

Supplementary Table 1 DAPs in germinated soybean under NaCl treatment.

No ^a	Fold change ^b	Description ^c	Score ^d	Cov ^e	MW ^f	pI ^g
Defense/Stress						
C6TBQ4	0.35±0.05	Peroxidase	0.00	17.39	27.6	6.87
I1NH59	0.51±0.04	Ran-binding protein 1 homolog b	14.30	23.28	27.4	5.29
B3TDK7	0.64±0.12	Lipoxygenase	49.37	14.90	94.9	5.96
D4N5G2	0.65±0.06	Rubisco activase	3.87	19.74	15.2	5.60
I1LKF8	1.61±0.19	Late embryogenesis abundant protein D-34-like	5.71	9.01	37.6	7.36
C6T5C9	1.69±0.14	Stress responsive alpha-beta barrel domain-containing protein	6.41	17.32	18.2	4.41
I1JFL5	1.69±0.15	Subtilisin-like protease SBT3.3	6.61	22.37	16.7	5.36
I1JP97	1.83±0.23	S-(hydroxymethyl)glutathione dehydrogenase	126.53	46.64	27.6	5.39
Q7M1R5	2.10±0.35	Superoxide dismutase [Cu-Zn]	101.03	26.55	23.7	6.58
Q9XER5	2.16±0.31	Seed maturation protein PM22	4.65	16.13	6.9	12.03
P05046	2.20±0.18	Lectin (Agglutinin) (SBA)	6.74	6.63	103.3	6.76
C6TDF5	2.34±0.13	Formate dehydrogenase, mitochondrial	7.10	23.53	14.7	6.52
C6SWE8	2.37±0.68	Superoxide dismutase [Cu-Zn]	9.29	7.53	52.4	5.96
Q9XF18	2.37±0.22	Peroxidase	28.32	10.49	81.7	5.34
I1N747	2.65±1.25	P24 oleosin isoform A	2.51	10.62	23.6	8.94
I1L849	2.65±0.84	Late embryogenesis abundant protein D-34-like	116.28	45.67	41.9	7.36
A1KR24	3.03±1.01	Dehydrin	20.63	12.31	35.5	9.00
K7LDT9	3.21±0.16	Low-temperature-induced 65 kDa protein	9.59	28.51	25.4	6.61
P26413	3.33±0.75	Heat shock 70 kDa protein	38.05	20.16	70.8	5.49
P26987	4.01±1.21	Stress-induced protein SAM22	23.43	39.49	16.6	4.82
B2YDR0	4.06±1.67	Gly m Bd 28K allergen	4.36	13.00	24.7	4.86
Q39805	4.63±0.94	Dehydrin-like protein	105.10	29.23	50.7	6.19
C6TEP1	4.65±1.35	40S ribosomal protein S30	7.00	13.98	39.6	6.60
I1LHP6	5.24±0.93	Vicilin-like antimicrobial peptides 2-2	13.24	36.84	15.2	6.24
Carbohydrate metabolism						
I1J4J6	0.43±0.09	Malic enzyme	13.76	15.91	65.0	6.15
Q1W376	0.45±0.10	Phosphomannomutase	4.43	1.98	114.2	6.70
I1LKM5	0.46±0.01	Apoptosis-inducing factor homolog A	41.31	47.97	32.1	6.96
I1M307	0.52±0.05	Epidermis-specific secreted glycoprotein EP1-like	10.57	14.29	37.8	6.55
K7MZJ1	0.54±0.10	Sucrose synthase	5.49	5.81	26.5	5.88
I1KWM7	0.56±0.10	6-phosphogluconate dehydrogenase, decarboxylating	15.10	20.73	45.6	7.15
I1KQ93	0.63±0.01	Phosphoglucomutase, cytoplasmic-like	15.09	11.51	63.4	5.53
I1L6Y9	1.54±0.14	Alpha-galactosidase 1-like	0.00	5.12	40.7	9.38
I1J6Z7	1.63±0.13	Aldo-keto reductase family 4 member C9	0.00	7.50	39.3	9.42
I1N4B8	1.70±0.46	Aldose 1-epimerase	3.07	2.55	43.6	6.37
I1KC66	1.72±0.23	Glyceraldehyde-3-phosphate dehydrogenase	0.00	2.65	85.1	6.09
I1KEA0	2.01±0.33	Probable aldo-keto reductase 2	21.11	10.08	53.5	6.48
C6TJM8	2.56±0.52	Alpha-galactosidase	0.00	5.67	28.0	6.24
I1KZ09	3.77±1.52	Enoyl-[acyl-carrier-protein] reductase [NADH] 2, chloroplastic-like	5.12	10.54	34.9	6.65
P10743	3.78±0.08	aldo-keto reductase 1	8.54	4.66	48.9	8.70
I1NFH5	4.11±0.52	Dihydrolipoyllysine-residue acetyltransferase component 4 of pyruvate dehydrogenase complex	1.97	10.18	41.7	8.51
I1JXQ5	4.33±1.05	Alpha-mannosidase	6.28	4.37	48.8	6.64
Nucleotide metabolism						
I1L5R2	0.36±0.01	UMP-CMP kinase	2.00	4.04	22.4	5.87

I1LBH6	0.49±0.10	Benzyl alcohol O-benzoyltransferase-like	10.78	11.55	50.5	5.00
P04670	0.50±0.20	Uricase (Nod-35)	0.00	15.68	18.0	8.12
I1K081	0.51±0.04	Nucleoside diphosphate kinase	3.96	1.34	57.2	6.25
C6TK65	0.64±0.02	31 kDa ribonucleoprotein, chloroplastic	2.23	10.67	25.0	8.85
Q8GV25	1.60±0.06	Nucleoside diphosphate kinase	26.74	19.69	29.1	4.75
I1MDY5	1.62±0.11	Dihydropyrimidinase	0.00	3.97	41.3	8.53
C6SZE4	1.65±0.01	4-hydroxy-4-methyl-2-oxoglutarate aldolase	7.07	18.77	35.1	8.29
I1K893	1.66±0.13	RNA-binding protein 1-like	7.73	33.13	17.7	6.79
I1JWB7	1.67±0.25	Methyl-CpG-binding domain-containing protein 10-like	23.11	30.20	16.3	7.50
K7KHJ7	1.72±0.25	Glycine-rich RNA-binding protein GRP1A-like	3.00	6.97	32.1	4.88
E9KNA4	2.03±0.35	14-3-3 protein SGF14h [Glycine max]	11.17	19.67	32.8	4.70
Energy						
K7KNL2	0.30±0.08	Carbonic anhydrase	5.34	4.33	68.7	5.58
P00865	0.33±0.04	Ribulose biphosphate carboxylase small chain 1	13.02	13.43	38.9	8.16
I1KTM3	0.34±0.07	ADP,ATP carrier protein 1, mitochondrial	3.09	8.84	15.6	4.82
P27066	0.40±0.03	Ribulose biphosphate carboxylase large chain	35.05	20.04	63.9	7.37
I1NFS4	0.46±0.12	ATP synthase subunit beta	0.00	3.48	59.9	6.98
I1JPX8	0.47±0.03	Fructose-biphosphate aldolase	65.17	33.09	59.8	6.15
C6T1J0	0.48±0.09	Ferredoxin	152.23	33.47	52.6	6.43
Q38IX1	0.49±0.23	Glyceraldehyde-3-phosphate dehydrogenase	33.07	28.21	38.3	7.53
O81279	0.50±0.08	Malate dehydrogenase	2.76	3.54	43.3	7.74
I1KNH5	0.50±0.07	Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit beta (PF6P)	16.08	17.88	38.5	6.79
D7EYG6	0.52±0.01	V-type proton ATPase catalytic subunit A	5.72	18.41	25.6	8.12
Q2PMS8	0.53±0.11	ATP synthase subunit alpha	2.43	4.56	49.8	9.16
Q9LLR1	0.57±0.08	Acetyl-CoA carboxylase	0.00	2.37	79.6	7.81
I1JBV5	0.60±0.04	Pyruvate dehydrogenase E1 component subunit alpha	5.02	8.76	42.0	9.61
K7MH04	0.60±0.11	Ferredoxin--NADP reductase	7.09	7.42	58.7	7.50
P45458	0.65±0.01	Malate synthase	2.83	8.67	70.3	6.30
G0T440	1.59±0.14	Purple acid phosphatase	27.47	24.72	20.1	8.66
I1M6P9	1.77±0.19	dihydrolipoyllysine-residue succinyltransferase	32.21	20.84	43.2	8.25
I1MB71	2.86±0.43	Fructose-biphosphate aldolase	19.01	15.00	27.3	5.73
K7MAP7	4.21±0.36	Pentatricopeptide repeat-containing protein At5g19020, mitochondrial	21.48	15.49	55.7	5.21
F4JLP5	67.13±5.98	Dihydrolipoyl dehydrogenase 2, chloroplastic	3.01	8.96	21.9	5.55
Amino acid metabolism						
Q42792	0.39±0.01	Asparagine synthetase	11.48	12.00	34.3	5.77
K7MQ84	0.41±0.01	Asparagine synthetase 1	8.07	1.11	70.5	4.72
A8C8H5	0.43±0.12	Glutamate decarboxylase	48.35	17.27	65.2	6.64
I1K3S5	0.44±0.15	Adenosylhomocysteinase	4.30	3.90	51.9	6.93
I1KG03	0.45±0.24	Methylenetetrahydrofolate reductase	7.48	8.90	48.0	5.49
I1LH18	0.59±0.06	Acetylornithine deacetylase-like	4.47	8.07	62.8	6.58
I1NFX7	1.55±0.07	D-3-phosphoglycerate dehydrogenase	17.73	30.38	27.0	5.71
I1NA39	1.57±0.03	Glutathione S-transferase L3	9.04	9.97	32.3	5.87
I1JW29	1.73±0.24	Probable protein arginine N-methyltransferase 3	43.50	14.85	53.2	5.88
I1J6Q1	1.84±0.03	Methionine aminopeptidase	7.37	5.17	57.2	5.82
C6TIP9	1.93±0.13	Cysteine synthase	28.39	19.00	65.2	6.73
Q8W1A0	2.58±0.96	Cysteine synthase	19.50	19.38	34.2	5.82
Signal transduction						
H1AD80	0.65±0.05	Truncate phytochrome A2 protein	5.46	4.08	84.0	6.71
I1MCF0	1.68±0.15	SNF1-related protein kinase regulatory subunit	7.83	10.17	45.2	6.43

gamma-like PV42a

Cell growth/division						
I1K2I1	0.39±0.04	Tubulin alpha chain	56.52	36.16	50.4	4.83
C6TJ78	0.51±0.24	Actin-11	15.89	21.22	41.8	5.40
I1K7J4	0.59±0.11	Tubulin beta chain	34.99	20.76	90.8	5.24
I1NGB7	0.62±0.25	RAN GTPase-activating protein 2-like	2.21	0.40	261.5	5.03
I1LDR2	0.65±0.09	Tubulin beta-1 chain	5.45	23.89	12.8	4.94
I1JXA0	1.64±0.09	Cell division cycle protein 48 homolog	3.20	2.07	57.9	4.72
I1KYK0	2.00±0.03	Fasciclin-like arabinogalactan protein 1	2.50	3.61	43.7	6.24
I1L957	2.56±0.65	Embryonic protein DC-8-like	34.77	33.41	48.8	6.42
C6T5I8	2.75±0.04	Tubulin-specific chaperone A	25.39	23.11	49.6	5.10
P04347	10.73±0.93	Phragmoplast orienting kinesin 2 isoform X3	4.29	13.33	11.5	5.60
I1JLC8	11.82±4.07	Protein SLE2	31.89	26.56	50.4	4.87
Proteolysis						
I1NBK8	0.53±0.10	Cathepsin B	10.02	32.65	27.7	7.27
I1JWD2	0.55±0.05	Carboxypeptidase	0.00	4.00	33.4	7.01
K7N0R1	0.58±0.05	Carboxypeptidase	9.88	11.16	46.9	8.54
C6SXU0	1.88±0.26	Cysteine proteinase inhibitor	20.63	14.04	39.4	6.27
I1JW44	2.63±0.06	Protein ASPARTIC PROTEASE IN GUARD CELL 2-like	2.49	2.28	54.8	6.14
Protein destination and storage						
P10742	0.64±0.08	Stem 31 kDa glycoprotein	34.66	17.88	67.9	6.58
C6K8D0	0.65±0.04	Trypsin inhibitor 26 kDa isoform	134.77	59.84	29.3	7.21
K7MIV6	1.55±0.02	Kunitz-type elastase inhibitor BrEI-like	6.15	8.67	18.9	5.60
Q9SPJ6	2.02±0.27	Maturation protein pPM32	296.44	62.39	53.6	6.07
Q7XXT2	2.03±0.10	Prepro beta-conglycinin alpha prime subunit	719.70	46.59	63.1	4.96
Q9XET0	2.08±0.29	Seed maturation protein PM30	141.92	31.29	55.7	6.55
Q8RVH5	2.10±0.07	Basic 7S globulin 2	310.93	46.60	54.4	5.58
Q9XIS8	2.42±0.36	Trypsin inhibitor p20 precursor	541.89	46.25	63.6	5.55
C6K8D1	2.48±0.63	Seed biotinylated protein 68 kDa isoform	21.05	20.59	25.9	8.32
Q9XET1	2.64±1.09	Seed maturation protein PM31	217.55	46.12	57.9	5.90
P25974	2.76±1.12	Beta-conglycinin	192.38	39.29	54.2	5.97
P11828	3.11±1.70	Glycinin G3	55.84	24.84	17.7	6.55
O22120	3.40±0.36	Alpha subunit of beta conglycinin	598.59	52.87	47.8	8.15
I1LE33	4.50±0.94	Beta-conglycinin, beta chain-like	9.43	26.17	23.6	7.33
P04405	5.93±1.26	Glycinin G2 precursor	40.92	21.71	47.2	8.25
P13917	6.13±2.13	Chain D, Crystal Structure Of Basic Globulin	538.33	47.60	47.9	5.92
P04776	6.66±1.05	Glycinin G1	1.72	3.88	22.6	5.58
Q84V19	7.84±0.65	Sucrose-binding protein 2	41.00	18.32	68.2	6.32
P04347	10.73±1.55	Glycinin	20.57	24.29	15.1	8.90
Q9S9D0	14.75±2.68	Glycinin G4 subunit	37.65	20.35	43.7	8.48
Transporters						
C6T9E5	0.45±0.03	ADP,ATP carrier protein 1, mitochondrial	5.64	1.89	53.8	4.60
Q13367	0.54±0.05	Coatomer subunit beta'-2	4.46	2.83	24.2	8.81
Q9FQE4	0.54±0.13	Glutathione S-transferase GST 14	22.11	12.22	25.1	6.42
C6T9M6	3.57±0.50	Reticulon-like protein	0.00	5.48	25.3	7.59
C6T1R3	6.26±1.91	GTP-binding nuclear protein	4.65	11.05	42.1	9.70
Protein synthesis/folding						
I1JGR4	0.25±0.09	Eukaryotic translation initiation factor isoform 4G-1-like	5.03	9.05	25.9	10.15
I1KRD4	0.39±0.05	26S proteasome non-ATPase regulatory subunit 8 homolog A-like	6.00	14.55	11.1	4.32

Q2PMQ0	0.45±0.13	30S ribosomal protein S8	3.40	5.22	111.7	9.33
I1KQE3	0.51±0.09	40S ribosomal protein S16-like	41.35	27.27	30.0	10.23
I1KZJ9	0.55±0.10	Glycine--tRNA ligase, mitochondrial 1	3.32	11.49	10.2	10.84
K7KIC0	0.55±0.17	Eukaryotic translation initiation factor subunit B (eIF3b) (eIF-3-eta) (eIF3 p110)	3 4.80	5.45	46.9	5.96
I1LDE9	0.57±0.18	60S ribosomal protein L3	3.59	8.22	16.7	10.92
K7MV98	0.58±0.13	Eukaryotic translation initiation factor subunit H (eIF3h)	3 2.69	5.68	25.8	4.87
I1M6M4	0.60±0.13	Trigger factor-like protein TIG, Chloroplastic	5.18	2.86	68.8	5.97
I1K970	0.61±0.10	26S proteasome non-ATPase regulatory subunit 11 homolog	10.01	18.46	7.5	11.17
K7M7B5	0.61±0.03	60S ribosomal protein L10-like	2.28	10.05	20.7	7.64
I1MJL6	1.57±0.09	60S ribosomal protein L6	5.38	10.12	29.2	4.60
I1L1H7	1.62±0.12	Translation machinery-associated protein 22	5.94	12.20	23.8	11.44
I1L3W4	1.67±0.05	Eukaryotic translation initiation factor subunit J	3 5.71	7.05	34.0	9.29
I1KA65	1.68±0.03	Ubiquitin-fold modifier 1	19.48	15.12	50.6	6.67
C6SYM3	1.72±0.16	50S ribosomal protein L31	2.09	11.94	15.7	10.30
I1LL59	1.76±0.24	Protein disulfide isomerase	8.50	2.81	86.1	8.00
I1JSC6	2.02±0.50	50S ribosomal protein L3, chloroplastic-like	3.68	13.53	14.9	9.54
C6SZ18	2.04±0.46	40S ribosomal protein S28	14.18	6.45	17.4	10.20
C6TN03	2.04±0.04	40S ribosomal protein S4	8.82	17.22	44.4	10.17
I1JYI8	2.11±0.04	60S acidic ribosomal protein P1	4.99	13.31	28.8	10.45
Q39871	2.65±0.86	Maturation polypeptide	2.76	2.70	60.8	8.22
K7MYU5	3.13±1.09	Eukaryotic translation initiation factor subunit A	3 2.54	20.27	7.9	8.76
K7N3S3	3.39±0.64	60S ribosomal protein L36	2.78	4.95	64.8	4.79
I1NB91	3.43±0.03	Ribosomal protein L19	6.94	11.74	61.2	5.21
I1JAL4	3.75±0.74	Probable acyl-activating enzyme peroxisomal	1, 0.00	15.84	11.7	9.52
I1M3C1	5.00±1.70	60S ribosomal protein L5	6.73	6.07	81.0	7.39
I1M290	5.41±2.00	60S ribosomal protein L26-1-like	7.08	13.48	30.9	5.08
Q6VEV1	13.80±1.34	40S ribosomal protein S25	3.02	10.64	10.5	10.76
Secondary metabolism						
Q70EW1	0.39±0.16	Amine oxidase	6.63	14.89	20.9	9.04
I1JE17	0.47±0.12	Glycosyltransferase	6.55	8.86	51.4	6.09
I1MTH5	0.51±0.03	1-deoxy-D-xylulose 5-phosphate reductoisomerase, chloroplastic-like	17.52	27.17	41.7	5.78
I1J637	0.59±0.12	Alpha-1,4-glucan-protein synthase	1.73	2.32	53.1	5.86
C6TBV6	0.65±0.14	Pathogenesis-related protein	33.28	18.42	75.6	7.40
Uncharacterized proteins						
I1KAJ5	0.45±0.03	Hypothetical protein GLYMA_06G122600	16.20	17.80	36.9	6.15
C6SYI8	0.44±0.27	Uncharacterized protein	5.16	16.08	28.8	6.79
C6T3M1	0.45±0.22	Uncharacterized protein	1.67	13.75	17.3	8.19
C6TG30	0.45±0.21	Uncharacterized protein	15.63	30.52	23.5	6.21
I1JYG3	0.46±0.06	Hypothetical protein GLYMA_04G226900	6.05	9.39	34.7	6.37
I1MGM0	0.60±0.06	Hypothetical protein GLYMA_15G148900	2.80	8.81	31.5	6.24
K7M9Q4	0.61±0.08	Hypothetical protein GLYMA_15G052500	13.95	33.98	26.2	4.89
I1JEI0	0.61±0.14	Hypothetical protein GLYMA_02G120900	4.04	9.57	20.1	7.72
C6T7G4	0.63±0.11	Uncharacterized protein	2.28	14.41	24.1	6.15
I1LCM6	0.64±0.04	Hypothetical protein GLYMA_10G197700	6.41	16.49	29.9	6.61
I1JWW7	0.64±0.05	Hypothetical protein GLYMA_04G171400	2.04	9.29	25.3	9.51
C6SXS9	0.65±0.07	Uncharacterized protein	12.10	6.80	34.6	6.19
C6TKQ3	0.65±0.16	Uncharacterized protein	41.71	27.89	31.6	6.84
K7MVK8	0.66±0.08	Uncharacterized protein	7.09	38.76	14.0	6.15
I1NJA4	1.57±0.12	Hypothetical protein GLYMA_20G245300	11.48	24.19	33.9	5.88

C6T4P6	1.58±0.07	Uncharacterized protein	7.01	18.60	10.3	10.35
C6SWP9	1.65±0.16	Uncharacterized protein	14.13	14.71	18.6	5.02
C6TF55	1.70±0.30	Uncharacterized protein	27.27	55.47	26.0	5.02
C6TE70	1.71±0.14	Uncharacterized protein	18.45	24.79	12.7	9.44
C6T3K3	1.93±0.12	Uncharacterized protein	52.23	30.97	17.8	6.38
I1KRG4	1.94±0.07	Hypothetical protein GLYMA_08G084800	4.71	14.29	31.4	8.22
C6TEA3	1.99±0.44	Uncharacterized protein	9.22	19.90	23.7	10.27
C6THQ1	1.99±0.24	Uncharacterized protein	5.00	12.07	24.8	9.85
C6TG59	2.11±0.72	Uncharacterized protein	3.08	4.98	44.1	7.62
C6T9C2	2.13±0.59	Uncharacterized protein	19.22	22.69	28.6	6.35
C6TKH0	2.16±0.53	Uncharacterized protein	5.36	6.40	58.1	7.02
C6TMV9	2.30±0.28	Uncharacterized protein	8.78	16.77	19.0	4.73
C6T0B5	2.45±0.51	Uncharacterized protein	3.93	8.10	44.1	7.65
C6SYA7	2.48±0.13	Uncharacterized protein	7.73	8.84	49.7	5.68
C6TB98	2.49±0.50	Uncharacterized protein	230.35	30.95	58.0	6.49
K7L353	2.76±1.05	Hypothetical protein GLYMA_07G219500	5.86	18.29	18.4	6.34
I1LFE1	2.84±0.22	Hypothetical protein GLYMA_10G291500	7.61	17.11	17.6	6.74
I1J7G5	2.94±0.07	Uncharacterized protein	6.58	24.28	29.7	9.06
I1NGG4	3.01±0.73	Hypothetical protein GLYMA_20G147600	14.61	9.29	21.5	10.21
I1L4K5	3.57±1.20	Hypothetical protein GLYMA_09G192800	9.98	26.56	21.7	9.50
I1LE41	1.57±0.94	Hypothetical protein GLYMA_10G247500	78.54	24.05	18.5	5.24
I1L860	5.01±1.32	Hypothetical protein GLYMA_10G028300	10.23	17.19	15.0	10.17
C6T1Q7	5.15±2.40	Uncharacterized protein	4.86	20.92	41.5	5.97

a Accession number according to the UniProtKB database

b The abundance ratio of proteins in soybeans under NaCl treatment compared to water

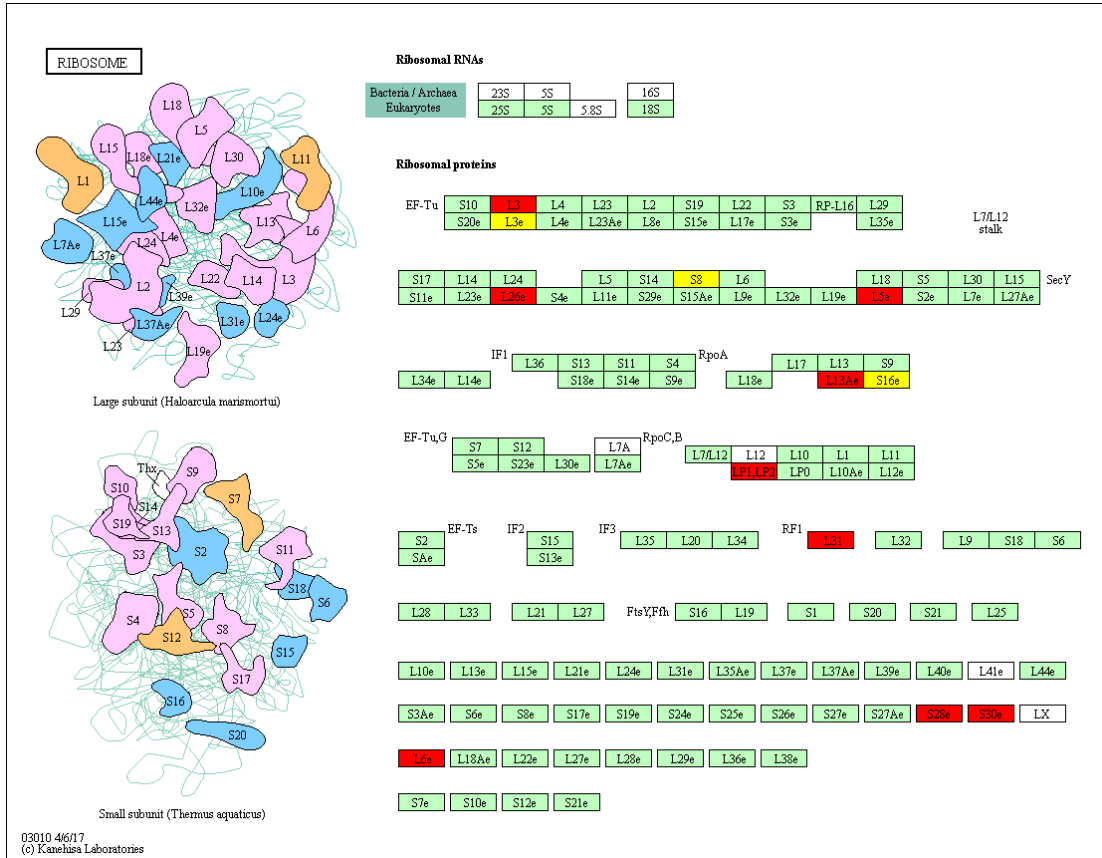
c Description, Homologue protein name obtained using Arabidopsis database from the UniProtKB

d Mascot score

e Sequence coverage

f MW, Theoretical molecular weight

g pI, Theoretical isoelectric point



Supplementary Fig. S1 Schematic presentation of salinity stress-responsive proteins involved in ribosome pathway in soybeans. Red and yellow boxes indicate increased and decreased DAPs, respectively.