

Table S1: the function annotation of clone sequences may be involved in salt stress

Gene-id	Source	accession	Putative-description	Species	E-value	Ref-PMID
S04106_01_A03	NR	ADY11192.1	early salt-stress induced 2-2	Triticum aestivum	4.00E-53	nonpublished
S04106_01_B11	NR	EMT00621	Histone H1(H1_5)	Aegilops tauschii	1.67E-30	25063323
S04106_01_C02	NR	AAM74069	CONSTANS-like protein	Hordeum vulgare subsp. vulgare	1.84E-88	25073793
S04106_01_C08	NR	XP_003569021.1	predicted ABC transporter G family member 1	Brachypodium distachyon 3e-21	7.95E-24	21663998
S04106_01_E07	KEGG	K02144	V-type H ⁺ -transporting ATPase subunit-H(ATPeVIH)	-	-	25222556
S04106_01_F05	NR	EMT04135	Monodehydroascorbate reductase	Aegilops tauschii	1.68E-170	17043889
S04106_01_F10	NR	EMT00621.1	Histone H1(H1_5)	Aegilops tauschii	2.00E-30	25063323
S04106_01_H03	NR	XP_003563177	PREDICTED: probable aquaporin PIP2-1	Brachypodium distachyon	4.82E-168	15356390
S04106_02_B06	NR	EMT04698	MADS-box transcription factor 27	Aegilops tauschii	3.99E-105	23632855
S04106_02_B02	NR	EMS55427	ATP-dependent zinc metalloprotease FTSH 2, chloroplastic	Triticum urartu	3.30E-163	11972783
S04106_02_C08	COG	COG1278	cspA,cold shock protein (beta-ribbon-CspA family)-	-	-	-
S04106_02_E02	NR	ACV65038	Cu/Zn superoxide dismutase	Deschampsia antarctica	1.18E-90	26339977/26353406
S04106_02_F11	NR	EMT00621	Histone H1	Aegilops tauschii	5.22E-30	25063323
S04106_02_G02	NR	EMS55466.1	S-adenosylmethionine synthase 1	Triticum urartu	0	8018871
S04106_02_G06	NR	CAI99406	P-type ATPase	Flabellia petiolata	1.67E-89	-
S04106_03_A01	NR	EMS49467	Aquaporin PIP1-2	Triticum urartu	0	18956193(cotton)
S04106_03_F10	NR	AJC64140	auxin-repressed protein	Triticum aestivum	3.00E-44	20499123/18506580
S04106_05_A06	NR	AAK55324	thaumatin-like protein TLP6	Hordeum vulgare	1.79E-121	26442045/10608717
S04106_05_A10	NR	XP_010232378	PREDICTED: glutathione S-transferase 1	Brachypodium distachyon	1.02E-139	11092907/15012285
S04106_05_B05	NR	ADD70015	S-adenosyl-L-methionine decarboxylase 2	Leymus chinensis	6.52E-62	16642382
S04106_05_C02	NR	EMS45815	putative aquaporin TIP1-1	Triticum urartu	6.72E-17	16183846
S04106_05_C11	NR	BAG06230	plasma membrane intrinsic protein	Hordeum vulgare	1.87E-146	21640804/25544590
S04106_05_D01	NR	AAV49759	non-specific lipid transfer protein 6	Hordeum vulgare subsp. vulgare	7.14E-40	12869521
S04106_05_D03	NR	XP_003559966	PREDICTED: serine hydroxymethyltransferase1,mitochondrial	Brachypodium distachyon	0.00E+00	15659103/22587350
S04106_05_F09	NR	EMT25919	Cell division protease ftsH-like protein, chloroplastic	Aegilops tauschii	5.35E-128	11972783
S04106_05_F10	NR	BAB88645	alternative oxidase	Triticum aestivum	1.95E-134	19941623
S04106_05_G07	NR	AHZ35571	LEA protein	Triticum aestivum	7.05E-26	16023228
S04106_05_H04	NR	BAK05489.1	Calreticulin	Triticum urartu	5.00E-155	26469859
S04106_05_H06	NR	BAG54794	plasma membrane protein 3	Puccinellia tenuiflora	3.67E-24	18593528
S04106_06_A09	NR	XP_010229208	PREDICTED: calmodulin-binding receptor-like cytoplasmic kinase 2	Brachypodium distachyon	0	15292241
S04106_06_B05	NR	EMT21270	Mitochondrial uncoupling protein 3	Aegilops tauschii	1.63E-145	21912606
S04106_06_C04	NR	XP_006643957	PREDICTED: LOW QUALITY PROTEIN: salt stress root protein RS1-like	Oryza brachyantha	4.98E-49	-
S04106_06_E11	NR	XP_003558722	PREDICTED: cyclic dof factor 1-like	Brachypodium distachyonm	3.29E-134	24399177/25636232

Continued Table S1

Gene-id	Source	accession	Putative-description	Species	E-value	Ref-PMID
S04106_06_F04	NR	AF18617	cation/H ⁺ exchanger	<i>Puccinellia tenuiflora</i>	3.52E-124	-
S04106_06_F07	NR	EMS65202	Bowman-Birk type trypsin inhibitor	<i>Triticum urartu</i>	6.15E-46	18433440
S04106_06_H05	NR	NP_001052879.1	Auxin response factor 9	<i>Oryza sativa Japonica Group</i>	4.00E-57	20499123/18506580
S04106_06_H09	NR	XP_003559852	PREDICTED: F-box protein SKIP5	<i>Brachypodium distachyon</i>	3.78E-157	25877816
S04106_07_A09	NR	EMS47319	Zinc finger CCCH domain-containing protein 65	<i>Triticum urartu</i>	6.47E-27	19402879/25074582
S04106_07_B06	NR	P23957	vacuolar-type H ⁺ -ATPase 16 kDa subunit c	<i>Puccinellia tenuiflora</i>	2.35E-71	-
S04106_07_B07	NR	EMS53884	Pathogenesis-related protein STH-21	<i>Triticum urartu</i>	1.33E-61	25173686
S04106_07_B12	NR	XP_010232378	PREDICTED: glutathione S-transferase 1	<i>Brachypodium distachyon</i>	1.02E-139	11092907/15012285
S04106_07_D06	NR	EMS49467	Aquaporin PIP1-2	<i>Triticum urartu</i>	0	21441236
S04106_07_G08	NR	BAI66439	tonoplast intrinsic protein TIP1;3	<i>Hordeum vulgare</i>	1.27E-150	-
S04106_08_C02	NR	ADD70015	S-adenosyl-L-methionine decarboxylase 2	<i>Leymus chinensis</i>	6.52E-62	16642382
S04106_08_D06	NR	AAB67991	Cu/Zn superoxide dismutase	<i>Triticum aestivum</i>	1.51E-92	26339977/26353406
S04106_08_E02	NR	EMT05501	SKP1-like protein 1B	<i>Aegilops tauschii</i>	3.06E-75	25477077
S04106_09_D08	NR	XP_004955675	PREDICTED: auxin-responsive protein IAA24-like	<i>Setaria italica</i>	3.81E-71	20499123/18506580/
S04106_09_F12	NR	NP_001174278	BURP domain-containing protein 6	<i>Oryza sativa Japonica Group</i>	6.35E-110	19363683
S04106_10_E08	NR	ABF50675	vacuolar ATPase subunit G	<i>Triticum aestivum</i>	8.23E-38	-
S04106_10_H05	NR	EMT05501	SKP1-like protein 1B	<i>Aegilops tauschii</i>	3.06E-75	25477077
S04106_11_A07	NR	EMT05585	Pathogenesis-related protein 1	<i>Aegilops tauschii</i>	4.07E-85	-
S04106_11_B06	NR	XP_003561285	PREDICTED: glycerol-3-phosphate dehydrogenase [NAD(+)], chloroplastic isoform X1	<i>Brachypodium distachyon</i>	1.45E-108	-
S04106_11_B12	NR	XP_003560016	PREDICTED: CBS domain-containing protein CBSX3, mitochondrial	<i>Brachypodium distachyon</i>	7.24E-135	22302312
S04106_11_D01	NR	CAJ85945	mitogen-activated protein kinase homolog 1	<i>Festuca arundinacea</i>	0	-
S04106_11_D03	NR	EMT02551	Calreticulin	<i>Aegilops tauschii</i>	8.67E-153	25995067
S04106_11_E04	NR	XP_010232378	PREDICTED: glutathione S-transferase 1	<i>Brachypodium distachyon</i>	1.02E-139	11092907/15012285
S04106_11_F12	NR	XP_003580542	PREDICTED: probable potassium transporter 11	<i>Brachypodium distachyon</i>	1.31E-102	-
S04106_12_A01	NR	NP_001152280	ras-related protein Rab-18	<i>Zea mays</i>	4.00E-125	20018899
S04106_12_B01	NR	XP_004952783	PREDICTED: two-component response regulator ARR4-like	<i>Setaria italica</i>	7.21E-77	9607306
S04106_12_E11	NR	BAF33069	aquaporin	<i>Hordeum vulgare</i>	5.90E-175	21441236
S04106_12_F04	NR	AFW60589.1	heat shock protein binding protein	<i>Zea mays</i>	1.48E-99	-
S04106_12_G05	NR	XP_006643957	PREDICTED: LOW QUALITY PROTEIN: salt stress root protein RS1-like	<i>Oryza brachyantha</i>	2.91E-50	-
S04106_12_G06	NR	XP_003572098	PREDICTED: cyclic nucleotide-gated ion channel 1-like isoform X1	<i>Brachypodium distachyon</i>	1.09E-143	18823330
S04106_12_H02	NR	ABX10014	vacuolar H ⁺ -pyrophosphatase	<i>Triticum aestivum</i>	3.53E-149	21762382
S04106_12_H10	NR	ABX39195	C2H2 zinc finger protein	<i>Triticum aestivum</i>	4.66E-29	26237514

Continued Table S1

Gene-id	Source	accession	Putative-description	Species	E-value	Ref-PMID
S04106_13_C04	NR	ACG28224	stress responsive protein	<i>Zea mays</i>	7.17E-18	-
S04106_13_C12	NR	BAJ89536	predicted protein	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	1.96E-145	-
S04106_13_D06	NR	A6XMY9	S-adenosylmethionine synthase 1	<i>Triticum monococcum</i>	0	8018871
S04106_13_D12	NR	EMT17394	Putative calcium-binding protein CML18	<i>Aegilops tauschii</i>	1.92E-77	26550992
S04106_13_E03	NR	NP_001148857	sheat shock protein binding protein	<i>Zea mays</i>	1.24E-105	-
S04106_13_E07	NR	EMS52570	putative glutathione S-transferase GSTU1	<i>Triticum urartu</i>	1.00E-42	11092907/15012285
S04106_13_F10	NR	XP_003570765	PREDICTED: two-component response regulator ARR10	<i>Brachypodium distachyon</i>	3.47E-122	-
S04106_14_A05	NR	AFV92901	putative PIP-type aquaporin	<i>Lolium perenne</i>	0	21441236
S04106_14_B01	NR	EMT14050	Protein ETHYLENE INSENSITIVE 3	<i>Aegilops tauschii</i>	2.38E-143	22209220
S04106_14_C05	NR	O24528	<i>Festuca rubra</i>	Metallothionein-like protein 1	2.91E-11	16912923
S04106_14_C08	NR	O24528	<i>Festuca rubra</i>	Metallothionein-like protein 1	2.91E-11	16912923
S04106_14_E01	NR	XP_006643957	PREDICTED: LOW QUALITY PROTEIN: salt stress root protein RS1-like	<i>Oryza brachyantha</i>	-	-
S04106_14_E08	NR	EMT00621	Histone H1	<i>Aegilops tauschii</i>	3.47E-29	25063323
S04106_14_E10	NR	ACV65038	Cu/Zn superoxide dismutase	<i>Deschampsia antarctica</i>	1.43E-92	25867355
S04106_15_B06	NR	XP_009629758	PREDICTED: ADP-ribosylation factor 2 isoform X1	<i>Nicotiana tomentosiformis</i>	1.98E-128	24247851
S04106_15_B07	NR	AFV92901	putative PIP-type aquaporin	<i>Lolium perenne</i>	0	21441236
S04106_15_D11	NR	ACV52081	S-adenosylmethionine decarboxylase 3	<i>Sorghum bicolor</i>	3.04E-54	8018871
S04106_15_G05	NR	XP_004955675	PREDICTED: auxin-responsive protein IAA24-like	<i>Setaria italica</i>	4.56E-72	20499123/18506580
S04106_16_A03	NR	XP_003562171	PREDICTED: auxin-repressed 12.5 kDa protein-like	<i>Brachypodium distachyon</i>	1.93E-46	20499123/18506580
S04106_16_A07	NR	ABF50675	vacuolar ATPase subunit G	<i>Triticum aestivum</i>	7.06E-38	-
S04106_16_E02	NR	O24528	Metallothionein-like protein 1	<i>Festuca rubra</i>	6.51E-10	16912923
S04106_17_C08	NR	P46524	Cold-induced COR410 protein	<i>Triticum aestivum</i>	8.76E-37	-
S04106_17_D01	NR	ADP37001	jacalin-related lectin 1	<i>Triticum aestivum</i>	2.26E-98	10872230
S04106_17_E12	NR	AHZ35571	LEA protein	<i>Triticum aestivum</i>	1.11E-34	16023228
S04106_17_G02	NR	XP_003577085	PREDICTED: serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform isoform X1	<i>Brachypodium distachyon</i>	3.29E-129	25281708
S04106_18_A08	NR	XP_003560412	PREDICTED: myb family transcription factor APL-like isoform X1	<i>Brachypodium distachyon</i>	3.75E-79	22140235
S04106_21_E10	NR	AHZ35571	LEA protein	<i>Triticum aestivum</i>	2.12E-09	16023228
S04106_18_E07	NR	AEV53588	light-induced protein 1-like protein	<i>Puccinellia tenuiflora</i>	4.33E-84	-
S04106_18_F04	NR	EMT08035	Heat stress transcription factor A-5	<i>Aegilops tauschii</i>	9.14E-137	-
S04106_18_F11	NR	ADP37001	jacalin-related lectin 1	<i>Triticum aestivum</i>	7.32E-101	10872230
S04106_18_H08	NR	AAY1679	early salt stress and cold acclimation-induced protein 2-1	<i>Lophopyrum elongatum</i>	1.57E-55	-
S04106_19_A03	NR	XP_003573692	PREDICTED: CBS domain-containing protein CBSX1, chloroplastic-like	<i>Brachypodium distachyon</i>	4.20E-83	22302312
S04106_19_B06	NR	ABB90544	dehydration responsive element binding protein	<i>Triticum aestivum</i>	8.43E-115	19005655

Continued Table S1

Gene-id	Source	accession	Putative-description	Species	E-value	Ref-PMID
S04106_19_B10	NR	XP_003557725	PREDICTED: glucose-6-phosphate 1-dehydrogenase, chloroplastic-like	Brachypodium distachyon	3.03E-129	17952457
S04106_19_D06	NR	O24528	Metallothionein-like protein 1	Festuca rubra	7.38E-13	16912923
S04106_19_H01	NR	CAB64671	S-adenosylmethionine decarboxylase 1, partial	Oryza sativa Indica Group	7.99E-57	16642382
S04106_19_H04	NR	AFV92901	putative PIP-type aquaporin	Lolium perenne	0	21441236
S04106_20_B06	NR	ABI84118	betaine aldehyde dehydrogenase	Oryza sativa Japonica Group	2.00E-153	25150410(rice)
S04106_20_C07	NR	EMT31119	Zinc finger A20 and AN1 domain-containing stress-associated protein 4	Aegilops tauschii	8.47E-95	18588956
S04106_20_C10	NR	XP_004962473	PREDICTED: probable calcium-binding protein CML21-like	Setaria italica	7.07E-38	26550992
S04106_20_D12	NR	AAK55324	thaumatin-like protein TLP6	Hordeum vulgare	1.24E-121	16203714
S04106_20_E10	NR	XP_003563517	PREDICTED: Bowman-Birk type trypsin inhibitor-like	Brachypodium distachyon	2.91E-29	18433440
S04106_20_H09	NR	XP_010227523	PREDICTED: ras-related protein Rab11C	Brachypodium distachyon	1.24E-150	20018899
S04106_20_H04	NR	Q00434	Oxygen-evolving enhancer protein 2, chloroplastic	Triticum aestivum	3.57E-133	15221768
S04106_21_C11	NR	XP_010232378	PREDICTED: glutathione S-transferase 1	Brachypodium distachyon	1.33E-139	11092907/15012285
S04106_21_D04	NR	XP_003568950	PREDICTED: probable calcium-binding protein CML21 isoform X1	Brachypodium distachyon	6.56E-151	26550992
S04106_21_E10	NR	AHZ35571	LEA protein	Triticum aestivum	2.12E-09	16023228
S04106_21_E12	NR	XP_00170324	myo-inositol-1-phosphate synthase	Chlamydomonas reinhardtii	5.00E-144	12624775
S04106_21_G04	NR	O24528	Metallothionein-like protein 1	Festuca rubra	2.29E-10	16912923
S04106_21_H04	NR	XP_010232479	PREDICTED: ADP-ribosylation factor 2 isoform X2	Brachypodium distachyon	7.37E-127	24247851
S04106_21_H09	NR	XP_003560016	PREDICTED: CBS domain-containing protein CBSX3, mitochondrial	Brachypodium distachyon	3.11E-134	22302312
S04106_22_C09	NR	XP_010227582	PREDICTED: dehydrin DHN3-like	Brachypodium distachyon	7.57E-18	22608523
S04106_22_F07	NR	ACV65038	Cu/Zn superoxide dismutase	Deschampsia antarctica	1.44E-92	25867355
S04106_22_H02	NR	AAY16796	early salt stress and cold acclimation-induced protein 2-3	Lophopyrum elongatum	1.90E-48	-
S04106_22_H11	NR	CAB64671	S-adenosylmethionine decarboxylase 1, partial	Oryza sativa Indica Group	5.44E-54	16642382
S04106_23_A09	NR	AFV92901	putative PIP-type aquaporin	Lolium perenne	0	21441236
S04106_23_B11	NR	O24528	Metallothionein-like protein 1	Festuca rubra	3.04E-11	16912923
S04106_23_C01	NR	ABC65853	drought-responsive factor-like transcription factor DRFL1a	Triticum aestivum	7.22E-17	-
S04106_23_C03	NR	EMT26943	Serine/threonine protein phosphatase 2A 55 kDa regulatory subunit B beta isoform	Aegilops tauschii	1.04E-139	25281708
S04106_23_E10	NR	XP_003567630	PREDICTED: S-adenosylmethionine synthase 3-like	Brachypodium distachyon	0	8018871
S04106_23_F02	NR	EMS65202	Bowman-Birk type trypsin inhibitor	Triticum urartu	5.92E-48	18433440

Continued Table S1

Gene-id	Source	accession	Putative-description	Species	E-value	Ref-PMID
S04106_23_F06	NR	BAJ8672	predicted protein(GstA)	Hordeum vulgare subsp. vulgare	5.65E-125	11092907/15012285
S04106_24_A09	NR	XP_001699660	2-cys peroxiredoxin	Chlamydomonas reinhardtii	7.34E-113	23053072
S04106_24_D04	NR	AAL67139	thioredoxin H	Triticum aestivum	1.50E-49	22010108 (rice)
S04106_24_F02	NR	XP_003575573	PREDICTED: CBS domain-containing protein CBSX1, chloroplastic-like	Brachypodium distachyon	3.16E-91	22302312
S04106_24_F07	NR	AAY16798	early salt stress and cold acclimation-induced protein 2-1	Lophopyrum elongatum	3.37E-54	-
S04106_24_G07	NR	EMS68484	Zinc finger A20 and AN1 domain-containing stress-associated protein 8	Triticum urartu	2.10E-94	22961664
S04106_25_B09	NR	XP_003558174	PREDICTED: low temperature-induced protein It101.2	Brachypodium distachyon	9.29E-23	-
S04106_25_B01	NR	BAF99133	basic region/leucine zipper protein	Triticum aestivum	3.18E-50	7476849
S04106_25_E08	NR	XP_010230700	PREDICTED: zinc finger CCCH domain-containing protein 3	Brachypodium distachyon	4.65E-66	25074582/19402879
S04106_25_G10	NR	ABI84118	betaine aldehyde dehydrogenase	Oryza sativa Japonica Group	2.00E-153	25150410(rice)
S04106_25_H12	NR	XP_010232090	PREDICTED: ketol-acid reductoisomerase, chloroplastic-like	Brachypodium distachyon	1.19E-134	22930436
S04106_26_B07	NR	ACV65038	Cu/Zn superoxide dismutase	Deschampsia antarctica	1.51E-89	25867355
S04106_26_D12	NR	EMS50250	Thioredoxin H-type	Triticum urartu	5.67E-31	22010108 (rice)
S04106_26_C04	NR	CAB64671	S-adenosylmethionine decarboxylase 1, partial	Oryza sativa Indica Group	3.28E-52	16642382
S04106_26_F03	NR	XP_003579861	PREDICTED: zeaxanthin epoxidase, chloroplastic	Brachypodium distachyon	1.27E-99	26573680
S04106_26_F09	NR	AFF18616	ammonium transporter	Puccinellia tenuiflora	3.21E-138	-
S04106_26_G02	NR	XP_003575573	PREDICTED: CBS domain-containing protein CBSX1, chloroplastic-like	Brachypodium distachyon	1.51E-89	22302312
S04106_27_A04	NR	CAZ64535	sucrose synthase(Cation_ATPase)	Hordeum vulgare subsp. vulgare	0	24482191
S04106_27_A11	NR	A3BOY1	Metallothionein-like protein 3B	Oryza sativa Japonica Group	1.11E-16	16912923
S04106_27_B10	NR	XP_003563776	PREDICTED: ras-related protein RIC2	Brachypodium distachyon	1.97E-151	20018899
S04106_27_C03	NR	BAK23261	Na+/H+ exchanger	Puccinellia tenuiflora	6.03E-123	-
S04106_27_D01	NR	EMT18074	RING finger protein 165	Aegilops tauschii	8.24E-37	-
S04106_27_E02	NR	XP_006643957	PREDICTED: LOW QUALITY PROTEIN: salt stress root protein RS1-like	Oryza brachyantha	7.42E-51	-
S04106_27_E11	NR	ACT65562	70 kDa heat shock protein	Triticum aestivum	1.40E-159	-
S04106_27_F12	NR	Q00434	Oxygen-evolving enhancer protein 2, chloroplastic	Triticum aestivum	1.21E-132	15221768
S04106_27_F03	NR	A3BOY1	Metallothionein-like protein 3B(OsMT-I-3b)	Oryza sativa Japonica Group	7.79E-16	16912923
S04106_27_H05	NR	XP_003568882	PREDICTED: universal stress protein A-like protein	Brachypodium distachyon	4.62E-72	-
S04106_27_H12	NR	XP_003558228	PREDICTED: heat shock cognate 70 kDa protein 2-like	Brachypodium distachyon	3.47E-168	-

Continued Table S1

Gene-id	Source	accession	Putative-description	Species	E-value	Ref-PMID
S04106_28_A02	NR	ACV86035	glyceraldehyde-3-phosphate dehydrogenase 2	Festuca arundinacea	2.23E-127	24737077
S04106_28_A09	KEGG	K13946	AUX1, LAX, auxin influx carrier (AUX1/LAX family)	Arabidopsis thaliana	-	11864575/20110325
S04106_28_E02	NR	EMS55466	S-adenosylmethionine synthase 1	Triticum monococcum	3.33E-175	8018871
S04106_28_F11	NR	BAH01721	cation/H ⁺ exchanger	Puccinellia tenuiflora	1.13E-151	-
S04106_29_A04	NR	XP_003569277	PREDICTED: probable V-type proton ATPase subunit d	Brachypodium distachyon	1.71E-177	8980504
S04106_29_A09	NR	AAQ17506	calcium dependent protein kinase 3	Oryza sativa Japonica Group	7.00E-88	-
S04106_29_B04	NR	EMT00621	Histone H1	Aegilops tauschii	6.50E-30	25063323
S04106_29_C01	NR	XP_003573856	PREDICTED: probable calcium-binding protein CML8	Brachypodium distachyon	3.55E-72	26550992
S04106_29_C07	NR	ACN54194	HVA22-like protein	Triticum aestivum	8.07E-94	12081371/11292078
S04106_29_D08	NR	AGW23429	ascorbate peroxidase	Puccinellia tenuiflora	6.80E-35	25644292
S04106_29_D09	NR	XP_003574676	PREDICTED: heat shock cognate 90 kDa protein-like	Brachypodium distachyon	1.46E-145	-
S04106_29_D10	NR	ACV60508	aquaporin	Triticum aestivum	4.29E-173	21441236
S04106_29_D11	NR	ABG75753	salt stress-responsive protein	Triticum aestivum	5.03E-81	-
S04106_29_E09	NR	CAA81231	alanine aminotransferase	Hordeum vulgare subsp. vulgare	1.81E-180	-
S04106_29_H02	NR	EMS63241	Late embryogenesis abundant protein Lea14-A	Triticum urartu	1.30E-126	16023228
S04106_30_B07	NR	P23957	vacuolar-type H ⁺ -ATPase 16 kDa subunit c	Puccinellia tenuiflora	1.87E-71	-
S04106_30_C09	NR	ACN67534	cellulose synthase-like protein H1	Hordeum vulgare subsp. vulgare	2.68E-142	20409003
S04106_30_G02	NR	A6XMY9	S-adenosylmethionine synthase 1	Triticum monococcum	0	8018871
S04106_30_G03	NR	EMS58299	Dehydrin Rab15	Triticum urartu	4.46E-24	19398349
S04106_30_H05	NR	AIR07415	glutathione S-transferase	Alopecurus japonicus	2.49E-143	11092907/15012285
S04106_30_D08	NR	O24528	Metallothionein-like protein 1	Festuca rubra	2.77E-11	16912923
S04106_30_G04	NR	CAD31225	glutathione s-transferase, partial	Oryza sativa Japonica Group	2.22E-78	11092907/15012285
S04106_30_H05	NR	AIR07415	glutathione S-transferase	Alopecurus japonicus	2.49E-143	11092907/15012285
S04106_31_A05	NR	XP_003578375	PREDICTED: CSC1-like protein HYP1	Brachypodium distachyon	1.70E-158	12552141
S04106_31_A11	NR	EMT00621	Histone H1	Aegilops tauschii	3.86E-30	25063323
S04106_31_B05	NR	O24528	Metallothionein-like protein 1(MT-1)	Festuca rubra	9.26E-11	16912923
S04106_31_D11	NR	BAJ90885	predicted protein(glyceraldehyde-3-phosphate dehydrogenase A)	Hordeum vulgare subsp. vulgare	2.11E-176	24737077
S04106_31_C09	NR	NP_001105490	calmodulin	Zea mays	9.08E-98	15292241
S04106_31_F07	NR	XP_003577566	PREDICTED: probable WRKY transcription factor 75	Brachypodium distachyon	6.70E-65	26106823
S04106_32_C06	NR	BAA23745	HvPIP1;3	Hordeum vulgare subsp. vulgare	2.63E-176	21441236
S04106_32_G02	NR	XP_010230849	S-adenosylmethionine synthase 1	Triticum monococcum	1.11E-135	8018871