

Supplemental Table 1. Differentially expressed genes in *L. mollis* drought SSH library.

Clone ID	Accession	Homology	Organism	Identity %	E-value	Accession
Lm1_G03_47	JK317151	Dehydrin	<i>Hordeum vulgare</i>	71	1e-114	AAF01690
Lm2_F06_87	JK317162	Harpin inducing protein	<i>Oryza sativa</i>	66	2e-13	ABR25843
Lm3_F04_62	JK317173	Ribulose-bisphosphate carboxylases	<i>Arabidopsis thaliana</i>	92	3e-39	ATCG00490
Lm4_F03_46	JK317184	Xylanase inhibitor	<i>Triticum aestivum</i>	100	5e-11	BAF74364
Lm5_E03_45	JK317194	Putative senescence-associated protein	<i>Pisum sativum</i>	85	1e-14	BAB33421
Lm6_E01_10 ^a	JK317205	Aquaporin 2.1	<i>Triticum turgidum</i>	85	8e-21	EU182655
Lm7_D04_59	JK317216	NADPH quinone oxidoreductase 1	<i>Zea mays</i>	73	1e-57	ACG47380
Lm8_D03_43	JK317227	Putative senescence-associated protein	<i>Lilium longiflorum</i>]	98	4e-57	ABO20851
Lm9_D02_24	JK317238	Putative diacylglycerol kinase	<i>Oryza sativa</i>	77	3e-33	AAS07206
Lm11_C02_22	JK317142	Annexin	<i>Zea mays</i>	96	3e-24	NP_001105728
Lm12_C01_6	JK317143	Transaldolase 2	<i>Oryza sativa</i>	89	6e-66	ABR25370
Lm13_H01_4	JK317144	UDP-glucosyl transferase	<i>Arabidopsis thaliana</i>	41	0.002	AT3G53160
Lm14_G06_43 ^a	JK317145	Thioredoxin h	<i>Triticum aestivum</i>	96	9e-12	EU706448
Lm15_G02_11	JK317146	(1,3;1,4) beta-glucanase	<i>Triticum aestivum</i>	91	4e-13	ABB96917
Lm16_F01_2	JK317147	Putative fructose 1-,6-biphosphate aldolase	<i>Triticum aestivum</i>	88	8e-72	CAD12665
Lm17_D03_16	JK317148	Putative diacylglycerol kinase	<i>Oryza sativa</i>	82	7e-27	AAS07206
Lm18_D02_8	JK317149	Xyloglucan endotransglucosylase/hydrolase	<i>Arabidopsis thaliana</i>	65	8e-04	AT5G57550
Lm19_H06_86	JK317150	Putative rubisco activase	<i>Vigna unguiculata</i>	84	1e-34	CAO02538
Lm20_H04_61	JK317152	Putative carbonic anhydrase	<i>Hordeum vulgare</i>	55	0.060	P40880
Lm21_H01_14	JK317153	Actin-depolymerizing factor 6	<i>Zea mays</i>	90	2e-62	NP_001148357
Lm22_G06_85	JK317154	Purple acid phosphatase 27	<i>Arabidopsis thaliana</i>	68	2e-36	AT5G50400
Lm23_G03_42	JK317155	ABC2 transporter homolog 13	<i>Arabidopsis thaliana</i>	75	7e-23	AT5G64940
Lm24_G01_13	JK317156	Chloroplast inositol phosphatase-like protein	<i>Triticum aestivum</i>	99	2e-57	AAU82110
Lm25_F04_55	JK317157	Ribulose-1,5-bisphosphate carboxylase activase	<i>Triticum aestivum</i>	100	1e-22	AAP72270
Lm26_F02_25	JK317158	Ferredoxin-NADP(+)-oxidoreductase 1	<i>Arabidopsis thaliana</i>	88	2e-71	AT5G66190
Lm27_F01_11	JK317159	HPP integral membrane protein	<i>Zea mays</i>	90	9e-48	NP_001150258
Lm28_E06_83	JK317160	Lipoxygenase 3	<i>Arabidopsis thaliana</i>	48	8e-07	AT1G17420
Lm29_E05_71	JK317161	Lipoamide dehydrogenase	<i>Capsicum annuum</i>	95	1e-18	AAS47493
Lm30_D05_70 ^a	JK317163	Predicted protein	<i>Hordeum vulgare</i>	71	2e-28	AK355638
Lm31_D04_53	JK317164	Putative carbonic anhydrase	<i>Hordeum vulgare</i>	95	4e-80	P40880
Lm32_D03_33	JK317165	Type II metacaspase	<i>Triticum aestivum</i>	95	4e-134	ACY82389
Lm33_D02_22	JK317166	Phosphoethanolamine methyltransferase	<i>Triticum aestivum</i>	97	1e-53	AAL40895

Supplemental Table 1. (continued)

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Lm34_D01_9	JK317167	Putative carbonic anhydrase	<i>Hordeum vulgare</i>	96	5e-82	P40880
Lm35_C06_78	JK317168	Nucleotide pyrophosphatase/phosphodiesterase	<i>Hordeum vulgare</i>	90	1e-52	CAE46394
Lm36_C03_32	JK317169	Glycine decarboxylase P-protein 1	<i>Arabidopsis thaliana</i>	85	1e-70	AT4G33010
Lm37_C02_21	JK317170	Galactose mutarotase-like superfamily protein	<i>Arabidopsis thaliana</i>	80	5e-68	AT5G66530
Lm38_C01_8	JK317171	Ribulose 1,5-biphosphate carboxylase/ oxygenase	<i>Triticum aestivum</i>	95	3e-62	P26667
Lm39_B05_68	JK317172	translation initiation factor 5A1	<i>Triticum aestivum</i>	98	2e-32	AAZ95171
Lm40_B02_17	JK317174	Methyljasmonate-inducible lipoxygenase 2	<i>Hordeum vulgare</i>	87	1e-25	P93184
Lm41_B01_4	JK317175	Chlorophyll binding protein	<i>Helianthus annuus</i>	94	1e-15	ACJ13835
Lm42_A03_30	JK317176	ETTIN-like auxin response factor	<i>Triticum aestivum</i>	99	6e-45	AAQ86960
Lm43_A02_15	JK317177	Photosystem I reaction center subunit N	<i>Hordeum vulgare</i>	100	1e-54	P31093
Lm44_A01_3	JK317178	Chloroplast RNA binding	<i>Arabidopsis thaliana</i>	96	5e-09	AT1G09340
Lm45_H11_95	JK317179	Histidine kinase	<i>Sorangium cellulosum</i>	45	0.55	YP_001613592
Lm46_H07_91	JK317180	Cell wall-associated hydrolase	<i>Microscilla marina</i>	55	9e-08	ZP_01689674
Lm47_H03_87	JK317181	No significant homology				
Lm48_F10_70 ^a	JK317182	Arabinogalactan protein 18	<i>Arabidopsis thaliana</i>	100	0.012	AT4G37450
Lm49_F09_69	JK317183	No significant homology				
Lm50_F07_67	JK317185	No significant homology				
Lm51_E06_54 ^a	JK317186	ARM repeat superfamily protein	<i>Arabidopsis thaliana</i>	92	0.73	AT5G27010
Lm52_D02_38	JK317187	No significant homology				
Lm53_C11_35	JK317188	Similar to PDZ domain containing 6	<i>Ciona intestinalis</i>	48	0.42	XP_002122300
Lm54_B11_23	JK317189	Nucleotidyltransferase family protein	<i>Arabidopsis thaliana</i>	50	0.22	AT3G45760
Lm55_A07_7	JK317190	No significant homology				
Lm56_H08_102	JK317191	Serine/threonine protein kinase	<i>Cryptococcus gattii</i>	36	0.06	XP_003193882
Lm57_H01_8	JK317192	Predicted protein	<i>Oryza sativa</i>	41	0.008	CAE03625
Lm58_G09_109	JK317193	RNA polymerase II, second largest subunit	<i>Hordeum vulgare</i>	99	5e-49	AAB94059
Lm59_F10_116	JK317239	No significant homology				
Lm60_F05_57	JK317195	Amylo-alpha-1,6-glucosidase	<i>Micromonospora carbonacea</i>	37	0.24	ZP_04609345
Lm61_F04_43	JK317196	No significant homology				
Lm62_E09_107	JK317197	B-box zinc finger family protein	<i>Arabidopsis thaliana</i>	100	0.52	AT4G39070
Lm64_B02_11	JK317199	Putative retrotransposon protein	<i>Phyllostachys edulis</i>	31	0.029	ADB85430

Supplemental Table 1. (continued)

Clone ID	Accession	Homology	Organism	Identity %	E-value	Accession
Lm65_A09_103	JK317200	DNA-3-methyladenine glycosylase	<i>Streptomyces hygroscopicus</i>	36	0.68	ZP_07298831
Lm66_A08_94	JK317201	Putative gag-pol precursor	<i>Zea mays</i>	48	7e-06	AAL66751
Lm67_E06_86	JK317202	Hypothetical protein	<i>Oryza sativa</i>	44	0.099	BAD69283
Lm68_A03_38	JK317203	Predicted protein	<i>Populus trichocarpa</i>	95	8e-37	XP_002338056
Lm69_E01_1 ^a	JK317204	Predicted protein	<i>Hordeum vulgare</i>	78	3e-18	AK368418
Lm71_H05_74 ^a	JK317207	Predicted protein	<i>Hordeum vulgare</i>	98	7e-14	AK359580
Lm72_H02_29	JK317208	Ribulose biphosphate carboxylase small chain	<i>Arabidopsis thaliana</i>	63	2e-11	AT1G67090
Lm73_G04_58	JK317209	No significant homology				
Lm74_A05_65	JK317210	Predicted protein	<i>Hordeum vulgare</i>	93	1e-48	BAJ91862
Lm75_G08_80	JK317211	LETM1-like protein	<i>Arabidopsis thaliana</i>	66	8e-07	AT5G06220
Lm76_G05_77	JK317212	MATE efflux family protein	<i>Arabidopsis thaliana</i>	43	0.28	AT2G38330
Lm77_F11_71	JK317213	Hypothetical protein	<i>Sorghum bicolor</i>	28	0.86	AAD27567
Lm78_H08_92 ^a	JK317214	A genome HMW glutenin A gene locus	<i>Triticum turgidum</i>	74	5e-13	FN564428
Lm79_E07_55	JK317215	SER/ARG-rich protein 34A	<i>Arabidopsis thaliana</i>	27	0.36	AT3G49430
Lm80_E05_53	JK317217	No significant homology				
Lm81_C10_34	JK317218	Galactose oxidase/kelch repeat superfamily protein	<i>Arabidopsis thaliana</i>	95	0.37	AT5G60570
Lm82_C08_32	JK317219	Glycine-rich protein	<i>Arabidopsis thaliana</i>	100	0.12	AT5G46730
Lm83_D01_37	JK317220	Unknown protein	<i>Arabidopsis thaliana</i>	59	6e-08	AT5G53930
Lm85_A02_2	JK317222	Nuclear pore complex protein	<i>Arabidopsis thaliana</i>	47	0.27	AT5G05680
Lm86_H05_61	JK317223	Diacylglycerol kinase1	<i>Arabidopsis thaliana</i>	68	3e-20	AT5G07920
Lm87_H04_45	JK317224	Pheophytinase	<i>Arabidopsis thaliana</i>	100	0.42	AT5G13800
Lm88_G08_101	JK317225	No significant homology				
Lm89_E08_99	JK317226	No significant homology				
Lm90_D05_49	JK317228	AtAPY1, apyrase 1	<i>Arabidopsis thaliana</i>	82	0.044	AT3G04080
Lm91_D04_41	JK317229	Prolyl oligopeptidase family protein	<i>Arabidopsis thaliana</i>	71	1e-14	AT5G24260
Lm92_C08_97	JK317230	Glutathione S-transferase	<i>Arabidopsis thaliana</i>	71	2e-12	AT5G42150
Lm93_C05_48	JK317231	Hypothetical protein	<i>Oryza sativa</i>	59	4e-35	EEC80601
Lm94_A06_62	JK317232	Putative harbinger transposase-derived nuclease	<i>Arabidopsis thaliana</i>	36	1e-07	AT2G13770
Lm95_A04_36	JK317233	PAS/PAC sensor hybrid histidine kinase	<i>Pseudomonas fulva</i>	43	0.84	YP_004473704
Lm96_F03_63	JK317234	Retrotransposon protein (Ty3-gypsy subclass)	<i>Oryza sativa</i>	62	6e-49	ABA98107

Supplemental Table 1. (continued)

Clone ID	Accession	Homology	Organism	Identity %	E-value	Accession
Lm97_E11_59	JK317235	Putative Transposase (TNP2 family)	<i>Oryza sativa</i>	41	2e-40	AAX95379
Lm98_E08_56	JK317236	Putative retrotransposon protein	<i>Oryza sativa</i>	66	6e-08	ABB47084
Lm99_E04_52	JK317237	Retrotransposon protein	<i>Oryza sativa</i>	72	2e-56	ABA93936
Lm100_B08_20	JK317124	Transposon protein (CACTA, En/Spm sub-class)	<i>Oryza sativa</i>	37	2e-12	ABF99296
Lm101_B02_14	JK317125	TNP2-like transposase protein	<i>Hordeum vulgare</i>	56	2e-29	CAG30726
Lm102_H09_110	JK317126	Putative retrotransposon protein	<i>Oryza sativa</i>	62	2e-18	ABA97489
Lm103_H06_74	JK317127	Putative retrotransposon protein	<i>Phyllostachys edulis</i>	46	0.009	ADB85414
Lm104_F08_100	JK317128	Putative retrotransposon protein (Ty3-gypsy)	<i>Oryza sativa</i>	39	2e-08	ABA98154
Lm105_E05_51	JK317129	Putative retrotransposon protein	<i>Oryza sativa</i>	64	1e-10	NP_001065797
Lm106_H03_48	JK317130	Late embryogenesis abundant protein (LEA)	<i>Arabidopsis thaliana</i>	55	2e-05	AT3G15670
Lm107_E01_10	JK317131	No significant homology				
Lm108_G02_36	JK317132	NAD(P)H:plastoquinone dehydrogenase	<i>Arabidopsis thaliana</i>	78	6e-33	AT4G37925
Lm109_G01_13	JK317133	Xyloglucan endotransglycosylase 6	<i>Arabidopsis thaliana</i>	77	2e-17	AT4G25810
Lm110_B07_76	JK317135	No significant homology				
Lm111_C07_31	JK317136	Protein kinase superfamily protein	<i>Arabidopsis thaliana</i>	100	0.75	AT5G11410
Lm112_B07_19 ^a	JK317137	Retrotransposon	<i>Triticum monococcum</i>	85	3e-16	AF326781
Lm113_H02_18 ^a	JK317138	Predicted protein	<i>Hordeum vulgare</i>	88	6e-28	AK354795
Lm114_G05_35	JK317139	Allene oxide cyclase 3	<i>Hordeum vulgare</i>	90	4e-19	AK365667
Lm115_F03_18	JK317140	No significant homology				
Lm116_C03_15	JK317141	ARR4, MEE7, ATRR1 response regulator 4	<i>Arabidopsis thaliana</i>	100	0.032	AT1G10470

^a indicates homology search was carried using nucleotide-nucleotide BLAST (blastn).