Table S1. Quantitative shotgun proteomic analysis of developing seeds of MSD1OE and WT at 4 and 10 DAF under hot and control conditions.

WT, Nipponbare wild type; MSD1OE, Nipponbare MSD1 overexpressor. Hot condition = 33/28 °C (12/12 h); control condition = 28/23 °C (12/12 h). Numerical values in blue and red indicate ≧2-fold upregulation and downregulation, respectively, in MSD1OE.

cTP: chloroplast transit peptide
mTP: mitochondrion transit peptide
SP: signal peptide
NTS: nuclear transport signal
PTS: peroxisome targeting signal

Stress response

	hot (light 12h, 33℃ / dark 12h, 28℃)				control (light 12h, 28℃ / dark 12h, 23℃)						
Accession	Coverage	Peptide	Ratio (MSD1OE/WT for 4days)	Ratio (MSD1OE/WT for 10days)	Coverage	Peptide	Ratio (MSD1OE/WT for 4days)	Ratio (MSD1OE/WT for 10days)	Description		Sorting signal (localization predicted)
reactive oxygen scavenging											
P0C5C9	37.29	29	0.562	0.132	30.91	20	1.343	1.967	1-Cys peroxiredoxin A OS=Oryza sativa subsp. japonica GN=Os07g0638300 - [REHYA_ORYSJ]		NTS (nucleus)
P0C5D5	7.83	2	2.022	1.756	15.21	12	1.067	1.121	Peroxiredoxin Q, chloroplastic OS=Oryza sativa subsp. japonica GN=Os06g0196300 - [PRXQ_ORYSJ]		cTP (plastid)
P93407	30.33	15	2.989	3.078	34.60	27	1.003	1.067	Superoxide dismutase [Cu-Zn], chloroplastic OS=Oryza sativa subsp. japonica GN=SODCP - [SODCP_ORYSJ]		unclear (plastid, cytoplasm)
Q0D840	48.36	41	1.179	2.383	40.98	60	1.301	0.788	Thioredoxin H1 OS=Oryza sativa subsp. japonica GN=TRXH - [TRXH1_ORYSJ]		none (cytoplasm)
Q10N21	42.80	20	3.993	5.523	54.40	68	1.492	0.987	L-ascorbate peroxidase 1, cytosolic OS=Oryza sativa subsp. japonica GN=APX1 - [APX1_ORYSJ]		none (cytoplasm)
Q6AUK5	4.80	1	2.054	3.986	16.59	7	1.267	0.974	Peptide methionine sulfoxide reductase B3, chloroplastic OS=Oryza sativa subsp. japonica GN=MSRB3 - [MSRB3_ORYSJ]		cTP (plastid)
Q6ER94	26.44	9	1.843	2.329	31.42	40	1.628	1.010	2-Cys peroxiredoxin BAS1, chloroplastic OS=Oryza sativa subsp. japonica GN=BAS1 - [BAS1_ORYSJ]		cTP (plastid)
Q6ZJ08	1.61	1	5.117	4.124	26.21	18	1.657	0.774	Monodehydroascorbate reductase OS=Oryza sativa subsp. japonica GN=OJ1150_A11.25 - [Q6ZJ08_ORYSJ]		SP (ER)
Q6ZJJ1	13.75	5	2.029	4.853	28.52	18	1.772	0.995	Probable L-ascorbate peroxidase 4 OS=Oryza sativa subsp. japonica GN=APX4 - [APX4_ORYSJ]		mTP (mitochondrion)
Q7F8S5	4.89	1	2.614	3.754	44.00	12	1.404	1.197	Peroxiredoxin-2E-2, chloroplastic OS=Oryza sativa subsp. japonica GN=PRXIIE-2 - [PR2E2_ORYSJ]		cTP (plastid)
Q7XZW1	4.04	1	1.866	4.315	5.38	4	1.836	1.267	NADH-ubiquinone oxidoreductase 23 kDa subunit, mitochondrial, putative, expressed OS=Oryza sativa subsp. japonica GN=OSJNBb0094O03.18 - [Q7XZW1_ORYSJ]		mTP (mitochondrion)
Q8H8D6	3.13	1	3.239	2.758	N. D	N. D	N. D	N. D	Glutathione S-transferase, N-terminal domain containing protein, expressed OS=Oryza sativa subsp. japonica GN=OJ1006F06.9 - [Q8H8D6_ORYSJ]		SP (ER)
Q8RZT1	2.42	1	0.447	1.147	2.42	6	1.513	0.998	Os01g0316100 protein OS=Oryza sativa subsp. japonica GN=B1012D10.43 - [Q8RZT1_ORYSJ]	Putative L-pipecolic acid oxidase	unclear
Q9FE01	38.25	9	2.569	3.760	40.64	56	1.562	1.001	L-ascorbate peroxidase 2, cytosolic OS=Oryza sativa subsp. japonica GN=APX2 - [APX2_ORYSJ]		none (cytoplasm)
Q9FR35	13.58	2	1.953	2.011	51.23	28	1.389	0.982	Peroxiredoxin-2C OS=Oryza sativa subsp. japonica GN=PRXIIC - [PRX2C_ORYSJ]		none (cytoplasm)
chaperone, heat shock protein							N. D				
Q53NM9	26.35	55	1.807	2.385	55.62	251	1.705	1.086	DnaK-type molecular chaperone hsp70-rice OS=Oryza sativa subsp. japonica GN=Os11g0703900 - [Q53NM9_ORYSJ]		NTS (nucleus)
Q53RJ5	4.19	11	0.299	0.410	7.62	34	0.755	N. D	DnaK protein OS=Oryza sativa subsp. japonica GN=Os03g0710500 - [Q53RJ5_ORYSJ]		SP (secretory)
Q5VRY1-1	17.47	4	1.772	2.036	16.87	6	1.653	0.836	Isoform 1 of 18.0 kDa class II heat shock protein OS=Oryza sativa subsp. japonica GN=HSP18.0 - [HSP18_ORYSJ]		none (cytoplasm)
Q5Z9N8	4.19	6	2.290	2.741	28.82	47	1.722	0.832	Heat shock protein 90 OS=Oryza sativa subsp. japonica GN=P0481E08.35 - [Q5Z9N8_ORYSJ]		SP (secretory)
Q69Y99	23.41	6	0.997	3.395	51.59	40	1.304	1.019	Putative chaperonin 21 OS=Oryza sativa subsp. japonica GN=P0528E04.36-1 - [Q69Y99_ORYSJ]		cTP (plastid)
Q6K7E9	7.56	3	0.984	0.248	6.40	1	1.472	1.324	18.6 kDa class III heat shock protein OS=Oryza sativa subsp. japonica GN=HSP18.6 - [HS186_ORYSJ]		none (cytoplasm)
Q6Z7B0	47.52	114	0.382	0.793	52.78	316	1.389	0.982	Dnak-type molecular chaperone Bip OS=Oryza sativa subsp. japonica GN=P0036E06.29 - [Q6Z7B0_ORYSJ]		SP (secretory)
Q6Z7L1	17.23	16	1.647	3.257	27.98	48	1.500	1.084	Os02g0774300 protein OS=Oryza sativa subsp. japonica GN=OJ1448_G06.10 - [Q6Z7L1_ORYSJ]	Putative DnaK-type molecular chaperone	mTP (mitochondrion)
Q6Z7V2	22.73	6	1.602	2.646	5.91	1	1.110	0.695	24.1 kDa heat shock protein, mitochondrial OS=Oryza sativa subsp. japonica GN=HSP24.1 - [HS24M_ORYSJ]		unclear
Q6ZCV7	4.97	6	1.738	2.107	21.15	40	4.469	1.093	Os08g0487800 protein OS=Oryza sativa subsp. japonica GN=P0028A08.21 - [Q6ZCV7_ORYSJ]	Putative heat-shock protein	cTP (plastid)
Q75I57	4.48	8	1.177	2.021	14.67	17	1.437	0.943	Putative heat shock protein, 5'-partial (Fragment) OS=Oryza sativa subsp. japonica GN=OSJNBa0083F15.25 - [Q75I57_ORYSJ]		unclear
Q8H3I7	6.12	1	1.217	2.194	16.33	13	1.176	1.285	10 kDa chaperonin OS=Oryza sativa subsp. japonica GN=P0524G08.116 - [Q8H3I7_ORYSJ]		mTP (mitochondrion)
Q8H903	22.65	18	1.576	2.021	41.29	69	1.512	1.073	Mitochondrial chaperonin-60 OS=Oryza sativa subsp. japonica GN=OSJNBa0071K18.10 - [Q8H903_ORYSJ]		mTP (mitochondrion)
Q943E6	18.00	9	1.659	0.243	12.00	1	N. D	N. D	16.9 kDa class I heat shock protein 2 OS=Oryza sativa subsp. japonica GN=HSP16.9B - [HS16B_ORYSJ]		none (cytoplasm)
Q9SLY8-1	38.44	28	2.484	4.276	34.43	45	1.399	0.954	Isoform 1 of Calreticulin OS=Oryza sativa subsp. japonica GN=Os07g0246200 - [CALR_ORYSJ]		SP (secretory)
stress related											
O04226	2.37	2	2.945	N. D	6.42	6	1.574	0.829	Delta-1-pyrroline-5-carboxylate synthase OS=Oryza sativa subsp. japonica GN=P5CS - [P5CS_ORYSJ]		none (cytoplasm)
Q0JMY8	5.52	1	4.795	3.210	22.07	3	1.299	0.689	Salt stress-induced protein OS=Oryza sativa subsp. japonica GN=SALT - [SALT_ORYSJ]		none (cytoplasm)
Q67X37	6.82	2	1.150	2.329	10.71	2	1.473	0.869	Os06g0231300 protein OS=Oryza sativa subsp. japonica GN=P0525F01.37 - [Q67X37_ORYSJ]	Putative salt tolerance protein 5	cTP (plastid)
Q6ESR4	4.14	2	0.801	2.244	N. D	N. D	N. D	N. D	Dehydration-stress inducible protein 1 OS=Oryza sativa subsp. japonica GN=P0684A08.9-1 - [Q6ESR4_ORYSJ]		NTS (nucleus)
Q6H660	20.70	15	1.116	2.128	36.16	46	1.202	1.281	Os02g0644100 protein OS=Oryza sativa subsp. japonica GN=OJ1282_H11.17 - [Q6H660_ORYSJ]	Putative stress-induced protein sti1	none (cytoplasm)
Q6YUR8	25.31	9	1.981	4.368	29.05	10	1.127	1.114	Cold shock domain protein 1 OS=Oryza sativa subsp. japonica GN=OSJNBb0088N06.21 - [Q6YUR8_ORYSJ]		none (cytoplasm)
Q6Z4N4	9.80	1	1.966	2.335	9.80	1	1.643	1.262	Os07g0684000 protein OS=Oryza sativa subsp. japonica GN=OSJNBa0060O17.15 - [Q6Z4N4_ORYSJ]	Ricin B-related lectin domain containing protein.	unclear
Q6ZBK6	1.99	1	0.256	0.279	3.10	2	1.812	0.965	Os08g0519400 protein OS=Oryza sativa subsp. japonica GN=P0689E12.19 - [Q6ZBK6_ORYSJ]	Putative stress related-like protein interactor	SP (secretory)
Q75LL0	33.52	10	0.428	0.264	19.78	22	1.623	1.423	Putative stress-related protein OS=Oryza sativa subsp. japonica GN=OSJNBa0047E24.27 - [Q75LL0_ORYSJ]		none (cytoplasm)
Q7XUY5	74.52	83	2.059	3.846	79.62	146	1.295	1.196	OSJNBb0048E02.12 protein OS=Oryza sativa subsp. japonica GN=OSJNBb0048E02.12 - [Q7XUY5_ORYSJ]	Pathogenesis-related protein	none (cytoplasm)
Q84UR8	41.62	24	1.670	3.357	48.73	16	0.765	1.249	Cold shock domain protein 2 OS=Oryza sativa subsp. japonica GN=P0582D05.112 - [Q84UR8_ORYSJ]		none (cytoplasm)

Metabolism

	hot				control					
Accession	Coverage	Peptide	Ratio (MSD1OE/WT for 4days)	Ratio (MSD1OE/WT for 10days)	Coverage	Peptide	Ratio (MSD1OE/WT for 4days)	Ratio (MSD1OE/WT for 10days)	Description	Sorting signal (localization predicted)
glycometabolism, glycolysis										
P15280-2	30.27	32	0.344	0.845	48.85	98	1.356	1.146	Isoform 2 of Glucose-1-phosphate adenylyltransferase small subunit, chloroplastic/amyloplastic OS=Oryza sativa subsp. japonica GN=AGPS - [GLGS_ORYSJ]	cTP (plastid)
P27934-2	4.29	2	0.351	0.082	N. D	N. D	N. D	N. D	Isoform 2 of Alpha-amylase isozyme 3E OS=Oryza sativa subsp. japonica GN=AMY1.4 - [AMY3E_ORYSJ]	SP (secretory)
P29421	13.50	4	0.202	0.124	21.00	12	1.200	1.185	Alpha-amylase/subtilisin inhibitor OS=Oryza sativa subsp. japonica GN=RASI - [IAAS_ORYSJ]	SP (secretory)

P42863	1.59	1	0.953	**2.315**	14.64	9	1.753	0.725	Glucose-6-phosphate isomerase, cytosolic B OS=Oryza sativa subsp. japonica GN=Os06g0256500 - [G6PIB_ORYSJ]		none (cytoplasm)
Q01401-1	23.66	31	**0.114**	0.685	28.66	84	1.272	0.659	Isoform 1 of 1,4-alpha-glucan-branching enzyme, chloroplastic/amyloplastic OS=Oryza sativa subsp. japonica GN=SBE1 - [GLGB_ORYSJ]		cTP (plastid)
Q0D3D2	2.04	1	1.830	**2.146**	4.77	5	1.977	1.089	Pyruvate decarboxylase isozyme 3 OS=Oryza sativa subsp. japonica GN=PDC3 - [PDC3_ORYSJ]		none (cytoplasm)
Q0J8A4	33.23	34	1.686	**2.210**	59.35	164	**2.051**	0.899	Glyceraldehyde-3-phosphate dehydrogenase, cytosolic OS=Oryza sativa subsp. japonica GN=GAPC - [G3PC_ORYSJ]		none (cytoplasm)
Q40677	16.49	9	**2.461**	**2.338**	29.64	41	1.846	1.175	Fructose-bisphosphate aldolase, chloroplastic OS=Oryza sativa subsp. japonica GN=Os11g0171300 - [ALFC_ORYSJ]		cTP (plastid)
Q5JK10	9.49	4	**2.053**	1.960	27.31	28	1.913	0.694	Os01g0926300 protein OS=Oryza sativa subsp. japonica GN=OSJNBa0093F16.14 - [Q5JK10_ORYSJ]	Putative transaldolase	unclear
Q5NBP9	1.30	1	**2.594**	**4.814**	N. D	N. D	N. D	N. D	Os01g0276800 protein OS=Oryza sativa subsp. japonica GN=P0038F12.26 - [Q5NBP9_ORYSJ]	Protein kinase C substrate 80K-H isoform 2-like	SP (secretory)
Q5VNT5	3.31	3	**0.372**	1.057	37.74	84	1.377	1.313	Glucose-1-phosphate adenylyltransferase OS=Oryza sativa subsp. japonica GN=P0663E10.9 - [Q5VNT5_ORYSJ]		none (cytoplasm)
Q5VNW1	5.37	4	**2.791**	1.058	28.12	68	1.768	0.834	Putative transketolase 1 OS=Oryza sativa subsp. japonica GN=P0001H02.3 - [Q5VNW1_ORYSJ]		NTS (nucleus)
Q60EY9	3.92	3	**2.036**	**2.178**	25.16	15	1.936	0.666	Os05g0208000 protein OS=Oryza sativa subsp. japonica GN=OJ1430_B02.7 - [Q60EY9_ORYSJ]	Putative 2-oxoglutarate/malate translocator	mTP (mitochondrion)
Q653V7	1.47	1	**0.110**	N. D	13.56	19	1.463	1.382	Probable alpha-glucosidase Os06g0675700 OS=Oryza sativa subsp. japonica GN=Os06g0675700 - [AGLU_ORYSJ]		SP (secretory)
Q69K00	8.88	4	**3.120**	**2.710**	25.00	18	1.557	1.044	Triose phosphate isomerase OS=Oryza sativa subsp. japonica GN=P0569E11.2-1 - [Q69K00_ORYSJ]		cTP (plastid)
Q6EN36	1.81	1	**0.398**	**7.427**	N. D	N. D	N. D	N. D	Os02g0256100 protein OS=Oryza sativa subsp. japonica GN=OSJNBa0052K15.27 - [Q6EN36_ORYSJ]	Putative polygalacturonase	SP (secretory)
Q6EUF8	11.00	4	1.676	**2.058**	8.20	3	1.817	**0.449**	Citrate synthase OS=Oryza sativa subsp. japonica GN=OJ1705_E12.26 - [Q6EUF8_ORYSJ]		unclear
Q6H6P8	7.52	8	0.667	**2.082**	24.24	77	1.381	0.759	Branching enzyme-3 OS=Oryza sativa subsp. japonica GN=P0475F05.16 - [Q6H6P8_ORYSJ]		cTP (plastid)
Q6Z5N4	10.77	5	1.691	**2.152**	17.95	24	1.730	0.889	Os02g0739600 protein OS=Oryza sativa subsp. japonica GN=P0684F11.25 - [Q6Z5N4_ORYSJ]	Putative pyruvate dehydrogenase E1 alpha subunit	mTP (mitochondrion)
Q6Z9C3	7.65	4	**0.500**	1.047	N. D	N. D	N. D	N. D	Probable 6-phosphogluconolactonase 3, chloroplastic OS=Oryza sativa subsp. japonica GN=Os08g0547100 - [6PGL3_ORYSJ]		cTP (plastid)
Q6ZBH2	12.47	16	**0.237**	0.583	27.10	67	1.357	1.248	Os08g0545200 protein OS=Oryza sativa subsp. japonica GN=P0623F08.37 - [Q6ZBH2_ORYSJ]	Putative sorbitol dehydrogenase	unclear
Q75K90	17.10	6	**2.752**	0.984	44.84	42	2.093	1.028	Phosphoglycerate kinase OS=Oryza sativa subsp. japonica GN=OJ1118_C04.1 - [Q75K90_ORYSJ]		none (cytoplasm)
Q7FAH2	35.31	41	**2.256**	**2.998**	48.66	187	1.873	0.885	Glyceraldehyde-3-phosphate dehydrogenase OS=Oryza sativa subsp. japonica GN=OJ000223_09.15 - [Q7FAH2_ORYSJ]		unclear
Q7X8A1	7.46	3	**3.835**	**2.516**	28.61	42	**2.024**	0.910	OSJNBa0036B21.24 protein OS=Oryza sativa subsp. japonica GN=OSJNBa0036B21.24 - [Q7X8A1_ORYSJ]	glucose metabolic process related protein	cTP (plastid)
Q8H3Q7	8.77	5	**2.116**	**3.116**	30.48	34	1.776	0.912	Xylose isomerase OS=Oryza sativa subsp. japonica GN=P0625E02.119 - [Q8H3Q7_ORYSJ]		SP (secretory)
Q8H4V1	1.54	2	**3.583**	1.746	28.32	50	1.685	0.675	Os08g0366000 protein OS=Oryza sativa subsp. japonica GN=OJ1484_G09.129-1 - [Q8H4V1_ORYSJ]	Phosphoenolpyruvate carboxylase	unclear
Q94JJ0	6.95	2	**2.877**	**2.770**	9.02	8	1.961	0.885	Fructose-bisphosphate aldolase OS=Oryza sativa subsp. japonica GN=P0494A10.15 - [Q94JJ0_ORYSJ]		unclear
Q9AUQ4	22.68	27	1.095	**2.004**	44.85	105	1.665	0.935	Phosphoglucomutase OS=Oryza sativa GN=OSJNBb0033N16.5 - [Q9AUQ4_ORYSA]		PTS(peroxisome)
Q9FRX7	4.74	3	**2.259**	1.558	26.96	34	1.738	0.902	Aldehyde dehydrogenase ALDH2b OS=Oryza sativa subsp. japonica GN=Aldh2b - [Q9FRX7_ORYSJ]		mTP (mitochondrion)
Q9SNK3	14.41	7	**2.494**	**2.030**	30.63	44	1.868	1.063	EST C74302(E30840) corresponds to a region of the predicted gene OS=Oryza sativa subsp. japonica GN=Os03g0129300 - [Q9SNK3_ORYSJ]	Glyceraldehyde-3-phosphate dehydrogenase B,	cTP (plastid)
energy metabolism											
P0C522	9.63	6	**2.664**	**4.095**	46.56	132	1.804	0.860	ATP synthase subunit alpha, mitochondrial OS=Oryza sativa subsp. japonica GN=ATPA - [ATPAM_ORYSJ]		mitochondrial gene
P12085	14.26	22	**2.063**	**2.056**	65.46	178	1.850	1.082	ATP synthase subunit beta, chloroplastic OS=Oryza sativa subsp. japonica GN=atpB - [ATPB_ORYSJ]		chloroplastic gene
Q01859	46.74	63	**2.046**	**2.436**	56.70	212	1.586	1.190	ATP synthase subunit beta, mitochondrial OS=Oryza sativa subsp. japonica GN=ATPB - [ATPBM_ORYSJ]		mTP (mitochondrion)
Q5TKF4	25.10	8	**2.070**	**2.402**	21.34	14	1.644	0.901	Nucleoside diphosphate kinase OS=Oryza sativa subsp. japonica GN=OSJNBa0030I14.12 - [Q5TKF4_ORYSJ]		cTP (plastid)
Q8S7T5	11.53	6	**2.822**	**2.007**	N. D	N. D	N. D	N. D	ATP synthase subunit alpha OS=Oryza sativa subsp. japonica GN=OSJNBb0005J14.21 - [Q8S7T5_ORYSJ]		none (cytoplasm)
Q6K9N6	11.37	6	1.874	**2.564**	30.33	22	1.630	1.094	Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial OS=Oryza sativa subsp. japonica GN=Os02g0621700 - [SUCB_ORYSJ]		mTP (mitochondrion)
lipid metabolism											
Q10EK7	37.79	17	**0.422**	**0.121**	18.60	6	1.343	1.967	Oleosin 18 kDa OS=Oryza sativa subsp. japonica GN=OLE18 - [OLEO2_ORYSJ]		unclear
Q42980	7.43	2	0.954	**0.384**	7.43	4	1.139	1.683	Oleosin 16 kDa OS=Oryza sativa subsp. japonica GN=OLE16 - [OLEO1_ORYSJ]		unclear
Q6YY47	2.73	2	**3.469**	**4.556**	1.34	1	**2.004**	1.091	Os02g0588500 protein OS=Oryza sativa subsp. japonica GN=OSJNBb0046O12.21 - [Q6YY47_ORYSJ]	Putative GPI-anchored protein	SP (plasma membrane)
Q6YZX6	4.90	4	**3.413**	**3.178**	23.39	73	1.623	0.983	Putative aconitate hydratase, cytoplasmic OS=Oryza sativa subsp. japonica GN=Os08g0191100 - [ACOC_ORYSJ]		none (cytoplasm)
Q6Z0I4	21.33	9	1.210	**2.222**	14.93	7	1.795	0.981	Os08g0327400 protein OS=Oryza sativa subsp. japonica GN=OSJNBa0049I01.2 - [Q6Z0I4_ORYSJ]	Putative enoyl-ACP reductase	cTP (plastid)
Q75GN2	10.14	1	**0.213**	**0.224**	10.14	2	1.505	1.543	Non-specific lipid-transfer protein OS=Oryza sativa subsp. japonica GN=OSJNBa0018K15.7 - [Q75GN2_ORYSJ]		SP (secretory)
Q75LC6	2.72	3	**5.639**	N. D	2.45	3	1.856	0.579	GDSL-motif lipase/hydrolase family protein, putative, expressed OS=Oryza sativa subsp. japonica GN=OSJNBa0032G11.17 - [Q75LC6_ORYSJ]		SP (secretory)
Q7F280	2.67	1	**4.106**	N. D	30.83	25	1.838	0.753	Isocitrate dehydrogenase [NADP] OS=Oryza sativa subsp. japonica GN=OSJNBb0006H05.32 - [Q7F280_ORYSJ]		PTS(peroxisome)
Q8S0E1	3.41	3	**2.049**	0.951	N. D	N. D	N. D	N. D	Pyruvate kinase OS=Oryza sativa subsp. japonica GN=OJ1014_E09.29-2 - [Q69WE5_ORYSJ]		Mitochondrion
nucleotide and amino acid metabolism											
P14656	3.09	1	**2.847**	**3.026**	29.21	19	1.549	0.998	Glutamine synthetase cytosolic isozyme 1-1 OS=Oryza sativa subsp. japonica GN=GLN1-1 - [GLN11_ORYSJ]		PTS(peroxisome)
P37833	9.83	7	**0.491**	0.958	47.42	78	1.538	0.712	Aspartate aminotransferase, cytoplasmic OS=Oryza sativa subsp. japonica GN=Os01g0760600 - [AATC_ORYSJ]		none (cytoplasm)
Q0DKY4	13.38	6	**3.404**	**2.219**	38.13	42	1.652	1.363	S-adenosylmethionine synthase 1 OS=Oryza sativa subsp. japonica GN=SAM1 - [METK1_ORYSJ]		none (cytoplasm)
Q6ATY5	8.84	1	1.595	**2.468**	9.52	5	1.685	1.188	Putative N'-5'-phosphoribosyl-formimino-5-aminoimidazole-4-carboxamide ribonucleotide isomerase OS=Oryza sativa subsp. japonica GN=OSJNBa0035J16.8 - [Q6ATY5_ORYSJ]		none (cytoplasm)
Q6K1R5	10.56	2	1.846	**2.459**	39.30	55	1.785	0.944	Putative adenosine kinase OS=Oryza sativa subsp. japonica GN=B1215B07.34 - [Q6K1R5_ORYSJ]		SP (ER)
Q7F1F2	6.38	5	1.855	**2.350**	16.90	18	1.524	1.099	Os08g0525600 protein OS=Oryza sativa subsp. japonica GN=OJ1191_A10.119 - [Q7F1F2_ORYSJ]	Putative 70 kDa peptidyl-prolyl isomerase	none (cytoplasm)
Q94HC5	10.54	13	**0.425**	0.998	43.60	105	1.329	0.998	Putative alanine aminotransferase OS=Oryza sativa subsp. japonica GN=OSJNBb0061I18.10 - [Q94HC5_ORYSJ]		none (cytoplasm)
secondary metabolite											
Q5VR12	3.54	1	**2.328**	**3.321**	17.04	6	1.704	0.986	Os01g0174300 protein OS=Oryza sativa subsp. japonica GN=OSJNBa0089K24.21 - [Q5VR12_ORYSJ]	Flavoprotein pyridine nucleotide cytochrome reductase domain containing protein	mTP (mitochondrion)
Q6ATP8	8.06	2	**8.291**	**8.456**	N. D	N. D	N. D	N. D	Dirigent-like protein, expressed OS=Oryza sativa subsp. japonica GN=OSJNBa0028F23.22 - [Q6ATP8_ORYSJ]		SP (secretory)
Q6Z6B5	3.48	1	**3.218**	**4.937**	11.50	6	1.693	0.973	Os02g0328300 protein OS=Oryza sativa subsp. japonica GN=P0622F08.20 - [Q6Z6B5_ORYSJ]	Phenol hydroxylase reductase family protein	cTP (plastid)
Q6Z8I7	4.49	2	**8.293**	N. D	21.03	24	1.823	0.801	Os02g0752200 protein OS=Oryza sativa subsp. japonica GN=P0431B06.43 - [Q6Z8I7_ORYSJ]	Similar to Beta-D-xylosidase	SP (plasma membrane)
Q8W3D0	4.47	2	**2.087**	**2.404**	N. D	N. D	N. D	N. D	Probable pyridoxal biosynthesis protein PDX1.2 OS=Oryza sativa subsp. japonica GN=PDX12 - [PDX12_ORYSJ]		none (cytoplasm)
photosynthesis											
P0C358	1.63	8	**4.091**	1.941	15.94	34	1.689	0.882	Photosystem I P700 chlorophyll a apoprotein A2 OS=Oryza sativa subsp. japonica GN=psaB - [PSAB_ORYSJ]		chloroplastic gene

P0C367	11.63	7	**3.297**	1.696	24.52	39	1.953	0.972	Photosystem II CP43 chlorophyll apoprotein OS=Oryza sativa subsp. japonica GN=psbC - [PSBC_ORYSJ]		chloroplastic gene
P0C434	6.80	4	**4.586**	2.025	20.96	47	1.728	1.082	Photosystem Q(B) protein OS=Oryza sativa subsp. japonica GN=psbA - [PSBA_ORYSJ]		chloroplastic gene
P0C512	19.92	46	**2.653**	1.308	37.32	232	1.739	0.722	Ribulose bisphosphate carboxylase large chain OS=Oryza sativa subsp. japonica GN=rbcL - [RBL_ORYSJ]		chloroplastic gene
P93431-2	7.16	3	**3.430**	1.518	51.96	114	1.763	0.973	Isoform 2 of Ribulose bisphosphate carboxylase/oxygenase activase, chloroplastic OS=Oryza sativa subsp. japonica GN=RCA - [RCA_ORYSJ]		cTP (plastid)
Q0DFC9	5.19	2	**2.396**	1.950	20.78	8	0.751	1.652	Plastocyanin, chloroplastic OS=Oryza sativa subsp. japonica GN=PETE - [PLAS_ORYSJ]		cTP (plastid)
Q10HD0	24.71	8	**2.799**	1.653	24.71	49	1.760	0.906	Chlorophyll a-b binding protein, chloroplastic OS=Oryza sativa subsp. japonica GN=RCABP89 - [CB23_ORYSJ]		cTP (plastid)
Q6AVA8-2	20.63	61	**0.312**	1.373	52.83	274	1.208	1.143	Isoform 2 of Pyruvate, phosphate dikinase 1, chloroplastic OS=Oryza sativa subsp. japonica GN=PPDK1 - [PPDK1_ORYSJ]		cTP (plastid)
Q6Z411	4.83	3	**2.297**	1.547	20.34	50	1.937	0.892	Chlorophyll a/b-binding protein OS=Oryza sativa subsp. japonica GN=P0567H04.14 - [Q6Z411_ORYSJ]		cTP (plastid)
Q6ZF30	6.77	3	**3.005**	**2.689**	17.67	22	**2.040**	0.889	Os07g0562700 protein OS=Oryza sativa subsp. japonica GN=P0406F06.32 - [Q6ZF30_ORYSJ]	Putative chlorophyll A-B binding protein of LHCII type III	cTP (plastid)
Q6ZFJ9	11.04	29	1.584	**6.532**	27.09	58	1.718	1.313	Os02g0102900 protein OS=Oryza sativa subsp. japonica GN=OJ1435_F07.26 - [Q6ZFJ9_ORYSJ]	60 kDa chaperonin beta subunit	cTP (plastid)
Q7X9A7	11.82	16	**2.208**	**2.875**	57.02	115	1.396	1.130	Putative Rubisco subunit binding-protein alpha subunit (60 kDa chaperonin alpha subunit) OS=Oryza sativa subsp. japonica GN=OSJNBa0033P04.2 - [Q7X9A7_ORYSJ]		cTP (plastid)
Q7XM78	5.84	2	**3.704**	**2.649**	55.84	45	1.983	0.957	OSJNBa0079C19.2 protein OS=Oryza sativa GN=OSJNBa0079C19.2 - [Q7XM78_ORYSA]		SP (plasma membrane)
Q84PB4	18.72	3	1.758	**2.215**	44.33	23	1.563	0.991	Chloroplast photosystem I reaction center subunit II-like protein OS=Oryza sativa subsp. japonica GN=Os08g0560900 - [Q84PB4_ORYSJ]		cTP (plastid)
Q8GTK4	20.47	13	**2.845**	**2.449**	46.46	48	1.576	0.988	Os07g0141400 protein OS=Oryza sativa subsp. japonica GN=OJ1351_C05.112 - [Q8GTK4_ORYSJ]	Probable photosystem II oxygen-evolving complex protein 2	cTP (plastid)
Q8S7H8	4.24	1	**3.191**	1.671	22.46	12	1.751	1.129	Photosystem I reaction center subunit III, chloroplast, putative, expressed OS=Oryza sativa subsp. japonica GN=OSJNBa0010I09.4 - [Q8S7H8_ORYSJ]		cTP (plastid)
Q943W1	23.72	20	**2.864**	**2.384**	43.54	99	1.467	1.227	Os01g0501800 protein OS=Oryza sativa subsp. japonica GN=B1080D07.27 - [Q943W1_ORYSJ]	Putative 33kDa oxygen evolving protein of photosystem II	cTP (plastid)
Q9LWT6	29.95	49	1.537	**2.565**	50.92	121	1.415	1.135	Os06g0114000 protein OS=Oryza sativa subsp. japonica GN=P0541H01.20 - [Q9LWT6_ORYSJ]	Rubisco subunit binding-protein beta subunit	cTP (plastid)

Storage protein

	hot				control						
Accession	Coverage	Peptide	Ratio (MSD1OE/WT for 4days)	Ratio (MSD1OE/WT for 10days)	Coverage	Peptide	Ratio (MSD1OE/WT for 4days)	Ratio (MSD1OE/WT for 10days)	Description		Sorting signal (localization predicted)
P07728	37.47	384	**0.196**	**0.197**	41.68	439	1.305	0.887	Glutelin type-A 1 OS=Oryza sativa subsp. japonica GN=GLUA1 - [GLUA1_ORYSJ]		SP (protein body)
P07730	34.87	330	**0.423**	0.882	43.29	383	1.255	0.527	Glutelin type-A 2 OS=Oryza sativa subsp. japonica GN=GLUA2 - [GLUA2_ORYSJ]		SP (protein body)
P14323	46.09	351	**0.073**	**0.271**	41.28	566	1.215	1.160	Glutelin type-B 1 OS=Oryza sativa subsp. japonica GN=GluB1-A - [GLUB1_ORYSJ]		SP (protein body)
P14614	56.60	356	**0.068**	**0.137**	46.80	459	0.950	0.893	Glutelin type-B 4 OS=Oryza sativa subsp. japonica GN=GLUB4 - [GLUB4_ORYSJ]		SP (protein body)
Q02897	46.87	335	**0.023**	**0.285**	37.78	484	1.221	0.893	Glutelin type-B 2 OS=Oryza sativa subsp. japonica GN=GLUB2 - [GLUB2_ORYSJ]		SP (protein body)
Q09151	34.48	255	**0.193**	**0.174**	41.53	333	1.055	0.577	Glutelin type-A 3 OS=Oryza sativa subsp. japonica GN=GLUA3 - [GLUA3_ORYSJ]		SP (protein body)
Q42465	33.77	82	0.904	**0.280**	33.77	50	**0.479**	0.597	Prolamin PPROL 14P OS=Oryza sativa subsp. japonica GN=PROLM20 - [PRO20_ORYSJ]		SP (protein body)
Q5W695	39.19	56	N. D	**0.019**	N. D	N. D	N. D	N. D	Putative prolamin 7 OS=Oryza sativa subsp. japonica GN=OSJNBa0051L16.21 - [Q5W695_ORYSJ]		SP (protein body)
Q5W6A3	38.67	39	N. D	**0.033**	48.67	75	0.762	**0.273**	Prolamin OS=Oryza sativa subsp. japonica GN=OSJNBa0051L16.13 - [Q5W6A3_ORYSJ]		SP (protein body)
Q5W6A5	18.11	10	**0.245**	**0.148**	N. D	N. D	N. D	N. D	Putative prolamin 7 OS=Oryza sativa subsp. japonica GN=OSJNBa0051L16.9 - [Q5W6A5_ORYSJ]		unclear
Q65XA1	13.93	4	**2.029**	1.591	27.88	50	1.689	0.986	Os05g0116000 protein OS=Oryza sativa subsp. japonica GN=OJ1654_B10.17 - [Q65XA1_ORYSJ]	Putative legumin	unclear
Q6ESW6	26.65	197	**0.149**	0.708	35.47	243	1.056	0.547	Glutelin OS=Oryza sativa subsp. japonica GN=P0503B05.14 - [Q6ESW6_ORYSJ]		SP (protein body)
Q6K508	25.21	203	**0.121**	**0.235**	32.44	205	1.313	1.032	Glutelin OS=Oryza sativa subsp. japonica GN=OSJNBa0011N12.22 - [Q6K508_ORYSJ]		SP (protein body)
Q6K7K6	43.33	110	**0.170**	**0.349**	46.27	275	1.238	1.068	Glutelin OS=Oryza sativa subsp. japonica GN=P0533E11.34-1 - [Q6K7K6_ORYSJ]		SP (protein body)
Q8GVK5	80.79	79	**0.479**	N. D	N. D	N. D	N. D	N. D	13 kDa prolamin OS=Oryza sativa subsp. japonica GN=OSJNBa0031C24.138 - [Q8GVK5_ORYSJ]		SP (protein body)
Q8GVK7	80.79	79	**0.496**	N. D	58.94	33	N. D	0.583	13 kDa prolamin OS=Oryza sativa subsp. japonica GN=OSJNBa0031C24.134 - [Q8GVK7_ORYSJ]		SP (protein body)
Q8S0E1	3.41	3	**0.066**	**0.077**	N. D	N. D	N. D	N. D	Os01g0898500 protein OS=Oryza sativa subsp. japonica GN=P0506A10.18 - [Q8S0E1_ORYSJ]	Putative patatin-like protein	unclear

Functional protein expression

	hot				control						
Accession	Coverage	Peptide	Ratio (MSD1OE/WT for 4days)	Ratio (MSD1OE/WT for 10days)	Coverage	Peptide	Ratio (MSD1OE/WT for 4days)	Ratio (MSD1OE/WT for 10days)	Description		Sorting signal (localization predicted)
proteolysis											
P52428	2.59	1	**2.018**	1.828	22.96	10	**2.025**	1.016	Proteasome subunit alpha type-1 OS=Oryza sativa subsp. japonica GN=PAF1 - [PSA1_ORYSJ]		none (cytoplasm)
Q5SMV5	3.10	2	1.719	**2.038**	N. D	N. D	N. D	N. D	Os06g0186400 protein OS=Oryza sativa subsp. japonica GN=P0470C02.1 - [Q5SMV5_ORYSJ]	Similar to Serine carboxypeptidase II-2 precursor	SP (secretory)
Q5SNJ4	1.58	3	1.536	**2.507**	7.52	6	1.954	0.960	Os01g0191500 protein OS=Oryza sativa subsp. japonica GN=P0710E05.34 - [Q5SNJ4_ORYSJ]	Putative mitochondrial processing peptidase	mTP (mitochondrion)
Q5VMN4	3.25	1	**2.547**	**2.719**	17.33	8	1.767	0.736	Proteasome subunit beta type OS=Oryza sativa subsp. japonica GN=OSJNBa0085L11.4 - [Q5VMN4_ORYSJ]		unclear
Q5VPF1	4.47	2	**2.259**	**2.544**	N. D	N. D	N. D	N. D	Proteasome subunit beta type OS=Oryza sativa subsp. japonica GN=OSJNBa0041F13.35 - [Q5VPF1_ORYSJ]		none (cytoplasm)
Q5ZAM8	4.06	5	**0.462**	0.914	2.13	2	1.635	0.511	Os01g0767100 protein OS=Oryza sativa subsp. japonica GN=OSJNBb0053G03.16 - [Q5ZAM8_ORYSJ]	Putative prolyl carboxypeptidase, isoform 1	unclear
Q6H852	5.96	1	1.581	**2.804**	N. D	N. D	N. D	N. D	Proteasome subunit alpha type OS=Oryza sativa subsp. japonica GN=OJ1626_B09.4 - [Q6H852_ORYSJ]		none (cytoplasm)
Q6K669	4.01	3	**2.337**	0.911	34.28	36	1.702	1.238	Leucine aminopeptidase 2, chloroplastic OS=Oryza sativa subsp. japonica GN=Os02g0794700 - [AMPL2_ORYSJ]		cTP (plastid)
Q6YT00	4.42	1	**2.443**	**2.537**	25.70	15	1.992	1.033	Proteasome subunit alpha type-7-A OS=Oryza sativa subsp. japonica GN=Os08g0548900 - [PSA7A_ORYSJ]		none (cytoplasm)
Q6Z6L4	3.76	4	**3.861**	N.D.	15.38	18	1.501	0.716	Os02g0218200 protein OS=Oryza sativa subsp. japonica GN=P0027A02.7 - [Q6Z6L4_ORYSJ]	Putative aminopeptidase M	unclear
Q6ZL89	5.19	3	**4.527**	**2.499**	14.29	31	1.445	0.767	Os07g0578300 protein OS=Oryza sativa subsp. japonica GN=OJ1065_B06.27 - [Q6ZL89_ORYSJ]	Putative subtilisin-like serine protease	SP (ER)
Q8H5C3	7.32	1	1.857	**3.573**	7.32	2	1.083	1.688	Putative Skp1 OS=Oryza sativa subsp. japonica GN=OJ1343_B12.137 - [Q8H5C3_ORYSJ]		none (cytoplasm)
Q8RZW7	4.36	3	1.661	**6.911**	27.39	35	1.783	0.875	Os01g0916400 protein OS=Oryza sativa subsp. japonica GN=P0413C03.8 - [Q8RZW7_ORYSJ]	Putative selenium binding protein	PTS(peroxisome)
Q9LST6	5.19	1	1.527	**2.112**	33.49	9	1.965	0.806	Proteasome subunit beta type-2 OS=Oryza sativa subsp. japonica GN=PBD1 - [PSB2_ORYSJ]		unclear
Q9LSU3	4.07	1	**2.710**	1.522	24.80	21	1.750	0.929	Proteasome subunit alpha type-6 OS=Oryza sativa subsp. japonica GN=PAA1 - [PSA6_ORYSJ]		none (cytoplasm)
protein folding											
Q53LQ0	61.72	94	**0.494**	1.022	60.94	279	1.162	1.005	Protein disulfide isomerase-like 1-1 OS=Oryza sativa subsp. japonica GN=PDIL1-1 - [PDI11_ORYSJ]		SP (ER)
Q5N801	17.09	3	1.339	**3.919**	17.09	4	1.252	1.238	Os01g0915800 protein OS=Oryza sativa subsp. japonica GN=P0004D12.26 - [Q5N801_ORYSJ]	Putative immunophilin	SP (secretory)

Q5Z9H9	28.18	17	0.912	**2.114**	39.55	24	1.545	0.969	Peptidyl-prolyl cis-trans isomerase OS=Oryza sativa subsp. japonica GN=P0655A07.5-1 - [Q5Z9H9_ORYSJ]		mTP (mitochondrion)
Q653F6	1.61	1	**2.297**	1.167	6.43	7	1.543	0.905	Putative t-complex protein 1 theta chain OS=Oryza sativa subsp. japonica GN=P0623A10.31 - [Q653F6_ORYSJ]		none (cytoplasm)
Q67IX6	29.13	36	**0.299**	0.755	40.50	92	1.217	1.195	Protein disulfide isomerase-like 1-4 OS=Oryza sativa subsp. japonica GN=PDIL1-4 - [PDI14_ORYSJ]		SP (ER)
Q6ZH98	26.74	11	1.898	**2.201**	22.09	66	1.544	1.001	Peptidyl-prolyl cis-trans isomerase OS=Oryza sativa subsp. japonica GN=OJ1020_C02.14 - [Q6ZH98_ORYSJ]		PTS(peroxisome)
Q75M08-1	19.40	13	1.971	**2.714**	37.70	36	1.571	1.012	Isoform 1 of Protein disulfide isomerase-like 2-1 OS=Oryza sativa subsp. japonica GN=PDIL2-1 - [PDI21_ORYSJ]		SP (secretory)
Q75M32	15.60	6	**2.106**	1.983	32.40	30	1.469	1.057	Peptidyl-prolyl cis-trans isomerase OS=Oryza sativa subsp. japonica GN=P0668H12.6 - [Q75M32_ORYSJ]		unclear
phosphorylation											
P48489	3.11	1	**3.895**	N.D.	N.D.	N.D.	N.D.	N.D.	Serine/threonine-protein phosphatase PP1 OS=Oryza sativa subsp. japonica GN=Os03g0268000 - [PP1_ORYSJ]		none (cytoplasm)
Q06967	14.23	15	**2.080**	**2.724**	62.31	99	1.878	0.820	14-3-3-like protein GF14-F OS=Oryza sativa subsp. japonica GN=GF14F - [14336_ORYSJ]		none (cytoplasm)
Q69QZ0	3.39	1	**0.141**	**0.207**	7.34	3	1.037	1.500	Probable protein phosphatase 2C 27 OS=Oryza sativa subsp. japonica GN=Os02g0799000 - [P2C27_ORYSJ]		none (cytoplasm)
Q6H3Z1	1.51	2	1.148	**0.338**	N.D.	N.D.	N.D.	N.D.	Os02g0650500 protein OS=Oryza sativa subsp. japonica GN=OSJNBb0012J10.12 - [Q6H3Z1_ORYSJ]	Similar to Protein kinase-like (Protein serine/threonine kinase).	unclear
Q6ZGJ8	15.36	4	**2.136**	**3.662**	27.27	19	1.447	1.117	Putative inorganic pyrophosphatase OS=Oryza sativa subsp. japonica GN=OJ1767_D02.15-2 - [Q6ZGJ8_ORYSJ]		mTP (mitochondrion)
Q7XTT9	0.71	1	**0.384**	**0.084**	N.D.	N.D.	N.D.	N.D.	OSJNBa0058K23.13 protein OS=Oryza sativa subsp. japonica GN=OSJNBa0058K23.13 - [Q7XTT9_ORYSJ]	Belongs to the protein kinase superfamily	SP (plasma membrane)
enzyme											
Q60EJ3	12.68	2	**2.478**	N.D.	22.44	18	**2.047**	1.501	putative 1,4-benzoquinone reductase' OS=Oryza sativa subsp. japonica GN=OSJNBa0017K09.5 - [Q60EJ3_ORYSJ]		unclear
Q69QR4	16.67	2	**2.170**	N. D	21.32	9	1.978	0.931	Os09g0481400 protein OS=Oryza sativa subsp. japonica GN=P0463D04.22 - [Q69QR4_ORYSJ]		none (cytoplasm)
Q6L4R5	7.43	3	**4.280**	**3.042**	24.14	13	1.712	0.861	Os05g0593100 protein OS=Oryza sativa subsp. japonica GN=P0663C08.13 - [Q6L4R5_ORYSJ]	Putative vacuolar ATP synthase subunit C	unclear
Q84R32	19.02	5	1.926	**2.422**	29.27	11	1.576	1.193	CBS domain containing protein, expressed OS=Oryza sativa subsp. japonica GN=OSJNBb0016H12.19 - [Q84R32_ORYSJ]		cTP (plastid)
Q8GRU7	1.96	1	**2.749**	**8.813**	1.96	1	1.468	N.D.	Os07g0640200 protein OS=Oryza sativa subsp. japonica GN=P0524G08.102 - [Q8GRU7_ORYSJ]		none (cytoplasm)
Q8GTK7	9.76	6	1.730	**2.527**	9.76	9	1.322	1.074	Os07g0495200 protein OS=Oryza sativa subsp. japonica GN=OJ1457_D07.102 - [Q8GTK7_ORYSJ]	Putative ATP synthase delta' chain, mitochondrial	mTP (mitochondrion)
Q8LQS5	15.30	4	**2.182**	1.687	9.61	10	1.503	1.048	Carboxymethylenebutenolidase-like protein OS=Oryza sativa subsp. japonica GN=P0702H08.32 - [Q8LQS5_ORYSJ]	Putative beta-D-xylosidase	mTP (mitochondrion)
others											
Q0JR25	6.69	3	1.494	**0.279**	N.D.	N.D.	N.D.	N.D.	Bowman-Birk type bran trypsin inhibitor OS=Oryza sativa subsp. japonica GN=RBBI3.3 - [IBBR_ORYSJ]		SP (secretory)
Q5TKJ2	1.20	1	1.346	**2.269**	20.85	17	1.706	0.802	Os05g0429400 protein OS=Oryza sativa subsp. japonica GN=OSJNBb0048I21.5 - [Q5TKJ2_ORYSJ]	Phosphatidylinositol transfer protein-like, N-terminal domain containing protein	NTS (nucleus)
Q67VZ1	3.15	1	**2.114**	1.310	34.07	26	1.696	0.892	Os06g0221200 protein OS=Oryza sativa subsp. japonica GN=P0516A04.15 - [Q67VZ1_ORYSJ]	Putative annexin	none (cytoplasm)
Q6YUA1	12.75	6	1.272	**2.793**	19.61	19	1.224	1.006	Os02g0100300 protein OS=Oryza sativa subsp. japonica GN=B1370C05.2 - [Q6YUA1_ORYSJ]	Putative tetratricopeptide repeat (TPR)-containing protein	NTS (nucleus)
Q6Z8S1	6.29	2	1.176	**2.370**	7.43	2	1.870	1.062	Os08g0442300 protein OS=Oryza sativa subsp. japonica GN=P0708B04.3-1 - [Q6Z8S1_ORYSJ]	Putative Calcineurin B subunit	none (cytoplasm)
Q75GX9	42.70	113	1.257	**0.345**	32.92	82	1.416	0.995	Cupin family protein, expressed OS=Oryza sativa subsp. japonica GN=OSJNBa0034D21.12 - [Q75GX9_ORYSJ]		SP (secretory)
Q7G8G4	0.86	1	1.463	**2.716**	N.D.	N.D.	N.D.	N.D.	NB-ARC domain containing protein, expressed OS=Oryza sativa subsp. japonica GN=OSJNBa0020E23.2 - [Q7G8G4_ORYSJ]		unclear
Q84VG0	36.49	15	1.569	**3.154**	70.27	31	1.183	1.159	Probable calcium-binding protein CML7 OS=Oryza sativa subsp. japonica GN=CML7 - [CML7_ORYSJ]		PTS(peroxisome)
Q851Y1	2.57	1	**2.765**	1.302	15.43	5	1.652	0.889	Ankyrin repeat domain protein 2, putative, expressed OS=Oryza sativa subsp. japonica GN=OSJNBa0015N08.20 - [Q851Y1_ORYSJ]		unclear
Q8H8B0	11.96	2	1.255	**0.247**	7.61	2	N.D.	N.D.	Os03g0159600 protein OS=Oryza sativa subsp. japonica GN=OJ1134F05.19 - [Q8H8B0_ORYSJ]	Putative abscisic acid-induced protein	none (cytoplasm)
Q9FTY4	4.10	1	**3.122**	**2.721**	18.28	6	1.171	0.906	Os01g0104400 protein OS=Oryza sativa subsp. japonica GN=P0436E04.19 - [Q9FTY4_ORYSJ]	Ricin B-related lectin domain containing protein	PTS(peroxisome)

Translation, Transcription

	hot				control						
Accession	Coverage	Peptide	Ratio (MSD1OE/WT for 4days)	Ratio (MSD1OE/WT for 10days)	Coverage	Peptide	Ratio (MSD1OE/WT for 4days)	Ratio (MSD1OE/WT for 10days)	Description		Sorting signal (localization predicted)
translation											
P31674	27.92	13	1.281	**2.395**	N.D.	N.D.	N.D.	N.D.	40S ribosomal protein S15 OS=Oryza sativa subsp. japonica GN=RPS15 - [RS15_ORYSJ]		ribosome
P40978	36.30	17	0.993	**2.033**	N.D.	N.D.	N.D.	N.D.	40S ribosomal protein S19 OS=Oryza sativa subsp. japonica GN=RPS19A - [RS19_ORYSJ]		ribosome
P49216	6.77	1	1.554	**3.508**	6.77	2	1.058	0.856	40S ribosomal protein S26 OS=Oryza sativa subsp. japonica GN=RPS26 - [RS26_ORYSJ]		ribosome
P49398	22.64	8	1.806	**2.369**	27.55	18	1.292	**0.390**	40S ribosomal protein S4 OS=Oryza sativa subsp. japonica GN=RPS4 - [RS4_ORYSJ]		none (cytoplasm)
P51431	39.35	60	1.478	**2.721**	N.D.	N.D.	N.D.	N.D.	Ubiquitin-40S ribosomal protein S27a-2 OS=Oryza sativa subsp. japonica GN=RPS27AB - [R27AB_ORYSJ]		none(cytoplasm), NTS (nucleus)
P56724	20.17	3	1.283	**4.007**	20.17	17	0.795	1.636	60S acidic ribosomal protein P3 OS=Oryza sativa subsp. japonica GN=Os06g0701400 - [RLA3_ORYSJ]		ribosome
Q0DK10	5.49	2	1.824	**2.361**	24.73	14	1.655	**0.417**	60S ribosomal protein L11 OS=Oryza sativa subsp. japonica GN=RPL11 - [RL11_ORYSJ]		cytoplasm
Q53JG0	2.06	2	**2.828**	0.853	20.82	16	1.382	**0.467**	60S ribosomal protein L3, putative, expressed OS=Oryza sativa subsp. japonica GN=RPL3B - [Q53JG0_ORYSJ]		ribosome
Q5Z9S4	5.80	1	**2.216**	**3.757**	25.36	6	1.517	0.636	40S ribosomal protein S24 OS=Oryza sativa subsp. japonica GN=P0458E11.17 - [Q5Z9S4_ORYSJ]		ribosome
Q6H541	5.80	1	**2.605**	**2.053**	N.D.	N.D.	N.D.	N.D.	40S ribosomal protein S24 OS=Oryza sativa subsp. japonica GN=OSJNBb0035N08.11 - [Q6H541_ORYSJ]		ribosome
Q6ZFJ5	10.38	3	**2.076**	**3.322**	N.D.	N.D.	N.D.	N.D.	Putative 60S ribosomal protein L9 OS=Oryza sativa subsp. japonica GN=OJ1435_F07.31 - [Q6ZFJ5_ORYSJ]		ribosome
Q6ZLB8	22.22	14	1.400	**2.152**	52.84	76	1.516	**0.455**	Putative 60S ribosomal protein L4/L1 OS=Oryza sativa subsp. japonica GN=OJ1014_E09.28 - [Q6ZLB8_ORYSJ]		ribosome
Q75G91	5.70	4	**2.184**	1.574	33.77	22	1.927	0.557	40S ribosomal protein S3, putative, expressed OS=Oryza sativa subsp. japonica GN=Os03g0577000 - [Q75G91_ORYSJ]		ribosome
Q7F5L2	2.51	1	1.507	**2.476**	5.85	2	1.598	1.244	Os01g0196600 protein OS=Oryza sativa subsp. japonica GN=P0419B01.3 - [Q7F5L2_ORYSJ]	Putative nucleotide diphosphatase	unclear
Q8H2J8	6.52	1	0.929	**2.088**	12.32	12	1.544	0.964	40S ribosomal protein S12 OS=Oryza sativa subsp. japonica GN=OSJNBa0016A21.128-2 - [Q8H2J8_ORYSJ]		ribosome
Q8L4F2	20.42	5	1.474	**2.039**	11.97	7	1.178	**0.261**	40S ribosomal protein S23 OS=Oryza sativa subsp. japonica GN=P0460C04.38 - [Q8L4F2_ORYSJ]		
Q8L5X0	15.45	2	1.200	**3.108**	N.D.	N.D.	N.D.	N.D.	60S ribosomal protein L36 OS=Oryza sativa subsp. japonica GN=P0408C03.28 - [Q8L5X0_ORYSJ]		ribosome
Q9AY43	8.82	2	**2.356**	**2.477**	22.79	4	1.525	**0.408**	60S ribosomal protein L27 OS=Oryza sativa GN=OSJNBa0027P10.10 - [Q9AY43_ORYSA]		ribosome
Q9LWS2	9.62	4	1.469	**2.329**	26.44	14	0.982	1.105	60S ribosomal protein L13 OS=Oryza sativa subsp. japonica GN=P0541H01.38 - [Q9LWS2_ORYSJ]		ribosome
Q9ZST1	5.52	1	**3.051**	**2.919**	N.D.	N.D.	N.D.	N.D.	30S ribosomal protein S17, chloroplastic OS=Oryza sativa subsp. japonica GN=RPS17 - [RR17_ORYSJ]		unclear
Protein biosynthesis											
O64937	17.00	27	2.011	**2.646**	28.64	71	**2.076**	**0.496**	Elongation factor 1-alpha OS=Oryza sativa subsp. japonica GN=REFA1 - [EF1A_ORYSJ]		NTS (nucleus)
P29545	46.88	39	1.032	**2.137**	58.04	65	0.881	1.305	Elongation factor 1-beta OS=Oryza sativa subsp. japonica GN=Os07g0662500 - [EF1B_ORYSJ]		NTS (nucleus)

P35683	12.08	13	1.877	**2.313**	37.92	75	1.882	0.763	Eukaryotic initiation factor 4A-1 OS=Oryza sativa subsp. japonica GN=Os06g0701100 - [IF4A1_ORYSJ]		ribosome
Q40680	29.69	31	1.033	**2.153**	42.36	44	1.225	1.065	Elongation factor 1-delta 1 OS=Oryza sativa subsp. japonica GN=Os07g0614500 - [EF1D1_ORYSJ]		none (cytoplasm)
Q5Z627	10.82	5	1.855	**2.420**	26.20	25	1.759	0.611	Elongation factor 1-gamma 3 OS=Oryza sativa subsp. japonica GN=Os06g0571400 - [EF1G3_ORYSJ]		unclear
Q688X1	3.93	3	**2.246**	1.966	8.72	7	1.750	0.814	Os05g0566500 protein OS=Oryza sativa subsp. japonica GN=OJ1781_H11.6 - [Q688X1_ORYSJ]	Putative eukaryotic translation initiation factor (EIF3d)	none (cytoplasm)
Q6H4L2	12.81	28	**2.010**	**2.587**	40.21	157	1.710	0.673	Elongation factor 2 OS=Oryza sativa subsp. japonica GN=P0461D06.32 - [Q6H4L2_ORYSJ]		unclear
Q6K2P9	2.22	2	1.527	**3.272**	N.D.	N.D.	N.D.	N.D.	Os09g0326900 protein OS=Oryza sativa subsp. japonica GN=P0706E03.4-1 - [Q6K2P9_ORYSJ]	Putative eukaryotic translation initiation factor 5	NTS (nucleus)
Q6YSX0	30.00	17	1.498	**2.260**	24.62	7	0.937	0.713	Os07g0674200 protein OS=Oryza sativa subsp. japonica GN=P0037D09.3 - [Q6YSX0_ORYSJ]	Putative 60S ribosomal protein L22	ribosome
Q7XHW8	13.06	5	1.578	**2.096**	N.D.	N.D.	N.D.	N.D.	Os07g0681000 protein OS=Oryza sativa subsp. japonica GN=OSJNBa0008J01.17 - [Q7XHW8_ORYSJ]	Putative translation initiation factor eIF-2 beta chain	NTS (nucleus)
Q7XIK5	1056.00	3	**2.357**	**6.595**	6.21	4	1.043	**0.347**	Os04g0613600 protein OS=Oryza sativa subsp. japonica GN=OJ1773_H01.103 - [Q7XIK5_ORYSJ]	Putative 40S ribosomal protein S11	ribosome
Q7Y1V2	14.58	4	1.132	**2.665**	22.92	3	1.512	0.826	Eukaryotic translation initiation factor 1A OS=Oryza sativa subsp. japonica GN=eif-1a-OF2 - [Q7Y1V2_ORYSJ]		none (cytoplasm)
Q84ZK1	11.25	8	1.344	**2.799**	18.75	16	1.335	1.046	Os07g0597000 protein OS=Oryza sativa subsp. japonica GN=P0453E05.118 - [Q84ZK1_ORYSJ]	Translation initiation factor 5A	none (cytoplasm)
Q8H684	8.70	5	**0.489**	0.895	3.68	1	1.712	1.102	OSEYA1 OS=Oryza sativa subsp. japonica GN=OSJNBa0004I20.20 - [Q8H684_ORYSJ]		none (cytoplasm)
Q8LNW1	4.27	1	1.374	**4.337**	18.29	2	0.985	1.308	Os10g0483000 protein OS=Oryza sativa subsp. japonica GN=OSJNBa0012L23.32 - [Q8LNW1_ORYSJ]	Transcription factor BTF3, putative, expressed	NTS (nucleus)
nucleosome assembly											
Q2RAD9	6.62	1	**2.766**	**5.586**	5.15	1	1.434	**0.425**	Histone H3.2 OS=Oryza sativa subsp. japonica GN=Os01g0866200 - [H32_ORYSJ]		NTS (nucleus)
Q53WK4	14.56	9	1.172	**2.461**	24.73	15	1.324	0.945	Os05g0539700 protein OS=Oryza sativa subsp. japonica GN=OSJNBa0052K01.18 - [Q53WK4_ORYSJ]	Putative nucleosome assembly protein	NTS (nucleus)
Q5VND6	11.64	6	1.223	**2.532**	20.90	16	1.138	1.344	Os06g0149400 protein OS=Oryza sativa subsp. japonica GN=P0710H01.4 - [Q5VND6_ORYSJ]	Putative nucleosome assembly protein 1	NTS (nucleus)
Q688F7	17.85	10	**2.068**	**4.682**	7.74	4	0.918	**0.318**	Putative histone deacetylase HD2 OS=Oryza sativa subsp. japonica GN=OSJNBa0035I01.3 - [Q688F7_ORYSJ]		none (cytoplasm)
Q69JW2	29.76	7	**3.086**	**9.999**	34.52	12	1.398	1.018	Os02g0576700 protein OS=Oryza sativa subsp. japonica GN=B1342F01.10 - [Q69JW2_ORYSJ]		none (cytoplasm)
Q6AVQ4	7.77	2	**0.421**	0.681	19.08	8	1.090	N.D.	Putative prohibitin OS=Oryza sativa subsp. japonica GN=OSJNBa0075M12.18 - [Q6AVQ4_ORYSJ]		unclear
Q6F362	28.95	7	**2.094**	**3.652**	N.D.	N.D.	N.D.	N.D.	Histone H2B.9 OS=Oryza sativa subsp. japonica GN=H2B.9 - [H2B9_ORYSJ]		NTS (nucleus)
nucleic acid binding											
Q5W6H1	5.34	2	**2.036**	1.976	25.95	31	1.538	0.921	Os05g0350500 protein OS=Oryza sativa subsp. japonica GN=OSJNBa0077J17.8 - [Q5W6H1_ORYSJ]	Putative DNA-binding protein GBP16	unclear
Q5ZDX8	1.79	1	1.521	**2.651**	8.05	2	0.812	2.357	Heterogeneous nuclear ribonucleoprotein A2/B1-like OS=Oryza sativa subsp. japonica GN=P0410E01.38 - [Q5ZDX8_ORYSJ]		NTS (nucleus)
Q60DW3	10.85	2	1.412	**2.231**	3.10	1	1.862	0.965	Os05g0419100 protein OS=Oryza sativa subsp. japonica GN=P0426G01.9 - [Q60DW3_ORYSJ]	Putative nucleic acid binding protein	none (cytoplasm)
Q6ASX7	16.05	7	1.003	**2.649**	32.72	36	1.410	1.017	Glycine-rich RNA binding protein OS=Oryza sativa subsp. japonica GN=B1130H05.5 - [Q6ASX7_ORYSJ]		unclear
Q6K6Z4	7.29	2	1.775	**2.900**	16.03	7	1.542	0.885	KH domain-containing protein NOVA-like OS=Oryza sativa subsp. japonica GN=P0474F11.35 - [Q6K6Z4_ORYSJ]		cTP (plastid)
Q6YYV1	4.23	3	1.256	**2.132**	28.55	40	1.550	1.071	Os09g0115400 protein OS=Oryza sativa subsp. japonica GN=OJ1310_F05.15 - [Q6YYV1_ORYSJ]	Poly(A)-binding protein	cTP (plastid)
Q6Z1C0	1.22	1	1.282	**2.147**	N.D.	N.D.	N.D.	N.D.	Os08g0192900 protein OS=Oryza sativa subsp. japonica GN=OSJNBa0056O06.24 - [Q6Z1C0_ORYSJ]	Putative nucleolin	unclear
Q7F2X8	14.67	4	**3.486**	**10.360**	25.33	10	1.290	1.057	Os01g0916600 protein OS=Oryza sativa subsp. japonica GN=P0004D12.37 - [Q7F2X8_ORYSJ]	OsGRP2	cTP (plastid)
Q8W0D1	23.95	10	1.229	**2.184**	N.D.	N.D.	N.D.	N.D.	Os01g0721900 protein OS=Oryza sativa subsp. japonica GN=P0690B02.26-1 - [Q8W0D1_ORYSJ]	Putative nuclear RNA binding protein A	none (cytoplasm)
Q94D20	2.60	2	**4.390**	**3.837**	8.20	4	1.868	0.564	Nucleoid DNA-binding protein cnd41-like OS=Oryza sativa subsp. japonica GN=P0025A05.25 - [Q94D20_ORYSJ]		SP (secretory)
Q9FW37	20.15	2	1.707	**2.741**	8.21	2	1.535	1.003	Os05g0100800 protein OS=Oryza sativa subsp. japonica GN=P0036D10.5 - [Q9FW37_ORYSJ]	Putative uncharacterized protein	none (cytoplasm)
Q9FWK8	5.82	1	**2.840**	**4.303**	12.28	13	1.308	1.148	Putative RNA binding protein OS=Oryza sativa GN=OSJNBa0079L16.15 - [Q9FWK8_ORYSA]		unclear
DNA recombination, repair, replication											
Q5Z6P9	9.44	13	1.269	**3.021**	29.24	12	1.352	1.271	Os06g0264300 protein OS=Oryza sativa subsp. japonica GN=OJ1001_B06.1 - [Q5Z6P9_ORYSJ]	Similar to RAD23	none (cytoplasm)
Q6H734	9.88	4	1.087	**2.304**	21.93	17	1.440	1.075	Os02g0198600 protein OS=Oryza sativa subsp. japonica GN=P0026H03.19 - [Q6H734_ORYSJ]	Putative DNA-damage inducible protein	none (cytoplasm)
Q7F953	2.55	2	**0.128**	**0.483**	N.D.	N.D.	N.D.	N.D.	OSJNBb0002J11.12 protein OS=Oryza sativa GN=OSJNBb0002J11.12 - [Q7F953_ORYSA]	mismatch repair	unclear
Q7XD67	0.74	1	**3.021**	**4.260**	0.74	1	1.751	0.813	DNA ligase OS=Oryza sativa subsp. japonica GN=B1288B10.3 - [Q7XD67_ORYSJ]		NTS (nucleus)
Q8H0A5	1.16	1	**0.107**	N.D.	1.160	1	N.D.	N.D.	Retrotransposon protein, putative, unclassified OS=Oryza sativa subsp. japonica GN=LOC_Os10g37940 - [Q8H0A5_ORYSJ]		NTS (nucleus)
RNA splicing											
Q0JM17-2	3.49	3	**2.553**	1.686	N.D.	N.D.	N.D.	N.D.	Isoform 2 of DEAD-box ATP-dependent RNA helicase 56 OS=Oryza sativa subsp. japonica GN=Os01g0549700 - [RH56_ORYSJ]		unclear
Q6EUD5	1.52	4	1.785	**3.489**	3.91	2	N.D.	1.743	Os02g0245000 protein OS=Oryza sativa subsp. japonica GN=OJ1134_F06.6 - [Q6EUD5_ORYSJ]	Putative splicing factor 3a	NTS (nucleus)
others											
Q53QG2	6.48	1	**0.495**	1.313	N.D.	N.D.	N.D.	N.D.	Os11g0153800 protein OS=Oryza sativa subsp. japonica GN=Os11g0153800 - [Q53QG2_ORYSJ]	Ribonucleoprotein	ribosome
Q6YTE9	5.65	1	**0.179**	1.248	N.D.	N.D.	N.D.	N.D.	Epstein-Barr virus EBNA-1-like protein OS=Oryza sativa subsp. japonica GN=P0025F02.34 - [Q6YTE9_ORYSJ]		unclear
Q7XI40	8.01	3	**2.231**	**4.010**	N.D.	N.D.	N.D.	N.D.	Os07g0624700 protein OS=Oryza sativa subsp. japonica GN=P0524E08.133 - [Q7XI40_ORYSJ]	UMP/CMP kinase a	none (cytoplasm)
Q7XXR8	9.76	6	1.556	**2.721**	N.D.	N.D.	N.D.	N.D.	Nascent polypeptide associated complex alpha chain OS=Oryza sativa subsp. japonica GN=Os05g0373700 - [Q7XXR8_ORYSJ]		none (cytoplasm)

Transport

	hot				control						
Accession	Coverage	Peptide	Ratio (MSD1OE/WT for 4days)	Ratio (MSD1OE/WT for 10days)	Coverage	Peptide	Ratio (MSD1OE/WT for 4days)	Ratio (MSD1OE/WT for 10days)	Description		Sorting signal (localization predicted)
P31691	13.55	11	**2.318**	**2.039**	29.84	50	1.761	0.639	ADP, ATP carrier protein, mitochondrial OS=Oryza sativa subsp. japonica GN=Os02g0718900 - [ADT_ORYSJ]		unclear
Q53MW2	11.11	2	0.637	**0.401**	11.11	1	1.599	1.602	Non-specific lipid-transfer protein OS=Oryza sativa subsp. japonica GN=Os11g0427800 - [Q53MW2_ORYSJ]		SP (secretory)
Q5N7W3	1.58	2	**2.530**	N. D	3.87	2	1.709	0.950	Os01g0911200 protein OS=Oryza sativa subsp. japonica GN=P0470A12.10 - [Q5N7W3_ORYSJ]	Putative ribophorin II	unclear
Q651T8	4.35	3	**2.508**	0.958	36.45	52	1.818	0.888	Os06g0662000 protein OS=Oryza sativa subsp. japonica GN=OSJNBa0051O02.43 - [Q651T8_ORYSJ]	Putative vacuolar proton-ATPase	none (cytoplasm)
Q65XV6	26.71	5	**0.358**	**0.431**	49.32	22	1.521	1.239	Os05g0111200 protein OS=Oryza sativa subsp. japonica GN=P0016H04.12 - [Q65XV6_ORYSJ]	Putative amino acid selective channel protein	none (cytoplasm)
Q69TX3	7.61	5	**2.831**	1.080	15.76	18	1.166	N.D.	Os06g0210500 protein OS=Oryza sativa subsp. japonica GN=P0021C04.12 - [Q69TX3_ORYSJ]	Putative mitochondrial phosphate transporter	mTP (mitochondrion)

Q6Z782	17.65	13	**0.359**	0.918	31.53	45	1.229	0.501	Os02g0202400 protein OS=Oryza sativa subsp. japonica GN=P0419A09.38 - [Q6Z782_ORYSJ]	Putative Brittle-1 protein, chloroplast	unclear
Q7F270	4.42	4	**2.457**	2.325	43.65	41	1.467	0.965	ADP-ribosylation factor 1 OS=Oryza sativa subsp. japonica GN=OJ1118_B03.103 - [Q7F270_ORYSJ]		unclear
Q8H852	0.90	1	1.280	**2.216**	7.69	8	1.684	0.753	Coatomer subunit gamma-1 OS=Oryza sativa subsp. japonica GN=Os03g0227000 - [COPG1_ORYSJ]		none (cytoplasm)
Q9FWV2	3.44	4	0.623	**3.086**	18.72	33	1.703	1.264	Putative chloroplast inner envelope protein OS=Oryza sativa subsp. japonica GN=OSJNBa0051D19.7 - [Q9FWV2_ORYSJ]		cTP (plastid)
Q9FWV6	17.05	2	**0.372**	N. D	N. D	N. D	N. D	N. D	Probable aquaporin TIP3-1 OS=Oryza sativa subsp. japonica GN=TIP3-1 - [TIP31_ORYSJ]		unclear

Cell wall, cytoskeleton

	hot				control						
Accession	Coverage	Peptide	Ratio (MSD1OE/WT for 4days)	Ratio (MSD1OE/WT for 10days)	Coverage	Peptide	Ratio (MSD1OE/WT for 4days)	Ratio (MSD1OE/WT for 10days)	Description		Sorting signal (localization predicted)
P28752	14.00	12	**2.723**	**5.167**	36.89	71	1.721	0.772	Tubulin alpha-1 chain OS=Oryza sativa subsp. japonica GN=TUBA1 - [TBA1_ORYSJ]		none (cytoplasm)
P45960	17.23	21	**2.800**	**3.339**	40.27	123	1.528	0.619	Tubulin beta-4 chain OS=Oryza sativa subsp. japonica GN=TUBB4 - [TBB4_ORYSJ]		none (cytoplasm)
Q40665-1	19.96	28	1.950	**2.578**	N. D	N. D	N. D	N. D	Isoform 1 of Tubulin beta-3 chain OS=Oryza sativa subsp. japonica GN=TUBB3 - [TBB3_ORYSJ]		none (cytoplasm)
Q53M52	13.97	14	**3.383**	**3.835**	38.36	96	1.704	0.617	Tubulin alpha-2 chain OS=Oryza sativa subsp. japonica GN=TUBA - [TBA2_ORYSJ]		none (cytoplasm)
Q53NL5	19.66	8	**0.134**	0.902	30.00	25	1.233	0.796	Xylanase inhibitor protein 2 OS=Oryza sativa subsp. japonica GN=Chib3H-h - [XIP2_ORYSJ]		SP (secretory)
Q75LL2	0.71	1	**0.193**	0.552	1.74	3	1.760	1.744	Kinesin-like protein OS=Oryza sativa subsp. japonica GN=OSJNBa0047E24.25 - [Q75LL2_ORYSJ]		NTS (nucleus)

Morphogenesis (embryogenesis, flowering, seed set)

	hot				control						
Accession	Coverage	Peptide	Ratio (MSD1OE/WT for 4days)	Ratio (MSD1OE/WT for 10days)	Coverage	Peptide	Ratio (MSD1OE/WT for 4days)	Ratio (MSD1OE/WT for 10days)	Description		Sorting signal (localization predicted)
P46520	51.58	10	**0.185**	**0.120**	12.63	1	N. D	4.371	Embryonic abundant protein 1 OS=Oryza sativa subsp. japonica GN=EMP1 - [EMP1_ORYSJ]		none (cytoplasm)
Q656A5	6.82	1	**0.265**	**0.366**	18.18	3	1.254	1.822	Os06g0498800 protein OS=Oryza sativa subsp. japonica GN=P0596H06.13 - [Q656A5_ORYSJ]	Putative terminal flower 1	NTS (nucleus)
Q656J2	4.91	2	0.606	**0.193**	16.23	6	1.596	1.171	Os06g0503400 protein OS=Oryza sativa subsp. japonica GN=P0564B04.17 - [Q656J2_ORYSJ]	Putative 24 kDa seed maturation protein	unclear
Q6KA29	15.29	10	0.703	**0.258**	2.76	1	N. D	N. D	Os02g0250600 protein OS=Oryza sativa subsp. japonica GN=OJ1113_G05.23 - [Q6KA29_ORYSJ]	Putative late embryogenesis abundant domain-containing protein	unclear
Q6YZA9	14.03	11	1.259	**0.452**	9.95	14	1.544	1.229	Germin-like protein 8-2 OS=Oryza sativa subsp. japonica GN=GER3 - [GL82_ORYSJ]		SP (secretory)
Q6Z0I0	20.00	3	0.790	**0.361**	N. D	N. D	N. D	N. D	Os08g0327700 protein OS=Oryza sativa subsp. japonica GN=OSJNBa0049I01.9 - [Q6Z0I0_ORYSJ]	Putative seed maturation protein	unclear
Q6ZK46	7.91	15	1.905	**0.172**	13.56	13	1.299	1.573	Os08g0127900 protein OS=Oryza sativa subsp. japonica GN=OJ1163_G08.32 - [Q6ZK46_ORYSJ]	Putative early embryogenesis protein	SP (secretory)
Q8H8H1	14.66	6	0.973	**2.950**	14.66	1	0.857	0.843	Agamous-like MADS box protein AGL14, putative, expressed OS=Oryza sativa subsp. japonica GN=OJ1126B12.10 - [Q8H8H1_ORYSJ]		NTS (nucleus)

Allergen

	hot				control						
Accession	Coverage	Peptide	Ratio (MSD1OE/WT for 4days)	Ratio (MSD1OE/WT for 10days)	Coverage	Peptide	Ratio (MSD1OE/WT for 4days)	Ratio (MSD1OE/WT for 10days)	Description		Sorting signal (localization predicted)
Q01881	16.25	68	0.512	**0.380**	24.38	54	1.185	1.557	Seed allergenic protein RA5 OS=Oryza sativa subsp. japonica GN=RA5 - [RA05_ORYSJ]		SP (secretory)
Q01882	6.02	14	**0.247**	**0.135**	6.02	11	1.217	**2.144**	Seed allergenic protein RAG2 OS=Oryza sativa subsp. japonica GN=RAG2 - [RAG2_ORYSJ]		SP (secretory)
Q6ZD29	14.57	3	**0.137**	**0.236**	68.87	29	1.117	1.021	Os08g0374000 protein OS=Oryza sativa subsp. japonica GN=P0690C12.27 - [Q6ZD29_ORYSJ]	Bet v I allergen family protein.	unclear
Q7X7E6	5.70	11	**0.175**	**0.144**	11.39	29	1.409	1.682	Os07g0216600 protein OS=Oryza sativa subsp. japonica GN=OJ1080_F08.102 - [Q7X7E6_ORYSJ]	Cereal seed allergen, trypsin/alpha-amylase inhibitor family protein.	SP (secretory)
Q8H4L8	18.47	7	**0.100**	**0.063**	10.19	8	1.724	1.702	Allergen RA16 OS=Oryza sativa subsp. japonica GN=OJ1116_C08.118 - [Q8H4L8_ORYSJ]		SP (secretory)
Q8H4M4	13.13	10	**0.188**	**0.054**	10.00	11	1.404	1.940	Allergenic protein OS=Oryza sativa subsp. japonica GN=OJ1116_C08.108 - [Q8H4M4_ORYSJ]		SP (plasma membrane)
Q8H559	8.55	2	**0.477**	0.716	15.79	8	1.912	0.845	Os07g0159800 protein OS=Oryza sativa subsp. japonica GN=OJ1714_H10.115 - [Q8H559_ORYSJ]	E1 protein and Def2/Der2 allergen family protein	SP (secretory)

Cell organization

	hot				control						
Accession	Coverage	Peptide	Ratio (MSD1OE/WT for 4days)	Ratio (MSD1OE/WT for 10days)	Coverage	Peptide	Ratio (MSD1OE/WT for 4days)	Ratio (MSD1OE/WT for 10days)	Description		Sorting signal (localization predicted)
Q6K8D4	5.36	1	1.663	**3.196**	30.36	8	1.618	1.085	Os02g0760300 protein OS=Oryza sativa subsp. japonica GN=OJ1175_B01.15 - [Q6K8D4_ORYSJ]	Putative immunophilin	PTS(peroxisome)
Q6Z347	4.51	4	1.698	**3.208**	20.68	4	1.860	1.171	Os02g0726000 protein OS=Oryza sativa subsp. japonica GN=B1121A12.6 - [Q6Z347_ORYSJ]	Putative fasciclin-like arabinogalactan-protein	SP (plasma membrane)

Unknown

	hot				control						
Accession	Coverage	Peptide	Ratio (MSD1OE/WT for 4days)	Ratio (MSD1OE/WT for 10days)	Coverage	Peptide	Ratio (MSD1OE/WT for 4days)	Ratio (MSD1OE/WT for 10days)	Description		Sorting signal (localization predicted)
Q5W645	5.51	3	**2.936**	**3.647**	3.81	2	N. D	N. D	Os05g0349500 protein OS=Oryza sativa subsp. japonica GN=OSJNBb0052F16.17 - [Q5W645_ORYSJ]		none (cytoplasm)
Q5W6H0	24.80	7	**2.096**	**3.292**	22.40	7	1.628	1.122	Putative uncharacterized protein OSJNBa0077J17.9 OS=Oryza sativa subsp. japonica GN=OSJNBa0077J17.9 - [Q5W6H0_ORYSJ]		unclear
Q657K0	5.15	1	**0.126**	**0.293**	5.15	2	0.683	1.367	Os01g0567200 protein OS=Oryza sativa subsp. japonica GN=P0002B05.18 - [Q657K0_ORYSJ]		NTS (nucleus)

Q69LX0	3.64	1	**3.697**	**12.378**	3.64	1	**2.018**	0.781	Putative uncharacterized protein OSJNBa0057D11.11 OS=Oryza sativa subsp. japonica GN=OSJNBa0057D11.11 - [Q69LX0_ORYSJ]	unclear
Q69RX0	7.22	1	**2.637**	**4.227**	N. D	N. D	N. D	N. D	Putative uncharacterized protein OS=Oryza sativa subsp. japonica GN=OSJNBa0058D03.120 - [Q69RX0_ORYSJ]	none (cytoplasm)
Q6K316	15.15	1	**0.144**	**0.219**	N. D	N. D	N. D	N. D	Putative uncharacterized protein OSJNBb0066C12.15 OS=Oryza sativa subsp. japonica GN=OSJNBb0066C12.15 - [Q6K316_ORYSJ]	unclear
Q6YYB0	3.29	1	**2.684**	**3.960**	5.16	3	1.288	1.156	Uncharacterized protein Os08g0359500 OS=Oryza sativa subsp. japonica GN=Os08g0359500 - [Y8359_ORYSJ]	PTS(peroxisome)
Q6Z4T7	1.96	1	1.613	**2.470**	N. D	N. D	N. D	N. D	Os08g0175200 protein OS=Oryza sativa subsp. japonica GN=OSJNBa0054L03.38 - [Q6Z4T7_ORYSJ]	none (cytoplasm)
Q6ZB13	6.25	1	**0.322**	**0.373**	N. D	N. D	N. D	N. D	Putative uncharacterized protein OJ1449_H02.17 OS=Oryza sativa subsp. japonica GN=OJ1449_H02.17 - [Q6ZB13_ORYSJ]	unclear
Q6ZHP6	36.63	2	**0.149**	**0.383**	36.63	9	1.634	1.607	Os02g0715400 protein OS=Oryza sativa subsp. japonica GN=OJ1191_G08.15 - [Q6ZHP6_ORYSJ]	unclear
Q7EZB3	7.08	1	**2.141**	**2.918**	N. D	N. D	N. D	N. D	Putative uncharacterized protein P0689E12.5 OS=Oryza sativa subsp. japonica GN=P0700D12.129 - [Q7EZB3_ORYSJ]	unclear
Q7EZS5	13.79	1	**2.570**	**3.306**	N. D	N. D	N. D	N. D	Putative uncharacterized protein OJ1163_G08.42 OS=Oryza sativa subsp. japonica GN=P0582D05.141 - [Q7EZS5_ORYSJ]	unclear
Q7XU87	1.18	1	**3.155**	**3.350**	N. D	N. D	N. D	N. D	OSJNBa0029H02.25 protein OS=Oryza sativa GN=OSJNBa0029H02.25 - [Q7XU87_ORYSA]	NTS (nucleus)
Q84MQ0	2.99	1	**2.206**	**2.209**	8.98	2	1.605	0.638	Putative uncharacterized protein OSJNBb0036F07.11 OS=Oryza sativa subsp. japonica GN=OSJNBb0036F07.11 - [Q84MQ0_ORYSJ]	none (cytoplasm)
Q9FU80	2.65	2	**2.187**	**3.675**	15.91	10	1.218	1.095	Os01g0143300 protein OS=Oryza sativa subsp. japonica GN=P0019D06.31 - [Q9FU80_ORYSJ]	mTP (mitochondrion)