1	ACCTGGGTAGCTTAGTTGGTAGAGCATTGGACTTTTAATTTGAGGGCCCAG GTTTCAAGTCCCTGTTTGGGTG
ex3_56 76503_ x1	CM00066 3.2/16520 658- 16520585	14	0.004	28.2	1	GTCTCTGTGGCGCAATCGGTTAGCGCGTTCCGGCTGTTAACTGAAAGGTTG GTGGTTCGAGCCCACCCAGGGACG

ex3_56 76802_ x1	KZ208915 .1/326654 0- 3266610	14	0.004	28.2	1	GGGGGTAGAATTCGGGGTAGAACATTTGACTGCAGATCAAGAGGTCCCCG CTTCGAATCTGGGTACCCCCT
ex3_56 77528_ x1	CM00067 1.2/84246 500- 84246559	13	0.008	26.3	1	GGTTCATGGTGTAATGGTGAGCACTCTGGACTCAGAATCCAGAAGTAGT GCTGGAACAA
ex3_56 78217_ x1	CM00068 4.2/36172 857- 36172789	14	0.006	28.2	1	GAGAAAGTCAGAGTGATTATGAAGCTCGTTTGAACCAGTTTTAGGAGGTT TGATTCCTTCCTTTCTCG
ex3_56 80876_ x1	CM00067 3.2/11356 2356- 11356227 3	13	0.01	26.3	1	ACCAGGATGGCCAAGTAGTTAAAGGCACTGGACTTAAGAGCCAATGGACA TATGTCTGTGTGGGTTTGAACCCCACTCCTGGTG
ex3_56 80944_ x1	CM00067 1.2/50964 82- 5096410	15	0.0005	30.2	1	TAGATTGAAGCCAGTTGATTAGGGTATTTAGCTGTAACTAAATTTTTGTGG GTTTGAATTCCACCGATCTAG
ex3_56 81479_ x1	CM00066 3.2/14373 5993- 14373592 0	13	0.008	26.3	1	GTCTCTGTGGCGCAATGGGTTAGCGCGTTTCGGCTGTAAACCGAAAGGTTG GTGGTTCGAGCCCATCCAGGGACG
ex3_56 81525_ x1	CM00066 9.2/57187 832- 57187767	13	0.008	26.3	1	GGTAAAAAGGCCGGGTAAGCATTAGACTGTAAATCTAAAGACAGAGGTCA AGGCCTCTTTTAGCA
ex3_56 82907_ x1	CM00066 6.2/11629 7743- 11629781 3	15	0.0009	30.2	1	GTTAATGTAGCTTAATTATTCAAAGCAAGACACTGAAAATGTCTAGATGGAT CCGCACAACCCTATAAACA
ex3_56 82975_ x1	CM00066 8.2/27293 892- 27293965	26	#####	52	1	GGCCGGTTAGCTCAGTTGGTTAGAGCGTGCTGCTACTAATGCCAGGGTCG AGGTTTCGATCCCCGTACGGGCCT

ex3_56 84497_ x1	CM00066 3.2/23794 1311- 23794137 9	13	0.008	26.3	1	AAGGGCTTAGCTTAATTAAGTGGTTGATTTGCATTCAATTGATGCAGAATA GAGTCTCGCAGTCCTTA
ex3_56 85020_ x1	CM00067 2.2/55597 818- 55597888	13	0.009	26.3	1	GTTAATGTAGCTTAATTATTTAAAGCAAGGCACTGAAAATGCCTAGATGGG TCGCAAAACCCCATAAACA
ex3_56 88472_ x1	CM00066 3.2/93516 349- 93516277	26	#####	52	1	GGGGGTATAGCTCAGGTGGTAGAGCATTGACTGCAGATCAAGAGGTCCC CGGTTCAAATCCGGGTGCCCCCT
ex3_56 89575_ x1	CM00066 8.2/57793 617- 57793545	17	0.008	26.3	1	GGGGATTAGCTCAAGCGGTAGAGCGCCTGCTTAGCATGCAAGAGGTAG CAGGATCGATGCCTGCATTCTCCA
ex3_56 89670_ x1	CM00068 1.2/31995 809- 31995876	14	0.003	28.2	1	GTTTCCATGGTGTAATGGTGAGCACTCTGGACTCTGAATCCAGAAATACAT TCAAAGAATTAAGAACA
ex3_56 90234_ x1	CM00066 3.2/23794 3730- 23794365 6	20	0.0002	32.2	1	GTTAAGATGGCAGAGCCCAGCAATTGCATAAACTTAAACTTTACAATCA GAGGTTCAACTCCTCTTCTTAACA
ex3_56 91109_ x1	CM00067 6.2/88979 098- 88979170	19	#####	38.2	1	GGGGAATTAGCTCAAGTGGTAGAGCGCTCGCTTAGCATGCGAGAGGTAGT GGGATCGATGCCCGCATTCTCCA
ex3_56 95351_ x1	CM00066 4.2/11702 4867- 11702493 5	14	0.005	28.2	1	AGAAATATGTCTGACAAAAGAATTACTTTGATAGAGTAAATAATAGAGATTA AATTCCTCTTATTTCTA
ex3_56 96504_ x1	CM00066 4.2/14021 7492- 14021756 0	15	0.0005	30.2	1	GAGGGCTTAGCTTAATTAAGTGGCTGATTTGTGTTCAATTGATGCAGAAT AGAGTCTTGACAGTCCTTA

ex3_57 04314_ x1	CM00067 0.2/70237 343- 70237274	15	0.0007	30.2	1	GGCAGTGTCTAGAGGTAAGAGTACAGGCTTAGAGTCAGACAGCGCGG GTTCAAATCCTGCTTCTGCCA
ex3_57 07409_ x1	CM00067 6.2/20663 285- 20663192	17	0.008	26.3	1	CCTTCGATAGCTCAGCTGGTAGAGCGGAGGACTGTAGATTGTACAGACAT TTGCGGACATCCTTAGGTTCGCTGGTTTCGATTCCGGCTCGAAGGA
ex3_57 07821_ x1	CM00068 4.2/44150 657- 44150743	24	#####	48.1	1	GCTCGGATGATCCTCAGTGGTCTGGGGTGCAGGCTTCAAACCTGTAGCTG TCTAGTGACAGAGTGGTTCAATTCCACCTTTGTAGGC
ex3_57 08207_ x1	CM00066 8.2/27583 528- 27583457	16	0.0002	32.2	1	TCCTCGTTAGTATAGTGGTGAGTGTCCCCGTCTGTCACGCGGGAGACCGG GGTTCGATTCCCCGACGGGGAG
ex3_57 11485_ x1	CM00067 4.2/49817 479- 49817409	14	0.003	28.2	1	TAGGATGTGGTGTGATAGGTAGCATGGAGAATTTTGGATTCTCAGGGGTA GGTTCAATTCCTATATTCTAG
ex3_57 14527_ x1	CM00066 9.2/14180 3557- 14180362 8	14	0.002	28.2	1	TAGGACGTGGTGTAGTAGGTAGCATGGAGAATGTTGAATTCTCAGGGGTA GGTTCAATTCCTATAGTTCTAG
ex3_57 17520_ x1	CM00066 4.2/11702 6500- 11702643 5	14	0.003	28.2	1	GGTAAATGACTGAGTAAGCGTTAGACTGTAAATCAAAGATGGAGGTCAA GGCCTCCTTTACCA
ex3_57 19633_ x1	CM00067 1.2/80564 882- 80564950	13	0.008	26.3	1	AAGGGCTTAGCTTAATTAAGTGGTTGATTTGTGTTCAATTGATGCAGAAC AGAGTCTTGCAGTCCTTA
ex3_57 20245_ x1	CM00067 0.2/66113 367- 66113459	24	#####	48.1	1	CCTTCGATAGCTCAGCTGGTAGAGCGGAGGACTGTAGCTACTTCCTCAGC AGGAGACATCCTTAGGTTCGCTGGTTTCGATTCCGGCTCGAAGGA
ex3_57 20851_ x1	CM00066 8.2/26568	13	0.009	26.3	1	CCTTCGATAGCTCAGTTGGTAGAGCGGAGGACTGTAGTTGGCTGTGTCCT TAGACATCCTTAGGTTCGCTGGTTTCGAATCCGGCTCGAAGGA

x1	858- 26568948						
ex3_57 21047_ x1	CM00066 3.2/14380 0111- 14380004 1	16	0.0001	32.2	1	GCACTGGTGGTTCAGTGGTAGGGTTCTCGCCTCACACGCGGGAGACCCG GGTTCAATTCCCGGTCAAGGCA	
ex3_57 21922_ x1	CM00066 3.2/24887 4248- 24887431 9	20	#####	40.1	1	TCCCTGGTGGTCTAGTGGTTAGGATTCGGCGCTCTCACCGCCGCGGCC GGTTTCGATTCCCGGTCAGGAAA	
ex3_57 27083_ x1	CM00066 4.2/11702 3841- 11702391 5	13	0.009	26.3	1	GTAAAGATGGCAGAGCCCAGCAATTGCATAAATCTTAAACTTTATAATCA GAGTTTCGACTCCTCTTCTTAACA	
ex3_57 27638_ x1	KI270803. 1/667733- 667803	14	0.002	28.2	1	GTAAATGTAGCTTAATTATTTAAAGCAAGACACTGAAAATGTCTAGATGGGC TTATACAGCCCCATAAACA	
ex3_57 28171_ x1	CM00068 5.2/39153 03- 3915230	26	#####	44.1	1	GGCCGGTTAGCTCAGTTGGTAAGAGCGTGGTGCTGATAACACCAAGGTGCG CGGGCTCGACTCCCGCACCGGCCA	
ex3_57 28385_ x1	CM00066 6.2/40906 798- 40906726	13	0.008	26.3	1	GACCATGTGGCCTAAGGGAAAAGACATCTCACTTTGGGTCAGAAGATTGA GGTTCAAGTCCTTTCATGGTCA	
ex3_57 31720_ x1	CM00066 6.2/15546 1250- 15546131 5	22	#####	44.1	1	GGTAAAGTGGCTGAATAAGCATTAGACTGTAAATCTAAAGACAGAGGTCAA GCCTCTTTTTAGCA	
ex3_57 34442_ x1	CM00066 3.2/14837 8989- 14837891 6	14	0.004	28.2	1	GTCTCTGTGGCACAATCGGTTAGCGCGTTCGGCTGTTAATCTAGAGGTTG GTGGTTAGAGCCCACTGAGGGATG	

ex3_57 35455_ x1	CM00067 8.2/33698 13- 3369884	13	0.009	26.3	1	TAGGACTTGGTGTAATGGGTAGCACAGAGAATTTTGGATTCTCAGGGGTG GGTTCAATTCCTTTCGTCCTAG
ex3_57 39076_ x1	CM00066 8.2/57870 417- 57870345	14	0.005	28.2	1	GGGGAATTAGCCCAAGTGGTAGAGCGCTTGCTTAGCATGCAAGAGGTAGT GGGATCGATGCCACATTCTCCA
ex3_57 40339_ x1	CM00066 8.2/69204 486- 69204568	13	0.01	26.3	1	ACTCATTGGCTGAGTGGTTAAGGCATTGGACTTAAGATCCAATGGAGTAG TGGCTGTGTGGGTTAAACCCACTACTGGTA
ex3_57 45328_ x1	CM00067 2.2/19747 745- 19747689	13	0.01	26.3	1	TGGTGTAATAGGTAGCACAGAGAATTCTGGATTCTCAGGGGTAGGTTCAAT TCCTAT
ex3_57 46011_ x1	CM00066 6.2/15546 3900- 15546382 6	13	0.01	26.3	1	GTAAAGATGGCAGAGCCTGGTAATTGCATAAACTTAAAATTTTATAATCAG AGGTTCAACTCCTCTTCTTAACA
ex3_57 48544_ x1	CM00067 0.2/66113 988- 66114076	13	0.008	26.3	1	CCTTCGATAGCTCAGCTGGTAGAGCGGAGGACTGTAGGCGCGCGCCCGT GGCCATCCTTAGGTCGCTGGTTCGATTCCGGCTCGAAGGA
ex3_57 50555_ x1	CM00068 5.2/55178 915- 55178987	14	0.003	28.2	1	TAGATTGAAGCCAGTTGATTAGGGTGTTTAGCTGTTAACGAAATTTTCGTG GTTTTGAATTCCACCAATCTAG
ex3_57 53884_ x1	CM00067 8.2/31939 18- 3193990	18	0.004	28.2	1	GCCCCAGTGGCCTGATGGATAAGGTAAGTGGCCTCCTAAGCCAGGGATTGT GGGTTGAGTTCCACCTGGGGTA
ex3_57 56847_ x1	CM00066 3.2/16162 1675- 16162174 8	24	#####	48.1	1	GTTTCTGTAGCGCGATCGGTTAGCGCCTTCGGCTGTTAAACGAAAGGTTG GTGGTTCGTTCCACCCCGGGACA
ex3_57 57187_ x1	CM00066 7.2/26198	13	0.008	26.3	1	GCCCGACTACCTCAGTCGGTGGAGCATGGGACTCTTCATCCCAGGGTTGT GGTTCGAGCCCCACATTGGGCA

x1	502- 26198430						
ex3_57 57366_ x1	CM00067 9.2/64530 873- 64530800	25	#####	50.1	1	AGCACCATGGCTTAGCTGGTTAAAGCACCTGTCTAGTAAACAGGAGATCCT GAGTTTCAATTCCAATGGTGCCT	
ex3_57 59246_ x1	CM00066 8.2/28989 002- 28989083	17	0.008	26.3	1	GGTAGCGTGGCCGAGCGGTCTAAGGCGCTGGATTAAGGCTCCAGTCTCTT CGGGGGCGTGGGTTCAAATCCCACCGCTGCCA	
ex3_57 59452_ x1	CM00066 3.2/55373 438- 55373506	20	0.0003	32.2	1	GAGAAAGTCATCGTAGTTACGAAGTTGGCTTAAACCCAGTTTTGGGAGGTT CAATTCCTTCTTTCTCT	
ex3_57 60063_ x1	GL00025 5.2/88972 -88899	14	0.002	28.2	1	GCCGAAATAGCTCAGTTGGGAGAGCGTTAGACCGAAGATCTTAAAGGTCC CTGGTTCAATCCCGGTTTTCGGCA	
ex3_57 62777_ x1	CM00066 3.2/16161 2718- 16161278 9	13	0.01	26.3	1	GCGTTGGTGGTGTAGTGGTGAGCACAGCTGCCTTTCAAGCAGTTAACGCG GGTTCGATTCCCGGGTAACGAA	
ex3_57 63390_ x1	CM00067 9.2/22527 153- 22527081	16	0.0001	32.2	1	TAGATTGAAGCCAGTTGATTAAGGTATTTAGCTGTAAACCAAATTTTTGTGG GTTAAGTCCCATTGATCTAG	
ex3_57 64687_ x1	CM00066 3.2/16872 583- 16872654	15	0.0008	30.2	1	TCCCTGGTGGTCTAGTGGCTAGGATTCGGCGCTTTCACCGCCGCGGCC GGTTCGATTCCCGGCCAGGGAA	
ex3_57 66530_ x1	CM00067 1.2/92539 385- 92539457	18	0.006	28.2	1	TAGATTGAAGCCAGTTGATTAGGGTATTTAGCTGTAACTACATTTTTATGG GTTTGAGTCCCATTATCTAG	
ex3_57 69284_ x1	CM00067 2.2/12581 9937- 12581987 4	13	0.01	26.3	1	GGTAAATGGCAGAGCAAGCATTAGACTGTAAATCTAGAGACAGGTTGAG CCCTCTTTTTACCA	

ex3_57 72834_ x1	CM00067 0.2/11093 4801- 11093486 9	23	#####	46.1	1	GAGGGCTTAGCTTAATTAAGTAGTTGATTTGCGTTCAATTGATGCAGAGT GGAGTCTTGCAGTCCTTA
ex3_57 77346_ x1	CM00067 6.2/20677 100- 20677019	13	0.01	26.3	1	GGTAGTGTGGTTGAATGGTCTAAGGCACTGAATTTAGGCTCCAGTCTCTTT GGGGACGTGGGTTTAAATCCCCTGCTGCAA
ex3_57 79437_ x1	CM00066 4.2/13138 5560- 13138563 1	13	0.009	26.3	1	TAGGACGTGGTGTGATAGGTAGCACGGAGAATTTTGGATTCTCAGGGATG GGTTCAATTCCTGTAGTTCTAG
ex3_57 80488_ x1	CM00066 9.2/14935 6723- 14935666 5	22	0.003	28.2	1	ATAGCTCAGTGGTAGAGCATTAACTGTAGATCAAGAGGTCCCTGGATCAA CTCTGGGT
ex3_57 87509_ x1	CM00066 9.2/97141 638- 97141584	14	0.004	28.2	1	GCTAGTCAGTAGAGCATGAGACTCTTAATCTCAGGGTCGTGGGTTGAGC CCCAC
ex3_57 94886_ x1	CM00067 6.2/83589 111- 83589041	13	0.01	26.3	1	GTTAATGTAGCTTAATTATTCAAAGCAAGACACTGAAAATGTCTAGATGGGT TTACACAATTCCATAAACG
ex3_57 96267_ x1	GL00025 6.2/52365 -52293	13	0.008	26.3	1	GGCCGCGTGGCCTAATGGATAAGGCGTCTGATTCCGGATCAGAAGATTGA GGGTTAGAGTCCCTTCGTGGTCCG
ex3_57 99641_ x1	CM00066 3.2/16535 350- 16535279	23	#####	46.1	1	TCCCTGGTGGTCTAGTGGCTAGGATTCGGCGCTTTCACCGCCGCGGCC GGGTTGATTCCCGGTCAGGGAA
ex3_57 99788_ x1	CM00066 5.2/10690 2102- 10690203 1	16	0.0003	32.2	1	TAGGATGTGGTGTATTAGGTAGCACAGAGAATTTTGGATTCTCAGGGGTAG GTTCGATTCCATAATTCTAC

ex3_58 00888_ x1	CM00066 8.2/28478 704- 28478623	15	0.0005	30.2	1	GGTAGCGTGGCCGAGTGGTCTAAGACGCTGGATTAAGGCTCCAGTCTCTT CGGGGGCGTGGGTTTGAATCCCACCGCTGCCA
ex3_58 01937_ x1	CM00066 6.2/15546 2873- 15546280 5	13	0.008	26.3	1	GGAAATATGTCAGACAAAAGAATTACTTTGATAGAGTAAACAATAGAGGTT AAAATCCTCTAATTTCTA
ex3_58 02290_ x1	CM00066 5.2/17699 968- 17699905	15	0.0008	30.2	1	GTATATCTCAGGGGGCAGAGCATTGACTGCAGATCAAGAGGTCCCCGGT TGAAATCCGGGTGC
ex3_58 10632_ x1	CM00066 3.2/14515 7157- 14515722 9	16	0.0001	32.2	1	GTTTCCGTAGTGTAGTGGTTATCATGTTTCGCCTCACACGCGAAAGGTCCC CGGTTTCGAAACTGGATGGAAACA
ex3_58 11844_ x1	CM00066 3.2/23794 2562- 23794263 3	13	0.009	26.3	1	TAGGACTTGGTGTAATAGGTAGCACGAAGAGATTTGGATTCTCAGGGGTA GGTTCAATTCCTATAGTTCTGG
ex3_58 13753_ x1	CM00068 3.2/88455 58- 8845492	14	0.004	28.2	1	GGTAAAATGACTGAGTAGGGCATTAGACTGTACATCTAAAAACAGAGGTCA ACGCCTGTTTTTACCA
ex3_58 14596_ x1	CM00066 8.2/28489 066- 28488993	13	0.009	26.3	1	GGCTCTATGGCTTAGTTGGTTAAAGCGCCTGTCTCGTAAACAGGAGATCCT GGGTTTCGACTCCCAGTGGGGCCT
ex3_58 17009_ x1	AC00867 0.6/83725 -83795	13	0.009	26.3	1	ACUUUUAAAAGGAUAACAGCCAUCCGUUGGUCUUAGGCCCCAAAAUUUU GGUGCAACUCCAAAUAAAAGUA
ex3_58 22328_ x1	GL00025 3.2/73472 -73400	13	0.01	26.3	1	GCCGAGATAGCTCAGTTGGGAGAGCGTTAGACTGAAGATCTAAAGATCCC TGTTCAATCCCGGGTTTCGGCA
ex3_58 25943_ x1	CM00067 8.2/31961 53-	13	0.009	26.3	1	GCCCAGCTAGCTCAGCCGGTAGAGCACAAAGACTCTTAATCTCAGGGTCGT GGTTTTGAGCCCTGTGTTGAGCA

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ex3_58 27416_ x1	CM00066 3.2/14804 8589- 14804851 6	20	0.0004	32.2	1	GTCTCTGTGGCGCAATCGGTTAGCGCGTTCGGCTGTAACTGAAAGGTTA GTGGTTCGAGCCCACCCGGGGACG
ex3_58 33284_ x1	CM00067 9.2/40082 752- 40082680	13	0.009	26.3	1	GATTCTATAGTGTAGCAGTTATCACATCTGCTTTACATGCAGAAGGTCCTA GGTTTGAGCCGCGGTGGAACCA
ex3_58 36127_ x1	CM00066 8.2/57842 286- 57842214	13	0.01	26.3	1	GCCCTCTTAGTGCAGCTGGCAGCGCGTCAGTTTCATAATCTGAAAGTCCT GAGTTCAAGCCTCAGAGAGGGCA
ex3_58 37463_ x1	CM00067 9.2/19598 561- 19598631	14	0.002	28.2	1	GTTAATGTAGCTTAATTATTCAAAGCAAGACACTGAAAATGTCTAGATGGGT CTGCACATCCCCATAAACA
ex3_58 37558_ x1	CM00066 3.2/14835 3561- 14835363 2	15	0.001	30.2	1	GGTTCATGGGTAAATGGTGAGCACCCCTGGACTCTGAATCAAGCGATCCG AGTTCAAATCTCGGTGGTACCT
ex3_58 40339_ x1	CM00066 3.2/16532 471- 16532398	27	#####	54	1	GTCTCTGTGGTGCAATCGGTTAGCGCGTTCGGCTGTAAACCATAAGGTTG GTGGTTACAGACCACCCAGGGACG
ex3_58 43731_ x1	CM00067 0.2/11093 4549- 11093461 4	17	#####	34.2	1	GGTAAAATGGCTGAGTAAACATTAGACTGCAAATCTGAAGATGGAGGTTAA GCCTCTTTTTACCA
ex3_58 52111_ x1	CM00066 4.2/14022 1556- 14022148 5	13	0.009	26.3	1	GCTAAGATGGCAGAGCCCGGCAATTGCATAAACTTAAACTTTATAATCT GAGGTTCAACTCCTCTTAACA

ex3_58 52426_ x1	CM00067 1.2/54433 01- 5443364	17	#####	34.2	1	TGCACAATAGTTAAGAGCATAAACACTGGAACCAGATGTCTGGGTTCGAAT CCCAGCTGTGCTA
ex3_58 55051_ x1	CM00066 4.2/13027 2409- 13027233 8	17	0.01	26.3	1	TAGGACGTGGTGTGATAGGTAGCATGGAGAATTTTGGATTCTCAGGGATG GGTTC AATTCCTATAGTCCTAG
ex3_58 61314_ x1	CM00067 5.2/36065 681- 36065610	13	0.008	26.3	1	TAGGATGTGGTGTGACAGGTAGCATGGAGAATTTTGGATTCTCAGGGTTA GGTTC AATTCCTATAGTTCTAG
ex3_58 64767_ x1	CM00066 9.2/14180 2320- 14180238 8	15	0.001	30.2	1	AAGGGTTTAGCTTAGTTAAAGTGGTTGATTTGCATTCAACTGATGCAGAAT AGAGTCTGGCAGTCCTTA
ex3_58 68643_ x1	CM00066 3.2/54957 941- 54957869	30	#####	60	1	GCCCAGCTAGCTCAGTCGGTAGAGCATGAGACTCTTAATCTCAGGGTCAT GGGTTTGAGCCCCACGTTTGGTG
ex3_58 68660_ x1	CM00066 9.2/14966 4824- 14966489 5	13	0.008	26.3	1	GGGGGTATAGCTCACAGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCC GGTTC A AATCTGGGTGCCCCCT
ex3_58 77017_ x1	GL00025 1.2/28053 0-280459	26	#####	52	1	GGGGGTGTAGCTCAGTGGTAGAGCGCATGCTTTGCATGTATGAGGTCCCG GGTTCGATCCCCGCCACCTCCA
ex3_58 78576_ x1	CM00066 4.2/13027 5520- 13027545 1	14	0.002	28.2	1	GAGAAGGTCACAGAGGTTATGGGATTGGCTTGAAACCAGTCTGTGGGGG GTTCGATTCCCTCCTTTTTCA
ex3_58 79275_ x1	CM00067 1.2/12035 5157- 12035507 5	14	0.004	28.2	1	GTCAGGGTGGCTGAGCAGTCTGAGGGGCTGCGTTCAGGTCGCAGTCTGC CCTGGAGGCGTGGGTTTCAATCCCCTCCTGAAA

ex3_58 81865_ x1	CM00066 9.2/14935 5746- 14935567 5	16	0.0001	32.2	1	GGGGGTATAGCTCAGGGGTAGAGCATTGACTGCAGATCAAGAGGTCCCC AGTTCAAATCTGGGTGCCCCCT
ex3_58 81928_ x1	CM00066 8.2/27162 271- 27162344	13	0.008	26.3	1	GGCCCTGTGGCTTAGCTGGTCAAAGCGCCTGTCTAGTAAACAGGAGATCC TGGTTTCGAATCCCAGCGGGGCCT
ex3_58 86017_ x1	CM00068 5.2/55178 753- 55178818	14	0.007	28.2	1	GGTAAATGGCTGGGTAAGCATTAGACTGTAAATCTAAAGACAGAGGCCA AGGCCGCTTTTATAGCA
ex3_58 88434_ x1	CM00066 3.2/14383 1781- 14383170 8	15	0.0009	30.2	1	GTCTCTGTGGCGCAATCGGCTAGCGGTTTGGCTGTAACTAAAAAGTTG GTGGTTCGAACACACCCAGAGGCG
ex3_58 91501_ x1	CM00066 3.2/23794 1237- 23794130 9	13	0.008	26.3	1	TAGATTGAAGCCAGTTGATTAGGGTATTTAGCTGTAACTAAGTTTTCATGG GTTTGAATCCCACCGATCTAG
ex3_58 92700_ x1	CM00067 3.2/10340 4238- 10340430 7	13	0.008	26.3	1	CAAGAAATTCATAGAGGTTATGGGATTGGCTAGAAACCAGTTTCAGGAGGT TCGATTCCTTCCTTTTTGG
ex3_59 06282_ x1	CM00066 6.2/15546 2736- 15546280 7	13	0.008	26.3	1	TAGGACGTGGTGTGATAGGTAGCACAGAGAATTTTGGATTCTCAGGGGTA GTTAAATTCCTATAGTACTAG
ex3_59 09145_ x1	CM00066 8.2/26673 362- 26673434	19	0.001	30.2	1	GGGGAATTAGCTCAAGTGGTAGAGCGCTTGCTTAGCATGCAAGAGGTAGT GGGATCAATGCCACATTCTCCA
ex3_59 09173_ x1	CM00067 9.2/22527 306-	14	0.004	28.2	1	GGTAAGATGGCTGAGCAAAGCATTAGACTGTAAATCTAAAACTCTTTTT ACCA

ex3_59 10134_ x1	22527251 CM00068 5.2/10277 3201- 10277327 5	13	0.008	26.3	1	GTAAAGATGGTAGAGCCTGGTAATTGCATAAACTTGAAATTTTATAATCAG AGGTTCAATTACTCTTCTTTTAA
ex3_59 15573_ x1	CM00066 9.2/14940 6135- 14940606 4	13	0.008	26.3	1	GGGGGTATAGCTGAGGAGTAAACCATTTGGCTGCAGATCAAGTGGTCCCT GTTCAAATATGGGTGCCCTCT
ex3_59 17200_ x1	CM00067 1.2/92539 198- 92539263	13	0.009	26.3	1	GGTAAAATGGCTGAGTAAAGCATTAGACTGTAAATCTAAGGACAGAGGCTA AACCTCTTTTACCA
ex3_59 22691_ x1	CM00066 4.2/13138 5697- 13138562 9	15	0.0006	30.2	1	AGAAATATGTCTGACAAAAGAATTACTTTGACAGAGTAAACAACAGAGGTT AAAATCCTCATATTTCTA
ex3_59 22886_ x1	CM00066 8.2/26305 570- 26305493	14	0.003	28.2	1	GAGGCCTGGCCGAGTGGTTAAGGCGATGGACTGCTAATCCATTGTGCTCT GCACGCGTGGGTTTCAATCCCATCCTCG
ex3_59 24225_ x1	CM00066 8.2/26721 065- 26720992	18	0.003	28.2	1	GGCCGGTTAGCTCAGTTGGTCAGAGCGTGGTGCTAATAACGCCAAGGTCG CGGGTTCGATCCCCGTACGGGCCA
ex3_59 28764_ x1	CM00067 1.2/74903 145- 74903074	15	0.001	30.2	1	TCCTCGTTAGTATGGTGGTGGTATCCCTGCCTGTCACGCGGGAGACCGG GGTTCGATTCCCAACGGGGAG
ex3_59 30597_ x1	CM00067 2.2/69595 484- 69595416	14	0.004	28.2	1	AGAAATATGTCCGATAAAAGAGTTACATTGATAGAATAAATAATAGAGGTTT AAATCCTCTTATTTCTA
ex3_59 31472_ x1	CM00066 3.2/14512 9239- 14512931	25	#####	50.1	1	GTCTCTGTGGCGCAATCGGCTAGCGCGTTTGGCTGTTAACTAAAAGGTTG GCGGTTTCAACCCACCCAGAGGCG

2

ex3_59 37476_ x1	CM00066 3.2/12104 8505- 12104843 2	14	0.002	28.2	1	GTCTCTGTGGCGCAATCGGCTAGCGCTTTTGGCTGTAACTAAAAGGTTG GTGGTTTGAACCCACCCAGAGGCG
ex3_59 41921_ x1	CM00067 0.2/46827 965- 46828036	14	0.004	28.2	1	TACGACATGGTGTAATAAGTAGCACAGAGAATTTTGGGTTCTCAGGGGTAG GTTCAATTCCCATAGTTCTAG
ex3_59 42220_ x1	CM00067 8.2/10721 693- 10721625	13	0.009	26.3	1	GTAATATAGTTTAAACCAAACATTAGACTATGAATCTAACAATAGAAGCCC GCAACTTCTTATCTACC
ex3_59 42967_ x1	GL00025 4.2/29263 -29190	14	0.004	28.2	1	GCTGAAATAGCTCAGTTGGGAGAGCGTTAGACTGAAGATCTTAAAGTTCCC TGTTCAACCCTGGGTTTCAGCC
ex3_59 55317_ x1	CM00067 2.2/36434 555- 36434485	14	0.002	28.2	1	ACTTTTAAAGTATAAGAGCGACCCATTGGTCTTAGGAACCAAAAATATTGG TGCAACTCCAAATAAAAGTA
ex3_59 60246_ x1	CM00066 3.2/16559 6913- 16559698 5	14	0.003	28.2	1	GTCTAGCTAGATCAGTTGGTAGAGCATAAGACTCTTAATCTCAGGGTCATG GGTTTGAGCCCTACGTTGGGCG
ex3_59 68528_ x1	CM00067 3.2/54759 373- 54759316	14	0.003	28.2	1	TAGCTTAGTTGATGAAGCGTGAGACTCTTAATCTCAGGGTAGTGGGTTCAA GCCCCAC
ex3_59 74922_ x1	CM00067 0.2/46828 102- 46828034	13	0.009	26.3	1	GGAAATATGTTCAACAAAAGAATTACTTTGATAGACTAAACAATGGAGGTTA AAATCCTCTTATTTCTA
ex3_59 82080_ x1	CM00066 7.2/13218 0779- 13218083 8	19	0.002	30.2	1	AGGGGTATAGCTCAGTGGTAGAGCATTTGACTGCAGATCAAAAAAAAAAAG TTTCCCCCG

ex3_59 83262_ x1	CM00066 8.2/15654 7986- 15654791 2	13	0.01	26.3	1	GTTAAGACGGCAGAGCCCGGCAATTGCGTAAAATTTACAACCTTTATGGGCA GAGGTTCAATTCCTCTCTTAACA
ex3_59 95369_ x1	CM00066 8.2/27631 421- 27631514	14	0.004	28.2	1	GCTCCAGTGGCGCAATCGGTTAGCGCGCGGTACTTATACAACAGTATATG TCCGGGTGATGCCGAGGTTGTGAGTTCGAGCCTCACCTGGAGCA
ex3_59 97393_ x1	CM00066 9.2/14960 8376- 14960844 7	14	0.002	28.2	1	GGGTGTATGGCTCAGGGGTAGAGAATTTGACTAGAGATCAAGAGGTCCCT GGTCAAATCCAGGTGCCCCCT
ex3_60 02730_ x1	CM00068 5.2/55181 396- 55181322	14	0.004	28.2	1	GTTAAGATGGCAGAGCCCGGCAATTGCATAAGACTTAAAACCTTTATAATCA GAGGTTCAACTCCTCTCATTAACA
ex3_60 09060_ x1	CM00066 8.2/27209 849- 27209930	30	#####	60	1	GCTGTGATGGCCGAGTGGTTAAGGCGTTGGACTCGAAATCCAATGGGGTC TCCCCGCGCAGGTTCAAATCCTGCTCACAGCG
ex3_60 18723_ x1	CM00068 2.2/30746 051- 30746117	13	0.009	26.3	1	GGTAAATGACTGAGTAGGGCATTAGACTGTACATCTAAAAACAGAGGTCA AGTCCTGTTTTTACCA
ex3_60 28422_ x1	CM00066 4.2/13138 4241- 13138431 3	18	0.003	28.2	1	TAGATTGAAGCCAGTTGATTAGGGTGTTTAGCTGTTAATTAATTTTCGTGG GTTAAGTCCCGTCAATCTAG
ex3_60 41109_ x1	CM00066 8.2/27532 208- 27532289	15	0.001	30.2	1	GTAGTCGTGGCCGAGTGGTTAAGGCGATGGACTAGAAATCCATTGGGGTT TCCCCACGCAGGTTCAATCCTGCCGACTACG
ex3_60 49787_ x1	CM00066 3.2/14970 8730- 14970866 0	15	0.0006	30.2	1	GCAGTGGTGGTTCAGTGGTAGGGTTCTCGCCTCACACGCGGGAGACCCG GGTCAAATCCCGGTCAAAGCA

ex3_60 57824_ x1	CM00066 3.2/23794 1074- 23794113 9	14	0.002	28.2	1	GGTAAATGACTGAGTAAGCATTAGACTATAAATCTAAAGACAGAGGTCAA GACCTCTTTTTACCA
ex3_60 86981_ x1	CM00066 9.2/14958 4725- 14958479 6	21	#####	34.2	1	GGGGGTATAGCTCAGGGGTAGAGCATTGACTGCAGATCAAGAGGTCTCT GTTCAAATCCAGGTGCCCCCT
ex3_60 90119_ x1	CM00066 9.2/64110 164- 64110229	13	0.008	26.3	1	GGTAAATGGCTGAGTAAGCATTAGACTGTAAATCTAAAGACAGAGGTCAA GCCTCTTTTTTCCT
ex3_60 90541_ x1	KI270879. 1/243806- 243735	13	0.01	26.3	1	TAGGATGTGGTGTATTATGTAGCACGGAGAATTTTGGATTCTCATGGGTAG GTTCAATTCCTGTAATTCTAG
ex3_61 03961_ x1	CM00067 4.2/27690 373- 27690445	14	0.002	28.2	1	ACCCAGATAGCTCAGTCAGTAGAGCATCAGACTTTTAATCTGAGGGTCCAA GTTTCATGTCCCTTTTTGGGTG
ex3_61 16175_ x1	CM00067 0.2/33015 199- 33015128	14	0.005	28.2	1	TAGTACATAGTGTAATAGGTAGCACAGATAATTTTGGATTCTCAGGGGTAG GTTCAATTCTTATAGTTCTAG
ex3_61 41787_ x1	CM00066 4.2/15526 3939- 15526401 1	14	0.004	28.2	1	TAGATTGAAGCCACTTGATTAGGGTATTTAGCTGTAACTAAATTTTTGTGG GTTAAGTCCCGTTAATCTAG
ex3_61 43180_ x1	CM00066 3.2/16875 463- 16875536	13	0.01	26.3	1	GTCTCTGTGGTGCAATCGGTTAGCGCGTTCGGCTGTTAACCATAAGGTTG GTGGTTAGAGACCACCAGGGACG
ex3_61 50395_ x1	CM00066 8.2/26687 257- 26687329	21	#####	42.1	1	GGGAATTAGCTCAAGTGGTAGAGCGCTTGCTTAGCACGCAAGAGGTAGT GGGATCGATGCCACATTCTCCA
ex3_61 66629_ x1	CM00066 9.2/64110	14	0.002	28.2	1	TAGATTGAAGCCAGTTGATTAGGGTGTTTAGCTGTAACTAAATTTTCGTG GTTAAGTCCCACCAATCTAG

x1	327- 64110398						
ex3_61 84109_ x1	CM00067 1.2/78741 572- 78741640	14	0.005	28.2	1	AAGAGCTTAGCTTAATTAAGTGGTTGATTTGTGTTCAATTGATGCAGAATA GAGTCTTGCAGTCCTTA	
ex3_62 10314_ x1	CM00066 9.2/57194 203- 57194273	13	0.008	26.3	1	AGTTGTAGAGGATAAGAGCTATCCATTGGTCTCAGGAACCAAAAATATTGG TGCAACTCCAAATACAAGTA	
ex3_62 13134_ x1	CM00067 8.2/33699 50- 3369882	15	0.001	30.2	1	GGAAATATGTCCGACACAAGAATTACTTTGATAGAGTAAACAATAAAGGTTT AAATCCTCTCATTCTA	
ex3_62 26588_ x1	GL00025 3.2/68435 -68365	18	0.003	28.2	1	GGGGGTGTAGCTCAGTGGTAGAGCGCATGCTTTGCATGTATGAGGCCTCG GTTCGATCCCCGACACCTCCA	
ex3_62 35967_ x1	GL00025 1.2/23841 2-238484	16	0.0002	32.2	1	GCCTGGATAGCTCAGTTGGTAGAACATCAGACTTTTAATCTGACGATGCAG GGTTCAAGTCCCTGTTTCAGGCC	
ex3_62 37537_ x1	CM00067 8.2/70778 281- 70778211	41	#####	73.8	1	GCATTGGTGGTTCAGTGGTAGAATTCTCGCCTGCCACGCGGGAGGCCCG GGTTTGATTCCCGGCCAGTGCA	
ex3_62 53735_ x1	CM00066 8.2/27605 745- 27605638	13	0.008	26.3	1	GTCAGGATGGCCGAGTGGTCTAAGGCGCCAGACTCAAGCTTACTGCTTCC TGTGTTCCGGTCTTCTGGTCTCCGTATGGAGGCGTGGGTTCGAATCCCAC TTCTGACA	
ex3_62 59611_ x1	CM00066 3.2/16154 0241- 16154031 4	35	#####	69.9	1	GTCTCTGTGGCGCAATCGGTTAGCGGTTCCGGCTGTTAACCGAAAGGTTG GTGGTTTCGATCCCACCCAGGGACG	
ex3_62 61570_ x1	CM00066 3.2/14955 8493- 14955841 9	13	0.008	26.3	1	GTCTCTGTGGCGCAATTGGTTAGCGGTTCCGGTTGTTAACCGTAAAGGTT GGTGGTTTCGAGCCCACCCAGGAACG	

ex3_62 67923_ x1	CM00066 8.2/27576 067- 27576139	14	0.002	28.2	1	ACCTGGGTAGCTCAGTAGGTAGAACATCAGACTTTTAATCTGAGGGTCTAG GGTTCAAGTCCCTGTCCAGGCG
ex3_62 91923_ x1	CM00066 4.2/21177 8006- 21177793 8	13	0.008	26.3	1	AAGGGCTTAGCTTAATTAAGTGGTTTATTTGCGTTCAACTGATGCAGAATA GAGTCTTGCAGCCCTTA
ex3_63 26101_ x1	CM00066 9.2/57186 344- 57186273	16	0.0003	32.2	1	TAGGACGTGGTGTGATAGGTAGCATGGGGAATTTTGGATTCTCAGGGGTG GGTTCAATTCCTATAGTTCTAG
ex3_63 56549_ x1	CM00067 3.2/10341 1122- 10341105 2	14	0.006	28.2	1	GTTAATGTAGCTTAATTAATTTAAAGGAAGACACTGAAAATGTCTAGATGGGT TTGCACAACCCCATAAACA

(b)

Qseqid	Sseqid	NT	Evalue	Bitscore	Number	Sequence
co3_131898 4_x14055	AC092686.3/296 31-29561	30	#####	60	14055	GCAUUGGUGGUUCAGUGGUAGAAUUCUCGCCUGCCACGCG GGAGGCCCGGGUUCGAUUCGCCGCAUGCA
co3_140152 2_x13170	GL000253.2/247 759-247830	30	#####	60	13170	TCCCTGGTGGTCTAGTGGTTAGGATTCGGCGCTCTACCGCC GCGGCCCGGGTTCGATTCCCGGTCAGGGAA
co3_147909 9_x12667	AF347001.1/160 15-15948	20	#####	40.1	12667	CAGAGAAUAGUUUAAAUUAGAAUCUAGCUUUGGGUGCUAA UGGUGGAGUUAAGACUUUUUCUCUGA
co3_185684 9_x8797	ENST00000387 461.2	17	#####	34.2	8797	CAGAGAATAGTTTAAATTAGAATCTTAGCTTTGGGTGCTAATG GTGGAGTTAAAGACTTT
co3_213255 2_x6512	AF347015.1/160 4-1672	17	#####	34.2	6512	CAGAGUGUAGCUUAACACAAAGCACCCAACUACACUJAGG AGAUUUAACUUAACUUGACCGCUCUGA
co3_240741 3_x5455	AC093311.2/140 036-139968	31	#####	61.9	5455	GUUCUUGUAGUUGAAUACAACGAUGGUUUUCAUAUCAUU GGUCGUGGUUGUAGUCCGUGCGAGAAUA
co3_323672 7_x3090	ENST00000387 441.1	22	#####	44.1	3090	GTAAATATAGTTTAAACAAAACATCAGATTGTGAATCTGACAA CAGAGGCTTACGACCCC
co3_324290 6_x3085	ENST00000387 342.1	17	#####	34.2	3085	CAGAGTGTAGCTTAACACAAAGCACCCAATTACACTTAGGA GATTTCAACTTAACTTGA
co3_355114 7_x2550	CM000678.2/31 91501-3191573	40	#####	79.8	2550	GCCCGGCTAGCTCAGTCGGTAGAGCATGGGACTCTTAATCTC AGGGTCGTGGGTTTCGAGCCCCACGTTGGGCG

co3_359915 6_x2502	ENST00000387 449.1	25	#####	50.1	2502	GAGAAAGCTCACAAGAACTGCTAACTCATGCCCCCATGTCTA ACAACATGGCTTTCTCA
co3_361410 7_x2478	CM000663.2/14 8302805- 148302734	26	#####	52	2478	GCCGTGATCGTATAGTGGTTAGTACTCTGCGTTGTGGCCGCA GCAACCTCGGTTCTGAATCCGAGTCACGGCA
co3_437415 5_x1469	GL000252.2/133 42-13414	34	#####	36.2	1469	GCCTGGATAGCTCAGTTGGTAGAACATCAGACTTTTAATCTGA CGGTGCAGGGTTCAAGTCCCTGTTCAGGCG
co3_446501 2_x1366	ENST00000387 421.1	20	#####	40.1	1366	CACTGTAAAGCTAACTTAGCATTAACTTTTAAGTTAAAGATTA AGAGAACCAACACCTC
co3_468900 9_x1180	AF382005.1/581 -651	30	#####	60	1180	GUUUAUGUAGCUUACCUCCUCAAGCAAUACACUGAAAAUG UUUAGACGGGCUCACAUCACCCCAUAAACA
co3_473880 7_x1138	AC007298.17/14 5366-145295	38	#####	75.8	1138	UCCUCGUUAGUAGUAGUGGUGAGUAUCCCCGCCUGUCACGC GGGAGACCGGGUUCGAUUCCCCGACGGGGAG
co3_486830 9_x1036	CM000663.2/14 5459658- 145459729	32	#####	63.9	1036	GGTTCATGGTGTAAATGGTGAGCACTCTGGACTCTGAATCCA GCGATCCGAGTTCGAGTCTCGGTGGAACCT
co3_497921 8_x963	ENST00000387 377.1	14	#####	28.2	963	AGTAAGGTCAGCTAAATAAGCTATCGGGCCCATACCCCGAAA ATGTTGGTTATAACCCTC
co3_531494 9_x769	CM000666.2/54 88322-5488403	23	#####	30.2	769	GATTTTATGGTGTAAATGGTGAGCACTCTGGACTTGGAATCCA GAATTAACAAACAGAACATCCTGCAATTTTATTAAGAGCA
co3_545869 2_x705	CM000664.2/20 2614781- 202614713	13	0.008	26.3	705	AAGAGAGTCATAGAAGTTATGGGATTGGCTTGAACCAATTC TGGAAGTTCAATTCCTTCTTTCTTG

co3_562622 7_x635	AC006449.19/19 6857-196784	23	1E-08	46.1	635	GUCUCUGUGGCGCAAUCGGUJAGCGCGUUCGGCUGUUAAC CGAAAGGUJGGUGGUUCGAGCCCACCCAGGGACG
co3_656413 7_x325	CM000668.2/28 658308- 28658237	20	#####	40.1	325	GGGGATGTAGCTCAGTGGTAGAGCGCATGCTTAGCATGCAT GAGGTCCCGGGTTCGATCCCCAGCATCTCCA
co3_658576 0_x320	CM000685.2/18 674981- 18674909	35	#####	69.9	320	GGTTCATAGTGTAGTGGTTATCACGTCTGCTTTACACGCAG AAGTCTCGGGTTCGAGCCCCAGTGGAAACCA
co3_665542 2_x303	CM000678.2/10 721693- 10721625	26	#####	28.2	303	GTAATATAGTTTAAACAAAACATTAGACTATGAATCTAACAAT AGAAGCCCGCAACTTCTTATCTACC
co3_677739 3_x274	AC008443.10/43 006-42934	23	#####	46.1	274	GUUUCGUGUAGUGUAGUGGUUAUCACGUUCGCCUCACACGC GAAAGGUCCCCGGUUCGAAACCGGGCGGAAACA
co3_681552 0_x266	CM000681.2/41 242309- 41242237	29	#####	34.2	266	GCCAGGATAGTTCAGGTGGTAGAGCATCAGACTTTTAACTG AGGGTTCAGGGTTCAAGTCTCTGTTTGGGCG
co3_684496 1_x260	CM000669.2/14 9691252- 149691181	24	#####	32.2	260	GGGGATATAGCTCAGGGGTAGAGCATTTGACTGCAGATCAAG AGGTCCCCGGTTCAAATCCGGGTGCCCCCC
co3_689431 8_x249	CM000663.2/16 1612718- 161612789	16	0.0003	32.2	249	GCGTTGGTGGTGTAGTGGTGAGCACAGCTGCCTTTCAAGCA GTTAACGCGGGTTCGATTCCCGGGTAACGAA
co3_692837 8_x242	ENST00000387 409.1	32	#####	63.9	242	GGTAAATGGCTGAGTGAAGCATTGGACTGTAAATCTAAAGA CAGGGGTTAGGCCTCTTT
co3_699745 4_x228	CM000681.2/45 478687- 45478602	22	#####	44.1	228	GCCCGGATGATCCTCAGTGGTCTGGGGTGCAGGCTTCAAAC CTGTAGCTGTCTAGCGACAGAGTGGTTCAATTCCACCTTTCCG GGC

co3_719623 6_x190	AL163195.5/370 2-3774	18	#####	28.2	190	GGCUCCAUAGCUCAGGGGUUAGAGCACUGGUCUUGUAAAC CAGGGGUCGCGAGUUCAAUCUCGCGGGGCCU
co3_725411 7_x181	AF346992.1/158 90-15955	29	#####	58	181	GUCCUUGUAGUAAAACUAAUACACCAGUCUUGUAAACCGG AGAUGAAAACCUUUUJCCAAGGACA
co3_739392 1_x159	AF381996.2/426 5-4333	17	#####	34.2	159	AGAAUAUGUCUGAUAAAAGAGUUACUUUGAUAGAGUAAAU AAUAGGAGCUUAAACCCCUUAAUUUCUA
co3_739771 7_x158	AF347015.1/582 7-5762	17	#####	34.2	158	AGCUCCGAGGUGAUUUUCAUUAUUGAAUUGCAAUUCGAAGA AGCAGCUCAAACCUGCCGGGGCUU
co3_742741 5_x153	ENST00000387 365.1	17	#####	34.2	153	AGAAATATGTCTGATAAAAGAGTTACTTTGATAGAGTAAATAA TAGGAGCTTAAACCCCC
co3_743686 5_x152	CM000678.2/33 69813-3369884	18	#####	28.2	152	TAGGACTTGGTGTAAATGGGTAGCACAGAGAATTTTGGATTCT CAGGGGTGGGTTCATTCCTTTTCGTCCTAG
co3_745534 1_x149	CM000669.2/13 9340700- 139340772	21	#####	42.1	149	GCCCCAGTGGCCTAATGGATAAGGCATTGGCCTCCTAAGCCA GGGATTGTGGGTTCGAGTCCCATCTGGGGTG
co3_746186 0_x148	ENST00000387 405.1	14	#####	28.2	148	AGCTCCGAGGTGATTTTCATATTGAATTGCAAATTCGAAGAAG CAGCTCAAACCTGCCG
co3_747677 7_x145	CM000668.2/27 777885- 27777956	21	#####	42.1	145	AGCAGAGTGGCGCAGCGGAAGCGTGCTGGGCCATAACCCA GAGGTCGATGGATCTAAACCATCCTCTGCTA
co3_751010 8_x140	GL000256.2/253 971-254043	22	#####	44.1	140	GCCTCCTTAGCGCAGTAGGCAGCGCGTCAGTCTCATAATCTG AAGTCCTGAGTTCGAACCTCAGAGGGGGCA

co3_756071 8_x133	CM000663.2/15 0045476- 150045406	20	#####	32.2	133	GGGGGTGTAGATCAGTGGTAGGGCGCACGCTTAGCATGCAT GAGGCCCTGGGTCAATCCCCAGCACCTCCA
co3_766146 5_x120	ENST00000387 456.1	37	#####	73.8	120	ACTTTTAAAGGATAACAGCTATCCATTGGTCTTAGGCCCCAAA AATTTTGGTGCAACTCC
co3_775409 8_x108	AF346999.1/440 2-4331	32	#####	63.9	108	UAGGAUGGGGUGUGAUAGGUGGCACGGAGAAUUUUGGAUU CUCAGGGAUGGGUUCGAUUCUCAUAGUCCUAG
co3_778768 1_x104	CM000663.2/16 1440242- 161440171	19	#####	30.2	104	GCGTTGGTGGTATAGTGGTGAGCATAGTTGCCTTCCAAGCAG TTGACCCGGGCTCGATTCCCGCCCAACGCA
co3_784054 7_x97	CM000663.2/93 847573- 93847657	34	#####	67.9	97	GGCTCCGTGGCGCAATGGATAGCGCATTGGACTTCTAGAGG CTGAAGGCATTCAAAGGTTCCGGGTTGAGTCCCGGCGGAG TCG
co3_791212 0_x89	AC005329.1/704 3-6971	22	#####	44.1	89	GCCGAAAUAGCUCAGUUGGGAGAGCGUUAGACUGAAGAUC UAAAGGUCCUGGUUCGAUCCCGGGUUUCGGCA
co3_791692 6_x89	ENST00000386 347.1	27	#####	54	89	GTTAAGATGGCAGAGCCCGGTAATCGCATAAACTTAAACT TTACAGTCAGAGGTTCAA
co3_795618 3_x85	AC008443.10/82 40-8321	20	#####	40.1	85	GGUAGCGUGGCCGAGCGGUCUAAGGCGCUGGAUUAAGGCU CCAGUCUCUUCGGGGCGUGGGUUCGAAUCCACCGCUGC CA
co3_797018 7_x83	CM000678.2/10 721565- 10721495	38	#####	28.2	83	ACTTTTAAAGGATAAGAGTTATCCATTGGTCTCAGGAACCAAA AACATCGGTGCAACTCCAATAAAAGTA

co3_802363 2_x78	CM000676.2/20 683273- 20683361	15	#####	30.2	78	CCTTCGATAGCTCAGCTGGTAGAGCGGAGGACTGTAGTACTT AATGTGTGGTCATCCTTAGGTCGCTGGTTCGATTCCGGCTCG AAGGA
co3_810758 0_x70	AL352978.6/119 697-119770	22	#####	36.2	70	GGCCGGUUAGCUCAGUUGGUUAGAGCGUGGUGCUAAUAAC GCCAAGGUCGCGGGUUCGAUCCCCGUACGGGCCA
co3_812181 5_x69	GL000251.2/124 019-123948	24	#####	32.2	69	GTGGATGTAGTTTAGTGGTAGAACGCGCGCTTTGCATGTATG AGTCCCAGTTTTCGATCCCTGGCGTTTCCA
co3_818350 1_x63	CM000676.2/20 677100- 20677019	15	#####	30.2	63	GGTAGTGTGGTTGAATGGTCTAAGGCACTGAATTTAGGCTCC AGTCTCTTTGGGGACGTGGGTTTAAATCCCCTGCTGCAA
co3_822052 0_x60	CM000670.2/67 585468- 67585398	23	#####	46.1	60	ACTTTTAAAGGATGAGAGTCATCCGTTGGTCTTAAGAACCAAA AACACTGGTGCAACTCCAATAAAAGTA
co3_822130 0_x60	CM000670.2/13 3755832- 133755767	16	#####	32.2	60	GGTAAATGACTGAATAAGCCTTAGACTGTAAATCTGAAGACA GAGGTCAAGGCCTCTTTTACCA
co3_824517 2_x58	ENST00000387 439.1	21	#####	42.1	58	TGGTATATAGTTTTAAACAAAACGAATGATTTGACTCATTAAAT TATGATAATCATATTT
co3_825611 1_x57	AC018638.5/469 4-4623	22	#####	44.1	57	GGCUCGUUGGUCUAGGGGUUAUGAUUCUCGCUUAGGGUGC GAGAGGUCCCCGGUUCAAAUCCCGGACGAGCCC
co3_827084 0_x56	CM000664.2/22 3321669- 223321597	26	#####	28.2	56	GTTGGGGTAACTCAGTTGGTAGAGTAGCAGACTTTTCATCTG AGGGTCCAGGGTTTAAGTCCATGTCCAGGCA
co3_829610 0_x54	CM000674.2/49 817479- 49817409	27	3E-06	38.2	54	TAGGATGTGGTGTGATAGGTAGCATGGAGAATTTTGGATTCT CAGGGGTAGGTTCAATTCCTATATTCTAG

co3_835501 1_x50	GL000252.2/861 6-8544	18	0.002	28.2	50	GGCCGCGTGGCCTAATGGATAAGGCGTCTGATTCCGGATCA GAAGATTGAGGGTTCGAGTCCCTTCGTGGTCCG
co3_837374 2_x49	CM000674.2/98 504252- 98504323	19	#####	38.2	49	GACCTCGTGGCGCAACGGTAGCGCGTCTGACTCCAGATCAG AAGGCTGCGTGTTTCAATCACGTCCGGGTCA
co3_845278 4_x43	CM000676.2/72 962971- 72963042	21	#####	34.2	43	GGGGGTATAGCTCAGGGGTAGAGCATTGACTGCAGATCAA GAGGTCCCCGGTTCAAATCCGGGTGCCCCCT
co3_846528 3_x42	CM000666.2/15 5461250- 155461315	13	#####	26.3	42	GGTAAAGTGGCTGAATAAGCATTAGACTGTAAATCTAAAGACA GAGGTCAAGGCCTCTTTTTAGCA
co3_847015 5_x42	CM000679.2/81 39525-8139452	34	#####	67.9	42	GGCGCCGTGGCTTAGCTGGTTAAAGCGCCTGTCTAGTAAACA GGAGATCCTGGGTTTCAATCCCAGCGGTGCCT
co3_847897 5_x42	CM000681.2/39 412260- 39412168	21	#####	42.1	42	GCTCCAGTGGCGCAATCGGTTAGCGCGCGGTACTTATATGAC AGTGCGAGCGGAGCAATGCCGAGGTTGTGAGTTCGATCCTC ACCTGGAGCA
co3_848350 6_x41	CM000665.2/45 689071- 45688999	15	#####	30.2	41	GGGCCAGTGGCGCAATGGATAACGCGTCTGACTACGGATCA GAAGATTCTAGGTTTCAATCCCTTCGTGGTCCG
co3_852940 2_x38	CM000668.2/26 299677- 26299749	14	#####	28.2	38	GACCACGTGGCCTAATGGATAAGGCGTCTGACTTCGGATCAG AAGATTGAGGGTTCGAATCCCTTCGTGGTTA
co3_855478 9_x37	CM000676.2/20 657557- 20657464	17	#####	26.3	37	CCTTCGATAGCTCAGCTGGTAGAGCGGAGGACTGTAGATTGT ATAGACATTTGCGGACATCCTTAGGTCGCTGGTTCGATTCCA GCTCGAAGGA
co3_857395 4_x36	CM000669.2/67 399631- 67399560	16	#####	32.2	36	GGCCTCATGGTGCAACAGTAGTGTGTCTGACTCCAGATCAGA AGTTGTATGTTCAAATCACGTAGGGGTCA

co3_857818 4_x35	J01415.2/7514- 7446	21	#####	42.1	35	GAAAAAGTCATGGAGGCCATGGGGTTGGCTTGAAACCAGCTT TGGGGGTTTCGATTCCTTCCTTTTTTG
co3_858602 4_x35	CM000668.2/27 293892- 27293965	33	#####	42.1	35	GGCCGGTTAGCTCAGTTGGTTAGAGCGTGCTGCTACTAATGC CAGGGTTCGAGGTTTCGATCCCCGTACGGGCCT
co3_858644 4_x35	CM000686.2/83 71587-8371660	13	#####	26.3	35	GTTAAGATGGCAGAACCTGGCAGTTTCATAAACTTAAAGTTT ATAATCAGAGGTTCAACTCCTCTTCTTAACA
co3_864081 5_x32	CM000673.2/59 551755- 59551837	24	#####	40.1	32	ACCAGAATGGCCGAGTGGTTAAGGCGTTGGACTTAAGATCCA ATGGATTCATATCCGCGTGGGTTTGAACCCCACTTCTGGTA
co3_864225 5_x32	ENST00000387 392.1	30	#####	60	32	AAGGGCTTAGCTTAATTAAGTGGCTGATTTGCGTTCAGTTGA TGCAGAGTGGGGTTTTG
co3_864777 0_x31	ENST00000387 419.1	20	#####	40.1	31	AAGGTATTAGAAAAACCATTTTCATAACTTTGTCAAAGTTAAATT ATAGGCTAAATCCTAT
co3_864987 8_x31	CM000664.2/45 710374- 45710302	14	#####	28.2	31	GGCTGTGTACCTCAGTGGGCAAGGGTATGGACTTTGAAGCC AGACTATTTGGGTTCAAATCCCAGCTTGGCCT
co3_865006 4_x31	GL000250.2/777 22-77651	30	#####	44.1	31	GGGGGTATAGCTCAGCGGTAGAGCGCGTGCTTAGCATGCAC GAGGTCCTGGGTTCAATCCCCAATACCTCCA
co3_867168 3_x30	CM000665.2/10 6894213- 106894143	14	#####	28.2	30	ACTTTTAAAGGATAGGAGTTATCTATTGATCTTAGGAACCAAA AACATTGGTTCAACTCCAAGTAAAGGTA
co3_868421 2_x29	CM000668.2/27 664766- 27664841	27	#####	30.2	29	GCCGAAATAGCTCAATTGGGAGAGTGTTAGACTGAAGATCTT CTGCAGGTCTCTGGTTCATTCCGGGTTTCGACA

co3_872062 8_x28	CM000663.2/14 9558493- 149558419	28	#####	56	28	GTCTCTGTGGCGCAATTGGTTAGCGCGTTCGGTTGTTAACCG TAAAGGTTGGTGGTTCGAGCCCACCCAGGAACG
co3_872294 6_x27	CM000684.2/36 179392- 36179460	30	#####	52	27	GGAAATATGTCTGATAAGAGAGTTACTTTGACAGAGTAAATTA CAGAGGTTTTAAATCTTCCTATTTCTA
co3_873944 3_x27	CM000669.2/14 9556711- 149556780	18	#####	36.2	27	GGCGTATAGCTCAGGGGTAGAGCATTGACTGCAGATCAA GAGGTCCCAGTTCAAATCTGGGTGCCCA
co3_873984 8_x27	CM000664.2/21 8245826- 218245918	21	#####	34.2	27	CCTTCAATAGTTCAGCTGGTAGAGCAGAGGACTATAGCTACT TCCTCAGTAGGAGACGTCCTTAGGTTGCTGGTTCGATTCCAG CTTGAAGGA
co3_876114 5_x26	CM000666.2/75 04618-7504555	18	#####	28.2	26	GGCTGGGAAGCCAGCCCTGGGGTCCAGAGCCAGATGGATGT GGTTCAAATCCCACCACAGCCA
co3_877051 3_x25	CM000664.2/30 054702- 30054774	16	#####	32.2	25	GGCCAGTGGCTCAATGGATAATGCGTCTGACTAAGAATCAG AAGATTCCAGCCTTGACTCCTGGCTGGCTCA
co3_877398 8_x25	CM000670.2/46 827965- 46828036	34	#####	28.2	25	TACGACATGGTGTAAATAAGTAGCACAGAGAATTTTGGGTTCTC AGGGGTAGGTTCAATTCCCATAGTTCTAG
co3_878221 3_x25	CM000671.2/11 0198523- 110198595	14	#####	28.2	25	GGCCGTGTGGCCTAATGGATAAGGCGTCTGACTTCGGATCAA AAGATTGCAGGTTTGAGTTCTGCCACGGTCG
co3_880144 1_x24	AF134583.1/159 9-1666	23	#####	46.1	24	AGAAUUUAGGUUAAAUACAGACCAAGAGCCUUCAAAGCCC UCAGUAAGUUGCAAUACUAAUUUCUG
co3_883520 4_x22	CM000668.2/26 687257- 26687329	25	#####	34.2	22	GGGAATTAGCTCAAGTGGTAGAGCGCTTGCTTAGCACGCAA GAGGTAGTGGGATCGATGCCACATTCTCCA

co3_883725 0_x22	CM000668.2/27 545689- 27545770	46	#####	91.7	22	GTAGTCGTGGCCGAGTGGTTAAGGCGATGGACTTGAAATCCA TTGGGGTTTTCCCCGCGCAGGTTTCAATCCTGCCGACTACG
co3_884576 4_x22	CM000679.2/40 117373- 40117300	20	#####	32.2	22	GACCGTGTGGCCTTAATGGATAAGGTGTCTGACTTCAGATCA GAAGATTGAGGGTTTGAGTCCCTTTGTGGTCA
co3_885547 1_x21	CM000663.2/14 8246758- 148246831	39	#####	30.2	21	GTCTCTGTGGCGCAATCGGTCAGAGCGTTTCGGCTATTAACCG AACGGTGAGTAGTTCAAGACCACCCAGGGACG
co3_886376 6_x21	CM000668.2/27 618356- 27618429	13	0.009	26.3	21	GGCCCTGTAGCTCAGCGGTTGGAGCGCTGGTCTCGTAAACC TAGGGGTCGTGAGTTCAAATCTCACCAGGGCCT
co3_888770 8_x20	CM000673.2/11 3562356- 113562273	14	#####	28.2	20	ACCAGGATGGCCAAGTAGTTAAAGGCACTGGACTTAAGAGCC AATGGACATATGTCTGTGTGGGTTTGAACCCCACTCCTGGTG
co3_888844 8_x20	AF134583.1/181 6-1744	19	#####	38.2	20	UAGAUUGAAGCCAGUUGAUUAGGGUGCUUAGCUGUUAACU AAGUGUUUGUGGGUUUAAGUCCCAUUGGUCUAG
co3_893819 7_x18	CM000668.2/26 705377- 26705449	14	#####	28.2	18	GGGAATTAGCTCAAGCGGTAGAGCGCTTGCTTAGCATGCAA GAGGTAGTGGGATCGATGCCACATTCTCCA
co3_894870 7_x17	CM000674.2/26 572619- 26572687	27	0.001	30.2	17	AAGGAGTTAGCTCAATTAAGTGATTGATTTGCATTCAGTTGA TGTAAGATAAGATCTTGACAGTCCTTA
co3_899087 0_x16	CM000666.2/40 906798- 40906726	34	#####	44.1	16	GACCATGTGGCCTAAGGGAAAAGACATCTCACTTTGGGTCAG AAGATTGAGGGTTCAAGTCTTTTCATGGTCA
co3_899717 4_x16	CM000663.2/23 7942562- 237942633	28	0.0004	32.2	16	TAGGACTTGGTGTAATAGGTAGCACGAAGAGATTTGGATTCT CAGGGGTAGGTTCAATTCCTATAGTTCTGG

co3_900074 2_x16	CM000663.2/22 2465005- 222465077	19	#####	30.2	16	GGCTCCATAGCTCAGTGGTTAGAGCACTGGTCTTGTAACCA GGGGTCGCGAGTTCGATCCTCGCTGGGGCCT
co3_900466 8_x15	CM000668.2/15 6547986- 156547912	15	#####	30.2	15	GTTAAGACGGCAGAGCCCGGCAATTGCGTAAAATTTACA TTATGGGCAGAGGTTCAATTCCTCTTCTTAACA
co3_902214 3_x15	CM000679.2/64 530873- 64530800	16	0.0001	32.2	15	AGCACCATGGCTTAGCTGGTTAAAGCACCTGTCTAGTAAACA GGAGATCCTGAGTTTCAATTCGAATGGTGCCT
co3_902449 8_x15	CM000681.2/12 188561- 12188634	34	#####	28.2	15	GGCTCTGTGGCTTTGTGGGTTAAAGTACTTGTCTGGCAAACA GGAGATGCTGGATTTCAATCCAGCAGGGCCT
co3_905407 6_x14	CM000676.2/20 613862- 20613790	22	#####	36.2	14	GGCTCCATAGCTCAGGGGTTAGAGCGCTGGTCTTGTAACCA GGGGTCGCGAGTTCGAATTCGCTGGGGCCT
co3_909912 2_x12	CM000664.2/13 0273728- 130273656	16	#####	32.2	12	TAGATTGAAGCCAGTTGATTAGGGTGTATCTGTAAATTTAA TGTTCTGGGTTTAAAGTCCCATCAATCTAG
co3_914925 3_x11	CM000685.2/14 3434095- 143434024	18	0.004	28.2	11	TAGGATATGGTATATTAGGTAGCACAAAGAATTTGAATTCTC AGGGGTAGATTCAATTCCTATAATTCTAG
co3_919844 3_x10	CM000679.2/22 528921- 22528853	22	#####	36.2	10	GAAAAAGTCATAGGGGTTATGAGGCTGGCTTGAAACCAGCCT TAGGAGGTTCAATTCCTTCTTTTTTG
co3_921103 2_x9	CM000678.2/14 285893- 14285964	35	#####	61.9	9	GGCGCGGTGGCCAAGTGGTAAGGCGTCGGTCTCGTAAACCG AAGATCACGGGTTTGAACCCCGTCCGTGCCT
co3_921269 7_x9	CM000670.2/65 697384- 65697297	22	#####	28.2	9	TCTTCAATAGCTCAGCTGGTAGAGCGGAGGACTGTAGGTGCA CGCCCGTGGCCATTCTTAGGTGCTGGTTTGATTCCGACTTGG AGAG

co3_927764 2_x8	CM000676.2/88 979098- 88979170	18	#####	28.2	8	GGGAATTAGCTCAAGTGGTAGAGCGCTCGCTTAGCATGCG AGAGGTAGTGGGATCGATGCCCGCATTCTCCA
co3_927996 4_x7	CM000673.2/10 9165312- 109165393	13	#####	26.3	7	TGAGTTGTAGCTGAGTGGTTAAGGCAACGAGCTAGAAATTCG TTGGTTTCTCTCTGTGCAGGTTTGAATCCTGCTAATTATG
co3_928046 8_x7	CM000670.2/66 114189- 66114261	23	1E-08	46.1	7	GGGGATTAGCTCAAATGGTAGAGCGCTCGCTTAGCATGCG AGAGGTAGCGGGATCGATGCCCGCATCCTCCA
co3_930525 5_x7	CM000673.2/92 75243-9275316	28	#####	32.2	7	GCCTCCTTAGTG CAGTAGGTAGCGCATCAGTCTCAAATCTG AATGGTCCTGAGTTCAAGCCTCAGAGGGGGCA
co3_931276 6_x7	ENST00000387 429.1	21	#####	42.1	7	ACTCTTTTAGTATAAATAGTACCGTAACTTCCAATTAAGT TTTGACAACATTCAA
co3_932103 3_x7	ENST00000387 400.1	27	#####	54	7	TAGATTGAAGCCAGTTGATTAGGGTGCTTAGCTGTAACTAAG TGTTTGTGGGTTTAAGT
co3_933021 4_x6	CM000668.2/69 204486- 69204568	18	#####	28.2	6	ACTCATTGGCTGAGTGGTTAAGGCATTGGACTTAAGATCCA ATGGAGTAGTGGCTGTGTGGGTTTAAACCCCACTACTGGTA
co3_935002 0_x6	CM000683.2/35 891030- 35891100	13	#####	26.3	6	GAGGATTTAGTTTAAATTAATGTTTGTATTGCATTCAATTGAT GTAAGATAGAGAGTGTGCAGTCCTTA
co3_936440 8_x6	CM000669.2/14 1803557- 141803628	22	#####	28.2	6	TAGGACGTGGTGTAGTAGGTAGCATGGAGAATGTTGAATTCT CAGGGGTAGGTTCAATTCCTATAGTTCTAG
co3_938024 8_x5	CM000663.2/14 6488866- 146488936	20	0.0002	32.2	5	GCGTCAGTGGTTTAGTGGTGAATTCCTGCCTCCCATGCACG AGATCCGTGTTCAACTCCTGGTTGGTGCA

co3_938186 3_x5	CM000685.2/55 178915- 55178987	35	8E-11	54	5	TAGATTGAAGCCAGTTGATTAGGGTGTTTAGCTGTTAACGAAA TTTTCGTGGGTTTGAATTCCACCAATCTAG
co3_939353 3_x5	CM000665.2/10 6894340- 106894273	13	0.008	26.3	5	GTAGTTATAGTTTAATTAACATTAGATTGTGGATCTAATAATA GAAGTCTACAGCTTCTTACCTACC
co3_942889 8_x5	CM000668.2/57 861238- 57861166	21	#####	26.3	5	GGGAATTAGCGCAAGTGGTAGAGTGCTTGCTTAGCATGCAA GAGGTAGTGGGATCGATGCCACATTCTCCA
co3_943475 8_x5	CM000685.2/10 2010285- 102010355	13	#####	26.3	5	GTTAGTGTAGCTTAATATGGTAAAGCAAGGCACTGAAAGTGC GTAGATGAGTTCATGTAACTCCATAACA
co3_943779 8_x5	CM000669.2/14 9406135- 149406064	32	#####	32.2	5	GGGGGTATAGCTGAGGAGTAAACCATTTGGCTGCAGATCAAG TGGTCCCTGGTTCAAATATGGGTGCCCTCT
co3_944419 6_x4	CM000669.2/14 9363270- 149363207	22	#####	28.2	4	GTGGATATAGTCTGCATTTGACTGCAAATTAAGAAGTCTCTG GTTCAAATCCAGCTGTCCCCT
co3_945595 2_x4	CM000664.2/11 7026500- 117026435	17	#####	26.3	4	GGTAAATGACTGAGTAAGCGTTAGACTGTAAATCAAAGAT GGAGGTCAAGGCCTCCTTTTACCA
co3_946446 0_x4	KI270803.1/6677 33-667803	15	#####	30.2	4	GTTAATGTAGCTTAATTATTTAAAGCAAGACTGAAAATGTC TAGATGGGCTTATACAGCCCCATAACA
co3_948082 4_x4	CM000672.2/36 434683- 36434615	33	#####	34.2	4	GTAATATAGTTTGTAGTCAAATATTAGATTGTGGATCTGATAAT AGAAGTCTGTAACCTTCTTATTTACT
co3_952478 8_x3	CM000670.2/79 428812- 79428742	14	#####	28.2	3	GGCACTGTAGTTTGGATTGAGAAACACAGGCTTTAGAGGCAG AAGTTCTGGGTTCAAACCCAGCATTGCCA

co3_957686 8_x3	CM000672.2/55 597818- 55597888	13	#####	26.3	3	GTTAATGTAGCTTAATTATTTAAAGCAAGGCACTGAAAATGCC TAGATGGGTCCGCAAACCCCATAAACA
co3_958251 1_x3	CM000669.2/68 098326- 68098258	13	#####	26.3	3	GAGAAGGTCATAGAGGTTATGGGATTGGCTTGAAACCAGTTT CTGGAGGTTCCATTCTTTCTTTTTTCG
co3_962305 0_x3	CM000685.2/11 9603898- 119603966	15	#####	30.2	3	GCAGCTGTGGCTCAGTGGAAAGAGCATCAGTCTGGGTATCA GAAGACCTAGGTCTAGCCCCAGCTGTA
co3_967836 9_x2	CM000676.2/61 184426- 61184490	15	#####	30.2	2	GACAGTTTGGCTTAGTGGTTAAGAGCTTTGGTACCAGATGGA ATGGGTTCAAATCCCAACTCT
co3_968127 5_x2	CM000671.2/64 046744- 64046678	21	#####	26.3	2	GGTAAAATGACTGAGTAGGGCATTAGACTGTACATCTAAAAA CAGAGGTCAAGGCCTGTTTTTACCA
co3_972240 9_x2	CM000673.2/63 489530- 63489598	18	#####	36.2	2	ATTAAGGTAGTATAGTAGAGTAAATACTTCGAAGCCAAAAGA TCTAGGTTTGAATCCTAGCTTTCATG
co3_972316 9_x2	CM000685.2/10 2786742- 102786669	18	#####	28.2	2	TAGAATATAGTGTATCAGGTAGCACAAAGATTTTTGAATTCTT AAGAGAGTAGGTTCAATTCCTATAATCCTGT
co3_973215 1_x2	CM000685.2/25 262043- 25261972	14	0.003	28.2	2	AGTCAAGTGGTTTTAGTGGAAAGAACATTGGATTGGAAGTCAA GAGGCCTGGATTCTTGCTCCAGCTTCACCA
co3_973574 1_x2	CM000670.2/70 237343- 70237274	15	0.0005	30.2	2	GGCAGTGTCTAGAGGTAAAGAGTACAGGCTTAGAGTCAGAC AGCGCGGGTTCAAATCCTGCTTCTGCCA
co3_983329 5_x2	CM000670.2/88 133080- 88133007	14	#####	28.2	2	GGTACAGTGTTAAAGGGGAGAAAATTGCTGACTTTGAATAC AGTAGACCTAGGTTTGAATCCTGGCTTTACCA

co3_98714 83_x2	CM000666.2/8 4855315- 84855245	14	##### #	28.2	2	AATATAGTACTGAGTGATGAAGAGCCTGGCTTGGAATC AGATAGATGTAGTTTTAAATTCTGTCTGTATTG
co3_98776 29_x2	CM000670.2/1 8537373- 18537307	13	##### #	26.3	2	GGTAATATAGCTTAAGAGCCGTGGGTTTTGAACTCAGAT TGCCTTGGTTCAAATCCGAGTTTTCATTT
co3_99941 67_x2	CM000672.2/4 7633857- 47633927	18	##### #	28.2	2	GTTAATGTAGCTTAATTATTTAAAGCAAGGCACTGAAAA TGCCTAGATGGGTCCGCACAACCCGGTAAACA
co3_10040 725_x1	CM000664.2/8 2819272- 82819338	17	9E-05	34.2	1	GCCCTTGTAGTATAATTCAATACTCTGGTCTTGTAACC AGAAATGGAGGATCTCCTCCCCAGGACA
co3_10046 439_x1	CM000665.2/1 66233278- 166233208	14	##### #	28.2	1	GTTGATGTGGTTTAATATGTTAAAACAAGGCATTGAAAA TGTCTAGATGAGTTCTCATAGCTCCATAAACA
co3_10140 946_x1	CM000668.2/2 6728053- 26728125	23	##### #	46.1	1	GGGGAATTGGCTCAAGCGGTAGAGCGCTTGCTTAGCAT GCAAGAGGTAGCAGGATCGACGCCTGCACTCTCCA

Table S3. The list of identified glycosylated snoRNA in paracancerous tissue (PCA) and cancer tissue (CA). (a) N-linked glycosylated snoRNAs from PCA, (b) N-linked glycosylated snoRNAs from CA

(a)

Qseqid	Sseqid	NT	Evalue	Bitscore	Number	Sequence
ex3_16_03268_x2330	ENST0000364281.1	14	##### ##	28.2	2330	CTAAAACAATGTCAATAGTTTTTCATCAACAGCAGTTGAACCTAGTAAGTGTGCGATACTTT
ex3_16_07924_x2326	CM000664.2/231456523-231456444	17	##### ##	34.2	2326	TGGATATGATGACTGATTACCTGAGAAATAATTGATGAAATCTCAAGAAAATTCCTCTAGATAGTCAAGTTCTGATCCAG
ex3_19_90113_x1412	CM000673.2/62853395-62853325	20	##### ##	40.1	1412	CTCACCAGTGATGAGTTGAATACCGCCCCAGTCTGATCAATGTGTGACTGAAAGGTA TTTTCTGAGCTGTG
ex3_20_57856_x1303	ENST0000627253.1	20	##### ##	40.1	1303	AAGACTATACTTTTCAGGGATCATTCTATAGTTTGTTACTAGAGAAGTTTCTCTGAACGT
ex3_21_14424_x1214	AY349606.1/1-85	15	##### ##	30.2	1214	CCCCUAUCUCUCAUGAUGAACACAU AUGCCUCUGAGCUGCUGUGAUUUUCUGGCUU CAAAGUAAACGCUCUGAAGAAGAGAUGGGG
ex3_21_78138_x1108	AJ224028.1/3-79	28	##### ##	56	1108	CAGAAUACAUGAUGAUCUCAAUCCAACUUGAACUCUCUCACUGAUUACUUGAUGAC AAUAAAAUAUCUGAUUUCUG

ex3_22 45872_ x1006	ENST0 000036 2607.1	26	#### ##	52	1006	CTGCATCCACTGATAGACCTTGAACAATTTACTGTTGTTCTTTTGGTTTGCCTAGGA TG
ex3_23 19852_ x914	CM000 663.2/7 578707 2- 757871 50	14	#### ##	28.2	914	GGTCAATGATGAGTTGGCATGTATTCTGAATCTAAAGTTGATTATTACTACTTTAGCTC TAGAATTACTCTGAGACCTG
ex3_23 32579_ x902	ENST0 000058 0533.1	30	#### ##	60	902	AAGACTATACTTTCAGGGATCATTCTATAGTGTGTTACTAGAGAAGTTTCTCTGAAC GT
ex3_24 01130_ x832	CM000 672.2/8 906113 1- 890610 31	14	#### ##	28.2	832	ATTCTTTTGTATCTCACAAGTGTGACTGGGTTTTTAGGCTCATGTGTGAGATGAGCTT CCCTCAAAAATTGTTGTGACTGTGGCATGTTACCTGTGTGATG
ex3_24 10212_ x819	ENST0 000038 4048.1	16	#### ##	32.2	819	ATTCGTGATGACTGATCATTCTTCACTTTGACCAGATGTCTACTGAAGAAAGCCTGC GT
ex3_24 68755_ x767	ENST0 000038 4320.2	14	#### ##	28.2	767	CTGGTTGCATGATGAATAAAATCAAATCACCATCTTTCGGCTGAGTTCGTGATGGATT TG
ex3_25 97573_ x661	AB061 820.1/3 401- 3472	28	#### ##	56	661	UCAAAAUGAUGAGAUUCCACUUAUUUGGUCCGUGUUUCUGAAACACAUGAUUUU GUGGAAAUUCUGACUUG
ex3_26 11343_ x649	ENST0 000044 8188.1	29	#### ##	58	649	TGGAGGTGATGAACTGTCTGAGCCTGACCTTGTAGAATGGAGGCCAAAAAACTGATT TAA
ex3_27 44568_ x548	AJ5433 25.1/2- 85	28	#### ##	56	548	CUGAGUCCAUGAUGAUUUCAAGUUAUCCUGUCUGAAGGCAAAGAAAGGCCUUUC UGUGUGGAAUUUGAAUAUCUGAAACUCAG

ex3_27 82515_ x524	ENST0 000036 4155.1	45	#### ##	65.9	524	GTTTCTGATGAAGCCTATGTTGGTAGGGACA ACTAAGGTTGTTGATGAATGCTAACA GCT
ex3_27 89313_ x520	AC104 446.2/1 45501- 145577	35	#### ##	69.9	520	AAUGUGAAGCAAUGAUGAUAAACUGGAUC UGACUGACUGUGGCUGAGUCUGUUCA AUCCAACCCUGAGCUUCAUGUU
ex3_28 15960_ x505	AK096 147.1/7 39-811	20	#### ##	40.1	505	GUUUGAAUGAUGACUUUAAUUGUCGGAU ACCCCUUCACUCCUUUUUAUGAGUGAAA CAUAAGAGUCUGACAAAC
ex3_28 51113_ x485	AJ6094 83.1/2- 129	28	6E-11	56	485	CUGGAGGACUAAGAAGGCUGAGUCUGAU GAAGUAAGACUUUGCUGAUACAUCCU CCUAGAAAAAAGGGUUGGAGAGAGCAGCC UUCACUGAAGAGUAUCACAGGGCUGA CUGUACUACCCAACACUC
ex3_29 58900_ x429	ENST0 000036 4921.1	19	0.002	30.2	429	ATGCAGGTACTGTTATAACTGAAGTGTTTT ACGGTTTTTTCTTCCTGCTTAAAGCACTT G
ex3_29 73373_ x423	AF020 531.1/1 04-320	24	#### ##	48.1	423	AAGACUAUACUUUCAGGGAUCAUUUCUAU AGUGUGUUACUAGAGAAGUUUCUCUG AACGUGUAGAGCACCGAAAACCACGAGGA AGAGAAGUAGCGUUUUCUCCUGAGCG UGAAGCCGGCUUUCUGGCGUUGCUUGGC UGUAACUGCCGUCAGCCAUUGAUGAU CGUUCUUCUCCCCGUAUUGGGGAGUGAG AGGGAGAGAACGCGGUCUGAGUGGU

ex3_30 29161_ x397	AC092 174.5/1 56814- 156683	23	#### ##	46.1	397	CUUCCCAUUUAAUUUGCUGCUUAAUAGUCUCACUGUGAUUAGAGCAAUUUAUACACAU GGGAUAAAAUAAUUAUUGAGCCACUGUAAAUUGAGAUGAAGUAACCGUUUUUCAUUAU CUUCUGCAUGGACUAGACAUUG
ex3_30 76021_ x377	CM000 673.2/6 285373 2- 628536 63	24	#### ##	48.1	377	GTTTGTGATGACTTACATGGAATCTCGTTCGGCTGATGACTTGCTGTTGAGACTCTGA AATCTGATTTTC
ex3_31 21870_ x356	CM000 679.2/1 911263 6- 191124 20	30	#### ##	60	356	AAGGCTATACTTTTCAGGGATCATTCTATAGTGTGTTACTAGAGAAGTTTCTTTGAAC GTGTAGAGCACCGAAAACCCCGAGGAAGAGAGGTAGCGTTTTCTCCTGAGCGTGAA GCCGGCTTTCTGGCGTTGCTTGGCTGCAACTGCCGTCAGCCATTGATGATCGTTCTT CTCTCCGTATTGGGGAGTGAGAGGGGAGAGAACGCGGTCTGAGTGGT
ex3_32 02744_ x322	CM000 682.2/1 796294 6- 179627 10	29	#### ##	58	322	GTGAAATGATGATTCAGTTTATCCATTCGCTGAGTGCGCTGCACTGACCTTCTTCCAA GCCTCAGTTCCTGTTCTAGGAACTTGAGGCTATGTAGCCTGAAAATGCCCTGCAGTC TGCAGTGTTCTACTGTGAACTGCTTGTGTGTTGGCAGGCTACCGGTAAGAATGGTTG GTGTCAGCAGGGACGGGGCCCTCTGAGACCCATCTCACAAGATGAGTGGTGAAAA TCTGATCAC

ex3_32 18399_ x317	CM000 668.2/8 567736 8- 856772 94	25	#### ##	50.1	317	TATCTGTGATGATCTTATCCCGAACCTGAACTTCTGTTGAAAAAAAAAACTTTTACG GATCTGGCTTCTGAGAT
ex3_32 38119_ x309	ENST0 000045 9342.1	24	1E-08	48.1	309	G TTCAGATGATGAATTTAACTGTTCAACTGCTGAATGATAACGGGCATGAACTAAAAC TT
ex3_32 63969_ x300	CM000 685.2/1 197874 84- 119787 353	23	#### ##	46.1	300	AAAGCAGGTTGCAATTACAGTGCTTCATTTTGTGGAAGTACTGCCATTATCCTGCTGA AAGAAAAGCCGTGTTAATCATTTTTGATTTTGCCTTTATGAGGGTAAAATCATGACAG ATTGACATGGACAATT
ex3_32 65168_ x299	ENST0 000039 1079.1	14	#### ##	28.2	299	AAATGATGAAATCACCCAAAATAGCTGGAATTACCGGCAGATTGTGTAGTGGTGAAC CTA
ex3_32 98669_ x289	AADC0 110290 1.1/154 89- 15356	19	#### ##	38.2	289	CUGUCAGGUGGGUAUACCCUUCUCCUGUUCUCCGUUUGGAGGGCAGAUAGAACA UGAUGACUGGAGAUGCAUGAAAUGUGACUAAUGUCUCUGUGUAAUCAGGACUUGC AACACCCUGAUUGCUCCUAUCUGAU
ex3_33 43463_ x272	CM000 663.2/4 477649 0- 447765 93	26	#### ##	52	272	AAGTAGGGTGATGAAAAAGAATCCTTAGGGCGTGGTTGTGGCCGTCTTGGTCACCTGT GTGCCACTTGCCAATGCAAGGACTTGTCATAGTTACACTGACTGTTG

ex3_34 25819_ x247	CM000 667.2/5 807018 8- 580702 91	17	#### ##	34.2	247	ATCCTTTTGTAGTTTACGAGCATGATGATTGAGTGTTACACACACGGATGTGATATGTG CCACCCTCAAACCTTGTTACGACTTCAGCTTATTACCCAAGTACC
ex3_34 41946_ x242	AJ2388 53.1/1- 62	25	#### ##	50.1	242	CACAGAUGAUGAACUUAUUGACGGGCGGACAGAAACUGUGUGCUGAUUGUCACGU UCUGAUU
ex3_34 66325_ x236	AP001 273.4/3 902- 3830	35	#### ##	69.9	236	CGAUGUUAUGAUGAUGGGCGAAAUGUUAACUGCUCUGAAGGGGCUGAAUGAAAA UGGCCUUUCUGAACAUCC
ex3_34 74528_ x233	AJ6094 88.1/1- 73	21	#### ##	42.1	233	GUUCAGAUGAUGAAUUUAACUGUUAACUGCUGAAUGAUAAACGGGCAUGAACUAA AACUUAAUUCUGACAGAG
ex3_34 81725_ x231	CM000 674.2/5 664375 0- 566436 80	24	#### ##	48.1	231	CCTCACTGATGAGTACGTTCTGACTTTCGTTCTTCTGAGTTTGCTGAAGCCAGATGCA ATTTCTGAGAAGG
ex3_35 37711_ x213	ENST0 000062 9536.1	26	#### ##	52	213	AAGCACTGCCTTTGAACCTGATGTGTCTTGTTTGTAGCTTCACGGGCCAAGCAACAG TGC
ex3_35 49990_ x209	AK303 222.1/6 47-788	21	#### ##	42.1	209	GCUCUGUGAUGGAGCCCAUGCGUGUCAUCUGAGCCUCUGGCUUCCUGCCAGUG CAGCCCUGGCAGUGUCCUACUUCCAGGGCUGUUGUCUGCCUGGCGGGAAGGUC CUGGGCAAAGGAUCAGUCUUUGUACUCUGAGAGC
ex3_35 62651_ x206	ENST0 000038 4147.1	35	#### ##	69.9	206	CTACGGGGATGATTTTACGAACTGAACTCTCTTTTCTGATGGATTAGTGGAGAAAAC AG

ex3_35 95851_ x197	CM000 665.2/1 854422 19- 185442 319	15	#### ##	30.2	197	ATTCTTTTGTGATTCATAAGCATGACTGGGTGTTCCCCTCACGGGTGAGATGTGCC TCCCTCCAACCTTGTACGACGTCACCACATTACCTGTCTGACA
ex3_36 24250_ x190	AB061 820.1/2 178- 2249	28	#### ##	56	190	CAGUAGUGAUGAAAUCCACUUCAUUGGUCCGUGUUUCUGAACCACAUGAUUUUC UCGGAUGUUCUGAUGCU
ex3_36 30119_ x189	AC006 597.2/8 154- 8065	14	#### ##	28.2	189	UCACUGUGAUGAUGGUUUUCCAACAUUCGCAGUUUCCACCAGAAAGGUUUUCCUU AGUGUUGGGUAAACCUUCCUUGGAUGUCUGAGUGA
ex3_36 34440_ x187	AJ0106 66.1/3- 73	20	#### ##	40.1	187	AGCACAAAUGAUGAAUAACAAAGGGACUUAUACUGAAACCAGAUGUUACAUUGUA GUGUGCUGAUGUGCU
ex3_36 36497_ x187	AJ6094 30.1/1- 139	29	#### ##	58	187	GACCUCCUGGGAUCGCAUCUGGAGAGUGCCUAGUAUUCUGCCAGCUUCGGAAAG GGAGGGAAAGCAAGCCUGGCAGAGGCACCCAUUCCAUCCCAGCUUGCUCGGUA GCUGGCGAUUGGAAGACACUCUGCGACAGUG
ex3_37 04649_ x171	AJ6094 50.1/1- 137	29	#### ##	58	171	GGGCAUACUCGUAGACCUUGCCUGACUGUGUCUCAUGUCCAGGCAGGGGGGACAG UGUAUGCAAGAAUAAUUGGAGUUCUGCCAGCUCUAACCAGCUUCAUCAGUGGC UGGAUAAAUUGCAGGACUCUAAACAUUU
ex3_37 17530_ x168	ENST0 000040 8061.1	31	#### ##	61.9	168	GGGCTCCCATGATGTCCAGCACTGGGCTCTGATCACCCCTGAGGACACAGTGCACC CCAG

ex3_37 21212_ x167	ENST0 000036 3836.1	14	#### ##	28.2	167	GGTCAATGATGTAATGGCATGTATTAGCTGAATCCAGAGTTGATATGAGTTCTAAAAT TA
ex3_37 29173_ x165	CM000 679.2/8 173587 - 817345 4	20	#### ##	40.1	165	TCGTCAGGTGGGATAATCCTTACCTGTTCTCCTCCGGAGGGCAGATTAGAACATGA TGATTGGAGATGCATGAAACGTGATTAACGTCTCTGCGTAATCAGGACTTGCAACAC CCTGATTGCTCCTGTCTGAT
ex3_37 30159_ x164	AC025 362.12/ 104594 - 104663	40	#### ##	79.8	164	GCUGUGAUGACAUUCCAAUUAAGCACGUGUUAGACUGCUGACGCGGGUGAUGC GAACUGGAGUCUGAGC
ex3_37 43959_ x161	ENST0 000036 3981.1	21	#### ##	42.1	161	ACTCCATGATGAACACAAAATGACAAGCATATGGCTGAACTTTCAAGTGATGTCATCT TA
ex3_37 60941_ x157	CM000 663.2/2 850855 9- 285087 62	24	#### ##	48.1	157	CCAACGTGGATACCCTGGGAGGTCACTCTCCCCAGGCTCTGTCCAAGTGGCATAGG GGAGCTTAGGGCTCTGCCCATGATGTACAGTCCCTTTCCACAACGTTGAAGATGAA GCTGGGCCTCGTGTCTGCGCCTGCATATTCCTACAGCTTCCCAGAGTCCTGTGGAC AATGACTGGGGAGACAAACCATGCAGGAAACATAT
ex3_37 87417_ x151	AB061 820.1/4 174- 4242	27	#### ##	54	151	UUGUUAUGAUGAGAUUCCACUUAAGGUCCGUGUUUCUGAAACAAAUGAUUUUGUG GAAGUUCUGAUUUA
ex3_37 90585_ x150	ENST0 000040 8493.2	23	#### ##	46.1	150	ACCTTCTTGATAAGCACTGTGCTAAAATTGCAGACACTAGGACCATGTCTTGGTTTT TG

ex3_37 92235_ x150	ENST0 000036 4805.1	14	#### ##	28.2	150	GAGGTCAGTGATGAGCAACATTCACCATCTTTCGTTTGAGTCTCACGGCCATGAGAT CAA
ex3_38 02049_ x147	AC117 503.8/2 09801- 209669	25	#### ##	50.1	147	UAGCAAGCCUCCAGCGUGCUUGGGUCUGCAGUGACCCCGUGGAUCCUACAGGG CUUGCCAGAACAGUUUUGAAAUGGUUUGAGGCCUUGCCGUGCUCCAUGUAGAGC AAGGUUAUAGAAUUUCAGACAAUG
ex3_38 32570_ x141	AC093 484.2/1 60294- 160365	23	#### ##	46.1	141	UGUCCUGAUGAUACUUGUAAUAGGAAGUGCCGUCAGAAGCGAUAACUGACGACGU CUAAUGUCUAUCUGACC
ex3_38 52233_ x138	ENST0 000051 6404.1	19	#### ##	38.2	138	TCCAGCTGTAGGCAGCTGCCTAGGTTGTCTTGTACCTAGGCAAGTGTTACACTGCTG GGA
ex3_38 61227_ x135	ENST0 000036 4722.1	29	2E-11	58	135	GATCAATGATGAAACTAGCCAAATCTGAGCATCAGAAGGCTTTCGGTCTACCTGAT GCA
ex3_38 67822_ x134	CM000 679.2/1 918801 6- 191882 32	34	2E-14	67.9	134	AAGACTATACTTTCAGGGATCATTCTATAGTGTGTTACTAGAGAAGTTTCTCTGAAC GTGTAGAGCACCGAAAACACGAGGAAGAGAGGTAGCGTTTTCTCCTGAGCGTGAA GCCGGCTTCTGGCGTTGCTTGGCTGCAACTGCCGTCAGCCATTGATGATCGTTCTT CTCTCCGTATTGGGGAGTGAGAGGGAGAGAACGCCGTCTGAGTGGT
ex3_38 68626_ x134	ENST0 000062 5943.1	23	#### ##	46.1	134	TCTCAGTGATGAAAACCTTGTCCAGTTCTGCTACTGACAGTAAGTGAAGATAAAGTGT GT

ex3_38 69832_ x134	AY349 593.1/1 -137	32	#### ##	63.9	134	CAGGCUGUGAUGAUUGGCAGGGGUACGGACCUCAGCUGAGUCAUGGGAGCUG AAUGUAUGUGUUUCUCCUUUGUCCUGCAUGUGGCAGGCUGAUGGGGAGCACUUA CAUGAGACUGUUGCCUCAAUUCUGAGCCUG
ex3_38 73031_ x133	AY349 604.1/4 -89	41	#### ##	81.8	133	UCUGGCAAUGAUGACCCACUUGCCCUCACUGAGAACAAGUUCGGUAAUGAGAAU CUUUGUUAUGGACUCAAGUUCUGAGCCAGC
ex3_38 79510_ x131	CM000 664.2/2 061618 78- 206161 956	22	#### ##	44.1	131	CTGGTTGCATGATGAATAAAATCAAATCACCATCTTTTCGGCTGAGTTCGTGATGGATT TGCTTTTTCTGATTAAGCCA
ex3_39 03542_ x127	ENST0 000058 3861.1	23	#### ##	46.1	127	CACAGATGATGAACTTATTGACGGGCGGACAGAACTGTGTGCTGATTGTCACGTTC TGA
ex3_39 10624_ x126	ENST0 000045 9163.1	51	#### ##	85.7	126	AAGTGAAATGATGGCAATCATCTTTTCGGGACTGACCTGAAATGAAGAGAATACTCATT GC
ex3_39 11632_ x126	ENST0 000038 4229.1	51	#### ##	46.1	126	TGCTCTGATGAAATCACTAATAGGAAGTGCCGTCAGAAGCGATAACTGACGAAGACT ACT
ex3_39 18628_ x124	ENST0 000036 3214.1	41	#### ##	65.9	124	TGATGACATTCTCCGGAATCGCTGTACGGCCTTGATGAAAGCACATTTGAACCCTTTT CC

ex3_39 19000_ x124	AL449 212.1/1 7376- 17238	23	#### ##	46.1	124	GACCUCCUGGGAUCGCAUCUGGAGACUGCCUAGUAUUCUGCCAGCUUCGGAAAG GGAGGGAAAGCAAGCCUGGCAGAGGCACCCAUUCCAUUCCCAGCUUGCUCGGUA GCUGGUGAUUGGAAGACACUCUGCGACAGUG
ex3_39 22844_ x123	CM000 679.2/1 919024 5- 191900 29	23	#### ##	46.1	123	AAGACTATACTTTTCAGGGATCATTCTATAGTGTGTTACTAGAGAAGTTTCTCTGAAC GTGTAGAGCACCGAAAACCACGAGGAAGAGAGGTAGCGTTTTCTCCTGAACGTGAA GCCGGCTTTCTGGCGTTGCTTGGCTGCAACTGCCGTCAGCCATTGATGATCGTTCTT CTCTCCGTATTGGGGAGTGAGAGGGAGAGAACGCGGTCTGAGTGGT
ex3_39 32654_ x122	CM000 682.2/2 656939 - 265701 0	17	#### ##	34.2	122	TGGAGGTGATGAACTGTCTGAGCCTGACCTTGTAGAATGGAGGCCAAAAAACTGATT TAATGAGCCTGATCC
ex3_39 43630_ x120	CM000 672.2/6 875517 2- 687552 38	28	#### ##	56	120	GAGTTATGATGTGTGTAATCCTATTCCATTGCTGAAATGCAGTGTGGAACACAATGA ACTGAACTC

ex3_39 45182_ x119	CM000 685.2/7 084629 5- 708460 80	15	#### ##	30.2	119	AAGACTATACTTTTCAGGGATCATTTCTATAGTTTGTTACTAGAGAAGTTTCTCTGAACG TGTATAGCACTGAAAACCACAAAGAAGAGGTGCAGCATTATCTCCTAAGTGTAAGC CGGCTCTTGATGTTGCTTTGCTGCAACTGCCATTTGCCATTGATGATCGTTCTTTTCT TCCTTTGGGAGACTGGGAAGGAAAGGATGCAATCTGAGTGGT
ex3_39 51830_ x118	ENST0 000038 4214.1	32	#### ##	63.9	118	CTTCGATGAAGAGATGATGACGAGTCTGACTTGGGGATGTTCTCTTTGCCAGGTGG CCT
ex3_39 65257_ x116	ENST0 000036 4938.1	43	#### ##	85.7	116	CCAACGTGGATACACCCGGGAGGTCACTCTCCCCGGGCTCTGTCCAAGTGCGTAG GGGA
ex3_39 91858_ x111	ENST0 000038 4769.1	33	#### ##	50.1	111	AGCTTAATGATGACTGTTTTTTTTGATTGCTTGAAGCAATGTGAAAAACACATTTACC G
ex3_39 99465_ x110	ENST0 000051 6236.1	20	#### ##	40.1	110	ATGGAGGCTGCAGTGAGCAGAGATGGCGCCACTGCACTCCAGCCTGAGCGACAAC GAGAC
ex3_40 04167_ x109	ENST0 000038 4176.1	24	#### ##	48.1	109	CTCCATGTATCTTTGGGACCTGTCAAGTGTGGCAGTCTCCCTTCTTGCCATGGAAG AGC
ex3_40 05257_ x109	AC007 066.4/1 64516- 164622	34	#### ##	67.9	109	AAGUUUUCUAAGUGUCUAAUGAUGAAUUUCAUAGGGCAGAUUCUGAGGUGAAAAU UUAAUUCAUACUGAUACUCCUACUGUGGAAUCUGAAGACACUUGAAAACGU
ex3_40 32731_ x104	ENST0 000038 4027.1	37	#### ##	58	104	GTTTGAATGATGACTTTAATTGTCGGATACCCCTTCACTCCTTTTATGAGTGAAACATA A

ex3_40 38295_ x103	AC104 066.3/5 1055- 51176	25	#### ##	50.1	103	GUGCCCUUUUAAGGUUGACCCAGUGCUUUUAAGAGGCCUAACACAGAAGGGUAAAGU AAGUCUCCAUA AAAACCCAGAGAAGAGACUGGAAAGCUCCUCUUUGGAUCCUGUCU GGAGUCACAACU
ex3_40 57732_ x100	ENST0 000038 4220.1	20	#### ##	40.1	100	CTTCCCATTTATTTGCTGCTTATAGTCTCACTGTGATATGAGCAATTATACACATGGG AT
ex3_40 95189_ x93	ENST0 000058 3032.1	29	#### ##	58	93	AGTGATGATGACCCCAGGTA ACTCTGAGTGTGTGCTGATGCCATCACCGCAGCGC TCTG
ex3_41 09281_ x91	ENST0 000057 9879.1	47	#### ##	54	91	GGGGCGGTGATGACCCCAACATGCCATCTGAGTGTGCGGTGCTGAAATCCAGAGGCT GTTT
ex3_41 30956_ x88	AC008 443.10/ 63918- 63851	28	#### ##	56	88	GGGGCGGUGAUGACCCCAACAUGCCAUCUGAGUGUCGGUGCUGAAAUCCAGAGG CUGUUUCUGAGCUG
ex3_41 39376_ x87	CM000 679.2/4 838258 6- 483823 71	18	#### ##	28.2	87	AAGACTATACTTT CAGGGATCATTCTATAGTTAGTTGCTAGAGAAGTTTCTCTGGAC ATGTGGAGCACCCAGAAACCATGAGAAGGAGATGTAGTGTTCTCTCCGGAGCATGAA GCTGGCTCTTGTTGTTGCTTCGCTGCACCTGCCATTTGCCATTGACAATCATTCTTCT CTTCTCTGGGAGAGTAAGGAGGAGAGGACACAGTCTGAGTGGT
ex3_41 48537_ x86	AB061 837.1/2 430- 2563	28	#### ##	56	86	UGGUCCAUCCUAAUCCUGCCGGUCCAUCUGUGGCCUGCCAGGUUUCGCUUGUG GACCAGAGCACCCUAGAAGCCUCACCCGAGGAGUGAGCAGGGCUCCAGUGGGCU CACGUCAUGGGCACUUCUAGACACUC

ex3_41 52729_ x85	CM000 663.2/1 738644 45- 173864 369	23	#### ##	46.1	85	AACCAATGATGTAATGATTCTGCCAAATGAAATATAATGATATCACTGTAAAACCGTTC CATTTTGATTCTGAGGTT
ex3_41 54344_ x85	ENST0 000038 4584.1	29	#### ##	58	85	CAGCATGTTTCCAAGGGCTGTGGCTGGTCATAGCCATGGGATCTCCAAGTGCATGCA AGA
ex3_41 75367_ x82	ENST0 000038 3875.1	46	#### ##	83.8	82	CTGCAGTGATGACTTTCTTAGGACACCTTTGGATTACCGTGAAAATTAATAAATTCT GA
ex3_42 10891_ x77	AC013 283.23/ 46245- 46493	38	#### ##	75.8	77	AACAUGCUUCCUUAGAUCACCCUUUGUGGAUGAAUCUUGAACUGAGUUCCACUUG UAAACUUCUUGUUUCUUGUGGUUCCAGUAGUCAAGAAACAUCAGCAACUUUUU UGGUUGUAUAGUCAAGGUGCUUGAGUCAUUGGCAUGUAAGAGAAAUUACCUGC AUGUUAGUCUACGUUCUGAUAGAAUAGACAUUGCAUUUAUGCUGCCAUUUGUUAC UAUCAGGACUCGACUCGUGUGCGGACAUU
ex3_42 13894_ x77	ENST0 000036 3484.1	20	#### ##	40.1	77	ACCTGTATTCGAAAGTGATCGTGGGCTGCCTGTGCCCTGGTCATTGATAGTGCAGG GAGA

ex3_42 17282_ x77	BK005 568.1/1 -420	28	6E-11	56	77	GUUUUAGGGAGGGAGAGCGGCCUGGGUCCUGGGUGUUGUGUGCGGAGCUGUGG CGUCGCGUGUGAGGCGCGUGCAGGGUGAGUGAGUGGACGCGUGAGUGUGUG AGUGUGCGCGCUUGGAGCGUGUUAGGCGAGUGCGUGCGCCACCCUGCGCCCC UCCUCCCGCUUACACUUUGAUCUUUUUGAUCGGAUCGUGACCCAGCCCCGCCG GGCCGACCCGAAAUGAAAAGCUCUCCUCCUGCGAAGCCCCUCGGGGCGCUGUG CAGCGAGGCCCUUAGGCGGCGGCCACGCUGUGGUCCCCGAGGUCCCCGAGCUG GCCUUGCGGGGCCCGGCGCUCAGAAGUGAUGAAUUGAUCAGAUAGACGAGGCCG GGCUUGUCCCCGCCACUGAUUAUCGAGGCGAUUCUGAUCUGG
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ex3_42 23227_ x76	CM000 668.2/3 183526 3- 318353 26	33	#### ##	65.9	76	AGTGATGATGACCCAGGTAACCTTGAGTGTGTCGCTGATGCCATCACCGCAGCG CTCTGACC
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ex3_42 33396_ x75	CM000 665.2/5 269137 8- 526914 53	33	#### ##	65.9	75	AAGAAATGAAGAACTAAAATTGGTCTTAGTATTGAAGTGAAGACACTGAGATCCAAC TCTGATCTTGCCCTAAAC
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ex3_42 72183_ x70	ENST0 000038 4662.1	26	#### ##	52	70	CTTCCCATTATTTGCTGCTTGTAGTCTCACAGTGATACGAGCAGTTATACGCATGGG AT
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ex3_42 73998_ x69	CM000 668.2/1 328168 02- 132816 877	28	6E-11	56	69	GCTGTACATGATGACAACCTGGCTCCCTCTACTGAACTGCCATGAGGAACTGCCATG TCACCCTTCTGATTACAGC
ex3_42 88263_ x68	ENST0 000036 3217.1	19	#### ##	38.2	68	CCAACGTGGATACCCTGGGAGGTCACTCTCCCCAGGCTCTGTCCAAGTGGCATAGG GGAG
ex3_42 92981_ x67	L36587 .1/100- 167	21	5E-07	42.1	67	UUCCUAUGAUGAGGACCUUUUCACAGACCUGUACUGAGCUCGUGAGGAUAAGUA ACUCUGAGGAGAU
ex3_42 95862_ x67	CM000 670.2/3 351347 5- 335135 78	24	#### ##	48.1	67	ATCCTTTTGTAGTTCATGAGCGTGATGATTGGGTGTTTCATACGCTTGTGTGAGATGTG CCACCCTTGAACCTTGTTACGACGTGGGCACATTACCCGTCTGACC
ex3_43 08009_ x65	ENST0 000036 4113.1	26	#### ##	52	65	ATCGAGGCTAGAGTCACGCTTGGGTATCGGCTATTGCCTGAGTGTGCTAGAGTCCTC GAA
ex3_43 16573_ x64	CM000 673.2/1 230594 22- 123059 335	21	5E-07	42.1	64	TCGCTGTGATGAGTGATTGTTAAACATTCGTAGTTTCCACCAAAGCTTGGCTAATGA TGGCAACACCTTCCTTGGATGTCTGAGCGA
ex3_43 17021_ x64	CM000 663.2/1 738656 86- 173865 622	21	#### ##	42.1	64	GTGTAATGATGTTGATCAAATGTCTGACCTGAAATGAGCATGTAGACAAAGGTAACAC TGAAGAA
ex3_43 19773_ x64	AC018 761.6/4 8391- 48315	26	#### ##	52	64	GGCCUCAAGUGAUGGAGAGCAAUACCCGGGGAUGACUGUGACCACAUUGGGAUG UAUUCGUACUGUCUGAUGGGGCC

ex3_43 24189_ x64	ENST0 000036 4884.1	25	#### ##	50.1	64	GGGAATGATGATTTACAGACTAGAGTCTCCGATGCTGGTCATGATGTCAAACCTAA GTT
ex3_43 31950_ x63	ENST0 000042 6867.1	35	5E-15	69.9	63	TCTCAGTGATGTAATTCCAATAGATCCTTCTGACCCTCCACTGTGGACTCAATAGCAG GG
ex3_43 42047_ x61	CM000 663.2/9 283728 9- 928373 83	28	#### ##	56	61	GCTGAATGATGATATCCCACTAACTGAGCAGTCAGTAGTTGGTCCTTTGGTTGCATAT GATGCGATAATTGTTTCAAGACGGGACTGATGGCAGC
ex3_43 42840_ x61	ENST0 000036 2883.1	20	#### ##	40.1	61	GCTGTGATGACATTCCAATTAAGCACGTGTTAGACTGCTGACGCGGGTGATGCGAA CTG
ex3_43 50038_ x61	CM000 679.2/8 034584 - 803448 7	14	#### ##	28.2	61	ATCCTTTTGTACTTGGTAAGCATGATGATTGGGTTTTTATGCTTATATATGAGACATGC TTGTCTCAAATCTTGTTACAGCACATTACCCTTCTACT
ex3_43 50343_ x61	ENST0 000040 8564.2	21	#### ##	42.1	61	GTGGCCCTGACTGAAGACCAGCAGTTGTAAGTGTGGCTGTTGGTTTCAAGCAGAGGC CTAA
ex3_43 55812_ x60	ENST0 000038 4339.1	26	#### ##	52	60	CTGCGAATATTCTCGCTGTTCTGATTTTGTAAATAGTCAGGACAGGCTAAACATTGCT AT
ex3_43 58812_ x60	ENST0 000038 4792.1	25	3E-09	50.1	60	GTGCAAACCTCGATCACTAGCTCTGCGTGATGTGGCAGAAGCGAAGGGAACCAGGTT TGCA
ex3_43 64273_ x59	AC010 653.10/ 104059 - 104144	29	#### ##	58	59	UGUGUGUUGGAGGAUGAAAGUACGGAGUGAUCCAUCGGCUAAGUGUCUUGUCAC AAUGCUGACACUCAAACUGCUGACAGCACACG

ex3_43 66751_ x59	ENST0 000038 6847.1	32	#### ##	63.9	59	TGTCCCTGACCTGGGTAGAGTGGCATCTGGTTGGT GATGCCCATCTCATATCAGCCA GGG
ex3_43 75338_ x58	ENST0 000038 4581.1	36	#### ##	71.9	58	ATCCTCCTGATCCCTTTCCCATCGGATCTGAACACTGGTCTTGGTGGTCGTAAAAGG AGG
ex3_43 85832_ x57	ENST0 000038 3903.1	20	#### ##	40.1	57	AGTCTGTGATGAATTGCTTTGACTTCTGACACCTCGTATGAAA ACTGCACGTGCAGTC TG
ex3_43 87713_ x57	ENST0 000036 5161.1	21	#### ##	42.1	57	TCTCGTGATGAAA ACTCTGTCCAGTTCTGCTACTGAAGGGAGAGAGATGAGAGCCTT TTA
ex3_44 02448_ x55	CM000 673.2/6 285563 2- 628555 64	21	#### ##	42.1	55	CTTCCTATGATGAGGACCTTTTCACAGACCTGTACTGAGCTCCGTGAGGATAAATAA CTCTGAGGAGAT
ex3_44 05583_ x55	AC023 950.6/1 58570- 158435	25	3E-09	50.1	55	UGCCCCAUUCUCAAAAGAGAAUAGGCACUGUUGAUCAUGCGAUCCAGAGAUUGUUA AUGGGGCUGCAUUGAGAAACAAGCUAUGUUUCCAUUCACAGCAAACACAUCGCAG UGGUGACAAUGAGACCUGUAACAUIIU
ex3_44 08622_ x54	AC006 435.7/2 333- 2239	15	0.002	30.2	54	CUUAAGAGCCAAUGAUGUUUUUAUUCAAAUGUCUGAACCGUCUGAAGCAUCCC AGUGAUGCAACUUCUGUGUGAUACUGAGGCUUUUUUGCCA
ex3_44 09486_ x54	AC104 446.2/1 43509- 143592	22	1E-07	44.1	54	UUUUGGUUGAAAUUGAUGAGUGUACAAAUCUUGAUUUUAAGUGAAUGAAAAUUA CAAGAUCCAACUCUGAUUUUCAGCCAGAG

ex3_44 14022_ x54	ENST0 000036 5530.1	36	#### ##	48.1	54	AGCACAAATGATGAATAACAAAGGGACTTAATACTGAAACCTGATGTTACATTGTAGT GT
ex3_44 28608_ x52	CM000 682.2/3 842533 1- 384251 98	26	#### ##	52	52	CCCTGTATTTCGAAAGTGATCGTGGGCTGCCTTTGCCCTGGTCATTGATAGTGCAGGG AGAGGAATCAATGAAAGCGCTTCCCCGTGTTTGAAGGGTCCACTCCTATCCCTTCCA AACTCTGGAGCTTTCGTACA
ex3_44 38135_ x51	AY349 607.1/2 -78	33	#### ##	65.9	51	GUAAAUGAUGACUUCACUUUUUUCCCCAUCAGAUUCGACAAUGCUGACGUCUUUAU UUUUGCCAGUUAGUUCUGAUAC
ex3_44 42266_ x51	CM000 680.2/4 949172 9- 494916 64	21	#### ##	42.1	51	CTGCGATGATGGCATTCTTAGGACACCTTTGGATTAATAATGAAAACA ACTACTCTC TGAGCAGC
ex3_44 44000_ x51	ENST0 000051 6528.1	26	#### ##	52	51	ATGCATCTATTTGACAGACCTGGAGCAGTTAGTGTGTGCTGCTAAGTTTCTACCTCT AG
ex3_44 55305_ x50	CM000 663.2/1 759685 40- 175968 398	31	#### ##	61.9	50	AATGGAAGCTGCTGGAACCAGCCATGTGGACAAATGAAAAAATGCCTTTTGTCTACA GATTGCAGCGATCCTACATAAATATATGGAGGTCTCTGTCTGGCTTAGGACAGCTGG CTAAGTCTGATCGTCCCCCTCCGTACAGC
ex3_44 60561_ x49	ENST0 000036 2874.1	27	#### ##	30.2	49	TTGCAATGATGTGAATCTCTCACTGAATTCAACCTTGAAGTGCGAATCCATGAGCTTT TT

ex3_44 82071_ x47	CM000 682.2/2 654212 - 265428 6	27	#### ##	54	47	TTGCAGTGATGACTTGCGAATCAAATCTGTCAATCCCCTGAGTGCAATCACTGATGTC TCCATGTCTCTGAGCAA
ex3_44 85267_ x47	CM000 663.2/3 096823 6- 309681 64	27	#### ##	54	47	ACTGGCAAGGATGATACACACTTGCCCTCACTTAGACTATAGTTCACTGATGAGAGC ATTGTTCTGAGCCAGT
ex3_44 96683_ x45	ENST0 000038 4574.1	19	#### ##	38.2	45	TGCACTGCATGGTATCTGCACTCAGCAGTTTACACCTGCTAGGGTGTTCAAAGGTCA GTG
ex3_45 06533_ x44	AF141 346.1/1 052- 1111	37	#### ##	73.8	44	AGCCUGUGAUGCUIUUAAGAGUAGUGGACAGAAGGGAUUUCUGAAAUUCUAUUCUG AGGCU
ex3_45 16521_ x44	CM000 681.2/5 713426 0- 571340 49	17	#### ##	34.2	44	CACTTTATACTTTTAGGGATGATTTCTATAATTCATGAGTGGAGAGGTTTCTCTAGAG GTGTAGGGGACTGGAAACCACATCCAGGAAGTACAGCTTTCTCTCCTGAGCATGAAG GTATCTTGGCATTCTTCACTGCAATTGCCATTTGCCTTTTTGTTTTTCTTTTGAGA TAGGGTGTACCTGTTGCCAGGCTGGAGGGCAGTGGT
ex3_45 19077_ x43	CM000 673.2/6 285396 8- 628539 04	23	#### ##	46.1	43	TTTCTATGATGAATCAAACCTAGCTCACTATGACCGACAGTGAAAATACATGAACACCT GAGAAAC

ex3_45 23506_ x43	CM000 663.2/1 542597 27- 154259 862	28	#### ##	56	43	GGGCATACCCGTAGACCTTGTCTGACTGTGCTCATGGCCAGGCAGGGGGGACAGTG TATGCAAGAGTAATGTGGAGTTTGTGCTAACTCTAGCCAGCTTAATTAGTGACTGGAT AAATTGCACAACCTCTCACATTC
ex3_45 25140_ x43	AC010 361.3/2 3932- 23994	26	#### ##	52	43	GUGCAUGUGAUGAAGCAAAUCAGUAUGAAUGAAUUCAUGAUACUGUAAACGCUUU CUGAUGUA
ex3_45 26043_ x43	CM000 663.2/4 477586 4- 447759 43	23	4E-08	46.1	43	CGTGTATGATGACAACCTCGGTAATGCTGCATACTCCCGAGTGCGCGGTGGGGAAGC CAACCTTGAGAGCTGAGCGTGCG
ex3_45 37956_ x42	AJ2240 26.1/1- 80	29	2E-11	58	42	GUGCCCUGCCUCUGAUGAAGCCUGUNUUGGUAGGGACAUCUGAGAGUAAUGAUG AAUGCCAACCGCUCUGAUGGUGGCAC
ex3_45 39636_ x42	CM000 682.2/4 928031 9- 492804 09	33	#### ##	65.9	42	GCTGGCATATATGATGACTTAGCTTTTTTCCCGACAGATCGACTATGTTGATCTAAC TTTTCTAAGCCAGTTTCTGTCTGATATGCCAGC
ex3_45 44282_ x41	ENST0 000040 8376.1	20	#### ##	40.1	41	TGATGACTGTTCTTCCTGTTGCCTTCAGACCTGGCATTAGGATTTAGGTCATCATAA AT
ex3_45 47193_ x41	ENST0 000038 4693.1	22	#### ##	44.1	41	GTTTGTGATGACTTACATGGAATCTCGTTCGGCTGATGACTTGCTGTTGAGACTCTGA AA

ex3_45 48915_ x41	AF141 346.1/1 275- 1356	28	#### ##	56	41	UGCCACAAUGAUGACAGUUUUAUUUGCUACUCUUGAGUGCUAGAAUGAUGAGGAUC UUAACCACCAUUAUCUUAACUGAGGCA
ex3_45 51523_ x40	ENST0 000045 9433.1	31	1E-12	61.9	40	GGTTCATGATGACACAGGACCTTGTCTGAACATAATGATTTCAAATTTGAGCTTAAA AA
ex3_45 66668_ x39	AC006 435.7/3 490- 3399	27	#### ##	54	39	UAGAGAAGUCAAUUGAUGGUUUUAUUCUAUUCGUCUGAACCUGUCUGAAGCAUCUC AGUGAUGCAAUCUCUGUGUGGUUCUGAGACUUCUCCA
ex3_45 67526_ x39	AF141 346.1/3 076- 3157	48	#### ##	56	39	CCGAUACAAUGAUGAUACAUAAGUUCAGCAGACUAACGCUGAUGAGCAAUAUUAAG UCUUUCGCUCCUAUCUGAUGUAUCUG
ex3_45 67565_ x39	CM000 663.2/1 738660 28- 173865 968	35	5E-15	69.9	39	CCTGGATGATGATAAGCAAATGCTGACTGAACATGAAGGTCTTAATTAGCTCTAACTG ACT
ex3_45 71348_ x39	CM000 682.2/4 928068 3- 492807 72	29	#### ##	58	39	GCCTTTGCAGCTGATGATACAGCTTCTTTCCCATCAGATCGACCCTGTTGATCTCTA CACTATTGGCCAGTTTTGTCTGATGCATTGGC
ex3_45 71738_ x39	AB061 826.1/4 476- 4547	23	#### ##	46.1	39	AGCUUAAUGAUGACUGUUUUUUUUGAUUGCUUGAAGCAAUGUGAAAAACACAUUU CACCGGCUCUGAAAGCU
ex3_45 72362_ x39	ENST0 000038 4072.1	25	#### ##	50.1	39	TGGTCATTACCAAGGCTTTTAGAATGCAGTTTCTCATTTGCTGTGGACATGACCATAA AA

ex3_45 75363_ x38	CM000 673.2/6 285469 5- 628546 21	27	#### ##	54	38	GTCAGATGATTTGAATTGATAAGCTGATGTTCTGTGAGGTACAAAAGTTAATAGCATG TTAGAGTTCTGATGGCA
ex3_45 84027_ x38	AM055 745.1/1 -178	28	#### ##	56	38	ACCUUCUUGUAUAAGCACUGUGCUAAAAUUGCAGACACUAGGACCAUGUCUUGGU UUUUGCAAUAUUGCUUGCAGAGUACACACAAGAAGAAAAGUAACAGCACUAGAUUG UAAAGACUGGGGUGGACCUCUUUCUUAUUGUCCAAUGUCCUUUGUCUUAAGAUUU GGUGCAAUAUCU
ex3_45 95578_ x37	ENST0 000040 8587.1	38	1E-16	75.8	37	CAGCCTGAAGTGATGATTCACATTCATGTCTCTTCTCTGATAAATTCTTGAAGAAAATT T
ex3_45 97576_ x37	ENST0 000038 4096.1	27	#### ##	54	37	CTCCATGTATCTTTGGGACCTGTCAGCCGTGGCAGTCTCCCTTCCTAGCCATGGAAG AGC
ex3_45 98242_ x37	AB017 710.1/1 702- 1771	24	#### ##	48.1	37	AAUCAAUUGAUGAAACCUAUCCCGAAGCUGAUAAACCUGAAGAAAAUAAGUACGGAU UCGGCUUCUGAGAU
ex3_45 98575_ x37	CM000 684.2/2 933325 8- 293331 63	14	#### ##	28.2	37	ACCCCTGGCAGCCCTCCTGATGATTCTTCTTCCTGAGCACGCTCATGATGAGCAAA CTGAGCCTCTAAGAAGTTGACTGAAGGGGCTGCTTCCCC
ex3_45 98649_ x37	ENST0 000039 0994.1	34	#### ##	67.9	37	AGCTTATCAGTGATGTTGTAAAAATAAATGTCTGAACATATGAATGCAGTATTGATTC A

ex3_45 99877_ x36	AC093 484.2/1 62015- 162087	21	#### ##	42.1	36	AAAUGAUGAAAUCACCCAAAAUAGCUGGAAUUACCGGCAGAUUGUGUAGUGGUGA ACCUAUGGUUUUCUGAAG
ex3_46 01461_ x36	ENST0 000036 5444.1	51	#### ##	61.9	36	CGATGTTATGATGATGGGCGAAATGTTCAACTGCTCTGAAGGGGCTGAATGAAAATG GCC
ex3_46 02577_ x36	AJ0106 76.1/1- 70	24	#### ##	48.1	36	GCUGUGAUGACAUUCCAAUJAAAGCACGUGUUAGACUUCUGACGCGGGUGAUGC GAACUGGAGUCUGAGC
ex3_46 12047_ x35	CM000 678.2/2 155105 - 215502 3	20	2E-06	40.1	35	AGTCTGTGATGAATTGCTTTGACTTCTGACACCTCGTATGAAAAGTGCACGTGCAGTC TGATTATTTAGCAAGACTGAGGCTT
ex3_46 13622_ x35	ENST0 000058 1525.1	39	0.008	30.2	35	CGTGTATGATGACAACCTCGGTAATGCTGCATACTCCCGAGTGCGCGGTGGGGAAGC CAAC
ex3_46 14812_ x35	ENST0 000045 9004.1	20	2E-06	40.1	35	TTGCATGTGGAAATGTCTGCTTCTCATTCTTGGGAGCAGGAATATGTTCATAACATG CT
ex3_46 20657_ x35	ENST0 000060 6769.1	17	#### ##	34.2	35	AAGCAACACTCTGTGGCAGATGATCAAACTGTCTGACACAATTTGAGCTTGCTATAG CA
ex3_46 29699_ x34	ENST0 000051 6624.1	24	#### ##	48.1	34	ATGCATCTATTTGACAGACCTGGAGTAGTTACTGTCTGCTGCTAAGGTTTCCACTACA GA
ex3_46 32045_ x34	ENST0 000040 8189.1	31	#### ##	61.9	34	TTGCAGTGATGACTTGCGAATCAAATCTGTCAATCCCCTGAGTGCAATCACTGATGTC TC

ex3_46 32657_ x34	L44140 .1/7071 6- 70850	43	#### ##	85.7	34	CCGCAGCCAAUUAAGCCGACUGAGUUCUUCUCAUGGGGACCCAGUGUGCGA UGGCUGCACACAGCAGCUUCCUUGGUAGUGUACGCAGCCUGUUGGUUGUAUGGG UUGCUCUAAGGGACCUUGGAGACAGGC
ex3_46 38765_ x33	CM000 677.2/2 507411 4- 250742 15	14	0.008	28.2	33	AGGTTGATGATGACTTACATATATACGTTTTTTTTTTTTTTTTTTGGAAAGGTGAACAAA TGAGTGAAACTCAGTACCATCATCCTCATCTAACTGAGGTCC
ex3_46 39920_ x33	ENST0 000038 3884.1	30	5E-07	44.1	33	TGCAGATGATGTAAAAGAATATTTGCTATCTGAGAGATGGTGATGACATTTTAAACCA CC
ex3_46 48830_ x33	GL000 250.2/3 167878 - 316794 0	40	7E-18	79.8	33	AGTGATGATGACCCCAGGTA ACTCTGAGTGTGTCGCTGATGCCATCACCGCAGCGC TCTGACC
ex3_46 50638_ x32	ENST0 000041 0557.1	24	#### ##	48.1	32	TGATGGCTGTTCCCTCTCACTGCTTGAAGCCTTAGGCAGTGGGATTTTGATCCATCATA TA
ex3_46 51214_ x32	ENST0 000051 6327.1	14	#### ##	28.2	32	AGTTACTGTCTGCTGCTAATGTTTCCACTACAGATAACAAGAAAAAGTCTCTTCACACT TT

ex3_46 53966_ x32	L07382 .1/2- 208	23	4E-08	46.1	32	CCAACGUGGAUACACCCUGGGAGGUCACUCUCCCCGGGCUCUGUCCAAGUGGCG UAGGGGAGCAUAGGGCUCUGCCCAUGAUGUACAAGUCCCUUCCACAACGUUG GAAAUAAAGCUGGGCCUCGUGUCUGCGCCUGCAUAUUCUACAGCUUCCAGAGU CCUGUCGACAAUUACUGGGGAGACAAACCAUGCAGGAAACAGCC
ex3_46 56334_ x32	ENST0 000038 6148.1	38	5E-07	44.1	32	GATCCTGGTGATGACAGACGACATTGTCAGCCAATCCCCATGTGGTAGTGAGGACAT GTC
ex3_46 59662_ x32	ENST0 000036 5607.2	35	#### ##	69.9	32	CTTCCTATGATGAGGACCTTTTCACAGACCTGTACTGAGCTCCGTGAGGATAAATAA CTC
ex3_46 62923_ x31	AJ6094 59.1/1- 132	32	#### ##	56	31	CUUCCCAUUUAAUUUGCUGCUUGUAGUCUCACAGUGAUACGAGCAGUUUACGCAU GGGAUAAAAUAACAUUGGGCCACUGUAAAUUGAGAUGAAGUAACCAUUUUCUUCU CUUCUGCAGGGACUAGACAUUG
ex3_46 64349_ x31	ENST0 000041 0433.1	21	#### ##	42.1	31	GCTGGCATATATGATGACTTAGCTTTTTTCCCCGACAGATCGACTATGTTGATCTAAC TT
ex3_46 65372_ x31	ENST0 000038 3893.1	33	#### ##	65.9	31	GGTCAATGATGAGTTGGCATGTATTCTGAATCTAAAGTTGATTATTACTACTTTAGCTC T
ex3_46 70611_ x31	ENST0 000038 4512.1	33	1E-13	65.9	31	GGTCAATGATGTGTTGGCATGTATTATCTGAATCTATTGCTGATGTGTAATAACACTTT A

ex3_46 78773_ x30	AF141 346.1/1 960- 2019	26	#### ##	52	30	CCUGGAUGAUGAUAGCAAUUGCUGACUGAACAUAGAAGGUCUUAUUAGCUCUAAC UGACU
ex3_46 97177_ x29	CM000 672.2/4 341743 8- 434172 49	15	#### ##	30.2	29	TAGGCGGCTTTCAGGGATCATTCTATAGTCTGCTACTAGAGTACTTTCTGTGAAAGT GTAGAGCCCCCGAAACGACAGGAGGTGCAGTTTTCTCCTGAGTGTGAAGCCGGCG CTTGGTGTGCTTTCGCCATTGAGGTTTCTTCTCCTCCGTGGGGGAATGAGAGGGAG AGGACACAGGCTGAATGGT
ex3_46 97641_ x29	ENST0 000036 3961.1	22	#### ##	44.1	29	TTGCAGTGATGTAAAATTTCTTGGCCTGAAATTACTGTGAAGAGTAAAACCGAGCTTT TT
ex3_47 10446_ x28	AJ2240 27.1/1- 88	19	#### ##	38.2	28	UACUGUUAGUGAUGAUUUUAAAAUUAAAAGCAGAUGGGAAUCUCUCUGAGAAAGA AAAUGGGAGAUUAAUCCUUAACCUGAAACAGUA
ex3_47 14702_ x28	ENST0 000036 2761.1	27	2E-10	54	28	GCGGCCGGTGATGAGAACTTCTCCCACTCACATTCGAGTTTCCCGACCATGAGATGA CTC
ex3_47 15710_ x28	CM000 673.2/6 285536 6- 628552 92	21	5E-07	42.1	28	CTACGGGGATGATTTTACGAACTGAACTCTCTTTCTGATGGATTAGTGGAGAAAAC AGAAAATTCTGAGTAGC
ex3_47 15794_ x28	KN196 479.1/1 75490- 175564	38	1E-16	75.8	28	TGCAGATGATGTAAAAGAATATTTGCTATCTGAGAGATGGTGATGACATTTTAAACCA CCAAGATCGCTGATGCA
ex3_47 16522_ x28	ENST0 000036 5223.1	38	3E-14	67.9	28	TTGCTGTGATGACTATCTTAGGACACCTTTGGAATAACTATGAAAGAAAATTTCTG AG

ex3_47 17334_ x28	CM000 664.2/2 892798 3- 289280 60	26	8E-10	52	28	TTGCTGTGATGACTATCATTGGGTTTTCGCATGTTGCTGAGTTCAGTGATGCCTCTTT TCTCTTGGCTGTCTGAGCAA
ex3_47 18849_ x27	ENST0 000038 4550.1	26	#### ##	52	27	TGGATATGATGACTGATTACCTGAGAAATAATTGATGAAATCTCAAGAAAATTCCTCT AG
ex3_47 19713_ x27	AC078 797.20/ 67061- 67136	27	#### ##	54	27	UUCCUCUGAUGACUCCUGUUAGUGCCACGUGUCUGGGCCACUGAGACACCAUG AUGGAACUGAGGAUCUGAGGAA
ex3_47 21900_ x27	CM000 665.2/1 867847 96- 186784 864	39	3E-17	77.8	27	AAGTGAAATGATGGCAATCATCTTTTCGGGACTGACCTGAAATGAAGAGAATACTCATT GCTGATCACTT
ex3_47 22656_ x27	AC011 031.12/ 168663 - 168575	20	2E-06	40.1	27	GCUGGCACAAUGAUGACUAAAAUUACUUUUUGCCGUUUACCCAGCUGAGGUUGUC UUUGAAGAAAUAUUUUUAAGACUGAGAUGCCAGU
ex3_47 23790_ x27	AC097 720.5/9 9784- 99861	25	3E-09	50.1	27	AUGCUAUGAUGACAUCCAUUUGGUUUCGCUGCUGGCUGAGUUUCAGAGAUGACAC CUUUCUCUUGGCUGUCUGAGCAU
ex3_47 31782_ x27	ENST0 000040 8813.1	29	2E-11	58	27	TGGCCAAGGATGAGAACTCTAATCTGATTTTATGTGCTTCTGCTGTGATGGATTAAAG GA
ex3_47 33115_ x26	ENST0 000038 4674.1	21	5E-07	42.1	26	ACTCTCTCGGCTCTGCATAGTTGCACTTGGCTTCACCCGTGTGACTTTCGTAACGGG GAG

ex3_47_34207_x26	ENST0000516652.1	16	0.0006	32.2	26	GCTACTCTTGAACCTCCTGACCTCAACTGATCCACCCGCCTCGGCCTCCCAAAGTATGAAA
ex3_47_34727_x26	ENST0000384762.1	23	#### ##	46.1	26	AGCACTATATTTAAACCTGTGGATGGGAATATTCCCCATTCTTGGTTACGCTGTAGTGCA
ex3_47_35247_x26	AC097720.5/86379-86467	36	#### ##	71.9	26	UGGUGCUGUGAUGAUGCCUAAAUUUUGUGGUUUCGACUCACUGAGAGUAAAAUGAGGACCUACAAUCCUUGGCUGUGUCUGAGCACCC
ex3_47_36677_x26	ENST0000390856.1	21	#### ##	42.1	26	TTCCTCTGATGACTTCCTGTTAGTGCCACGTGTCTGGGCCACTGAGACACCATGATGGAA
ex3_47_41045_x26	AF492209.1/1-275	28	6E-11	56	26	AAUCUGUAGUCUUGGAGCCGCACAGGGUUGGUGGUACCCUCGAGCACACCAGACUUGCAGAAAAAGCAUACUCCAGAGGAAGCUGAGGCAUGCCUGCUCGAGAGCCAGCUGUCCAUGUGCAAUUUCCUCUGAUAGUUUCUGGUCACUGUUGCCACGGUGAAUGACUGGGCUAUGUCAUUUCUAUCCGCCAACAGUAAGAGAAGCUUUGCAGUCGAGAUUUUGUUUAGCAGAUGGAGUGUUUUCUGUUGAACACUAAGUACUGCCACAA GU
ex3_47_42007_x26	ENST0000386910.1	29	2E-11	58	26	CCCCTATCTCTCATGATGAACACATATGCCTCTGAGCTGCTGTGATTTCTGGCTTCAAAG
ex3_47_43619_x26	ENST0000439232.2	21	5E-07	42.1	26	ACTCACTCACTGCCCTATTTTGTCCCTGTATTTCGAAAGTGATCGTGGGCTGCCTTTGCC

ex3_47 51321_ x25	CM000 681.2/3 982572 - 398250 7	32	3E-13	63.9	25	ATTCGTGATGACTGATCATTCTTCACTTTGACCAGATGTCTACTGAAGAAAGCCTGC GTCTGAGG
ex3_47 51446_ x25	ENST0 000038 6307.1	47	#### ##	54	25	GCTGGTGTAATGATGACTTCACTTTTTTCCCATCAGATCGACAATGCTGACGTCTT AT
ex3_47 54496_ x25	L36588 .1/797- 921	25	3E-09	50.1	25	UCCCAAUGAAGAAACUUUCACAUGUCUUACUCUCUGUCCUAGUCCAGAGCCUGU AAAGGUGAACCACUGGGACUGGCUGGGGGGAGAAGAGGAAGAUUUGUCCAGAAG GAACUGUCUGAGGGAU
ex3_47 54746_ x25	ENST0 000062 8590.1	28	#### ##	56	25	ACGCGCTGTCTTTGAGCCCCGCCGAGCTTCTCGTGGCGCCGGGGTCAATCTGC AGCG
ex3_47 58471_ x25	GL000 250.2/3 169692 - 316975 8	27	#### ##	54	25	GGGAATGATGATTTACAGACTAGAGTCTCCGATGCTGGTCATGATGTCAAACCTAA GTTCTGACTC
ex3_47 58846_ x25	ENST0 000036 5382.1	25	3E-09	50.1	25	TCGCTGTGATGAGTGATTGTAAACATTCGTAGTTTCCACAAAAGCTTGGCTAATGA TG
ex3_47 63971_ x25	ENST0 000036 4432.1	24	#### ##	48.1	25	CCCGCCACTGCACCTGACCAGGTCTCTGTTGGCTGGTGCAATCCAGTGGTGAGCTG ATAG
ex3_47 64246_ x25	ENST0 000036 5493.1	20	#### ##	40.1	25	TGTGCACATTGTTAGAGCTTGGAGTTGAGGCTACTGACTGGCCGATGAACTCGCAAG TGT

ex3_47 66864_ x24	ENST0 000045 8770.1	23	#### ##	46.1	24	CCACATGCGGCTGATGACAGCACTTCTGCTGAGACGCTGTGATTGCTCTGTCCAAAG TAA
ex3_47 67536_ x24	CM000 664.2/2 314604 40- 231460 371	26	8E-10	52	24	AGCACAAATGATGAATAACAAAGGGACTTAATACTGAAACCTGATGTTACATTGTAGT GTGCTGATGTGC
ex3_47 74352_ x24	AY077 740.1/1 -330	21	#### ##	42.1	24	UGGAAAUGAUGAAAUAGAGAUAAUUGGGUGUUGAAUGUUGUAUGACUGGAAUUU UUAAUAUGUAUUAUUGUAAUUCUUUAUAAGUUUAGUGUUUUUAUAGGUACUUAAUA GAGAGUGUGUAUGCAUGUGUGUGUCUUGUGGGUGGCUAUGGAAAGGGGACUG ACUGGUGAUGCUGAUUAUUGGAGUGCAUCUGAGGCUGUUGUAGAAAUAACAUGGG UUGUUGAUUACAACAUUGCCAAUGAUUAUAACCCAAGAACAGCUCACCUAACUAGC CUGGCACCCUAAAAUCUCUAACAGGUUCAUUAUUAAUUGGUCCUGUGAUCUGAUCCA A
ex3_47 77088_ x24	ENST0 000036 3753.1	14	0.008	28.2	24	CAGTAGTGATGAAATTCCACTTCATTGGTCCGTGTTTCTGAACCACATGATTTTCTCG GA
ex3_47 89817_ x23	CM000 682.2/3 843399 8- 384338 65	25	#### ##	50.1	23	ACCTGTATTGAAAAGTGATCGTGGGCTGCCTGTGCCCTGGTCATTGATAGTGCAGG GAGAGAAATCGCGGAAAGTGCTTCCCCGTGTTTGGAGGGTCCGCTCCTGTCCCTTT CAAACCTCTGGAGCTTTCTCACA

ex3_47 93957_ x23	ENST0 000038 4567.1	29	#### ##	58	23	ATGCGATGATGAGTGAAGTAGAGCCTGACCTGGTATTGCCATTGCTTCACTGTTGGC TTT
ex3_47 96395_ x23	CM000 667.2/1 812418 92- 181241 814	28	6E-11	56	23	GGTCCTGGTGATGACAGATGGCATTGTCAGCCAATCCCCAAGTGGGAGTGAGGACA TGTCCTGCAATTCTGAAGGGATT
ex3_47 98777_ x22	ENST0 000050 5219.1	27	#### ##	54	22	GGGCATACTCGTAGACCTTGCCTGACTGTGCTCATGTCCAGGCAGGGGGGACAGTG TATG
ex3_48 01615_ x22	ENST0 000038 4323.1	27	#### ##	54	22	TACCCCTTTTCACTTTGCCAGTTGGACTTATGTCTTTATTGGTCATTCAAGTGGGGC AA
ex3_48 04387_ x22	CM000 667.2/1 385611 10- 138561 043	31	1E-12	61.9	22	GTGCAATGATGTATTTTATTCAACACATCATTCTGAAAGAACGTGTGGAAAATAATG ACTGAGCACA
ex3_48 09733_ x22	AK095 849.1/8 03-874	28	#### ##	56	22	ACUCCAUGAUGAACACAAAAUGACAAGCAUAUGGCUGAACUUUCAAGUGAUGUCAU CUUACUACUGAGAAGU
ex3_48 09887_ x22	AB061 824.1/2 400- 2464	22	#### ##	44.1	22	CUGCAGUGAUGACUUUCUUGGGACACCUUUGGAUUUACCGUGAAAAUUAAUAAU UCUGAGCAGC
ex3_48 10745_ x22	AF019 618.1/4 8-114	21	#### ##	42.1	22	GGAUUUGUGAUGAGCUGUGUUUACUGAGCAUGAUGAAGUAAAGCUCACGUGAUU ACUCUGAAGUCC
ex3_48 15311_ x21	ENST0 000038 4714.1	21	5E-07	42.1	21	CTTCAGTGATGACACGATGACGAGTCAGAAAGGTCACGTCTGCTCTTGGTCCTTGT CAG

ex3_48 22136_ x21	ENST0 000038 4304.1	32	#### ##	63.9	21	CCTTCTATGATGATTTTATCAAATGACTTTCGTTCTTCTGAGTTTGCTGAAGCCACAT T
ex3_48 24320_ x21	AJ6094 86.1/1- 187	21	5E-07	42.1	21	ACGGUCUGGGGAAAGGCUCCUGUGUUGUUGAGCCUGCCAAGUUGUGGGUGCAGC AUGGUACCAGGCAGCCCAACCCUGACCUAAAAGUAAAUJCCCGGAAGAAGUCUUUC CUGGGUUUUGAAUUUGCAGUAAACAGGUGUGAGCAUUCUAGCAGCAGUUUGAUGA UCAUGUAUGAUACUGCAAACAGGA
ex3_48 29213_ x21	AC018 607.12/ 34735- 34867	31	#### ##	61.9	21	AGCCUCAUGCUAGAUGAGAAUGGGCACUGUUGAUCAAGGUGUCCAAAAUAGUUA AUGUGGCUAAAUUGAGAUAGGUUAUGCUUCCAUCACAGUAUGCAUUAUUGCAGUGG UGACAAUGAGACCUGUAACAUUU
ex3_48 35196_ x20	ENST0 000036 4578.1	19	#### ##	38.2	20	AAGCAGGATTCAGACTACAATATAGCTGTAAAGTGCTGTATTGTCATTCCCCCTGCTC AA
ex3_48 39376_ x20	CM000 682.2/2 656624 - 265669 4	21	5E-07	42.1	20	CCACAATGATGGCAATATTTTTTCGTCAACAGCAGTTCACCTAGTGAGTGTTGAGACTC TGGGTCTGAGTGA
ex3_48 41036_ x20	AJ6094 65.1/1- 134	35	5E-15	69.9	20	UGGUAAUGGAUUUAUGGUGGGUCCUUCUCUGUGGGCCUCUCAUAGUGUACCCAU GCCAUAGCAAUUGGCAGCCUCGAACCAUUGCCCAGUCCCCUACCUGUGGGCUGU GAGCACUGAAGGGGGUUGCACAGUG

ex3_48 44496_ x20	ENST0 000036 4089.1	30	#### ##	60	20	TCCAGCGGTTGTCAGCTATCCAGGCTCATGTGGTGCCTGTGATGGTGTACTACTGTT GGA
ex3_48 47276_ x20	AJ6094 67.1/1- 135	29	2E-11	58	20	AGCACUAUAUUUAAACCUGUGGAUGGGAAUAUUCCCCAUUCUUGGUUACGCUGUA GUGCAAAGAAUUCCUGGCUCUCUGUUGCACAGCUGACUUGUGCCAUUCUGCUG UUGCUGUAUAGAGUUAAGGAACAUGG
ex3_48 52496_ x19	ENST0 000038 4342.2	23	4E-08	46.1	19	CCCTTGGCCCTTATCGAAGCTGCAGCTGCTTCCGCATAGCTGCTGTGGTCAAAAAGG AGC
ex3_48 53560_ x19	AJ0077 33.1/1- 97	22	1E-07	44.1	19	AUGCGAUGAUGAGUGAAGUAGAGCCUGACCUGGUUAUUGCCAUUGCUUCACUGUU GGCUUUGACCAGGGUAUGAUCUCUUAUCUUCUCUCUGAGCUG
ex3_48 58766_ x19	ENST0 000036 4849.1	24	1E-08	48.1	19	GCTGGCACAATGATGACTTAAATTACTTTTTGCCGTTTACCCAGCTGAGGTTGTCTTT GA
ex3_48 58861_ x19	ENST0 000060 7313.1	36	1E-15	71.9	19	CTGCGATGATGGCATTCTTAGGACACCTTTGGATTAATAATGAAAACAACACTACTCTC TG
ex3_48 60020_ x19	AC092 123.4/2 4307- 24224	23	4E-08	46.1	19	UGAUGACAUUCUCCGGAAUCGCUGUACGGCCUUGAUGAAAGCACAUUUGAACCCU UUUCCAUCUGAUUGCUGAGGCUUUUAUC
ex3_48 63687_ x19	AJ2240 23.1/1- 67	31	1E-12	61.9	19	GUGCAUAUGAUGGAAAAGUUUUAUCUCCUGACACUUGUGAUGUCUUCAAAGGAA CCACUGAUGCAC
ex3_48 67031_ x19	CM000 679.2/1 644003 6-	26	#### ##	52	19	TGCTCTGATGAAATCACTAATAGGAAGTGCCGTCAGAAGCGATAACTGACGAAGACT ACTCCTGTCTGATT

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ex3_48 67981_ x19	ENST0 000038 4252.1	27	2E-10	54	19	GCTATGATGAATTTGATTGCATTGATCGTCTGACATGATAATGTATTTTTGTCCTCTAA G
ex3_48 68779_ x19	ENST0 000038 4384.1	23	4E-08	46.1	19	GGGTCATTTCAAAGAGGGCTTATGAGGCTGTGAAACCCAGAGCTCTTAACGCTGTGA CCA
ex3_48 74957_ x18	AK025 846.1/2 178- 2094	25	#### ##	50.1	18	UACUGUUAGUGAUGAUUUUAAAAUUAAAGCAGAUGGGAAUCUCUCUGAGAAAGAA AAUGGAGAUUAAUCUUAACUGAAACAGUA
ex3_48 78377_ x18	AC055 855.9/1 10736- 110601	22	2E-07	44.1	18	GUGACUGUCCUGGUUUUGAUUGCAUUUGUUAGUUGUACAGUGCAACCAUAGACA GUCACACACAUUAAAACAGAUGGUUCCUGCCGACAGGGUCUGUAUAGUUUAUCAGA UUUUCUGUGCGAUGGCUCCAUACAUG
ex3_48 86819_ x18	ENST0 000057 8179.1	18	3E-05	36.2	18	GCAGACTCACTCTGCATCTGACTATACTTCCAGGCGGGTGCTTTTTTCTGTCTGCCAG ATA
ex3_48 86909_ x18	ENST0 000038 4262.1	24	1E-08	48.1	18	GTGCAATGATGTATTTTATTCAACACATCATTCTGAAAGAACGTGTGGAAAATAATG AC
ex3_48 86981_ x18	AJ6094 71.1/1- 132	38	1E-16	75.8	18	GUUGAGGUCUAUCCCGAUGGGGCUUUUCCUGUAGCCUGCACAUUCGUUGGAAACG CCUCAUAGAGUAACUCUGUGGUUUUACUUUACUCACAGGACUAUUGUUAGAUCUG UGGGAAGGAAUUACAAGACAGUU

ex3_48 97027_ x17	AC102 799.9/5 3508- 53611	37	4E-16	73.8	17	UGGUCUCAAGGAAGGGAUGAUGUJCCAGUUGAGACUCAAGAAAAGGAUUCUGAGC CUCAGAGCUUUGAAGGAGCCACUUGGUCCUGACCUUCCUAGAGGCAAA
ex3_49 02841_ x17	ENST0 000036 3548.1	24	1E-08	48.1	17	ATGCAGGTACTGTTACAATACTGATGTGTTTTGTTGTCGTTCCCCCTGCTTAAAG CA
ex3_49 05323_ x17	ENST0 000039 1305.1	26	8E-10	52	17	GCCGAGACTAGAGTCACATCCTGACACAACCTTTGTCCTGGTGTGCTAGAGTACTCG AAG
ex3_49 06003_ x17	AC079 951.35/ 128361 - 128226	16	0.000 5	32.2	17	UUGGCCUGAAUCAAGGCCAGCAGUUUGCUGAAGCUGUUGGUUUC AAGCAGGAG CCUAAAAGAAUUGUCUUUCUAUGGUCUGUUGGCCAUUUCAUAACUUUGGAAAUGUA AUGGUCAAUUCAUUAGAAAGAAACAUG
ex3_49 10702_ x16	AJ6094 83.1/1- 129	30	#### ##	60	16	ACUGGAGGACUAAGAAGGCUGAGUCUGAUGAAGUAAGACUUUGCUGAUACAUUCC UCCUAGAAAAAAGGUUGGAGAGAGCAGCCUUCACUGAAGAGUAUCACAGGGCUG ACUGUACUACCCAACACUC
ex3_49 12190_ x16	ENST0 000039 1002.1	33	#### ##	58	16	GCCTTTGCAGCTGATGATACAGCTTCTTTCCCATCAGATCGACCCTGTTGATCTCTA CA
ex3_49 14062_ x16	CM000 676.2/6 347927 2- 634794 13	14	0.008	28.2	16	GGCCTCTCTCCCATGGTGCTGTGGGTGGGGGAGGAGGGGTGCTTTTCTCCTCAGCG AAGACTGGAGGCAGACATCACCCCTCAAGGATCATCCTCAGAACTGCCACGTGCTG GACAGCCTTGTTTTTCTACCTCACACATTT

ex3_49 18926_ x16	GL000 250.2/2 868998 - 286892 3	42	5E-19	83.8	16	GCCAAATGATGTTTATTTGAAACAGGAGCACCTCAGTGCAAGGACGACTCTTATCTAT CACCCATGACTGATGGCT
ex3_49 22414_ x16	ENST0 000036 3664.1	30	4E-12	60	16	AAGCCAGCCAATGAATCTGCTTACCTGATTGTGTTTGTGCAGACATACTTTAAAAACT GG
ex3_49 22782_ x16	ENST0 000040 8314.1	29	2E-11	58	16	GGGCCTCCATGATGTCCAGCACTGGGCTCCGACTGCCACTGAGGACACGGTGCCC CCCGG
ex3_49 23758_ x16	AC013 416.4/5 5441- 55577	22	#### ##	44.1	16	UGCAGUCAAGUCAAAUUCAGUGCCCGUUUCUGUCAUAGCGGGGGCUGGCCCAGA UGGCUGCCACAGCAAGCUCCACAGCUCAUGGGCCCUGGGUCACCUACCCUGGGA CCUGGGGAUAAGUUUGGCUGUGGACAGUG
ex3_49 25102_ x16	ENST0 000063 7869.1	15	#### ##	30.2	16	TTTATTATTATTGTTGTTGTTATTTTGGAGTAGGACTCTCACTGTGTTGGCCAGGCTGG AG
ex3_49 26926_ x16	ENST0 000051 6978.2	19	8E-06	38.2	16	GAGAAATGATGAGGGTCAACATTCTTCATACCAAAGTGAAGACATGAGATCCAACCTC TGA
ex3_49 28126_ x16	AJ6094 80.1/1- 137	21	5E-07	42.1	16	GAGCACCUGAAUCUUUCCAUUCCUUGCUGCCUCGUGCCGGUGUGGGGACAGAU GGUGCUACAGAAUGAGCAGAGGAAAUCCAGACAGGUUGUUUCCAUUUGUCUUGG GGCCUGUCUCUACAGCUCUGCCACAUUU

ex3_49 30498_ x15	CM000 684.2/3 931530 7- 393152 13	41	2E-18	81.8	15	GCTGTTCGTTGATGAGGCTCAGAGTGAGCGCTGGGTACAGCGCCCGAATCGGACAG TGTAGAACCATTCTCTACTGCCTTCCTTCTGAGAACAGC
ex3_49 30903_ x15	CM000 671.2/1 274486 30- 127448 501	32	3E-13	63.9	15	CCCGCCACTGCACCTGACCAGGTCTCTGTTGGCTGGTGCAATCCAGTGGTGAGCTG ATAGTAAACCCCAGCTTAGGAAACAGGGTTGTTCTTCATGTGGATGACTCTGTGCCG AAAGCATGGGAACAGCC
ex3_49 31293_ x15	AJ6094 85.1/1- 127	22	1E-07	44.1	15	CUGGAGACUAAGAAAAUAGAGUCCUUGAAAUCAAGCUGACUCUGCUUUUAGCCUC CUAAAUGAAAAGGUAGAUAGAACAGGUCUUGUUUGCAAAAUAAAUUCAAGACCUAC UUAUCUACCAACAGCA
ex3_49 32478_ x15	ENST0 000038 3885.1	23	4E-08	46.1	15	TAGGCCCTGAATCAAGACCAATGGTTTGCTGTAGCTGTTGGTTTCAAACAGGAGCTA AGA
ex3_49 34638_ x15	AJ6094 66.1/1- 132	23	#### ##	46.1	15	CAGCAUGUUUCCAAGGGCUGUGGCUGGUCAUAGCCAUGGGAUCUCCAACUGCAU GCAAGAGCAACCUGGAAAGACUUUGACAGCGCAGGUCAGUACAAUACCUGCAAGC UGCCACUCAGCUUCCUAUAAUG
ex3_49 45813_ x15	CM000 670.2/9 931823 - 993172 0	14	0.008	28.2	15	GTCCTTTTGTGGTTCATAAGCATGATGATTGGGTTTTTCAGGCCGATTGTGTGAGATGTG CCTCATTGAAACCTTGTTACGATGTCTGCCATTACCCATCTGATG

ex3_49 51861_ x14	ENST0 000062 6886.1	24	1E-08	48.1	14	GCTGTCCTGGACCTGTTGGCACCACAGACAGTTGCTCTGCTGTGCCTGTGGCCTCG GGGC
ex3_49 54829_ x14	D8801 0.1/291 9-3009	21	5E-07	42.1	14	UCACUAUGAUGAUUGGUUGCCAGACAUUCGCAGUUUCCACCAGAAAUGUUUUUCC UUAUGUUGGCCAGUUCUUCUUGGAUGUCUGAGUGA
ex3_49 59589_ x14	AL121 809.6/1 72081- 172016	21	#### ##	42.1	14	CUGUGAUGAUGGCAUUUCUUAGGACAAUUUUGGAUUAAUUUAUGAAAACAACUACU CUCUGAGCAAU
ex3_49 62165_ x14	ENST0 000039 1145.1	34	2E-14	67.9	14	TTATAAGTTTTCTAAGTGTCTAATGATGAATTTTCATAGGGCAGATTCTGAGGTGAAAAT T
ex3_49 62767_ x14	CM000 663.2/7 578788 9- 757879 72	30	4E-12	60	14	GGTCAATGATGTGTTGGCATGTATTATCTGAATCTATTGCTGATGTGTAATAACACTTT AGCTCTAGAATTACTCTGAGACCTT
ex3_49 63649_ x14	ENST0 000039 1100.1	24	3E-06	40.1	14	TCCAGCAGTAGTCAGCCATCCGGACAGAACCGTTCCTGTGATGGTGTTACTGCTG GGA
ex3_49 66785_ x14	AC006 064.10/ 138690 - 138555	34	2E-14	67.9	14	UUGUCCUGGCCUAUUUUUCUGCUCCCCUGUGCUCAGUUCUAACAGGGUAGUCUG GCAGGACACACAGCAAUCCUCUCAGUUUAGGAGGGCCGUCCUAAGAAUAGGGC UGGCUCUUAAGGCACGAGAGGACAAU
ex3_49 69277_ x14	AC064 836.7/3 1785- 31868	28	6E-11	56	14	GUGUCAAUGAUGAUUUUCUAUUUGUUUGCCUGAUUUCCUUUUGGAUAAUGAAGGC AUCUUUAGUCACUACCUCUUCUGAGACAC

ex3_49 70103_ x14	AJ6094 54.1/1- 139	32	#### ##	63.9	14	UGCACUGCAUGGUAUCUGCACUCAGCAGUUUACACCUAGCUAGGGUGUUCAAAGGU CAGUGCUAUAGAAAUUCAGUAUCUGGCAUCGUUGGUUUUCUUGGCUUUGUGCUU GUUAAACCUAGGUAUUUCUACUGAUACAGUA
ex3_49 71461_ x14	AB020 236.1/2 404- 2533	22	1E-07	44.1	14	AUCGAGGCUAGAGUCACGCUUGGGUAUCGGCUAUUGCCUGAGUGUGCUAGAGUC CUCGAAGAGUAAACUGCUGACCUUAUUCACUGGCUUGGGCCUUAUGGCACAGUCA GUCACCAGGUUAGAGACAUGC
ex3_49 71629_ x14	ENST0 000039 1150.1	21	5E-07	42.1	14	AATGTGAAGCAAATGATGATAAACTGGATCTGACTGACTGTGCTGAGTCTGTTCAATC CA
ex3_49 71965_ x14	AB061 824.1/4 441- 4504	20	#### ##	40.1	14	UUGCUGUGAUGACUAUCUUAAGGACACCUUUGGAAUAACUAUGAAAGAAAACUAAU CUGAGCAAC
ex3_49 74525_ x13	AJ5433 24.1/2- 73	34	#### ##	67.9	13	ACAAGCCUAUGAUGGUUAGUUAUCCUGUCUGAAAAUCUGGACUGAGGGAAAUAA UCUAUUCUGAGGCUAA
ex3_49 75318_ x13	ENST0 000038 4170.1	26	8E-10	52	13	TAGCAAGCCTCCAGCGTGCTTGGGTCTGCAGTGACCCCGTGGATTCCTACAGGGCT TGCC
ex3_49 78711_ x13	AC106 804.4/7 4513- 74420	24	#### ##	48.1	13	CAGCCUGAAAUGAUGACUCUUUAAAAUUUCAUGUCUCUUCUCUGACAUUUUUC UCUGGACACAGUUUUUGCCUUAUGAAUCUGAUCAGGCUG
ex3_49 79179_ x13	ENST0 000057 9969.1	51	3E-05	38.2	13	ATGCTATGATGACATCCATATGGTTTTGCTGCTGGCTGAGTTTCAGAGATGACACCTT TC

ex3_49 88539_ x13	ENST0 000036 4646.1	24	1E-08	48.1	13	GCCCTCCTGGTGCTTACCACAGGCTGTGTTCTTACACTGACTGTATAGAATGAGAAG GTA
ex3_49 88552_ x13	AK095 288.1/7 48-880	22	1E-07	44.1	13	CCCCUUUUAAAAGCACUCAAUUGGGCCUGUGGCUAAUGACCUAUUGAGCCGUCAA GAAAGGGGAGAGUGAAAACAUCGCUUUUGGGUGAAGUGGCAACAUGUGUUGUUU GCUUCAAUUCGGUGGUGUGACAAGG
ex3_49 89319_ x13	ENST0 000036 3450.1	34	#### ##	67.9	13	AAGCAGGATTCAGACTACAATATAGCTGCTAAGTGCTGTGTTGTCGTTCCCCCTGCT TAA
ex3_49 89579_ x13	AC016 868.8/2 1258- 21186	24	0.000 6	32.2	13	GUGUGAUGAAAUCACCCCAAUAGCUGGAAUUACCAGCAGAUUGUGUAGUGGUGA ACCUACAUUUUUCUGAAG
ex3_49 93752_ x13	ENST0 000038 4334.1	18	3E-05	36.2	13	GCATGGCTGAATACTGTGTTCTTTTATCAGTAGTTTACACAGCCAGACACCATGCAAA AG
ex3_49 94961_ x13	CM000 673.2/1 230589 95- 123058 909	25	7E-07	42.1	13	TCGCTATGATGATGGATTCCAAAACCATTCGTAGTTTCCACCAGAAAGTCTTATGTTG GCCAGTTCCTTCCTTGGATGTTTGAGCGA
ex3_50 00185_ x12	ENST0 000036 4953.1	25	3E-09	50.1	12	AGTGATGATGACCCCAGGTA ACTCTTGAGTGTGTCGCTGATGCCATCACCGCAGCG CTCT
ex3_50 03425_ x12	AL355 075.6/1 93439- 193515	28	6E-11	56	12	AGUUUGCCAUGAUGAAAUGCAUGUUAAGUCCGUGUUUCAGCUGAUCAGCCUGAUU AAACACAUGCUCUGAGCAGACU

ex3_50 05633_ x12	ENST0 000036 3946.1	25	#### ##	50.1	12	TCCTCCTACAAAGGCGTGTCTGTGGTTCCTGTCTTTGGACACGTAAGAATTGGAGG AAA
ex3_50 17825_ x12	ENST0 000038 4416.1	20	2E-06	40.1	12	GTTGAGGTCTATCCCGATGGGGCTTTTCCTGTAGCCTGCACATCGTTGGAAACGCCT CAT
ex3_50 18725_ x12	ENST0 000040 8716.1	35	6E-15	69.9	12	GCAGACTCACTATGCACCTGACTGTACTTCCAGGCAGGTGCTTTTTCTGTCTGCCAG AGA
ex3_50 20117_ x12	CM000 677.2/6 650291 0- 665028 12	28	#### ##	56	12	TGCAATGATGTCGTAATTTGCGTCTTACTCTGTTCTCAGCGACAGTTGCCTGCTGTCA GTAAGCTGGTACAGAAGGTTGACGAAAATTCTTACTGAGCA
ex3_50 20309_ x12	AB028 893.1/4 087- 4152	20	2E-06	40.1	12	CGUCCAUGAUGUCCGCAACUACCUACAUUGUUUGAUCCUCAUGAAAGCAGCACU GGCUGAGACGC
ex3_50 21461_ x12	ENST0 000045 9174.1	43	1E-19	85.7	12	GGTGCAGATGATGACACTGTAAAGCGACCAAAGTCTGAACAAAGTGATTGGTACCTC GTT
ex3_50 21737_ x12	ENST0 000036 4995.1	38	1E-16	75.8	12	AATCAATGATGAAACCTATCCCGAAGCTGATAACCTGAAGAAAAATAAGTACGGATTC GG
ex3_50 22553_ x12	U4390 1.2/401 1-4161	21	5E-07	42.1	12	GCUGCACACUAUUAAAGCUCAGGGUGGAGGCCAGUCUUGGCUCAUGAACUUCUGA GUGUCGGAAGUGUGCUAUUAUCAAUGGCAGGAUUUUCGCUAACACCAGUAGAGCUU GCCUCUAUGACUGGAGUUUGGUAGUACUCGCUGCCACAUAG

ex3_50 27872_ x11	AC018 761.6/5 1237- 51168	28	6E-11	56	11	UGGGAAGUGAUGACACCCUGUGACUGUUGAUGUGGAACUGAUUUUAUCGCGUAUUC GUACUGGCUGAUCCUG
ex3_50 27883_ x11	ENST0 000038 4423.1	21	5E-07	42.1	11	ATCCAAGGTGATTCCCTCTCCAAGGGGACATCAGTGCCTCTCAGGAAAGTAGCAGCT TGG
ex3_50 28994_ x11	ENST0 000036 5128.1	14	#### ##	28.2	11	GCTGTAATGTGTGCATAGGTTTCATCTGTGTCTGGTAGCAGTGTCTGTCTGTGTTTT CA
ex3_50 30985_ x11	ENST0 000038 4215.1	33	#### ##	65.9	11	TAGCAAGCCTCCAGCGTGCTTGGGTCTGCGGTGACCCTATGCATTCCTTCAGTGCTT GCT
ex3_50 32635_ x11	CM000 667.2/1 392787 81- 139278 978	37	4E-16	73.8	11	TCCAGCGGTTGTCAGCTATCCAGGCTCATGTGGTGCCTGTGATGGTGTACACTGTT GGAAGAGCAAACACTGTCTTTATTGAGGTTTGGCTCCAAGCACTGTTTTGGTGTGTA GCTGAGTACCTTTGGGCAGTGTTTTGCACCTCTGAGAGTGAATGACTCCTGTGGAG TTGATCCTAGTCTGGGTGCAAACAAT
ex3_50 35066_ x11	ENST0 000038 8090.1	23	4E-08	46.1	11	TGCACTTATGTATGTTTTTGTTTAACGTGGACAAAGACTTACAGATAGGTGCAAAAA TA
ex3_50 48629_ x11	ENST0 000045 9155.1	24	1E-08	48.1	11	CAGGCTGATGAGACTAAGGCGAATGCGACTCCGTGCTCTCTGGCCCTTGGCTCCTT GTTG

ex3_50 51308_ x10	L07383 .1/1- 153	30	4E-12	60	10	UGUGCACAUUGUUAGAGCUUGGAGUUAGAGGCUACUGACUGGCCGAUGAACUCGC AAGUGUAGGUAGUGUGCUACAUGAGGGGCAAGUUUCGCUAACACCACAAGGGUC UCUGGCCCAAUGAGUGGAGUUUGAUAGUAAUUCUUGCUACAAGU
ex3_50 51988_ x10	ENST0 000045 9577.1	30	4E-12	60	10	TGGTCTCAAGGAAGGGATGATGTTCCAGTTGAGACTCAAGAAAAGGATTCTGAGCCT CAG
ex3_50 53918_ x10	ENST0 000041 3522.1	26	8E-10	52	10	CCACAATGATGGCAATATTTTTTCGTCAACAGCAGTTCACCTAGTGAGTGTTGAGACTC TG
ex3_50 54028_ x10	ENST0 000036 2803.1	20	2E-06	40.1	10	TGCAATGATGTCGTAATTTGCGTCTTACTCTGTTCTCAGCGACAGTTGCCTGCTGTCA GT
ex3_50 55098_ x10	CM000 666.2/5 414726 4- 541474 61	22	0.009	28.2	10	AAGACTCTACTTCCAGGTATAATTTCTATGGTTTATTACTGGAAAAGTTTCTCTAAATA TGTGGATCGCTGGAAATAAGAGGAAGCACAGGGTTCTCCGAGTGAAGCTGGCTTTT GGAATTACTTGGCTGCAACTGTCATTTGCTACTTTAAGATTTTACTTATTGATTTTTTTT TTTGAGACAGAGTCTCACTCTGT
ex3_50 57008_ x10	AF250 841.1/2 261- 2352	21	5E-07	42.1	10	GGAUCGAUGAUGACUUCCAUAUGUACAUUCUUGGAAAGCUGAACAAAAUGAGUG AAAACUCUAUACCGUCAUCCUCGUCGAACUGAGGUCC
ex3_50 59798_ x10	ENST0 000038 6062.1	25	#### ##	50.1	10	AATAAGTGATGAAAAAAGTTTCGGTCCCAGATGATGGCCAGTGATAACAACATTTTTTC TG

ex3_50 62638_ x10	ENST0 000038 6745.1	23	4E-08	46.1	10	GCTGTTCAGTGATGAGGCCTGGAATGTGCGCTGGGCACAGCGCCCGAGACAGACT GCGGA
ex3_50 62938_ x10	ENST0 000038 3870.1	40	7E-18	79.8	10	CCTCCTTTTCTTGGCGGGGATCGGGCTTGTGGTGCCGCTCCCCGTAATGTACGGAG GAAG
ex3_50 63198_ x10	AJ6094 77.1/1- 132	30	#### ##	60	10	GGCCUCCUGGUGCUUACCACAGGCUGUGUUCUUACACUGACUGUAUAGAAAGAG GAGGUAGAGUAAACCUACCCCAUUAUACACCUCAGCUCAGGCCUUGCCUGGUCU GUAUUGUGAAUGGGGGAACAUAG
ex3_50 64198_ x10	ENST0 000040 8454.1	31	1E-12	61.9	10	GGGACCCCGTGATGTCCAGCACTGGGCTCTGACTGCCCTGAGGACACGGTGCAC CCCGG
ex3_50 68968_ x10	ENST0 000038 4356.1	20	2E-06	40.1	10	CTGTGAATATTCTCGCTGTTCTGATTTTGTATAATCACGATGGGCTAACATTCGCA AT
ex3_50 69588_ x10	ENST0 000038 4033.1	34	2E-14	67.9	10	GCTGCACACTATTAAAGCTCAGGGTGGAGGCCAGTCTTGGCTCATGAACTTCTGAGT GTC
ex3_50 69998_ x10	ENST0 000051 6231.1	30	1E-04	36.2	10	TGAGATGAGATCATGCCATTGCACTCCAGCCTGGACGACAGAGCGAGACTTCATCTC AAA
ex3_50 70598_ x10	AB028 893.1/3 145- 3226	35	5E-15	69.9	10	AGGUCAGUGAUGAGCAACAUUCACCAUCUUUCGUUUGAGUCUCACGGCCAUGAGA UCAACCCCAUGCACCGCUCUGAGACCU
ex3_50 71048_ x10	ENST0 000038 4360.1	25	3E-09	50.1	10	GACCTCCTGGGATCGCATCTGGAGACTGCCTAGTATTCTGCCAGCTTCGGAAAGGG AGGG

ex3_50 72938_ x10	BL000 002.1/9 801851 9- 980187 14	30	#### ##	60	10	AGAGAAGCAAAGUGAUGAGUAAUACUGGCUGGAGCCCCAAAGAGGCACGUGUGUG UGUUUGUGUGUGUGUGUAUAUGCUUGUCAGUGCAUGCACGUGUAUGUCUGGGAG UACAAAUGGGUGCGACUGGUUGUAGGGAACUAGCUAUGUGCCUUCUAUUAGGCC AUGACAGUCAAACUGAUAGAUCUGAUUGCUUC
ex3_50 73588_ x10	CM000 663.2/2 202006 76- 220200 546	23	4E-08	46.1	10	TTCCAAAGTGTTAAGTTCAGTTCAGGGTAGCTTCCCTGCTCTGTTAATTAACCTTTGG AACATTGAACTGGCTAGGGAAAATGATTGGATAGAACTATTATTCTATTCATTTATC CCCAGCCTACAAAA
ex3_50 73928_ x10	ENST0 000038 3953.1	20	2E-06	40.1	10	GCTGAATGATGATATCCCCTAACTGAGCAGTCAGTAGTTGGTCCCTTTGGTTGCATAT GA
ex3_50 75628_ x10	CM000 677.2/6 434256 6- 643426 98	14	0.009	28.2	10	TGTTACTCTCTAGCTTAAGAACCCTTTAATGTGGTGATGTCCATCTCATGTCATCCAGG GATAAAGCAACCCTTGTTTATCCCATCTTGGCTCTTGGTCTGTGCCCATGGCTGGTT CGTGCCTTGGATACATGG
ex3_50 77258_ x10	ENST0 000036 2541.1	22	1E-07	44.1	10	TCTTAGTGACATAATTCTAATAGTTTGTTCGACCTTCCACTGTGGACTCAATAGCAG GG
ex3_50 78736_ x9	AL132 709.5/1 55570- 155499	33	#### ##	65.9	9	UGGAUCGAUGAUGACUGCUGGUGGCGUAUGAGUCUJACAUGAUGAAUACGUGUC UGGAACUCUGAGGUCCAU
ex3_50 82174_ x9	ENST0 000038 4583.1	43	1E-19	85.7	9	TTGGCCCTGAATCAAGGCCAGCAGTTTGTGAAGCTGTTGGTTTCAAGCAGGAGCCT AAA

ex3_50 85927_ x9	CM000 673.2/7 540442 1- 754045 66	21	5E-07	42.1	9	CTTCAGTGATGACACGATGACGAGTCAGAAAGGTCACGTCCTGCTCTTGGTCCTTGT CAGTGCCATGTTCTGTGGTGTGTGCACGAGTTCCTTTGGCAGAAGTGTCTATTTA TTGATCGATTTAGAGGCATTTGTCTGAGAAGG
ex3_50 86287_ x9	ENST0 000038 4437.1	28	6E-11	56	9	ATTGCACCTAAACCCAAGAATCACTGTTTCTTATAGCGGTGGTTTAAACAGAGGTGCA AA
ex3_50 86944_ x9	CM000 675.2/4 533644 7- 453363 14	22	1E-07	44.1	9	ATGCATCTATTTGACAGACCTGGAGCAGTTGCTATCTGCTGCTATGGTTTCCACCACA GATGCAAGAAGAACATGTCCTTGCGCTTCCGTCTGTCTAATTGTGGCAGCTGAGAT TGAATAGAGGAATACAGGA
ex3_50 88519_ x9	ENST0 000036 4968.1	24	#### ##	48.1	9	ACAAGCCTATGATGGTTAGTTATCCCTGTCTGAAAATCTGGACTGAGGGAAATAATCT AT
ex3_50 93037_ x9	AC020 931.6/9 5709- 95787	15	0.002	30.2	9	CCACAUGC GG CUGAUGACAGCACUUCUGCUGAGACGCUGUGAUUGCUCUGUCCA AAGUAAACGCCUGACGCACUGUGG
ex3_50 93235_ x9	AB028 893.1/4 355- 4440	31	1E-12	61.9	9	GGCAGAUGAUGUCCUUAUCUCACGAUGGUCUGCGGAUGUCCCUGUGGGAAUGGC GACAAUGCCAAUGGCUUAGCUGAUGCCAGGAG
ex3_51 00183_ x9	AL132 709.5/1 75950- 175879	21	#### ##	42.1	9	UGGAUCAAUGAUGAGUACCCUGGGGUGUCUGAAUCUUGGAUUUUGAUUAAACCCU AUAACUCUGAGGUCCA
ex3_51 05052_ x9	ENST0 000036 2423.1	21	5E-07	42.1	9	CCCCTTTTAAAGCACTCAATGGGCCTGTGGCTAATGACCTATTGAGCCGTCAAGAA AGG

ex3_51 08912_ x8	AK090 585.1/1 147- 1282	33	8E-14	65.9	8	GCUGUCCUGGACCUGUUGGCACCACAGACAGUUGCUCUGCUGUGCCUGUGGCCU CGGGCAAAGAGAAAGUGGCGAUUUCUACACUCAGUGCUCGGGAACCAGUGGGC ACUGAGAAUGGUUUAUGGCCUGACAUA
ex3_51 13544_ x8	ENST0 000036 4915.1	33	8E-14	65.9	8	GCCAAATGATGTTTATTTGAAACAGGAGCACCTCAGTGCAAGGACGACTCTTATCTAT CA
ex3_51 13880_ x8	AJ6094 41.1/1- 130	21	5E-07	42.1	8	CUGCAUCCACUGAUAGACCUUGAACAAUUUACUGUUGUUCUUUUGGUUUGCACUA GGAUGCAAAAAGAAAGAAUCCUGCGCUUUCUGUCUGUCUUUGUGGGCGGCCAGA UUGAAUUGGGGAAUACAUCU
ex3_51 17992_ x8	AJ6094 73.1/1- 130	35	5E-15	69.9	8	AAGCCAGCCAAUGAAUCUGCUUACCUGAUUGUGUUUGUGCAGACAUACUUUAAAA ACUGGCAAUAGUAAAAGCCAUGUUACGAGCCUUAAGGACAUUGAAGUCGUUAAGGU CCCUGAGAAUGGCUAUAACA
ex3_51 18072_ x8	CM000 673.2/7 540039 1- 754005 38	20	2E-06	40.1	8	CTTCGATGAAGAGATGATGACGAGTCTGACTTGGGGATGTTCTCTTTGCCAGGTGG CCTACTCTGTGCTGCGTTCTGTGGCACAGTTTAAAGAGCCCTGGTTGAAGTAATTC CTAAAGATGACTTAGAGGCATTTGTCTGAGAAGG
ex3_51 20904_ x8	CM000 663.2/1 791964 73- 179196 579	20	0.000 8	32.2	8	ATCCAAGGTGATTCCTTCTCCAAGGGGGACATCCAGTGACCCTCTCAGGAAGTAGCA ACTTGGAATAGAATAGTCCAGGAGTTCCAGGACCAGCCTGGCCAATATGG

ex3_51 21136_ x8	AF308 283.1/1 -330	25	#### ##	50.1	8	GCCACAUGAUGAUUCAAGGCUGUUGUGAUUCAGUUGGUUUUGGCUAAGCCCAGG GACCUUUUGGCCUGUUAAAAGGUCUGUAAUCUUGGUGGGCGAUACAGAGUUUAUGUG UGUUCACUGUAAGGGCAGACCAACAAGAACUUUUUCCUACUUUUUGAGCUACCUCU UUUUAUAGGGGUGAUUCUUCAGUUGCUGGAGAGAAAUUGUGGUAACUGGAGU GAGAGAGUAGGAACAGGGCAUGUUCAGGGUAUCAGGGCCAAGGGUCCUAAAGGA CUUAGCUUGUGUUAUGGCCACUGAGAGAUGAAACACAGAUCUUUGGUAAUCUGAU GGCU
ex3_51 21720_ x8	AF001 689.1/3 146- 3209	24	1E-08	48.1	8	GGGGUAAUGAUGGAAAAUCAUUUAUUGGAAAAGAAUGACAUGAACAAAGGAACCAC UGAAGUGC
ex3_51 26008_ x8	AF141 346.1/2 40-319	37	4E-16	73.8	8	GUGCCCUGCCUCUGAUGAAGCCUGUGUUGGUAGGGACAUCUGACAGUAAUGAUG AAUGCCAACCGCUCUGAUGGUGGCAC
ex3_51 26224_ x8	CM000 671.2/3 393437 6- 339342 96	25	3E-09	50.1	8	CTGGAAAAGACAATGATGTTTTATTTCCAAGCACATATCTGAGTTGTATGTGTGGACA GCACTGAGACTGAGTCTTTCCAC
ex3_51 26616_ x8	ENST0 000045 9579.1	33	#### ##	65.9	8	GCTCTGTGATGGAGCCCATGCGTGTCATCTGAGCCTCTGGCTTCCCTGCCAGTGCA GCCC

ex3_51 26648_ x8	CM000 684.2/3 931391 1- 393138 19	41	2E-18	81.8	8	GCTGTTCAGTGATGAGGCCTGGAATGTGCGCTGGGCACAGCGCCCGAGACAGACT GCGGAACCGTTCCTTGTTGCCTTCCTTCTGAGAACAGC
ex3_51 27552_ x8	ENST0 000045 9255.1	35	5E-15	69.9	8	GCCACATGATGATATCAAGGCTGTTGTGATTGAGTTGGTTTGGCTAAGCCCAGGGAC CTT
ex3_51 28824_ x8	ENST0 000040 8573.1	33	0.000 5	34.2	8	GCTGTACATGATGACAACCTGGCTCCCTCTACTGAACTGCCATGAGGAAACTGCCATG TCA
ex3_51 34552_ x8	CM000 671.2/3 395285 0- 339527 69	27	2E-10	54	8	GTCCAGAAAACAATGATGTGGTAATTTCCAAGCACATATCTGATGATTCCATGTGGAA TTTAACTACCTGAGTTTCCTGGAC
ex3_51 34840_ x8	CM000 663.2/1 554216 5- 155423 04	19	0.006	30.2	8	TGGCTCGGTTTCCTGGGGGGTGGGCTCAGTCTACACCACCTCCCCTCAGCCAAGCC TACAGTAGAGGGCCCAGGCATCCTCCCGTATGGGAGAGGCGTTTGAGTAAGGAGCC TCACCTGGGGTGTCTAGCCTCACATTT
ex3_51 36320_ x8	CM000 671.2/1 314904 86- 131490 571	19	8E-06	38.2	8	TCTCAGTGATGTAATTCCAATAGATCCTTCTGACCCTCCACTGTGGACTCAATAGCAG GGAGATGAAGAGGACAGTGACTGAGAGA
ex3_51 36560_ x8	CM000 679.2/8 329583 - 832971 9	21	5E-07	42.1	8	AAAGCAAGCTGGAATTACAGTGCTTCATTTTGTGAAATACTAAATACCATCATTATGCT GCTGAAAGAAAAGCTGTTTTAATGATTTTTGATTTGTCTTTGTGAGAGTAAATCACGA CAGATTGACATGGACAATT

ex3_51 37120_ x8	CM000 668.2/1 368558 31- 136855 698	14	0.009	28.2	8	TACCCTCTTTCCACTTTGCCAACTGGATGTATGTCTTTACTGGTCATTCCAGTGGGGC AAACGAAATATCCTTTTTAAACTCAGGCAAACCTGGGTGTTTGTTCATGGTCATGTATC CTGTCAGAGAAAACAAAC
ex3_51 39400_ x8	CM000 663.2/1 738663 68- 173866 301	24	1E-08	48.1	8	ATACTATGATGGTTGCATAGTTTCAGCAGATTTAATCATGAAGAGATGTACTATCTGTC TGATGTATCT
ex3_51 42433_ x7	ENST0 000036 3389.1	27	2E-10	54	7	GGCAGATGATGTCCTTATCTCACGATGGTCTGCGGATGTCCCTGTGGGAATGGCGA CAAT
ex3_51 42909_ x7	CM000 681.2/1 786258 8- 178627 20	25	3E-09	50.1	7	ATTGCACCTAAACCCAAGAATCACTGTTTCTTATAGCGGTGGTTTAAACAGAGGTGCA AACAGCAAGCGGATCTTGTCGCCTTTGGGGGGCTGTGGCCGTGCCCTCAAAGTGA ATTTGGAGGTTCCACAAC
ex3_51 43784_ x7	ENST0 000036 4804.2	22	2E-07	44.1	7	AAGACTATTTTCAAGGTTCAATTTCTATAGTTCACTACTGGAGAAGTTTCTCTGAACATG T
ex3_51 44568_ x7	AC064 836.7/1 5165- 15252	28	#### ##	56	7	UUCGUUGUUGUCAAUGAUGUAUUCUUCUUGGAACUGAAUCUAAGUGAUCUGACUC AAUAUUCGUCACUACCACUGAGACAACGAUGAA
ex3_51 46227_ x7	ENST0 000036 2396.1	29	2E-11	58	7	ACCTGCATTCAAAAATGATCACGGGCTGCCTGTGCTCTGGTCATCAATAACGCAGGG AGA

ex3_51 47298_ x7	BC063 011.1/4 24-557	26	8E-10	52	7	ACUCUCUCGGCUCUGCAUAGUUGCACUUGGCUUCACCCGUGUGACUUUCGUAAC GGGGAGAGAGAGAAAAGAUCUCCUCAGGACCUCGGAUGGGCCUUACUGUGGCCU CUCUUUCCUUGAGGGGUGCAACAGGC
ex3_51 48964_ x7	L07384 .1/2- 133	22	#### ##	44.1	7	AAGCAGGAUUCAGACUACAAUUAUAGCUGCUAAGUGCUGUGUUGUCGUUCCCCUG CUUAAAAUAAAGUUGUUUCUUAACUUAUACCUGUCUGCUAUUCUCCUGUAGCAGCC AGGGACGCUUGGUCUCAUCAU
ex3_51 49069_ x7	ENST0 000063 6377.1	22	1E-07	44.1	7	GAGTTATGATGTGTGTAATCCTATTCCATTGCTGAAATGCAGTGTGGAACACAATGA AC
ex3_51 53073_ x7	CM000 677.2/2 507043 2- 250705 26	30	4E-12	60	7	GGATCGATGATGAGTCCTCCAAAAAACATTCTTGAAAAGCTGAACAAAATGAGT GAGAACTCATACCGTCGTTCTCATCGGAACTGAGGTCC
ex3_51 54823_ x7	ENST0 000058 5078.1	21	#### ##	42.1	7	GTGCTGTGATGATGCCTTAATATTGTGGTTTCGACTCACTGAGAGTAAAATGAGGAC CTA
ex3_51 68760_ x7	AJ6094 26.1/1- 135	23	4E-08	46.1	7	UAGGCCUGAAUCAAGACCAAUGGUUUGCUGUAGCUGUUGGUUUCAAACAGGAGC UAAGAGUGAUGUCUCCUUGUGGUCUGUUGGCUAUUCAGUAUCCAGUGCGAAU UGCCAAUUCAGUUGGAAGAAACAUAG

ex3_51_69551_x7	AK128_061.1/3_770-3890	34	2E-14	67.9	7	UGGUCAUUACCAAGGCUUUUJAGAAUGCAGUUUCUCAUUUGCUGUGGACAUGACCA UAAAAAAAAUUUCCAGUAGGUUUUCUAUCUGCUACUUUGCUGCAAUCAGCUU GGGGAACAGUU
ex3_51_71952_x7	AJ6094_55.1/1-133	29	#### ##	58	7	AGCCUUUGUGUUGCCCAUUCACUUUGGAAACUAGUGAAUGUGGUGUCAAAAAAGG CGUAAUUAAACGCUUUGCAGCCUUUCCUGCCCUUAAAUUUGAUACCUUUGGUG UAGGAGCUGCAUAAGUAACAGUU
ex3_51_76572_x7	AP001_458.6/7_2689-72837	26	#### ##	52	7	CCUCCUUUUCUUGGCGGGGAUCGGGCUUGUGGUGCCGCUCCCCGUAUUGUACGG AGGAAGAGGGAAAGGGCUCUGGCCCCUCGGCGUCAUGUCUUCGGUGCUGGCGG CUUCCAUCCGCUGGUUCUAUCCUCAACGCCGGGACACCG
ex3_51_78677_x6	ENST0_000038_4391.2	19	8E-06	38.2	6	AAGAGTATAATTTTCAGGCATCAATTCTGTAGTTCCTTACTAGAGAAGTTTCTCTTAACA T
ex3_51_79271_x6	AJ6094_79.1/1-123	21	#### ##	42.1	6	GAGCACUGUUCGUAACCCGUUAGCCUGGCUGUAGCUAAUGGGUUCCAUUCGGU GCAAUAGCAUUCCAGCGACACAUGACUGACUGGUGGCUUUCAGUUUCAGG UCUUGGAGACAAU
ex3_51_80801_x6	ENST0_000038_4111.1	29	2E-11	58	6	TGCAGCCGTGTCAAATTCAGTACCTGTCCTATGCATGGTAGGCACTGGCCCAGAAG GCTG
ex3_51_82469_x6	ENST0_000036_5633.1	27	2E-10	54	6	TGGCGTCCATGATGTTCCGCAACTACCTACATTGTTTGATCCTCATGAAAGCAGCACT GG

ex3_51 83315_ x6	ENST0 000038 3966.1	31	1E-12	61.9	6	CGGCAGACAGTTATCCCTTTCTAGTCTGGCTCGTGGGACTCTAGAGGGAGTCAGTCT GCA
ex3_51 85475_ x6	AC025 362.12/ 104850 - 104982	23	4E-08	46.1	6	GCGCUGUCUUUGAGCCCCGCCGAGCUUCCUCGUGGCGCCGGGGGUCAAUCUGC AGCGCUAGAGCAUGUGCUUUGCAGUAACUGGGGCGCCUGGCCUCCCGCGGGCG GCCUUUUUAACCGCGAGCGACAAGA
ex3_51 85577_ x6	ENST0 000038 4756.1	31	1E-12	61.9	6	TCCCAATGAAGAACTTTACATGTCTTACTCTCTGTCCTAGTCCCAGAGCCTGTAAA GG
ex3_51 86741_ x6	ENST0 000058 4302.1	26	8E-10	52	6	CTACCAAAAGTTAGCTTTTTGGGGGCAGGTTTTTAAGTAACCTTTGCCAACTTGGG CTA
ex3_51 88805_ x6	ENST0 000040 8139.1	26	8E-10	52	6	CAGCCTGAAATGATGACTCTTTAAAAAATTCATGTCTCTTCTCTGACATTTTTCTCTG G
ex3_51 92177_ x6	ENST0 000040 8684.1	23	4E-08	46.1	6	TACATTCCATGATGTCCAGCACTGGGCTCTGATCACTCCGGAGGACACAGTTTTCCC CAA
ex3_51 92543_ x6	ENST0 000039 1232.1	32	3E-13	63.9	6	TTCGTTGTTGTCAATGATGTATTCTTCTTGGAAGTGAATCTAAGTGATCTGACTCAATA T
ex3_51 94211_ x6	CM000 680.2/2 171211 9- 217119 50	19	1E-05	38.2	6	AACTTCCTGTATAAGCACTGTGCTAAAATCGCAGAACTAGGACCATATCTTGGTTTT TGTGATAATGCTAGCAGAGTACACAGAAGAATAAACGTAACAGCATTGGATTATAAAG ACTAGGGTGAGGCCAGGCGCAGTGGCTCACACGTGTAATCCCAGCACTTTGGGA

ex3_51_94445_x6	AK092_096.1/8_24-956	37	4E-16	73.8	6	UGGCCCUUAUCGAAGCUGCAGCUGCUUCCGCAUAGCUGCUGUGGUCAAAAAGGA GCCAGAGUGACAGUUUUCUUGACGGUCGCCGUUCUGUUUGUUAACUGAUC UGCAACAUUUUGGAAAAUACAGUU
ex3_51_96629_x6	AF266_720.1/1_61-233	26	#### ##	52	6	GCUAUGAUGAAUUUGAUUGCAUUGAUCGUCUGACAUGAUAAUGUAUUUUUGUCCU CUAAGAAGUUCUGAGCUU
ex3_51_97241_x6	ENST0_000038_4281.1	22	1E-07	44.1	6	GAGCACTGTTCGTAACCCGTTAGCCTGGCTGTAGCTAATGGTTCCATTCCGGTGCA ATA
ex3_51_98513_x6	AL132_709.5/1_91680-191609	23	4E-08	46.1	6	UAGACCAAUGAUGAGUAUUCUGGGGUGUCUGAAUCAUGAUUUUGAUUAAACCCU GUAACUCUGAGGUCCAU
ex3_51_98753_x6	CM000_666.2/1_595074_58-159507_372	21	#### ##	42.1	6	AAGACTCTACTTTCAGGGATCACTTCTATAGTCCATCCCTAGAGAAGTTTCTCTGAAA GTGTAGAGCAGCAGTCCCCAGTCCCTGGG
ex3_51_99191_x6	ENST0_000036_4259.1	27	2E-10	54	6	GGGCATACCCGTAGACCTTGTCTGACTGTGCTCATGGCCAGGCAGGGGGGACAGTG TATG
ex3_51_99947_x6	AJ6094_51.1/1-130	25	3E-09	50.1	6	AUCCUCCUGAUCCCUUCCCAUCGGAUCUGAACACUGGUCUUGGUGGUCGUAAAA GGAGGAAAAGUAAUAGUGAAGCUGGCCUAAAUGUUGUAAUCUGGUUAUAUGGCAUG UGGGCUAGUUUCAGACAGGU

ex3_52 00295_ x6	AC064 836.7/1 6842- 16926	25	3E-09	50.1	6	UUCAAUGUUGUCAAUUGAUGCAUUCUUAUUGGAACUGAAUUUAAGUGAUCUGACUC AUUCGUCACUACCACUGAGACAACAUUGAG
ex3_52 00877_ x6	ENST0 000038 4390.1	20	#### ##	40.1	6	TCGCTATGATGATGGATTCCAAAACCATTCGTAGTTTCCACCAGAAAGTCTTATGTTG GC
ex3_52 02953_ x6	ENST0 000045 9386.1	28	3E-08	48.1	6	GTCCAGAAAACAATGATGTGGTAATTTCCAAGCACATATCTGATGATTCCATGTGGAA TT
ex3_52 03067_ x6	CM000 664.2/2 314559 36- 231455 800	26	8E-10	52	6	GTCTTCTCATTGAGCTCCTTTCTGTCTATCAGTGGCAGTTTATGGATTTCGCACGAGAA GAAGAGAGAATTACAGAACTAGCATTATTTTACCTTCTGTCTTTACAGAGGTATATTT AGCTGTATTGTGAGACATTC
ex3_52 03583_ x6	AY077 742.1/1 -131	25	3E-09	50.1	6	UGGGAGGCUGAUACACAAAUUGGGCUGAAAUACUGCUCUACUUGUCACCAUGCCU CCCUAGAAUAAACUGCCUUUUGAUGACCGGGACGAAUUGAGUGAAUUCGUAACGG ACAGAUACGGGGCAGACAGAU
ex3_52 06991_ x6	ENST0 000038 4675.1	26	8E-10	52	6	TTCCACAGCTACTGGTCTGCAGCTGTTCTTATGGTAGCAGTTGTGGCATTCTCTGT GGG
ex3_52 07033_ x6	AJ0030 41.1/11 9-186	25	#### ##	50.1	6	UUGCCAAUGAUGGUUAAGAAUUUCUUCACCUGAAUAAACCAUGUGGUCAGCAUUG CAUCUGAGGCAAA
ex3_52 14581_ x6	ENST0 000036 4043.1	28	6E-11	56	6	AAGTAGGGTGATGAAAAGAATCCTTAGGCGTGGTTGTGGCCGTCTTGGTCACCTGT GTG

ex3_52 18406_ x5	CM000 663.2/9 284071 9- 928408 51	25	3E-09	50.1	5	GTGCAAACCTCGATCACTAGCTCTGCGTGATGTGGCAGAAGCGAAGGGAACCAGGTT TGCAAAAAGTAACTGTGGTGATGGAAATGTGTTAGCCTCAGACACTACTGAGGTGGTT CTTTCTATCCTAGTACAGTC
ex3_52 19041_ x5	AJ6094 31.1/1- 133	41	2E-18	81.8	5	UAGCAAGCCUCCAGCGUGCUUUGGGUCUGCGGUGACCCUAUGCAUUCUUCAGUG CUUGCUAGAACAGUUUUGAAACGGUUUGAGGCCUUGCCUGCUCCAUCCAGAGCA AGGUUAUAGAAAUUUCAGACAAUG
ex3_52 23066_ x5	AL132 709.5/1 78148- 178075	27	2E-10	54	5	UGGACCAAUGAUGAGAUUGGAGGGUGUCUGAAUCAAAAAUUUUGAUUAAAGCCAU CUGUAACUCUGAGGUCCA
ex3_52 23341_ x5	ENST0 000036 5659.1	27	2E-10	54	5	TCAAAATGATGAGATTCCACTTAATTGGTCCGTGTTTCTGAAACACATGATATTTGTG GA
ex3_52 23676_ x5	AC132 192.3/7 1954- 71776	21	#### ##	42.1	5	GUAAUGUGUGCAUAGGUUUCAUCUGUGUCUGGUAGCAGUGUCUGUCUGUGUUUU UCAUUCAGAUUCUUGCUAUCCACACAAACAUCAUGCGGCCAAAGAGUAACUUGGGA UCAUAGUACUGGUCUAGUGUUUGUCUCUGGACACAUCUACCACUGGCCAGCCUCCA AAUUCCACACACAG
ex3_52 24631_ x5	AC068 213.7/1 0987- 11117	25	3E-09	50.1	5	CUCCAUGUAUCUUUGGGACCUGUCAAGUGUGGCAGUCUCCCUUCCUUGCCAUGG AAGAGCAUAUUCUUGUUUACCAGCAAAGCUGUCACCAUUUAAUUGGUAUCAGAUU CUGACUUGCACAAGUAACAUC

ex3_52 27311_ x5	AC090 227.10/ 15359- 15277	20	2E-06	40.1	5	UGGCCGAUGAUGACGAGACCACUGCGCAAUCUGAGUUCUGGGAACCAGGUGAUG GAGUAUGUUCUGAGAACAGACUGAGGCCG
ex3_52 29301_ x5	ENST0 000057 7887.1	44	#### ##	71.9	5	TTGCTGTGATGACTATCATTGGGTTTCGCATGTTGCTGAGTTCAGTGATGCCTCTTT TC
ex3_52 30256_ x5	ENST0 000038 6967.1	22	1E-07	44.1	5	TGGGAAGTGATGACACCTGTGACTGTTGATGTGGAAGTATTTATCGCGTATTCGTA CTG
ex3_52 30481_ x5	CM000 684.2/3 931911 3- 393190 50	30	4E-12	60	5	CACAGATGATGAACTTATTGACGGCGGACAGAACTGTGTGCTGATTGTCACGTTC TGATTTG
ex3_52 30556_ x5	ENST0 000045 9187.1	22	#### ##	44.1	5	TTGCCCGATGATTATAAAAAGACGCGTTATTAAGAGGACTTTATGCTGGAGTTCTTGA CG
ex3_52 30646_ x5	ENST0 000051 6165.1	24	0.000 6	32.2	5	CTGGTCAACAGAGAGAGACTCTGTCTCAAAAAAAGAAAGAAAAGATTTCTGATGTG CTA
ex3_52 34636_ x5	ENST0 000036 4993.1	21	#### ##	42.1	5	AGCCACCGCACCCGCGGGCTGTATTCTTACACTGACTGTATAGAAAGAGGAGAT AGAG
ex3_52 39511_ x5	ENST0 000038 5573.1	24	1E-08	48.1	5	TGCACTTATGTATGTTTTTGTAACTTGTGGACAAAGACTTATGGATAGGTGCAAAA AA
ex3_52 40186_ x5	CM000 673.2/1 020569 27- 102057 017	15	0.005	30.2	5	ATTTTTATTTTTATATGCCTATTTTTATCCTTTGCTGACATGTGCCACCCTCAAACCTT GTGATGATGTCAGCACATTACCCTTCTGACA

ex3_52 40196_ x5	CM000 667.2/1 722524 78- 172252 334	17	0.000 1	34.2	5	CCTCGCTTTCTTTGCAGGGAGCAGGTATGTATGTTCCCTATTATGTCTGGAGGCAGA GGGAAAAGGCTTCAGTCCCCTGGGCATCATGTCTTTGGTGCCGCTGGCTTCCTGTCT GCCAATTCTATCCTCAAGCACTGGGACACAG
ex3_52 42786_ x5	ENST0 000060 9620.2	33	8E-14	65.9	5	TAGAGAAGTCAATGATGGTTTTATTTCATATCGTCTGAACCTGTCTGAAGCATCTCAGT GA
ex3_52 42861_ x5	ENST0 000051 7258.1	15	0.003	30.2	5	GACTAGTACCACCTCACACCCGCAGAGCACTGGGCCCTGCCTGGGGTGAAATGCCA GTTG
ex3_52 43126_ x5	AC079 951.35/ 115286 - 115150	20	2E-06	40.1	5	GUGGCCCUAGACUGAAGACCAGCAGUUGUACUGUGGCUGUUGGUUUCAGCAGAG GCCUAAAGGACUGUCUUCUGUGGUCUGUUGGCUGUUCUGGGACCUCAGUAGGG AAUGGCUAUUUCAUUUGGAAGAAACAACC
ex3_52 43146_ x5	BC042 667.1/5 32-663	35	5E-15	69.9	5	ACUGCCCCUAGAGGCGUUGCAGCUGUGGCUGCCGUGUCACAUCUGUGUCAUUAA GUGGCAGAGAUUAGAGAGGCCU AUGUCUACGCUCAGCGUUCUGCCCCGUGAACGU UUGAAUGUUUGAUAGUCUCACACU
ex3_52 44461_ x5	AC007 318.4/8 0306- 80504	14	0.008	28.2	5	UCCAGCAGUCGUUAGCUCUCCUGGCUAGUGUGAUGCCUGUGAUGGUGUUUCACU GUUGGAACAGCAAGCACUGUCUAAUUGAGGCUUGGCUCGGGUGCUGUUUUGG UGUGGGGCCAAGUAUACCUUUGGGCAGUGUUUUGCACUUCUGAGAGUGAAAUGA CUCCUGUGGAGUCGGUCCUAAUCUGAGUGCAAACAAU

ex3_52_44511_x5	ENST0000516733.1	28	6E-11	56	5	TGCCAATGATGGTTAAGAATTTCTTCACCTGAATAAACCATGTGGTCAGCATTGCATCTG
ex3_52_45331_x5	KN196479.1/176189-176262	21	#### ##	42.1	5	TTGCAGTGATGTAAAATTTCTTGGCCTGAAATTACTGTGAAGAGTAAAACCGAGCTTTTAAACACTGAGTCAGC
ex3_52_45366_x5	CM000672.2/100237302-100237156	20	2E-06	40.1	5	AGTTGTGGTGGTTTTCTTTTTGGCACATTTGTAAAGTTTTCAAATGGGCCTAACTCTGCCACATATATAATATCGGAGATGGCAAAGCCTTGTGACGGAGATATCTCTCTTAAGCCTTTCCTGCATCAGAGAATGGCTCCCACATGT
ex3_52_47701_x5	CM000663.2/75789548	20	#### ##	40.1	5	GGTCAATGATGTAATGGCATGTATTAGCTGAATCTAAAGTTGATGTGAGTTCTAAAAT TAACTGAGACCTT
ex3_52_47706_x5	D00591.1/3109-3311	31	1E-12	61.9	5	CCAACGUGGAUACCCUGGGAGGUCACUCUCCCCAGGCUCUGUCCAAGUGGCAUA GGGGAGCUUAGGGCUCUGCCCAUGAUGUACAGUCCCUUCCACAACGUUGAAGA UGAAGCUGGGCCUCGUGUCUGCGCCUGCAUAUCCUACAGCUUCCCAGAGUCCU GUGGAUAAUGAUAGGGGAGACAAACCAUGCAGGAAACAUAU
ex3_52_48221_x5	ENST0000458862.1	22	2E-07	44.1	5	TGGAGGACTGAGAAGGTGAGGCAGTTTTGCCCGTGCTGCCTTCCACCGGTTAAGACCTC
ex3_52_51961_x5	CM000666.2/151103827-	25	3E-09	50.1	5	AATAAGTGATGAAAAAAGTTTTCGGTCCCAGATGATGGCCAGTGATAACAACATTTTTCTGATGTT

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ex3_52 52761_ x5	AL132 709.5/1 34553- 134482	24	1E-08	48.1	5	UGGAUCGAUGAUGAGCACUGGUGGAGUAUGAGUCACAUACGAUGAAUACGUGUCU GGAACUCUGAGGUCCAU
ex3_52 53771_ x5	AJ6094 68.1/1- 136	38	1E-16	75.8	5	AAGCACUGCCUUUGAACCGAUGUGUCUUGUUUGUAGCUUCACGGGCCAAGCAAC AGUGCUAGAGCAUAACGACUUGUUUAUACUGGGGCUCUUCAGCUCUCAACUGAAC UGCUCUUUUAAAAACAAGGUACAUUU
ex3_52 54701_ x5	ENST0 000038 4289.1	22	1E-07	44.1	5	TTCCAAAGTGTTGAGTTCAGTCCAGGGCAGCTTCCCTGTTCTGTTAATTAACCTTTGG GA
ex3_52 55096_ x5	ENST0 000039 0981.1	28	6E-11	56	5	ACTGAGGAATGATGACAAGAAAAGGCCGAATTGCAGTGTCTCCATCAGCAGTTTGCT CTC
ex3_52 56806_ x5	AC010 325.7/1 35083- 134993	31	1E-12	61.9	5	GGGCUCCCAUGAUGUCCAGCACUGGGCUCUGAUCACCCCUGAGGACACAGUGCA CCCCAGGACCUUUGACACCUUGGGGGUCUGAGGGGCC
ex3_52 57086_ x5	AL121 809.6/1 49441- 149356	26	#### ##	52	5	UGGCAACUGUGAUGAAAGAUUUGGUCUGUAUGUAAUAGAUUUUUAUUACUAAAUGA GGACAACAGUCCCUCUAAACUGAUGUUGCCA
ex3_52 57201_ x5	CM000 673.2/6 285303 5- 628529 10	21	5E-07	42.1	5	TCCAATGAAGAACTTTTACATGTCTTACTCTCTGTCCTAGTCCCAGAGCCTGTAAA GGTGAACCCACTGGGACTGGCTGGGGGAGAAGAGGAAGATTTGTTCCAGAAGGAAC TGTCTGAGGGAT

ex3_52 57521_ x5	AK123 993.1/1 023- 1100	29	2E-11	58	5	CUGAGCUGAGGAUGAUUUAAAGUUAUCCUGUCUGAAAUGGUAUCUUUUGUGAGG AGGUCUGACUUGCUGAGGCUCAG
ex3_52 57686_ x5	ENST0 000062 8922.1	22	2E-07	44.1	5	AAGACTATACTTTGAGGGATCATTTCTATAGTTTGTTACTGGAGAAGTTTCTCTGAATA T
ex3_52 59561_ x5	CM000 668.2/6 721048 0- 672104 08	18	0.008	28.2	5	AAACGATGAACTCACCTAAAATAGCTGTAATAACCAGCAGATTATGTAATGGCAAACC TACAGTTTTCTGAAT
ex3_52 63951_ x4	ENST0 000051 7061.1	19	0.005	30.2	4	GCTTAGGGAGGGTGCTCTGCCAGGTTCCAATCCTGGTTCCACTGCATATGAGCCTT GTA
ex3_52 64267_ x4	AC087 863.10/ 61455- 61585	23	4E-08	46.1	4	CCCUCCUACAAAGGCAUGUCUAUAAUCCUUGUCUUUGGACAUGUAAGAAUUGGA GGGACAGAAAUGUGGACUUGGAGAAAUCUGGGGCCAGCUUUCUCAUCACAGGCU CAACAUCAACCAUGCCACAUAG
ex3_52 64283_ x4	CM000 665.2/1 540075 02- 154007 367	22	#### ##	44.1	4	TCGTCAGGTGGGAGAATTCTTACATGTTCCCTCCTTTTGCAAGGCAGATTAGAACATGA TGATTGGGGTTTCGCATAATATGTGATTAACGTTTCTGTGTAATCAGGACTTGCAACAT CCCGAATGCCCTTACCTGAC
ex3_52 64291_ x4	ENST0 000063 0737.1	23	4E-08	46.1	4	GAGCACTGCTTTAGAGCCTCTGCGTGTCTGGCTGTGGCCTCAGGGGTCTAGCAGCA GTGC

ex3_52 64611_ x4	AC079 802.6/8 0721- 80594	23	4E-08	46.1	4	UAGACUUGUGCAUGUUUUUGCUUAACUUGUGGAUAAAGUCUUACAGACAGGUGCA AAAAUAAAUCCUCUUUUUGCAACCCAGAACUCAUUGUUCAGUAUGAGUUUUGAUAC AUUAUAGAAAGGACAUU
ex3_52 65395_ x4	ENST0 000036 4133.1	22	1E-07	44.1	4	GGGCATACCCGTAGACCTTGCCTGACTGTGCTCATGTCCAGGCAGGGGGGACATTG TATT
ex3_52 65523_ x4	CM000 671.2/1 333504 56- 133350 528	20	2E-06	40.1	4	TTGCAATGATGTGAATCTCTCACTGAATTCAACCTTGAAGTGCGAATCCATGAGCTTT TTAACCTGAGCAAT
ex3_52 67183_ x4	ENST0 000036 4533.1	30	4E-12	60	4	TCACTGTGATGATGGTTTTCCAACATTCGCAGTTTTCCACCAGAAAGGTTTTCTTAGT GT
ex3_52 67459_ x4	AL138 976.5/1 50375- 150500	39	3E-17	77.8	4	AAGCAACACUCUGUGGCAGAUGAUCAAACUGUCUGACACAAUUUGAGCUUGCUA UAGCAAGAAAGUCUAACCUAUUCCGGUGUUCUCUCUCCAUGAGACAAGCCGUUA UAUAGACUAAAACAGU
ex3_52 67487_ x4	AC114 402.2/3 8652- 38776	23	4E-08	46.1	4	GCAGACUCACUAUGCACCUGACUGUACUUCAGGCAGGUGCUUUUUCUGUCUGC CAGAGAAACAUUCCAGGGUGCUGUGGCUGCCUCACCUAUCCAGGGCGAUGCAGC UCCCUGGGGACACAGGU
ex3_52 67839_ x4	ENST0 000060 6420.1	29	2E-11	58	4	GGCCTCCTGGTGCTTACCACAGGCTGTGTTCTTACACTGACTGTATAGAAAGAGGAG GTA

ex3_52 67995_ x4	ENST0 000038 3895.1	20	2E-06	40.1	4	AAAGCAGGTTGCAATTACAGTGCTTCATTTTGTGGAAGTACTGCCATTATCCTGCTGAA
ex3_52 69203_ x4	ENST0 000063 0429.1	29	2E-11	58	4	ACTGCCCCTAGAGGCGTTGCAGCTGTGGCTGCCGTGTCACATCTGTGTCATTAGGT GGCA
ex3_52 69699_ x4	CM000 684.2/3 778552 6- 377856 33	15	0.002	30.2	4	ATCCTTTTGTCTTCATAAGCATGACGATTGGGCTTTCATGCTCATGCATGAGATGGG CCTCCCTTCAGTCTTGTTACAGGCCGGCTCTGTGGCTCATGCCTGTAATC
ex3_52 70331_ x4	AJ2431 99.1/1- 78	21	6E-07	42.1	4	GCCAUUAUGAUGUUUUCUUUUCGAAAGGUGAGCGCUUUGCGCAGUGAUGACCCUC AUCUAUCACCCUUGACUGAUGGCU
ex3_52 70931_ x4	AC016 876.10/ 19660- 19526	20	2E-06	40.1	4	UGUCCCUGACCUGGGUAGAGUGGCAUCUGGUUGGUGAUGCCCAUCUCAUAUCAG CCAGGGACAAAGCAACUCCUUGUUCAUCCCAGCUUGGCUUUUGAUCGUGCCCAU GCCUGGUUCAUGCCUUGGACACAUAG
ex3_52 71447_ x4	ENST0 000036 3593.1	30	4E-12	60	4	TCGTCAGGTGGGATAATCCTTACCTGTTCCCTCCCGGAGGGCAGATTAGAACATGA TGA
ex3_52 75599_ x4	ENST0 000045 8893.1	32	3E-13	63.9	4	GTGCATATGATGGAAAAGTTTTAATCTCCTGACACTTGTGATGTCTTCAAAGGAACCA CT
ex3_52 76495_ x4	CM000 663.2/1 738677 50- 173867 671	39	3E-17	77.8	4	GTGCCCTGCCTCTGATGAAGCCTGTGTTGGTAGGGACATCTGAGAGTAATGATGAAT GCCAACCGCTCTGATGGTGGCAC

ex3_52_79935_x4	CM000 682.2/3 842744 2- 384273 09	34	#### ##	67.9	4	TCCTGCATCCGAAAGTGATCATAGGCTGCCTGTGCCTAGGTCATTGATAGTGCAGGG AGAGGAACGCTGAAAGAGGTTGTCCCCGTGTTTGGAGGGTCCACCCTATCCCATCC GAACCCTGAAGCTTTCACACA
ex3_52_82363_x4	CM000 667.2/6 887395 4- 688740 87	22	#### ##	44.1	4	CCCAAAGTGCTGGGATAACCCTTACCTGTTTCTCCTTTGCAGGGCAGATAGAACATG ATAATTGGAGATGCATGAAACGTGATTAATCTCTCTGTATAATCAGGACTTGCAACAC ACTTAATTTTTTTTTTAAT
ex3_52_83215_x4	ENST0 000062 8177.1	30	4E-12	60	4	GTCTGTGATGAATTGCTTTGACTTCTGACACCTCGTATGAAAACCTGCACGTGCAGTCT GA
ex3_52_84063_x4	ENST0 000038 6157.1	22	#### ##	44.1	4	CTTCCTCAGCCTTACTCCAGGGACTTTTTGTTGCCTGTAAAGTGCTCTGGCATTGCCT GA
ex3_52_85083_x4	ENST0 000036 2704.1	22	1E-07	44.1	4	TTGTTATGATGAGATTCCACTTAAGGTCCGTGTTTCTGAAACAAATGATTTTGTGGAA GT
ex3_52_85271_x4	BK005 567.1/2 84-353	23	4E-08	46.1	4	GGGCAAUGAUGAAAAGGUUUUACUACUGAUCUUUGUAACUAUGAUGGUUUUCUACA CUUGACCUGAGCUCA
ex3_52_92499_x4	AJ6094 61.1/1- 133	32	3E-13	63.9	4	GGGUCAUUUCAAGAGGGCUUAUGAGGCUGUGAAACCCAGAGCUCUUAACGCUGU GACCAAAGAUGGAAGUUCUCUAUAGGAAGCCAUAGCACUCCUAAUGUUUGGUGCU AUGUUUCCUGAGGAGAUUAAA

ex3_52_92571_x4	CM000 663.2/4 477839 0- 447784 58	21	#### ##	42.1	4	TCTCAGTGATGAAAACCTTTGTCCAGTTCTGCTACTGACAGTAAGTGAAGATAAAGTGT GTCTGAGGAGA
ex3_52_93663_x4	AJ2240 25.1/2- 73	21	5E-07	42.1	4	GGUGCAAUUGAUGCAUAUGUUAGCGACCAAAGCCUGAUCUUUGCUGAUUAGUCAU AAUUAACUGACUGCACC
ex3_52_94595_x4	AK027 016.1/1 395- 1517	26	#### ##	52	4	UGGUCAUUACCAAGGCUUUUJAGAAUGCAGUUUCUCAUUUGCUGUGGACAUGACCA UAAAAAAAAAUUCCAGUAGGUUUUCUAUCUGCUACGUUGCUGCAAUCAGCUU AUUGGGAACAGUU
ex3_52_95627_x4	ENST0 000051 7238.1	20	0.000 6	32.2	4	CAAAGTTCTGGAATTACAGGTGTGAGCCACCGTGCCAGCATTAAAATTTAATATG TA
ex3_52_95671_x4	ENST0 000040 8789.1	25	3E-09	50.1	4	GGGGTGTGCTCAGAGCAGGGGGCCCAAAGAATGGCTCCTCTGTTTACAACACACCC AACA
ex3_52_97311_x4	CM000 682.2/3 842980 3- 384296 70	27	2E-10	54	4	CCCTGCATTGAAAGTGATCATGAGCTGCCCGTGCCCTGGTCATTGGTAGTGCAGG GAGAGGAACTGCCGAGAGCACTTCCCCGTGTTTGGAGGGTCCACTCCTGTCTCTTC CAAACCCTGGAGCTTTCCACA
ex3_52_97547_x4	ENST0 000036 2915.1	25	3E-09	50.1	4	TGGTCCATCCTAATCCCTGCCGGTCCATCTGTGGCCTGCCAGGTTTCGCTTGTGGAC CAG

ex3_52 98439_ x4	CM000 674.2/6 967606 - 696733 7	24	1E-08	48.1	4	CAGGCTGATGAGACTAAGGCGAATGCGACTCCGTGCTCTCTGGCCCTTGGCTCCTT GTTGGGGGTGGGGACTACAGATGAGATCTGAAATCTTAGTGGTAGTACCTGAGCCAT GACTCCCCACTGTAAGGCCAGATCAATAGCATTGGTGGCCTTGCCTTCATTTCTGGT GCTGCCCTAGTTCCTGGCAGCAGCCTGCAGGGAGGCCACAGGTGGGGTCCACG GTAGGGCTGGGCACAAGCCACCTGAGCGCAACCTTGGATCTGACA
ex3_53 03639_ x4	AL132 709.5/1 46793- 146719	30	4E-12	60	4	UGGACCAAUGAUGACAAAUGGUGGCAUUGGAGUUAUGGACGAUGAAUGAUUAUGUG UCUGAAACUCUGAGGUCCAA
ex3_53 04043_ x4	ENST0 000036 4902.1	28	6E-11	56	4	TGCAGTCAAGTCAAATTCAGTGCCCGTTTCTGTCATAGCGGGGGCTGGCCCAGATG GCTG
ex3_53 04423_ x4	CM000 670.2/1 897961 9- 189797 72	14	0.009	28.2	4	TATTCTTCTTGTTAGAGCTCGGAGTTGAGGCCAGTGACTGGCCAATGAACTCACAAG TGTAGACAGGGTGTTACGCAAGGGACAAGTTTTTCACTAACACCACAAGAGTCTCTG GCCCAATGAGAGGAGTTTAATAGAAATTCTTGCTACAAC
ex3_53 05127_ x4	ENST0 000045 8790.1	23	4E-08	46.1	4	AGCCTTTGTGTTGCCCATTCACCTTTGGAAACTAGTGAATGTGGTGTCAAAAAGGCG TAA
ex3_53 05883_ x4	ENST0 000038 4365.1	22	1E-07	44.1	4	GGATCGATGATGAGTCCTCCAAAAAACATTCTTGGAAAAGCTGAACAAAATGAGT GAG

ex3_53 06631_ x4	ENST0 000060 7547.2	14	0.009	28.2	4	AAGACTATACTTTTCAGGGATCATTCTCTAGTTCAATACTACAGAAGTTTCTCTGAAG GT
ex3_53 09115_ x4	ENST0 000039 1007.1	52	2E-15	71.9	4	TTCAATGTTGTCAATGATGCATTCTTATTGGAAGTGAATTTAAGTGATCTGACTCATTC G
ex3_53 09771_ x4	AC010 553.6/7 12-633	20	2E-06	40.1	4	CAGCCUGAAGUGAUGAUUCACAUUCAUGUCUCUUCUCUGAUAAAUUCUUGAAGAA AAUUUUUGUGUGUCUGAUCAGGCCU
ex3_53 10635_ x4	ENST0 000038 4706.1	19	0.008	30.2	4	GTCAGATGATTTGAATTGATAAGCTGATGTTCTGTGAGGTACAAAAGTTAATAGCATG TT
ex3_53 11903_ x4	AC115 088.6/1 23021- 122911	21	5E-07	42.1	4	UGUGAGAGUGAUGAGUUGCACACUGGUGGAGCCAUGGUAUCAGGUGAUACAGGC ACCACUCAGUAUCACCCUGGUGACAAAUAAGUGCACAGGGGCCAUCUGACUCA CA
ex3_53 12379_ x4	ENST0 000038 4452.1	24	1E-08	48.1	4	CTGCATTCTTAAACCCTCTTGGTAGCTTCGTTCTAAGTGCTTCCAAGATATGAGTGAA TG
ex3_53 13667_ x4	CM000 685.2/1 547685 28- 154768 659	28	6E-11	56	4	TTCCAAAGTGTTGAGTTCAGTCCAGGGCAGCTTCCCTGTTCTGTTAATTAACCTTTGG GACATTAATAATGGGCTAAGGGAGATGATTGGGTAGAAAGTATTATTCTATTCATTTGC CTCCCAGCCTACAAAA
ex3_53 14835_ x4	ENST0 000051 6890.1	31	1E-12	61.9	4	CCTCTTCTCAGAACACTTCTGGGTCTGATTGGTGGCCCAGGGAGCTGTCAGAGAA GAGC

ex3_53 15159_ x4	ENST0 000036 5570.1	50	5E-07	44.1	4	TAGCATATGATGGAAAAATCTTAATCTTCTGAGACTTGTGATGTCTTCAAAGGAACCA CT
ex3_53 15399_ x4	ENST0 000036 2567.2	20	#### ##	40.1	4	CCTGGACCTGTTGGCACCACAGACAGTTGCTCTGCTGTGCCTGTGGCCTCGGGGCA AAGA
ex3_53 15555_ x4	CM000 665.2/1 834525 67- 183452 732	19	9E-06	38.2	4	ACCTTCTTGTTTAAGCTCTGTACTAAAATTGCAGAACTAGTATCGTGTCTTACCATTT GTAATAAAGCTATCAGAGAAAACCCAAGGAAAAAACAGCTGTACCAGATAGAAAA CTGAGTTGAACCTTTTTTTTTTCTTTTTTTTAGATGGAGTCTCACTCTGT
ex3_53 16495_ x4	ENST0 000036 3064.1	20	2E-06	40.1	4	GAAAATACATGATGATCTCACTCCAACCTGGAACCTCTCACTGATTACTTGATAACAA TA
ex3_53 17615_ x4	ENST0 000045 9229.1	21	5E-07	42.1	4	GCCCTGTGGTTGCTGGATGCTGTTGTGCATGGACAGCTCTCCAGTGGATTTCGATGG GCCA
ex3_53 17767_ x4	AB070 559.1/4 340- 4471	31	1E-12	61.9	4	CUGCGAAUUAUUCUCGUCUGUUCUGAUUUUGUAAUAGUCAGGACAGGCUAAACAUUC GCUAUUAUUAAGACCAUGCAUGUGUCCCCAAACCUAGUUCUUUCCCUAGGUCUGGU UUUAUAAAUGCUGGUGAUAAAC
ex3_53 18363_ x4	CM000 663.2/1 714819 07- 171482 009	14	0.009	28.2	4	ATCCTTTTGTAGTTCATAAGTGTGATGATTCAGTGTTCACATGAATCTATGAGATGCG CCAACCTCAAACCTTGTTATGACGTGGTCCATTACCCATCTGATG

ex3_53 20910_ x3	ENST0 000041 0438.1	23	4E-08	46.1	3	TTCCAAAGTGTTAAGTTCAGTTCAGGGTAGCTTCCCTGCTCTGTTAATTAACCTTTG AA
ex3_53 21276_ x3	Z15025 .1/1294 5- 12815	14	0.008	28.2	3	UCCUCCUACAAAGGCGUGUCUGUGGUUCCUGUCUUUGGACAUGUAAGAAUUGG AGAAAAUAAAUGUGGAUUUGGGAAACUUUGAGGCCAGCUUGCUUCUUGCAGGCUC AUGAUCAACCAAUCUCACAUAA
ex3_53 21618_ x3	ENST0 000045 9157.1	22	1E-07	44.1	3	ATCCTTTTGTAGTTCATGAGCGTGATGATTGGGTGTTACATGCATGTGTGAGATGTG CC
ex3_53 22956_ x3	ENST0 000039 1141.1	22	1E-07	44.1	3	AACATGCTTCCTTAGATCCACCTTTGTGGATGAATCTTGAAGTACTGAGTTCCACTTGTA AC
ex3_53 23415_ x3	CM000 679.2/4 402522 3- 440250 20	15	0.003	30.2	3	AAGCTTGTAAGTCTCAGTGATCATTGCTGTAGTTACGAGATAAGCTTCTCTGAACATGC AGAGCAGTGGTAACTATGAGGAGGCACAGTCTCTCCTGAGCATGACTCTGGCTGTT GGTGTGGCTTTGCTGCAGCTGCCGTGTGCCATTGATGATCCTGCTCCTCTTCCTTCG GAAAAGTAAGAGGGAGAGAACAGTCTGAGTGGG

ex3_53 23568_ x3	CM000 677.2/3 685264 0- 368528 59	14	0.008	28.2	3	AAGACGATACTTTCAAGAATCATGATCATTCTATACAGTTCATTACTAGAAAAGTTTCT CTAAACATGTAGAGCGCTGGAAGCCATGAGGAGGAGTCTCAGTGTTGTTGCCTGAG CATGAAGCAGACTCTTGTTGCTTCACTGCAACCACCATGTACCATTGATGATGGTTCT TCTCTTCTCCAGGAGAGTAAGAGGGAAAGAATTCAGTCTGAGTGGT
ex3_53 24168_ x3	AJ6094 64.1/1- 132	28	6E-11	56	3	UUCCACAGCUACUGGUCUGCAGCUGUUCUUAUGGUAGCAGUUGUGGCAUCCUC UGUGGGAAAGAAACUGUUAACACAAACACCUCUUUCUUAAGCAAACAGAAAGUGG GUAUUAUUGUGUGACAGACACAA
ex3_53 26193_ x3	ENST0 000060 6526.1	27	2E-10	54	3	TCACTATGATGATTGGTTGCCAGACATTCGCAGTTTCCACCAGAAATGTTTTTCCTTA TG
ex3_53 26697_ x3	ENST0 000051 6419.1	20	#### ##	32.2	3	TACTCCAGCCTGGATGACAGAGCCAGACTCTGTCTCGAAAAAAAAAAAAAAAAAAGC TTA
ex3_53 27180_ x3	AL132 709.5/1 53488- 153414	20	2E-06	40.1	3	UGGACCAGUGAUGGUGACUGGUGGUGUGUGAGUCAUGCACAGUGAAUAUCAUGU GUCUGGAACUCUGAGGUCCAA
ex3_53 27267_ x3	ENST0 000040 8569.2	16	0.000 8	32.2	3	TTGTATTTTTTGTAGAGATGGGGTCTCTCCCATGGGCACAGTCTCATTGTTTCTATAG TT

ex3_53_27285_x3	AJ6094_52.1/1-137	15	0.005	30.2	3	UACCAAAAGUUAGCUUUUUGGGGGGCAGGUUUUUAAGUAACCUUUGCCAACUUGG GCUAUUUUGGAAGAGUAAAAGACCACACUCCACAGUGGGCUAUACCACUUAGUAUA GUUCGCUACUAAUUUUGUGGCCUACAUG
ex3_53_29685_x3	AY055_806.1/1-75	29	2E-11	58	3	GGUUCAUGAUGACACAGGACCUUGUCUGAACAUAAUGAUUUUCAAUUUUGAGCUU AAAAUGACACUCUGAAAUC
ex3_53_30039_x3	AM055_743.1/3-203	25	3E-09	50.1	3	UCCAGCAGUAGUCAGCCAUCGGACAGAACCGUCCUGUGAUGGUGUUACACUGC UGGGAGAGGAAUGUCUUGUCUUCAUCCGGUUGCCUGCGCCACUGUUCUGGUGGC GUCUGGCACUGGUGCAAGACAGAGCUGUGCUUCCCCGAGAGUGUGCUAAGCAUU CACUUUGGCUGCUUAGUUCUAGUCUGGGAGCAGACAGA
ex3_53_30738_x3	CM000_672.2/5-659603-1-565959-63	20	#### ##	40.1	3	TGATGAATTGATGACAGTCATCTTTTGAGAGTGACCCAAAATGAAAAGAATACTCATT GCTGATCACTT
ex3_53_31167_x3	AP005_270.2/1-24772-124639	20	2E-06	40.1	3	UGCCUCUGACCUUGGGUAGAGUGGCAUCUGGCUGUGACAUUCAUCUCAUAUCAGC CAGGGACAAAGCAACCCCUUGUUUAUUUCAGCUUGGCCUUUUGUCUGUGCCAUG CCUGGUUCAUGCCUUGGACACACUA

ex3_53 32196_ x3	AC104 360.8/6 2127- 61997	39	3E-17	77.8	3	GCCGAGACUAGAGUCACAUCCUGACACAACUCUUGUCCUGGUGUGCUAGAGUACU CGAAGAGAAUCUACUGGUCUUGAUUACUGGUGGGGGCAGUCGGUGCCCCCGUU AGUGCCCAGAU CAGAAACAUAC
ex3_53 32235_ x3	CM000 667.2/8 030636 8- 803062 35	14	0.008	28.2	3	ATACATCTGTTTGACAGACCTAGTGCAATTACTGGGTGCTGCTAAGGTTCTCACTACA GATGCAAGAAAAAGGTGTCATTGTCCTTTCTGTCTGTCTTATTGTGGTAGCCAAGACT GAATAGAGGAAAACAGAG
ex3_53 32679_ x3	ENST0 000038 6037.1	20	2E-06	40.1	3	CAGGCTGTGATGATTGGCGCAGGGGTACGGACCTCAGCTGAGTCATGGGAGCTGAA TGTA
ex3_53 33174_ x3	AJ6094 39.1/1- 126	30	5E-12	60	3	UACCCCUUUUCACUUGCCAGUUGGACUUAUGUCUUUAUUGGUCAUUAAGUGG GGCAAAGGAAUAUCCUUUUAAAACUCAGGCAAACUGGGUGUUUGUCUGUAUCCU GUCAGAGGAAACAAAU
ex3_53 33282_ x3	AY077 737.1/2 -276	21	5E-07	42.1	3	GGUCGUGAUGAUUGGUAAAAGGUCUGAUUGCACUGAAUGUCACAGUCCCUUUGU UGCCCUAACUCCAGCAGCCCAUUUUUCCCUCCCGUCACAUUAAGUCAUGUG UAUGGGAUCAUGGAGCAGCUGAUAAUUUGGGAUUCUGUCAGUGUGUUUCUGA GAGUGAUCGACUCACAGCUGACGAGUAUCCAACAAAACCAGUUACACAGGAGACU GACGAGUGGCAGUCAUGGGUGUGAUGGUGCAUGAUCUCAAGUUUUCAAUCUGAG ACC

ex3_53 33480_ x3	ENST0 000039 1112.1	25	#### ##	50.1	3	ATACTATGATGGTTGCATAGTTCAGCAGATTGAATTCATGAAGAGATTTACAATGTCT GA
ex3_53 35010_ x3	ENST0 000063 6729.1	18	0.009	28.2	3	ATCATTATTGTTATTATTATATTTTTGAGAAGGAATCTCACTCTGTGCGCCAGGCTGGA G
ex3_53 35274_ x3	AJ6094 70.1/1- 125	15	0.004	30.2	3	GCGCUCACUAAGGCUCGGUCCUCUCCACGUGGUCCUGACCUGUCCUCUGUGAGC AAGAGAAACAGGACUGGUUUUGGGGUGUCCUGUCUCAGUGGACACAGGACACCA CGGUUUUCAGUACAACA
ex3_53 35703_ x3	CM000 681.2/3 305140 3- 330515 04	20	2E-06	40.1	3	AAGACTGTACTTCCAGGGATCATTCTACAGTTCGTTACTAGAGAAGTTTCTCTGTAC GTGTACAGCAACCGTTTATATTAGTGTGGCACACACCTATCTGA
ex3_53 40992_ x3	ENST0 000058 4275.1	30	4E-12	60	3	GCCATATGATGTTTTCTTTTCGAAAGGTGAGCGCTTTGCGCAGTGATGACCCTCATCT AT
ex3_53 42183_ x3	AC121 336.3/1 55535- 155667	14	0.008	28.2	3	UUGGGCAGUGAACACCCAAGUGUGCUUUUAUAGUCCUUUGGCUUUGACUUUGUG CUAGAGCAAUGUCUGUUAUUUUUCUCUGCAUUGAAAGGAGCAUUUAUCCUUUUAA AUGUAUUCAGAAAGCCAGUACAUU
ex3_53 42216_ x3	AF001 689.1/2 296- 2367	28	6E-11	56	3	GGUGCAGAUGAUGACACUGUAAAGCGACCAAAGUCUGAACAAAGUGAUUGGUACC UCGUUGUCUGAUGCACC

ex3_53 43884_ x3	AJ6094 84.1/1- 166	22	#### ##	44.1	3	CAGCACUUGAUACUAACCGAGCUGUCUAUAUCCUAGCCUUGUGUCAAGGCUUGU GAUGUGUUGUGAUAGCUGGGUUUAAGAAGUGCAAUAUAAAACAAAAGCCAUGAG UCUUUUAAGCCCAGUGUGUAAAGAUACACUCUGAGUUUAACUCAGAGGCACAAC U
ex3_53 44556_ x3	CM000 678.2/5 694655 7- 569464 46	14	0.008	28.2	3	AAGACTATACTTTTCAGGGATCATTCTGTGGTTGGTTACCAGAGAAGTTTCTCTGAAC ATGTAGAGCACTGGTAAAAAAAAATAAATAAGAAATCATTATTTATTTTTTGA
ex3_53 44850_ x3	AK027 197.1/1 806- 1940	21	#### ##	42.1	3	CCGCAGCCAAUUAAGCCGACUGAGUUCUUCUUCUCAUGGGGACCCAGUGUGCGA UGGCUGCACACAGCAGCUUCCUUGGUAGUGUACGCAGCCUGUUGGUUGUAUGGG UUGCUGUAAGGGACCUUGGAGACAGGC
ex3_53 46206_ x3	AM055 742.1/1 -134	14	0.009	28.2	3	UUGCAUGUGGAAAUGUCUGCUUCUCAUUCUUGGGAGCAGGAAUAUGUUCAUAAC AUGCUACAUUAACAAAGGAGUUCUCAGGGCUGCCAACCUUCUAGUAAAGGUUGAG UGGUAGUAUUAUUUCUCCAACAUA
ex3_53 46824_ x3	ENST0 000040 8237.1	24	1E-08	48.1	3	GGGGTGTGCTCAGAGCAGGGGGCCTAAAGAATGGCTCCTCTGTTTATAACACACCC AACA
ex3_53 47712_ x3	CM000 685.2/2 350731 3- 235072 11	16	0.001	32.2	3	ATCCCTTTATAGTTCCCAGCATGACGATTGGGTGTTACATGCATGTGTGAGATGT ACCACCCTCGCATCTTGTTAGACGTTGGCACATTACCCGTCTGACC

ex3_53_49062_x3	AL132_709.5/1_33438-133369	15	0.005	30.2	3	UGGUUCAGUGUUGACUACUGGUGUCGUGUGAGUCAUACAAUGAAUACAUGUCUG GAACUCUGAGGCCCAU
ex3_53_49551_x3	BA000_025.2/1_06547-106465	35	5E-15	69.9	3	UGGGAGUGGUAAUGAUGAUCUGGUUUGGACAAGAGUCUCUGAGCUUUUCUCUGAG GAUCUUUGAACCCACCUGAUCCACCUUCA
ex3_53_50328_x3	AC005_682.2/1_10683-110610	21	5E-07	42.1	3	UGGCCAAGGAUGAGAACUCUAAUCUGAUUUUAUGUGCUUCUGCUGUGAUGGAUUA AAGGAUUUACCUGAGGCCA
ex3_53_54342_x3	AK095_831.1/7_58-827	35	5E-15	69.9	3	GGUGAAAUGAUGAAUUCUGGGGCGCUGAUUCAUGUGACUUGAAAAUGCCAUC AUUUCUGAUUCACC
ex3_53_55161_x3	ENST0_000038_6683.1	51	3E-24	101	3	GGATTTGTGATGAGCTGTGTTTACTGAGCATGATGAAGTAAAGCTCAACGTGATTACT CT
ex3_53_55389_x3	CM000_677.2/9_241754_7-924176_89	14	0.009	28.2	3	AAGCATGGCACACTGGATGGGCGTTCTGCTTCTCTTTAAAGAGCATGGATTTATCCA TACCATGTGACATGAATGAAATGAGGAGTTTTTCAGGGCTGCCAACCTCTTGTTAAG GTTCTGTGTAGTATATTTCTCCTACAATA
ex3_53_57768_x3	ENST0_000036_5074.1	14	0.008	28.2	3	CTGCAGATATTCTCACTGTTTTGATTTTGTAAATAGTCAGGACAGGCTAACCATTCACT TT
ex3_53_59205_x3	ENST0_000045_9159.1	25	3E-09	50.1	3	TGGCGATGAGGAGGTACCTATTGTGTTGAGTAACGGTGATAATTTTATACGCTATTCT GA
ex3_53_59622_x3	ENST0_000039_0930.1	32	3E-13	63.9	3	GTGAAATGATGATTCAGTTTATCCATTCGCTGAGTGCGCTGCACTGACCTTCTTCCAA GC
ex3_53_60951_x3	ENST0_000038_4744.1	23	4E-08	46.1	3	GCATGGTAATGGATTTATGGTGGGTCCTTCTCTGTGGGCCTCTCATAGTGTACCCAT GCC
ex3_53_66009_x3	AL132_709.5/1_48004-	22	1E-07	44.1	3	UGGACCAAUUAUGACUACUGGUGUGAGUCACGCAUAAUGAACACCACGUGUCUGG AACUCUGAGGUCCAA

	147935						
ex3_53_66444_x3	ENST0000606577.1	33	8E-14	65.9	3	GGTCCTGGTGATGACAGATGGCATTGTCAGCCAATCCCCAAGTGGGAGTGAGGACA TGTC	
ex3_53_68949_x3	CM000673.2/1193234	15	0.006	30.2	3	GTTGGATGAAAATCATCCCAGGGCTTTGCCAGTGGCCGCGAGTGCCCAGAGCTTCCA GGGGCCTCAGCTCACCATGCACTGCCCCGTGTGTGGCAGTGAAACCCAGGCCCTGA CAGGC	
ex3_53_71481_x3	CM000675.2/4623577	14	0.008	28.2	3	ATCCTTTAGTAGTTCATAAGCATGATGATTGGCTTTTTATGCTCATGAATAAAATATGC CTCCCTCAAGCCTTTTTATGACATTGGCACATTACCCATCTGACG	
ex3_53_71553_x3	CM000679.2/1955756	30	4E-12	60	3	GCCCAGGGTATGTTACGGGGCGATGCTGCCCTCCCAGCTGGCCCATGGGTGACC CTGGGAACATTAAGTGCCTCACAAACGTTTGTGCCTCAGTTACCCGTAGATGTAGTGA GGGTAACAATACTTACTCTCGTTGGTGATAAGGAACAGCT	
ex3_53_72723_x3	AJ609482.1/1-130	24	1E-08	48.1	3	UGGACAUUUUUUUUUUUUUCAGUUUCUUCUCAAGGUGAAGAUAAACUCUUUGUAAAU GUCCUACAGAAAUAUAGUAGCUUUCUGUUCUUCUUUGCAAGUAAAAAGGGUGGG UCGUCCACUACUGACAUUU	
ex3_53_75912_x3	AC010582.6/81476-81337	14	0.008	28.2	3	UGAUGACUGUUCUUCUGUUGCCUUCAGACCUGGCAUUAGGAUUUUUAGGUCAUCA UAAAUUAAAAUUUGAUUUUCUUCACUCAGAGAAUUAUUAGGAUAAUGGAGUUAUCUG UUCUCUGAAAUUUGCGGAUCAACAUGU	
ex3_53_76545_x3	ENST0000384183.1	14	0.008	28.2	3	TTTCTCATTTGACTACCACATTTTCTCCTAATAATAGATTTTAGTGGCTATGCTTATGG G	
ex3_53_77472_x3	ENST0000363524.1	22	1E-07	44.1	3	CCCTCCTACAAAGGCATGTCTATAGTTCCTTGTCTTTGGACATGTAAGAATTGGAGGC AA	
ex3_53_78771_x3	AJ609427.1/1-137	14	0.008	28.2	3	UUGGCCUGAAUCAAGGCCAGCAGUUUGCUGAAGCUGUUGGUUUCAAGCAGGAG CCUAAAGAAUUGUCUUUCUAUGGUCUGUUGGCCAUUUUCAUAAACUUUGGAAUUGUA AUGGUCAAUUCAUUAGAAAGAAACAUGA	
ex3_53_80508_x3	AP001324.4/9	18	3E-05	36.2	3	ACAGAUGAUGAACUCAUUGACAGACAUACAGAGACUGUGUGCUGAUUGUCAUGUU CUGACUUA	

x3	5881-95819						
ex3_53_81276_x3	ENST0000364729.1	21	5E-07	42.1	3	TCCTGCATCCGAAAGTGATCATAGGCTGCCTGTGCCTAGGTCATTGATAGTGCAGGGAGA	
ex3_53_84213_x3	ENST0000459083.1	36	1E-15	71.9	3	GGTGCAAATGATGCATATGTTAGCGACCAAAGCCTGATCTTTGCTGATTAGTCATAATA	
ex3_53_84429_x3	CM000670.2/99292971-99293049	25	3E-09	50.1	3	AAGACTATACTTTTCAGGGATCATTCTATAGTTTGTACTAGAGAAGTTTCTCTGAACGTGTAAAGCACCATTTAAAGT	
ex3_53_84639_x3	BC028232.1/151-277	15	0.006	30.2	3	GUUGGUUGAAAAUCGCCCCCGCCUUUGCCGUGGCCGCGGGUGAGAUUCGGCGCCAGAGCCCCCGGGGCCUCAGCUCACCCGCGCGCUGCCCCAUGUGCGGCGGUGA	
ex3_53_87045_x3	AL132709.5/183412-183335	29	2E-11	58	3	UGGAUCA AUGAUGAGUAUUGGUGGAGGUGUCUGAAUCAACACUUUUGAUUAAGCC CUCUGUGUAACUCUGAGAUCUGU	
ex3_53_87750_x3	ENST0000515966.1	14	0.009	28.2	3	GCCCTATGTTAAAATTTTAATTCTGCACTTACTAACTATCTTGGGAACCTTGGGCAAGTA	
ex3_53_88677_x3	ENST0000365465.1	22	1E-07	44.1	3	AATCAATGATGAAACCTATCCCAAAGCTGATGACCTGAAGAAAAATACGTACAGATTCAG	
ex3_53_89316_x3	CM000685.2/100822620	21	1E-06	42.1	3	TAGCAAGCCTCCAGCATGCTTAGGTCTGCAGTGACCCTATGCATCCCTACAGTGCTTGCCAGAACAGTTTTGAAACGGTTTGAGGCCTTGCCCTGCTCCATCCAGAGCAAGGGTATAGAAATTTTCAGACAATT	
ex3_53_89364_x3	AB028893.1/10920-11006	23	4E-08	46.1	3	GGCAGAUGAUGUUUGUUUUCACGAUUGGUCUUCAGAUGCCCACGUGGGCACUGCUGAGAAAGCCACUUGGUAAAACUGAUGCCGAAA	
ex3_53_89583_x3	ENST0000362805.1	21	5E-07	42.1	3	GGGCAATGATGAAAAGGTTTTACTACTGATCTTTGTA ACTATGATGGTTTCTACTTGA	

ex3_53 90084_ x3	AJ0103 96.1/58 4-712	34	2E-14	67.9	3	CGGCAGACAGUUAUCCCUUUCUAGUCUGGCUCGUGGGACUCUAGAGGGAGUCAG UCUGCAACAGUAAGUGGUGAGUUCUUCUGUCCAGCGUCAGUAUUUUGAUGGUGG CUUUAGACUUGCCAGAUACA
ex3_53 90909_ x3	AY349 597.1/1 -142	37	4E-16	73.8	3	UUGCCCGAUGAUUUAUAAAAGACGCGUUUAUAAGAGGACUUUAUGCUGGAGUUCU UGACGUUUUUCUCUCUUUUCUAUACUUCUUUUUCUUUCUUUGAAUGUCCAGCGUC CUGUGAGCGAAGAUUAUGAGAUUAUGAGGGCAA
ex3_53 91206_ x3	CM000 676.2/6 365149 9- 636512 96	15	0.002	30.2	3	AAGACCATATTTTCAGGGATCATTTCTATAGTTCATTACTAGAGAAGTTTCTCTG AACATGCAGGGCACCGCAAACCATGAGGAAGAGGCACAGCATTCTTCTGAGCCT GAAGCCAGCTCTTCTTGCTTCACTGCCATTTGCCCTTCATGATCATTCTCTTCTGCA GGAGAGTAAGAAAGGATGCAGTCTGAGTGGT
ex3_53 92031_ x3	ENST0 000036 3315.1	36	1E-10	56	3	CTGAGCTGAGGATGATTTAAAGTTATCCCTGTCTGAAATGGTATCTTTTGTGAGGAGG TC
ex3_53 94563_ x3	CM000 673.2/9 373064 6- 937305 13	33	8E-14	65.9	3	GGGTCATTTCAAAGAGGGCTTATGAGGCTGTGAAACCCAGAGCTCTTAACGCTGTGA CCAAAGATGGAAGTTCTCTATAGGAAGCCATAGCACTCCTAATGTTTGGTGCTATGTT TTCCTGAGGAGATATAAAA
ex3_53 95136_ x3	CM000 681.2/4 994952 7- 499493 16	16	0.000 8	32.2	3	AAGATGACACTTTGAGGCATCGTGTCTATGGTTCATTACTACAGAAGCTTCTCTGGAT GTGTAAGCACAGGAAACCAGGCAGAGGAGGCACAGGGTGCTCTCCAGAACGAGAA GCCAGCTCCTGGAGTTGTTTGCTGCAACTGCCATTCCCGTTGATGACCATGCTCTT CCTTCAGAAGAGGGAGAGTGAGAGGACCAAGTCCAAGTGGT
ex3_53 95412_ x3	CM000 673.2/6 699562 5- 669954 78	18	0.008	28.2	3	AGGACTGTACTTTCAAGGATCATTTCTATAGTTTATTACTAAAGAAGTTTCTCTGAACA TATAAAGCAAACATTTTTTAAGAAGAAAAAATAGACCAGATGCTGTGGCTGCACTT GTAGTCCCAGCACTTGGGTAGGCTGAGGTAG
ex3_54 00827_ x3	AY841 870.1/3 444- 3579	28	6E-11	56	3	GCAUGGGUUUGGAUUUAUGACAGGCCCGUCACCCUGGGCCUGUCAUAGUACCCC AUGCCAGAGCAAACUGUGUCCCCGAACCAUUGCCUGGCCUCUGUGCCCGUAGGC UGCUGGCACUGAAGUGGGUUGCACAGUG
ex3_54 00968_ x3	CM000 668.2/8 871443	25	3E-09	50.1	3	TCAGCTTGAGTCACTCTTCCCAGGCTTTATCCAGGTGGCTTAGGTTAGCTAGGGCTG TGTCCCCTGATGTACAGTCCCTTTACACAATGTTGGAGATAAACTTGGCCTCATGTC TTGCTTCATATCCACAGCCTCTCAGAGTCCTGTGGACAATGACTAGGGAGACAAA

	0- 887142 42					CCATGCAAGCAACATAT
ex3_54 01379_ x3	AJ6094 53.1/1- 134	21	5E-07	42.1	3	UGCAGCCGUGUCAAAUUCAGUACCUGUCCUAUGCAUGGUAGGCACUGGCCAGAA GGCUGCCACAGAAACACUGUGACUCAUGGGCCUGUUCUGUGUCCAGGCUCA GGGAUAAAUUUGGUUACAGACAUCA
ex3_54 01580_ x3	CM000 668.2/5 314792	15	0.004	30.2	3	AAGACTATACTTTCAGGGATCATTCTATAGTTTGTACTAGAGAAATTTCTCTGGACA TCTAGAGCACACAAAAAAGAAAAAGGAACTTCATTCTTA
ex3_54 02579_ x3	KV880 768.1/1 517190 - 151695 3	15	0.002	30.2	3	AGTCACCTTTAAAAAAGGCAGGTCCCCAGCAGCCCATTTTTTTTTTCTCCCATCAC ATTTAAGTCATGTGTATGGGATCATGAAGGAGGTGATAATTTGGGGTTTTTTCAGTGT ATGTTTCTGAGAGTGAATGGTTCACAGCTGACGAGTATCCAACAGAACCAGTTACAC AGGAGATTGAGGAGTGGCTGTGATGGCTGTGACAGTGCATGATCTCAAGTTTTCAAT CTGAGACC
ex3_54 03236_ x3	AM055 729.1/1 -131	28	6E-11	56	3	GGGGUGUGCUCAGAGCAGGGGGCCCAAAGAAUGGCUCCUCUGUUUACAACACAC CCAACAGGAAUCUGGGGUCAUUGUGAUGAGGGCGUCAAAUCUUGUGGCUCUCCUA UGAACAAACGUCCCCAACACCU
ex3_54 03299_ x3	ENST0 000039 1196.1	34	2E-14	67.9	3	GATCACGGTGATGGCTGACCAGGGCTCCCTGACCTATACAGGCCTCTGCTATGGGG GTGA
ex3_54 03677_ x3	AJ6094 57.1/1- 135	30	4E-12	60	3	CUGCAUUCUUAACCCUCUUGGUAGCUUCGUUCUAAGUGCUUCCAAGAUUAGAGU GAAUGCUAUAGAAUUGCAGGGGAGUCCAAAGGGCUGCGCUUCUCCCGUGGCUC AGUCUUUUUUAUACCUUGCGACAUCU
ex3_54 04349_ x3	ENST0 000036 3497.1	26	8E-10	52	3	TGGACCAATGATGAGATTGGAGGGTGTCTGAATCAAAAATTTTGATTAAGCCATCTG TA
ex3_54 04622_ x3	AL445 624.3/8 0903- 80775	20	2E-06	40.1	3	CUAGCAUUUUCACAGGUCCUCCCUCAGGCUAUGGGGCCAGGAUUUGGUAGCUGG UGCUGAGAGAAAACGCUUGAUUGCAUCCUUGCCUUGGGACUGUGCCAGUGGCAG CUGUCACUCAUUGGGACAAU
ex3_54 04958_ x3	ENST0 000038 4158.1	26	8E-10	52	3	GTCTTCTCATTGAGCTCCTTTCTGTCTATCAGTGGCAGTTTATGGATTTCGCACGAGAA GA
ex3_54 05183_ x3	CM000 682.2/4 927894	21	5E-07	42.1	3	GCTGGTGTAATGATGACTTCACTTTTTTCCCATCAGATCGACAATGCTGACGTCTT ATATTTTGCCAGTTAGTTCTGATACATCGGC

	0- 492790 28						
ex3_54 05762_ x3	ENST0 000045 9584.1	20	2E-06	40.1	3	GGGCTAATGATGGAAAAATCATTATTGGAAAAGAATGACATGAACAAAGGAACCACT GAA	
ex3_54 06020_ x3	CM000 663.2/8 559228	19	1E-05	38.2	3	GAAAATACATGATGATCTCACTCCAACCTGGAACCTCTCTCACTGATTACTTGATAACAA TAAATATCTGATATTCTG	
	0- 855923 56						
ex3_54 06245_ x3	CM000 667.2/1 385590	23	4E-08	46.1	3	GTGCCGTGATGTATTTGTCAACACATCACTCTGAAGAAAAGTATGTGGTGACTTTCTG TGACTGAGCATG	
	39- 138558 970						
ex3_54 07261_ x2	AC007 448.14/ 61996- 61858	24	1E-08	48.1	2	UGCACUGCAUGGCAUCUGCACCCAGCAGUUUACUCUUGCUAAGGUGUUCAAAGGU CAGUGCUAUAGAAUUCAGUAUCUGGCAUCAUUGGUUUUCUUGACUUUGUGCUUG UUAACCUAGUAUUUCUAUUGAUACAGUA	
ex3_54 07571_ x2	AB028 893.1/3 795- 3879	20	2E-06	40.1	2	GCGGCCGGUGAUGAGAACUUCUCCACUCACAUUCGAGUUUCCCGACCAUGAGAU GACUCCACAUGCACUACCAUCUGAGGCCAC	
ex3_54 07589_ x2	AC104 843.3/8 1519- 81640	14	0.009	28.2	2	GCACCCUUUAAGGCUGAUGCAAUGCUUUAAGAGGCCUAACACAGAAGGGUGAAGC CAGUCUCCUUAAAACCCAAAGAAGAGAUUGUAAAACUUCUCUUUGGCUCCUGUCU GGAGUCACAGCU	
ex3_54 08009_ x2	CM000 667.2/1 496959	15	0.004	30.2	2	AAGACTCTACTCTCAGGGCTCATTTCTGTCAATCAATACTAGAGAAGTTTCTCTGAAT GTTTAGAGCACTGGAAACCAACGGAGGAGGCCGGGCATTCTTTCTGAGCATGCAG CCAGCTCATAGTGTTGTTTTGTTGCAGCTGCCGCTTGCCATTGATGATCCTTCTTCTC TTCCTTCAGGGGAGTAAGGAGACGACGCGGTCTTAGTGGT	
	59- 149695 748						
ex3_54 08443_ x2	CM000 672.2/4 995421	20	3E-06	40.1	2	TCCAGCAGTAGTCAGCTGTCTGGACAGAACCATTCTGGGATGGTGTTACACTGCTG GGAGAAGAATGTCTTCTCTTCATCCAGTTGCCTCCATCACTGTTCTGGTGGTGTCTG GCACTGGTGCAAGGCAGAAGTGTGCTTCTTGAGAGTGTGCTGAGCATTACCTTG GCTGCTTGGTTCTAGTCTGGGAGCAGACACA	
	4-						

	499544						
	14						
ex3_54_08831_x2	ENST0_000036_4597.1	14	0.009	28.2	2	GGCGGCCCTTATCACAGCTGCAGCTGCTTCCACATAGCTGCTGCGGTCAAAAAGGA GCCC	
ex3_54_09069_x2	ENST0_000036_5609.1	14	0.009	28.2	2	TCACTGTGATGATGGTTTTTCAACGTTTCCACCAGAAAGATTTTCCTTAGT GT	
ex3_54_09663_x2	ENST0_000045_8892.1	15	0.006	30.2	2	TGGCAACTGTGATGAAAGATTTGGTCTGTATGTAATAGATTTTATTACTAAATGAGGA CA	
ex3_54_09675_x2	AL132_709.5/1_80473-180397	26	8E-10	52	2	UGGAUCAAUGAUGAGUAUGCGUGGGGCAUCUGAAUCAAAUUAUUCUGAUUAUACCC UGUCUGUAUCUCUGAGGUCCAU	
ex3_54_09861_x2	ENST0_000051_6310.1	14	0.008	28.2	2	GTTGGATGAAAATCATCCCGGGCTTTGCCAGTGGCCGCGAGTGCCCAGAGCTTCCA GGGG	
ex3_54_09925_x2	ENST0_000038_4418.1	26	2E-07	44.1	2	GCCCGCCTTGGCCTCCCAAAGTGCTGGGATTCTTACATCGACTGCATAGAAAGAGG AGAG	
ex3_54_10175_x2	AC112_907.7/6_2863-62686	27	2E-10	54	2	ACCUUCUUGUAUAAGCACUGUGCUAAAAUUGCAGACACUAGGACCAUGUCUUGGU UUUUGCAAUAUAGCUAGCAGAGUACACACAAGAAGAAAAGUAACAGCACUAGAUUG UAAAGACUGGGGUGGACCUCUUUCUUAUUGUCCAAUGUCCUUUGUCUUAAGAUUU GGUGCAAUAUCU	
ex3_54_10383_x2	AP000_033.1/3_1795-31930	29	2E-11	58	2	GCAUGGGUUUGGAUUUAUGAUGGGCCCGUCCCCUGGACCUCUCAUAGUACCCC AUGCCAGAGCAAACUGUAGCCCUGAACCAUUGCCUGGCCUCUGUCCCCGUAGGCU GCUGGCACUGAAGUGGGUUGCACAAUA	
ex3_54_10609_x2	CM000_681.2/1_143915_9-114392_75	17	0.000 1	34.2	2	AGCCTCCCAAAGTGCTAAGCCGCCGCGCTTGGCCACGATGATTAGTTTTTATGCAC GTGTGAGAGATACGCCTCCCTTAAACCTTGTTGCGACCTTGGCGCATTACCTGTCTG ATA	
ex3_54_10617_x2	AL132_709.5/1_82043-181969	36	1E-15	71.9	2	UGGACCAGUGAUGAAUAUCAUGGGGUUUCUGAAACAACAUUUUUGAUUAAACCCA UCUGCAACUCUGAGGUCCAU	
ex3_54	CM000	35	6E-15	69.9	2	AAGACTATACTTTCAGGGATCATTCTATAGTTTGTACTAGAGAAGTTTCTCTGAACG	

10853_x2	676.2/8 527193 2- 852720 10					TGTAGAGCACTAAAATGCTA
ex3_54_11467_x2	AC093 462.11/ 145947 -	21	5E-07	42.1	2	UGAGCACUUUCACAGGUCCUCCCUCAGGCUGUGGGGCCAGGAUUUGGUAGCUGG UGCUGAGAGAAAACCUUUGUUGGCAUCCUUGCCCUGGGACUGUGCCAGUGGCAG CUGUCAUUCAAUGGGACAAUU
ex3_54_11513_x2	146075 CM000 663.2/2 857882 2- 285787 49	38	1E-16	75.8	2	ACTGGTCCAGGATGAAACCTAATTTGAGTGGACATCCATGGATGAGAAATGCGGATA TGGGACTGAGACCAGCT
ex3_54_11583_x2	CM000 668.2/2 543528 0- 254354 01	16	0.000 7	32.2	2	ATCCTTTTGTAGTTCATGAGGGTGATGGTTGGGTGTTACGCACGTATGTGAGATGT GCTACCCTCGAACCTTGTTAAAGAAAAAAAAAAGCTAATATTGTATTAGTATATATCTGT GTGACT
ex3_54_12957_x2	AL132 709.5/1 37723- 137652	40	7E-18	79.8	2	UGGAUCGAUGAUGACUACUGGUGGCGUAUGAGUCAUAGACAAUGAAUACGUGUCU GGAACUCUGAGGUCCA
ex3_54_13501_x2	ENST0 000039 1286.1	22	1E-07	44.1	2	GTGCCCTTTTAAGGTTGACCCAGTGCTTTAAGAGGCTAACACAGAAGGGTAAAGTAA GTC
ex3_54_13671_x2	ENST0 000036 4957.1	25	0.000 2	34.2	2	ACTCCAGCCTGGCTGACAGAGTGGGACCCCATCTCAAAAAAAAAAAAAAAAAAATTAAGC TGG
ex3_54_13851_x2	CM000 678.2/6 863035 4- 686302 23	31	2E-05	38.2	2	TGAGATGAGATCATGCCATTGCACTCCAGCCTGGACGACAGAGCGAGACTTCATCTC AAAAAAAAAAAGGATCCTCAGGGCTGCCAACCTTATAGTAGAAGTTGAGGTGGTAG TGGATTTCTCCTACACAA
ex3_54_14627_x2	AL132 709.5/1	22	1E-07	44.1	2	UGGACCAAUGAUGACCACUGGUGGCGUUUGAGUCAUGGACGAUGAAUACUACGU GUCUGAAACUCUGAGGUCCA

x2	68250-168176						
ex3_54	CM000	15	0.004	30.2	2	AAGACTCCTTTCAGGAATCATTCTTTAGTTCCCTACTAGAGAGGCTTCTCTTAACATGT	
14695_	668.2/9					GGAGCGCTGGAAACCACAAAGAGGAGGTGCAGCATTTCAGTTCTAAGTGTGAAGTGG	
x2	279045					ATTCTTGGTGTGGCTGTGCTGCAACTGCCATTTGCTAATGATGACCTTGCTTTTCTTA	
	3-927906					CTTAGAGTAAGACAGAGAGACAGCAGTCAGCCTAAGCGGT	
	65						
ex3_54	ENST0	29	2E-11	58	2	ATGTAATAATGTTTCATCAAATGTCTGACCTGAAATGAGCATGTAGACAAGTTAATTTAA	
15311_	000039					C	
x2	1076.1						
ex3_54	ENST0	14	0.009	28.2	2	CAAATACATGATGATCTCACCTCAGTTTGAACCTCTCTCACTGATCACTTGATGACAAT	
15465_	000036					AA	
x2	5153.1						
ex3_54	ENST0	15	0.002	30.2	2	GTGCACATTGTTACATTGGGAGAAAAGATATTTCTGATGTGATGAATAAATTTTTGGA	
15705_	000051					GA	
x2	6013.1						
ex3_54	CM000	18	0.008	28.2	2	AAGACTATACTTTCAGGAATTGTTTCTGTAGTACATTACTAGAGAATGTCCTCTGAAT	
16847_	685.2/1					GTGCAGAGCACAGAAAATAACAAAATAATAAATTCCAAATCAGCTATCTGAGTA	
x2	509021						
	21-150902						
	235						
ex3_54	ENST0	22	1E-07	44.1	2	GGGCAATGATGTAAAGGTTTTACGACTGACCTTTGTAACATGAAGTTTTCTACACTT	
17493_	000036					GA	
x2	5012.1						
ex3_54	ENST0	18	0.009	28.2	2	GGGTGGTGATGAGAACCTTGTATTCTTCTGAAGAGAGGTGATGACTTAAAAACCATG	
18063_	000036					CTC	
x2	3931.1						
ex3_54	ENST0	46	2E-21	91.7	2	GGATCGATGATGAGTCCCCAAAAAACATTCCTTGGAAAAGCTGAACAAAATGAGT	
18453_	000038					GAA	
x2	4274.1						
ex3_54	CM000	15	0.004	30.2	2	AAGACTATACTTTCAGGGATCATTCTATAGTTCGTCCTACTAGAGAAGTTTCTCTGAAC	
18865_	665.2/1					GTGTAGAGCACTGATGCAGCCAAAAACACATGAAAAATGCTCATCATCACTGGC	
x2	831750						
	07-183174						
	894						
ex3_54	ENST0	14	0.009	28.2	2	TGGACCAGTGATGGTGACTGGTGGTGTGTGAGTCATGCACAGTGAATATCATGTGTC	
19015_	000036					TGG	

x2	3738.1					
ex3_54 20585_ x2	AC068 057.5/6 2929- 63057	15	0.002	30.2	2	CUGAGAAUAUCUUGCUGUUCUGAUUUUGUAAUAGGACAGGCCUAUAAAGAUUGGCU AUUUUAAGGCCACGCACAUGUCCCCAGACUUAUUUCUUUCCCUAGGUCUGUUUU AUAAACUCUGGUAAUAAAC
ex3_54 20709_ x2	ENST0 000036 5032.1	22	2E-07	44.1	2	GCCTGCATTTCGTAAGTGATCACGGGCTGCCCGTGCCTGGTCATTGGTAGTGCAGG CAGA
ex3_54 21799_ x2	CM000 685.2/1 508112 74- 150811 384	18	0.009	28.2	2	AAGACTCTACTTTTCAGGGATCATTCTGTAGTTTGTATTAGAGAAGATTCTCTGAAG GTGTAGAGCATCAAAAATAAAAATAAAATTTTAAAAAGGAAATAGAAAATCTGA
ex3_54 21973_ x2	AF250 841.1/4 124- 4215	28	6E-11	56	2	GGAUCGAUGAUGACCUCAAUACAUGCAUUCUUGGAAAGCUGAACAAAAUGAGUG AAAACUCUAUACCGUCGUCCUCGUCAAACUGAGGUCC
ex3_54 22077_ x2	ENST0 000039 1162.1	30	4E-12	60	2	AGTTGTGGTGGTTTTCTTTTTGGCACATTTGTTAAGTTTTCAAATGGGCCTAACTCTG CC
ex3_54 22787_ x2	AC013 722.8/1 84033- 183920	27	2E-10	54	2	ACUGAGGAAUGAUGACAAGAAAAGGCCGAAUUGCAGUGUCUCCAUCAGCAGUUUG CUCUCCAUGGGCACACGAUGACAAAUAUCCUGAAGCGAACACUAGUCUGACCU CAGU
ex3_54 23065_ x2	AF250 841.1/6 375- 6466	31	1E-12	61.9	2	GGAUCGAUGAUGACUUUUUAUACAUGCAUUCUUGGAAAGCUGAACAAAAUGAGUG AAAACUCUAUACCGUCAUCUUCGUUGAACUGAGGUCC
ex3_54 23559_ x2	ENST0 000038 4765.1	35	5E-15	69.9	2	GACCTCCTGGGATCGCATCTGGAGAGTGCCTAGTATTCTGCCAGCTTCGGAAAGGG AGGG
ex3_54 24695_ x2	CM000 668.2/1 342065 14- 134206 411	15	0.002	30.2	2	ATCCCTTTGTCGTTTATAAGTGTGATGATTGGGTTTTTCATGTTCTGTGTGAGATATG CCTCCTTCAAGCCTTGTTATGATGTCTGCACATTACCTGCCTGTCA
ex3_54 24967_	CM000 663.2/1	15	0.004	30.2	2	AAGACTATACTTTTCAGGGATCATTATATGATTTGTGGCTACAGAAGTTTCTCAGCGT GAGGAGCCCCAGAAACCATGAGGAGGAGACGCAGCATTCTCTGTGGCGCGTGAGG

x2	162786 06- 116278 821					CCAGCTCTTGGTTTTACTTCGCTACAACCTGCATTTGCCATTGGTGATCGTTCTTCTCT CATCTCAGGGAGAGTAGAAGGGAGAGAAGATGCAGCCTGAGTGAT
ex3_54 25441_ x2	CM000 664.2/2 153027 66- 215302 864	14	0.008	28.2	2	ATCCTTTTGCAGTTCATAAGCATGAAGTTTGGGTTTTACATGCATCTGTGAGAAATA CCTTCCTCAAACCCTGTTACAATGGTGGCTCACATCTGTAA
ex3_54 26487_ x2	ENST0 000038 6747.1	37	4E-16	73.8	2	GCTGTTCGTTGATGAGGCTCAGAGTGAGCGCTGGGTACAGCGCCCGAATCGGACAG TGTA
ex3_54 26797_ x2	CM000 675.2/3 242051 6- 324203 90	15	0.005	30.2	2	AATTGGGATCAAAGATGCAGCCGCCTTCCCATTAAAGCAGCACAGACAGCCCAAAGT GACAGTTTTCTGTACAGTTACTCTTCTGTTATCTGTAAGTCTATGACATTTTGGG AAAAACAGCC
ex3_54 27505_ x2	ENST0 000051 7059.1	16	0.000 6	32.2	2	TCAAATGAGCCTGAGCTGACATTGTAGAGGATGTAGATGGCTGAAGAACTGTTTCAG CTG
ex3_54 27525_ x2	AC005 214.1/1 4143- 14018	21	5E-07	42.1	2	AAACCCUGUUCACUUUGCCAAAUGGAUUUGUGUCUUUAUUGCUCAUUAAUUGGG GCAAAGGAAAUUCCUUUUAAAACUCAGGCAAACUGAGUGUUUGUCUUGUAUCCU GUCAGAGGAAAGAAAU
ex3_54 27585_ x2	ENST0 000036 4009.1	21	5E-07	42.1	2	TCACAATGATGAATGGTCCAAAACATTCGCGGTTTCCACCAGAATTCAAGGTGTTGG CAA
ex3_54 27709_ x2	ENST0 000036 4672.1	16	0.001	32.2	2	AAGGCAGCATTGTTGTAGATGATTTGAAAGATTTTAAAGGTATAAGCTCACAAGTGT AG
ex3_54 28301_ x2	ENST0 000051 6006.1	15	0.005	30.2	2	GGATCGATGATGACTATAAAAAAATGGATCTCATCGGAATCTGAACAAAATGAGTGA CC
ex3_54 28433_ x2	CM000 672.2/6 122619 6- 612262	17	0.000 2	34.2	2	AGTGTATGATGACACCTTGGTAATGCTGCAGACTCCTCAGTGTGCAGTGAAGAGGTG AACTTTGAAGAGTCACA

	69						
ex3_54_28729_x2	CM000 663.2/2 868966 5- 286897 94	14	0.008	28.2	2	TGGACATTTATTTTTATTCAGTTTTTTCTCAAGGTGAAGGTAAGTGTGGTAGATGTCC TAGAGAAATATTGTAGCTTTCTGTTCAACCTTTGCAACTAAAAAGCATGGACTGTTCC ACTACTGAGATTT	
ex3_54_29451_x2	ENST0 000040 8473.2	15	0.002	30.2	2	TAGGCGGCTTTCAGGGATCATTCTATAGTCTGCTACTAGAGTACTTTCTGTGAAAGT GT	
ex3_54_30489_x2	CM000 674.2/5 664510 1- 566450 27	22	1E-07	44.1	2	CCTTCTATGATGATTTTATCAAATGACTTTTCGTTCTTCTGAGTTTGTGGAAGCCACAT TTAGGTAAGTACTGAGAAGG	
ex3_54_31049_x2	ENST0 000045 9477.1	15	0.003	30.2	2	CTGCATGTGGAAATGTCTGTTCTTCATTCTTTTAGGAGCAGGAATACATATAGATATA AA	
ex3_54_31075_x2	CM000 665.2/1 560088 80- 156008 801	15	0.003	30.2	2	TAGACTATACTTTTCAGGGATCATTCTACAGTTTGTACTAGAGAAGTTTCTCTGAATG TATAGAGCACCGAAGACAAGC	
ex3_54_31615_x2	AY077 738.1/1 -265	25	3E-09	50.1	2	GGUCAUGAUGAAUGGUAAAAGGUCUGAGUCCUCAGAUCCCCUCCCGGCAUCCCA GUUAUCCCCAGCUGCCUCUCCUCCAUCGCACUUCAGAAGUGCUGCGAUGGGCAG AAGGGCAGCUGACACUCCGUGAUGUCCCUCAUUCUGUGUCCUCCGUGAGCUCA GGGAAGACACUGGUUGGCAUCCAACAGCUUAGUCACAAAGGGAUUUGAUUUGUUGG GAGUGCUGGUAUCUGUGGCUAUGAUCUGCCUUGUUAAGCUGAGACC	
ex3_54_32217_x2	CM000 665.2/1 834538 14- 183453 944	14	0.009	28.2	2	AGGCAGGATCTAGTTACATTGTAGCTGTGAAGTGTGCTGCATTGTCTTTGCCCCCTGCT CAAAATAAACTGTTACCTTTCAAGCCCTGTCTGCCATGGTGCTGTAGCAGCAGGGA TGTTTGGTCTCATAACAT	
ex3_54_32317_x2	ENST0 000051 6449.1	18	0.009	28.2	2	TCCCATCTCTTAAATAAAAAGATTTTTTTTTTTAAGAAGTTGTACATGTGCAATGGCTGC A	
ex3_54	AJ6094	46	2E-21	91.7	2	CUCCAUGUAUCUUUGGGACCUGUCAGCCGUGGCAGUCUCCCUUCCUAGCCAUGG	

32435_x2	78.1/1-124					AAGAGCAUAUCCUUGUUUUAUUGGCAAAGCUGUCACCAUUUAAUUGGUAUCAGAUUCUGACUUGCACAAGU
ex3_54_32591_x2	AC112 497.4/53124	15	0.004	30.2	2	UACCUCCCAGGAUGGCAUCUGGAAGUGGAUAGUAUUCUGCCAGCUUUGGAAACUGGAUGAAAAGCAAUCUGGCAGAGGUACCCAUUUCAUUCCCAGCUUGCUCAGUAGCUGGUGAUUGGAAGAAACUCUGCAACAGUG
ex3_54_32727_x2	AC008 083.23/27997-28128	14	0.009	28.2	2	GGCCUCUCAGUGCCGCUJAAUCACACAGGUCCAGUGUGUGCUUGGUGUCUUUUCUGGGAGGCAGAGGAAGGCUCUCCUAAUCACAACAGACCUGCCCAGAAGGGCCUCUCUAUUUCUAGGAGUAUGAUAGCU
ex3_54_32943_x2	CM000 668.2/51464690-51464765	14	0.008	28.2	2	GTCCTCTGATGACTTCATGTTAGTGCCACCTGTCTGGGCCACGGAGAACCCATGATGGAAGTCTGAGGAA
ex3_54_33091_x2	CM000 676.2/2032326-20323179	28	6E-11	56	2	TGATGGCTGTTCTCTCACTGCTTGAAGCCTTAGGCAGTGGGATTTTATCCATCATAATCAAAAATGGCTTATCTTCACTCAGGGCACCATGAGGATGGGCTGGCTGTCCGTTAGTGCCTTCTGATTTTTGCGGAGTCAAACAATT
ex3_54_33467_x2	ENST0 0000391075.1	15	0.005	30.2	2	GTAGGTGACGACCAATATTTTTTTTACTTTGACTTGATGTCTATTGAAGAAATCTAGCAT
ex3_54_34207_x2	AL132 709.5/152651-152577	35	7E-15	69.9	2	UGGACCAAUGAUGACAAAUACCGGCGUAUGAGUCUUGGAUGAUGAAUAAUACGUGUCUGGAACUCUGAGGUCCAU
ex3_54_35349_x2	ENST0 0000408535.2	32	3E-13	63.9	2	GCGCTGTCTTTGAGCCCCCGCCGAGCTTCTCGTGGCGCCGGGGTCAATCTGCA GCGCT
ex3_54_35655_x2	CM000 679.2/7577955-7578091	21	5E-07	42.1	2	ATCCAAGGTGATTCCCTCTCCAAGGGGACATCAGTGCCTCTCAGGAAAGTAGCAGCTTGGAATAGAATCTGGCATGCCTAAGGCCTTTGGGGAAGTGGGATGCTTATTTCTCTGCCTTCCTTGCTGCCACATGG
ex3_54_36555_x2	ENST0 000039	15	0.005	30.2	2	GTCCTCTGATGACTTCATGTTAGTGCCACCTGTCTGGGCCACGGAGAACCCATGATGGAA

x2	1230.1						
ex3_54 37409_ x2	AL132 709.5/1 67225- 167151	14	0.008	28.2	2	UGAGCCAGUGAUGAAAACUGGUGGCAUAGAAGUCAAGGAUGCUGAAUAAUGUGUG UCUAGAACUCUGAGGUUCA	
ex3_54 38505_ x2	ENST0 000060 7417.1	15	0.004	30.2	2	CAGCATTGTGCAATGGCCTTTGGTTTTTCTTGTAACCAGTTAGGTCTGAAACCAATGC AA	
ex3_54 38555_ x2	ENST0 000038 3906.1	23	5E-08	46.1	2	GCATGGGTTTGGATTTATGACAGGCCCGTCACCCTGGGCCTGTCATAGTACCCCATG CCA	
ex3_54 39005_ x2	ENST0 000045 9623.1	28	6E-11	56	2	TTTTGGTTGAAATATGATGAGTGACAAAATCTTGATTTAAGTGAATGAAAAATTACAA G	
ex3_54 39241_ x2	ENST0 000045 9473.1	29	2E-11	58	2	GGTGAAAATGATGAATTCTGGGGCGCTGATTCATGTGACTTGAAAAATGCCATCCAT TTC	
ex3_54 39803_ x2	ENST0 000038 4107.1	26	8E-10	52	2	TGCCTCATTCTAGAGAATGGGCACTGTTGATCATGGTGTCCAAAAATAGTTAATGTGG CT	
ex3_54 40045_ x2	AK124 098.1/2 478- 2557	21	1E-06	42.1	2	AGCUUAUCAGUGAUGUUGUAAAAUAAAUGUCUGAACAUUAUGAAUGCAGUAUUGA UUUCAGCAUUUAACUGAGAUAAAGCG	
ex3_54 41163_ x2	ENST0 000036 4749.1	22	1E-07	44.1	2	ATCCAAGGTGATTCCCTCTCCAAGGGGAACATCCAGTGCCCCTCTCAGGAAAGTAGC AAC	
ex3_54 41517_ x2	ENST0 000036 3807.1	14	0.008	28.2	2	CTATTATGATGAGATTACGCTCTGTGGTCCGTGTTTCTGAAACACAGGATTTTGTGGA AG	
ex3_54 41635_ x2	ENST0 000036 4027.1	14	0.008	28.2	2	TTTAGGAACAGCCTTTGAGGAAGCCTGTGTTTGTAGGGACATCTGAGAGTGTTGATG AAT	
ex3_54 41789_ x2	ENST0 000036 3922.1	39	3E-17	77.8	2	GCATGGGTTTGGATTTATGATGGGCCCGTCCCCCTGGACCTCTCATAGTACCCCATG CCA	
ex3_54 42331_ x2	CM000 679.2/2 977761	17	0.000 2	34.2	2	CTACAACCAGCTACTGGTTGATCTTACATTTGATCTGGTGTGCAATGGCTGCAACA GCAGCCTCCTTGGTGGTGTTCGAGCCTGTTGCTTGTATGAGTTGCCCTAATGGACC TTGGAGACAGCC	

	297777						
	44						
ex3_54	CM000	14	0.009	28.2	2	GCCCGCCTTGGCCTCCCAAAGTGCTGGGATTCTTACATCGACTGCATAGAAAGAGG	
42489_	683.2/4					AGAGAACATAACCTACCTACCCCGTACATACTTCAGCCCAGGTCTGTGCCTCATCT	
x2	051314					GTAATATGAATGAAGAGACATGG	
	4-						
	405132						
	79						
ex3_54	CM000	23	5E-08	46.1	2	AAGACTATACTTTTCAGGGATCATTCTATAGTTCGTTACTAAAGAAGTTTCTCTGAACG	
42941_	671.2/8					TGTAGAGCACCGGTACAAACAAATG	
x2	837426						
	9-						
	883743						
	52						
ex3_54	CM000	14	0.009	28.2	2	GTCCACTTGTAGTTCATAAGCAACATGATTTGGTTTTTCATGCTGATGTGTGAGATGTG	
43537_	663.2/2					CCTCCCTCAAACCTTGTTACTATGTTGGCACATTACAAGTTTGACA	
x2	229119						
	47-						
	222911						
	844						
ex3_54	CM000	15	0.002	30.2	2	TGCACCTGTTTGAGGAATAAAGGAATTAAACTCCCAAAGAGGACAAATATTAACAA	
44323_	679.2/6					AAATGTATGGACAGACGCAAAAAACAAATCCTCATTGCAACCCAGAATAATTGTT	
x2	935528					TAGTATGATTTTTGACACATATAAGAAGGAGTATT	
	3-						
	693551						
	33						
ex3_54	CM000	15	0.004	30.2	2	TAGACGATACTTTCAAGGATCATTCTATAGTTTGTACTAGAGAAATTGCTCTGAATG	
44541_	680.2/5					TGTAGAGCAGCAGAAATCACAAAGAGGAGGCGCAGCATCCTCCCCTGAGCATGTTG	
x2	695727					CTTCCCTTCAACTGCGCTTTGCCATTACTGATGGTTCTTCTCTTCTCTGCGAGAGTA	
	0-					AGAGGGAGAGGATGCAGTCTGAATGGG	
	569574						
	69						
ex3_54	ENST0	15	0.003	30.2	2	TGCACTTGTGTTTTTGTAACTGTGAACAAAGACTTATAGAGAAGTGCAAAAAATAAA	
44813_	000039					T	
x2	0964.1						
ex3_54	CM000	16	0.001	32.2	2	CTCCTTTTGCGGTTTATAAGCATGATGATTGGGTTTTTCATGTGTGAGATGTGTCTCCC	
44887_	677.2/9					TCAAATCTTTTTATGAAGTAGATGCATTGTCTGTCTGACA	
x2	183537						
	9-						
	918354						

	76						
ex3_54_45655_x2	ENST0000515921.1	15	0.003	30.2	2	CTATCTAGCAAATTTGGTTT	AGAGGGAAAGTTTATAGTAGACTTTGCCAGCTGAAGTTG
ex3_54_45859_x2	CM000672.2/87994695-87994618	15	0.002	30.2	2	CAGTCCAGCCTCTGATGAAGCCTATGTTAGTAGGCACATCTGAGTGGTAATGAATGC	CAGCAGCTCTGATGAAAAAAA
ex3_54_46043_x2	CM000678.2/726951-7726841	24	0.001	32.2	2	AGCACTTGTATGTTTTAACATGTGGACATTTATAGACAGGTTCAAAAAGTCCTCTTGC	AACCCAGAACTCGTTGTTTCAGTATGAGTCTTGATACGTGTAAGAAGGGATTTG
ex3_54_46301_x2	AC116348.3/101703-101837	40	7E-18	79.8	2	GCAUGGGUUUGGAUUUAUGAUGGGCUGGAUJCCCUAGGCCUCUCAUAGUACCCC	AUGCCAGAGCAAACUGUAGCCCCAACCAUUGCCGGGCCUCUAUGCCUGUAGGCUGCUGGCACUGAAGUGGGUUGCACAGUA
ex3_54_47029_x2	ENST0000580726.1	36	2E-15	71.9	2	TCCAGCAGTAGTCAGCTGTCTGGACAGAACCATTCTGGGATCATGTTACACTGCTG	GGA
ex3_54_47921_x2	ENST0000363181.1	44	9E-18	79.8	2	GGTCAATGATGAGCTGACATGTATTCTGAATCTAAAGTTGATTATTAGTACTTTAGTTC	T
ex3_54_48117_x2	AC004125.1/88446-88314	14	0.008	28.2	2	AGCCUCUUUCUAGAUGAGAAUGGGCACUGUCGAUCAUGGUGUCUGAAAAUUGUAA	GUGGCUAAAUUGAAACACAGGUUAUGCUUCCAUAAGAGUAUAUGUAUUGCAGUGGUGACAAUGAGACCUGUAACACUU
ex3_54_48173_x2	ENST0000458800.1	14	0.008	28.2	2	ATTCAGATGCTGAATTTAACTGTTCAACTGCTGAACCACTCAACAGACATGAACGAAA	GC
ex3_54_49933_x2	CM000663.2/11237104-112371107	15	0.006	30.2	2	ATCCTTTTACAGTTCATAAGAGTGATGACTGGGTTTTCACTTTTCATGTGTAAGATGTG	CCTCCCTGAAACCTTGTTACAACATTGGCACATTACCCATCTGATG
ex3_54	ENST0	14	0.009	28.2	2	ACCAAGATTCAAGTCACATTCCGAGTGTCCCGGTGTGCTAGGGCACTTGCAGAGAAT	

50145_	000040					CTG
x2	8166.1					
ex3_54	ENST0	14	0.008	28.2	2	AAGACTATTCTTTCAGGGATCATTTCATGCTTTGCTACTAGAAAGTTTCTCTGAAAGTGT
50491_	000039					A
x2	1296.2					
ex3_54	CM000	22	1E-07	44.1	2	AAGCAGGATTCAGACTACAATATAGCTGTAAAGTGCTGTATTGTCATTCCCCCTGCTC
50947_	663.2/3					AAATTAAGTTGTTTCTTAACATAACCCATCTGCTATTCTGTAGCAGCCAGGGATGCT
x2	641857					TGGTCACATACAT
	8-					
	364184					
	50					
ex3_54	CM000	14	0.009	28.2	2	CTGCCAATATTCTCATTGCTCTGATTTTGTAAATAGTCAGGACAGCCTAACATTTGCT
51195_	670.2/1					ATATTTTTTAAATTTTAAATTTTAAATTTTGTGGGTATAACATTCACTATATTAAGATCAT
x2	314329					GCATGTGCCCCCAAACCTAATTCCTTTCTTAAGTCTAGTTTTATAAATGCTAATGATGA
	55-					AC
	131432					
	776					
ex3_54	CM000	19	0.003	30.2	2	AGCGTGAAGCTGGCTCTTGGTGCTCCTTCACTGAAAATGCCATTTGCCATTGATGAT
51671_	663.2/1					CGCTCTTCCCTTCTCTGGGAGGAT
x2	937319					
	40-					
	193731					
	859					
ex3_54	CM000	30	4E-12	60	2	ATCCTTTTGTAGTTCATAAACATAATGGTTGGGTGTTACGTGCGTGTGTGAAATGTGC
51711_	673.2/5					CACCCTCCAGCCTTGTTACGATGTTGACACATTACCCATCTGACA
x2	732896					
	1-					
	573288					
	59					
ex3_54	KZ208	14	0.008	28.2	2	AAGACGATACTTTCAGGGATCATTCTGTAGTTTGCTACTAGAGAAGTTCCTCTAAAC
52371_	915.1/4					GTGTAGAGAAAAAATGTTAAACAGGAATACATGAAGATCATCAAAGAATGGA
x2	293352					
	-					
	429346					
	2					
ex3_54	BX640	14	0.008	28.2	2	AGGUCACUCAAAGAGGGGCUUGUGGGGCGUGUGAAACCAAGGGGUCUUAACAGUA
52495_	788.1/4					UGACCAAAAACUGAAGUUCUCUAUAGGAUGCUGUAGCACUCAUUGGUGCUAUGUU
x2	49-324					UUCUCAGGAGAUUGA
ex3_54	ENST0	20	2E-06	40.1	2	TGGTCAGGTGGAATAATCCTTATCTGTTTCTCCTTTTGAAGGGCAGATTAGAACATGA
52729_	000036					TA

x2	4940.1						
ex3_54 53469_	ENST0 000040	14	0.008	28.2	2	TCTGAGACTAGAGTCACATCCTGACACGGCTCTTCTCCAATGTGCTGGAGTCCTCAG CAT	
x2	8712.1						
ex3_54 53557_	ENST0 000051	14	0.008	28.2	2	TTTAGTTCCATTAACAAAATCTAAAGTTGATTTATAGGCAGGTACAAAAAATCAATCC T	
x2	6379.1						
ex3_54 54057_	ENST0 000062	32	3E-13	63.9	2	AAAATGATGAGATTCCACTTAATTGGTCCGTGTTTCTGAAACACATGATATTTGTGGA AA	
x2	9629.1						
ex3_54 54849_	ENST0 000041	31	1E-12	61.9	2	TGGACCAATGATGTGAATGGAATGCATCTGAATAAAAATTATGATCAATCAGTTTTTG GA	
x2	0253.1						
ex3_54 55817_	ENST0 000045	33	8E-14	65.9	2	AGTTTGCCATGATGAAATGCATGTTAAGTCCGTGTTTCAGCTGATCAGCCTGATTAAA CA	
x2	9475.1						
ex3_54 56003_	AJ6094 34.1/1-	22	1E-07	44.1	2	ACUGCCCCUAGAGGCGUUGCAGCUGUGGCUGCCGUGUCACAUCUGUGUCAUUAG GUGGCAGAGAUUAGAGAGGCUAUGUCUACGCUCAGCGUUCUGCCCCGUGAACGU UUGAAUGUUUGAUAGUCUCACACU	
x2	132						
ex3_54 56343_	CM000 677.2/2	31	1E-12	61.9	2	GGATCGATGATGAGTCCTCCAAAAAACATTCTTGGAAAAGCTGAACAAAATGAG TGAAACTCATAACCGTCATTCTCATCGGAACTGAGGTCC	
x2	506502						
	6-						
	250651						
	21						
ex3_54 56381_	CM000 667.2/1	14	0.008	28.2	2	AACTTTGCAGTCCATGCACGTGATGATTGGGTGTTTCACACACGTGTGAGGTGTACCC ACCTCGAACCTTGTTATGATCTCAGCACATTACCTACCTGACA	
x2	505436						
	89-						
	150543						
	590						
ex3_54 56931_	CM000 677.2/2	31	1E-12	61.9	2	GGATCGATGATGAGTCCCCTATAAAAAACATTCTTGGAAAAGCTGAACAAAATGAGT GAGAACTCATAACGTCAATTCTCATCGGAACTGAGGTCC	
x2	505147						
	7-						
	250515						
	71						
ex3_54 57649_	AC007 374.6/1	23	0.003	30.2	2	GGGUGUGCUCAGAGCAGGGGGCCCGAAGAAUGCCUCCUCUGUUUACAACACACC CAAUAGGAAUCUGGGGUCAUUGUGACAAGGGACACAGAGCUUGUGACCUCUUAC AAACAAAUGCCCUACACA	
x2	22865-						

	122739						
ex3_54 57719_ x2	AC011 749.2/6 4633- 64502	15	0.004	30.2	2	CUUCCCAUUUAAUUUGCUGGUAAUAAUGAUACAAUGAUUAGAGCAGUUUACUCUUU GGAAAAAAUAAUUAUUGGGCCAUUGUAAAUUGACAUGAAGUAAGUAAUUUUAUAUCA UCUGCAAUGGACUAGAUGUUG	
ex3_54 58357_ x2	CM000 677.2/4 571081 5- 457108 73	15	0.002	30.2	2	AGAGTGCTGGTGGCTGATGAGCCCAGGGCTGCTCTTGCTCACTTTGCTGACAGCAC TCG	
ex3_54 58839_ x2	ENST0 000036 5321.1	15	0.006	30.2	2	GTGAGTGATGAATAGTTCTGTGGCATATGAATCATTAAATTTTGATTAAACCCTAAACTC T	
ex3_54 59471_ x2	ENST0 000036 4642.1	35	5E-15	69.9	2	CCCTGCATTGAAAGTGATCATGAGCTGCCCGTGCCCTGGTCATTGGTAGTGCAGG GAGA	
ex3_54 60679_ x2	CM000 668.2/1 137814 64- 113781 311	15	0.004	30.2	2	AAGACTATACTTCCCAGCATCATTGCTATGGTTCATTAAGTAAAGTTTCTCCAATT TGTAGAGCACTAGGAGCCAGAAGGAGGAGGTGCAGTGTCTCTTTAGTGTGAAG CCAGCTTTGCTCTTCGGGAAGGAATGCAGTCTGAGCGAT	
ex3_54 60813_ x2	CM000 666.2/1 859460 83- 185946 186	14	0.008	28.2	2	ATCCTTTTGGGGTTGATAGGTGTGATGATTGGGTTTCTATGCATGTGTGTGACATGTG TCTCCCTCAAAGCTTGTTACCACATCCGTACAGCACCCATAGGATG	
ex3_54 61131_ x2	CM000 681.2/4 476497 6- 447651 00	14	0.009	28.2	2	ATGAACACTAGTCAAGCTAATTGTGCTCCTCTCCTCCTATGCAGTGGCGGCAAACAG CAGTGCCCTCAGTAGTATACGCAGCCTGCTGCGTGTAGCGGTGGCCTTAAGAGACC TTGGAGATAGCC	
ex3_54 61551_ x2	AP005 857.3/1 35498- 135653	15	0.003	30.2	2	UCUCGUGGUAGUUUUUUUUUGGCACAUUUGUUAAGUUUUCAAUUGGGCCUAACA CUGCCACAUGUAUUUAUACUGGAGUUGGCAAAGGCCUGUGACAAUGAGAUUUCUCU CAAGCCUUUCACGCCUUUCCUCUAUCAGAGAAUUGGCUCCCACAUGU	
ex3_54	KZ208	14	0.009	28.2	2	CTCCTTTTGTAGTTCAGGAGAATGATTTGGTGTGTTTGTGCCTAAGTGTGATATGTGCCT	

61625_x2	908.1/6 6317- 66216					CCCTCTGAACCTTGTTACAGCGCTGGCACATTACCCATCCAACC
ex3_54 61911_x2	CM000 664.2/6 952017 4- 695200 43	20	2E-06	40.1	2	TTCCAAAGTGTTGAGTTCAGTCCAGGGCAGCTTCCCTGTTCTGTTAATTAACCTTTGG GACATTGAAATGGGCTAGGGGAGATGATTGGGTAGAAAGCATTATTTTATTCATTTGC CTCCCAGCCTACAAAA
ex3_54 62011_x2	CM000 680.2/2 181762 4- 218178 28	14	0.009	28.2	2	CCAATGTGTAATATCCTGGGATATCATTTTTTCTAGGCTTTGTCCACATGGCTTAGGG GAGCATAGGGCTCTGCCCCATGATGTACAGTCCCTTTCCTCAGTGTTGGAGATGAAG CTGGGTCTGGTGTTCACATTTTCATTTCTGTAGCTTCTCAGAATCCTGTGGACAGT GACTGGGGAGACAAACCATGCAGGAAATATGT
ex3_54 62507_x2	ENST0 000039 1226.1	14	0.008	28.2	2	AAGACAACGTAAATATATGTATAAAGAGTATCTTCAGGAGACGTAATAATGTAAAAAT CA
ex3_54 62831_x2	ENST0 000040 8784.1	15	0.003	30.2	2	GGCCAGTGATGGTTTTAAAGTAATGGACAGAAGGTTTCTGAAATTCTATTTTGAAGTT
ex3_54 63215_x2	AF067 016.1/5 46-676	14	0.008	28.2	2	UUCCAAAGUGUUGAGUUCAGUCCAGGGCAGCUUCCCUGUUCUGUUAUUAAACUU UGGGACAUUAAAUGGGCUAAGGGAGAUGAUUGGGUAGAAAGUUAUUUAUUCUAUUC AUUUGCCUCCCAGCCUACAAA
ex3_54 63811_x2	ENST0 000039 1308.2	24	1E-08	48.1	2	AAGACTATACTTTTCAGGGATTATTTTCAGATAAACTTCTAGAGTTTCTCTGAACCTGTAG A
ex3_54 63815_x2	AL132 709.5/1 71766- 171695	21	5E-07	42.1	2	UGGACCUAUGAUGAUGACUGGUGGCGUAUGAGUCAUUGACGGUGAAUACAGGUC UGGAAGUCUGAGGUCCAA
ex3_54 63999_x2	CM000 679.2/2 801877 0- 280189 07	19	0.005	30.2	2	TGTCTCATTTTTGTAGATCAGGACACTGGGAGGCTCCCTTTTCTCCTTAGCCATGGCT GGAGGCCAAGTCCAGCCCTCAAGGATCATTGTCAGGACCAACACAAGCTGGACAGC CTTGTTTTCTACCTCAGATGGGA
ex3_54 65147_x2	CM000 680.2/5 607959	14	0.009	28.2	2	CCAACATGGATACCCTGGGAAGTCACTCTCCCCAGGCTCTGTCTAAATGGCATAGGG GAGCATAGGGTCCCATCCCAGGATGTACTGTCTTTGCCACAAGTTAGAGATGAAGC TGGGTCTGGTGTCTGTGCCTGAATATTCCTACAGCTTCTGAGTCTGTGGACAATGA

	4- 560793 94					CAGAGGAGACAGACCATGCAGGAAATTTGT
ex3_54 65933_ x2	ENST0 000060 7595.1	15	0.003	30.2	2	TCCAGCAGTCGTTAGCTCTCCTGGCTAGTGTGATGCCTGTGATGGTGTTCCTACTGTT GGA
ex3_54 66671_ x2	ENST0 000036 3863.1	15	0.004	30.2	2	TGTCAGTGCTGAAACTTTGTCAAGTTATGCTACTGACATGAAGTAATGATACAGTATA TC
ex3_54 68731_ x2	AB061 842.1/1 832- 1898	20	2E-06	40.1	2	UGGCGAUGAGGAGGUACCUAUUGUGUUGAGUAACGGUGAUAAUUUUUAUACGCUAU UCUGAGCCAGCA
ex3_54 68851_ x2	CM000 683.2/3 445623	16	0.001	32.2	2	GGGGTGCCTCAGGGCAGGGGGCTTGAAGAACGGCTCCTCTGTTTACGACACACTC AACAGGGGTGTGAGGTCACAGTGATGAGAGGCCCAAACCTTGTGGCCTCCCCGTGAA CAAATGCCCTACACAT
ex3_54 69843_ x2	7- 344561 10 CM000 672.2/1 214566	15	0.002	30.2	2	ATGCTTTCGTAGTCCGTAGATGTGATGATTGGATCTTCACGCTCGTGTGTGAGATGT GCCTCTCTCCAGCCTTGTTAGGATGTTGGAACATTACCCATCTGACA
ex3_54 70023_ x2	3- 121457 66 CM000 674.2/9 254498	14	0.008	28.2	2	ATTCTCCAAAGCATGATGATTGGGTTTTTCATGCTAATGTGTGAAATGTGCCTCCCTCA AACCTTGTTACGACAAATAAAATTCTCCCCAGGTGATT
ex3_54 70815_ x2	7- 925448 92 CM000 676.2/3 575632	15	0.002	30.2	2	ATGCATCTACTATGTGACAGACCTGGAGCAGTTCCTGTCTGCTGCTAAGGTTTCCAC TACAGATGCAAGAAAACATGTCCTTGTACTTTCTGTCTTTTTTATTGTGGCAGCCAA GGATGAATAGAGGGATACAGGG
ex3_54 72635_ x2	7- 357564 63 ENST0 000060 8459.2	17	0.000 1	34.2	2	TTAGAGGTATTTTCAGTACTCTGGCTTAAGAGCCAATGATGTTTTTATTCAAATGTCT G

ex3_54 76059_ x2	CM000 676.2/9 171513 0- 917149 15	14	0.008	28.2	2	AAAATTATACTTTTCAGCAATCATCTCTATAGTTTGTACTAGAGAAGCTTCTGTGAATG TGTAGAGCACCGGAAACCACAAGGCAAAGGCTCAGCATTCTCTCCTAAGCGCGAAG CTGGCTCCTGGTGTGGTTGGCCGCAACTGCCATTTGCCATTGATGATCATTCTTCT CTTCTGTGGTAGAGGAAGAGGGAGAGAATGCAGTTTGAGTGGT
ex3_54 76323_ x2	CM000 682.2/4 136971 4- 413696 13	14	0.009	28.2	2	AAGACTATACTTTTCAGGGATCATTCTACAGTTCATGACTAGAGAAGTTTCTCTCTGT AGAGCACATTTGGTTGCTGGGATCAGAAACCCATTCAAGCTAGC
ex3_54 77429_ x2	ENST0 000051 6848.1	15	0.002	30.2	2	CTACAACCAGCTACTGGTTGATCTTACATTTGATCTGGTGTGCAATGGCTGCAAACA GCA
ex3_54 80513_ x2	CM000 663.2/1 222127 1- 122211 48	14	0.009	28.2	2	CTAGAAAAATTGAAGATTTGGCCACTCTGGAAACTGCTGAGGGCCCCATGTGTAATG GCTGCAAACAGCTTCCTTTGTTGTGTAGACAGCCTGAGTTTTTCTCTAAGGGACTATG GAGACAGCC
ex3_54 81947_ x2	CM000 678.2/1 229732 3- 122971 97	18	0.008	28.2	2	ATTACTTGAAAATCACTCCCAGGCTTTGGCCATGGCAGCAGGTGAGATTCAAGGCC AGAGCCTCCAGGGCCTCAGCTCACCGCACACTGCCCGTGTGTGGTGGGGAAACC CAGACCCCAACAGGT
ex3_54 83349_ x2	AC020 918.6/1 65518- 165651	14	0.008	28.2	2	GGCCUCCUGGUGCUUACAAGCAGCUGUGUCUUGCAUUGACUGUACAGAAAAAAA GAGAUAGAGUAAACACACCCCGUAUACAACUCAGCCCAGGUCCUGUGCCUUGUCU AUUUUGUGAAUAGGGGGGACAUAG
ex3_54 84167_ x2	CM000 685.2/8 814879 2- 881489 18	14	0.008	28.2	2	GTTGGTTGTGAATAACCCTTGGCTTTGATTGTGGCTGTGGATGAAATTCAGCACCTA CAGCCACCAGTAGCCTTAGCTCACCACCCACTGTCTCAATATCATGGGTAAAACCCA GGCTCTGACAGGC
ex3_54 84451_ x2	ENST0 000036 4339.1	15	0.005	30.2	2	CAGCCCTAAAATGGAAAAATTTAAAATTACTTAGACAATGTGATGTCATCAAAGGAA CC

ex3_54 85725_ x2	AK024 486.1/3 319- 3428	23	4E-08	46.1	2	UGCCCAGUGAUGACACCAUCCUUGCUCCCCGUGCCCCCAGGGGCUAUGGGCGA CACCAUGGCUGCCCCUGGGCUGGGCCAGUGGGGCCAAUGCCCAGGGGCUGAGG GCA
ex3_54 86785_ x2	CM000 669.2/1 290615 31- 129061 634	15	0.005	30.2	2	ATTCTTTTGTAGCTGATAAGCATGATGACTGGAGTTTCACGTGCATGTGTGAGATATA CCTCCCTCCAACCTTGTTACCACATCTGCACATTACCTGCCTGATG
ex3_54 86847_ x2	ENST0 000036 5363.2	14	0.009	28.2	2	GAGATTATACTTTCAGGGATCAATTCTATAGTTTGTACTAGGGAAGTTTCTCTGAAT GC
ex3_54 89479_ x2	CM000 684.2/1 764151 9- 176414 06	14	0.009	28.2	2	ATCCTTTTGC GGTT CATAAAGAACCAAGATGACTGGGTTTCATGCTAATGCATGACAT GTGCCTCCCTCAAATCATGTTGCCTCATGGGCTTATTGGCACATTACCGTCTGAGG
ex3_54 89571_ x2	AC073 149.5/3 8723- 38590	14	0.009	28.2	2	UGUUCUGACAUGGGAAGAGUAGCUUCUGGUUGGUGGAGCCCAUCUCACAUUAGC CAGAGACAAAGCAACACCUUGUUUAUCCCGGCUUGGCUUUUGGCCUGUGUCCAUG ACUGGUCCAUAACCUUGGACACAUGG
ex3_54 90129_ x2	AC099 676.2/7 9107- 79241	21	5E-07	42.1	2	CUGCAGCCAAUUAAGCCGACUGAGUUCUUCUCAUGGGGGCCCAGUGUGCAA UGGCUGUAAAUAGCAGCUUCCUUGGUAGUGUAUGCAGCCUGUUUGUUGUAUGGG UUGCUCUAAGGGACCUUGGAGACAGUC
ex3_54 90759_ x2	AC090 227.10/ 15587- 15444	19	8E-06	38.2	2	CUUUCGGGUCCCCAUUGCAGCCCCCGGAUGAGCCCGCAGUAUUUCCUUAUAUG AUCAGGUCCCAUUGC GGGCGGCGCCGCUUGCCCGGAGCCUGAGAGGUAUAUGAA AACGUGGC GAGCGAAUUGGGGCCAGGGGACCUGGAG
ex3_54 91107_ x2	ENST0 000038 4436.1	21	5E-07	42.1	2	CCGCAGCCAATTAAGCCGACTGAGTTCCTTTCTCATGGGGACCCAGTGTGCGATG GCTG
ex3_54 91125_ x2	ENST0 000051 6131.1	27	2E-10	54	2	GCCAGGTACCATGCAAAAGCAATCTTCCCTTTAGAATGACTGATGGTATGCTAAGGT TTT
ex3_54 91285_ x2	ENST0 000040 8746.2	14	0.009	28.2	2	AAGACTTTATCCCCCACCCCGCAAAGAAAAGGAAGAAGAAGAGTTTTTAAATGGCG CAG

ex3_54 91757_ x2	AL132 709.5/1 28363- 128289	15	0.004	30.2	2	UGAGCAAGCGAUGACAGCCGGUGUGUGAGUCAUGGAGGAUGAAUACUAAGU GCCUGGAACUCUGAGGUUCAA
ex3_54 92699_ x2	CM000 680.2/2 290162 6- 229015 24	15	0.007	30.2	2	GTTCTTTTGTGTTTCATAAAGTAATGATTGTGTTTTCACATTATTGTGTGAGGTGTGCC TCCCTCAGACCTTGATACCAGTCTGCACATTACCTGATGTGAAG
ex3_54 94789_ x2	CM000 686.2/5 714796 5- 571478 90	28	6E-11	56	2	AAGACTATACTTTCAGGGATTATTTCTATAGTTTGTTAATTATTTGTACTAATAGTAGTA ATTGACACTAACTAGT
ex3_54 95535_ x2	ENST0 000036 4699.1	43	1E-19	85.7	2	TGGACCAATGATGACAAATGGTGGCATTGGAGTTATGGACGATGAATGATATGTGTC TGA
ex3_54 96043_ x2	AC104 763.12/ 68286- 68156	15	0.003	30.2	2	UGCCUCUCUCCCAUGGGCUUUGGGGGGUCCUGUUCUCCUAGCCAAGGCUGGA GGCCAAGAGCAGCCCUCGAGGAUCGUCGUCAGGACUGCCACGAGUGGGGCAGCC UUGUUUUCUGCCUCAGACAUGU
ex3_54 96437_ x2	CM000 669.2/2 426171 4- 242616 09	15	0.003	30.2	2	ATCCTTTTGTAGTTTGTAAGTGTGATGATTGGGTTTTTTCACGCTCATGTGTGAGATAT GCCTTCCTTAAAGTTTGTTACATCATCAGCACATTACCCATCTGACA
ex3_54 97001_ x2	AC090 821.13/ 147314 -	16	0.000 9	32.2	2	UGCACUUAUGUAUGUUUUUGUUUAAACUGUGGACAAAGACUUAUGGAUAAGUACA AAAAUAAAUCCUCUUUUGCAACCCAGAACUCAUUGUUCAGUAUGAGUUUUAUAC AUUAAGCCAGGGAAAUU
ex3_54 98959_ x2	CM000 669.2/1 111093 57- 111109 268	14	0.009	28.2	2	ATGCTTTTGTAGTTCGTAAGCATGATGATTGGGTTTTTCTTGCTCTTGTATGAGATGTG CCTCCGTCATACCTTGAAACCTGACTTGA

ex3_54 99153_ x2	ENST0 000040 8528.2	14	0.009	28.2	2	AAGACTCCTTTCAGGAATCATTCTTTAGTTCTACTAGAGAGGCTTCTCTTAACATGT G
ex3_55 00887_ x2	ENST0 000040 8612.1	15	0.003	30.2	2	ACTGGTCCAGGATGAAACCTAATTTGAGTGGACATCCATGGATGAGAAATGCGGATA TGG
ex3_55 01069_ x2	ENST0 000036 2493.1	32	3E-13	63.9	2	AGGCAGGATCTAGTTACATTGTAGCTGTGAAGTGCTGCATTGTCTTTGCCCCCTGCT CAA
ex3_55 01869_ x2	AB017 549.1/4 52-542	18	5E-05	36.2	2	UGCUGGUGGUGAAGCUCUCCUCUCUCCGAGCACUGGGCCCUGCCUGGGGGCUCUCC GGGAGCCAGGGGAGAUGCACCUCCGGAAGCUGAAGCG
ex3_55 02825_ x2	CM000 672.2/2 148563 8- 214857 22	15	0.004	30.2	2	AAGACTGTATTTTCAGAGCTCATTCTGTAGTTCATTACTATGGAAGTTTCTGTAAATA TATAGAGGTCTACAAAACAAAAAAGT
ex3_55 02989_ x2	CM000 674.2/6 476097 3- 647608 68	20	0.000 8	32.2	2	ATCCTTTTGTGGTTCATAAGCCTGATGATTGGGTTTTTCATGCTATTGTGTGAGTTACC ACCCCTACCTCAAACCTTGTTAGGACTCCGCGCATTACCCCTCTGTGT
ex3_55 03441_ x2	CM000 663.2/1 539981 51- 153998 067	15	0.002	30.2	2	TTGACTATACTTTTCAGGGATCATTCTATAGTTCATTACTAGAGAAGTTTCTCAGAATG TATAGAGAAAAAAAAGAATCCACAGA
ex3_55 04457_ x2	AC104 794.4/7 2269- 72155	14	0.008	28.2	2	GUGCCUAAGGUUAACACAGCGCCUUAAGAGGCUAACACAGAAGGGCAAAGUAAGU CUCCAUAAAACCCAGAGAAGACUGUGAACCCUUCUCUGGAUCCUGUCUGGAGUCA CAGCU
ex3_55 05425_ x2	ENST0 000039 1322.1	15	0.003	30.2	2	GTGCCCTTTTAAGGTTGACGCAGTGCTTTAAGGGGCTAACACAGAAGGGTAAAGGAA GTC
ex3_55 05807_ x2	CM000 668.2/9 211942	15	0.003	30.2	2	AAGGCTATACTTTTCAGGAATCATTCTATAGTTTGTACAAGAGAAGTTTCTCTGAATG TGTAGAGCACCAGAAACCACGACGAGGACGAGAAGGCACAGCATTCTTTCTAAATG TGAAGCCAGCTCTTGGTGTGCTTCAACTGCCACTTGCCATTAATGACAGTTCTTCTT

	3- 921196 33					TCCCCTGGGAGAATAAAAAGGAGAGAATGCAGTCCT
ex3_55 06225_ x2	CM000 663.2/9 065775 0- 906579 64	15	0.003	30.2	2	AAGACTATATTTTCAGGGATCATTCTACAGTGCCTACTAGAGAAGTTTCTGTGAAC TTGTAGAGCACCGGAAACCATGAGCAGGAAGTGCAGCGTTCTCTCTGAGCATGAA GCCGGCTCTTGGTGTGGCTTCGCTGCAACTGCCATTGGCCATTGATGATCGTTCTTC TCTTCTCTGGGAGAGTAAGAGAGAGAGGACACAGTCTGAGTGGT
ex3_55 06903_ x2	ENST0 000040 8318.1	14	0.008	28.2	2	GGGGTGTGCTCAGAGCAGGGGGCTGAAGAATGGCTCCTCTGTTTATAACACATGGA ACAG
ex3_55 07449_ x2	ENST0 000038 3910.1	20	2E-06	40.1	2	CTGCAGCCAATTAAGCCGACTGAGTTCCTTTCTCATGGGGGCCAGTGTGCAATG GCTG
ex3_55 08683_ x2	ENST0 000045 9538.1	26	8E-10	52	2	ACCCCTGGCAGCCCCTCCTGATGATTCTTCTTCTGAGCACGCTCATGATGAGCAAA CTG
ex3_55 08837_ x2	ENST0 000058 1572.1	30	1E-09	52	2	TACTCCAGCCTGGATGACAGAGCCAGACTCTGTCTCGAAAAAAAAAAAAAAAAAAG CTT
ex3_55 08845_ x2	CM000 671.2/9 229259 3- 922924 61	30	4E-12	60	2	GCCCTGTGGTTGCTGGATGCTGTTGTGCATGGACAGCTCTCCAGTGGATTTCGATGG GCCATAGCAATCCTGTGATTTATGCATGGAGGCTGCTTCTCCTCAGCAGCTGCCATA GCCCGGTCGCTGGTACATGA
ex3_55 09565_ x2	ENST0 000041 0734.2	15	0.002	30.2	2	AGGACTGTGCTTTCAGAGTTCATGTCCACAGCTCATTGCGGGGGCAGTTTCTCTGAT CGT
ex3_55 09777_ x2	ENST0 000040 8471.1	16	0.001	32.2	2	GGGGTGCCTCAGGGCAGGGGGCTTGAAGAACGGCTCCTCTGTTTACGACACACTC AACA
ex3_55 12381_ x2	ENST0 000036 2913.1	16	0.001	32.2	2	CCGCAGTGACAGCAATATTTTTCATCCACAGTTCACCTCATGAATGTTGTCACTTTGG GT
ex3_55 12585_ x2	ENST0 000038 4084.1	43	1E-19	85.7	2	GGTCTCTCAGCTCCGCTTAACCACACGGGTCCAGTGTGTGCTTGGCGTGTTCAGG GAG
ex3_55	ENST0	14	0.008	28.2	2	ATTCATGTTTTAAAGGCATAATGATGTCACTGACTGGCTGATGAAATCCCAAGCGTA

12805_	000036					GG
x2	5504.1					
ex3_55	CM000	15	0.005	30.2	2	ATCCTTTTCATAGTTCATATGCGTGCTGATTGGGGTTTCATGCTCTGGTGTGAGATGT
13721_	666.2/7					GCTTCCCTCAAGCCTTGTTAAGACATGAGCACATTACCATCTGATA
x2	864010					
	0-					
	786402					
	02					
ex3_55	CM000	34	2E-14	67.9	2	ATGCAGGTACTGTTACAATACTGATGTGTTTTGTTGTCGTTCCCCCTGCTTAAAG
15853_	665.2/1					CACTTGATGCATAACTCTGTCTACCTTCATTCCGTAGTAAGACAGAGACGCTTGGCTT
x2	867863					CAGACAT
	23-					
	186786					
	445					
ex3_55	CM000	14	0.009	28.2	2	ATTCTTTTATGGCTTTTATGGTGCATAAGCATGATGATAGGGTTTTTATGCTCATGTGT
16383_	680.2/3					GAGACACACGTCTCTCAAACCTTATTACGACAACAGTACATTACCTGTATGACT
x2	107249					
	5-					
	310726					
	07					
ex3_55	ENST0	15	0.003	30.2	2	AGACTCCCAGCTCTGCCAGTTACACTAGGCTTCGCCTGTGTGGCTTCTGTAATGGG
16687_	000036					GAG
x2	5647.1					
ex3_55	ENST0	22	4E-05	36.2	2	ATGCATCTATTTGACAGACCTGGAGCAGTTGCTATCTGCTGCTATGGTTTCCACCACA
18681_	000051					GA
x2	7242.1					
ex3_55	CM000	14	0.008	28.2	2	ATCCTTTTGTAGTTCATAAGTGTGATTGGGTATTCAAATGAAGGTGTGAGAGGTGCCA
18779_	676.2/1					CTCTGAAACCTTGTTATGACGTCGGCACATTACCCATATGACA
x2	027895					
	91-					
	102789					
	491					
ex3_55	ENST0	44	3E-20	87.7	2	TCCTCCTACAAAGGCGTGTCTGTGGTTCCTGTCTTTGGACATGTAAGAATTGGAGG
18981_	000057					AAA
x2	8065.1					
ex3_55	ENST0	25	4E-09	50.1	2	GGGGTGTGCTCAGAGCAGGGGGCCTGAAGAATGGCTCCTCTGTTTACAACACACCC
19615_	000040					AACA
x2	8548.1					
ex3_55	AC092	20	2E-06	40.1	2	UUGCACAGUGAACACCCAAGUGUGCUUUUAUAGUUCUUUGGCUUUGACCCUGUGC
19987_	579.3/1					UAGAGCAUUCAUUACCUUGUUCUUCUGCUCUGCAUUGAAAGGAAUUAUUUGUCCUUU

x2	14744-114881					UAAAUGUAUUCAGAAAGCCAGCACAUUA
ex3_55 24439_	ENST0 000045	15	0.002	30.2	2	AAGACTATCCTCTCAGTGATGATTTCTATAGTTCGTTACTAGAGAAGTTTCTCTAAACA T
x2	8938.2					
ex3_55 24883_	ENST0 000036	16	0.000 7	32.2	2	AAGACTATACTTTCAGGGATCATTCTGTAGTTCATTATTAGAGAGGTCTCTCTGAAT GA
x2	4476.2					
ex3_55 25687_	CM000 669.2/9	15	0.002	30.2	2	ATCCTTTTGTAAATTCATGAGTGTGCTTGGGTGTTACATCCATGTGTGAGACATGCCA CTCTCAAACCTTGTCAACAACGTTGGCACATTACCCATGTGACA
x2	941407 8- 994139 78					
ex3_55 25717_	CM000 683.2/3	14	0.008	28.2	2	ACTTTATTGTATATAAGCACTGTGCTAAAATTGCAGGAACTGGGACCATATCCTGATT TTTGTAAATAATGCCAGCAGAGTACACACAAGAAAAGTAACTGCACTAGATTGTGAAGA CTGGGGTGGACCTGCTTCTGAAGGTCCAGTGCCCTTTGTCTTAAGATTTGGTGTAGT GTGT
x2	166430 6- 316644 82					
ex3_55 26691_	CM000 664.2/6	15	0.002	30.2	2	ATCCTTTTGTAGCTTGTAAAGCGTGATGATTGGATGTTTGCAGGAGCGTGTGTGATGT GCCACCTCGCACCTTGCTACAACATCGGCACAGTAGCTGTGTGACA
x2	995564 5- 699557 47					
ex3_55 26737_	CM000 663.2/3	33	8E-14	65.9	2	TCTGGCAATGATGACCCACTTGCCCTCACTGAGAACAAAGTTTCGGTAATGAGAATCT TTGTTAATGGACTCAAGTTCTGAGCCAGA
x2	093577 3- 309356 88					
ex3_55 27279_	CM000 663.2/1	14	0.009	28.2	2	AGGACTTGCCTCATTAGTAATACAACCAAGCTGATAGGGTAGTTTGGCAGGACACAC AGCCATTTCCCTCTCAGCTTAGGAAGGCTGTCATAAGACTAGGACTAGCTCTGCAAG GCAAGAGAAGGACAAT
x2	369619 9- 136960 70					
ex3_55 27355_	CM000 678.2/6	18	8E-05	36.2	2	TAGTGTGGAAGTGTCTACTCCTCATTCTGTGGAAGCAGGAATACATTATAACATGC TCCATTAATAAAGGAGTTCTAGGCCAGGCAGCGTGCCTCATGCCTGG

x2	863096 8- 686308 64					
ex3_55 29171_ x2	AC095 353.9/7 5194- 75323	22	4E-05	36.2	2	CUUCCCAUUUUAUUUGCUGGUUAUAGUCUCACAAUGAUUAUGGCCAGUUUAUACUUAUG GGAAAAAUAUAUUUGGCCAUUCGUUAUUUGACAUGAGUAACUAAUUUUCACCUCU UCUGCAUGGACUAUCUAUUAU
ex3_55 31133_ x2	AC006 534.10/ 104122 -	35	5E-15	69.9	2	CCCUCUACAAAGGCAUGUCUAUAGUUCUUGUCUUUGGACAUGUAAGAAUUGGA GGCAAAGAAAUGUGGACUUGGAGAAAUCUGGGGCCAGCUUGCUCUCCGCAGGCU CAAGAUCAACCAUCCCAUAG
ex3_55 34331_ x2	104252 CM000 672.2/2 840825 1- 284080 39	14	0.009	28.2	2	AGGACTGTGCTTTCAGAGTTCATGTCCACAGCTCATTGCGGGGGCAGTTTCTCTGAT CGTGTGGAGCTGGATGCCAGGAGCAGGACACACTGTGTTCTTTCCTGAGCATGAAG CCAGCTCTCGGAGTTGTTTTGTTGCACCTGCCATTAGGCGTTGATGATGTTCTTTCTT TCCTCCGGTAGGGTAAGAAGGAGAGGACGCAGTCCAAGTGGT
ex3_55 34549_ x2	ENST0 000038 4529.1	42	5E-19	83.8	2	GGATCGATGATGACTTCCATATATACATTCCCTTGGAAGCTGAACAAAATGAGTGAAA AC
ex3_55 34591_ x2	CM000 663.2/2 263161 64- 226316 061	14	0.008	28.2	2	ATCCTTTTGTAGCTCCTGAGCACGATGATTGTGTGTTTCATGCTCATGTGTGAGATGTC CCACCCTTGAACCTTGTTACAACATCGGCATATTACCTGTCTGACA
ex3_55 37033_ x2	ENST0 000051 6069.1	14	0.008	28.2	2	TTATATTAGTGATGGCTTTTAAAGTTCTCACAGACAGGCATCTCTCTGAAAGACAGCG AA
ex3_55 38623_ x2	CM000 677.2/2 508128 7- 250813 78	37	4E-16	73.8	2	GGATCGATGATGACTTCCATATATACATTCCCTTGGAAGCTGAACAAAATGAGTGAAA ACTCTATACCGTCATCCTCGTCAAACCTGAGGTCC
ex3_55 39431_ x2	AC004 830.1/5 8886-	15	0.003	30.2	2	CUAUCAAAAGUUACUUUUUUGUGGGGUGGAAGUUUUUAAAAUAACCUUUACCUACG UGGGCUGUUUUUGAAAAUAAAGAAAAGACCACACUCAGCAGAGGGGCUAUACCCCU UAGUAUAGUUCACCACUAUUUUUGCAGCUUAUUAU

	58743						
ex3_55_39591_x2	KV880 768.1/1 215368	16	0.001	32.2	2	ATCCTTTTGTAAAGATAAGCATAATGATTGGGTTTTTATGTTACATGTTTGATATGC CTCCCTCAAATCCTCTTATGATGTCGGCACATGACCCATCTGAGG	
	- 121547 1						
ex3_55_39893_x2	CM000 677.2/6 945814	14	0.008	28.2	2	AAGAGTATAATTTTCAGGCATCAATTCTGTAGTTCCTTACTAGAGAAGTTTCTCTTAACA TGTACAACACTGGAAACCATGAGGAGGTGGCAGCACAGCATTCTCTGCTGAGCGTG AGGTTGGCTCTTGGTGTGCTTTGCTGCAACTGTCATTTGCCATTGATGATGGTTCTT CTCTTCTCCGAGGGAGAGAATGCAGTCTGAGTGGG	
	9- 694579 41						
ex3_55_39921_x2	AC055 866.19/ 124993	16	0.001	32.2	2	UGCACUUAUGUAUGUUUUUGUUUAACUUGUGGACAAAGACUUAUGGAUAGGUGCA ACAAAUAUCCUCUUUUGCAACCCAGAUCUAUUGUUCAGCAUGAGUUUUGAUAC AUACAGGAAGGGAUUU	
	- 124866						
ex3_55_40979_x2	AJ6094 56.1/1- 134	22	2E-07	44.1	2	UGCAUUCUUAACCCUCUUGGUGGCUUCCUGUAAAUGCUUCCAAGAUUAGAGCG AAUGCUAUAGAAUUGCAGGAAAGUCCAAGGGCUGCGCUGUCUCCUGUGGCUCAG UCUUUUUCAUACCUGCAACAUCU	
ex3_55_41093_x2	AL161 747.5/8 490- 8387	40	7E-18	79.8	2	CCCCUGUGAUGAGUUUGCAUAAUACGGAGACACCAGGUAGGGAGUUUUACCC UAACUUGGGUGUUGUUUGAAUAAACUCUUUCUGUAAAUGCUGAGGGGC	
ex3_55_41363_x2	KN538 363.1/2 21065- 221340	31	1E-12	61.9	2	GGTCGATGATGATTGGTAAAAGGTCTGATTGCACTGAATGTCACGGTCCCTTTGTTG CCCTCAACTCCCAGCAGCCCATTTTTTCCCTCCCGTACATTTAAGTCATGTGTATGG GATCATGGAGCAGCTGATAATTTGGGATTCTGTCAGTGTGTGTTTCTGAGAGTGATC GGCTCACAGCTGACGAGTATCCAACAAAACAGTTACACAGGAGACTGACGAGTGG CAGTCATGGGTGTGATGGTGCATGATCTCAAGTTTTCAATCTGAGACC AGGTCTTGTGGACAAAGACTTACGGACAGGTGCAAAACATAAATCCTCTTCTGCAAC CCAGAACTTATTGTTTCAGTATGAGTTTTGATACATGTAAGAAGGGATATT	
	4- 239721 88						
ex3_55_44117_x2	AL132 709.5/1 38673- 138602	33	8E-14	65.9	2	UGGAUCGAUGAUGACUACCGGUGGCGUAUGAGUCAUAUGUGAUGAAUACGUGUU UGGAACUCUGAGGUCCA	

ex3_55_44655_x2	ENST0000517283.1	19	0.004	30.2	2	ACCTTCTTGTTTAAGCTCTGTACTAAAATTGCAGAACTAGTATCGTGTCTTACCATTG
ex3_55_44725_x2	CM000663.2/26246754-26246847	15	0.005	30.2	2	AAGACTGTATTTTCAGGGATCGTTTCTGTAGTATGTTACTAGAGAAGTTTTCTGAATGTGTAGAGCACCGTTAAGAAAAAGAAAATAAAATGA
ex3_55_45405_x2	CM000664.2/232678963-232679065	14	0.008	28.2	2	ATCCTTTTGCGGTTTCATAATGTGATGACTAGGTTTTTCATGTCCATGTGTGAAGTGCGCCTTCCTCCAATCCTGTTAAGATGTCAGCACATTTGCCTTCTGACA
ex3_55_46693_x2	ENST0000363762.1	32	3E-13	63.9	2	TGGATCAATGATGAGTATGCGTGGGGCATCTGAATCAAATATTCTGATTATACCCTGCT
ex3_55_50007_x2	ENST0000516650.1	15	0.004	30.2	2	CACTCCCCTTTCATTTTACCATTGAGGCTTATGTCTTTATTGGTTGTTCAAGTAGGGCAA
ex3_55_50331_x2	CM000667.2/140527428-140527352	15	0.005	30.2	2	GGTCAATGATGAGCTGACATGTATTCTGAATCTAAAGTTGATTATTAGTACTTTAGTTCTAGAATTACTGAGACATG
ex3_55_51443_x2	CM000667.2/175450816	14	0.009	28.2	2	ATCCTTTTGTGGTTCATAAGCATGATGATTGGGTTTTTCATGCTTATGTGTGTGATGTGCTGCCTTAAACCTTGTTACAGTGTCAGCACGTCACTCATCTGATG
ex3_55_51753_x2	ENST0000364969.1	22	1E-07	44.1	2	TGGACCAATGATGACCACTGGTGGCGTTTGAGTCATGGACGATGAATACTACGTGCTGA
ex3_55_52021_x2	CM000666.2/57106345-	15	0.004	30.2	2	ATCCTTTTGTAGTTCATAAGCATGATGATTGAGTGTTTCATACACATGTGTGAGGTATGTCGCCCCCAAACCTTTTATGACATTGGCACATTACCTGTCTGACA

	571062						
	43						
ex3_55	AJ3118	40	7E-18	79.8	2	GAUCACGGUGAUGGCUGACCAGGGCUCUCCUGACCUAUACAGGCCUCUGCUAUGG	GGGUGAUGGCCAGUCCUGGUGUCUGAGUGAUU
52237_	53.1/1-						
x2	86						
ex3_55	ENST0	33	8E-14	65.9	2	GGATCGATGATGACTTCCATATGTACATTCTTGAAAGCTGAACAAAATGAGTGAAA	AC
52317_	000038						
x2	4430.1						
ex3_55	CM000	33	8E-14	65.9	2	GGATCGATGATGACTTCCATATATACATTCTTGAAAGCTGAACAAAATGAGTGAAA	ACTCTATACCGTCATTCTCGTCGAACTGAGGTCC
52569_	677.2/2						
x2	508014						
	2-						
	250802						
	33						
ex3_55	CM000	33	8E-14	65.9	2	ATCCTTTTGTAAATACATAAGCATAATGATTGGTTTTTATGTTACATGTTTGATATGC	CTCCCTCAAATCCTCTTATGATGTCGGCACATGACCCATCTGAAG
54591_	678.2/2						
x2	953936						
	5-						
	295392						
	62						
ex3_55	ENST0	40	7E-18	79.8	2	GCACCTGAATCTTTCCATTCTTGCTGCCTCGTGCCGGTGTGGGGACAGATGGTG	CTAC
54605_	000036						
x2	4587.1						
ex3_55	AL132	33	8E-14	65.9	2	UGGAUCAAUGAUGACCACUGGUGGCGUAUGAGUCAUAUGUGAUGAAUACGUGUCU	GGAACUCUGAGGUCCAC
56305_	709.5/1						
x2	39624-						
	139553						
ex3_55	ENST0	18	4E-05	36.2	2	CAGTCCAGCCTCTGATGAAGCCTATGTTAGTAGGCACATCTGAGTGGTAATGAATGC	CAG
58303_	000036						
x2	4021.1						
ex3_55	CM000	15	0.004	30.2	2	GTCCTTTTGTAGTTCTTCAGCAGGATGACTGGGTGTTTCATGCTCCTATGTGAGATGT	GCTTTCTCAAACCTCAAACCTTGCTGGCAAGCAGTGAGTCAAGGCTGTTCTGAGT
58697_	664.2/7						
x2	093041						
	5-						
	709303						
	03						
ex3_55	CM000	19	0.003	30.2	2	CTCATACCTAAACCCAAGAATCACTTTCTTATAGTGATGATTTAAACAGATGCAAACA	GCGAGCACATCTTGTACACCTTTGCGGGACTGTGGCTGTGCCCTCGCAGTAAATTTG
58713_	667.2/1						
x2	592301						
	94-						

	159230						
	322						
ex3_55	ENST0	16	0.000	32.2	2	TGTGTATGATGAGATTTCACTTCATGGTCTGTGTTTCTGAAACACATGATGTTGTGGA	
60379_	000045		8			AG	
x2	9604.1						
ex3_55	ENST0	15	0.002	30.2	2	CTTGCCAGCCCCATAGACACAGTTGCTGTGCTGTGCCTGTACTATTGGAGCAAAGAA	
61921_	000036					AAA	
x2	5346.2						
ex3_55	AC012	15	0.006	30.2	2	AUCCAAGGGGAUUCCCUCUCCAAGGGAACAUGCAGUGCCCCUCUCAGGAAAGUAA	
63101_	119.8/9					CAACCUGGAAUAGAAUCUGGCAUGCCUAAGGUCUUUGAGGAAUAGAGGAAUAGAG	
x2	2875-93023					GAUGCUUGUUUCCUCUGCCUUCUUGGCUGCCUACAUGG	
ex3_55	AJ6094	29	2E-11	58	2	UCCUCCUACAAAGGCGUGUCUGUGGUUCCCUGUCUUUGGACACGUAAGAAUUGG	
63185_	74.1/1-132					AGGAAAAUAAAUGUGGAUUUGGGAAACUUUGAGGCCAGCUUGCUUCUUGCAGGCU	
x2						CAUGAUC AACCAUCUCACAUAA	
ex3_55	ENST0	14	0.008	28.2	2	TTTATCAATGGCATGATTTTAAAGCTGTTTCACCCGAGTACACAGCAGGGAAGCCATC	
63751_	000062					CT	
x2	0099.1						
ex3_55	ENST0	21	6E-07	42.1	2	CTTCCCATTTATTTGCTGCTATAGTCTCATAATGATACAAGCAGTTATATGCATGGGAT	
64073_	000038					A	
x2	3922.1						
ex3_55	ENST0	20	2E-06	40.1	2	ATCCTTTTGTAGTTCATGAGCGTGATGATTGGGTGTTTCATACGCTTGTGTGAGATGTG	
64109_	000045					CC	
x2	9299.1						
ex3_55	CM000	15	0.004	30.2	2	TAGAAGTGACTGGAGTTGTTGATGGATGGACAGAGACATCGTGCTGATTGCCATGTT	
65127_	685.2/9					CTGATTGA	
x2	414717						
	0-						
	941472						
	34						
ex3_55	CM000	17	0.000	34.2	2	AAGATTATATTTCCAGGGGTCATTTCTGTGGTTCATTAAGGAGTTTCCCAAG	
65151_	665.2/6		3			TGTGTAGAGCACTGGAAACACAGGAAGATATGCAATGTTCTCTCCCGAGCACGAAG	
x2	085660					CTCGTTCTTGGTGTGCTTCATTGCAACTGCCATTTGCCATTGATCATTGTTTTTTCT	
	5-					TCCTTTGGGGAGATTAAGAGGAAGAGGACACAGTCTGAGTGAT	
	608563						
	89						
ex3_55	CM000	20	2E-06	40.1	2	AAGACTATGCTTTCAGGGATCATTCTATAGTTCGTTACTCGGGAAGTTTCTCTGAAC	
65261_	672.2/8					GTGTAAAGCACCCGAACAAA	
x2	705024						
	6-						

	870503						
	22						
ex3_55	CM000	14	0.009	28.2	2	CCTCCTTTTCTTGTGTCAGGGACTGAGTGTGTGGTCCTGCTCCTGTTATGTATGGAGGC	
65861_	667.2/4					AAAGGGAAAGGGCTCCGGCCCCCTCAAATCATGTCTTTGGTGCCAGCCGGTTCTG	
x2	079020					TTCTCAGTCACCTGGATACTG	
	4-						
	407900						
	71						
ex3_55	ENST0	15	0.004	30.2	2	GGGTCAATGATGAGAACCCTATATTGTGTTGAAGAGAGGTGATGACTTAAATTACCA	
65901_	000036					TG	
x2	4461.1						
ex3_55	ENST0	14	0.009	28.2	2	AAGCTTGTACTCTCAGTGATCATTGCTGTAGTTACGAGATAAGCTTCTCTGAACATGC	
66507_	000040					AG	
x2	8117.2						
ex3_55	CM000	15	0.003	30.2	2	ATTCTTTTGTGGCTCATAAGCTTGGGATTTTACACTAAACATTTTTAACTCATGAGGT	
67595_	667.2/1					TGGGACTTACATTAATCTCTAATCTTTGAGATTGCCTCCCTCAAACCTTGCTACAGT	
x2	227960					ATTGGCACATTACCCATCTCACA	
	88-						
	122796						
	227						
ex3_55	CM000	14	0.009	28.2	2	AAGACTGTACTTTCAGGGATCATTCTGTTGTTTGCTACTAGAGAAGCTTCTCTGAAT	
68037_	670.2/2					GTGTACAGCATGTGGACATGTGTGCACACATG	
x2	878245						
	0-						
	287825						
	39						
ex3_55	ENST0	17	0.000	34.2	2	AAGACTGTACGTTCCAAGATTGTTTCTATAGTTGGTTGTGAGAGAAGTTTCTCTGAAC	
68977_	000039		1			TT	
x2	1065.2						
ex3_55	AC016	49	4E-23	97.6	2	GGUCUCUCAGCUCUGCUUAACCACACGGGUCCAGUGUGUGCUUGGCGUGUUUUC	
69293_	907.6/1					AGGGAGGCAGAGAAAGGCUCUCCUAAUGCACGACAGACCCGCCAGAAUGGCCUC	
x2	86868-					UCUGUUCCUAGGAGUGUGACAAUU	
	187000						
ex3_55	CM000	22	1E-07	44.1	2	ATTCTTTTCGTAGTTTCGTAAGCTGGATTATTGAGTATTCACACACGTGTGTGAGATGTG	
69531_	669.2/1					CCACCCTTGAACCTTGTTACAACGTGGGCACATTATCACTTGACA	
x2	403756						
	66-						
	140375						
	563						
ex3_55	ENST0	16	0.001	32.2	2	CTGATTCAACTATGATTTTTATTTGTTTGACTGATTTTCTTTTGGATAATGAAGGTATC	

69977_	000045					T
x2	9482.1					
ex3_55	AC010	14	0.008	28.2	2	CUACCAAAGUUAAUUUUUUUAUGGGGAAGGCUUUCUAAAUAACCUUUACCAAUUU
70487_	746.8/1					GGGCUAUUUUGGGAGAGUAAAGGAAAGACCACACUCCACAGCGGGCUAUACCAAUA
x2	40334-140470					GUUCACUACUAAUUUGUGGUCUACAUU
ex3_55	AC020	26	1E-09	52	2	UGCACUUAUGUAUGUUUUUGUUUAACUUGUGGACAAAGACUUAUGGAUAGGUGCA
70667_	602.6/1					AAAAUAAAUCCUCUUUUUGCAACCCAGAACUCAUUGUUCAGUAUGAGUUUUGAUAC
x2	36573-136700					AUAUAAGAAGGGAUUU
ex3_55	ENST0	16	0.001	32.2	2	TAGACTTGTGCATGTTTTTGTCTTAACCTTGTGGATAAAGTCTTACAGACAGGTGCAAAA
72471_	000039					AA
x2	1153.1					
ex3_55	CM000	15	0.003	30.2	2	ATCCTTTTGTAGTTCATAAATGTGATAATTGGGTGTTACGTGCATGTATGAGATGTC
73291_	674.2/1					TGAGTCCCTCAAACCTTGTTACAACATTGGTACATTACCCATTTTACC
x2	00402145-100402250					
ex3_55	CM000	16	0.000	32.2	2	TCACATTTTATCAACCAAATGAATTAGGGAAAAAAGTTCATGCCCAGGGGTGAGACTA
74901_	667.2/6		8			TAGTGCCAGAACACTTGCTTGTGCATAATTAAGGCCACTTGCCCTCTTCAGGTAGCC
x2	5961319-65961183					CTTTTAACTGGGAGCAAAGTGA
ex3_55	ENST0	14	0.009	28.2	2	GAGGTACGAGGAAACAGTCTGATAGTCACTGAAGACTGATTAGATCCAACCTCTGATC
78639_	000039					TCA
x2	1191.1					
ex3_55	CM000	19	0.004	30.2	2	ATCCTTTTATAGCTCATAAGTGTGATAACTGGATTTTCACTCTCCTGTGTGAGATGTG
78941_	677.2/6					CTTCCCTCAAACCTTGTTACATCAGCACATTACGTGTCTGATT
x2	5571073-65570973					
ex3_55	CM000	18	0.008	28.2	2	GTCCTTCTGTAGTTCATGAGCGTGAAGATTGGGTGCTCACGGGCACATGTGAAATGT
79689_	664.2/2					GCCACCCTCTGAACCTTGTTACAACATCGGCACATTACCCATCTGACC
x2	22698000-222697896					

ex3_55 80153_ x2	ENST0 000036 2763.1	14	0.009	28.2	2	ATGCAGGTA CTGTTACA ATGACTGA AGTGATTT GTTGTCAT TTCCCCTG CTTAAAG CC
ex3_55 80831_ x2	CM000 675.2/9 521034 4- 952104 48	14	0.009	28.2	2	ATCCTTTT GTAGTTC ATGAGCAT GATAATCG GGGTGTT CACGCACT TGTGTGAG ATGTGCC ACCCTTGA ATTTTGT TATGATG TTTCCACA AATAGCCC ATCTGACA
ex3_55 81971_ x2	CM000 664.2/1 856617 74- 185661 906	14	0.008	28.2	2	TTATCAGCT GGGATAAT CTTTACCT GTTCTTCT TTTTGGAG GGGCAAAT TAGGACAT GATTGGGG TTCACATAG TATGCGATT AACGTCTCT GAGTAATC AGGACTTCC AGTACCCT GATTGTGC CTATCTGAT
ex3_55 83081_ x2	ENST0 000045 9452.1	15	0.004	30.2	2	ATCCTTTT GCAGTTC ATGAACAT GATGATTG GGGTGTT CATGCTCAT GTGTGAG ATGTGCC CC
ex3_55 83991_ x2	CM000 670.2/7 060453 2- 706046 37	16	0.001	32.2	2	ACCCTTTT GTAGTTC ACAAGTGT GATGATTG GGGTTT CACGCTT ATATGTG AGATGTG TCTCTCC CTCAAAC TTTGTTC TGACCTG AGCACCT TACCTGT CATAAA
ex3_55 84183_ x2	ENST0 000036 4773.1	31	1E-12	61.9	2	TTGCATTCT TAAACCCT CTTGGTGG CTTCCCTG TAAATGCT TCCAAGAT ATGAGCGAA TG
ex3_55 84259_ x2	ENST0 000036 4632.1	14	0.008	28.2	2	ATGTGATGC CTCTGATG AAGCCTAT GTTAGTAG AGACATCT GAGAGTGT AGATGAAT GCC
ex3_55 84603_ x2	CM000 666.2/1 683106 92- 168310 795	15	0.004	30.2	2	ATCCTTTT GTAGTTC ATAAATGT GATGATTG GGTTTT CATGTGT ATGTGTTG GATGTGCC CTACTCA ATCCTTG TTACAAAG TTATCTCA TTATCCGG CTGGCA
ex3_55 85011_ x2	ENST0 000058 4451.1	20	0.001	32.2	2	CATGTATA ATGATATA TTGGTAAC ACTGCAG ACTTGGGG AAGCCAG CCAACCT TGGAAT GAT
ex3_55	CM000	15	0.004	30.2	2	ATCTTTT GTAGTTC CTAAGTGT GATGATTG GGGTGTT CACAGGC ATGTGTG AGATGGC

85539_x2	669.2/9 527658 6- 952766 84					CTCCCTCAAACCTTGTTATGACATTGGCATAACCCAAAAAAA
ex3_55_85775_x2	CM000 663.2/2 047279 91- 204728 106	19	0.002	30.2	2	CGCCTTTCTCCCATGGGCTGTGTGGGGTCCCTGTTCTTCGCAGCTAAGGCTGGAGG CCAAGATCAGCCTTTGAGGACTGTCATCAGAATTGCCTTGCTTTCCTGCCTCAGATG TGA
ex3_55_85805_x2	CM000 664.2/1 140056 55- 114005 440	29	4E-09	50.1	2	AAGACTGTAGTTTCAGGGATTGTTTCTATAGTTTGCTACTAGAGAAGTTTCTCTGAAC GTGTAGAGCCCCGAAACCCCGGGTGGTGGTGCAGCATCCTCTCTTGAGGTGAAG CCGGCTTTTGGTGTTCCTCACTGCAACTACCTTTTGCCATGGATGATTGTCCTTCTC CTCCTCTGGCAGAGGGAGAGGGAGAGGACATAAGTCTGAGTGGT
ex3_55_88125_x2	ENST0 000038 4614.1	42	5E-19	83.8	2	TTGCACAGTGAACACCCAAGTGTGCTTTATAGTTCCTTGGCTTTGACCCTGTGCTA GAG
ex3_55_88193_x2	ENST0 000038 4504.1	40	7E-18	79.8	2	TGAGCACTTTCACAGGTCCTCCCTCAGGCTGTGGGGCCAGGATTTGGTAGCTGGTG CTGA
ex3_55_89545_x2	ENST0 000036 4172.1	28	6E-11	56	2	CCCTCCTACAAAGGCATGTCTATAATTCCTTGTCTTTGGACATGTAAGAATTGGAGGG AC
ex3_55_89817_x2	ENST0 000036 5075.1	18	0.009	28.2	2	CTACAGCCAACCTCAGCTGGCTGAGTTCCTCGCCTCATGGGGGACGTGTGCAATGGC TGCA
ex3_55_92301_x2	CM000 672.2/6 017194 - 601705 4	14	0.009	28.2	2	ATGCATCTTAGAACATCCAGGAGACAGTCTTCTAAAATACCAGTGAGTGGCAAGATAT GAGTAAATTCACAGGAAAAGGAAGGCAGTCCAAAGGGCTGTGCTTCTCCTGTGGC TCAGTGTTATTCATAGCTGTGACATCT
ex3_55_93299_x2	AL132 709.5/1 64433- 164362	21	6E-07	42.1	2	UGGAUCAUGAUGUCCACUGGUGGCGUAUAAAUCAUUAUUUGGUGAAUUAUGUCU GGAACUCUGAGGUCCAA
ex3_55	AB007	22	1E-07	44.1	2	GGUCUCUCAGCUCCGCUUAACCACACGGGUCCAGUGUGUCUUGGCGUGUUUUC

93959_	147.1/1					AGGGAGGCAGAGAAAGGCUCUCCUAAUGNACGACAGACCCGCCAGAAUGGCCUC
x2	04-236					UCUGUCCUAGGAGUGCGACAAUU
ex3_55	ENST0	16	0.001	32.2	2	AACATAGAGTACACATTTTCTGTTTTGTTTAAGAATTATTCTCTTGCAGACCTATGTTT
94171_	000057					T
x2	8183.1					
ex3_55	ENST0	15	0.005	30.2	2	AGCGCTGACTCCCACATATGCATTCCTTAGAAAGCTGAACAAAATGAGCAAAAAACC
95249_	000051					TCT
x2	7176.1					
ex3_55	CM000	15	0.002	30.2	2	TTGTGAAGACTATTTTCAAGGTTTCAATTTCTATAGTTCACTACTGGAGAAGTTTCTCTGA
95413_	685.2/1					ACATGTGGAACACCAGGAAACATGAGGAAGAAGCACAGCATTCTCTCTAAATGTGA
x2	139444					AGCCAGCTGTTGGTGTGGCTTTGCTATAACTGCTATTTGCCATTGATGATTATTTTCT
	04-					CTTCTTCCCAGAGAGTAAGAGGGAGAGGATGCAGTCTGTGTGGT
	113944					
	186					
ex3_55	ENST0	20	2E-06	40.1	2	TGGACCAATGATGAGACAGTGTTTATGAACAAAAGATCATGATTAATCCAGTTCTGCA
96869_	000045					CA
x2	8974.1					
ex3_55	ENST0	14	0.008	28.2	2	TATGGCCTTTATCAAAGCTGCAGCTGCTTCCATGTAGCTGCTGTGGTCAAAAAGAAG
97019_	000036					CCA
x2	4674.1					
ex3_55	CM000	15	0.003	30.2	2	ATCCTTTTGTAGTTCGTAAGCATGACGATCGGGTTTTTACATACATGTCTCAGAAGTG
97945_	677.2/4					CCTCTCTCAAACCTTGTTACGTCAGCACATTACCTGTCTTACA
x2	270879					
	2-					
	427086					
	92					
ex3_55	CM000	15	0.002	30.2	2	GCATGGTAGTGGGTTTCAATGGGGGCCCTTCTCTGTGGCCTCATAGCGTACCCATG
98321_	663.2/1					CCAGTGTAACCTTGAGCCTTGAACCATTGCCAGCCTCCTTCCCATGGGCTGTGTGT
x2	156220					AGCGAAGGGGGTTGCACAGTG
	05-					
	115621					
	872					
ex3_55	AC137	28	6E-11	56	2	CUUCCUCAGCCUUACUCCAGGGACUUUUUGUUGCCUGUAAAGUGCUCUGGCAUU
98585_	590.2/6					GCCUGAGGAUAGAUGAGAAAGCACAUAUCCUCCCCAGUAAGACGCUGUUUUCUU
x2	1748-					UUGGGGCCUACAAGUUGAGCUGACAGU
	61613					
ex3_55	CM000	14	0.008	28.2	2	AAGACTATTCTTTTCAAGGATCATTATGCGAGAAGTTTTTCTGAATGCCTAAAGAACCA
98679_	663.2/1					GAAAACCATGAGGACAGACAGCAGCATTCTCTCTGAGCTTGAAGCTGGCTCTTGGC
x2	639236					ACTGGTTTGTGCAACTGCCGTTTGCATTGCTGATCATTTTTCTCTTCTTTGGGAG
	70-					AGTGAGGGGAAGAGAATGCAATCTGAGTGAT

	163923						
	873						
ex3_55	ENST0	14	0.008	28.2	2	AAGACTGTATTTTCAGGGATCATGTCTATAGGTCATTTCTAGAGAAGCTTCTCTGAAC	
99201_	000040					AT	
x2	8706.2						
ex3_55	AC096	18	0.009	28.2	2	GCUAUCCUGGACUUGCCAGCCCAUAGACACAGUUGCUGUGCUGUGCCUGUACU	
99781_	587.1/2					AUUGGAGCAAAGAAAAAGUGGCUAUUUCUAUGCUCAGUGUUCACAAACCAGUGAG	
x2	5864- 25727					CACUAAGAAUGGUUUUAGCCUGACAUUU	
ex3_55	CM000	15	0.003	30.2	2	AAGACTATACTTTTCAGGGATCATTTCTATAGTTTGTTCCTAGAGAAGTTTCTCCGAATG	
99791_	677.2/3					TGTAGAGCACTGCTTAATCTTTTAAATTTAGA	
x2	901581 1- 390159 01						
ex3_55	CM000	15	0.002	30.2	2	ATCCTTTTGTAGTTTCTAAGCGGGATGATTGGGTGTTACGCGCATGCGTGAGATGT	
99849_	681.2/5					GCCTCCCTCAAACCTTGTTACGACATCGGCACATTACTCTTCTGACA	
x2	516717 1- 551672 74						
ex3_56	ENST0	18	0.009	28.2	2	CCTGCCAGCTGCACAGATGCAGATGCTCTGCTATGCCTGTAACATCGGGGCGAAGT	
00125_	000036					GAAA	
x2	2945.2						
ex3_56	ENST0	26	8E-10	52	2	GGTCAATGATGTAATGGCATGTATTAGCTGAATCTAAAGTTGATGTGAGTTCTAAAAT	
01945_	000036					TA	
x2	4617.1						
ex3_56	AC015	19	0.003	30.2	2	GGUUGUGGUGGUUUUCUUUCUGGUACAUUUGUUAAGUUUUCAAAUGAGCCUAAC	
02709_	982.9/4					UCUGCCACAUUAUCAUAUAGGAGCUGGCAAAGGCUUGAUGACAAAGAGAUCUCU	
x2	5601- 45748					CUCAAGCCUUUCCACAUCAGAGGCUGGCUUUCACACAC	
ex3_56	CM000	14	0.009	28.2	2	GCAGACTCACTGTGCACCTGGCTGCAGGCCAGGTGGGTGCTCGTTCCCTCTGCAA	
02851_	677.2/6					GAGAAACAAACATTCCAGGGTGCTGTGGCTGCCTGACCTATAAGGGCGATGCAGCT	
x2	932542 0- 693252 93					GCCTGGGGATAGACAG	
ex3_56	CM000	18	4E-05	36.2	2	CTGCATCCACTGATAGACCTTGGACAGTTTGCTGTTTTTTTTTTGTTTGTGTTTGTGTT	
03237_	664.2/4					GTTTGTGTTTGTGTTGCTCTGGGGATGCAAAAGAGGGAAATCCCTGCACTTCTCTCTG	
x2	827155					TCTTTGTGGCAGCCGGGATTGAATTGGGGAATGCATCT	

	-					
	482700					
	1					
ex3_56	CM000	15	0.002	30.2	2	ATCCAAGGTGATTCCCTCTCCAAGGGGAACATCCAGTGCCCCTCTCAGGAAAGTAGC
03525_	663.2/1					AACCTGGAACAGAATCTGGCATGCCTAAGGCATTTGGGGAACAGGGCTGGTTATTC
x2	792014					CTCTGCCTTCCTTGGCTGCCTACATGG
	87-					
	179201					
	627					
ex3_56	ENST0	15	0.007	30.2	2	CCCTATATTCGAAAGTTATCCTGGTCATTGACAGTGCAGGGAGAGAACTGCTGAAA
03993_	000036					GCA
x2	4523.1					
ex3_56	AC007	25	3E-09	50.1	2	GGCCUCCUGGUACUUACCCACAGGCUGCGUUCUUACACUGGCUGUACAGAAAGAG
05161_	240.2/1					GAGCUAGAGUAAACCUACC UAAUACACCUCAGCCCAGGCCUGUGCCUGGUCU
x2	63812-					GUAUUGUGAAUGGGGGGGACA UAG
	163679					
ex3_56	AC090	15	0.002	30.2	2	UCAUCAGGUGGGAUAAUCCUUACCUUGUCCUUGUUUGGAGGGCAGAUAGAACAG
06081_	233.16/					GAUAAUUGGAGUUUGCAUGAUCCAUGAUUAAUGUCUCUGUGUAAUCAGGACUUGC
x2	1998-					AAACUCUGAUUGUUCAUAUCUGAU
	1865					
ex3_56	CM000	19	0.006	30.2	2	AAGATTATACTTTTCAGGAATCATTTCTATAGTTTGTACTAGAGAAAGTTCTCTGAATG
06365_	665.2/6					TGTAAAGCATGAAAAACCACAAGGAGACACAGTGTCTGCTCCTGACTGAAAAGCCAG
x2	407201					CTCTTGGTGTGCTCTGCTGCAACTGCTATTTGCCATTGATAACCATTCTTCTCTTCC
	9-					TCTGGGATAGTAAGAGGGAGAGACTGCAGTCTGAGTGGT
	640718					
	07					
ex3_56	CM000	15	0.002	30.2	2	TTGATCACAGGACCCCTTTACACTCGTAAATAAATTATTGATGTACCAGACAGCCTGA
07659_	673.2/1					CCCTGACCTCAAGTAAATTCCCAGGAGACGCCTTTCTGGGTTTTGAATTTGCCGTA
x2	290498					ACAGGTGTGAGCATTCTAGCAGCAGTTTGGTGTATCATGTACGATACTGCAAACAGGA
	8-					
	129048					
	17					
ex3_56	AL132	29	2E-11	58	2	UGGAUCGAUGAUGACUACUGGUGGCGUAUGAGUCAUCUACAGUGAAUACGUCUCU
09065_	709.5/1					GGAACUCUGAGGUCUGU
x2	40595-					
	140524					
ex3_56	ENST0	16	0.000	32.2	2	ATGCATCTACTATGTGACAGACCTGGAGCAGTTCCTGTCTGCTGCTAAGGTTCCAC
09219_	000051		9			TAC
x2	7250.1					
ex3_56	CM000	14	0.008	28.2	2	ATACTTTTGTAGCTCATAAGCATGATGATTCAGTGTCCAAGTGCATGCATGAGATGTG

09411_ x2	664.2/2 181850 82- 218184 979					CCTCCCTCAAACCTTGTCAACAACATCAGCACGTTGCTCATCTGACA
ex3_56 10151_ x2	BK005 567.1/2 9-108	47	6E-22	93.7	2	GAUCAAUGAUGAAACUAGCCAAAUCUGAGCAUCAGAAGUCUUUCCAGUCUACCUG AUGCAUGAUCUCUACAGUUCUGAGA
ex3_56 10999_ x2	CM000 679.2/5 024500 4- 502448 96	16	0.001	32.2	2	ATTCTTTTGCTGTTTCGTAAGCATAAGGATCAGGTATTCATGGTCATGTGTAAGACGTG CCTCCCTCAAACCTTGTTACGATGTGGACGTCAGCACATACCCATTTGATG
ex3_56 11493_ x2	CM000 669.2/2 526465 6- 252648 82	14	0.009	28.2	2	GAGATTATACTTTTCAGGGATCAATTCTATAGTTTGTTACTAGGGAAGTTTCTCTGAAT GCGTACAGACCTGCAGAAGAGCAGCAGAACCCATGAGGAGAAGGCCGAGGATGAT CCTGAGCATGAAGCTGGCTCATGGAGTTGCTTTGCTGCTACTGTCACTTGCCATTGA TGATCGTTCTTCTTCTTTGAGAGGAAGAGGGGGAGAAAGCAGTTGGAGTGG T
ex3_56 14629_ x2	CM000 670.2/2 203235 0- 220324 52	15	0.004	30.2	2	AGGCTCTTGTCATTTATAAGTGTGATGATTGGGGTTTCACGCTCGTGTGTAAGGTGT GCCTCCCACAAACCTGGTTACGAGTTGGCACATCACCTGTCTGATG
ex3_56 15069_ x2	CM000 672.2/1 190611 11- 119060 983	17	0.000 3	34.2	2	GTGCACATTTTCATTGTCTTTTTTCTTTATTTCAAGAGAAAAGATATATCTGATGTGCTC AGCAAACCTTTGGAGGTTAATTAGCAGCATGACTAATTTAGCCATTGCTGCCAGTCAC CTTCAAACAAGT
ex3_56 16101_ x2	CM000 663.2/2 057313 52- 205731 221	15	0.002	30.2	2	CTGCAGATATTCTCACTGTTTTGATTTTGTAAATAGTCAGGACAGGCTAACCATTCACT TTATTAAGACCATGCATATATCCCAGAAGTCTTTCTGAGGTCTAGTTTTATAA ATGTTGCTGATAAAC
ex3_56 16697_ x2	CM000 680.2/2	15	0.002	30.2	2	AAGACTATACTTTTCAGGGATCATTCTATAGTTCTTTACTAGAGAAGTTTCTCTGAACA TGTAGAGCACTGTGCCTTAAAAAAGAAAAAAAAAAGGGC

x2	629925						
	5-						
	262991						
	58						
ex3_56	AL132	14	0.008	28.2	2	AAGAUCAAUGAUGACUACUGUUAGUGUAUGAGUUACACAUGAUGAAUACAUGUCU	
17237_	709.5/1					GAAACUCUGAGGUCCAU	
x2	54547-						
	154476						
ex3_56	ENST0	14	0.008	28.2	2	CCCAAAGTGCTGGGATAACCCTTACCTGTTTCTCCTTTGCAGGGCAGATAGAACATG	
18115_	000039					ATA	
x2	0947.2						
ex3_56	CM000	15	0.005	30.2	2	AGTTCCTTGAAGTTAAAGGTTAAGCTTAAGGACTGATTCAAAGGCAGGTGCAAAAA	
18367_	669.2/9					ATAAACCTCTTTTGTAACCCAGAACTCATTTTTCAGTATGAGTTTTGATACATATAAG	
x2	995203					AAGGAAAAGCT	
	3-						
	999521						
	58						
ex3_56	ENST0	15	0.005	30.2	2	CCCCTGTGATGAGTTGCCATGCTAATACGGAGACACCAGGTAGGGAGTTTTACCCTA	
18663_	000036					ACT	
x2	2566.1						
ex3_56	CM000	14	0.008	28.2	2	ATCCTTTTGTAGTTCATAAGCATAATGACTGGGTGCTTACACACATGTGAGATGTGCC	
19971_	674.2/4					ACCCTCAAACCTTGTTACATTGGCACACTATCCATTTGACA	
x2	896083						
	6-						
	489607						
	38						
ex3_56	ENST0	15	0.007	30.2	2	CTGCAACCAATTAAGCCGACCTAGTTCCTTTCTCCTTTGGGGCCTGGTGTTC AATAG	
20705_	000038					CTG	
x2	4492.1						
ex3_56	AL132	21	5E-07	42.1	2	UGGACCAAUGAUGACAACUGCCGGCGUAUGAGUGUUGGGUGAUGAAUAAUACGU	
23903_	709.5/1					GUCUAGAACUCUGAGGUCCAA	
x2	49496-						
	149422						
ex3_56	ENST0	15	0.002	30.2	2	AAACCCCTGTTCACTTTGCCAAATGGATTTGTGTCTTTATTGCTCATT AATTGGGGCA	
24363_	000036					AA	
x2	3365.1						
ex3_56	CM000	19	0.004	30.2	2	AAGACTATACTTTTCAGGGATTATTTTCAGATAAACTTCTAGAGTTTCTCTGAACCTGTAG	
24625_	663.2/2					AGCACCAGAAACCATGAAAAGAGGGTGTAGCATTCTCTCCTGCGTGTGAGGCCGGC	
x2	185418					TCTTGGTGCTACCTCACTGAAACTGCCATTGCCACGGATGATCATTCTTCTTACTC	
	99-					TGAGAGAGAAAAGAGAGAGAGAATACAGTCTGAGTGGT	

	218541						
	690						
ex3_56	CM000	19	2E-05	38.2	2	AAGACTATACTTTTCAGGGATCATTCCCTATAGTTTCATCATTAGAGAAGTTCTCTGAACAT	
24929_	670.2/2					GTAGAGCACCCGAGACAAGAAATAACTAAGATCAGA	
x2	061492						
	6-						
	206148						
	33						
ex3_56	ENST0	14	0.009	28.2	2	ATCCTTTTGTAGTTCATAAGCATGATGATTGGGTTTTTCATGCTTGTGTGTGAGATGTG	
24931_	000045					CT	
x2	9407.1						
ex3_56	ENST0	17	0.000	34.2	2	GACTTCTCACTGAGCTTCTTTCTGTCTGTTGCTGGCAGCTTATGGATTCATATGAGCA	
26035_	000039		2			GA	
x2	1318.1						
ex3_56	ENST0	16	0.000	32.2	2	GGCAGCCATGTCAAATTCAGTGCCTGCCCTGTCTATGGTAGGCACTGGCCCAGAAG	
27255_	000036		6			ACTG	
x2	3786.1						
ex3_56	ENST0	14	0.009	28.2	2	AAGCTAGCCAATGAATCTGCTTACCTAAACATGTTTCTGCAGAAATTTTTATTTTAAAA	
28329_	000036					A	
x2	5413.1						
ex3_56	CM000	14	0.008	28.2	2	TTCTAAAGTGTTGAGTTCAGTCCAGGGTGGATCCCCTGCTCTGTTAATTGAACTGGA	
28449_	664.2/2					ACATTTAAACTGGCTAGGCAAATGCCTACATAGAAAGCATTACTCTTTATTCATCCC	
x2	764216					CAGCCTACAAAA	
	9-						
	276420						
	43						
ex3_56	CM000	19	0.006	30.2	2	ATCCTTTTGTAGTTCAGGTGCATGTGTGAGTTGTGCCTCCCTCAAACCTTGTTACAAA	
30971_	663.2/5					GTCAGCACATTACCTGTCTATCA	
x2	241144						
	2-						
	524115						
	22						
ex3_56	CM000	15	0.002	30.2	1	ATCCTTTATGGTTCATAAATATGATGAATGGGTTTTACGCTGCTGTGTGAGATATAT	
32199_	665.2/4					CTCCTTCAAACCTTATATAATTTATATGTTATAATATAATGACCTTTTTATGATGTCAG	
x1	708860					CATATGAATGACCCAGCTGATA	
	8-						
	470887						
	47						
ex3_56	CM000	15	0.005	30.2	1	AAGACGACGCTTGCAGGGATTGTTTCTATAGCTCACTACCAGATAAGTTTCTCCGAA	
32364_	683.2/2					CATGTAGAGCACCCAGAAACCACATGCAGCGGTGCAGCGCTCTCTCGGGAGCCTGAC	

x1	918063					ACTGGCTCTGGGTGCTGCTTCACTGCAACTTCCATTTGCCATTGAGAACTGTTCCGC
	9-					TCTTCCTCTGGGAAAGTAAGAGAGAGAGGGTGCAATCTGAGGGGT
	291804					
	25					
ex3_56	ENST0	15	0.004	30.2	1	ATATAGTTGGACTCAACACCTCTCTATCAGAAATGGACAGATCCAGATCATGAAGAGA
32445_	000051					TT
x1	6158.1					
ex3_56	CM000	14	0.009	28.2	1	ATCTTTTTGTAGTTCATAAGCTTATGATGACGTAAGTGTGACGACATTGGGTTTTTAC
32719_	685.2/7					GTTTCATGTGTGAGATGTGCCTCCCTCAAGCCTTATTACAATGCCAGTACATTTTTTTT
x1	144064					CCACATCTGATG
	4-					
	714405					
	17					
ex3_56	ENST0	14	0.008	28.2	1	TTGTGGGTATAACATTCACTATATTAAGATCATGCATGTGCCCCAAACCTAATTCTTT
32950_	000051					T
x1	6349.1					
ex3_56	ENST0	14	0.008	28.2	1	GATCGATGATGAAAATAAGCAAGTTTGAGCATCAGAAGACCTTCCAGTCTACTTGATG
33117_	000036					CA
x1	2361.1					
ex3_56	AC079	14	0.008	28.2	1	GUUGAGGUCUAUCCCGAUAGGUCUUUUCUGUAGCCUGCACGUUGUUGGAAAUG
33832_	969.5/1					CCUCAUAGAGUAACUCUGUGAUUUUACUUUACUUACAGGACUAUUGUUACAUCUG
x1	16696-					UGGGAAGGAACCAACAAGACAGUU
	116565					
ex3_56	CM000	14	0.009	28.2	1	AACCAATTGTGCCAGTGGGGCTATGGGTGGCCCTTTTCTCCTCAGTCAGGGCTGG
34785_	677.2/7					AGGCCAAGATCAGCCTTTGAGGATTATCAGGGCTGCCACAAGCTGGGCAGCCTTGT
x1	512166					TTTCCTACCTCAGACATTT
	6-					
	751215					
	36					
ex3_56	ENST0	15	0.002	30.2	1	TCCTGGCTTTAATTTATATGCCTTTTTTCAAATTCTGACTGGTTGCATGATGAATAAAAT
34821_	000062					C
x1	5269.1					
ex3_56	CM000	14	0.009	28.2	1	AAGACTATACTTTGAGGGATCATTCTATAGTTTGTACTGGAGAAGTTTCTCTGAATA
35606_	665.2/3					TGTAGAGCACCACAAATCACGAGGAAAAGCGCAGCATTCTCTCCTGAGCATGAAGC
x1	030453					CAGTTTTCAGTGTTGCTTCGATGTAAGTGCCTTCTGCCCTTGATGATCATTCTTCTCT
	6-					CCTCCCTGGAGAGTAAGAGGGAGAGGAGGCAGTCTGAGTGGT
	303043					
	21					
ex3_56	ENST0	19	2E-05	38.2	1	AAGACTATACTTTGAGGGATCATTCTATAGTTCATTACTAGAGAAGTTTCTCTGAATG
35796_	000036					G

x1	2986.2						
ex3_56_35887_x1	AK096_147.1/2_233-2308	24	1E-08	48.1	1	GCUGUACAUGAUGACAACUGGGCUCUACUGAACUGCCAUGAGGAAACUGCCAUGUCACCCUUCUGACUACAGC	
ex3_56_35905_x1	ENST0_000038_4442.1	15	0.002	30.2	1	GGCTTGCTGGTGCTTACCACAGGCTGAATTCTTACACTGACTATATAGAAAAGGAGGTAG	
ex3_56_36645_x1	ENST0_000040_8876.1	20	3E-06	40.1	1	TGCCCAGTGATGACACCATCCTTGCTCCCCGTGCCCCCAGGGGCTATGGGCGACACCAT	
ex3_56_36980_x1	CM000_666.2/1_118884	14	0.009	28.2	1	TGTCCTTGGCCTGGGTAGAGTGGCACCTAGTTGGTGGTGCCCATATTAGCCAGGGACAAAGCAACCCTTTGTTTCATCCCAGCTTGGCTTTTGTATCTGTACCTATACCTGGTTCTGCCTTAGACACATGG	
	-						
	1119013						
ex3_56_37670_x1	CM000_673.2/6_2854285-62854161	15	0.003	30.2	1	CTCCAATGAGGAGGAAACATCCTGCCTTACCCCTGTTTTAGCCTGGGAACCAGTAATTGTGAACTCACCAGGGTTAACATGAAGAGGGCATGAGAGCTTATTCCATAAGGAATTGTCTGAGACAT	
ex3_56_37908_x1	ENST0_000036_5080.1	32	3E-13	63.9	1	TGGATCAATGATGAGTACCCTGGGGTGTCTGAATCTTGGATTTTGATTAAACCCTATAAC	
ex3_56_38053_x1	ENST0_000051_6035.1	19	0.007	30.2	1	TTTCTATTTTATCTGATTCTTCCTCTATGCACAACTCAGCTTCAGTCATTAGTATCATT	
ex3_56_38182_x1	ADDF0_113389_94.1/3988-3917	14	0.009	28.2	1	UGGGCAUGUGAUGUGACCUUCCUGAGCCUGCAUUCCUCACCUGGAAAUGAUGAGCAGUUACUGAUGCCACA	
ex3_56_38337_x1	CM000_685.2/2_0136135-20136066	33	8E-14	65.9	1	GGGCAATGATGTAAAGGTTTTACGACTGACCTTTGTA ACTATGAAGTTTTCTACTTGACCTGAGCTCA	

ex3_56 38690_ x1	ENST0 000051 7184.1	15	0.003	30.2	1	TGGTTTAAAGCCAACCTCTGGGCTCCCATCAGAAGGAAGGAGATGAATGCTATGACCA AAG
ex3_56 39905_ x1	ENST0 000051 6792.1	16	0.000 5	32.2	1	GAGGAGGTCCATTTTAAAAAGAATAGATTGGAAATGCCTCATAGAGTAACTCTGTG GTT
ex3_56 40134_ x1	CM000 682.2/1 698303 3- 169828 31	14	0.009	28.2	1	AAGATTATATTTTCAGGGATCATTCTATAGTTTGTCACTAGGGAAGTTCCTCTGAATG TGTAGAGCACCAGAAACATGAGGAAGAGGCACAGGGTTCTCTCCTGAGTGTGAAGC TGGCTCTTGGCGCTGCTTTCCTGCAACTGCTATTTGCCATTCGTGATTGTGGAGAGT CAGAGGGAGAGGATGATGCAGTCTGAGTGGT
ex3_56 40464_ x1	ENST0 000036 4977.1	19	1E-05	38.2	1	ACCACCAGTGATGAGTTGAATACTGCCCCAGTCTGATCAACATGCGTGAAAGATATT TTC
ex3_56 41320_ x1	CM000 682.2/3 844808 4- 384482 15	14	0.009	28.2	1	GCCTGCATTTCGTAAGTGATCACGGGCTGCCCGTGTCTGCTCATTGGTAGTGCAGG CAGAGGAAATGCGGGAAAGGTTGCTGTGTTTGGAGGGTCCACATCTTCACCCTCCT GTCCCAGGAGCTTTCCTACA
ex3_56 41715_ x1	CM000 682.2/5 121539 - 512141 7	15	0.003	30.2	1	GTTCCCTTTTAAGGCTGACCCAGTGCTTTAAGAGGCTGATACAGAAGGGTAAAGTTA AGTCTCCACAAAATCCAGGGAAGAGACTGTGAAACTCATCTTAGAACCTTGTATGGA GTCACAGCT
ex3_56 42085_ x1	CM000 685.2/2 013638 5- 201363 06	23	4E-08	46.1	1	GATCAATGATGAAACTAGCCAAATCTGAGCATCAGAAGGCTTTCGGTCTACCTGAT GCATGATCTCTACAGTTCTGAGA
ex3_56 42446_ x1	AC034 186.5/1 19166- 119029	14	0.008	28.2	1	GCUGUCCUGGACCUGCCAGCUGCACAGAUGCAGAUGCUCUGCUAUGCCUGUAAC AUCGGGGCGAAGUGAAAGUGGCUAUUUCUACACUCAGUGUUCAGAAAACACUGAA CAACAAGAAUGGAUAAUAGCCUGACAUUU
ex3_56 42701_ x1	ENST0 000051 7111.1	14	0.008	28.2	1	ATGCATCTATCTGACATGCCTGGAGCAGGTATTGTCTGCTGCTAAAGTTTCCACCAC AGA

ex3_56 43282_ x1	CM000 674.2/1 037210 44- 103720 942	14	0.009	28.2	1	ATCCTTTTGTGGTTCATTAGCTTGATATTGGGTTTTACACTATTCTATGAGATGTGCC TCCCTCAAACCTTGTTACAACATTGACACATTACCCTTCTGATG
ex3_56 43384_ x1	CM000 685.2/4 747560 9- 474757 80	14	0.009	28.2	1	GGCCTCCTGGTGCTTACCACAGGCTGTGTTCTTACACTGACTGTATAGAAAAGAAG TGGGCCTGCCTTCTCTGTTCTTGTACTGACTGTATAGAAAGAGAAGAGCTCCTACCC TATATACACCTCTGCCCAGGCTCTAGTCCTGGTCTGAATTGTGAATGGAGGGACATG G
ex3_56 43477_ x1	ENST0 000038 4458.1	15	0.006	30.2	1	GGTCTCTCAGCTCTGCTTAACCACACGGGTCCAGTGTGTGCTTGGCGTGTTCAGG GAG
ex3_56 44189_ x1	AC005 995.3/2 6676- 26542	33	8E-14	65.9	1	GCAUGGGUUUGGAUUAUGACAGGCCCAUCCCCUGGACCUCUCAUAGUGCCCCA UGCCAGAGCAAACUGUGGCCCCGAACCAUUGCCUGGCUUCUGUACCCGUGGGCC ACUGGCACUGAAGAGGGUUACACAGUG
ex3_56 45549_ x1	CM000 663.2/1 930574 15- 193057 281	14	0.009	28.2	1	TTGCATGTGGTAATGTCTGCTCTTCATTCTTTGGGAGCAGAAATACATCCATAACAC GCTAAATTA AAAAAGGAGTTCTCAGGGCTGCCAACCTTACAGTAGAGGTTGAGTGGT AGTATATTACTCCTACATAA
ex3_56 45900_ x1	ENST0 000036 3660.1	17	0.000 1	34.2	1	GGCAGATGATGTTTGTTCACGATGGTCTTCAGATGCCACGTGGGCACTGCTGAG AAA
ex3_56 46734_ x1	ENST0 000036 4079.1	19	0.006	30.2	1	GGGTCAATGATGAGAACCTGATATTGCCCTGAAGAGAGATGATGACTTAAAAATCAT GTT
ex3_56 46981_ x1	ENST0 000041 1292.1	33	8E-14	65.9	1	TGTGTGTTGGAGGATGAAAGTACGGAGTGATCCATCGGCTAAGTGTCTTGTACAAT GCT
ex3_56 48029_ x1	AJ6094 76.1/1- 135	15	0.002	30.2	1	CUUCCUCAGCCUACUCCAGGGACUUUUGUUGCCUGUAAAGUGCUCUGGCAUUG CCUGAGGAUAGAUGAGAAAGCACAUUCCCUCCCAGUAAGACGCUGUUUUUUUU UGGGGCCUACAAGUUGAGCUGACAGU
ex3_56 48632_ x1	CM000 663.2/1 116961	16	0.001	32.2	1	ATCCTTTTGTATACATTTATGCATGATGATTGGGTTTTTACCATCATATGTGGTGAGAT GTGTCTCCCTCAAACCTTGTTATCACGTCAGCATGTGATCAGTCTGACA

	3- 111695 07						
ex3_56 48720_ x1	ENST0 000036 5028.1	21	5E-07	42.1	1	TTTAGAATGTCAA AATTGATTTTGT AATAGTCAGGACAGGATAAACAGTCGCTATATTA A	
ex3_56 48826_ x1	ENST0 000040 8175.1	20	0.000 5	32.2	1	GGGGTGTGCTCAGAGCAGGGGGCCCGAAGAATGCCTCCTCTGTTTACAACACACCC AATA	
ex3_56 49119_ x1	CM000 663.2/1 565293	19	0.002	30.2	1	ATACTTTTGTAGGTCATAAGCTGAGGATTGGGTTTTTCATGCTCTTGTGTGAGATATGC TTCTCTCAAACCTTCTGACCTGGGCACATTACCCAGCTAATG	
	30- 156529 429						
ex3_56 49345_ x1	CM000 671.2/1 931069	14	0.009	28.2	1	ATCTTCTTATAGTTGATAAGCGTTGATGATTGGATGTTCCACGCACATGTGTGAGATGT GCCTCCTACAACCTTGATGTTGGCATATTACCTGTCTGATG	
	1- 193107 88						
ex3_56 49364_ x1	KZ208 915.1/6 242092	19	0.005	30.2	1	AAGACTGTACTTTTCAGGGGTCATTTCTGTAGTTCATTAATATAGTTTTCTGAGCATGTA GAGCACCAAAAAAAT	
	- 624201 9						
ex3_56 49857_ x1	AC084 794.3/2 15294- 215169	14	0.008	28.2	1	AGAUCAUUUCAAGAGGGGCUCGUGGGGCUAUGAAACCAUGAGCUCUUA AUGCUAU GACCAAAGACUGAAGUUCUCUAUAGGACGCCAUAGCACUCA AUGGUGCUGUUUUC CUGAGGAGACAUAGA	
ex3_56 49868_ x1	CM000 667.2/4 065496	14	0.008	28.2	1	ACGCAGGATTCAGACTAGAATATAGCTGTTAAGTGCTGTGTTGTCATTCTCCCTGCTT AAAATAAAGTTTTTTTTCTTAAC TATACCTGTCTGCTATCTGCTGTAGCAGCCAGGGAT GCTTGGTTTTCATACAT	
	3- 406550 94						
ex3_56 50130_ x1	ENST0 000039 1306.1	14	0.008	28.2	1	TGAAC TTTAAAATGCAAGTTCATAGTTCTTTAAGAGACTAACACAGAAAGCTAAAGTA AT	

ex3_56 50258_ x1	CM000 668.2/1 614844 5- 161483 65	18	7E-05	36.2	1	AAGACTATACTCTCAAGGATCATTTCTATAGTTTGTTACTAAAGAAGTTTCTCTGAATT TGTAGAGCACCGAAATTATTA
ex3_56 50549_ x1	CM000 666.2/5 412320 4- 541231 00	14	0.009	28.2	1	ATCTTTTTTGTAGTTCATAAATGCGATGATTGGGTTTTTCATGTTTATGTGTGAGATGTG CTTCCCTCAAACCTTGTTATGATGTCAGTACGTTATCCATCTGATG
ex3_56 50700_ x1	ENST0 000039 1093.1	15	0.004	30.2	1	TTTACAAGGGAAAAGCAACCCCATTA AAAAGTGGGCAAAGTAAGGTCTTTGGGGAAC AGG
ex3_56 50794_ x1	ENST0 000036 3424.1	16	0.001	32.2	1	TTCCAAAGAATTGAGTTCAGTTC AAGGCAGCTTCCCTGTTCTGTTAACGAACTTTGG GA
ex3_56 51079_ x1	ENST0 000036 4514.1	18	0.009	28.2	1	AGGCAACTCTTAGAAGATGGATAGCTTCTCTTTTGCTGTGGGTGTGGCCACAAAACG TTT
ex3_56 51623_ x1	ENST0 000036 3552.1	14	0.008	28.2	1	GGTCAATGATGTAATGGCATGTATTAGCTGAATCCAAAGTTGAAGTGAATTCTAAAAT TA
ex3_56 52164_ x1	CM000 679.2/4 281844 - 428176 9	14	0.008	28.2	1	AAGACTATCCTTTCAGGGATCATTTCTATAGTTTGTTACTATAGAAGTTTTCTGAAGGT GTAGAGCACCAAAGGAT
ex3_56 52305_ x1	ENST0 000045 8802.1	15	0.002	30.2	1	AGTTTTCTGTGGTTCATAAGCATGATGATTGGGTTTTTCATGCTTATGTGTGAGATGTG CC
ex3_56 52832_ x1	ENST0 000036 2582.1	16	0.000 5	32.2	1	TCTTGTATCCAAAAGTGATCATGGGTTGCCTGTGTCCCGATCATTAAACAGTGCAGGG GTA
ex3_56 52880_ x1	AF250 841.1/1 -91	37	4E-16	73.8	1	GAUCGAUGAUGACUCCAUAUAUACAUUCCUUGGAAAGCUGAACAAAAUGAGUGA AAACUCUAUACUGUCAUCCUCGUCGAACUGAGGUCC
ex3_56	ENST0	21	5E-07	42.1	1	TGTGAGAGTGATGAGTTGCACACTGGTGGAGCCATGGTATCAGGTGATACAGGCAC

52933_	000039					CACT
x1	0833.1					
ex3_56	AC006	15	0.002	30.2	1	GCAGACUCACUCUGCAUCUGACUAUACUUCAGGCGGGUGCUUUUUCUGUCUGC
53218_	549.28/					CAGAUAAACAUUCAGGGUGCUGUGGCCGCCUCACGUAUCCAGAGUGAUGCAGCU
x1	5389-5513					CCCUGGGGACACAGGU
ex3_56	ENST0	15	0.003	30.2	1	GGATCGATGATGACTTAAAGATTTATCTAATTTAAATCTGAACAAAATGAGTGACCAA
53231_	000051					AA
x1	6087.1					
ex3_56	CM000	17	0.000	34.2	1	AAGACTATACTCTCAGGAATCATTCTATAGTTTTTACTAGAGAAATTTCTCTGAACG
53742_	670.2/9		1			TGTAGAGCACTGGAAACCGTGAGGAGAAGCTGCCTTCTCTTCTGAGCATGAAGTGA
x1	735826					GCTCTCAGTGTGCTTCTCTGCAACTGCCATTTGCCATTGATGATCGTTCTTCTCTTC
	5-97358478					CTCTGGGAGAGTAAAAGGGTACAGGATGCAGTCTGAGTAAT
ex3_56	CM000	15	0.004	30.2	1	ATCCTTCTGTAGTTCACAAGCATGATGATTGGGTTTTTACACTTACATGAGATGTGCC
54322_	664.2/4					TCCCCTCAGCCTTGTTACTACATTATCCACCTGATA
x1	423966					
	1-44239568					
ex3_56	CM000	15	0.003	30.2	1	GGTCAAAATGTGTTGACATGTATTACCTGAATTTATTGCTGATGTATAATAACACTTCA
54883_	663.2/2					ACTCTAAAATAATATAGCTTTTTGG
x1	173074					
	71-217307389					
ex3_56	ENST0	22	4E-07	44.1	1	GTGTTCAATGATGATTTCTATTTGTTTGCCTGATTTCTTTTGGATAATGAAGGCATCT
54895_	000045					T
x1	9124.2					
ex3_56	ENST0	20	0.001	32.2	1	CATATCTATTTGACAGACCTGGAGCAGTTACTGTCTGCTGCTAAGGTTTCCACTACAG
54979_	000051					AT
x1	6771.1					
ex3_56	CM000	15	0.005	30.2	1	GTCCTTTTATAGTTGATGAGCATGATGATTGGGTGTTACACGCATGTGTGAAATGTC
56654_	667.2/6					CCACCCTCAAATCTTGTTACAATATTGGCACATTACCCATCTGACA
x1	953926					
	4-69539161					
ex3_56	CM000	28	6E-11	56	1	ATCCTTTTGTAGTTCATGAGTGTGATGATTGTGTGTTTCATACGCTTGTGTGAGATGTG

57671_x1	665.2/4 725062 6- 472505 23					CCACCCTTGAACCTTGTTACGACATTGGCACATTACCCGTCTGATC
ex3_56_58211_x1	CM000 670.2/7 589290 4- 758928 00	15	0.003	30.2	1	ATCCTCTTGCAGTTCATAAGCATGATGATTGGGTTTTTCACACTCCTGTGTGAAATGTA CCTTCCTCAAACCTTTTTATAACATCAGCACATTACCGAACATGAAA
ex3_56_58270_x1	AC073 210.8/1 34490- 134624	26	8E-10	52	1	GCAUGGCUGAAUACUGUGUUCUUUUUAUCAGUAGUUUACACAGCCAGACACCAUGC AAAAGCAGUCUJCCCUIIUAGAAUGACUGAUGGUAUGCUAAGGUUUUUCAUAGCAU AUCAUUUUAAAGGUGAAUACAAAU
ex3_56_58426_x1	ENST0 000036 3418.1	14	0.008	28.2	1	TTTGAGGTCTTTCCCGATGGGACTTTTTCTGTAGGCTGCACATCATTGGAAACGCCTC ATA
ex3_56_58550_x1	CM000 666.2/1 831769 40- 183176 760	14	0.009	28.2	1	AAGTCACGCTTAGCTTCTGCAAGTATTTGTTTTGCAGTATTGAAAACTCCTCCATGA GGAGGGCACAGCGTTCTGCCTGGAGTGTGAGGCCGGTGTGCTTGGCTGCAGCTG CCATTTGCCACTGATGATCATTCTTCTCTTCCCCTGTGAGAGTAAGGAGAGGATGCA GTCTGAGTGGT
ex3_56_59086_x1	CM000 685.2/8 085720 2- 808570 76	16	0.000 6	32.2	1	ATTGGTTGAATATCACCCCTGGCTTTGGCCATGGCCATGGGAGAGATTTGGCACCCA GAGCCTCCAGGGGCCTCAGCTCAATGTGCACTGCCCCATGTGCAGCTGTGAAACCC AGGCCCTGATGGGC
ex3_56_59179_x1	ENST0 000051 6395.1	19	0.002	30.2	1	ATGACCTGTGAAACCAAGGGCTCCTAATGCTATGACCAAAGACTGAAGCTCTCTATG AGA
ex3_56_59207_x1	ENST0 000045 8762.1	15	0.006	30.2	1	TGATGAATTGATGACAGTCATCTTTTGAGAGTGACCCAAAATGAAAAGAATACTCATT GC
ex3_56_59842_x1	ENST0 000041 1362.1	14	0.008	28.2	1	GCCAAATGATGCTTATTTGACTCTGGTGCCTTCAGTGTAAGGATGATTTATAATCTG TC
ex3_56	ENST0	19	0.004	30.2	1	TGTCAAAAATTCCCAATCCTATTTCTGACACTTCATATGAAAGCTGCATGTGCAGTC

60957_	000051					TT
x1	6883.1					
ex3_56	ENST0	36	1E-15	71.9	1	GCATGGGTTTGGATTATGACAGGCCCATCCCCCTGGACCTCTCATAGTGCCCCATGC
61076_	000038					CAG
x1	4488.1					
ex3_56	CM000	15	0.005	30.2	1	ATTCTTTTATAGTTTATAAGTGTGATGATTGAGTTTTTCATGCTCAGGCATGAGATGTGT
61566_	679.2/1					CACCTCAAACCTTGCTAAACATCAGCACAAAGACCAGACG
x1	814655					
	2-					
	181466					
	51					
ex3_56	AL132	37	4E-16	73.8	1	UGGAUCGAUGAUGACUACUGGUGGCGUAUGAGUCUUUUGCGAUGAAUACGUGUC
61933_	709.5/1					UAGAACUCUGAGGUCCGU
x1	35542-					
	135471					
ex3_56	ENST0	14	0.008	28.2	1	CTCCATGTGTCTTTGGAACCTGTCAGCTGTGGCAGTTGCCCTTCCTAGCCATGGAAG
63520_	000038					AGT
x1	4401.1					
ex3_56	ENST0	25	3E-09	50.1	1	AAGAAATGAAGAACTAAAATTGGTCTTAGTATTGAAGTGAAGACACTGAGATCCAAC
64048_	000041					TC
x1	0413.1					
ex3_56	AC068	15	0.004	30.2	1	AUAGUCUGUGGAAAGGCUACUGUGUUGUUGAACUUGCCCAGCUGUGGGUGCAGC
64763_	544.7/1					CAUGUACCAGGCAGCCCAAGCCUGACAUAAGUAAAUUCCCAGGAGAAGUCUUUC
x1	02252-					CUGGGUUUUGAAUUUGCAGUAACAGGUGUAAGCAUUCAGCAGCAGUUUGUUGAU
	102068					CAUGUGAUAUUCAGAAAUGCAA
ex3_56	CM000	15	0.004	30.2	1	GACCTCTCTCATAGGGCTGTAGGGGATCTTTTTTCTCTTCAGCCAGGGTTGGAGG
65899_	673.2/8					CCAAGATGGCCCTTGAGAATCATCATCATGACTGCTGAGAGCTGGGCAGCCTTGTTT
x1	555016					ACCTCCCTTGGGCATTT
	-					
	855514					
	6					
ex3_56	AL121	18	0.009	28.2	1	GGGGUGUGCUCAGAGCAGGGGGCCCGAAGAAUGCCUCCUCUGUUUACAACACAC
66123_	784.5/1					CAAUAGGAAUCUGGGGUCAUUGUGACAAGGGACACAGAGCUUGUGACCUCUCCUA
x1	00385-					CAAACAAUUGCCCUACACAU
	100257					
ex3_56	CM000	14	0.009	28.2	1	ATAAACAAAAGAACACCAATTGTGCTCCTTTCCTCCTGGGGCCCAGTGTGCAATGGC
66952_	665.2/1					TGCAAACAGCTGCCTCCTTGGTAGTATACATGGCCTGTTGCTTGTATGGGTTGGCCT
x1	085745					AAGAAACCTGAGAGACAGCC
	65-					
	108574					

ex3_56 67440_ x1	698 CM000 666.2/8 776858 1- 877684 85	14	0.009	28.2	1	ATCCTTTTGTGGTTTGTAAAGAATGATGACTGTGTTTTACTCAAGATGTGCCTTTCTC AAACCTTATTACCATGTTGGCACATTACCTGTCTGATG
ex3_56 67448_ x1	ENST0 000051 6873.1	14	0.008	28.2	1	ACTCACTGATGAGTAGCTTCTGACTTTCATTCTGAGTTTGCTGAACCCAGATGCCATT CC
ex3_56 67515_ x1	AC009 967.8/2 6053- 26184	14	0.009	28.2	1	GGCUUCCUAGUACUUAACCAUGGUCUGUGUUUCUACGCUGACUGUAUAGAAACAGG AGGCAGAGUAAACCGACCCCACAUAUACCUCAGCCCAGGCCUGUGCUGCGUCUG UAUUGUGAAUCAGGAGACAUGG
ex3_56 68452_ x1	ENST0 000051 6629.1	15	0.002	30.2	1	GAGCAGTTTGGCATATGTTCTGAATCTGAGGTTGATTATTATTCCTTTAGCGCTAGTA TT
ex3_56 69346_ x1	CM000 667.2/5 600062 1- 560005 18	16	0.000 7	32.2	1	ATTCTTTTGTAGTTTATAAGCCTGATGATTGGGTTTTTCATGTGCATGTGTGAGATGTG CCTCCCGCAAACCTTGTTACGACGTTGGCACATTACCCATCTGATG
ex3_56 70017_ x1	CM000 666.2/7 355923 4- 735593 11	14	0.008	28.2	1	AAGAGTATACTTTCAGGGATCATTCTATAGTTTGTTATTAATAGGTGGCTGCTAAAAT GTAGAAACCATTAATAGT
ex3_56 70080_ x1	CM000 674.2/6 265117 5- 626512 78	14	0.009	28.2	1	ATCCTTTTGTAGTTCATAAGCTTGATGTTTGAGTTTTACACTTACGTGTGAAATGTGC CTCCCTAAACCTTGTTACTACGTCAGCACATTACCCATGAGACA
ex3_56 70281_ x1	CM000 675.2/7 258668 0- 725868	14	0.009	28.2	1	TGGCAAGCCTCCAGCGTGCGTGGGTCTGTGGTGATGTGTGCATTCCCTACACTGCTT GCCAGAACAGTATTGAAATAGTGGAGCGTTTTGTCTGCTCCATCCAGAGCAAGGTTA TAGAAATTTTCAGACAATT

ex3_56 70353_ x1	10 CM000 669.2/5 610065 9- 561007 52	14	0.008	28.2	1	ATCCTTTTGTAGTTAAGTGTGATGACAGGGTTTTTCACACTCATGAAGTGTGCCTCCCT CAAAACTGGTTGCATTGACACACTACCCATCTGACA
ex3_56 70476_ x1	CM000 673.2/3 208176 4- 320819 73	15	0.002	30.2	1	AAGACTATACTTTTCAGGGATCATTCTATAGTTCATTACTAAAGAAGTCTATCTGAACA TGTAGAACACATGACACCATAAGGAGGAGGCACAACATTCTCCCTAGAGCCTGAAGC TGGCTCTTGGTGTTCATGACTACAGCAGCCATTTGCCACTGATGACTGTTCTCTTCC AGGAGAATAAGAAGGAGAAGATGCAGTTTTGGGTTGT
ex3_56 70971_ x1	CM000 676.2/4 159446 2- 415945 91	15	0.004	30.2	1	TTTATTTATCTGACAGACCTGCAGCAGTTACTGGATGCTGTTAAAGTTTCCACTACAG ATGCAAGAAAAGTGTCCACACTTTCTGTCTGTCTGATTGTGACAGCTAAGATTAAT CAGGTAGGACAGTA
ex3_56 71061_ x1	CM000 673.2/4 675887 3- 467587 66	14	0.009	28.2	1	TATAAATGTGATGAATTGCACACTCGCAGAGTCATAGCATTAGGGGATGCAGGCAGT GTTTCATACTTTCCCGAGGAAAGAAATGCACAGGTGCCACTCAGTCATCAC
ex3_56 71243_ x1	CM000 663.2/2 263042 62- 226304 363	15	0.006	30.2	1	ACCCTTCTTAGTTCATAAGCATGATGATTGGGTTTTTCATACTCATGTGTGAGATGTGT CTCTCTCAAACCTTTGTGAAAAGTCAGCACATGACCCATCTGATG
ex3_56 71539_ x1	ENST0 000051 7180.1	15	0.004	30.2	1	TTGCAGATGCAAGAAAAAAGTGTCCCTCATGCTTTCTTTCTGATGGTGGCAGCTGAGA CTG
ex3_56 71644_ x1	CM000 665.2/9 887218 0- 988720 83	16	0.000 6	32.2	1	AAGACTATACTTTTCAGAGATCACTTCTGTAGTTTATTATTAGAAAAGTTTCTCTGAATGT GTAGAACAAGTGGAAAAAATGATCTAAGACTACTGTGAAT

ex3_56 71648_ x1	CM000 665.2/1 729752 42- 172975 142	16	0.000 8	32.2	1	ACCATGTTGTGGTTCACAAGCATGATAACTCTGTTTTTACGCTCACATGTGAGACATG CCTCCTTCCAATCTTGTTATGTCAGCACATTATCCATCTGATG
ex3_56 72498_ x1	CM000 664.2/1 045327 73- 104532 985	14	0.009	28.2	1	AAGACTATTCTTCTAGGGATCTTTTCTATAGTTCAGTACCAGAGATGGTTCTCTGACA GTGTGGAGCACCAGAAACCATGAGAAGGAGGCACAGCAATCTCTCCTGAGCATGGA GCCTGCTCTTGGTGTTGTTTTGCTGCAGCTGCTGTTTGCCATTGATGATCGTTCTCTT CTTTCAGGAGAGTAAGAAGGCGAGGATGCAGTCTGAGTGGT
ex3_56 73688_ x1	CM000 669.2/1 368411 96- 136841 093	15	0.003	30.2	1	ATCATTTTGCAGCTTATACATGTGATGACTGGGTTTTTTAACTCATAAGTGAGATGTG CCTTTCTTACATCTTATTATGACATTAGTACATTACCCATTTGATA
ex3_56 74144_ x1	CM000 668.2/3 820727 4- 382073 45	15	0.004	30.2	1	GGTCAATGATGTAATGGCATGTATTAGCTGAATCCAGAGTTGATATGAGTTCTAAAAT TACACTGAAGCTGG
ex3_56 74161_ x1	CM000 663.2/3 531027 4- 353104 25	15	0.004	30.2	1	AAGGCAGCATTGTTGTAGATGATTTGAAAGATTTTAAAAGGTATAAGCTCACAAAGTGT AGGTAGTGTGCTACATGAGGGGCAAGTTTTTCACTAATATTACAAGGGTCTCTGATC CAGTGAGTGGAGTTTGATAGTAATTTTTGATACAAGT
ex3_56 74217_ x1	CM000 670.2/7 181562 5- 718154 94	14	0.009	28.2	1	TCCACAGGTGAGATCATCCTTACCTGTTCTTCTTTTGGAGGGCAGAGTTCACGATG ACTAGAGTTTACATGATATGTGATTAATTCTCTGCATAATCAGGATTTGCAACATTCTG TTTGCTCCTACCTGAT
ex3_56 74371_ x1	BC036 582.1/1 156- 1210	18	5E-05	36.2	1	GGGGUGAUGAAGGCCUGCACCUGGUCCCCUCCCCAACUCUGCUCUGCUCCUGAA G

ex3_56 74630_ x1	CM000 680.2/3 025567 - 302543 4	14	0.009	28.2	1	ATCCCATCTCTTAAATAAAAAGATTTTTTTTTTTAAGAAGTTGTACATGTGCAATGGCTG CAAACAGCAGCTTCCTTGGCAGTGTGTGCAGCCTGTTTCTTGTATGGGTTGCTCTAA GGGACCTTGGAGACAGGC
ex3_56 76479_ x1	ENST0 000036 3791.1	22	7E-05	36.2	1	AGGTTGATGATGACTTACATATATACGTTTTTTTTTTTTTTTTTTGGAAAGGTGAACAAAA T
ex3_56 76933_ x1	ENST0 000036 5519.1	14	0.008	28.2	1	TAGAAGCCAATTAAGCCAAGTGGTGTGCCATGG CTG
ex3_56 77417_ x1	ENST0 000038 4533.1	15	0.003	30.2	1	GGATCGATGATGACTTTTCATACATGCATTCCTTGGAAAGCTGAACAAAATGAGTGAAA AC
ex3_56 77735_ x1	CM000 664.2/8 634719 5- 863470 62	25	7E-07	42.1	1	TCATCAGGTGGGATAATTCTTACCTGTTTCTCCTTTTGGAGGGCAGGAAGAATAGGC TGATTGGAGATGCATGAAATGTGGTTAATGTCTCTGCGTAATCAGGACTTGCAACAC CCCGATTACTCCTTTCTGAT
ex3_56 77790_ x1	CM000 669.2/1 381761 54- 138176 282	15	0.002	30.2	1	ATCTTTTTGTAATTCCTAAGCATGATGGTTGATTCGGCTCTCACACTTGATGATTGGG CTTTCACCTGGATCTGTGAGATGTGCCTCCCTCAACCCTTCTGCGAAGTCAGCACA TTACCTGACAGAAA
ex3_56 77873_ x1	CM000 685.2/7 272633 7- 727261 22	15	0.008	30.2	1	AGGGCTATACTTTCAGGGGTAATTTCTATAGTTCATTAAGTGTGTTCTCTGAAT GTGTAGGGTGCCAGAAACCACAAGGAGGAGGCACAGCATTCTCTAGTGAGTGTGAA GCCGGCTGTTGGTGTGCTTCGCTGAAACTGCCATTTGCCACTGATAATCGTTCCTC TTTTCCATCAGGAGACTAAGAGGTAGAAAACGCAGTCTGAGTGGT
ex3_56 78039_ x1	ENST0 000036 4166.1	21	1E-06	42.1	1	TGGACTGTTGATGACAAGTGGTGGCTTATGTGGTTGTACATGCTGGTTGTATATGAA GAA
ex3_56 78304_ x1	CM000 671.2/6 235828 5-	15	0.004	30.2	1	CTACAATCAATTAAGCCACATGGGGCCTGGTGTGCAAGGGCTGCAAACAGCATCATC CTAGGTAGTGTACAGCAGCCTGTTCCCTTGCGTACAACA

	623581						
	91						
ex3_56	CM000	14	0.009	28.2	1	TTGTCCTGGCCTATGCTTTTTCTACTCCCCTCTGCTTTTTTGGTCCCCCTGTGCTCAG	
80225_	673.2/1					TTCTAACAAGGTAGTCTGGCAGGACACACAGCAGTCTCCTTCAGTTTAGGAGGACTG	
x1	172637					TCTTTAGAATAGAGCTGTCCCAAGGCACAAGATTACAAT	
	99-						
	117263						
	952						
ex3_56	ENST0	14	0.009	28.2	1	GCTGTCCTGGACCTGCCAGCACACAGACACAGTTGCTCCTGCGTGCCTGTAACAC	
80949_	000051					CGGG	
x1	7240.1						
ex3_56	CM000	15	0.004	30.2	1	AAGACTATACTTTTCAGGGATCATTCTATAGTTCATTACTAGAGAAGTTTCTCTGAAG	
81249_	684.2/2					GTGTAGAGCACCCCTC	
x1	094664						
	5-						
	209467						
	18						
ex3_56	CM000	17	0.000	34.2	1	AATCAATGATGAAACCTATCCCAAAGCTGATGACCTGAAGAAAATACGTACAGATTC	
82184_	674.2/1		2			AGCTTCTGAGAT	
x1	104964						
	21-						
	110496						
	352						
ex3_56	CM000	15	0.002	30.2	1	AAGACTTTACTTTTCAGGGGTCATTTCTATAGTTTGTTTCAGAAGTTTCTCTGAATGTGTA	
82546_	669.2/9					GAGCAAAAAGT	
x1	838982						
	4-						
	983897						
	55						
ex3_56	CM000	15	0.004	30.2	1	ATTATTTTGTGGTTCATAAATGTGAAACACACTTACAGTTTTTCATGCTCATGTGTGAG	
82644_	663.2/2					ATATCCATCCTTTAAACCTTGTTACAATGTTGGCACATTACCTGTCCGATA	
x1	308955						
	41-						
	230895						
	432						
ex3_56	CM000	15	0.003	30.2	1	AAGACTATACTTTTCAGGGATCATTCTATAGCTCATTACTAGAGAAGTTCCCCTGAAC	
83093_	667.2/3					GTGTAGAACACTGGCAACCATGAGGAGGACATGCAGTGTTCTGTCCTGAGTGTGAA	
x1	542906					GCTGGGTCTTGGTGTTGCTTTGCTGCAAGTACCATTTGCCACTGATGATTGTTTTTGT	
	4-					CTCCCTCTGGGACAGTAAGGGAAAGGACACAGTCTGAGTGAT	
	354292						

Accession	Gene	Length	Score	GC	GC3	GC4	Sequence
ex3_56_83576_x1	ENST0000458908.1	15	0.005	30.2	1		TAGCACTGTTGCCTGAGCCATTGGTGCTCCCTGGTACTAGCTCAGTTTTAATGCAGTGCA
ex3_56_83716_x1	CM000672.2/19598247-19598463	14	0.009	28.2	1		AAGACTGTGCTTTCAGGGATCATGTCTATAGTTTGCCACTAGAGAAGTTTTTTTGAACATGTAGTAGGGCACCAGAAGCACAAGGAAGAGGCACAGCCTTCTCCTGAGCATGAATCTGGCTCTTGGTCTTGGCTTTGTTCCAGCTACCATTTGCCATTGATTATGTCCTTCTTTCCTTCCAGAAAGTAAAAGGGAGAGAATGCAGTCTGAGTGGT
ex3_56_84392_x1	CM000667.2/142626305-142626169	14	0.008	28.2	1		CAATGCCTTGAGTTCAGTCGAGGACAGCTTCCCTTTTCTGTTAATTAACCTTTGGAATGTTGGGGCATTAAAACAGGCTAGGGTAGGTGATTGCACAGAGAATACTATTCTATTCATTCCTTCCAGAAAAACA
ex3_56_84513_x1	CM000671.2/128749358-128749461	19	0.002	30.2	1		ATCCTTTCGTAGTTTATAAGAGTGATGATTAGGTCTTCATGCTCATGTGTGAAATGTGCCTCCCTCAAACCATGTTAGGACGTTGGCATATTGCCCATCTGAAA
ex3_56_84806_x1	AL132709.5/129680-129609	15	0.003	30.2	1		UGGAUCAUCAUGACUACUGGUAUUGGAUGGGUCUUCGUCAGUGAAUGCCUAUCUGGAACUCUGAGGUCCAU
ex3_56_85138_x1	CM000684.2/19249840-19249966	14	0.008	28.2	1		TCAAAGCTGATTTTAAAAGCTTAAAAAATAATCGCCAGGTACCATGCAAAAGCAATCTTCCCTTTAGAATGACTGATGGTATGCTAAGGTTTTTTCGTGGCATATTATTATAAAGGTGAATACAAAT
ex3_56_86363_x1	CM000664.2/147323971-147324075	14	0.008	28.2	1		ATCTTTTTGTAGTTCATGAGCACGATGATTGGGTTTTTACAAGAATGTGTGAGATGTGCCACCCTCTGAACCTTTTTATGATCTTGGCACATTACCCATCTGACC
ex3_56_87119_x1	CM000670.2/1	15	0.004	30.2	1		ATTCTTTTTTAGTTTTAAAAGTGTGATGATTAGGTTTTTCACTTGTGTGAGATGTGCCTTCCTCAAACCTTGTTACAACGCTGCACATTACCCATCGGACA

x1	125639 76- 112563 875					
ex3_56 87293_ x1	AC008 581.11/ 95393- 95256	27	2E-10	54	1	UGGAGGACUGAGAAGGUGAGGCAGUUUUGCCCCGUGCUGCCUCCACCGGUUAA GACCUCCAAAAUCGAAGGGCUGCCCAGGCAGAGGAUGUCCCCUUGCCACCCUUG GAGGGGCAGCGCUGUGCUGGCCGACAUUUG
ex3_56 87461_ x1	CM000 668.2/1 109634 66- 110963 569	15	0.004	30.2	1	ATCTTTTTGTAGTTCATAAGCATGATGATTATGTTTTTACATTCATGTGTAAGATGTGC CTCCCTCAAACCTTGTTATGATGTCAGCATATTACCTGTCTGATG
ex3_56 88031_ x1	ENST0 000038 4737.1	15	0.004	30.2	1	GTGCACATTTTCATTGACCTGCTTTCTTTTATGTGAGTAGTGTTATTTCTTATGTGCTAT A
ex3_56 88617_ x1	ENST0 000039 0977.2	19	0.004	30.2	1	ATACTGTGACAGTTGCATCGTTCAGCAGATTGAGTCACGAAGAGATGTATACCATCT GTC
ex3_56 88722_ x1	AC010 325.7/1 32197- 132107	23	4E-08	46.1	1	GGGCCUCCAUGAUGUCCAGCACUGGGCUCCGACUGCCACUGAGGACACGGUGCC CCCCGGGACCUUUGACACCCGGGGGUCUGAGGGGCC
ex3_56 88963_ x1	ENST0 000045 9128.1	14	0.009	28.2	1	GGATCGATGATGAGAATAATTGTCTGAGGATGCTGAGGGACTCATTCCAGATGTCAA TCT
ex3_56 89140_ x1	CM000 674.2/8 418344 8- 841833 24	14	0.009	28.2	1	GCTGACACTAGAGTAACATCCTGACACAGCTCTTGTCTGGTGTGCTAGAGTTCTCG ATGAATCTACTGGTCTTGATTCAGTGGCAGGAGCAGTGACTGTGTTAGTATGCGTAT CTGAAACATGG
ex3_56 90067_ x1	AC107 390.4/3 3836- 33915	14	0.009	28.2	1	UUGAUCUACCUCUGAUGAAACCUGUGUUGGUGGGGACAUCUGAGAGUGUUGAUG AAUGCCAGUGACUCUGAUAGAAAAA
ex3_56 90121_ x1	CM000 679.2/2 802246	14	0.008	28.2	1	TAGAAGCCAATTAAGCCAACTGAGTTTCTTTCCTCACAGGGACCTGGTGTGCCATGG CTGCAAACAGCAGCTTCTTGTGTCAGGGTACGCAGACTGTTTCTTGGATGGGTTGCTC TAAGGGACCTTGGAGACAGGC

	4- 280223 30						
ex3_56 90457_ x1	AC079 121.5/4 2943- 42813	18	6E-05	36.2	1	UUCCAAAGUGUUGAGUUCAGUCCAGGGCAGCUUCCCUGUUCUGUUAAUUAACUU UGGGACAUUGAAAUGGGCUAGGGGAGAUGAUUGGGUAGAAAGCAUUUUUUUUC AUUUGCCUCCCAGCCUACAAA	
ex3_56 91149_ x1	X8737 3.1/278 6-2857	15	0.004	30.2	1	AAUGAAUGAUGACAAAAUGUUUCAGUCCCAAUGAUACAUCUGAUUUUACCAUUA UAUUUAUCCUGACAUU	
ex3_56 91163_ x1	ENST0 000039 0962.1	17	0.000 2	34.2	1	AAATAATGAAATCACCCAAAATAGCTGGAATTACTGGCAGATTGTGTAGCAATAACC TA	
ex3_56 93450_ x1	CM000 685.2/1 351833 06- 135183 190	14	0.008	28.2	1	AAGACTATACTTGCAGGGATCATTCTGTAGTTGGTTACTAGAGAAGTTTCTGTGACA GGGCACAGTACCAAATTTTAAAAGAATGCACTTCAAATCTTCAAAGTTAGGATTGGAG A	
ex3_56 94803_ x1	ENST0 000038 3961.1	14	0.009	28.2	1	GGATCGATGATGACTTCCTTATATACATTTCCTTGGAAAGCTGAACAAAATGAGTGAAA AC	
ex3_56 94950_ x1	CM000 668.2/6 866524 5- 686651 28	31	2E-12	61.9	1	AAGACTATACTTTTCAGGGATCATTCTATAGTTTGTACTAGAGAAGTTTCTCTGAACG TGTAGAGCACCGAGAACCTACAAAATACCATGAAATGAGAAGTGATGATAAAGAGTG GT	
ex3_56 95184_ x1	ENST0 000061 5323.1	18	1E-04	36.2	1	AACACTTCCATGCACCATTTCTATAGTTTCTTACCAGAGAAGTTTCTCTGAACATGTG GA	
ex3_56 96037_ x1	CM000 663.2/6 710277 9- 671026 45	14	0.008	28.2	1	ATGCATCTATTTGACAGACCTGGAGTAGTTACTGTCTGCTGCTAAGGTTTCCACTACA GATGCAAGAAAAAATATTCTCGAGTTTTCTGTCTGTCTGATTGTGGCCTCTGAGAT TGAATAGAGGAATACAGTG	
ex3_56 96049_ x1	AC073 210.8/1 29951-	14	0.008	28.2	1	UUGCACAGUGAACACCCAAGUGUGCUUUUAGUUCUUUGGCUUUGACCCUGUGC UAGAGCAUUGCCUGUCUCUUCUCCUCUGCAUUGAAAGGAAUAAUUUUCUUUAAA UGUAUUCAGAAAGCCAGCACAUUA	

ex3_56_97017_x1	130084 CM000 685.2/4 808176 7- 480818 70	14	0.008	28.2	1	ATCCTTTTGTAGTTCCTAAGCATGATGATTGGGTGTTTCATGTGCTTATGTGAGATGTG CCTTTCTCAAACCTTGTTATGACATCAGCACATTATTCATCTGATA
ex3_56_97159_x1	CM000 665.2/4 878702 - 487859 9	14	0.008	28.2	1	ATTCTTCTATAGTTCATGAGCATGATGATTGGGTGTTTCATGACATGTGTGAGATGTGC CACCCCTCTGAACCTTGTTCCCACATCGGCACATTATCCATCTAACC
ex3_56_98399_x1	CM000 669.2/1 483896 45- 148389 859	14	0.009	28.2	1	TAGTAACACTTCCATGCACCATTTCTATAGTTTCTTACCAGAGAAGTTTCTCTGAACAT GTGGAGCACCGGAAACCACGAGGAGGCGGCTCAGCATTCACTCCTGAGCATGAAGC TGGCTCTTGGTGGTGCTTCTCTGCAATTGCCTTTTGCTGCTGATGATCACTCTTCTCT TCCTTTGGGAGAGTGAAAGGGAAAGGAAGCCATCTGAAGGGT
ex3_56_98480_x1	ENST0 000038 4234.1	15	0.003	30.2	1	GGCTTCCTAGTACTTACCATGGTCTGTGTTCTTACGCTGACTGTATAGAAACAGGAG GCA
ex3_56_98613_x1	ENST0 000038 4053.1	16	0.000	32.2	1	GGCTTCTCATTGAGCTCCTTTCTGTCCATTGATGGCAGTTGATGGATTTGCATGAGAA GA
ex3_56_99346_x1	AC011 120.11/ 127524 -	16	0.000	32.2	1	CAGACAUUCAUUUUUAUCCAGUUUCUUCUCAAGUGAAGAUAAUUUUUGUAAA GUCCUAAAGUCAUGUAGAAUGUAGUAGCUUUCUGUUCACACUGUACAAUAAAA GGAUGGAUCAUUCUACAACUGACAUUA
ex3_56_99447_x1	ENST0 000051 7218.1	16	0.000	32.2	1	TTGCAGGTTTGCTCCAAGGTTTAAACATGAACACTAGTCAAGCTAATTGTGCTCCTCT CC
ex3_57_00798_x1	ENST0 000036 4393.1	14	0.009	28.2	1	TGGATCAATGATGTCCACTGGTGGCGTATAAATCATATTTGGTGAATATATGTCTGGA AC
ex3_57_01199_x1	ENST0 000036 4946.1	14	0.008	28.2	1	CCAACATGGATACCCTGGGAAGTCACTCTCCCCAGGCTCTGTCTAAATGGCATAGGG GAG
ex3_57	ENST0	17	0.000	34.2	1	GCTGACACTAGAGTAACATCCTGACACAGCTCTTGTCCTGGTGTGCTAGAGTTCTCG

02423_	000040		2			ATG
x1	8221.1					
ex3_57	ENST0	18	0.008	28.2	1	AGGACATTTCAATGCGGGCTCATGGGGCTGTGAAGCCAAGAGCTATTAACACTATGA
02573_	000036					CCA
x1	2522.1					
ex3_57	ENST0	18	3E-05	36.2	1	GCATGGCCGAATACTGTGTTTTATCAGTAGTTTACACAGCCAGACACCCATGCAAAA
02583_	000038					GCA
x1	4439.1					
ex3_57	CM000	15	0.003	30.2	1	ATCCCTTCGTAGTTCATAAGCGTGATGACTGGTTTTACGCTCACGTGTGAGATGTTC
02617_	663.2/2					CTCAAACCTATGATGACATTGTCACGTTACCAGTCTGATG
x1	388225					
	5-					
	238823					
	52					
ex3_57	AC020	25	3E-09	50.1	1	UGCAGCUGUGUCAAAUUUGGUGCCUGCCCUGCCUGUGUAGGCACUGACCCAGAA
02713_	634.16/					GGCUGCCACAGAAACACUGACUCAUGGGCCUGUCCUGUGUCUCGGGCUCAGG
x1	18995-					GAUAAUUUGGUUACAGAUACCA
	18865					
ex3_57	ENST0	14	0.009	28.2	1	CTGCATTTTACCCTCCCTGATGGGGCTCAGTGTGCAGCAGCTGGAAAAAGTAGATGC
02789_	000051					CCT
x1	7233.1					
ex3_57	ENST0	14	0.009	28.2	1	TTGCATGAGGAAGTATCTGCTCTTCATTCCTTTGGGAGGAGAAATACATCCATAACAT
03094_	000045					GC
x1	9316.1					
ex3_57	CM000	16	0.001	32.2	1	GCACCCCTTTAAGGCTGATGCAATGCTTTAAGAGGCTAACGCAGAAGGGTGAAGCC
03586_	669.2/1					AGTCTCCTTAAAACCCAAAGAAGAGATTGTAACCTTCTCTTTGGATCCTGTCTGGAG
x1	526093					TCACAGCT
	13-					
	152609					
	434					
ex3_57	ENST0	21	5E-07	42.1	1	TGATGGCAATGATGATTTTTTACACTTATTGTTGTTACCTGATAACATAAATATGAGGG
03853_	000060					T
x1	7707.1					
ex3_57	ENST0	14	0.009	28.2	1	AAGACCCTTCAGCTGCAAACAACAGCTTCCTTGGTAGTTTATGCAGCCTGTTTCTTGT
04791_	000051					AT
x1	6717.1					
ex3_57	ENST0	15	0.007	30.2	1	TTCCTAAAGATTCACAATGAACATTATTATTTAAGAGCTTTTTGAAGTGCAAATCCATG
05101_	000051					A
x1	7285.1					
ex3_57	CM000	15	0.004	30.2	1	ATTCTTTTTTGGTTCATAAGTGTGATGATTTTCGTTTTTCATGTTAAAGTGTGAGATCAGC

05153_x1	666.2/1 835823 01- 183582 195					CTCCCTCAAACCTTGTTACTACATCAACACCACATTATCCATCCAATG
ex3_57_05352_x1	AJ6094 35.1/1- 128	33	8E-14	65.9	1	GUGCACAUUUCAUUGACCUGCUUUCUUUUUAUGUGAGUAGUGUUUUUUUCUUAUGUG CUAUACAAUAAUUGAAGGCUAAUUAGCAGUAUAACUAUAAAUAGUAAUGCUGCCA GUCUCCUUCAGACAAAA
ex3_57_05814_x1	ENST0 000060 7261.1	14	0.008	28.2	1	TGGATCAATGATGAGTATTGGTGGAGGTGTCTGAATCAACACTTTTGATTAAGCCCTC TG
ex3_57_06112_x1	ENST0 000039 1302.1	15	0.005	30.2	1	TGCCCCTGACCTGGGAAGAGAGGGGCCTGGCTGGTGGTATCCATCTCATACCAGCT AGGG
ex3_57_06295_x1	AC080 089.5/4 2226- 42352	15	0.003	30.2	1	GGGGUGUGCUCAGAGCAGGGGGCUGAAGAAUGGCUCCUCUGUUUUAUAACACAUG GAACAGGCAUCUGAGGUCACUGUGACAAGGGGCACAAAACUUGUGACUCCCUAAG AACAAAUGUCCUACAAGU
ex3_57_06497_x1	ENST0 000036 3883.1	15	0.002	30.2	1	CTACAAAGATAGCAACACTTTTCATCAACAGCAGTTCACCTAGAGAGAGTCGACACTT TT
ex3_57_07351_x1	CM000 669.2/1 386251 88- 138625 060	18	3E-05	36.2	1	AATACTTCATTTAGTTCCATTAACAAAATCTAAAGTTGATTTATAGGCAGGTACAAAA AATCAATCCTCTTTTGCAATCCAGAACTCATTGTTTCAGTATAAGTTTTGCTACAAATA GAAGGGGTATT
ex3_57_08289_x1	ENST0 000039 1143.1	16	0.000 8	32.2	1	TGTCCTTGACTTGGGTAGAGTGATGTCTGGTTGGTGCTGCCTATCTCATATAAGCCA GGG
ex3_57_09568_x1	CM000 668.2/4 354414 4- 435442 70	16	0.000 6	32.2	1	CTGAAGACTAAGAAAATAGAGTCCTTAAAGTCAAGCTGAGTCTGCTGTTAGCCTCCTA AATGAAAGGATAGACAGAACAGGTCTGTTTGCAAATAAATTCAAGACCTACTTATC TACCGACAGCA
ex3_57_10013_x1	CM000 672.2/1 012808 97-	15	0.006	30.2	1	AAGACTGTACTTTTCAGGGATCATTTCTTTAGTTCATTACTAGATAAGTTTCTCTGAATA TGTAGAGCGCTGAATTATAAT

	101280						
	976						
ex3_57	CM000	19	0.003	30.2	1	ACTCTTTTCATCTTTTTTGTGATGACTGGATTTTCATGCTGTTATGTGAGATGTGCCTCC	
10020_	685.2/1					CTCAAACCTTGTGATGACATCTTGGCACATTACCCATCTGATG	
x1	241332						
	76-						
	124133						
	377						
ex3_57	ENST0	15	0.006	30.2	1	AATTCTATACTTTGAGGAGCCATTTTCATAGTTTGTACTAGAGAAGTTTCTCTGAACA	
10244_	000040					T	
x1	8405.2						
ex3_57	AL132	15	0.004	30.2	1	UUGAUGAUUAUGAUGGCCACUGGUGGCUUAUGAGUCUUAUACAGUGAAUACAUGUU	
10364_	709.5/1					UGAAACUCUGAGGUCUGU	
x1	56819-						
	156747						
ex3_57	ENST0	14	0.008	28.2	1	AAGATTATACTTTTCAGGAATCATTCTATAGTTTGTACTAGAGAAAGTTCTCTGAATG	
10647_	000036					T	
x1	3352.2						
ex3_57	CM000	14	0.008	28.2	1	AAGACTATATTTTCAGGGGTCACCTTCTATAGTTTGTACTAGAGAAGTTTCTCTGAACA	
11358_	685.2/1					GGTAAAGATAAAAAGCACATATGTACTGTGT	
x1	205894						
	41-						
	120589						
	530						
ex3_57	ENST0	15	0.006	30.2	1	AGGCCAATGCTGAATTATTATCTTGACGAGAAATGATGACGTAAAAATTAAGCTTAGT	
14425_	000039					AG	
x1	1109.1						
ex3_57	CM000	14	0.009	28.2	1	TAGCACTGTTGCCTGAGCCATTGGTGTCCCTGGTACTAGCTCAGTTTTAATGCAGT	
15008_	685.2/1					GCAATAGGAATTCTTTGTTTCCACAAGGCCTTGTCTGCTGTGGGCTGCTCCTTCCC	
x1	187380					ACAGTTGGACCTTG	
	55-						
	118738						
	182						
ex3_57	ENST0	22	4E-05	36.2	1	AAGACTCTACTCTCAGGGCTCATTCTGTCAATCAACTAGAGAAGTTTCTCTGAAT	
16138_	000040					GT	
x1	8116.2						
ex3_57	CM000	14	0.009	28.2	1	CCAACATGGATAGTCTGGGAGGTCACTCTCCCCAGGCTCTGTGGAAGTGGTGTGG	
16509_	670.2/5					GGAGCATAGACGTTTGGTCCATGACGTACAGTACAGCCCCTTCCACAATGCTGGAG	
x1	433068					ATGAAGCTGGGTCTCCTGTCTGCGCCTGCATATTCCTATAGCTTCCCTGAGTCCTGT	
	7-					GGATGATGACTGGTGAGACAAATCGTGCAGGAAACAAGT	

	543308						
	95						
ex3_57	CM000	16	0.001	32.2	1	ATCCTTTTCGTAATTCATAAGCATGATTTGGGTGTTTATACTCAGATATGAGATAAGCCT	
16605_	685.2/3					TTCTCTAAACTTATGATGTTGGCACACTACCCATTTGATA	
x1	284800						
	5-						
	328479						
	07						
ex3_57	CM000	14	0.009	28.2	1	ATCCTTTTGTAGTTCATAAGCATGATGAGTGGGTTTTCCACTGCTGTGTGAGATGTG	
16755_	679.2/6					CCTTCCTCAAGCCTCGTTACAATGTCAGCACATTATCCATCTGATG	
x1	096189						
	3-						
	609617						
	90						
ex3_57	CM000	15	0.002	30.2	1	ATCCTTTTGTGCTTCATAAATGTGGGTTTTCCAACGTGCATGAGATGGCCCTCAAACCT	
18161_	668.2/1					TGTTACAACGATGCACTTTACTCGTTTGATG	
x1	572913						
	99-						
	157291						
	311						
ex3_57	CM000	15	0.005	30.2	1	ATCCTTTTGTAGTTCATGAGGATGATGGTTGGGTGTTTCACACATGTGTGTGAAATGT	
18870_	675.2/4					ACCACCCTCAAACCTTGTTACAATGTCAGCACATTACCTGCCTGACC	
x1	462867						
	3-						
	446285						
	69						
ex3_57	CM000	18	4E-05	36.2	1	ACCTGCATTCAAAAATGATCACGGGCTGCCTGTGCTCTGGTCATCAATAACGCAGGG	
18891_	682.2/3					AGAGGAATTGCTGAAAGCCGTTTCCCGTGTTTGGAGGGTTCACACCTGTCCCTTTCA	
x1	844937					AATGCTGGCGCTTTCACACA	
	0-						
	384495						
	03						
ex3_57	CM000	14	0.009	28.2	1	AAGACTATCCTCTCAGTGATGATTTCTATAGTTCGTTACTAGAGAAGTTTCTCTAAACA	
18940_	669.2/1					TGTAGAGAGCATCAGAAACCACAAAAAAGAGGTGCAGCGGTCTCTCCTGAGTGTGAA	
x1	079999					GCTGGCTCTTGGTATTGCTTCTTGGTTCTTCTTCTTCTTTGGGAGAGTAAGAGGAAG	
	82-					AGGATGCAGTCTTAGTAGT	
	107999						
	791						
ex3_57	ENST0	14	0.008	28.2	1	CCAATGTGGATACACCAGGAGGTCACTCTCTCCCAGGCTGTGTCCAAGTAGCATA	
18958_	000036					GGG	

x1	4478.1					
ex3_57_18988_x1	AC007_240.2/2_2839-22705	42	5E-19	83.8	1	UAGGCCCUCAAUCAAGACUAGUGUUUUGCUGUAGCUGUUGGUUUCAAACAGGAUC CGAGAGUGAUGUCUUCUUGUGGUCUGUUCACUGCUCAGUAUCCCAGUGUCAGU GGCCAAUUCAGUUGGAAGCAACAUGG
ex3_57_19181_x1	CM000_679.2/5_863183_6-586316_41	19	0.008	30.2	1	AAGACTATATTTTGGAGGGATAATTTCTATAGTGTGTTTCTCGAGGAGTATATCTGAAC GTGTAGAACGCTGGAAACCGCGAGAGGGAGATATTTGTGTTCTCTCACGAGTGGGA TAGCAGTGTGGTGTGGCGTTATTCTAACTGCTGTTGCTGTTGGTACCCTTCTTC TCTAGAGAAGGCAGTCTGAGTAGT
ex3_57_19272_x1	CM000_675.2/5_655962_4-565597_25	15	0.004	30.2	1	ATCCATTTGTAGTTCAGAAACATGACTATTGTCTTTTCAAGCTTATATGAGATCTGGCT CCCTCAATCCTTGCTATGATATCAGTACATTACCTGTCTGATG
ex3_57_19673_x1	CM000_679.2/4_888084_0-488809_67	14	0.008	28.2	1	GTCGCACTTAAACTTAAGACTCTTTTTCTTGCAGCAGTGGTTTAAACAGAGGAACAAA CAGGAAGATCTTGTGCCTTTGAGGGGCTGTGGTTGGGCCCTCAAAGTGACTTTG GAGTTCTACGCCA
ex3_57_20990_x1	ENST0_000057_9995.1	23	1E-05	38.2	1	AACTATTGAGAACAAGATGCAACATACCACTCGAGTGTGCAGTGGGGAAGCCAACC TTG
ex3_57_21740_x1	CM000_682.2/3_384229_-338444_0	16	0.000 5	32.2	1	AAGACTATACTTTCAGGGATCATTCTGTAGTTCATTATTAGAGAGGTCTCTCTGAAT GAGTAGAGCACTAGAAACCACAGAAGGAGGCACAGTGGTCTCTCCTGAGCATAAAG CTGGTTTTTGATGTTGCTTTGCTGCAACTGCCATTCGTCACTGATGACTGTTTTCTTC CTCTGGGAGAGTAAGAGGGAGAGGACACTATCTGAGTGTT
ex3_57_21995_x1	ENST0_000039_1291.1	15	0.003	30.2	1	CACTAGAAGACAGAATTCACAGAAGTAGCATTTCACCTTTTGCCTTTACAGAAGTATA TT
ex3_57_22055_x1	ENST0_000036_2412.1	14	0.008	28.2	1	TGGCAAGCCTCCAGCGTGCCTGGGTCTGTGGTGTGTTGATGTGTGCATTCTACTGCTT GCCA
ex3_57_22506_x1	ENST0_000039	16	0.001	32.2	1	GTTTCATGATAAGTAACATTTCTTCAATTTGACCTGATGTGTATTGAAGAAAACCAGCAT C

x1	0968.1					
ex3_57 22886_ x1	AC104 581.22/ 69359- 69497	22	2E-07	44.1	1	UGGCUCGAUUUCCUGGGGGGUGGUCUCAGCCCACUCCACCUCCCCUCAGCCGAG CCUAGAGUAGAGGGGGCCAGGCAUCCUCCCCAGGGGAGGGGCGUUUAAGCAAGGA GCCUCUCCUGGGCUGUCCUAGCCUCACAUUU
ex3_57 23525_ x1	CM000 672.2/1 588635 8- 158864 65	21	0.000 2	34.2	1	ATCCTCTGGTAGTTTGTAAAGTGTGATGATTGAGTATTCACATGCATGCATGTGTGAGA TGTGTCACTCCCAAACCTTATTGCAACATGGGCACATTACCCATCTCACA
ex3_57 23699_ x1	ENST0 000036 4630.1	14	0.008	28.2	1	TGGACCAATGATGATGACTGGTGGTGTATGAGTTAAAGGTGATGAATAGTAAGTGTC TTT
ex3_57 24033_ x1	CM000 675.2/4 118008 7- 411799 81	15	0.002	30.2	1	ATCCTTTTGTAGTTTATAAGCGTGATGACTGGGGTTTCACGTGCATGTGTGAAATGTG CCTTCCCCAAGCCTTGTTATGACCTCATTGGAACATTACCCCTTTGACA
ex3_57 24547_ x1	ENST0 000039 1095.1	18	0.008	28.2	1	ATTCTTAAATGAATGATGAAATACCAAAAAGAAAAATAAGCAAAGAACAGATAACAGA AA
ex3_57 24680_ x1	ENST0 000041 1005.1	21	5E-07	42.1	1	GTGCCGTGATGTATTTGTCAACACATCACTCTGAAGAAAAGTATGTGGTGACTIONCTG TG
ex3_57 25233_ x1	ENST0 000036 5398.2	18	0.008	28.2	1	AATTGTATACTTTCAGGGATCATTCCATAGGTTGTTACTAGAGAAGTTTTTTTAGATGT G
ex3_57 25410_ x1	ENST0 000051 6391.1	14	0.008	28.2	1	TGGTCAGGCTGTGGCTGTGGCACAGCACTTGGCTTTCTCCTGGGGGCACTGGGGAG CCAT
ex3_57 26360_ x1	AC078 860.19/ 16828- 16700	16	0.001	32.2	1	AUUUUACAUAAGCGCUGCAGAUGUGGCUGCUGUGUCACAUUUGUGUUUUUAGGUG GCAGAGAGAAGAGAGGCUAUGUCUAUGCUCAGUGUUCUGCCCCAUGAACAUUUGA AUGUUUAAUAGUCAGACACU
ex3_57 26510_ x1	ENST0 000036 4099.1	14	0.009	28.2	1	CGGGTGGTGTGATGACCCCAACATTCCATCTGAATGCCTGTGCTGAAACCCAGAGGCT GTTT
ex3_57	CM000	15	0.005	30.2	1	ATCCTCCTGTAGTTCCTGAGCGTGACGACGGGGTGTTCGTGCGCGTGTGAGATGTG

26864_x1	674.2/1 308153 53- 130815 450					CCACCCTCGAACCTCATTACATCAGCACATCACCCACTGGCC
ex3_57_26868_x1	ENST0 000045 8890.1	14	0.008	28.2	1	ATCCTTCTTTAGTTCATAAGCATGATGATTGGGTTTTTCATGTACATGTGTGAGATGTGCC
ex3_57_27140_x1	CM000 683.2/9 907916 - 990801 0	16	0.001	32.2	1	CTACAATCAATTAAGCCACATGGGACCTGGTGTGCAAGGGCTGCAAACAGCAGCATCCTAGGTAGTGTACAGCAGCCTGTTCCTTGTGTACAACA
ex3_57_28357_x1	CM000 666.2/1 684714 09- 168471 539	14	0.008	28.2	1	GGCTTGCTGGTGTACCACAGGCTGAATTCTTACACTGACTATATAGAAAAGGAGGTAGAGTAAACCTACCCAATATACCCCTCAGCCCAGGCTCTGTGCCTGATCTATATTGTGAATGTGGGAACATAG
ex3_57_28615_x1	ENST0 000051 5935.1	16	0.001	32.2	1	AGGTCATTTTGTAGGGCTTGTGGGCTGTGAAACCAAGAGCTCTTAACGCTATGACCA AAT
ex3_57_29057_x1	AC069 157.8/6 5923- 65741	15	0.002	30.2	1	AUGGUCUGGGGAAAGGCUCCUGUGUGGCUGAACCCUGCCCAGCUGUGGGUGCAGCCUUGUACCAGGCACCCCAACCCUGACCUAAAGUAAAUCCAGGAGAAGUCUUUCUGGGAUUUUGAAUUUGCAGUACAGGUGUGAACAUUCUAGCGCAGUUUGAUCAUUAUGAUACUAAAACAGGA
ex3_57_29866_x1	CM000 665.2/4 189925 3- 418991 11	16	0.000 7	32.2	1	TAGTCAGGCAGGATAATCCCTATCTGTTCCTCCTTTTGGAGGGCAGTAGAATGTGGTAATTGGAGTGGCATAATACTTGATTAATAATTGTGCACTTTCCAATTCATGCTATTATGGCTTCCTGGAGTGGTGTCTTCTCTGAT
ex3_57_30264_x1	CM000 685.2/1 228404 26- 122840 645	16	0.001	32.2	1	AAGGCTATACTTTTCAGGGATCATTTTTATAGCTTATTACTAGAGGAGTTAATGTGAATGTGTAGAGCACCAGAAACCTTGAGGAGGAGGTGCAGCGTTCTCTCCTGAGCATAAAGCTGGCCCAGTATTGTGTTGCCTCACTGCAACTGCCATTTGCCATTGATGATGATGTGTTCTCTTTCCTGAGAGAGTAAGAGGACAGGATGCATTCTAACTGGC
ex3_57	CM000	14	0.009	28.2	1	ATCTTTTCGTAGTTCATAAGTGTGATTGGGTTTTTACACGCATGTGTGAGATGTGCTT

30413_	677.2/4					TCTTCAAAC TTTGTTACGATGTTGGCACATTATACATCTGACA
x1	060731					
	2-					
	406072					
	12					
ex3_57	ENST0	14	0.008	28.2	1	AGGTGATTTCAAAAAGGACTTGTGGGCTGTGAATCCAGGCACTCAACACTTTGAAAG
30860_	000060					TCT
x1	7153.1					
ex3_57	CM000	16	0.000	32.2	1	ATCCTTTTGTAGTTCGTAAGTGTGATGATTGGGTTTGCACACGCATGTTTGAGATGTG
31149_	664.2/5		5			CCTCCCTCAAACCTGTATTAGTCCATTTTACACAGCTA
x1	383982					
	9-					
	538397					
	33					
ex3_57	CM000	14	0.009	28.2	1	TTCCTGTTGGTTCCTAAGTGTGATGATTGGGTTTTTACATTCATGTGTGACATGTGCC
31938_	669.2/3					TCCCTCAAATCTTGTGATGATGTGCGGCACGTGACCCATCTGACG
x1	716977					
	9-					
	371696					
	78					
ex3_57	AC091	14	0.008	28.2	1	CUGCAGCCAAUUGAGUUGACCGAGCUCUUUUUCCUCCUGGGGGCUUGGUGUGCAA
32385_	826.3/1					UGGCUGCAAACAGCAGAUUCCUUGGUAGUGUAUGCAGCCUGCUUCUUGUAUGGG
x1	2688-					UUGCCUCUAAGGGACCUUGAAGGCAGCC
	12823					
ex3_57	CM000	15	0.004	30.2	1	ACAGACTCACTTTGCACCTGGCTGCAGCCTCATGGGGGTGCTTTTTCCATGTGCCAG
33029_	663.2/8					GGAAACATTCTGGGGTGTGTGGCTGCCTGACCTATCAAGGGTGTGATGCAGCTGTCT
x1	511919					GGGATACAGGA
	-					
	851179					
	5					
ex3_57	ENST0	15	0.003	30.2	1	TCCTCACATGGGATAATTTTTACTTTATTCTCCCTTTGGAGGTCAGGTTAAACAAGAT
33226_	000045					T
x1	9141.1					
ex3_57	ENST0	17	0.000	34.2	1	ATAGCCAATCATTAGTATTCTGAGCTGTAGGAATCAAAGATTTTGATTAGATTCTGTAA
34026_	000039		2			C
x1	1082.1					
ex3_57	ENST0	16	0.000	32.2	1	TCCACAGGTGAGATCATCCTTACCTGTTCTTCTTTTGGAGGGCAGAGTTCACGATG
35243_	000036		5			ACT
x1	3321.1					
ex3_57	CM000	15	0.004	30.2	1	AAGACTGTATTTTTCAGGGATCATGTCTATAGGTCATTTCTAGAGAAGCTTCTCTGAAC

35306_x1	665.2/1 090191 16- 109018 909					ATTTAGGGCACAGGAAACCACGAGGAGGCGCAGCATTCTCTCCTGAGCATGGAACC GGTGTGCTTCACTGCAACTGGCCGTTCAATTTGCTCTTGGTGATCATTCTCTCTTCC TTTGGGAGAGGAATAGGGAGAGGACACAGTCGAGGA
ex3_57_35751_x1	ENST0 000039 0976.1	14	0.009	28.2	1	TTGGATATACGATAATCTCACTCCGACTTAACTCTCTCACTGATTATTTGATAATAAC A
ex3_57_36528_x1	ENST0 000036 2600.1	14	0.008	28.2	1	ACACTCTCAGCTATGTATAGTTACACCTGGCTTCACTTGTGTGACTTTTGCAATGGGA AG
ex3_57_36556_x1	ENST0 000045 9428.1	21	5E-07	42.1	1	ATCCTTTTGTAGTTCATGAGCATGATGATTGGGTGTTACGAGTGTGTGTGAGATGT GCC
ex3_57_37986_x1	CM000 673.2/4 756645 - 475679 7	14	0.008	28.2	1	ATTGCACGTTGTTGGAGCTTGGAGTTGGTGCTCTAACTGGCTGATAAACTTGCAAGT GTAGGTAGTATGCTATGTGAGGGGCAAATTTTTTCAGTAACATGACAAAGGTCTTTGG CCTAGTGAGTAGAGTTTGACAATAATCCTCGCTGCAAGT
ex3_57_39058_x1	CM000 672.2/1 013719 52- 101371 852	15	0.003	30.2	1	ATCCTTTTGTAGTTTGTAAGCATGACGATTGGGTTTTTCAGCCTCATGTGTGAGGTGTG CCTCCCTCAAACCTTGTTACATAGGCACATTACCTGTCTGGCA
ex3_57_39848_x1	CM000 668.2/4 183285 4- 418329 93	15	0.005	30.2	1	TGCATTGCCATGGTATCTGCACTCAGTAGTTTATTCCTGCTGGGTGTCCAAAGATCA GTGCCATAGAAATTCAGTATCTAGCATCACTGATTTTCTTGGCTTTGTGCTTGTTAAAA CTTGGTATTTCTATTGACACAGTA
ex3_57_39996_x1	CM000 666.2/1 760981 63- 176098 285	18	5E-05	36.2	1	GCCCTCCTGGTGCTTACCACAGGCTGTGTTCTTCACTGACTGTATAGAATGAGAAG GTAGAATAAATCTACCCCATATGCACTTCAGCCCAACTGAAGTGTGTTGTTCTGGG CCAAAAAGA
ex3_57_40379_x1	AC093 157.2/1	15	0.006	30.2	1	AUGGUUUGGGAAAGGCUCUUGUGUUGUUGAACCUGCUCAGUUGUGGGUGCAGC CUUGUACCAGGCAGCCCAACCCUGACCUAAAGUAAAUUCCAGGAAAAGUCUUUC

x1	50637-150823					CUAGGUUGUGAAUUJGCAGUAAUAGGUGUGUGCAUCCUAGCAGCAGUUUGAUGA UCAUGUAUGAAACUGCAAACAGGA
ex3_57 41783_	ENST0 000038	21	0.000 2	34.2	1	CTGTGAATATTCTCTGTGTTCTGATTATGTGAGAGCCAGGACAGGCTAAACATTTGCT AC
x1	4174.1					
ex3_57 42997_	CM000 682.2/1	15	0.005	30.2	1	ATCCTTTTGTAGTTCGCGTGACGATGGGGTGTTCACACGCATGTGTGAGATGTGCCA CCCTTGAACCTTGTTATGATGTCGTACATTACCCATCCAACA
x1	834689 8- 183469 97					
ex3_57 43286_	ENST0 000036	14	0.009	28.2	1	AGATAACTTCAAAGAGGGCTTGCGGAGCTGCAAACCAAGAGCTTTTAATGTATTACT GA
x1	2326.1					
ex3_57 43685_	AJ6094 45.1/1-	40	7E-18	79.8	1	UGCACUUAUGUAUGUUUUUGUUUAACGUGGACAAAGACUACAGAUAGGUGCAAA AAAUAAAUCCUCUUUUUGCAACCCAGAACUCAUUGUUCAGUAUGAGUUUUGAUACAU AUAAGAAGGGAUUAU
x1	126					
ex3_57 43992_	CM000 664.2/2	16	0.001	32.2	1	AAGCCTATGCATTCTGGGATCATTTTCGATAGCTCGTTCCTGGAGAAGTTTCTCTGAG CACCAGAAGCCACAAGGAGCAGGCCAGCATTCCCTCCCGAGCAGGCCAGCGTT CCCTCCCGAGCAGGAGCCGTCTGTGTTGCTTCCCTGCAAGTACCATTGCGCCAC TGATGACCATTCTTCTGTTCTCTGGGAGAGTAAGAGGGAGAGGATGTAGTCTGAGA GGT
x1	402892 16- 240289 443					
ex3_57 44068_	ENST0 000062	15	0.002	30.2	1	GCGCTGCCTTTGTACCCACCGTGCCTCCGCCTGGTGTCTGGGGTCAGGTTGCAGT GCCA
x1	7561.1					
ex3_57 45265_	CM000 674.2/1	25	0.000 2	34.2	1	TTTAGGAACAGCCTTTGAGGAAGCCTGTGTTTGTAGGGACATCTGAGAGTGTTGATG AATGCCAACGGCTCTGATGGAAAAA
x1	073747 47- 107374 829					
ex3_57 45395_	CM000 663.2/4	17	0.000 2	34.2	1	TCTCGTGATGAAAACCTCTGTCCAGTTCTGCTACTGAAGGGAGAGAGATGAGAGCCTT TTAGGCTGAGGAA
x1	477784 3- 447779 12					
ex3_57 46101_	CM000 666.2/6	15	0.002	30.2	1	ATTTTCATGTTTTAAAGGCATAATGATGTCACTGACTGGCTGATGAAATCCCAAGCGTA GGTAGTATGCTACATGAGGGGTGAGTTTTTTGCTAACACCACAAAGGTCTCTGGCCC

x1	774723					AATGAGTGGAGTTTGATAGGAGTTCTTGTGACAAGT
	6- 677473 86					
ex3_57 46491_	ENST0 000039	14	0.009	28.2	1	AAGACTGTAGTTTCAGGGATTGTTTCTATAGTTTGCTACTAGAGAAGTTTCTCTGAAC GT
x1	0880.2					
ex3_57 47265_	ENST0 000057	14	0.008	28.2	1	CTGCAGACAGTTAAGCCAACTGAGTTCCTTTCTCAGGGAGGCCAGTGACAATGG CTG
x1	8836.1					
ex3_57 48112_	ENST0 000036	31	3E-10	54	1	TGGACCAATGATGAGTACCATGGGGTATCTGAAACAGGATTTTTGATTAAACCCATAT GC
x1	4802.1					
ex3_57 48446_	CM000 665.2/1	15	0.005	30.2	1	ATCCTTTTGCAATTCATGAGCATGATGATGTGGTATCACACTTACGTGTGAGATGTGC CTCCCTCAAACCTTCTTCTACAGGTTGGCACTTTGCCACCTGACA
x1	500778 31- 150077 727					
ex3_57 48469_	ENST0 000036	18	9E-05	36.2	1	CTGCAGCTAGTTAACCTGACTTGTCCACCTCCCTGCTGGGGGCTCAGTGTGCAATG GTTG
x1	4506.1					
ex3_57 48547_	ENST0 000036	14	0.009	28.2	1	TGCTGGAGTGATGAAAAAGTATCTTCAGGTGTGGCTGTGGCCACCTTGGCCACCTGT GTG
x1	4139.1					
ex3_57 48717_	CM000 679.2/5	16	0.001	32.2	1	CTGTATTTGTAGTTCATGAGCATGGTATTGGGTGTTTCATGCAGGTGTGTGAGATAT GCCACCCTTGAACCTTGTTACAACACTGGCACATTCTCAGACCTGAAA
x1	109827 8- 510981 74					
ex3_57 48762_	CM000 678.2/2	14	0.008	28.2	1	ATCTTTTTGTAGTTCATAAACGTGATGACTGTGTTTCCATGCTCATGCGTGAGTTGCA CCTCCCTCAAACCTTGTTTTGACATTGACACATTATCTGCCTGATG
x1	906635 8- 290662 55					
ex3_57 48848_	ENST0 000036	23	0.003	30.2	1	AGGCCATTTTAAAGAGGGCTCATGGGACTATGAAACCAAGAGCTCTTAATGCTGTGA CCA
x1	5507.1					

ex3_57 49319_ x1	CM000 669.2/5 226956 9- 522694 37	14	0.008	28.2	1	TCCATCTGTTTGGCAGACCTGGAGCAGTTAGTGTCTGCTGCTAAGGTTTCCATTACA GATGTGAGAAAAAAGTGTCTTCTGCTTTCTGTCTGTCTCAGTGGCAACCAAGATT GAATGGGGGATATGAGAG
ex3_57 51738_ x1	CM000 674.2/7 568930 5- 756891 43	15	0.002	30.2	1	TTCCATTTTCAGAAAGCCGAGGTCAAATAATGAGTCCTGGGGAATTCAAACCTTGTGTT AAGAAAATGTGTCCCAGTGTGCAATGGCTGCAAACAGCAGCTTCCTTGGTAGTGTAT GCAGCCTGTTTGTGTACGGGTTGCTCTAAAGGGCCTTGGAGACAGTC
ex3_57 52429_ x1	ENST0 000040 8532.1	15	0.003	30.2	1	GGGGTGTGCTCAGAGCAGGGGGCCTGAAGAATGCTTCTTCTGTTTACAACACACCC AATA
ex3_57 52930_ x1	CM000 676.2/1 023743 19- 102374 238	20	2E-06	40.1	1	AAGGCTGTGCTTTCTGGGATCATTCTATAGTTCATTAAGTACTAGAGAAGTTTCTCTGAAT GTGTAGAGCAAAGAAAAAATATT
ex3_57 55737_ x1	CM000 685.2/1 428740 63- 142873 960	17	0.000 1	34.2	1	GTAATTTTCGTAGTTCATAAGCATGATGATTGGGTGTTACACACATGCGTGAGATACG CCACCCTCCCACCTTGTTAAGATGTTGGCACATAACCCGTCTTACA
ex3_57 56298_ x1	CM000 677.2/2 510157 5- 251016 66	20	2E-06	40.1	1	GGATCGATGATGACTTAAAGATTTATCTAATTTAAATCTGAACAAAATGAGTGACCAA AACACTTCTGTACCACTTCTGTGAGCTGAGGTCC
ex3_57 56741_ x1	ENST0 000040 8571.1	16	0.001	32.2	1	GCAGACTCCCTCAGCATCCAGCGGGTGCTTTTTCGGTCTGCCAGTGAGCATTCCATG GTG
ex3_57 57759_ x1	AF250 841.1/1 59716- 159797	14	0.009	28.2	1	GGGUCGAUGAUGAGAACCUUAUUAUUGUUCUGAAGAGAGGUGAUGACUAAAAAUC AUGCUCAAUAGGAUUACGCUGAGGCC

ex3_57 58131_ x1	ENST0 000036 3666.1	15	0.005	30.2	1	AAGTCATTTCAAAGAGGGCTTGGATGGCTATGAAACCAGAGCTCTTAAGGTTATAATA AG
ex3_57 59026_ x1	ENST0 000036 3280.1	16	0.000 7	32.2	1	TGAATCAATGGTGACCACTGGTGGCATATAAGTCATGGATGATGAATATGAGAAGAA AAG
ex3_57 59263_ x1	CM000 675.2/3 985722 7- 398571 35	15	0.004	30.2	1	AGATTGATGATGGCACCCCCATAAAACCATTCCCTTAGGAAATCTGAACAAAATGAGTG AAAACCTACTAGTTGTTCTCATTGAGGCTGGGCC
ex3_57 59630_ x1	ENST0 000036 4595.1	15	0.005	30.2	1	AGCCTCCTGGTGCTCAGCACAGGATGTGTTCTTACCCTAACCAAATAGAAAGAGTAG GCT
ex3_57 61199_ x1	AL132 709.5/1 85108- 185034	35	5E-15	69.9	1	UGGACCAAUGAUGAGUACCAUGGGGUAUCUGAAACAGGAUUUUUGAUUAAACCCA UAUGCAAUUCUGAGGUCCAU
ex3_57 61207_ x1	ENST0 000038 4000.1	14	0.008	28.2	1	GGATCGATGATGAGTCCCCATAAAAACATTCCCTTGAAAAGCTGAACAAAATGAGT GAG
ex3_57 61645_ x1	CM000 668.2/7 339401 3- 733939 13	18	0.008	28.2	1	ATCCTTTTGTAAAGTCATAAGTGTGATTGGGTTTTTCATGCTCTTGTGTCAAATGTGCCT CCCTCAAACCTTGTTACGAAGTGGGCACACTACCCACCTGATG
ex3_57 61781_ x1	ENST0 000040 8823.1	18	6E-05	36.2	1	GGGGTGCGCTCAGAGCAGAGGGCCTTAAGAATGGCTCCTCTGTTTACAACACACCCC AACA
ex3_57 62098_ x1	ENST0 000051 6632.1	21	0.000 3	34.2	1	AGGGGTGGTCTCCTCCCTTACTCTTTGGGAACTCAGATTGGCCTTATGGTGGCCTCT CTT
ex3_57 62485_ x1	CM000 674.2/1 035921 12- 103592 243	14	0.009	28.2	1	TCATCAGATGGGATAACTTTTACCTGTTCCCTCTTTTGGAGGTTAGATTCTAATACGA TGATTGAAGTTCGTATGATACGTGATTAATGTCTCTGCATAATCAGGACTTGTAACAC CTTGATTGCTTCTGAT

ex3_57 62661_ x1	CM000 670.2/1 231805 25- 123180 310	16	0.000 6	32.2	1	GAGACTATACTCTCAGTGACCAGTTCCTGAGTTCATTA CTAGAGAAGTTTCTCTGAAC GTGTAGAGCACGGGGAGCCAGGAGGGGAAGGTGAGCG TTTTCTCCTGAGCATGAG GTGGCTTTAGATATTGCTTCATGGCAATTTGGCAACT GCCATGTGCCATTGAAGATG GTTGTTATCTTCCTCTGGAAGAGGAAGAGGACACAGT CTGAGTGGT
ex3_57 63075_ x1	ENST0 000041 1034.1	14	0.009	28.2	1	AGTTCCTTGGAAAGTTAAAGGTTAAGCTTAAGGACTG ATTCAAAGGCAGGTGCAAAAA ATA
ex3_57 63126_ x1	CM000 678.2/1 887026 9- 188701 66	15	0.004	30.2	1	ATCCTTTTGTAAACATAAGCATAATGATTGGGTTTTT ATTTTCACATGTTTGATATGC CTCCCTCAAATCCTCTTATGATGTCAGCACATTACCC ATCTGAGG
ex3_57 65938_ x1	CM000 665.2/1 014115 0- 101412 47	15	0.002	30.2	1	GACTTTTTGTACTTTTATAAGCGTGATGATTGGGTGT TCCCCTGTGAGATGCGCCACC CTCGAACCTTGTTACGACGTCGGCACATTGCGCGTCT GACA
ex3_57 66165_ x1	CM000 664.2/1 615585 44- 161558 646	15	0.005	30.2	1	ACCCTTTTGTAGTTCATGAGCATGATGATTGGGTGTT CACACACATGTGTGAAATGTG CCACCCTCAACCTTATTATGAGGTCAGCACATTACCC ATCTGACA
ex3_57 66245_ x1	AC002 069.2/2 1330- 21191	15	0.002	30.2	1	AUCCAAGGCGAUUCCCUCUCCAAGGGGACAUCUAGUG CCCCUCUCAGGAAAGUAG CAACUUGGAAUAGAAUCUGGCAUGCCUAAGGUCUUU GAGGAACAGGGAUGCUUUA UCCUCUGCCUUCUUGGCUGCCUACAUAAG
ex3_57 66252_ x1	CM000 681.2/5 166940 5- 516695 08	16	0.001	32.2	1	ATCCTTTTGTAGTTCATAAGTGTGAGGACTGGGTTTT CAGGCTCGTGTATAAGATGTG CCTCCCTCACTCCTTGTTACAACATCGGCATATTACT CATCTGAAT
ex3_57 66280_ x1	ENST0 000036 4937.1	15	0.004	30.2	1	TACCCTCTTCCACTTTGCCAACTGGATGTATGTCTTT ACTGGTCATTCCAGTGGGGC AA

ex3_57 67215_ x1	AC020 553.4/1 38195- 138051	16	0.000 6	32.2	1	AAUCUCCUGGGAUUGUGUCUGGCGAGUGCCCAGUAUUCUGCCACCUUCAGAAGG AAGGGAAAGCAAACCUUCAUGAAAGCAGAGGCAUUCUCCAUUCCCAGCUUGCU CCAGAUCUGGCAGUUGGAAGACAUCUGCAACAAUG
ex3_57 67841_ x1	ENST0 000062 0104.1	15	0.002	30.2	1	AAAAAAGTGTCTTGAGCTTTCTGTCTGATTGTGGCAGCCAAGATTGAATAGAGGA
ex3_57 68772_ x1	CM000 678.2/8 245432 0- 824544 32	15	0.006	30.2	1	ATCCTTTTGTGGTTCCTAAGTGTGATGATTGGGTTTTTCATACTCATGTGTGAAATGTA CCTCCCTCAAGCCTTGTTATGATGTGGCGGGCACATTACCCTTACCCATCTGATG
ex3_57 69232_ x1	AF067 020.1/9 80- 1114	14	0.008	28.2	1	CGGCAAACAGUUAUCCCCUUCUAGUCUGGCUCUCCUGGGAACUCUAGAAGGGAAUC AGUCUGCCACAAGUAAGUGGGUGAAUUCUUCUGUCCACGUCAGUAUUUUGAUGG GUNGCUUNAAAACUUGCCAGAUAAACC
ex3_57 69288_ x1	ENST0 000036 4263.1	15	0.003	30.2	1	CTATCAAAAAGTTACTTTTTGTGGGGTGAAGTTTTTAAAATAACCTTTACCTACGTGG GC
ex3_57 70659_ x1	CM000 676.2/1 011456 95- 101145 480	14	0.008	28.2	1	AAGACTATACTTTCAGGGATCATTCTATAGTTTCATTACTAGAGAAGTTTCTCTGAATG TG TAGAGCACCAGAACTATGAGGAGGAGGCACAGAGTTCTCTCCTGAGCATGAAG CTGGCACTTGGTGTGCTTTGCTGTCAGCTGCCACTTACCATTGGTGATTGTTCTTGTC TTCCTCTTGGAGAGTAAGAGAAAAGAGAATGCAGTCTGAGAGGT
ex3_57 72395_ x1	CM000 670.2/1 036652 95- 103665 394	15	0.003	30.2	1	ATTCTTTCATAGTTCATAAGTGTGATTGGGTGTTTAAACGCTCATTGAGATGTTCCCTCC CTCAAACCTTGGTATTATGTTTGCACATTACACATCTGATG
ex3_57 72451_ x1	ENST0 000045 9301.1	15	0.002	30.2	1	ATCCTTTTGTAGTTCATAGCATGATGATTGGGTGTTACATGCATGTGTGAAATGTGC CA
ex3_57 72531_ x1	CM000 663.2/1 126525 88- 112652	20	0.000 8	32.2	1	ATCCTTTTGTAGTTCATAAGTGTGATGGTTGAGTTTTTACATGCATGTGTGAGATGTG CCTCCCTCAAACCTTGTTATGTTGGCACATTACCTGTCTGACA

Gene	Transcript	Length	Score	Position	Count	Sequence
688						
ex3_57_72642_x1	ENST0000390832.1	15	0.006	30.2	1	TACACTTGTTTATATTTTTGTTTAACTTGTGGACAAAGATTTATAGACAGGTGCAAAAA A
ex3_57_72971_x1	CM000664.2/88307360-88307463	15	0.004	30.2	1	ATCCTTTTGCAGCTCATAAGTGTGATGATTGGGTTTTCACACTCATGTGTAAGATGTG TTTCCCTCAAACCTTGCTATGATATCAGCACAGTACCTATCTGACA
ex3_57_73859_x1	ENST0000515993.1	14	0.009	28.2	1	TTGCATCTATTTGACAGACTAGAATAATTACTATCTGCTGCTAAGGTTTCCCTGCAG AT
ex3_57_74841_x1	ENST0000391132.2	17	0.0004	34.2	1	AAGACTATACTTTCAGGGATCATTCTATAGTTTATTACTGGAGAAGTTTCTTTGAATG T
ex3_57_75429_x1	CM000664.2/18394936-183949333	14	0.009	28.2	1	ATCTTTTTGTGGTTCACAAGTGTGATGATTAGGTTTTTCAGACTCATGTGTGAGACATG CCTTCCCTCAAACCTTCTTATGCTATCAGCACATAATCTGGCTGACA
ex3_57_76340_x1	CM000668.2/28015568-28015777	16	0.001	32.2	1	AAGACTATACTTTCAGGGATCATTCTACATTTCCGGTAATTTCTTTGAACATGTGG AGCACCGGAAACCACCAGGAGGAGGCACAGCATTCTCTGGAGCGTGAAGCCAGT TCTTGGTGTGCTGCATAGCAACTGCCATTTGCCTTTGATGATCATTCTTTCTTTCTT TAGGAGAATAAGAGGGGGAGAACCCAGTCTGAGGGAT
ex3_57_76546_x1	CM000663.2/9082879	14	0.009	28.2	1	ATGGTCTGGGGAAAGGCTCCTATGTTTTTGAACCTGCCAGTTGTGGGTGCAATCTT GCACCAGGCAGCCCAACCCTGACCTAAAGTAAATCCCAGAAGTCTTTCTGGGTTT TGAATTTGCAGTAACAGCTGTGGGCATTCTAGCAGCAGTTCGATGATCATGTATGGT ACTGCAAACAGGA
ex3_57_76775_x1	ENST0000384645.1	33	8E-14	65.9	1	GGATCGATGATGACCTCAATACATGCATTCTTGGAAAGCTGAACAAAATGAGTGAA AAC
ex3_57_79653_x1	CM000680.2/2774846	14	0.009	28.2	1	ATCTTGGTGGACTTGACTTTGAACAAGAATGCTTGTGATGATTGGGTGTTACGCAC ATGCGTGAGATATGCCACCCTTGAACCTTGTTACTGTTGGCACATTACCTGTCTGA CC

	-					
	277496					
	3					
ex3_57	CM000	15	0.002	30.2	1	AAGACTACACTTTTCAGGGATCCTTTCTTCAGTTCGTTACTAGAGGTTTCTCTGAATAT
80561_	668.2/7					GTAGAGCACCAGAAACCACTAGAAGGAAATGCAGTGTGCTCTCTCCAGAGTGTGAA
x1	112710					GCCAACCCTTGGTGTTGCTTGGCTGCAACTGCCGTTTACCATTGACAATTGTTCTCTT
	5-					CCTCAAGAAGAATGAGAGGGGAAAGAAGGCAGTCTGTGTGAT
	711268					
	93					
ex3_57	ENST0	16	0.001	32.2	1	CTACAATCAATTAAGCCACATGGGGCCTGGTGTGCAAGGGCTGCAAACAGCATCATC
80979_	000051					CTA
x1	6324.1					
ex3_57	AC012	19	0.004	30.2	1	CCCUAUUAUUCGAAAGUUAUCCUGGUCAUUGACAGUGCAGGGAGAGAAACUGCUGA
81082_	560.5/1					AAGCAUUCUUUUUGGAGGGUCCACUCCUGUCCCUUCUAAACUCUGGAGUU
x1	66192-					UCCACA
	166076					
ex3_57	CM000	15	0.004	30.2	1	ATCCTTTTGAAGTTCATAAGCATGGTATTGGGTTTTTCACTCATGTGTGAGATGTA
81240_	674.2/6					CCACCCTTAAAGCTTGTTATGATGTAGGCACATTACCCATCTGACA
x1	435586					
	5-					
	643557					
	62					
ex3_57	CM000	15	0.006	30.2	1	TGTTTAATGACTAAGGAAGTCCCTGTCCCCGCCAGGGGCTGTGAGCAACACCATG
81982_	680.2/2					GCTGCCCCAGGGCTGGCCAATTGGGCAGATGCCAGGGGCTGAGAACA
x1	145075					
	6-					
	214506					
	53					
ex3_57	CM000	15	0.002	30.2	1	AAGACTAAACTTTTCAGGGGTCATTTCTATAGTTCATTACTAGAGAAGTTTCTCTGAAT
82735_	664.2/1					GTGTGGAAAAATAAGTCAAT
x1	647463					
	12-					
	164746					
	389					
ex3_57	ENST0	14	0.008	28.2	1	TCCTCGCATGGGATAATTTTTACTTTATTCTCCCTTTGGAGGTCAGGTTAAACATGA
83377_	000045					TT
x1	9095.1					
ex3_57	CM000	14	0.008	28.2	1	ATCTTTTTGTAGTGTAAGTTTGATCATTGGATTTTCATGCTCACGTGTGATACGTGCCT
84277_	672.2/6					CCTTCAAACCTTGTTATGACACTAGCACATTATTCATATGACA
x1	661533					

ex3_57 84380_ x1	8- 666152 37 CM000 675.2/1 987518	15	0.003	30.2	1	ATCCTTTTGGAGTTCATGAGTGTGAGAACTGGGTGTTACCCGCATGTGTGAGATGT GCCACCCGCAAACCTTGTTATGACATCAGCACATTACTGAAA
ex3_57 84751_ x1	7- 198752 85 CM000 676.2/3 130652	15	0.004	30.2	1	AAGACTCTACTTTCAGGGATCATTCTATAGTTCATTACTAGGGAAGTTTCTCTCAATG TG TAGAGCACAAAAAGTAAAT
ex3_57 84769_ x1	0- 313066 00 CM000 676.2/5 084462	14	0.008	28.2	1	TGAGTTTTGGGATGAGACCCTGGAATAAGTGCTGGACACAGTGCCTGAATCAGACTG TGGAAATATTAATGTATTTTATTTTACTTA
ex3_57 85262_ x1	5- 508447 12 CM000 664.2/3 075772	15	0.004	30.2	1	ATCCTTTTGTGATTCATAAGCGTGATGATTGGGTTTTTCATGCTCATGTGTGAGATATG CCTCTCTCAAGCCTTGTTACAACATCACATTACCTGTCTGATG
ex3_57 85399_ x1	- 307567 2 AC023 490.5/1 21842- 121984	14	0.009	28.2	1	UUCUCAGGUCGCCAGUGCAGCCCCAAGAUGAGCCUGCAGUAUUUUCCUUACAUGA UCUGGUCCUACUGUGGGCAGCGCUGCUGCCCAGAGCCUGAGAGGAUUAUGAAAA CAUGGCAACGGAAGUGAGGCCAGGGGACACAGCA
ex3_57 85404_ x1	AL591 067.35/ 160576	16	0.001	32.2	1	UGGUCAUUACCAAGGCUUUUJAGAAUGCAGUUUCUCAUUUGCUGUGGACAUGACCA UAAAGAAAAUUCCAUGAGGUUUUUAUUAUGCUACUUGACUAGCAGUUAACCGU UUGGGAACACGU
ex3_57 87420_ x1	- 160455 CM000 677.2/5 876068 1-	16	0.001	32.2	1	AAGACTATACTTTCAGGGATCATTGTATAGTTCGTTACTAGAGAATTTTCTCTGAATG TG TAGAACACCAGAAACCACAAGGAGGAGGCGCAGCGTTCTCTCCTGAGCGTGAAG CCGGGTCTGGTGTGCTTCACTGCAACTGCCATTTGCCATTGATGATTGTTCTTCTC TTCTTTGGGAGAGTAAGAGGGCAAAGGATGCAGTCTGAATGGT

	587604						
	66						
ex3_57	CM000	15	0.003	30.2	1	TTCTTACAAATCTAAATGTGCTTTGATGCAAGTATATTTGAATCCCTTTCCATCTGATA	
87442_	679.2/1					ACTGAGCAAATAATA	
x1	894399						
	9-						
	189440						
	73						
ex3_57	CM000	14	0.009	28.2	1	ATCCTTTTGTGGTTCATAAGCATGATGATTGGGTTTTTCATGCTGTGTGAGGTGTGCCT	
87872_	663.2/1					CCCTCAGACCTTGTTATGACATTAGTATATTACCTGTCTGACA	
x1	591089						
	7-						
	159109						
	97						
ex3_57	AC009	16	0.000	32.2	1	UGGCAUGAUUUCCUGCAGGUUGAGCUCAGCCAAGUACCACCCUCAGUAAGCCUA	
88367_	228.4/5		9			GAGUAGAGGGGCCUGACAUCCUUUCCUUAAAUAACAAGGAGCCUUAUCCAGGU	
x1	9361-					UGUCCUAGUCUCAUACUU	
	59234						
ex3_57	ENST0	15	0.005	30.2	1	GCATGGTAGTGGGTTTCATTGGGGGCCCTTCTCTGTGGGCCTCATAGCGTACCCATG	
88494_	000038					CCAG	
x1	4771.1						
ex3_57	CM000	15	0.005	30.2	1	ATCCTTTTGTAGTTTTTAAGTGTCATGATGGGGTGTCCATGCACATGTGTAAGATGTG	
90276_	677.2/5					CCACTCTTGAAGCTTGTTACAACATGGGCAGATTACCAATCTCACA	
x1	595580						
	4-						
	559557						
	01						
ex3_57	CM000	14	0.008	28.2	1	ATCCTTTTGTGGTTC AAGAGCGTGATGATTGGGTTTTACGCTCATGTGTGAGAAGT	
90404_	669.2/2					GCCTCCCTCGAATCTTGTTATGACTCCATGTTGGCAAATTATGTCTGAAG	
x1	389513						
	4-						
	238950						
	28						
ex3_57	CM000	15	0.003	30.2	1	GACTTCTCACTGAGCTTCTTTCTGTCTGTTGCTGGCAGCTTATGGATTCATATGAGCA	
90544_	666.2/7					GAGAGAATCACAGA ACTAGCATTACTTTTGTCTTTACAGGAGTATATTTGGCTGTCTT	
x1	984310					GTGAGATATTA	
	2-						
	798432						
	28						
ex3_57	ENST0	15	0.008	30.2	1	ATAAACAAAAGAACACCAATTGTGCTCCTTTCCTCCTGGGGCCAGTGCAATGGC	

91198_	000036					TGC
x1	5509.1					
ex3_57	ENST0	14	0.009	28.2	1	AGGTCATTTCAAAGAAGGTTACAGTGGCTGTGAGACCAAGAACGCTTAATGCTGTTA
92609_	000051					CCA
x1	6741.1					
ex3_57	ENST0	23	4E-08	46.1	1	TGGACCTATGATGATGACTGGTGGCGTATGAGTCATTGACGGTGAATACAGGTCTGG
94453_	000036					AAG
x1	2705.1					
ex3_57	ENST0	15	0.003	30.2	1	TGAACTAGTGGTGGTGGCTTGTGGCATATTTAGTCACAGATGATGAATAAATACATGC
95125_	000036					CT
x1	2520.1					
ex3_57	ENST0	15	0.003	30.2	1	TCCACATTCTAAAAACAATCCACTCTGTGAGGTGCAACAGTTAATAGCATGTTAGAGT
96057_	000051					TC
x1	6475.1					
ex3_57	CM000	15	0.005	30.2	1	AAGACTATGCTTTTCAGGGATCATTTCTACAGTTTGTTACTAGAGAATTTCTCTGAACAT
96325_	663.2/1					GTAGTTTTCAAAAAAAAAATTAGATT
x1	240925					
	1-					
	124091					
	68					
ex3_57	ENST0	14	0.008	28.2	1	ATGCATCTATTTGACAGACCTGGAACAGTTATTTTTTGGCCACTAAGATTTCTACTACAG
96805_	000051					A
x1	6241.1					
ex3_57	CM000	16	0.000	32.2	1	ATCTTCTGTAGTTCATCAGTATGATACCTGGGTGTTTCACACACATGTGAGATGAGTC
96864_	665.2/4		8			ATTCTTGAACCTTGTTATGATGTCAGCACTACCCATCTAACC
x1	746634					
	9-					
	474664					
	48					
ex3_57	ENST0	15	0.004	30.2	1	CCAACATGGATAGTCTGGGAGGTCCTCTCCCCAGGCTCTGTGGAAGTGGTGTGG
98067_	000036					GGAG
x1	2342.1					
ex3_57	CM000	14	0.008	28.2	1	ATCCTTTGTAGTTAATAACATGATGATTGTGTTTTCACACTCTCGTGTGAGATATGCCT
98322_	680.2/3					CCCTCAAATCTTGGCACATTACCCATCTGACA
x1	424349					
	-					
	342425					
	9					
ex3_57	ENST0	15	0.002	30.2	1	GGATCGATGATGACTTTTATACATGCATTCCTTGGAAAGCTGAACAAAATGAGTGAAA
99681_	000038					AC

x1	4549.1						
ex3_58_00284_x1	ENST0000516178.1	15	0.003	30.2	1	GTGTGGGATGTGTGTCTAAACACGACAATCTGAAGACAGAGGTGTAGAAATTGGCAAGTT	
ex3_58_00831_x1	AL132709.5/169743-169666	15	0.004	30.2	1	GGGACCAAUGAUAAUGACUGUUGGGGUAUGAGUCAGUGAGGUUGAAUAACAGUUUGUAUCUGGAAAUCUGAGGUCCAA	
ex3_58_01402_x1	CM000663.2/51724896-51724775	19	0.007	30.2	1	GTGCCCTTTTAAGGTTGACGCAGTGCTTTAAGGGGCTAACACAGAAGGGTAAAGGAA GTCTCCATAAACCCCAGAGAAGAGATTGTAAAGCTCCTCTTTAGAACCTTTCTGGAGT CACACCT	
ex3_58_01827_x1	CM000669.2/152069005-152068900	20	0.002	32.2	1	ATTCTTTTGTAGTTCATAAGTGTGGTGAAGTGGGTTTTTCATGTGCTTGTGGGAAATATG CCTCCCTCAAATCTTATTACGAAGTCAGCCATTTTACTTGTCTGACA	
ex3_58_02130_x1	CM000679.2/44303998-44304203	20	0.001	32.2	1	GGGCACAGTCTCATTGTTTCTATAGTTTATTACCAGAAAAGTTTCTCAGAATGTGTAG AGCACTGGAAACCATGAGGAAGAGGCATAGCGTTCTCTTTGAGCATCAAGTTGGCT GTTGGTGTGCTTTGCTGCAAACGCCATTTGTCATTGTCTTCCTTGTCTTCCTTTAGG AGAGTAAGAGGGAGAGGACACAGTCTGGGTAGT	
ex3_58_02263_x1	ENST0000611947.1	15	0.003	30.2	1	AAGCCTATGCATTCTGGGATCATTTCGATAGCTCGTTCCTGGAGAAGTTTCTCTGAG CAC	
ex3_58_02482_x1	CM000673.2/11562708285-115627082	14	0.008	28.2	1	GTCCTTTTGTAGTTCATAAGCGAGATGATTGGGTGTTTCAGGCACATGTGTGAGATGT GCCTCCTTCAAACCTTGTTACAACGTCAGCACATTACCCGCCTGACA	
ex3_58_02973_x1	ENST0000384004.1	15	0.004	30.2	1	TTCTAAAGTGTTGAGTTCAGTCCAGGGTGGATCCCCTGCTCTGTTAATTGAACTGGA ACA	
ex3_58_03452_x1	ENST000036	21	5E-07	42.1	1	TGGACCAATGATGACAAATACCGGCGTATGAGTCTTGGATGATGAATAATACGTGTC TGG	

x1	5400.1						
ex3_58 04481_ x1	ENST0 000036 5087.1	16	0.000 6	32.2	1	AGGTCACCTTCAAAGAGGGCTTGTGGGGCTGTGAAACCAAGAGGTCTTAACAGTATGA CCA	
ex3_58 04516_ x1	CM000 667.2/1 338509	15	0.004	30.2	1	ATCTTTTGTGTTTCCTAAGTGTGATGATTGAGTTTTCAAACCTCACTTGAGGTGTGCCT CCCTTAAACCTCATTATGACATCAGCATATTACCCATCTGACG	
	57- 133850 857						
ex3_58 04850_ x1	CM000 665.2/1 874233	14	0.009	28.2	1	ATCCTTTTGCAGTTCATGAACATGATGATTGGGTGTTTCATGCTCATGTGTGAGATGTG CCACCCTCTGAATCTTGTTATGACATCAGCACATTATCCATCTGACC	
	15- 187423 419						
ex3_58 05836_ x1	AL049 840.8/4 9457- 49533	21	7E-07	42.1	1	AUUGUUACAUUGAUAAAAUCAAAUCACCAUCUUUUUAGCUAAGCUUGUGCUGGAUU UGCUUUUUUUCUGAUAAAGAUG	
ex3_58 06011_ x1	CM000 667.2/8 431560	15	0.003	30.2	1	AAGACTATACTTTTCAGGGATCATTCTATGGTTCATTACTAGGGAAGTTTCCCTGAAT GTGTAGAGCACCCGAAAACACTCTTCAGG	
	5- 843156 90						
ex3_58 06379_ x1	CM000 685.2/1 704451	15	0.003	30.2	1	GGCGGCCCTTATCACAGCTGCAGCTGCTTCCACATAGCTGCTGCGGTCAAAAAGGA GCCCAGAGTCAGTTTCCCTTGACCATCACCATTCTGTTTGCTATAAGTGATCTGTAACA TTTTGCGAAAATACAGTT	
	1- 170443 80						
ex3_58 06981_ x1	CM000 671.2/1 145653	15	0.002	30.2	1	ATCCTTTTGTAGTTCATAAGGATGATGACTGAGTGTTCCACTCGTGTGTGAGATGTG CCACCCTCAGACCTTGAAATCTTCAGTCACTCTTGTTAAGTGAAC	
	52- 114565 250						
ex3_58 07236_ x1	CM000 671.2/1	16	0.000 7	32.2	1	ATGCATCTATTTGACAGCCCCAGAGCAGTTACTGTCTGCTAAGGTTTCCACTACAGAT GCAAAAACAGCGTCCCTGTGCTTTCTCTCTGACTGCTTTCTGCTTTCTGTGGCAGCC	

x1	310213 06- 131021 168					GAGATTGAATAGAGGAATCCAGGA
ex3_58 07293_ x1	CM000 672.2/1 639875 9- 163986 55	15	0.002	30.2	1	ATCCTTTTGTAGTTCATGAGCATGACCATCGAGTGTACATGCATGTGTGAGATATG ACACCTTCTGAACCTTGTTACGGAGTTGGCATGTTACCCATCTAACC
ex3_58 07810_ x1	ENST0 000051 6831.1	15	0.006	30.2	1	TAGTGTGGAAGTGTCTACTCCTCATTCTGTGGAAGCAGGAATACATTCATAACATGC TC
ex3_58 08545_ x1	ENST0 000051 6965.1	15	0.005	30.2	1	TTACCTTGAATACATACAGATACTTCTGTTACTCTCTAGCTTAAGAACCTTTAATGTG G
ex3_58 08602_ x1	ENST0 000036 3205.1	14	0.009	28.2	1	AGGATATATCAAAGAGACTTTCTGGGGCTGGGAAACCAGGATCTCGTAATGCTATGA CCA
ex3_58 08885_ x1	ENST0 000051 6634.1	14	0.009	28.2	1	GATTCACAGCAGAAAGACAGCTAATCTAGTGTGCTAGCTGTAGAGCAAGTTTGCTGC AAA
ex3_58 09911_ x1	CM000 663.2/2 156301 17- 215630 026	14	0.008	28.2	1	AGATCATTGATGACTTCCATATATCCATTCTTGGAAAGCTGAACAACATGAGTGAAA ACTCTACTGAAAAAAGAAAAGAAATGGGAGGCCG
ex3_58 11206_ x1	CM000 681.2/3 834911 0- 383490 09	15	0.003	30.2	1	ATCTTCTTGTAGTTTCTACGTGTGGCGATTGGGTTTTACCGTCATCTGAGATGTGTC TCCCTCAAGCCTTGTTATGGTGTGCGCCATTACCTGTCTGACA
ex3_58 11793_ x1	ENST0 000036 3915.1	21	5E-07	42.1	1	TCCCAATGATGAGTTGCCATGCTAATACTGAGCCACCAGGTAGGGCAGTGTTGCCCT GGT
ex3_58 11980_ x1	CM000 683.2/3 934545	14	0.008	28.2	1	ATCCTTTTCATAAGCTTGAAGATTGGGGTTTACGCTCATGTGTGAGATGTCCCTCTCT CAAACCTTACTATGAAGTCAGCACCCTGGGCACATTACTTGTCTGACA

	7-						
	393453						
	51						
ex3_58	ENST0	14	0.009	28.2	1	TCCATCTGTTTGGCAGACCTGGAGCAGTTAGTGTCTGCTGCTAAGGTTTCCATTACA	
12322_	000051					GAT	
x1	7219.1						
ex3_58	AP000	18	8E-05	36.2	1	GAGCUUCCAGGAUCACCCUUGCAGAGUGGCUAAUUAUUCUGCCAGCUUCGGAAAGG	
13648_	577.5/6					GAGGGGAAGCAAGCCUGGCAGAGGCACCCAUUCCAUUCUCCAGCUUGCUUAGUAG	
x1	9612- 69474					CUGGCCAUGGGAAGACACUGUGCAACACUG	
ex3_58	ENST0	17	0.000	34.2	1	GGCCTTTTGGTGCTTACCACAGACTGTGCTCTTTCCTGACTGAATAGAGAGAGGAG	
13711_	000038		3			GCA	
x1	4151.1						
ex3_58	ENST0	15	0.002	30.2	1	CTTCCCATTATTTGCTGGTATAGTCTCACAATGATATGGCCAGTTATACTTATGGGA	
13849_	000036					AA	
x1	4790.1						
ex3_58	ENST0	20	3E-06	40.1	1	AAGACTATACTTTCAGGGATCATTCTATAGTTAGTTGCTAGAGAAGTTTCTCTGGAC	
14153_	000036					AT	
x1	3668.2						
ex3_58	ENST0	14	0.009	28.2	1	ATCCTTTCACAGTTCATAAGAGTGATGACTGGGTTTTCACTTTCATGTGTAAGATGTG	
14274_	000045					CC	
x1	9350.1						
ex3_58	ENST0	15	0.006	30.2	1	AAGACTATACTCTCAGGAATCATTCTATAGTTTTTTACTAGAGAAATTTCTCTGAACG	
14840_	000038					T	
x1	4486.2						
ex3_58	ENST0	14	0.008	28.2	1	AAAGCAAGCTGGAATTACAGTGCTTCATTTTGTGAAATACTAAATACCATCATTATGCT	
15998_	000039					G	
x1	0904.1						
ex3_58	CM000	14	0.008	28.2	1	GGACCAATGATGACTTCCATACATGCATTCCCTTGAAAGCTGAACAAAATGAGTGGG	
16479_	677.2/2					AACTCTGTACTATCATCTTAGTTGAACTGAGGTCC	
x1	507905						
	8-						
	250791						
	49						
ex3_58	ENST0	28	6E-11	56	1	AATGAATGATGACAAAATGTTTCAGTCCCAAATGATACATACTGATTATACCATTATAT	
16619_	000036					T	
x1	4394.1						
ex3_58	CM000	15	0.005	30.2	1	ATCCTTTTGTAGTTCATAAGCTGATGGTTGGGTTTTACGCTCATGTGTGAGATGTGT	
16750_	668.2/4					TCCTTCATATCTGTCAACACACTACCGGGCTGTTG	
x1	643762						

	-						
	464385						
	4						
ex3_58	CM000	14	0.008	28.2	1	GATCAGCTTTTTCAAAGGTTTACTGCATTTTTACCCTCCCTGATGGGGCTCAGTGTGCG	
17333_	686.2/2					CAGCTGGAAAAAGTAGATGCCCTGGTTATGCATGCAGCTCATTTGTTGTACATGTTG	
x1	624738					CTTTAAGGGACCTTGAAGACTCTT	
	4-						
	262475						
	21						
ex3_58	CM000	14	0.008	28.2	1	AAGACTTTATCCCCCACCCCGCAAAGAAAAGGAAGAAGAAGAGTTTTTAAATGGCG	
17449_	663.2/2					CAGCCCTGGAATCCACAAGGAGGAGGTTTCAGTATTCTCTCCTGAGCGTGAAGTTGGT	
x1	199626					TCTTGGCATTGCTTCACTGCAACTGCTATTTGCCATTGATGATTGTTCTTCTCTTCTC	
	52-					TGAGAGAGTAAGAGGGAGAGGATGCATGCAGTCTGAGTGGT	
	219962						
	865						
ex3_58	CM000	14	0.008	28.2	1	AAGACCCTTCAGCTGCAAACAACAGCTTCCTTGGTAGTTTATGCAGCCTGTTTCTTGT	
17839_	678.2/5					ATGGGCTGCTCTAAGGGACCATGGAGACAGGC	
x1	015173						
	1-						
	501516						
	42						
ex3_58	ENST0	14	0.009	28.2	1	CTTCTGCTAAGGTTTACACTATAGATGCAGGAAAAAAATGTCCTCACACTGTCTGTC	
19324_	000051					TG	
x1	6029.1						
ex3_58	AJ6094	23	4E-08	46.1	1	CUGGCACUUUCACAGUUCUUCCCCAGGCAGUGGGGCCAGGAUUUGGUAGCUGG	
19516_	40.1/1-					UGCUGAGAGAAAACCCUUGAUUGUAUUCUUGCCCUGGGAUUUAUACCAGUGGCAAC	
x1	129					UGUCACUCAAUUGGGACAGUG	
ex3_58	CM000	18	0.009	28.2	1	ATCTTTTTGTAGTTCATAAACGTGATGACTGTGTTTTTCATGCTCATGCGTGAGTTGCA	
19691_	678.2/2					CCTCCCTCAAACCTTGTTTTGACATTGACACATTATCTGCCTGATG	
x1	867233						
	6-						
	286722						
	33						
ex3_58	CM000	14	0.008	28.2	1	ATCCTTTTATAGTTCATAAACATAGTAATTAGGTGTTCCCATTGCATGTATGAGATGTG	
21579_	664.2/6					CCTCCCAAAGAGCTTGTTACAGCGTTAGTACATTACCTGTCTGATA	
x1	991269						
	5-						
	699127						
	99						
ex3_58	ENST0	14	0.009	28.2	1	AAGACTACACTTTCAGGGATCCTTTCTTCAGTTCGTTACTAGAGGTTTCTCTGAATAT	

21706_	000040					GT
x1	8418.2					
ex3_58	ENST0	15	0.004	30.2	1	TTGCATGTGGTAATGTCTGCTCTTCATTCCCTTTGGGAGCAGAAATACATCCATAACAC
21750_	000045					GC
x1	8806.1					
ex3_58	CM000	16	0.001	32.2	1	AGCACTTGTGTTTGGCTTTTGTGTTGACTTGTGGACAAAGACTTATAGTAGACAGGCACG
22125_	667.2/1					AAAAAATAAATCCTCTTTTGGCAACCCATGAGTTGTTATACATGCAAGAAGGAATATT
x1	680332					
	05-					
	168033					
	091					
ex3_58	ENST0	14	0.008	28.2	1	CAGTCAGTGTGCGAGAACCTTATATTGTTCTGAAGAGAGGTGGTGACTTAAAAATCATG
22184_	000036					CT
x1	3528.1					
ex3_58	ENST0	15	0.004	30.2	1	GTGTGATGAAATCACCCCAAATAGCTGGAATTACCAGCAGATTGTGTAGTGGTGAAC
22343_	000045					CTA
x1	9126.1					
ex3_58	CM000	19	0.005	30.2	1	AAGACTATACTTTTCAGGGATCATTCTATAGTTCATTACTAGAGAAGTTTCTCTGAATG
22702_	680.2/7					GGTAGAGCACTGGAAACCATGAGGAGGAGGCACAGTGTTCTCTCCTGAGCATGAAG
x1	995570					CTGACTCTTGGTGTGCTTCACTGCACCTGCCATGTGCCACTGATGATTGTTCTTGTCT
	-					TTCCTCTGGGAGAGTAAGACGGAGAGCATGCAGTCTGAGTGCT
	799578					
	5					
ex3_58	CM000	14	0.009	28.2	1	ATCCCTTTGTAGTTCATAAGCATGATAATTGGGGTTTCCCTCGCATGTGTGAGACATG
25207_	679.2/1					CTTCCCTCAAACCTTGTTACGAAGCTGGCACAGTATCCATCTGATG
x1	616295					
	-					
	161619					
	2					
ex3_58	CM000	14	0.008	28.2	1	CCAATGTGGATACACCCAGGAGGTCACTCTCTCCCAGGCTGTGTCCAAGTAGCATA
25327_	682.2/8					GGGAGCACAGGGCTCTGTCCCATGATGTAAGTGTCTTTTCCATGACATTGGAGAT
x1	831186					GAAGCTGGACCTCAACTCTGCACATGCATATTCCTACAATTCTCAGAGTCTGTGG
	-					ATAATGACGGAGGAGAGAAACCATGCAGGAAACAGCC
	883139					
	3					
ex3_58	CM000	14	0.009	28.2	1	TGGACCAGTGATAAGAATGTGTTAGGAACCAAAGATTAGGAGTAATCTAGTTTTGTAT
25406_	670.2/4					ATCTGAGGTCCATT
x1	204357					
	5-					
	420435					

ex3_58 25474_ x1	04 CM000 684.2/2 823282 3- 282327 56	15	0.003	30.2	1	CAGCCCTAAAATGGAAAAATTTAAAATTACTTAGACAATGTGATGTCATCAAAGGAA CCCTAAGTAA
ex3_58 26044_ x1	ENST0 000036 4528.1	14	0.008	28.2	1	TCGTCAGGTGGGAGAATTCTTACATGTTCCCTCCTTTTGCAAGGCAGATTAGAACATGA TG
ex3_58 26727_ x1	ENST0 000039 0863.2	15	0.004	30.2	1	AAGATTATATTTTCAGGGATCATTCTATAGTTTGTCACTAGGGAAGTTCCTCTGAATG T
ex3_58 27757_ x1	CM000 663.2/1 515279 38- 151527 831	14	0.009	28.2	1	TATAGTGTGGCCATGGGATCTCCAACCTGCATGCAAGAGCAACCTGGAGAGACTTTGA CAGAACAGGTCAGACAATCCCTGCAGCTGCCACTTGTCTTTCGTGTGTGT
ex3_58 27901_ x1	AC087 763.10/ 29854- 29985	15	0.002	30.2	1	CUGCAGCCAAUUGAGCUGAUGGAGUUCCUUUCCUCCUGGGGCCAGUGUGCAA AGCUGCAAACAGCAGCUUCCUUGGUAGUGUACGCAGCCUGUUUCUUUAUUGGGU UGCUCUAAGGGACCUUGGAGACAG
ex3_58 29919_ x1	CM000 674.2/1 200484 30- 120048 528	14	0.009	28.2	1	ATCTTTTTGTAGTTCATAAACATGATGATTGGGCTTTCACACTTGTTTGAGGTGTGTCT TCCTCAAACCTTATAGTGTGTCAGCACATTGCCTGTCTGATG
ex3_58 30278_ x1	CM000 670.2/5 612135 2- 561212 42	14	0.009	28.2	1	ACCAAGATTCAAGTCACATTCCGAGTGTCCCGGTGTGCTAGGGCACTTGCAGAGAAT CTGCTGGTCTTGATTCACTGGTGGGGGCAATCGGTGCCAGATTAGGAACATGC
ex3_58 32426_ x1	ENST0 000051 6421.1	18	0.009	28.2	1	TTTCCAGAATTACGGGTTTGACAAACCAAACATTCAATTATTTTCTCTCTAGAGAGAG TT
ex3_58 32519_ x1	ENST0 000060	16	0.000 5	32.2	1	TGTGTGCTCCACAAGGAGCACATTTTGCCTAACACCACAAGAGTCTGGCTCAGTGA ATG

x1	6322.1						
ex3_58 33900_ x1	CM000 670.2/4 337829 8- 433785 10	15	0.003	30.2	1	AATGCTATACTTTTCATGGGTCATTTCTATAGTTTGTATTAGAGAAGTTTCTCTGAATG TGTTGAGCACCAGAAACCACGAGGAGATGCAGCATTCTCCTGAACGGGAAGCCA GCTTTTGGCATTGCTTTGATGCAACTACCATTTGCCATTGATGGCAATGCATCGCTTC CTCTAGGAGTGTAAAGAGGGAGTGGATGCAGTCAGAGTGGT	
ex3_58 34004_ x1	AC064 836.7/3 0066- 30155	23	6E-08	46.1	1	UGAUGGCAAUGAUGAUUUUUACACUUAUUGUUGUUCACCUGAUACAUAUAUAUG AGGGUGUUCAGUCACUACCUCAUCUGAUGCCAUCA	
ex3_58 34060_ x1	ENST0 000040 8133.1	15	0.002	30.2	1	AGGGTTTGCTTAGGGCAGGGAGGTTGAAGAGTGGCTCCTCTGTTTACAATACACCAA ACA	
ex3_58 34405_ x1	CM000 684.2/3 694848 0- 369485 61	19	0.004	30.2	1	ATTATTTTGTAAATTCATAGACGTGATGATTGGGTGTTCCCTATGCATGTGTGAGATGTG CCACCTTCAAACCTTGTTACTGTA	
ex3_58 37189_ x1	ENST0 000036 4359.1	19	1E-05	38.2	1	AGGTTGGATTTCATTGTTACAATATAGCTGTGAAGTGCTATGTTGTCCTTGCCCCCTGC TC	
ex3_58 37646_ x1	ENST0 000038 4159.1	14	0.009	28.2	1	CTGCAGTCAATTAAGCCAGCTGTACTCCTTTCTCACAGGGGCTCGGTGTAATGGCT GCA	
ex3_58 37856_ x1	CM000 680.2/3 209450 4- 320946 06	14	0.008	28.2	1	ATCCTTTTGC GGTTTCATAGTGTGATGATTGAGTGTTCCACAGGCATGTGTGAGATATGC CATCCTCAAACCTTGTTACAGGGTCAGCACATTACCCATCTGACA	
ex3_58 37898_ x1	CM000 677.2/2 489374 7- 248938 48	16	0.000 6	32.2	1	ATTCTTTTCATGGTTCTTTATCGGTATGGTGATAGGGTTTTTCATATTCATGTGTGAGATG TGCTCCCTCAGTCCTTGTTATGACATCATTACGTGTCTGACA	
ex3_58 37914_ x1	ENST0 000039	15	0.004	30.2	1	TTCTTATTGAGCTCCTTTCTGTCTACTGGTGGCAGTCTATGGATTTGCACAAGACAAA AC	

x1	1278.1						
ex3_58 38718_ x1	CM000 672.2/2 686816 5- 268682 64	14	0.009	28.2	1	ATCCTTTTCATAGTTCATAAGCATGATTGGGTTTTTCACACTATGTGTAAGATGTGCCTC CATCAAACCTTGTTAGGATGTTGGCATATCACCCATCTGATG	
ex3_58 38988_ x1	CM000 668.2/1 495946 25- 149594 759	15	0.003	30.2	1	TAGGCCCTGAATCAAGAAACGTGATGGTTTGCCATTGTAGCTATTGGTTTCAAACAAG AGCCAAGATTGATGTCTTTCTTATGGTCTGTTGGCTAATCCCAGTATGAATGGCCAGT TCAGCTAGAAGAAACAAAC	
ex3_58 40365_ x1	AF250 841.1/1 8857- 18939	14	0.008	28.2	1	GGAUCGAUGAUGACUUAUUUUUUUUGGAAACCUUGGAAUUCUGAACAAAAUGAGUGA CCAAGACACUUCUGUGAGCUGAGGUCC	
ex3_58 40873_ x1	CM000 666.2/1 587006 91- 158700 909	26	6E-05	36.2	1	AAGACTATACTTTTCAGGGATCATTCTCTAGTTCAATACTACAGAAGTTTCTCTGAAG GTGTAGCAAGCACCAGAAACCACGAGGAAAGTGCAGTATTCTCTCCAAGTGTGATG CCGCCCGTCTCTTGATGTTGCTTTGCTCAGCTGCCATTCCGGCATTGATGATTGTTTTA TCCTTCCTTAGGAAGAGTGAGAGGGAAAGGATGCAGTCCAAGTGGC	
ex3_58 41028_ x1	CM000 665.2/1 716932 11- 171693 314	15	0.002	30.2	1	ATCCTTTTGTAGTTCATGAGCATGATGATTGTGTGTTACACACAAGCGTGAGATGTG CCCACTCGAACCTTCTTACGACGTCTGCACATTACCCATCTCATC	
ex3_58 41284_ x1	ENST0 000051 6773.1	18	7E-05	36.2	1	ATGCATCTATTTGACAGCCCCAGAGCAGTTACTGTCTGCTAAGGTTTCCACTACAGAT GC	
ex3_58 41977_ x1	CM000 679.2/1 207716 8- 120770 77	15	0.005	30.2	1	AAGACTATACTTTTCAGGGGTCAATTTCTATAGTTCATTACTAGAGAAGTTTCTCTGAACA TGCAGAGCACCTAAGATGTTTCCGTTCTCCTGA	
ex3_58 42159_ x1	CM000 672.2/6	16	0.000 8	32.2	1	ATCTGTTTGTAGTCATAATTGTGATGGTTGAGTTTTTCATGTGTGAGATGTGTATCACT CAAGCCTTTTTACAATGTCGGTATATTGCCGGGTGCGGTG	

x1	871295 8- 687130 55						
ex3_58 43287_ x1	CM000 685.2/1 533514 73- 153351 576	14	0.009	28.2	1	ATCCTTTTGTAGTTCATACACATGACAATTGGGTTTCCACGCACGTGCATGAGATGTT CCTCCTTCAAACCTTGTTACTATGTCAGCACATTAAGTGCCTGGCA	
ex3_58 43404_ x1	ENST0 000038 3865.1	15	0.006	30.2	1	GTGGAGGTCTATTCCAATGGGGCTTTTCTGTAGCTGCATGTTGTTGGAAACTCCTC ATA	
ex3_58 44058_ x1	ENST0 000036 3091.1	20	2E-06	40.1	1	CTGAGTCCATGATGATTTCAAGTTATCCCTGTCTGAAGGCAAAGAAAGGCCTTTCTGT GT	
ex3_58 44478_ x1	AL161 747.5/1 3638- 13529	22	2E-07	44.1	1	UCCCAAUGAUGAGUUGCCAUGC UAAUACUGAGCCACCAGGUAGGGCAGUGUUGCC CUGGUUUGGGUGCCAGUGAGUUUAACAAAACUUCUCACAUGAAGAUCUGAGGGGC	
ex3_58 44534_ x1	CM000 664.2/1 721561 39- 172156 029	24	0.001	32.2	1	ATTCTCCTAAGGACTGTGCAACCTGAGCATGATGATTGGGTATTCACGTGCATGTGT GAGATCTGCCACCCTTGAACCTTGTTATGACGTTAGCACATTACCCATCTGACA	
ex3_58 44650_ x1	ENST0 000036 4830.3	19	0.003	30.2	1	TAGACCAATGATGAGTATTCTGGGGTGTCTGAATCAATGATTTTGATTAACCCTGTA AC	
ex3_58 44769_ x1	CM000 666.2/4 730603 7- 473059 34	14	0.008	28.2	1	TTCCTTTTGTAGTACATGAGCATGATGATTTAATTTTACACACATGTGTAAGACATGC CTCTCTCAAACCTTTGTTATGAGGTCAGCACATTACCTTTCTGATA	
ex3_58 44923_ x1	ENST0 000038 4785.1	18	0.009	28.2	1	TTCCACCACTATTGGTCTGCAGCTCTTCTTATGGTAGCAGTTGTTGCATTTCTCTGTG GG	
ex3_58 45388_ x1	ENST0 000051	15	0.002	30.2	1	CAGACTTACAGATAAGTTCGAGAAATAAACCCCTGTTTTGCAACCCAGAGCACATTGTT CA	

x1	5895.1						
ex3_58_45430_	ENST0_000036	16	0.0006	32.2	1	GATCAAGGATGAAAATACCCAAATTTGAGTATCAGAAGACCTTCCAGTCTACTTGATGCA	
x1	3024.1						
ex3_58_45737_	AF141_346.1/2	15	0.002	30.2	1	UACUGUUAGUGAUGAUUUUAAAAUUAAAGCAGAUGGGAAUCCCUCUGAGAAAGAA AAUGGAGAUUAAUCUUAACUGAAACAGUA	
x1	553-2637						
ex3_58_46128_	ENST0_000041	15	0.003	30.2	1	GTGCACATTTTCATTGTCTTTTTTCTTTATTTCAAGAGAAAAGATATATCTGATGTGCTCA	
x1	0656.1						
ex3_58_46751_	CM000_667.2/7	16	0.001	32.2	1	ATCCTTTTGTAGTTCAAGAGCATAATGATCGGGCGTTCACATGCGTGTGTCAGATGT GCCACCTCGAACCTTGTTAGGATGTTGGCACATTACCTGTCTGACA	
x1	6784096-76784199						
ex3_58_46874_	CM000_665.2/1	33	9E-14	65.9	1	ATACTTTTATAGTTCATAAGTCTGATGATTGGGTGTCATGCTCATGTGTGAGACATGC CTCCCTTAAGCCTTGTTATGACGTGAGCATATTACCTGTCTAGATA	
x1	22750372-122750475						
ex3_58_48062_	CM000_671.2/8	14	0.008	28.2	1	GTGCCCTTTTAAGGTAGACGCAGTTTCGTAAGAGGCTAACACATAAGGGTAAATTAA AGTAAGTCTCCATAAAACCCAGAGAAGAGACAGAAGAGACTGTGAAACTCCTCTTTG GACCCCATCTGGAGCCACAGCA	
x1	7260450-87260585						
ex3_58_48551_	ENST0_000038	15	0.002	30.2	1	TGGTAATTACCAAGATTTTTAGAATGCAGTTTCTCATTTGCCAGGGAAATGACCATAA AA	
x1	4049.1						
ex3_58_48805_	ENST0_000038	25	3E-09	50.1	1	CTGGCACTTTTCACAGTTCCTTCCCCAGGCAGTGGGGCCAGGATTTGGTAGCTGGTG CTGA	
x1	4028.1						
ex3_58_49416_	ENST0_000057	15	0.005	30.2	1	GCCGTGTGAGGCCACCTCTGCCATGCTGCAGGCTCCCCAGCACGCAGTGGGGAAC CCAAC	
x1	9216.1						
ex3_58_50908_	ENST0_000039	14	0.008	28.2	1	ATACTATGATGTTTGCATAGTTCAGCAGATTGAATTATGAAGAGATCTACCATTTGTCT G	

x1	1113.1						
ex3_58 51752_ x1	AC026 355.13/ 69334- 69207	14	0.009	28.2	1	UUUGAGGUCUUUCCCGAUGGGACUUUUCUGUAGGCUGCACAUCAUUGGAAACGC CUCAUAGAGUUAACUCUGUGUUUUACUUUACUCACAGGACUCUUGUUAGAUCUG UGGGAACUACAAGACAGUU	
ex3_58 54331_ x1	CM000 668.2/1 186518 - 118662 0	14	0.009	28.2	1	GTTCTTTTGTGGTTCATAAGTGTGATGATTGGGTTTTTTGCTCATGTGTGAGATGTGC CTCCCTCAAACCTCGTTATGATGTCGGCACATCACCCATCTGACT	
ex3_58 54515_ x1	ENST0 000036 3336.1	19	0.002	30.2	1	GTTTCTGATGAAGCCTATGTTGGTAGAGACATCTGAGAGTATTGATGAATGCCAACA GCT	
ex3_58 54758_ x1	ENST0 000036 3193.1	15	0.006	30.2	1	TGGGCCCTTTCACAGGCCCTCCCCTCGGCAGTGGGGCCAGGATTGGGTTGCTGGT GCTGA	
ex3_58 55486_ x1	CM000 668.2/1 009571 60- 100957 263	15	0.002	30.2	1	ATCCTTTTGTAAATTTATAAGCATCATGGTTAGGATTTAATGCTCATATGTGAGCTGAGC CTCCCTCAAACATTGTTAGGACATCAACACAATACCAGTCTGATA	
ex3_58 55701_ x1	CM000 664.2/1 203037 2- 120303 03	21	7E-07	42.1	1	TGTGTATGATGAGATTTCACTTCATGGTCTGTGTTTCTGAAACACATGATGTTGTGGA AGTTCTGATTTG	
ex3_58 55957_ x1	CM000 666.2/7 326396 0- 732640 84	19	0.003	30.2	1	TCTGAGACTAGAGTCACATCCTGACACGGCTCTTCTCCAATGTGCTGGAGTCCTCAG CATCTGCTGGTCTTGATTCACTGATGGGGGCAACCAGTGTCCCCTTAAGTGTCCGGG CAGAAACATAC	
ex3_58 56973_ x1	CM000 670.2/2 775512 2- 277550	14	0.008	28.2	1	ATCCTTCTGTAGTTTATGAGTGTGATGATTGGCTGTTTCATGTGCATGTATGAGATGTG CCACCCTTGAACCTTGTCATGTCTGATGTGAAA	

ex3_58 60465_ x1	32 CM000 673.2/1 020584 08- 102058 305	15	0.005	30.2	1	ATCCTTTTGTAGTTTATGAGCATGATGACTGGGTTTTTCACAGGTATGTGTGAGATGTG CCATCCTCGAACCTTGTTATGATGTGCGGCATATTGTCAGTCTGACA
ex3_58 62695_ x1	CM000 680.2/1 253352 5- 125334 24	15	0.003	30.2	1	ATCCTTTTGCAGTTCCTAAGCGTGATGATTGGATATTCACACTTGTGTGCGAGATGTT CCTTTTTCTAAACCTTGTTATGTCAGCACATTACTCATCTGATG
ex3_58 62811_ x1	CM000 673.2/8 284388 5- 828439 85	14	0.008	28.2	1	AACCATGAATGCAAGAAGCGTATGATTGGGTTTTTCATGCTCACGTGTGAAATGGACC ACCCTCAAACCTGGTTATGCTATCAGCACATTACCTGTCTGATG
ex3_58 63197_ x1	ENST0 000036 5172.1	30	4E-12	60	1	TGTCCTGATGATACTTGTAAATAGGAAGTGCCGTCAGAAGCGATAACTGACGACGTCT AAT
ex3_58 63333_ x1	ENST0 000045 8838.1	25	3E-09	50.1	1	CTGGAAAAGACAATGATGTTTTATTTCCAAGCACATATCTGAGTTGTATGTGTGGACA GC
ex3_58 63586_ x1	CM000 665.2/9 042623 5- 904263 56	20	0.000 8	32.2	1	AAGACTGTACTTTTCAGGGATCATTCTATAGTTTGTACAAAAAGAGTGCTTCAAACCT CCTCTACCAAAGGAAGGTTCAACTCTTTGAGTTGAATGCACACATAAAAAAGAAGTT TCTGA
ex3_58 64527_ x1	AC021 733.12/ 63797- 63917	15	0.002	30.2	1	GGUAAUUACCAAGAUUUUUUAGAAUGCAGUUUCUCAUUUGCCAGGGAAAUGACCAU AAAAUAAUUUCCACUAGAUUUUUUUUAUCUGUUACCUUGCUAGCAAGCAGUCUAU UGGGAACAUUU
ex3_58 65462_ x1	CM000 663.2/1 502616 94- 150261	14	0.009	28.2	1	ATCCTTTTGTAGTTCATGGGCATGATGATGGGGTGTTCCTGAGCATGCGTAAGATGT GCCGCCCTCAAATCTTGCAAGATGTTGGCACATTACCCATCTGACA

Accession	Gene	Length	Score	Start	End	Sequence
ex3_58_65739_x1	ENST0000408163.1	15	0.004	30.2	1	GGGATGTGCTCAGAGCAGGGGGCCTGAGGAATGGCTCCTCTGTTTACAACACACCC AACA
ex3_58_66728_x1	CM000685.2/4 028509 6- 402851 99	14	0.009	28.2	1	ATCCTTTTATGGTTCATAAGTATGTTGATTATGTTTTTCATGCTATTGTGTGAGATGTAC CTCCCTCAAACCTTGTTATGATGTCAGCACATTATCCATCTGATG
ex3_58_67733_x1	CM000668.2/1 214436 17- 121443 693	19	0.004	30.2	1	AAGACTATACTTTTCAGGGATCATTCTATAGTTTGTACTAGAATGTAAATAAACTTAG TGATGAATTACTATAAGC
ex3_58_68192_x1	CM000669.2/1 076033 63- 107603 507	15	0.003	30.2	1	CTGCATGTGGAAATGTCTGTTCTTCATTCTTTTAGGAGCAGGAATACATATAGATATA AAAAACATCCCATATTTTAAAAGGAATTCTTAGGGCTTGCCAATCTTGTAGTAAAGGT TGAATTAGCAGTATATGTCTTCTACATAA
ex3_58_68586_x1	CM000682.2/3 842177 4- 384216 47	14	0.008	28.2	1	TCTTGATCCAAAAGTGATCATGGGTTGCCTGTGTCCCGATCATTAACAGTGCAGGG GTAGGAGTGCTGAAAGACATCTTCCCTGCGTTGGTCCAGCCTTCCCTTTCAAACCCT GGAGCTTCCACG
ex3_58_70717_x1	CM000667.2/1 230096 40- 123009 542	15	0.003	30.2	1	ATCCTTGTGTAGTGCATAAGTGTGATGACTGGGTTTTCCCACTCTTGTGAGGTGTGC CTCCTGCAAATCTTATGATGTCTGCATATGACTTGTTTGACA
ex3_58_75145_x1	CM000665.2/9 003028 4- 900304 95	15	0.006	30.2	1	AAGACTATTCTTTCAGGGATCATTTTTATGCTTTGTTACTAGAAGTTTCTCTGAAAGTGT AGAGCACCATCAACTATGGGAAAGGGGCACAGCATTGTCTCCTAAGCATGAAGCCA GCTCTCTGTGTTGTGTTGCTGCAACTGCACTTGGTATTGATGATCATTCTTCCCTC CCTCAAAGAATAAGAGGGGAGGATGAAGTCTGAGAGGT

ex3_58 77178_ x1	AC015 550.19/ 39913- 40054	15	0.004	30.2	1	CUGCAGCCUAAUUAAGCCAACUGAGUJCCUJCCUCAUGGGGGGGCCAGUGUGC AAUGGCUGCAAACAGCAGCUUCCUUGGUAGUGUAUGCAGCCUGUGUGUUGUAAU GUAUGGGUUGCUCUAAGGGACCCUGGAGACAGUC
ex3_58 79588_ x1	CM000 679.2/8 214166 3- 821417 73	14	0.009	28.2	1	ATCCTTTTGTGGTTCATCCGCCTGATGATTGGGTTTTTCATGCAGACGTGTGAGCTGT GCCTCCCTCAAGCCTTGTTACAACATCCGACATCCGCACATTACCTGTCTGATG
ex3_58 80522_ x1	ENST0 000039 1236.2	18	0.009	28.2	1	AAGACTATTCTTTCAGGGATCATTATGCGAGAAGTTTTTCTGAATGCCTAAAGAACCA GA
ex3_58 80649_ x1	ENST0 000036 4796.1	14	0.009	28.2	1	CAGCCTCTGATGAAATTTATCTTGATAGGGACATCTGAAAGTGTGATGAATGCCAAG GA
ex3_58 80930_ x1	CM000 667.2/5 685714 0- 568572 51	14	0.008	28.2	1	AACATTTAATTGCAGTAATTCATAAGTGTAATGATTGGGTTTTCACATGCATGCATAAG ATGTGCGTTTTCTCCAACCTTTGTTACAGTGTCAGCATGTTATCCTCATTGACA
ex3_58 80976_ x1	ENST0 000036 3694.1	15	0.004	30.2	1	GGGTCAATGATGAGAATCTTATATTGTCCTGAAGAGAGGTGATGACTTAAAAATCATG CT
ex3_58 82114_ x1	CM000 664.2/5 701616 4- 570160 61	15	0.004	30.2	1	ATATTTTTGTGATTCATAAGTATAATGATGGAGTTTTCAAATTCACGTGTGTGATGTGC CCCCCTCAAACCTCTTTATGATGTCAGCATATTGCTCATCTGACA
ex3_58 82235_ x1	CM000 677.2/2 506233 3- 250624 27	14	0.009	28.2	1	GGATCGATGATGAGTCCCCATAAAAACATTCTTGAAAAGCTGAACAAAATGAGT GAGAACTCATACCGTCGTTCTCATCAGAACTGAGGTCC
ex3_58 84010_ x1	ENST0 000036 3243.1	15	0.002	30.2	1	GGCCTCCTGGTGCTTACCAAGGCTGTCTTCTTACACTGACTGAAGCAGAGAAAGAGG AAG

ex3_58 85653_ x1	CM000 664.2/1 830643 46- 183064 235	14	0.008	28.2	1	GCAGACTCCCTCAGCATCCAGCGGGTGCTTTTTCGGTCTGCCAGTGAGCATTCCATG GTGCTGTGACCATTTTGACCTCTCTAGGGTGATGCAGCTGCCTGGGGACACAGAG
ex3_58 85789_ x1	CM000 675.2/3 410083 8- 341007 11	18	0.008	28.2	1	AGATAACTTCAAAGAGGGCTTGCGGAGCTGCAAAACCAAGAGCTTTTAATGTATTACT GAATATTGAAGTTCTCCGTAGGATGCCATAGTCACTCAGTAGTGCTATATCTTCCTAA GCAGATATAAGA
ex3_58 86497_ x1	AL132 709.5/1 45774- 145703	14	0.008	28.2	1	UAGAUCAGUGAUGACUACUGUUGGUGUAUGAGUCAUUAUACGAUGAAUACAUGUCU GAAAUUCUGAGGUCCAA
ex3_58 87684_ x1	CM000 670.2/5 913750 2- 591373 72	15	0.005	30.2	1	AGCCTCCTGGTGTTTTAACACAGCTGTGTTCTTATACTGACTGTGTAGAAAGAGAAGG AAATAAACCTTACCCCATATGCATTTTCATCCCCGGACCCTGCACCTCGTCTATATTGT GAATAGGGAAATATGG
ex3_58 87898_ x1	CM000 664.2/2 186198 01- 218619 887	16	0.001	32.2	1	AAGACTACACTTTCAGGGATAATTTCTATAGTTCATTACTAGAGAAGTTTCTCTGAATG TGTAGAGCACCATAAAATACATTTTATT
ex3_58 88397_ x1	ENST0 000040 8534.2	25	3E-09	50.1	1	GAGACTATACTCTCAGTGACCAGTTCCTGAGTTCATTACTAGAGAAGTTTCTCTGAAC GT
ex3_58 89235_ x1	AC013 416.4/5 4383- 54515	16	0.000 7	32.2	1	UGGCAGCCAUGUCAAAUUCAGUGCCUGCCCUGUCUAUGGUAGGCACUGGCCCCAG AAGACUGCCACAGAAACAGUGACUCACAGGCCUGUUACUGUGUCCCAGGCUCAG GGAUAAAUUUGGUUACAGACACCA
ex3_58 89275_ x1	CM000 667.2/8 750719 7- 875073	15	0.003	30.2	1	AAGACTACACTTTCAGGGATTATTTCTATAGTTCATTCTAGAGAAATTTCTCTGAACA TGTAGAGCATGAAAACTAATTATGGAAAGGGAAGACCATTACCAGCCAGT

	06						
ex3_58 90134_ x1	CM000 672.2/2 678901 7- 267891 57	14	0.009	28.2	1	CCTCATTTCCTTGGCAGGAACTTGTAGTCCCCTCCCTGTTATGTACAGAGGCAAAG GGAAGAGCTCTGGCCCCCTTGGCATGTCTTTGGAGCCATGCAGCTTCCCGTCTGCC AGTTCTATCCTCAAGCACCAGGACACCA	
ex3_58 90637_ x1	CM000 663.2/1 192590 41- 119259 141	14	0.008	28.2	1	ATTCTTTTGTAGTTCAAGAGTGTGATGATTGGCTGTTTCATGAGCATGTATGAGATATG CCACCCTTGAACCTTGTTACATCAGCACATTATCTGCCTTACC	
ex3_58 91156_ x1	ENST0 000036 2701.1	14	0.009	28.2	1	TTGGGCAGTGAACACCCAAGTGTGCTTTATAGTTCCTTTGGCTTTGACTTTGTGCTAG AG	
ex3_58 91501_ x1	ENST0 000051 6599.1	20	0.000 5	32.2	1	TGTCAGTGATGAAAGCTTAGTCCCGTTCTGCTACTAATGTTAAGTGATGATAAAGTTA TG	
ex3_58 91640_ x1	ENST0 000036 5313.1	14	0.008	28.2	1	TTACCAAAAGTTAATGTTTTAGAGAATGCTTTGGTTAAAAGCCTTTACCAACTTGG GC	
ex3_58 92907_ x1	AC016 708.11/ 153795 - 153929	43	1E-19	85.7	1	CUGCAGCCAAUUAAGCCAACUGAGUUCUUCUUGUGGGGGCCAGUGUGCAA UGGCUGCACACAGCAGCUUCCUUGGUAGUGUACACAGCCUGUUGGUUGUAUGGG UUGCUCUGAGGGACCUUGGAGACAGGC	
ex3_58 95935_ x1	ENST0 000039 1284.1	15	0.002	30.2	1	ACCTCTGCTGGGGTGTTTAAAGGTCAGCGCTGTAGATATTCAGCATCTGGCATCTTG GCT	
ex3_58 96177_ x1	CM000 680.2/2 226057 6- 222606 77	15	0.002	30.2	1	ATCTTCTGTGGTTTCTAAGTGTGATGATTGGGTTTTACACAGTTGTGTGAGGTGTGC CACCTCAAACCTTGTTATGACGTCGACACTTACCCATCTGACA	
ex3_58 97252_ x1	ENST0 000036 5473.1	14	0.009	28.2	1	TAGGCCCTGAATCAAGAAACGTGATGGTTTGCCATTGTAGCTATTGGTTTCAAACAAG AG	
ex3_59	ENST0	18	7E-05	36.2	1	GGGTCGATGATGAGAACCTTATATTTTCCTGAAGAGAGGTGATGACTTAAAATCATG	

00043_	000060					CT
x1	6510.1					
ex3_59	ENST0	14	0.009	28.2	1	TGCACTGCATGGCATCTGCACCCAGCAGTTTACTCTTGCTAAGGTGTTCAAAGGTCA
00165_	000038					GTG
x1	4679.1					
ex3_59	AC023	14	0.009	28.2	1	AGCCUCAUUCUAGAUGAGAAUGGGUACUGCUGAUCUAGGUGUCCAAAAACUUUA
00265_	271.11/					UGUGGCUAAAUUGAGACACAGGCUAUGCUUCCAUCACAGUACACAUUUGCAGUG
x1	39009- 38876					GUGACAAUGAAACCGUAACAUUU
ex3_59	CM000	15	0.002	30.2	1	ATCCTTTTGTGGTTGATAAGTGTGATGATTCAGTTTTTCATGCTCATGTATGAGATGTG
01289_	665.2/3					CCCCAATCAAACCTTGTCACAACATCTGCTTATTATCAGACA
x1	217265 6- 321727 55					
ex3_59	CM000	15	0.002	30.2	1	CTGGAGACTAAGAAACCAGTCCTTGAAGTCAAGCTGACTCTGCTTTTAGCCTCCTAA
03130_	682.2/4					ATTAAGATAGATAGAATAGGTCTTGTTTGCAAATAAATTCAAGATCTACTCATCTA
x1	330455 5- 433046 79					TCAATAGCA
ex3_59	AL132	22	4E-05	36.2	1	UGGAUCGAUGAUGACUACUGGUAGCAUGAGUCAUUAACAGUGAAUACAUGUCUGG
03433_	709.5/1					AACUCUGAGGUCUGU
x1	31508- 131439					
ex3_59	ENST0	14	0.009	28.2	1	AGCCTCATTCTAGATGAGAATGGGTACTGCTGATCATGGTGTCCAAAAAAGTTTATGT
05623_	000036					GG
x1	5189.1					
ex3_59	CM000	15	0.005	30.2	1	GTTTCTGATGAAGCCTATGTTGGTAGAGACATCTGAGAGTATTGATGAATGCCAACA
06161_	677.2/8					GCTTAAATGGAGAAAA
x1	617327 0- 861731 98					
ex3_59	CM000	18	5E-05	36.2	1	AGTCTTTTGTAGTTTGCAAGCATGATGATTCGGTTTTGAGAGGTGCCTCCCTCAAACC
06892_	665.2/1					TTGTAGACGTCGTCATCGGCACATTACCTGCCTGATG
x1	973395 51- 197339 457					

ex3_59 07171_ x1	ENST0 000036 5612.2	19	0.003	30.2	1	AGGGCTATACTTTCAGGGGTAATTTCTATAGTTCATTACTAGAGTAGTTTCTCTGAAT GT
ex3_59 09573_ x1	CM000 670.2/1 232667 45- 123266 642	15	0.003	30.2	1	ATCCTTTTGTAGTTCCTTAAGTGTGATGATTGGGTTTTTCATGCTTATGTGTGAAATGTGC CTTTCTCAAACCTTGTTATGACACTGGCACATTACCTGTGTGACG
ex3_59 10185_ x1	ENST0 000039 1209.2	15	0.004	30.2	1	AAGACGATACTTTCAAGAATCATGATCATTCTATACAGTTCATTACTAGAAAAGTTTCT C
ex3_59 10686_ x1	CM000 666.2/1 595070 29- 159506 894	17	0.000 3	34.2	1	GCGAGGAGGAGGCACAGGGTTCTCCCCTGAGAGCCAGGCCAGCTCTTAGTGTGTTGCT TCGCTGCAGGTGCCATTTGGCATTGAGGATTGTTTTTCTCTTCCTCCGGCAAAGTAA GAGGGAGAGGACACAGTCTGAGT
ex3_59 10973_ x1	CM000 679.2/1 906413 6- 190639 20	31	1E-12	61.9	1	AAGACTATACTTTCAGGGATCATTCTATAGTGTGTTACTAGAGAAGTTTCTCTGAAC GTGTAGAGCACCGAAAACCCCGAGGAAGAGAGGTAGCGTTTTCTCCTGAGCGTGAA GCCGGCTTTCTGGCGTTGCTTGGCTGCAACTGCCGTCAGCCATTGATGATCGTTCTT CTCTCCGTATTGGGGAGTGAGAGGGAGAGAACGCGGTCTGAGTGGT
ex3_59 13585_ x1	CM000 668.2/1 170981 9- 117099 60	15	0.002	30.2	1	ATCCAAGGTGAGTCTCTCTCCAAGGGGCTGACTAGTGCCTCTCTTAGGACAGTAGCA AGTTGGAATAAAAATCTGGCATGCCTAAGGTCTTTAAGGAACAGGGGATGCTTACTTC TTTTGCGTTCCTCTGGCGGCCTACATAG
ex3_59 15019_ x1	ENST0 000039 1215.1	19	0.005	30.2	1	GTTCCCTTTTAAGGCTGACCCAGTGCTTTAAGAGGCTGATACAGAAGGGTAAAGTTA AGT
ex3_59 16454_ x1	AJ2432 22.1/1- 109	14	0.008	28.2	1	UCCCAAUGAUGAGUUGCCAUGC UAAUACUGAGCCACCAGGUAGGGCAGUGUUGCC UGGUUUGGGUGCCAGUGAGUUUAACAAAACUUCUCACAUGAAGAUCUGAGGGGU
ex3_59 18008_ x1	CM000 665.2/1 322806 18-	14	0.008	28.2	1	ATCCTTTTGTAGTTCATAACAGTGATTACTGGGTTTTTCACGTTTCATGTGTGAGATGTG CCTTTCTTTTTTTTTGTT

	132280						
	693						
ex3_59_18053_x1	AC104_446.2/1_42006-142080	20	0.0005	32.2	1	CAUGGGUGAGGUACGAGGAAACAGUCUGAUAGUCACUGAAGACUGAUUAGA UCCA ACUCUGAUCUCAGCAAAGCC	
ex3_59_18100_x1	ENST0_000038_4470.1	14	0.008	28.2	1	TCTTAGTGATGAAAAC TTTGTCCAGTTCTGCTAATGACTTTAAGTGATGATAAACTATG T	
ex3_59_18305_x1	ENST0_000038_3920.1	15	0.004	30.2	1	TAGGCCCTGAATCAAGACTAGTGTTTTGCTGTAGCTGTTGGTTTCAAACAGGATCCG AGA	
ex3_59_18726_x1	ENST0_000038_4225.3	23	4E-08	46.1	1	GCACTGCCTTTGAACCTGATGTGTCTTGT TTTGTAGCTTCACGGGCCAAGCAACAGTG CTA	
ex3_59_18866_x1	CM000_673.2/6_643276	15	0.006	30.2	1	GATGCCTTCCGGAACATGCCAGCACCGCAGATGCTGGCAGTCTGCTGTGCCCGTGA TATTGGGCAAAGAGGAAGTGGCTATTTCTACACTTGGTGTT CAGAAACCAGTGAGCT CTAAGAATGGTTTATAGCCTGACATTT	
	3-66432902						
ex3_59_20097_x1	AC016_710.7/5_8672-58803	15	0.002	30.2	1	CUGUGAAUAUUCUCUGUGUUCUGAUUAUGUGAGAGCCAGGACAGGC UAAACAUUU GCUACAUUAAGACCAUGCAUGUGUACCCAGAUGUAGCCCAU UCCCUAGCUCUGGU CUUAUAAAUGCUGGUGAUAAAC	
ex3_59_21333_x1	CM000_677.2/5_939020	15	0.006	30.2	1	ATCCTTTTGTAGTT CATAAGCGTGATGACTGTGGTTTCATGCTTGTGTGTGAGAGATG GGTGGGCCTCCCTCAAACCTTGTTACGACGTAGGCCCAT TACCCATCTGACA	
	8-59390317						
ex3_59_22272_x1	CM000_669.2/1_022279	14	0.009	28.2	1	AAGATGATACTTT CAGTGATCTTTTTTTCAGTTTATTACTAGAAAAGTGTCTCTGAACCT GGAGAGCACCCAGAAACCAAGAGGAGGAGATGTAGCGCTCTCTCTCTGAGCTTAAAGC TGGCTCTTGGTTTTGCTTTGCTGCAACTGCTTTTTGCCATTGATGATCATTCTTCTCTT CCTCTGGGAAGTAAGAGAGAGAAGATGCAGCACGAATGGT	
	7-10223011						
ex3_59_22571_x1	ENST0_000060_6412.1	20	2E-06	40.1	1	TGGATCAATGATGACCACTGGTGGCGTATGAGTCATATGTGATGAATACGTGTCTGG AAC	

ex3_59 23429_ x1	CM000 674.2/8 886664 3- 888667 63	16	0.001	32.2	1	TGTCTCTGACCTGGTTAAAGTGGCATCTGGTTGGTGGCACTTATCTCAAATCGCAA GACATAAGGCAACCTCTTGTATCCAGCTTGGCTTTTTGTTTTTGTAGACA GGGTC
ex3_59 23758_ x1	CM000 663.2/1 530126 14- 153012 482	14	0.008	28.2	1	ATGCATCTATCTGACATGCCTGGAGCAGGTATTGTCTGCTGCTAAAGTTTCCACCAC AGATGCAAGAAGAAAATGTCCTCATGCTTTTTGTCTGTGATTGTGGCAGCCAAGATT GACTAGAGGAATGCAGAG
ex3_59 25488_ x1	CM000 685.2/2 892406 9- 289241 38	14	0.009	28.2	1	CAGCCTCTGATGAAATTTATCTTGATAGGGACATCTGAAAGTGTGATGAATGCCAAG GACTCTAATGGA
ex3_59 25809_ x1	CM000 665.2/1 805427 01- 180542 836	14	0.008	28.2	1	TGGTCAGGTGGAATAATCCTTATCTGTTTCTCCTTTTGAAGGGCAGATTAGAACATGA TAATTGGAGTTCACATGATACATGATTAAAGTCTCTGTGTAATCATGACTTACAATATC CTGATTATTCCTATCTTAT
ex3_59 25891_ x1	CM000 677.2/6 569693 6- 656968 33	28	6E-11	56	1	ATCCTTTTGTAGTTTATGAGCATGATGATTGGGTATTCATCCATGTTTGTGAGATGTG CCACCCTTGAACCTTGTTACGACATCAGCACATTACCCATCTGACC
ex3_59 26019_ x1	CM000 669.2/3 741962 8- 374197 67	15	0.002	30.2	1	GGCCTCCTGGTGCTTACCAAGGCTGTCTTCTTACACTGACTGAAGCAGAGAAAGAGG AAGCAGAGTAAACCTATACCATGTGCACCTCAGCCCAGGCCCTGTGTGTGTGCCTG GTCTGTATTGTAAATGCAGGGAAATGG
ex3_59 27339_ x1	CM000 675.2/2 096931 8-	16	0.001	32.2	1	ATCATTTTGTACCTTTTAAGCATGACCATTGGGTTTTCACACTCATATGGGAGGTGCC TCCCTCAAACCTTTGTACATTGGCACATGACTCATCTGATG

	209694						
	16						
ex3_59	CM000	15	0.008	30.2	1	GATCCTGGTGATGACAGACGACATTGTCAGCCAATCCCCATGTGGTAGTGAGGACAT	
28063_	685.2/1					GTCTGCAGTTCTGAAGGGATT	
x1	102250						
	63-						
	110224						
	985						
ex3_59	ENST0	14	0.009	28.2	1	ATCCTTTTGTAGTTCGTAAGCATGATGATTGGGTGTTACGTGTATGTGTGAGATGTG	
28184_	000045					CC	
x1	9180.1						
ex3_59	ENST0	23	4E-08	46.1	1	AAGGCTATACTTTCAGGGATCATTTTTATAGCTTATTACTAGAGGAGTTAATGTGAAT	
28629_	000039					GT	
x1	1019.2						
ex3_59	CM000	16	0.000	32.2	1	ATCCTTTTGTAGTTCATAAGCCTGATGATTGGATTTTCATGCTCATGTGTGCGATCTT	
29429_	668.2/7		9			CCTCCCTCAGCCTTGTTAATGTGTTGGCACATTACTCATCTGACG	
x1	586596						
	4-						
	758660						
	66						
ex3_59	ENST0	17	0.000	34.2	1	AATTGGGATCAAAGATGCAGCCGCCTTCCCATTTAAGCAGCACAGACAGCCCAAAGT	
30592_	000039		4			GAC	
x1	0991.1						
ex3_59	CM000	14	0.009	28.2	1	ATCCTTTTGTAGTTCATGAGTGTAATGATTGAGTGTTTCATGCACATGTGTGAGATATG	
30896_	673.2/8					CCACCCTTGAACCTTGTTACACCGTTGTCACATTGCCCGTTTGACA	
x1	609419						
	2-						
	860942						
	95						
ex3_59	CM000	16	0.000	32.2	1	TGCCCTGACCTGGGAAGAGAGGGGCCTGGCTGGTGGTATCCATCTCATACCAGCT	
31930_	677.2/2		8			AGGGATGAAGAAACCGCTTGCTCATCCCAGCCTGGCTCCTGGTCTATGCCCATGCC	
x1	600907					TGGTTCGTGCCTTGGACATATCA	
	4-						
	260089						
	40						
ex3_59	CM000	21	1E-06	42.1	1	AAGACTATACTTTCAGGGATCATTTCTATAGTTTGTACTAGAGAAGTTTCTCTGAACG	
32096_	681.2/4					TGTAGAGCACCGAGGCATGGGCAAGGACTTCATGTCCA	
x1	011470						
	5-						
	401146						

ex3_59_32114_x1	CM000 667.2/8 023958 9- 802394 87	15	0.005	30.2	1	TTCCTTTTTAGTTCATAAGCATGATGATTGGGTTTTTCATGCTTGTCTGTGAGATGTGC CTCCCTTAAATCTTGTGCATGTCGTTGGTACATTACCCATGTGACA
ex3_59_35128_x1	AC008 474.9/1 13719- 113587	15	0.003	30.2	1	UUCUCACCUAAAACCCAAGAAUCACUGUUUCUUAUAGCGGUGGUUUAACAGAGGU GCAAACAGCAAGUGAAUCUCGUCGCCUUUGCGGGGCUGUGGCCAUGCCCCUCA AGGAAUUUGGAGGCUCUACAGCC
ex3_59_35585_x1	ENST0 000039 1249.2	14	0.009	28.2	1	AAGACTATACTTTCAGGGATCATTCTATAGTTCATTACTAAAGAAGTCTATCTGAACA T
ex3_59_35779_x1	AJ6094 25.1/1- 130	20	2E-06	40.1	1	UGCCUCAUUCUAGAGAAUGGGCACUGUUGAUCAUGGUGUCCAAAAUAGUUAUG UGGCUAAAUUGAGACAGGUUAUGCUUCCAUCACAGUAUGCAUUAUUGCAGUGGUGA CAAUGAGACCUGUAACAUUU
ex3_59_36599_x1	CM000 681.2/4 948996 5- 494900 48	20	2E-06	40.1	1	GAGGTCAGTGATGAGCAACATTCACCATCTTTCGTTTGAGTCTCACGGCCATGAGAT CAACCCCATGCACCGCTCTGAGACCTG
ex3_59_38617_x1	ENST0 000036 3219.1	15	0.003	30.2	1	TGAGCAAGCGATGACAGCCGGTGGTGTGTGAGTCATGGAGGATGAATACTAAGTGC CTGG
ex3_59_42240_x1	ENST0 000036 2500.2	19	1E-05	38.2	1	TAGTAACACTTCCATGCACCATTTCTATAGTTTCTTACCAGAGAAGTTTCTCTGAACAT G
ex3_59_42446_x1	CM000 678.2/6 831334 0- 683132 39	14	0.009	28.2	1	ATCGTTTTGTAGTTCATAAGCGTGATGACTGGGTGTTTCATGTGCCTGTGTCAGACGT GCCTCCCTCAAACCTTTACTACATTGGCACGTTACCCATTTGAAC
ex3_59_42542_x1	AC090 527.3/1 7174- 17301	15	0.006	30.2	1	UUCACCACUAUUGGUCUGCAGCUCUUCUUAUGGUAGCAGUUGUUGCAUUUCUCU GUGGGAAAAGAAAGAGGAUUAACACCUCUUUCUUAUGCAAAACAGAGAGUAGGCA UAUGUGUGACAGACAAA
ex3_59	ENST0	16	0.000	32.2	1	TGCCTCTGACCTGGGTAGAGTGGCATCTGGCTGTGACATTCATCTCATATCAGCCAG

42546_	000039		5			GGA
x1	1324.1					
ex3_59	CM000	14	0.009	28.2	1	ATCCTTTTGCAGTTATGCATAATGACTGGGTTTTACGCTTATGAATGAGATGTGCCT
42905_	664.2/6					CCCTCAAACATTGTTATATGTCAGCACATTATGCATCTGACA
x1	490868					
	6-					
	649085					
	87					
ex3_59	CM000	14	0.009	28.2	1	GTCTTTTTATAGTTCATAAGTGTGATGATTGGGTTTTATGCTCTTGTATGTGATGCC
43368_	664.2/1					CTCTCCTCAAATCTTGTGATGATGTTGGCACATTACCCATCTGATG
x1	564221					
	95-					
	156422					
	299					
ex3_59	CM000	15	0.006	30.2	1	ATTATTTTGTGTTTCATAAGTGTAAATGATTGGATTTTCATGCACATGTATGAGATGTGC
43655_	679.2/3					CTCCATCAAGCCTTGTTACTACAAAGTCAGTGCATTACCCATCTGATG
x1	505449					
	4-					
	350543					
	88					
ex3_59	CM000	14	0.009	28.2	1	ATCCTTTTGTAGTCCATAAGCGTGATGATTGAGTGTTCACACTTATGTGAGACACGTG
44460_	668.2/3					CCCTCCCTCAAACCTTGTTATGACATTGGCACATTATTTCTCTGATG
x1	468279					
	8-					
	346829					
	02					
ex3_59	ENST0	15	0.004	30.2	1	AGGTCATTTCAAAGAGGTCTTGTGAGGCTGTGAAACCAAGAGCTCTTAACACTGCGA
46051_	000036					CCA
x1	4831.1					
ex3_59	ENST0	15	0.002	30.2	1	CTGCAGCCAATTAAGCTGACTGAATTCCTTTCCCTTATGGGGTCCAGTGTGCAATGG
47981_	000038					CTG
x1	4210.1					
ex3_59	ENST0	15	0.002	30.2	1	GGGTCGATGATGAGAACTTTATATTGTTCTGAAGAGAGGTGATGACTTAAAAATCATG
48208_	000036					CT
x1	3810.1					
ex3_59	CM000	15	0.003	30.2	1	ATCCTTTTGTAGTTCATAAGCATGATGATTATGTGTTACACACGTTCCCATGTAAGAT
49332_	684.2/2					GTGCCACCTTCAAATATTTTTTTT
x1	141105					
	0-					
	214111					

32

ex3_59_50688_x1	AC141 001.6/1 1830-11964	33	8E-14	65.9	1	UUUCCCUGACCUGGGUAGAGUGGCAUCCAGUUGGUGGUGCCCAUCUCAUAUCAG CCAGGGACAAAGCAACCCCUUGUUCUCCAGCUUGGCUUUUCAUCUGUGCCUUAU GCCUGGUUCAUGCCUUGGACACAUUU
ex3_59_50976_x1	ENST0 000045 9171.1	14	0.009	28.2	1	ATTACTTGAAAATCACTCCCAGGCTTTGGCCATGGCAGCAGGTGAGATTCAAGGCC AGA
ex3_59_51529_x1	ENST0 000036 4446.1	16	0.000 8	32.2	1	AATCTCCTGGGATTGTGTCTGGCGAGTGCCCAGTATTCTGCCACCTTCAGAAGGAAG GGA
ex3_59_51985_x1	CM000 677.2/2 505953 8-250596 33	14	0.008	28.2	1	GGATCGATGATGAGTCCCCCAAAAAACATTCTTGAAAAGCTGAACAAAATGAG TGAAAACATACCGTCTGTTCTCAGCGGAACTGAGGTCC
ex3_59_52429_x1	CM000 672.2/2 316698 5-231671 01	23	0.005	30.2	1	AGCATTAATCTACTGAAGATATCCACATCCTTAGACAGACGCAAAAAATAAATTCTC TTTTGCAACTCAGAGCTCATTGTGCGGTATGAGCTTTGATACATATAAGAAGGAATAT T
ex3_59_53858_x1	AL132 709.5/1 41607-141533	18	0.008	28.2	1	UAGAACAACGAUAACAAUAGUAGUGCAGGAGUCAUAAACUAUGAGUAAUAUGUGU GUGGAACUCUGAGCAUCA
ex3_59_54948_x1	ENST0 000051 6021.1	15	0.003	30.2	1	CTCGAGGGTGATGAAAAAGCATCCCTAGGTGTGGTTGTGGCATCTTGGTCACCTATG TGC
ex3_59_54989_x1	ENST0 000039 1156.1	15	0.003	30.2	1	TGTCCTTGGCCTGGGTAGAGTGGCACCTAGTTGGTGGTGCCCATATTAGCCAGGGA CAAA
ex3_59_55135_x1	CM000 666.2/1 394364 94-139436 368	19	0.004	30.2	1	ATTGGTTGAAAATCACCCCCGGCTTTGGCCATGGCAGCGGGTGAGATTGGCGCC CAGAGCCTCCAGGGGCTCAGCTCACCGCACGCTGACACATGTGCGGCGGTGAAA CCCAGCCCCAACAGGC
ex3_59	CM000	15	0.006	30.2	1	ATTCTTTTGTAGTTCAAAGCATGATGATTGGGTGTTACAGGCATGTGTAAGACGTG

56868_x1	671.2/7 252723 6- 725273 39					ACACCCTCTGAACCTCCTTATGACCCGGTACATTACCTGTCTGACC
ex3_59_57840_x1	ENST0 000038 4381.1	15	0.003	30.2	1	TGTCAGTGATGAAAATTTTGTCTAGTTCTGCTACTGACATTAAGTTATGATAAAGTCTGT
ex3_59_61419_x1	CM000 674.2/1 283984 08- 128398 522	18	0.009	28.2	1	GTCCTTTTGTAGTTCATAAGGGTGAACCTTTGTAGTTCATAAGGTTTTTCATCCTCATGT GTGAGACATGTCTCCCTCAGACCTTGTTATGATGTTGGCACGTTGCCCGTCTGATG
ex3_59_63148_x1	ENST0 000045 9326.1	30	4E-12	60	1	GCCCAGGGTATGTTACGGGGCGATGCTGCCCTCCCAGCTGGCCCATGGGTGACC CTGGG
ex3_59_63222_x1	KN538 374.1/2 557483 -	20	0.001	32.2	1	TAGTCAGGCGGGATAATCCTTACCTGTGCCTCCTTTTGGAGGGCAGTAGAATGTGGT AGTTGGAGTTGCATGATACTTGATTCATATCTCTGTGTAATGATGGCATGCAATACCC TGACTGCTCCTTTTGAAT
ex3_59_64296_x1	AC022 107.8/6 6266- 66397	15	0.006	30.2	1	GCGCUGCCUUUGUACCCCACCGUGCCUCCGCCUGGUGUCUGGGGUCAGGUUGCA GUGCCAGAGCACGUGCUUGCGCAUAAAUGGGGCAGCCUGGCCCCCUGCGGAUGG UCCUUUUAACCGCGAGCAACAAGG
ex3_59_67601_x1	AADB0 201611 5.1/249 55- 25031	15	0.003	30.2	1	UGGACCAAUGAUGAGACAGUGUUUAUGAACAAAAGAUGAUGAUUAAUCCAGUUCU GCACAAAACACUGAGGUCCAUU
ex3_59_68756_x1	CM000 664.2/1 217060 80- 121705 967	14	0.009	28.2	1	ACCCACTTGTGGATTTGTTTCAAACCTTAGTTTGTAGATCTTTTGTAGTTTTTACATTCGTG TGAGATGTGCCTCCCTCAAACCTTGTTACTACCTTGGCACATTACATATCTGATG
ex3_59_69245_x1	CM000 677.2/2	24	1E-08	48.1	1	GGATCGATGATGACTTTTAAATGGATCTCATCGGAATCTGAACAAAATGAGTGACCAA ATCACTTCTGTGCCACTTCTGTGAGCTGAGGTCC

x1	509766						
	3-						
	250977						
	54						
ex3_59	ENST0	15	0.002	30.2	1	ATCCTTTTGTAGTTCAGAATCATGATGATTGGGTTTTTCATGCTCATGTGTGAGATGTG	
70310_	000045					CC	
x1	9372.1						
ex3_59	CM000	14	0.008	28.2	1	AGCTTTTTGTAGTTCATAAGCGTGATGACTGGGTGTACACACATGTGTAAGATGTACC	
70674_	677.2/1					TCCCTCACACCTCGGTACAACATTGGCATATTACCCACCCACA	
x1	016835						
	15-						
	101683						
	616						
ex3_59	CM000	14	0.008	28.2	1	GCCAAATGATGCTTATTTGACTCTGGTGCACTTCAGTGTAAGGATGATTTATAATCTG	
71445_	674.2/6					TCACTCATGATTGAAGGCC	
x1	457566						
	5-						
	645757						
	41						
ex3_59	ENST0	20	2E-06	40.1	1	ATCCTTTTGTAGTTCATGAGTGTGATGATTGTGTGTTTCATACGCTTGTGTGAGATGTG	
71468_	000045					CC	
x1	9492.1						
ex3_59	CM000	20	0.000	32.2	1	AGTTTTCTGTGGTTCATAAGCATGATGATTGGGTTTTTCATGCTTATGTGTGAGATGTG	
72920_	685.2/1		6			CCTCCCTCAAACCTTGTTACGACATTGGCACATTACCCATCTGATG	
x1	735793						
	0-						
	173580						
	33						
ex3_59	ENST0	19	0.003	30.2	1	ATTCATTTTCAAATATTTGCTGACTAAATGATACACACATGACTAAAACCTTAATCCTGA	
73545_	000060					C	
x1	7246.1						
ex3_59	KV766	15	0.007	30.2	1	AAGACTATACTTCCGGATATCACTTCTATAGTTTGTACTAGAGAAGTTTTTCTGAACG	
75058_	198.1/1					TGTAGAGCACGGGAAAGCACAAAGGGAGAAATGTAGTTTTTTTTCTGAGCGTGAAAA	
x1	32915-					TGGTTTTTTGTTGTTGCTTTCATTGCAAGTACGATTTGCCATTGACGATCGTTCTTACT	
	133131					GTTCTCTTTGGAGGGTAAGAGGAAGAGAACGCGGTCTGAGTG	
ex3_59	CM000	14	0.009	28.2	1	ATCCTTTTGTAGTTCATAAGCATGATGATCGGGTGTTTCATGTCCGAGCATGAGATGTG	
75813_	670.2/1					CCTCCCTCAAACCTTGTTGTGACGTTGGCACATTTCCCATCTGATG	
x1	226712						
	91-						
	122671						

	394						
ex3_59_76696_x1	CM000 664.2/2 020818 75- 202081 978	19	3E-05	38.2	1	ATCCTTTTGTAGTTCATAAGCATGATGATTGGGTGTTACATGCATGTGTGAATGTGC CACCTCTGAACCTCGTTACAACATCAACACATTACCTGTCTGACC	
ex3_59_77377_x1	ENST0 000045 8953.1	15	0.004	30.2	1	AAGCATGGCACACTGGATGGGCGTTCTGCTTCTCTTTAAAGAGCATGGATTTATCCA TAC	
ex3_59_78078_x1	CM000 675.2/9 788580 9- 978859 12	15	0.005	30.2	1	ATCCTCTTGTAGCTCCTAAGTGTGACGATTGGGTTTTTCAGGCTCATATGTGAGATGTG CCTCCCTCAGATCTTGTTACGATGTTGGCACATTACCCATCTGATG	
ex3_59_79976_x1	CM000 672.2/1 138204 59- 113820 590	17	0.000 3	34.2	1	ACTGCCCTGGAGGCATTGCAGATGTGGCTGCTGTGTGCACATTTGTGTCATTAGGTA GCAGCGATTAGAGAGGCTATGTCTATGCTCAGCGTTCTGTCCCATGAACATTTGAAT GTTTAATAGTCTGACTCT	
ex3_59_82910_x1	ENST0 000051 6190.1	14	0.009	28.2	1	TTGCGTCTATTTGACAGACTAGAATAATTAATCTATCTGCTGCTAAGGTTTCCCCTGCAG AT	
ex3_59_83508_x1	ENST0 000038 4250.1	18	0.008	28.2	1	TGCATTGCCATGGTATCTGCACTCAGTAGTTTATTCTGCTGGGTGTCCAAAGATCA GTG	
ex3_59_83881_x1	ENST0 000051 7031.1	20	2E-06	40.1	1	TATAGTGTGGCCATGGGATCTCCAAGTGCATGCAAGAGCAACCTGGAGAGACTTTGA CAG	
ex3_59_83996_x1	AJ6094 42.1/1- 121	34	2E-14	67.9	1	UGGUCAUUACCAAGGCUUUUAGAAUGCAGUUUCUCAUUUGCUGUGGACAUGACCA UAAAAAAAAUUUCCAGUAGGUUUUCUAUCUGCUACUUUGCUAGCAAUCAGCUUUAU UGGGAACAGUU	
ex3_59_86614_x1	CM000 680.2/2 668952 9- 266893 16	14	0.008	28.2	1	AAGACTGTACGTTCCAAGATTGTTTCTATAGTTGGTTGTGAGAGAAGTTTCTCTGAAC TTGCAGAGCACGGGAAACCAGGAGGAGGAGGCTCAGGGTGCTCTCCACACGTGTG AAACCGGCTGTGGGTGTTGCTTTCCTGTGACTGCCATTTGCCACTGATGATCTTCTC TTCCTCTGGAAGAGTAAGAGGGGGGAAGGACACAGTTTCAGTGCT	

ex3_59 87036_ x1	ENST0 000039 1287.1	14	0.008	28.2	1	ACTGCCCTGGAGGCATTGCAGATGTGGCTGCTGTGTCACATTTGTGTCATTAGGTA GCA
ex3_59 87979_ x1	BC021 677.1/1 965- 1834	14	0.009	28.2	1	GUGGAGGUCUAUUCOAUGGGGCUUUUCCUGUAGCUGCAUGUUGUUGGAAACUC CUCAUAGACUACUCUGUGUUUUUGCUUUACUCACAGGACUAAUAGUUAGGUCUG UGGGAAGGAACUACAAGACAGUU
ex3_59 88219_ x1	ENST0 000051 6313.1	14	0.009	28.2	1	AAGATTCGACAGATACCCTACTGCCTCTCTTTGTGGCGGCGGGGCTCAGGCTGCAG CACC
ex3_59 90453_ x1	ENST0 000038 4171.1	14	0.009	28.2	1	GGCCTCCTGGTACTTACCCACAGGCTGCGTTCTTACACTGGCTGTACAGAAAGAGGA GCT
ex3_59 90464_ x1	AC079 945.21/ 34878- 35012	15	0.005	30.2	1	CUCCAUGUGUCUUUGGAACCGUCAGCUGUGGCAGUUGCCCUUCCUAGCCAUGG AAGAGUAAGUAUUAUCUUGUUUAUUGGCAAAGCUGUCACCAUUUCAUUGGUUAUCA GAUUCUGACUUGCACAAGUAACAUUC
ex3_59 90544_ x1	ENST0 000038 4448.1	15	0.003	30.2	1	GGCCTCCTGGTGCTTACAAGCAGCTGTGTGCTTGCATTGACTGTACAGAAAAAAGA GAT
ex3_59 91398_ x1	AL132 709.5/1 42597- 142509	14	0.008	28.2	1	UGGACUGUUGAUGACAAGUGGUGGCUUAUGUGGUUGUACAUGCUGGUUGUAUUAU GAAGAAUUAUACAUAUCUGAAACUUUGAGGUCCAA
ex3_59 91833_ x1	ENST0 000040 8792.1	14	0.008	28.2	1	GCCGAGACTAAGTCGCATGCTGACACAGCTCTTGGTGTGCTACGGTACTTGGAGAG AATC
ex3_59 93607_ x1	CM000 671.2/1 371236 08- 137123 509	19	0.003	30.2	1	ATTTTTTGTAGTTCCTCAGTGTGATGATTTGGTTTCACACTCATGTGAGATGTGCTTTT CTCAAACCTTCTTACAAAGTCAGCGCCTTACCCATCTGACC
ex3_59 95256_ x1	CM000 663.2/2 201371 64- 220137 266	14	0.008	28.2	1	ATCCTTTTGTGATTCGTAAGCGTGATGATTGGGTTTTCGCACTATTGTGTGAGGTGTG CCTCCCTCAAACCTTGTACAGTGTGGCACATTGCTGTCTGAAG
ex3_59	ENST0	16	0.001	32.2	1	AAACGATGAACTCACCTAAAATAGCTGTAATAACCAGCAGATTATGTAATGGCAAACC

95771_	000039					TA
x1	0927.1					
ex3_59	CM000	14	0.009	28.2	1	CTGTGAATATTCTCGCTGTTCTGATTTTGTAAATAATCACGATGGGCTAAACATTTCGCA
97722_	665.2/1					ATATTAAGACCATGTATGTATCCCTAGACCTAGTTCTTTCCCCAGGTCTGGTTTTATAA
x1	606969					ATGCTGGTGATAAAC
	29-					
	160697					
	060					
ex3_59	ENST0	15	0.005	30.2	1	TTCAGATGATTTGAATTGATAAGCTGAGGTTCTGTGAGGAATGACAGTTAAGAGCATG
98109_	000039					TT
x1	0993.1					
ex3_59	ENST0	16	0.001	32.2	1	TCAATAATGAAATCTTCTGATTTGGTGAGAAATAATGCCTTAAAATTACACTCAATAGG
99126_	000039					A
x1	0982.1					
ex3_60	ENST0	20	2E-06	40.1	1	ACCCTTTTGTAGTTCATGAGCATGATGATTGGGTGTTACACACATGTGTGAAATGTG
01230_	000045					CC
x1	8927.1					
ex3_60	CM000	19	0.005	30.2	1	AGCCTTTGGTAGTTCATGAGCATGATGATTGGGTGTTACGCATGGGGGTGAGATGT
03497_	682.2/3					GCCGCCTTCAAACCTTGTTACAATGTACAATGTGAACGCATTACCTGTCTGACA
x1	612096					
	2-					
	361210					
	72					
ex3_60	CM000	23	0.003	30.2	1	AGGTTATTTCAAAGAGGGCTCATGAGGCTATGAAACCAAGA ACTCTTAATGCTATGAC
04083_	675.2/9					CAAAGATTGAAGTTCTCTATAGAATGCCATAGCACTCAATAATGTTATGTTTTCTTGAG
x1	978398					GCATATAAGA
	3-					
	997838					
	57					
ex3_60	CM000	14	0.009	28.2	1	ATCCTTTTTTAATTCCTAAGTGTGATGACTGGGTTTCCACACTCATGTGTGAGATGTG
04394_	664.2/8					CTTTCCTCAAACCTTTTTTACAACATCAGCACACTACCTATCTGTTA
x1	978895					
	-					
	897899					
	9					
ex3_60	CM000	16	0.000	32.2	1	ATCCTTTTGTACTTCTTAAGCATAAGGATTAGGTGTTACACACAGGTGTGAGATGGG
04445_	665.2/5		5			CCATCCTGAAACATTGCTACAATGTGCGCATATTACCTGTCTGACA
x1	328329					
	9-					
	532831					

	96						
ex3_60_04465_x1	ENST0000515906.1	15	0.003	30.2	1	TTCACAATGTCTATTGAAGGATCTCATCACCTTTAGAGAGCTGTGGTCATGCCCTTAA	
ex3_60_05994_x1	CM000663.2/20703800-207038694	15	0.002	30.2	1	ATCCTTTTGTAGTTCATAAGTGTGATGATTGGGGTTTTGCACTTATGTGTGGGATGTGATGACTCTCTCAAACCTTGTTATGACATCAGCACATTACCTGTCTGATG	
ex3_60_06906_x1	ENST0000363626.1	15	0.003	30.2	1	CTGTCAGGTGGGATAACCCTTCCCTGTTCCCTCCGTTTGGAGGGCAGATAGAACATGATGA	
ex3_60_07357_x1	CM000675.2/21527900-21527800	15	0.003	30.2	1	ATTTATTCATCTTAAGTGTGATGACTGGGTTTTTCACATTGATGAGTGAGATGCGCCTCCCTCAAACCTTGTTTACAAGGACAACATATTGGTTGTCTGACG	
ex3_60_08297_x1	ENST0000583665.1	29	1E-06	42.1	1	TACTCCAGCCTGGATGACAGAGCCAGACTCTGTCTCGAAAAAAAAAAAAAAAAAAGCTTAA	
ex3_60_08565_x1	AC092324.3/97410-97533	16	0.0007	32.2	1	AACCCUUUUUCACUUUGCCAAUUGGACUUUAUGUCUUUAUUGAUCAUUCAAGUGAGCAAAGGAAAUACGCUUUUAAAACUCAGGCAAACGGUGUUUGUCUUGUAUCCCGUCAGAGGAAACAAAU	
ex3_60_08835_x1	CM000663.2/19532274-19532170	15	0.007	30.2	1	ATCCTTTTGCAGTTCATGAGCATGATGATTGGGTGTTTATGTGTATGTGTGAGATCTGCCACTCTCTGAACCTTGTTACAACATTGTCACATTACCCGTCTAACC	
ex3_60_11511_x1	CM000666.2/14129778-141297774	16	0.001	32.2	1	ATCCTTTTGTAGTTCATGAGCATAATGATTGGGTGTTTCGCATACATGTGTGAGATGTGCCACCCTCTGAACCTAGTTACAATGTGGGGATATTACCTGTCTGACC	
ex3_60_13182_x1	ENST000039	14	0.009	28.2	1	TAGACGATACTTTCAAGGATCATTCTATAGTTTGTACTAGAGAAATTGCTCTGAATGT	

x1	1237.2						
ex3_60 14131_ x1	AC010 325.7/1 31787- 131697	20	2E-06	40.1	1	GGGACCCCGUGAUGUCCAGCACUGGGCUCUGACUGCCCCUGAGGACACGGUGCA CCCCGGGACCUUUGACAUCCGGGGUUCUGAGGGGCC	
ex3_60 16036_ x1	ENST0 000039 0893.2	19	0.002	30.2	1	AAGACTATATTTTGGAGGGATAATTTCTATAGTGTGTTTCTCGAGGAGTATATCTGAAC GT	
ex3_60 17790_ x1	CM000 679.2/2 330370	35	7E-15	69.9	1	TAGAGAAGTCAATGATGGTTTTATTCATATCGTCTGAACCTGTCTGAAGCATCTCAGT GATGCAATCTCTGTGTGGTTCTGAGACTTCTCCAAGT	
	- 233027 6						
ex3_60 18992_ x1	CM000 685.2/1 352124 41- 135212 513	14	0.009	28.2	1	AAGACTATACTTGCAGGGATCATTCTGTAGTTGGTTACTAGAGAAGTTTCTTGTCTG TAGTTGGTTATTAGA	
ex3_60 19071_ x1	ENST0 000036 3448.2	15	0.003	30.2	1	AAGACTATACTTTCAGGGATCATTGTATAGTTCGTTACTAGAGAATTTTCTCTGAATG T	
ex3_60 21684_ x1	ENST0 000039 0971.1	16	0.001	32.2	1	TGCACTTATGTATGTTTTGTTTAACTGTGGACAAAGACTTATGGATAAGTACAAAAA A	
ex3_60 22513_ x1	CM000 673.2/1 334370 39- 133436 938	18	5E-05	36.2	1	GTGCTTCTGTGGTTCATAAGGGTGATGGCTGGGCTCATGCGGATGTGTGAGATGTG CTACCCTGGAACTGGTTATGACGTCGGCACATTACCCATCTGACA	
ex3_60 22683_ x1	ENST0 000051 6213.1	19	0.004	30.2	1	CCACACAGGACGAAGGGTAGATATACTTGTACCAAATGAATGTTTCAGCAATCTGAGA TAA	
ex3_60 22906_ x1	CM000 668.2/7 539906 7- 753988	14	0.009	28.2	1	AATTCTATACTTTGAGGAGCCATTTTCATAGTTTGTACTAGAGAAGTTTCTCTGAACA TGGAGTGTACCAGAAAGCATGAGGAGGAAGTGCAGTGCTCTCGCCTTAGCTGTGAA ATCAGTTGCTTCATTGTAACCACCATTTTTTCATTGATGGCCCATCTTCTCTCCTTTGG GAGAATAAGAAGGGGAAGATGCAGTCTGAGTGGT	

ex3_60 24436_ x1	60 CM000 664.2/6 226499 5- 622650 98	14	0.008	28.2	1	ATCCTTCTGTAGTTCATAAGCATCATGCCTGGGTTTTTCGCGTTCCCATGTGAGCTGTG CCTCCCTCAAACCTTGTTATGGCATCGGCACATTATCCATCTGATG
ex3_60 24612_ x1	CM000 669.2/4 689480 - 468958 3	14	0.008	28.2	1	ATCCTTTTGTGTTTCATGAGCATGACAATTGGGTGTTTTTCATGCAGCGAGTGAGATGT GCCACCCTGGAACCTTGTTACGACGTTCGCATGTTACCTGTCTGACC
ex3_60 27527_ x1	ENST0 000051 6390.1	15	0.005	30.2	1	CTACAATCAATTAAGCCACATGGGACCTGGTGTGCAAGGGCTGCAAACAGCAGCATC CTA
ex3_60 28018_ x1	CM000 676.2/7 379901 5- 737991 18	15	0.002	30.2	1	ATCCTTTTGTAGTTCATAAGCATGACGATTGGCTTTTCACTTTCATGTGTGAGATGTG CCTCACTCAAACCTTGTTATATTGTCAGCACATTACCCATCTGATG
ex3_60 30203_ x1	CM000 667.2/2 907049 6- 290706 10	14	0.008	28.2	1	GAGGAGGTCCATTTTAAAAAAGAATAGATTGGAAATGCCTCATAGAGTAACTCTGTG GTTTTATTTTACCCACAGGACTATGGTTAAATATGTGGGAAAGAACTACAAGACAGTT
ex3_60 30509_ x1	ENST0 000051 6202.1	15	0.006	30.2	1	AGGACGTCAAACCATCATAAAGTATAGATCTCCACAGGATGCCATAGTGAATAGTGC TAT
ex3_60 31766_ x1	ENST0 000036 2796.2	17	0.000 1	34.2	1	AAGACTATATTTTTCAGGGATCATTTCTACAGTGCACTACTAGAGAAGTTTCTGTGAAC TT
ex3_60 32978_ x1	ENST0 000036 4537.1	15	0.002	30.2	1	CTTGCACCTAAACCCAAAGAATCACTGTTTCTTGAAGTGGTGGTTTAAACAAGGTGCA AA
ex3_60 33639_ x1	CM000 674.2/7 716302	15	0.004	30.2	1	ATCCTTTTGTGGTTCATAAGCATGATGATTGGGTTTCCACATTCTTGTGAGATGGGCC TCCCTCAAACCTTGTTATGATGTCAGCACATTACCCCTTGACG

	5- 771629 26						
ex3_60 35158_ x1	ENST0 000039 1256.1	15	0.004	30.2	1	GTGCCTAAGGTTAACACAGCGCCTTAAGAGGCTAACACAGAAGGGCAAAGTAAGTCT CCA	
ex3_60 35463_ x1	AC011 891.3/5 4747- 54616	15	0.004	30.2	1	ACACUCUCAGCUAUGUAUAGUUACACCCUGGCUUCACUUGUGUGACUUUUGCAAUG GGAAGAGAGAGAGAAGGUCCCCUUGGUACCUCAGCUCGGCCUUAUGGUGGCCUC UUUCCUUGAAGGGUGCAACAAAA	
ex3_60 37202_ x1	AY270 787.1/1 35-13	14	0.009	28.2	1	ACUGGAGGACUAAGGAGGCUGGGUCUGAUGAGGCAAGAUUUUGCUGAUACAUUG CUCCUAGAAAAAGGGUUGGCAAGAGCAGCCCUGGAGACUCACACGGCUGACUGU UCUACCCAACACUC	
ex3_60 41392_ x1	CM000 674.2/1 297205 3- 129721 43	14	0.008	28.2	1	TACATTCCATGATGTCCAGCACTGGGCTCTGATCACTCCGGAGGACACAGTTTTCCC CAAGACCATGGCTACCTGGGGATCTGAGAGAAAA	
ex3_60 41594_ x1	ENST0 000051 6361.2	14	0.009	28.2	1	TGGACCAATGATGAGAGCATGTCACAAAACAAGGCTTATGATTAATCCAGTTCTGTAC AC	
ex3_60 44034_ x1	AC069 351.5/3 7957- 38002	14	0.008	28.2	1	AGCUGAAGAGCUGAUGAUGUUUCCCCUAAAGCUGAAGCUCUUAAGCU	
ex3_60 44618_ x1	ENST0 000036 2963.1	16	0.000 6	32.2	1	GGGTCGATGATGAGAACCTTATATTTTCTGAAGAGAGGTGATGACTTAAAAATCATGC TC	
ex3_60 46763_ x1	ENST0 000038 6104.1	15	0.005	30.2	1	CAGCACTGCCAAGTGACCCATTGGGCTCCATCTTGACCAACTGGGCATCAAGCGGT GCAA	
ex3_60 48989_ x1	ENST0 000038 4520.1	15	0.002	30.2	1	CTGAGAATATCTTGCTGTTCTGATTTTGTAATAGGACAGGCTATAAAGATTGGCTATA TT	
ex3_60 49726_ x1	ENST0 000036 3072.1	14	0.009	28.2	1	TGGATCAATGATAAACTTGCTGGCATATGAATCTTGATAATGGATGATACGTGTGT GG	
ex3_60 49981_ x1	CM000 667.2/5	18	0.009	28.2	1	ATCCTTTTGTAGTTCATAAACAGGATGATAGGGTTTTTACATTTATTGTGAGATGTGCT TCCCTCCAACCTTGTTATGATGTTGATGCATTATCCATCTGATA	

x1	132198						
	3-						
	513220						
	85						
ex3_60	CM000	15	0.004	30.2	1	AGCCTCCCAAAGCACTGGGAGTGTGATGACTAGGTTTTCACACTGGGTTTTCATGTG	
53925_	669.2/6					TGAGATATGCCTTGCTCAAACCTTGTTACAGCACTGGCACATTGCCTGTCCGATG	
x1	643450						
	7-						
	664346						
	18						
ex3_60	CM000	14	0.008	28.2	1	TTCCCTGTGACACATCAGCAGGATGACTGGGCTTTCATCCTCCTGGGTGGGACATGC	
57238_	683.2/4					CTCCCTCAAGCCTTGCTGCTGGGCACATTATCTGTCCAACA	
x1	160468						
	3-						
	416045						
	86						
ex3_60	ENST0	15	0.002	30.2	1	AGCACTTGTGTTTGCTTTTGTGGACTTGTGGACAAAGACTTATAGTAGACAGGCACG	
57496_	000051					AA	
x1	7256.1						
ex3_60	CM000	14	0.008	28.2	1	AAGACTATACTTTCAGGGATCATTCTATAGTTTATTACTGGAGAAGTTTCTTTGAATG	
59775_	685.2/6					TATAGAGCACTAAAAACCATATTATCTCCCAAGTGAAAGCTGCCTCTTGGTGTGGT	
x1	969295					TTACTTCAGTTGCCATTTGCCATTAATGATTGTTCTTCTTTTCTTTGGGGAGAATAAGA	
	6-					GACAGAGGACACAGTCTGGGTGGG	
	696931						
	55						
ex3_60	CM000	14	0.009	28.2	1	GGGGTGTGCTCAGAGCAGGGGGCCTGAAGAATGCTTCTTCTGTTTACAACACACCC	
60545_	685.2/4					AATAGGAATCTGGGGTCATTGTGACGGGGGGCACAAAACCTTGTGACCTCTCTATGAA	
x1	738864					CAAATGCCCCACATGT	
	9-						
	473887						
	77						
ex3_60	AC092	15	0.005	30.2	1	UUGUCCUGGCCUAGGCCAUUUCUGCUCCCCCGCGCUCAGUCCUAGCAGAGUAGU	
60784_	184.7/5					CUGGCAGGACGCACAGCAAUCUCCUCUCAGUUUAGGAGGGCCGUCUCCUAAGAA	
x1	0327-					UAGGGCUGGCAGGAAAGGACAAU	
	50196						
ex3_60	ENST0	16	0.000	32.2	1	GATCAATGATGAAACTAGCCAAATCTGAGCATCAGAAGTCTTCCAGTCTACCTGATG	
62185_	000036		5			CA	
x1	4329.1						
ex3_60	ENST0	17	0.000	34.2	1	AAGATTATATTTCCAGGGGTCATTTCTGTGGTTCATTAAGGAGTTTCCCAAG	
62229_	000039		3			TG	

x1	0909.2						
ex3_60 62545_ x1	CM000 669.2/1 327530 23- 132753 126	15	0.003	30.2	1	TGCTGGAGTGATGAAAAAGTATCTTCAGGTGTGGCTGTGGCCACCTTGGCCACCTGT GTGTCACTTGCCAATGCAAGGACTTGTATAGTTACACTGACTGTTA	
ex3_60 64328_ x1	CM000 668.2/2 416627 3- 241663 74	14	0.008	28.2	1	CTCGAGGGTGATGAAAAAGCATCCCTAGGTGTGGTTGTGGCATCTTGGTCACCTATG TGCCACCTGCCAGTGCAAGGATTTGTATAGTTATAGTGACCGTG	
ex3_60 66079_ x1	CM000 685.2/1 331527 54- 133152 892	15	0.004	30.2	1	TGCACTGCGTGGTATCTGCACTCAGCAGTTTACTCCTGCTAGGGTGTTCAAAGGTCA GTGCCATAGAAATCCAGTATCTGGTTTCATTGGTTTTCTTGGCTTTGTGCTTGTTAAA CCTGGTATTTCTATTGATACAGCA	
ex3_60 66291_ x1	CM000 679.2/1 966200 0- 196620 90	14	0.009	28.2	1	CTGATTCTTTGTACTAGGATGCAAAAGAAAACAATCCTTGTGCCTTCTATCTCTCTTG GTGGCAGCCCAGATTGAATTGGGAATACATCT	
ex3_60 67389_ x1	ENST0 000036 2451.1	19	0.002	30.2	1	AGGTTGTGATGAATTGCTTTAATTTCTGACACCTCATATGAAAGCTGCACTTGCAGTC TT	
ex3_60 68998_ x1	ENST0 000039 1265.1	15	0.003	30.2	1	CCTCCTTTTCTTGTCAGGGACTGAGTGTGTGGTCCTGCTCCTGTTATGTATGGAGGC AAA	
ex3_60 71810_ x1	CM000 669.2/9 888509 0- 988849 90	14	0.009	28.2	1	ATCCTTTTGTAGTTTGTAAGGGTGATGATTGGGGTTTCATGCTTATATGTGAGACATG CCTCCCTCAAACCTTGTTATGTCAGCACATTACCCATCTGATG	
ex3_60 77303_ x1	CM000 685.2/1 205443	14	0.008	28.2	1	ATCCTTTTGTAGTTGAGAAGCATGATGATTGGGGTTTTTATGCTCATATATGAGATGTG CTTCCTTCAAACCTTGTTATGACATCAGCACATTACCTGTCTGATG	

	15- 120544 418						
ex3_60 79394_ x1	ENST0 000051 6468.1	18	0.009	28.2	1	GGATTGACGATGACTTTAAAAAATAATCTCATTGAAATCTGAAAAAATGAGTGA CC	
ex3_60 84257_ x1	AC026 161.4/8 9260- 89123	14	0.008	28.2	1	GCUGUCCUGGACCUGCCAGCUGCACAGAUGCAGAUGCUCUGCUAUGCCUGUAAC AUCGGGGCGAAGUGAAAGUGGCUAUUUUCUACACUCAGUUUUCAGAAAACAGUGAA CAACAAGAAUGGAUAAUAGCCUGACAUUU	
ex3_60 84583_ x1	ENST0 000051 6910.1	14	0.009	28.2	1	GGAAAGGTTACTAAAAGAACACTGCATTCTGTAGCCTGCACGTCCTTAGAAACACC TCA	
ex3_60 85393_ x1	CM000 668.2/3 469278 0- 346928 83	15	0.004	30.2	1	ATCCTTTTGTAAATTCAGATGCGTGATGATTGGGTGTTTACATGCATGTATGAGACGTG CCAACCTTGAATCTTGTATATAACGTGCACATTACCCGTCTGACA	
ex3_60 85660_ x1	AC026 222.5/2 6043- 25912	15	0.003	30.2	1	GGCCUCUCAGUCCGCUJAAUCACACAGGUCCAGUGUGUGCUUGGUGUCUUUUC UGGGAGGCAGAGGAAGGCUCUCCUAAUCACAACAGACCUGCCCAGAAGGGCCUCU CUAUUUUCUAGGAGUAUGAUAGCU	
ex3_60 86113_ x1	CM000 670.2/1 298687 16- 129868 590	16	0.001	32.2	1	AGGATATATCAAAGAGACTTTCTGGGGCTGGGAAACCAGGATCTCGTAATGCTATGA CCAAAGATTGAAGTTTTGCATAGGATACCGTAGTCACTCAGTAGTGCTGTTTTCTGA GGAAATACAAGA	
ex3_60 86610_ x1	CM000 668.2/4 250560 6- 425055 00	15	0.003	30.2	1	ATCCGTTTGTGATTCATAAGGGTGATGATTGGGTTTTCATGCTAATATGTGAGATGTG ACTCCTTCAAACCTTCTTGTATGACATCAGCACATTACTCATCTGATG	
ex3_60 86874_ x1	ENST0 000036 5579.1	14	0.009	28.2	1	AGGCAGGTACTGTTAGAATATAACTGAAGTGTTTTATTGTTATTGTCATTGCTTAAAGC A	
ex3_60 87337_ x1	CM000 663.2/3	19	0.002	30.2	1	ATCCTTTTGTAGTTTGCAAGTGTGATGATTGGGGATTCACTCGTATGTGAGATGTG TCACCCCGAACCTTTTACGTTGGCAAATACCCATCTGACA	

x1	775020 2- 377503 02						
ex3_60 88084_ x1	CM000 674.2/5 048856 6- 504884 84	18	3E-05	36.2	1	AAGACTATACTTTTCAGGGATCATTTCATAGTTTGTTACTAGAGAAGTTTCTCTGAGC ATGTGGAGCACTGAAATATCTAAGA	
ex3_60 88561_ x1	CM000 684.2/2 251778 0- 225178 75	16	0.000 8	32.2	1	ATCCTTTTGTGAGGATAAGCGTGATGCTTGGGTTTTCACTCATGTGAGATGTGCTTCC CTCAAACCTTGTTATATCAGCATGTTAACATCTGATG	
ex3_60 89355_ x1	ENST0 000045 9332.1	14	0.008	28.2	1	GCTTAATGATGAGAATCATTATTTCTTGAATTGGATGACACTTTCCATTCTGCAAAG GG	
ex3_60 90811_ x1	ENST0 000038 4249.1	15	0.004	30.2	1	GGCCTCCTGGGATCCCATCTGGAAAGTGCTTAGTATTCTGCCTGCTTCACAAAGGGA GGG	
ex3_60 96143_ x1	CM000 685.2/1 241977 43- 124197 849	15	0.003	30.2	1	TGTAACCTTGTGGACAAGGCTTATTGACAGGTGCAAAAATAAATAATCTTTTGCCACT CAGAACTCATTGTTTCAGTATGAGTTTTGATACACATAAGAAGGAATATT	
ex3_60 96539_ x1	CM000 665.2/7 257296 5- 725730 68	15	0.005	30.2	1	ATCCTTTTGTAGTTCTTGAGTGTGATGATCGGGTGCTCACACTCATGTGTGAGATATG CCACCCTCGAACCTCATTTTGAAGTCAGCACGTTACCTGTCTGACA	
ex3_60 97634_ x1	ENST0 000041 0213.1	15	0.005	30.2	1	TCAGCTTGAGTCACTCTTCCCAGGCTTTATCCAGGTGGCTTAGGTTAGCTAGGGCTG TGT	
ex3_61 04312_ x1	AC094 019.2/4 7367-	20	2E-06	40.1	1	AGGUCAUUUCAAGAGGUCUUGUGAGGCUGUGAAACCAAGAGCUCUUAACACUGC GACCAAAGAUGGAAGUUCUCUAUAGGAUGCCAUGGCAUUUGAUGGUGCUAUGUUU UCUUGAGGAGAUUAAGA	

	47494						
ex3_61_06739_x1	ENST0000516618.1	15	0.005	30.2	1	TATAAATGTGATGAATTGCACACTCGCAGAGTCATAGCATTAGGGGATGCAGGCAGTGTT	
ex3_61_07625_x1	CM000668.2/103583135-103583268	16	0.0007	32.2	1	AAGCTAGCCAATGAATCTGCTTACCTAAACATGTTTCTGCAGAAATTTTTATTTTAAAAAGCTGGTAATAGTAAAGCCATTTATGAGCCTTAAGTATATTGAAGTTGTTAAGATCCC TGAAAATGGCTATAACA	
ex3_61_08129_x1	CM000665.2/11187915-111879311	14	0.009	28.2	1	AAGACTATACTTTTCAGGGATCATTCTATACTTCATTACTAGAGAAGTTTCTCTGAATGTGTAGAGTACCAACTTCTACGCAAATAAACTAGAAAATCTAGAAGA	
ex3_61_09950_x1	CM000683.2/36258426	15	0.004	30.2	1	ATTCATCTGCAGTTCATTAGTGTGATGATTGGGTGTTACGCACATGCGTGATATGTGCCACCCTCAAACTTTGTTACAATGGTCGGCACATTGTCTGATGTGAAA	
ex3_61_13292_x1	CM000664.2/10057769-100577557	15	0.003	30.2	1	CTCATTTTGTGGTTCATAAGTACGATCACGTATGTGAGATGTGCCCCCTCAAATATCGTTAGGCTGTTGGCACATTACCCATATGACA	
ex3_61_14708_x1	CM000671.2/38147561	15	0.005	30.2	1	TCGATGGGTGGGATAATCCTTACCTGTTCTCGTTTTGGAGGGCAGATAGAACATGATGATTGGAGATGCATGAAATGTGATTAATGCCTCTGCCTAATCAGGACTTGCAACACCCTGAGTACTCCTCTCTGAT	
ex3_61_14805_x1	CM000677.2/25099594	33	8E-14	65.9	1	GGATCGATGATGACTATAAAAAAATGGATCTCATCGGAATCTGAACAAAATGAGTGA CCAAATCATTCTGTGCCACTTCTGTGAGCTGAGGTCC	

ex3_61 15069_ x1	CM000 672.2/1 043997 90- 104399 903	14	0.009	28.2	1	ATATAATTGCAATTAATAATTACATGATTTGATCTTGACTGGGTGTTACATGTATGTG TAAGATATGCCTCCCTCAAACCTTATCACGATGTGCGCACATTACCCATCCAACA
ex3_61 15982_ x1	CM000 663.2/1 717680 70- 171768 175	15	0.003	30.2	1	CACCCCTTTTCTCCTCAGCCAAGGCTAGAGGCCAAGATCAGCCCTCAGGGATCATCA TCAGGACTGCCATGAGCTGAGCTGCCTTGTTCCTGCCGCAAACATGT
ex3_61 17829_ x1	CM000 665.2/8 062807 3- 806279 61	15	0.002	30.2	1	GAGGAGGAGATATTTGTGTTCTCTCATGAGCGTGAAAACAGCGTTTGGTGTTCGTT ATTCCAAGTCCATTTGCTATTGGTGATCGTTCTTCTCTAGAGAATGCGCAACCTA
ex3_61 20865_ x1	ENST0 000036 2981.2	14	0.009	28.2	1	AAGACTATACTTTCAGGGATCATTTCTACATTTCCGGTAATTTCTTTGAACATGTGG AG
ex3_61 21251_ x1	ENST0 000039 1069.1	15	0.004	30.2	1	GGTCATATAAGTAGAAACCACTGAGTGAATCTTACTAGAAAAGTGAATGGCCATTCTT GG
ex3_61 22281_ x1	ENST0 000058 1669.1	14	0.008	28.2	1	TGCTGGTGGTGAAGCTCCCTCTCTCCGAGCACTGGGCCCTGCCTGGGGTAAGGCT
ex3_61 22703_ x1	CM000 670.2/8 491991 3- 849198 18	14	0.009	28.2	1	AGACTCAGTGAATGTGATGATTGAATTTTCACACTCATGTGTGAGATGTGCCTCCCTC AAATCTTGTTATGATATTGGCACATTACCTGTCTAACA
ex3_61 23259_ x1	ENST0 000051 6319.1	14	0.008	28.2	1	ACTCCATGATGAACCCAAAATGCCAAGTATATGACTGAACTTACAAGTGATACCATCT TA
ex3_61 29116_ x1	AC092 590.2/3 5181- 35054	14	0.009	28.2	1	AGGCCAUUUUAAAGAGGGCUCAUGGGACUAUGAAACCAAGAGCUCUUAUGCUGU GACCAAAGAUUGAAGUUCUCUAUAGGUUGCCAAAGCACUCAGUGGUGCUGUGUUU UCCUGAGGAGAUUAAGA

ex3_61 29816_ x1	CM000 674.2/1 013588 49- 101358 748	14	0.009	28.2	1	ATGCTTCATAATTTATAAGTGTGATGGTTGGGTTTCTATGTTTATGGGTGAGATATGT CTCCCTCAACCTTGTTACAACAGTTGGGCATTATCTGCCTGATG
ex3_61 32896_ x1	CM000 670.2/1 018473 60- 101847 256	16	0.001	32.2	1	ATCCTGTTGTAGCTCATGAGCGTGATAATTGGGTGTTTCATGTGCGTGTGTGAGATGT GCCACCCTCTGAACCTTGTTACGACATTGGCACATTACCTGTCTGACC
ex3_61 35498_ x1	ENST0 000051 6084.2	14	0.008	28.2	1	TCCATTTTCAGAAAGCCGAGGTCAAATAATGAGTCCTGGGGAATTCAAACCTTGTGTTA AG
ex3_61 36471_ x1	ENST0 000045 9536.1	18	0.008	28.2	1	TTCTCATGTGGGATAGTTTTCACTTGTTCCCTTCTTTGGAGGGCAGATTAGAACATGA TG
ex3_61 36508_ x1	CM000 674.2/1 147377 04- 114737 798	14	0.009	28.2	1	CACTCCCCTTTTCATTTTACCATTGAGGCTTATGTCTTTATTGGTTGTTCAAGTAGGGC AAAGGAAATGGCCTTTTAAACTCAGAGGCCAGGTAC
ex3_61 37313_ x1	ENST0 000039 1316.1	15	0.002	30.2	1	TTCTTACAAATCTAAATGTGCTTTGATGCAAGTATATTTGAATCCCTTTCCATCTGATA A
ex3_61 37856_ x1	ENST0 000039 1130.1	15	0.006	30.2	1	GCCATGATGCTCTTCGGTTTAGGAGCAATTAATGACTACAGATTGGTGGCAGTTTA TG
ex3_61 38718_ x1	ENST0 000051 6639.1	15	0.004	30.2	1	AAGCAGAACTCAGACTACAATATAGCCGTCAACTGCTGTTTTGTCATATTCTCTGCTC AA
ex3_61 39213_ x1	CM000 677.2/4 521503 3- 452149 06	14	0.009	28.2	1	GGGATGTGCTCAGAGCAGGGGGCCTGAGGAATGGCTCCTCTGTTTACAACACACCC AACAGGAATCTGGGATCATTGTGACGAGAGGTACCAAACCTTGTAGGCTTCCTACGA ACAAACTGTACATGT
ex3_61	AL132	34	2E-14	67.9	1	UGGACCAGUGAUGACCACUGGUGGCAUAUGAGUCAUACACAUGAACACCAUGUUU

40472_x1	709.5/1 51720-151647					CUAGAACUCUGAGGUCCAA
ex3_61_46245_x1	CM000 684.2/3 370492 0-33704786	22	1E-07	44.1	1	GCACTGCTTTAGAGCCTCTGCGTGTCTGGCTGTGGCCTCAGGGGTCTAGCAGCAGT GCTAGAGCAGACCCAGCTTGTGATCCGGGGCTGCTTAGAGGCCACCTAAGTGAT TCCTTTGGCAGCAAGCAACATTC
ex3_61_49277_x1	CM000 675.2/9 978415 7-99784054	15	0.005	30.2	1	ATCCTTTTGTGGTTCACAAGCATGATGATTGACTTCTCATGCTATTGTGTGAGATGTA CCTCCTTCAAATCTTGCTGCAACGTTGGCACATTACAGATCTGATG
ex3_61_52853_x1	CM000 684.2/4 207616 1-42076058	14	0.009	28.2	1	ATCCTTTTGTAGTTCATGAGCGTGATGATTGGGTGTTACATGCATGTGTGAGCTGT GCCACCCTCGAACCTTGTTACCATGTAGGCACATTACCGATCTGACA
ex3_61_52957_x1	CM000 663.2/2 363009 80-236301051	16	0.001	32.2	1	ATCCTTTTGTAGCTCATAAGCATGATGATTGAGGTTTCACACACATTAATGAAATGTG CCTCCCTCAGACTG
ex3_61_53058_x1	ENST0 000036 4671.1	14	0.008	28.2	1	AGCCTCTTTCTAGATGAGAATGGGCACTGTCGATCATGGTGTCTGAAAATTGTAAGT GGC
ex3_61_55092_x1	ENST0 000039 0859.1	14	0.008	28.2	1	GGATTTATAATGAGCTGTGTTTACTGAGCATTATGAAGTAAAGTTCAATATGATTACTC T
ex3_61_55270_x1	ENST0 000036 4939.1	18	9E-05	36.2	1	TCATCAGGTGGGATAATCTTTTCCTGTTCTTCTTTTGGAGGACAGATTATAACATGA TT
ex3_61_57588_x1	ENST0 000039 1263.1	15	0.002	30.2	1	GTCGCACTTAACTTAAGACTCTTTTTCTTGCAGCAGTGGTTTAAACAGAGGAACAAA CA
ex3_61	CM000	14	0.008	28.2	1	TATGGCCTTTATCAAAGCTGCAGCTGCTTCCATGTAGCTGCTGTGGTCAAAAAGAAG

58143_x1	663.2/2 123528 16- 212352 950					CCAAGAGTGACAGTTTTTCCTTGATGGTCATAGTTCTGTTTGCTGTAAGTCTGCAA GATTTTGGGAAAATACCATT
ex3_61 62227_x1	CM000 666.2/1 589094 42- 158909 373	15	0.002	30.2	1	TGGCATGATTTTAAAGCTGTTTCACCCGAGTACACAGCAGGGAAGCCATCCTTGGAG AGCTGAACATGCA
ex3_61 62920_x1	AC016 394.13/ 8497- 8370	16	0.000 5	32.2	1	GGGGUGUGCUCAGAGCAGGGGGCCUAAAGAAUGGCUCCUCUGUUUAUACACAC CCAACAGGAAUCUGGGGUCAAUGUGAUGAGAGGCACAAAGCUUGUGGCCUCCCUA CAAACAAUAGCCUACAUGU
ex3_61 63229_x1	ENST0 000038 4516.1	25	3E-09	50.1	1	GGATCGATGATGACTTAAAAAATGGAAACCTTGAAATCTGAACAAAATGAGTGAC CAA
ex3_61 63619_x1	ENST0 000036 3536.1	15	0.002	30.2	1	TGGATCGATGATGACTACTGGTGGCGTATGAGTCATAGACAATGAATACGTGTCTGG AAC
ex3_61 64089_x1	CM000 672.2/4 598461 0- 459848 10	14	0.008	28.2	1	TCCAGCAGTAGTCAGCTGTCTGGACAGAACCATTCTGGGATCATGTTACACTGCTG GGAGAAGAATGTCTTCTCTTCATCCAGTTGCGTCCATCACTGTTCTGGTGGTGTCTG GCACTGGTGAAGGCAGAACTGTGCTTCCTTGAGAGTGTGCTGAGCATTACCTTG GCTGCTTGGTTCTAGTCTAGGAGCAGACACA
ex3_61 68713_x1	ENST0 000051 6728.1	15	0.004	30.2	1	TATATCTATTTGAGAGACCTAGTACAGTTACTGTCTGTGGCTGAGGTTTCCACTACAG AT
ex3_61 71797_x1	ENST0 000051 7079.1	14	0.008	28.2	1	ATGCCTCTATTTGACACATGAAACAGTTACTGCCTGCTGCTATGGTTTCCACTACAGA TG
ex3_61 71970_x1	CM000 669.2/2 991252 8- 299126 32	20	2E-06	40.1	1	ATCCTCTTGTAGTTCATGAGCGTGATGATTGAGTATTCATGTGCATGTGTGAGATGTG CCTCTCTGAACCTTGTTACAACCTTGGCACATTACCTGTCTGACC
ex3_61	CM000	15	0.004	30.2	1	AACCTAAACATGACAACTGGGTTTTTCATGCTATTGCATGATACCTGCCTCCCTCAAAA

72722_	678.2/1					CTTGTTACATCATCATATCACTCACCTGATA
x1	146764					
	1-					
	114677					
	29					
ex3_61	ENST0	14	0.008	28.2	1	CTACAGATATTTTCTGAATTGGCAAGTCCACCAAGAACTATAAAAATGTGTGTGTGC
73830_	000036					AA
x1	3367.1					
ex3_61	ENST0	15	0.006	30.2	1	GTTGAGGTCTAACACGATAGGGCTTTATCTGTAGCCACACCATCTGGAAACATCTAG
74619_	000051					TGT
x1	6440.1					
ex3_61	ENST0	15	0.005	30.2	1	CTCCAATGAGGAGGAAACATCCTGCCTTACCCCTGTTTTAGCCTGGGAACCAGTAAT
76284_	000051					TGT
x1	6331.1					
ex3_61	CM000	16	0.001	32.2	1	TTGCTTTTGTAGCTTAAGTGTGATGATTGAGTTTGTATGTGCATGTGTGAGATGTGCC
77251_	663.2/1					ACCCTCGAACCTTATTATAGCATGGGCACATTACCCATCTGACA
x1	670414					
	35-					
	167041					
	536					
ex3_61	CM000	14	0.009	28.2	1	ATCCTTTTGTAGTTCATAAGCATGATAACTGGGTTTTTCACACACATATGAGATGTGCC
81508_	663.2/1					TCCCTCAAACCTTGCTACAGCATTGGTACATTATCTGTCTAACA
x1	742002					
	30-					
	174200					
	129					
ex3_61	ENST0	18	0.009	28.2	1	GGTTGTGGTGGTTTTCTTTCTGGTACATTTGTTAAGTTTTCAAATGAGCCTAACTCTG
81589_	000039					CC
x1	0873.1					
ex3_61	ENST0	19	0.004	30.2	1	CTGTGATGATGGCATTCTTAGGACAATTTTGGATTAATTATGAAAACAACACTACTCTCT
82930_	000039					G
x1	1313.1					
ex3_61	CM000	16	0.000	32.2	1	ATCCTTTTGCAGCTCATGAGTGTGACGATTGGGTGTTTCATGCATGTGTGTGAGGTGT
82962_	673.2/6		7			GCCACCCTCTGAACCTTGTTACAACATCAGCACATTACGTCTCTGAAC
x1	615262					
	1-					
	661527					
	25					
ex3_61	CM000	15	0.004	30.2	1	CTGCAGCTAGTTAACCTGACTTGTCCACCTCCCTGCTGGGGGCTCAGTGTGCAATG
83056_	676.2/5					GTTGCAAATGGAGATTCCCTGGTTGTGTATACACCTCATTTCTTGAATGTGTTGCTT

x1	124409					TAAGGGTTCTTGAAGACATTA
	0-					
	512442					
	24					
ex3_61	CM000	14	0.009	28.2	1	ATTCTTTTGTAAATTCATAAGCATGATGACTCGGTATTCACGTGCATGTGTGAGATGTG
83216_	663.2/5					CCACCCTGGAACCTTGTTGCAACGTCAGCACATTATGGGTCTGACA
x1	123135					
	6-					
	512312					
	53					
ex3_61	CM000	14	0.008	28.2	1	ATCTTTATACTTTTCAGGGATCAATTCTATAGTAGGTTACTAGAGAAATGTTTCTGAACA
84102_	664.2/7					GAGTAGGGGGAGAAATCTCAATGAAAAGCTGCAGTAGCTCTCCTGAGCATGAAGCT
x1	562795					GGCAGGTGGTGCCACCTGGTGGTAGCCACTGCTTGCTGTTCGATGACCGTTCTTTGC
	3-					TCCTTGGACAAGGATAAGAGAGAGAGAGAGAACAACAAGCTGCGGGTT
	756281					
	68					
ex3_61	ENST0	25	1E-06	42.1	1	TACTCCAGCCTGGATGACAGAGCCAGACTCTGTCTCGAAAAAAAAAAAAAAAAAAGCTT
84107_	000057					AAT
x1	9231.1					
ex3_61	CM000	15	0.002	30.2	1	ATCCTTTTGTAGTTCATAAGCACAAATGATTGAATTTTCATGCTCATGTGTGAGATATGC
84117_	672.2/5					CTCACTCCAGTCTTGTTACAGTGTTAGCACATTACCTATCTGATA
x1	823876					
	0-					
	582386					
	57					
ex3_61	ENST0	14	0.009	28.2	1	AGATCATTTCAAAGAGGGCTCGTGGGGCTATGAAACCATGAGCTCTTAATGCTATGA
84217_	000036					CCA
x1	3782.1					
ex3_61	CM000	15	0.002	30.2	1	TTTAGAATGTCAA AATTGATTTTGTAAATAGTCAGGACAGGATAAACAGTCGCTATATTA
85060_	663.2/2					AGACCATGTACGTGTCCCTAGACCTAGTTCCTTCCCTACGTCTGTTTTTATAAATGCT
x1	241796					GGTGATAAAC
	41-					
	224179					
	767					
ex3_61	CM000	14	0.009	28.2	1	ATCCTTTTGTAAATTCATAGGTGTGATTATTGGGTTTTTCATGCTCATGTGTGAGAGGTA
87252_	663.2/1					CCTCCTCAAACCTTGTTACAACACGGGCACATTTCTGTCTGTTG
x1	736602					
	00-					
	173660					
	097					

ex3_61 89662_ x1	CM000 666.2/4 008298 3- 400831 06	14	0.009	28.2	1	AGCCACCGCACCCGGCCGGGCTGTATTCTTACACTGACTGTATAGAAAGAGGAGAT AGAGTAAACCTACCCCGTATACTTCAGCCCACGCCCTGTGCCTGTTCTGTATTATGA AGCGGGGTTGG
ex3_61 93266_ x1	ENST0 000045 9339.1	15	0.003	30.2	1	CTGTGTGTAGAAATGTTTGCTCCTCTATCCTTTGGGAACAGGAATACATTTCATAACAT GC
ex3_61 93759_ x1	CM000 679.2/2 655679 - 265578 2	15	0.002	30.2	1	ATTCTTTTGTAGTTGCTACGTGTGACGACAGGGTGTTACACACACATGTGTAAGATGTA CCACCCTCCAGCCTTGTTACAATGTCGTACATTACCCGACCGATG
ex3_61 95510_ x1	CM000 666.2/1 732088 2- 173207 46	19	0.004	30.2	1	GGCTTCTCATTGAGCTCCTTTCTGTCCATTGATGGCAGTTGATGGATTTGCATGAGAA GAAGAGAGAATTACAGAACTAGCGTTATTTTACTTTCTGTCTTTACAGAGGTATATTT GGCTGTTTTGTGAGACATTC
ex3_61 96875_ x1	ENST0 000038 3923.1	24	1E-08	48.1	1	CTGCAGCCTATTAAGCCAAGTTCCTTTTCTCATGGGGGGGCCAGTGTGCAAT GGC
ex3_61 97314_ x1	CM000 663.2/5 680952 - 568102 6	15	0.002	30.2	1	CTCAGCTGGGCTTTTTTTAAGTAACAAGTACTGGGCCACTGACATGTAAAGAGGGA AGTGAGGTGCTCCTGGAG
ex3_61 97636_ x1	CM000 674.2/9 326573 2- 932656 29	16	0.000 9	32.2	1	ATCCTTTTGTAGTTCATAAGCATGATAATTGGGTTTTTCATGCTCATGTGTGAGCTGTA CCTCCCTTAAACCTCGTTATGATGTTGACACATTACCTGTCTGACA
ex3_62 02566_ x1	ENST0 000036 3572.1	15	0.004	30.2	1	GGTCAATGATGTCGTGGCATGTATCAGCTGAATCCAAAGTTGATGTGAGTTCCAAAA TTA
ex3_62	ENST0	14	0.009	28.2	1	TTGATCTACCTCTGATGAAACCTGTGTTGGTGGGGACATCTGAGAGTGTTGATGAAT

05430_	000036					GCC
x1	4129.1					
ex3_62	CM000	17	0.000	34.2	1	ATCCTGAGATTCATGAGTGTGATGGATTGGGTGTTTCGTATGCATGTGTGAGATGCCG
14202_	677.2/3		2			CACCATTGAACCTTGTTAAGATATGGACACATTACCTGTCTGACA
x1	289520					
	0-					
	328953					
	01					
ex3_62	CM000	14	0.008	28.2	1	ATCCTTTTGTGGTTCATGAGTGCGATGATTGGTTTTTACACATATATGTGAGATGTG
14418_	685.2/1					CCTCCCTCAAACCTTGTTAGGAGTAGAAGGTAGGCACATTACCTATCTGACG
x1	130011					
	28-					
	113001					
	019					
ex3_62	CM000	18	0.008	28.2	1	CTGTGTGTAGAAATGTTTGCTCCTCTATCCTTTGGGAACAGGAATACATTACATAACAT
15927_	664.2/7					GCTACATGTAAAAAGGACTCCCCAGGGTGGCCAATCTTATGGTAGAGGTTGTATGGT
x1	548957					AATATATTTCTCCTTCATAA
	6-					
	754897					
	10					
ex3_62	AC099	15	0.002	30.2	1	AGACUCCCAGCUCUGCCCAGUUACACUAGGCUUCGCCUGUGUGGCUUCUGUAAU
17519_	331.2/1					GGGGAGGGAGAGAAAGGAUCUCCCCAGGACCUCAGAUUGGCUUUACUGUGGCAU
x1	40721-					CUCUUUCCUUGAGGGACACAAUAGGU
	140854					
ex3_62	CM000	14	0.008	28.2	1	GGCCTTTTGGTGCTTACCACAGACTGTGCTCTTTCACTGACTGAATAGAGAGAGGAG
18426_	663.2/2					GCAGAGTAAACCTATCCTATATACACCTCAGTCCAAGCCTGGTCTGTATTATGAATGG
x1	286524					GGCAACATGG
	36-					
	228652					
	560					
ex3_62	ENST0	14	0.009	28.2	1	TGGTTGTTACCAAGGCATTTAGCATGCAATTTCTCATTTGCTGTGGACACGACGAGAA
22057_	000038					GA
x1	4772.1					
ex3_62	ENST0	15	0.004	30.2	1	AACCCCTTTTCACTTTGCCAATTGGACTTATGTCTTTATTGATCATTCAAGTGAGCAA
23312_	000036					A
x1	2604.1					
ex3_62	CM000	14	0.008	28.2	1	AGCCTTGAAACTGACTCAAACAATAGGTTTTTATATTTATGTGTGAGATGTGCCTCT
28538_	685.2/1					TTCAAACCTTGTTACAACCTTTGGCACATTACCCATCTGATG
x1	249285					
	19-					

	124928						
	617						
ex3_62	AC092	14	0.008	28.2	1	AUGCCCUUUUAAGGUUGAUGUGGUGUCUUUAAGAAGCUAACAUAGAAGGAUAAAGU	
32579_	814.2/1					AAGUCUCUACAAAACCCAGAGAAGAGACUGGAAAACUCCUCUCUGGAUCCUGCCU	
x1	36717- 136838					GGAGUCACAGCU	
ex3_62	ENST0	18	0.009	28.2	1	AGATTGATGATGGCACCCCCATAAAACCATTCTTAGGAAATCTGAACAAAATGAGTG	
32934_	000039					AA	
x1	1251.1						
ex3_62	ENST0	14	0.008	28.2	1	TGGATCGATGGTGACTGTTGATGGCATATGACTCACATATGATGAGTACGTATCTGG	
33437_	000036					AAC	
x1	5029.1						
ex3_62	CM000	14	0.008	28.2	1	CATGTATAATGATATATTGGTAACACTGCAGACTTGGGGAAGCCAGCCAACCTTGA	
37696_	673.2/1					GATCTGAGTGTGAG	
x1	092635 64- 109263 494						
ex3_62	CM000	14	0.009	28.2	1	ATCCTTTTGTAGTTCATGAATGTGATGATTGGGCATTCACGTGGATGTGTGAGTGCTA	
38857_	665.2/1					CCCTCGAAGCTTGTTTCAACATTGGCACATTATGCATCTGACT	
x1	215912 94- 121591 394						
ex3_62	CM000	15	0.003	30.2	1	CATCTGTGATTATCCTATTCTGAACCTGAATTTCTACTAGAAAAAATTATATGAATCT	
40625_	666.2/7					GGCTTCTGAGAT	
x1	640207 6- 764021 46						
ex3_62	CM000	14	0.009	28.2	1	ATCGTTTTGTAGTCTATTATAAGCGTGATGATTGGGTGTTTCATATGCATATGTGAGAT	
42081_	670.2/1					GTGCCACCCTCAAATCTTGTTATGACGTCATCAGCACGTTACTCTTCTGATA	
x1	023886 35- 102388 526						
ex3_62	ENST0	17	0.000	34.2	1	GGGTCAGTGATGAGAACCTTATATTGTCCTGAAGAAAGGTGATGACTTAAAAATCATG	
48640_	000036		3			CT	
x1	5318.1						
ex3_62	ENST0	20	0.000	32.2	1	TAATGCTATACTTTTCATGGGTCATTTCTATAGTTTGTTATTAGAGAAGTTTCTCTGAAT	

49115_	000036		6			G
x1	4459.2					
ex3_62	CM000	16	0.001	32.2	1	ATTCTTTAGTAGTTCATAATGCTATGATTGGGTTTCCATGTGCACATGTAAGATGTGC
50012_	682.2/5					CTCTCTCAAGCCTTGTTGTGACATCAGCACATTACCCATCTGATG
x1	647564					
	3-					
	564757					
	45					
ex3_62	ENST0	14	0.009	28.2	1	TACCTCCCAGGATGGCATCTGGAAGTGGATAGTATTCTGCCAGCTTTGGAAACTGGA
50099_	000036					TGA
x1	3750.1					
ex3_62	ENST0	15	0.004	30.2	1	ATTTCTATGGAAAAGAGGTGAAGTGGACAGAAGGGATGTCTGAAATTCTATCCTGAG
51737_	000040					GCT
x1	8373.1					
ex3_62	CM000	14	0.008	28.2	1	ATCTTTTTGTAGTTCATGAGCGTGATGACTGAGTGTTTCATGTGCATGTGTGAGGCGT
51744_	669.2/1					GCCACCCTTAAACCTTGTTATAACATCAGCACATTACCCACATGACA
x1	381210					
	88-					
	138121					
	191					
ex3_62	ENST0	16	0.000	32.2	1	CCTCATTTTCTTGGCAGGAACTTGTAGTCCCCTCCCTGTTATGTACAGAGGCAAAG
53614_	000041		7			GGA
x1	1095.1					
ex3_62	ENST0	38	1E-16	75.8	1	TGGACCAGTGATGAATATCATGGGGTTTCTGAAACAACATTTTTGATTAAACCCATCT
58773_	000036					GC
x1	3345.3					
ex3_62	CM000	15	0.006	30.2	1	ATCCTCCTATAGTTCCTCAATGTGATGACTGGGTGTTCACTCATTGGCGAGATGT
59216_	669.2/5					GCCTCTCTCAAACCTTGTTTCAGATGCTGCAGACACATTACCCATCAGATG
x1	485395					
	-					
	548550					
	1					
ex3_62	CM000	17	0.000	34.2	1	ATCCCTTTGTAGCTCATAAGCAAGATGACTGGGTGTTACGCACATGTGTGAGGTGT
62472_	673.2/1		3			GCCTCCCTTAAACCTTGTTAAGGGTTGTTACCCGTGTGATG
x1	262816					
	57-					
	126281					
	754					
ex3_62	ENST0	14	0.009	28.2	1	TGTTCCCGATCTGGTAGAGTAGCATCTGGTTGGTGGTGACCATCTAATACCAGCCAG
63111_	000039					GGA

	6- 241333 17						
ex3_62 82896_ x1	ENST0 000039 1159.1	15	0.003	30.2	1	ATTTTACATAGCGCTGCAGATGTGGCTGCTGTGTCACATTTGTGTTATTAGGTGGCA GAG	
ex3_62 82950_ x1	AL132 709.5/1 32469- 132398	31	3E-10	54	1	UGGAUCGAUGAUGACUGCUGGUGGGCGUAUGAGUCAUAUGCGAUGAAUACGUGUC UAGAACUCUGAGGUCCAU	
ex3_62 83062_ x1	CM000 672.2/1 105763	14	0.008	28.2	1	GTCCTTTTGTAAATGCATAAGCACGATGATTGGGTTTTTCGTGTTTCATGTGAGTCATGCC TCCCTCAAACCTTGTTAGGACATTGGCACATTACCAATGTGATG	
	60- 110576 461						
ex3_62 86778_ x1	ENST0 000036 5391.1	23	4E-08	46.1	1	GGGTCAATGATGAGAACCTTATATTGTCCTGAAGAGCGGTGATGACTTAAAAATCAT GCT	
ex3_62 91112_ x1	CM000 671.2/8 345227	15	0.002	30.2	1	ATCTCTTTGTAGTTCACAAGCATGGTGATTGGGTGCTCAAGCCCATGTGTGAGGTGT GCCTCCCTCAAACCTTGTTACAACGTAGGCACAGCATCACCTGACG	
	3- 834523 75						
ex3_62 91609_ x1	ENST0 000038 4300.1	15	0.003	30.2	1	ATCCAAGGGGATTCCCTCTCCAAGGGAACATGCAGTGCCCTCTCAGGAAAGTAACA ACC	
ex3_62 96585_ x1	CM000 665.2/4 525562	15	0.004	30.2	1	AATTGTATACTTTCAGGGATCATTCCATAGGTTGTTACTAGAGAAGTTTTTTTAGATGT GTAGAACACTGGAAACCACGAGGAGGAGGCGCAGCATTCTCTCTTGACCATGAAGC CGGCTCTTGGTGTTGTTTCATTGCAACTGTCATTTGCCATTGATGATCGTTCTCTTCC TCTGGGAGAGTAAGAGGGGAGAGGACACAGTTTGAGTGGT	
	0- 452554 09						
ex3_62 96758_ x1	CM000 665.2/3 269424	14	0.009	28.2	1	AAGACTACACTTTCAGGGATCATTCTACAGTTTGTTACTGGAGAAGTTTCTCTGAAA GTGTAGAGTACCAAACACT	
	0- 326941 64						

ex3_62 96902_ x1	CM000 680.2/3 573043 - 357294 0	15	0.004	30.2	1	ATCTTTTTGTGATTCATCAGCATGATGATTGGGTCTTCACACAAAAGTTTAAGATGTG CCTCCCTCACATCTTATTATCGTGTGTCAGCATATTTCTGTCTGAAG
ex3_62 98692_ x1	CM000 663.2/1 012287 65- 101228 664	16	0.000 7	32.2	1	ATCCTTTTGTAGTTCATAAGCGTGATCACTGGGTGTTTACGCACGTGTGAGATATGCC ATCCTTGAACCTTGTTATGATGTCAGCACATTACCCATCTGACA
ex3_62 99991_ x1	ENST0 000040 8198.2	20	0.000 5	32.2	1	AAGATGACACTTTGAGGCATCGTGTCTATGGTTCATTACTACAGAAGCTTCTCTGGAT GT
ex3_63 02708_ x1	CM000 676.2/1 023589 02- 102358 799	15	0.004	30.2	1	ATTCTTTTGTAGTTCATAGGCATAATGATTGGGTTTTTCATGCTCATGTATGACCTGTG CCTTCCTCAAACCTTTGCTATGATGTTGGCACATTACCTAGCTGATA
ex3_63 03324_ x1	ENST0 000051 6123.1	14	0.008	28.2	1	GGATGGATGACGACTTAAAAATGAATCTCGTTGGAATCTGAGCAAAACGAGTGAGCA AAC
ex3_63 06129_ x1	CM000 663.2/1 561921 76- 156192 063	14	0.009	28.2	1	TTGCCGCCACACAACCAAATTAATAACACAGAAGGGTAAGGTAAGTCTCCATT AAACCCAGGAAAGAGACTGGAAAACCTCCTCTTTGGAGCCTGTCTATAGTCACAGGT
ex3_63 06246_ x1	ENST0 000051 6303.1	23	1E-05	38.2	1	GTGTTTAGAAGACCACATCTTCATCCTGAAAGCACAGATGTGTGGAAACCAATGACC GAG
ex3_63 08527_ x1	CM000 677.2/2 035218 1- 203520 86	16	0.001	32.2	1	ATCCTTCTGTGGCTGATATGTGTGATGAGGGGGTTTTTCACACTCTTGCGTGGGACGT GCAACCTCTTTAGAACAGTGGCACATTACCTGTCCTACA
ex3_63	CM000	15	0.003	30.2	1	CTGCAACCAATTAAGCCGACCTAGTTCCTTTCTCTTTGGGGCCTGGTGTTC AATAG

19045_x1	673.2/8 304159 8- 830414 64					CTGCAAACAGCAGCTTCCTTGGTAGTGTATGCAGCCTGTTTCTTGTATGGGTTGCTC TAAAGGACCTTGGAGACAGCC
ex3_63_28416_x1	CM000 663.2/2 243367 91- 224336 889	16	0.000 7	32.2	1	ATCCTTTTGTAGTTCCTAAGTGTGAAGAATGGGTGTTTCATGCAGAAGGATAAGATGTG CTACCCTCAAACCTTGTTCCGTGCATATTACACGTCTGACA
ex3_63_29390_x1	ENST0 000036 4764.1	15	0.004	30.2	1	GGGTCAATGATGAGATGTTACCTTGAAGAGAAATGATGACGTAAAAATTAAGTTCAGT TG
ex3_63_30461_x1	ENST0 000036 2917.1	36	1E-15	71.9	1	GCATGGGTTTGGATTTATGATGGGCTGGATTCCCTAGGCCTCTCATAGTACCCCATG CCA
ex3_63_30836_x1	CM000 682.2/4 171260 0- 417124 79	14	0.009	28.2	1	GTGTCCTTTTAAGGTTGACACAGTGCTTTAAGAGCCTAACACAGAAAGGTAAAGTAA GTTTCCGTAAAACCCAGAAATGATATTGCAAATTCCTCTTTGAATCATGTCTGGAGT CACAGCT
ex3_63_31636_x1	CM000 663.2/1 121954 94- 112195 606	15	0.003	30.2	1	ATCAGTTTAACATTTAAAAAATGTATCAAGGCGTGGTGATTAGGTTTTCACACTCAT GTGTGAGATGTGCCTCCCTTGAACCTTGTTACATTGGCACTTACCCATTTGACA
ex3_63_32022_x1	ENST0 000045 9368.1	21	1E-06	42.1	1	ATCCTCTTGTAGTTCATGAGCGTGATGATTGAGTATTCATGTGCATGTGTGAGATGTG CC
ex3_63_32624_x1	CM000 676.2/6 365911 9- 636591 92	24	0.001	32.2	1	TAGACTGTACTTTTCAGGGATCATTCTGTAATTCGTTACTAGAGAAATTTCTCTGAATG TGTAGAGCAGTTAAT
ex3_63_34634_x1	AC010 653.10/	15	0.002	30.2	1	CUGCAGACAGUUAAGCCAACUGAGUJCCUJCCUCAGGGAGGCCAGUGUACA GGCUGCCCACAGCAGCUUCCUUGGUAGCGUACUCAGCCUGUUUCUUGUAUGGGU

x1	163838					UGCUCUAAGGGACCUUAGAGACAGGC
	-					
	163972					
ex3_63	ENST0	15	0.004	30.2	1	CTACAATCATGGCAATATTTTTGTCAACAGCGGTTACCTAGTGAATGTTGATACTTT
34823_	000038					G
x1	4713.1					
ex3_63	CM000	15	0.005	30.2	1	TTACAGTCAATTAAGCCAATCATGTTCCCTTTCTTGTAAAGGGCCAGGTGTGCCATGG
37957_	666.2/4					CTGCGAACAGCAGCCTTCTCGGTAGTATGTGCACCGTGTTGCTTGTATGTTGTAAGC
x1	893638					ATTGCCCTAAGGACCTTGGAGACAGCC
	1-					
	489365					
	21					
ex3_63	CM000	14	0.009	28.2	1	TGCACTTGTGTTTTGTTAACTGTGAACAAAGACTTATAGAGAAGTGCAAAAAATAAA
38144_	663.2/1					TCCTCTTTTGCAACCCAGAACTCATTGTTTAGTAAGGGTTTTGATACATATAAAAGAG
x1	176887					ATATT
	42-					
	117688					
	621					
ex3_63	ENST0	15	0.003	30.2	1	GATGCCTTCCGGAACATGCCAGCACCGCAGATGCTGGCAGTCTGCTGTGCCCGTGA
42356_	000036					TATT
x1	4863.1					
ex3_63	ENST0	14	0.008	28.2	1	CCTGGGTGATGATAAGCAAATGATGCCTGAATGTGAAGGTCATACTCGGCTTTAGCT
42760_	000036					GAT
x1	3202.1					
ex3_63	ENST0	14	0.009	28.2	1	ATCCTGTTGTAGTTCATAAGCATGATGATTTGGTGTTCACGTGCATGTGTGGGATGTG
44942_	000045					CC
x1	8863.1					
ex3_63	CM000	15	0.007	30.2	1	AGCCTCCTGGTGTCTCAGCACAGGATGTGTTCTTACCCTAACCAAATAGAAAGAGTAG
45138_	669.2/1					GCTGAATTAACCTATGCCATATACACCTCAACCCAGGCCCTGCAACTCCTCTGTATTG
x1	381881					TCAATGGGTGGACATGG
	29-					
	138187					
	998					
ex3_63	CM000	15	0.003	30.2	1	ATCCTTTTGTAGTTGATGAACAATGATGATTGGGTGTTTCATGCACATGCGTGAGATGT
45416_	671.2/1					GTCACCCTCAAACCCTTACGTGGCAGGTTACCCATCTGACG
x1	330930					
	52-					
	133093					
	151					
ex3_63	KV766	15	0.002	30.2	1	ATCCTTTTATAGTTCATAAGCATGATGATTGGGTTTTTGCACACGTGTAATATGTGCCT

49352_x1	194.1/1 8640- 18741					CCCTCAAACCATGTTATGACCTCAGCATATTACCTGTCTGATA
ex3_63_49389_x1	CM000 675.2/1 027218 02- 102721 905	16	0.002	32.2	1	ATCCTTTTGTGGTTCATACATGTGGTGATTGGGTTTTCACACTCACATGTGAGATGTG CCTCCCTCCAACCTTGTTATGATGTCAGCACATTACCCATCTGACA
ex3_63_51480_x1	ENST0 000051 6329.1	14	0.009	28.2	1	AGCACTTGTATGTTTTAACATGTGGACATTTATAGACAGGTTCAAAAAGTCCTCTTGC AA
ex3_63_52698_x1	CM000 667.2/6 623123 2- 662311 29	14	0.009	28.2	1	ATCCTTTTGTGGTTGGTAAGCATGATAACTGGATTTTCACATTCATGTGTGAAATGTG CCTCCTCAAGGCTTGTTACCATGTAGGCACATTACCCAACCTGATG
ex3_63_54001_x1	ENST0 000036 3622.2	20	2E-06	40.1	1	AAGGCTATACTTTCAGGAATCATTCTATAGTTTGTTACAAGAGAAGTTTCTCTGAATG T
ex3_63_57901_x1	CM000 664.2/1 294274 22- 129427 525	15	0.004	30.2	1	ATGTTTTTGTGGTTTATGAATGTGATGATTGGGTTTTCACACTCAAGTGTGAGACGTG CCTCTCTCAGATCTTGTTCCAATGTCAGTACATTACCGATCTGACA
ex3_63_58809_x1	CM000 684.2/3 195340 4- 319535 06	14	0.008	28.2	1	ATCTTTTTGTAGTTCATAAGTGTGATGATTGGGTTTTGACATGCAGGTGTGAGATGTG CCACCCTCAAACCTTGTTACAACATAGACATGTGACCCTCTGATG
ex3_63_61713_x1	CM000 671.2/7 567690 7- 756770 16	14	0.008	28.2	1	ATCCTTTTGGGGTTCATAAGCGTGATGACTGGGTTTTTGCACACTCATGTGTGAGATG CACTTCTCTCAAACCTTTTTGCAATGTTGGCATACTATCATACCTGCTTGATG

(b)

Qseqid	Sseqid	NT	Evalue	Bitscore	Number	Sequence
co3_23_63374_x5590	CM0006 64.2/231 456523- 2314564 44	18	#####	36.2	5590	TGGATATGATGACTGATTACCTGAGAAATAATTGATGAAATCTCAAGAAAATTC CTCTAGATAGTCAAGTTCTGATCCAG
co3_28_21260_x4135	ENST00 0003642 81.1	14	#####	28.2	4135	CTAAAACAATGTCAATAGTTTTTCATCAACAGCAGTTGAACCTAGTAAGTGTCG ATACTTT
co3_29_85674_x3730	ENST00 0003843 20.2	14	#####	28.2	3730	CTGGTTGCATGATGAATAAAATCAAATCACCATCTTTCGGCTGAGTTCGTGAT GGATTTG
co3_29_93122_x3717	ENST00 0003840 48.1	16	#####	32.2	3717	ATTCGTGATGACTGATCATTCTTCACTTTGACCAGATGTCTACTGAAGAAAG CCTGCGT
co3_33_55757_x2884	CM0006 73.2/628 53395- 6285332 5	20	#####	40.1	2884	CTCACCAGTGATGAGTTGAATACCGCCCCAGTCTGATCAATGTGTGACTGAAA GGTATTTTCTGAGCTGTG
co3_40_65880_x1811	AY34960 6.1/1-85	15	#####	30.2	1811	CCCCUAUCUCUCAUGAUGAACACAUAUGCCUCUGAGCUGCUGUGAUUUUCU GGCUUCAAGUAAACGCUCUGAAGAAGAGAUGGGG
co3_43_66794_x1475	ENST00 0006272 53.1	21	#####	42.1	1475	AAGACTATACTTTTCAGGGATCATTCTATAGTTTGTTACTAGAGAAGTTTCTCT GAACGT
co3_45_57968_x1281	AB06182 0.1/3401- 3472	28	#####	56	1281	UCAAAAUGAUGAGAUUCCACUUAUUUGGUCCGUGUUUCUGAAACACAUGAU AUUUGUGGAAAUUCUGACUUG

co3_47 70375_ x1115	ENST00 0004481 88.1	29	#####	58	1115	TGGAGGTGATGAACTGTCTGAGCCTGACCTTGTAGAATGGAGGCAAAAAAC TGATTTAA
co3_48 12047_ x1078	AJ60948 3.1/2-129	28	#####	56	1078	CUGGAGGACUAAGAAGGCUGAGUCUGAUGAAGUAAGACUUUGCUGAUACA UCCUCCUAGAAAAAGGGUUGGAGAGAGCAGCCUUCACUGAAGAGUAUCA CAGGGCUGACUGUACUACCCAACACUC
co3_48 17430_ x1075	CM0006 85.2/135 212441- 1352125 13	18	#####	36.2	1075	AAGACTATACTTGCAGGGATCATTTCTGTAGTTGGTTACTAGAGAAGTTTCTT GTCTGTAGTTGGTTATTAGA
co3_50 20108_ x938	CM0006 73.2/628 53732- 6285366 3	24	#####	48.1	938	GTTTGTGATGACTTACATGGAATCTCGTTCGGCTGATGACTTGCTGTTGAGAC TCTGAAATCTGATTTTC
co3_51 18822_ x875	AC09217 4.5/1568 14- 156683	23	#####	46.1	875	CUUCCCAUUUAAUUUGCUGCUUAUAGUCUCACUGUGAUUAGAGCAAUUUAC ACAUGGGAUAAAAUAAUUAUUGAGCCACUGUAAAUUGAGAUGAAGUAACCGU UUUCAUAUCUUCUGCAUGGACUAGACAUUG
co3_51 63667_ x849	AJ23885 3.1/1-62	25	#####	50.1	849	CACAGAUGAUGAACUUAAUUGACGGGCGGACAGAAACUGUGUGCUGAUUGU CACGUUCUGAUU
co3_51 88031_ x833	AC02536 2.12/104 594- 104663	40	#####	79.8	833	GCUGUGAUGACAUCCAAUUAAAGCACGUGUUAGACUGCUGACGCGGGUG AUGCGAACUGGAGUCUGAGC

co3_53 76913_ x742	ENST00 0003641 55.1	45	#####	65.9	742	GTTTCTGATGAAGCCTATGTTGGTAGGGACA ACTAAGGTTGTTGATGAATGCT AACAGCT
co3_54 28064_ x720	CM0006 79.2/428 1844- 4281769	25	#####	34.2	720	AAGACTATCCTTTCAGGGATCATTCTATAGTTT GTTACTATAGAAGTTTTCTG AAGGTGTAGAGCACCAAAGGAT
co3_54 33817_ x717	ENST00 0003626 07.1	26	#####	52	717	CTGCATCCACTGATAGACCTTGAACAATTTACT GTTGTTCTTTTGGTTTGC ACTAGGATG
co3_54 50915_ x708	AJ22402 8.1/3-79	28	6E-11	56	708	CAGAAUACAUGAUGAUCUCAAUCCAACUUGAAC UCUCUCACUGAUUACUUG AUGACAAUAAAAUAUCUGAUUUCUG
co3_54 65725_ x701	CM0006 82.2/179 62946- 1796271 0	29	2E-11	58	701	GTGAAATGATGATTTCAGTTTATCCATTCGCTGAG TGCGCTGCACTGACCTTCT TCCAAGCCTCAGTTCCTGTTCTAGGAACTTGAGG CTATGTAGCCTGAAAATGC CCTGCAGTCTGCAGTGTCTACTGTGAACTGCTT GTGTGTTGGCAGGCTACC GGTAAGAATGTTGGTGTGTCAGCAGGGACGGGG CCCTCTGAGACCCATCTCA CAAAGATGAGTGGTAAAATCTGATCAC
co3_55 65224_ x663	AC10444 6.2/1455 01- 145577	35	#####	69.9	663	AAUGUGAAGCAAUGAUGAUAAACUGGAUCUGAC UGACUGUGCUGAGUCU GUUCAAUCCAACCCUGAGCUUCAUGUU

co3_55 84997_ x654	CM0006 72.2/890 61131- 8906103 1	14	#####	28.2	654	ATTCTTTTGTATCTCACAAGTGTGACTGGGTTTTTAGGCTCATGTGTGAGATGA GCTTCCCTCAAAAATTGTTGTGACTGTGGCATGTTACCTGTGTGATG
co3_56 57610_ x621	AP00127 3.4/3902- 3830	35	#####	69.9	621	CGAUGUUAUGAUGAUGGGCGAAAUGUUCAACUGCUCUGAAGGGGCUGAAU GAAAUGGCCUUUCUGAACAUCC
co3_57 21359_ x592	CM0006 63.2/757 87072- 7578715 0	14	#####	28.2	592	GGTCAATGATGAGTTGGCATGTATTCTGAATCTAAAGTTGATTATTACTACTTT AGCTCTAGAATTACTCTGAGACCTG
co3_57 49504_ x581	AJ54332 5.1/2-85	28	#####	56	581	CUGAGUCCAUGAUGAUUUCAAGUUAUCCUGUCUGAAGGCAAAGAAAGGCC UUUCUGUGUGAAUUUGAAUAUCUGAAACUCAG
co3_57 77102_ x571	AC01876 1.6/4839 1-48315	26	#####	52	571	GGCCUCAAGUGAUGGAGAGCAAUACCCGGGGAUGACUGUGACCACAUUGG GAUGUAUUCGUACUGUCUGAUGGGGCC
co3_58 33308_ x552	AJ60943 0.1/1-139	30	4E-12	60	552	GACCUCCUGGGAUCGCAUCUGGAGAGUGCCUAGUAUUCUGCCAGCUUCGG AAAGGGAGGGAAAGCAAGCCUGGCAGAGGCACCCAUUCCAUUCAGCUU GCUCCGUAGCUGGCGAUUGGAAGACACUCUGCGACAGUG
co3_59 22158_ x519	CM0006 68.2/121 443617- 1214436	29	#####	50.1	519	AAGACTATACTTTTCAGGGATCATTCTATAGTTTGTACTAGAAATGTAATAAA CTTAGTGATGAATTACTATAAGC

co3_60 17443_ x490	ENST00 0003649 21.1	19	#####	30.2	490	ATGCAGGTACTGTTATAACTGAAGTGTTTTACGGTTTTTTCTTCCTGCTTAAAG CACTTG
co3_60 51763_ x477	ENST00 0006295 36.1	26	#####	52	477	AAGCACTGCCTTTGAACCTGATGTGTCTTGTGTTGTAGCTTCACGGGCCAAGCA ACAGTGC
co3_61 78992_ x433	AK30322 2.1/647- 788	21	#####	42.1	433	GCUCUGUGAUGGAGCCCAUGCGUGUCAUCUGAGCCUCUGGCUUCCCUGCC AGUGCAGCCCUGGCAGUGUCCUACUUCCCAGGGCUGUUGUCUGCCUGGC GGGAAGGUCCUGGGCAAAGGAUCAGUCUUUGUACUCUGAGAGC
co3_62 72551_ x407	CM0006 65.2/185 442219- 1854423 19	15	#####	30.2	407	ATTCTTTTGTGATTCATAAGCATGACTGGGTGTTCCCACTCACGGGTGAGATG TGCCTCCCTCCAACCTTGTTACGACGTCAACACATTACCTGTCTGACA
co3_63 76397_ x375	AB06182 0.1/2178- 2249	21	#####	42.1	375	CAGUAGUGAUGAAAUCCACUUCAUUGGUCCGUGUUUCUGAACCACAUGAU UUUCUCGGAUGUUCUGAUGCU

co3_63 92775_ x369	CM0006 63.2/285 08559- 2850876 2	24	#####	48.1	369	CCAACGTGGATACCCTGGGAGGTCACTCTCCCCAGGCTCTGTCCAAGTGGCA TAGGGGAGCTTAGGGCTCTGCCCCATGATGTACAGTCCCTTTCCACAACGTT GAAGATGAAGCTGGGCCTCGTGTCTGCGCCTGCATATTCCTACAGCTTCCA GAGTCCTGTGGACAATGACTGGGGAGACAAACCATGCAGGAAACATAT
co3_64 12609_ x365	AK09614 7.1/739- 811	20	#####	40.1	365	GUUUGAAUGAUGACUUUAAUUGUCGGAUACCCCUUCACUCCUUUUAUGAG UGAAACAUAAGAGUCUGACAAAC
co3_64 94947_ x344	CM0006 74.2/566 43750- 5664368 0	24	#####	48.1	344	CCTCACTGATGAGTACGTTCTGACTTTCGTTCTTCTGAGTTTGCTGAAGCCAG ATGCAATTTCTGAGAAGG
co3_65 06924_ x340	CM0006 65.2/988 72180- 9887208 3	19	#####	30.2	340	AAGACTATACTTTTCAGAGATCACTTCTGTAGTTTATTATTAGAAAGTTTCTCTG AATGTGTAGAACACTGGAAAAATGATCTAAGACTACTGTGAAT
co3_65 21144_ x336	ENST00 0003913 08.2	18	#####	28.2	336	AAGACTATACTTTTCAGGGATTATTTTCAGATAAACTTCTAGAGTTTCTCTGAACC TGTAGA
co3_65 32530_ x333	ENST00 0003630 64.1	49	#####	65.9	333	GAAAATACATGATGATCTCACTCCAACCTGGAACCTCTCTCACTGATTACTTGATA ACAATA

co3_65 53032_ x328	CM0006 85.2/119 787484- 1197873 53	23	#####	46.1	328	AAAGCAGGTTGCAATTACAGTGCTTCATTTTGTGGAAGTACTGCCATTATCCT GCTGAAAGAAAAGCCGTGTTAATCATTTTTGATTTTGCCTTTATGAGGGTAAAA TCATGACAGATTGACATGGACAATT
co3_66 17765_ x313	AY34959 3.1/1-137	30	#####	60	313	CAGGCUGUGAUGAUUGGCGCAGGGGUACGGACCUCAGCUGAGUCAUGGGA GCUGAAUGUAUGUGUUUCUCCUUUGUCCUGCAUGUGGCAGGCUGAUGGG GAGCACUUACAUGAGACUGUUGCCUCAAUUCUGAGCCUG
co3_66 31786_ x310	AJ01066 6.1/3-73	20	#####	40.1	310	AGCACAAAUGAUGAAUAACAAAGGGACUUAUACUGAAACCAGAUGUUACA UUGUAGUGUGCUGAUGUGCU
co3_66 65387_ x301	CM0006 63.2/447 76490- 4477659 3	26	#####	52	301	AAGTAGGGTGATGAAAAAGAATCCTTAGGCCGTGGTTGTGGCCGTCTTGGTCA CCTGTGTGCCACTTGCCAATGCAAGGACTTGTGCATAGTTACACTGACTGTTG
co3_66 78235_ x297	ENST00 0003637 53.1	18	#####	36.2	297	CAGTAGTGATGAAATTCCACTTCATTGGTCCGTGTTTCTGAACCACATGATTTT CTCGGA
co3_67 71615_ x276	AC10406 6.3/5105 5-51176	25	#####	50.1	276	GUGCCCUUUUAAGGUUGACCCAGUGCUUUUAAGAGGCUAACACAGAAGGGU AAAGUAAGUCUCCAUAAAACCCAGAGAAGAGACUGGAAAGCUCUCCUUUGG AUCCUGUCUGGAGUCACAACU

co3_68 20038_ x265	ENST00 0004084 93.2	23	#####	46.1	265	ACCTTCTTGTATAAGCACTGTGCTAAAATTGCAGACACTAGGACCATGTCTTG GTTTTTG
co3_68 58134_ x257	AJ60945 0.1/1-137	29	#####	58	257	GGGCAUACUCGUAGACCUUGCCUGACUGUGCUCAUGUCCAGGCAGGGGGG ACAGUGUAUGCAAGAAUAAUUUGGAGUUCUGCCAGCUCUAACCAGCUUCA UCAGUGGCUGGAUAAAUUGCAGGACUCUAAACAUUU
co3_68 71168_ x254	AB06182 0.1/4174- 4242	35	#####	69.9	254	UUGUUUGAUGAGAUUCCACUUAAGGUCCGUGUUUCUGAAACAAAUGAUUU UGUGGAAGUUCUGAUUUU
co3_68 76996_ x253	AY34960 4.1/4-89	41	#####	81.8	253	UCUGGCAAUGAUGACCCACUUGCCCUCACUGAGAACAAGUUCGGUAAUGA GAAUCUUUGUUAAUGGACUCAAGUUCUGAGCCAGC
co3_68 78261_ x253	AL04984 0.8/4945 7-49533	15	#####	30.2	253	AUUGUUACAUGAUAAAAUCAAAUCACCAUCUUUUAGCUAAGCUUGUGCUG GAUUUGCUUUUUUCUGAUAAAGAUG

co3_69 20620_ x243	BK00556 8.1/1-420	28	#####	56	243	GUUUUAGGGAGGGAGAGCGGCCUGGGUCCUGGGUGUUGUGUGCGGAGCU GUGGCGUCGCGUGUGAGGCGCGUGCAGGGUGAGUGUGAGUGGACGCGUG AGUGUGUGAGUGUGCGCGCUUGGAGCGUGUUAGGCGAGUGCGUGCGCCC ACCCUGCGCCCCUCCUCCCGCUUACACUUUGAUCUUUUUGAUCGGAUC GUGACCCAGCCCCGCCGGGCCACCCGAAAUGAAAAGCUCUCCUCCUGC GAAGCCCCUCGGGGCGCUGUGCAGCGAGGCCCCUUAGGCGGCGGCCAC GCUGUGGUCCCCGAGGUCCCGGAGCUGGCCUUGCGGGGCCCGGCGCUCA GAAGUGAUGAAUUGAUCAGAUAGACGAGGCCGGGCUUGUCCCCGGCCACU GAUUAUCGAGGCGAUUCUGAUCUGG
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co3_69 56354_ x236	CM0006 68.2/856 77368- 8567729 4	25	#####	50.1	236	TATCTGTGATGATCTTATCCCGAACCTGAACTTCTGTTGAAAAAAAAAACTTT TACGGATCTGGCTTCTGAGAT
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co3_69 84369_ x231	ENST00 0003639 81.1	21	#####	42.1	231	ACTCCATGATGAACACAAAATGACAAGCATATGGCTGAACTTTCAAGTGATGT CATCTTA
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co3_70 24787_ x223	ENST00 0003910 79.1	14	#####	28.2	223	AAATGATGAAATCACCCAAAATAGCTGGAATTACCGGCAGATTGTGTAGTGGT GAACCTA
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co3_70 27683_ x222	ENST00 0003649 38.1	43	#####	85.7	222	CCAACGTGGATACACCCGGGAGGTCCTCTCCCCGGGCTCTGTCCAAGTGG CGTAGGGGA
co3_70 43145_ x219	AADC01 102901.1 /15489- 15356	19	#####	38.2	219	CUGUCAGGUGGGAUAAACCCUUCCUGUUCUCCGUUUGGAGGGCAGAUAG AACAUGAUGACUGGAGAUGCAUGAAAUGUGACUAAUGUCUCUGUGUAAUCA GGACUUGCAACACCCUGAUUGCUCUCCUAUCUGAU
co3_70 87608_ x210	AC09348 4.2/1602 94- 160365	23	#####	46.1	210	UGUCCUGAUGAUACUUGUAAUAGGAAGUGCCGUCAGAAGCGAUAAACUGAC GACGUCUAAUGUCUAUCUGACC
co3_71 05529_ x207	AF14134 6.1/1052- 1111	38	1E-16	75.8	207	AGCCUGUGAUGCUIIUAAAGAGUAGUGGACAGAAGGGAUUUCUGAAAUUCUA UUCUGAGGCU
co3_71 59131_ x197	ENST00 0004591 63.1	51	1E-19	85.7	197	AAGTCAAATGATGGCAATCATCTTTTCGGGACTGACCTGAAATGAAGAGAATAC TCATTGC
co3_71 77660_ x193	L44140.1 /70716- 70850	43	#####	85.7	193	CCGACGCCAAUUAAGCCGACUGAGUUCUUCUCCUCAUGGGGACCCAGUGU GCGAUGGCUGCACACAGCAGCUUCCUUGGUAGUGUACGCAGCCUGUUGGU UGUAUGGGUUGCUCUAAGGGACCUUGGAGACAGGC

co3_72 20697_ x186	CM0006 63.2/116 278606- 1162788 21	22	#####	36.2	186	AAGACTATACTTTTCAGGGATCATTTATATGATTTGTGGCTACAGAAGTTTCTCA GCGTGAGGAGCCCCAGAAACCATGAGGAGGAGACGCAGCATTCTCTGTGGC GCGTGAGGCCAGCTCTTGGTTTTACTTCGCTACAACCTGCATTTGCCATTGGTG ATCGTTCTTCTCTCATCTCAGGGAGAGTAGAAGGGAGAGAAGATGCAGCCTG AGTGAT
co3_72 34765_ x184	ENST00 0006259 43.1	23	#####	46.1	184	TCTCAGTGATGAAAACCTTTGTCCAGTTCTGCTACTGACAGTAAGTGAAGATAA AGTGTGT
co3_72 38261_ x184	ENST00 0003842 29.1	51	#####	46.1	184	TGCTCTGATGAAATCACTAATAGGAAGTGCCGTCAGAAGCGATAACTGACGA AGACTACT
co3_72 42291_ x183	ENST00 0004080 61.1	31	#####	61.9	183	GGGCTCCCATGATGTCCAGCACTGGGCTCTGATCACCCCTGAGGACACAGT GCACCCAG
co3_72 85684_ x176	ENST00 0003842 14.1	32	#####	63.9	176	CTTCGATGAAGAGATGATGACGAGTCTGACTTGGGGATGTTCTCTTTGCCCA GGTGGCCT
co3_72 94957_ x174	CM0006 82.2/417 12600- 4171247 9	23	#####	30.2	174	GTGTCCTTTTAAGGTTGACACAGTGCTTTAAGAGCCTAACACAGAAAGGTAAA GTAAGTTTCCGTAAAACCCAGAAATGATATTGCAAAATTCCTCTTTGAATCATG TCTGGAGTCACAGCT
co3_72 97045_ x174	AC00844 3.10/639 18-63851	28	#####	56	174	GGGGCGGUGAUGACCCCAACAUGCCAUCUGAGUGUCGGUGCUGAAAUCCA GAGGCUGUUUCUGAGCUG

co3_73 22653_ x169	ENST00 0004593 42.1	24	#####	48.1	169	G TTCAGATGATGAATTTAACTGTTCAACTGCTGAATGATAACGGGCATGAACT AAA ACTT
co3_73 32773_ x168	AC00706 6.4/1645 16- 164622	25	#####	50.1	168	AAGUUUUCUAAGUGUCUAAUGAUGAAUUUCAUAGGGCAGAUUCUGAGGUG AAAAUUUAAUUCACUGAUACUCCUACUGUGGAAUCUGAAGACACUUGA AAACGU
co3_73 44163_ x167	CM0006 74.2/103 592112- 1035922 43	19	#####	30.2	167	T CATCAGATGGGATAACTTTTACCTGTTCCCTCTTTTGGAGGTTAGATTCTAAT ACGATGATTGAAGTTTCGTATGATACGTGATTAATGTCTCTGCATAATCAGGAC TTGTAACACCTTGATTGCTTCTGAT
co3_73 61860_ x164	ENST00 0003840 27.1	37	#####	58	164	G TTTGAATGATGACTTTAATTGTCGGATACCCCTTCACTCCTTTTATGAGTGAA ACATAA
co3_73 76969_ x161	CM0006 72.2/687 55172- 6875523 8	26	#####	52	161	G AGTTATGATGTGTGTAAATCCTATTCCATTGCTGAAATGCAGTGTGGAACAC AATGAACTGAACTC
co3_73 95189_ x158	ENST00 0003841 47.1	35	#####	69.9	158	C TACGGGGATGATTTTACGAACTGAACTCTCTCTTTCTGATGGATTAGTGGAG AAAACAG
co3_74 17108_ x155	ENST00 0003632 14.1	41	#####	65.9	155	T GATGACATTCTCCGGAATCGCTGTACGGCCTTGATGAAAGCACATTTGAACC CTTTTCC

co3_74 30475_ x153	AC01328 3.23/462 45-46493	38	#####	75.8	153	AACAUGC <u>U</u> CCU <u>U</u> AGA <u>U</u> CCACCU <u>U</u> UGUGGAUGAAUCUUGAACUGAGU <u>U</u> CCA CUUGUAAACUUCUUGUUUCUUGUGGU <u>U</u> CCAGUAGUCAAAAGAAACA <u>U</u> CCAGC AACUUUUUUGGUUGUAUAGUCAAAAGGUGCUUGAGUCAUUGGCAUGUAAGA GAAAU <u>U</u> ACCUGCAUGUUAGUCUAACGUUCUGAUAGAA <u>U</u> GACAUGCAUUU AUGCUGCCA <u>U</u> UUUGUUACUAUCAGGACUCGACUCGUGUGCGGACAUU
co3_74 43214_ x151	AC00643 5.7/3490- 3399	32	#####	63.9	151	UAGAGAAGUCA <u>U</u> GAUGGUUUU <u>U</u> AU <u>U</u> CAU <u>U</u> ACGUCUGAACCU <u>U</u> GUCUGAAGCA UCUCAGUGAUGCAAUCUCUGUGUGGUUCUGAGACUUCUCCA
co3_74 48471_ x150	ENST00 0006072 46.1	19	#####	30.2	150	ATTCATTTTCAAATATTTGCTGACTAAATGATACACACATGACTAAA <u>U</u> ACTTAATC CTGAC
co3_74 50121_ x150	AC00659 7.2/8154- 8065	14	#####	28.2	150	UCACUGUGAUGAUGGUUUUCCAACA <u>U</u> UCGCAGUUUCCACCAGAAAGGUUU UCCUUAGUGUUGGGUAAACCU <u>U</u> CCUUGGAUGUCUGAGUGA
co3_74 85294_ x144	ENST00 0003847 69.1	33	#####	50.1	144	AGCTTAATGATGACTGTTTTTTTTGATTGCTTGAAGCAATGTGAAAAACACATT TCACCG
co3_74 92741_ x142	AC01876 1.6/5123 7-51168	18	#####	28.2	142	UGGGAAGUGAUGACACCUGUGACUGUUGAUGUGGAACUGAUUU <u>U</u> AUCGCGU AUUCGUACUGGCUGAUCCUG

co3_75_00969_x141	CM0006 68.2/132 816802- 1328168 77	28	#####	56	141	GCTGTACATGATGACAACTGGCTCCCTCTACTGAACTGCCATGAGGAACTG CCATGTCACCCTTCTGATTACAGC
co3_75_30425_x137	ENST00 0003638 36.1	14	#####	28.2	137	GGTCAATGATGTAATGGCATGTATTAGCTGAATCCAGAGTTGATATGAGTTCT AAAATTA
co3_75_72074_x131	ENST00 0003838 75.1	46	#####	83.8	131	CTGCAGTGATGACTTTCTTAGGACACCTTTGGATTTACCGTGAAAATTAATAAA TTCTGA
co3_75_87083_x130	CM0006 68.2/318 35263- 3183532 6	37	#####	73.8	130	AGTGATGATGACCCAGGTA ACTCTTGAGTGTGTGCTGATGCCATCACCGC AGCGCTCTGACC
co3_75_90831_x129	D88010. 1/2919- 3009	18	#####	36.2	129	UCACUAUGAUGAUUGGUUGCCAGACAUUCGCAGUUUCCACCAGAAAUGUUU UUCUUAUGUUGGCCAGUUCUUCUUGGAUGUCUGAGUGA
co3_76_35999_x123	ENST00 0005164 04.1	19	#####	38.2	123	TCCAGCTGTAGGCAGCTGCCTAGGTTGTCTTGTACCTAGGCAAGTGTTACAC TGCTGGGA
co3_76_39197_x123	ENST00 0003634 84.1	20	#####	40.1	123	ACCTGTATTCGAAAGTGATCGTGGGCTGCCTGTGCCCTGGTCATTGATAGTG CAGGGAGA
co3_76_89802_x116	AC01036 1.3/2393 2-23994	26	#####	52	116	GUGCAUGUGAUGAAGCAAUCAGUAUGAAUGAAUUCAUGAUACUGUAAACG CUUUCUGAUGUA
co3_77_51177_x109	ENST00 0003845 84.1	29	#####	58	109	CAGCATGTTTCCAAGGGCTGTGGCTGGTCATAGCCATGGGATCTCCA ACTGC ATGCAAGA

co3_77 55934_ x108	CM0006 70.2/206 14926- 2061483 3	27	#####	30.2	108	AAGACTATACTTTTCAGGGATCATTCCCTATAGTTCATCATTAGAGAAGTTCTCTG AACATGTAGAGCACCGAGACAAGAAATAACTAAGATCAGA
co3_77 67930_ x106	CM0006 64.2/289 27983- 2892806 0	26	#####	52	106	TTGCTGTGATGACTATCATTGGGTTTCGCATGTTGCTGAGTTCCAGTGATGCC TCTTTTCTCTTGGCTGTCTGAGCAA
co3_77 96258_ x103	ENST00 0003648 84.1	25	8E-09	50.1	103	GGGAATGATGATTTTCACAGACTAGAGTCTCCGATGCTGGTCATGATGTCAAAA CTAAGTT
co3_77 99851_ x102	CM0006 65.2/154 007502- 1540073 67	22	#####	28.2	102	TCGTCAGGTGGGAGAATTCTTACATGTTCCCTCTTTTGAAGGCAGATTAGAA CATGATGATTGGGGTTCGCATAATATGTGATTAACGTTTCTGTGTAATCAGGA CTTGCAACATCCC GAATGCCCTTACCTGAC
co3_78 18441_ x100	ENST00 0004083 76.1	20	#####	40.1	100	TGATGACTGTTCTTCTGTTGCCTTCAGACCTGGCATTAGGATTTTAGGTCAT CATAAAT
co3_78 51658_ x96	CM0006 67.2/580 70188- 5807029 1	17	#####	34.2	96	ATCCTTTTGTAGTTTACGAGCATGATGATTGAGTGTTCCACACACGGATGTGAT ATGTGCCACCCTCAAACCTTGTTACGACTTCAGCTTATTACCCAACCTGACC
co3_78 62259_ x95	CM0006 63.2/193 731940- 1937318 59	18	0.009	28.2	95	AGCGTGAAGCTGGCTCTTGGTGCTCCTTCACTGAAAATGCCATTTGCCATTGA TGATCGCTCTTCCCTTCTCTGGGAGGAT

co3_78 92782_ x91	AJ60946 5.1/1-134	34	#####	67.9	91	UGGUA AUGGAUUUAUGGUGGGUCCUUCUCUGUGGGCCUCUCAUAGUGUAC CCAUGCCAUAJGCAAUUGGCAGCCUCGAACCAUUGCCCAGUCCCCUACCUG UGGGCUGUGAGCACUGAAGGGGGUUGCACAGUG
co3_78 94238_ x91	ENST00 0004085 64.2	21	5E-07	42.1	91	GTGGCCCTGACTGAAGACCAGCAGTTGTA CTGTGGCTGTTGGTTTTCAAGCAG AGGCCTAA
co3_79 03132_ x90	ENST00 0005162 36.1	16	#####	32.2	90	ATGGAGGCTGCAGTGAGCAGAGATGGCGCCACTGCACTCCAGCCTGAGCGA CAACGAGAC
co3_79 06192_ x90	CM0006 71.2/381 47428- 3814756 1	35	#####	38.2	90	TCGATGGGTGGGATAATCCTTACCTGTTCTCGTTTTGGAGGGCAGATAGAA CATGATGATTGGAGATGCATGAAATGTGATTAATGCCTCTGCCTAATCAGGAC TTGCAACACCCTGAGTACTCCTCTCTGAT
co3_79 06462_ x90	CM0006 67.2/140 527428- 1405273 52	20	0.0009	32.2	90	GGTCAATGATGAGCTGACATGTATTCTGAATCTAAAGTTGATTATTAGTACTTT AGTTCTAGAATTACTGAGACATG
co3_79 10692_ x90	ENST00 0003841 76.1	24	#####	48.1	90	CTCCATGTATCTTTGGGACCTGTCAAGTGTGGCAGTCTCCCTTCTTGCCATG GAAGAGC
co3_79 11497_ x89	CM0006 63.2/309 68236- 3096816 4	27	#####	54	89	ACTGGCAAGGATGATACACACTTGCCCTCACTTAGACTATAGTTCACTGATGA GAGCATTGTTCTGAGCCAGT

co3_79 25679_ x88	ENST00 0003845 81.1	36	#####	71.9	88	ATCCTCCTGATCCCTTTCCCATCGGATCTGAACACTGGTCTTGGTGGTCGTAA AAGGAGG
co3_79 33133_ x87	ENST00 0003839 03.1	20	2E-06	40.1	87	AGTCTGTGATGAATTGCTTTGACTTCTGACACCTCGTATGAAAACCTGCACGTG CAGTCTG
co3_79 42071_ x86	CM0006 83.2/291 80639- 2918042 5	23	#####	30.2	86	AAGACGACGCTTGCAGGGATTGTTTCTATAGCTCACTACCAGATAAGTTTCTC CGAACATGTAGAGCACCCAGAAACCACATGCAGCGGTGCAGCGCTCTCTCGG GAGCCTGACACTGGCTCTGGGTGCTGCTTCACTGCAACTTCCATTTGCCATT GAGAACTGTTCCGCTCTTCCTCTGGGAAAGTAAGAGAGAGAGGGTGCATCT GAGGGGT
co3_79 70021_ x83	ENST00 0003843 04.1	15	#####	30.2	83	CCTTCTATGATGATTTTATCAAATGACTTTCGTTCTTCTGAGTTTGCTGAAGC CACATT
co3_79 80835_ x82	AF01961 8.1/48- 114	21	#####	42.1	82	GGAUUUGUGAUGAGCUGUGUUUACUGAGCAUGAUGAAGUAAAGCUCAACG UGAUUACUCUGAAGUCC
co3_79 88024_ x81	AJ60948 6.1/1-187	26	#####	52	81	ACGGUCUGGGGAAAGGCUCCUGUGUUGUUGAGCCUGCCAAGUUGUGGGU GCAGCAUGGUACCAGGCAGCCCAACCCUGACCUGAAAGUAAAUCCCGGAAG AAGUCUUUCCUGGGUUUUGAAUUUGCAGUAACAGGUGUGAGCAUUCUAGC AGCAGUUUGAUGAUCAUGUAUGAUACUGCAAACAGGA

co3_80 20434_ x78	ENST00 0004590 04.1	23	#####	46.1	78	TTGCATGTGAAATGTCTGCTTCTCATTCCCTTGGGAGCAGGAATATGTTTCATA ACATGCT
co3_80 21604_ x78	ENST00 0003655 30.1	36	3E-08	48.1	78	AGCACAAATGATGAATAACAAAGGGACTTAATACTGAAACCTGATGTTACATT GTAGTGT
co3_80 34210_ x77	AL12180 9.6/1720 81- 172016	19	#####	38.2	77	CUGUGAUGAUGGCAUUUCUUAGGACAAUUUUGGAUUAAUUUAUGAAAACAAC UACUCUCUGAGCAAU
co3_80 35827_ x77	CM0006 68.2/241 66273- 2416637 4	19	#####	30.2	77	CTCGAGGGTGATGAAAAAGCATCCCTAGGTGTGGTTGTGGCATCTTGGTCAC CTATGTGCCACCTGCCAGTGCAAGGATTTGTCATAGTTATAGTGACCGTG
co3_80 37591_ x76	ENST00 0003845 83.1	43	#####	85.7	76	TTGGCCCTGAATCAAGGCCAGCAGTTTGCTGAAGCTGTTGGTTTCAAGCAGG AGCCTAAA
co3_80 45799_ x76	AP00057 7.5/6961 2-69474	23	#####	30.2	76	GAGCUUCCAGGAUCACCCCUGCAGAGUGGCUAAUUAUUCUGCCAGCUUCGG AAAGGGAGGGGAAGCAAGCCUGGCAGAGGCACCCAUUCCAUCCAGCUU GCUUAGUAGCUGGCCAUGGGAAGACACUGUGCAACACUG
co3_80 54380_ x75	CM0006 85.2/235 07313- 2350721 1	20	#####	40.1	75	ATCCCTTTATAGTTCCCGAGCATGACGATTGGGTGTTACATGCATGTGTGAG ATGTACCACCTCGCATCTTGTTAGACGTTGGCACATTACCCGTCTGACC

co3_80 76170_ x73	ENST00 0006067 69.1	17	#####	34.2	73	AAGCAACTCTGTGGCAGATGATCAAACACTGTCTGACACAATTTGAGCTTGC TATAGCA
co3_80 79236_ x73	ENST00 0005162 31.1	14	0.008	28.2	73	TGAGATGAGATCATGCCATTGCACTCCAGCCTGGACGACAGAGCGAGACTTC ATCTCAAA
co3_80 87971_ x72	ENST00 0003868 47.1	21	5E-07	42.1	72	TGTCCCTGACCTGGGTAGAGTGGCATCTGGTTGGTGATGCCCATCTCATATC AGCCAGGG
co3_80 93898_ x71	CM0006 82.2/265 4212- 2654286	27	2E-10	54	71	TTGCAGTGATGACTTGCGAATCAAATCTGTCAATCCCCTGAGTGCAATCACTG ATGTCTCCATGTCTCTGAGCAA
co3_81 04920_ x70	CM0006 63.2/928 37289- 9283738 3	28	#####	56	70	GCTGAATGATGATATCCCCTAACTGAGCAGTCAGTAGTTGGTCCTTTGGTTG CATATGATGCGATAATTGTTTCAAGACGGGACTGATGGCAGC
co3_81 10030_ x70	CM0006 74.2/888 66643- 8886676 3	30	#####	36.2	70	TGTCTCTGACCTGGTTAAAGTGGCATCTGGTTGGTGGCACTTATCTCAAATCG CAAAGACATAAGGCAACCTCTTGTTTATCCCAGCTTGGCTTTTTGTTTTTGT TTTTAGACAGGGTC
co3_81 24851_ x69	CM0006 63.2/175 968540- 1759683 98	31	#####	61.9	69	AATGGAAGCTGCTGGAACCAGCCATGTGGACAAATGAAAAAATGCCTTTTGTG TACAGATTGCAGCGATCCTACATAAATATATGGAGGTCTCTGTCTGGCTTAGG ACAGCTGGCTAAGTCTGATCGTTCCTCCGTACAGC

co3_81 33838_ x68	AC02055 3.4/1381 95- 138051	41	#####	34.2	68	AAUCUCCUGGGAUUGUGUCUGGCGAGUGCCCAGUAUUCUGCCACCUUCAG AAGGAAGGGAAAGCAAACCUUCAUGAAAGCAGAGGCAUUCAUUCCAUUCCC AGCUUGCUC CAGAUCUGGCAGUUGGAAGACAUCUGCAACAAUG
co3_81 34314_ x68	ENST00 0005165 99.1	33	#####	42.1	68	TGTCAGTGATGAAAGCTTAGTCCCGTTCTGCTACTAATGTTAAGTGATGATAA AGTTATG
co3_81 40390_ x67	CM0006 73.2/628 55632- 6285556 4	21	#####	42.1	67	CTTCCTATGATGAGGACCTTTTCACAGACCTGTACTGAGCTCCGTGAGGATAA ATAACTCTGAGGAGAT
co3_81 51870_ x66	ENST00 0004587 70.1	23	#####	46.1	66	CCACATGCGGCTGATGACAGCACTTCTGCTGAGACGCTGTGATTGCTCTGTC CAAAGTAA
co3_81 64796_ x65	ENST00 0004594 33.1	31	#####	61.9	65	GGTTCATGATGACACAGGACCTTGTCTGAACATAATGATTTCAAATTTGAGC TTAAAAA
co3_81 67461_ x65	ENST00 0003846 74.1	46	#####	91.7	65	ACTCTCTCGGCTCTGCATAGTTGCACTTGGCTTCACCCGTGTGACTTTCGTAA CGGGGAG
co3_81 68501_ x65	AC01065 3.10/104 059- 104144	29	#####	58	65	UGUGUGUUGGAGGAUGAAAGUACGGAGUGAUCCAUCGGCUAAGUGUCUUG UCACAAUGCUGACACUCAAAACUGCUGACAGCACACG
co3_81 73787_ x64	ENST00 0003649 77.1	21	#####	34.2	64	ACCACCAGTGATGAGTTGAATACTGCCCCAGTCTGATCAACATGCGTGAAAG ATATTTTC

co3_81 78907_ x64	AF14134 6.1/3076- 3157	48	#####	56	64	CCGAUACAAUGAUGAUACAUAAGUUCAGCAGACUACGCUGAUGAGCAAUA UUAAGUCUUUCGCUCCUAUCUGAUGUAUCUG
co3_81 84950_ x63	ENST00 0006285 90.1	24	#####	48.1	63	ACGCGCTGTCTTTGAGCCCCGCGAGCTTCCTCGTGGCGCCGGGGTCAA TCTGCAGCG
co3_81 89297_ x63	CM0006 72.2/565 96031- 5659596 3	27	#####	46.1	63	TGATGAATTGATGACAGTCATCTTTTGGAGAGTGACCCAAAATGAAAAGAATAC TCATTGCTGATCACTT
co3_81 95389_ x62	CM0006 63.2/154 259727- 1542598 62	27	#####	54	62	GGGCATACCCGTAGACCTTGTCTGACTGTGCTCATGGCCAGGCAGGGGGGA CAGTGTATGCAAGAGTAATGTGGAGTTTGTGCTAACTCTAGCCAGCTTAATTA GTGACTGGATAAATTGCACAACCTCTCACATTC
co3_81 98799_ x62	CM0006 63.2/447 75864- 4477594 3	23	4E-08	46.1	62	CGTGTATGATGACAACCTCGGTAATGCTGCATACTCCCGAGTGCGCGGTGGGG AAGCCAACCTTGGAGAGCTGAGCGTGCG
co3_82 00287_ x62	ENST00 0005799 69.1	29	3E-11	58	62	ATGCTATGATGACATCCATATGGTTTTGCTGCTGGCTGAGTTTCAGAGATGAC ACCTTTC
co3_82 01713_ x62	AC00643 5.7/2333- 2239	15	#####	30.2	62	CUUAAGAGCCAAUGAUGUUUUUAUUCAAAAUGUCUGAACCUGUCUGAAGCA UCCCAGUGAUGCAACUUCUGUGUGAUACUGAGGCUUUUUUGCCA

co3_82 11668_ x61	AB01771 0.1/1702- 1771	24	#####	48.1	61	AAUCAAUGAUGAAACCUAUCCCGAAGCUGAUAACCUGAAGAAAAUAAGUAC GGAUUCGGCUUCUGAGAU
co3_82 15145_ x61	ENST00 0003910 81.1	19	#####	30.2	61	TGTTCCCGATCTGGTAGAGTAGCATCTGGTTGGTGGTGACCATCTAATACCA GCCAGGGA
co3_82 19080_ x60	ENST00 0003843 39.1	26	#####	52	60	CTGCGAATATTCTCGCTGTTCTGATTTTGTAAATAGTCAGGACAGGCTAAACAT TCGCTAT
co3_82 27540_ x60	CM0006 84.2/293 33258- 2933316 3	14	0.009	28.2	60	ACCCCTGGCAGCCCCTCCTGATGATTCTTCTTCTCCTGAGCACGCTCATGATGA GCAAACCTGAGCCTCTAAGAAGTTGACTGAAGGGGCTGCTTCCCC
co3_82 32884_ x59	ENST00 0005166 52.1	15	#####	30.2	59	GCTACTCTTGAACCTCCTGACCTCAACTGATCCACCCGCCTCGGCCTCCCAA GTATGAAA
co3_82 35598_ x59	AC07879 7.20/670 61-67136	27	#####	54	59	UCCUCUGAUGACUCCUGUUAGUGCCACGUGUCUGGGCCACUGAGACAC CAUGAUGGAACUGAGGAUCUGAGGAA
co3_82 43606_ x58	CM0006 65.2/526 91378- 5269145 3	22	1E-07	44.1	58	AAGAAATGAAGAACTAAAATTGGTCTTAGTATTGAAGTGAAGACACTGAGAT CCAACCTCTGATCTTGCCCTAAAC
co3_82 49116_ x58	CM0006 82.2/265 6624- 2656694	20	#####	40.1	58	CCACAATGATGGCAATATTTTTTCGTCAACAGCAGTTCACCTAGTGAGTGTTGA GACTCTGGGTCTGAGTGA
co3_82 54684_ x58	ENST00 0003846 62.1	26	#####	52	58	CTTCCCATTTATTTGCTGCTTGTAGTCTCACAGTGATACGAGCAGTTATACGC ATGGGAT

co3_82 72744_ x56	AC09023 3.16/199 8-1865	40	#####	32.2	56	UCAUCAGGUGGGAUAAUCCUUACCUGUUCCUCGUUUUGGAGGGCAGAUAG AACAGGAUAAUUGGAGUUUGCAUGAUCCAUGAUUAAUGUCUCUGUGUAAUC AGGACUUGCAAACUCUGAUUGUUCAUAUCUGAU
co3_82 78285_ x55	ENST00 0003838 70.1	40	#####	79.8	55	CCTCCTTTTCTTGCGGGGATCGGGCTTGTGGTGCCGCTCCCCGTAATGTAC GGAGGAAG
co3_82 84995_ x55	CM0006 79.2/803 4584- 8034487	14	#####	28.2	55	ATCCTTTTGTACTTGGTAAGCATGATGATTGGGTTTTTATGCTTATATATGAGA CATGCTTGTCTCAAATCTTGTTACAGCACATTACCCTTCCTACT
co3_82 93508_ x54	KN19647 9.1/1754 90- 175564	38	1E-16	75.8	54	TGCAGATGATGTAAAAGAATATTTGCTATCTGAGAGATGGTGATGACATTTTAA ACCACCAAGATCGCTGATGCA
co3_83 07683_ x53	CM0006 82.2/384 21774- 3842164 7	21	#####	34.2	53	TCTTGTATCCAAAAGTGATCATGGGTTGCCTGTGTCCCGATCATTAAACAGTGC AGGGGTAGGAGTGCTGAAAGACATCTCCCTGCGTTGGTCCAGCCTTCCCTT TCAAACCCTGGAGCTTTCCACG
co3_83 08372_ x53	ENST00 0003627 61.1	27	#####	54	53	GCGGCCGGTGATGAGAACTTCTCCCACTCACATTTCGAGTTTCCCGACCATGA GATGACTC
co3_83 08743_ x53	ENST00 0005815 25.1	39	#####	30.2	53	CGTGTATGATGACAACCTCGGTAATGCTGCATACTCCCGAGTGCGCGGTGGGG AAGCCAAC

co3_83 27968_ x52	ENST00 0004084 18.2	15	#####	30.2	52	AAGACTACACTTTCAGGGATCCTTTCTTCAGTTCGTTACTAGAGGTTTCTCTGA ATATGT
co3_83 39923_ x51	AB06183 7.1/2430- 2563	27	#####	54	51	UGGUCCAUCCUAAUCCUGCCGGUCCAUCUGUGGCCUGCCAGGUUUCGCU UGUGGACCAGAGCACCCUAGAAGCCUCACCCGAGGAGUGAGCAGGGCUCC AGUGGGCUCACGUCAUGGGCACUUCUAGACACUC
co3_83 48861_ x50	ENST00 0005165 28.1	26	#####	52	50	ATGCATCTATTTGACAGACCTGGAGCAGTTAGTGTGTGCTGCTAAGGTTTCTA CCTCTAG
co3_83 52111_ x50	CM0006 81.2/571 34260- 5713404 9	17	#####	34.2	50	CACTTTATACTTTTAGGGATGATTTCTATAATTCATGAGTGGAGAGGTTTCTCT AGAGGTGTAGGGGACTGGAAACCACATCCAGGAAGTACAGCTTTCTCTCCTG AGCATGAAGGTATCTTGCCATTTCTTCACTGCAATTGCCATTTGCCTTTTTTGT TTTTCTTTTGAGATAGGGTGTACCTGTTGCCAGGCTGGAGGGCAGTGGT
co3_83 63746_ x49	ENST00 0003628 74.1	27	0.008	30.2	49	TTGCAATGATGTGAATCTCTCACTGAATTCAACCTTGAAGTGCGAATCCATGA GCTTTTT
co3_83 72468_ x49	ENST00 0003908 56.1	21	5E-07	42.1	49	TTCCTCTGATGACTTCCTGTTAGTGCCACGTGTCTGGGCCACTGAGACACCAT GATGGAA
co3_83 83177_ x48	ENST00 0005167 08.1	17	0.0005	34.2	48	CCTCATTGATTAGTAGCTTCTGACTTTTGTCTGAGTTTGTGCTGAAGCTAGATGC CATTCC

co3_83 93459_ x47	L36588.1 /797-921	25	#####	50.1	47	UCCCAAUGAAGAAACUUUCACAUGUCUUACUCUCUGUCCUAGUCCCAGAGC CUGUAAAGGUGAACCACUGGGACUGGCUGGGGGAGAAGAGGAAGAUUUUGU UCCAGAAGGAACUGUCUGAGGGAU
co3_84 12319_ x46	AC00606 4.10/138 690- 138555	34	#####	67.9	46	UUGUCCUGGCCUAAAAAAAAUCUGCUCCCCUGUGCUCAGUUCU AACAGGGUAG UCUGGCAGGACACACAGCAAUUCUCCUCUCAGUUUAGGAGGGCCGUCCUAA GAAUAGGGCUGGCUCUUAAGGCACGAGAGGACAAU
co3_84 30901_ x45	ENST00 0004105 57.1	24	#####	48.1	45	TGATGGCTGTTCTCTCACTGCTTGAAGCCTTAGGCAGTGGGATTTTGATCCA TCATATA
co3_84 40797_ x44	CM0006 63.2/173 864445- 1738643 69	23	#####	46.1	44	AACCAATGATGTAATGATTCTGCCAAATGAAATATAATGATATCACTGTAAAC CGTTCCATTTTGATTCTGAGGTT
co3_84 45197_ x44	AC09772 0.5/8637 9-86467	20	2E-06	40.1	44	UGGUGCUGUGAUGAUGCCUAAUAUUGUGGUUUCGACUCACUGAGAGUAA AAUGAGGACCUACAAUUCUUGGCUGUGUCUGAGCACCC
co3_84 52053_ x43	ENST00 0003654 93.1	24	1E-08	48.1	43	TGTGCACATTGTTAGAGCTTGGAGTTGAGGCTACTGACTGGCCGATGAACTC GCAAGTGT
co3_84 53472_ x43	AJ22402 7.1/1-88	19	3E-05	38.2	43	UACUGUUAGUGAUGAUUUUAAAAUAAAAGCAGAUGGGAAUCUCUCUGAGA AAGAAAAUGGGAGAUUAAUCCUUAACCUGAAACAGUA

co3_84 62932_ x43	AC11750 3.8/2098 01- 209669	25	#####	50.1	43	UAGCAAGCCUCCAGCGUGCUUGGGUCUGCAGUGACCCCGUGGAUUCUAC AGGGCUUGCCAGAACAGUUUUGAAAUGGUUUGAGGCCUUGCCGUGCUCCA UGUAGAGCAAGGUUAUAGAAAUUUCAGACAAUG
co3_84 63491_ x43	ENST00 0003847 92.1	27	#####	54	43	GTGCAAACCTCGATCACTAGCTCTGCGTGATGTGGCAGAAGCGAAGGGAACCA GGTTTGCA
co3_84 66375_ x42	ENST00 0003845 12.1	33	1E-13	65.9	42	GGTCAATGATGTGTTGGCATGTATTATCTGAATCTATTGCTGATGTGTAATAAC ACTTTA
co3_84 66585_ x42	ENST00 0003913 05.1	26	8E-10	52	42	GCCGAGACTAGAGTCACATCCTGACACAACCTTTGTCCTGGTGTGCTAGAGT ACTCGAAG
co3_84 67551_ x42	ENST00 0003641 13.1	26	#####	52	42	ATCGAGGCTAGAGTCACGCTTGGGTATCGGCTATTGCCTGAGTGTGCTAGAG TCCTCGAA
co3_84 77463_ x42	ENST00 0003912 09.2	18	#####	28.2	42	AAGACGATACTTTCAAGAATCATGATCATTCTATACAGTTCATTACTAGAAAAG TTTCTC
co3_84 86212_ x41	ENST00 0003840 72.1	25	#####	50.1	41	TGGTCATTACCAAGGCTTTTAGAATGCAGTTTCTCATTGCTGTGGACATGAC CATAAAA
co3_84 97528_ x41	ENST00 0003861 48.1	38	#####	44.1	41	GATCCTGGTGATGACAGACGACATTGTCAGCCAATCCCCATGTGGTAGTGAG GACATGTC

co3_84 98899_ x40	AY07774 0.1/1-330	22	1E-07	44.1	40	UGGAAAUGAUGAAAUAGAGAUAAUUGGGUGUUGAAUGUUGUAUGACUGGA AAUUUUUAAUAUGUAUUAUUGUAAUUCUUAUAAGUUUAGUGUUUUUJAGG UACUUAUAGAGAGUGUGUAUGCAUGUGUGUGUCUUGUGGUGGCUAUGG AAAGGGGGCACUGACUGGUGAUGCUGAUAAUUGGAGUGCAUCUGAGGCUGU UGUAGAAAUAACAUGGGUUGUUGAUUACAACAUUGCCAAUGAUUUAACCC AAGAACAGCUCACCUAACUAGCCUGGCACCCUAAAUCUCUAACAGGUUCA UUAAAUGGUCCUGUGAUCUGAUCCAA
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co3_85 04299_ x40	ENST00 0005778 87.1	17	#####	34.2	40	TTGCTGTGATGACTATCATTGGGTTTCGCATGTTGCTGAGTTCAGTGATGCC TCTTTTC
co3_85 15184_ x39	ENST00 0003843 84.1	23	#####	46.1	39	GGGTCATTTCAAAGAGGGCTTATGAGGCTGTGAAACCCAGAGCTCTTAACGC TGTGACCA
co3_85 18967_ x39	CM0006 79.2/440 25223- 4402502 0	15	#####	30.2	39	AAGCTTGTACTCTCAGTGATCATTGCTGTAGTTACGAGATAAGCTTCTCTGAA CATGCAGAGCAGTGGTAACTATGAGGAGGCACAGTCTCTCCTGAGCATGACT CTGGCTGTTGGTGTGGCTTTGCTGCAGCTGCCGTGTGCCATTGATGATCCTG CTCCTCTTCCTTCGGGAAAGTAAGAGGGAGAGAACAGTCTGAGTGGG

co3_85 34190_ x38	ENST00 0003845 67.1	43	#####	85.7	38	ATGCGATGATGAGTGAAGTAGAGCCTGACCTGGTATTGCCATTGCTTCACTGT TGGCTTT
co3_85 36394_ x38	ENST00 0003642 87.1	23	2E-05	38.2	38	TATTCTTCTTGTTAGAGCTCGGAGTTGAGGCCAGTGACTGGCCAATGAACTCA CAAGTGT
co3_85 40042_ x38	ENST00 0003631 07.1	15	0.005	30.2	38	CCAATGTGTAATATCCTGGGATATCATTTTTTCTAGGCTTTGTCCACATGGCTT AGGGGA
co3_85 42474_ x38	CM0006 74.2/110 496421- 1104963 52	43	4E-10	54	38	AATCAATGATGAAACCTATCCCAAAGCTGATGACCTGAAGAAAAATACGTACA GATTCAGCTTCTGAGAT
co3_85 49498_ x37	AY07774 2.1/1-131	25	3E-09	50.1	37	UGGGAGGCUGAUACACAAAUUGGGCUGAAAUACUGCUCUACUUGUCACCA UGCCUCCCUAGAAUAAACUGCCUUUUGAUGACCGGGACGAAUUGAGUGAAA UCGUAACGGACAGAUACGGGGCAGACAGAU
co3_85 75610_ x36	CM0006 73.2/628 53968- 6285390 4	33	1E-13	65.9	36	TTTCTATGATGAATCAAACCTAGCTCACTATGACCGACAGTGAAAATACATGAA CACCTGAGAAAC
co3_85 76654_ x36	CM0006 63.2/156 192176- 1561920 63	21	#####	34.2	36	TTGCCGCCACACAACCAAATTAATAACACAGAAGGGTAAGGTAAGTCT CCATTAAACCCAGGAAAGAGACTGGAAAACCTCCTTTGGAGCCTGTCTATAG TCACAGGT

co3_85 76834_ x36	CM0006 71.2/127 448630- 1274485 01	43	#####	85.7	36	CCCGCCACTGCACCTGACCAGGTCTCTGTTGGCTGGTGCAATCCAGTGGTGA GCTGATAGTAAACCCCAGCTTAGGAAACAGGGTTGTTCTTCATGTGGATGACT CTGTGCCGAAAGCATGGGAACAGCC
co3_85 79164_ x35	CM0006 67.2/151 10920- 1511078 6	41	0.0005	34.2	35	TCATCAGGTGGGATCATCCTTACCTGTTTCTCCTTTTGGAGGGCAGATCAGAA CATGATGATTGGAGAAGAATGAAACGTGATTAATAACTCTGTGTAATCAGGCC TTGCAGCACCCCAATTGAGCCTTTCTGAT
co3_85 82209_ x35	AJ60946 7.1/1-135	22	1E-07	44.1	35	AGCACUAUAUUUAAACCUGUGGAUGGGAAUAUUCCTTCAUUCUUGGUUACGC UGUAGUGCAAAGAAUUCUGGCUCUCUGUUGCACAGCUGACUUGUGCCA UUCUGCUGUUGCUGUAUAGAGUUAAGGAACAUGG

co3_85 95759_ x34	AF49220 9.1/1-275	28	6E-11	56	34	AAUCUGUAGUCUUGGAGCCGCACAGGGUUGGUGGUACCCUCGAGCACACC AGACUUGCAGAAAAAGCAUACUCCAGAGGAAGCUGAGGCAUGCCUGCUCGA GAGCCAGCUGUCCAUGUGCAAUUUCCUCUGAUAGUUUCUGGUCACUGU UGCCACGGUGAUAAUGACUGGGCUAUGUCAUUAUCUAUCCGCCAACAGUAA GAGAAGCUUUGCAGUCGAGAUUUGUUUAGCAGAUGGAGUGUUUUCUGUU GAACACUAAGUACUGCCACAAGU
co3_86 03307_ x34	CM0006 63.2/173 866028- 1738659 68	40	7E-18	79.8	34	CCTGGATGATGATAAGCAAATGCTGACTGAACATGAAGGTCTTAATTAGCTCT AACTGACT
co3_86 20086_ x33	ENST00 0003629 81.2	15	0.007	30.2	33	AAGACTATACTTTTCAGGGATCATTCTACATTTCCGGGTAATTTCTTTGAACAT GTGGAG
co3_86 23353_ x33	ENST00 0003911 45.1	33	8E-14	65.9	33	TTATAAGTTTTCTAAGTGTCTAATGATGAATTTATAGGGCAGATTCTGAGGTG AAAATT
co3_86 26092_ x33	AC09218 4.7/5032 7-50196	17	#####	34.2	33	UUGUCCUGGCCUAGGCCAUUUCUGUCUCCCCGCGCUCAGUCCUAGCAGAG UAGUCUGGCAGGACGCACAGCAAUCUCCUCUCAGUUUAGGAGGGCCGUC UCCUAAGAAUAGGGCUGGCAGGAAAGGACAAU
co3_86 31343_ x32	ENST00 0005170 31.1	18	#####	28.2	32	TATAGTGTGGCCATGGGATCTCCAAGTGCATGCAAGAGCAACCTGGAGAGAC TTTGACAG

co3_86 33423_ x32	CM0006 73.2/115 627185- 1156270 82	18	#####	28.2	32	GTCCTTTTGTAGTTCATAAGCGAGATGATTGGGTGTTCAGGCACATGTGTGAG ATGTGCCTCCTTCAAACCTTGTTACAACGTCAGCACATTACCCGCCTGACA
co3_86 42831_ x32	AC01686 8.8/2125 8-21186	24	0.0006	32.2	32	GUGUGAUGAAAUCACCCCAAUAGCUGGAAUUACCAGCAGAUUGUGUAGUG GUGAACCUACAAUUUUCUGAAG
co3_86 49537_ x31	CM0006 77.2/250 70432- 2507052 6	33	8E-14	65.9	31	GGATCGATGATGAGTCCTCCAAAAAACATTCTTGAAAAGCTGAACAAAAT GAGTGAGAACTCATACCGTCGTTCTCATCGGAACTGAGGTCC
co3_86 68293_ x30	ENST00 0003867 45.1	23	4E-08	46.1	30	GCTGTTTCAGTGATGAGGCCTGGAATGTGCGCTGGGCACAGCGCCCGAGACA GACTGCGGA
co3_86 68983_ x30	AC10279 9.9/5350 8-53611	37	4E-16	73.8	30	UGGUCUCAAGGAAGGGAUGAUGUCCAGUUGAGACUCAAGAAAAGGAUUC UGAGCCUCAGAGCUUUGAAGGAGCCACUUGGUCCCUGACCUUCCUAGAGG CAAA
co3_86 69463_ x30	CM0006 67.2/138 561110- 1385610 43	31	#####	61.9	30	GTGCAATGATGTATTTTATTCAACACATCATTCTGAAAGAACGTGTGGAAAAT AATGACTGAGCACA
co3_86 69943_ x30	CM0006 67.2/181 241892- 1812418 14	32	3E-13	63.9	30	GGTCCTGGTATGACAGATGGCATTGTCAGCCAATCCCCAAGTGGGAGTGAG GACATGTCCTGCAATTCTGAAGGGATT

co3_86 71953_ x30	CM0006 73.2/628 54695- 6285462 1	22	#####	44.1	30	GTCAGATGATTTGAATTGATAAGCTGATGTTCTGTGAGGTACAAAAGTTAATA GCATGTTAGAGTTCTGATGGCA
co3_86 73843_ x30	ENST00 0003911 43.1	22	#####	28.2	30	TGTCCTTGACTTGGGTAGAGTGATGTCTGGTTGGTGCTGCCTATCTCATATAA GCCAGGG
co3_86 88417_ x29	ENST00 0003653 82.1	20	2E-06	40.1	29	TCGCTGTGATGAGTGATTGTTAAACATTCGTAGTTTCCACCAAAGCTTGGCT AATGATG
co3_86 91230_ x29	ENST00 0003842 81.1	22	#####	44.1	29	GAGCACTGTTCGTAACCCGTTAGCCTGGCTGTAGCTAATGGGTTCCATTCCG GTGCAATA
co3_86 97784_ x29	AJ60948 0.1/1-137	33	#####	65.9	29	GAGCACCUGAAUCUUUCCCAUUCUUGCUGCCUCGUGCCGGUGUGGGGAC AGAUGGUGCUACAGAAUGAGCAGAGGAAAUCCAGACAGGUUGUUUCCAU UUGUCUUGGGGCCUGUCUCUACAGCUCUGCCACAUUU
co3_87 13180_ x28	AC02395 0.6/1585 70- 158435	26	#####	52	28	UGCCCAUUCUCAAAAGAGAAUAGGCACUGUUGAUCAUGCGAUCCAGAGAUU GUUAAUGGGGCUGCAUUGAGAAACAAGCUAUGUUUCCAUUCACAGCAAACA CAUCGCAGUGGUGACAAUGAGACCUGUAACAUUU
co3_87 19984_ x28	ENST00 0003845 33.1	15	0.008	30.2	28	GGATCGATGATGACTTTTCATACATGCATTCTTGAAAGCTGAACAAAATGAG TGAAAAC

co3_87 21076_ x28	AJ60947 1.1/1-132	38	#####	75.8	28	GUUGAGGUCUAUCCCGAUGGGGCUUUUCCUGUAGCCUGCACAU CGUUGGA AACGCCUCAUAGAGUAACUCUGUGGUUUUACUUUACUCACAGGACU AUUGU UAGAUCUGUGGGAAGGAAUUACAAGACAGUU
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co3_87 27050_ x27	AF30828 3.1/1-330	25	3E-09	50.1	27	GCCACAUGAUGAUUCAAGGCUGUUGUGAUUCAGUUGGUUUUGGCUAAGCC CAGGGACCUUUGGCCUGUUAAGGUCUGUAAUCUUGGUGGGCGAUACAGA GUUAUGUGUGUUCACUGUAAGGGCAGACCAACAAGAACUUUUUCCUACUUU UGAGCUACCUCUUUUUAAUAGGGGUGAUUCUCCAGUUGCUGGAGAGAAA UUGUGGUAACUGGAGUGAGAGAGUAGGAACAGGGCAUGUUCAGGGUAUCA GGCCAAGGGUCCUAAAGGACUUAGCUUGUGUUAUGGCCACUGAGAGAUG AAACACAGAUCUUUGGUAUCUGAUGGCU
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co3_87 38687_ x27	AC01103 1.12/168 663- 168575	20	#####	40.1	27	GCUGGCACAAUGAUGACUUAUUUACUUUUUGCCGUUUACCCAGCUGAGG UUGUCUUUGAAGAAUAAUUUUUAAAGACUGAGAUGCCAGU
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co3_87 39362_ x27	ENST00 0003845 74.1	19	#####	38.2	27	TGCACTGCATGGTATCTGCACTCAGCAGTTTACACCTGCTAGGGTGTTCAAAG GTCAGTG
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co3_87 45493_ x26	CM0006 82.2/492 80319- 4928040 9	46	2E-21	91.7	26	GCTGGCATATATGATGACTTAGCTTTTTTCCCCGACAGATCGACTATGTTGAT CTAACTTTTCTAAGCCAGTTTCTGTCTGATATGCCAGC
co3_87 52825_ x26	ENST00 0005850 78.1	15	#####	30.2	26	GTGCTGTGATGATGCCTTAATATTGTGGTTTCGACTCACTGAGAGTAAAATGA GGACCTA
co3_87 62237_ x26	ENST00 0003909 62.1	44	#####	56	26	AAATAATGAAATCACCCAAAATAGCTGGAATTACTGGCAGATTGTGTAGCAAT AAACCTA
co3_87 64913_ x25	ENST00 0003842 52.1	27	2E-10	54	25	GCTATGATGAATTTGATTGCATTGATCGTCTGACATGATAATGTATTTTTGTCC TCTAAG
co3_87 68563_ x25	ENST00 0003913 09.1	21	#####	34.2	25	ATACATGATGACTTACATGGACTCTCATTGAGCTAATGACTTGCTGCTGAAAC ATGAAA
co3_87 69513_ x25	ENST00 0005172 83.1	19	#####	30.2	25	ACCTTCTTGTTTAAGCTCTGTACTAAAATTGCAGAACTAGTATCGTGTCTTAC CATTTG
co3_87 71588_ x25	ENST00 0004087 16.1	35	#####	69.9	25	GCAGACTCACTATGCACCTGACTGTACTTCCAGGCAGGTGCTTTTTCTGTCTG CCAGAGA
co3_87 79488_ x25	CM0006 84.2/393 15307- 3931521 3	41	2E-18	81.8	25	GCTGTTGTTGATGAGGCTCAGAGTGAGCGCTGGGTACAGCGCCCGAATCG GACAGTGTAGAACCATTCTCTACTGCCTTCTTCTGAGAACAGC
co3_87 95969_ x24	ENST00 0003639 61.1	22	#####	44.1	24	TTGCAGTGATGTAAAATTTCTTGGCCTGAAATTACTGTGAAGAGTAAAACCGA GCTTTTT
co3_87 96209_ x24	ENST00 0003911 00.1	24	3E-06	40.1	24	TCCAGCAGTAGTCAGCCATCCGGACAGAACCGTTCCTGTGATGGTGTACAC TGCTGGGA

co3_87 96833_ x24	AC05585 5.9/1107 36- 110601	18	#####	36.2	24	GUGACUGUCCUGGUUUAUUGAUUUGCAUUUGUUAGUUGUACAGUGCAACCAU AGACAGUCACACACAUUAAAACAGAUGGUUCCUGCCGACAGGGUCUGUAUA GUUAUCAGAUUUUCUGUGCGAUGGCUCCAUACAUG
co3_88 01777_ x24	CM0006 75.2/211 39957- 2113988 6	39	#####	38.2	24	ACTCCATGATGAACCCAAAATGCCAAGTATATGACTGAACTTACAAGTGATAC CATCTTACGACTGAAGAGT
co3_88 08853_ x23	ENST00 0005052 19.1	27	2E-10	54	23	GGGCATACTCGTAGACCTTGCCTGACTGTGCTCATGTCCAGGCAGGGGGGA CAGTGTATG
co3_88 12372_ x23	ENST00 0006268 86.1	40	7E-18	79.8	23	GCTGTCCTGGACCTGTTGGCACCACAGACAGTTGCTCTGCTGTGCCTGTGGC CTCGGGGC
co3_88 20077_ x23	AC01341 6.4/5544 1-55577	21	#####	42.1	23	UGCAGUCAAGUCAAAUUCAGUGCCCGUUUCUGUCAUAGCGGGGGCUGGCC CAGAUGGCUGCCACAGCAAGCUCCACAGCUCAUGGGCCCUGGGUCACCUA CCCUGGGACCUGGGGAUAAGUUUGGCUGUGGACAGUG
co3_88 21411_ x23	ENST00 0004268 67.1	35	5E-15	69.9	23	TCTCAGTGATGTAATTCCAATAGATCCTTCTGACCCTCCACTGTGGACTCAAT AGCAGGG
co3_88 24999_ x23	ENST00 0004085 87.1	38	1E-16	75.8	23	CAGCCTGAAGTGATGATTCACATTCATGTCTCTTCTCTGATAAATTCTTGAAGA AAATTT
co3_88 30980_ x22	CM0006 69.2/140 375666- 1403755 63	19	0.004	30.2	22	ATTCTTTTCGTAGTTTCGTAAGCTGGATTATTGAGTATTCACACACGTGTGTGAG ATGTGCCACCCTTGAACCTTGTTACAACGTGGGCACATTATTCACTTGACA
co3_88 33620_ x22	ENST00 0003843 42.2	23	4E-08	46.1	22	CCCTTGGCCCTTATCGAAGCTGCAGCTGCTTCCGCATAGCTGCTGTGGTCAA AAAGGAGC
co3_88 34038_ x22	ENST00 0004088 13.1	29	2E-11	58	22	TGGCCAAGGATGAGAACTCTAATCTGATTTTATGTGCTTCTGCTGTGATGGAT TAAAGGA

co3_88 35842_ x22	CM0006 77.2/665 02910- 6650281 2	29	2E-11	58	22	TGCAATGATGTCGTAATTTGCGTCTTACTCTGTTCTCAGCGACAGTTGCCTGC TGTCAGTAAGCTGGTACAGAAGGTTGACGAAAATTCTTACTGAGCA
co3_88 43938_ x22	ENST00 0005159 69.1	20	0.001	32.2	22	TTCAAAAAAGACCATATATCCTTGAAGAGTAACTGCTGAACTTATTCACTGGCA GTGGGC
co3_88 47392_ x22	CM0006 73.2/754 04421- 7540456 6	21	#####	42.1	22	CTTCAGTGATGACACGATGACGAGTCAGAAAGGTCACGTCCTGCTCTTGGTC CTTGTCAGTGCCATGTTCTGTGGTGCTGTGCACGAGTTCCTTTGGCAGAAGT GTCCTATTTATTGATCGATTTAGAGGCATTTGTCTGAGAAGG
co3_88 49724_ x22	AB02889 3.1/4087- 4152	21	5E-07	42.1	22	CGUCCAUGAUGUUCGCAACUACCUACAUUGUUUGAUCCUCAUGAAAGCAG CACUGGCUGAGACGC
co3_88 59839_ x21	ENST00 0004596 23.1	16	0.001	32.2	21	TTTTGGTTGAAATATGATGAGTGTACAAAATCTTGATTTAAGTGAATGAAAAAT TACAAG
co3_88 63787_ x21	ENST00 0003863 07.1	47	#####	54	21	GCTGGTGTAATGATGACTTCACTTTTTTCCCATCAGATCGACAATGCTGAC GTCCTTAT
co3_88 80268_ x20	CM0006 63.2/517 24896- 5172477 5	22	0.009	28.2	20	GTGCCCTTTTAAGGTTGACGCAGTGCTTTAAGGGGCTAACACAGAAGGGTAA AGGAAGTCTCCATAAACCCAGAGAAGAGATTGTAAGCTCCTCTTTAGAACC TTTCTGGAGTCACACCT
co3_88 80648_ x20	ENST00 0003843 60.1	25	3E-09	50.1	20	GACCTCCTGGGATCGCATCTGGAGACTGCCTAGTATTCTGCCAGCTTCGGAA AGGGAGGG
co3_88 82288_ x20	ENST00 0003880 90.1	23	4E-08	46.1	20	TGCACTTATGTATGTTTTTGTTTAACGTGGACAAAGACTTACAGATAGGTGCAA AAAATA

co3_88 90208_ x20	ENST00 0003910 02.1	33	3E-11	58	20	GCCTTTGCAGCTGATGATACAGCTTCTTTCCCATCAGATCGACCCTGTTGAT CTCTACA
co3_88 93428_ x20	ENST00 0003845 50.1	23	4E-08	46.1	20	TGGATATGATGACTGATTACCTGAGAAATAATTGATGAAATCTCAAGAAAATTC CTCTAG
co3_89 03557_ x19	ENST00 0003869 10.1	16	0.001	32.2	19	CCCCTATCTCTCATGATGAACACATATGCCTCTGAGCTGCTGTGATTTCTGGC TTCAAAG
co3_89 07376_ x19	ENST00 0003847 72.1	18	5E-05	36.2	19	TGGTTGTTACCAAGGCATTTAGCATGCAATTTCTCATTTGCTGTGGACACGAC GAGAAGA
co3_89 13057_ x19	CM0006 67.2/139 278781- 1392789 78	37	4E-16	73.8	19	TCCAGCGGTTGTCAGCTATCCAGGCTCATGTGGTGCCTGTGATGGTGTTACA CTGTTGGAAGAGCAAACACTGTCTTTATTGAGGTTTGGCTCCAAGCACTGTTT TGGTGTGTAGCTGAGTACCTTTGGGCAGTGTGTTTGCACCTCTGAGAGTGGA ATGACTCCTGTGGAGTTGATCCTAGTCTGGGTGCAAACAAT
co3_89 23041_ x18	ENST00 0003855 73.1	14	#####	28.2	18	TGCACTTATGTATGTTTTTGTGTTAACTTGTGGACAAAGACTTATGGATAGGTGC AAAAAA
co3_89 23599_ x18	U43901. 2/4011- 4161	21	#####	42.1	18	GCUGCACACUAUJAAAGCUCAGGGUGGAGGCCAGUCUJGGCUCAUGAACU UCUGAGUGUCGGAAGUGUGCUAUUAUCAUUGGCAGGAUUUCGCUAACACC AGUAGAGCUJGCCUCUAUGACUGGAGUUUGGUAGUACUCGCUGCCACAU A G
co3_89 30241_ x18	CM0006 69.2/152 595923- 1525960 30	31	1E-07	46.1	18	AGGCCCTGTAGTTCCCGAGCACGATGACTGGGTGTTTACGTGCACGTGTG GGATGTGCCACCCTCTGAACCTTGTTACGATGTTGGCACATTACCCTGGACC TGACC
co3_89 37585_ x18	ENST00 0006378 69.1	15	0.003	30.2	18	TTTATTATTATTGTTGTTGTTATTTTGGAGTAGGACTCTCACTGTGTTGGCCAGG CTGGAG

co3_89 43975_ x18	AF25084 1.1/2261- 2352	33	8E-14	65.9	18	GGAUCGAUGAUGACUCCAUUAUGUACAUUCCUUGGAAAGCUGAACAAAAUG AGUGAAAACUCUAUACCGUCAUCCUCGUCGAACUGAGGUCC
co3_89 47593_ x18	ENST00 0003645 78.1	22	1E-07	44.1	18	AAGCAGGATTCAGACTACAATATAGCTGTTAAGTGCTGTATTGTCATTCCCC TGCTCAA
co3_89 50407_ x17	ENST00 0003644 60.1	37	#####	65.9	17	TGGATTGGTGATGAGCAACAATCACCATCTTTCGTTTGAGTCTCATGGCCATG AGACCAA
co3_89 52124_ x17	AJ60948 5.1/1-127	22	#####	44.1	17	CUGGAGACUAAGAAAAUAGAGUCCUUGAAAUCAAGCUGACUCUGCUUUUAG CCUCCUAAAUGAAAAGGUAGAUAGAACAGGUCUUGUUUGCAAAAUAAAUUC AAGACCUACUUAUCUACCAACAGCA
co3_89 60777_ x17	ENST00 0004591 74.1	43	1E-19	85.7	17	GGTGCAGATGATGACACTGTAAAGCGACCAAAGTCTGAACAAAGTGATTGGT ACCTCGTT
co3_89 64313_ x17	ENST00 0003867 47.1	20	5E-06	40.1	17	GCTGTTTCGTTGATGAGGCTCAGAGTGAGCGCTGGGTACAGCGCCCGAATCG GACAGTGTA
co3_89 65945_ x17	CM0006 82.2/384 49370- 3844950 3	32	0.001	32.2	17	ACCTGCATTCAAAAATGATCACGGGCTGCCTGTGCTCTGGTCATCAATAACGC AGGGAGAGGAATTGCTGAAAGCCGTTTCCCGTGTTTGGAGGGTTCACACCTG TCCCTTTCAAATGCTGGCGCTTTCACACA
co3_89 70892_ x17	ENST00 0003628 03.1	44	3E-20	87.7	17	TGCAATGATGTCGTAATTTGCGTCTTACTCTGTTCTCAGCGACAGTTGCCTGC TGTCAGT
co3_89 71844_ x17	ENST00 0003843 34.1	18	3E-05	36.2	17	GCATGGCTGAATACTGTGTTCTTTTATCAGTAGTTTACACAGCCAGACACCAT GCAAAAG
co3_89 74038_ x16	CM0006 73.2/117 263799- 1172639 52	14	0.009	28.2	16	TTGTCCTGGCCTATGCTTTTTTCTACTCCCCTCTGCTTTTTTGGTCCCCCTGTGC TCAGTTCTAACAAGGTAGTCTGGCAGGACACACAGCAGTCTCCTTCAGTTTAG GAGGACTGTCTTTAGAATAGAGCTGTCCCAAGGCACAAGATTACAAT

co3_89 77238_ x16	ENST00 0003847 62.1	23	#####	46.1	16	AGCACTATATTTAAACCTGTGGATGGGAATATTCCCATTCTTGGTTACGCTG TAGTGCA
co3_89 87286_ x16	ENST00 0003861 57.1	24	1E-08	48.1	16	CTTCCTCAGCCTTACTCCAGGGACTTTTTGTTGCCTGTAAAGTGCTCTGGCAT TGCCTGA
co3_89 88150_ x16	ENST00 0003842 50.1	16	0.0006	32.2	16	TGCATTGCCATGGTATCTGCACTCAGTAGTTTATTCTGCTGGGTGTCCAAAG ATCAGTG
co3_89 88742_ x16	ENST00 0004081 89.1	18	0.0001	36.2	16	TTGCAGTGATGACTTGCGAATCAAATCTGTCAATCCCCTGAGTGCAATCACTG ATGTCTC
co3_89 89670_ x16	ENST00 0005167 33.1	17	#####	34.2	16	TGCCAATGATGGTTAAGAATTTCTTCACCTGAATAAACCATGTGGTCAGCATT GCATCTG
co3_89 91174_ x16	AJ60947 3.1/1-130	38	1E-16	75.8	16	AAGCCAGCCAAUGAAUCUGCUUACCUGAUUGUGUUUGUGCAGACAUACUUU AAAAACUGGCCAAUAGUAAAGCCAUGUUACGAGCCUUAAGGACAUUGAAGUC GUUAAGGUCCCUGAGAAUGGCUAUAACA
co3_89 94646_ x16	ENST00 0003644 32.1	20	2E-06	40.1	16	CCCGCCACTGCACCTGACCAGGTCTCTGTTGGCTGGTGCAATCCAGTGGTGA GCTGATAG
co3_90 03123_ x15	CM0006 66.2/159 507029- 1595068 94	14	0.009	28.2	15	GCGAGGAGGAGGCACAGGGTTCTCCCCTGAGAGCCAGGCCAGCTCTTAGTG TTGCTTCGCTGCAGGTGCCATTTGGCATTGAGGATTGTTTTCTCTTCCCTCCG GCAAAGTAAGAGGGAGAGGACACAGTCTGAGT
co3_90 06048_ x15	ENST00 0003640 43.1	27	2E-10	54	15	AAGTAGGGTGATGAAAAAGAATCCTTAGGCGTGGTTGTGGCCGTCTTGGTCA CCTGTGTG
co3_90 09108_ x15	CM0006 85.2/150 902121- 1509022 35	40	0.001	32.2	15	AAGACTATACTTTTCAGGAATTGTTTCTGTAGTACATTACTAGAGAATGTCCTCT GAATGTGCAGAGCACAGAAAAATACAAAATAATAATAAATTCAAATCAGCTAT CTGAGTA

co3_90 11898_ x15	ENST00 0003633 89.1	27	#####	54	15	GGCAGATGATGTCCTTATCTCACGATGGTCTGCGGATGTCCCTGTGGGAATG GCGACAAT
co3_90 17013_ x15	ENST00 0003625 41.1	21	5E-07	42.1	15	TCTTAGTGACATAATTCTAATAGTTTGTTCGACCTTCCACTGTGGACTIONAATA GCAGGG
co3_90 24888_ x15	AJ60947 7.1/1-132	30	4E-12	60	15	GGCCUCCUGGUGCUUACCACAGGCUGUGUUCUUACACUGACUGUAUAGAA AGAGGAGGUAGAGUAAACCUACCCCAUUAACACCUCAGCUCAGGCCUGUG CCUGGUCUGUAUUGUGAAUGGGGGAACAUAG
co3_90 29223_ x15	AL13270 9.5/1555 70- 155499	34	#####	67.9	15	UGGAUCGAUGAUGACUGCUGGUGGCGUAUGAGUCUUACAUGAUGAAUACG UGUCUGGAACUCUGAGGUCCAU
co3_90 30228_ x15	ENST00 0003860 37.1	25	#####	50.1	15	CAGGCTGTGATGATTGGCGCAGGGGTACGGACCTCAGCTGAGTCATGGGAG CTGAATGTA
co3_90 30808_ x14	ENST00 0003847 14.1	21	5E-07	42.1	14	CTTCAGTGATGACACGATGACGAGTCAGAAAGGTCACGTCCTGCTCTTGGTC CTTGTCAG
co3_90 31676_ x14	ENST00 0005161 90.1	14	#####	28.2	14	TTGCGTCTATTTGACAGACTAGAATAATTACTATCTGCTGCTAAGGTTTCCCCT GCAGAT
co3_90 35638_ x14	AL13270 9.5/1781 48- 178075	27	2E-10	54	14	UGGACCAAUGAUGAGAUUGGAGGGUGUCUGAAUCAAAAAUUUUGAUUAAAG CCAUCUGUAACUCUGAGGUCCAU
co3_90 40342_ x14	CM0006 84.2/377 85526- 3778563 3	16	0.0005	32.2	14	ATCCTTTTGTTCGTTTCATAAGCATGACGATTGGGCTTTCATGCTCATGCATGAG ATGGGCCTCCCTTCAGTCTTGTTACAGGCCGGCTCTGTGGCTCATGCCTGTA ATC
co3_90 42960_ x14	ENST00 0004112 92.1	16	0.001	32.2	14	TGTGTGTTGGAGGATGAAAGTACGGAGTGATCCATCGGCTAAGTGTCTTGTG ACAATGCT

co3_90 43394_ x14	CM0006 63.2/173 865686- 1738656 22	21	#####	42.1	14	GTGTAATGATGTTGATCAAATGTCTGACCTGAAATGAGCATGTAGACAAAGGT AACACTGAAGAA
co3_90 47902_ x14	ENST00 0005163 27.1	14	0.008	28.2	14	AGTTACTGTCTGCTGCTAATGTTTCCACTACAGATACAAGAAAAAGTCTCTTCA CACTTT
co3_90 49134_ x14	ENST00 0003840 33.1	20	2E-06	40.1	14	GCTGCACACTATTAAGCTCAGGGTGGAGGCCAGTCTTGGCTCATGAACTTC TGAGTGTC
co3_90 53362_ x14	AJ24319 9.1/1-78	22	1E-07	44.1	14	GCCAUUGAUGUUUUCUUUUCGAAAGGUGAGCGCUUUGCGCAGUGAUGAC CCUCAUCUAUCACCCUUGACUGAUGGCU
co3_90 57044_ x14	ENST00 0003631 81.1	32	2E-08	48.1	14	GGTCAATGATGAGCTGACATGTATTCTGAATCTAAAGTTGATTATTAGTACTTT AGTTCT
co3_90 57590_ x14	ENST00 0003913 16.1	23	0.003	30.2	14	TTCTTACAAATCTAAATGTGCTTTGATGCAAGTATATTTGAATCCCTTTCCATCT GATAA
co3_90 57954_ x14	ENST00 0003654 73.1	17	#####	34.2	14	TAGGCCCTGAATCAAGAAACGTGATGGTTTGCCATTGTAGCTATTGGTTTCAA ACAAGAG
co3_90 62028_ x13	ENST00 0003640 89.1	30	4E-12	60	13	TCCAGCGGTTGTCAGCTATCCAGGCTCATGTGGTGCCTGTGATGGTGTTACA CTGTTGGA
co3_90 63913_ x13	BL00000 2.1/9801 8519- 9801871 4	28	6E-11	56	13	AGAGAAGCAAAGUGAUGAGUAAUACUGGCUGGAGCCCCAAAGAGGCACGU GUGUGUGUUUGUGUGUGUGUGUUAUAGCUUGUCAGUGCAUGCACGUGUA UGUCUGGGAGUACAAAUGGGUGCGACUGGUUGUAGGGAACUAGCUAUGUG CCUUCUAUUAGGCCAUGACAGUCAACUGAUUAGAUCUGAUUGCUUC
co3_90 65330_ x13	CM0006 68.2/388 22401- 3882230 7	33	#####	58	13	TCTGCTGGGGTGTTTAAAGGTCAGCGCTGTAGATATTCAGCATCTGGCATCTT GGCTTCTGCTTGTAAACCTGGTATTTTTACTGATACAGTA

co3_90 79695_ x13	ENST00 0003911 41.1	23	4E-08	46.1	13	AACATGCTTCCTTAGATCCACCTTTGTGGATGAATCTTGAAGTGAAGTTCCACTT GTAAAC
co3_90 85935_ x13	ENST00 0003651 28.1	14	0.008	28.2	13	GCTGTAATGTGTGCATAGGTTTCATCTGTGTCTGGTAGCAGTGTCTGTCTGTG TTTTTCA
co3_90 87625_ x13	AC06483 6.7/3178 5-31868	24	1E-08	48.1	13	GUGUUCAAUGAUGAUUUUCUAAUUUGUUUGCCUGAUUUCCUUUUUGGAUAAUG AAGGCAUCUUUAGUCACUACCUCUUCUGAGACAC
co3_90 91616_ x13	ENST00 0003648 49.1	24	1E-08	48.1	13	GCTGGCACAATGATGACTTAAATTACTTTTTGCCGTTTACCCAGCTGAGGTTG TCTTTGA
co3_90 95366_ x12	AC09346 2.11/145 947- 146075	43	1E-19	85.7	12	UGAGCACUUUCACAGGUCCUCCUCAGGCUGUGGGGCCAGGAUUUGGUAG CUGGUGCUGAGAGAAAACCUUUGUUGGCAUCCUUGCCUGGGACUGUGCC AGUGGCAGCUGUCAUUCUAAUGGGACAAUU
co3_90 98498_ x12	ENST00 0003647 22.1	29	2E-11	58	12	GATCAATGATGAAACTAGCCAAATCTGAGCATCAGAAGGCTTTCCGGTCTACC TGATGCA
co3_91 00838_ x12	ENST00 0003909 68.1	23	#####	30.2	12	GTTTCATGATAAGTAACATTTCTTCAATTTGACCTGATGTGTATTGAAGAAAACC AGCATC
co3_91 01006_ x12	CM0006 63.2/163 923670- 1639238 73	20	#####	32.2	12	AAGACTATTCTTTTCAGGGATCATTATGCGAGAAGTTTTTCTGAATGCCTAAAGA ACCAGAAAACCATGAGGACAGACAGCAGCATTTCCTGAGCTTGAAGCTG GCTCTTGGCACTGGTTTGCTGCAACTGCCGTTTGCCATTGCTGATCATTTTTTC TCTTCCTTTGGGAGAGTGAGGGGAAGAGAATGCAATCTGAGTGAT
co3_91 03046_ x12	ENST00 0003650 74.1	23	0.004	30.2	12	CTGCAGATATTCTCACTGTTTTGATTTTGTAATAGTCAGGACAGGCTAACCATT CACTTT
co3_91 08530_ x12	AC06483 6.7/3006 6-30155	18	0.009	28.2	12	UGAUGGCAAUGAUGAUUUUUACACUUUUUGUUGUUCACCUGAUACAUAUAAA UAUGAGGGUGUUCAGUCACUACCUCUUCUGAUGCCAUCA
co3_91 12658_ x12	ENST00 0004591 55.1	24	1E-08	48.1	12	CAGGCTGATGAGACTAAGGCGAATGCGACTCCGTGCTCTCTGGCCCTTGGCT CCTTGTTG

co3_91 13438_ x12	CM0006 76.2/634 79272- 6347941 3	14	0.009	28.2	12	GGCCTCTCTCCCATGGTGCTGTGGGTGGGGGAGGAGGGGTGCTTTTCTCCT CAGCGAAGACTGGAGGCAGACATCACCCCTCAAGGATCATCCTCAGAAGTGC CACGTGCTGGACAGCCTTGTTTTTCTACCTCACACATTT
co3_91 15394_ x12	ENST00 0005164 29.1	14	0.008	28.2	12	TTGCTCTGGGGATGCAAAAGAGGGAAATCCCTGCACTTCCTCTCTGTCTTTGT GGCAGCC
co3_91 15838_ x12	AC09022 7.10/153 59-15277	20	2E-06	40.1	12	UGGCCGAUGAUGACGAGACCACUGCGCAAUCUGAGUUCUGGGAACCAGGU GAUGGAGUAUGUUCUGAGAACAGACUGAGGCCG
co3_91 16030_ x12	CM0006 81.2/499 49527- 4994931 6	15	0.008	30.2	12	AAGATGACACTTTGAGGCATCGTGTCTATGGTTCATTACTACAGAAGCTTCTC TGGATGTGTAAAGCACAGGAAACCAGGCAGAGGAGGCACAGGGTGCTCTCC AGAACGAGAAGCCAGCTCCTGGAGTTGTTTGCTGCAACTGCCATTCCCCGTT GATGACCATGCTCTTCCTTCAGAAGAGGGAGAGTGAGAGGACCAAGTCCAAG TGGT
co3_91 20134_ x12	CM0006 66.2/677 47236- 6774738 6	35	2E-05	38.2	12	ATTTTCATGTTTTAAAGGCATAATGATGTCACTGACTGGCTGATGAAATCCCAA GCGTAGGTAGTATGCTACATGAGGGGTGAGTTTTTTGCTAACACCACAAAGG TCTCTGGCCAATGAGTGGAGTTTGATAGGAGTTCTTGTGACAAGT
co3_91 24658_ x12	CM0006 85.2/115 545637- 1155457 17	26	5E-05	36.2	12	AGGGGTGGTCTCCTCCCTTACTCTTTGGGAACTCAGATTGGCCTTATGGTGG CCTCTCTTTCCTTGAGGGGCACAACAGGT

co3_91 24898_ x12	AJ22402 3.1/1-67	32	#####	63.9	12	GUGCAUAUGAUGGAAAAGUUUUAAUCUCCUGACACUUGUGAUGUCUUCAAA GGAACCACUGAUGCAC
co3_91 34557_ x11	ENST00 0004595 77.1	44	3E-20	87.7	11	TGGTCTCAAGGAAGGGATGATGTTCCAGTTGAGACTCAAGAAAAGGATTCTG AGCCTCAG
co3_91 37021_ x11	CM0006 66.2/541 47264- 5414746 1	22	0.009	28.2	11	AAGACTCTACTTCCAGGTATAATTTCTATGGTTTATTACTGGAAAAGTTTCTCT AAATATGTGGATCGCTGGAAATAAGAGGAAGCACAGGGTTCTCCGAGTGAAG CTGGCTTTTGGAACTTACTTGGCTGCAACTGTCATTTGCTACTTTAAGATTTTAC TTATTGATTTTTTTTTTTGAGACAGAGTCTCACTCTGT
co3_91 37285_ x11	AL13270 9.5/1467 93- 146719	21	#####	34.2	11	UGGACCAAUGAUGACAAAUGGUGGCAUUGGAGUUAUGGACGAUGAAUGAU AUGUGUCUGAAACUCUGAGGUCCAA
co3_91 37505_ x11	ENST00 0004592 55.1	32	3E-13	63.9	11	GCCACATGATGATATCAAGGCTGTTGTGATTGATTGGTTTGGCTAAGCCCAG GGACCTT
co3_91 37582_ x11	ENST00 0003654 05.1	22	0.0001	36.2	11	ATTGTTACATTGATAAAATCAAATCACCATCTTTTAGCTAAGCTTGTGCTGGAT TTGCTT
co3_91 41520_ x11	ENST00 0004592 29.1	20	2E-06	40.1	11	GCCCTGTGGTTGCTGGATGCTGTTGTGCATGGACAGCTCTCCAGTGGATTGCG ATGGGCCA

co3_91 42312_ x11	CM0006 71.2/872 60450- 8726058 5	43	0.007	30.2	11	GTGCCCTTTTAAGGTAGACGCAGTTTCGTAAGAGGCTAACACATAAGGGTAAA TTAAAGTAAGTCTCCATAAAACCCAGAGAAGAGACAGAAGAGACTGTGAAACT CCTCTTTGGACCCCATCTGGAGCCACAGCA
co3_91 43291_ x11	ENST00 0003843 23.1	45	8E-21	89.7	11	TACCCCTTTTCACTTTGCCAGTTGGACTTATGTCTTTATTGGTCATTCAAGTG GGCAA
co3_91 50980_ x11	ENST00 0003840 49.1	25	6E-09	50.1	11	TGGTAATTACCAAGATTTTTAGAATGCAGTTTCTCATTTGCCAGGGAAATGAC CATAAAA
co3_91 52289_ x11	CM0006 64.2/231 455936- 2314558 00	26	#####	52	11	GTCCTTCTCATTGAGCTCCTTTCTGTCTATCAGTGGCAGTTTATGGATTCGCAC GAGAAGAAGAGAGAATTCACAGAAGTAGCATTATTTACCTTCTGTCTTTACA GAGGTATATTTAGCTGTATTGTGAGACATTC
co3_91 53070_ x11	AK12399 3.1/1023- 1100	29	2E-11	58	11	CUGAGCUGAGGAUGAUUUAAAGUUUAUCCUGUCUGAAAUGGUAUCUUUUG UGAGGAGGUCUGACUUGCUGAGGCUCAG
co3_91 55083_ x11	ENST00 0003910 61.1	19	1E-05	38.2	11	TGCGTGACATGTATGTTTTTGTTTAACTTGTATACAAAGGCTTATGGATAGGTG CAAAAA
co3_91 56491_ x11	ENST00 0003643 75.1	32	2E-08	48.1	11	AGGTTATTTCAAAGAGGGCTCATGAGGCTATGAAACCAAGAAGACTCTTAATGCT ATGACCA
co3_91 60836_ x11	ENST00 0003650 28.1	28	1E-08	48.1	11	TTTAGAATGTCAAAATTGATTTTGTAAATAGTCAGGACAGGATAAACAGTCGCTA TATTAA

co3_91 62243_ x10	AC13219 2.3/7195 4-71776	23	#####	46.1	10	GUAAUGUGUGCAUAGGUUUCaucugugucugguagcagugucugucugug UUUUUCAUUCAGAUUCUUGCUAUCCACACAAACAUCAUGCGGCCAAAGAGUA ACUUGGGAUCAUAGUACUGGUCUAGUGUUGUCUCUGGACACAUCUACCAC UGCCAGCCUCCAAAUUCCACACACAG
co3_91 64963_ x10	ENST00 0006096 20.2	23	1E-07	46.1	10	TAGAGAAGTCAATGATGGTTTTATTCATATCGTCTGAACCTGTCTGAAGCATCT CAGTGA
co3_91 66233_ x10	ENST00 0003641 21.1	16	0.002	32.2	10	AGGTCATTTCAAAGAGGCTGCAAAACCAAGAGCTCTTAACGCTGTGAGCAAA GATGGAAG
co3_91 67533_ x10	ENST00 0004081 75.1	44	3E-20	87.7	10	GGGGTGTGCTCAGAGCAGGGGGCCCGAAGAATGCCTCCTCTGTTTACAACA CACCCAATA
co3_91 68053_ x10	ENST00 0003634 85.1	31	0.004	30.2	10	TTATGAATATACTCACCGTTTTGATTTTATAATAGTAACGACAAGCTAAACATT CACTAT
co3_91 68683_ x10	CM0006 71.2/339 34376- 3393429 6	28	#####	56	10	CTGGAAAAGACAATGATGTTTTATTTCCAAGCACATATCTGAGTTGTATGTGTG GACAGCACTGAGACTGAGTCTTTCCAC
co3_91 73043_ x10	ENST00 0004587 90.1	21	5E-07	42.1	10	AGCCTTTGTGTTGCCATTCACTTTGGAACTAGTGAATGTGGTGTCAAAAA GGCGTAA
co3_91 73573_ x10	ENST00 0003645 97.1	23	0.003	30.2	10	GGCGGCCCTTATCACAGCTGCAGCTGCTTCCACATAGCTGCTGCGGTCAAAA AGGAGCCC

co3_91 84223_ x10	ENST00 0005159 26.1	24	#####	32.2	10	AAAATATATTTTAGTTTGTGGGCTGGGAAACCAAGAGCTCTTAATGCTATACC CAAAGAC
co3_91 89173_ x10	CM0006 63.2/155 42165- 1554230 4	14	0.009	28.2	10	TGGCTCGGTTTCCTGGGGGTGGGCTCAGTCTACACCACCTCCCCTCAGCC AAGCCTACAGTAGAGGGCCAGGCATCCTCCCGTATGGGAGAGGCGTTTGA GTAAGGAGCCTCACCTGGGGTGTCTAGCCTCACATTT
co3_91 91123_ x10	ENST00 0003860 62.1	20	2E-06	40.1	10	AATAAGTGATGAAAAAAGTTTCGGTCCCAGATGATGGCCAGTGATAACAACAT TTTTCTG
co3_91 96843_ x10	ENST00 0003842 89.1	23	4E-08	46.1	10	TTCCAAAGTGTTGAGTTCAGTCCAGGGCAGCTTCCCTGTTCTGTTAATTAAC TTTGGGA
co3_91 97403_ x10	ENST00 0003649 15.1	26	2E-09	52	10	GCCAAATGATGTTTATTTGAAACAGGAGCACCTCAGTGCAAGGACGACTCTTA TCTATCA
co3_92 03940_ x9	ENST00 0003623 96.1	21	5E-07	42.1	9	ACCTGCATTCAAAAATGATCACGGGCTGCCTGTGCTCTGGTCATCAATAACGC AGGGAGA
co3_92 04480_ x9	CM0006 64.2/215 302766- 2153028 64	19	0.003	30.2	9	ATCCTTTTGCAGTTCATAAGCATGAAGTTTGGGTTTTTCACATGCATCTGTGAG AAATACCTTCTCAAACCCTGTTACAATGGTGGCTCACATCTGTAA
co3_92 07729_ x9	CM0006 81.2/178 62588- 1786272 0	25	3E-09	50.1	9	ATTGCACCTAAACCCAAGAATCACTGTTTCTTATAGCGGTGGTTTAAACAGAG GTGCAAACAGCAAGCGGATCTTGTGCGCCTTTGGGGGGCTGTGGCCGTGCC CTCAAAGTGAATTTGGAGGTTCCACAAC

co3_92 09862_ x9	ENST00 0003844 18.1	15	#####	30.2	9	GCCCGCCTTGGCCTCCCAAAGTGCTGGGATTCTTACATCGACTGCATAGAAA GAGGAGAG
co3_92 10933_ x9	ENST00 0003650 32.1	15	0.003	30.2	9	GCCTGCATTCGTAAGTGATCACGGGCTGCCCGTGTCTGCTGATTCATTGGTAGTG CAGGCAGA
co3_92 16126_ x9	ENST00 0003844 37.1	27	2E-10	54	9	ATTGCACCTAAACCCAAGAATCACTGTTTCTTATAGCGGTGGTTTAAACAGAG GTGCAA
co3_92 18727_ x9	ENST00 0003636 64.1	30	4E-12	60	9	AAGCCAGCCAATGAATCTGCTTACCTGATTGTGTTTGTGCAGACATACTTTAA AAACTGG
co3_92 20014_ x9	ENST00 0003624 23.1	23	#####	46.1	9	CCCCTTTTAAAAGCACTCAATGGGCCTGTGGCTAATGACCTATTGAGCCGTCA AGAAAGG
co3_92 23803_ x9	AC06483 6.7/1684 2-16926	36	1E-15	71.9	9	UUCAUGUUGUCAUUGAUGCAUUCUUAUUGGAACUGAAUUUAAGUGAUCUG ACUCAUUCGUCACUACCACUGAGACAACAUUGAG
co3_92 26413_ x9	CM0006 77.2/463 51745- 4635166 2	28	0.0008	32.2	9	TGATTCAACTATGATTTTTATTTGTTTGACTGATTTCTTTTGGATAATGAAGGT ATCTTTAGTCACCATATCTTCTGAGACAT
co3_92 27016_ x9	CM0006 75.2/724 60628- 7246051 9	18	5E-05	36.2	9	CAGTCACCATTGTTTGTCAATTATTTCTTCACAATGTCTATTGAAGGATCTCAT CACCTTTAGAGAGCTGTGGTCATGCCCTTAAAGTGAATTTGGAGGTTTTATA CCC
co3_92 31264_ x9	ENST00 0003910 76.1	14	0.009	28.2	9	ATGTAATAATGTTTCATCAAATGTCTGACCTGAAATGAGCATGTAGACAAGTTAA TTTAAC

co3_92 33658_ x9	ENST00 0003643 59.1	27	0.006	30.2	9	AGGTTGGATTCAATTGTTACAATATAGCTGTGAAGTGCTATGTTGTCCTTGCCC CCTGCTC
co3_92 36646_ x9	ENST00 0003639 46.1	22	1E-07	44.1	9	TCCTCCTACAAAGGCGTGTCTGTGGTTCCCTGTCTTTGGACACGTAAGAATTG GAGGAAA
co3_92 45202_ x8	AL13270 9.5/1759 50- 175879	27	5E-08	46.1	8	UGGAUCAAUUGAUGAGUACCCUGGGGUGUCUGAAUCUUGGAUUUUGAUUAA ACCCUAUAACUCUGAGGUCCAU
co3_92 51626_ x8	ENST00 0004135 22.1	24	2E-08	48.1	8	CCACAATGATGGCAATATTTTTTCGTCAACAGCAGTTCACCTAGTGAGTGTTGA GACTCTG
co3_92 55754_ x8	ENST00 0003843 90.1	30	4E-12	60	8	TCGCTATGATGATGGATTCCAAAACCATTTCGTAGTTTCCACCAGAAAGTCTTA TGTTGGC
co3_92 56562_ x8	ENST00 0003908 32.1	20	5E-06	40.1	8	TACACTTGTTTATATTTTTGTTAACTTGTGGACAAAGATTTATAGACAGGTGC AAAAAA
co3_92 59138_ x8	ENST00 0004593 86.1	28	3E-08	48.1	8	GTCCAGAAAACAATGATGTGGTAATTTCCAAGCACATATCTGATGATTCCATG TGGAATT
co3_92 62202_ x8	ENST00 0004081 13.2	20	2E-06	40.1	8	AAGACTATACTTTCAGGGATCATTTATATGATTTGTGGCTACAGAAGTTTCTCA GCGTGA
co3_92 65122_ x8	ENST00 0003844 16.1	23	#####	46.1	8	GTTGAGGTCTATCCCGATGGGGCTTTTCCTGTAGCCTGCACATCGTTGGAAA CGCCTCAT
co3_92 72914_ x8	ENST00 0003841 70.1	27	2E-10	54	8	TAGCAAGCCTCCAGCGTGCTTGGGTCTGCAGTGACCCCGTGGATTCCCTACAG GGCTTGCC
co3_92 75218_ x8	ENST00 0003649 68.1	24	1E-08	48.1	8	ACAAGCCTATGATGGTTAGTTATCCCTGTCTGAAAATCTGGACTGAGGGAAAT AATCTAT

co3_92 75418_ x8	CM0006 72.2/100 237302- 1002371 56	33	#####	65.9	8	AGTTGTGGTGGTTTTCTTTTTGGCACATTTGTTAAGTTTTCAAATGGGCCTAAC TCTGCCACATATATAATATCGGAGATGGCAAAGGCTTGTGACGGAGATATCTC TCTTAAGCCTTTCTGCATCAGAGAATGGCTCCCACATGT
co3_92 76242_ x8	ENST00 0003656 33.1	14	0.009	28.2	8	TGGCGTCCATGATGTTCCGCAACTACCTACATTGTTTGATCCTCATGAAAGCA GCACTGG
co3_92 77018_ x8	AL13270 9.5/1851 08- 185034	32	0.001	32.2	8	UGGACCAAUGAUGAGUACCAUGGGGUAUCUGAAACAGGAUUUUUGAUUAAA CCCAUUGCAAUUCUGAGGUCCAU
co3_92 81126_ x7	CM0006 67.2/172 252478- 1722523 34	17	#####	34.2	7	CCTCGCTTTCTTTGCAGGGAGCAGGTATGTATGTTCCCTATTATGTCTGGAGG CAGAGGGAAAAGGCTTCAGTCCCCTGGGCATCATGTCTTTGGTGCCGCTGGC TTCCTGTCTGCCAATTCTATCCTCAAGCACTGGGACACAG
co3_92 81616_ x7	AL13270 9.5/1517 20- 151647	14	0.008	28.2	7	UGGACCAGUGAUGACCACUGGUGGCAUAUGAGUCAUACACAUGAACACCAU GUUUCUAGAACUCUGAGGUCCAA
co3_92 83954_ x7	BC04266 7.1/532- 663	33	8E-14	65.9	7	ACUGCCCCUAGAGGCGUUGCAGCUGUGGCUGCCGUGUCACAUCUGUGUCA UUAAGUGGCAGAGAUUAGAGAGGCCUAUGUCUACGCUCAGCGUUCUGCCCC GUGAACGUUUUGAAUGUUUGAUAGUCUCACACU

co3_92 84514_ x7	AY34959 7.1/1-142	27	#####	54	7	UUGCCCGAUGAUUUAUAAAAAGACGCGUUUUAUUAAGAGGACUUUAUGCUGGAG UUCUUGACGUUUUUCUCUCUUUUUCUAUACUUCUUUUUCUUUCUUUGAAUG UCCAGCGUCCUGUGAGCGAAGAUUAUGAGAUUAUGAGGGCAA
co3_92 85256_ x7	ENST00 0003654 00.1	33	#####	65.9	7	TGGACCAATGATGACAAATACCGGCGTATGAGTCTTGGATGATGAATAATACG TGTCTGG
co3_92 89211_ x7	CM0006 77.2/250 99499- 2509959 4	29	2E-11	58	7	GGATCGATGATGACTATAAAAAAATGGATCTCATCGGAATCTGAACAAAATG AGTGACCAAATCATTCTGTGCCACTTCTGTGAGCTGAGGTCC
co3_92 90947_ x7	ENST00 0003909 47.2	15	#####	30.2	7	CCCAAAGTGCTGGGATAACCCTTACCTGTTTCTCCTTTGCAGGGCAGATAGAA CATGATA
co3_92 95329_ x7	ENST00 0004588 92.1	24	1E-08	48.1	7	TGGCAACTGTGATGAAAGATTTGGTCTGTATGTAATAGATTTTATTACTAAATG AGGACA
co3_92 98612_ x7	ENST00 0003910 75.1	27	3E-05	38.2	7	GTAGGTGACGACCAATATTTTTTTTACTTTGACTTGATGTCTATTGAAGAAATC TAGCAT
co3_93 04310_ x7	AL13270 9.5/1568 19- 156747	27	0.004	30.2	7	UUGAUGAUUAUGAUGGCCACUGGUGGCUUAUGAGUCUUAUACAGUGAAUAC AUGUUUGAAACUCUGAGGUCUGU

co3_93 05304_ x7	AC07314 9.5/3872 3-38590	19	0.002	30.2	7	UGUUCUGACAUGGGAAGAGUAGCUUCUGGUUGGUGGAGCCCAUCUCACAU UAGCCAGAGACAAAGCAACACCUUGUUUAUCCCGGCUUGGCUUUUGGCCU GUGUCCAUGACUGGUCCAUAACCUUGGACACAUGG
co3_93 16049_ x7	CM0006 67.2/407 90204- 4079007 1	23	1E-05	38.2	7	CCTCCTTTTCTTGTCAGGGACTGAGTGTGTGGTCCTGCTCCTGTTATGTATGG AGGCAAAGGGAAAGGGCTCCGGCCCCCTCAAATCATGTCTTTGGTGCCAGC CGGTTCTGTTCTCAGTCACCTGGATACTG
co3_93 16056_ x7	AC01211 9.8/9287 5-93023	15	0.008	30.2	7	AUCCAAGGGGAUUCCUCUCCAAGGGAACAUGCAGUGCCCCUCUCAGGAA AGUAACAACCUUGGAAUAGAAUCUGGCAUGCCUAAGGUCUUUGAGGAAUAGA GGAAUAGAGGAUGCUUGUUUCCUCUGCCUUCUUGGCUGCCUACAUGG
co3_93 18023_ x7	ENST00 0003649 40.1	20	2E-06	40.1	7	TGGTCAGGTGGAATAATCCTTATCTGTTTCTCCTTTTGAAGGGCAGATTAGAA CATGATA
co3_93 34618_ x6	ENST00 0003647 96.1	32	7E-06	40.1	6	CAGCCTCTGATGAAATTTATCTTGATAGGGACATCTGAAAGTGTTGATGAATG CCAAGGA
co3_93 35122_ x6	ENST00 0003839 53.1	20	2E-06	40.1	6	GCTGAATGATGATATCCCACTAACTGAGCAGTCAGTAGTTGGTCCTTTGGTTG CATATGA
co3_93 36022_ x6	ENST00 0003644 46.1	40	7E-06	40.1	6	AATCTCCTGGGATTGTGTCTGGCGAGTGCCCAGTATTCTGCCACCTTCAGAA GGAAGGGA

co3_93 36298_ x6	ENST00 0003909 94.1	38	1E-16	75.8	6	AGCTTATCAGTGATGTTGTAAAAATAAATGTCTGAACATATGAATGCAGTATTG ATTTCA
co3_93 36682_ x6	AC09658 7.1/2586 4-25727	29	#####	42.1	6	GCUAUCCUGGACUUGCCAGCCCAUAGACACAGUUGCUGUGCUGGCCUG UACUUAUUGGAGCAAAGAAAAAGUGGCUAUUUCUAUGCUCAGUGUUCACAAA CCAGUGAGCACUAAGAAUGGUUUUAUAGCCUGACAUUU
co3_93 56458_ x6	ENST00 0003635 24.1	39	1E-07	46.1	6	CCCTCCTACAAAGGCATGTCTATAGTTCCTTGTCTTTGGACATGTAAGAATTG GAGGCAA
co3_93 61264_ x6	CM0006 79.2/763 24196- 7632429 9	15	0.006	30.2	6	ATCATTGTTGTAGTTCATAAGTGTGATCATTGGGTGTTACGCTTACATGTGAGA TGTGCCATCCTTGAACCTTGTTAGAACATCAGTACATCACCTGGCTGACA
co3_93 61276_ x6	ENST00 0004591 57.1	21	#####	42.1	6	ATCCTTTTGTAGTTCATGAGCGTGATGATTGGGTGTTACATGCATGTGTGAG ATGTGCC
co3_93 62182_ x6	ENST00 0003646 46.1	21	5E-07	42.1	6	GCCCTCCTGGTGCTTACCACAGGCTGTGTTCTTACACTGACTGTATAGAATGA GAAGGTA
co3_93 62518_ x6	ENST00 0003844 23.1	21	5E-07	42.1	6	ATCCAAGGTGATTCCCTCTCCAAGGGGACATCAGTGCCTCTCAGGAAAGTAG CAGCTTGG
co3_93 62698_ x6	ENST00 0003627 05.1	14	0.008	28.2	6	TGGACCTATGATGATGACTGGTGGCGTATGAGTCATTGACGGTGAATACAGG TCTGGAAG

co3_93 64714_ x6	AC02210 7.8/6626 6-66397	20	#####	32.2	6	GCGCUGCCUUUGUACCCACCGUGCCUCCGCCUGGUGUCUGGGGUCAGG UUGCAGUGCCAGAGCACGUGCUUGCGCAUAAAUGGGGCAGCCUGGCCCCC UGCGGAUGGUCCUUUUAACCGCGAGCAACAAG
co3_93 64726_ x6	ENST00 0005161 31.1	22	1E-07	44.1	6	GCCAGGTACCATGCAAAAGCAATCTTCCCTTTAGAATGACTGATGGTATGCTA AGGTTTT
co3_93 65254_ x6	ENST00 0005172 58.1	14	0.009	28.2	6	GACTAGTACCACCTCACACCCGCAGAGCACTGGGCCCTGCCTGGGGTGAAA TGCCAGTTG
co3_93 67948_ x6	ENST00 0006201 04.1	19	0.003	30.2	6	AAAAAAGTGTCTTGAGCTTTCTGTCTGATTGTGGCAGCCAAGATTGAATAG AGGA
co3_93 70636_ x6	ENST00 0005171 11.1	28	0.001	32.2	6	ATGCATCTATCTGACATGCCTGGAGCAGGTATTGTCTGCTGCTAAAGTTTCCA CCACAGA
co3_93 71074_ x6	AL13270 9.5/1834 12- 183335	20	#####	40.1	6	UGGAUCAAUGAUGAGUAUUGGUGGAGGUGUCUGAAUCAACACUUUUGAUU AAGCCCUCUGUGUAACUCUGAGAUCUGU
co3_93 71464_ x6	ENST00 0006306 15.1	51	3E-24	101	6	TCCTGTGTGAGAAATGATGAGGGTCAACATTCTTCATACCAAAGTGAAGACAT GAGATCC
co3_93 72352_ x6	ENST00 0003838 95.1	20	2E-06	40.1	6	AAAGCAGGTTGCAATTACAGTGCTTCATTTTGTGGAAGTACTGCCATTATCCT GCTGAAA
co3_93 75160_ x6	ENST00 0004595 07.1	18	0.008	28.2	6	ATCCTGTTGTAGCTCATGAGCGTGATAATTGGGTGTTTCATGTGCGTGTGTGAG ATGTGCC

co3_93 79893_ x5	ENST00 0005172 38.1	22	0.009	28.2	5	CAAAGTTCTGGAATTACAGGTGTGAGCCACCGTGCCAGCATTAAATTTTA ATATGTA
co3_93 83978_ x5	CM0006 76.2/698 04331- 6980420 3	30	3E-07	44.1	5	AGGGTTTGCCTTAGGGCAGGGAGGTTGAAGAGTGGCTCCTCTGTTTACAATAC ACCAAACAGGAATCTGGGGTCATTGTGACAAGGGGGCACAAAACCTTGTGTCCT CCCTACATGTGAAAAAAAAAAAAAGA
co3_93 84153_ x5	ENST00 0003847 13.1	19	#####	30.2	5	CTACAATCATGGCAATATTTTTTGTCAACAGCGGTTACCTAGTGAATGTTGAT ACTTTG
co3_93 86608_ x5	ADDF01 1338994. 1/3988- 3917	15	0.004	30.2	5	UGGGCAUGUGAUGUGACCUUCCUGAGCCUGCAUUCCUCACCUUGGAAAUG AUGAGCAGUUACUGAUGCCACA
co3_93 88683_ x5	CM0006 77.2/643 42566- 6434269 8	14	0.008	28.2	5	TGTTACTCTCTAGCTTAAGAACCTTTAATGTGGTGATGTCCATCTCATGTCATC CAGGGATAAAGCAACCCTTGTTTATCCCATCTTGGCTCTTGGTCTGTGCCAT GGCTGGTTCGTGCCTTGGATACATGG
co3_93 89253_ x5	AB02889 3.1/1092 0-11006	44	#####	87.7	5	GGCAGAUGAUGUUUGUUUUCACGAUGGUCUUCAGAUGCCCACGUGGGCAC UGCUGAGAAAGCCACUUGGUAAAACUGAUGCCGAAA
co3_93 90878_ x5	ENST00 0003847 56.1	16	0.001	32.2	5	TCCCAATGAAGAACTTTACATGTCTTACTCTCTGTCCTAGTCCCAGAGCCT GTAAAGG

co3_93 91998_ x5	AC11508 8.6/1230 21- 122911	20	2E-06	40.1	5	UGUGAGAGUGAUGAGUUUGCACACUGGUGGAGCCAUGGUUAUCAGGUGAUAC AGGCACCACUCAGUAUCACCCUGGUGACAAAAUCAAGUGCACAGGGGCCAU CUGACUCACA
co3_93 92073_ x5	CM0006 75.2/565 59624- 5655972 5	15	#####	30.2	5	ATCCATTTGTAGTTCAGAAACATGACTATTGTCTTTTCAAGCTTATATGAGATC TGGCTCCCTCAATCCTTGCTATGATATCAGTACATTACCTGTCTGATG
co3_93 93508_ x5	AF14134 6.1/1275- 1356	25	3E-09	50.1	5	UGCCACAAUGAUGACAGUUUUAUUUGCUACUCUUGAGUGCUAGAAUGAUGA GGAUCUUAACCACCAUUUAUCUUAACUGAGGCA
co3_93 93713_ x5	ENST00 0003647 29.1	25	#####	34.2	5	TCCTGCATCCGAAAGTGATCATAGGCTGCCTGTGCCTAGGTCATTGATAGTG CAGGGAGA
co3_93 94568_ x5	ENST00 0003645 33.1	21	0.0005	34.2	5	TCACTGTGATGATGGTTTTCCAACATTCGCAGTTTCCACCAGAAAGGTTTTCC TTAGTGT
co3_93 95428_ x5	ENST00 0004085 69.2	18	0.008	28.2	5	TTGTATTTTTTTGTAGAGATGGGGTCTCTCCCATGGGCACAGTCTCATTGTTTCT ATAGTT
co3_93 95698_ x5	ENST00 0006072 61.1	22	3E-07	44.1	5	TGGATCAATGATGAGTATTGGTGGAGGTGTCTGAATCAACACTTTTGATTAAG CCCTCTG
co3_93 97198_ x5	CM0006 63.2/285 78822- 2857874 9	35	5E-15	69.9	5	ACTGGTCCAGGATGAAACCTAATTTGAGTGGACATCCATGGATGAGAAATGC GGATATGGGACTGAGACCAGCT
co3_93 98613_ x5	ENST00 0003913 06.1	18	0.009	28.2	5	TGAACTTTAAAATGCAAGTTCATAGTTCTTTAAGAGACTAACACAGAAAGCTAA AGTAAT

co3_94 02158_ x5	ENST00 0005166 29.1	31	0.008	30.2	5	GAGCAGTTTGGCATATGTTCTGAATCTGAGGTTGATTATTATTCCTTTAGCGCT AGTATT
co3_94 02793_ x5	CM0006 64.2/276 42169- 2764204 3	14	0.009	28.2	5	TTCTAAAGTGTTGAGTTCAGTCCAGGGTGGATCCCCTGCTCTGTTAATTGAAC TGGAACATTTAAACTGGCTAGGCAAAATGCCTACATAGAAAGCATTACTCTTT ATTCATCCCCAGCCTACAAAA
co3_94 05003_ x5	ENST00 0003908 59.1	22	2E-07	44.1	5	GGATTTATAATGAGCTGTGTTTACTGAGCATTATGAAGTAAAGTTCAATATGAT TACTCT
co3_94 06833_ x5	ENST00 0003869 67.1	18	5E-05	36.2	5	TGGGAAGTGATGACACCTGTGACTGTTGATGTGGAAGTATTATCGCGTATT CGTACTG
co3_94 08028_ x5	CM0006 65.2/183 453814- 1834539 44	23	#####	30.2	5	AGGCAGGATCTAGTTACATTGTAGCTGTGAAGTGCTGCATTGTCTTTGCCCC TGCTCAAATAAACTGTTACCTTTCAAGCCCTGTCTGCCATGGTGCTGTAGC AGCAGGGATGTTTGGTCTCATACAT
co3_94 10823_ x5	ENST00 0005168 83.1	30	0.0001	36.2	5	TGTCAAAAATCCCCAATCCTATTTCTGACACTTCATATGAAAGCTGCATGTGC AGTCTT
co3_94 19098_ x5	ENST00 0005799 95.1	28	#####	40.1	5	AACTATTGAGAACAAAGATGCAACATACCACTCGAGTGTGCAGTGGGGAAGC CAACCTTG
co3_94 19168_ x5	ENST00 0003910 89.1	31	0.005	30.2	5	TGTTCTGACATGGGAAGAGTAGCTTCTGGTTGGTGGAGCCCATCTCACATTA GCCAGAGA

co3_94 20933_ x5	ENST00 0004595 38.1	26	8E-10	52	5	ACCCCTGGCAGCCCCTCCTGATGATTCTTCTTCCTGAGCACGCTCATGATGA GCAAACCTG
co3_94 27308_ x5	ENST00 0003646 30.1	31	1E-07	46.1	5	TGGACCAATGATGATGACTGGTGGTGTATGAGTTAAAGGTGATGAATAGTAAG TGTCITT
co3_94 34063_ x5	ENST00 0003844 42.1	24	0.0006	32.2	5	GGCTTGCTGGTGCTTACCACAGGCTGAATTCTTACACTGACTATATAGAAAAG GAGGTAG
co3_94 35718_ x5	ENST00 0003630 91.1	27	3E-05	38.2	5	CTGAGTCCATGATGATTTCAAGTTATCCCTGTCTGAAGGCAAAGAAAGGCCTT TCTGTGT
co3_94 37178_ x5	ENST00 0003845 04.1	24	1E-08	48.1	5	TGAGCACTTTCACAGGTCCTCCCTCAGGCTGTGGGGCCAGGATTTGGTAGCT GGTGCTGA
co3_94 40298_ x5	ENST00 0003841 22.1	29	1E-06	42.1	5	GTTGAGGTCTATCCCGATAGGTCTTTTCCTGTAGCCTGCACGTTGTTGGAAAT GCCTCAT
co3_94 43112_ x4	ENST00 0003841 51.1	28	0.001	32.2	4	GGCCTTTTGGTGCTTACCACAGACTGTGCTCTTTCACTGACTGAATAGAGAGA GGAGGCA
co3_94 45496_ x4	ENST00 0003839 06.1	22	#####	44.1	4	GCATGGGTTTGGATTTATGACAGGCCCGTCACCCTGGGCCTGTCATAGTACC CCATGCCA
co3_94 46848_ x4	ENST00 0003653 21.1	15	0.003	30.2	4	GTGAGTGATGAATAGTTCTGTGGCATATGAATCATTAAATTTGATTAAACCCTA AACTCT
co3_94 48728_ x4	ENST00 0004588 62.1	26	9E-10	52	4	TGGAGGACTGAGAAGGTGAGGCAGTTTTGCCCGTGCTGCCTTCCACCGGTT AAGACCTC
co3_94 48940_ x4	ENST00 0003629 15.1	25	3E-09	50.1	4	TGGTCCATCCTAATCCCTGCCGGTCCATCTGTGGCCTGCCAGGTTTTCGCTTG TGGACCAG

co3_94 49240_ x4	ENST00 0004595 79.1	33	8E-14	65.9	4	GCTCTGTGATGGAGCCCATGCGTGTGTCATCTGAGCCTCTGGCTTCCCTGCCAG TGCAGCCC
co3_94 52388_ x4	AY07773 7.1/2-276	24	1E-08	48.1	4	GGUCGUGAUGAUUGGUAAAAGGUCUGAUUGCACUGAAUGUCACAGUCCCU UUGUUGCCCUCAACUCCAGCAGCCAUUUUUUCCCUCCCGUCACAUUUAA GUCAUGUGUAUGGGAUCAUGGAGCAGCUGAUAAUUUGGGAUUCUGUCAGU GUGUGUUUCUGAGAGUGAUCGACUCACAGCUGACGAGUAUCCAACAAAACC AGUUACACAGGAGACUGACGAGUGGCAGUCAUGGGUGUGAUGGUGCAUGA UCUCAAGUUUCAAUCUGAGACC
co3_94 55664_ x4	ENST00 0006367 29.1	22	4E-05	36.2	4	ATCATTATTGTTATTATTATATTTTTGAGAAGGAATCTCACTCTGTCGCCCAGG CTGGAG
co3_94 55856_ x4	AJ60945 3.1/1-134	20	#####	40.1	4	UGCAGCCGUGUCAAAUUCAGUACCUGUCCUAUGCAUGGUAGGCACUGGCC CAGAAGGCUGCCACAGAAACACUGUGACUCAUGGGCCCUGUUCCUGUGUC CCAGGCUCAGGGAUAAAUUUGGUUACAGACAUCA
co3_94 55892_ x4	ENST00 0003646 99.1	24	1E-08	48.1	4	TGGACCAATGATGACAAATGGTGGCATTGGAGTTATGGACGATGAATGATAT GTGTCTGA

co3_94 56344_ x4	CM0006 79.2/280 18770- 2801890 7	16	0.001	32.2	4	TGTCTCATTTTTGTAGATCAGGACACTGGGAGGCTCCCTTTTCTCCTTAGCCA TGGCTGGAGGCCAAGTCCAGCCCTCAAGGATCATTGTCAGGACCAACACAAG CTGGACAGCCTTGTTTTCTACCTCAGATGGGA
co3_94 57056_ x4	AL13270 9.5/1585 45- 158469	15	0.006	30.2	4	UGAACUAGUGGUGAUGGCUUGUGGCAUUAUUUAGUCACAGAUGAUGAAUAA AUACAUGCCUGAGACUCUGAGGUUAGU
co3_94 57820_ x4	ENST00 0003649 57.1	23	0.002	30.2	4	ACTCCAGCCTGGCTGACAGAGTGGGACCCCATCTCAAAAAAAAAAAAAAAAAAATT AAGCTGG
co3_94 63472_ x4	ENST00 0003847 06.1	19	2E-05	38.2	4	GTCAGATGATTTGAATTGATAAGCTGATGTTCTGTGAGGTACAAAAGTTAATA GCATGTT
co3_94 64316_ x4	ENST00 0003638 83.1	25	2E-06	42.1	4	CTACAAAGATAGCAACACTTTTCATCAACAGCAGTTCACCTAGAGAGAGTCGA CACTTTT
co3_94 64956_ x4	ENST00 0006304 29.1	23	4E-08	46.1	4	ACTGCCCTAGAGGCGTTGCAGCTGTGGCTGCCGTGTCACATCTGTGTCATT AGGTGGCA
co3_94 70200_ x4	ENST00 0003844 36.1	26	9E-10	52	4	CCGCAGCCAATTAAGCCGACTGAGTTCCTTTCTCATGGGGACCCAGTGTGC GATGGCTG

co3_94 73196_ x4	AJ60948 4.1/1-166	22	1E-07	44.1	4	CAGCACUUGAUACUAACCGAGCUGUCUAUAUCCUAGCCUUGUGUCAAGGC UUGUGAUGUGUUGUGAUAGCUGGGUUUAAGAAGUGCAAUAUJAAAACAAAA GCCAUGAGUCUUUUAAGCCCAGUGUGUAAAGAUACACUCUGAGUUUAACU CAGAGGCACAACU
co3_94 73780_ x4	ENST00 0006312 70.1	15	0.004	30.2	4	GCTGTCCTGGACCTGCCAGCTGCACAGATGCAGATGCTCTGCTATGCCTGTA ACATCGGG
co3_94 75580_ x4	ENST00 0003845 49.1	22	1E-07	44.1	4	GGATCGATGATGACTTTTTATACATGCATTCCTTGAAAGCTGAACAAAATGAG TGAAAAC
co3_94 76496_ x4	ENST00 0005164 19.1	21	0.0001	34.2	4	TACTCCAGCCTGGATGACAGAGCCAGACTCTGTCTCGAAAAAAAAAAAAAAAAA AAGCTTA
co3_94 77336_ x4	ENST00 0003652 72.1	26	9E-05	36.2	4	TAGATCAGTGATGACTACTGTTGGTGTATGAGTCATATACGATGAATACATGT CTGAAAT
co3_94 84496_ x4	CM0006 85.2/124 197743- 1241978 49	22	1E-07	44.1	4	TGTAAC TTGTGGACAAGGCTTATTGACAGGTGCAAAAAATAAATAATCTTTTGC CACTCAGAACTCATTGTTTCAGTATGAGTTTTGATACACATAAGAAGGAATATT
co3_94 89036_ x4	ENST00 0004594 73.1	20	2E-06	40.1	4	GGTGAAAATGATGAATTCTGGGGCGCTGATTCATGTGACTTGAAAATGCCAT CCATTTT
co3_94 94680_ x4	ENST00 0005842 75.1	22	3E-07	44.1	4	GCCATATGATGTTTTCTTTTCGAAAGGTGAGCGCTTTGCGCAGTGATGACCCT CATCTAT

co3_94 95112_ x4	ENST00 0003653 46.2	22	#####	36.2	4	CTTGCCAGCCCCATAGACACAGTTGCTGTGCTGTGCCTGTACTATTGGAGCA AAGAAAAA
co3_94 95332_ x4	ENST00 0003645 87.1	22	#####	44.1	4	GCACCTGAATCTTTCCCATTCCTTGCTGCCTCGTGCCGGTGTGGGGACAGAT GGTGCTAC
co3_94 95628_ x4	AB00714 7.1/104- 236	38	1E-16	75.8	4	GGUCUCUCAGCUCCGCUUAACCACACGGGUCCAGUGUGUGCUUGGCGUGU UUUCAGGGAGGCAGAGAAAGGCUCUCCUAAUGNACGACAGACCCGCCAG AAUGGCCUCUCUGUCCUAGGAGUGCGACAAU
co3_94 98548_ x4	AC01372 2.8/1840 33- 183920	28	#####	56	4	ACUGAGGAAUGAUGACAAGAAAAGGCCGAAUUGCAGUGUCUCCAUCAGCAG UUUGCUCUCCAUGGGCACACGAUGACAAAAUAUCCUGAAGCGAACCACUAG UCUGACCUCAGU
co3_94 99568_ x4	CM0006 76.2/963 23787- 9632369 1	19	8E-06	38.2	4	ATTCTTTTGTGGTTCATAAGCGTGATGATTGGGTGTTACATGAATGTGTGAG ATGTGTCACCCTCAAACCTTGTGTGCTATTTTTCTGCCTGCCT
co3_95 00392_ x4	CM0006 73.2/129 04988- 1290481 7	23	1E-05	38.2	4	TTGATCACAGGACCCCTTTACACTCGTAAATAAATTATTGATGTACCAGACAG CCTGACCCTGACCTCAAGTAAATTCAGGAGACGCCTTTCTGGGTTTTGAA TTTGCCGTAACAGGTGTGAGCATTCTAGCAGCAGTTTGGTGATCATGTACGAT ACTGCAAACAGGA

co3_95 10120_ x4	AJ60943 5.1/1-128	22	1E-07	44.1	4	GUGCACAUUUCAUUGACCUGCUUUCUUUUAUGUGAGUAGUGUUUUUUUU AUGUGCUAUACAAAUAUUUGAAGGCUAAUUAGCAGUAUAACUAUAAAUAGU AAUGCUGCCAGUCUCCUUCAGACAAAA
co3_95 18652_ x4	ENST00 0003656 09.1	14	#####	28.2	4	TCACTGTGATGATGGTTTTTCAACGTTACAGTTTCCACCAGAAAGATTTTCCT TAGTGT
co3_95 20680_ x4	ENST00 0003846 75.1	23	4E-08	46.1	4	TTCCACAGCTACTGGTCTGCAGCTGTTCTTATGGTAGCAGTTGTGGCATTCT CTGTGGG
co3_95 24041_ x3	CM0006 69.2/102 194205- 1021940 76	26	#####	52	3	TGCCTCTTTTTGTTAAAGATAATTTGCTTTTTGGTAGTGCCCATCTCCTATCAG TCAGGGATGAAGCAATCCCTTGTTTCATCCCCAGCTTGGCTTTTGATCTATGCC TGGTTCATGCCTTGGACACATGG
co3_95 24647_ x3	CM0006 68.2/134 206514- 1342064 11	15	0.003	30.2	3	ATCCCTTTGTCGTTTATAAGTGTGATGATTGGGTTTTTCATGTTCCCTGTGTGAGA TATGCCTCCTTCAAGCCTTGTTATGATGTCTGCACATTACCTGCCTGTCA
co3_95 27341_ x3	ENST00 0003913 22.1	17	0.0002	34.2	3	GTGCCCTTTTAAGGTTGACGCAGTGCTTTAAGGGGCTAACACAGAAGGGTAA AGGAAGTC
co3_95 28949_ x3	ENST00 0003841 58.1	29	2E-11	58	3	GTCTTCTCATTGAGCTCCTTTCTGTCTATCAGTGGCAGTTTATGGATTTCGCAC GAGAAGA
co3_95 31985_ x3	ENST00 0003912 15.1	28	3E-08	48.1	3	GTTCCCTTTTAAGGCTGACCCAGTGCTTTAAGAGGCTGATACAGAAGGGTAAA GTTAAGT

co3_95 32051_ x3	AJ60947 0.1/1-125	15	0.005	30.2	3	GCGCUCACUAAGGCUCGGUCCUCUCCACGUGGUCCUGACCUGUCCUCUGU GAGCAAGAGAAAACAGGACUGGUUUUGGGGGUGUCCUGUCUCAGUGGACACA GGACACCACGGUUUUCAGUACAACA
co3_95 32486_ x3	ENST00 0003847 44.1	29	2E-11	58	3	GCATGGTAATGGATTTATGGTGGGTCCTTCTCTGTGGGCCTCTCATAGTGTAC CCATGCC
co3_95 32561_ x3	ENST00 0005165 17.1	42	5E-19	83.8	3	GGATCGATGATGACTTTAAAATGGATCTCATCGGAATCTGAACAAAATGAGTG ACCAAAT
co3_95 35420_ x3	AC09052 7.3/1717 4-17301	14	0.008	28.2	3	UCCACCACUAUUGGUCUGCAGCUCUUCUUAUGGUAGCAGUUGUUGCAUU UCUCUGUGGGAAAGAAAAGAGGAUUAACACCUCUUUCUAGCAAAACAGA GAGUAGGCAUAUGUGUGACAGACACAA
co3_95 35492_ x3	AC10458 1.22/693 59-69497	21	6E-07	42.1	3	UGGCUCGAUUUCCUGGGGGGUGGUCUCAGCCCACUCCACCUCCCCUCAGC CGAGCCUAGAGUAGAGGGGCCAGGCAUCCUCCCCAGGGGAGGGGCGUUG AAGCAAGGAGCCUCUCCUGGGCUGUCCUAGCCUCACAUUU
co3_95 40571_ x3	ENST00 0003630 24.1	16	0.0005	32.2	3	GATCAAGGATGAAAATACCCAAATTTGAGTATCAGAAGACCTTCCAGTCTACT TGATGCA
co3_95 41066_ x3	ENST00 0003841 11.1	28	6E-11	56	3	TGCAGCCGTGTCAAATTCAGTACCTGTCCTATGCATGGTAGGCACTGGCCCA GAAGGCTG

co3_95 43628_ x3	ENST00 0006075 95.1	19	0.005	30.2	3	TCCAGCAGTCGTTAGCTCTCCTGGCTAGTGTGATGCCTGTGATGGTGTTCAC TGTTGGA
co3_95 51137_ x3	CM0006 77.2/751 21666- 7512153 6	16	0.001	32.2	3	AACCAATTGTGCCAGTGGGGCTATGGGTGGCCCCTTTTCTCCTCAGTCAGGG CTGGAGGCCAAGATCAGCCTTTGAGGATTATCAGGGCTGCCACAAGCTGGG CAGCCTTGTTTTCTACCTCAGACATTT
co3_95 52556_ x3	ENST00 0003631 56.1	20	2E-06	40.1	3	TCGATGGGTGGGATAATCCTTACCTGTTCCCTCGTTTTGGAGGGCAGATAGAA CATGATGA
co3_95 54266_ x3	ENST00 0005166 16.1	26	0.0001	36.2	3	TTAAATGTCCATCACAGGAAACACCTTTAGAGTAACTCTGTGGTTTTGCTTTAT TCACAG
co3_95 56936_ x3	ENST00 0003841 42.1	25	0.0002	34.2	3	CTGCAGTCAATTAAGTGTACTGAGTTCCTTTCTTATGGGGGCCAGTGTGCA ATGGCTG
co3_95 57341_ x3	ENST00 0003839 66.1	32	3E-13	63.9	3	CGGCAGACAGTTATCCCTTTCTAGTCTGGCTCGTGGACTCTAGAGGGAGTC AGTCTGCA
co3_95 59702_ x3	ENST00 0003912 87.1	29	0.0002	34.2	3	ACTGCCCTGGAGGCATTGCAGATGTGGCTGCTGTGTCACATTTGTGTCATTA GGTAGCA
co3_95 60770_ x3	ENST00 0003912 92.1	15	0.002	30.2	3	TCATCAGATGGGATAACTTTTACCTGTTCCCTTTTGGAGGTTAGATTCTAAT ACGATG
co3_95 62390_ x3	ENST00 0003843 00.1	54	#####	54	3	ATCCAAGGGGATTCCCTCTCCAAGGGAACATGCAGTGCCCCTCTCAGGAAAG TAACAACC

co3_95 65915_ x3	CM0006 63.2/260 06216- 2600629 9	21	0.0004	34.2	3	TGGCCAGTGATGAAGTCACCATTAGTGCAGTCTGAGTTCTGGGAACCAGGTG ATGGAGTGTGTTCCAAGAATGGACTGAGGGCC
co3_95 67508_ x3	ENST00 0003909 30.1	28	6E-11	56	3	GTGAAATGATGATTCAGTTTATCCATTCGCTGAGTGCGCTGCACTGACCTTCT TCCAAGC
co3_95 70835_ x3	AL35507 5.6/1934 39- 193515	21	5E-07	42.1	3	AGUUUGCCAUGAUGAAAUGCAUGUUAAGUCCGUGUUUCAGCUGAUCAGCC UGAUUAAACACAUGCUCUGAGCAGACU
co3_95 71657_ x3	ENST00 0003840 28.1	41	7E-09	50.1	3	CTGGCACTTTCACAGTTCCTTCCCCAGGCAGTGGGGCCAGGATTTGGTAGCT GGTGCTGA
co3_95 75071_ x3	CM0006 70.2/277 55122- 2775503 2	16	0.0008	32.2	3	ATCCTTCTGTAGTTTATGAGTGTGATGATTGGCTGTTTCATGTGCATGTATGAG ATGTGCCACCCTTGAACCTTGTGCATGTCTGATGTGAAA
co3_95 76118_ x3	ENST00 0006084 59.2	22	3E-07	44.1	3	TTAGAGGTATTTTCAGTACTCTGGCTTAAGAGCCAATGATGTTTTTATTCAAAA TGTCTG
co3_95 78092_ x3	CM0006 79.2/196 62000- 1966209 0	33	2E-11	58	3	CTGATTCTTTGTACTIONAGGATGCAAAGAAAACAATCCTTGTGCCTTCTATCTCT CTTGGTGGCAGCCCAGATTGAATTGGGAATACATCT
co3_95 80648_ x3	ENST00 0005168 84.1	14	0.008	28.2	3	TGTAACCTTGTGGACAAGGCTTATTGACAGGTGCAAAAAATAAATAATCTTTTGC CACTCA

co3_95 85970_ x3	BK00556 7.1/284- 353	32	3E-13	63.9	3	GGCAAUGAUGAAAAGGUUUUACUACUGAUCUUUGUAACUAUGAUGGUUU CUACACUUGACCUGAGCUCA
co3_95 86507_ x3	CM0006 77.2/220 60827- 2206072 7	18	0.008	28.2	3	ATCCCTTCGTAGTTCATAAGCGTGATGACTGAGTTTTTGCCTCCTGTGTGAA ATGTACCTCCCTCAAACCTTATGACATATATACATTACCTGACTCACA
co3_95 87260_ x3	ENST00 0003641 39.1	35	0.007	30.2	3	TGCTGGAGTGATGAAAAAGTATCTTCAGGTGTGGCTGTGGCCACCTTGGCCA CCTGTGTG
co3_95 89828_ x3	ENST00 0003908 43.2	24	0.0008	32.2	3	TAGTCAGGCAGGATAATCCCTATCTGTTCCTCCTTTTGGAGGGCAGTAGAATG TGGTAAT
co3_95 89891_ x3	AC02091 8.6/1655 18- 165651	30	8E-05	36.2	3	GGCCUCCUGGUGCUUACAAGCAGCUGUGCUUGCAUUGACUGUACAGAA AAAAAGAGAUAGAGUAAACACACCCCGUAUACAACUCAGCCCAGGUCCUGU GCCUUGUCUAUUAUUGUGAAUAGGGGGGACAUAG
co3_95 97850_ x3	ENST00 0003847 85.1	30	#####	52	3	TTCCACCACTATTGGTCTGCAGCTCTTCTTATGGTAGCAGTTGTTGCATTTCTC TGTGGG
co3_96 01135_ x3	ENST00 0003630 90.1	14	0.008	28.2	3	GGGTCGATGATGAGAACTTATATTGTCTGAAGAGAGGTGATGACTTAAAAAT CATGCTC
co3_96 01837_ x3	ENST00 0003840 84.1	23	9E-08	46.1	3	GGTCTCTCAGCTCCGCTTAACCACACGGGTCCAGTGTGTGCTTGGCGTGTTT TCAGGGAG

co3_96 04834_ x3	AY07773 8.1/1-265	24	1E-08	48.1	3	GGUCAUGAUGAAUGGUAAGGUCUGAGUCCUCAGAUCUCCUCCCGGCA UCCAGUUAUCCCGAGCUGCCUCUCCUCAUCGCACUUCAGAAGUGCUGC GAUGGGCAGAAGGGCAGCUGACACUCCGUGAUGUCCCUCAUUCUGUGUUC CUCCGUGAGCUCAGGGAAGACACUGGUUGGCAUCCAACAGCUUAGUCACA AAGGGAUUUGAUUGUUGGGAGUGCUGGUAUCUGUGGCUAUGAUCUGCCUU GUUCAAGCUGAGACC
co3_96 05323_ x3	CM0006 78.2/279 6532- 2796408	24	2E-08	48.1	3	GCCGAGACTAAGTCGCATGCTGACACAGCTCTTGGTGTGCTACGGTACTTGG AGAGAATCTACTGGTCTTGATTCACTGGTGGGGGCAGTTGTTGCTTCCTTTAG TGCCAGATCAGAAACATAC
co3_96 06556_ x3	ENST00 0004588 38.1	16	0.0009	32.2	3	CTGGAAAAGACAATGATGTTTTATTTCCAAGCACATATCTGAGTTGTATGTGTG GACAGC
co3_96 08623_ x3	CM0006 75.2/228 03145- 2280322 4	21	#####	42.1	3	TTCCTAAAGATTCACAATGAACATTATTATTTAAGAGCTTTTTGAAGTGCAAAT CCATGAGCTTTTTAACCCTGAGCAAT
co3_96 08851_ x3	ENST00 0004591 28.1	14	0.009	28.2	3	GGATCGATGATGAGAATAATTGTCTGAGGATGCTGAGGGACTCATTCCAGAT GTCAATCT
co3_96 18832_ x3	ENST00 0003847 37.1	26	8E-10	52	3	GTGCACATTTATTGACCTGCTTTCTTTTATGTGAGTAGTGTTATTTCTTATGT GCTATA

co3_96 19288_ x3	CM0006 75.2/411 80087- 4117998 1	22	0.009	28.2	3	ATCCTTTTGTAGTTTATAAGCGTGATGACTGGGGTTTCACGTGCATGTGTGAA ATGTGCCTTCCCCAAGCCTTGTTATGACCTCATTGGAACATTACCCCTTTGAC A
co3_96 23452_ x3	ENST00 0003627 01.1	14	0.009	28.2	3	TTGGGCAGTGAACACCCAAGTGTGCTTTATAGTTCCTTTGGCTTTGACTTTGT GCTAGAG
co3_96 26239_ x3	ENST00 0003635 48.1	25	3E-09	50.1	3	ATGCAGGTACTGTTACAATACTGATGTGTTTTGTTGTCGTTCCCCCTGCTT AAAGCA
co3_96 28090_ x3	AJ60948 2.1/1-130	24	1E-08	48.1	3	UGGACAUUUUUUUUUUUUUCAGUUUCUUCUCAAGGUGAAGAUAACUCUUUGU AAAUGUCCUACAGAAUUAUAGUAGCUUUCUGUUCUUCUUUGCAAGUAAAA AGGGUGGGUCGUUCCACUACUGACAUUU
co3_96 29443_ x3	AL13270 9.5/1804 73- 180397	18	#####	28.2	3	UGGAUCAAUGAUGAGUAUGCGUGGGGCAUCUGAAUCAAAUUAUUCUGAUUA UACCCUGUCUGUAUCUCUGAGGUCCA
co3_96 36247_ x3	ENST00 0003648 02.1	28	5E-06	40.1	3	TGGACCAATGATGAGTACCATGGGGTATCTGAAACAGGATTTTTGATTAAACC CATATGC
co3_96 37981_ x3	ENST00 0004594 75.1	16	0.0008	32.2	3	AGTTTGCCATGATGAAATGCATGTAAAGTCCGTGTTTCAGCTGATCAGCCTGA TTAAACA

co3_96 42187_ x3	CM0006 72.2/231 66985- 2316710 1	22	0.0001	36.2	3	AGCATTAAATCTACTGAAGATATCCACATCCTTAGACAGACGCAAAAAATAAAT TCTCTTTTGCAACTCAGAGCTCATTGTGCGGTATGAGCTTTGATACATATAAG AAGGAATATT
co3_96 45772_ x3	ENST00 0004592 01.1	22	0.009	28.2	3	ATCATTTTGTAGTTCATAAGCATGATGATTGGGCATTCACATGGATGTGTGAA ATGTGCC
co3_96 46633_ x3	CM0006 63.2/512 31356- 5123125 3	45	8E-09	50.1	3	ATTCTTTTGTAAATTCATAAGCATGATGACTCGGTATTCACGTGCATGTGTGAGA TGTGCCACCCTGGAACCTTGTTGCAACGTCAGCACATTATGGGTCTGACA
co3_96 47374_ x3	ENST00 0003844 52.1	40	7E-18	79.8	3	CTGCATTCTTAAACCCTCTTGGTAGCTTCGTTCTAAGTGCTTCCAAGATATGA GTGAATG
co3_96 52192_ x3	CM0006 68.2/927 90453- 9279066 5	31	#####	30.2	3	AAGACTCCTTTCAGGAATCATTCTTTAGTTCCTACTAGAGAGGCTTCTCTTAA CATGTGGAGCGCTGGAACCACAAAGAGGAGGTGCAGCATTCAAGTCTAAGT GTGAAGTGGATTCTTGGTGTGCTGTGCTGCAACTGCCATTTGCTAATGATGA CCTTGCTTTTCTTACTTAGAGTAAGACAGAGAGACAGCAGTCAGCCTAAGCG GT
co3_96 54991_ x2	ENST00 0003841 07.1	15	0.004	30.2	2	TGCCTCATTCTAGAGAATGGGCACTGTTGATCATGGTGTCCAAAAATAGTTAA TGTGGCT
co3_96 55031_ x2	ENST00 0005164 82.1	19	#####	30.2	2	ATGCACATCTGCTGCTATGGTTTCCACTACAGATGCAAGGAAAAAGTGTCTC GTCCTTT

co3_96 56437_ x2	ENST00 0005172 33.1	15	0.003	30.2	2	CTGCATTTTACCCTCCCTGATGGGGCTCAGTGTGCAGCAGCTGGAAAAAGTA GATGCCCT
co3_96 57267_ x2	ENST00 0003645 06.1	15	0.007	30.2	2	CTGCAGCTAGTTAACCTGACTTGTCCACCTCCCTGCTGGGGGCTCAGTGTGC AATGGTTG
co3_96 57311_ x2	ENST00 0003625 35.1	20	5E-06	40.1	2	AGCCTCATGCTAGATGAGAATGGGCACTGTTGATCAAGGTGTCCAAAAATAGT TAATGTG
co3_96 63145_ x2	ENST00 0003910 00.1	26	2E-07	44.1	2	AGGGAAGTGATGACAACTGTGACTGTTGTGTGACACTGATTTCTCTCATATTT GTACTGG
co3_96 64297_ x2	CM0006 64.2/699 12695- 6991279 9	15	0.004	30.2	2	ATCCTTTTATAGTTCATAAACATAGTAATTAGGTGTTCCCATTGCATGTATGAG ATGTGCCTCCCAAAGAGCTTGTTACAGCGTTAGTACATTACCTGTCTGATA
co3_96 64691_ x2	ENST00 0003640 09.1	20	0.001	32.2	2	TCACAATGATGAATGGTCCAAAACATTCGCGGTTTCCACCAGAATTCAAGGTG TTGGCAA
co3_96 67629_ x2	CM0006 72.2/121 45663- 1214576 6	14	0.008	28.2	2	ATGCTTTCGTAGTCCGTAGATGTGATGATTGGATCTTCACGCTCGTGTGTGAG ATGTGCCTCTCTCCAGCCTTGTTAGGATGTTGGAACATTACCCATCTGACA
co3_96 69043_ x2	CM0006 78.2/114 67641- 1146772 9	14	0.008	28.2	2	AACCTAAACATGACAACTGGGTTTTTCATGCTATTGCATGATACCTGCCTCCCT CAAACTTGTTACATCATCATATCACTCACCTGATA

co3_96 70257_ x2	CM0006 75.2/324 20516- 3242039 0	34	0.0001	36.2	2	AATTGGGATCAAAGATGCAGCCGCCTTCCCATTTAAGCAGCACAGACAGCCC AAAGTGACAGTTTTCTGTACAGTTACTCTTCTGTTATCTGTAAGTACTGATCTATG ACATTTTGGGAAAAAACAGCC
co3_96 70475_ x2	CM0006 79.2/195 57560- 1955771 1	25	3E-09	50.1	2	GCCCAGGGTATGTTACGGGGCGATGCTGCCCTCCCAGCTGGCCCATGGGT GACCCTGGGAACATTAAGTGCCTCACAACGTTTGTGCCTCAGTTACCCGTAG ATGTAGTGAGGGTAACAATACTTACTCTCGTTGGTGATAAGGAACAGCT
co3_96 71365_ x2	CM0006 65.2/129 074095- 1290742 02	14	0.009	28.2	2	AGCCTTTTGTAGTTTATAAGTGTGATGATTGGCTTTTCTCATTCTTGTGTGAGT GAGAACTTCTTTTCTCAAACCTTGTTATGATGTCAGCACATTACCTACCAGACA
co3_96 72219_ x2	AC02063 4.16/189 95-18865	16	0.0006	32.2	2	UGCAGCUGUGUCAAAUUUGGUGCCUGCCCUGCCUGUGUAGGCACUGACCC AGAAGGCUGCCACAGAAACACUGACUCAUGGGCCCUGUUCUGUGUCUCG GGCUCAGGGAUAAAUUUGGUUACAGAUACCA
co3_96 72987_ x2	CM0006 84.2/215 45125- 2154520 7	24	3E-06	40.1	2	CAGCCAATGATGACGTGGCCACCGCACAACTGAGTTCTGGGAACCATGTGA TGGAATGTGTTCTGGGAATAGACTGCAGCCA

co3_96 73379_ x2	CM0006 64.2/218 185082- 2181849 79	14	0.009	28.2	2	ATACTTTTGTAGCTCATAAGCATGATGATTCAGTGTCCAAGTGCATGCATGAG ATGTGCCTCCCTCAAACCTTGTCAACATCAGCACGTTGCTCATCTGACA
co3_96 74549_ x2	CM0006 63.2/122 21271- 1222114 8	22	0.009	28.2	2	CTAGAAAAATTGAAGATTTGGCCACTCTGGAAACTGCTGAGGGCCCCATGTG TAATGGCTGCAAACAGCTTCCTTTGTTGTGTAGACAGCCTGAGTTTTTCTCTAA GGGACTATGGAGACAGCC
co3_96 75351_ x2	ENST00 0003626 96.1	42	2E-09	52	2	GGCCTCTCAGTGCCGCTTAATCACACAGGTCCAGTGTGTGCTTGGTGTCTTTT CTGGGAG
co3_96 76467_ x2	ENST00 0004085 28.2	15	0.006	30.2	2	AAGACTCCTTTCAGGAATCATTCTTTAGTTCCTACTAGAGAGGCTTCTCTTAA CATGTG
co3_96 79169_ x2	ENST00 0003909 04.1	14	0.008	28.2	2	AAAGCAAGCTGGAATTACAGTGCTTCATTTTGTGAAATACTAAATACCATCATT ATGCTG
co3_96 79543_ x2	CM0006 63.2/491 51390- 4915150 3	14	0.008	28.2	2	ATAGTTTAAAAAATTTGTTAAGCATGATGATTAACTTTTTACAATAATGCAATAA TGTGTGAGCTATGCCTCTCTCAAACCTTATTATGATGTTGGCCATTACCCAT CTGATG
co3_96 80181_ x2	ENST00 0003909 93.1	14	0.008	28.2	2	TTCAGATGATTTGAATTGATAAGCTGAGGTTCTGTGAGGAATGACAGTTAAGA GCATGTT

co3_96 80471_ x2	CM0006 69.2/138 482583- 1384824 80	17	0.0002	34.2	2	ATCCTTTTGTGGTTCATAAGCATGATGATCAGGTTTTTCAGGCATATGTGTACG ATGTGCCTCCTTCAAACCTTTGTTAGGATGCTACCACGCTACCCATCTGACT
co3_96 81185_ x2	BA00002 5.2/1065 47- 106465	20	2E-06	40.1	2	UGGGAGUGGUAAUGAUGAUCUGGUUGGACAAGAGUCUCUGAGCUUUUCUC UGAGGAUCUUUGAACCCACCUGAUCCACCUUCA
co3_96 81695_ x2	ENST00 0005788 36.1	18	4E-05	36.2	2	CTGCAGACAGTTAAGCCAACTGAGTTCCTTTTCCTCAGGGAGGCCCAAGTGTAC AATGGCTG
co3_96 81757_ x2	ENST00 0006307 37.1	31	1E-12	61.9	2	GAGCACTGCTTTAGAGCCTCTGCGTGTCTGGCTGTGGCCTCAGGGGTCTAGC AGCAGTGC
co3_96 83337_ x2	CM0006 67.2/138 559039- 1385589 70	24	1E-08	48.1	2	GTGCCGTGATGTATTTGTCAACACATCACTCTGAAGAAAAGTATGTGGTGACT TTCTGTGACTGAGCATG
co3_96 85657_ x2	CM0006 63.2/171 768070- 1717681 75	15	0.003	30.2	2	CACCCCTTTTCTCCTCAGCCAAGGCTAGAGGCCAAGATCAGCCCTCAGGGAT CATCATCAGGACTGCCATGAGCTGAGCTGCCTTGTTTTCTGCCGAAACAT GT
co3_96 86409_ x2	BC02823 2.1/151- 277	26	8E-10	52	2	GUUGGUUGAAAAUCGCCCCCGGCUUUGGCCGUGGCCGCGGGUGAGAUUC GGCGCCCAGAGCCCCCGGGGGCCUCAGCUCACCGCGCGCUGCCCCAUGU GCGGCGGUGAAACCCAGGCCCCGACAGGC

co3_96 91283_ x2	CM0006 85.2/881 48792- 8814891 8	14	0.008	28.2	2	GTTGGTTGTGAATAACCCTTGGCTTTGATTGTGGCTGTGGATGAAATTCAGCA CCTACAGCCACCAGTAGCCTTAGCTCACCACCCACTGTCTCAATATCATGGGT AAAACCCAGGCTCTGACAGGC
co3_96 92659_ x2	ENST00 0003844 92.1	15	0.003	30.2	2	CTGCAACCAATTAAGCCGACCTAGTTCCTTTCTCTTTGGGGCCTGGTGTTCA ATAGCTG
co3_96 92801_ x2	ENST00 0005160 87.1	17	0.0002	34.2	2	GGATCGATGATGACTTAAAGATTTATCTAATTTAAATCTGAACAAAATGAGTGA CCAAAA
co3_96 94563_ x2	CM0006 78.2/686 30968- 6863086 4	27	0.006	30.2	2	TAGTGTGGAAGTGTCTACTCCTCATTCTGTGGAAGCAGGAATACATTCATAA CATGCTCCATTAATAAAGGAGTTCTAGGCCAGGCAGCGTGCCTCATGCCTGG
co3_97 01909_ x2	CM0006 74.2/645 75665- 6457574 1	16	0.001	32.2	2	GCCAAATGATGCTTATTTGACTCTGGTGCACTTCAGTGTAAGGATGATTTATA ATCTGTCACTCATGATTGAAGGCC
co3_97 03327_ x2	CM0006 72.2/601 7194- 6017054	15	0.007	30.2	2	ATGCATCTTAGAACATCCAGGAGACAGTCTTCTAAAATACCAGTGAGTGGCAA GATATGAGTAAATTCACAGGAAAAGGAAGGCAGTCCAAAGGGCTGTGCTTC TCCTGTGGCTCAGTGTTATTCATAGCTGTGACATCT
co3_97 03849_ x2	ENST00 0005843 02.1	26	8E-10	52	2	CTACCAAAGTTAGCTTTTTGGGGGCAGTTTTTAAGTAACCTTTGCCAACT TGGGCTA

co3_97 05133_ x2	ENST00 0004590 83.1	34	2E-14	67.9	2	GGTGCAAATGATGCATATGTTAGCGACCAAAGCCTGATCTTTGCTGATTAGTC ATAATTA
co3_97 06143_ x2	AK02448 6.1/3319- 3428	23	4E-08	46.1	2	UGCCCAGUGAUGACACCAUCCUUGCUCCCCCGUGCCCCCAGGGGCUAUGG GCGACACCAUGGCUGCCCCUGGGCUGGGCCAGUGGGGCCAAUGCCCAGG GGCUGAGGGCA
co3_97 06733_ x2	ENST00 0005816 69.1	14	0.009	28.2	2	TGCTGGTGGTGAAGCTCCCTCTCTCCGAGCACTGGGCCCTGCCTGGGGTAA GGCT
co3_97 08441_ x2	CM0006 70.2/561 21352- 5612124 2	31	4E-10	54	2	ACCAAGATTCAAGTCACATTCCGAGTGTCCCGGTGTGCTAGGGCACTTGCCAG AGAATCTGCTGGTCTTGATTCACTGGTGGGGCAATCGGTGCCCAGATTAGG AACATGC
co3_97 08937_ x2	ENST00 0003838 65.1	17	0.0001	34.2	2	GTGGAGGTCTATTCCAATGGGGCTTTTCCTGTAGCTGCATGTTGTTGGAAACT CCTCATA
co3_97 10099_ x2	ENST00 0003911 96.1	45	6E-16	73.8	2	GATCACGGTGATGGCTGACCAGGGCTCCCTGACCTATACAGGCCTCTGCTAT GGGGGTGA
co3_97 10481_ x2	CM0006 78.2/122 97323- 1229719 7	15	0.003	30.2	2	ATTACTTGAAAATCACTCCCAGGCTTTGGCCATGGCAGCAGGTGAGATTCAA GGCCCAGAGCCTCCAGGGCCTCAGCTCACCGCACACTGCCCCGTGTGTGGT GGGAAACCCAGACCCCAACAGGT

co3_97 11173_ x2	CM0006 79.2/350 54494- 3505438 8	15	0.002	30.2	2	ATTATTTTGTGTTTCATAAGTGTAATGATTGGATTTTCATGCACATGTATGAGAT GTGCCTCCATCAAGCCTTGTTACTACAAAGTCAGTGCATTACCCATCTGATG
co3_97 13057_ x2	ENST00 0003645 95.1	29	0.0002	34.2	2	AGCCTCCTGGTGCTCAGCACAGGATGTGTTCTTACCCTAACCAAATAGAAAGA GTAGGCT
co3_97 15043_ x2	CM0006 69.2/664 34507- 6643461 8	16	0.0006	32.2	2	AGCCTCCCAAAGCACTGGGAGTGTGATGACTAGGTTTTCCACTGGGTTTTTC ATGTGTGAGATATGCCTTGCTCAAACCTTGTTACAGCACTGGCACATTGCCTG TCGGATG
co3_97 19117_ x2	ENST00 0003639 15.1	22	1E-07	44.1	2	TCCCAATGATGAGTTGCCATGCTAATACTGAGCCACCAGGTAGGGCAGTGTT GCCCTGGT
co3_97 19989_ x2	ENST00 0003840 04.1	23	5E-08	46.1	2	TTCTAAAGTGTTGAGTTCAGTCCAGGGTGGATCCCCTGCTCTGTTAATTGAAC TGGAACA
co3_97 23867_ x2	CM0006 85.2/714 40644- 7144051 7	20	0.0007	32.2	2	ATCTTTTTGTAGTTCATAAGCTTATGATGACGTAAGTGTGACGACATTGGGTTT TCACGTTTCATGTGTGAGATGTGCCTCCCTCAAGCCTTATTACAATGCCAGTAC ATTTTTTTTCCACATCTGATG
co3_97 24929_ x2	CM0006 82.2/564 75643- 5647574 5	15	0.007	30.2	2	ATTCTTTAGTAGTTCATAATGCTATGATTGGGTTTCCATGTGCACATGTAAGAT GTGCCTCTCTCAAGCCTTGTTGTGACATCAGCACATTACCCATCTGATG

co3_97 28625_ x2	CM0006 72.2/101 371952- 1013718 52	33	0.0004	34.2	2	ATCCTTTTGTAGTTTGTAAAGCATGACGATTGGGTTTTTCAGCCTCATGTGTGAG GTGTGCCTCCCTCAAACCTTGTTACATAGGCACATTACCTGTCTGGCA
co3_97 33119_ x2	AC10476 3.12/682 86-68156	20	2E-06	40.1	2	UGCCUCUCUCCCAUGGGCUUUGGGGGGUCCCUGUUCUCCUUAGCCAAGGC UGGAGGCCAAGAGCAGCCCUCGAGGAUCGUCGUCAGGACUGCCACGAGUG GGCAGCCUUGUUUCCUGCCUCAGACAUGU
co3_97 37289_ x2	ENST00 0005163 13.1	15	0.006	30.2	2	AAGATTCGACAGATAACCCTACTGCCTCTCTTTGTGGCGGCGGGGCTCAGGCT GCAGCACC
co3_97 38139_ x2	CM0006 78.2/188 70269- 1887016 6	19	0.006	30.2	2	ATCCTTTTGTAAATACATAAGCATAATGATTGGGTTTTTATTTTCACATGTTTGTAT ATGCCTCCCTCAAATCCTCTTATGATGTCAGCACATTACCCATCTGAGG
co3_97 42435_ x2	ENST00 0003844 48.1	15	0.003	30.2	2	GGCCTCCTGGTGCTTACAAGCAGCTGTGTGCTTGCATTGACTGTACAGAAAA AAAGAGAT
co3_97 43871_ x2	ENST00 0004102 53.1	15	0.002	30.2	2	TGGACCAATGATGTGAATGGAATGCATCTGAATAAAAATTATGATCAATCAGTT TTTGGAT
co3_97 45063_ x2	ENST00 0003626 03.1	27	0.004	30.2	2	GTGCATGTACTGTTACAATCTAACTGAAGTATTTTATTGTTACCCCTGCTTAAA GCAGTA
co3_97 56573_ x2	ENST00 0004588 63.1	31	2E-05	38.2	2	ATCCTGTTGTAGTTCATAAGCATGATGATTTGGTGTTCACGTGCATGTGTGGG ATGTGCC
co3_97 57403_ x2	ENST00 0003909 81.1	26	8E-10	52	2	ACTGAGGAATGATGACAAGAAAAGGCCGAATTGCAGTGTCTCCATCAGCAGT TTGCTCTC
co3_97 60825_ x2	ENST00 0005167 92.1	19	0.004	30.2	2	GAGGAGGTCCATTTTAAAAAAGAATAGATTGAAATGCCTCATAGAGTAACTC TGTGGTT

co3_97 66385_ x2	CM0006 64.2/709 30415- 7093030 3	15	0.002	30.2	2	GTCCTTTTGTAGTTCTTCAGCAGGATGACTGGGTGTTTCATGCTCCTATGTGAG ATGTGCTTTTCTCAAACCTCAAACCTTGCTGGCAAGCAGTGAGTCAAGGCTGT TCTGAGT
co3_97 69245_ x2	ENST00 0004591 24.2	22	1E-07	44.1	2	GTGTTCAATGATGATTTCTATTTGTTTGCCTGATTTCTTTTGGATAATGAAGG CATCTT
co3_97 74633_ x2	CM0006 64.2/754 89576- 7548971 0	14	0.008	28.2	2	CTGTGTGTAGAAATGTTTGTCTCTATCCTTTGGGAACAGGAATACATTCAT AACATGCTACATGTAAAAAGGACTCCCCAGGGTGGCCAATCTTATGGTAGAG GTTGTATGGTAATATATTTCTCCTTCATAA
co3_97 76839_ x2	ENST00 0003843 70.1	25	0.0003	34.2	2	CTGCAACCAATTAAGCTGACTGAATTCCTTTCTCCCGGGGGCCAGGTGTGC AATGGCTG
co3_97 79939_ x2	AB06184 2.1/1832- 1898	35	5E-15	69.9	2	UGGCGAUGAGGAGGUACCUAUUUGUGUUGAGUAACGGUGAUAAUUUUUAUAC GCUAUUCUGAGCCAGCA
co3_97 84327_ x2	AF25084 1.1/1768 78- 176958	14	0.009	28.2	2	GGGGCAAUAUGGAGAUGUUUAUUAUUGUCUUCGACAGGGAAGAUGACAUAAAA AUUAUGUUCAAUAGGAUUUAUGUGGAGACUU
co3_97 91267_ x2	CM0006 77.2/406 07312- 4060721 2	19	0.004	30.2	2	ATCTTTTCGTAGTTTCATAAGTGTGATTGGGTTTTTCACACGCATGTGTGAGATGT GCTTTCTTCAAACCTTTGTTACGATGTTGGCACATTATACATCTGACA
co3_97 93117_ x2	CM0006 84.2/249 01214- 2490114 7	19	0.007	30.2	2	CCGCAGTGACAGCAATATTTTTTCATCCACAGTTCACCTCATGAATGTTGTAC TTTGGGTCTGAGTGA

co3_97 93625_ x2	ENST00 0003908 33.1	23	4E-08	46.1	2	TGTGAGAGTGATGAGTTGCACACTGGTGGAGCCATGGTATCAGGTGATACAG GCACCACT
co3_97 97917_ x2	ENST00 0003632 19.1	15	0.003	30.2	2	TGAGCAAGCGATGACAGCCGGTGGTGTGTGAGTCATGGAGGATGAATACTAA GTGCCTGG
co3_98 04627_ x2	CM0006 64.2/183 064346- 1830642 35	24	3E-06	40.1	2	GCAGACTCCCTCAGCATCCAGCGGGTGCTTTTTCGGTCTGCCAGTGAGCATT CCATGGTGCTGTGACCATTTTGACCTCTCTAGGGTGATGCAGCTGCCTGGGG ACACAGAG
co3_98 07709_ x2	ENST00 0003624 93.1	24	1E-08	48.1	2	AGGCAGGATCTAGTTACATTGTAGCTGTGAAGTGCTGCATTGTCTTTGCCCC TGCTCAA
co3_98 16233_ x2	CM0006 72.2/100 019594- 1000196 99	27	0.003	30.2	2	GTCATTTTGTAGGTCATAAGCATGATGATTGAGTTTTTCATGCTCATGCGTGAG ATGTACCTCCCTCAAACCTTGCTACAACATTGGTAATGTACCAATGTCTGACA
co3_98 18833_ x2	AADB02 016115.1 /24955- 25031	15	0.005	30.2	2	UGGACCAAUGAUGAGACAGUGUUUAUGAACAAAAGAUCAUGAUUAAUCCAG UUCUGCACAAAACACUGAGGUCCAUU
co3_98 24971_ x2	CM0006 66.2/139 436494- 1394363 68	21	1E-06	42.1	2	ATTGGTTGAAAATCACCCCCGGCTTTGGCCATGGCAGCGGGTGAGATTCCGG CGCCCAGAGCCTCCAGGGGCCTCAGCTCACCGCACGCTGACACATGTGCGG CGGTGAAACCCAGCCCCAACAGGC
co3_98 28857_ x2	ENST00 0006275 61.1	17	0.0004	34.2	2	GCGCTGCCTTTGTACCCACCGTGCCTCCGCCTGGTGTCTGGGGTCAGGTT GCAGTGCCA
co3_98 33797_ x2	CM0006 73.2/628 54285- 6285416 1	14	0.009	28.2	2	CTCCAATGAGGAGGAAACATCCTGCCTTACCCCTGTTTTAGCCTGGGAACCA GTAATTGTGAACTCACCAGGGTTAACATGAAGAGGGCATGAGAGCTTATTCCA TAAGGAATTGTCTGAGACAT

co3_98 35943_ x2	AF25084 1.1/1432 08- 143289	28	6E-11	56	2	GGGUCAAUGAUGAGAACCGUAUUAUUGUCCUGAAGAGCGGUGAUGACUJAA AAAUAAUGCUCAAUAGGAUUACGCUGAGGCC
co3_98 36487_ x2	ENST00 0003842 75.1	21	0.0004	34.2	2	TGCAGCTGTGTCAAATTTGGTGCCTGCCCTGCCTGTGTAGGCACTGACCCAG AAGGCTGC
co3_98 40517_ x2	CM0006 72.2/267 89017- 2678915 7	15	0.003	30.2	2	CCTCATTTCCTTGGCAGGAACCTTGTAGTCCCCTGTTATGTACAGAGGC AAAGGGAAGAGCTCTGGCCCCCTTGGCATGTCTTTGGAGCCATGCAGCTTCC CGTCTGCCAGTTCTATCCTCAAGCACCAGGACACCA
co3_98 42255_ x2	ENST00 0003647 64.1	14	0.009	28.2	2	GGGTCAATGATGAGATGTTACCTTGAAGAGAAATGATGACGTAAAAATTAAGT TCAGTTG
co3_98 44811_ x2	CM0006 65.2/608 56605- 6085638 9	15	0.008	30.2	2	AAGATTATATTTCCAGGGTCAATTTCTGTGGTTCATTAATAAGGAGTTTCCC CAAGTGTGTAGAGCACTGGAAACCACAGGAAGATATGCAATGTTCTCTCCCG AGCACGAAGCTCGTTCTTGGTGTGCTTCATTGCAACTGCCATTTGCCATTGA TCATTGTTTTTTCTTCTTTGGGGAGATTAAGAGGAAGAGGACACAGTCTGA GTGAT
co3_98 57099_ x2	AC00702 5.2/1358 7-13714	14	0.008	28.2	2	CAGCACUGCCAAGUGACCCAUUGGGCUCCAUCUUGACCAACUGGGCAUCA AGCGGUGCAAAGCAAUCCUCUCAAGCUGGGAGAGUCACACCGUGGG CUACUCCUGCAUGCAGCUGGGUACAUAU
co3_98 62255_ x2	ENST00 0005170 59.1	16	0.001	32.2	2	TCAAATGAGCCTGAGCTGACATTGTAGAGGATGTAGATGGCTGAAGAACTG TTCAGCTG
co3_98 65421_ x2	ENST00 0003911 26.1	15	0.004	30.2	2	GGGTCATGAGGAGGTTTGTAGACATAAAAATTATGCTCATAAGTATTATGCTG AGACCC
co3_98 65425_ x2	ENST00 0005172 63.1	15	0.005	30.2	2	TGATGACACTCTCTGGAATTGTTACTACTACCATAATTAAGTGCCTGAATCTT TTTCTA

co3_98 66683_ x2	ENST00 0003912 84.1	23	0.003	30.2	2	ACCTCTGCTGGGGTGTTTAAAGGTCAGCGCTGTAGATATTCAGCATCTGGCA TCTTGGCT
co3_98 77153_ x2	ENST00 0004087 46.2	15	0.002	30.2	2	AAGACTTTATCCCCCACCCCGCAAAGAAAAGGAAGAAGAAGAGTTTTTAAAT GGCGCAG
co3_98 88217_ x2	ENST00 0005166 18.1	16	0.001	32.2	2	TATAAATGTGATGAATTGCACACTCGCAGAGTCATAGCATTAGGGGATGCAG GCAGTGTT
co3_98 91115_ x2	ENST00 0005164 40.1	36	0.001	32.2	2	GTTGAGGTCTAACACGATAGGGCTTTATCTGTAGCCACACCATCTGGAAACAT CTAGTGT
co3_98 92605_ x2	ENST00 0005161 78.1	17	0.0001	34.2	2	GTGTGGGATGTGTGTCTAAACACGACAATCTGAAGACAGAGGTGTAGAAATT GGCAAGTT
co3_98 98399_ x2	CM0006 64.2/232 678963- 2326790 65	14	0.009	28.2	2	ATCCTTTTGCGGTTCCATAATGTGATGACTAGGTTTTTCATGTCCATGTGTGAAGT GCGCCTTCTCCAATCCTGTTAAGATGTCAGCACATTTGCCTTCTGACA
co3_99 03973_ x2	CM0006 69.2/561 00659- 5610075 2	14	0.009	28.2	2	ATCCTTTTGTAGTTAAGTGTGATGACAGGGTTTTTCACACTCATGAAGTGTGCC TCCCTCAAACACTGGTTGCATTGACACACTACCCATCTGACA
co3_99 04717_ x2	ENST00 0005162 02.1	14	0.009	28.2	2	AGGACGTCAAACCATCATAAAGTATAGATCTCCACAGGATGCCATAGTGAATA GTGCTAT
co3_99 04763_ x2	CM0006 72.2/214 85638- 2148572 2	14	0.009	28.2	2	AAGACTGTATTTTCAGAGCTCATTTCTGTAGTTCATTACTATGGAAGTTTCTGT AAATATATAGAGGTCTACAAAACAAAAAAGT

co3_99 06443_ x2	ENST00 0003846 14.1	15	0.004	30.2	2	TTGCACAGTGAACACCCAAGTGTGCTTTATAGTTCCCTTGGCTTTGACCCTGT GCTAGAG
co3_99 09739_ x2	ENST00 0003912 56.1	15	0.003	30.2	2	GTGCCTAAGGTTAACACAGCGCCTTAAGAGGCTAACACAGAAGGGCAAAGTA AGTCTCCA
co3_99 10211_ x2	BC03658 2.1/1156- 1210	16	0.0008	32.2	2	GGGGUGAUGAAGGCCUGCACCUGGUCCCCUCCCCAACUCUGCUCUGCUCC UGAAG
co3_99 16043_ x2	ENST00 0003653 13.1	15	0.003	30.2	2	TTACCAAAAGTTAATGTTTTAGAGAATGCTTTGGTTAAAAAGCCTTTACCAAC TTGGGC
co3_99 17627_ x2	ENST00 0005165 40.1	15	0.003	30.2	2	CTGATTCTTTGTACTAGGATGCAAAGAAAACAATCCTTGTGCCTTCTATCTCT CTTGGT
co3_99 27243_ x2	CM0006 68.2/100 957160- 1009572 63	15	0.006	30.2	2	ATCCTTTTGTAAATTTATAAGCATCATGGTTAGGATTTAATGCTCATATGTGAGC TGAGCCTCCCTCAAACATTGTTAGGACATCAACACAATACCAGTCTGATA
co3_99 27449_ x2	CM0006 67.2/122 796088- 1227962 27	15	0.003	30.2	2	ATTCTTTTGTGGCTCATAAGCTTGGGATTTTCACTAAACATTTTAACTCAT GAGGTTGGGACTTCACATTAATCTCTAATCTTTGAGATTGCCTCCCTCAAACC TTGCTACAGTATTGGCACATTACCCATCTCACA
co3_99 31167_ x2	ENST00 0005159 87.1	15	0.003	30.2	2	GATCAGCTTTTCAAAGGTTTACTGCATTTTACCCTCCCTGATGGGGCTCAGTG TGCGCAG
co3_99 31405_ x2	CM0006 69.2/548 5395- 5485501	19	0.003	30.2	2	ATCCTCCTATAGTTCCTCAATGTGATGACTGGGTGTTCACTCATTGGCGAG ATGTGCCTCTCTCAAACCTTGTTAGATGCTGCAGACACATTACCCATCAGAT G
co3_99 41009_ x2	ENST00 0005164 68.1	28	0.001	32.2	2	GGATTGACGATGACTTTAAAAAAAAAAAAATCTCATTGAAATCTGAAAAAATGA GTGACC

co3_99 43255_ x2	ENST00 0004590 70.1	15	0.005	30.2	2	ATTGGTTGAATATCACCCCTGGCTTTGGCCATGGCCATGGGAGAGATTTGGC ACCCAGAG
co3_99 45737_ x2	ENST00 0004589 74.1	22	1E-07	44.1	2	TGGACCAATGATGAGACAGTGTTTATGAACAAAAGATCATGATTAATCCAGTT CTGCACA
co3_99 48399_ x2	CM0006 79.2/693 55283- 6935513 3	27	0.003	30.2	2	TGCACCTGTTTGAGGAATAAAGGAATTA AAACTCCCAAAGAGGACAAATATT AACAAAAATGTATGGACAGACGCAAAAAACAAATCCTCATTGCAACCCAGA ACTAATTGTTTAGTATGATTTTTGACACATATAAGAAGGAGTATT
co3_99 53483_ x2	ENST00 0004593 73.1	19	0.004	30.2	2	GTTGGTTGAAAATCGCCCCGGCTTTGGCCGTGGCCGCGGGTGAGATTCGG CGCCAGAG
co3_99 57335_ x2	ENST00 0005159 06.1	19	1E-05	38.2	2	TTCACAATGTCTATTGAAGGATCTCATCACCTTTAGAGAGCTGTGGTCATGCC CCTTAAA
co3_99 60053_ x2	ENST00 0006074 17.1	20	2E-06	40.1	2	CAGCATTGTGCAATGGCCTTTGGTTTTTCTTGTAACCAGTTAGGTCTGAAACC AATGCAA
co3_99 67585_ x2	ENST00 0003908 89.1	27	0.004	30.2	2	AAATAATTAATTTCTCCAATAGCTGGAGTTACTGGCAAATTGTTTAGTGCCA AACATG
co3_99 69105_ x2	CM0006 85.2/118 738055- 1187381 82	14	0.008	28.2	2	TAGCACTGTTGCCTGAGCCATTGGTGCTCCCTGGTACTAGCTCAGTTTTAATG CAGTGCAATAGGAATTCCTTTGTTTCCACAAGGCCTGTCTGTGGGCTGC TCCTTCCCACAGTTGGACCTTG
co3_99 75207_ x2	ENST00 0005781 83.1	14	0.009	28.2	2	AACATAGAGTACACATTTTCTGTTTTGTTAAGAATTATTCTCTTGCAGACCTAT GTTTT
co3_99 80723_ x2	ENST00 0005172 85.1	15	0.002	30.2	2	TTCCTAAAGATTCACAATGAACATTATTATTTAAGAGCTTTTTGAAGTGCAAAT CCATGA

co3_99 82125_ x2	ENST00 0005171 60.1	16	0.0008	32.2	2	CTAGAAAAATTGAAGATTTGGCCACTCTGGAAACTGCTGAGGGCCCCATGTG TAATGGCT
co3_99 83939_ x2	ENST00 0003656 47.1	14	0.009	28.2	2	AGACTCCCAGCTCTGCCAGTTACACTAGGCTTCGCCTGTGTGGCTTCTGTA ATGGGGAG
co3_99 84365_ x2	ENST00 0004592 78.1	14	0.009	28.2	2	ATCCTTTTGTAGCTCATAAGCAGGATGACTGGGTTTTCCACTCAGGTGTGAG ATGTGCC
co3_99 85511_ x2	ENST00 0003651 89.1	23	0.003	30.2	2	AGCCTCATTCTAGATGAGAATGGGTACTGCTGATCATGGTGTCCAAAAAATT TATGTGG
co3_99 93327_ x2	AC02349 0.5/1218 42- 121984	16	0.0007	32.2	2	UUCUCAGGUCGCCAGUGCAGCCCCAAGAUGAGCCUGCAGUAUUUCCUUA CAUGAUCUGGUCCUACUGUGGGCAGCGCUGCUGCCAGAGCCUGAGAGGA UUAUGAAAACAUGGCAACGGAAGUGAGGCCAGGGGACACAGCA
co3_99 94299_ x2	AC09022 7.10/155 87-15444	20	2E-06	40.1	2	CUUUCGGGUCCCCAUUGCAGCCCCCGGAUGAGCCCGCAGUAUUUCCUUA UAUGAUCAGGUCCCCAUUGC GGGCGGCCGCUUGCCCGGAGCCUGAGAG GAUUAUGAAAACGUGGCGAGCGAAAUGGGGCCAGGGGACCUGGAG
co3_99 95207_ x2	CM0006 73.2/855 5016- 8555146	14	0.009	28.2	2	GACCTCTCTCATAGGGCTGTAGGGGATCTTTTTCTCTTCAGCCAGGGTTG GAGGCCAAGATGGCCCTTGAGAATCATCATGACTGCTGAGAGCTGGGCA GCCTTGTTTACCTCCCTTGGGCATT
co3_99 98483_ x2	ENST00 0005163 29.1	14	0.008	28.2	2	AGCACTTGATGTTTTAACATGTGGACATTTATAGACAGGTTCAAAAAGTCCTC TTGCAA
co3_99 98713_ x2	CM0006 63.2/568 0952- 5681026	14	0.009	28.2	2	CTCAGCTGGGCTTTTTTAAAGTAACAAGTGACTGGGCCACTGACATGTAAAGA GGGAAGTGAGGTGCTCCTGGAG
co3_10 001378 _x1	ENST00 0006127 41.1	15	0.006	30.2	1	CTACAATCAATTAAGCCACATGGGGCCTGGTGTGCAAGGGCTGCAAACAGCA GCATCCTA

co3_10 003567 _x1	ENST00 0005161 58.1	16	0.0007	32.2	1	ATATAGTTGGACTCAACACCTCTCTATCAGAAATGGACAGATCCAGATCATGA AGAGATT
co3_10 003769 _x1	CM0006 67.2/659 61319- 6596118 3	15	0.005	30.2	1	TCACATTTTATCAACCAAATGAATTAGGGAAAAAAGTTCATGCCCAGGGGTGA GACTATAGTGCCAGAACACTTGCTTGTGCATAATTAAGGCCACTTGCCCTCTT CAGGTAGCCCTTTTAACTGGGAGCAAAGTGA
co3_10 006260 _x1	CM0006 73.2/927 29415- 9272933 0	14	0.008	28.2	1	GTCCATTTGCAGTTCATAAGTGTGATGACTGGGTTTTCCACACGTGAGAGAT GTGTCTCCCTCAAATCTTATTACCCATCTGATG
co3_10 006288 _x1	ENST00 0004593 16.1	14	0.009	28.2	1	TTGCATGAGGAAGTATCTGCTCTTCATTCCCTTTGGGAGGAGAAATACATCCAT AACATGC
co3_10 009678 _x1	ENST00 0005164 49.1	15	0.005	30.2	1	TCCCATCTCTTAAATAAAAAGATTTTTTTTTTAAGAAGTTGTACATGTGCAATG GCTGCA
co3_10 011491 _x1	CM0006 85.2/328 48005- 3284790 7	14	0.008	28.2	1	ATCCTTTCGTAATTCATAAGCATGATTTGGGTGTTTATACTCAGATATGAGATA AGCCTTCTCTAAACTTATGATGTTGGCACACTACCCATTTGATA
co3_10 013325 _x1	ENST00 0005163 20.1	15	0.008	30.2	1	GCCAGCAGTCGCCAGGTGTCTCTCACGCTGCTGGGAGAGGAATGTCTCGTC TTCTTCATC
co3_10 015707 _x1	ENST00 0003911 59.1	22	0.009	28.2	1	ATTTTACATAGCGCTGCAGATGTGGCTGCTGTGTACATTTGTGTTATTAGGT GGCAGAG
co3_10 021566 _x1	ENST00 0004081 98.2	14	0.009	28.2	1	AAGATGACACTTTGAGGCATCGTGTCTATGGTTCATTACTACAGAAGCTTCTC TGGATGT

co3_10 022634 _x1	ENST00 0003910 95.1	19	0.004	30.2	1	ATTCTTAAATGAATGATGAAATACCAAAAAGAAAAATAAGCAAAGAACAGATAA CAGAAA
co3_10 023187 _x1	CM0006 85.2/485 61801- 4856170 2	14	0.009	28.2	1	ATCCTTTTGTAAATCAACAATGTGATGATTGGGCTTTCACACTTGTGTGAGATG CACCTCGCTCAAACCTTGTTAACATCTGCACGGTACCTGTCTGAAG
co3_10 026103 _x1	ENST00 0005163 10.1	16	0.0008	32.2	1	GTTGGATGAAAATCATCCCGGGCTTTGCCAGTGGCCGCGAGTGCCCAGAGC TTCCAGGGG
co3_10 026839 _x1	CM0006 84.2/176 41519- 1764140 6	15	0.005	30.2	1	ATCCTTTTGCGGTTCATAAAGAACCAAGATGACTGGGTTTCATGCTAATGCAT GACATGTGCCTCCCTCAAATCATGTTGCCTCATGGGCTTATTGGCACATTACC GTCTGAGG
co3_10 030747 _x1	ENST00 0005160 84.2	15	0.003	30.2	1	TCCATTTTCAGAAAGCCGAGGTCAAATAATGAGTCCTGGGGAATTCAAACCTTG TGTTAAG
co3_10 031791 _x1	CM0006 63.2/204 727991- 2047281 06	16	0.0005	32.2	1	CGCCTTTCTCCCATGGGCTGTGTGGGGTCCCTGTTCTTCGCAGCTAAGGCTG GAGGCCAAGATCAGCCTTTGAGGACTGTCATCAGAATTGCCTTGCTTTCCTG CCTCAGATGTGA
co3_10 032062 _x1	ENST00 0005164 27.1	17	0.0003	34.2	1	GGTCTCTTGTGTCGGCACCTGGGTGGCTTGCCGCCACACAACCAAATTA AAATAACA
co3_10 032252 _x1	ENST00 0003650 37.1	16	0.0007	32.2	1	GGGTCAATGATGAGAACCTTACATTGTCCTGAAGAGAGATGATGACTTAAAA TCATGCT
co3_10 038023 _x1	ENST00 0003635 28.1	15	0.004	30.2	1	CAGTCAGTGTGAGAACCTTATATTGTTCTGAAGAGAGGTGGTACTTAAAA TCATGCT
co3_10 040085 _x1	ENST00 0005168 48.1	15	0.003	30.2	1	CTACAACCAGCTACTGGTTGATCTTACATTTGATCTGGTGTGCAATGGCTGCA AACAGCA

co3_10 043969 _x1	CM0006 63.2/136 96199- 1369607 0	15	0.003	30.2	1	AGGACTTGCCTCATTAGTAATACAACCAAGCTGATAGGGTAGTTTGGCAGGA CACACAGCCATTTCCCTCTCAGCTTAGGAAGGCTGTCATAAGACTAGGACTA GCTCTGCAAGGCAAGAGAAGGACAAT
co3_10 048336 _x1	CM0006 71.2/623 58285- 6235819 1	14	0.008	28.2	1	CTACAATCAATTAAGCCACATGGGGCCTGGTGTGCAAGGGCTGCAAACAGCA TCATCCTAGGTAGTGTACAGCAGCCTGTTCCCTTGCGTACAACA
co3_10 051202 _x1	CM0006 64.2/883 07360- 8830746 3	15	0.005	30.2	1	ATCCTTTTGCAGCTCATAAGTGTGATGATTGGGTTTTCACACTCATGTGTAAG ATGTGTTTCCCTCAAACCTTGCTATGATATCAGCACAGTACCTATCTGACA
co3_10 053017 _x1	ENST00 0005162 07.1	14	0.009	28.2	1	GTTGGTTGTGAATAACCCTTGGCTTTGATTGTGGCTGTGGATGAAATTCAGCA CCTACAG
co3_10 059331 _x1	ENST00 0003841 59.1	15	0.003	30.2	1	CTGCAGTCAATTAAGCCAGCTGTACTCCTTTCCTCACAGGGGCTCGGTGTAAT GGCTGCA
co3_10 062447 _x1	CM0006 74.2/101 358849- 1013587 48	14	0.009	28.2	1	ATGCTTCATAATTTATAAGTGTGATGGTTGGGTTTCTATGTTTATGGGTGAGAT ATGTCTCCCTCAACCTTGTTACAACAGTTGGGCATTATCTGCCTGATG
co3_10 063514 _x1	ENST00 0004107 34.2	15	0.005	30.2	1	AGGACTGTGCTTTCAGAGTTCATGTCCACAGCTCATTGCGGGGGCAGTTTCT CTGATCGT
co3_10 063842 _x1	ENST00 0004085 71.1	20	0.0005	32.2	1	GCAGACTCCCTCAGCATCCAGCGGGTGCTTTTTTCGGTCTGCCAGTGAGCATT CCATGGTG

co3_10 064028 _x1	CM0006 83.2/416 04683- 4160458 6	15	0.004	30.2	1	TTCCCTGTGACACATCAGCAGGATGACTGGGCTTTCATCCTCCTGGGTGGGA CATGCCTCCCTCAAGCCTTGCTGCTGGGCACATTATCTGTCCAACA
co3_10 067821 _x1	ENST00 0003648 63.1	14	0.008	28.2	1	GATGCCTTCCGGAACATGCCAGCACCGCAGATGCTGGCAGTCTGCTGTGCC CGTGATATT
co3_10 067912 _x1	ENST00 0004082 12.1	15	0.007	30.2	1	TGTTTAATGACTAAGGAAGGTCCCTGTCCCCGCCAGGGGCTGTGAGCAACAC CATGGCTG
co3_10 068360 _x1	ENST00 0003649 61.1	15	0.003	30.2	1	GTGTTGATGATGAGAACCTTATATTATCCTGAAGAGAGGTGATGACTTAAAAA TCATGCT
co3_10 069328 _x1	ENST00 0003643 94.1	45	8E-21	89.7	1	AATGAATGATGACAAAATGTTTCAGTCCCAAATGATACATACTGATTATACCAT TATATT
co3_10 073829 _x1	ENST00 0005168 90.1	24	1E-08	48.1	1	CCTCTTCTCAGAACACTTCCTGGGTCTGATTGGTGGCCCAGGGAGCTGTGAG AGAAGAGC
co3_10 076055 _x1	ENST00 0005170 61.1	14	0.008	28.2	1	GCTTAGGGAGGGTGCTCTGCCAGGTTCCAATCCTGGTTCCACTGCATATGA GCCTTGTA
co3_10 083072 _x1	ENST00 0003629 63.1	15	0.005	30.2	1	GGGTGATGATGAGAACCTTATATTTTCTGAAGAGAGGTGATGACTTAAAAAT CATGCTC
co3_10 084484 _x1	AC06935 1.5/3795 7-38002	14	0.009	28.2	1	AGCUGAAGAGCUGAUGAUGUCCCCUAAAGCUGAAGCUCUUAAGCU
co3_10 084901 _x1	CM0006 67.2/119 069400- 1190692 97	14	0.009	28.2	1	ATACTTTTTAGTTCATAAGTGGGATGATTGTGTGTTCACTTGTGTGAGACGT CCCTCCCTCAAACCTTGTTGCGCCATCATCTGCACATTACCCATCTGATG

co3_10 085428 _x1	CM0006 79.2/821 41663- 8214177 3	16	0.0006	32.2	1	ATCCTTTTGTGGTTCATCCGCCTGATGATTGGGTTTTTCATGCAGACGTGTGAG CTGTGCCTCCCTCAAGCCTTGTTACAACATCCGACATCCGCACATTACCTGTC TGATG
co3_10 088162 _x1	ENST00 0004081 17.2	23	0.003	30.2	1	AAGCTTGTACTCTCAGTGATCATTGCTGTAGTTACGAGATAAGCTTCTCTGAA CATGCAG
co3_10 091319 _x1	ENST00 0003649 02.1	26	8E-10	52	1	TGCAGTCAAGTCAAATTCAGTGCCCGTTTCTGTCATAGCGGGGGCTGGCCCA GATGGCTG
co3_10 093728 _x1	ENST00 0005159 66.1	16	0.0008	32.2	1	GCCCTATGTTAAAATTTTAATTCTGCACTTACTAACTATCTTGGGAACCTTGGG CAAGTA
co3_10 096195 _x1	ENST00 0003629 45.2	15	0.003	30.2	1	CCTGCCAGCTGCACAGATGCAGATGCTCTGCTATGCCTGTAACATCGGGGCG AAGTGAAA
co3_10 098971 _x1	CM0006 63.2/202 197731- 2021976 28	47	0.008	30.2	1	ATACTTTTGTAGTTAAGAAGTGTGACAATTGGGTTTTTCGTGCTCACATGTGAG AAGTGCCTCCCTCAAACCTTGTTATGAAGTCAGCACATTACTGGTCTTCTT
co3_10 108121 _x1	CM0006 69.2/129 061531- 1290616 34	19	0.005	30.2	1	ATTCTTTTGTAGCTGATAAGCATGATGACTGGAGTTTCACGTGCATGTGTGAG ATATACCTCCCTCCAACCTTGTTACCACATCTGCACATTACCTGCCTGATG
co3_10 112589 _x1	CM0006 75.2/110 414205- 1104143 06	14	0.008	28.2	1	GTCCTTTTGTGGGTCATCAGCATGATGCTGGGGCGTTCACACTCGTGTGAGA CATGCCTCTCTCAAACCTTGTTAAGATGTCAGCACATGACCCATCTCACA

co3_10 115536 _x1	CM0006 80.2/357 3043- 3572940	16	0.0006	32.2	1	ATCTTTTTGTGATTCATCAGCATGATGATTGGGTCTTCACACAAAAGTTTAAGA TGTGCCTCCCTCACATCTTATTATCGTGTGTCAGCATATTCCTGTCTGAAG
co3_10 119633 _x1	CM0006 65.2/474 66349- 4746644 8	14	0.008	28.2	1	ATCTTCTGTAGTTCATCAGTATGATACCTGGGTGTTTCACACACATGTGAGAT GAGTCATTCTTGAACCTTGTTATGATGTCAGCACTACCCATCTAACC
co3_10 120475 _x1	CM0006 63.2/224 336791- 2243368 89	37	0.0003	34.2	1	ATCCTTTTGTAGTTCCTAAGTGTGAAGAATGGGTGTTTCATGCAGAAGGATAAG ATGTGCTACCCTCAAACCTTGTTCCGTGCATATTACACGTCTGACA
co3_10 121214 _x1	ENST00 0005163 91.1	15	0.003	30.2	1	TGGTCAGGCTGTGGCTGTGGCACAGCACTTGGCTTTCTCCTGGGGGCACTG GGGAGCCAT
co3_10 125715 _x1	AC01074 6.8/1403 34- 140470	22	5E-05	36.2	1	CUACCAAAGUUAAUUUUUUUAUGGGGAAGGCUUUCUAAAUAACCUUUACCA AUUUGGGCUAUUUGGGAGAGUAAAGGAAAGACCACACUCCACAGCGGGCU AUACCAAUAGUUCACUACUAAUUUUGUGGUCUACAUU
co3_10 127798 _x1	CM0006 72.2/104 399790- 1043999 03	14	0.009	28.2	1	ATATAATTGCAATTAATAATTACATGATTTGATCTTGACTGGGTGTTTCACATGT ATGTGTAAGATATGCCTCCCTCAAACCTTATCACGATGTCGGCACATTACCCA TCCAACA
co3_10 128686 _x1	ENST00 0003910 93.1	15	0.004	30.2	1	TTTACAAGGGAAAAGCAACCCCATTA AAAAGTGGGCAAAGTAAGGTCTTTGG GGAACAGG
co3_10 133677 _x1	CM0006 84.2/225 17780- 2251787 5	15	0.002	30.2	1	ATCCTTTTGTGAGGATAAGCGTGATGCTTGGGTTTTCACTCATGTGAGATGTG CTTCCCTCAAACCTTGTTATATCAGCATGTTTAACATCTGATG

co3_10 135805 _x1	ENST00 0005171 36.1	15	0.004	30.2	1	TGAGTTTTGGGATGAGACCCTGGAATAAGTGCTGGACACAGTGCCTGAATCA GACTGTGG
co3_10 140685 _x1	ENST00 0004594 45.2	14	0.008	28.2	1	TCATATATTAAGTGCTTTATAACGAATTCTTGCAAATGGATTTAACAGAACAT GACGAC
co3_10 140765 _x1	ENST00 0003649 41.1	15	0.003	30.2	1	GTCTGCATTTGAAAGTGATCATCAGCTAGCCTGTGTCTTCGTCATCGATAGTA CAGGCCG
co3_10 141872 _x1	ENST00 0003645 14.1	14	0.009	28.2	1	AGGCAACTCTTAGAAGATGGATAGCTTCTCTTTTGCTGTGGGTGTGGCCACAA AACGTTT
co3_10 143386 _x1	CM0006 83.2/444 39035- 4443911 0	14	0.008	28.2	1	TGTTGACCTGCCTCCGTCCTCTGTCTGTCCAGGGCTCCCGGGAGCCAGGGG AGATGCTACCTCGGAAGCTGAAGCG
co3_10 145116 _x1	ENST00 0004081 66.1	14	0.008	28.2	1	ACCAAGATTCAAGTCACATTCCGAGTGTCCCGGTGTGCTAGGGCACTTGCAG AGAATCTG
co3_10 145687 _x1	ENST00 0004596 13.1	14	0.008	28.2	1	ATTGGTTGAAAATCACCCCGGCTTTGGCCATGGCAGCGGGTGAGATTCGG CGCCCAGA
co3_10 155696 _x1	CM0006 65.2/163 178975- 1631788 74	14	0.009	28.2	1	GTACTTTTGTGGTTCATAAGTGTGATATATGAGTTTTTCATGCTCATGTATGAGA TGTGCCTCCCTCAAAGCTTAGGACTTCAGCACATTGCCTAATACGAAA
co3_10 155821 _x1	ENST00 0006200 99.1	15	0.003	30.2	1	TTTATCAATGGCATGATTTTAAAGCTGTTTCACCCGAGTACACAGCAGGGAAG CCATCCT
co3_10 156256 _x1	CM0006 66.2/183 582301- 1835821 95	15	0.004	30.2	1	ATTCTTTTTTGGTTCATAAGTGTGATGATTTTCGTTTTTCATGTTAAAGTGTGAGAT CAGCCTCCCTCAAACCTTGTTACTACATCAACACCACATTATCCATCCAATG

co3_10 160679 _x1	ENST00 0003629 87.1	16	0.0005	32.2	1	CATCTGTGATTATCCTATTCTGAACCTGAATTTCTACTAGAAAAACTTATATG AATCTG
co3_10 176372 _x1	KV88076 8.1/1215 368- 1215471	15	0.006	30.2	1	ATCCTTTTGTAAATAGATAAGCATAATGATTGGGTTTTTATGTTACATGTTTGAT ATGCCTCCCTCAAATCCTCTTATGATGTCGGCACATGACCCATCTGAGG
co3_10 179296 _x1	CM0006 75.2/209 69318- 2096941 6	15	0.006	30.2	1	ATCATTTTGTACCTTTTAAAGCATGACCATTGGGTTTTTCACTCATATGGGAGG TGCCTCCCTCAAACCTTTGTTACATTGGCACATGACTCATCTGATG
co3_10 184894 _x1	CM0006 83.2/393 45457- 3934535 1	15	0.005	30.2	1	ATCCTTTCATAAGCTTGAAGATTGGGGTTTTCACGCTCATGTGTGAGATGTCCC TCTCTCAAACCTTACTATGAAGTCAGCACCACTGGGCACATTACTTGTCTGAC A
co3_10 186261 _x1	ENST00 0003632 80.1	18	0.009	28.2	1	TGAATCAATGGTGACCACTGGTGGCATATAAGTCATGGATGATGAATATGAGA AGAAAAG
co3_10 196913 _x1	ENST00 0005158 95.1	19	0.004	30.2	1	CAGACTTACAGATAAGTTCGAGAAATAAACCTGTTTTGCAACCCAGAGCACA TTGTTCA
co3_10 197121 _x1	ENST00 0003911 12.1	15	0.004	30.2	1	ATACTATGATGGTTGCATAGTTCAGCAGATTGAATTCATGAAGAGATTTACAAT GTCTGA
co3_10 198179 _x1	CM0006 63.2/174 49763- 1744986 3	15	0.003	30.2	1	ACACTTATGTGGTTCATAAAAGTGATTGAGTTTTTTCATGTTTCATGTGTTGAATGT GCCTCCCTCAAACCTTGTTAAGTCATCAGCACATTACCCATTTGATG

co3_10 200244 _x1	CM0006 69.2/138 176154- 1381762 82	15	0.002	30.2	1	ATCTTTTTGTAATTCCTAAGCATGATGGTTGATTCGGCTCTCACACTTGATGAT TGGGCTTTCACTTGGATCTGTGAGATGTGCCTCCCTCAACCCTTCCTGCGAA GTCAGCACATTACCTGACAGAAA
co3_10 201741 _x1	ENST00 0003842 31.1	15	0.004	30.2	1	CTGCAGCCAATTGAGTTGACCGAGCTCTTTTCCTCCTGGGGGCTTGGTGTGC AATGGCTG
co3_10 202035 _x1	AC00922 8.4/5936 1-59234	14	0.009	28.2	1	UGGCAUGAUUUCCUGCAGGUUGAGCUCAGCCAAGUACCACCCUCAGUAA GCCUAGAGUAGAGGGGCCUGACAUCUUUCCUUAAAUAACAAGGAGCCU UAUCCAGGUUGUCCUAGUCUCAUACUU
co3_10 202388 _x1	ENST00 0003912 91.1	20	0.0006	32.2	1	CACTAGAAGACAGAATTCACAGAAGTAGCATTTCACCTTTTGCCTTTACAGAA GTATATT
co3_10 205575 _x1	ENST00 0005160 35.1	17	0.0002	34.2	1	TTTCTATTTTATCTGATTCTTCCTCTATGCACAACTCAGCTTCAGTCATTAGTA TCATT
co3_10 205607 _x1	CM0006 71.2/942 33478- 9423358 1	14	0.009	28.2	1	ATCCTTTTGTATCTCATAAACATGATGATTGGGTTTTTCACACACACATGTAAGA TGTGTCACCATCAATCCTTGTTATGACATCAGCACATTACCCATCTAACA
co3_10 207715 _x1	CM0006 63.2/173 660200- 1736600 97	14	0.008	28.2	1	ATCCTTTTGTAAATTCATAGGTGTGATTATTGGGTTTTTCATGCTCATGTGTGAGA GGTACCTCCTTCAAACCTTGTTACAACACGGGCACATTTCTGTCTGTTG
co3_10 208128 _x1	AC01112 0.11/127 524- 127388	19	0.005	30.2	1	CAGACAUUCAUUUUUAUCCAGUUUCUUCUCAAGUGAAGUAACUUUUUGU AAAUGUCCUAAAGUCAUGUAGAAUGUAGUAGCUUUCUGUUCACACUGUACA AAUAAAAAGGAUGGAUCAUUCUACAACUGACAUUA
co3_10 214535 _x1	ENST00 0005166 32.1	20	3E-06	40.1	1	AGGGGTGGTCTCCTCCCTTACTCTTTGGGAACTCAGATTGGCCTTATGGTGG CCTCTCTT

co3_10 216520 _x1	CM0006 65.2/861 25216- 8612528 7	14	0.008	28.2	1	AAATGTTATGATATGAGCAAAATGTTCAACTATTCCAAATGGGCTGAGTGAAA ATAGGTTTTCTGAGCATCC
co3_10 217693 _x1	CM0006 77.2/918 35379- 9183547 6	14	0.008	28.2	1	CTCCTTTTGCGGTTTATAAGCATGATGATTGGGTTTTTCATGTGTGAGATGTGT CTCCCTCAAATCTTTTTATGAAGTAGATGCATTGTCTGTCTGACA
co3_10 217729 _x1	CM0006 72.2/687 12958- 6871305 5	14	0.008	28.2	1	ATCTGTTTGTAGTCATAATTGTGATGGTTGAGTTTTTCATGTGTGAGATGTGTAT CACTCAAGCCTTTTTACAATGTCGGTATATTGCCGGGTGCGGTG
co3_10 223655 _x1	ENST00 0004593 50.1	24	0.0009	32.2	1	ATCCTTTCACAGTTCATAAGAGTGATGACTGGGTTTTCACTTTCATGTGTAAGA TGTGCC
co3_10 229144 _x1	CM0006 65.2/321 72656- 3217275 5	15	0.008	30.2	1	ATCCTTTTGTGGTTGATAAGTGTGATGATTCAGTTTTTCATGCTCATGTATGAGA TGTGCCCCCAATCAAACCTGTCACAACATCTGCTTATTATCAGACA
co3_10 231700 _x1	AC00483 0.1/5888 6-58743	14	0.008	28.2	1	CUAUCAAAAGUUACUUUUUGUGGGGUGGAAGUUUUUAAAAUAACCUUUUACC UACGUGGGCUGUUUUGGAAAAUAAAGAAAAGACCACACUCAGCAGAGGGCU AUACCCCUUAGUAUAGUUCACCACUUUUUGCAGCUUAUAUU
co3_10 234184 _x1	ENST00 0003655 09.1	15	0.003	30.2	1	ATAAACAAAAGAACACCAATTGTGCTCCTTTCCTCCTGGGGCCCAGTGTGCAA TGGCTGC
co3_10 239247 _x1	ENST00 0005171 84.1	15	0.004	30.2	1	TGGTTTAAAGCCAACTCTGGGCTCCCATCAGAAGGAAGGAGATGAATGCTAT GACCAAAG
co3_10 239584 _x1	ENST00 0003911 77.2	14	0.008	28.2	1	AAGACGACGCTTGCAGGGATTGTTTCTATAGCTCACTACCAGATAAGTTTCTC CGAACAT

co3_10 241922 _x1	AJ60947 2.1/1-140	15	0.006	30.2	1	UUUCUCAUUUGACUACCACAUUUUCUCCUAAUAAUAGAUUUUAGUGGCUAU GCUUAUGGGAUAGAUUAAACUUGCCAUGAUCUGAAGAGGGAGGGUUUUUU CAUGUCCUCCUCCUAUAUGAAAUGGCUGAACGGAUUUA
co3_10 243836 _x1	ENST00 0004591 41.1	16	0.001	32.2	1	TCCTCACATGGGATAATTTTTACTTTATTCTCCCTTTGGAGGTCAGGTTAAAC AAGATT
co3_10 245707 _x1	CM0006 63.2/286 89665- 2868979 4	31	2E-05	38.2	1	TGGACATTTATTTTTATTCAGTTTTTTCTCAAGGTGAAGGTAAGTGTGATGAT GTCCTAGAGAAATATTGTAGCTTTCTGTTACCCTTTGCAACTAAAAAGCATG GACTGTTCCACTACTGAGATTT
co3_10 251860 _x1	ENST00 0006077 07.1	27	2E-10	54	1	TGATGGCAATGATGATTTTTTACACTTATTGTTGTTACCTGATAACATAAATAT GAGGGT
co3_10 252753 _x1	CM0006 67.2/568 57140- 5685725 1	14	0.008	28.2	1	AACATTTAATTGCAGTAATTCATAAGTGAATGATTGGGTTTTTCACATGCATGC ATAAGATGTGCGTTTTCTCCAACCTTTGTTACAGTGTGAGCATGTTATCCTCATTT GACA
co3_10 255235 _x1	ENST00 0005165 43.1	24	0.001	32.2	1	TGGACAGACGCAAAAAACAAATCCTCATTGCAACCCAGAACTAATTGTTTA GTATGAT
co3_10 258655 _x1	ENST00 0003913 02.1	15	0.006	30.2	1	TGCCCTGACCTGGGAAGAGAGGGGCCTGGCTGGTGGTATCCATCTCATA CAGCTAGGG
co3_10 261942 _x1	ENST00 0003909 91.1	15	0.003	30.2	1	AATTGGGATCAAAGATGCAGCCGCCTTCCCATTTAAGCAGCACAGACAGCCC AAAGTGAC
co3_10 262949 _x1	CM0006 67.2/119 469055- 1194689 59	15	0.003	30.2	1	ATACAATGAATAAAGTGTGATGACTGAGTGTTCACTCGTGTAAGATATGCC TCCCTCAAACGTTGTCATGAAATAAGCACATTGCCCAACTGATA
co3_10 266412 _x1	ENST00 0005167 41.1	14	0.008	28.2	1	AGGTCATTTCAAAGAAGGTTACGTGGCTGTGAGACCAAGAACGCTTAATGC TGTTACCA

co3_10 269083 _x1	CM0006 64.2/156 410246- 1564101 44	14	0.009	28.2	1	ATCCTTCTGTAGTTTATAAGCATGATGACTGAGTATTCACCCGCATGTGTGAG ACGTGCTGCCCTTAAACTTTGTTATGGTGTACACACTGCTAGCCTGAAA
co3_10 270133 _x1	ENST00 0005834 96.1	14	0.009	28.2	1	TGTTGACCTGCCTCCGTCCTCTGTCTGTCCAGGGCTCCCGGGAGCCAGGGG AGATGCTAC
co3_10 270347 _x1	ENST00 0003912 88.1	17	0.0005	34.2	1	GCACCCCTTTAAGGCTGATGCAATGCTTTAAGAGGCTAACGCAGAAGGGTGA AGCCAGTC
co3_10 271082 _x1	CM0006 66.2/408 68970- 4086886 4	19	0.008	30.2	1	ATCTTTTAGTAGTTCGTAAGCATGGTGATTGGCTTTTCATGTGCATGTGTGAAA TGTGCCTTCCACAAACCTTGTTACAAAGTTGGCACACTACCATTGATGTGAAA
co3_10 272949 _x1	ENST00 0004088 76.1	14	0.008	28.2	1	TGCCCAGTGATGACACCATCCTTGCTCCCCGTGCCCCCAGGGGCTATGGG CGACACCAT
co3_10 285387 _x1	CM0006 65.2/470 88608- 4708874 7	15	0.003	30.2	1	ATCCTTTATGGTTCATAAATATGATGAATGGGTTTTACAGCTGCTGTGTGAGAT ATATCTCCTTCAAACCTTATATAATTTATATGTTATAATATATAATGACCTTTTTAT GATGTCAGCATATGAATGACCCAGCTGATA
co3_10 285925 _x1	CM0006 81.2/447 64976- 4476510 0	14	0.009	28.2	1	ATGAACACTAGTCAAGCTAATTGTGCTCCTCTCCTCCTATGCAGTGGCGGCAA ACAGCAGTGCCCTCAGTAGTATACGCAGCCTGCTGCGTGTAGCGGTGGCCTT AAGAGACCTTGGAGATAGCC
co3_10 294448 _x1	ENST00 0003649 39.1	16	0.0005	32.2	1	TCATCAGGTGGGATAATCTTTTCCTGTTCTTCCTTTTGGAGGACAGATTATAAC ATGATT
co3_10 313284 _x1	CM0006 65.2/175 739271- 1757393 76	15	0.002	30.2	1	ATCCTTTTGTGGTTCATATTTGTGACGATTTCGGTTGTCAGGCCAATGTGTGAG ATTTACCTCCTTCAAACCTTGTTAGCACATTGGCACATTTCAATTGTCTGACA

co3_10 315001 _x1	ENST00 0005167 17.1	15	0.004	30.2	1	AAGACCCTTCAGCTGCAAACAACAGCTTCCTTGGTAGTTTATGCAGCCTGTTT CTTGTAT
co3_10 315048 _x1	ENST00 0003909 77.2	19	0.002	30.2	1	ATACTGTGACAGTTGCATCGTTCAGCAGATTGAGTCACGAAGAGATGTATACC ATCTGTC
co3_10 336492 _x1	ENST00 0003644 61.1	15	0.006	30.2	1	GGGTCAATGATGAGAACCCTATATTGTGTTGAAGAGAGGTGATGACTTAAAAT TACCATG
co3_10 369114 _x1	ENST00 0003653 91.1	14	0.008	28.2	1	GGGTCAATGATGAGAACCCTTATATTGTCCTGAAGAGCGGTGATGACTTAAAAA TCATGCT
co3_10 369599 _x1	ENST00 0005792 16.1	14	0.009	28.2	1	GCCGTGTGAGGCCACCTCTGCCATGCTGCAGGCTCCCCAGCACGCAGTGGG GAACCCAAC
co3_10 369974 _x1	CM0006 80.2/381 1317- 3811420	14	0.009	28.2	1	ATCCTTTTGTGGATCATAATCATAATGATTGAGTTTTACAGTAATATATGAGA TGTGCTTCCTTCAAACCTTGTTATGATGTTGGCACACTATCCGTCTTACA
co3_10 378998 _x1	ENST00 0005160 13.1	15	0.003	30.2	1	GTGCACATTGTTACATTGGGAGAAAAGATATTTCTGATGTGATGAATAAATTTT TGGAGA
co3_10 384031 _x1	ENST00 0003910 82.1	19	0.006	30.2	1	ATAGCCAATCATTAGTATTCTGAGCTGTAGGAATCAAAGATTTTGATTAGATTC TGTAAC
co3_10 384818 _x1	ENST00 0003648 40.1	19	0.002	30.2	1	TAGAACAACGATAACAAATAGTAGTGCAGGAGTCATAAACTATGAGTAATATG TGTGTGG
co3_10 385811 _x1	ENST00 0003639 31.1	16	0.001	32.2	1	GGGTGGTGATGAGAACCCTTGATTCTTCTGAAGAGAGGTGATGACTTAAAAAC CATGCTC
co3_10 400973 _x1	CM0006 72.2/295 75306- 2957538 1	18	0.009	28.2	1	AGGCCAATGCTGAATTATTATCTTGACGAGAAATGATGACGTAAAAATTAAGC TTAGTAGGATTACACTGAGGCC

co3_10 402151 _x1	CM0006 67.2/150 029452- 1500293 49	14	0.008	28.2	1	ATCCTTTTATAGCTCACAAGTATGACAATCTGGTATTCATGCACATGGGTGAG ATGTGCCTCCCTCAAACCTCATTATAACGTGAGCACATTACCCATTTGACA
co3_10 402483 _x1	ENST00 0004589 08.1	15	0.004	30.2	1	TAGCACTGTTGCCTGAGCCATTGGTGCTCCCTGGTACTAGCTCAGTTTTAATG CAGTGCA
co3_10 409940 _x1	ENST00 0005166 34.1	14	0.008	28.2	1	GATTCACAGCAGAAAGACAGCTAATCTAGTGTGCTAGCTGTAGAGCAAGTTTG CTGCAAA
co3_10 417757 _x1	CM0006 66.2/185 946083- 1859461 86	16	0.0006	32.2	1	ATCCTTTTGGGGTTGATAGGTGTGATGATTGGGTTTCTATGCATGTGTGTGAC ATGTGTCTCCCTCAAAGCTTGTTACCACATCCGTACAGCACCCATAGGATG
co3_10 420620 _x1	ENST00 0003632 05.1	16	0.0006	32.2	1	AGGATATATCAAAGAGACTTTCTGGGGCTGGGAAACCAGGATCTCGTAATGC TATGACCA
co3_10 421255 _x1	ENST00 0003643 93.1	22	0.0001	36.2	1	TGGATCAATGATGTCCACTGGTGGCGTATAAATCATATTTGGTGAATATATGT CTGGAAC
co3_10 423027 _x1	ENST00 0005162 13.1	17	0.0001	34.2	1	CCACACAGGACGAAGGGTAGATATACTTGTACCAAATGAATGTTTCAGCAATCT GAGATAA
co3_10 431164 _x1	ENST00 0003650 75.1	15	0.005	30.2	1	CTACAGCCAACTCAGCTGGCTGAGTTCCTCGCCTCATGGGGGACGTGTGCAA TGGCTGCA
co3_10 431979 _x1	ENST00 0003637 23.1	19	0.004	30.2	1	GGGTCAATGATGAGAACCGTATATTGTCCTGAAGAGCGGTGATGACTTAAAAA TAATGCT
co3_10 436715 _x1	ENST00 0004589 53.1	15	0.005	30.2	1	AAGCATGGCACACTGGATGGGCGTTCTGCTTCTCTTTAAAGAGCATGGATTTA TCCATAC

co3_10 463514 _x1	ENST00 0005160 69.1	15	0.003	30.2	1	TTATATTAGTGATGGCTTTTAAAGTTCTCACAGACAGGCATCTCTCTGAAAGAC AGCGAA
co3_10 464412 _x1	ENST00 0005168 31.1	41	0.0005	34.2	1	TAGTGTGGAAGTGTCTACTCCTCATTCTGTGGAAGCAGGAATACATTCATAA CATGCTC
co3_10 467234 _x1	ENST00 0005163 95.1	36	0.001	32.2	1	ATGACCTGTGAAACCAAGGGCTCCTAATGCTATGACCAAAGACTGAAGCTCT CTATGAGA
co3_10 468026 _x1	CM0006 79.2/181 46552- 1814665 1	15	0.003	30.2	1	ATTCTTTTATAGTTTATAAGTGTGATGATTGAGTTTTTCATGCTCAGGCATGAGA TGTGTCACCCTCAAACCTTGCTAAAACATCAGCACAAAGACCAGACG
co3_10 469588 _x1	ENST00 0003909 82.1	15	0.003	30.2	1	TCAATAATGAAATCTTCTGATTTGGTGAGAAATAATGCCTTAAATTACTCA ATAGGA
co3_10 470423 _x1	CM0006 72.2/996 01780- 9960188 0	19	0.002	30.2	1	ATCCTTTTGTAGCCCGTGAACATGATGATTTGGGTTTTTCACACACATGTGAGA TGTGCCTCCTTCAAACCTTAAGACATCAGCATGTTACCTGACGTGAAA
co3_10 471981 _x1	CM0006 81.2/383 49110- 3834900 9	15	0.003	30.2	1	ATCTTCTTGTAGTTTCTACGTGTGGCGATTGGGTTTTTCACCGTCATCTGAGAT GTGTCTCCCTCAAGCCTTGTTATGGTGTGCGCCCATACCTGTCTGACA
co3_10 474175 _x1	ENST00 0004110 95.1	20	0.0007	32.2	1	CCTCATTTTCTTGGCAGGAACTTGTAGTCCCACTCCCTGTTATGTACAGAGGC AAAGGGA
co3_10 486821 _x1	CM0006 77.2/457 10815- 4571087 3	14	0.008	28.2	1	AGAGTGCTGGTGGCTGATGAGCCCAGGGCTGCTCTTGCTCACTTTGCTGACA GCACTCG

co3_10 486979 _x1	AL13270 9.5/1425 97- 142509	18	0.009	28.2	1	UGGACUGUUGAUGACAAGUGGGUGGCUUAUGUGGUUGUACAUGCUGGUUGU AUAUGAAGAAUAAUUAUCAUAUCUGAAACUUUGAGGUCCAA
co3_10 516611 _x1	ENST00 0003646 72.1	14	0.009	28.2	1	AAGGCAGCATTGTTGTAGATGATTTGAAAGATTTTAAAAGGTATAAGCTCACA AGTGTAG
co3_10 521466 _x1	ENST00 0003911 30.1	14	0.009	28.2	1	GCCATGATGCTCTTCGGTTTAGGAGCAATTAATGACTACAGATTGGTGGCA GTTTATG
co3_10 533341 _x1	CM0006 82.2/357 16471- 3571657 0	14	0.008	28.2	1	AAATTTTAGGAGTACCTAAGTGTGATGATTTGGTTTTTACATTCATGTGTGAGC TGTGCCTGCCTTTTGTACAAGGGCATATTACCCTTTGTTGTGAAA
co3_10 534332 _x1	ENST00 0005170 95.1	16	0.001	32.2	1	TCACATTTTATCAACCAAATGAATTAGGGAAAAAAGTTCATGCCCAGGGGTGA GACTATA
co3_10 548984 _x1	CM0006 63.2/111 69613- 1116950 7	14	0.009	28.2	1	ATCCTTTTGTATACATTTATGCATGATGATTGGTTTTTACCATCACATGTGGT GAGATGTGTCTCCCTCAAATTGTTATCACGTCAGCATGTGATCAGTCTGACA
co3_10 549560 _x1	ENST00 0005170 15.1	39	0.006	30.2	1	CATCTCCTATCAGTCAGGGATGAAGCAATCCCTTGTTTCATCCCCAGCTTGGCT TTTGATC
co3_10 559256 _x1	ENST00 0003633 67.1	15	0.005	30.2	1	CTACAGATATTTTCTGAATTGGCAAGTCCACCAAGAACTATAAAAATGTGTGT GTGCAA
co3_10 564810 _x1	ENST00 0004106 72.2	14	0.009	28.2	1	TACTTCCAACCTCTAGGATAGCATCATGCAATAAGAAAAGTATGACAGAGGTAC CCATTCC
co3_10 568728 _x1	ENST00 0004087 92.1	19	0.007	30.2	1	GCCGAGACTAAGTCGCATGCTGACACAGCTCTTGGTGTGCTACGGTACTTGG AGAGAATC

co3_10 574026 _x1	ENST00 0005166 64.1	15	0.005	30.2	1	ACCCAGGGGGTTCCCTCTCAGGGGACAGTTCGTATACTCAAGAATGTGGCCA CTTGGAGA
co3_10 598609 _x1	ENST00 0005161 13.1	16	0.0006	32.2	1	ATGCATCTTAGAACATCCAGGAGACAGTCTTCTAAAATACCAGTGAGTGGCAA GATATGA
co3_10 606757 _x1	ENST00 0004593 39.1	15	0.004	30.2	1	CTGTGTGTAGAAATGTTTGCTCCTCTATCCTTTGGGAACAGGAATACATTCAT AACATGC
co3_10 618223 _x1	CM0006 79.2/797 13731- 7971382 6	14	0.008	28.2	1	ATCCTTCTGTGGCTGATATGTGTGATGAGGGGGTTTTTCACACTCTTGCGTGG GACGTGAAACGTCTTTAGAACAGTGGCACGTTACCTGTCTTACA
co3_10 630550 _x1	ENST00 0003645 40.1	15	0.004	30.2	1	AAATGTTATGATATGAGCAAAATGTTCAACTATTCCAAATGGGCTGAGTGAAA ATAGGTT
co3_10 631794 _x1	CM0006 80.2/229 01626- 2290152 4	15	0.005	30.2	1	GTTCTTTTGTGTTTCATAAAGTAATGATTGTGTTTTTCACATTATTGTGTGAGGT GTGCCTCCCTCAGACCTTGATACCAGTCTGCACATTACCTGATGTGAAG
co3_10 657483 _x1	ENST00 0003623 26.1	15	0.002	30.2	1	AGATAACTTCAAAGAGGGCTTGCGGAGCTGCAAACCAAGAGCTTTTAATGTA TACTGA
co3_10 658573 _x1	CM0006 65.2/101 201832- 1012019 35	15	0.007	30.2	1	ATTCTTTTGTGGTTTATAAGCATAATGGTTGGGTTTTTATATGCATGTGTGAAA TGTA CTCCCTCAAACCTTGTTACAATGTCAGCACATTACCCACCTGACA
co3_10 660956 _x1	CM0006 65.2/197 339551- 1973394 57	16	0.0007	32.2	1	AGTCTTTTGTAGTTTGCAAGCATGATGATTCGGTTTTGAGAGGTGCCTCCCTC AAACCTTG TAGACGTCGTCATCGGCACATTACCTGCCTGATG

co3_10 671950 _x1	ENST00 0006071 53.1	19	0.004	30.2	1	AGGTGATTTCAAAAAGGACTTGTGGGCTGTGAATCCAGGCACTCAACACTTTG AAAGTCT
co3_10 697710 _x1	ENST00 0004590 14.1	31	3E-10	54	1	GTTGGTTGAAAATCACCCCGGTTTTGGCCGTGGCCGCGGGTGAAATTCGGC GCGCAAGA
co3_10 698029 _x1	CM0006 64.2/649 08686- 6490858 7	15	0.003	30.2	1	ATCCTTTTGCAGTTATGCATAATGACTGGGTTTTACGCTTATGAATGAGATGT GCCTCCCTCAAACATTGTTATATGTCAGCACATTATGCATCTGACA
co3_10 707122 _x1	ENST00 0003912 63.1	16	0.0005	32.2	1	GTCGCACTTAAACTTAAGACTCTTTTTCTTGCAGCAGTGGTTTAAACAGAGGA ACAAACA
co3_10 726530 _x1	ENST00 0005170 79.1	19	1E-05	38.2	1	ATGCCTCTATTTGACACATGAAACAGTTACTGCCTGCTGCTATGGTTTCCACT ACAGATG
co3_10 735735 _x1	ENST00 0005163 61.2	14	0.008	28.2	1	TGGACCAATGATGAGAGCATGTCACAAAACAAGGCTTATGATTAATCCAGTTC TGACAC
co3_10 742577 _x1	ENST00 0004110 34.1	15	0.002	30.2	1	AGTTCCTTGGAAGTTAAAGGTTAAGCTTAAGGACTGATTCAAAGGCAGGTGCA AAAAATA
co3_10 757644 _x1	CM0006 79.2/674 07946- 6740784 3	14	0.009	28.2	1	ATCCTTTTGTGGTTCACAAGCACAGCGATTGGGTTTTCACACTCATGTCTGAG ATGTGCCGCTCTCAAACCTTACTATGACATCAGCACATTGCCTATCTGATG
co3_10 766965 _x1	ENST00 0005160 29.1	20	0.0007	32.2	1	CTTCTGCTAAGGTTTACACTATAGATGCAGGAAAAAATGTCCTCACACTGT CTGTCTG
co3_10 771144 _x1	ENST00 0003911 09.1	16	0.001	32.2	1	AGGCCAATGCTGAATTATTATCTTGACGAGAAATGATGACGTAAAAATTAAGC TTAGTAG

co3_10 775197 _x1	ENST00 0003642 63.1	16	0.0007	32.2	1	CTATCAAAGTTACTTTTTGTGGGGTGAAGTTTTTAAAATAACCTTTACCTAC GTGGGC
co3_10 805386 _x1	ENST00 0005163 03.1	15	0.002	30.2	1	GTGTTTAGAAGACCACATCTTCATCCTGAAAGCACAGATGTGTGGAAACCAAT GACCGAG
co3_10 815734 _x1	CM0006 64.2/179 125637- 1791255 36	15	0.006	30.2	1	ATCCTTTTGTAGTTTATAAGCATGATGATGGGTGCTCACACTCATCTGAGATG TGCTCCCTCTAAGCCTTGTAACAACATCAGCACGTTACCCTTCTGATG
co3_10 818840 _x1	ENST00 0005163 49.1	16	0.0008	32.2	1	TTGTGGGTATAACATTCACTATATTAAGATCATGCATGTGCCCCAAACCTAAT TCTTTT
co3_10 851764 _x1	ENST00 0003912 27.1	15	0.007	30.2	1	CCTCGCTTTCTTTGCAGGGAGCAGGTATGTATGTTCCCTATTATGTCTGGAGG CAGAGGG
co3_10 860635 _x1	ENST00 0005164 21.1	15	0.006	30.2	1	TTCCAGAATTACGGGTTTGACAAACCAAACATTCATTATTTTCTCTCTAGAG AGAGTT
co3_10 861041 _x1	ENST00 0003912 65.1	14	0.009	28.2	1	CCTCCTTTTCTTGTCAGGGACTGAGTGTGTGGTCCTGCTCCTGTTATGTATGG AGGCAA
co3_10 872963 _x1	ENST00 0004102 13.1	14	0.009	28.2	1	TCAGCTTGAGTCACTCTTCCCAGGCTTTATCCAGGTGGCTTAGGTTAGCTAGG GCTGTGT
co3_10 878069 _x1	ENST00 0005172 04.1	19	0.004	30.2	1	ATGCACCCATTTGACTAACTTGCAGCAGCTAATGTCTGCTGCCAAGGTTTCCT CTCCAGA
co3_10 893412 _x1	ENST00 0005169 65.1	16	0.001	32.2	1	TTACCTTGAATACATACAGATACTTCTGTTACTCTCTAGCTTAAGAACCTTTA ATGTGG

co3_10 899850 _x1	ENST00 0004593 26.1	16	0.001	32.2	1	GCCCAGGGTATGTTACAGGGGCGATGCTGCCCTCCCAGCTGGCCCATGGGT GACCCTGGG
co3_10 905384 _x1	ENST00 0005159 21.1	17	0.0003	34.2	1	CTATCTAGCAAAAATTTGGTTTAGAGGGAAAGTTTATAGTAGACTTTGCCAGCT GAAGTTG
co3_10 948961 _x1	ENST00 0003910 78.1	15	0.007	30.2	1	GGGGCAATATGGAGATGTTATATTGTCTTCGACAGGGAAGATGACATAAAAAT TATGTTC
co3_10 957393 _x1	ENST00 0003645 23.1	14	0.009	28.2	1	CCCTATATTCGAAAGTTATCCTGGTCATTGACAGTGCAGGGAGAGAAACTGCT GAAAGCA
co3_10 961095 _x1	ENST00 0003653 06.1	16	0.0005	32.2	1	GGGTCAATGAGAACCTTATATTGTCCTGAAGAGAGGTGATAACTTAAAAATCA TGCTCAA
co3_11 015004 _x1	CM0006 67.2/133 850957- 1338508 57	14	0.009	28.2	1	ATCTTTTGTGTTTCCTAAGTGTGATGATTGAGTTTTCAAACCTCACTTGAGGTGT GCCTCCCTTAAACCTCATTATGACATCAGCATATTACCCATCTGACG
