

**S1 Table 1. GO enrichment analysis about mRNA**

GO_ID	Description	GeneRatio	pvalue	qvalue	geneID	GO_domain
GO:005090	leukocyte migration	49/875	1.85E-10	7.48E-07	ATP1B2/AZU1/CCL3/CCR2/CCR5/CCR7/CD34/CD58/CEACAM1/CEACAM6/CEACAM8/CMKLR1/CX3CR1/CXCL10/CXCL2/CXCL5/CXCR1/CXCR2/CXCR4/ELANE/EPS8/GCSAM/GPR15/ICAM1/IFNG/IL12A/IL6/ITGA1/ITGAV/ITGAX/LGALS9/MERTK/OLR1/P2RY12/PDE4B/PDGFB/PF4/PODXL2/PPBP/PROS1/PTGER4/ROCK1/RPS19/SBDS/SIRPG/SLC7A5/SPNS2/TNF/TRPM4	Biological Process
GO:0009617	response to bacterium	61/875	6.84E-10	1.38E-06	ALPL/AZU1/BMP6/BPI/CAMP/CCL3/CCR5/CCR7/CD180/CLEC4D/COCH/CTSG/CX3CR1/CXCL10/CXCL2/CXCL5/DEFA1/DEFA1B/DEFA3/DEFA4/ELANE/EPPIN/FASLG/GNLY/HLA-DRB5/ICAM1/IFNG/IL12A/IL6/IRAK3/ISG15/JUND/LCN2/LGALS9/LTF/MAPK14/MAPK3/MUC5B/NCF1/NLRC4/NLRP6/PDE4B/PF4/PGLYRP1/PLD1/PPBP/PRDM1/PROS1/PTGER4/RBPJ/RIPK2/SLPI/SOCS1/SPARC/TICAM2/TLR1/TLR5/TNF/TNFAIP3/TNFSF4/TNFSF8	Biological Process
GO:0031640	killing of cells of other organism	12/875	1.60E-08	1.62E-05	BCL2L11/CAMP/CTSG/DEFA1/DEFA1B/DEFA3/DEFA4/ELANE/FCER2/GNLY/IFNG/NCF1	Biological Process
GO:0044364	disruption of cells of other organism	12/875	1.60E-08	1.62E-05	BCL2L11/CAMP/CTSG/DEFA1/DEFA1B/DEFA3/DEFA4/ELANE/FCER2/GNLY/IFNG/NCF1	Biological Process
GO:0050663	cytokine secretion	25/875	5.15E-07	0.000298	AIM2/ALOX15B/CAMP/CASP5/CCL3/CCR7/CD34/CD58/CHI3L1/CLEC5A/HLA-DRB5/IFNG/IL6/LGALS9/MAPK14/NLRC4/PTGER4/RBPJ/SCAMP5/SOCS1/TLR1/TLR10/TNF/TNFRSF21/TNFSF4	Biological Process
GO:0071216	cellular response to biotic stimulus	25/875	1.71E-06	0.000577	APAF1/BMP6/CCL3/CCR5/CD180/CX3CR1/CXCL10/ICAM1/IFNG/IL12A/IL6/LCN2/LTF/MAPK14/MAPK3/PDE4B/PRDM1/RIPK2/TICAM2/TLR1/TLR5/TNF/TNFAIP3/TNFSF4/TXNIP	Biological Process
GO:0050707	regulation of cytokine secretion	22/875	2.02E-06	0.000594	AIM2/ALOX15B/CAMP/CASP5/CCL3/CCR7/CD34/CD58/CLEC5A/HLA-DRB5/IFNG/IL6/LGALS9/MAPK14/PTGER4/SCAMP5/SOCS1/TLR1/TLR10/TNF/TNFRSF21/TNFSF4	Biological Process
GO:0006914	cellular defense	14/875	2.67E-06	0.000691	CCR2/CCR3/CCR5/CLEC5A/CX3CR1/CXCR2/GNLY/ITK/KIR3DL2/KLRC2/KLRG1/LGALS3BP/N	Biological Process

68	response				CF1/SH2D1A	Process
GO:0001906	cell killing	19/875	3.02E-06	0.000691	BCL2L11/CAMP/CTSG/DEFA1/DEFA1B/DEFA3/DEFA4/ELANE/FCER2/GNLY/ICAM1/IFNG/IL12A/KIR3DL1/LAG3/LGALS9/NCF1/SH2D1A/STX7	Biological Process
GO:0070098	chemokine-mediated signaling pathway	16/875	3.07E-06	0.000691	CCL3/CCR2/CCR3/CCR5/CCR7/CMKLR1/CX3CR1/CXCL10/CXCL2/CXCL5/CXCR1/CXCR2/CXCR4/PF4/PPBP/ROBO1	Biological Process
GO:0032609	interferon-gamma production	18/875	4.48E-06	0.000907	AZI2/CCR2/CCR7/EOMES/HLA-DPB1/HLA-DRB5/IL12A/IL18R1/ISG15/ITK/LGALS9/PDE4B/PGLYRP1/RIPK2/TICAM2/TLR8/TNF/TNFSF4	Biological Process
GO:0015671	oxygen transport	7/875	5.02E-06	0.000967	HBA1/HBA2/HBB/HBD/HBG1/HBG2/IPCEF1	Biological Process
GO:0031643	positive regulation of myelination	6/875	7.93E-06	0.001361	DICER1/HGF/NRG1/PARD3/TENM4/WASF3	Biological Process
GO:0002292	T cell differentiation involved in immune response	12/875	8.41E-06	0.001361	CLEC4D/EOMES/IFNG/IL18R1/IL6/LEF1/LGALS9/MYB/PTGER4/RELB/RIPK2/TNFSF4	Biological Process
GO:0031646	positive regulation of neurological system process	7/875	1.38E-05	0.001864	DICER1/HGF/IL6/NRG1/PARD3/TENM4/WASF3	Biological Process
GO:0007431	salivary gland development	10/875	3.25E-05	0.003549	EDAR/HGF/IL6/LAMA5/NFIB/NRP1/NTN4/TFCP2L1/TGM2/TNF	Biological Process
GO:0015701	bicarbonate transport	10/875	3.25E-05	0.003549	CA1/CA14/HBA1/HBA2/HBB/SLC26A2/SLC26A6/SLC4A1/SLC4A10/SLC4A3	Biological Process
GO:0001525	angiogenesis	42/875	3.42E-05	0.003645	APOLD1/ARHGAP24/BTG1/CALCRL/CCR2/CCR3/CD34/CEACAM1/CHI3L1/COL4A3/CX3CR1/CXCL10/CYP1B1/DICER1/EGF/EPGN/EPHA2/EPHB1/FASLG/FGF2/FGF9/HGF/HOXA5/HOXB3/IL	Biological Process

					6/ITGAV/LAMA5/LEF1/MAPK14/NRARP/NRCAM/NRP1/PF4/PTGIS/RBPJ/ROBO1/ROCK1/ROCK2/SERPINF1/SPARC/TMIGD2/TNFAIP3	
GO:0032680	regulation of tumor necrosis factor production	16/875	3.56E-05	0.003691	AZU1/BPI/CCL3/CCR2/CD34/ERRFI1/IFNG/IRAK3/LGALS9/LTF/ORM1/PF4/RIPK2/TBC1D23/TLR1/TNFAIP3	Biological Process
GO:0003158	endothelium development	17/875	3.93E-05	0.003974	ACVR2B/APOLD1/BMP6/BTG1/CD34/CXCL10/ICAM1/LAMA5/NRG1/NRP1/PTPRS/RBPJ/RDX/ROCK1/ROCK2/STK3/TNF	Biological Process
GO:0007159	leukocyte cell-cell adhesion	46/875	4.55E-05	0.004278	AZI2/CCR2/CCR7/CD83/CD8B/CLEC4D/EOMES/FLT3/HLA-DMA/HLA-DPB1/HLA-DQA2/HLA-DQB1/HLA-DRB5/ICAM1/ICOSLG/IFNG/IL12A/IL18R1/IL6/ITK/LAG3/LEF1/LGALS9/MAFB/MAIP3K8/MYB/NCK2/NRARP/PATZ1/PDE5A/PODXL2/PTGER4/RELB/RIPK2/ROCK1/SATB1/SIRPG/SIT1/SPTA1/TMIGD2/TNF/TNFRSF21/TNFSF4/TNFSF8/VNN1/ZC3H8	Biological Process
GO:0042063	gliogenesis	26/875	5.68E-05	0.004788	ARHGEF10/AZU1/CCL3/CDK5R1/CXCR4/DICER1/EGR2/HMBS/LEF1/NFIB/NFIX/NRG1/P2RY12/PARD3/PHGDH/PICK1/PRKCI/S100B/SERPINE2/SH3TC2/SOX5/SRGAP2/TENM4/TNFRSF21/TSPAN2/WASF3	Biological Process
GO:0044110	growth involved in symbiotic interaction	7/875	9.60E-05	0.006582	CAMP/CTSG/ELANE/IFNG/MPO/PGLYRP1/TNF	Biological Process
GO:0044116	growth of symbiont involved in interaction with host	7/875	9.60E-05	0.006582	CAMP/CTSG/ELANE/IFNG/MPO/PGLYRP1/TNF	Biological Process
GO:1902105	regulation of leukocyte differentiation	27/875	0.000118	0.007678	CCL3/CD83/FAM213A/FLT3/FLT3LG/GPR68/HLA-DMA/IFNG/IL12A/IL6/LEF1/LGALS9/LTF/MAFB/MYB/NME1/NRARP/OGT/PF4/PGLYRP1/PPARGC1B/PRDM1/RIPK2/TNF/TNFSF4/VNN1/ZC3H8	Biological Process
GO:19037	positive regulation of	21/875	0.00012	0.007678	CD83/FLT3LG/GPR68/HLA-DMA/HOXA5/IFNG/IL12A/IL6/ISG15/LEF1/LGALS9/MAPK14/MYB/	Biological

08	hemopoiesis				OGT/PF4/PPARGC1B/PRDM1/RIPK2/TNF/TNFSF4/VNN1	Process
GO:00512 22	positive regulation of protein transport	41/875	0.00013	0.008234	AIM2/AKAP6/ALOX15B/ASPH/BMP6/C2CD5/CAMP/CASP5/CCL3/CD34/CD38/CD58/CDK5R1/CLC5A/DAB2/DACT1/EDAR/EGF/GOLPH3L/GPR68/HLA-DRB5/IFNG/IL18R1/IL6/ITGAX/JUP/KANK1/LGALS9/MAPK14/NLGN2/NRG1/PLK3/PTGER4/RHOU/RPL28/SCAMP5/STOM/TNF/TNFSF4/TRIP6/UGCG	Biological Process
GO:00069 59	humoral immune response	24/875	0.000141	0.008615	A2M/AZU1/C1QA/CAMP/CCR7/CD83/CFH/DEFA1/DEFA1B/DEFA3/DEFA4/FCER2/HLA-DQB1/HLA-DRB5/IFNG/IL6/LTF/PROS1/RBPJ/SH2D1A/SLPI/SPNS2/TNF/TNFRSF21	Biological Process
GO:00441 46	negative regulation of growth of symbiont involved in interaction with host	6/875	0.000161	0.009462	CAMP/CTSG/ELANE/IFNG/MPO/TNF	Biological Process
GO:00433 72	positive regulation of CD4-positive; alpha-beta T cell differentiation	7/875	0.000177	0.009975	CD83/IFNG/IL6/LGALS9/MYB/RIPK2/TNFSF4	Biological Process
GO:00457 85	positive regulation of cell adhesion	36/875	0.000198	0.010844	AZU1/CCR2/CCR7/CD83/FBLN2/HLA-DMA/HLA-DPB1/HLA-DQA2/HLA-DQB1/HLA-DRB5/ICL6/IFNG/IL12A/IL6/ITGAV/LEF1/LGALS9/LIMS1/MAP3K8/MYB/MYO10/NCK2/NET1/NINJ1/NRG1/OLFM4/RIPK2/ROCK1/SIRPG/SPTA1/TGM2/TMIGD2/TNF/TNFSF4/TPM1/VNN1	Biological Process
GO:00450 73	regulation of chemokine biosynthetic process	5/875	0.000238	0.012177	AZU1/ELANE/IFNG/IL6/TNF	Biological Process
GO:00454 46	endothelial cell differentiation	14/875	0.000257	0.012896	ACVR2B/APOLD1/BMP6/BTG1/ICAM1/LAMA5/NRG1/NRP1/PTPRS/RBPJ/RDX/ROCK1/ROCK2/TNF	Biological Process

GO:00425 52	myelination	15/875	0.000265	0.013088	ARHGEF10/CXCR4/DICER1/EGR2/HGF/IFNG/MAL/NRG1/PARD3/PMP22/SH3TC2/TENM4/TNFRSF21/TSPAN2/WASF3	Biological Process
GO:00512 49	regulation of lymphocyte activation	36/875	0.000273	0.013263	CCR2/CCR7/CD38/CD83/FLT3/FLT3LG/HLA-DMA/HLA-DPB1/HLA-DQA2/HLA-DQB1/HLA-DRB5/ICOSLG/IFNG/IL12A/IL6/LAG3/LGALS9/MAP3K8/MERTK/MYB/NCK2/NRARP/PDE5A/PGLYRP1/PRDM1/RIPK2/SIRPG/SIT1/SPTA1/THOC1/TMIGD2/TNFAIP3/TNFRSF21/TNFSF4/VNN1/ZC3H8	Biological Process
GO:19034 09	reactive oxygen species biosynthetic process	13/875	0.000309	0.014541	CD34/CLCN3/CYP1B1/ESR1/HBB/ICAM1/IFNG/IL6/MPO/NCF1/PTGIS/TLR5/TNF	Biological Process
GO:00972 85	cell-type specific apoptotic process	40/875	0.000334	0.015478	AGRN/APAF1/BAG3/BCL2L11/BTG1/CCL3/CCR7/CD248/CDK5R1/CLEC5A/COL4A3/DICER1/FAM134B/FASLG/GCLM/GIMAP8/ICAM1/IFNG/IL12A/IL6/ITGA1/LEF1/LGALS9/LGMN/MERTK/NAIP/NEFL/NLRC4/NRBP2/NRG1/NRP1/PRKCI/ROCK1/RYR2/STK3/TNF/TNFAIP3/TNFRSF21/TSN2/SC22D3/ZC3H8	Biological Process
GO:00713 96	cellular response to lipid	37/875	0.000337	0.015478	BMP6/CCL3/CCR5/CD180/CX3CR1/CXCL10/ERRFI1/ESR1/FBXO32/FECH/HMBS/ICAM1/IFNG/IL12A/IL6/KANK2/KLF9/LCN2/LEF1/LTF/MAPK14/MAPK3/NME1/OGT/PDE4B/PID1/PRDM1/RIPK2/ROCK2/SERPINF1/SREBF1/THRB/TICAM2/TLR5/TNF/TNFAIP3/TNFSF4	Biological Process
GO:19001 82	positive regulation of protein localization to nucleus	15/875	0.000367	0.01574	AKAP6/BMP6/CDK5RAP3/DAB2/DACT1/EDAR/EGF/IL18R1/IL6/JUP/KANK1/LGALS9/MAPK14/TNF/TRIP6	Biological Process
GO:00420 33	chemokine biosynthetic process	5/875	0.00037	0.01574	AZU1/ELANE/IFNG/IL6/TNF	Biological Process
GO:00107 99	regulation of peptidyl-threonine	8/875	0.000391	0.01623	AZU1/CHI3L1/DDIT4/EGF/PARD3/RIPK2/SPRY2/STOX1	Biological Process

	phosphorylation					
GO:00509 21	positive regulation of chemotaxis	16/875	0.000397	0.01623	AZU1/CCL3/CCR2/CCR7/CMKLR1/CXCL10/CXCL2/CXCL5/FGF2/IL12A/IL6/LGALS9/NRP1/PD GFB/PF4/PPBP	Biological Process
GO:00423 07	positive regulation of protein import into nucleus	14/875	0.000408	0.016453	AKAP6/BMP6/DAB2/DACT1/EDAR/EGF/IL18R1/IL6/JUP/KANK1/LGALS9/MAPK14/TNF/TRIP6	Biological Process
GO:19030 35	negative regulation of response to wounding	19/875	0.000428	0.016831	CALCRL/CD34/CX3CR1/ELANE/FGF2/IER3/NLRP6/PDGFB/PGLYRP1/PLAUR/PRKG1/PROS1/P TGER4/PTGIS/RPS19/SERPINB2/SERPINE2/SERPINF1/TNFAIP3	Biological Process
GO:19016 54	response to ketone	19/875	0.000505	0.019042	AVPR1A/CCR7/CD38/ERRFI1/FBXO32/FECH/HMBS/IL6/KLF2/KLF9/NEFL/NME1/ROCK2/SERP INF1/SOCS1/SREBF1/TNFSF4/TXNIP/TYMS	Biological Process
GO:00507 55	chemokine metabolic process	5/875	0.00055	0.019866	AZU1/ELANE/IFNG/IL6/TNF	Biological Process
GO:00459 32	negative regulation of muscle contraction	6/875	0.00059	0.02057	CALCRL/GUCY1A3/NCF1/PDE5A/PRKG1/TNNT1	Biological Process
GO:00550 23	positive regulation of cardiac muscle tissue growth	6/875	0.00059	0.02057	AKAP6/FGF2/FGF9/MAPK14/NRG1/RBPJ	Biological Process
GO:19011 84	regulation of ERBB signaling pathway	12/875	0.000771	0.025786	AFAP1L2/EGF/EPGN/ERRFI1/FASLG/ITGA1/LGMN/NCK2/PLAUR/RBPJ/SH3TC2/SPRY2	Biological Process
GO:00083 60	regulation of cell shape	17/875	0.000915	0.029391	ARHGAP18/CCL3/CDC42EP1/CDC42EP3/COCH/EPB42/EPS8/FGD4/ICAM1/IL6/MYO10/PALM/R DX/RHOU/S100B/SPTA1/WASF3	Biological Process
GO:00454 28	regulation of nitric oxide biosynthetic	9/875	0.000949	0.029544	CD34/ESR1/HBB/ICAM1/IFNG/IL6/PTGIS/TLR5/TNF	Biological Process

	process					
GO:00514 53	regulation of intracellular pH	10/875	0.000968	0.029544	ATP6V0E2/AVPR1A/CLCN3/FASLG/SLC26A2/SLC26A6/SLC4A1/SLC4A10/SLC4A3/TMEM165	Biological Process
GO:00609 96	dendritic spine development	10/875	0.000968	0.029544	ACSL4/CAPRIN2/CDK5R1/CUX2/EPHB1/NCK2/PALM/PLK2/SHANK1/SRGAP2	Biological Process
GO:00026 90	positive regulation of leukocyte chemotaxis	12/875	0.000971	0.029544	CCL3/CCR2/CCR7/CMKLR1/CXCL10/CXCL2/CXCL5/IL12A/IL6/LGALS9/PF4/PPBP	Biological Process
GO:00026 83	negative regulation of immune system process	34/875	0.000999	0.029952	A2M/BPI/CCL3/CCR2/FLT3/GCSAM/GPR68/HIST1H4A/HLA-DRB5/HOXA5/IRAK3/LAG3/LGALS9/LTF/MAFB/MERTK/NLRP6/NME1/NRARP/OLFM4/PDE5A/PF4/PGLYRP1/PRDM1/PTGER4/RPS19/THOC1/TICAM2/TNF/TNFAIP3/TNFRSF21/TNFSF4/TSC22D3/ZC3H8	Biological Process
GO:00068 09	nitric oxide biosynthetic process	10/875	0.001107	0.032028	CD34/CYP1B1/ESR1/HBB/ICAM1/IFNG/IL6/PTGIS/TLR5/TNF	Biological Process
GO:00971 91	extrinsic apoptotic signaling pathway	24/875	0.001108	0.032028	BAG3/BCL2L11/CTTN/CX3CR1/FASLG/GCLM/ICAM1/IFI6/IFNG/IL12A/ITGAV/ITM2C/LCN2/MAL/MOAP1/NRG1/NRP1/PF4/SH3RF1/STK3/TICAM2/TNF/TNFAIP3/TNFSF10	Biological Process
GO:00072 49	I-kappaB kinase/NF-kappaB signaling	26/875	0.001251	0.033703	AZI2/BIRC3/CCR7/EDAR/EEF1D/ESR1/FASLG/IL18R1/LGALS9/LTF/NLRP6/OLFM4/PER1/PLK2/RELB/RIPK2/ROCK1/ROCK2/S100B/TIAF1/TICAM2/TLR8/TNF/TNFAIP3/TNFSF10/TRIP6	Biological Process
GO:00715 49	cellular response to dexamethasone stimulus	6/875	0.001277	0.033703	ERRFI1/FBXO32/FECH/HMBS/IL6/SERPINF1	Biological Process
GO:00321 02	negative regulation of response to external stimulus	25/875	0.001367	0.035009	CALCRL/CD34/CX3CR1/ELANE/FGF2/IER3/KANK2/LTF/NLRP6/NRBP2/NRP1/PDGFB/PGLYRP1/PLAUR/PRDM1/PRKG1/PROS1/PTGER4/PTGIS/ROBO1/RPS19/SERPIN2/SERPINE2/SERPINF1/TNFAIP3	Biological Process

GO:00314 97	chromatin assembly	18/875	0.001424	0.036235	ASF1B/CENPQ/CENPT/CENPV/H1FX/H3F3A/HIST1H1A/HIST1H2BL/HIST1H2BN/HIST1H2BO/ HIST1H3A/HIST1H3B/HIST1H3C/HIST1H4A/HIST2H3A/HIST2H3C/HMGA1/MCM2	Biological Process
GO:19016 55	cellular response to ketone	10/875	0.001627	0.038931	ERRFI1/FBXO32/FECH/HMBS/IL6/KLF2/KLF9/ROCK2/SERPINF1/TNFSF4	Biological Process
GO:00507 27	regulation of inflammatory response	26/875	0.001646	0.038931	A2M/BIRC3/CALCRL/CASP5/CCL3/CCR2/CCR7/CFH/CX3CR1/ELANE/IER3/IL6/MAPK14/NLRP 6/PER1/PGLYRP1/PROS1/PTGER4/PTGIS/RPS19/SERPINF1/TBC1D23/TLR10/TNF/TNFAIP3/TNF SF4	Biological Process
GO:00329 70	regulation of actin filament-based process	30/875	0.001833	0.042133	ADD2/ARFIP1/ARHGAP18/ARHGEF10/CCR7/CDC42EP1/CDC42EP3/CDK5R1/CFL2/CTTN/DIXD C1/EPS8/ICAM1/JUP/KANK1/LIMA1/NCK2/PARD3/PDE4B/PICK1/PTGER4/RDX/ROCK1/ROCK2 /RYR2/SHANK1/SPTA1/SPTBN5/SYNPO/TPM1	Biological Process
GO:00001 83	chromatin silencing at rDNA	8/875	0.00193	0.043638	H3F3A/HIST1H3A/HIST1H3B/HIST1H3C/HIST1H4A/HIST2H3A/HIST2H3C/TAF1A	Biological Process
GO:00468 24	positive regulation of nucleocytoplasmic transport	14/875	0.001972	0.044081	AKAP6/BMP6/DAB2/DACT1/EDAR/EGF/IL18R1/IL6/JUP/KANK1/LGALS9/MAPK14/TNF/TRIP6	Biological Process
GO:00431 54	negative regulation of cysteine-type endopeptidase activity involved in apoptotic process	12/875	0.00204	0.0451	BIRC3/FASLG/HERPUD1/HGF/IFI6/IL6/LEF1/NAIP/NLRC4/PLAUR/SH3RF1/TNFSF10	Biological Process
GO:00080 15	blood circulation	37/875	0.002061	0.045127	ACSM3/ACTA2/ADRB1/AKAP9/ASPH/AVPR1A/AZU1/CD34/CD38/COL4A3/CTSG/CXCL10/EPH X2/FGFBP3/GCLM/GUCY1A3/HBB/ICAM1/IER3/IFNG/ITGA1/JUP/MME/NTSR1/OLR1/OPRL1/P DE3A/PDE4B/PDE5A/PDGFB/PRKG1/RYR2/SMAD5/SREBF1/THRB/TPM1/TRPM4	Biological Process

GO:00485 20	positive regulation of behavior	16/875	0.002073	0.045127	AZU1/CCL3/CCR2/CCR7/CMKLR1/CXCL10/CXCL2/CXCL5/FGF2/IL12A/IL6/LGALS9/NRP1/PD GFB/PF4/PPBP	Biological Process
GO:00327 76	DNA methylation on cytosine	7/875	0.002074	0.045127	H3F3A/HIST1H3A/HIST1H3B/HIST1H3C/HIST1H4A/HIST2H3A/HIST2H3C	Biological Process
GO:00450 17	glycerolipid biosynthetic process	24/875	0.002213	0.047475	ABHD5/ACSL4/AGPAT4/ELOVL7/ETNK1/ETNK2/FAR1/FGF2/LPL/OCRL/PDGFB/PHOSPHO1/PI GF/PLA2G12A/PLA2G4A/PLA2G4B/PLA2G4C/PLAUR/PLD1/PLD4/SACM1L/SIK1/SREBF1/SYNJ 1	Biological Process
GO:00217 95	cerebral cortex cell migration	8/875	0.002241	0.047475	CCDC141/CDK5R1/CX3CR1/DIXDC1/MDGA1/NRP1/ROBO1/SRGAP2	Biological Process
GO:00305 20	intracellular estrogen receptor signaling pathway	8/875	0.002241	0.047475	DEFA1/DEFA1B/DEFA3/ESR1/KANK2/PHB2/PPARGC1B/ZNF366	Biological Process
GO:00329 56	regulation of actin cytoskeleton organization	26/875	0.002258	0.047592	ADD2/ARFIP1/ARHGAP18/ARHGEF10/CCR7/CDC42EP1/CDC42EP3/CDK5R1/CFL2/CTTN/DIXD C1/EPS8/ICAM1/KANK1/LIMA1/NCK2/PICK1/PTGER4/RDX/ROCK1/ROCK2/SHANK1/SPTA1/S PTBN5/SYNPO/TPM1	Biological Process
GO:00513 84	response to glucocorticoid	17/875	0.002305	0.048084	ALPL/AVPR1A/BMP6/ERRF1/FBXO32/FECH/HMBS/IL6/KLF9/NEFL/PPARGC1B/PTGDS/S100B /SERPINF1/SPARC/TNF/TYMS	Biological Process
GO:00068 85	regulation of pH	11/875	0.002329	0.048323	ATP6V0E2/AVPR1A/CLCN3/FASLG/SLC26A2/SLC26A6/SLC4A1/SLC4A10/SLC4A3/SLC9A4/TM EM165	Biological Process
GO:00456 01	regulation of endothelial cell differentiation	6/875	0.002452	0.050261	APOLD1/BMP6/BTG1/ROCK1/ROCK2/TNF	Biological Process
GO:00313	regulation of cell	9/875	0.002514	0.050867	BCL2L11/FCER2/ICAM1/IFNG/IL12A/LAG3/LGALS9/SH2D1A/STX7	Biological

41	killing					Process
GO:000176	leukocyte homeostasis	11/875	0.002585	0.05153	BCL2L11/FLT3/IFNG/IL6/LGALS9/PDE4B/SPNS2/SPTA1/TNFAIP3/TSC22D3/ZC3H8	Biological Process
GO:0007585	respiratory gaseous exchange	10/875	0.002611	0.05153	BPGM/CSF2RB/GLS/HOXA5/MAFB/NLGN2/NTSR1/SLC5A3/TRAF4/TSHZ3	Biological Process
GO:0030278	regulation of ossification	19/875	0.002666	0.052361	ACVR2B/BMP6/CCL3/DHRS3/EGR2/HGF/ID3/IFITM1/IL6/JUND/KL/LTF/PBX1/PHOSPHO1/PTGER4/RBPJ/SMAD5/TNF/TOB1	Biological Process
GO:0043244	regulation of protein complex disassembly	12/875	0.002726	0.052758	ADD2/ASPH/CFL2/EPS8/IRAK3/LIMA1/RDX/SBDS/SPTA1/SPTBN5/SYNJ1/TNF	Biological Process
GO:0045161	neuronal ion channel clustering	4/875	0.002738	0.052758	AGRN/CNTNAP2/NRCAM/PICK1	Biological Process
GO:0090150	establishment of protein localization to membrane	33/875	0.002837	0.053776	BCL2L11/C2CD5/CACNB1/CDK5R1/DYNLL1/EPHA2/JUP/LAMA5/MOAP1/NCF1/PACSIN1/PALM/PARD3/PID1/PRKCI/RDX/ROCK1/ROCK2/RPL18/RPL18A/RPL28/RPL8/RPS15/RPS18/RPS19/RPS26/RPS4X/RPS5/SRP54/STOM/TNF/WRB/ZDHHC18	Biological Process
GO:0051702	interaction with symbiont	8/875	0.002979	0.054119	CAMP/CCL3/CTSG/ELANE/LEF1/LTF/NCF1/STOM	Biological Process
GO:0032103	positive regulation of response to external stimulus	25/875	0.003061	0.055289	AZU1/BMP6/CCL3/CCR2/CCR7/CD180/CMKLR1/CXCL10/CXCL2/CXCL5/FGF2/IL12A/IL6/LGALS9/NRP1/PDGFB/PF4/PPBP/PTGER4/RPS19/SCARF1/TLR10/TNF/TNFSF4/WDFY3	Biological Process
GO:2001057	reactive nitrogen species metabolic process	11/875	0.003164	0.056718	CD34/CYP1B1/ESR1/HBB/ICAM1/IFNG/IL6/MARC1/PTGIS/TLR5/TNF	Biological Process
GO:00026	regulation of immune	35/875	0.003275	0.057715	A2M/AIM2/BIRC3/CCR2/CD8B/CFH/ELMOD2/FAM131B/FANCL/FCER2/FCGR3B/HIST1H3A/HI	Biological

97	effector process				ST1H3B/HIST1H3C/ICAM1/IFNG/IL12A/IL6/IRAK3/LAG3/LGALS9/MYB/MYLK/PGLYRP1/PRO S1/RIPK2/RPS19/SH2D1A/STOM/STX7/THOC1/TNF/TNFAIP3/TNFSF4/TRPM4	Process
GO:00096 36	response to toxic substance	19/875	0.003424	0.05946	ALPL/AQP10/CCL3/CYP1B1/EPHX2/FECH/GUCY1A3/HMBS/IL6/LCN2/MAPK3/MARC1/MGMT/ MPO/NEFL/PLA2G4A/TRPM6/TYMS/ZC3H8	Biological Process
GO:00217 00	developmental maturation	23/875	0.003546	0.061058	AGRN/BFSP1/BLOC1S5/CDK5R1/CLCN3/CNTNAP2/EPB42/HOXA5/KLF2/LTF/NRCAM/NTN4/P ALM/PDE3A/PHOSPHO1/PICK1/RBPJ/SCARF1/SEPT4/SHANK1/SLC26A6/TFCP2L1/TYMS	Biological Process
GO:00108 93	positive regulation of steroid biosynthetic process	4/875	0.003791	0.063122	BMP6/IFNG/SREBF1/TNF	Biological Process
GO:00485 05	regulation of timing of cell differentiation	4/875	0.003791	0.063122	FGF9/RBPJ/SERPINE2/SOX5	Biological Process
GO:00600 33	anatomical structure regression	4/875	0.003791	0.063122	CD248/LEF1/NINJ1/SMAD5	Biological Process
GO:00352 65	organ growth	15/875	0.003924	0.064213	ACVR2B/AKAP6/BCL2L11/CACNA2D2/DUSP6/ESR1/FGF2/FGF9/LY6E/MAPK14/NRG1/RBPJ/SP RY2/STK3/TENM4	Biological Process
GO:00970 61	dendritic spine organization	7/875	0.003949	0.064213	CAPRIN2/CDK5R1/CTTN/CUX2/EPHB1/PICK1/SHANK1	Biological Process
GO:00092 14	cyclic nucleotide catabolic process	5/875	0.004104	0.065126	PDE3A/PDE4B/PDE5A/PDE7B/PDE9A	Biological Process
GO:00070 15	actin filament organization	28/875	0.004132	0.065309	ADD2/ARFIP1/ARHGAP18/ARHGEF10/CCR7/CDC42EP1/CDC42EP3/CFL2/CTTN/EPS8/ICAM1/K ANK1/LIMA1/MYLK/NCK2/PICK1/PPARGC1B/PRKCI/PTGER4/RDX/ROCK1/ROCK2/SHANK1/ SPTA1/SPTBN5/SYNPO/TPM1/WASF3	Biological Process
GO:00604	regulation of cell	14/875	0.004422	0.068063	AGRN/ARHGAP24/ATP8B1/CCR7/CDC42EP1/CDC42EP3/EPHA2/FNBP1L/ICAM1/KANK1/MYO	Biological

91	projection assembly				10/PALM/PLD1/RDX	Process
GO:0019369	arachidonic acid metabolic process	9/875	0.00455	0.068627	ALOX15B/CYP1B1/EPHX2/MAPK3/PLA2G4A/PLA2G4B/PLA2G4C/PTGDS/PTGIS	Biological Process
GO:0070555	response to interleukin-1	13/875	0.004579	0.068627	CCL3/CD38/CHI3L1/ICAM1/IL6/IRAK3/KLF2/LCN2/LGALS9/MAPK3/PRKCI/PTGIS/RIPK2	Biological Process
GO:0031349	positive regulation of defense response	35/875	0.004629	0.06912	AIM2/BIRC3/CCL3/CCR2/CCR7/CLEC4C/CLEC4D/COCH/DUSP6/IL12A/IL6/IRAK3/LAG3/LGMN/LTF/MAP3K8/MAPK14/MAPK3/NLRC4/NLRP6/PGLYRP1/PSMC6/PTGER4/RELB/RIPK2/RPS19/SH2D1A/TICAM2/TLR1/TLR10/TLR5/TLR8/TNF/TNFAIP3/TNFSF4	Biological Process
GO:0046434	organophosphate catabolic process	17/875	0.004828	0.071039	DDIT4/IER3/LIPC/NAPEPLD/NTSR1/NUDT1/OGT/PDE3A/PDE4B/PDE5A/PDE7B/PDE9A/PLA2G4A/PLA2G4B/PLA2G4C/PLD1/SYNJ1	Biological Process
GO:0001649	osteoblast differentiation	20/875	0.004994	0.072955	ACVR2B/ALPL/BMP6/CCL3/CLEC5A/EPHA2/FBL/FGF9/HGF/ID3/IFITM1/IL6/JUND/LEF1/LTF/RPS15/SMAD5/TMEM119/TNF/TOB1	Biological Process
GO:1902932	positive regulation of alcohol biosynthetic process	5/875	0.005084	0.072994	BMP6/IFNG/NTSR1/SREBF1/TNF	Biological Process
GO:0040034	regulation of development; heterochronic	4/875	0.005087	0.072994	FGF9/RBPJ/SERPINE2/SOX5	Biological Process
GO:0065004	protein-DNA complex assembly	19/875	0.005799	0.081762	ASF1B/CENPQ/CENPT/CENPV/H1FX/H3F3A/HIST1H1A/HIST1H2BL/HIST1H2BN/HIST1H2BO/HIST1H3A/HIST1H3B/HIST1H3C/HIST1H4A/HIST2H3A/HIST2H3C/MCM2/PSMC6/RAD52	Biological Process
GO:0002224	toll-like receptor signaling pathway	16/875	0.005917	0.082564	BIRC3/DUSP6/IRAK3/LGMN/LTF/MAP3K8/MAPK14/MAPK3/NLRP6/RIPK2/TICAM2/TLR1/TLR10/TLR5/TLR8/TNFAIP3	Biological Process
GO:00330	muscle cell	15/875	0.005959	0.082791	CALCRL/ELANE/FGF2/FGF9/IFNG/IL12A/IL6/MAPK14/NRG1/PAXBP1/PDGFB/RBPJ/TENM4/T	Biological

02	proliferation				NF/TNFAIP3	Process
GO:00435 76	regulation of respiratory gaseous exchange	5/875	0.006217	0.084704	GLS/NLGN2/NTSR1/SLC5A3/TSHZ3	Biological Process
GO:00973 06	cellular response to alcohol	12/875	0.006472	0.085302	ERRFI1/ESR1/FBXO32/FECH/HMBS/IL6/JUP/KANK2/KLF2/KLF9/ROCK2/SERPINF1	Biological Process
GO:19015 68	fatty acid derivative metabolic process	12/875	0.006472	0.085302	ALOX15B/AVPR1A/CYP1B1/CYP4F22/EPHX2/MAPK3/NCF1/PLA2G4A/PLA2G4B/PLA2G4C/PT GDS/PTGIS	Biological Process
GO:00703 71	ERK1 and ERK2 cascade	22/875	0.006526	0.085665	CCL3/CCR7/CHI3L1/DUSP6/EGF/EPHA2/EPHB1/ERRFI1/FGF2/ICAM1/IL6/ITGAV/LGALS9/MA PK3/NLRP6/NRP1/PDGFB/PHB2/PTGER4/RIPK2/SPRY2/TNF	Biological Process
GO:00347 28	nucleosome organization	17/875	0.006558	0.085665	ASF1B/CENPQ/CENPT/H1FX/H3F3A/HIST1H1A/HIST1H2BL/HIST1H2BN/HIST1H2BO/HIST1H3 A/HIST1H3B/HIST1H3C/HIST1H4A/HIST2H3A/HIST2H3C/HMGA1/MCM2	Biological Process
GO:00022 27	innate immune response in mucosa	5/875	0.007517	0.092456	CAMP/DEFA1/DEFA1B/DEFA3/LTF	Biological Process
GO:00343 68	protein-lipid complex remodeling	5/875	0.007517	0.092456	ABCA5/APOM/LIPC/LPL/MPO	Biological Process
GO:00343 69	plasma lipoprotein particle remodeling	5/875	0.007517	0.092456	ABCA5/APOM/LIPC/LPL/MPO	Biological Process
GO:00516 07	defense response to virus	28/875	0.007788	0.09521	AIM2/AZU1/BIRC3/CD8B/CXCL10/DDIT4/DEFA1/DEFA1B/DEFA3/DICER1/ELMOD2/FAM131B/ FANCL/FCGR3B/HIST1H3A/HIST1H3B/HIST1H3C/IFIT1B/IFIT2/IFITM1/IFITM2/IFNG/IL6/ISG15 /MYLK/STOM/TLR8/TNFAIP3	Biological Process
GO:00970 06	regulation of plasma lipoprotein particle	8/875	0.00796	0.096429	ABCA5/APOM/FECH/LIPC/LMF1/LPL/MPO/MYLIP	Biological Process

	levels					
GO:000606	protein import into nucleus	23/875	0.008162	0.097137	AKAP6/BMP6/DAB2/DACT1/EDAR/EGF/FGF9/IFNG/IL18R1/IL6/JUP/KANK1/LGALS9/MAPK14/MAPK3/PHB2/PRICKLE1/RANBP17/SFRP5/TNF/TOB1/TRIP6/TXNIP	Biological Process
GO:1902593	single-organism nuclear import	23/875	0.008162	0.097137	AKAP6/BMP6/DAB2/DACT1/EDAR/EGF/FGF9/IFNG/IL18R1/IL6/JUP/KANK1/LGALS9/MAPK14/MAPK3/PHB2/PRICKLE1/RANBP17/SFRP5/TNF/TOB1/TRIP6/TXNIP	Biological Process
GO:0000028	ribosomal small subunit assembly	4/875	0.008501	0.099701	RPS15/RPS19/RPS5/RRP7A	Biological Process
GO:0010888	negative regulation of lipid storage	4/875	0.008501	0.099701	ABHD5/IL6/ITGAV/TNF	Biological Process
GO:0043393	regulation of protein binding	16/875	0.008554	0.099794	ADD2/CAPRIN2/DAB2/HERPUD1/IFIT2/LEF1/MAPK3/NRG1/NRP1/PDGFB/PLK2/ROCK1/SLPI/PTA1/STK3/TRAF4	Biological Process
GO:0045669	positive regulation of osteoblast differentiation	8/875	0.008867	0.102031	ACVR2B/BMP6/HGF/IFITM1/IL6/JUND/LTF/SMAD5	Biological Process
GO:0002544	chronic inflammatory response	5/875	0.008996	0.102031	CAMP/CX3CR1/TNF/TNFAIP3/VNN1	Biological Process
GO:0006779	porphyrin-containing compound biosynthetic process	5/875	0.008996	0.102031	ALAS2/FECH/HMBS/SLC25A39/SPTA1	Biological Process
GO:0030509	BMP signaling pathway	14/875	0.009503	0.106807	ACVR2B/BMP6/FKBP8/FSTL1/LEF1/MAPK3/RBPJ/RGMB/RYR2/SKOR1/SMAD5/TOB1/ZCCHC12/ZFYVE16	Biological Process
GO:0046683	response to organophosphorus	14/875	0.009503	0.106807	AKAP6/AKAP9/ASPH/EGR2/JUND/NME1/P2RY12/PDE3A/PER1/PPARGC1B/SLC26A6/SPARC/SREBF1/TYMS	Biological Process

GO:0014074	response to purine-containing compound	15/875	0.010526	0.113793	AKAP6/AKAP9/ASPH/EGR2/IL6/JUND/NME1/P2RY12/PDE3A/PER1/PPARGC1B/RYR2/SLC26A6/SPARC/SREBF1	Biological Process
GO:0050673	epithelial cell proliferation	28/875	0.010638	0.113793	BMP6/CCR3/CD34/CDKN2B/EPGN/EPHA2/ERRFI1/ESR1/FGF2/FGF9/HOXA5/IFNG/IL6/IRF6/KLF9/LIMS2/NFIB/NME1/NRARP/NRP1/PDGFB/PHB2/ROBO1/SERPINF1/SPARC/STOX1/TNF/TNF AIP3	Biological Process
GO:0015697	quaternary ammonium group transport	4/875	0.010658	0.113793	CPT1B/PRKAB2/SLC22A16/SLC25A29	Biological Process
GO:0020027	hemoglobin metabolic process	4/875	0.010658	0.113793	AHSP/ALAS2/EPB42/FECH	Biological Process
GO:0009395	phospholipid catabolic process	6/875	0.010771	0.114096	LIPC/NAPEPLD/PLA2G4A/PLA2G4B/PLA2G4C/PLD1	Biological Process
GO:0001909	leukocyte mediated cytotoxicity	10/875	0.011088	0.116535	CTSG/ELANE/ICAM1/IL12A/KIR3DL1/LAG3/LGALS9/NCF1/SH2D1A/STX7	Biological Process
GO:0045445	myoblast differentiation	10/875	0.011088	0.116535	BTG1/CXCL10/DICER1/FLT3LG/ID3/MAPK14/NRG1/PRICKLE1/RBPJ/TNF	Biological Process
GO:0006323	DNA packaging	18/875	0.012126	0.12453	ASF1B/CENPQ/CENPT/CENPV/H1FX/H3F3A/HIST1H1A/HIST1H2BL/HIST1H2BN/HIST1H2BO/HIST1H3A/HIST1H3B/HIST1H3C/HIST1H4A/HIST2H3A/HIST2H3C/HMGA1/MCM2	Biological Process
GO:0031348	negative regulation of defense response	14/875	0.012207	0.125051	A2M/CALCRL/CX3CR1/ELANE/IER3/IRAK3/LGALS9/NLRP6/PGLYRP1/PTGER4/PTGIS/RPS19/SERPINF1/TNFAIP3	Biological Process
GO:0033598	mammary gland epithelial cell proliferation	5/875	0.012528	0.125219	EPHA2/ESR1/HOXA5/PHB2/ROBO1	Biological Process

GO:00024 37	inflammatory response to antigenic stimulus	7/875	0.012542	0.125219	CCR7/ELANE/HLA-DRB5/ICAM1/NLRP6/RBPJ/TNF	Biological Process
GO:00301 95	negative regulation of blood coagulation	7/875	0.012542	0.125219	CD34/PDGFB/PLAUR/PRKG1/PROS1/SERPINB2/SERPINE2	Biological Process
GO:19000 47	negative regulation of hemostasis	7/875	0.012542	0.125219	CD34/PDGFB/PLAUR/PRKG1/PROS1/SERPINB2/SERPINE2	Biological Process
GO:00060 66	alcohol metabolic process	31/875	0.012939	0.12566	ACER3/BMP6/CYP1B1/DHRS3/EPHX2/ERLIN1/FECH/FGF2/GK5/IFNG/IPMK/LEPR/LGMN/LIPC /LMF1/MINPP1/NTSR1/OCRL/PHOSPHO1/PLA2G12A/PLA2G4A/PLA2G4B/PLA2G4C/PLCH1/PL D4/SCARF1/SLC5A3/SREBF1/SYNJ1/TNF/TNFSF4	Biological Process
GO:00516 42	centrosome localization	4/875	0.01314	0.12566	ASUN/CCDC141/DYNC1LI2/PARD3	Biological Process
GO:00197 30	antimicrobial humoral response	8/875	0.013284	0.12566	AZU1/CAMP/DEFA1/DEFA1B/DEFA3/DEFA4/LTF/SLPI	Biological Process
GO:00017 71	immunological synapse formation	3/875	0.013392	0.12566	CCR7/EPHB1/NCK2	Biological Process
GO:00026 79	respiratory burst involved in defense response	3/875	0.013392	0.12566	MPO/NCF1/RPS19	Biological Process
GO:00465 01	protoporphyrinogen IX metabolic process	3/875	0.013392	0.12566	ALAS2/FECH/HMBS	Biological Process
GO:00515 97	response to methylmercury	3/875	0.013392	0.12566	FECH/HMBS/S100B	Biological Process
GO:19012	regulation of neuron	21/875	0.013942	0.12744	AGRN/BCL2L11/CCL3/CD34/CDK5R1/DDIT4/EPHB1/FAM134B/FASLG/GCLM/IL6/TTGA1/LGM	Biological

14	death				N/NAIP/NEFL/NLRC4/NRBP2/NRP1/PRKCI/ROCK1/SERPINF1	Process
GO:00029 20	regulation of humoral immune response	7/875	0.013984	0.12744	A2M/CCR7/CFH/FCER2/PROS1/SPNS2/TNF	Biological Process
GO:00001 86	activation of MAPKK activity	21/875	0.014564	0.131022	AKAP9/CSF2RB/DUSP5/DUSP6/EGF/FGF2/FGF9/FRS3/IL3RA/KL/MAP3K6/MAP3K8/MAPK3/NEFL/NRG1/PDGFB/PSMC6/RASGEF1A/SPTA1/SPTBN5/STK3	Biological Process
GO:00096 12	response to mechanical stimulus	18/875	0.014774	0.131962	BAG3/BMP6/CASP5/CHI3L1/CNTNAP2/CXCL10/IL6/JUND/JUP/LOXHD1/MAPK14/MAPK3/PTGER4/RYR2/SERPINE2/TLR5/TLR8/TXNIP	Biological Process
GO:00706 63	regulation of leukocyte proliferation	18/875	0.014774	0.131962	CCR2/CD38/HLA-DPB1/HLA-DRB5/ICOSLG/IFNG/IL12A/IL6/LGALS9/NCK2/PDE5A/PRDM1/RIPK2/SPTA1/TMIGD2/TNFAIP3/TNFRSF21/TNFSF4	Biological Process
GO:00725 11	divalent inorganic cation transport	33/875	0.015297	0.13604	AKAP6/ASP/CACHD1/CACNA2D2/CACNB1/CALCRL/CCL3/CCR5/CCR7/CXCL10/EGF/EPPIN/FGF2/ICAM1/ITGAV/LOXHD1/MCOLN2/MYB/MYLK/NIPA1/NIPA2/NIPAL2/NTSR1/OPRL1/P2RY12/PDE4B/PDGFB/RYR2/SMDT1/TCN1/TMEM165/TRPM4/TRPM6	Biological Process
GO:00717 72	response to BMP	14/875	0.015476	0.136401	ACVR2B/BMP6/FKBP8/FSTL1/LEF1/MAPK3/RBPJ/RGMB/RYR2/SKOR1/SMAD5/TOB1/ZCCHC12/ZFYVE16	Biological Process
GO:00717 73	cellular response to BMP stimulus	14/875	0.015476	0.136401	ACVR2B/BMP6/FKBP8/FSTL1/LEF1/MAPK3/RBPJ/RGMB/RYR2/SKOR1/SMAD5/TOB1/ZCCHC12/ZFYVE16	Biological Process
GO:00706 61	leukocyte proliferation	23/875	0.015526	0.136401	AZI2/CCR2/CD180/CD38/FLT3/HLA-DPB1/HLA-DRB5/ICOSLG/IFNG/IL12A/IL6/LEF1/LGALS9/NCK2/PDE5A/PRDM1/RIPK2/SATB1/SPTA1/TMIGD2/TNFAIP3/TNFRSF21/TNFSF4	Biological Process
GO:00508 19	negative regulation of coagulation	7/875	0.01554	0.136401	CD34/PDGFB/PLAUR/PRKG1/PROS1/SERPINB2/SERPINE2	Biological Process
GO:00100 02	cardioblast differentiation	4/875	0.015962	0.137333	EOMES/NRG1/PRICKLE1/RBPJ	Biological Process
GO:00709	neuron death	23/875	0.016816	0.141262	AGRN/APAF1/BCL2L11/CCL3/CD34/CDK5R1/DDIT4/EPHB1/FAM134B/FASLG/GCLM/IL6/ITGA	Biological

97					1/LGMN/NAIP/NEFL/NLRC4/NRBP2/NRP1/PRKCI/ROCK1/SERPINF1/TNFRSF21	Process
GO:0014808	release of sequestered calcium ion into cytosol by sarcoplasmic reticulum	5/875	0.016897	0.141262	AKAP6/ASPH/CCL3/CCR5/RYR2	Biological Process
GO:1903514	calcium ion transport from endoplasmic reticulum to cytosol	5/875	0.016897	0.141262	AKAP6/ASPH/CCL3/CCR5/RYR2	Biological Process
GO:0000302	response to reactive oxygen species	18/875	0.017041	0.142172	CCR7/CYP1B1/HBA1/HBA2/HBB/HGF/IL6/KLF2/LCN2/MPO/NET1/NME8/PLK3/PPARGC1B/SEN1/TNFAIP3/TPM1/TXNIP	Biological Process
GO:0003157	endocardium development	3/875	0.017699	0.143808	NRG1/RBPJ/STK3	Biological Process
GO:0045721	negative regulation of gluconeogenesis	3/875	0.017699	0.143808	IL6/LEPR/SIK1	Biological Process
GO:2000095	regulation of Wnt signaling pathway; planar cell polarity pathway	3/875	0.017699	0.143808	DAB2/DACT1/NPHP3	Biological Process
GO:0008286	insulin receptor signaling pathway	27/875	0.017825	0.144254	AKAP9/ATP6V0E2/C2CD5/CSF2RB/DUSP5/DUSP6/EGF/FGF2/FGF9/FRS3/GRB10/IL3RA/KANK1/KL/MAPK3/NEFL/NRG1/OGT/PDGFB/PID1/PRKAB2/PSMC6/RASGEF1A/SOCS1/SPTA1/SPTBN5/SREBF1	Biological Process
GO:0034341	response to interferon-gamma	15/875	0.018431	0.147636	CCL3/CD58/HLA-DPB1/HLA-DQA2/HLA-DQB1/HLA-DRB5/ICAM1/IFITM1/IFITM2/IFNG/IRF6/KYNU/LGALS9/SLC26A6/SOCS1	Biological Process

GO:0018107	peptidyl-threonine phosphorylation	9/875	0.018575	0.147636	AZU1/CDK5R1/CHI3L1/DDIT4/EGF/PARD3/RIPK2/SPRY2/STOX1	Biological Process
GO:0006979	response to oxidative stress	29/875	0.018608	0.147636	BTG1/CCR7/CD38/CYP1B1/DGKK/GCLM/HBA1/HBA2/HBB/HGF/IL6/IPCEF1/KLF2/LCN2/MGMT/MPO/NET1/NME8/NUDT1/PLK3/PPARGC1B/RAD52/RCAN2/SESN1/STOX1/TNFAIP3/TPM1/TXNIP/VNN1	Biological Process
GO:0050777	negative regulation of immune response	12/875	0.019773	0.152979	A2M/CCR2/IRAK3/LGALS9/NLRP6/OLFM4/PGLYRP1/RPS19/THOC1/TNF/TNFAIP3/TNFSF4	Biological Process
GO:0070613	regulation of protein processing	9/875	0.021674	0.163628	A2M/BIRC3/CFH/LDLRAD3/NAIP/NLRC4/PLGRKT/PROS1/SERPINE2	Biological Process
GO:0090066	regulation of anatomical structure size	34/875	0.022196	0.163628	ACTA2/ADD2/ADRB1/AQP10/ARFIP1/ARHGAP18/AVPR1A/CCR7/CD38/CDC42EP1/CDC42EP3/CDK5R1/CFL2/CLCN3/CTTN/EPHX2/EPS8/GCLM/GUCY1A3/HBB/ICAM1/ITGA1/KANK1/LIMA1/NCK2/NEFL/NRCAM/NRP1/PICK1/PRKG1/RDX/SPTA1/SPTBN5/TRPM4	Biological Process
GO:0072599	establishment of protein localization to endoplasmic reticulum	12/875	0.022309	0.163628	RPL18/RPL18A/RPL28/RPL8/RPS15/RPS18/RPS19/RPS26/RPS4X/RPS5/RYR2/SRP54	Biological Process
GO:0040017	positive regulation of locomotion	29/875	0.022615	0.163628	AZU1/CCL3/CCR2/CCR7/CMKLR1/CXCL10/CXCL2/CXCL5/DAB2/FGF2/HGF/ICAM1/IFNG/IL12A/IL6/ITGAV/LEF1/LGALS9/LGR6/MYLK/NRP1/PDGFB/PF4/PPBP/RDX/ROCK2/SPARC/TNF/TRIP6	Biological Process
GO:0002824	positive regulation of adaptive immune response based on somatic recombination of immune receptors	8/875	0.022646	0.163628	CCR2/FCER2/IFNG/IL12A/RIPK2/STX7/TNF/TNFSF4	Biological Process

	built from immunoglobulin superfamily domains					
GO:1904037	positive regulation of epithelial cell apoptotic process	4/875	0.022672	0.163628	CD248/FASLG/IL6/PRKCI	Biological Process
GO:0001774	microglial cell activation	3/875	0.022686	0.163628	AZU1/CX3CR1/TLR8	Biological Process
GO:0051969	regulation of transmission of nerve impulse	3/875	0.022686	0.163628	AVPR1A/IFNG/IL6	Biological Process
GO:0072109	glomerular mesangium development	3/875	0.022686	0.163628	ACTA2/CD34/PDGFB	Biological Process
GO:1902603	carnitine transmembrane transport	3/875	0.022686	0.163628	CPT1B/PRKAB2/SLC22A16	Biological Process
GO:0030168	platelet activation	21/875	0.023864	0.170301	A2M/DGKK/EGF/F2RL2/GNAI1/HBB/HGF/IL6/MAPK14/MAPK3/MERTK/MMRN1/P2RY12/PDGFB/PF4/PLA2G4A/PPBP/PRKG1/PROS1/SERPINE2/SPARC	Biological Process
GO:0060205	cytoplasmic membrane-bounded vesicle lumen	18/945	2.79E-07	7.40E-05	A2M/CLCN3/DEFA1/DEFA1B/DEFA3/EGF/FASLG/HBA1/HBA2/HBB/HGF/LTF/MMRN1/PDGFB/PF4/PPBP/PROS1/SPARC	Cellular Component
GO:0031983	vesicle lumen	18/945	3.38E-07	7.40E-05	A2M/CLCN3/DEFA1/DEFA1B/DEFA3/EGF/FASLG/HBA1/HBA2/HBB/HGF/LTF/MMRN1/PDGFB/PF4/PPBP/PROS1/SPARC	Cellular Component

GO:0005833	hemoglobin complex	7/945	7.39E-07	0.000108	AHSP/HBA1/HBA2/HBB/HBD/HBG1/HBG2	Cellular Component
GO:0005766	primary lysosome	7/945	8.84E-06	0.000774	AZU1/DEFA1/DEFA1B/DEFA3/DEFA4/MPO/STX7	Cellular Component
GO:0042582	azurophil granule	7/945	8.84E-06	0.000774	AZU1/DEFA1/DEFA1B/DEFA3/DEFA4/MPO/STX7	Cellular Component
GO:0032588	trans-Golgi network membrane	9/945	0.000988	0.035359	ARFIP1/GOLPH3L/HLA-DPB1/HLA-DQA2/HLA-DQB1/HLA-DRB5/LGR6/SCAMP5/TMEM165	Cellular Component
GO:0022627	cytosolic small ribosomal subunit	8/945	0.001048	0.035359	HBA1/HBA2/RPS15/RPS18/RPS19/RPS26/RPS4X/RPS5	Cellular Component
GO:0000786	nucleosome	14/945	0.001098	0.035359	H1FX/H3F3A/HIST1H1A/HIST1H2AK/HIST1H2AL/HIST1H2BL/HIST1H2BN/HIST1H2BO/HIST1H3A/HIST1H3B/HIST1H3C/HIST1H4A/HIST2H3A/HIST2H3C	Cellular Component
GO:0042613	MHC class II protein complex	5/945	0.001126	0.035359	HLA-DMA/HLA-DPB1/HLA-DQA2/HLA-DQB1/HLA-DRB5	Cellular Component
GO:0009897	external side of plasma membrane	24/945	0.00113	0.035359	CCR5/CCR7/CD34/CD69/CD83/CD8B/CLCN3/CXCL10/FASLG/FCER2/FLT3/FLT3LG/HLA-DRB5/ICAM1/IFNG/IL6/ITGA1/ITGAV/LAG3/NRCAM/P2RY12/SCNN1A/SERPINE2/TNF	Cellular Component
GO:0001726	ruffle	18/945	0.001519	0.041769	C2CD5/CTTN/EPHA2/EPH2/EPH3/EPH4/FRMD4B/ITGAV/KANK1/LAYN/MYO10/NME1/PACSIN1/PDE9A/RDX/ROCK1/S100B/SPRY2/TPM1	Cellular Component
GO:0044815	DNA packaging complex	14/945	0.001906	0.046377	H1FX/H3F3A/HIST1H1A/HIST1H2AK/HIST1H2AL/HIST1H2BL/HIST1H2BN/HIST1H2BO/HIST1H3A/HIST1H3B/HIST1H3C/HIST1H4A/HIST2H3A/HIST2H3C	Cellular Component
GO:0098552	side of membrane	36/945	0.002444	0.056327	CCR5/CCR7/CD34/CD69/CD83/CD8B/CLCN3/CXCL10/ERRFI1/FASLG/FCER2/FLT3/FLT3LG/GNAI1/GNG11/HLA-DPB1/HLA-DQA2/HLA-DQB1/HLA-DRB5/ICAM1/IFNG/IL6/ITGA1/ITGAV/ITK/JUP/LAG3/NRCAM/NTSR1/P2RY12/RGS9/SCNN1A/SERPINE2/SPTA1/STYK1/TNF	Cellular Component

GO:0005925	focal adhesion	34/945	0.00316	0.069196	ARHGAP24/CASS4/CDC42EP1/CTTN/DAB2/DIXDC1/EPHA2/FZD2/HMGA1/ICAM1/ITGA1/ITGAV/JUP/LAYN/LIMA1/LIMS1/LIMS2/MAPK3/MME/NEXN/NRP1/PLAUR/RDX/RHO/RPL18/RPL8/RPS15/RPS18/RPS19/RPS4X/RPS5/TGM2/TRIP6/TSPAN4	Cellular Component
GO:0030055	cell-substrate junction	34/945	0.004515	0.085951	ARHGAP24/CASS4/CDC42EP1/CTTN/DAB2/DIXDC1/EPHA2/FZD2/HMGA1/ICAM1/ITGA1/ITGAV/JUP/LAYN/LIMA1/LIMS1/LIMS2/MAPK3/MME/NEXN/NRP1/PLAUR/RDX/RHO/RPL18/RPL8/RPS15/RPS18/RPS19/RPS4X/RPS5/TGM2/TRIP6/TSPAN4	Cellular Component
GO:0032993	protein-DNA complex	17/945	0.007353	0.121278	H1FX/H3F3A/HIST1H1A/HIST1H2AK/HIST1H2AL/HIST1H2BL/HIST1H2BN/HIST1H2BO/HIST1H3A/HIST1H3B/HIST1H3C/HIST1H4A/HIST2H3A/HIST2H3C/JUND/JUP/LEF1	Cellular Component
GO:0032587	ruffle membrane	10/945	0.007478	0.121278	C2CD5/EPHA2/EP8/ITGAV/KANK1/NME1/PACIN1/PDE9A/SPRY2/TPM1	Cellular Component
GO:0005938	cell cortex	21/945	0.012955	0.171909	ASPH/C2CD5/CALD1/CLIC5/CTTN/CYTIP/EPB42/EP8/FNBP1L/MYO10/MYO5B/PARD3/PDZD4/PLA2G4C/RDX/SCNN1A/SEPT6/SLC4A1/SPTA1/SPTBN5/STOX1	Cellular Component
GO:0014701	junctional sarcoplasmic reticulum membrane	3/945	0.013595	0.175098	AKAP6/ASPH/RYR2	Cellular Component
GO:0031225	anchored component of membrane	15/945	0.014736	0.184362	ALPL/CD58/CEACAM6/CEACAM8/FCGR3B/LPL/LY6E/LYPD3/MDGA1/MMP25/PLAUR/RGMB/TFPI/TNFRSF10C/VNN1	Cellular Component
GO:0005868	cytoplasmic dynein complex	5/945	0.017274	0.208155	DNAH8/DYNC1LI2/DYNLL1/DYNLT3/NME8	Cellular Component
GO:0034704	calcium channel complex	8/945	0.018063	0.208155	AKAP6/ASPH/CACNA2D2/CACNB1/HERPUD1/PDE4B/RYR2/SMDT1	Cellular Component
GO:0032420	stereocilium	5/945	0.022655	0.243255	ATP8B1/CLIC5/EP8/LOXHD1/RDX	Cellular Component

GO:19025 55	endoribonuclease complex	4/945	0.02309	0.243255	CLP1/DICER1/POP1/RPP40	Cellular Component
GO:00725 62	blood microparticle	13/945	0.026346	0.256375	A1BG/A2M/CFH/HBA1/HBA2/HBB/HBD/HBG2/LGALS3BP/ORM1/PROS1/SLC4A1/STOM	Cellular Component
GO:00319 01	early endosome membrane	11/945	0.028667	0.27289	ATP9A/CD8B/CLCN3/EPHB1/LAMP5/OCRL/PLA2G4B/STX7/TICAM2/TMEM165/ZFYVE16	Cellular Component
GO:00053 44	oxygen transporter activity	7/872	2.65E-06	0.000679	HBA1/HBA2/HBB/HBD/HBG1/HBG2/IPCEF1	Molecular Function
GO:00016 37	G-protein coupled chemoattractant receptor activity	9/872	2.76E-06	0.000679	CCR2/CCR3/CCR5/CCR7/CMKLR1/CX3CR1/CXCR1/CXCR2/CXCR4	Molecular Function
GO:00049 50	chemokine receptor activity	9/872	2.76E-06	0.000679	CCR2/CCR3/CCR5/CCR7/CMKLR1/CX3CR1/CXCR1/CXCR2/CXCR4	Molecular Function
GO:00510 18	protein kinase A binding	9/872	0.000222	0.03275	AKAP3/AKAP6/AKAP9/C2orf88/DACT1/PRKAR1B/PRKAR2B/RDX/RYR2	Molecular Function
GO:00055 39	glycosaminoglycan binding	22/872	0.000636	0.050937	AGRN/AZU1/CFH/COL5A3/CTSG/CXCL10/ELANE/FGF2/FGF9/FGFBP3/FSTL1/LAYN/LIPC/LPL /LTF/MPO/NELL2/NRP1/PF4/PGLYRP1/PODXL2/SERPINE2	Molecular Function
GO:00051 64	tumor necrosis factor receptor binding	7/872	0.000752	0.050937	FASLG/LTB/TNF/TNFSF10/TNFSF4/TNFSF8/TRAF4	Molecular Function
GO:00082 01	heparin binding	18/872	0.000756	0.050937	AZU1/CFH/COL5A3/CTSG/CXCL10/ELANE/FGF2/FGF9/FGFBP3/FSTL1/LIPC/LPL/LTF/MPO/NE LL2/NRP1/PF4/SERPINE2	Molecular Function
GO:00199 56	chemokine binding	5/872	0.000759	0.050937	A2M/CCR5/CCR7/CXCR1/CXCR2	Molecular Function

GO:00452 36	CXCR chemokine receptor binding	5/872	0.001433	0.088138	CXCL10/CXCL2/CXCL5/PF4/PPBP	Molecular Function
GO:00046 20	phospholipase activity	12/872	0.002544	0.122439	CCR5/F2RL2/LIPC/LPL/NAPEPLD/PLA2G12A/PLA2G4A/PLA2G4B/PLA2G4C/PLCH1/PLD1/PLD4	Molecular Function
GO:00352 50	UDP-galactosyltransferase activity	5/872	0.00315	0.136734	B3GALNT1/B3GALT2/B4GALT2/UGT8/WDFY3	Molecular Function
GO:00080 47	enzyme activator activity	37/872	0.004649	0.180559	AFAP1L2/AGAP1/AGFG1/AHSA2/APAF1/ARHGAP18/ARHGAP23/ARHGAP24/ARHGAP29/ATP1B2/CCL3/CDC42EP1/CDC42EP3/CDK5R1/DNAJB1/EGF/ELMOD2/ERRFI1/LTF/MAL/MOB1B/NRG1/OCRL/OGT/PDGFB/RGS1/RGS18/RGS9/RIN2/SPRY2/SRGAP1/SRGAP2/STK3/SYDE2/TBC1D16/TBC1D8B/TIAM2	Molecular Function
GO:00469 06	tetrapyrrole binding	15/872	0.005163	0.190476	CYP1B1/CYP4F22/FECH/GUCY1A3/HBA1/HBA2/HBB/HBD/HBG1/HBG2/MPO/MUT/PGRMC1/PTGIS/TCN1	Molecular Function
GO:00080 81	phosphoric diester hydrolase activity	11/872	0.006208	0.218148	CCR5/F2RL2/NAPEPLD/PDE3A/PDE4B/PDE5A/PDE7B/PDE9A/PLCH1/PLD1/PLD4	Molecular Function
GO:19016 81	sulfur compound binding	21/872	0.006947	0.232862	AGRN/AZU1/CD34/CFH/COL5A3/CTSG/CXCL10/ELANE/FGF2/FGF9/FGFBP3/FSTL1/LIPC/LPL/LTF/MPO/NELL2/NRP1/PF4/RYR2/SERPINE2	Molecular Function
GO:00170 49	GTP-Rho binding	4/872	0.008254	0.234258	CDC42EP1/CDC42EP3/NET1/ROCK2	Molecular Function
GO:00305 51	cyclic nucleotide binding	6/872	0.010358	0.255493	PDE3A/PDE4B/PDE5A/PRKAR1B/PRKAR2B/PRKG1	Molecular Function
GO:00198 25	oxygen binding	7/872	0.010734	0.255493	CYP1B1/HBA1/HBA2/HBB/HBD/HBG1/HBG2	Molecular Function
GO:00508	extracellular matrix	7/872	0.010734	0.255493	AGRN/CD248/FBLN2/ITGAV/LYPD3/NTN4/SPARC	Molecular

40	binding					Function
GO:0005080	protein kinase C binding	7/872	0.014895	0.297061	AVPR1A/DACT1/ITGAV/NELL2/PARD3/PICK1/SDPR	Molecular Function
GO:0019843	rRNA binding	7/872	0.014895	0.297061	ERI1/RPF2/RPL8/RPS18/RPS4X/RPS5/SBDS	Molecular Function
GO:0015643	toxic substance binding	3/872	0.017303	0.327386	AZU1/EPHX2/TMEM181	Molecular Function
GO:0015106	bicarbonate transmembrane transporter activity	4/872	0.018606	0.343231	SLC26A2/SLC26A6/SLC4A1/SLC4A10	Molecular Function
GO:0016209	antioxidant activity	8/872	0.02752	0.425979	APOM/FAM213A/HBA1/HBA2/HBB/IPCEF1/MPO/TXNRD3	Molecular Function
GO:0070402	NADPH binding	3/872	0.027739	0.425979	CBR3/CBR4/CRYZ	Molecular Function
GO:1901981	phosphatidylinositol phosphate binding	11/872	0.027825	0.425979	APBA1/ARFIP1/GOLPH3L/KCNJ1/MYO10/NCF1/OGT/PARD3/SH3PXD2B/SYTL2/ZFYVE16	Molecular Function
GO:0005096	GTPase activator activity	21/872	0.028734	0.425979	AGAP1/AGFG1/ARHGAP18/ARHGAP23/ARHGAP24/ARHGAP29/CDC42EP1/CDC42EP3/ELMOD2/ERRFI1/OCRL/RGS1/RGS18/RGS9/RIN2/SRGAP1/SRGAP2/SYDE2/TBC1D16/TBC1D8B/TIAM2	Molecular Function
GO:0030246	carbohydrate binding	22/872	0.029426	0.425979	CD248/CD34/CD69/CHI3L1/CLEC11A/CLEC4C/CLEC4D/CLEC5A/CRYBG3/DCBLD1/FCER2/KLRC2/KLRG1/LAYN/LGALS2/LGALS9/LGALS9B/LGALSL/NOMO3/OLR1/PAM/PLOD2	Molecular Function
GO:0003823	antigen binding	10/872	0.032715	0.45588	HLA-DMA/HLA-DPB1/HLA-DQB1/HLA-DRB5/KIR2DL3/KLRC2/LAG3/LILRA2/SLC7A5/TSPAN4	Molecular Function
GO:00150	magnesium ion	3/872	0.033958	0.45588	NIPA1/NIPA2/NIPAL2	Molecular

95	transmembrane transporter activity					Function
GO:00342 36	protein kinase A catalytic subunit binding	3/872	0.033958	0.45588	PRKAR1B/PRKAR2B/RYR2	Molecular Function
GO:00305 52	cAMP binding	4/872	0.034602	0.45588	PDE3A/PDE4B/PRKAR1B/PRKAR2B	Molecular Function
GO:00605 89	nucleoside-triphosphat ase regulator activity	24/872	0.038218	0.463553	AGAP1/AGFG1/AHSA2/ARHGAP18/ARHGAP23/ARHGAP24/ARHGAP29/ATP1B2/CDC42EP1/C DC42EP3/DNAJB1/ELMOD2/ERRF1/OCRL/RGS1/RGS18/RGS9/RIN2/SRGAP1/SRGAP2/SYDE2/ TBC1D16/TBC1D8B/TIAM2	Molecular Function
GO:00153 01	anion:anion antiporter activity	5/872	0.038472	0.463553	SLC26A2/SLC26A6/SLC4A1/SLC4A10/SLC4A3	Molecular Function
GO:00168 66	intramolecular transferase activity	4/872	0.039538	0.463553	BPGM/MUT/PGM3/RPUSD2	Molecular Function
GO:00420 56	chemoattractant activity	4/872	0.039538	0.463553	CCL3/FGF2/HGF/PDGFB	Molecular Function
GO:00168 54	racemase and epimerase activity	3/872	0.040834	0.463553	AMACR/DSEL/RPE	Molecular Function
GO:00527 45	inositol phosphate phosphatase activity	3/872	0.040834	0.463553	MINPP1/OCRL/SYNJ1	Molecular Function

**Table 2. GO enrichment analysis about circRNA**

GO_ID	Description	GeneRatio	pvalue	qvalue	geneID	GO_domain
GO:0006997	nucleus organization	10/257	2.38E-05	0.047335	ZMPSTE24/NUP107/USPL1/SYNE2/AGFG1/UBXN2A/CCNB1/TBPL1/SYNE1/NUPL2	Biological Process
GO:0018205	peptidyl-lysine modification	17/257	5.23E-05	0.047335	ASH1L/ARID4B/SMYD3/MGEA5/NUP107/USPL1/SETDB2/CREBBP/UBA2/PHC3/SETD2/LEF1/SENAP2/ENP6/KMT2C/NUPL2/AUTS2/EHMT1	Biological Process
GO:0016571	histone methylation	9/257	6.73E-05	0.047335	ASH1L/ARID4B/SMYD3/SETDB2/SATB1/SETD2/KMT2C/AUTS2/EHMT1	Biological Process
GO:0034968	histone lysine methylation	8/257	7.28E-05	0.047335	ASH1L/ARID4B/SMYD3/SETDB2/SETD2/KMT2C/AUTS2/EHMT1	Biological Process
GO:0038095	Fc-epsilon receptor signaling pathway	15/257	0.000128	0.049414	PTEN/UBC/RASA3/NF1/MALT1/NFATC2/CSF2RB/PAK2/EGF/SKP1/UBE2D2/RICTOR/AKAP9/PTK2/SH2B3/TK2/MAPKAP1	Biological Process
GO:1903364	positive regulation of cellular protein catabolic process	11/257	0.000133	0.049414	RFWD2/PTEN/VPS11/UBC/ARIH1/RNF138/EGF/SKP1/CCNB1/PTK2/UBE2V2	Biological Process
GO:0016569	covalent chromatin modification	17/257	0.000348	0.082174	ASH1L/SKI/ARID4B/SMYD3/MGEA5/ATM/SETDB2/CREBBP/SATB1/SETD2/LEF1/SKP1/CCNB1/UBR2/KMT2C/AUTS2/EHMT1	Biological Process
GO:0071044	histone mRNA catabolic process	3/257	0.000411	0.082174	ATM/DCP2/PAPD4	Biological Process
GO:0042059	negative regulation of epidermal growth factor receptor	5/257	0.000518	0.088335	AP2A2/CBL/UBC/EGF/SH3KBP1	Biological Process

	signaling pathway					
GO:19011 85	negative regulation of ERBB signaling pathway	5/257	0.000577	0.088335	AP2A2/CBL/UBC/EGF/SH3KBP1	Biological Process
GO:00313 96	regulation of protein ubiquitination	12/257	0.000816	0.113685	PTEN/ATM/UBC/MALT1/UBXN2A/EGF/DCUN1D4/SKP1/CCNB1/PTK2/DNAJA1/CDC14B	Biological Process
GO:00069 98	nuclear envelope organization	6/257	0.000881	0.114605	ZMPSTE24/NUP107/SYNE2/UBXN2A/CCNB1/NUPL2	Biological Process
GO:00085 43	fibroblast growth factor receptor signaling pathway	13/257	0.001202	0.133791	SHOC2/PTEN/CBL/UBC/RASA3/NF1/CSF2RB/EGF/RICTOR/AKAP9/PTK2/MAPKAP1/SETX	Biological Process
GO:00063 52	DNA-templated transcription; initiation	13/257	0.001311	0.133791	TRIM33/SKI/PTEN/MED17/UBC/CREBBP/MED13/SMAD2/GLS/NR2C2/TBPL1/PRKAG2/SETX	Biological Process
GO:00400 23	establishment of nucleus localization	3/257	0.00147	0.133791	SYNE2/SYNE1/PTK2	Biological Process
GO:00900 68	positive regulation of cell cycle process	11/257	0.001614	0.133791	RFWD2/PKN2/PTEN/ATM/UBC/CREBBP/SPAST/LEF1/EGF/CCNB1/CSPP1	Biological Process
GO:00614 18	regulation of transcription from RNA polymerase II promoter in response to hypoxia	4/257	0.001636	0.133791	UBC/CREBBP/BACH1/UBE2D2	Biological Process
GO:00511	nuclear export	8/257	0.002314	0.158359	UPF2/BUD13/NUP107/MALT1/AGFG1/SETD2/PHAX/NUPL2	Biological

68						Process
GO:00717 74	response to fibroblast growth factor	13/257	0.002381	0.158811	SHOC2/PTEN/CBL/UBC/RASA3/NF1/CSF2RB/EGF/RICTOR/AKAP9/PTK2/MAPKAP1/SETX	Biological Process
GO:00434 84	regulation of RNA splicing	6/257	0.002634	0.160168	DYRK1A/MBNL1/HNRNPA2B1/PTBP3/SETX/AFF2	Biological Process
GO:00000 86	G2/M transition of mitotic cell cycle	9/257	0.002652	0.160168	ATM/UBC/CEP192/BACH1/CEP70/SKP1/CCNB1/CDK14/AKAP9	Biological Process
GO:00064 05	RNA export from nucleus	6/257	0.002786	0.160168	UPF2/BUD13/NUP107/AGFG1/SETD2/PHAX	Biological Process
GO:00022 23	stimulatory C-type lectin receptor signaling pathway	7/257	0.002836	0.160168	UBC/CREBBP/MALT1/NFATC2/PAK2/SKP1/UBE2D2	Biological Process
GO:00719 01	negative regulation of protein serine/threonine kinase activity	7/257	0.00297	0.160168	PDCD4/PTEN/NF1/CD300A/STK38/PRKAG2/DNAJA1	Biological Process
GO:00480 25	negative regulation of mRNA splicing; via spliceosome	3/257	0.00299	0.160168	DYRK1A/HNRNPA2B1/PTBP3	Biological Process
GO:00313 31	positive regulation of cellular catabolic process	12/257	0.003024	0.160168	RFWD2/PTEN/VPS11/UBC/ARIH1/RNF138/TBC1D5/EGF/SKP1/CCNB1/PTK2/UBE2V2	Biological Process
GO:00448	cell cycle G2/M phase	9/257	0.003054	0.160168	ATM/UBC/CEP192/BACH1/CEP70/SKP1/CCNB1/CDK14/AKAP9	Biological

39	transition					Process
GO:00022 20	innate immune response activating cell surface receptor signaling pathway	7/257	0.003252	0.160168	UBC/CREBBP/MALT1/NFATC2/PAK2/SKP1/UBE2D2	Biological Process
GO:00506 57	nucleic acid transport	8/257	0.003321	0.160168	UPF2/BUD13/NUP107/AGFG1/SETD2/PHAX/NUPL2/HNRNPA2B1	Biological Process
GO:00506 58	RNA transport	8/257	0.003321	0.160168	UPF2/BUD13/NUP107/AGFG1/SETD2/PHAX/NUPL2/HNRNPA2B1	Biological Process
GO:00512 36	establishment of RNA localization	8/257	0.003321	0.160168	UPF2/BUD13/NUP107/AGFG1/SETD2/PHAX/NUPL2/HNRNPA2B1	Biological Process
GO:00019 33	negative regulation of protein phosphorylation	13/257	0.003378	0.160168	ASH1L/SMYD3/PDCD4/PTEN/NF1/CD300A/STK39/PAK2/PDE4D/CCNB1/STK38/PRKAG2/DNAJ A1	Biological Process
GO:00702 07	protein homotrimerization	3/257	0.003478	0.161552	SKI/NELL2/ATXN10	Biological Process
GO:00466 21	negative regulation of organ growth	3/257	0.004012	0.173911	PTEN/PTK2/WWC3	Biological Process
GO:00427 87	protein ubiquitination involved in ubiquitin-dependent protein catabolic process	8/257	0.004318	0.181138	PTEN/UBC/ARIH1/EGF/SKP1/CCNB1/UBE3C/PTK2	Biological Process

GO:0005813	centrosome	19/266	0.000108	0.03021	RFWD2/SKI/PKN2/ANKRD26/C2CD3/NUP107/CEP128/CEP192/CTDP1/SPAST/CCDC14/CEP70/MBNL1/SCLT1/PDE4D/CCNB1/AKAP9/VPS37A/CSPP1	Cellular Component
GO:0005795	Golgi stack	8/266	0.000562	0.078627	CSGALNACT2/SGMS1/SCFD1/GOSR1/RAB27B/ASAP2/B4GALT5/AKAP9	Cellular Component
GO:0005667	transcription factor complex	12/266	0.001707	0.159278	SKI/MED17/CREBBP/RBL2/SMAD2/SATB2/GTF3C2/REL/NFATC2/LEF1/SMAD5/TBPL1	Cellular Component
GO:0005801	cis-Golgi network	4/266	0.003521	0.197172	SCFD1/GOSR1/UBXN2A/AKAP9	Cellular Component
GO:0016604	nuclear body	12/266	0.005746	0.221504	RFWD2/SKI/PTEN/USPL1/CREBBP/PRPF40A/SP3/DYRK1A/SATB1/RAD54L2/PHAX/AFF2	Cellular Component
GO:0005635	nuclear envelope	13/266	0.006259	0.221504	CEPT1/ATF6/ZMPSTE24/NUP107/SYNE2/BNIP2/AGFG1/C2orf42/CEP70/SYNE1/NUPL2/CDC14B/TXLNG	Cellular Component
GO:0031965	nuclear membrane	10/266	0.007157	0.221504	CEPT1/ZMPSTE24/NUP107/SYNE2/C2orf42/CEP70/SYNE1/NUPL2/CDC14B/TXLNG	Cellular Component
GO:0000151	ubiquitin ligase complex	9/266	0.008445	0.221504	MED17/ARIH1/PHC3/DCUN1D4/SKP1/UBE2D2/OTULIN/UBR2/DNAJA1	Cellular Component
GO:0031010	ISWI-type complex	2/266	0.009289	0.221504	BAZ1A/BPTF	Cellular Component
GO:0030122	AP-2 adaptor complex	2/266	0.011242	0.221504	AP2A2/TBC1D5	Cellular Component
GO:1902911	protein kinase complex	5/266	0.012408	0.221504	ERC1/TBC1D5/MAP3K5/PRKAG2/CDK14	Cellular Component
GO:00301	clathrin coat of	2/266	0.013358	0.221504	AP2A2/TBC1D5	Cellular

28	endocytic vesicle					Component
GO:0038201	TOR complex	2/266	0.013358	0.221504	RICTOR/MAPKAP1	Cellular Component
GO:0098562	cytoplasmic side of membrane	7/266	0.013448	0.221504	PTEN/ATP2B1/RASA3/NF1/ESYT2/PTK2/DNAJA1	Cellular Component
GO:0000940	condensed chromosome outer kinetochore	2/266	0.015632	0.243169	CREBBP/CCNB1	Cellular Component
GO:0043218	compact myelin	2/266	0.018059	0.266138	PTEN/MBP	Cellular Component
GO:0031235	intrinsic component of the cytoplasmic side of the plasma membrane	2/266	0.020634	0.271784	RASA3/NF1	Cellular Component
GO:0030136	clathrin-coated vesicle	6/266	0.022762	0.271784	DENND1B/AP2A2/VPS11/RAB27A/RAB27B/TBC1D5	Cellular Component
GO:0030132	clathrin coat of coated pit	2/266	0.023352	0.271784	AP2A2/TBC1D5	Cellular Component
GO:0017053	transcriptional repressor complex	4/266	0.023923	0.271784	SKI/MIER1/SP3/APPL1	Cellular Component
GO:0008047	enzyme activator activity	21/262	9.78E-06	0.003704	RABGAP1L/RAB4A/RASA3/BNIP2/NF1/ACAP1/TBCD/MALT1/UBA2/CFLAR/AGFG1/AHSA2/SAP2/DEPDC5/TBC1D5/PAK2/EGF/RICTOR/IQGAP2/PRKAG2/ASAP1	Molecular Function
GO:0018024	histone-lysine N-methyltransferase	6/262	6.19E-05	0.011732	ASH1L/SMYD3/SETDB2/SETD2/KMT2C/EHMT1	Molecular Function

	activity					
GO:00420 54	histone methyltransferase activity	6/262	0.000243	0.018432	ASH1L/SMYD3/SETDB2/SETD2/KMT2C/EHMT1	Molecular Function
GO:00605 89	nucleoside-triphosphat ase regulator activity	14/262	0.000437	0.027608	RABGAP1L/RAB4A/RASA3/BNIP2/NF1/ACAP1/TBCD/AGFG1/AHSA2/ASAP2/DEPDC5/TBC1D5 /IQGAP2/ASAP1	Molecular Function
GO:00048 42	ubiquitin-protein transferase activity	14/262	0.001199	0.051118	TRIM33/RFWD2/CBL/MED17/RNF10/ARIH1/UBE2G1/RNF138/MALT1/SKP1/UBE2D2/UBR2/UB E3C/UBE2V2	Molecular Function
GO:00170 16	Ras GTPase binding	10/262	0.002469	0.07196	RABGAP1L/ERC1/EXOC5/DAAM1/FMNL1/PAK2/IQGAP2/RHOBTB3/MAPKAP1/DOCK11	Molecular Function
GO:00167 80	phosphotransferase activity; for other substituted phosphate groups	3/262	0.003114	0.084276	CEPT1/SGMS1/PIGN	Molecular Function
GO:00085 65	protein transporter activity	6/262	0.003337	0.0843	RAB4A/AP2A2/SEC62/ASCC3/SEC63/NUPL2	Molecular Function
GO:00353 26	enhancer binding	6/262	0.003912	0.092644	FLI1/SMAD2/REL/BACH1/LEF1/BACH2	Molecular Function
GO:00168 74	ligase activity	14/262	0.006715	0.123046	TRIM33/TARS2/RFWD2/CBL/MYCBP2/ARIH1/UBE2G1/RNF138/UBA2/MARCH7/SUCLG2/UBE2 D2/UBR2/UBE3C	Molecular Function
GO:00316 25	ubiquitin protein ligase binding	10/262	0.006819	0.123046	SKI/CCT2/ARIH1/UBE2G1/SMAD2/USP25/SMAD5/PDE4D/UBE2V2/DNAJA1	Molecular Function
GO:00050	transforming growth	2/262	0.01025	0.146773	SMAD2/SMAD5	Molecular

72	factor beta receptor; cytoplasmic mediator activity					Function
GO:00156 43	toxic substance binding	2/262	0.012398	0.161238	PHAX/TMEM181	Molecular Function
GO:00434 22	protein kinase B binding	2/262	0.012398	0.161238	CCDC88A/APPL1	Molecular Function
GO:00321 83	SUMO binding	2/262	0.014724	0.161238	USPL1/USP25	Molecular Function
GO:00704 10	co-SMAD binding	2/262	0.014724	0.161238	TRIM33/SMAD2	Molecular Function
GO:00055 47	phosphatidylinositol-3; 4,5-trisphosphate binding	3/262	0.014912	0.161238	IQGAP2/ASAP1/MAPKAP1	Molecular Function
GO:00047 22	protein serine/threonine phosphatase activity	4/262	0.015611	0.161238	PTEN/CTDPI/ILKAP/CDC14B	Molecular Function
GO:00012 27	transcriptional repressor activity; RNA polymerase II transcription regulatory region sequence-specific	7/262	0.015837	0.161238	CREBBP/MNT/SP3/NFATC2/BACH1/SATB1/BACH2	Molecular Function

	binding					
GO:00082 34	cysteine-type peptidase activity	7/262	0.01783	0.173245	USP1/USPL1/MALT1/CFLAR/USP25/OTULIN/SEN6	Molecular Function
GO:00046 74	protein serine/threonine kinase activity	13/262	0.020928	0.193426	AKT3/PKN2/ATM/CDKL1/TAOK1/STK39/LTBP1/DYRK1A/PAK2/MAP3K5/STK38/PRKAG2/CDK14	Molecular Function
GO:00040 12	phospholipid-translocating ATPase activity	2/262	0.025687	0.202795	ATP8B4/ATP9B	Molecular Function
GO:00152 78	calcium-release channel activity	2/262	0.025687	0.202795	TPCN1/RASA3	Molecular Function
GO:00428 09	vitamin D receptor binding	2/262	0.025687	0.202795	MED17/MED13	Molecular Function
GO:00314 89	myosin V binding	2/262	0.028814	0.214099	RAB27A/RAB27B	Molecular Function
GO:00436 21	protein self-association	3/262	0.030084	0.216943	CCDC88C/MALT1/DYRK1A	Molecular Function
GO:00036 82	chromatin binding	13/262	0.033452	0.231622	ASH1L/SKI/FLI1/CREBBP/MNT/SMAD2/SP3/SATB2/REL/NFATC2/SATB1/LEF1/AUTS2	Molecular Function
GO:00312 10	phosphatidylcholine binding	2/262	0.035493	0.231622	NF1/ESYT2	Molecular Function
GO:00167 63	transferase activity; transferring pentosyl groups	3/262	0.035762	0.231622	XYLT1/PARP8/PARP12	Molecular Function

GO:0000149	SNARE binding	5/262	0.036673	0.231622	RAB4A/VPS11/SCFD1/GOSR1/TXLNG	Molecular Function
GO:0017124	SH3 domain binding	5/262	0.036673	0.231622	DNAJC6/CBL/FMN1/PDE4D/SH3KBP1	Molecular Function
GO:0019003	GDP binding	3/262	0.046357	0.255354	RAB4A/RAB27A/RAB27B	Molecular Function

**Table 3. GO enrichment analysis about lncRNA**

GO_ID	Description	GeneRatio	pvalue	qvalue	geneID	GO_domain
GO:0030670	phagocytic vesicle membrane	9/978	0.002228	0.742977	ATP6V0E2/HLA-A/ANXA3/CYBB/HLA-E/RAB22A/RAB43/RILP/TLR6	Cellular Component
GO:0071437	invadopodium	4/978	0.003168	0.742977	SVIL/AFAP1L1/FSCN1/NOX1	Cellular Component
GO:0031201	SNARE complex	8/978	0.005619	0.742977	BET1L/STXBP5/NAPA/BNIP1/CPLX1/SNAP47/VAMP2/VTI1A	Cellular Component
GO:0005875	microtubule associated complex	16/978	0.005827	0.742977	DISC1/KIF20B/WDR81/ACTR10/ACTR1A/ACTR1B/DNAH8/DNAH9/DNAL4/DYNLL1/HAUS5/KIF21A/KLC2/NDEL1/SPTBN5/STAU1	Cellular Component
GO:0045335	phagocytic vesicle	10/978	0.011207	0.96332	ATP6V0E2/HLA-A/SRGA2/ANXA3/CYBB/HLA-E/RAB22A/RAB43/RILP/TLR6	Cellular Component
GO:0030684	preribosome	7/978	0.017091	0.96332	RRP1/IMP4/MPHOSPH10/PIN4/RPS7/RRP1B/WDR3	Cellular Component
GO:00058	proteasome core	4/978	0.021834	0.96332	PSMA3/PSMB8/PSMA1/PSMB9	Cellular

39	complex					Component
GO:00081 80	COP9 signalosome	5/978	0.036991	0.96332	BASP1/DYNLL1/GPS1/HSPA5/TMOD1	Cellular Component
GO:00306 86	90S preribosome	4/978	0.040278	0.96332	IMP4/MPHOSPH10/RPS7/WDR3	Cellular Component