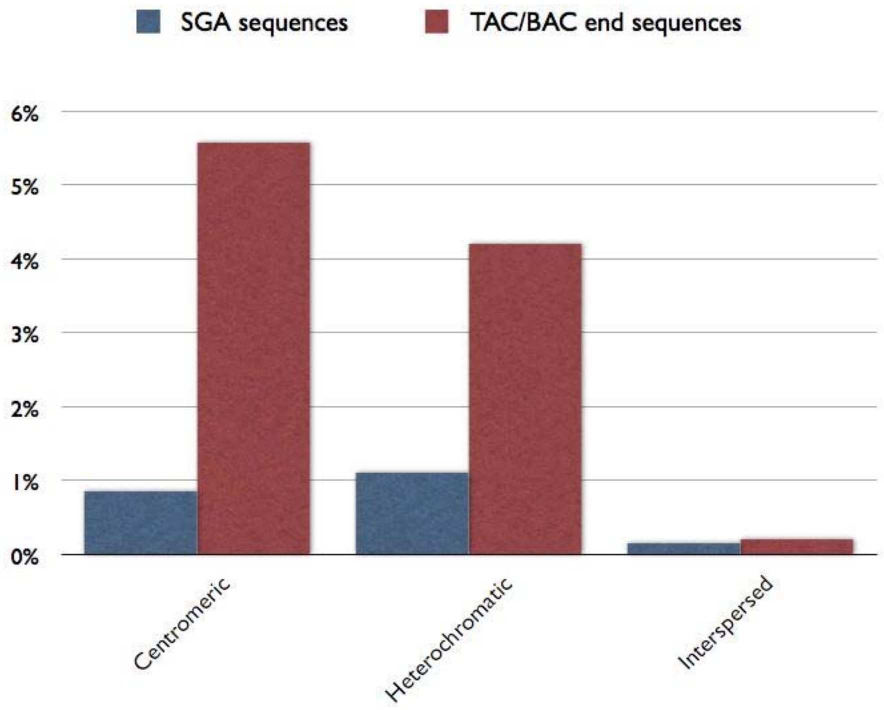
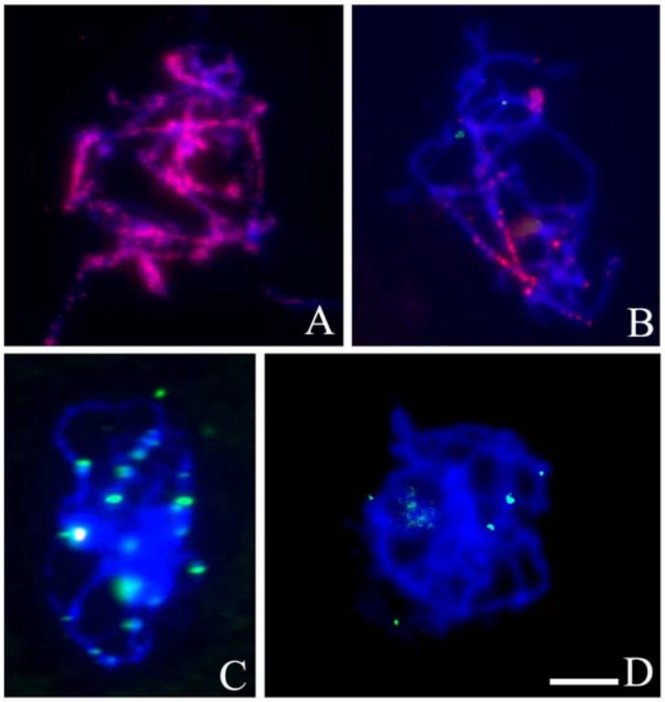
Supplemental Figures

Supplemental Figure 1. Ratio of repetitive sequences in SGA and TAC/BAC end sequences.

The ratios of the centromeric repeat sequence (LjRE2), heterochromatic repeat sequence (LjTR1) and interspersed repeat (LjRE1) in SGA sequences (blue) and TAC/BAC end sequences (red) were plotted.



Supplemental Figure 2. FISH images of repetitive sequences on pachytene chromosomes of *L. japonicus*. **A;** LjRE1 (red) exists throughout the entire *L. japonicus* genome. **B;** LjRE2 (red) was detected in the centromeric region. **C**; LiTR1 (green) was detected on major heterochromatin blocks. **D**; LjTR4 (green) was detected in subteromeric regions. Bar represents 5 µm.



Supplemental Table 1. List of sequenced TAC and BAC clones.

marker	marker type	chr	map position (cM)	contig name	clone name	phase	sequence redundancy	clone selection	Accession number
			0.0	CM0088	LjT12M01	1	x3	seed	DF093247
TM0088	SSR	1	0.0	CM0088	LjT15K21	1	x5	seed	DF093247
		1		CM0088	LjB26M21	1	x3	walking	DF093247
TM0224	dCAPS	1	0.0	CM0088	LjT13A11	3	x5	seed	DF093247
TM0358	SSR	1	0.0	CM0088	LjT48G05	3	x5	seed	DF093247
		1		CM0591	LjT21K10	1	x5	seed	DF093453
TM0771	SSR	1	0.0	CM0591	LjT13P11	1	x3	seed	DF093453
TM0591	SSR	1	0.0	CM0591	LjT01F11	1	x5	seed	DF093453
TM1473	SSR	1	0.0	CM0591	LjT39D07	1	x3	seed	DF093453
TM1049	SSR	1	0.0	CM0289	LjT39O15	1	x3	seed	DF093367
TM0289	SSR	1	0.0	CM0289	LjT16P18	3	x5	seed	DF093367
		1		CM0289	LjT45I09	1	x3	seed	DF093367
TM0145	SSR	1	0.0	CM0145	LjT43O24	3	x5	seed	DF093289
		1		CM0145	LjT62O12	1	x3	walking	DF093289
		1		CM0016	LjT02L12	1	x3	walking	DF093190
TM0016	SSR	1	0.0	CM0016	LjT13O04	3	x5	seed	DF093190
TM0189	SSR	1	0.0		LjT10H09	3	x5	seed	AP009657
TM0078	SSR	1	0.0	CM0078	LjT18O13	3	x5	seed	DF093241
		1		CM0078	LjT46D24	3	x3	walking	DF093241
		1		CM0078	LjT24A17	3	x5	walking	DF093241
		1		CM0078	LjB03H14	3	x5	walking	DF093241

		1		CM0171	LjB26G22	3		x5	walking	DF093305
		1		CM0171	LjT40A22	3		x5	walking	DF093305
		1		CM0171	LjB18I12	3		x5	walking	DF093305
TM1792	SSR	1	0.0	CM0171	LjT14A18	3		x5	walking	DF093305
TM0171	SSR	1	0.0	CM0171	LjT31H17	3		x5	seed	DF093305
		1		CM0171	LjB13J20	1		x3	walking	DF093305
		1		CM0171	LjB03E14	1		x3	walking	DF093305
		1		CM1785	LjT15F15	3		x5	walking	DF093527
		1		CM1785	LjT09P16	3		x5	walking	DF093527
TM0166	SSR	1	0.0	CM0166	LjT47G03	3		x5	seed	DF093302
BM1741	SSR	1	0.0	CM0166	LjB05K22	3		x5	walking	DF093302
		1		CM0166	LjB18D01	3		x5	walking	DF093302
		1		CM0166	LjB359B10	2		x5	walking	DF093302
		1		CM1956	LjT29F22	2		x5	walking	DF093535
		1		CM1956	LjB20A06	3		x5	walking	DF093535
BM2032	SSR	1	0.0	CM1956	LjB12K02	3		x5	walking	DF093535
		1		CM1956	LjB370E11	3		x5	walking	DF093535
		1		CM1956	LjT10M20	3		x5	walking	DF093535
		1		CM1956	LjB05K02	3		x5	walking	DF093535
		1		CM1956	LjB19O14	3		x5	seed	DF093535
BM1737	SSR	1	0.0		LjB20D08	3		x5	seed	AP009633
		1		CM0174	LjB15M15	1		x3	walking	DF093308
TM0174	dCAPS	1	0.0	CM0174	LjT45O19	3		x5	seed	DF093308
TM0092	dCAPS	1	0.0		LjT03K08	3		x5	seed	AP009651
TM1475	SSR	1	0.0		LjT16B05	1		x3	seed	AP010202

TM0454	SSR	1	0.0		LjT29N14	1	x3	seed	AP009985
TM1703	SSR	1	0.0		LjT48M07	3	x5	seed	AP009696
		1		CM0192	LjT11J08	1	x3	walking	DF093319
TM0192	dCAPS	1	0.0	CM0192	LjT40L14	3	x5	seed	DF093319
		1		CM0192	LjT43D23	1	x3	seed	DF093319
TM0252	SSR	1	0.0		LjT39K18	3	x5	seed	AP009805(a), AP009806(b), AP009807(c), AP009808(d)
TM1436	SSR	1	0.0	CM0668	LjT37F08	1	x3	seed	DF093465
		1		CM0668	LjT01M22	1	x3	seed	DF093465
TM1542	SSR	1	0.0		LjT32B13	1	x3	seed	AP010217
TM1841	SSR	1	0.0		LjT10G23	3	x5	seed	AP009730
TM1840	SSR	1	0.0		LjT06C08	3	x5	seed	AP009729
TM1868	SSR	1	0.0		LjT14B18	3	x5	seed	AP009740
BM1966	SSR	1	0.0		LjB17A22	3	x5	seed	AP009638
TM1842	SSR	1	0.0		LjT08C17	3	x5	seed	AP009731
BM1991	SSR	1	0.0		LjB21G05	3	x5	seed	AP009641
TM0103	SSR	1	0.0		LjT26E16	3	x5	seed	AP009652
TM0023	SSR	1	0.0	CM0023	LjT17G08	3	x5	seed	DF093196
		1		CM0023	LjT41O15	1	x3	walking	DF093196
		1		CM0123	LjT11C12	1	x3	walking	DF093274
TM0123	SSR	1	0.0	CM0123	LjT42E10	3	x5	seed	DF093274
		1		CM0123	LjT21O21	1	x3	walking	DF093274
TM1265	SSR	1	0.0		LjT31L11	1	x3	seed	AP010176
		1		CM0027	LjB03D13	3	x3	walking	DF093200

TM0027	SSR	1	0.0	CM0027	LjT08B24	3	x5	seed	DF093200
TM0181	SSR	1	0.0	CM0181	LjT09A07b	3	x5	seed	DF093315
		1		CM0181	LjT45E22	1	x3	walking	DF093315
TM0507	SSR	1	0.4		LjT46M16	1	x3	seed	AP009997
TM0496	SSR	1	0.8	CM0496	LjT34N02	1	x3	seed	DF093435
TM1046	SSR	1	0.8	CM0496	LjT05F14	1	x3	seed	DF093435
TM1305	SSR	1	0.8		LjT43O05	1	x3	seed	AP010180
		1		CM0039	LjT15E08	1	x3	walking	DF093209
TM0039	dCAPS	1	1.2	CM0039	LjT02D01	3	x5	seed	DF093209
		1		CM0039	LjT46N01	1	x3	walking	DF093209
TM0207	dCAPS	1	1.2		LjT41E18	3	x5	seed	AP009658
TM0320	dCAPS	1	1.2	CM0320	LjT29O08	3	x5	seed	DF093385
		1		CM0320	LjT17N12	1	x3	walking	DF093385
TM0653	SSR	1	1.2	CM0320	LjT14F08	1	x3	seed	DF093385
		1		CM0476	LjT12G04	1	x3	walking	DF093433
TM0476	SSR	1	1.2	CM0476	LjT33P04	3	x5	seed	DF093433
		1		CM0476	LjT18E21	1	x5	seed	DF093433
TM1394	SSR	1	1.2	CM0794	LjT25M20	1	x3	seed	DF093483
		1		CM0794	LjT28E14	1	x3	seed	DF093483
TM1003	SSR	1	1.2	CM0248	LjT13P21	3	x5	seed	DF093349
		1		CM0248	LjT38J20	2	x5	seed	DF093349
		1		CM0248	LjT26F07	1	x3	walking	DF093349
TM0248	dCAPS	1	1.6	CM0248	LjT10I22	3	x5	seed	DF093349
		1		CM0248	LjT21D14	1	x3	walking	DF093349
		1		CM0125	LjB07E24	1	x3	walking	DF093276

TM0125	SSR	1	1.6	CM0125	LjT19C08	3	x5	seed	DF093276
		1		CM0032	LjT05K14	1	x3	walking	DF093204
TM0032	SSR	1	1.6	CM0032	LjT05P21	3	x5	seed	DF093204
		1		CM0032	LjT12B03	1	x3	walking	DF093204
		1		CM0032	LjT07E21	3	x3	walking	DF093204
TM1730	SSR	1	1.6		LjT07G07	3	x5	seed	AP009852(a), AP009853(b)
TM0862	SSR	1	2.8		LjT27C19	1	x3	seed	AP010115
TM0036	SSR	1	2.8	CM0036	LjT03K03	3	x5	seed	DF093207
		1		CM0036	LjT22N16	1	x3	walking	DF093207
TM0955	SSR	1	3.6	CM0955	LjT14P03	1	x3	seed	DF093500
		1		CM0955	LjT29A16	2	x5	walking	DF093500
TM1968	SSR	1	3.8		LjT35H06	3	x5	seed	AP009780
		1		CM0094	LjT17D12	3	x5	walking	DF093250
TM0510	SSR	1	4.0	CM0094	LjT18G06	1	x5	seed	DF093250
BM1800	SSR	1	4.0	CM0094	LjB19C13	3	x5	walking	DF093250
TM0094	dCAPS	1	4.0	CM0094	LjT10J03	3	x5	seed	DF093250
		1		CM0094	LjT58K23	1	x3	walking	DF093250
TM1306	SSR	1	4.0	CM0094	LjT41G02	1	x3	seed	DF093250
		1		CM0063	LjT44E03	1	x3	walking	DF093230
TM0063	SSR	1	4.8	CM0063	LjT09L22	3	x5	seed	DF093230
		1		CM0063	LjT36H16	1	x3	walking	DF093230
TM1410	SSR	1	5.6		LjT40H13	1	x3	seed	AP010187
		1		CM0982	LjB141J17	1	x3	walking	DF093502
TM0982	SSR	1	7.6	CM0982	LjT10N18	1	x3	seed	DF093502

TM0523	SSR	1	8.0		LjT39K06	1	x3	seed	AP010002
TM1894	SSR	1	8.0		LjT20M22	2	x5	seed	AP009879
TM0050	SSR	1	8.8	CM0050	LjT03J05	3	x5	seed	DF093219
		1		CM0050	LjB08A07	1	x3	walking	DF093219
TM0671	SSR	1	8.8		LjT45O14	1	x3	seed	AP010043
		1		CM0133	LjB25H22	3	x5	walking	DF093282
TM0349	SSR	1	11.3	CM0133	LjT16F22	3	x5	seed	DF093282
		1		CM0133	LjT47B11	1	x3	walking	DF093282
TM1929	SSR	1	11.7	CM0133	LjT12P09	3	x5	seed	DF093282
		1		CM0133	LjT61C17	3	x5	walking	DF093282
TM0154	SSR	1	12.1	CM0133	LjT26D17	3	x5	seed	DF093282
		1		CM0133	LjT32A11	1	x5	seed	DF093282
TM0133	SSR	1	12.1	CM0133	LjT34I04	3	x5	seed	DF093282
		1		CM0133	LjT12P07	1	x3	walking	DF093282
TM1507	SSR	1	12.1	CM0133	LjT12K04	1	x3	walking	DF093282
		1		CM0133	LjT37F06	3	x5	walking	DF093282
TM0433	SSR	1	12.1	CM0433	LjT04F10	1	x3	seed	DF093421
		1		CM0433	LjT59O05	1	x3	walking	DF093421
TM0498	SSR	1	12.1		LjT33H07	1	x3	seed	AP009994
TM1633	SSR	1	12.1		LjT03I11	1	x3	seed	AP010233
TM0534	SSR	1	12.5		LjT04O21	1	x3	seed	AP010005
TM0442	SSR	1	12.5	CM0442	LjT45E10	1	x3	seed	DF093424
TM1621	SSR	1	12.5	CM0442	LjT43J12	1	x3	seed	DF093424
BM1404	SSR	1	12.9	CM0760	LjB24D20	3	x3	seed	DF093479
		1		CM0760	LjT47A24	1	x3	walking	DF093479

TM0372	SSR	1	13.3		LjT36G06	3	x5	seed	AP009819(a), AP009820(b)
TM0483	SSR	1	13.3		LjT12B11	1	x3	seed	AP009991
TM1767	SSR	1	13.3		LjT35C22	3	x5	seed	AP009709
TM0487	SSR	1	14.5		LjT04O06	3	x5	seed	AP009674
TM0334	SSR	1	16.1	CM0233	LjT02G18	3	x5	seed	DF093339
TM0670	SSR	1	16.9	CM0233	LjT16H21	1	x3	seed	DF093339
TM0233	dCAPS	1	17.3	CM0233	LjT30O01	3	x5	seed	DF093339
		1		CM0195	LjB21A21	1	x3	walking	DF093321
TM0195	SSR	1	17.7	CM0195	LjT39G11	3	x5	seed	DF093321
		1		CM0195	LjB16H08	1	x3	walking	DF093321
TM0275	dCAPS	1	17.7	CM0275	LjT29K22	3	x5	seed	DF093359
		1		CM0275	LjB06G06	1	x3	walking	DF093359
TM0952	SSR	1	17.7		LjT34C24	3	x5	seed	AP009682
		1		CM0121	LjB12P10	1	x3	walking	DF093272
TM0121	dCAPS	1	20.1	CM0121	LjT35I07	3	x5	seed	DF093272
		1		CM0178	LjB18G14	1	x3	walking	DF093312
TM0193	SSR	1	20.1	CM0178	LjT29P11	3	x5	seed	DF093312
		1		CM0178	LjB04J07	1	x3	walking	DF093312
		1		CM0178	LjB73O17	1	x3	walking	DF093312
TM0178	dCAPS	1	20.1	CM0178	LjT43N05	3	x5	seed	DF093312
		1		CM0178	LjT10P24	1	x3	walking	DF093312
BM1732	SSR	1	20.1		LjB18K24	2	x5	seed	AP009864
TM1078	SSR	1	20.9		LjT01D01	1	x3	seed	AP010155
TM0386	SSR	1	21.7		LjT45A19	1	x3	seed	AP009963

TM1844	SSR	1	22.5		LjT09E07	3	x5	seed	AP009732
TM1255	SSR	1	23.3	CM1255	LjT43J08	3	x5	seed	DF093511
		1		CM1255	LjB20B09	3	x5	seed	DF093511
TM1854	SSR	1	23.3		LjT06I14	3	x5	seed	AP009733
TM0101	SSR	1	24.4	CM0101	LjT02F07	3	x5	seed	DF093256
		1		CM0101	LjB15P21	1	x3	walking	DF093256
BM1485	SSR	1	26.1	CM0284	LjB07M21	1	x3	walking	DF093365
		1		CM0284	LjT30A24	3	x5	walking	DF093365
TM1486	SSR	1	26.1	CM0284	LjT56G08	1	x3	seed	DF093365
		1		CM0284	LjT23I21	2	x3	walking	DF093365
TM0284	SSR	1	26.1	CM0284	LjT34J23	3	x5	seed	DF093365
TM1444	SSR	1	27.7		LjT10B06	1	x3	seed	AP010195
TM1671	SSR	1	28.1		LjT08E15	1	x5	seed	AP010250
TM1635	SSR	1	28.1		LjT16J16	1	x3	seed	AP010235
		1		CM1413	LjT34K15	1	x3	seed	DF093515
TM1602	SSR	1	28.5	CM1413	LjT44I03	1	x3	seed	DF093515
		1		CM1413	LjT21N08	1	x5	seed	DF093515
TM0393	SSR	1	28.9	CM0393	LjT14E18	1	x3	seed	DF093409
TM0575	SSR	1	28.9	CM0393	LjT43J06	1	x3	seed	DF093409
TM0051	dCAPS	1	29.3	CM0051	LjT13M13	3	x5	seed	DF093220
TM0199	SSR	1	29.3	CM0051	LjT40C04	3	x5	seed	DF093220
		1		CM0051	LjT46I06	1	x3	walking	DF093220
TM1869	SSR	1	29.3		LjT29L18	2	x5	seed	AP009877
		1		CM0141	LjT58F09	1	x3	walking	DF093287
TM0141	SSR	1	29.7	CM0141	LjT28H14	3	x5	seed	DF093287

		1		CM0141	LjT45L12	1	x3	walking	DF093287
TM1325	SSR	1	29.7	CM0315	LjT18C12	1	x3	seed	DF093381
		1		CM0315	LjT46B03	1	x3	walking	DF093381
TM0315	SSR	1	29.7	CM0315	LjT39B10	3	x5	seed	DF093381
TM0187	dCAPS	1	30.1		LjT11G20	1	x5	seed	AP009955
BM1745	SSR	1	30.9	CM0410	LjB15M22	3	x5	walking	DF093415
		1		CM0410	LjT09A08	3	x5	walking	DF093415
TM0410	SSR	1	30.9	CM0410	LjT30G19	1	x3	seed	DF093415
TM1701	SSR	1	31.3	CM0410	LjT26M18	3	x5	walking	DF093415
		1		CM0410	LjT30G14	1	x3	seed	DF093415
TM1168	SSR	1	31.3		LjT34H22	1	x3	seed	AP010162
TM0163	dCAPS	1	31.7	CM0163	LjT35J19	3	x5	seed	DF093299
BM1196	SSR	1	31.7	CM0163	LjB70O07	1	x3	walking	DF093299
		1		CM0163	LjT37G03	1	x3	seed	DF093299
		1		CM0215	LjT56C20	1	x3	walking	DF093330
TM0215	SSR	1	33.3	CM0215	LjT36C05	3	x5	seed	DF093330
BM1697	SSR	1	33.7		LjB10L14	3	x5	seed	AP009628
TM1612	SSR	1	34.5		LjT14I13	1	x3	seed	AP010230
TM0688	SSR	1	34.9		LjT23O20	1	x3	seed	AP010048
TM0637	SSR	1	35.3		LjT36P09	1	x3	seed	AP010032
TM1124	SSR	1	37.8		LjT41J07	1	x3	seed	AP010158
TM0220	SSR	1	38.2		LjT23D08	3	x5	seed	AP009660
		1		CM0017	LjT37O24	1	x3	seed	DF093191
		1		CM0017	LjT40C16	1	x3	seed	DF093191
TM0117	SSR	1	40.2	CM0017	LjT43B20	3	x5	seed	DF093191

		1		CM0017	LjT09F06	2	x5	seed	DF093191
TM0017	SSR	1	42.2	CM0017	LjT06I17	3	x5	seed	DF093191
		1		CM0017	LjT47H11	1	x3	walking	DF093191
		1		CM0231	LjT04A18	1	x3	walking	DF093338
TM0231	SSR	1	42.2	CM0231	LjT09O08	3	x5	seed	DF093338
		1		CM0231	LjB26C21	1	x3	walking	DF093338
		1		CM0231	LjT25J06	1	x3	walking	DF093338
TM0240	SSR	1	42.6		LjT37A17	3	x5	seed	AP009664
		1		CM0150	LjT46G03	1	x3	seed	DF093292
		1		CM0150	LjT16L24	1	x3	walking	DF093292
TM0438	SSR	1	42.6	CM0150	LjT44N06	3	x5	seed	DF093292
		1		CM0150	LjT19F13	1	x3	walking	DF093292
TM0150	dCAPS	1	42.6	CM0150	LjT20G22	3	x5	seed	DF093292
		1		CM0150	LjT10D09	1	x3	walking	DF093292
		1		CM0113	LjB16L15	1	x3	walking	DF093265
TM0113	SSR	1	42.6	CM0113	LjT43P05	3	x5	seed	DF093265
		1		CM0113	LjT55F02	1	x3	walking	DF093265
TM0309	SSR	1	42.6	CM0113	LjT15N15	3	x5	seed	DF093265
		1		CM0113	LjT02B05	1	x3	walking	DF093265
		1		CM0147	LjB03L08	1	x3	walking	DF093290
TM0342	SSR	1	44.2	CM0147	LjT05H03	3	x5	seed	DF093290
		1		CM0147	LjT30B08	1	x3	walking	DF093290
TM0147	SSR	1	44.2	CM0147	LjT34B12	3	x5	seed	DF093290
TM0185	SSR	1	44.2	CM0147	LjT11J24	3	x5	seed	DF093290
		1		CM0147	LjT04O18	1	x3	walking	DF093290

TM0430	SSR	1	44.2		LjT43D18	1	x3	seed	AP009975
TM1284	SSR	1	44.2		LjT44L17	1	x3	seed	AP010177
TM1666	SSR	1	44.6		LjT36F23	1	x3	seed	AP010248
TM1516	SSR	1	44.6		LjT46N10	1	x3	seed	AP010208
TM0800	SSR	1	45.0	CM0800	LjT43C21	1	x3	seed	DF093484
		1		CM0800	LjB66I07	1	x3	walking	DF093484
		1		CM0800	LjT48M16	1	x5	walking	DF093484
		1		CM0800	LjT03A07	1	x3	seed	DF093484
TM0989	SSR	1	45.4		LjT36I17	1	x3	seed	AP010144
TM0316	SSR	1	46.2	CM0316	LjT02I08	3	x5	seed	DF093382
		1		CM0316	LjB13J04	1	x3	walking	DF093382
		1		CM0001	LjT48G21	1	x3	seed	DF093176
		1		CM0001	LjT16O19	1	x3	walking	DF093176
TM0001	SSR	1	47.0	CM0001	LjT09C23	3	x5	seed	DF093176
		1		CM0001	LjT02F04	3	x5	seed	DF093176
TM1818	SSR	1	47.0	CM0001	LjT28C03	3	x5	walking	DF093176
TM0805	SSR	1	47.5		LjT16O03	1	x5	seed	AP010091
		1		CM0064	LjT05I18	1	x3	walking	DF093231
TM0064	dCAPS	1	49.0	CM0064	LjT06B17	3	x5	seed	DF093231
TM0356	SSR	1	51.4		LjT08H21	1	x5	seed	AP009960
TM1880	SSR	1	51.4	CM1880	LjT41E05	3	x5	seed	DF093533
		1		CM1880	LjT23N18	2	x5	seed	DF093533
BM1186	SSR	1	51.8	CM0593	LjB69F06	1	x3	walking	DF093454
		1		CM0593	LjT09H02	3	x5	seed	DF093454
TM1207	SSR	1	52.2	CM0593	LjT38O19	1	x3	walking	DF093454

TM0222	SSR	1	52.2	CM0222	LjT15D21	3	x5	seed	DF093333
		1		CM0222	LjT31I13	1	x3	walking	DF093333
		1		CM0104	LjB04M10	1	x3	walking	DF093258
		1		CM0104	LjT35D17	3	x5	seed	DF093258
TM0107	SSR	1	52.6	CM0104	LjT28G12	3	x5	seed	DF093258
		1		CM0104	LjT44L12	1	x3	walking	DF093258
TM0236	SSR	1	53.8		LjT38H23	1	x5	seed	AP009956
TM0371	SSR	1	53.8	CM0371	LjT46E19	3	x5	seed	DF093403
		1		CM0371	LjT05K01	3	x5	walking	DF093403
TM1640	SSR	1	55.8	CM1409	LjT02P18	1	x3	seed	DF093514
TM1418	SSR	1	55.8	CM1409	LjT34J20	1	x3	seed	DF093514
		1		CM1409	LjT02K05	1	x3	seed	DF093514
		1		CM0098	LjT19C10	1	x3	walking	DF093253
TM0098	SSR	1	56.6	CM0098	LjT04C07	3	x5	seed	DF093253
		1		CM0098	LjT43M09	1	x3	walking	DF093253
TM1911	SSR	1	56.6		LjT01M20	3	x5	seed	AP009755
		1		CM0269	LjT34P12	1	x3	seed	DF093357
TM0269	SSR	1	57.0	CM0269	LjT04I09	3	x5	seed	DF093357
		1		CM0269	LjT40N03	1	x3	seed	DF093357
		1		CM0816	LjB05C24	3	x5	walking	DF093487
TM0816	SSR	1	57.0	CM0816	LjT09K12	1	x3	seed	DF093487
		1		CM0816	LjT06H19	3	x5	walking	DF093487
		1		CM0816	LjT02K21	3	x5	walking	DF093487
TM1438	SSR	1	57.0	CM0816	LjT15P18	1	x3	seed	DF093487
		1			LjB20I01	2	x5	walking	AP009865

		1		CM0009	LjT35G21	1	x3	walking	DF093184
TM0009	SSR	1	57.4	CM0009	LjT13B22	3	x5	seed	DF093184
		1		CM0009	LjB15J13	1	x3	walking	DF093184
TM0276	SSR	1	57.8	CM0009	LjT03B16	3	x5	seed	DF093184
TM0509	SSR	1	57.8		LjT38G13	1	x3	seed	AP009999
		1		CM0398	LjT20K12	1	x3	seed	DF093411
TM0398	SSR	1	57.8	CM0398	LjT47K05	1	x3	seed	DF093411
		1		CM0318	LjT02I22	1	x3	walking	DF093383
TM0318	SSR	1	59.8	CM0318	LjT45A23	3	x5	seed	DF093383
		1		CM0318	LjT45H04	1	x3	walking	DF093383
TM0221	SSR	1	60.2		LjT38A19	3	x5	seed	AP009661
TM0812	SSR	1	60.2		LjT05B18	1	x3	seed	AP010097
TM0322	SSR	1	60.6	CM0322	LjT17D07	3	x5	seed	DF093386
		1		CM0322	LjT11I07	2	x3	walking	DF093386
TM0935	SSR	1	60.6	CM0375	LjT03B08	1	x3	seed	DF093405
TM0605	SSR	1	60.6	CM0375	LjT37I21	1	x3	seed	DF093405
TM0375	SSR	1	60.6	CM0375	LjT45D03	3	x5	seed	DF093405
TM1643	SSR	1	61.0	CM0295	LjT30B06	1	x3	seed	DF093369
TM0295	SSR	1	61.4	CM0295	LjT47J05	1	x3	seed	DF093369
TM0332	SSR	1	61.4	CM0295	LjT27M11	3	x5	seed	DF093369
		1		CM0295	LjT23A03	1	x3	walking	DF093369
		1		CM0295	LjT06I08ab	3	x5	seed	DF093369
		1		CM0295	LjB22E06	1	x3	walking	DF093369
TM2017	SSR	1	61.8	CM0295	LjT18M13	3	x5	seed	DF093369
		1		CM0295	LjT27B01	3	x5	walking	DF093369

		1		CM0033	LjT18M23	2	x5	walking	DF093205
		1		CM0033	LjT35G11	2	x5	walking	DF093205
		1		CM0033	LjT58D09	3	x5	walking	DF093205
BM1994	SSR	1	62.2	CM0033	LjB05O03	3	x5	seed	DF093205
		1		CM0033	LjB07N04	3	x5	walking	DF093205
TM2015	SSR	1	62.2	CM0033	LjT45O08	3	x5	walking	DF093205
TM1322	SSR	1	62.2	CM0033	LjT35E02	1	x3	seed	DF093205
TM0033	SSR	1	62.2	CM0033	LjT07E11	3	x5	seed	DF093205
		1		CM0033	LjT16A03	3	x5	seed	DF093205
TM2016	SSR	1	62.2	CM0033	LjT38C06	3	x5	walking	DF093205
		1		CM0012	LjT13H23	1	x3	seed	DF093187
TM0908	SSR	1	63.4	CM0012	LjT46L16	1	x3	seed	DF093187
TM0422	SSR	1	63.4	CM0012	LjT12O19	1	x3	seed	DF093187
TM0012	SSR	1	63.8	CM0012	LjT03H13	3	x5	seed	DF093187
		1		CM0012	LjT49G12	1	x3	walking	DF093187
TM0705	SSR	1	65.4	CM0010	LjT41J08	1	x3	seed	DF093185
TM0010	SSR	1	65.4	CM0010	LjT01I13	3	x5	seed	DF093185
		1		CM0010	LjT38A06	1	x3	walking	DF093185
		1		CM0361	LjT25O07	1	x3	walking	DF093402
TM0980	SSR	1	65.4	CM0361	LjT29P14	1	x3	seed	DF093402
TM1391	SSR	1	65.4	CM0361	LjT41E03	3	x5	seed	DF093402
		1		CM0361	LjT43G12	1	x3	seed	DF093402
		1		CM0361	LjT33P08	1	x3	walking	DF093402
		1		CM0361	LjT34C12	3	x5	seed	DF093402
TM0378	dCAPS	1	65.4	CM0378	LjT45M12	3	x5	seed	DF093406

		1		CM0378	LjT19I13	1	x3	seed	DF093406
		1		CM0378	LjT08H16	1	x3	seed	DF093406
TM0785	SSR	1	65.8	CM0029	LjT16N20	1	x3	seed	DF093202
TM0029	SSR	1	65.8	CM0029	LjT11C13	3	x5	seed	DF093202
		1		CM0029	LjT09K14	1	x3	seed	DF093202
		1		CM0206	LjT36M24	1	x3	walking	DF093325
TM0223	SSR	1	66.2	CM0206	LjT44A10	3	x5	seed	DF093325
		1		CM0206	LjT04P23	1	x3	walking	DF093325
		1		CM0206	LjT36E14	1	x3	walking	DF093325
TM0206	dCAPS	1	66.2	CM0206	LjT16D13	3	x5	seed	DF093325
		1		CM0206	LjT56M23	1	x3	walking	DF093325
TM0144	SSR	1	66.2	CM0122	LjT27L02	3	x5	seed	DF093273
TM0143	SSR	1	66.2	CM0122	LjT20J05	3	x5	seed	DF093273
TM0122	SSR	1	66.2	CM0122	LjT45F11	3	x5	seed	DF093273
		1		CM0122	LjB15E24	1	x3	walking	DF093273
		1		CM0122	LjT36K23	1	x3	seed	DF093273
		1		CM0544	LjB12K22	3	x5	seed	DF093443
		1		CM0544	LjT54J01	1	x3	walking	DF093443
TM0544	SSR	1	67.0	CM0544	LjT44N05	3	x5	seed	DF093443
		1		CM0544	LjB140D10	1	x3	walking	DF093443
		1		CM0109	LjB04D14	1	x3	walking	DF093261
TM0109	SSR	1	67.0	CM0109	LjT25N10	3	x5	seed	DF093261
TM0811	SSR	1	67.0		LjT29L06	1	x3	seed	AP010096
TM1573	SSR	1	67.0		LjT30M08	2	x5	seed	AP009873
TM0600	SSR	1	69.0	CM0600	LjT46P11	1	x3	seed	DF093455

		1		CM0600	LjT05A19	1	x5	seed	DF093455
		1		CM0600	LjT09K09	1	x3	walking	DF093455
TM0835	SSR	1	69.4		LjT14G19	3	x5	seed	AP009681
		1		CM0579	LjT07K15	2	x5	seed	DF093450
BM1229	SSR	1	69.4	CM0579	LjB18B20	1	x3	walking	DF093450
TM1636	SSR	1	69.4	CM0579	LjT17N03	1	x3	seed	DF093450
TM0750	SSR	1	69.4		LjT43L07	1	x5	seed	AP010074
		1		CM0105	LjT42H23	1	x3	walking	DF093259
		1		CM0105	LjT36D11	1	x3	walking	DF093259
TM0105	SSR	1	71.0	CM0105	LjT17M09	3	x5	seed	DF093259
		1		CM0105	LjT62O06	3	x5	walking	DF093259
		1		CM0105	LjT02K14	3	x5	walking	DF093259
TM1494	SSR	1	71.0	CM0105	LjT45I15	3	x5	seed	DF093259
		1		CM0105	LjT20F11	3	x5	walking	DF093259
		1		CM0105	LjT46G19	1	x5	walking	DF093259
TM0067	SSR	2	0.0	CM0067	LjT12O09	3	x5	seed	DF093234
		2		CM0067	LjT41O24	3	x5	walking	DF093234
TM0808	SSR	2	0.4		LjT44B19	1	x3	seed	AP010093
		2		CM0237	LjB64M03	1	x3	walking	DF093341
TM0237	SSR	2	0.4	CM0237	LjT30K08	3	x5	seed	DF093341
		2		CM0262	LjT15A20	1	x3	walking	DF093356
TM0262	dCAPS	2	0.4	CM0262	LjT03H18	3	x5	seed	DF093356
		2		CM0262	LjT42L09	1	x3	walking	DF093356
TM0847	SSR	2	0.4		LjT07F03	1	x3	seed	AP010109
TM0712	SSR	2	0.4		LjT10F02	1	x3	seed	AP010057

TM1761	SSR	2	0.4		LjT45D13	3	x5	seed	AP009856(a), AP009857(b)
TM1637	SSR	2	0.8		LjT44M20	1	x3	seed	AP010236
BM2030	SSR	2	0.8		LjB11M03	3	x5	seed	AP009647
BM1950	SSR	2	0.8		LjB26H15	3	x5	seed	AP009637
TM1981	SSR	2	0.8		LjT09A11	3	x5	seed	AP009783
BM1699	SSR	2	1.2		LjB17A04	3	x5	seed	AP009630
TM0838	SSR	2	2.4		LjT17A07	1	x3	seed	AP010103
TM1655	SSR	2	2.4		LjT43N03	1	x3	seed	AP010242
TM0413	SSR	2	2.8		LjT44L24	1	x3	seed	AP009967
TM0134	SSR	2	3.2		LjT34H20	3	x5	seed	AP009654
TM1756	SSR	2	3.2		LjT11L13	3	x5	seed	AP009704
TM1860	SSR	2	3.2		LjT12G08	3	x5	seed	AP009737
TM1038	SSR	2	3.6		LjT24G10	1	x3	seed	AP010149
TM1456	SSR	2	4.0	CM0904	LjT09D03	1	x3	seed	DF093495
		2		CM0904	LjT33P02	1	x3	walking	DF093495
TM0368	SSR	2	4.0		LjT39I14	3	x5	seed	AP009816(a), AP009817(b), AP009818(c)
TM1583	SSR	2	4.0		LjT40P05	1	x3	seed	AP010227
TM1171	SSR	2	5.2		LjT45I07	1	x3	seed	AP010164
TM0875	SSR	2	6.0		LjT16I15	1	x3	seed	AP010120
TM0074	SSR	2	6.2	CM0074	LjT18E24	3	x5	seed	DF093238
		2		CM0074	LjB16D22	1	x3	walking	DF093238
TM0383	SSR	2	6.4		LjT16L14	3	x5	seed	AP009672
TM0564	SSR	2	8.4		LjT37J22	1	x3	seed	AP010013

		2		CM0312	LjT02L01	1	x3	walking	DF093379
TM0312	dCAPS	2	8.8	CM0312	LjT29F18	3	x5	seed	DF093379
TM0348	SSR	2	8.8	CM0312	LjT40O04	3	x5	seed	DF093379
TM0435	SSR	2	8.8		LjT47G24	1	x3	seed	AP009977
TM0490	SSR	2	8.8		LjT01N23	3	x5	seed	AP009675
TM0053	SSR	2	9.6		LjT01H08	3	x5	seed	AP009650
TM0254	dCAPS	2	9.6		LjT16L07	3	x5	seed	AP009665
TM0310	SSR	2	10.8	CM0310	LjT33E11	3	x5	seed	DF093377
		2		CM0310	LjT04O04	1	x3	walking	DF093377
TM0153	SSR	2	10.8	CM0153	LjT28L17	3	x5	seed	DF093294
		2		CM0153	LjT49J19	1	x3	walking	DF093294
TM0610	SSR	2	11.6		LjT17O14	3	x5	seed	AP009831(a), AP009832(b)
TM1996	SSR	2	12.0		LjT41F02	3	x5	seed	AP009785
TM0660	SSR	2	12.8	CM0660	LjT07O13	1	x3	seed	DF093464
TM1782	SSR	2	12.8	CM0660	LjT15B05	3	x5	seed	DF093464
		2		CM0065	LjB26D18	1	x3	walking	DF093232
TM0065	SSR	2	14.0	CM0065	LjT11D15	3	x5	seed	DF093232
TM0479	SSR	2	14.0		LjT43I20	1	x3	seed	AP009989
TM1405	SSR	2	14.0	CM0783	LjT22I07	1	x3	walking	DF093480
		2		CM0783	LjT43M11	1	x3	seed	DF093480
TM0915	SSR	2	14.0	CM0373	LjT07A18	1	x3	seed	DF093404
TM0535	SSR	2	14.0	CM0373	LjT10F01	2	x5	seed	DF093404
		2		CM0373	LjT53O13	3	x5	walking	DF093404
TM1329	SSR	2	14.0	CM0373	LjT41G23	1	x3	seed	DF093404

		2		CM0373	LjT24O01	3	x5	walking	DF093404
TM0373	SSR	2	14.4	CM0373	LjT16A21	3	x5	seed	DF093404
		2		CM0373	LjT43B09	1	x5	seed	DF093404
		2		CM0373	LjT02A17	3	x5	walking	DF093404
		2		CM0373	LjT24F03	3	x5	walking	DF093404
TM1491	SSR	2	17.7	CM0373	LjT47H03	1	x3	seed	DF093404
TM1561	SSR	2	18.9		LjT18H02	3	x5	seed	AP009692
TM1827	SSR	2	18.9		LjT32G18	3	x5	seed	AP009720
TM0263	SSR	2	19.3		LjT30P12	3	x5	seed	AP009666
		2		CM0201	LjT13J14	1	x3	seed	DF093324
TM0201	dCAPS	2	20.5	CM0201	LjT47H13	3	x5	seed	DF093324
TM0400	SSR	2	21.7	CM0201	LjT45A22	3	x5	seed	DF093324
		2		CM0201	LjT13C22	1	x3	seed	DF093324
TM1766	SSR	2	22.9	CM0081	LjT14B16	3	x5	seed	DF093244
TM0081	dCAPS	2	24.6	CM0081	LjT01G01	3	x5	seed	DF093244
		2		CM0081	LjT06B24	1	x5	walking	DF093244
		2		CM0225	LjT06K23	3	x5	seed	DF093334
TM0225	SSR	2	25.8	CM0225	LjT27K02	3	x5	seed	DF093334
		2		CM0225	LjT04D07	1	x3	walking	DF093334
TM0377	SSR	2	27.4		LjT39I02	3	x5	seed	AP009821(a), AP009822(b)
TM1882	SSR	2	28.3		LjT16J19	3	x5	seed	AP009746
TM0338	SSR	2	30.2	CM0338	LjT05M24	3	x5	seed	DF093393
		2		CM0338	LjT36E22	1	x3	walking	DF093393
		2		CM0903	LjT43M02	1	x3	seed	DF093494

TM1455	SSR	2	31.0	CM0903	LjT11H20	1	x3	walking	DF093494
		2		CM0903	LjT40G15	1	x3	seed	DF093494
		2		CM0903	LjT01E20	1	x5	walking	DF093494
BM1626	SSR	2	31.8	CM0903	LjB18B24	1	x5	seed	DF093494
TM1731	SSR	2	32.6	CM1731	LjT28M24	3	x5	seed	DF093526
TM1963	SSR	2	32.6	CM1731	LjT29K03	3	x5	seed	DF093526
TM0655	SSR	2	33.0		LjT09H11	1	x3	seed	AP010042
TM1403	SSR	2	33.0	CM0749	LjT05O01	1	x3	walking	DF093478
		2		CM0749	LjT13J06	1	x3	seed	DF093478
		2		CM0749	LjT28N02	3	x5	walking	DF093478
TM1773	SSR	2	33.0		LjT47E17	3	x5	seed	AP009711
BM1721	SSR	2	33.4	CM0124	LjB24P14	3	x5	seed	DF093275
		2		CM0124	LjT48O14	1	x3	seed	DF093275
TM1263	SSR	2	33.4	CM0124	LjT39N23	1	x3	seed	DF093275
		2		CM0124	LjT15J21	1	x3	walking	DF093275
TM0124	SSR	2	33.8	CM0124	LjT26I01	3	x5	seed	DF093275
		2		CM0124	LjB13M05	1	x3	walking	DF093275
		2		CM0124	LjT08N18	3	x5	walking	DF093275
		2		CM0120	LjT04J16	3	x5	walking	DF093271
		2		CM0120	LjT57J16	1	x3	walking	DF093271
TM0120	SSR	2	36.5	CM0120	LjT32P24	3	x5	seed	DF093271
		2		CM0120	LjB21N24	1	x3	walking	DF093271
		2		CM0641	LjB15B24	3	x5	walking	DF093461
		2		CM0641	LjT46E17	3	x5	walking	DF093461
TM1805	SSR	2	37.9	CM0641	LjT20I14	3	x5	walking	DF093461

TM0641	SSR	2	38.7	CM0641	LjT06G07	1	x3	seed	DF093461
		2		CM0641	LjT10M19	3	x5	walking	DF093461
TM0736	SSR	2	40.3	CM0608	LjT33G24	1	x3	seed	DF093458
TM0608	SSR	2	40.3	CM0608	LjT33L05	1	x3	seed	DF093458
TM1534	SSR	2	40.3	CM0608	LjT38H08	3	x5	seed	DF093458
		2		CM1150	LjT04O12	1	x3	walking	DF093509
TM1150	SSR	2	40.7	CM1150	LjT33B06	1	x3	seed	DF093509
		2		CM1150	LjB23N09	1	x3	walking	DF093509
TM0028	SSR	2	42.3	CM0028	LjT12F12	3	x5	seed	DF093201
		2		CM0028	LjT23F19	1	x3	walking	DF093201
		2		CM0056	LjT09H18	1	x3	walking	DF093223
TM0056	SSR	2	42.3	CM0056	LjT16I03	3	x5	seed	DF093223
		2		CM0056	LjT43I15	1	x3	walking	DF093223
		2		CM0008	LjT11E07	1	x3	walking	DF093183
TM0008	SSR	2	44.2	CM0008	LjT10B11	3	x5	seed	DF093183
TM0242	SSR	2	45.6	CM0008	LjT34L23	3	x5	seed	DF093183
TM0076	SSR	2	46.0	CM0008	LjT13I21	3	x5	seed	DF093183
		2		CM0008	LjT42N20	1	x3	seed	DF093183
TM1901	SSR	2	46.5		LjT13P17	2	x5	seed	AP009881
		2		CM0177	LjB03D10	1	x3	walking	DF093311
TM0541	SSR	2	48.5	CM0177	LjT17H01	3	x5	seed	DF093311
		2		CM0177	LjT11E23	3	x5	seed	DF093311
TM0177	dCAPS	2	48.5	CM0177	LjT01N11	3	x5	seed	DF093311
TM0381	dCAPS	2	48.5	CM0177	LjT10N22	3	x5	seed	DF093311
TM0520	SSR	2	48.5	CM0177	LjT47I01	3	x5	seed	DF093311

TM0230	SSR	2	48.9		LjT41P23	3	x5	seed	AP009662
BM1153	SSR	2	48.9	CM0020	LjB02I05	1	x3	walking	DF093194
		2		CM0020	LjT20J15	3	x5	seed	DF093194
TM0020	SSR	2	48.9	CM0020	LjT02F05	3	x5	seed	DF093194
		2		CM0803	LjB11B14	3	x5	walking	DF093485
TM0974	SSR	2	49.3	CM0803	LjT12H02	1	x3	seed	DF093485
		2		CM0803	LjT14N05	3	x5	walking	DF093485
		2		CM0803	LjT12C04	3	x5	walking	DF093485
		2		CM0803	LjT10G21	3	x5	walking	DF093485
		2		CM0803	LjT40H03	1	x3	seed	DF093485
TM0803	SSR	2	50.1	CM0803	LjT39E07	1	x3	seed	DF093485
		2		CM0803	LjT23F22	1	x5	walking	DF093485
TM0886	SSR	2	51.7	CM0272	LjT35D16	1	x3	seed	DF093358
TM0272	SSR	2	51.7	CM0272	LjT03C14	3	x5	seed	DF093358
		2		CM0272	LjB65N09	1	x3	walking	DF093358
TM1421	SSR	2	52.1	CM0695	LjT16F09	1	x3	seed	DF093472
BM1375	SSR	2	52.9	CM0695	LjB04A13	3	x5	seed	DF093472
TM0695	SSR	2	52.9	CM0695	LjT02P19	1	x3	seed	DF093472
TM0737	SSR	2	53.7	CM0249	LjT39J09	1	x3	seed	DF093350
BM1206	SSR	2	55.2	CM0249	LjB13I10	1	x3	walking	DF093350
		2		CM0249	LjT17E09	3	x5	seed	DF093350
TM0249	SSR	2	55.7	CM0249	LjT34A19	3	x5	seed	DF093350
		2		CM0249	LjB69K05	1	x3	walking	DF093350
		2		CM0249	LjB13F12	1	x3	walking	DF093350
TM0257	SSR	2	56.1	CM0249	LjT29N11	3	x5	seed	DF093350

		2		CM0249	LjT17G09	1	x3	walking	DF093350
TM0549	SSR	2	56.6	CM0249	LjT20E01	3	x5	seed	DF093350
TM0374	SSR	2	58.1		LjT34P04	1	x5	seed	AP009961
TM0652	SSR	2	58.1		LjT16G06	1	x3	seed	AP010041
TM0559	SSR	2	58.9	CM0323	LjT01C03	3	x5	seed	DF093387
TM0323	dCAPS	2	58.9	CM0323	LjT18J10	3	x5	seed	DF093387
		2		CM0323	LjB06D23	3	x5	seed	DF093387
TM0522	SSR	2	58.9	CM0323	LjT13I23	1	x5	seed	DF093387
TM0250	SSR	2	60.1	CM0250	LjT08A24	3	x5	seed	DF093351
TM1037	SSR	2	60.1	CM0250	LjT42E19	1	x3	seed	DF093351
		2		CM0168	LjB20F05	1	x3	walking	DF093303
TM0168	SSR	2	60.5	CM0168	LjT33C05	3	x5	seed	DF093303
		2		CM0168	LjB16K06	1	x3	walking	DF093303
TM1389	SSR	2	60.9	CM0021	LjT41P09	1	x3	walking	DF093195
		2		CM0021	LjT09A07a	3	x3	walking	DF093195
TM0132	SSR	2	60.9	CM0021	LjT19K21	3	x5	seed	DF093195
		2		CM0021	LjT40A14	3	x3	walking	DF093195
		2		CM0021	LjB71C07	3	x5	walking	DF093195
		2		CM0021	LjT28I23	3	x5	walking	DF093195
		2		CM0021	LjT17M11	3	x5	seed	DF093195
TM0021	SSR	2	60.9	CM0021	LjT04I02	3	x5	seed	DF093195
		2		CM0021	LjT30A05	1	x3	walking	DF093195
TM0550	SSR	2	60.9	CM0021	LjT17H09	3	x5	seed	DF093195
TM0521	SSR	2	60.9	CM0021	LjT16A17	1	x5	seed	DF093195
		2		CM0304	LjT39E08	1	x3	walking	DF093374

TM0934	SSR	2	60.9	CM0304	LjT08G16	3	x5	seed	DF093374
BM1477	SSR	2	60.9	CM0304	LjB10A07	3	x5	seed	DF093374
		2		CM0304	LjT31J14	1	x3	walking	DF093374
TM0304	SSR	2	60.9	CM0304	LjT41D09	3	x5	seed	DF093374
		2		CM0304	LjT48N18	1	x3	seed	DF093374
		2		CM0304	LjT57N07	3	x3	walking	DF093374
TM0060	SSR	2	60.9	CM0060	LjT04G24	3	x5	seed	DF093227
		2		CM0060	LjT45N17	1	x5	walking	DF093227
		2		CM0060	LjT34D07	1	x5	walking	DF093227
TM0635	SSR	2	61.3	CM0060	LjT47B15	3	x3	seed	DF093227
TM0018	SSR	2	61.3	CM0018	LjT08D14	3	x5	seed	DF093192
		2		CM0018	LjB07J24	1	x3	seed	DF093192
		2		CM0018	LjT45I08	1	x3	seed	DF093192
TM0691	SSR	2	61.7	CM0018	LjT04L09	1	x3	seed	DF093192
TM0588	SSR	2	61.7	CM0018	LjT01O03	3	x5	seed	DF093192
TM0587	SSR	2	62.1	CM0018	LjT08P04	3	x5	seed	DF093192
TM0592	SSR	2	62.1	CM0018	LjT41D19	3	x5	seed	DF093192
TM0796	SSR	2	62.1	CM0018	LjT10F20	3	x5	seed	DF093192
TM0504	SSR	2	62.9	CM0504	LjT31E24	1	x3	seed	DF093438
TM1649	SSR	2	62.9	CM0504	LjT23I09	1	x5	seed	DF093438
TM0360	SSR	2	62.9	CM0360	LjT31L13	3	x5	seed	DF093401
		2		CM0360	LjT35G04	1	x3	seed	DF093401
		2		CM0346	LjB14B15	1	x3	walking	DF093397
TM0346	dCAPS	2	63.3	CM0346	LjT16J06	3	x5	seed	DF093397
TM0058	dCAPS	2	63.7	CM0058	LjT01K12	3	x5	seed	DF093225

		2		CM0058	LjT30C01	1	x3	walking	DF093225
TM0526	SSR	2	63.7	CM0058	LjT09P04	1	x3	seed	DF093225
		2		CM0058	LjT16E09	1	x3	walking	DF093225
TM0889	SSR	2	63.7		LjT09A09	1	x3	seed	AP010123
TM0329	SSR	2	63.7		LjT03F24	1	x3	seed	AP009959
TM1744	SSR	2	63.7	CM0788	LjT10O06	3	x5	seed	DF093481
		2		CM0788	LjT43A15	1	x3	seed	DF093481
		2		CM0011	LjT33N06	2	x5	seed	DF093186
		2		CM0011	LjT16J04	1	x3	walking	DF093186
TM0011	SSR	2	65.3	CM0011	LjT12K07	3	x5	seed	DF093186
		2		CM0011	LjB09K11	1	x3	walking	DF093186
TM0405	SSR	2	65.3	CM0405	LjT45O06	1	x3	seed	DF093413
		2		CM0405	LjT06A09	1	x3	walking	DF093413
TM0417	SSR	2	66.1		LjT13M01	1	x3	seed	AP009971
		2		CM0002	LjT31G14	1	x3	walking	DF093177
TM0002	SSR	2	67.3	CM0002	LjT06K11	3	x5	seed	DF093177
		2		CM0002	LjT14P21	1	x3	walking	DF093177
TM0204	SSR	2	67.3	CM0002	LjT39P22	3	x5	seed	DF093177
TM0313	SSR	2	67.3	CM0002	LjT45D08	3	x5	seed	DF093177
TM0871	SSR	2	67.3		LjT46G02	1	x3	seed	AP010117
		2		CM1032	LjT05O03	1	x3	seed	DF093504
TM1032	SSR	2	67.3	CM1032	LjT37H21	3	x5	seed	DF093504
		2		CM1032	LjT44N22	3	x5	seed	DF093504
		2		CM0826	LjT23D07	3	x5	walking	DF093488
TM0826	SSR	2	67.7	CM0826	LjT35G07	1	x3	seed	DF093488

TM1285	SSR	2	67.7		LjT24P12	1	x3	seed	AP010178
		2		CM0545	LjB08D08	1	x3	walking	DF093444
TM0546	SSR	2	68.1	CM0545	LjT02D13	3	x5	seed	DF093444
		2		CM0545	LjT211O02	3	x5	seed	DF093444
TM0545	SSR	2	68.1	CM0545	LjT05B16	3	x5	seed	DF093444
TM1679	SSR	2	68.1	CM0545	LjT26K22	3	x5	walking	DF093444
		2		CM0031	LjB19D18	1	x3	walking	DF093203
TM0031	dCAPS	2	68.5	CM0031	LjT16N13	3	x5	seed	DF093203
		2		CM0308	LjT26M19	1	x3	walking	DF093376
TM0308	dCAPS	2	69.3	CM0308	LjT15H15	3	x5	seed	DF093376
		2		CM0308	LjT42O06	1	x3	walking	DF093376
TM0370	SSR	2	69.3		LjT04L10	3	x5	seed	AP009671
TM1517	SSR	2	69.3		LjT36E17	1	x3	seed	AP010209
BM2010	SSR	2	69.3		LjB15M17	3	x5	seed	AP009645
TM0099	SSR	2	69.5	CM0099	LjT01B10	3	x5	seed	DF093254
		2		CM0099	LjT18D17	1	x3	walking	DF093254
TM0621	SSR	2	69.7		LjT02C03	1	x3	seed	AP010026
TM1646	SSR	2	70.5		LjT02E02	1	x3	seed	AP010240
TM1659	SSR	2	70.5		LjT42I05	1	x3	seed	AP010245
TM1885	SSR	2	70.5		LjT42A12	3	x5	seed	AP009748
TM0667	SSR	2	71.3		LjT03I05	3	x5	seed	AP009833(a), AP009834(b)
TM0512	SSR	2	71.3		LjT48A12	1	x3	seed	AP010000
		2		CM0210	LjB21C16	3	x5	walking	DF093327
TM0210	SSR	2	72.1	CM0210	LjT43I02	3	x5	seed	DF093327

		2		CM0210	LjT13C09	1	x3	walking	DF093327
		2		CM0191	LjT45D07	3	x5	seed	DF093318
		2		CM0191	LjT44M23	3	x5	walking	DF093318
		2		CM0191	LjB12E22	3	x5	walking	DF093318
TM0324	SSR	2	72.5	CM0191	LjT38O12	3	x5	seed	DF093318
		2		CM0191	LjB13K21	3	x5	walking	DF093318
		2		CM0191	LjT37A22	1	x3	seed	DF093318
TM0191	SSR	2	72.5	CM0191	LjT21K08	3	x5	seed	DF093318
TM0380	SSR	2	72.9	CM0102	LjT18K09	3	x5	seed	DF093257
		2		CM0102	LjT36K11	1	x3	seed	DF093257
		2		CM0102	LjB66E01	1	x3	walking	DF093257
TM0102	dCAPS	2	72.9	CM0102	LjT08G20	3	x5	seed	DF093257
		2		CM0102	LjT42I06	1	x3	seed	DF093257
TM0793	SSR	3	0.0		LjT23O13	1	x3	seed	AP010087
TM0916	SSR	3	0.4		LjT34H24	1	x3	seed	AP010130
TM1924	SSR	3	0.4		LjT40P18	3	x5	seed	AP009764
TM1208	SSR	3	1.6	CM0253	LjT23O04	1	x3	walking	DF093352
		3		CM0253	LjT06I23	3	x5	seed	DF093352
BM1187	SSR	3	2.4	CM0253	LjB72A14	1	x3	walking	DF093352
TM0745	SSR	3	2.4		LjT07H20	1	x3	seed	AP010071
		3		CM0106	LjB07H05	1	x3	walking	DF093260
TM0666	SSR	3	5.3	CM0106	LjT15I02	3	x5	seed	DF093260
		3		CM0106	LjT42E24	1	x3	walking	DF093260
		3		CM0106	LjT59K09	1	x3	walking	DF093260
TM0106	SSR	3	5.7	CM0106	LjT48I11	3	x5	seed	DF093260

TM0576	SSR	3	5.7		LjT02L14	1	x3	seed	AP010017
		3		CM0176	LjB21E20	3	x3	walking	DF093310
TM0176	SSR	3	6.9	CM0176	LjT35C03	3	x5	seed	DF093310
		3		CM0176	LjT32J02	1	x3	walking	DF093310
		3		CM0059	LjB03D19	1	x3	walking	DF093226
TM0059	SSR	3	6.9	CM0059	LjT13M14	3	x5	seed	DF093226
		3		CM0059	LjT32D03	1	x3	walking	DF093226
		3		CM0282	LjT48M13	1	x3	seed	DF093363
TM0340	SSR	3	7.7	CM0282	LjT31E21	3	x5	seed	DF093363
		3		CM0282	LjT27B17	1	x5	walking	DF093363
TM0282	SSR	3	8.1	CM0282	LjT34M22	3	x5	seed	DF093363
BM1673	SSR	3	8.1	CM0282	LjB14E23	3	x5	walking	DF093363
		3		CM0282	LjT02M11	3	x5	walking	DF093363
		3		CM0282	LjT41F22	3	x5	walking	DF093363
		3		CM0282	LjT18K24	3	x5	walking	DF093363
		3		CM0634	LjT22B13	3	x5	walking	DF093460
TM1715	SSR	3	9.7	CM0634	LjT20E20	3	x5	walking	DF093460
BM1487	SSR	3	9.7	CM0634	LjB25F18	1	x3	walking	DF093460
		3		CM0634	LjT39K19	1	x3	seed	DF093460
TM0704	SSR	3	9.7	CM0634	LjT06E12	3	x5	seed	DF093460
		3		CM0634	LjT03G11	3	x5	seed	DF093460
		3		CM0634	LjT37M22	1	x3	seed	DF093460
TM0634	SSR	3	10.1	CM0634	LjT13G15	3	x3	seed	DF093460
TM0365	SSR	3	10.5		LjT46L11	3	x5	seed	AP009669
TM0436	SSR	3	10.5		LjT13N17	3	x5	seed	AP009825(a),

									AP009826(b)
TM0984	SSR	3	11.7		LjT42M03	1	x3	seed	AP010142
		3		CM0080	LjT58P12	1	x3	walking	DF093243
TM0080	SSR	3	12.5	CM0080	LjT14G02	3	x5	seed	DF093243
TM0513	SSR	3	12.5	CM0080	LjT30L04	1	x5	seed	DF093243
BM1753	SSR	3	12.9	CM0574	LjB24P16	3	x5	walking	DF093449
TM0574	SSR	3	12.9	CM0574	LjT12B12	1	x3	seed	DF093449
		3		CM0590	LjB25M18	3	x5	walking	DF093452
		3		CM0590	LjT05N10	3	x5	walking	DF093452
		3		CM0590	LjT39P06	3	x5	walking	DF093452
		3		CM0590	LjB15I03	3	x5	walking	DF093452
TM1283	SSR	3	12.9	CM0590	LjT43F24	1	x3	seed	DF093452
		3		CM0590	LjT47I22	1	x3	walking	DF093452
TM0590	SSR	3	13.3	CM0590	LjT09I23	3	x5	seed	DF093452
		3		CM0590	LjT02A12	1	x3	walking	DF093452
TM0859	SSR	3	13.3		LjT01D08	1	x3	seed	AP010114
		3		CM0423	LjT08P05	1	x3	seed	DF093418
TM1270	SSR	3	13.3	CM0423	LjT26F06	3	x5	seed	DF093418
		3		CM0423	LjT14H06	1	x3	walking	DF093418
		3		CM0423	LjT17F04	3	x5	seed	DF093418
TM1185	SSR	3	13.3	CM0241	LjT30D02	1	x3	walking	DF093343
		3		CM0241	LjB06P24	3	x5	seed	DF093343
BM1204	SSR	3	13.3	CM0241	LjB68K10	1	x3	seed	DF093343
		3		CM0241	LjT08O21	3	x5	seed	DF093343
BM0531	SSR	3	13.8	CM0241	LjB15I15	3	x5	seed	DF093343

TM0450	SSR	3	15.3		LjT26B16	1	x3	seed	AP009983
TM0996	SSR	3	21.1	CM0996	LjT45D11	1	x3	walking	DF093503
		3		CM0996	LjT25F10	3	x5	walking	DF093503
		3		CM0279	LjT10L05	1	x3	walking	DF093361
TM0279	SSR	3	24.0	CM0279	LjT26P21	3	x5	seed	DF093361
TM0403	SSR	3	24.0	CM0279	LjT17N21	3	x5	seed	DF093361
		3		CM0279	LjT13G10	1	x3	seed	DF093361
BM1543	SSR	3	24.8		LjB23H05	1	x5	seed	AP009946
		3		CM0190	LjT39K15	1	x3	walking	DF093317
TM0190	SSR	3	25.8	CM0190	LjT14C19	3	x5	seed	DF093317
		3		CM0111	LjB70H17	1	x3	walking	DF093263
TM0111	SSR	3	26.8	CM0111	LjT40O02	3	x5	seed	DF093263
		3		CM0111	LjB05K10	1	x3	walking	DF093263
TM0538	SSR	3	27.2	CM0111	LjT04D19	1	x3	seed	DF093263
TM0035	SSR	3	28.8		LjT10E18	3	x5	seed	AP009649
TM0070	SSR	3	28.8	CM0070	LjT11L19	3	x5	seed	DF093235
TM0369	SSR	3	29.2	CM0070	LjT30L06	3	x5	seed	DF093235
TM0426	SSR	3	29.2		LjT42K05	1	x3	seed	AP009972
TM1970	SSR	3	30.0		LjT23E22	2	x5	seed	AP009887
TM0196	dCAPS	3	30.8	CM0196	LjT45P14	3	x5	seed	DF093322
TM0198	dCAPS	3	31.2	CM0196	LjT43M15	3	x5	seed	DF093322
		3		CM0196	LjT62K10	1	x3	walking	DF093322
		3		CM0155	LjT19K09	1	x3	walking	DF093295
TM0155	SSR	3	31.2	CM0155	LjT41A07	3	x5	seed	DF093295
		3		CM0116	LjT33K22	1	x3	walking	DF093268

TM0116	dCAPS	3	31.6	CM0116	LjT46B01	3	x5	seed	DF093268
		3		CM0116	LjB06D13	1	x3	walking	DF093268
TM1465	SSR	3	31.6		LjT35O23	1	x3	seed	AP010198
TM1089	SSR	3	31.6		LjT47G05	3	x5	seed	AP009837(a), AP009838(b)
TM0388	SSR	3	32.0		LjT14J20	3	x5	seed	AP009823(a), AP009824(b)
TM1587	SSR	3	32.0		LjT18H18	1	x3	seed	AP010228
TM1548	SSR	3	32.0		LjT24D06	1	x3	seed	AP010220
TM1907	SSR	3	32.0		LjT21L04	3	x5	seed	AP009752
		3		CM1220	LjB26D22	3	x5	seed	DF093510
TM1220	SSR	3	32.0	CM1220	LjT25N08	1	x3	seed	DF093510
TM1463	SSR	3	32.0		LjT04G21	1	x3	seed	AP010197
TM0022	SSR	3	32.0		LjT11G09	3	x5	seed	AP009648
TM0159	SSR	3	32.8		LjT09L18	3	x5	seed	AP009656
TM0209	dCAPS	3	32.8		LjT15N01	3	x5	seed	AP009659
TM0782	SSR	3	32.8		LjT09M07	1	x3	seed	AP010084
TM0619	SSR	3	32.8		LjT03D10	1	x3	seed	AP010025
BM1720	SSR	3	33.0		LjB09K03	3	x5	seed	AP009632
TM0978	SSR	3	33.2		LjT46J05	1	x3	seed	AP010141
TM0568	SSR	3	33.2		LjT33P07	3	x5	seed	AP009829(a), AP009830(b)
TM0602	SSR	3	33.2	CM0602	LjT31D07	3	x5	seed	DF093457
TM0673	SSR	3	33.2	CM0602	LjT11E06	3	x5	seed	DF093457
		3		CM0602	LjB67K08	1	x3	walking	DF093457
TM0110	SSR	3	33.2	CM0110	LjT40L13	3	x5	seed	DF093262

		3		CM0110	LjT23I13	2	x3	walking	DF093262
TM1675	SSR	3	33.2	CM0110	LjT38P03	1	x3	seed	DF093262
TM1676	SSR	3	33.2	CM0110	LjT06K13	1	x3	seed	DF093262
TM0585	dCAPS	3	33.6		LjT40O07	3	x5	seed	AP009678
BM1682	SSR	3	33.6	CM0005	LjB16H07	1	x3	walking	DF093180
		3		CM0005	LjT02H21	1	x3	walking	DF093180
TM0672	SSR	3	33.6	CM0005	LjT33A07	3	x5	seed	DF093180
TM0005	SSR	3	34.0	CM0005	LjT15H09	3	x5	seed	DF093180
BM1669	SSR	3	34.0	CM0005	LjB21P22	3	x5	seed	DF093180
		3		CM0005	LjT47I17	1	x5	seed	DF093180
		3		CM0690	LjT44C14	1	x3	walking	DF093469
TM0690	SSR	3	34.0	CM0690	LjT11M02	3	x5	seed	DF093469
		3		CM0690	LjT11N13	1	x3	walking	DF093469
TM0907	SSR	3	34.0		LjT14G01	1	x3	seed	AP010127
TM1367	SSR	3	34.0		LjT48P15	3	x5	seed	AP009688
TM0707	SSR	3	36.0		LjT02C24	1	x3	seed	AP010056
		3		CM0047	LjB69N03	1	x5	walking	DF093216
TM0083	SSR	3	36.8	CM0047	LjT06J16	3	x5	seed	DF093216
TM0047	dCAPS	3	36.8	CM0047	LjT01P23	3	x5	seed	DF093216
		3		CM0047	LjT43K04	1	x3	walking	DF093216
TM0129	SSR	3	37.6	CM0129	LjT34A24	3	x5	seed	DF093280
		3		CM0129	LjT17L01	1	x3	walking	DF093280
TM0604	SSR	3	37.6	CM0129	LjT38D05	1	x3	seed	DF093280
TM1658	dCAPS	3	38.4	CM0292	LjT11L01	3	x5	seed	DF093368
		3		CM0292	LjT138B03	3	x5	walking	DF093368

		3		CM0292	LjB16L08	1	x5	walking	DF093368
TM0293	dCAPS	3	39.2	CM0292	LjT07E09	3	x5	seed	DF093368
TM0292	dCAPS	3	39.2	CM0292	LjT03N08	3	x5	seed	DF093368
TM1250	SSR	3	39.2		LjT58I15	1	x3	seed	AP010173
TM0452	SSR	3	40.0	CM0452	LjT37D12	1	x3	seed	DF093425
		3		CM0452	LjT03B09	1	x3	seed	DF093425
TM1822	SSR	3	40.8		LjT34E16	3	x5	seed	AP009717
		3		CM0142	LjB140N13	1	x3	walking	DF093288
TM0142	SSR	3	40.8	CM0142	LjT48D11	3	x5	seed	DF093288
		3		CM0142	LjT05E13	1	x3	walking	DF093288
		3		CM0226	LjT43K13	1	x3	seed	DF093335
TM0226	SSR	3	41.6	CM0226	LjT36O13	3	x5	seed	DF093335
		3		CM0226	LjT32O12	3	x5	walking	DF093335
TM0820	SSR	3	42.0	CM0726	LjT46K03	1	x3	seed	DF093475
TM0726	SSR	3	42.0	CM0726	LjT33I01	1	x3	seed	DF093475
		3		CM0246	LjT48E11	1	x3	walking	DF093347
TM0246	SSR	3	42.0	CM0246	LjT34I09	3	x5	seed	DF093347
TM0213	SSR	3	44.4	CM0213	LjT36M08	3	x5	seed	DF093329
		3		CM0213	LjT07L21	1	x3	seed	DF093329
TM1468	SSR	3	47.8	CM1468	LjT48C20	1	x3	seed	DF093517
TM1648	SSR	3	48.2	CM1468	LjT02E20	1	x3	seed	DF093517
		3		CM0406	LjB10A22	1	x3	walking	DF093414
TM0406	SSR	3	49.4	CM0406	LjT24C17	1	x3	seed	DF093414
		3		CM0208	LjT11A16	1	x3	seed	DF093326
TM0208	SSR	3	52.7	CM0208	LjT47I16	3	x5	seed	DF093326

		3		CM0208	LjT06I06	1	x3	seed	DF093326
TM0416	SSR	3	53.9		LjT15F18	1	x3	seed	AP009970
TM0724	SSR	3	54.7	CM0724	LjT02G14	1	x3	seed	DF093474
		3		CM0724	LjB24E23	1	x3	walking	DF093474
		3		CM0115	LjB03J23	1	x3	walking	DF093267
TM0115	SSR	3	54.7	CM0115	LjT38E13	3	x5	seed	DF093267
		3		CM0049	LjB22J21	1	x3	walking	DF093218
TM0049	SSR	3	55.1	CM0049	LjT17K09	3	x5	seed	DF093218
		3		CM0355	LjT42E17	3	x5	walking	DF093398
		3		CM0355	LjT15F02	1	x3	seed	DF093398
BM1881	SSR	3	56.2	CM0355	LjB19K14	3	x5	seed	DF093398
TM1570	SSR	3	56.7	CM1570	LjT05I24	1	x3	seed	DF093520
		3		CM1570	LjT22C05	3	x5	seed	DF093520
TM1871	SSR	3	57.5		LjT36L08	3	x5	seed	AP009741
		3		CM0711	LjT56J20	1	x3	walking	DF093473
TM0948	SSR	3	58.3	CM0711	LjT02C15	3	x5	seed	DF093473
TM0711	SSR	3	59.1	CM0711	LjT42D01	1	x3	seed	DF093473
		3		CM0160	LjB25B09	3	x5	walking	DF093297
		3		CM0160	LjB05A24	3	x5	walking	DF093297
		3		CM0160	LjB13M20	3	x5	walking	DF093297
		3		CM0160	LjT29I08	3	x5	walking	DF093297
TM0702	SSR	3	59.9	CM0160	LjT14C14	1	x3	seed	DF093297
		3		CM0160	LjT11B06	1	x3	walking	DF093297
TM0160	SSR	3	60.7	CM0160	LjT12A10	3	x5	seed	DF093297
TM0468	SSR	3	63.6	CM0468	LjT38N14	1	x3	seed	DF093431

TM1420	SSR	3	64.0	CM0468	LjT39M15	1	x3	seed	DF093431
TM1899	SSR	3	64.0		LjT47O18	3	x5	seed	AP009750
TM0203	SSR	3	64.8	CM0152	LjT45C16	3	x5	seed	DF093293
		3		CM0152	LjB03I06	1	x3	walking	DF093293
TM0152	dCAPS	3	65.2	CM0152	LjT38N11	3	x5	seed	DF093293
		3		CM0152	LjT14A24	1	x3	seed	DF093293
		3		CM0243	LjT23L17	1	x3	walking	DF093344
TM0243	SSR	3	65.6	CM0243	LjT02A16	3	x5	seed	DF093344
		3		CM0243	LjT21A07	3	x5	seed	DF093344
TM0164	SSR	3	66.4	CM0164	LjT04B20	1	x5	seed	DF093300
		3		CM0164	LjT48I02	1	x3	seed	DF093300
TM1144	SSR	3	67.6	CM1144	LjT18I21	3	x5	seed	DF093508
		3		CM1144	LjT22O15	2	x5	seed	DF093508
TM0701	SSR	3	67.6	CM0396	LjT04F17	3	x5	seed	DF093410
		3		CM0396	LjT10P11	1	x5	seed	DF093410
TM1812	SSR	3	67.6	CM0396	LjT31C02	3	x5	seed	DF093410
TM1402	SSR	3	67.6	CM0396	LjT15E16	1	x3	walking	DF093410
		3		CM0396	LjT39B20	1	x3	seed	DF093410
		3		CM0396	LjT06M13	1	x3	walking	DF093410
TM1002	SSR	3	68.0	CM0396	LjT04O19	3	x5	seed	DF093410
TM0649	SSR	3	69.2		LjT44N20	1	x3	seed	AP010039
TM0616	SSR	3	70.4		LjT05P05	1	x3	seed	AP010024
TM0730	SSR	3	70.4		LjT33O20	1	x3	seed	AP010066
TM0786	SSR	3	70.4		LjT39G24	1	x3	seed	AP010085
TM0136	dCAPS	3	70.9	CM0136	LjT21I12	3	x5	seed	DF093284

		3		CM0136	LjT09B19	2	x5	walking	DF093284
TM1053	SSR	3	72.4	CM0792	LjT04H14	1	x3	seed	DF093482
TM1424	SSR	3	72.6	CM0792	LjT42K10	1	x3	walking	DF093482
		3		CM0792	LjT23O15	1	x3	walking	DF093482
TM0506	SSR	3	72.8		LjT37F23	1	x3	seed	AP009996
TM1768	SSR	3	74.0		LjT23H01	3	x5	seed	AP009710
TM1222	SSR	3	74.0		LjT29G18	1	x3	seed	AP010168
		3		CM0091	LjT42G23	3	x5	walking	DF093249
TM0091	SSR	3	74.8	CM0091	LjT07I01	3	x5	seed	DF093249
		3		CM0091	LjT27C23	3	x5	walking	DF093249
		3		CM0091	LjT20I08	1	x3	walking	DF093249
TM0217	SSR	3	74.8	CM0091	LjT09C16	3	x5	seed	DF093249
TM0527	SSR	3	75.6	CM0091	LjT03B23	1	x3	seed	DF093249
		3		CM0216	LjT44D07	1	x3	seed	DF093331
TM0268	SSR	3	75.6	CM0216	LjT34K09	3	x5	seed	DF093331
TM0258	SSR	3	75.6	CM0216	LjT09E01	3	x5	seed	DF093331
		3		CM0216	LjT18B05	3	x5	seed	DF093331
TM0216	SSR	3	75.6	CM0216	LjT25N16	3	x5	seed	DF093331
		3		CM0216	LjT15M04	1	x3	walking	DF093331
		3		CM0216	LjT35B05	1	x3	walking	DF093331
TM0112	dCAPS	3	77.2	CM0112	LjT46K10	3	x5	seed	DF093264
		3		CM0112	LjT46E05	1	x3	walking	DF093264
TM0135	SSR	3	78.4	CM0135	LjT20B10	3	x5	seed	DF093283
		3		CM0135	LjB09C10	1	x3	walking	DF093283
		3		CM0460	LjT04C21	3	x5	walking	DF093429

		3		CM0460	LjT07O23	1	x3	seed	DF093429
TM0460	SSR	3	80.0	CM0460	LjT12O20	1	x3	seed	DF093429
TM0407	SSR	3	81.6		LjT33M17	1	x3	seed	AP009965
TM1820	SSR	3	81.6	CM0127	LjT01J15	3	x5	walking	DF093278
TM1419	SSR	3	81.6	CM0127	LjT43H12	3	x3	seed	DF093278
TM1821	SSR	3	82.0	CM0127	LjT05L20	3	x5	walking	DF093278
TM1917	SSR	3	82.0	CM0127	LjT38M18	3	x5	walking	DF093278
		3		CM0127	LjT30G11	3	x3	seed	DF093278
TM0127	SSR	3	82.4	CM0127	LjT44D21	3	x5	seed	DF093278
		3		CM0127	LjB18N14	1	x3	walking	DF093278
TM1819	SSR	3	82.8	CM0127	LjT33C21	3	x5	walking	DF093278
TM1437	SSR	3	83.2		LjT40N08	1	x3	seed	AP010190
		3		CM0261	LjT22I03	1	x3	walking	DF093355
TM0261	SSR	3	83.2	CM0261	LjT23P21	3	x5	seed	DF093355
		3		CM0261	LjT62K04	1	x3	walking	DF093355
TM0797	SSR	3	84.0		LjT39D18	1	x3	seed	AP010089
TM0525	SSR	4	0.0	CM0525	LjT46D13	1	x3	seed	DF093439
TM0869	SSR	4	0.4	CM0525	LjT35A11	1	x3	walking	DF093439
TM1203	SSR	4	0.4		LjT24N17	3	x5	seed	AP009839(a), AP009840(b)
TM0529	SSR	4	0.8		LjT03F09	1	x3	seed	AP010003
TM0654	SSR	4	1.6	CM0288	LjT42B20	1	x3	seed	DF093366
TM0841	SSR	4	1.6	CM0288	LjT19L11	1	x3	seed	DF093366
		4		CM0288	LjT31P09	3	x5	walking	DF093366
TM0288	SSR	4	2.0	CM0288	LjT36E18	3	x5	seed	DF093366

TM0353	SSR	4	2.0	CM0288	LjT39G20	3	x5	seed	DF093366
		4		CM0288	LjT02O22	1	x3	walking	DF093366
		4		CM0026	LjB72C18	1	x3	walking	DF093199
TM0026	dCAPS	4	2.8	CM0026	LjT09I17	3	x5	seed	DF093199
		4		CM0026	LjB70G09	1	x3	walking	DF093199
TM1536	SSR	4	3.2	CM1334	LjT31E01	3	x5	seed	DF093513
TM1334	SSR	4	4.0	CM1334	LjT20N14	3	x5	seed	DF093513
BM1232	SSR	4	4.0	CM0256	LjB07M17	1	x3	walking	DF093353
		4		CM0256	LjT14P17	1	x3	seed	DF093353
TM0256	SSR	4	5.6	CM0256	LjT07D18	3	x5	seed	DF093353
TM1170	SSR	4	6.8	CM0007	LjT11M06	1	x3	seed	DF093182
TM1717	SSR	4	6.8	CM0007	LjT09C19	3	x5	seed	DF093182
TM0265	SSR	4	7.6	CM0007	LjT09E08	3	x5	seed	DF093182
		4		CM0007	LjB01K01	1	x3	walking	DF093182
TM0719	SSR	4	8.0	CM0007	LjT20D24	1	x3	seed	DF093182
TM0007	dCAPS	4	8.4	CM0007	LjT10J15	3	x5	seed	DF093182
		4		CM0007	LjB69I05	1	x3	walking	DF093182
TM0530	SSR	4	8.4	CM0337	LjT30I15	1	x3	seed	DF093392
TM0337	SSR	4	8.4	CM0337	LjT05L17	3	x5	seed	DF093392
		4		CM0337	LjT119A16	3	x5	walking	DF093392
		4		CM0337	LjB23J17	3	x5	walking	DF093392
		4		CM0337	LjT41G07	3	x5	walking	DF093392
TM1779	SSR	4	8.4	CM0337	LjT16M14	3	x5	seed	DF093392
TM1600	SSR	4	8.4	CM0337	LjT31F09	1	x3	seed	DF093392
TM0708	SSR	4	8.8	CM0182	LjT27D17	1	x3	seed	DF093316

		4		CM0182	LjT20B08	3	x5	walking	DF093316
TM0182	SSR	4	8.8	CM0182	LjT16B11	3	x5	seed	DF093316
		4		CM0182	LjB10F10	3	x5	walking	DF093316
TM0100	SSR	4	8.8	CM0100	LjT36C13	3	x5	seed	DF093255
		4		CM0100	LjT46I20	1	x3	seed	DF093255
		4		CM0100	LjT08P14	1	x3	walking	DF093255
		4		CM0100	LjT13B11	1	x3	seed	DF093255
TM0832	SSR	4	9.6	CM0832	LjT47B07	1	x3	seed	DF093490
TM1074	SSR	4	9.6	CM0832	LjT44J22	2	x3	seed	DF093490
TM1713	SSR	4	9.6	CM1616	LjT16G09	3	x5	seed	DF093524
TM1616	SSR	4	9.6	CM1616	LjT03A02	3	x5	seed	DF093524
TM0692	SSR	4	11.6	CM0692	LjT04D06	1	x3	seed	DF093470
		4		CM0692	LjT46B17	3	x5	walking	DF093470
		4		CM0692	LjB21M16	1	x3	walking	DF093470
		4		CM0692	LjT30M19	1	x3	seed	DF093470
TM1708	SSR	4	12.4		LjT233I03	2	x3	seed	AP009874
TM0432	SSR	4	12.4	CM0432	LjT09M24	1	x3	seed	DF093420
		4		CM0432	LjT46B12	1	x3	walking	DF093420
		4		CM0432	LjT30M02	1	x3	seed	DF093420
		4		CM0079	LjT12E07	1	x3	walking	DF093242
TM0079	dCAPS	4	13.6	CM0079	LjT13P22	3	x5	seed	DF093242
		4		CM0079	LjT28E12	1	x3	walking	DF093242
BM1279	SSR	4	14.0	CM0227	LjB21D13	1	x3	walking	DF093336
		4		CM0227	LjT46M07	1	x3	walking	DF093336
TM0227	SSR	4	14.0	CM0227	LjT01O24	3	x5	seed	DF093336

TM1846	SSR	4	14.4	CM0227	LjT02L05	3	x5	seed	DF093336
		4		CM0227	LjT34M17	3	x5	walking	DF093336
		4		CM0227	LjB08D05	3	x5	walking	DF093336
		4		CM0227	LjT04J20	1	x3	seed	DF093336
		4		CM0229	LjB13B18	3	x3	walking	DF093337
TM0229	SSR	4	14.8	CM0229	LjT28E04	3	x5	seed	DF093337
BM1979	SSR	4	14.8	CM0229	LjB07N07	3	x5	walking	DF093337
		4		CM0229	LjT10H08	3	x5	walking	DF093337
TM1309	SSR	4	14.8	CM0229	LjT05H14	1	x3	seed	DF093337
		4		CM0229	LjT45B04	3	x5	walking	DF093337
TM0075	SSR	4	14.8	CM0075	LjT16A13	3	x5	seed	DF093239
		4		CM0075	LjB18N06	1	x3	walking	DF093239
TM0347	SSR	4	15.6	CM0128	LjT10F06	3	x5	seed	DF093279
TM0330	SSR	4	16.0	CM0128	LjT14C18	3	x5	seed	DF093279
TM0128	SSR	4	16.0	CM0128	LjT28L24	3	x5	seed	DF093279
		4		CM0128	LjT61N09	1	x3	walking	DF093279
TM0157	dCAPS	4	16.0	CM0128	LjT21D16	3	x5	seed	DF093279
		4		CM0536	LjT30P13	1	x3	seed	DF093441
TM1870	SSR	4	16.6	CM0536	LjT09M02	3	x5	seed	DF093441
TM1335	SSR	4	16.8		LjT45J24	3	x5	seed	AP009687
TM0194	SSR	4	19.3	CM0194	LjT11O06	3	x5	seed	DF093320
		4		CM0194	LjB23E08	1	x3	walking	DF093320
		4		CM0659	LjT04J13	1	x3	seed	DF093463
TM1427	SSR	4	19.3	CM0659	LjT05E03	1	x3	walking	DF093463
		4		CM0659	LjT06G24	1	x3	walking	DF093463

		4		CM0165	LjT14P18	1	x3	walking	DF093301
		4		CM0165	LjT12O03	1	x3	walking	DF093301
TM0165	dCAPS	4	20.1	CM0165	LjT05F06	3	x5	seed	DF093301
		4		CM0165	LjT39H21	1	x3	walking	DF093301
TM0283	SSR	4	20.5	CM0283	LjT18E13	3	x5	seed	DF093364
TM1581	SSR	4	20.5	CM0283	LjT21C10	1	x3	walking	DF093364
TM0212	SSR	4	20.9	CM0131	LjT20N03	3	x5	seed	DF093281
		4		CM0131	LjT09M05	1	x3	walking	DF093281
		4		CM0131	LjB12M18	1	x3	walking	DF093281
TM0131	SSR	4	21.3	CM0131	LjT21G09	3	x5	seed	DF093281
		4		CM0119	LjT37I04	1	x3	walking	DF093270
TM0119	SSR	4	21.3	CM0119	LjT34D11	3	x5	seed	DF093270
TM0197	SSR	4	21.3	CM0119	LjT45A24	3	x5	seed	DF093270
		4		CM0119	LjB05I10	1	x3	walking	DF093270
		4		CM0247	LjT18B07	1	x3	walking	DF093348
TM0247	SSR	4	24.2	CM0247	LjT01N13	3	x5	seed	DF093348
TM0296	SSR	4	24.2		LjT08E06	3	x5	seed	AP009811(a), AP009812(b)
TM0570	SSR	4	24.2		LjT10E08	3	x5	seed	AP009677
TM0831	SSR	4	24.2	CM0831	LjT09E17	1	x3	seed	DF093489
		4		CM0831	LjT44O17	1	x3	seed	DF093489
TM0677	SSR	4	24.2		LjT21A22	1	x3	seed	AP010045
TM1251	dCAPS	4	24.4	CM0161	LjT06J02	1	x3	walking	DF093298
		4		CM0161	LjT22D23	3	x5	seed	DF093298
TM0161	dCAPS	4	24.4	CM0161	LjT35D23	1	x5	seed	DF093298

		4		CM0281	LjB10A06	1	x3	walking	DF093362
TM0281	SSR	4	24.6	CM0281	LjT22I23	3	x5	seed	DF093362
		4		CM0281	LjT08A19	3	x3	walking	DF093362
TM1642	SSR	4	24.6		LjT04K15	1	x3	seed	AP010238
TM0851	SSR	4	24.6		LjT38A20	1	x3	seed	AP010110
BM1376	SSR	4	25.0		LjB20H09	3	x5	seed	AP009626
		4		CM0126	LjB09G03	1	x3	walking	DF093277
TM0126	SSR	4	25.0	CM0126	LjT31E04	3	x5	seed	DF093277
		4		CM0126	LjB15F18	1	x3	walking	DF093277
		4		CM0126	LjB20H13	3	x5	walking	DF093277
TM1693	SSR	4	25.4	CM0126	LjT05K12	3	x5	walking	DF093277
TM1734	SSR	4	25.4	CM0126	LjT11L10	3	x5	walking	DF093277
		4		CM0126	LjT34M05	2	x5	walking	DF093277
		4		CM0126	LjB25P16	3	x5	walking	DF093277
		4		CM0126	LjT07P19	3	x3	seed	DF093277
		4		CM0126	LjT17O03	3	x5	walking	DF093277
		4		CM0126	LjB372N22	3	x5	walking	DF093277
		4		CM0126	LjT15P01	3	x5	walking	DF093277
		4		CM0126	LjB09F11	3	x5	walking	DF093277
		4		CM0126	LjT41L19	3	x5	walking	DF093277
BM1082	dCAPS	4	25.8	CM0173	LjB06M21	1	x3	walking	DF093307
TM0173	SSR	4	25.8	CM0173	LjT10G09	3	x5	seed	DF093307
BM1727	SSR	4	25.8	CM0173	LjB356P07	3	x5	walking	DF093307
TM0172	SSR	4	26.6	CM0172	LjT39H01	3	x5	seed	DF093306
		4		CM0172	LjT15K20	1	x3	seed	DF093306

TM1793	SSR	4	27.1		LjT30K03	3	x5	seed	AP009716
		4		CM0170	LjB23D15	1	x3	seed	DF093304
TM0170	dCAPS	4	28.2	CM0170	LjT28B04	3	x5	seed	DF093304
		4		CM0087	LjT45N13	1	x3	walking	DF093246
TM0087	SSR	4	28.6	CM0087	LjT14P20	3	x5	seed	DF093246
		4		CM0087	LjT21I10	1	x3	walking	DF093246
TM0093	SSR	4	29.0	CM0087	LjT13G01	3	x5	seed	DF093246
		4		CM0087	LjB11J20	1	x3	walking	DF093246
BM1397	SSR	4	29.0	CM0087	LjB26F10	1	x3	walking	DF093246
		4		CM0087	LjT01H14	1	x3	walking	DF093246
TM1411	SSR	4	29.0	CM0087	LjT46M09	1	x3	seed	DF093246
BM1890	SSR	4	29.0	CM0087	LjB21L22	3	x5	seed	DF093246
TM0500	SSR	4	29.4	CM0500	LjT36O16	1	x3	seed	DF093436
		4		CM0500	LjT17K02	1	x3	walking	DF093436
BM1698	SSR	4	30.2		LjB15O07	3	x5	seed	AP009629
TM1874	SSR	4	31.3		LjT07P17	3	x5	seed	AP009743
TM0234	SSR	4	31.8	CM0234	LjT09G09	3	x5	seed	DF093340
		4		CM0234	LjT09F09	1	x3	walking	DF093340
		4		CM0003	LjT33L07	1	x3	walking	DF093178
TM0003	dCAPS	4	31.8	CM0003	LjT09A24	3	x5	seed	DF093178
TM0030	SSR	4	32.2	CM0003	LjT06A20	3	x5	seed	DF093178
		4		CM0003	LjB08A14	1	x3	walking	DF093178
		4		CM0003	LjT06K06	1	x3	seed	DF093178
		4		CM0219	LjB13L02	1	x3	walking	DF093332
TM0219	SSR	4	32.7	CM0219	LjT32M04	3	x5	seed	DF093332

		4		CM0219	LjT06F24	1	x3	walking	DF093332
		4		CM0179	LjT05M10	1	x3	walking	DF093313
TM0542	SSR	4	34.7	CM0179	LjT34O13	1	x3	seed	DF093313
TM0179	SSR	4	34.7	CM0179	LjT11D24	3	x5	seed	DF093313
		4		CM0179	LjT58D12	1	x3	walking	DF093313
		4		CM0061	LjT41D18	1	x3	seed	DF093228
TM0061	dCAPS	4	38.3	CM0061	LjT01K08	3	x5	seed	DF093228
		4		CM0061	LjT13J15	1	x3	walking	DF093228
TM0421	SSR	4	39.2	CM0421	LjT12G06	1	x3	seed	DF093417
		4		CM0421	LjT44F21	3	x5	walking	DF093417
		4		CM0244	LjT60L22	1	x3	walking	DF093345
TM0244	SSR	4	39.2	CM0244	LjT37A01	3	x5	seed	DF093345
TM0664	SSR	4	40.0	CM0244	LjT37C07	1	x3	seed	DF093345
		4		CM0244	LjB24G06	2	x3	walking	DF093345
TM0303	SSR	4	40.0	CM0244	LjT05D12	3	x5	seed	DF093345
		4		CM0244	LjB23A24	1	x5	walking	DF093345
TM1039	SSR	4	40.4	CM0297	LjT09A16	1	x3	seed	DF093370
		4		CM0297	LjT56A04	1	x3	walking	DF093370
TM0297	dCAPS	4	40.8	CM0297	LjT23O19	3	x5	seed	DF093370
		4		CM0297	LjT45N19	1	x3	seed	DF093370
		4		CM0297	LjT36N01	1	x3	seed	DF093370
		4		CM0297	LjT39I23	1	x3	walking	DF093370
		4		CM0006	LjT07I09	1	x3	walking	DF093181
TM0006	dCAPS	4	41.6	CM0006	LjT17P02	3	x5	seed	DF093181
		4		CM0006	LjB06G16	1	x3	walking	DF093181

TM0264	dCAPS	4	41.6	CM0006	LjT04O07	3	x5	seed	DF093181
		4		CM0006	LjT31N02	3	x5	seed	DF093181
		4		CM0006	LjT19G04	1	x3	walking	DF093181
		4		CM0006	LjB09G07	3	x5	seed	DF093181
		4		CM0006	LjT25B05	1	x3	walking	DF093181
TM0343	SSR	4	41.6	CM0006	LjT27P02	3	x5	seed	DF093181
TM1509	SSR	4	44.1	CM0333	LjT11C16	1	x3	walking	DF093390
TM0333	SSR	4	44.1	CM0333	LjT36O22	3	x5	seed	DF093390
		4		CM0429	LjT17H04	1	x3	walking	DF093419
TM0429	SSR	4	44.5	CM0429	LjT22K06	3	x5	seed	DF093419
TM0238	SSR	4	47.0		LjT32J05	3	x5	seed	AP009663
TM1401	SSR	4	47.8	CM0739	LjT45O15	1	x3	walking	DF093477
		4		CM0739	LjT24B12	1	x3	walking	DF093477
TM0387	SSR	4	47.8	CM0387	LjT27F14	3	x5	seed	DF093408
TM1865	SSR	4	48.2	CM0387	LjT31N09	3	x5	seed	DF093408
TM1908	SSR	4	48.2	CM0387	LjT30P17	3	x5	seed	DF093408
TM0555	SSR	4	49.0		LjT16L01	1	x3	seed	AP010009
TM0044	SSR	4	50.2	CM0044	LjT04F23	3	x5	seed	DF093213
		4		CM0044	LjT40O09	1	x3	walking	DF093213
TM0108	SSR	4	51.0	CM0044	LjT42D17	3	x5	seed	DF093213
TM0399	SSR	4	51.8	CM0399	LjT35C17	3	x5	seed	DF093412
		4		CM0399	LjT41A05	1	x3	seed	DF093412
		4		CM0046	LjT15D03	1	x3	seed	DF093215
		4		CM0046	LjT33J12	1	x3	seed	DF093215
TM0162	SSR	4	53.0	CM0046	LjT44L05	3	x5	seed	DF093215

TM0404	SSR	4	53.8	CM0046	LjT41M05	3	x5	seed	DF093215
TM0046	SSR	4	53.8	CM0046	LjT07K08	3	x5	seed	DF093215
TM1884	SSR	4	55.4	CM0680	LjT05B12	3	x5	seed	DF093467
TM1747	SSR	4	55.8	CM0680	LjT20M06	3	x5	seed	DF093467
		4		CM0680	LjT25M06	3	x5	seed	DF093467
TM0597	SSR	4	55.8		LjT06I07	1	x3	seed	AP010020
TM0307	SSR	4	56.2	CM0307	LjT43O18	3	x5	seed	DF093375
		4		CM0307	LjT32H01	1	x3	walking	DF093375
TM1415	SSR	4	57.0		LjT13D08	1	x3	seed	AP010188
TM0844	SSR	4	57.8		LjT06B21	1	x5	seed	AP010106
TM1169	SSR	4	58.6		LjT12N18	1	x3	seed	AP010163
		4		CM0175	LjB21K13	1	x3	walking	DF093309
TM0175	SSR	4	59.0	CM0175	LjT10G08	3	x5	seed	DF093309
		4		CM0175	LjB09H01	1	x3	walking	DF093309
TM0266	SSR	4	59.4	CM0175	LjT39E03	3	x5	seed	DF093309
		4		CM0175	LjT56P09	1	x3	walking	DF093309
		4		CM0558	LjT33E19	1	x3	walking	DF093446
TM0558	SSR	4	59.9	CM0558	LjT04E19	3	x5	seed	DF093446
		4		CM0558	LjT31L19	1	x3	walking	DF093446
BM1174	SSR	4	61.9	CM0501	LjB10P09	1	x5	walking	DF093437
		4		CM0501	LjT38C17	1	x3	seed	DF093437
		4		CM0025	LjT39J02	1	x3	walking	DF093198
TM0025	dCAPS	4	64.4	CM0025	LjT08D16	3	x5	seed	DF093198
		4		CM0025	LjT17B18	1	x3	walking	DF093198
		4		CM0004	LjT45G06	1	x3	walking	DF093179

		4		CM0004	LjT11H18	1	x3	walking	DF093179
TM0004	dCAPS	4	65.6	CM0004	LjT15D01	3	x5	seed	DF093179
		4		CM0004	LjT25C04	1	x3	walking	DF093179
		4		CM0617	LjT35B18	1	x3	seed	DF093459
		4		CM0617	LjT27N01	1	x3	walking	DF093459
TM1545	SSR	4	67.2	CM0617	LjT10K03	1	x3	seed	DF093459
TM0617	SSR	4	67.6	CM0617	LjT20B07	1	x3	seed	DF093459
		4		CM0617	LjT41N05	1	x3	walking	DF093459
		4		CM0042	LjB10K11	1	x3	walking	DF093212
TM0214	SSR	4	67.6	CM0042	LjT03K19	3	x5	seed	DF093212
		4		CM0042	LjT46F18	1	x3	walking	DF093212
		4		CM0042	LjT15L12	1	x3	walking	DF093212
TM0073	SSR	4	67.6	CM0042	LjT16G15	3	x5	seed	DF093212
		4		CM0042	LjT29M06	1	x3	walking	DF093212
TM0097	SSR	4	67.6	CM0042	LjT15N19	3	x5	seed	DF093212
		4		CM0042	LjB20D23	3	x5	walking	DF093212
TM0069	SSR	4	68.8	CM0042	LjT13O11	3	x5	seed	DF093212
		4		CM0042	LjB15M24	3	x5	walking	DF093212
TM1769	SSR	4	68.8	CM0042	LjT08E22	3	x5	walking	DF093212
		4		CM0042	LjT09K24	1	x3	seed	DF093212
TM1749	SSR	4	68.8	CM0042	LjT06K07	3	x5	walking	DF093212
		4		CM0042	LjT17C24	2	x3	walking	DF093212
TM2002	SSR	4	68.8	CM0042	LjT63K02	3	x5	walking	DF093212
TM0042	dCAPS	4	69.2	CM0042	LjT10L16	3	x5	seed	DF093212
		4		CM0042	LjT49M15	3	x5	walking	DF093212

		4		CM0042	LjT16A19	1	x3	seed	DF093212
TM0146	SSR	5	0.0	CM0089	LjT34P02	3	x5	seed	DF093248
		5		CM0089	LjT44D16	1	x3	walking	DF093248
		5		CM0089	LjT32O11	1	x3	seed	DF093248
		5		CM0089	LjB74C16	1	x3	seed	DF093248
		5		CM0089	LjT44A18	1	x3	walking	DF093248
TM0089	dCAPS	5	0.4	CM0089	LjT14E05	3	x5	seed	DF093248
		5		CM0089	LjT36K21	1	x3	walking	DF093248
TM1392	SSR	5	0.4		LjT42D02	1	x3	seed	AP010184
		5		CM0077	LjT12P24	1	x3	walking	DF093240
TM0822	SSR	5	0.8	CM0077	LjT41A16	1	x3	seed	DF093240
		5		CM0077	LjT30J18	1	x3	walking	DF093240
		5		CM0077	LjT08B03	3	x3	walking	DF093240
TM0291	SSR	5	0.8	CM0077	LjT36H12	3	x5	seed	DF093240
TM0077	SSR	5	0.8	CM0077	LjT18O12	3	x5	seed	DF093240
		5		CM0335	LjB18O02	3	x3	walking	DF093391
TM0335	dCAPS	5	1.2	CM0335	LjT48J22	3	x5	seed	DF093391
		5		CM0335	LjT31F22	1	x3	seed	DF093391
		5		CM0335	LjT61A03	1	x3	walking	DF093391
TM0852	SSR	5	2.8	CM0852	LjT41B10	1	x3	seed	DF093492
		5		CM0852	LjT30K21	3	x5	walking	DF093492
TM0321	dCAPS	5	3.6	CM0096	LjT04J15	3	x5	seed	DF093252
		5		CM0096	LjT56L17	1	x3	walking	DF093252
TM0096	SSR	5	3.6	CM0096	LjT08M07	3	x5	seed	DF093252
		5		CM0096	LjT37I17	1	x3	walking	DF093252

		5		CM0096	LjB15L19	1	x3	walking	DF093252
TM1423	SSR	5	3.6	CM0096	LjT02H08	1	x3	seed	DF093252
		5		CM0569	LjT36J24	1	x3	walking	DF093447
TM0569	SSR	5	4.0	CM0569	LjT34K16	3	x5	seed	DF093447
TM0362	SSR	5	4.4	CM0019	LjT02J09	1	x5	seed	DF093193
TM0019	dCAPS	5	4.8	CM0019	LjT05B20	3	x5	seed	DF093193
TM0034	SSR	5	4.8	CM0034	LjT02M03	3	x5	seed	DF093206
		5		CM0034	LjT33A19	1	x3	walking	DF093206
TM0090	SSR	5	5.2		LjT01J10	3	x5	seed	AP009801(a), AP009802(b)
TM0455	SSR	5	5.2	CM0040	LjT28O20	1	x3	seed	DF093210
		5		CM0040	LjT36N08	3	x5	walking	DF093210
		5		CM0040	LjT40J13	1	x3	walking	DF093210
TM0043	SSR	5	5.6	CM0040	LjT01O22	3	x5	seed	DF093210
		5		CM0040	LjT02D17	1	x3	walking	DF093210
TM0040	dCAPS	5	5.6	CM0040	LjT16I07	3	x5	seed	DF093210
BM1799	SSR	5	5.6	CM0040	LjB01H03	3	x5	walking	DF093210
BM1988	SSR	5	5.6	CM0040	LjB17J16	3	x5	walking	DF093210
		5		CM0040	LjB11C22	2	x5	walking	DF093210
		5		CM0345	LjT10B19	3	x3	walking	DF093396
TM1980	SSR	5	5.6	CM0345	LjT25H19	3	x5	walking	DF093396
		5		CM0345	LjB67C16	1	x3	walking	DF093396
		5		CM0345	LjT48I12	1	x3	walking	DF093396
		5		CM0345	LjT06A03	3	x5	walking	DF093396
		5		CM0345	LjB24B17	1	x3	walking	DF093396

		5		CM0345	LjB21J19	3	x5	walking	DF093396
BM2025	SSR	5	5.6	CM0345	LjB355E10	3	x5	walking	DF093396
TM1989	SSR	5	5.6	CM0345	LjT08J01	3	x5	walking	DF093396
		5		CM0345	LjT06D17	3	x5	walking	DF093396
TM1859	SSR	5	5.6	CM0345	LjT27F16	2	x5	walking	DF093396
		5		CM0345	LjB03C01	3	x5	walking	DF093396
BM1787	SSR	5	5.6	CM0345	LjB06H02	3	x5	walking	DF093396
		5		CM0345	LjT01M08	1	x3	seed	DF093396
		5		CM0345	LjB21B04	3	x5	walking	DF093396
TM1575	SSR	5	6.8	CM0345	LjT06P20	3	x5	seed	DF093396
		5		CM0345	LjT03E08	3	x5	walking	DF093396
TM1786	SSR	5	6.8	CM0345	LjT08F11	3	x5	walking	DF093396
TM0963	SSR	5	7.2		LjT32I14	1	x3	seed	AP010138
TM0072	SSR	5	7.6	CM0072	LjT02A14	3	x5	seed	DF093237
		5		CM0072	LjT09M22	1	x3	seed	DF093237
TM0428	SSR	5	8.0		LjT23J23	1	x3	seed	AP009974
TM0696	SSR	5	9.6		LjT08O17	1	x5	seed	AP010051
TM1077	SSR	5	11.2		LjT09C21	1	x5	seed	AP010154
TM0657	SSR	5	11.6	CM0657	LjT29A12	3	x5	seed	DF093462
		5		CM0657	LjB26K13	1	x3	walking	DF093462
TM1547	SSR	5	11.6		LjT48O19	1	x3	seed	AP010219
TM0471	SSR	5	11.6	CM0359	LjT02H19	1	x3	seed	DF093400
TM0359	SSR	5	11.6	CM0359	LjT01C14	3	x5	seed	DF093400
BM1982	SSR	5	12.0		LjB09C24	3	x5	seed	AP009795(a), AP009796(b)

TM1496	SSR	5	12.0		LjT40M15	3	x5	seed	AP009843(a), AP009844(b), AP009845(c)
TM0743	SSR	5	12.4		LjT10N02	1	x3	seed	AP010069
BM1886	SSR	5	12.4	CM1813	LjB14G21	3	x5	walking	DF093529
		5		CM1813	LjT22C22	3	x5	seed	DF093529
TM1373	SSR	5	12.4		LjT12G17	3	x5	seed	AP009690
		5		CM0911	LjT40K06	1	x3	seed	DF093498
		5		CM0911	LjT20M23	1	x3	walking	DF093498
TM0911	SSR	5	12.4	CM0911	LjT39H15	1	x3	seed	DF093498
		5		CM0571	LjT25K24	1	x3	seed	DF093448
TM0571	SSR	5	12.4	CM0571	LjT29C08	1	x3	seed	DF093448
TM0765	SSR	5	12.4	CM0571	LjT18L04	1	x3	seed	DF093448
TM0562	SSR	5	12.4		LjT42I01	1	x3	seed	AP010012
		5		CM0278	LjB25L11	1	x3	walking	DF093360
TM0278	SSR	5	12.4	CM0278	LjT01K09	3	x5	seed	DF093360
		5		CM0278	LjT20M14	1	x3	walking	DF093360
		5		CM0813	LjT45B16	2	x5	walking	DF093486
		5		CM0813	LjT11B03	3	x5	walking	DF093486
TM0813	SSR	5	12.8	CM0813	LjT33J17	1	x3	seed	DF093486
		5		CM1125	LjT16E17	3	x5	walking	DF093507
		5		CM1125	LjT48B18	3	x5	walking	DF093507
TM1125	SSR	5	13.2	CM1125	LjT08L06	3	x5	seed	DF093507
		5		CM1125	LjT43O12	3	x5	walking	DF093507
		5		CM1125	LjT114C18	3	x5	walking	DF093507
		5		CM1125	LjT28L23	2	x5	seed	DF093507

		5		CM1125	LjT13I22	1	x3	walking	DF093507
		5		CM0024	LjT15B12	3	x5	walking	DF093197
TM2004	SSR	5	13.2	CM0024	LjT33B14	3	x5	walking	DF093197
TM0024	dCAPS	5	13.2	CM0024	LjT17D01	3	x5	seed	DF093197
		5		CM0024	LjT22B04	3	x5	walking	DF093197
		5		CM0024	LjT25M10	3	x5	walking	DF093197
BM1728	SSR	5	13.6	CM0024	LjB08F01	3	x5	walking	DF093197
		5		CM0024	LjT28I17	3	x5	walking	DF093197
		5		CM0024	LjT17C17	3	x5	walking	DF093197
		5		CM1574	LjT17J11	3	x5	walking	DF093521
TM1574	SSR	5	14.4	CM1574	LjT06F10	1	x3	seed	DF093521
		5		CM1574	LjT35C10	3	x5	walking	DF093521
BM1891	SSR	5	14.8	CM1574	LjB11L10	3	x5	walking	DF093521
TM1755	SSR	5	14.8		LjT15N12	3	x5	seed	AP009703
TM1743	SSR	5	14.8		LjT35F02	3	x5	seed	AP009702
		5		CM0494	LjT22J03	1	x3	walking	DF093434
TM0494	SSR	5	14.8	CM0494	LjT21E22	1	x3	seed	DF093434
BM1460	SSR	5	14.8	CM0494	LjB11K16	3	x5	walking	DF093434
TM0151	SSR	5	15.2		LjT45G21	3	x5	seed	AP009655
TM0341	SSR	5	15.6	CM0341	LjT09O10	3	x5	seed	DF093394
		5		CM0341	LjB26D17	1	x3	walking	DF093394
		5		CM0071	LjT11G02	1	x3	seed	DF093236
		5		CM0071	LjT45J13	1	x3	walking	DF093236
TM0071	dCAPS	5	16.8	CM0071	LjT12L11	3	x5	seed	DF093236
		5		CM0086	LjT02C18	1	x3	walking	DF093245

TM0086	dCAPS	5	16.8	CM0086	LjT15O18	3	x5	seed	DF093245
TM0744	SSR	5	18.8		LjT25P23	1	x3	seed	AP010070
TM0431	SSR	5	19.2		LjT41L03	1	x3	seed	AP009976
TM1634	SSR	5	20.0		LjT09B23	1	x3	seed	AP010234
TM0280	dCAPS	5	20.4		LjT29J15	3	x5	seed	AP009809(a), AP009810(b)
TM0186	SSR	5	20.4		LjT18P14	1	x5	seed	AP009954
TM1323	SSR	5	22.8		LjT15D05	1	x3	seed	AP010183
		5		CM0062	LjT06F01	1	x3	walking	DF093229
TM0062	SSR	5	23.2	CM0062	LjT10C05	3	x5	seed	DF093229
TM0211	SSR	5	24.0	CM0211	LjT48O21	3	x5	seed	DF093328
		5		CM0211	LjT24K19	1	x3	walking	DF093328
		5		CM0299	LjB03O04	1	x3	walking	DF093371
TM0299	SSR	5	24.4	CM0299	LjT25E08	3	x5	seed	DF093371
TM0350	SSR	5	24.4	CM0299	LjT48D16	1	x5	seed	DF093371
TM1598	SSR	5	26.4	CM1598	LjT34B21	1	x3	seed	DF093522
BM1888	SSR	5	26.4	CM1598	LjB16B21	3	x5	seed	DF093522
		5		CM0048	LjT09F11	2	x3	walking	DF093217
TM0048	SSR	5	27.6	CM0048	LjT05P01	3	x5	seed	DF093217
		5		CM0048	LjB65P04	1	x3	walking	DF093217
TM0714	SSR	5	28.0	CM0048	LjT14E15	1	x3	seed	DF093217
TM0158	SSR	5	28.9	CM0158	LjT21J12	3	x5	seed	DF093296
		5		CM0158	LjB22J23	1	x3	walking	DF093296
		5		CM0239	LjB10D03	1	x3	walking	DF093342
TM0239	SSR	5	30.8	CM0239	LjT37K17	3	x5	seed	DF093342

		5		CM0239	LjT09O18	1	x3	walking	DF093342
		5		CM0239	LjB25E16	2	x3	walking	DF093342
TM0849	SSR	5	31.6	CM0239	LjT46E22	1	x5	seed	DF093342
		5		CM0239	LjB03D07	3	x5	walking	DF093342
TM0951	SSR	5	31.6	CM0239	LjT25G01	3	x5	seed	DF093342
TM0773	SSR	5	32.0	CM0239	LjT36C12	1	x3	seed	DF093342
TM0913	SSR	5	33.2		LjT38I13	1	x3	seed	AP010128
TM1493	SSR	5	33.6		LjT17N18	1	x3	seed	AP010206
TM1774	SSR	5	33.6	CM0909	LjT30I13	3	x5	walking	DF093497
TM0909	SSR	5	34.0	CM0909	LjT46H07	1	x3	seed	DF093497
		5		CM0909	LjT45M19	3	x5	seed	DF093497
TM1816	SSR	5	34.8	CM0909	LjT135A04	3	x5	walking	DF093497
BM1817	SSR	5	34.8	CM0909	LjB21K15	3	x5	walking	DF093497
		5		CM0909	LjT14F05	3	x5	walking	DF093497
		5		CM0909	LjT34P16	3	x5	walking	DF093497
		5		CM0909	LjT23O16	3	x5	seed	DF093497
		5		CM0909	LjT25M07	3	x5	walking	DF093497
TM0138	dCAPS	5	36.8		LjT43D06	1	x5	seed	AP009951
		5		CM0311	LjT47C07	1	x3	walking	DF093378
TM0311	dCAPS	5	37.6	CM0311	LjT23C14	3	x5	seed	DF093378
TM0095	SSR	5	37.6	CM0095	LjT02L13	3	x5	seed	DF093251
		5		CM0095	LjT04H13	1	x3	walking	DF093251
TM0389	SSR	5	39.2		LjT17D03	1	x5	seed	AP009964
TM1667	SSR	5	42.5		LjT08L18	1	x3	seed	AP010249
		5		CM0344	LjB22E16	1	x3	walking	DF093395

TM0344	SSR	5	42.9	CM0344	LjT12L15	3	x5	seed	DF093395
TM1417	SSR	5	42.9	CM0344	LjT10A13	1	x3	seed	DF093395
TM0052	SSR	5	44.1	CM0052	LjT08O18	3	x5	seed	DF093221
		5		CM0052	LjT17A13	1	x3	seed	DF093221
		5		CM0052	LjT02N08	1	x3	seed	DF093221
		5		CM0456	LjT30D08	1	x3	seed	DF093426
TM0456	SSR	5	44.1	CM0456	LjT01K11	1	x3	seed	DF093426
		5		CM0148	LjT55H21	1	x3	walking	DF093291
TM0148	dCAPS	5	44.1	CM0148	LjT30P03	3	x5	seed	DF093291
		5		CM0148	LjT27I11	3	x3	walking	DF093291
TM0596	SSR	5	44.5	CM0148	LjT12O14	1	x3	seed	DF093291
TM1672	SSR	5	44.9	CM0953	LjT35J07	3	x5	walking	DF093499
TM0953	SSR	5	44.9	CM0953	LjT17N13	3	x5	seed	DF093499
		5		CM0953	LjT25I15	1	x3	walking	DF093499
		5		CM0357	LjT05F18	2	x5	seed	DF093399
		5		CM0357	LjB19F18	3	x5	walking	DF093399
TM1748	SSR	5	46.1	CM0357	LjT34P10	3	x5	walking	DF093399
		5		CM0357	LjT127E18	3	x5	walking	DF093399
		5		CM0357	LjT32M13	3	x5	walking	DF093399
TM0357	SSR	5	47.3	CM0357	LjT02P23	3	x5	seed	DF093399
TM1692	SSR	5	47.3	CM0357	LjT05J08	3	x5	walking	DF093399
TM0710	SSR	5	47.3	CM0357	LjT32K11	1	x3	seed	DF093399
TM1466	SSR	5	47.3		LjT25B19	1	x3	seed	AP010199
TM1563	SSR	5	47.3	CM0956	LjT06D07	3	x5	seed	DF093501
TM0956	SSR	5	47.3	CM0956	LjT07L11	1	x3	seed	DF093501

		5		CM0200	LjT01E18	1	x3	walking	DF093323
TM0218	SSR	5	47.7	CM0200	LjT47L09	3	x5	seed	DF093323
		5		CM0200	LjT42H18	1	x3	walking	DF093323
TM0200	SSR	5	48.5	CM0200	LjT09H13	3	x5	seed	DF093323
		5		CM0200	LjT09M14	1	x3	walking	DF093323
TM0327	dCAPS	5	49.7	CM0200	LjT33L13	3	x5	seed	DF093323
		5		CM0200	LjB26H09	1	x3	walking	DF093323
TM0290	SSR	5	49.7	CM0200	LjT43G19	3	x5	seed	DF093323
		5		CM0200	LjB21O22	1	x3	walking	DF093323
TM0366	SSR	5	49.7	CM0200	LjT31L14	3	x5	seed	DF093323
TM1834	SSR	5	49.7		LjT24B10	3	x5	seed	AP009725
TM0731	SSR	5	50.1		LjT04G07	1	x3	seed	AP010067
		5		CM0328	LjB141A22	1	x3	walking	DF093389
TM0703	SSR	5	50.1	CM0328	LjT11C19	1	x3	seed	DF093389
TM0328	SSR	5	50.1	CM0328	LjT38F20	3	x5	seed	DF093389
		5		CM0328	LjT21F24	1	x3	seed	DF093389
TM1733	SSR	5	52.5	CM1439	LjT04I06	1	x5	seed	DF093516
TM1439	SSR	5	52.5	CM1439	LjT02A04	1	x3	seed	DF093516
TM1780	SSR	5	52.5		LjT14K23	3	x5	seed	AP009858(a), AP009859(b)
TM0698	SSR	5	52.5		LjT02I10	1	x3	seed	AP010053
TM0872	SSR	5	52.5		LjT39E05	1	x3	seed	AP010118
TM0180	SSR	5	54.1	CM0180	LjT03D07	3	x5	seed	DF093314
		5		CM0180	LjT23A04	1	x3	walking	DF093314
TM0656	SSR	5	54.5	CM0260	LjT03M08	1	x3	seed	DF093354

		5		CM0260	LjT02L21	3	x3	walking	DF093354
TM0260	SSR	5	54.9	CM0260	LjT47K21	3	x5	seed	DF093354
		5		CM0260	LjT09O04	1	x3	walking	DF093354
TM1948	SSR	5	56.1		LjT42F22	3	x5	seed	AP009775
BM1714	SSR	6	0.0	CM1613	LjB23G22	3	x5	seed	DF093523
		6		CM1613	LjB02L14	3	x5	walking	DF093523
TM1613	SSR	6	1.3	CM1613	LjT35E20	1	x3	seed	DF093523
TM0082	SSR	6	1.3		LjT06I08c	3	x5	seed	AP009799(a)
TM0553	SSR	6	1.7		LjT21O06	1	x3	seed	AP010008
TM1383	SSR	6	1.7	CM0686	LjT26K12	1	x3	walking	DF093468
		6		CM0686	LjT44C06	1	x3	seed	DF093468
TM1004	SSR	6	2.9	CM0472	LjT32I13	3	x5	seed	DF093432
TM0472	SSR	6	3.3	CM0472	LjT08D18	1	x3	seed	DF093432
TM0722	SSR	6	4.1		LjT17I05	1	x3	seed	AP010063
		6		CM0679	LjT16E05	3	x5	seed	DF093466
TM1264	SSR	6	6.1	CM0679	LjT31L16	1	x3	seed	DF093466
TM0679	SSR	6	6.1	CM0679	LjT08J21	1	x3	seed	DF093466
TM0517	SSR	6	6.5		LjT19B22	1	x3	seed	AP010001
		6		CM0014	LjT08H23	1	x3	walking	DF093189
TM0014	SSR	6	7.7	CM0014	LjT17C05	3	x5	seed	DF093189
TM1597	SSR	6	7.7		LjT40F03	1	x3	seed	AP010229
TM0817	SSR	6	13.6	CM0738	LjT44P17	1	x3	seed	DF093476
TM0738	SSR	6	14.0	CM0738	LjT04I05	1	x3	seed	DF093476
		6		CM0738	LjB22G09	1	x3	walking	DF093476
TM0302	SSR	6	14.0	CM0302	LjT37I11	3	x5	seed	DF093373

		6		CM0302	LjT13O03	1	x3	walking	DF093373
BM1429	SSR	6	14.0		LjB02K20	1	x3	seed	AP009945
TM0306	SSR	6	16.0		LjT23A02	3	x5	seed	AP009667
TM0689	SSR	6	16.4		LjT34N14	1	x3	seed	AP010049
TM1261	SSR	6	17.2		LjT45M05	1	x3	seed	AP010174
TM0084	dCAPS	6	18.4		LjT18B08	1	x5	seed	AP009949
TM0169	SSR	6	18.8		LjT30N23	1	x5	seed	AP009953
TM1862	SSR	6	18.8		LjT13N05	3	x5	seed	AP009862(a), AP009863(b)
TM2023	SSR	6	20.8		LjT11E14	3	x5	seed	AP009789
TM0245	SSR	6	20.8	CM0245	LjT05I20	3	x5	seed	DF093346
		6		CM0245	LjT38C24	1	x3	walking	DF093346
TM1789	SSR	6	20.8	CM1789	LjT18K17	2	x5	seed	DF093528
		6		CM1789	LjT123N17	2	x5	walking	DF093528
TM1514	SSR	6	21.6	CM1514	LjT13L20	3	x3	seed	DF093519
		6		CM1514	LjT43E06	3	x3	seed	DF093519
		6		CM1514	LjB23M19	2	x5	walking	DF093519
TM0632	SSR	6	23.6		LjT15B22	1	x3	seed	AP010031
TM1091	SSR	6	24.4		LjT46B14	3	x5	seed	AP009686
TM0821	SSR	6	26.0		LjT41B02	1	x3	seed	AP010099
		6		CM0836	LjT02L19	1	x3	walking	DF093491
TM0836	SSR	6	27.2	CM0836	LjT24B05	3	x5	seed	DF093491
		6		CM0836	LjT48D13	1	x3	walking	DF093491
TM0057	SSR	6	27.6	CM0057	LjT03B03	3	x5	seed	DF093224
		6		CM0057	LjT43M06	1	x3	seed	DF093224

TM0331	SSR	6	27.6	CM0057	LjT30M07	3	x5	seed	DF093224
TM0085	dCAPS	6	27.6		LjT14A08	1	x5	seed	AP009950
TM1374	SSR	6	28.0		LjT34E09	3	x5	seed	AP009841(a), AP009842(b)
TM1650	SSR	6	28.8		LjT28D11	3	x5	seed	AP009848(a), AP009849(b)
		6		CM0041	LjT25M04	1	x3	walking	DF093211
TM0041	SSR	6	32.5	CM0041	LjT17H19	3	x5	seed	DF093211
		6		CM0041	LjT38I04	1	x3	walking	DF093211
		6		CM0037	LjT48H23	3	x5	walking	DF093208
		6		CM0037	LjT13E22	1	x3	walking	DF093208
TM0037	dCAPS	6	32.9	CM0037	LjT16K17	3	x5	seed	DF093208
		6		CM0037	LjB140B09	2	x3	walking	DF093208
		6		CM0037	LjT32L10	2	x5	walking	DF093208
		6		CM0037	LjT02F19	3	x5	walking	DF093208
		6		CM0037	LjB04H20	3	x5	walking	DF093208
		6		CM0037	LjT46O03	3	x5	walking	DF093208
		6		CM0037	LjT40N16	3	x5	walking	DF093208
		6		CM0037	LjB382I13	3	x5	walking	DF093208
		6		CM0037	LjB26B08	3	x5	walking	DF093208
TM0317	SSR	6	34.9	CM0037	LjT18F01	1	x5	seed	DF093208
		6		CM0037	LjT47N19	3	x5	walking	DF093208
		6		CM0037	LjT41F23	3	x5	seed	DF093208
		6		CM0037	LjT33N07	1	x3	walking	DF093208
TM0140	SSR	6	36.1	CM0037	LjT21P04	3	x5	seed	DF093208
TM1540	SSR	6	36.1		LjT45M04	1	x3	seed	AP010216

TM0440	SSR	6	36.1	CM0440	LjT24F06	3	x3	seed	DF093423
		6		CM0013	LjB74E12	1	x3	walking	DF093188
TM0013	SSR	6	36.9	CM0013	LjT14O07	3	x5	seed	DF093188
		6		CM0013	LjB11I22	1	x3	walking	DF093188
TM0420	SSR	6	36.9	CM0420	LjT01K23	1	x3	seed	DF093416
		6		CM0420	LjB26H19	1	x3	walking	DF093416
TM1546	SSR	6	37.7	CM0420	LjT02A23	1	x3	seed	DF093416
		6		CM0137	LjB11L23	1	x3	walking	DF093285
TM0137	dCAPS	6	37.7	CM0137	LjT46P17	3	x5	seed	DF093285
TM0778	SSR	6	38.5		LjT10I04	1	x3	seed	AP010082
TM0045	SSR	6	38.9	CM0045	LjT14B06	3	x5	seed	DF093214
		6		CM0045	LjT46L22	1	x3	walking	DF093214
TM0830	SSR	6	38.9		LjT36L14	1	x3	seed	AP010101
TM0880	SSR	6	41.7		LjT34O10	1	x3	seed	AP010122
TM0957	SSR	6	45.0		LjT35H04	1	x3	seed	AP010137
		6		CM0437	LjT40C18	1	x5	walking	DF093422
TM0437	SSR	6	46.6	CM0437	LjT04L20	3	x5	seed	DF093422
		6		CM0437	LjT34G23	1	x3	walking	DF093422
TM0367	SSR	6	46.6		LjT16B20	3	x5	seed	AP009670
TM0630	SSR	6	46.6		LjT02P05	1	x3	seed	AP010029
TM1657	SSR	6	46.6		LjT36O06	1	x3	seed	AP010244
		6		CM0139	LjT34J02	1	x3	seed	DF093286
TM1116	SSR	6	46.6	CM0139	LjT16M07	1	x3	walking	DF093286
		6		CM0139	LjB141N22	1	x3	walking	DF093286
TM0139	SSR	6	46.6	CM0139	LjT19B18	3	x5	seed	DF093286

		6		CM0139	LjT27H06	1	x3	walking	DF093286
TM1525	SSR	6	46.6	CM0139	LjT19N13	1	x3	walking	DF093286
		6		CM0539	LjT26K17	1	x3	walking	DF093442
TM1035	SSR	6	46.6	CM0539	LjT42E12	1	x3	seed	DF093442
		6		CM1829	LjT34E13	3	x5	walking	DF093530
TM1829	SSR	6	46.6	CM1829	LjT05H22	3	x5	seed	DF093530
		6		CM0066	LjT03J20	1	x5	walking	DF093233
TM0066	SSR	6	46.6	CM0066	LjT12N11	3	x5	seed	DF093233
TM0402	SSR	6	46.6	CM0066	LjT33G10	1	x3	seed	DF093233
		6		CM0066	LjT21L21	1	x5	walking	DF093233
BM1377	SSR	6	47.4	CM0066	LjB01J04	3	x5	seed	DF093233
TM0756	SSR	6	49.9		LjT15B19	1	x3	seed	AP010076
		6		CM0118	LjT56H16	1	x3	walking	DF093269
TM0228	SSR	6	51.1	CM0118	LjT31L24	3	x5	seed	DF093269
		6		CM0118	LjB13A04	1	x5	seed	DF093269
TM0118	SSR	6	51.1	CM0118	LjT48M22	3	x5	seed	DF093269
		6		CM0118	LjT06P22	1	x3	walking	DF093269
TM1763	SSR	6	55.2		LjT03K02	3	x5	seed	AP009707
TM0301	SSR	6	55.6	CM0114	LjT29C05	3	x5	seed	DF093266
		6		CM0114	LjT42C13	1	x3	walking	DF093266
TM0114	dCAPS	6	57.2	CM0114	LjT19M07	3	x5	seed	DF093266
TM0336	SSR	6	57.6		LjT04E21	3	x5	seed	AP009668
		6		CM0055	LjT25K23	1	x3	walking	DF093222
TM0055	SSR	6	61.5	CM0055	LjT05E07	3	x5	seed	DF093222
		6		CM0055	LjT07N01	1	x3	seed	DF093222

		6		CM0055	LjT30C23	1	x3	seed	DF093222
BM1484	SSR	6	63.4	CM0055	LjB69N14	1	x3	walking	DF093222
		6		CM0055	LjT13B14	1	x3	walking	DF093222
		6		CM0055	LjT23F02	3	x5	walking	DF093222
		6		CM0314	LjT29P24	1	x3	seed	DF093380
TM0314	SSR	6	65.3	CM0314	LjT13E04	3	x5	seed	DF093380
TM0582	SSR	6	66.2	CM0314	LjT40A10	1	x3	seed	DF093380
TM1825	SSR	6	66.6	CM0314	LjT04K06	3	x5	walking	DF093380
TM1240	SSR	6	66.6	CM0314	LjT33P12	1	x3	seed	DF093380
TM0508	SSR	6	67.0		LjT09E22	1	x3	seed	AP009998
		6		CM0885	LjT39N07	3	x5	walking	DF093493
TM0885	SSR	6	67.4	CM0885	LjT45B09	3	x3	seed	DF093493
BM1560	SSR	6	67.4	CM0885	LjB12M17	1	x3	walking	DF093493
				CM0300	LjT33M01	3	x5	seed	DF093372
				CM0300	LjB11F20	1	x3	walking	DF093372
				CM0319	LjT20H21	3	x5	seed	DF093384
				CM0319	LjT17K05	1	x3	walking	DF093384
				CM0325	LjT18C01	1	x3	walking	DF093388
				CM0325	LjT38O11	3	x5	seed	DF093388
				CM0385	LjT15M15	1	x3	seed	DF093407
				CM0385	LjT38I10	1	x3	seed	DF093407
				CM0457	LjT12L18	1	x3	seed	DF093427
				CM0457	LjB12F21	1	x3	walking	DF093427
				CM0458	LjT17P12	1	x3	seed	DF093428
				CM0458	LjT36F18	1	x5	seed	DF093428

				CM0466	LjT26I04	1	x3	seed	DF093430
				CM0466	LjB03D18	3	x5	walking	DF093430
				CM0528	LjT30D10	1	x3	seed	DF093440
				CM0528	LjT07F08	1	x3	walking	DF093440
				CM0547	LjT14A12	3	x5	seed	DF093445
				CM0547	LjT07M13	1	x3	seed	DF093445
				CM0584	LjB10M13	1	x3	walking	DF093451
				CM0584	LjT29K06	1	x3	seed	DF093451
				CM0584	LjT45B13	1	x3	seed	DF093451
				CM0601	LjT42G24	1	x3	seed	DF093456
				CM0601	LjT06P01	1	x3	seed	DF093456
				CM0693	LjT27N15	1	x3	walking	DF093471
				CM0693	LjT09F15	1	x3	seed	DF093471
				CM0905	LjT46C08	1	x3	seed	DF093496
				CM0905	LjT39N15	1	x5	seed	DF093496
				CM1092	LjT10F22	3	x5	seed	DF093505
				CM1092	LjT44E18	3	x5	seed	DF093505
				CM1102	LjT09P09	1	x3	seed	DF093506
				CM1102	LjT52I02	1	x3	walking	DF093506
				CM1324	LjT05G19	1	x3	seed	DF093512
				CM1324	LjT34I23	1	x3	seed	DF093512
				CM1489	LjT14H03	3	x5	seed	DF093518
				CM1489	LjT21K14	3	x5	seed	DF093518
				CM1729	LjT15F22	3	x5	seed	DF093525
				CM1729	LjT18K19	3	x5	seed	DF093525

				CM1835	LjT17J13	3	x5	seed	DF093531
				CM1835	LjT38M11	3	x5	seed	DF093531
				CM1875	LjT33A23	3	x5	walking	DF093532
				CM1875	LjT45G01	3	x5	seed	DF093532
				CM1875	LjT19P08	3	x5	walking	DF093532
				CM1887	LjT46I13	2	x5	seed	DF093534
				CM1887	LjT06N24	3	x5	seed	DF093534
				CM1983	LjT40J16	3	x5	seed	DF093536
				CM1983	LjT31L17	2	x5	seed	DF093536
					LjB17L21	1	x3	seed	AP009940
					LjB03J07	1	x3	seed	AP009941
					LjB18I11	1	x3	seed	AP009942
					LjB18O14	1	x3	seed	AP009943
					LjB01D01	3	x5	seed	AP009625
					LjB03P03	1	x3	seed	AP009944
					LjB15A13	1	x5	seed	AP009947
					LjB01J01	3	x5	seed	AP009627
					LjB12P21	3	x5	seed	AP009631
					LjB14K02	3	x5	seed	AP009793(a), AP009794(b)
					LjB25I10	2	x5	seed	AP009866
					LjB16I02	3	x5	seed	AP009634
					LjB08M07	3	x5	seed	AP009635
					LjB12N13	3	x5	seed	AP009636
					LjB06H14	3	x5	seed	AP009639

					LjB22H06	3	x5	seed	AP009640
					LjB06P23	3	x5	seed	AP009642
					LjB09A03	3	x5	seed	AP009643
					LjB15P09	3	x5	seed	AP009644
					LjB12O06	3	x5	seed	AP009646
					LjB10M19	2	x5	seed	AP009867
					LjB06N21	2	x5	seed	AP009868
					LjT12M13	3	x5	seed	AP009797(a), AP009798(b)
					LjT06N06	1	x5	seed	AP009948
					LjT33A04	3	x5	seed	AP009653
					LjT22N02	1	x5	seed	AP009952
					LjT18J11	3	x5	seed	AP009803(a), AP009804(b)
					LjT31N18	1	x3	seed	AP009957
					LjT26C04	1	x3	seed	AP009958
					LjT24P23	3	x5	seed	AP009813(a), AP009814(b), AP009815(c)
					LjT31F05	1	x3	seed	AP009962
					LjT02J24	3	x5	seed	AP009673
					LjT39P23	1	x3	seed	AP009966
					LjT34F04	1	x3	seed	AP009968
					LjT17O07	1	x3	seed	AP009969
					LjT41B20	1	x3	seed	AP009973
					LjT29P04	1	x3	seed	AP009978

					LjT39H03	1	x3	seed	AP009979
					LjT03K24	1	x3	seed	AP009980
					LjT28H23	1	x3	seed	AP009981
					LjT33C23	1	x3	seed	AP009982
					LjT10D02	1	x3	seed	AP009984
					LjT06M01	1	x3	seed	AP009986
					LjT45L18	1	x3	seed	AP009987
					LjT37C05	1	x3	seed	AP009988
					LjT06I09	1	x3	seed	AP009990
					LjT35E03	1	x3	seed	AP009992
					LjT02G13	3	x5	seed	AP009827(a), AP009828(b)
					LjT30I08	3	x5	seed	AP009676
					LjT25P15	1	x3	seed	AP009993
					LjT18N19	1	x3	seed	AP009995
					LjT34L13	1	x3	seed	AP010004
					LjT42G13	1	x3	seed	AP010006
					LjT35D08	1	x3	seed	AP010007
					LjT33K05	1	x3	seed	AP010010
					LjT30N04	1	x3	seed	AP010011
					LjT06C12	1	x3	seed	AP010014
					LjT13J03	1	x3	seed	AP010015
					LjT01F24	1	x3	seed	AP010016
					LjT41H24	1	x3	seed	AP010018
					LjT10A21	1	x3	seed	AP010019

					LjT35C01	1	x3	seed	AP010021
					LjT48C16	1	x3	seed	AP010022
					LjT46I09	1	x3	seed	AP010023
					LjT04C06	1	x3	seed	AP010027
					LjT44F13	1	x3	seed	AP010028
					LjT37D10	1	x3	seed	AP010030
					LjT34K24	1	x3	seed	AP010033
					LjT47I02	1	x3	seed	AP010034
					LjT35B07	1	x3	seed	AP010035
					LjT45A20	1	x3	seed	AP010036
					LjT10O10	1	x3	seed	AP010037
					LjT16H12	1	x3	seed	AP010038
					LjT35J12	1	x3	seed	AP010040
					LjT30N24	1	x3	seed	AP010044
					LjT39B13	3	x5	seed	AP009679
					LjT30N18	1	x3	seed	AP010046
					LjT04N09	1	x3	seed	AP010047
					LjT37O09	1	x3	seed	AP010050
					LjT15N18	1	x3	seed	AP010052
					LjT41D10	1	x3	seed	AP010054
					LjT17C10	1	x3	seed	AP010055
					LjT35E05	1	x3	seed	AP010058
					LjT05A08	1	x3	seed	AP010059
					LjT02K08	1	x3	seed	AP010060
					LjT38J19	1	x3	seed	AP010061

					LjT17B03	1	x3	seed	AP010062
					LjT13N04	1	x3	seed	AP010064
					LjT23J20	3	x5	seed	AP009680
					LjT46A12	1	x3	seed	AP010065
					LjT10P12	1	x3	seed	AP010068
					LjT03D12	1	x3	seed	AP010072
					LjT09A12	1	x3	seed	AP010073
					LjT38P01	1	x3	seed	AP010075
					LjT13F18	1	x3	seed	AP010077
					LjT33M20	1	x3	seed	AP010078
					LjT07P21	1	x3	seed	AP010079
					LjT10E17	1	x3	seed	AP010080
					LjT16L08	1	x3	seed	AP010081
					LjT10F13	1	x3	seed	AP010083
					LjT39N06	1	x3	seed	AP010086
					LjT16I12	1	x3	seed	AP010088
					LjT45D24	1	x3	seed	AP010090
					LjT36E16	1	x3	seed	AP010092
					LjT03L21	1	x3	seed	AP010094
					LjT29E04	1	x3	seed	AP010095
					LjT11B21	1	x3	seed	AP010098
					LjT19F24	1	x3	seed	AP010100
					LjT30L14	1	x3	seed	AP010102
					LjT44F11	1	x3	seed	AP010104
					LjT13K07	1	x3	seed	AP010105

					LjT45M09	1	x3	seed	AP010107
					LjT36B17	1	x3	seed	AP010108
					LjT48O18	1	x3	seed	AP010111
					LjT48K17	1	x3	seed	AP010112
					LjT29B06	1	x3	seed	AP010113
					LjT14M06	1	x3	seed	AP010116
					LjT15F17	1	x3	seed	AP010119
					LjT22M20	1	x3	seed	AP010121
					LjT16G18	1	x3	seed	AP010124
					LjT07P16	1	x5	seed	AP010125
					LjT43K05	1	x3	seed	AP010126
					LjT02N03	1	x3	seed	AP010129
					LjT38B24	1	x3	seed	AP010131
					LjT03D05	1	x3	seed	AP010132
					LjT10J09	1	x3	seed	AP010133
					LjT47D03	1	x3	seed	AP010134
					LjT14H02	1	x3	seed	AP010135
					LjT19A14	1	x3	seed	AP010136
					LjT46P10	1	x3	seed	AP010139
					LjT25F20	1	x3	seed	AP010140
					LjT38E08	1	x3	seed	AP010143
					LjT32M01	1	x3	seed	AP010145
					LjT04E07	3	x5	seed	AP009683
					LjT33L17	3	x5	seed	AP009835(a), AP009836(b)

					LjT18K22	3	x5	seed	AP009684
					LjT37H17	1	x5	seed	AP010146
					LjT10H22	1	x3	seed	AP010147
					LjT21I06	1	x3	seed	AP010148
					LjT20L14	1	x3	seed	AP010150
					LjT38L02	1	x3	seed	AP010151
					LjT42I15	1	x3	seed	AP010152
					LjT01E03	1	x5	seed	AP010153
					LjT37G19	3	x5	seed	AP009685
					LjT33J24	1	x3	seed	AP010156
					LjT48K13	1	x5	seed	AP010157
					LjT34B08	1	x3	seed	AP010159
					LjT48O01	1	x3	seed	AP010160
					LjT46F23	1	x3	seed	AP010161
					LjT07C14	1	x3	seed	AP010165
					LjT16O05	1	x3	seed	AP010166
					LjT08D05	1	x3	seed	AP010167
					LjT35F01	1	x3	seed	AP010169
					LjT05F15	1	x3	seed	AP010170
					LjT07J01	2	x3	seed	AP009869
					LjT31K10	1	x3	seed	AP010171
					LjT31M07	1	x3	seed	AP010172
					LjT15A14	1	x3	seed	AP010175
					LjT01P07	1	x3	seed	AP010179
					LjT47C13	1	x3	seed	AP010181

					LjT19N22	1	x3	seed	AP010182
					LjT40B16	3	x5	seed	AP009689
					LjT18L24	2	x5	seed	AP009870
					LjT06J23	1	x3	seed	AP010185
					LjT44J06	1	x3	seed	AP010186
					LjT22N06	1	x3	seed	AP010189
					LjT04I16	1	x3	seed	AP010191
					LjT12A09	1	x3	seed	AP010192
					LjT12E12	1	x3	seed	AP010193
					LjT01K14	1	x3	seed	AP010194
					LjT14E02	1	x3	seed	AP010196
					LjT41F16	1	x3	seed	AP010200
					LjT45I18	1	x3	seed	AP010201
					LjT22H07	1	x3	seed	AP010203
					LjT11H16	1	x3	seed	AP010204
					LjT05D15	1	x3	seed	AP010205
					LjT28H08	1	x3	seed	AP010207
					LjT03E06	1	x3	seed	AP010210
					LjT28K11	1	x3	seed	AP010211
					LjT09J04	1	x3	seed	AP010212
					LjT36K06	1	x3	seed	AP010213
					LjT22H02	3	x5	seed	AP009691
					LjT35F06	1	x5	seed	AP010214
					LjT17I13	1	x3	seed	AP010215
					LjT04D09	1	x3	seed	AP010218

					LjT28O03	2	x3	seed	AP009871
					LjT26P12	2	x3	seed	AP009872
					LjT01D09	1	x3	seed	AP010221
					LjT32E09	1	x3	seed	AP010222
					LjT48H14	1	x3	seed	AP010223
					LjT15I01	1	x3	seed	AP010224
					LjT17L12	1	x3	seed	AP010225
					LjT31N05	1	x3	seed	AP010226
					LjT24M05	3	x5	seed	AP009693
					LjT19D10	3	x5	seed	AP009694
					LjT35G18	1	x3	seed	AP010231
					LjT03L06	1	x3	seed	AP010232
					LjT02D24	3	x5	seed	AP009846(a), AP009847(b)
					LjT28I10	1	x3	seed	AP010237
					LjT03L03	1	x3	seed	AP010239
					LjT03D14	1	x5	seed	AP010241
					LjT44L11	1	x3	seed	AP010243
					LjT48F24	1	x3	seed	AP010246
					LjT22I05	1	x3	seed	AP010247
					LjT15O11	1	x3	seed	AP010251
					LjT07B02	1	x3	seed	AP010252
					LjT06P13	1	x3	seed	AP010253
					LjT04K03	1	x3	seed	AP010254
					LjT08P02	3	x5	seed	AP009695

					LjT10C23	3	x5	seed	AP009697
					LjT10I01	3	x5	seed	AP009850(a), AP009851(b)
					LjT02O17	3	x5	seed	AP009698
					LjT24A04	3	x5	seed	AP009699
					LjT48K02	3	x5	seed	AP009700
					LjT31G10	3	x5	seed	AP009701
					LjT43O20	2	x5	seed	AP009875
					LjT18C07	3	x5	seed	AP009854(a), AP009855(b)
					LjT02A08	3	x5	seed	AP009705
					LjT28B05	3	x5	seed	AP009706
					LjT32D02	3	x5	seed	AP009708
					LjT38E14	1	x5	seed	AP010255
					LjT14E23	3	x5	seed	AP009712
					LjT37K03	3	x5	seed	AP009713
					LjT08O01	3	x5	seed	AP009714
					LjT24E04	3	x5	seed	AP009860(a), AP009861(b)
					LjT11K12	3	x5	seed	AP009715
					LjT06I10	3	x5	seed	AP009718
					LjT28H07	3	x5	seed	AP009719
					LjT17C09	3	x5	seed	AP009721
					LjT42E21	3	x5	seed	AP009722
					LjT39G17	3	x5	seed	AP009723
					LjT43D04	3	x5	seed	AP009724

					LjT04G17	3	x5	seed	AP009726
					LjT13L04	3	x5	seed	AP009727
					LjT35D18	3	x5	seed	AP009728
					LjT13F07	2	x5	seed	AP009876
					LjT15D07	3	x5	seed	AP009734
					LjT37E04	3	x5	seed	AP009735
					LjT31N04	3	x5	seed	AP009736
					LjT06B16	3	x5	seed	AP009738
					LjT06I13	3	x5	seed	AP009739
					LjT43N20	3	x5	seed	AP009742
					LjT30L13	3	x5	seed	AP009744
					LjT25I18	3	x5	seed	AP009745
					LjT40A21	3	x5	seed	AP009747
					LjT43F20	2	x5	seed	AP009878
					LjT24E19	3	x5	seed	AP009749
					LjT36L22	2	x5	seed	AP009880
					LjT17E11	3	x5	seed	AP009751
					LjT04A22	3	x5	seed	AP009753
					LjT25G12	3	x5	seed	AP009754
					LjT38B21	3	x5	seed	AP009756
					LjT14D09	3	x5	seed	AP009757
					LjT18D07	3	x5	seed	AP009758
					LjT16E14	3	x5	seed	AP009759
					LjT39M20	3	x5	seed	AP009760
					LjT05F19	3	x5	seed	AP009761

					LjT01K02	3	x5	seed	AP009762
					LjT09J11	3	x5	seed	AP009763
					LjT21I18	3	x5	seed	AP009765
					LjT40J14	3	x5	seed	AP009766
					LjT39F13	3	x5	seed	AP009767
					LjT40E15	3	x5	seed	AP009768
					LjT13A22	3	x5	seed	AP009769
					LjT15D16	3	x5	seed	AP009770
					LjT20A21	3	x5	seed	AP009771
					LjT07I16	3	x5	seed	AP009772
					LjT09F21	3	x5	seed	AP009773
					LjT43M12	2	x5	seed	AP009882
					LjT31J09	2	x5	seed	AP009883
					LjT24C10	2	x5	seed	AP009884
					LjT10B22	2	x5	seed	AP009885
					LjT19C19	2	x5	seed	AP009886
					LjT01F21	3	x5	seed	AP009774
					LjT18N03	3	x5	seed	AP009776
					LjT13C08	3	x5	seed	AP009777
					LjT09J10	3	x5	seed	AP009778
					LjT34L14	3	x5	seed	AP009779
					LjT15C06	3	x5	seed	AP009781
					LjT26J05	3	x5	seed	AP009782
					LjT35F15	2	x5	seed	AP009888
					LjT01G11	2	x5	seed	AP009889

					LjT11A15	3	x5	seed	AP009784	
					LjT41D08	2	x5	seed	AP009890	
					LjT28A08	3	x5	seed	AP009786	
					LjT40K11	3	x5	seed	AP009787	
					LjT02J13	3	x5	seed	AP009788	
					LjT15P09	3	x5	seed	AP009790	
					LjT24E07	2	x5	seed	AP009891	
					LjT24M21	2	x5	seed	AP009892	
					LjT22N13	2	x5	seed	AP009893	
					LjT27E22	2	x5	seed	AP009894	
					LjT09I09	2	x5	seed	AP009895	
					LjT41N19	2	x5	seed	AP009896	
					LjT47N10	2	x5	seed	AP009897	
					LjT06N02	2	x5	seed	AP009898	
					LjT30J19	2	x5	seed	AP009899	
					LjT39M07	2	x5	seed	AP009900	
					LjT11L09	2	x5	seed	AP009901	
					LjT10C06	2	x5	seed	AP009902	
					LjT08G12	2	x5	seed	AP009903	
					LjT10I14	2	x5	seed	AP009904	
					LjT09C09	2	x5	seed	AP009905	
					LjT04K19	2	x5	seed	AP009906	
					LjT39O22	2	x5	seed	AP009907	
					LjT06B04	2	x5	seed	AP009908	
					LjT39A22	2	x5	seed	AP009909	

					LjT46F13	2	x5	seed	AP009910
					LjT13J19	2	x5	seed	AP009911
					LjT36I04	2	x5	seed	AP009912
					LjT09O11	2	x5	seed	AP009913
					LjT45C19	2	x5	seed	AP009914
					LjT07K13	2	x5	seed	AP009915
					LjT43G14	2	x5	seed	AP009916
					LjT47B05	2	x5	seed	AP009917
					LjT35M05	2	x5	seed	AP009918
					LjT07J23	2	x5	seed	AP009919
					LjT31F12	2	x5	seed	AP009920
					LjT07L17	2	x5	seed	AP009921
					LjT41B11	2	x5	seed	AP009922
					LjT47H21	2	x5	seed	AP009923
					LjT13L03	2	x5	seed	AP009924
					LjT15A10	2	x5	seed	AP009925
					LjT04M14	2	x5	seed	AP009926
					LjT36B24	2	x5	seed	AP009927
					LjT30M06	2	x5	seed	AP009928
					LjT37I20	3	x5	seed	AP009791
					LjT42M11	3	x5	seed	AP009792
					LjT41B04	2	x5	seed	AP009929
					LjT48C01	2	x5	seed	AP009930
					LjT15B14	2	x5	seed	AP009931
					LjT16B12	2	x5	seed	AP009932

					LjT46P06	2	x5	seed	AP009933
					LjT32C22	2	x5	seed	AP009934
					LjT10I07	2	x5	seed	AP009935
					LjT09F05	2	x5	seed	AP009936
					LjT09K03	2	x5	seed	AP009937
					LjT43K18	2	x5	seed	AP009938
					LjT38D03	2	x5	seed	AP009939

Supplemental Table 2. Statistical analysis of the *L. japonicus* TGS assembly.

Features	
Total length of supercontigs (bases)	315,073,275
GC content	37%
Distribution of supercontig length (bases)	
Min	276
1st quartile	1,001
Median	1,146
3rd quartile	1,504
Max	1,625,999
Mean	2,927
N50	92,311
Anchored supercontigs	
Number of anchored supercontigs	594
Length of anchored supercontigs (bases)	130,251,279
Unnchored supercontigs	
Number of unanchored supercontigs	110,346
Length of unanchored supercontigs (bases)	184,821,996

Supplemental Table 3. SSRs in the *L. japonicus* TGS.

SSR pattern	SSR numbers in TGS	frequency in 100kb				
		all TGS	exon*	intron*	5' UTR*	3' UTR*
AT	10,375	3.20	0.64	3.82	8.44	9.49
AG	4,881	1.50	0.55	3.00	8.30	8.21
AC	1,118	0.34	0.14	1.59	1.47	1.52
GC	4	0.00	0.00	0.00	0.00	0.00
AAG	4,125	1.27	3.44	0.80	5.46	5.23
AAT	3,301	1.02	0.27	1.47	3.05	3.37
GGT	2,665	0.82	3.00	0.43	1.68	1.95
ATC	1,648	0.51	2.04	0.42	2.22	2.11
AAC	1,383	0.43	1.95	0.95	1.66	1.66
GGA	1,103	0.34	1.66	0.17	0.89	0.55
AGC	329	0.10	1.10	0.04	0.21	0.20
GGC	209	0.06	0.45	0.03	0.17	0.10
ACT	166	0.05	0.16	0.10	0.23	0.30
ACG	63	0.02	0.15	0.00	0.06	0.12
AAAT	1,088	0.34	0.06	0.67	1.27	1.24
AAAG	354	0.11	0.04	0.20	0.62	0.37
AATT	250	0.08	0.00	0.11	0.39	0.39
AAAC	232	0.07	0.02	0.24	0.41	0.61
AATG	177	0.05	0.06	0.09	0.21	0.37
AATC	120	0.04	0.01	0.17	0.21	0.24
GGGA	49	0.02	0.01	0.02	0.04	0.04
AAGC	17	0.01	0.01	0.01	0.04	0.02
GGGT	16	0.00	0.00	0.01	0.00	0.04
GGAT	15	0.00	0.02	0.01	0.00	0.08
GAGC	14	0.00	0.01	0.00	0.08	0.00
AACG	9	0.00	0.01	0.00	0.04	0.02
GGCT	5	0.00	0.00	0.00	0.00	0.02
AGGT	3	0.00	0.00	0.01	0.00	0.00
GACT	3	0.00	0.00	0.00	0.00	0.00
GATC	3	0.00	0.00	0.00	0.02	0.00
GGAC	2	0.00	0.00	0.00	0.00	0.02
GGCA	2	0.00	0.00	0.00	0.00	0.00
AGGC	1	0.00	0.00	0.00	0.02	0.00
total	33,730					

* exon and intron sequences were extracted from completely modeled genes in the TGS.
5' UTR and 3' UTR sequences corresponds to 500bp upstream and downstream sequences of the completely modeled genes in the TGS.

Supplemental Table 4. Frequency of repetitive sequences in TAC/BAC end sequences, putative introns, and putative UTRs.

	Fraction of TGS (%)	Fraction of TAC/BAC end sequences (%)	Fraction of intron sequences (%)	Fraction of 3' UTR sequences (%)	Fraction of 5' UTR sequences (%)
Class I					
SINEs	0.01%	0.01%	0.04%	0.02%	0.00%
LINEs	1.19%	0.68%	0.19%	0.31%	0.52%
LTR: Ty1/copia	7.16%	10.76%	0.58%	1.04%	0.78%
LTR: Ty3/gypsy	8.81%	9.64%	0.53%	1.02%	0.88%
Other LTR	2.05%	1.74%	0.20%	0.43%	0.65%
total class I	19.23%	22.84%	1.36%	2.83%	2.84%
Class II					
coding class II	0.97%	0.57%	0.19%	0.52%	0.69%
MITE	2.33%	1.38%	2.43%	2.00%	2.65%
total class II	3.31%	1.95%	2.62%	2.52%	3.24%
Short tandem repeats	1.31%	9.93%	0.00%	0.01%	0.01%
Unclassified	10.43%	10.56%	4.92%	7.72%	4.61%

Supplemental Table 5.

Supplemental Table 5. tRNA genes in the *L. japonicus* TGS.

Anticodon	number of genes	gene name
Ala(AGC)	10	LjSGA_012590.1.1,LjSGA_014452.1.1,LjSGA_047922.0.1,LjSGA_057483.0.1,LjSGA_080936.0.1,chr1.CM0206.130.nd,chr1.CM0816.320.nc,chr3.CM0152.140.nc,chr4.CM0087.900.nd,chr4.CM0307.80.nc
Ala(CGC)	4	LjT41B04.130.nd,chr1.CM0039.110.nd,chr1.CM0544.330.nc,chr4.CM0025.370.nc
Ala(TGC)	10	LjSGA_009813.1.1,LjSGA_016546.0.1,LjSGA_037526.0.1,LjSGA_078531.0.1,LjSGA_079854.0.1,LjT30N24.190.nd,chr1.CM0123.210.nc,chr2.CM0021.350.nc,chr4.CM0042.1330.nc,chr4.CM0244.240.nc
Arg(ACG)	25	LjSGA_012029.0.2,LjSGA_034758.0.1,LjSGA_061637.0.1,LjSGA_080502.0.1,LjSGA_089458.0.1,LjSGA_092923.0.1,LjSGA_095410.1.1,LjSGA_095609.1.2,LjSGA_098408.0.1,LjSGA_099551.1.2,LjSGA_108027.0.1,LjSGA_114244.0.1,LjSGA_123151.0.1,LjSGA_123559.0.1,LjSGA_127506.1.2,LjSGA_127544.0.1,LjSGA_133159.0.1,LjSGA_138405.0.1,LjT39A22.40.nd,chr1.CM0269.330.nc,chr2.CM0021.320.nc,chr3.CM0279.40.nd,chr4.LjT13D08.150.nd,chr4.LjT13D08.160.nd,chr4.LjT13D08.220.nd
Arg(CCG)	2	chr1.LjT04O21.200.nd,chr2.CM0002.20.nd
Arg(CCT)	7	LjSGA_014645.0.1,LjSGA_142541.0.1,chr1.LjB20I01.120.nd,chr2.CM0018.80.nc,chr3.CM0160.1020.nc,chr5.CM0180.210.nd,chr5.CM0852.270.nc
Arg(TCG)	4	LjSGA_015112.0.1,LjSGA_021358.0.1,LjT03E06.160.nd,chr6.CM0885.80.nc
Arg(TCT)	7	LjSGA_006242.1.1,LjSGA_013337.0.1,LjSGA_038272.0.1,LjT08D05.170.nd,chr1.LjT07G07.90.nc,chr1.LjT33H07.110.nd,chr5.CM0311.110.nc
Asn(GTT)	44	LjSGA_000580.1.1,LjSGA_000581.1.1,LjSGA_000582.0.1,LjSGA_000856.2.1,LjSGA_000857.0.1,LjSGA_001531.0.1,LjSGA_027174.0.1,LjSGA_029655.0.1,LjSGA_033233.0.1,LjSGA_034758.0.2,LjSGA_036837.0.1,LjSGA_062270.0.1,LjSGA_062817.0.1,LjSGA_063468.0.1,LjSGA_064786.1.1,LjSGA_066507.0.2,LjSGA_077679.0.1,LjSGA_079831.0.1,LjSGA_089458.0.2,LjSGA_090879.1.1,LjSGA_094328.0.1,LjSGA_095609.1.1,LjSGA_099551.1.1,LjSGA_100259.1.1,LjSGA_100273.0.1,LjSGA_102138.0.1,LjSGA_106623.1.1,LjSGA_107510.1.1,LjSGA_112580.0.2,LjSGA_119639.1.1,LjSGA_122659.0.1,LjSGA_125973.0.1,LjSGA_127506.1.1,LjSGA_129700.0.1,LjSGA_139720.1.2,chr1.CM0088.580.nd,chr2.CM0120.280.nc,chr2.CM0153.130.nc,chr3.CM0690.60.nd,chr3.LjT07H20.40.nd,chr5.CM0040.590.nd,chr5.CM0239.700.nc,chr5.CM0299.510.nd,chr6.LjT02P05.140.nd
Asp(ATC)	1	LjSGA_118743.0.1
Asp(GTC)	28	LjB18I11.30.nd,LjSGA_000356.0.1,LjSGA_006063.2.2,LjSGA_011819.0.1,LjSGA_019714.0.1,LjSGA_024813.0.1,LjSGA_035242.0.1,LjSGA_058323.0.1,LjSGA_087375.0.1,LjSGA_096041.0.2,LjSGA_096992.0.1,LjSGA_132645.0.3,LjSGA_137751.0.1,LjSGA_142963.1.1,LjT10C06.100.nd,chr1.CM0122.740.nd,chr1.CM0122.770.nd,chr1.CM0133.610.nc,chr1.CM0375.40.nd,chr2.CM0008.690.nc,chr2.CM0058.440.nd,chr2.LjT44L24.260.nd,chr3.CM0253.130.nc,chr3.CM0355.260.nc,chr3.LjT34H24.130.nd,chr3.LjT34H24.150.nd,chr3.LjT40N08.210.nd,chr4.CM0042.430.nd
Cys(GCA)	26	LjSGA_000579.0.1,LjSGA_059390.0.1,LjSGA_067096.0.1,LjSGA_067096.0.2,LjSGA_087356.0.1,LjSGA_098615.0.1,LjSGA_101868.0.1,LjSGA_102130.0.1,LjSGA_105530.0.1,LjSGA_105544.0.1,LjSGA_105812.0.1,LjSGA_106677.0.1,LjSGA_113301.0.1,LjSGA_113954.0.1,LjSGA_116334.0.1,LjSGA_130586.0.1,LjSGA_146927.0.1,LjSGA_148219.0.1,LjT04A22.100.nc,LjT31F12.130.nd,LjT41B11.70.nd,chr1.CM0105.520.nc,chr3.CM0208.190.nc,chr4.CM0025.570.nd,chr4.CM0558.220.nc,chr5.CM0180.80.nc
Gln(CTG)	6	LjSGA_022963.0.1,LjT45C19.60.nd,chr1.LjT43L07.110.nd,chr2.CM0249.1360.nc,chr3.CM0091.730.nd,chr3.CM0164.180.nd
Gln(TTG)	10	LjSGA_000363.0.1,LjSGA_022855.0.1,LjSGA_048513.0.1,LjSGA_051155.0.1,LjSGA_064248.0.1,LjSGA_091737.0.1,LjSGA_096924.0.1,LjSGA_112714.0.1,LjSGA_135261.0.1,LjT10J09.50.nd
Glu(CTC)	17	CM0584.320.nd,LjSGA_020155.0.1,LjSGA_020970.1.1,LjSGA_026679.0.2,LjSGA_067537.0.1,LjSGA_074662.0.1,LjT27E22.140.nd,chr1.CM0105.240.nd,chr1.CM0231.120.nd,chr2.CM0021.1260.nd,chr2.CM0081.200.nc,chr3.CM0112.60.nc,chr3.CM0282.200.nd,chr3.CM0634.350.nd,chr4.CM0046.90.nd,chr4.CM0399.310.nd,chr5.CM0071.380.nd
Glu(TTC)	20	LjSGA_022264.0.1,LjSGA_025542.1.2,LjSGA_031613.0.1,LjSGA_047288.0.1,LjSGA_079855.0.2,LjSGA_084909.0.1,LjSGA_093934.0.1,LjSGA_094806.1.1,LjSGA_096041.0.5,LjSGA_096996.0.3,LjSGA_097414.0.1,LjSGA_106085.0.2,LjSGA_134613.0.2,LjSGA_141655.0.3,chr1.CM0150.630.nd,chr2.CM0695.180.nc,chr4.CM0165.530.nd,chr5.CM0299.300.nc,chr6.CM0057.210.nc,chr6.CM0057.270.nd
Gly(CCC)	6	LjSGA_010960.1.1,LjSGA_039414.1.1,LjSGA_052328.0.1,LjSGA_145128.0.1,LjT32E09.120.nd,chr2.CM0124.450.nc
Gly(GCC)	19	LjSGA_000010.0.1,LjSGA_000262.0.1,LjSGA_000263.0.1,LjSGA_004114.0.1,LjSGA_004115.0.1,LjSGA_011112.0.1,LjSGA_053847.0.1,LjSGA_137274.0.2,LjT30N24.150.nd,LjT39P23.130.nd,chr1.CM0593.270.nc,chr2.CM0249.390.nd,chr2.CM0545.680.nc,chr2.CM0788.140.nc,chr3.CM0160.370.nc,chr3.CM0282.400.nc,chr3.CM0634.250.nd,chr5.CM0909.870.nc,chr5.CM0956.90.nc
Gly(TCC)	11	LjSGA_009853.1.1,LjSGA_011860.0.2,LjSGA_022461.0.2,LjSGA_053446.0.1,LjSGA_081371.0.1,LjSGA_082919.0.1,LjSGA_090583.0.1,LjSGA_118011.0.1,chr2.CM0191.50.nc,chr3.LjT42M03.20.nd,chr4.CM0046.330.nd
His(GTG)	18	LjB06H14.40.nc,LjSGA_000359.0.1,LjSGA_000360.0.1,LjSGA_030018.0.1,LjSGA_031628.1.1,LjSGA_039555.0.1,LjSGA_112596.1.1,LjSGA_125143.1.1,LjSGA_137513.1.1,chr2.CM0124.780.nc,chr2.CM1731.120.nc,chr4.CM0126.1610.nc,chr4.CM0131.550.nc,chr4.CM0429.190.nc,chr6.CM0055.1120.nd,chr6.CM0055.940.nc,chr6.CM0066.280.nc,chr6.CM0539.150.nd
Ile(AAT)	16	LjSGA_009760.1.1,LjSGA_015360.0.1,LjSGA_029490.0.1,LjSGA_043921.0.1,LjSGA_055163.0.1,LjSGA_060360.0.1,LjSGA_088256.0.1,LjSGA_146451.0.2,LjT37I20.10.nc,chr1.CM0206.310.nc,chr2.CM0304.720.nc,chr2.CM0338.130.nc,chr2.CM0695.390.nd,chr3.CM0091.170.nc,chr4.CM0046.290.nd,chr6.CM0118.1030.nd
Ile(TAT)	8	CM1489.230.nc,LjSGA_039056.0.1,LjSGA_052416.0.1,LjSGA_065592.0.1,LjSGA_145049.0.1,LjSGA_145716.0.1,chr1.CM0206.690.nd,chr2.CM0249.1380.nc
Leu(AAG)	11	LjSGA_012029.0.1,LjSGA_045260.0.1,LjSGA_046608.0.1,LjSGA_106296.0.1,LjSGA_108559.0.1,LjSGA_144261.0.1,LjSGA_146211.0.1,LjT01K02.70.nc,chr1.CM0032.490.nc,chr3.CM0396.40.nc,chr4.CM0244.700.nd
Leu(CAA)	23	LjSGA_040096.1.2,LjSGA_054896.1.1,LjSGA_058143.0.2,LjSGA_061891.1.1,LjSGA_063461.0.1,LjSGA_067953.0.1,LjSGA_073228.0.2,LjSGA_074276.1.1,LjSGA_080766.1.2,LjSGA_087372.0.1,LjSGA_088278.0.1,LjSGA_092461.1.2,LjSGA_093118.1.1,LjSGA_096917.1.1,LjSGA_099243.0.1,LjSGA_124861.0.2,LjT03D05.170.nd,LjT03D14.230.nd,LjT15B14.170.nd,chr2.CM0031.220.nc,chr3.CM0155.160.nd,chr3.CM0216.1000.nd,chr4.CM0007.740.nd
Leu(CAG)	5	LjSGA_013886.0.1,LjSGA_048985.0.1,LjSGA_066544.0.1,LjSGA_071668.0.1,chr4.CM0288.530.nc

Supplemental Table 5.

Leu(TAA)	11	CM0466.60.nd,LjB15A13.110.nd,LjSGA_027060.0.1,LjSGA_039051.0.1,LjSGA_042995.0.1,LjSGA_054971.0.1,LjSGA_117094.0.1,chr1.CM0233.540.nc,chr1.CM0233.570.nc,chr3.CM0396.100.nc,chr6.CM0539.360.nd
Leu(TAG)	16	LjSGA_004021.1.1,LjSGA_026149.0.1,LjSGA_056035.1.1,LjSGA_082599.0.2,LjSGA_087331.0.1,LjSGA_091078.0.1,LjSGA_098766.0.1,LjSGA_105817.0.1,LjSGA_110434.0.2,LjSGA_113687.1.2,LjSGA_117593.1.2,LjSGA_131846.0.1,LjT15N18.260.nd,chr1.CM0361.70.nd,chr1.CM0668.200.nd,chr5.CM0956.140.nc
Lys(CTT)	17	LjSGA_012238.0.1,LjSGA_015731.0.1,LjSGA_016083.0.1,LjSGA_022597.1.1,LjSGA_050142.0.1,LjSGA_092561.0.1,LjSGA_108228.0.1,LjSGA_149378.0.1,LjT25G12.120.nc,LjT30N04.50.nd,chr1.CM0001.100.nd,chr1.CM1255.260.nc,chr2.CM0021.800.nc,chr2.CM0304.120.nd,chr3.CM0396.220.nc,chr4.CM0075.240.nd,chr4.CM0831.110.nd
Lys(TTT)	12	LjSGA_000268.0.2,LjSGA_009653.0.1,LjSGA_115635.0.1,LjT04M14.20.nd,chr1.CM0375.460.nc,chr1.CM0800.410.nd,chr1.LjT29L18.130.nd,chr1.LjT46N10.150.nd,chr2.CM0074.70.nc,chr2.CM0405.90.nd,chr3.CM0164.110.nd,chr3.CM0164.150.nd
Met(CAT)	44	LjB08M07.20.nc,LjB12O06.70.nc,LjB15P09.130.nc,LjSGA_000215.0.1,LjSGA_000216.0.1,LjSGA_007732.0.1,LjSGA_007733.0.1,LjSGA_026513.0.1,LjSGA_031613.0.3,LjSGA_036925.0.1,LjSGA_039722.0.1,LjSGA_043939.0.1,LjSGA_048983.0.1,LjSGA_066558.1.1,LjSGA_070365.0.1,LjSGA_074815.1.2,LjSGA_083295.0.1,LjSGA_085476.0.2,LjSGA_088277.0.1,LjSGA_089547.0.1,LjSGA_091178.0.2,LjSGA_100702.0.1,LjSGA_105545.0.1,LjSGA_113221.0.1,LjSGA_114936.0.2,LjSGA_116228.1.1,LjSGA_117580.0.1,LjSGA_122818.1.2,LjSGA_125730.0.1,LjSGA_137274.0.1,LjSGA_147240.0.1,LjSGA_148875.0.1,LjT04N09.90.nd,LjT15D16.40.nc,chr1.CM0295.880.nc,chr2.CM0020.290.nc,chr2.CM0056.370.nd,chr2.CM0177.800.nc,chr4.CM0046.410.nc,chr4.CM0126.1520.nc,chr4.CM0126.1640.nc,chr4.CM0128.70.nc,chr6.CM0836.520.nd,chr6.LjT41B02.100.nd
Phe(GAA)	20	LjB15P09.110.nc,LjSGA_001054.1.2,LjSGA_001055.0.1,LjSGA_009322.1.1,LjSGA_013124.2.1,LjSGA_084901.0.1,LjSGA_093263.0.1,LjSGA_099318.0.1,LjSGA_120327.0.1,LjSGA_128613.0.1,LjSGA_144678.0.1,LjT01P07.150.nd,LjT30N04.20.nd,chr3.CM0160.380.nc,chr3.CM0590.760.nc,chr4.CM0007.640.nd,chr4.CM0007.650.nd,chr4.CM0026.150.nd,chr4.CM0126.1480.nc,chr5.CM0158.150.nc
Pro(AGG)	11	LjB15A13.90.nd,LjSGA_013630.0.1,LjSGA_036107.1.1,LjSGA_052886.1.1,LjSGA_079009.0.1,chr4.CM0007.1020.nc,chr5.CM0200.310.nc,chr5.CM0200.330.nc,chr5.CM0200.350.nc,chr5.CM0200.360.nc,chr5.CM0311.30.nd
Pro(CGG)	3	CM0300.170.nd,chr1.CM0206.110.nd,chr3.CM0216.650.nc
Pro(TGG)	24	CM0385.250.nd,LjSGA_001055.0.3,LjSGA_071951.0.3,LjSGA_073258.2.1,LjSGA_088474.0.1,LjSGA_089360.0.2,LjSGA_090124.0.2,LjSGA_122660.0.1,LjSGA_132441.0.1,LjSGA_133154.0.1,LjSGA_147069.0.1,LjT32D02.110.nc,chr4.CM0739.220.nd,chr4.LjT32J05.190.nc,chr5.CM0096.680.nd,chr5.CM0200.240.nc,chr5.CM0200.250.nc,chr5.CM0200.260.nc,chr5.CM0200.270.nc,chr5.CM0200.280.nc,chr5.CM0200.290.nc,chr5.CM0200.320.nc,chr5.CM0200.340.nc,chr5.CM0200.370.nc
Ser(AGA)	6	LjSGA_020405.1.1,LjSGA_020643.0.1,LjSGA_059744.0.1,LjSGA_123704.0.1,chr1.CM0094.390.nc,chr3.CM0253.190.nc
Ser(CGA)	2	LjSGA_117851.0.1,chr3.CM0152.210.nc
Ser(GCT)	12	LjSGA_001052.0.1,LjSGA_001053.0.1,LjSGA_001054.0.1,LjSGA_030084.0.1,LjSGA_102143.0.1,LjSGA_103862.0.2,LjSGA_103963.0.1,LjSGA_113972.0.1,LjT38P01.220.nd,chr1.LjT05B18.210.nd,chr3.CM0106.200.nc,chr3.CM0396.190.nc
Ser(GGA)	9	LjSGA_039703.0.2,LjSGA_043991.0.1,LjSGA_044596.0.2,LjSGA_048988.0.2,LjSGA_050867.1.1,LjSGA_056478.0.2,LjSGA_100446.1.1,LjSGA_112914.0.2,LjSGA_135849.0.2
Ser(TGA)	8	LjSGA_034895.0.1,LjSGA_037552.1.2,LjSGA_055949.1.1,LjT28I10.10.nd,chr1.CM0544.290.nc,chr2.CM0021.30.nd,chr3.CM0091.460.nd,chr5.CM0211.100.nc
Thr(AGT)	6	LjSGA_088932.0.1,chr1.CM0361.750.nc,chr2.CM0018.980.nc,chr2.CM0749.160.nd,chr5.CM0096.580.nd,chr6.LjT16B20.100.nc
Thr(CGT)	3	LjSGA_082982.0.1,chr2.CM0373.610.nc,chr4.CM0500.340.nd
Thr(GGT)	8	LjSGA_077259.0.1,LjSGA_079855.0.1,LjSGA_090887.0.1,LjSGA_106085.0.1,LjSGA_106854.0.1,LjSGA_129947.0.1,LjSGA_134613.0.1,LjSGA_141487.0.1
Thr(TGT)	19	LjB15P09.100.nc,LjSGA_009212.0.1,LjSGA_012727.0.1,LjSGA_038955.0.1,LjSGA_045892.0.1,LjSGA_046739.0.1,LjSGA_104100.0.1,LjSGA_113651.0.2,LjSGA_127963.0.1,LjSGA_135427.0.1,LjT10A21.70.nd,chr1.CM0166.120.nc,chr2.CM0304.1030.nc,chr3.CM0106.240.nc,chr4.CM0079.340.nd,chr4.CM0126.1470.nc,chr4.CM0501.20.nd,chr6.CM0539.140.nd,chr6.CM1829.30.nc
Trp(CCA)	20	LjSGA_015436.0.1,LjSGA_028747.0.1,LjSGA_033058.0.1,LjSGA_038071.0.2,LjSGA_044437.0.1,LjSGA_055001.0.1,LjSGA_071951.0.2,LjSGA_088474.0.2,LjSGA_089360.0.1,LjSGA_090124.0.1,LjSGA_096806.0.1,LjSGA_121270.0.1,LjSGA_122394.0.1,LjSGA_129403.0.1,LjSGA_132441.0.2,LjT46I09.30.nd,chr3.CM0226.60.nd,chr4.CM0100.260.nd,chr4.CM1334.180.nc,chr6.CM0139.750.nd
Tyr(GTA)	24	LjSGA_000581.1.2,LjSGA_000582.0.2,LjSGA_018216.1.1,LjSGA_021859.0.1,LjSGA_036925.0.2,LjSGA_041959.0.1,LjSGA_042153.0.1,LjSGA_055655.0.1,LjSGA_063963.0.1,LjSGA_075457.0.1,LjSGA_079855.0.3,LjSGA_096041.0.4,LjSGA_096996.0.2,LjSGA_097246.0.1,LjSGA_097414.0.2,LjSGA_104166.0.1,LjSGA_108939.0.1,LjSGA_132645.0.1,LjSGA_141655.0.2,LjT30N04.230.nd,LjT45I18.110.nd,chr1.CM0105.730.nc,chr3.CM0152.190.nc,chr6.LjT02P05.90.nd
Val(AAC)	11	CM0458.130.nd,LjSGA_005135.0.1,LjSGA_030967.0.1,chr1.CM0105.110.nd,chr1.CM0318.390.nc,chr1.CM0378.30.nc,chr2.CM0021.870.nd,chr2.CM0304.740.nc,chr2.CM1150.140.nd,chr3.LjT05P05.110.nd,chr3.LjT39G24.220.nd
Val(CAC)	4	LjSGA_021944.0.1,LjSGA_028647.0.1,chr1.CM0147.980.nc,chr4.CM0558.130.nd
Val(GAC)	6	LjSGA_035805.0.1,LjSGA_038943.0.1,LjSGA_056059.0.1,LjSGA_096800.0.1,LjSGA_118999.0.1,LjSGA_148702.0.1
Val(TAC)	4	chr3.CM0070.350.nc,chr3.CM0160.120.nc,chr3.LjT34H24.40.nd,chr6.LjT04E21.170.nc

Supplemental Table 6. List of miRNA precursor-encoding genes and the putative targets.

Genome/EST	Sequence (5'→3')	Length	Conserved Arabidopsis miRNA	Putative target	Annotation
SPD025h11_f	UGACAGAAGAGAGUGAGCAC	20	ath-miR156a/b/c/d/e/f	LjT31M07.90.nd	Squamosa promoter binding like-protein
LjSGA_046440	UGCCUGGCUCCCUGUAUGCCA	21	ath-miR160a/b/c	chr3.LjT10E18.60.nc	putative auxin response factor 10
LjT02P05	UGCCUGGCUCCCUGAAUGCCA	21	ath-miR160a/b/c		
LjT38I13	UGGAGAAGCAGGGCACGUGCA	21	ath-miR164a/b	LjSGA_137192.1	NAM (no apical meristem)-like protein
LjT29L06	UGGAGAAGCAGGGCACGUGCA	21	ath-miR164a/b	chr4.CM0087.800.nd	NAM (no apical meristem)-like protein
LjSGA_043888	UGGAGAAGCAGGGCACGUGCA	21	ath-miR164a/b		
LjSGA_008866	UGGAGAAGCAGGGCACGUGCA	21	ath-miR164a/b		
CM0299	UGGAGAAGCAGGGCACGUGCA	21	ath-miR164a/b		
CM0955	UCGGACCAGGCUUCAUUCCCC	21	ath-miR166a/b/c/d/e/f	LjSGA_101583.1	HD-zip transcription factor
CM0591	UCGGACCAGGCUUCAUUCCCC	21	ath-miR166a/b/c/d/e/f	LjSGA_035832.1	HD-zip transcription factor
LjSGA_018333	UCGGACCAGGCUUCAUUCCCC	21	ath-miR166a/b/c/d/e/f	LjSGA_016228.1	HD-zip transcription factor
CM0375	UCGGACCAGGUUUCAUUCCCC	21	ath-miR166a/b/c/d/e/f	LjSGA_014333.2	HD-zip transcription factor
LjSGA_020966	UCGGACCAGGCUUCAUUCCCU	21	ath-miR166a/b/c/d/e/f	LjSGA_029320.1	HD-zip transcription factor
				LjSGA_086292.1	HD-zip transcription factor
				chr3.LjT10E18.20.nc	HD-zip transcription factor
CM0322	UGAAGCUGCCAGCAUGAUCUA	21	ath-miR167a/b	chr2.LjT43I20.180.nd	auxin response factor
CM0803	UCGCUUGGUGCAGGUCGGGAA	21	ath-miR168a/b	MPDL007e07_f	Argonaute protein
LjT12G06	CAGCCAAGGAUGACUUGCCGG	21	ath-miR169b/c	chr3.CM0724.30.nd	transcription factor
LjSGA_058357	AAGCCAAGGAUGACUUGCCGG	21	ath-miR169b/c		
LjSGA_017129	CAGCCAAGGAUGACUUGCCGG	21	ath-miR169b/c		
LjSGA_014343	CAGCCAAGGAUGACUUGCCGG	21	ath-miR169b/c		
LjSGA_043512	CAGCCAAGGAUGACUUGCCGG	21	ath-miR169b/c		
LjT16A19	UGAUUGAGCCGCGCCAAUAUC	21	ath-miR171a	LjSGA_036968.1	Scarecrow-like 6
LjSGA_041313	UGAUUGAGCCGUGCCAAUAUC	21	ath-miR171a		
CM0055	UGAUUGAGCCGCGUCAAUAUC	21	ath-miR171a		
LjSGA_017253	UGAUUGAGCCGUGCCAAUAUC	21	ath-miR171a		
LjSGA_147834	UGAUUGAGCCGUGCCAAUAUC	21	ath-miR171a		
LjSGA_087681	UUGAGCCGUGCCAAUAUCACG	21	ath-miR171b		
LjSGA_027480	AGAAUCUUGAUGAUGCUGCAG	21	ath-miR172c/d	chr3.LjT05P05.30.nd	AP2 domain transcription factor
LjSGA_063209	AGAAUCUUGAUGAUGCUGCAU	21	ath-miR172a/b		
LjSGA_146667	AGAAUCUUGAUGAUGCUGCAU	21	ath-miR172a/b		
LjT44N20	AGAAUCUUGAUGAUGCUGCAU	21	ath-miR172a/b		
LjSGA_025466	UUGGACUGAAGGGAGCUCCC	20	ath-miR319a/b	LjSGA_035803.1	MYB family transcription factor
LjSGA_062796	UUGGACUGAAGGGAGCUCCU	20	ath-miR319c	chr3.CM0005.370.nc	transcription factor GAMYB
LjSGA_076794	UUGGACUGAAGGGAGCUCCU	20	ath-miR319c		
CM0360	UUGGACUGAAGGGAGCUCCU	20	ath-miR319c		
CM0116	AAGCUCAGGAGGGAUAGCGCC	21	ath-miR390a/b		
LjT09A09	AAGCUCAGGAGGGAUAGCGCC	21	ath-miR390a/b		
CM0148	UCCAAAGGGAUCGCAUUGAUC	21	ath-miR393a/b	LjSGA_042978.1	transport inhibitor response protein
LjT13M01	UCCAAAGGGAUCGCAUUGAUC	21	ath-miR393a/b	LjSGA_023031.1	transport inhibitor response protein
LjSGA_012464	UUGGCAUUCUGUCCACCUCC	20	ath-miR394a/b	LjSGA_028803.1	F-box protein
LjSGA_010860	AUGAAGUGUUUGGGGGAACUC	21	ath-miR395a/d/e	chr6.LjT23A02.80.nc	sulfate transporter
LjT04O21	UUUCACAGCUUUCAUGAACUG	21	ath-miR396a		
CM0953	UUCCACAGCUUUCUUGAACUG	21	ath-miR396a		
CM0003	UUCCACAGCUUUCUUGAACUU	21	ath-miR396b		
LjSGA_002401	UUAUUGAGUGCAGCGUUGAUG	21	ath-miR397a	chr3.CM0792.230.nd	laccase
				LjSGA_075846.2	laccase
				chr2.CM0249.1200.nc	laccase
CB829453	UGUGUUCUCAGGUCACCCCUU	21	ath-miR398a	LjSGA_088497.0.1	Cytochrome c oxidase subunit Vb
LjSGA_144108	UGCCAAAGGAGAGUUGCCCUG	21	ath-miR399b/c	LjSGA_077849.1	inorganic phosphate transperter
CM0953	UGCCAAAGGAGAGUUGCCCUG	21	ath-miR399b/c		
CM0126	AGCCAAAGAAGAGUUGCCCUG	21	ath-miR399b/c		
CM0046	UGCCAAAGGAGAUUUGCUCAG	21	ath-miR399d		
CM0046	CGCCAAAGAAGAUUUGCCCGG	21	ath-miR399f		
CM0046	UGCCAAAGGAGAUUUGCCCUG	21	ath-miR399a		
LjSGA_142734	AUGCACUGCCUCUUCCCUGGC	21	ath-miR408	LjSGA_034638.1	basic blue copper protein
CM0420	AUGCACUGCCUUUUCCCUGGC	21	ath-miR408		

Supplemental Table 7. Features of the deduced protein-encoding genes in the *L. japonicus* HGS.

Features	*L. japonicus*	*A. thaliana*
Gene length (bp) including introns	39-24,972 (2,917)	78-17,203 (1,918)
Product length (amino acids)	12-2,378 (433)	25-4,706 (427)
Genes with introns	3,968 (76%)	4,906 (76%)
Number of intron/gene	0-48 (4.1)	0-48 (4.0)
Coding exon length (bp)	2-5,262 (256)	2-5,966 (256)
Intron length (bp)	27-8,862 (395)	23-2,989 (157)
GC content of exons	45%	44%
GC content of Introns	33%	32%

Supplemental Table 8. Top 50 InterPro domains in the *L. japonicus* TGS.

InterPro ID	InterPro difinition	Number of genes
IPR011009	Protein kinase-like	929
IPR000719	Protein kinase	906
IPR002290	Serine/threonine protein kinase	581
IPR008271	Serine/threonine protein kinase, active site	469
IPR002885	Pentatricopeptide repeat	433
IPR001611	Leucine-rich repeat	396
IPR001810	Cyclin-like F-box	375
IPR009057	Homeodomain-like	317
IPR008940	Protein prenyltransferase	310
IPR001245	Tyrosine protein kinase	304
IPR001128	Cytochrome P450	261
IPR001841	Zinc finger, RING-type	260
IPR000504	RNA-binding region RNP-1 (RNA recognition motif)	226
IPR001005	Myb, DNA-binding	218
IPR001680	WD-40 repeat	204
IPR011046	WD40-like	170
IPR012336	Thioredoxin-like fold	167
IPR013210	Leucine rich repeat, N-terminal	160
IPR012337	Polynucleotidyl transferase, Ribonuclease H fold	154
IPR002048	Calcium-binding EF-hand	150
IPR001471	Pathogenesis-related transcriptional factor and ERF	146
IPR007087	Zinc finger, C2H2-type	140
IPR002213	UDP-glucuronosyl/UDP-glucosyltransferase	127
IPR005123	2OG-Fe(II) oxygenase	121
IPR002401	Cytochrome P450, E-class, group I	120
IPR003591	Leucine-rich repeat, typical subtype	119
IPR002182	NB-ARC	117
IPR003593	AAA+ ATPase, core	117
IPR000157	Toll-Interleukin receptor	115
IPR001087	Lipolytic enzyme, G-D-S-L	115
IPR003439	ABC transporter related	112
IPR002016	Haem peroxidase, plant/fungal/bacterial	110
IPR008972	Cupredoxin	110
IPR010255	Haem peroxidase	109
IPR011043	Galactose oxidase, central	105
IPR000767	Disease resistance protein	104
IPR011598	Helix-loop-helix DNA-binding	103
IPR011050	Pectin lyase fold/virulence factor	102
IPR013830	Esterase, SGNH hydrolase-type	102
IPR013026	Tetratricopeptide region	99
IPR000823	Plant peroxidase	98
IPR007114	Major facilitator superfamily	98
IPR006527	F-box associated type 1	97
IPR009072	Histone-fold	96
IPR003441	No apical meristem (NAM) protein	95
IPR001757	ATPase, P-type, K/Mg/Cd/Cu/Zn/Na/Ca/Na/H-transporter	92
IPR001878	Zinc finger, CCHC-type	92
IPR002110	Ankyrin	92
IPR001623	Heat shock protein DnaJ, N-terminal	91
IPR013101	Leucine-rich repeat 2	91

Supplemental Table 9. List of transcription factor domains found in the *L. japonicus* and *A. thaliana* genomes.

	L. japonicus	*A. thaliana*
C3H	183	164
MYB	156	138
AP2-EREBP	142	128
bHLH	118	162
C2H2 (Zn)	107	102
MADS	95	110
bZIP	88	73
ARF	75	24
NAC	71	90
WRKY (Zn)	63	72
C2C2 (Zn)	53	100
HB	41	89
HSF	37	21
SBP	33	16
GRAS	31	33
G2-like	23	40
GARP	20	55
ABI3/VP1	20	20
CCAAT	19	35
TCP	19	26
TUB	17	10
CAMTA	16	6
CPP (Zn)	9	8
BPC	8	7
GRF/ENBP (C3H-type2; Zn)	7	9
EIL	7	6
E2F/DP	7	8
Alfin-like	5	7
GeBP	5	16
BZR	4	6
VOZ-9	2	2
Total	1481	1583

*Data of *A. thaliana* TF was retrieved from AGRIS database at http://arabidopsis.med.ohio-state.edu/.

Supplemental Table 10. Cytochrome P450 genes in the genomes of *L. japonicus* and *A.thaliana*.

CYP subfamily	*L. japonicus*	*A. thaliana*
CYP51G	1	2
CYP71A	15	17
CYP71B	37	37
CYP72A	7	9
CYP72C	2	1
CYP73A	4	1
CYP74A	5	1
CYP74B	1	1
CYP75B	8	1
CYP76C	26	8
CYP76G	2	1
CYP77A	1	6
CYP77B	1	1
CYP78A	6	6
CYP79A	6	3
CYP79B	2	3
CYP79C	0	5
CYP79F	0	2
CYP81D	6	10
CYP81F	1	4
CYP81G	0	1
CYP81H	0	1
CYP81K	0	2
CYP82C	23	3
CYP82F	0	1
CYP82G	1	1
CYP83A	0	1
CYP83B	13	1
CYP84A	5	2
CYP85A	1	2
CYP86A	4	5
CYP86B	4	2
CYP86C	0	4
CYP87A	3	2
CYP88A	9	2
CYP89A	5	7
CYP90A	1	1
CYP90B	4	1
CYP90C	3	1
CYP90D	1	1
CYP93C	10	1
CYP94B	6	3
CYP94C	2	1
CYP94D	2	3
CYP96A	8	14
CYP97A	1	1
CYP97B	1	1
CYP97C	1	1
CYP98A	1	3
CYP701A	5	1
CYP702A	0	8
CYP703A	1	1
CYP704A	5	2
CYP704B	2	1
CYP705A	1	33
CYP706A	6	7
CYP707A	9	4
CYP708A	0	4
CYP709B	1	3
CYP710A	3	4
CYP711A	2	1
CYP712A	3	2
CYP714A	3	2
CYP715A	4	1
CYP716A	12	2
CYP718A	3	1
CYP720A	0	1
CYP721A	4	1
CYP722A	4	1
CYP724A	3	1
CYP734A	1	1
CYP735A	1	2
total	313	272

Supplemental Table 11. Disease registance genes in the *L. japonicus* TGS.

chr	map postion	clone/contig name	non-TIR NBS-LRR type	TIR NBS-LRR type
1	0.0	CM0174		1
1	0.8	LjT43O05		1
1	2.8	LjT27C19		1
1	28.9	CM0393		1
1	29.7	CM0141		1
1	31.3	LjT34H22	1	
1	33.7	LjB10L14	1	
1	34.9	LjT23O20		2
1	35.3	LjT36P09		1
1	42.2	CM0231		1
1	44.2	CM0147		1
1	45.0	CM0800		1
1	47.5	LjT16O03		1
1	52.6	CM0104		2
1	56.6	CM0098	1	
2	6.0	LjT16I15	1	
2	8.4	LjT37J22		1
2	27.4	LjT39I02	1	
2	40.3	CM0608		3
2	40.7	CM1150	2	
2	42.3	CM0056		1
2	48.9	CM0020	4	
2	49.3	CM0803	1	
2	51.7	CM0272	1	
2	55.2	CM0249	1	
2	60.9	CM0304		1
2	63.3	CM0346		1
2	67.3	LjT46G02	1	
2	67.7	CM0826	1	
2	68.1	CM0545	1	
2	69.3	LjT04L10		2
2	69.5	CM0099		1
2	69.7	LjT02C03		6
2	70.5	LjT42I05		1
2	72.5	CM0191	1	
3	5.3	CM0106	1	
3	7.7	CM0282		1
3	12.9	CM0590		1
3	13.8	CM0241		5
3	31.6	CM0116		1
3	32.0	TM0388		1
3	32.0	TM1548		3
3	32.0	TM0022	1	
3	34.0	CM0005		1
3	34.0	CM0690	1	
3	34.0	TM1367	1	

Supplemental Table 11.

3	36.8	CM0047		1
3	55.1	CM0049		2
3	74.8	CM0091		1
3	82.4	CM0127	1	
4	8.4	CM0007	1	
4	9.6	CM0832	1	
4	34.7	CM0179		1
4	69.2	CM0042		3
5	0.0	CM0089	2	
5	6.8	CM0345	1	
5	12.4	CM0571	2	
6	6.5	LjT19B22		1
6	27.6	CM0057		1
6	57.6	LjT04E21	1	
6	61.5	CM0055	2	
unmapped clones		LjB12O06		2
		CM0528		1
		CM0693		1
		LjT39P23		2
		LjT41B20		2
		CM0533		7
		LjT37O09		3
		LjT07P21		1
		LjT47D03		4
		LjT36L22		2
		LjT21I18		1
		LjT41B11		3
		CM0809	1	
		LjT46F23	1	
		LjT15I01	1	
		LjT47H21	1	
LjSGA			18	91
Total gene number			55	174

Supplemental Table12. The most frequently observed InterPro domains in the genes that are conserved in legumes but not in other plant species.

InterPro ID	InterPro difinition	Number of genes
IPR001810	Cyclin-like F-box	61
IPR013101	Leucine-rich repeat 2	26
IPR000719	Protein kinase	22
IPR011009	Protein kinase-like	22
IPR006527	F-box associated type 1	16
IPR001611	Leucine-rich repeat	14
IPR000157	Toll-Interleukin receptor	13
IPR003612	Plant lipid transfer protein/seed storage/trypsin-alpha amylase inhibitor	11
IPR003871	Protein of unknown function DUF223, Arabidopsis thaliana	10
IPR012337	Polynucleotidyl transferase, Ribonuclease H fold	10
IPR010264	Plant self-incompatibility S1	9
IPR001841	Zinc finger, RING-type	8
IPR002100	Transcription factor, MADS-box	8
IPR002885	Pentatricopeptide repeat	8
IPR003340	Transcriptional factor B3	8
IPR006121	Heavy metal transport/detoxification protein	8
IPR001087	Lipolytic enzyme, G-D-S-L	7
IPR001128	Cytochrome P450	7
IPR001245	Tyrosine protein kinase	7
IPR013210	Leucine rich repeat, N-terminal	7
IPR000215	Proteinase inhibitor I4, serpin	6
IPR001471	Pathogenesis-related transcriptional factor and ERF	6
IPR004314	Protein of unknown function DUF239, plant	6
IPR013128	Peptidase C1A, papain	6
IPR000668	Peptidase C1A, papain C-terminal	5
IPR001395	Aldo/keto reductase	5
IPR001563	Peptidase S10, serine carboxypeptidase	5
IPR003480	Transferase	5
IPR008949	Terpenoid synthase	5
IPR008972	Cupredoxin	5
IPR011043	Galactose oxidase, central	5

Supplemental Table13. The most frequently observed InterPro domains in the *L. japonicus* genes that do not have a counterpart in the public DNA databases.

InterPro ID	InterPro difinition	Number of genes
IPR000504	RNA-binding region RNP-1 (RNA recognition motif)	25
IPR001810	Cyclin-like F-box	22
IPR008994	Nucleic acid-binding, OB-fold	15
IPR006032	Ribosomal protein S12/S23	13
IPR001878	Zinc finger, CCHC-type	11
IPR000823	Plant peroxidase	8
IPR002016	Haem peroxidase, plant/fungal/bacterial	8
IPR010255	Haem peroxidase	8
IPR007087	Zinc finger, C2H2-type	7
IPR003441	No apical meristem (NAM) protein	6
IPR009057	Homeodomain-like	6
IPR010666	Zinc finger, GRF-type	6
IPR003612	Plant lipid transfer protein/seed storage/trypsin-alpha amylase inhibito	5
IPR008972	Cupredoxin	5
IPR010264	Plant self-incompatibility S1	5
IPR001005	Myb, DNA-binding	4
IPR001128	Cytochrome P450	4
IPR001841	Zinc finger, RING-type	4
IPR003245	Plastocyanin-like	4
IPR007243	Autophagy protein Apg6	4
IPR011009	Protein kinase-like	4
IPR013128	Peptidase C1A, papain	4
IPR013201	Proteinase inhibitor I29, cathepsin propeptide	4

Supplemental Table 14. List of the genes conserved in legumes but not in other plant species.		
gene name	product size (aa)	Description
chr1.CM0017.390.nd	331	(A2Q377) Nucleic acid-binding, OB-fold - Medicago truncatula (Barrel medic)
chr1.CM0032.150.nc	191	(Q1SI42) F-box associated, putative - Medicago truncatula (Barrel medic)
chr1.CM0032.80.nd	138	(Q1S6Z0) Ribonuclease T2 - Medicago truncatula (Barrel medic)
chr1.CM0033.1190.nc	139	(Q1SRN1) Integrase, catalytic region - Medicago truncatula (Barrel medic)
chr1.CM0098.50.nd	118	(Q1SJS5) Zinc finger, RING-type; RINGv - Medicago truncatula (Barrel medic)
chr1.CM0101.180.nc	126	(Q52ZP9) Suppressor of CONSTANS 1a (Fragment) - Pisum sativum (Garden pea)
chr1.CM0104.210.nc	506	(Q2HRN3) Transcription factor, MADS-box - Medicago truncatula (Barrel medic)
chr1.CM0104.340.nd	116	(A2Q5R3) Thioredoxin domain 2; Thioredoxin fold - Medicago truncatula (Barrel medic)
chr1.CM0125.80.nc	396	(Q1RWX3) Zinc finger, CCHC-type; Zinc finger, SWIM-type - Medicago truncatula (Barrel medic)
chr1.CM0145.70.nc	554	(A2Q1D6) Ovarian tumour, otubain, related - Medicago truncatula (Barrel medic)
chr1.CM0147.1070.nd	183	(A2Q1T1) Ubiquitin - Medicago truncatula (Barrel medic)
chr1.CM0195.310.nc	335	(Q1S216) Cyclin-like F-box; FBD - Medicago truncatula (Barrel medic)

chr1.CM0206.750.nc	382	(Q1T2S5) Cyclin-like F-box; F-box protein interaction domain; Galactose oxidase, central - Medicago truncatula (Barrel medic)
chr1.CM0233.40.nc	175	(Q1S5R2) At4g32860 - Medicago truncatula (Barrel medic)
chr1.CM0233.420.nc	666	(A2Q377) Nucleic acid-binding, OB-fold - Medicago truncatula (Barrel medic)
chr1.CM0233.500.nc	574	(Q1RU36) Hypothetical protein - Medicago truncatula (Barrel medic)
chr1.CM0233.520.nc	480	(Q2HSZ7) Cyclin-like F-box; FAR1; Zinc finger, SWIM-type - Medicago truncatula (Barrel medic)
chr1.CM0316.70.nd	369	(Q1S216) Cyclin-like F-box; FBD - Medicago truncatula (Barrel medic)
chr1.CM0316.80.nd	375	(Q1S216) Cyclin-like F-box; FBD - Medicago truncatula (Barrel medic)
chr1.CM0371.310.nc	284	(A2Q5N8) YT521-B-like protein - Medicago truncatula (Barrel medic)
chr1.CM0375.140.nd	131	(Q2HUN6) RNA-directed DNA polymerase (Reverse transcriptase); Ribonuclease H - Medicago truncatula (Barrel medic)
chr1.CM0375.190.nd	131	(Q2HUN6) RNA-directed DNA polymerase (Reverse transcriptase); Ribonuclease H - Medicago truncatula (Barrel medic)
chr1.CM0393.500.nd	235	(Q1SN43) Nucleic acid-binding, OB-fold, subgroup - Medicago truncatula (Barrel medic)
chr1.CM0410.50.nc	68	(Q1SCF3) AT5g39050/MXF12_60 - Medicago truncatula (Barrel medic)
chr1.CM0476.170.nc	860	(Q1S8L3) Hypothetical protein - Medicago truncatula (Barrel medic)
chr1.CM0496.60.nd	297	(Q1SPF6) Hypothetical protein - Medicago truncatula (Barrel medic)
chr1.CM0544.310.nc	79	(A2Q5Z5) Hypothetical protein - Medicago truncatula (Barrel medic)
chr1.CM0544.350.nc	200	(A2Q5Z9) Hypothetical protein - Medicago truncatula (Barrel medic)
chr1.CM0600.120.nd	111	(Q0PJK0) MYB transcription factor MYB88 - Glycine max (Soybean)
chr1.CM0668.120.nd	69	(A2Q3S6) Terpene synthase-like; Terpenoid synthase (Fragment) - Medicago truncatula (Barrel medic)

chr1.CM0760.20.nc	88	(Q1SYJ6) Hypothetical protein - Medicago truncatula (Barrel medic)
chr1.CM1956.490.nc	778	(Q2HU05) Integrase, catalytic region; Zinc finger, CCHC-type; Peptidase aspartic, catalytic - Medicago truncatula (Barrel medic)
chr1.CM1956.700.nc	223	(Q8RVA9) Succinate dehydrogenase subunit 4 - Pisum sativum (Garden pea)
chr1.LjT03I11.110.nd	214	(A2Q377) Nucleic acid-binding, OB-fold - Medicago truncatula (Barrel medic)
chr1.LjT03K08.120.nc	188	(Q1T0C2) Protein kinase - Medicago truncatula (Barrel medic)
chr1.LjT06I08.100.nc	72	(Q1ST07) Hypothetical protein - Medicago truncatula (Barrel medic)
chr1.LjT23O20.120.nd	428	(Q8S4X3) TIR-similar-domain-containing protein TSDC - Pisum sativum (Garden pea)
chr1.LjT34H22.50.nd	185	(Q69F86) Serine-threonine kinase - Phaseolus vulgaris (Kidney bean) (French bean)
chr1.LjT35C22.120.nc	193	(Q2HSY3) Nucleic acid-binding, OB-fold, subgroup - Medicago truncatula (Barrel medic)
chr1.LjT36F23.80.nd	182	(Q1S668) Cyclin-like F-box; F-box protein interaction domain - Medicago truncatula (Barrel medic)
chr1.LjT44L17.50.nd	77	(Q1SZE6) Hypothetical protein - Medicago truncatula (Barrel medic)
chr2.CM0018.1020.nc	300	(Q1RTJ9) Cyclin-like F-box; F-box protein interaction domain - Medicago truncatula (Barrel medic)
chr2.CM0018.1030.nc	369	(Q1S2E0) Cyclin-like F-box; F-box protein interaction domain; Galactose oxidase, central - Medicago truncatula (Barrel medic)
chr2.CM0018.910.nc	399	(A2Q377) Nucleic acid-binding, OB-fold - Medicago truncatula (Barrel medic)
chr2.CM0021.300.nc	439	(Q1SCA5) Hypothetical protein - Medicago truncatula (Barrel medic)

chr2.CM0021.470.nc	379	(Q1S161) F-box protein interaction domain - Medicago truncatula (Barrel medic)
chr2.CM0021.980.nd	231	(A2Q1D6) Ovarian tumour, otubain, related - Medicago truncatula (Barrel medic)
chr2.CM0058.310.nd	333	(Q1SH60) Disease resistance protein; AAA ATPase - Medicago truncatula (Barrel medic)
chr2.CM0099.110.nc	100	(Q56NI2) MADS box protein M8 - Pisum sativum (Garden pea)
chr2.CM0177.250.nc	360	(Q1SST4) Polynucleotidyl transferase, Ribonuclease H fold - Medicago truncatula (Barrel medic)
chr2.CM0191.200.nc	184	(Q6KC90) FtsH-like protease - Pisum sativum (Garden pea)
chr2.CM0191.430.nc	87	(A1IHM7) Polyketide reductase - Lotus japonicus
chr2.CM0201.520.nd	242	(O24088) MtN24 protein - Medicago truncatula (Barrel medic)
chr2.CM0201.540.nd	247	(O24088) MtN24 protein - Medicago truncatula (Barrel medic)
chr2.CM0272.440.nd	380	(Q2HS67) Cyclin-like F-box; F-box protein interaction domain - Medicago truncatula (Barrel medic)
chr2.CM0338.270.nd	76	(A2Q516) SAM (And some other nucleotide) binding motif - Medicago truncatula (Barrel medic)
chr2.CM0545.190.nd	224	(A2Q1D6) Ovarian tumour, otubain, related - Medicago truncatula (Barrel medic)
chr2.CM0803.810.nd	76	(Q2MIY7) Cytochrome P450 monooxygenase CYP707A17 (Fragment) - Medicago truncatula (Barrel medic)
chr2.CM0826.30.nc	343	(Q1S223) Cyclin-like F-box; FBD - Medicago truncatula (Barrel medic)
chr2.CM0826.80.nc	342	(Q1S223) Cyclin-like F-box; FBD - Medicago truncatula (Barrel medic)
chr2.CM1032.180.nc	103	(Q1RXM5) Hypoxia induced protein conserved region - Medicago truncatula (Barrel medic)

chr2.LjT02E02.130.nd	128	(Q1ACB4) Homogentisate phytyltransferase VTE2-1 - Glycine max (Soybean)
chr2.LjT03I05.130.nc	102	(O24101) MtN5 protein precursor - Medicago truncatula (Barrel medic)
chr2.LjT03I05.160.nc	102	(O24101) MtN5 protein precursor - Medicago truncatula (Barrel medic)
chr2.LjT03I05.170.nc	102	(O24101) MtN5 protein precursor - Medicago truncatula (Barrel medic)
chr2.LjT10F02.180.nd	217	(Q1SCZ2) Transcriptional factor B3 - Medicago truncatula (Barrel medic)
chr2.LjT37J22.210.nd	240	(Q1RUJ1) Leucine-rich repeat - Medicago truncatula (Barrel medic)
chr3.CM0005.830.nd	341	(Q1SQ19) F-box protein interaction domain - Medicago truncatula (Barrel medic)
chr3.CM0049.110.nd	199	(Q1RW52) Cyclin-like F-box; F-box protein interaction domain - Medicago truncatula (Barrel medic)
chr3.CM0059.220.nc	248	(Q1SN43) Nucleic acid-binding, OB-fold, subgroup - Medicago truncatula (Barrel medic)
chr3.CM0070.210.nc	608	(Q1SJ05) Hypothetical protein - Medicago truncatula (Barrel medic)
chr3.CM0080.140.nd	141	(Q8LLR3) Ethylene-responsive element binding protein 1 - Glycine max (Soybean)
chr3.CM0091.420.nd	101	(Q41126) Non-specific lipid transfer-like protein - Phaseolus vulgaris (Kidney bean) (French bean)
chr3.CM0091.540.nc	112	(Q9FUP6) Suspensor-specific protein - Phaseolus coccineus (Scarlet runner bean)
chr3.CM0111.400.nd	67	(Q0GPF4) BZIP transcription factor bZIP132 - Glycine max (Soybean)
chr3.CM0111.80.nd	134	(Q1RVI4) Fasciclin domain, putative - Medicago truncatula (Barrel medic)
chr3.CM0112.250.nd	133	(Q84VH6) Gag-pol polyprotein - Glycine max (Soybean)

chr3.CM0116.220.nc	212	(Q1RY66) Hypothetical protein - Medicago truncatula (Barrel medic)
chr3.CM0127.720.nc	255	(Q1S8A0) Cyclin-like F-box; F-box protein interaction domain - Medicago truncatula (Barrel medic)
chr3.CM0127.870.nc	507	(Q2HRQ4) Transcription factor, MADS-box - Medicago truncatula (Barrel medic)
chr3.CM0142.50.nd	200	(Q1S6C8) VQ - Medicago truncatula (Barrel medic)
chr3.CM0155.350.nc	208	(Q1SN43) Nucleic acid-binding, OB-fold, subgroup - Medicago truncatula (Barrel medic)
chr3.CM0160.770.nd	91	(Q1RY21) Hypothetical protein - Medicago truncatula (Barrel medic)
chr3.CM0196.260.nc	157	(Q2HT06) Hypothetical protein - Medicago truncatula (Barrel medic)
chr3.CM0208.110.nd	1333	(Q1S7C5) Integrase, catalytic region - Medicago truncatula (Barrel medic)
chr3.CM0213.110.nc	287	(A2Q377) Nucleic acid-binding, OB-fold - Medicago truncatula (Barrel medic)
chr3.CM0241.270.nc	163	(Q1SYP3) Leucine Rich Repeat, putative - Medicago truncatula (Barrel medic)
chr3.CM0246.50.nd	108	(Q1S193) Alpha/beta hydrolase fold - Medicago truncatula (Barrel medic)
chr3.CM0292.290.nd	51	(Q84PE1) Multifunctional beta-amyrin synthase - Lotus japonicus
chr3.CM0355.80.nc	609	(Q1SJ05) Hypothetical protein - Medicago truncatula (Barrel medic)
chr3.CM0396.600.nc	314	(Q1S5X3) Cyclin-like F-box; FBD - Medicago truncatula (Barrel medic)
chr3.CM0574.20.nc	258	(Q1SMB9) Glucosyltransferase, putative - Medicago truncatula (Barrel medic)
chr3.CM0711.260.nc	157	(Q9SBR5) Putative wound-induced protein - Medicago varia (Alfalfa)
chr3.CM0792.200.nd	125	(Q2HS30) Hypothetical protein - Medicago truncatula (Barrel medic)
chr3.CM1144.20.nc	250	(Q1SHX0) Ribosomal protein S2; Oligopeptide transporter OPT superfamily - Medicago truncatula (Barrel medic)
chr3.LjT09M07.10.nd	261	(Q1SVR4) Hypothetical protein - Medicago truncatula (Barrel medic)

chr3.LjT11G09.20.nc	80	(Q75NI3) Type 2 metallothionein - Phaseolus aureus (Mung bean) (Vigna radiata)
chr3.LjT34H24.140.nd	79	(Q2HVX2) Embryo-specific 3 - Medicago truncatula (Barrel medic)
chr3.LjT39G24.230.nd	237	(Q1SE34) Cyclin-like F-box; tRNA-binding arm - Medicago truncatula (Barrel medic)
chr3.LjT42M03.80.nd	103	(Q1SGX5) Peptidase S10, serine carboxypeptidase - Medicago truncatula (Barrel medic)
chr4.CM0004.230.nd	78	(Q1SEA5) Hypothetical protein - Medicago truncatula (Barrel medic)
chr4.CM0042.2200.nc	352	(Q1SN01) Hypothetical protein - Medicago truncatula (Barrel medic)
chr4.CM0046.760.nc	304	(Q1SNE2) Expressed protein, putative - Medicago truncatula (Barrel medic)
chr4.CM0079.320.nc	192	(Q1SZJ0) Cyclin-dependent kinase inhibitor - Medicago truncatula (Barrel medic)
chr4.CM0100.350.nd	231	(Q1SFW1) Hypothetical protein - Medicago truncatula (Barrel medic)
chr4.CM0126.1450.nc	160	(Q1ST36) Agenet - Medicago truncatula (Barrel medic)
chr4.CM0126.650.nc	195	(Q1SUD8) Zinc finger, CCHC-type; Zinc finger, SWIM-type - Medicago truncatula (Barrel medic)
chr4.CM0165.330.nd	57	(Q0GPG1) BZIP transcription factor bZIP117 - Glycine max (Soybean)
chr4.CM0165.60.nd	193	(A2Q354) Harpin-induced 1 - Medicago truncatula (Barrel medic)
chr4.CM0170.110.nd	207	(A2Q2Z7) Contains similarity to reverse trancriptase , related - Medicago truncatula (Barrel medic)
chr4.CM0234.180.nc	448	(A2Q377) Nucleic acid-binding, OB-fold - Medicago truncatula (Barrel medic)

chr4.CM0333.140.nd	190	(Q1SWC3) T6A9.7 protein-Arabidopsis thaliana - Medicago truncatula (Barrel medic)
chr4.CM0337.190.nd	94	(Q9XHD6) Polygalacturonase inhibitor protein (Fragment) - Glycine max (Soybean)
chr4.CM0421.220.nd	251	(Q1T1H3) Cadmium-transporting ATPase; ATPase, E1-E2 type - Medicago truncatula (Barrel medic)
chr4.CM0558.40.nd	120	(Q9SBR6) Enod93 protein - Medicago varia (Alfalfa)
chr4.CM1616.400.nc	88	(Q5UB06) Wound-inducible putative chloroplast terpene synthase 3 - Medicago truncatula (Barrel medic)
chr4.LjT13D08.190.nd	275	(Q1T2M2) Protein kinase - Medicago truncatula (Barrel medic)
chr4.LjT233I03.20.nd	260	(Q1SDV9) Hypothetical protein - Medicago truncatula (Barrel medic)
chr5.CM0019.150.nd	164	(Q1RV67) Glycoside hydrolase, family 32 - Medicago truncatula (Barrel medic)
chr5.CM0040.790.nc	92	(Q1SCZ2) Transcriptional factor B3 - Medicago truncatula (Barrel medic)
chr5.CM0062.80.nd	61	(A2Q5Q4) Glycoside hydrolase, family 17; X8 - Medicago truncatula (Barrel medic)
chr5.CM0072.390.nd	64	(Q1SM56) Peptidase C19, ubiquitin carboxyl-terminal hydrolase 2; Ubiquitin carboxyl-terminal hydrolase, N-terminal region 1 - Medicago truncatula (Barrel medic)
chr5.CM0089.1240.nd	122	(Q6Y1E6) Cysteine protease 8 - Trifolium repens (Creeping white clover)
chr5.CM0095.160.nc	86	(Q1T152) IMP dehydrogenase/GMP reductase (Disease resistance protein; GTP-binding signal recognition particle SRP54, G-domain) - Medicago truncatula (Barrel medic)

chr5.CM0096.30.nc	72	(Q2HRI3) Hypothetical protein - Medicago truncatula (Barrel medic)
chr5.CM0148.230.nc	124	(A2Q5P6) Protein phosphatase inhibitor - Medicago truncatula (Barrel medic)
chr5.CM0158.40.nc	244	(Q1SN43) Nucleic acid-binding, OB-fold, subgroup - Medicago truncatula (Barrel medic)
chr5.CM0239.110.nd	141	(Q1RU09) Polynucleotidyl transferase, Ribonuclease H fold - Medicago truncatula (Barrel medic)
chr5.CM0239.50.nd	138	(Q1RU06) Polynucleotidyl transferase, Ribonuclease H fold - Medicago truncatula (Barrel medic)
chr5.CM0239.90.nd	203	(Q1RU09) Polynucleotidyl transferase, Ribonuclease H fold - Medicago truncatula (Barrel medic)
chr5.CM0335.310.nd	233	(Q41111) Dehydrin - Phaseolus vulgaris (Kidney bean) (French bean)
chr5.CM0335.60.nc	248	(Q2HSY3) Nucleic acid-binding, OB-fold, subgroup - Medicago truncatula (Barrel medic)
chr5.CM0357.700.nc	603	(Q1RU36) Hypothetical protein - Medicago truncatula (Barrel medic)
chr5.CM0569.110.nd	82	(Q4VYC7) Coiled-coil-helix-coiled-coil-helix domain containing protein - Medicago truncatula (Barrel medic)
chr5.CM0909.420.nc	707	(Q1SYZ2) Transposase - Medicago truncatula (Barrel medic)
chr5.CM0909.570.nc	287	(Q1SDV9) Hypothetical protein - Medicago truncatula (Barrel medic)
chr5.CM0911.110.nd	226	(Q1S2W5) NB-ARC domain, putative - Medicago truncatula (Barrel medic)
chr5.CM0953.370.nd	81	(Q1S104) Embryo-specific 3 - Medicago truncatula (Barrel medic)
chr5.CM1125.360.nc	276	(Q1S7I4) Helix-loop-helix DNA-binding - Medicago truncatula (Barrel medic)
chr5.CM1125.60.nc	145	(Q1S0T4) Cyclin-like F-box - Medicago truncatula (Barrel medic)
chr5.LjT10N02.230.nd	79	(Q9ZRY4) NDX1 homeobox protein - Lotus japonicus

chr5.LjT40M15.30.nc	138	(Q1RW23) Plant self-incompatibility S1 - Medicago truncatula (Barrel medic)
chr5.LjT41L03.130.nd	99	(Q1T3I5) Hypothetical protein - Medicago truncatula (Barrel medic)
chr6.CM0045.110.nc	257	(Q1T444) At1g16840/F17F16.27-related - Medicago truncatula (Barrel medic)
chr6.CM0066.460.nd	54	(Q2HST1) Ferric reductase-like transmembrane component - Medicago truncatula (Barrel medic)
chr6.CM0118.840.nc	350	(Q1SS60) RNA-directed DNA polymerase (Reverse transcriptase); Zinc finger, CCHC-type; Ribonuclease H - Medicago truncatula (Barrel medic)
chr6.CM0139.20.nd	80	(Q1W5W2) Adenylate isopentenyltransferase - Lotus japonicus
chr6.CM0302.50.nc	305	(A2Q5X7) Ovarian tumour, otubain, putative - Medicago truncatula (Barrel medic)
chr6.CM0314.200.nd	179	(Q1T553) Reverse transcriptase (RNA-dependent DNA polymerase), putative - Medicago truncatula (Barrel medic)
chr6.CM0437.350.nc	304	(Q1S4X6) Hypothetical protein - Medicago truncatula (Barrel medic)
chr6.LjT02P05.40.nd	71	(A2Q5G7) Heavy metal transport/detoxification protein - Medicago truncatula (Barrel medic)
chr6.LjT19B22.130.nd	115	(Q9M7D7) Lipid transfer protein - Pisum sativum (Garden pea)
chr6.LjT30N23.170.nd	216	(Q1RX94) IMP dehydrogenase/GMP reductase - Medicago truncatula (Barrel medic)
chr6.LjT34O10.30.nd	120	(Q1SM53) Hypothetical protein - Medicago truncatula (Barrel medic)
chr6.LjT36L14.120.nd	121	(A2Q3A4) Hypothetical protein - Medicago truncatula (Barrel medic)

chr6.LjT36L14.200.nd	143	(Q1SYX5) Protein kinase - Medicago truncatula (Barrel medic)
chr6.LjT45M04.270.nd	59	(Q2MJ13) Cytochrome P450 monooxygenase CYP83E9 - Medicago truncatula (Barrel medic)
CM0300.120.nd	326	(Q1T2T1) Cyclin-like F-box; F-box protein interaction domain - Medicago truncatula (Barrel medic)
CM0300.190.nd	234	(Q1SVM0) Cyclin-like F-box - Medicago truncatula (Barrel medic)
CM0385.320.nd	173	(A2Q147) Exostosin-like - Medicago truncatula (Barrel medic)
LjB14K02.80.nc	284	(Q1SIK3) Cyclin-like F-box; F-box protein interaction domain; Galactose oxidase, central - Medicago truncatula (Barrel medic)
LjT01D09.130.nd	174	(A2Q377) Nucleic acid-binding, OB-fold - Medicago truncatula (Barrel medic)
LjT01K02.120.nc	150	(Q1SMY2) Alcohol dehydrogenase superfamily, zinc-containing - Medicago truncatula (Barrel medic)
LjT02J13.110.nc	133	(Q1S1V9) Heavy metal transport/detoxification protein - Medicago truncatula (Barrel medic)
LjT02N03.50.nd	125	(Q1T3I5) Hypothetical protein - Medicago truncatula (Barrel medic)
LjT04D09.180.nd	84	(Q9SEL1) Seed maturation protein PM23 (Fragment) - Glycine max (Soybean)
LjT06I09.10.nd	116	(Q1SJ80) Cornichon - Medicago truncatula (Barrel medic)
LjT07J01.30.nd	199	(Q1SMB6) Cyclin-like F-box; F-box protein interaction domain - Medicago truncatula (Barrel medic)
LjT07J01.80.nd	189	(Q1S6B6) Cyclin-like F-box; F-box protein interaction domain - Medicago truncatula (Barrel medic)
LjT07J23.20.nd	170	(A2Q377) Nucleic acid-binding, OB-fold - Medicago truncatula (Barrel medic)

LjT10C06.90.nd	339	(Q1SHD0) Leucine Rich Repeat, putative - Medicago truncatula (Barrel medic)
LjT11L09.170.nd	92	(Q00M65) Expressed protein-like protein - Glycine max (Soybean)
LjT13A22.70.nc	136	(Q2HSY3) Nucleic acid-binding, OB-fold, subgroup - Medicago truncatula (Barrel medic)
LjT13L04.100.nc	327	(Q1SAG6) Cyclin-like F-box; FBD - Medicago truncatula (Barrel medic)
LjT13L04.50.nc	327	(Q1SAG6) Cyclin-like F-box; FBD - Medicago truncatula (Barrel medic)
LjT14E23.70.nc	259	(Q1SCZ2) Transcriptional factor B3 - Medicago truncatula (Barrel medic)
LjT15A10.50.nd	279	(Q1SUI8) Beta tubulin - Medicago truncatula (Barrel medic)
LjT15F17.140.nd	66	(Q1RV67) Glycoside hydrolase, family 32 - Medicago truncatula (Barrel medic)
LjT16H12.130.nd	96	(Q1RSC2) Pentatricopeptide repeat - Medicago truncatula (Barrel medic)
LjT16H12.280.nd	121	(Q1SWM3) Proteinase inhibitor, propeptide - Medicago truncatula (Barrel medic)
LjT17L12.190.nd	153	(Q1T3E8) Helix-turn-helix, AraC type; NAD-binding site; Fumarate lyase - Medicago truncatula (Barrel medic)
LjT18C07.90.nc	187	(Q2PER6) Putative Asp1 - Trifolium pratense (Red clover)
LjT21I06.100.nd	65	(Q1RZG7) Hypothetical protein - Medicago truncatula (Barrel medic)
LjT22N06.120.nd	227	(Q1S2G8) Cyclin-like F-box; FBD - Medicago truncatula (Barrel medic)
LjT22N06.140.nd	228	(Q1S2G8) Cyclin-like F-box; FBD - Medicago truncatula (Barrel medic)
LjT24M21.10.nd	348	(Q1SMB6) Cyclin-like F-box; F-box protein interaction domain - Medicago truncatula (Barrel medic)
LjT24M21.180.nd	348	(Q1SMB6) Cyclin-like F-box; F-box protein interaction domain - Medicago truncatula (Barrel medic)

LjT24M21.190.nd	348	(Q1SMB6) Cyclin-like F-box; F-box protein interaction domain - Medicago truncatula (Barrel medic)
LjT25G12.10.nc	113	(Q4VPE7) Lateral organ boundaries-like 4 (Fragment) - Lotus japonicus
LjT25I18.100.nc	395	(Q1S8I3) RNA-directed DNA polymerase (Reverse transcriptase); Expansin/Lol pI - Medicago truncatula (Barrel medic)
LjT30J19.180.nd	308	(A2Q377) Nucleic acid-binding, OB-fold - Medicago truncatula (Barrel medic)
LjT30J19.30.nd	138	(Q2HVD7) Nucleic acid-binding, OB-fold, subgroup - Medicago truncatula (Barrel medic)
LjT32M01.110.nd	197	(Q2HV31) Prefoldin - Medicago truncatula (Barrel medic)
LjT39N06.110.nd	59	(Q1T5H1) Multi antimicrobial extrusion protein MatE - Medicago truncatula (Barrel medic)
LjT41B11.140.nd	608	(Q1SJ05) Hypothetical protein - Medicago truncatula (Barrel medic)
LjT44L11.30.nd	60	(Q1T2K5) Alpha/beta hydrolase fold - Medicago truncatula (Barrel medic)
LjT45C19.100.nd	144	(Q1RW23) Plant self-incompatibility S1 - Medicago truncatula (Barrel medic)
LjT46F13.30.nd	69	(Q533S8) MADS box protein AP1a - Lotus japonicus
LjT46I09.80.nd	193	(Q1SBL6) Putative phytochrome kinase substrate 1, putative - Medicago truncatula (Barrel medic)
LjT46P06.100.nd	434	(Q1SVR4) Hypothetical protein - Medicago truncatula (Barrel medic)
LjT46P10.200.nd	138	(O04180) Pge1 protein - Lotus japonicus
LjT47D03.100.nd	148	(A2Q6G3) TIR; AAA ATPase - Medicago truncatula (Barrel medic)
LjT47H21.20.nd	283	(Q1SN43) Nucleic acid-binding, OB-fold, subgroup - Medicago truncatula (Barrel medic)
chr1.CM0001.150.nd	184	(Q8GYP3) Hypothetical protein At2g30280 - Arabidopsis thaliana (Mouse-ear cress)

chr1.CM0001.210.nd	139	(Q9FNC0) Gb|AAD10670.1 (Hypothetical protein) (Hypothetical protein At5g44060) (Hypothetical protein At5g44060/MRH10_17) - Arabidopsis thaliana (Mouse-ear cress)
chr1.CM0012.640.nd	96	(A3AE38) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr1.CM0016.200.nc	218	(Q1S6N3) Hypothetical protein - Medicago truncatula (Barrel medic)
chr1.CM0017.470.nc	52	(A3B432) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr1.CM0033.530.nc	115	(Q6NLG8) At4g33550 - Arabidopsis thaliana (Mouse-ear cress)
chr1.CM0078.60.nc	458	(Q681X9) Hypothetical protein At1g21560 - Arabidopsis thaliana (Mouse-ear cress)
chr1.CM0088.160.nd	93	(A2WTT4) Hypothetical protein - Oryza sativa (indica cultivar-group)
chr1.CM0094.430.nd	115	(Q6NLG8) At4g33550 - Arabidopsis thaliana (Mouse-ear cress)
chr1.CM0101.170.nc	320	(Q9LQJ0) F28G4.15 protein (Hypothetical protein) - Arabidopsis thaliana (Mouse-ear cress)
chr1.CM0104.80.nd	63	(Q1S020) 2OG-Fe(II) oxygenase - Medicago truncatula (Barrel medic)
chr1.CM0105.500.nc	110	(Q1SHH1) Ribosomal protein 60S - Medicago truncatula (Barrel medic)
chr1.CM0105.650.nc	102	(Q1SIU5) O-methyltransferase, family 2 - Medicago truncatula (Barrel medic)
chr1.CM0109.160.nd	64	(Q1RV36) Ribosomal protein L19e - Medicago truncatula (Barrel medic)
chr1.CM0113.240.nc	86	(A1C1I1) Apocytochrome b (Fragment) - Eichhornia azurea
chr1.CM0113.380.nd	210	(A3B010) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr1.CM0113.450.nd	182	(Q6VN49) Putative cysteine proteinase (Peptidase C1A, papain; Peptidase M14, carboxypeptidase A) - Medicago truncatula (Barrel medic)
chr1.CM0133.1230.nd	70	(Q9FIV1) Gb|AAF02153.1 - Arabidopsis thaliana (Mouse-ear cress)
chr1.CM0141.120.nd	68	(Q9MBG4) Lipoate protein ligase-like protein - Arabidopsis thaliana (Mouse-ear cress)

chr1.CM0145.100.nc	107	(Q1T4Z9) CTP synthase - Medicago truncatula (Barrel medic)
chr1.CM0145.350.nd	132	(Q4VSU3) Hcr9-OR2C - Solanum pimpinellifolium (Currant tomato) (Lycopersicon pimpinellifolium)
chr1.CM0147.30.nd	62	(Q0WLF7) Hypothetical protein (At1g61667) - Arabidopsis thaliana (Mouse-ear cress)
chr1.CM0147.690.nc	671	(Q9FNS1) MYB-like DNA-binding protein - Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle)
chr1.CM0147.740.nc	128	(Q1S2F4) UDP-glucose glucosyltransferase - Medicago truncatula (Barrel medic)
chr1.CM0147.920.nc	247	(Q65XA5) Hypothetical protein OJ1654_B10.13 (Hypothetical protein) (Os05g0115600 protein) (Unknow protein) - Oryza sativa (japonica cultivar-group)
chr1.CM0150.180.nd	80	(Q1S2B0) No apical meristem (NAM) protein - Medicago truncatula (Barrel medic)
chr1.CM0150.360.nc	166	(Q9ATD0) WD1521 - Gossypium hirsutum (Upland cotton) (Gossypium mexicanum)
chr1.CM0171.850.nd	125	(Q8GT65) Serpin-like protein (Fragment) - Citrus paradisi (Grapefruit)
chr1.CM0171.880.nd	226	(A2Q2N0) Proteinase inhibitor I4, serpin - Medicago truncatula (Barrel medic)
chr1.CM0178.160.nd	124	(Q1S7V9) At1g05410/T25N20_5 (Hypothetical protein) - Medicago truncatula (Barrel medic)
chr1.CM0192.120.nc	180	(A3CES3) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr1.CM0192.130.nc	76	(Q69UZ3) Putative ATP-dependent proteinase LON2 - Oryza sativa (japonica cultivar-group)
chr1.CM0206.1000.nd	125	(Q1SRV3) Pathogenesis-related transcriptional factor and ERF - Medicago truncatula (Barrel medic)

chr1.CM0248.440.nc	108	(Q2HTD6) RNA-binding region RNP-1 (RNA recognition motif); Calcium-binding EF-hand - Medicago truncatula (Barrel medic)
chr1.CM0269.30.nd	166	(Q7X8D0) OSJNBa0035M09.3 protein (Hypothetical protein) (OSJNBb0015N08.13 protein) - Oryza sativa (japonica cultivar-group)
chr1.CM0275.140.nd	95	(Q42792) Asparagine synthetase (EC 6.3.5.4) - Glycine max (Soybean)
chr1.CM0284.150.nd	384	(Q1RW53) Cyclin-like F-box; F-box protein interaction domain - Medicago truncatula (Barrel medic)
chr1.CM0284.170.nc	288	(Q2HV76) F-box protein interaction domain; Galactose oxidase, central - Medicago truncatula (Barrel medic)
chr1.CM0295.1070.nc	246	(A4GZJ9) HECT - Medicago truncatula (Barrel medic)
chr1.CM0295.330.nd	187	(Q43411) SRK3 gene - Brassica oleracea (Wild cabbage)
chr1.CM0315.70.nd	302	(A2WU16) Hypothetical protein - Oryza sativa (indica cultivar-group)
chr1.CM0316.40.nd	211	(Q1SVM0) Cyclin-like F-box - Medicago truncatula (Barrel medic)
chr1.CM0318.710.nd	76	(Q1SHW4) Hypothetical protein - Medicago truncatula (Barrel medic)
chr1.CM0320.110.nc	234	(Q9FN67) Gb|AAD56319.1 (Hypothetical protein At5g41330) (At5g41330) - Arabidopsis thaliana (Mouse-ear cress)
chr1.CM0322.100.nc	151	(A2Y959) Hypothetical protein - Oryza sativa (indica cultivar-group)
chr1.CM0361.40.nd	214	(Q38HU4) Thaliana 60S ribosomal protein L7 (At2g44120) - Solanum tuberosum (Potato)
chr1.CM0371.240.nc	88	(Q1RTR5) Hypothetical protein - Medicago truncatula (Barrel medic)
chr1.CM0393.320.nd	187	(Q9LPF6) T12C22.2 protein (Hypothetical protein At1g44750) (Hypothetical protein At1g44750; T12C22.2) - Arabidopsis thaliana (Mouse-ear cress)
chr1.CM0393.40.nd	81	(Q9FLK9) Leucine-rich repeat disease resistance protein-like (Cf-5 disease resistance protein-like) - Arabidopsis thaliana (Mouse-ear cress)

chr1.CM0442.400.nd	221	(Q1SIQ4) Transcription factor, MADS-box - Medicago truncatula (Barrel medic)
chr1.CM0579.360.nd	75	(Q9M308) Hypothetical protein F2A19.210 - Arabidopsis thaliana (Mouse-ear cress)
chr1.CM0591.290.nd	168	(Q3EA28) Protein At4g14805 - Arabidopsis thaliana (Mouse-ear cress)
chr1.CM0593.90.nd	123	(Q9LT84) Emb|CAB62003.1 - Arabidopsis thaliana (Mouse-ear cress)
chr1.CM1956.580.nc	71	(Q1S774) Hypothetical protein - Medicago truncatula (Barrel medic)
chr1.LjB10L14.60.nc	115	(Q7XHX6) Putative vacuolar targeting receptor (Hypothetical protein) (Os07g0680000 protein) - Oryza sativa (japonica cultivar-group)
chr1.LjB21G05.130.nc	120	(Q8H8M5) Putative kinase - Oryza sativa (japonica cultivar-group)
chr1.LjT04O21.120.nd	83	(Q1SD45) Hypothetical protein - Medicago truncatula (Barrel medic)
chr1.LjT08E15.170.nd	109	(Q9LZS6) Cucumisin-like protein - Arabidopsis thaliana (Mouse-ear cress)
chr1.LjT08H21.20.nd	104	(Q9M0R3) Hypothetical protein AT4g09150 - Arabidopsis thaliana (Mouse-ear cress)
chr1.LjT10B06.110.nd	77	(Q2HUD0) WD40-like - Medicago truncatula (Barrel medic)
chr1.LjT14B18.60.nc	150	(A2Z2A7) Hypothetical protein - Oryza sativa (indica cultivar-group)
chr1.LjT14G19.20.nc	346	(Q1SPD3) Cyclin-like F-box; F-box protein interaction domain - Medicago truncatula (Barrel medic)
chr1.LjT16J16.120.nd	142	(Q6IQZ0) Hypothetical protein - Mus musculus (Mouse)
chr1.LjT29L06.180.nd	122	(Q9ZUN5) Putative senescence-associated protein 5 (At2g19580) - Arabidopsis thaliana (Mouse-ear cress)

chr1.LjT29L18.10.nd	110	(Q8S8S4) Putative flavonol synthase - Arabidopsis thaliana (Mouse-ear cress)
chr1.LjT30M08.120.nd	72	(Q1SSA4) Hypothetical protein - Medicago truncatula (Barrel medic)
chr1.LjT34H22.260.nd	149	(Q1SF17) Heat shock protein Hsp70 - Medicago truncatula (Barrel medic)
chr1.LjT35H06.70.nc	717	(A3A4L0) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr1.LjT36G06.100.nc	98	(Q1S2B0) No apical meristem (NAM) protein - Medicago truncatula (Barrel medic)
chr1.LjT36G06.130.nc	167	(Q8GZD8) Neutral leucine aminopeptidase preprotein precursor (EC 3.4.11.1) - Solanum lycopersicum (Tomato) (Lycopersicon esculentum)
chr1.LjT36I17.90.nd	89	(A1L4U4) At5g64300 - Arabidopsis thaliana (Mouse-ear cress)
chr1.LjT36P09.120.nd	155	(Q8S4X3) TIR-similar-domain-containing protein TSDC - Pisum sativum (Garden pea)
chr1.LjT43L07.160.nd	128	(Q9STP2) Hypothetical protein T27E11.80 (At4g27840/T27E11_80) (Hypothetical protein AT4g27840) - Arabidopsis thaliana (Mouse-ear cress)
chr1.LjT44L17.210.nd	73	(Q1SHX0) Ribosomal protein S2; Oligopeptide transporter OPT superfamily - Medicago truncatula (Barrel medic)
chr1.LjT45O14.20.nd	130	(Q9C651) Hypothetical protein F9K23.1 - Arabidopsis thaliana (Mouse-ear cress)
chr1.LjT46N10.200.nd	189	(Q1S0T7) Cyclin-like F-box; F-box protein interaction domain; Galactose oxidase, central - Medicago truncatula (Barrel medic)
chr2.CM0008.600.nc	210	(Q1S8R3) Hypothetical protein - Medicago truncatula (Barrel medic)
chr2.CM0018.260.nd	94	(Q1T0B9) IMP dehydrogenase/GMP reductase - Medicago truncatula (Barrel medic)
chr2.CM0018.880.nc	163	(Q3EA10) Protein At4g16195 - Arabidopsis thaliana (Mouse-ear cress)

chr2.CM0020.20.nd	323	(Q2HW84) Cyclin-like F-box - Medicago truncatula (Barrel medic)
chr2.CM0020.40.nd	314	(Q2HW84) Cyclin-like F-box - Medicago truncatula (Barrel medic)
chr2.CM0021.1200.nd	69	(Q1W203) NAK-type protein kinase - Nicotiana tabacum (Common tobacco)
chr2.CM0021.400.nc	298	(A0MEP3) Hypothetical protein (Fragment) - Arabidopsis thaliana (Mouse-ear cress)
chr2.CM0031.10.nd	90	(Q2PHF4) Aldehyde oxidase 1 - Lactuca sativa (Garden lettuce)
chr2.CM0056.130.nd	91	(Q1S950) Zinc finger, RING-type; RINGv - Medicago truncatula (Barrel medic)
chr2.CM0056.200.nd	49	(Q1T048) Hypothetical protein - Medicago truncatula (Barrel medic)
chr2.CM0058.420.nd	178	(Q1SXV2) No apical meristem (NAM) protein - Medicago truncatula (Barrel medic)
chr2.CM0060.330.nd	164	(Q9FQZ4) Avr9/Cf-9 rapidly elicited protein 194 - Nicotiana tabacum (Common tobacco)
chr2.CM0081.350.nd	259	(Q2HTU0) Glycoside hydrolase, family 5; Ricin B-related lectin - Medicago truncatula (Barrel medic)
chr2.CM0081.410.nd	155	(Q1S510) Protein kinase - Medicago truncatula (Barrel medic)
chr2.CM0081.530.nd	255	(Q2HTU0) Glycoside hydrolase, family 5; Ricin B-related lectin - Medicago truncatula (Barrel medic)
chr2.CM0099.200.nd	982	(Q5XWR0) Hypothetical protein - Solanum tuberosum (Potato)
chr2.CM0124.150.nd	81	(Q9SB33) SRG1-like protein - Arabidopsis thaliana (Mouse-ear cress)
chr2.CM0124.260.nd	102	(Q9SB33) SRG1-like protein - Arabidopsis thaliana (Mouse-ear cress)
chr2.CM0177.730.nc	117	(A2Q3L5) Zinc finger, CCCH-type - Medicago truncatula (Barrel medic)
chr2.CM0191.190.nc	128	(Q1ENZ8) Hypothetical protein - Musa acuminata (Banana)

chr2.CM0201.380.nc	194	(Q1SHW9) Ribosomal protein S2; Oligopeptide transporter OPT superfamily - Medicago truncatula (Barrel medic)
chr2.CM0225.290.nd	118	(Q1S4Z8) AAA ATPase - Medicago truncatula (Barrel medic)
chr2.CM0225.80.nc	146	(Q1SHX1) Oligopeptide transporter OPT superfamily - Medicago truncatula (Barrel medic)
chr2.CM0249.1280.nc	191	(Q1XI26) PvLEA1 protein - Polypedilum vanderplanki (sleeping chironomid)
chr2.CM0249.1340.nc	107	(A2YSA4) Hypothetical protein - Oryza sativa (indica cultivar-group)
chr2.CM0249.310.nd	258	(A3AW23) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr2.CM0249.850.nd	145	(A3AYA2) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr2.CM0250.220.nd	52	(Q7PQY7) ENSANGP00000011061 - Anopheles gambiae str. PEST
chr2.CM0304.100.nd	129	(Q1RVC3) Hypothetical protein - Medicago truncatula (Barrel medic)
chr2.CM0323.170.nc	218	(Q8GVI7) Putative thaumatin-like protein - Oryza sativa (japonica cultivar-group)
chr2.CM0323.220.nc	160	(Q8LBP3) Hypothetical protein - Arabidopsis thaliana (Mouse-ear cress)
chr2.CM0405.80.nd	218	(Q9LHB3) Gb|AAB97123.1 - Arabidopsis thaliana (Mouse-ear cress)
chr2.CM0545.140.nd	147	(Q1SM53) Hypothetical protein - Medicago truncatula (Barrel medic)
chr2.CM0545.150.nd	96	(Q1S1E7) Hypothetical protein - Medicago truncatula (Barrel medic)
chr2.CM0545.160.nd	70	(Q1MX17) Aldehyde oxidase - Brassica campestris (Field mustard)
chr2.CM0545.690.nc	90	(Q84W73) Putative cell division-related protein - Arabidopsis thaliana (Mouse-ear cress)
chr2.CM0608.250.nd	110	(A2Q2R1) Thioredoxin domain 2; Thioredoxin fold - Medicago truncatula (Barrel medic)
chr2.CM0695.360.nd	73	(Q8H241) Hypothetical protein - Gossypium hirsutum (Upland cotton)

chr2.CM0749.120.nd	121	(Q1SGX6) Peptidase S10, serine carboxypeptidase - Medicago truncatula (Barrel medic)
chr2.CM0803.770.nd	82	(Q9LW56) Similarity to long chain fatty alcohol oxidase (At3g23410/MLM24_23) - Arabidopsis thaliana (Mouse-ear cress)
chr2.CM0904.190.nd	51	(Q9SUC7) Hypothetical protein T13K14.10 (Hypothetical protein AT4g20850) - Arabidopsis thaliana (Mouse-ear cress)
chr2.CM0904.70.nd	100	(Q1S0S9) Hypothetical protein - Medicago truncatula (Barrel medic)
chr2.CM1032.310.nc	72	(Q1S121) Heavy metal transport/detoxification protein - Medicago truncatula (Barrel medic)
chr2.LjT02C03.110.nd	122	(Q19PN4) TIR-NBS-LRR-TIR type disease resistance protein (Fragment) - Populus trichocarpa (Western balsam poplar)
chr2.LjT02C03.200.nd	189	(Q19PN4) TIR-NBS-LRR-TIR type disease resistance protein (Fragment) - Populus trichocarpa (Western balsam poplar)
chr2.LjT02E02.30.nd	111	(Q9C4Z6) Guanine nucleotide-binding protein, putative (Putative guanine nucleotide-binding protein) - Arabidopsis thaliana (Mouse-ear cress)
chr2.LjT10F02.130.nd	319	(Q1SCZ2) Transcriptional factor B3 - Medicago truncatula (Barrel medic)
chr2.LjT10F02.140.nd	281	(Q1SCZ2) Transcriptional factor B3 - Medicago truncatula (Barrel medic)
chr2.LjT13P17.210.nd	86	(Q1T3I5) Hypothetical protein - Medicago truncatula (Barrel medic)
chr2.LjT13P17.230.nd	372	(Q9FYK5) F21J9.25 (At1g24590) (Putative AP2/EREBP transcription factor) - Arabidopsis thaliana (Mouse-ear cress)
chr2.LjT17A07.210.nd	239	(Q9LZ03) Meiosis specific-like protein (At5g02820) (Topoisomerase 6 subunit A) (Putative topoisomerase VI subunit A) - Arabidopsis thaliana (Mouse-ear cress)

chr2.LjT36E17.20.nd	92	(Q6K5C8) Putative WD repeat protein (Os02g0294600 protein) - Oryza sativa (japonica cultivar-group)
chr2.LjT46G02.110.nd	220	(Q9M5M5) 60S acidic ribosomal protein PO (Fragment) - Euphorbia esula (Leafy spurge)
chr2.LjT47G24.10.nd	161	(Q6ZJW3) Putative blue copper binding protein (Hypothetical protein) - Oryza sativa (japonica cultivar-group)
chr2.LjT47G24.110.nd	155	(Q1SHX1) Oligopeptide transporter OPT superfamily - Medicago truncatula (Barrel medic)
chr2.LjT47G24.90.nd	181	unknown protein
chr3.CM0059.40.nd	325	(A0DBL2) Chromosome undetermined scaffold_44, whole genome shotgun sequence - Paramecium tetraurelia
chr3.CM0110.160.nc	184	(Q9LVV3) Genomic DNA, chromosome 5, P1 clone:MNB8 - Arabidopsis thaliana (Mouse-ear cress)
chr3.CM0116.440.nd	226	(A3BES0) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr3.CM0129.360.nd	128	(Q9ZRV4) MLH1 protein (Fragment) - Arabidopsis thaliana (Mouse-ear cress)
chr3.CM0135.20.nc	199	(A3B6L6) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr3.CM0155.220.nc	537	(Q94B16) Pectin methylesterase PME1 - Vitis vinifera (Grape)
chr3.CM0155.230.nc	268	(A2Q3Z2) Pectinesterase; Pectinesterase inhibitor - Medicago truncatula (Barrel medic)
chr3.CM0160.730.nd	148	(Q9ZWC2) F21M11.4 protein - Arabidopsis thaliana (Mouse-ear cress)
chr3.CM0160.950.nd	189	(O22443) Seed coat peroxidase precursor (EC 1.11.1.7) (Seed coat peroxidase) (Peroxidase precursor) - Glycine max (Soybean)
chr3.CM0164.270.nd	260	(Q680R1) NAC-domain protein-like - Arabidopsis thaliana (Mouse-ear cress)
chr3.CM0196.190.nc	176	(Q9SWB5) Seed maturation protein PM37 - Glycine max (Soybean)

chr3.CM0196.90.nc	162	(Q1SW46) Hypothetical protein - Medicago truncatula (Barrel medic)
chr3.CM0208.310.nc	237	(Q3E8M5) Protein At5g36905 - Arabidopsis thaliana (Mouse-ear cress)
chr3.CM0216.260.nc	258	(Q1S066) Arabidopsis conserved protein - Medicago truncatula (Barrel medic)
chr3.CM0216.950.nd	61	(Q2HTR2) Cyclin-like F-box - Medicago truncatula (Barrel medic)
chr3.CM0216.980.nd	71	(Q1S3A0) CAMP response element binding (CREB) protein - Medicago truncatula (Barrel medic)
chr3.CM0279.360.nc	132	(Q1SIS5) Immunoglobulin/major histocompatibility complex; Zinc finger, BED-type predicted; Zinc finger, C2H2-type - Medicago truncatula (Barrel medic)
chr3.CM0279.80.nd	111	(Q1SAU4) Helicase, C-terminal - Medicago truncatula (Barrel medic)
chr3.CM0406.270.nd	334	(Q9ZTA8) Homeodomain protein (Fragment) - Malus domestica (Apple) (Malus sylvestris)
chr3.CM0423.390.nc	140	(Q1SAR7) Eukaryotic aspartyl protease, putative - Medicago truncatula (Barrel medic)
chr3.CM0574.170.nd	101	(Q9FJ71) Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MTE17 - Arabidopsis thaliana (Mouse-ear cress)
chr3.CM0590.410.nd	82	(Q84PM9) Putative COP-1 interacting protein 7 (Fragment) - Gossypium hirsutum (Upland cotton)
chr3.CM0590.820.nc	165	(Q04129) Wound induced protein (Fragment) - Solanum lycopersicum (Tomato) (Lycopersicon esculentum)
chr3.CM0590.830.nc	168	(Q04129) Wound induced protein (Fragment) - Solanum lycopersicum (Tomato) (Lycopersicon esculentum)
chr3.CM0602.160.nc	214	(Q1S8I5) Probable Ta11-like non-LTR retroelement protein [imported]- Arabidopsis thaliana - Medicago truncatula (Barrel medic)
chr3.CM0602.400.nd	112	(O64515) YUP8H12R.2 protein - Arabidopsis thaliana (Mouse-ear cress)

chr3.CM0634.510.nc	194	(Q8RVP6) Gaiacol peroxidase (EC 1.11.1.7) - Gossypium hirsutum (Upland cotton)
chr3.CM0634.590.nc	194	(Q8RVP6) Gaiacol peroxidase (EC 1.11.1.7) - Gossypium hirsutum (Upland cotton)
chr3.CM0690.110.nd	123	(A3AHD9) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr3.CM0726.350.nd	118	(Q2HSU8) Cupin region - Medicago truncatula (Barrel medic)
chr3.CM1144.210.nc	130	(Q1S793) Plant self-incompatibility S1 - Medicago truncatula (Barrel medic)
chr3.LjT03D10.70.nd	61	(A2Q2W3) Hypothetical protein - Medicago truncatula (Barrel medic)
chr3.LjT03D10.80.nd	61	(A2Q2W3) Hypothetical protein - Medicago truncatula (Barrel medic)
chr3.LjT07H20.260.nd	68	(Q1SP72) Ferredoxin - Medicago truncatula (Barrel medic)
chr3.LjT13N17.100.nc	409	(A3AQC0) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr3.LjT13N17.120.nc	425	(A3AQC0) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr3.LjT26B16.190.nd	335	(Q8GW43) Putative 8-amino-7-oxononanoate synthase (At5g04620) - Arabidopsis thaliana (Mouse-ear cress)
chr4.CM0003.210.nc	147	(A3B5R3) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr4.CM0004.160.nd	72	(A1KXE2) Putative ribosomal protein L31 - Lactuca sativa (Garden lettuce)
chr4.CM0004.250.nd	164	(Q1S606) Heat shock protein DnaJ - Medicago truncatula (Barrel medic)
chr4.CM0006.490.nc	113	(Q73XI0) Bcp - Mycobacterium paratuberculosis
chr4.CM0006.500.nc	86	(Q9LMA2) T29M8.11 (Hypothetical protein At1g19240) - Arabidopsis thaliana (Mouse-ear cress)
chr4.CM0007.680.nd	56	(Q1SA81) Hypothetical protein - Medicago truncatula (Barrel medic)
chr4.CM0007.890.nd	86	(Q4U4M3) Subtilisin-like protease (Fragment) - Arachis hypogaea (Peanut)

chr4.CM0042.1020.nd	60	(Q9ZNU5) Hypothetical protein At2g01610 (At2g01610) - Arabidopsis thaliana (Mouse-ear cress)
chr4.CM0042.1980.nc	741	(A0ME24) Hypothetical protein (Fragment) - Arabidopsis thaliana (Mouse-ear cress)
chr4.CM0042.2590.nd	68	(A3BYM6) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr4.CM0042.820.nc	85	(Q1RYL4) Serine/threonine protein kinase, active site - Medicago truncatula (Barrel medic)
chr4.CM0042.910.nc	86	(A3B8R9) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr4.CM0044.130.nd	123	(A2ZET1) Hypothetical protein - Oryza sativa (indica cultivar-group)
chr4.CM0044.240.nd	121	(Q8LCV8) Hypothetical protein - Arabidopsis thaliana (Mouse-ear cress)
chr4.CM0044.280.nd	202	(Q9LDN0) Phragmoplast-associated kinesin-related protein 1 - Arabidopsis thaliana (Mouse-ear cress)
chr4.CM0046.420.nc	121	(Q9FQE4) Glutathione S-transferase GST 14 (EC 2.5.1.18) (Fragment) - Glycine max (Soybean)
chr4.CM0128.180.nc	460	(Q382P4) Hypothetical protein - Trypanosoma brucei
chr4.CM0131.630.nc	122	(Q6NLG8) At4g33550 - Arabidopsis thaliana (Mouse-ear cress)
chr4.CM0165.220.nd	96	(Q9M839) T27C4.13 protein - Arabidopsis thaliana (Mouse-ear cress)
chr4.CM0170.280.nc	307	(A2Q681) Ribonuclease H - Medicago truncatula (Barrel medic)
chr4.CM0175.140.nd	165	(Q9FIT8) GCN4-complementing protein homolog - Arabidopsis thaliana (Mouse-ear cress)
chr4.CM0175.250.nd	77	(Q8VZ20) Hypothetical protein At2g33550 - Arabidopsis thaliana (Mouse-ear cress)
chr4.CM0179.280.nc	669	(Q69P59) Hypothetical protein OJ1740_D06.20 - Oryza sativa (japonica cultivar-group)

chr4.CM0182.170.nc	83	(Q944L5) At1g26740/T24P13_11 - Arabidopsis thaliana (Mouse-ear cress)
chr4.CM0182.210.nd	92	(Q944L5) At1g26740/T24P13_11 - Arabidopsis thaliana (Mouse-ear cress)
chr4.CM0227.30.nd	76	(Q8VXZ5) Hypothetical protein At2g35610 - Arabidopsis thaliana (Mouse-ear cress)
chr4.CM0281.10.nd	60	(Q1SPA4) SAM (And some other nucleotide) binding motif - Medicago truncatula (Barrel medic)
chr4.CM0288.300.nd	232	(Q39814) Hypothetical protein (Fragment) - Glycine max (Soybean)
chr4.CM0337.260.nc	149	(Q17U53) DNA-directed RNA polymerase, putative - Solanum bulbocastanum (Wild potato)
chr4.CM0387.240.nc	140	(Q1RUQ0) Nonaspanin (TM9SF) - Medicago truncatula (Barrel medic)
chr4.CM0500.110.nd	88	(Q1SGK8) Leucine-rich repeat; Leucine-rich repeat, cysteine-containing subtype - Medicago truncatula (Barrel medic)
chr4.CM0558.110.nd	77	(Q1RY76) Mitochondrial substrate carrier - Medicago truncatula (Barrel medic)
chr4.CM0617.10.nd	83	(Q1SEA4) AT5g11700/T22P22_90 - Medicago truncatula (Barrel medic)
chr4.CM0617.450.nd	53	(A2ZXD7) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr4.CM0692.110.nd	115	(Q53YQ2) AS2 (At1g65620) - Arabidopsis thaliana (Mouse-ear cress)
chr4.CM0692.370.nd	270	(Q9CAS4) Hypothetical protein T17F3.6 - Arabidopsis thaliana (Mouse-ear cress)
chr4.CM0692.630.nd	80	(Q9SSM3) Similar to jacalin (At1g73040) - Arabidopsis thaliana (Mouse-ear cress)
chr4.CM1334.80.nc	130	(O49715) Hypothetical protein T8O5.130 (Hypothetical protein AT4g21920) - Arabidopsis thaliana (Mouse-ear cress)
chr4.CM1334.90.nc	132	(O49715) Hypothetical protein T8O5.130 (Hypothetical protein AT4g21920) - Arabidopsis thaliana (Mouse-ear cress)

chr4.LjT13D08.210.nd	154	(Q9XED4) Receptor-like protein kinase homolog RK20-1 - Phaseolus vulgaris (Kidney bean) (French bean)
chr4.LjT21A22.200.nd	60	(Q8VYC4) Putative sun protein fmu (Putative sun (Fmu) protein) - Arabidopsis thaliana (Mouse-ear cress)
chr4.LjT30K03.130.nc	267	(Q5N7S4) Receptor serine/threonine kinase PR5K-like - Oryza sativa (japonica cultivar-group)
chr4.LjT32J05.160.nc	144	(A0JPW5) At3g21490 - Arabidopsis thaliana (Mouse-ear cress)
chr4.LjT38A20.30.nd	114	(Q1RUQ0) Nonaspanin (TM9SF) - Medicago truncatula (Barrel medic)
chr4.LjT38A20.60.nd	91	(Q2A9D6) Hypothetical protein - Brassica oleracea (Wild cabbage)
chr4.LjT45J24.70.nc	70	(Q8LF02) Hypothetical protein (At1g73090) - Arabidopsis thaliana (Mouse-ear cress)
chr5.CM0019.110.nd	71	(Q1SX83) Hypothetical protein - Medicago truncatula (Barrel medic)
chr5.CM0019.410.nc	398	(Q9FYX4) BAC19.2 - Solanum lycopersicum (Tomato) (Lycopersicon esculentum)
chr5.CM0040.150.nd	143	(Q1SQL2) 4Fe-4S ferredoxin, iron-sulfur binding - Medicago truncatula (Barrel medic)
chr5.CM0040.620.nd	70	(Q8RXN4) Putative enoyl-CoA hydratase - Arabidopsis thaliana (Mouse-ear cress)
chr5.CM0052.160.nd	226	(Q1T0J6) Cupredoxin - Medicago truncatula (Barrel medic)
chr5.CM0052.330.nd	126	(Q1SFG0) Glycoside hydrolase, family 10; DNA repair protein RadA - Medicago truncatula (Barrel medic)
chr5.CM0089.1040.nd	51	(Q1S2L8) Transcriptional factor B3; Cupredoxin; TonB box, N-terminal - Medicago truncatula (Barrel medic)
chr5.CM0089.970.nd	191	(A1L4Y7) At4g10400 - Arabidopsis thaliana (Mouse-ear cress)

chr5.CM0095.330.nd	101	(Q2HTK4) Protein kinase; U box - Medicago truncatula (Barrel medic)
chr5.CM0148.150.nd	72	(A3A9W2) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr5.CM0158.310.nd	137	(Q7XVH0) OSJNBa0073L04.11 protein (Hypothetical protein) (Os04g0412800 protein) (OJ000126_13.3 protein) - Oryza sativa (japonica cultivar-group)
chr5.CM0211.30.nc	361	(A3BJL3) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr5.CM0239.860.nd	77	(Q9FV64) NTS1 protein - Nicotiana tabacum (Common tobacco)
chr5.CM0278.310.nc	64	(Q8RWQ5) AT5g54860/MBG8_12 - Arabidopsis thaliana (Mouse-ear cress)
chr5.CM0328.280.nd	557	(Q1SUB1) RNA polymerase Rpb2, domain 4; RNA polymerase Rpb2, domain 5 - Medicago truncatula (Barrel medic)
chr5.CM0345.470.nc	125	(Q9LRV8) Leucine-rich-repeat protein-like (Plant intracellular Ras-group-related LRR protein 2) (Hypothetical protein At3g26500) (Hypothetical protein At3g26500/MFE16_1) - Arabidopsis thaliana (Mouse-ear cress)
chr5.CM0456.160.nd	140	(Q2HY53) AtpE (Fragment) - Leucophyllum frutescens (Texas ranger) (Ceniza)
chr5.CM0456.400.nd	95	(Q1SHZ1) DNA binding protein E4/E8BP-1-tomato-related - Medicago truncatula (Barrel medic)
chr5.CM0494.330.nc	142	(Q1SCX0) Pathogenesis-related transcriptional factor and ERF - Medicago truncatula (Barrel medic)
chr5.CM0569.220.nc	352	(Q9FYX4) BAC19.2 - Solanum lycopersicum (Tomato) (Lycopersicon esculentum)
chr5.CM0571.220.nd	229	(Q9SSG7) F25A4.12 protein - Arabidopsis thaliana (Mouse-ear cress)
chr5.CM0813.360.nd	115	(Q1SXC6) Tetratricopeptide-like helical - Medicago truncatula (Barrel medic)
chr5.CM0909.540.nc	180	(Q2HV66) Zinc finger, RING-type - Medicago truncatula (Barrel medic)

chr5.CM0909.550.nc	163	(Q1T0Q0) Zinc finger, RING-type; RINGv - Medicago truncatula (Barrel medic)
chr5.CM0909.560.nc	166	(Q1T0Q0) Zinc finger, RING-type; RINGv - Medicago truncatula (Barrel medic)
chr5.CM0911.220.nd	94	(A2Q5Q4) Glycoside hydrolase, family 17; X8 - Medicago truncatula (Barrel medic)
chr5.CM0956.20.nc	234	(Q1SD46) Transcription factor, MADS-box - Medicago truncatula (Barrel medic)
chr5.CM1125.210.nc	190	(Q1SGL6) Hypothetical protein - Medicago truncatula (Barrel medic)
chr5.CM1125.590.nd	79	(Q9LV18) Emb|CAA16536.1 (Hypothetical protein At3g18215) - Arabidopsis thaliana (Mouse-ear cress)
chr5.CM1439.20.nd	106	(Q5DMV7) Pentatricopeptide (PPR) repeat protein-like - Cucumis melo (Muskmelon)
chr5.LjT08L18.120.nd	175	(Q9LNK3) F12K21.25 (Hypothetical protein F7P12.13) - Arabidopsis thaliana (Mouse-ear cress)
chr5.LjT09B23.60.nd	156	(Q53ML9) Endomembrane protein 70 (Hypothetical protein) - Oryza sativa (japonica cultivar-group)
chr5.LjT23J23.150.nd	87	(A4L9G5) Putative integral membrane protein - Gossypium raimondii (New World cotton)
chr6.CM0013.10.nd	162	(A3BZ52) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr6.CM0037.1440.nc	119	(Q9ZPJ5) Ran-related GTP binding protein (Fragment) - Zea mays (Maize)
chr6.CM0037.1760.nc	226	(A2Q681) Ribonuclease H - Medicago truncatula (Barrel medic)
chr6.CM0037.930.nc	227	(Q5Y381) Aldo/keto reductase - Fragaria ananassa (Strawberry)

chr6.CM0055.370.nd	173	(Q9SW15) Hypothetical protein F13M23.250 (Hypothetical protein AT4g25110) - Arabidopsis thaliana (Mouse-ear cress)
chr6.CM0055.460.nd	108	(Q9LVM0) Receptor-like protein kinase (At5g58299/At5g58299) (Hypothetical protein) - Arabidopsis thaliana (Mouse-ear cress)
chr6.CM0055.680.nd	125	(O24019) GTP cyclohydrolase II / 3,4-dihydroxy-2-butanone-4-phosphate synthase - Solanum lycopersicum (Tomato) (Lycopersicon esculentum)
chr6.CM0057.200.nc	217	(Q1SQA9) Hypothetical protein - Medicago truncatula (Barrel medic)
chr6.CM0057.280.nd	217	(Q1SQA9) Hypothetical protein - Medicago truncatula (Barrel medic)
chr6.CM0057.360.nd	311	(Q6H5N4) Hypothetical protein OJ1118_F11.28 (Hypothetical protein) (Os09g0384900 protein) - Oryza sativa (japonica cultivar-group)
chr6.CM0057.420.nc	114	(Q9LMX8) F21F23.14 protein (At1g13700) - Arabidopsis thaliana (Mouse-ear cress)
chr6.CM0057.430.nc	121	(Q9FJS0) Genomic DNA, chromosome 5, P1 clone:MQD22 - Arabidopsis thaliana (Mouse-ear cress)
chr6.CM0066.370.nc	151	(Q8L4S3) Hypothetical protein (At5g09390/T5E8_190) - Arabidopsis thaliana (Mouse-ear cress)
chr6.CM0139.50.nd	154	(A2Q377) Nucleic acid-binding, OB-fold - Medicago truncatula (Barrel medic)
chr6.CM0314.30.nd	98	(Q1SH78) K+ potassium transporter - Medicago truncatula (Barrel medic)
chr6.CM0314.530.nd	101	(Q1STS0) Peptidase S10, serine carboxypeptidase - Medicago truncatula (Barrel medic)
chr6.CM0314.560.nd	142	(A4GNA9) Phosphatidylserine decarboxylase - Arabidopsis thaliana (Mouse-ear cress)
chr6.CM0420.20.nd	98	(Q2HT48) HECT; Ubiquitin - Medicago truncatula (Barrel medic)
chr6.CM0437.310.nc	372	(Q1S4X3) IMP dehydrogenase/GMP reductase - Medicago truncatula (Barrel medic)

chr6.CM0437.400.nc	75	(Q1S4Y2) Berberine and berberine like, putative - Medicago truncatula (Barrel medic)
chr6.CM0437.430.nc	161	(Q1S4Y2) Berberine and berberine like, putative - Medicago truncatula (Barrel medic)
chr6.CM0472.180.nc	95	(Q2HUJ7) V-ATPase subunit C - Medicago truncatula (Barrel medic)
chr6.CM0539.180.nd	234	(Q9M8I9) F28L1.23 protein - Arabidopsis thaliana (Mouse-ear cress)
chr6.CM0679.150.nd	138	(Q6TF29) Rapid alkalinization factor 1 - Solanum chacoense (Chaco potato)
chr6.CM0686.240.nd	420	(Q9C6K1) Hypothetical protein F8A12.2 - Arabidopsis thaliana (Mouse-ear cress)
chr6.CM0836.470.nd	286	(Q9SJW6) Putative ARP2/3 protein complex subunit p41 (At2g31300/F16D14.14) - Arabidopsis thaliana (Mouse-ear cress)
chr6.CM0885.280.nc	79	(Q1SKV9) Bromodomain - Medicago truncatula (Barrel medic)
chr6.LjT06I08.70.nc	88	(Q9T0H6) Hypothetical protein T6G15.110 (Hypothetical protein At4g13560) (Hypothetical protein At4g13560/T6G15_110) - Arabidopsis thaliana (Mouse-ear cress)
chr6.LjT14A08.40.nd	80	(Q7XLZ1) OSJNBa0086O06.18 protein (Hypothetical protein) (Os04g0590400 protein) - Oryza sativa (japonica cultivar-group)
chr6.LjT14A08.80.nd	54	(Q7XLZ1) OSJNBa0086O06.18 protein (Hypothetical protein) (Os04g0590400 protein) - Oryza sativa (japonica cultivar-group)
chr6.LjT15B19.180.nd	97	(Q944N0) Acyl carrier protein - Olea europaea (Common olive)
chr6.LjT16B20.50.nc	104	(A3ADE6) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr6.LjT36L14.210.nd	109	(A2Q396) Galactose mutarotase-like - Medicago truncatula (Barrel medic)
chr6.LjT45M04.110.nd	123	(Q1SAR1) Annexin, putative - Medicago truncatula (Barrel medic)

CM0300.50.nc	55	(Q9FGT4) Genomic DNA, chromosome 5, TAC clone:K21L19 - Arabidopsis thaliana (Mouse-ear cress)
CM0319.110.nd	211	(Q9C6H1) Hypothetical protein T12I7.9 - Arabidopsis thaliana (Mouse-ear cress)
CM0385.120.nd	256	(Q1T0C7) IQ calmodulin-binding region; CG-1 - Medicago truncatula (Barrel medic)
CM0547.170.nd	92	(Q6VWJ5) Fructokinase 3 - Solanum lycopersicum (Tomato) (Lycopersicon esculentum)
CM0601.150.nd	123	(Q1SB03) Tyrosine protein kinase - Medicago truncatula (Barrel medic)
CM1983.70.nc	109	(Q9FHG9) Similarity to ankyrin - Arabidopsis thaliana (Mouse-ear cress)
LjB03J07.40.nd	51	(Q1SHN8) Hypothetical protein - Medicago truncatula (Barrel medic)
LjB03P03.190.nd	249	(Q2HTI8) AT3g20300/MQC12_5 - Medicago truncatula (Barrel medic)
LjB12O06.10.nc	54	(Q7XLZ1) OSJNBa0086O06.18 protein (Hypothetical protein) (Os04g0590400 protein) - Oryza sativa (japonica cultivar-group)
LjT01K02.40.nc	51	(Q1SUA5) Hypothetical protein - Medicago truncatula (Barrel medic)
LjT03E06.40.nd	465	(Q8L7V8) AT3g53540/F4P12_240 - Arabidopsis thaliana (Mouse-ear cress)
LjT03L06.20.nd	270	(Q9FIN6) Gb|AAD32909.1 - Arabidopsis thaliana (Mouse-ear cress)
LjT04N09.230.nd	132	(Q9LLZ7) Phytocyanin homolog - Pinus taeda (Loblolly pine)
LjT05D15.240.nd	106	(Q1SIQ4) Transcription factor, MADS-box - Medicago truncatula (Barrel medic)
LjT05F19.160.nc	959	(Q1RXG8) IMP dehydrogenase/GMP reductase - Medicago truncatula (Barrel medic)
LjT06B16.100.nc	443	(Q8H3K2) Hypothetical protein P0428D12.111 (Hypothetical protein) - Oryza sativa (japonica cultivar-group)
LjT06N02.140.nd	104	(Q9FPK9) Putative resistance protein - Glycine max (Soybean)

LjT06N06.260.nd	151	(Q6CKI0) Kluyveromyces lactis strain NRRL Y-1140 chromosome F of strain NRRL Y-1140 of Kluyveromyces lactis - Kluyveromyces lactis (Yeast) (Candida sphaerica)
LjT06N06.350.nd	129	(Q1RZB7) Hypothetical protein - Medicago truncatula (Barrel medic)
LjT06P13.130.nd	111	(A3B901) Hypothetical protein - Oryza sativa (japonica cultivar-group)
LjT07J01.40.nd	153	(Q1SAV3) Cyclin-like F-box; F-box protein interaction domain; Galactose oxidase, central - Medicago truncatula (Barrel medic)
LjT10B22.140.nd	121	(Q1SYP9) Myb, DNA-binding - Medicago truncatula (Barrel medic)
LjT10C06.140.nd	72	(Q84K13) Putative polygalacturonase - Arabidopsis thaliana (Mouse-ear cress)
LjT10C23.70.nc	192	(Q1SH03) Hypothetical protein - Medicago truncatula (Barrel medic)
LjT10D02.90.nd	77	(Q1S9W9) Auxin responsive SAUR protein - Medicago truncatula (Barrel medic)
LjT11L09.60.nd	113	(A3AAD6) Hypothetical protein - Oryza sativa (japonica cultivar-group)
LjT12M13.90.nc	156	(Q38706) Cysteine proteinase - Alnus glutinosa (Alder)
LjT13K07.90.nd	51	(Q9LY62) Hypothetical protein F27K19_10 (Hypothetical protein At3g55830) - Arabidopsis thaliana (Mouse-ear cress)
LjT14D09.70.nc	674	(Q2HVW1) Hypothetical protein - Medicago truncatula (Barrel medic)
LjT14H02.180.nd	81	(Q9LZ63) 8-amino-7-oxononanoate synthase-like protein - Arabidopsis thaliana (Mouse-ear cress)
LjT15D07.30.nc	111	(A0ELV0) Non-S-locus F-box-like protein 2011 (Fragment) - Petunia integrifolia subsp. inflata
LjT15F17.90.nd	243	(Q0PJM1) MYB transcription factor MYB54 - Glycine max (Soybean)
LjT17C10.70.nd	57	(Q1SRB6) Hypothetical protein - Medicago truncatula (Barrel medic)

LjT17E11.10.nc	949	(Q1RXG8) IMP dehydrogenase/GMP reductase - Medicago truncatula (Barrel medic)
LjT19C19.60.nd	170	(Q1SN20) Hypothetical protein - Medicago truncatula (Barrel medic)
LjT19N22.70.nd	290	(Q94KU0) ATP8 - Arabidopsis thaliana (Mouse-ear cress)
LjT19N22.90.nd	134	(Q8LJS7) Homeodomain protein GhHOX2 - Gossypium hirsutum (Upland cotton)
LjT20L14.90.nd	62	(Q1S8W5) Glycoside hydrolase, family 17 - Medicago truncatula (Barrel medic)
LjT21I06.50.nd	328	(Q1SHX0) Ribosomal protein S2; Oligopeptide transporter OPT superfamily - Medicago truncatula (Barrel medic)
LjT22H02.40.nc	138	(Q8W2N3) Cytochrome P450-dependent fatty acid hydroxylase - Vicia sativa (Spring vetch) (Tare)
LjT24M05.100.nc	932	(Q1RXG8) IMP dehydrogenase/GMP reductase - Medicago truncatula (Barrel medic)
LjT24M05.170.nc	96	(Q1SH78) K+ potassium transporter - Medicago truncatula (Barrel medic)
LjT30N18.300.nd	80	(Q94AG1) AT3g07470/F21O3_18 - Arabidopsis thaliana (Mouse-ear cress)
LjT32C22.120.nd	303	unknown protein
LjT32C22.130.nd	297	unknown protein
LjT33J24.50.nd	224	(Q6VN49) Putative cysteine proteinase (Peptidase C1A, papain; Peptidase M14, carboxypeptidase A) - Medicago truncatula (Barrel medic)
LjT35D08.240.nd	211	(Q10A46) Alcohol dehydrogenase 2, putative, expressed (Os10g0159800 protein) - Oryza sativa (japonica cultivar-group)
LjT35G18.20.nd	200	(Q1SRI1) RNA-directed DNA polymerase (Reverse transcriptase) - Medicago truncatula (Barrel medic)
LjT35J12.20.nd	232	(Q3EBG6) Protein At2g44120 - Arabidopsis thaliana (Mouse-ear cress)

LjT37C05.180.nd	155	unknown protein
LjT37C05.80.nd	107	(Q1G0Z1) Putative spindle disassembly related protein CDC48 - Nicotiana tabacum (Common tobacco)
LjT37D10.80.nd	99	(A3Z8T2) Photosystem I P700 chlorophyll a apoprotein subunit Ia (PsaA) - Synechococcus sp. RS9917
LjT37O09.360.nd	130	(Q1S6E3) Scarecrow-like protein 3 [imported]-Arabidopsis thaliana-related - Medicago truncatula (Barrel medic)
LjT38B21.40.nc	494	(Q1SGL6) Hypothetical protein - Medicago truncatula (Barrel medic)
LjT38B24.120.nd	82	(Q9SWS9) Ribosomal protein S26 - Pisum sativum (Garden pea)
LjT39P23.170.nd	183	(Q19PJ3) TIR-NBS-LRR type disease resistance protein - Populus trichocarpa (Western balsam poplar)
LjT39P23.40.nd	122	(Q1RSP6) TIR; Disease resistance protein; AAA ATPase; Winged helix repressor DNA-binding - Medicago truncatula (Barrel medic)
LjT40J14.110.nc	127	(Q9SA38) F3O9.19 protein (At1g16390/F3O9_19) - Arabidopsis thaliana (Mouse-ear cress)
LjT40J14.50.nc	571	(A3QRM4) Senescence-associated nodulin 1A - Glycine max (Soybean)
LjT41B11.170.nd	226	(A3QVH0) Toll interleukin receptor - Phaseolus vulgaris (Kidney bean) (French bean)
LjT41D10.70.nd	124	(Q1SWG9) Heavy metal transport/detoxification protein - Medicago truncatula (Barrel medic)
LjT41F16.130.nd	121	(Q2HTB8) Harpin-induced 1 - Medicago truncatula (Barrel medic)
LjT41N19.40.nd	50	(A4GGE0) Ribosomal protein S8 - Phaseolus vulgaris (Kidney bean) (French bean)
LjT42M11.120.nc	364	(Q9LP24) F14D7.1 protein - Arabidopsis thaliana (Mouse-ear cress)

LjT43N20.110.nc	62	(Q1S278) Proteinase inhibitor I13, potato inhibitor I - Medicago truncatula (Barrel medic)
LjT44J06.120.nd	86	(Q93X23) Putative chloroplast terpene synthase precursor - Quercus ilex (Holly oak)
LjT44J06.130.nd	124	(Q93X23) Putative chloroplast terpene synthase precursor - Quercus ilex (Holly oak)
LjT47D03.110.nd	254	(A2X6W8) Hypothetical protein - Oryza sativa (indica cultivar-group)
LjSGA_001771.2	381	(Q5GN36) Serpin (Fragment)
LjSGA_003943.1	243	(Q2HVE0) Disease resistance protein; AAA ATPase
LjSGA_004132.0.1	119	(Q9ZVD0) Expressed protein (Hypothetical protein At2g27100) (C2H2 zinc-finger protein SERRATE) (At2g27100/T20P8.15)
LjSGA_005129.0.1	54	(Q5Z845) Hypothetical protein P0468G03.24
LjSGA_005273.2	110	(Q2HUA2) Proteinase inhibitor I25, cystatin
LjSGA_005309.1	273	unknown protein
LjSGA_005477.1.1	54	(Q6K2P4) Methylenetetrahydrofolate dehydrogenase-like
LjSGA_005575.0.1	83	(O49896) Hypothetical protein
LjSGA_006494.1	92	(Q6NLR7) At5g04070
LjSGA_007172.1	176	(Q94CQ1) Putative RNA-binding like protein
LjSGA_007195.3	65	(O65884) Major latex-like protein
LjSGA_007644.1	90	(Q30D01) Putative 3-dehydroquinate synthase
LjSGA_007647.1	102	(Q9ZQT9) WERBP-1 protein
LjSGA_007648.1	125	(Q9ZQT9) WERBP-1 protein
LjSGA_007850.1	62	(Q9SK79) Hypothetical protein At2g20220
LjSGA_008112.1	84	(Q56SE1) Methyl jasmonate esterase
LjSGA_008600.2.1	146	(Q9SCA1) Calcium-binding protein

LjSGA_008663.1	86	(Q9AVC1) Chalcone synthase (EC 2.3.1.74)
LjSGA_008942.1	137	(Q2HS79) Cyclin-like F-box; Agenet
LjSGA_009738.0.1	109	(Q9FKF1) DNA-directed RNA polymerase subunit
LjSGA_009761.2	74	(Q2QWK0) Subtilisin inhibitor . [broad bean
LjSGA_010377.1	375	(Q93XX2) Hypothetical protein At3g01670; F4P13.21 (At3g01670)
LjSGA_010548.2	216	(O82711) Profucosidase precursor (EC 3.2.1.51)
LjSGA_010711.1	52	(Q942D2) Putative WRKY DNA binding protein (WRKY23) (WRKY transcription factor 23) (WRKY4)
LjSGA_011304.1	221	(Q9LXJ7) Hypothetical protein F3C22_70 (Fragment)
LjSGA_011595.2	283	(Q8W3F7) Pre-mRNA splicing factor, putative
LjSGA_011662.1	247	(Q9FNJ5) Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MDJ22
LjSGA_012121.1	134	(Q9LMI5) T2D23.4 protein
LjSGA_012185.1	227	(Q2QW52) Transposon protein, putative, CACTA, En/Spm sub-class
LjSGA_012355.2	212	(Q3EBU0) Protein At2g25850
LjSGA_013051.1	242	(Q2HSZ7) FAR1 family, putative
LjSGA_013091.2	154	(Q7XRX2) OSJNBb0032E06.5 protein
LjSGA_013115.1	234	(Q2HUI7) Cyclin-like F-box; FBD; Zinc finger, FYVE/PHD-type
LjSGA_013263.3	154	(Q9QZE4) Signal transducer and activator of transcription 2
LjSGA_013493.1	138	(Q6UQ08) Putative TIR-NBS type R protein 11
LjSGA_013527.1	344	(Q2HUN6) RNA-directed DNA polymerase (Reverse transcriptase); Ribonuclease H
LjSGA_013649.2	109	(Q9LUZ5) GblAAC80581.1
LjSGA_013917.1	89	(Q8GYK6) Hypothetical protein At2g32840

LjSGA_014070.2	231	(Q9FNJ1) Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MDJ22
LjSGA_014139.1	140	unknown protein
LjSGA_014142.2	74	(Q9LET5) Hypothetical protein T8M16_50
LjSGA_014321.1	74	(Q6L570) Hypothetical protein OJ1115_D04.1
LjSGA_014365.1	74	(Q9FG53) Gb|AAC80581.1
LjSGA_014391.0.1	115	(Q6Z8U6) Putative glutathione transporter
LjSGA_014467.1	108	unknown protein
LjSGA_014483.1	97	(Q8W0Y5) Enod8.1
LjSGA_014912.1.1	134	(Q9LP66) T1N15.20
LjSGA_015052.2	67	(Q9SJI6) Hypothetical protein At2g42700
LjSGA_015078.1	543	(Q9LRQ0) Emb|CAB39684.1
LjSGA_015103.1	151	(O49607) Subtilisin proteinase-like (Putative subtilisin serine protease) (Putative subtilisin serine proteinase)
LjSGA_015113.1	518	(Q9ZVX1) Putative ubiquitin-conjugating enzyme
LjSGA_015171.1	53	(Q5ENY3) Respiratory burst oxidase 2 (Fragment)
LjSGA_015400.1	67	(Q9FHA4) Subtilisin-type protease-like (At5g67090)
LjSGA_015418.1	61	(Q547H3) Tubulin folding cofactor A
LjSGA_015468.1	162	(Q9LFC1) Hypothetical protein F7J8_130
LjSGA_015473.1	216	(Q6ZHE3) Putative cyclic nucleotide-binding transporter 1
LjSGA_015496.1	148	(Q9SWG9) Inorganic phosphate transporter
LjSGA_015549.1	214	(Q69QY7) Hypothetical protein OJ1695_D07.22
LjSGA_015573.1	143	(Q2HS67) F-box associated, putative
LjSGA_015707.0.1	122	unknown protein
LjSGA_015906.1	623	(Q9W1X5) CG12781-PA, isoform A (Cg12781-pb, isoform b) (GH04942p)

LjSGA_015939.1	101	(Q6K852) Putative methyltransferase
LjSGA_015943.1.1	101	(Q40156) L.esculentum protein with leucine zipper
LjSGA_016033.2.1	77	(Q949H4) Leaf ubiquitous urease (EC 3.5.1.5)
LjSGA_016155.1	245	(Q9FNJ4) Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MDJ22
LjSGA_016204.1.1	120	(Q29PU4) At1g68795
LjSGA_016350.2	106	(Q852S5) Nucleoside diphosphate kinase
LjSGA_016388.2	108	(Q3EDK1) Protein At1g02850
LjSGA_016403.1	79	(Q6H889) Putative zinc-binding protein
LjSGA_016425.1	92	(O04518) F21M12.37 protein
LjSGA_016520.1	112	(Q2HVN4) Probable Na/H antiporter [imported]-Arabidopsis thaliana, putative
LjSGA_016674.1	198	(Q9LDH3) T12C24.5 (F5O11.25) (Hypothetical protein At1g12500/T12C24_29)
LjSGA_016728.2	171	unknown protein
LjSGA_016758.1	434	(Q2HSF7) Cyclin-like F-box; F-box protein interaction domain; Galactose oxidase, central
LjSGA_016896.1	50	(Q93XQ3) Putative beta-1,3-glucan synthase
LjSGA_017029.2	60	(Q8LFK2) Hypothetical protein (Hypothetical protein At3g03270)
LjSGA_017037.2.1	89	(O64470) Putative anthranilate N-hydroxycinnamoyl/benzoyltransferase
LjSGA_017136.1	82	(Q6NLT5) At3g21440
LjSGA_017463.1	86	(Q84ZX0) HEN4
LjSGA_017537.1.1	108	(Q9LYG5) Lysophospholipase-like protein
LjSGA_017637.1.1	127	(Q84VX5) At4g02100
LjSGA_017734.1	275	(Q2HV58) Hypothetical protein

LjSGA_018197.2	95	(Q8RXT2) Hypothetical protein At4g32350
LjSGA_018236.1	54	(Q9FJK3) Similarity to MADS-box DNA-binding protein (MADS-box family protein)
LjSGA_018295.1	282	(Q9ZUS6) Chloroplast lumen common protein family
LjSGA_018330.1	158	(Q42433) S3 self-incompatibility protein precursor
LjSGA_018382.1	120	(Q8S901) Syringolide-induced protein 14-1-1
LjSGA_018480.0.1	109	(Q84XL0) SP3D
LjSGA_018778.1	175	(Q93ZA0) AT4g13250/F17N18_140
LjSGA_018827.1	130	(Q9SS87) F4P13.22 protein (At3g01680)
LjSGA_018848.1.1	136	(Q7XC13) Expressed protein
LjSGA_019072.1	97	(Q6K8I3) Fertility restorer homologue A-like
LjSGA_019080.3	293	(Q2HVE0) Disease resistance protein; AAA ATPase
LjSGA_019091.2	173	(Q7XMI8) OSJNBb0006N15.11 protein
LjSGA_019149.1	117	(Q9FP50) Hypothetical protein P0475H04.20
LjSGA_019250.1	109	(Q65XE3) Putative cullin 1
LjSGA_019286.1	145	(Q6YNS0) Putative translation-initiation factor 3 subunit
LjSGA_019385.2	249	(Q8H9A2) Dehydratiion responsive element binding protein 1 like protein
LjSGA_019412.1.1	140	(Q949V7) Hypothetical protein At3g59300
LjSGA_019465.1	58	(Q84TF0) At2g37790
LjSGA_019506.1	154	(Q9C7J9) Hypothetical protein F14G9.15 (At1g56240)
LjSGA_019604.2	149	unknown protein
LjSGA_019700.2	162	(O65510) Putative receptor protein kinase
LjSGA_019725.2	197	(P93620) Phosphoinositide-specific phospholipase C (EC 3.1.4.11)
LjSGA_019790.0.1	128	(O48766) Putative glucanse (At2g32990)
LjSGA_020175.2	92	(Q940J9) Hypothetical protein At1g04430; F19P19.11

LjSGA_020518.0.1	155	(Q8GTR0) Sugar transporter
LjSGA_020534.1	117	(Q8H958) Peroxidase 1
LjSGA_020576.1	92	(Q9SLJ4) F20D21.22 protein
LjSGA_020611.1	135	(Q9SU88) Hypothetical protein T16L4.100 (Hypothetical protein AT4g29590)
LjSGA_020777.1	113	(Q6ZA15) Putative mitochondrial carrier protein
LjSGA_021301.1	73	(Q2QVE1) Transposon protein, putative, unclassified
LjSGA_021536.1	69	(Q8LBX6) Hypothetical protein
LjSGA_021547.1	159	(Q3LVQ7) TO24-123rc (Fragment)
LjSGA_021639.1	99	(Q9ZQI2) Hypothetical protein At2g27370
LjSGA_021748.1.1	55	(Q6DMZ6) Cinnamoyl CoA reductase (Fragment)
LjSGA_021829.1	110	(Q94IA6) CYP90D (Putative cytochrome P450)
LjSGA_021975.1	115	(Q2HSK0) Transcriptional factor B3
LjSGA_021983.1	228	(Q8LAM5) Protein disulfide isomerase-like
LjSGA_021991.1	113	(Q8H241) Hypothetical protein
LjSGA_022138.1	223	(Q8VYX4) Sucrose transporter SUC1
LjSGA_022221.2	82	(Q8RXG9) Hypothetical protein At4g33565/T16L1.1
LjSGA_022494.1	87	unknown protein
LjSGA_022704.3	113	(Q9SL64) Hypothetical protein At2g20170
LjSGA_022784.1	218	(Q8L7C2) Hypothetical protein At3g01370
LjSGA_022879.1	120	(Q6NLF7) At1g62790
LjSGA_023299.1	117	(O23207) Minor allergen
LjSGA_023592.2	73	(Q765H9) TATA box-binding protein associated factor 10
LjSGA_023901.2	152	(Q84UT8) Flavonol synthase
LjSGA_024000.1	53	(Q676Y2) Hypothetical protein (Fragment)

LjSGA_024007.1	98	(Q5CCP6) Beta-D-galactosidase (EC 3.2.1.23)
LjSGA_024344.1.1	105	(Q3EAL1) Protein At3g52525
LjSGA_024353.1	128	(Q94AT1) Hypothetical protein At5g53140 (Putative phosphatase 2C)
LjSGA_024617.1	248	(Q2R8W7) Leucine Rich Repeat, putative
LjSGA_024674.1	102	(Q9XIG1) Putative UDP-glucose:sterol glucosyltransferase (At1g43620)
LjSGA_024678.1	212	(O22952) Putative SF16 protein (Helianthus annuus)
LjSGA_024820.1	262	(Q4L0F8) Protein phosphatase 2c
LjSGA_024873.1	85	(Q9FR37) Amidase (At1g08980/F7G19_15)
LjSGA_025115.1	225	(Q9XGZ4) T1N24.4 protein
LjSGA_025170.2	44	(Q9SCS2) CDPK-related protein kinase
LjSGA_025344.2	482	(Q2KQ28) Resistance protein PLTR (Fragment)
LjSGA_025640.1	532	(Q2HUZ8) Helicase, C-terminal; Zinc finger, CCHC-type
LjSGA_025651.1.1	75	(Q9M2N9) Hypothetical protein T10K17.300
LjSGA_025689.1.1	182	(O23222) MADS-box protein AGL40 (Putative MADS-box protein)
LjSGA_025894.1	98	(Q8VWN6) Raffinose synthase (EC 2.4.1.82)
LjSGA_025910.2	161	(Q68GS0) SKP1
LjSGA_026078.1	105	(Q9FVV1) Putative GDSL-motif lipase/acylhydrolase; 82739-81282 (Putative GDSL-motif lipase/acylhydrolase) (At1g71250)
LjSGA_026433.2	112	(O82023) N7 protein (Fragment)
LjSGA_026475.1	142	(Q9LI65) Nodulin-like protein (Hypothetical protein At3g30340/T6J22_10)
LjSGA_026712.1	61	(Q501D2) At1g18840
LjSGA_026814.1	61	(Q9LP66) T1N15.20
LjSGA_026849.1	77	(O65152) Putative cinnamyl alcohol dehydrogenase
LjSGA_026864.1	125	(Q9FI75) Similarity to 5'-nucleotidase
LjSGA_027445.1	153	(Q6ESR6) Putative anter-specific proline-rich protein APG

LjSGA_027478.1.1	82	(Q5Z656) Putative ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1
LjSGA_027516.1	60	(Q6Z0F0) Putative GEKO1
LjSGA_027545.2	141	(Q9LP66) T1N15.20
LjSGA_027604.1	103	(Q6EP65) Hypothetical protein B1077E10.21 (Hypothetical protein P0638A12.10)
LjSGA_027781.1	116	(Q9LHW8) Putative esterase
LjSGA_027812.1.1	79	(Q7XKR2) OSJNBa0053B21.9 protein
LjSGA_028108.1	209	(Q9AV94) Hypothetical protein
LjSGA_028144.1	133	(Q9FK75) GDSL-motif lipase/hydrolase-like protein (AT5g45670/MRA19_6)
LjSGA_028206.1	248	(Q9FNJ4) Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MDJ22
LjSGA_028216.1	77	(Q3HLN2) Sucrose-phosphate synthase isoform B (EC 2.4.1.14)
LjSGA_028218.2	152	(Q9FQE9) Glutathione S-transferase GST 9 (EC 2.5.1.18)
LjSGA_028767.1	95	(Q2HUN2) TIR; Disease resistance protein
LjSGA_029016.1	113	(Q9LHL1) Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MJH23 (Hypothetical protein At3g13227)
LjSGA_029165.1.1	80	(Q9M2S1) Regulator of chromosome condensation-like protein
LjSGA_029238.1	117	(Q8S351) Auxin-induced SAUR-like protein
LjSGA_029271.1	68	(Q5JKB0) Putative replication licensing factor MCM4
LjSGA_029572.0.1	50	(Q9XH70) Hypothetical protein p69RF (Fragment)
LjSGA_029572.2	89	(O80851) Putative dioxygenase
LjSGA_029582.1	68	(Q6NMB2) Hypothetical protein At5g10320
LjSGA_029612.1	65	(Q9FG70) Gb|AAF04433.1
LjSGA_029724.1	170	(Q6Z3F5) Putative MYST1

LjSGA_029886.1	187	(Q6NLE5) At3g01516
LjSGA_029906.1	121	(Q337J6) Expressed protein
LjSGA_030032.2	134	(Q9SA38) F3O9.19 protein (At1g16390/F3O9_19)
LjSGA_030056.1	257	(O23360) Hypothetical protein AT4g15060
LjSGA_030070.1	111	(Q303Z0) Protein At5g53050
LjSGA_030143.2	122	(Q41251) Calmodulin-binding heat-shock protein
LjSGA_030160.1	68	(Q336T9) Flavin-containing monooxygenase, putative
LjSGA_030203.1	153	(Q2HUD3) Heat shock protein Hsp70
LjSGA_030339.1	88	(Q9M2F3) Hypothetical protein F14P22.230
LjSGA_030441.1	59	(Q6K9F7) Putative SET domain protein SUVR2
LjSGA_030495.0.1	48	(Q56WN0) Endoribonuclease/protein kinase IRE1
LjSGA_030680.1	149	(Q6V0J6) Reduced vernalization response 1
LjSGA_030719.2	87	(Q8W4Z5) Hypothetical protein f16
LjSGA_030798.2	140	(Q84YF4) Hypothetical protein 5
LjSGA_031016.1.1	109	(Q6L3G4) Putative plant disease resistant protein
LjSGA_031034.1	186	(Q2V4C9) Protein At1g72990
LjSGA_031058.2	78	(O80619) Homeotic protein AGL30
LjSGA_031321.1	128	(Q9SFV9) T1B9.4 protein
LjSGA_031368.1	128	(Q5XEY4) At5g53080
LjSGA_031426.2	80	(Q25AJ5) H0510A06.10 protein
LjSGA_031649.1.1	254	(Q9FGH9) Leucine zipper protein (AT5g58430/mqj2_20)
LjSGA_031726.2	83	(Q84X66) NBS-LRR type resistance protein (Fragment)
LjSGA_032158.1.1	170	(Q9LWA5) Putative TFIIIA (Or kruppel)-like zinc finger protein
LjSGA_032260.1	137	(Q6K4E1) Hypothetical protein OJ1506_A04.22 (Hypothetical protein OJ1001_G09.8)

LjSGA_032392.1	113	(Q71QH1) Cf-4/9 disease resistance-like protein (Fragment)
LjSGA_032481.1	83	(Q2HU26) CCT
LjSGA_032795.2.1	71	(Q93YP7) Polyprenyltransferase like protein (Para-hydroxy bezoate polyprenyl diphosphate transferase) (At4g23660)
LjSGA_032906.1	83	(Q8GT20) Benzoyl coenzyme A: benzyl alcohol benzoyl transferase
LjSGA_032985.1	73	(Q647I5) Putative RNA-dependent RNA polymerase SDE1
LjSGA_033075.1	134	(Q9LW22) Gb|AAD30245.1
LjSGA_033145.2	77	(Q677A2) Cold-induced protein (Fragment)
LjSGA_033178.1	105	(Q8VYW7) AT5g16210/T21H19_130
LjSGA_033312.1	116	(Q9FJD9) Similarity to RNaseP protein p30
LjSGA_033713.1	138	(Q5XWQ0) At3g17900/MEB5_12-like protein
LjSGA_033789.1	55	(O64489) F20D22.5 protein
LjSGA_033846.1	125	(Q42433) S3 self-incompatibility protein precursor
LjSGA_033901.1	178	unknown protein
LjSGA_033923.1	375	(Q2HTR6) RNA-directed DNA polymerase (Reverse transcriptase)
LjSGA_033967.1.1	70	(Q5SNH5) Putative 6-phospho-1-fructokinase
LjSGA_033972.1	162	(Q9M2Z5) Hypothetical protein T21J18_150 (Hypothetical protein At3g48880)
LjSGA_034219.1	91	(Q56I14) TPR-containing protein kinase
LjSGA_034329.1	101	(Q9C5S3) AtSPO11-1
LjSGA_034445.1	79	(Q9SZH4) Putative nucleic acid binding protein
LjSGA_034560.1	135	(Q9C7X8) Hypothetical protein F13N6.18
LjSGA_034862.1	84	(Q2V381) Protein At5g13750
LjSGA_035237.1	71	(Q9LYF1) Putative potassium transport protein
LjSGA_035304.1	106	(Q5Z825) Putative avrRpt2-induced AIG2 protein

LjSGA_035476.1	80	(Q2HUI4) Cystinosin/ERS1p repeat
LjSGA_035658.1	133	(Q599T8) Allene-oxide cyclase precursor (EC 5.3.99.6)
LjSGA_035868.1	76	(Q9C650) Peptidylprolyl isomerase, putative
LjSGA_035870.1	59	(Q9SX67) F11A17.11 (At1g48330)
LjSGA_035880.1.1	99	(Q7XIX3) Hypothetical protein OJ1136_D11.125
LjSGA_036127.1.1	99	(Q9MA41) T20M3.12 protein (Putative class I chitinase) (Chitinase-like protein 1)
LjSGA_036219.1	132	(Q9ZVN2) T22H22.2 protein (At1g54570) (Hypothetical protein) (Hypothetical protein At1g54570/T22H22_2)
LjSGA_036325.1	247	(Q8LEM2) Hypothetical protein
LjSGA_036392.1.1	87	(Q8LES9) Hypothetical protein
LjSGA_036522.1	112	(Q6Z390) Hypothetical protein P0417F02.15 (Hypothetical protein P0589E08.34)
LjSGA_036630.1	185	(Q9FJK3) Similarity to MADS-box DNA-binding protein (MADS-box family protein)
LjSGA_036811.1	145	(Q9FL05) Similarity to intracellular protein (AT5g40270/MSN9_170)
LjSGA_037347.1	91	(O49521) Hypothetical protein F28J12.190 (Hypothetical protein AT4g18530)
LjSGA_037647.1.1	96	(Q2HUT2) Amino acid/polyamine transporter II
LjSGA_038084.2	76	(Q9M817) Peptide transporter, putative
LjSGA_038153.1	146	(Q2PJR6) WRKY54
LjSGA_038349.1	108	(Q9FKS9) WD-repeat protein-like
LjSGA_038401.1	133	(Q7XQM5) OSJNBa0089K21.11 protein
LjSGA_038620.1	236	(O48807) F2401.16 (Hypothetical protein At1g62420/F24O1_44) (Hypothetical protein At1g62425)

LjSGA_038807.2	66	(Q304A8) Protein At4g05520
LjSGA_038968.1	69	(Q94IA6) CYP90D (Putative cytochrome P450)
LjSGA_039082.1	117	(Q9SL64) Hypothetical protein At2g20170
LjSGA_039202.2	91	(Q6K861) Putative GDSL-lipase
LjSGA_039212.1	207	(Q2YE87) NBS-LRR type disease resistance protein Rps1-k-2
LjSGA_039269.2	169	(Q9FJ30) Similarity to heat shock transcription factor HSF30
LjSGA_039636.1	181	(Q8GT65) Serpin-like protein (Fragment)
LjSGA_039685.1	143	(Q9LMI5) T2D23.4 protein
LjSGA_039898.2	133	(Q949G8) HcrVf2 protein
LjSGA_040104.1	128	(Q9FP50) Hypothetical protein P0475H04.20
LjSGA_040247.1	196	(Q38M54) Rieske iron-sulfur protein-like
LjSGA_040307.1	44	(Q2PEY2) Putative long chain acyl-CoA synthetase 9
LjSGA_040403.1.1	135	(Q9SSM2) Similar to (R)-mandelonitrile lyase isoform 1
LjSGA_040430.1	90	(Q9SZU6) Hypothetical protein F6G17.110 (Hypothetical protein AT4g37460)
LjSGA_040519.2	128	(Q6K963) Putative callose synthase 1 catalytic subunit
LjSGA_040652.1	81	(Q39820) Hsp22.5
LjSGA_040770.1	96	(Q9ZQ30) Hypothetical protein At2g24370
LjSGA_040863.1	89	(Q9FL22) Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MPL12
LjSGA_041028.3	114	(Q2HWC9) Hypothetical protein
LjSGA_041071.1	303	(Q84ZV0) R 14 protein
LjSGA_041349.1	143	(Q6SZ87) Nucleobase-ascorbate transporter 11
LjSGA_041622.1	198	(Q9STP5) Hypothetical protein T27E11.50 (Hypothetical protein AT4g27810)
LjSGA_041871.1.1	73	(Q9FYD4) Rec-like protein

LjSGA_041878.0.1	56	(Q9M1D6) Hypothetical protein T2O9.50
LjSGA_042000.1	82	(Q9M1J2) Hypothetical protein F24I3.160 (Hypothetical protein At3g57080/F24I3_160) (Hypothetical protein At3g57080)
LjSGA_042231.1	69	(Q2HTR2) Cyclin-like F-box
LjSGA_042393.1	158	(O23726) B-Zip DNA binding protein
LjSGA_042417.1	160	(Q2HSY3) Nucleic acid-binding, OB-fold
LjSGA_042493.2.1	49	(Q8LAU7) Hypothetical protein
LjSGA_042741.1	155	(Q9LVK5) Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC16
LjSGA_042772.1	76	(Q7XMI1) OSJNBb0004G23.4 protein
LjSGA_042990.2	128	(Q2HS79) Cyclin-like F-box; Agenet
LjSGA_043060.1	68	(Q9FZ04) Plastid terminal oxidase
LjSGA_043183.1	129	(Q8LC04) Hypothetical protein
LjSGA_043214.1	102	(Q2KNL3) Alcohol dehydrogenase-like protein
LjSGA_043231.1	314	(Q2HUI7) Cyclin-like F-box; FBD; Zinc finger, FYVE/PHD-type
LjSGA_043606.0.1	90	(Q9T0J2) Auxin-induced protein-like (At4g38840)
LjSGA_043640.3	133	(O82491) T12H20.3 protein (Putative transcriptional regulator)
LjSGA_044174.1.1	115	(Q6L459) Hypothetical protein PGEC589.7
LjSGA_044936.1	84	(Q9ZNX9) Sigma-like factor precursor (RNA polymerase sigma subunit SigE)
LjSGA_045035.1	186	(Q43521) Unknown protein
LjSGA_045070.1	168	(Q53NG8) Aldehyde dehydrogenase, putative
LjSGA_045216.1	125	(Q9LP66) T1N15.20
LjSGA_045471.3	282	(Q2HV76) F-box protein interaction domain; Galactose oxidase, central
LjSGA_045906.2	62	(Q3E9P8) Protein At4g36860

LjSGA_046038.1	202	(Q9FJJ4) Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K19B1
LjSGA_046103.1	97	(Q93XZ7) Hypothetical protein At5g42570; K16E1.4 (At5g42570)
LjSGA_046214.1	95	(Q4PSB2) Hypothetical protein
LjSGA_046400.1.1	107	(Q2L8Z5) RNA polymerase beta' subunit
LjSGA_046630.2	257	(Q6L3S8) Putative F-Box protein
LjSGA_046820.1	80	(Q2PES5) Hypothetical protein
LjSGA_046898.1.1	93	(Q75I70) Putative sesquiterpene synthase
LjSGA_047329.1	231	(Q9LJF8) Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MQP17
LjSGA_047358.1	82	(Q6X0N8) Putative spermine/spermidine synthase
LjSGA_047416.1	203	(Q9C5I9) Putative lipase
LjSGA_047781.1	103	(Q56YR0) Hypothetical protein At4g01290
LjSGA_048117.0.1	95	(Q9FM77) Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MDF20 (Hypothetical protein At5g55610)
LjSGA_048252.1	168	(Q3E936) Protein At5g26230
LjSGA_048703.1	71	(Q677F2) Ribosomal protein L19
LjSGA_048736.1	97	(O22633) NOI protein, nitrate-induced (Putative nitrate-induced NOI protein)
LjSGA_048814.1	260	(Q9ZW94) F5A8.4 protein
LjSGA_049059.1	154	(Q3E9S8) Protein At4g32330
LjSGA_050024.1	108	(Q9C7D6) Serine carboxypeptidase, putative; 18637-16038 (At3g12203)
LjSGA_050059.1	111	(O23269) Hypothetical protein dl3085w (Hypothetical protein AT4g14090)
LjSGA_050115.1.1	106	(Q6K6G8) Putative Importin 7<Ran-binding protein 7
LjSGA_050213.1	173	(O81731) Hypothetical protein F16G20.50 (Hypothetical protein AT4g23350)
LjSGA_050544.1	132	(Q8GTG4) WRKY transcription factor IId-2 (Fragment)

LjSGA_050616.1	86	(Q8LG03) Hypothetical protein
LjSGA_051239.1	175	(Q93YF1) Nucleic acid binding protein
LjSGA_051266.1	137	(Q8L9R6) Hypothetical protein (At1g68680)
LjSGA_051377.2	346	(Q53K97) Retrotransposon protein, putative, unclassified
LjSGA_051656.1	201	(Q9FJY3) Photoreceptor-interacting protein-like
LjSGA_051999.1	60	(O65023) Hypothetical protein
LjSGA_052124.1	113	(Q25AD4) H0201G08.9 protein
LjSGA_052190.1	259	(Q6ZD72) Hypothetical protein P0450B04.17
LjSGA_052243.1	72	(P93157) Annexin (Fragment)
LjSGA_052254.2	104	(Q9SR02) F7O18.23 protein (SWP1) (Struwwelpeter 1 protein)
LjSGA_053143.1	107	(Q8LFE2) Photosystem II
LjSGA_053245.1	192	(Q6L4X7) Hypothetical protein OSJNBb0108E17.2
LjSGA_053455.1.1	122	(Q6DXS9) Predicted protein
LjSGA_053489.1	84	(Q67VB0) Hypothetical protein OSJNBa0068B06.28 (Hypothetical protein OSJNBa0052G07.19)
LjSGA_053648.2	337	(Q2HWB4) Cyclin-like F-box; F-box protein interaction domain
LjSGA_053831.1	92	(Q3E9Q4) Protein At4g35987
LjSGA_053890.1	114	(Q84YP6) F-box protein-like protein
LjSGA_053986.1	108	(Q93X19) Urease (EC 3.5.1.5)
LjSGA_054078.1	73	(Q64EX4) MtN19-like protein
LjSGA_054328.1.1	91	(Q6NPR7) At1g29470
LjSGA_054339.2	153	(Q9AVC0) Chalcone synthase (EC 2.3.1.74)
LjSGA_054553.2	89	(Q9ZPH9) F15P23.1 protein (Hypothetical protein AT4g00750)
LjSGA_054994.1	120	(Q9LLZ7) Phytocyanin homolog
LjSGA_055018.1	216	(Q9M9R5) F14L17.26 protein

Supplemental Table 15. List of the *L. japonicus* genes without a counterpart in the databases.

gene name	product size (aa)	Status	Description
chr2.CM0225.90.nc	53	comp.	(Q6W2J4) VDAC1.2 - Lotus japonicus
LjSGA_039975.1	51	comp.	(Q53UK3) Ser/Thr protein kinase
LjSGA_043445.1	66	comp.	(Q53VE2) Ser/Thr protein kinase
LjSGA_091697.1	53	comp.	(Q40209) RAB5A
chr1.CM0033.550.nc	89	comp.	(Q1T2J3) DNA binding protein S1FA - Medicago truncatula (Barrel medic)
chr1.CM0064.450.nc	186	comp.	(Q1S3X4) Ribonuclease H - Medicago truncatula (Barrel medic)
chr1.CM0098.30.nd	77	comp.	(Q2HW84) Cyclin-like F-box - Medicago truncatula (Barrel medic)
chr1.CM0105.700.nc	146	comp.	(Q1SL48) Zinc finger, GRF-type - Medicago truncatula (Barrel medic)
chr1.CM0109.340.nc	189	comp.	(Q1SFZ0) At5g27860 (Vitellogenin, related) - Medicago truncatula (Barrel medic)
chr1.CM0125.60.nc	509	comp.	(Q2HUJ3) Hypothetical protein - Medicago truncatula (Barrel medic)
chr1.CM0171.670.nd	64	comp.	(Q1SKE5) Short-chain dehydrogenase/reductase SDR - Medicago truncatula (Barrel medic)
chr1.CM0233.120.nc	248	comp.	(Q1SR58) Hypothetical protein - Medicago truncatula (Barrel medic)
chr1.CM0233.460.nc	215	comp.	(Q1SU18) Hypothetical protein - Medicago truncatula (Barrel medic)
chr1.CM0295.510.nd	137	comp.	(Q1RW20) Plant self-incompatibility S1 - Medicago truncatula (Barrel medic)
chr1.CM0433.190.nd	151	comp.	(Q1SXA3) IMP dehydrogenase/GMP reductase - Medicago truncatula (Barrel medic)
chr1.CM1956.100.nd	146	comp.	(Q1SL48) Zinc finger, GRF-type - Medicago truncatula (Barrel medic)
chr1.LjT41J07.10.nd	256	comp.	(Q1SB14) Protein kinase - Medicago truncatula (Barrel medic)
chr1.LjT43O05.100.nd	171	comp.	(Q1S1M9) Hypothetical protein - Medicago truncatula (Barrel medic)
chr1.LjT43O05.140.nd	136	comp.	(Q4A185) Beclin 1 protein - Medicago truncatula (Barrel medic)
chr2.CM0058.60.nc	457	comp.	(Q1SZ19) Hypothetical protein - Medicago truncatula (Barrel medic)
chr2.CM0102.380.nc	278	comp.	(Q1SUL5) IMP dehydrogenase/GMP reductase - Medicago truncatula (Barrel medic)

chr2.CM0120.340.nc	142	comp.	(Q1SCP0) RNA-binding region RNP-1 (RNA recognition motif) - Medicago truncatula (Barrel medic)
chr2.CM0124.510.nc	121	comp.	(Q1SCR3) Pre-mRNA cleavage complex II Clp1 - Medicago truncatula (Barrel medic)
chr2.CM0153.110.nc	412	comp.	(Q1SCA3) Hypothetical protein - Medicago truncatula (Barrel medic)
chr2.CM0153.140.nc	405	comp.	(Q1SCA0) Hypothetical protein - Medicago truncatula (Barrel medic)
chr2.CM0177.590.nc	209	comp.	(Q1S546) Hypothetical protein - Medicago truncatula (Barrel medic)
chr2.CM0201.250.nc	321	comp.	(Q1SCA3) Hypothetical protein - Medicago truncatula (Barrel medic)
chr2.CM0201.70.nd	384	comp.	(Q1SCA3) Hypothetical protein - Medicago truncatula (Barrel medic)
chr2.CM0210.40.nc	101	comp.	(Q1S948) PGPS/D10 - Medicago truncatula (Barrel medic)
chr2.CM0272.460.nd	182	comp.	(Q1SI76) Cyclin-like F-box; F-box protein interaction domain (F-box associated, putative) - Medicago truncatula (Barrel medic)
chr2.CM0308.250.nc	101	comp.	(Q1S704) Hypothetical protein - Medicago truncatula (Barrel medic)
chr2.CM0338.240.nd	86	comp.	(Q1SR15) Zinc finger, RING-type; RINGv - Medicago truncatula (Barrel medic)
chr2.CM0749.290.nd	99	comp.	(Q1SBE2) Hypothetical protein - Medicago truncatula (Barrel medic)
chr3.CM0091.100.nc	267	comp.	(Q1RYG0) Zinc finger, CCHC-type; Plant MuDR transposase; Zinc finger, SWIM-type - Medicago truncatula (Barrel medic)
chr3.CM0091.250.nc	105	comp.	(Q1SI76) Cyclin-like F-box; F-box protein interaction domain (F-box associated, putative) - Medicago truncatula (Barrel medic)
chr3.CM0091.610.nd	88	comp.	(Q1S9F6) Hypothetical protein - Medicago truncatula (Barrel medic)
chr3.CM0110.90.nc	844	comp.	(Q1RXG8) IMP dehydrogenase/GMP reductase - Medicago truncatula (Barrel medic)
chr3.CM0135.210.nd	60	comp.	(Q1RSQ6) Metal-dependent phosphohydrolase, HD region (Metal-dependent phosphohydrolase, HD region; Putative DNA binding) - Medicago truncatula (Barrel medic)
chr3.CM0216.400.nc	92	comp.	(Q1SSK7) Peptidase C14, caspase catalytic subunit p20 - Medicago truncatula (Barrel medic)
chr3.CM0261.290.nc	155	comp.	(Q5UBY0) Wound-inducible putative cytosolic terpene synthase 1 - Medicago truncatula (Barrel medic)

chr3.CM0634.380.nd	84	comp.	(Q1STP0) Serine/threonine-specific protein phosphatase and bis(5-nucleosyl)-tetraphosphatase - Medicago truncatula (Barrel medic)
chr3.CM0711.470.nd	75	comp.	(Q1SAL1) Protein phosphatase 2C-like - Medicago truncatula (Barrel medic)
chr3.LjT29G18.130.nd	137	comp.	(Q1SYS3) Hypothetical protein - Medicago truncatula (Barrel medic)
chr3.LjT36L08.50.nc	137	comp.	(Q1RVQ7) Hypothetical protein - Medicago truncatula (Barrel medic)
chr4.CM0007.1340.nd	435	comp.	(Q1S4X3) IMP dehydrogenase/GMP reductase - Medicago truncatula (Barrel medic)
chr4.CM0007.220.nd	203	comp.	(Q2MJ18) Cytochrome P450 monooxygenase CYP72A59 - Medicago truncatula (Barrel medic)
chr4.CM0170.260.nc	55	comp.	(Q1SL61) Mov34-1; Flagellar motor switch protein FliG-like - Medicago truncatula (Barrel medic)
chr4.CM0173.100.nd	118	comp.	(Q1SNK5) Hypothetical protein - Medicago truncatula (Barrel medic)
chr4.CM0421.230.nd	100	comp.	(Q1T1H3) Cadmium-transporting ATPase; ATPase, E1-E2 type - Medicago truncatula (Barrel medic)
chr5.CM0096.90.nc	671	comp.	(Q1SJ05) Hypothetical protein - Medicago truncatula (Barrel medic)
chr5.CM0569.330.nc	656	comp.	(Q1SJ05) Hypothetical protein - Medicago truncatula (Barrel medic)
chr6.CM0055.1090.nd	78	comp.	(Q2HVA4) Centromere protein, putative - Medicago truncatula (Barrel medic)
chr6.CM0066.340.nc	378	comp.	(Q1SCA0) Hypothetical protein - Medicago truncatula (Barrel medic)
chr6.CM0137.190.nc	769	comp.	(A2Q4W6) RNA-binding region RNP-1 (RNA recognition motif) - Medicago truncatula (Barrel medic)
chr6.CM1514.40.nc	109	comp.	(O24101) MtN5 protein precursor - Medicago truncatula (Barrel medic)
CM0319.120.nd	71	comp.	(Q1T065) Cyclin-like F-box - Medicago truncatula (Barrel medic)
LjB03P03.280.nd	131	comp.	(Q1T670) Nitrate-induced NOI - Medicago truncatula (Barrel medic)
LjB18O14.10.nd	85	comp.	(Q1SRL4) Hypothetical protein - Medicago truncatula (Barrel medic)
LjT01F21.100.nc	101	comp.	(Q1S9F6) Hypothetical protein - Medicago truncatula (Barrel medic)
LjT07J01.170.nd	90	comp.	(Q93YX8) Phosphoinositide-specific phospholipase C (PLC) - Medicago truncatula (Barrel medic)

LjT10B22.70.nd	105	comp.	(Q1SKK1) Cellular retinaldehyde-binding/triple function, N-terminal - Medicago truncatula (Barrel medic)
LjT11A15.20.nc	145	comp.	(Q1SX51) Hypothetical protein - Medicago truncatula (Barrel medic)
LjT13L03.120.nd	85	comp.	(Q1S0I9) Plant lipid transfer/seed storage/trypsin-alpha amylase inhibitor - Medicago truncatula (Barrel medic)
LjT22M20.110.nd	74	comp.	(Q1T3U5) Haem peroxidase, plant/fungal/bacterial - Medicago truncatula (Barrel medic)
LjT28O03.30.nd	101	comp.	(Q1S9F6) Hypothetical protein - Medicago truncatula (Barrel medic)
LjT31F05.20.nd	501	comp.	(Q1SUL5) IMP dehydrogenase/GMP reductase - Medicago truncatula (Barrel medic)
LjT31J09.130.nd	146	comp.	(Q1SL48) Zinc finger, GRF-type - Medicago truncatula (Barrel medic)
LjT34F04.140.nd	110	comp.	(Q1SZY7) Hypothetical protein - Medicago truncatula (Barrel medic)
LjT34L13.40.nd	104	comp.	(Q1S492) TIR - Medicago truncatula (Barrel medic)
LjT34L14.110.nc	137	comp.	(Q1S796) Plant self-incompatibility S1 - Medicago truncatula (Barrel medic)
LjT35J12.250.nd	108	comp.	(Q1RYG7) Plant lipid transfer protein/Par allergen - Medicago truncatula (Barrel medic)
LjT37D10.210.nd	55	comp.	(Q1RVK3) Hypothetical protein - Medicago truncatula (Barrel medic)
LjT42G13.130.nd	231	comp.	(Q1SVM0) Cyclin-like F-box - Medicago truncatula (Barrel medic)
LjT42G13.30.nd	270	comp.	(Q1RT02) Cyclin-like F-box - Medicago truncatula (Barrel medic)
LjSGA_013309.2	82	comp.	(Q8GSM9) Squalene monooxygenase 2 (EC 1.14.99.7)
LjSGA_015717.1	92	comp.	(Q2HTV0) Zinc finger, RING-type; Transcription factor jumonji, jmjC; Zinc finger, C2H2-type
LjSGA_016981.1.1	579	comp.	(Q2HVW1) Hypothetical protein
LjSGA_027876.1	97	comp.	(Q2HSY3) Nucleic acid-binding, OB-fold
LjSGA_033871.1	79	comp.	(Q2HS79) Cyclin-like F-box; Agenet
LjSGA_035275.2	127	comp.	(Q2HV12) Plant lipid transfer/seed storage/trypsin-alpha amylase inhibitor; Pistil-specific extensin-like protein
LjSGA_036568.1	162	comp.	(Q2HW14) Zinc finger, CCCH-type; Sugar transporter superfamily
LjSGA_048115.1	107	comp.	(Q8W0Y5) Enod8.1
LjSGA_061912.1	101	comp.	(Q2MJ18) Cytochrome P450 monooxygenase CYP72B

LjSGA_068378.1	103	comp.	(Q2HUI7) Cyclin-like F-box; FBD; Zinc finger, FYVE/PHD-type
LjSGA_084113.1	88	comp.	(Q2MGR5) Glycoside hydrolase, family 28
LjSGA_100408.2	136	comp.	(Q4A185) Beclin 1 protein
LjSGA_119111.2	83	comp.	(Q8W0V0) Type IIB calcium ATPase
LjSGA_122476.1	55	comp.	(Q4A185) Beclin 1 protein
LjSGA_136168.1.1	136	comp.	(Q4A185) Beclin 1 protein
chr3.CM0711.70.nd	91	comp.	(Q9SBR5) Putative wound-induced protein - Medicago varia (Alfalfa)
LjSGA_052423.1	105	comp.	(Q9SBR5) Putative wound-induced protein
chr5.CM0278.300.nc	77	comp.	(Q41012) Endo-1,4-beta-glucanase precursor - Pisum sativum (Garden pea)
LjSGA_108514.1	49	comp.	(Q76JT3) RelA-SpoT like protein PsRSH1
LjSGA_117613.1	49	comp.	(Q76JT3) RelA-SpoT like protein PsRSH1
chr5.LjT08O17.180.nd	117	comp.	(Q2PEF7) Pseudo-response regulator 37 homologue - Lemna paucicostata
chr1.LjT08C17.50.nc	508	comp.	(Q35I38) Hypothetical protein - Bradyrhizobium sp. BTAi1
chr6.CM0055.1110.nd	118	comp.	(A0U939) Hypothetical protein precursor - Burkholderia cenocepacia MC0-3
chr6.CM0055.960.nc	118	comp.	(A0U939) Hypothetical protein precursor - Burkholderia cenocepacia MC0-3
LjSGA_026701.2	44	comp.	(Q84KS9) RelA homolog
LjSGA_042273.2	47	comp.	(Q95FJ6) ATP synthase beta subunit
LjSGA_040712.1	70	comp.	(Q9AVC0) Chalcone synthase (EC 2.3.1.74)
chr1.CM0496.320.nd	112	comp.	(Q6EMA7) Ribosomal protein S7 - Mahonia aquifolium
chr1.CM0275.130.nd	162	comp.	(A1Y2K6) VS-B (Fragment) - Vasconcellea stipulata
chr5.CM0911.160.nd	251	comp.	(Q5ICP0) RING-H2 subgroup RHE protein - Populus tremula x Populus alba
LjSGA_053007.1	78	comp.	(Q8H255) Myb-like transcription factor 6
chr1.CM0123.300.nc	341	comp.	(Q7Q1K5) ENSANGP00000010223 (Fragment) - Anopheles gambiae str. PEST
LjSGA_019745.1	233	comp.	(Q7Q1K5) ENSANGP00000010223 (Fragment)

chr1.CM0001.300.nd	93	comp.	(Q9LZS7) Hypothetical protein F17C15_30 (Putative lipase/acylhydrolase) (Hypothetical protein At5g03610) - Arabidopsis thaliana (Mouse-ear cress)
chr1.CM0033.1150.nc	107	comp.	(Q8S8L5) Expressed protein (Auxin-responsive family protein) - Arabidopsis thaliana (Mouse-ear cress)
chr1.CM0033.320.nc	149	comp.	(Q9LVU8) Gb|AAF27101.1 - Arabidopsis thaliana (Mouse-ear cress)
chr1.CM0174.40.nd	92	comp.	(Q5XF07) At3g48425 - Arabidopsis thaliana (Mouse-ear cress)
chr1.CM0206.40.nd	114	comp.	(Q5XVC1) Hypothetical protein - Arabidopsis thaliana (Mouse-ear cress)
chr1.CM0231.290.nc	189	comp.	(Q9M1L9) Hypothetical protein F18P9_20 (Hypothetical protein At3g42860) - Arabidopsis thaliana (Mouse-ear cress)
chr1.CM0231.460.nd	108	comp.	(Q9LDF5) 3-hydroxybutyryl-CoA dehydrogenase-like protein - Arabidopsis thaliana (Mouse-ear cress)
chr1.CM0233.410.nc	221	comp.	(Q9LJ70) Gb|AAC72857.1 - Arabidopsis thaliana (Mouse-ear cress)
chr1.CM0295.140.nd	133	comp.	(Q9LTC6) Similarity to ethylene response element binding protein EREBP (AP2/EREBP transcription factor) - Arabidopsis thaliana (Mouse-ear cress)
chr1.CM0295.770.nc	167	comp.	(Q9FNC0) Gb|AAD10670.1 (Hypothetical protein) (Hypothetical protein At5g44060) (Hypothetical protein At5g44060/MRH10_17) - Arabidopsis thaliana (Mouse-ear cress)
chr1.CM0361.250.nd	149	comp.	(Q9M9U9) F6A14.11 protein - Arabidopsis thaliana (Mouse-ear cress)
chr1.CM0393.130.nd	78	comp.	(Q9SRY1) F22D16.12 protein (Thiamin pyrophosphokinase, putative) - Arabidopsis thaliana (Mouse-ear cress)
chr1.CM0593.430.nd	184	comp.	(Q9FFY2) Emb|CAB86673.1 - Arabidopsis thaliana (Mouse-ear cress)
chr1.LjT01D01.160.nd	85	comp.	(Q9M011) Light-inducible protein ATLS1 - Arabidopsis thaliana (Mouse-ear cress)
chr1.LjT01D01.70.nd	73	comp.	(Q9M010) Hypothetical protein F7A7_180 - Arabidopsis thaliana (Mouse-ear cress)
chr1.LjT06I14.20.nc	106	comp.	(O22128) Expressed protein (At2g45450) (Hypothetical protein) - Arabidopsis thaliana (Mouse-ear cress)
chr1.LjT43L07.60.nd	102	comp.	(Q94A79) AT3g49250/F2K15_110 - Arabidopsis thaliana (Mouse-ear cress)
chr1.LjT46N10.20.nd	111	comp.	(Q9SFU9) T1B9.14 protein (At3g07190) - Arabidopsis thaliana (Mouse-ear cress)

chr2.CM0008.670.nc	123	comp.	(Q29Q81) At5g40460 - Arabidopsis thaliana (Mouse-ear cress)
chr2.CM0011.260.nc	194	comp.	(Q9SHT9) Hypothetical protein At2g05350 - Arabidopsis thaliana (Mouse-ear cress)
chr2.CM0018.1060.nc	191	comp.	(O65499) Putative zinc-finger protein (Zinc finger family protein) - Arabidopsis thaliana (Mouse-ear cress)
chr2.CM0099.240.nd	132	comp.	(Q9SJH0) Expressed protein (Helix-loop-helix protein) (Hypothetical protein At2g42870) (Hypothetical protein) - Arabidopsis thaliana (Mouse-ear cress)
chr2.CM0177.530.nc	137	comp.	(Q9LSK9) Genomic DNA, chromosome 5, TAC clone:K21L13 (Hypothetical protein At5g65660) (At5g65660) (Hypothetical protein) - Arabidopsis thaliana (Mouse-ear cress)
chr2.CM0237.340.nc	206	comp.	(O80986) Hypothetical protein At2g26110 (At2g26110) - Arabidopsis thaliana (Mouse-ear cress)
chr2.CM0249.970.nd	98	comp.	(O23230) Trichohyalin like protein - Arabidopsis thaliana (Mouse-ear cress)
chr2.CM0272.110.nd	295	comp.	(O81793) Hypothetical protein F8D20.120 (Hypothetical protein AT4g35610) - Arabidopsis thaliana (Mouse-ear cress)
chr2.CM0338.210.nd	100	comp.	(Q9SIF5) Putative GDSL-motif lipase/hydrolase - Arabidopsis thaliana (Mouse-ear cress)
chr2.LjT30P12.30.nc	90	comp.	(Q8L9P8) RALF (Hypothetical protein At4g15800) (At4g15800) - Arabidopsis thaliana (Mouse-ear cress)
chr3.CM0070.200.nc	163	comp.	(Q8S8L5) Expressed protein (Auxin-responsive family protein) - Arabidopsis thaliana (Mouse-ear cress)
chr3.CM0112.200.nd	131	comp.	(Q7XBI1) Metacaspase 7 (Metacaspase 4) - Arabidopsis thaliana (Mouse-ear cress)
chr3.CM0160.190.nc	66	comp.	(Q9M0H9) Hypothetical protein AT4g28290 (At4g28290) - Arabidopsis thaliana (Mouse-ear cress)
chr3.CM0160.990.nc	195	comp.	(Q8L7Z6) AT3g54680/T5N23_40 - Arabidopsis thaliana (Mouse-ear cress)
chr3.CM0164.70.nd	102	comp.	(Q9FNI1) Gb|AAF02129.1 (Putative B-type cyclin) (Hypothetical protein) - Arabidopsis thaliana (Mouse-ear cress)
chr3.CM0282.950.nc	246	comp.	(Q56YM7) Hypothetical protein - Arabidopsis thaliana (Mouse-ear cress)
chr3.CM0423.330.nc	274	comp.	(Q9LS28) Similarity to kinase - Arabidopsis thaliana (Mouse-ear cress)
chr3.CM0996.150.nd	103	comp.	(Q9M9V9) Putative translationally controlled tumor protein - Arabidopsis thaliana (Mouse-ear

			cress)
chr3.LjT02L14.150.nd	30	comp.	(Q9SCL3) PRE-MRNA SPLICING FACTOR SF2-like protein - Arabidopsis thaliana (Mouse-ear cress)
chr3.LjT37F23.70.nd	129	comp.	(O82343) Expressed protein (Hypothetical protein At2g46260) - Arabidopsis thaliana (Mouse-ear cress)
chr3.LjT40N08.110.nd	316	comp.	(Q0WT56) ZFP3 zinc finger protein - Arabidopsis thaliana (Mouse-ear cress)
chr4.CM0006.670.nd	99	comp.	(Q8VXY7) Hypothetical protein At1g70330 - Arabidopsis thaliana (Mouse-ear cress)
chr4.CM0025.320.nc	114	comp.	(Q8LC23) Hypothetical protein - Arabidopsis thaliana (Mouse-ear cress)
chr4.CM0042.2260.nc	148	comp.	(Q9C923) Putative GTP-binding protein; 106556-109264 - Arabidopsis thaliana (Mouse-ear cress)
chr4.CM0079.80.nd	56	comp.	(Q94B05) Hypothetical protein F1N21.15 (At1g67250) (Hypothetical protein) (Hypothetical protein At1g67250/F1N21_7) - Arabidopsis thaliana (Mouse-ear cress)
chr4.CM0288.140.nd	123	comp.	(Q84JS4) Hypothetical protein At5g47740 - Arabidopsis thaliana (Mouse-ear cress)
chr4.CM0500.150.nd	440	comp.	(Q9C908) Hypothetical protein F1O17.11 - Arabidopsis thaliana (Mouse-ear cress)
chr4.CM0558.310.nc	408	comp.	(Q9FG24) Receptor-like protein kinase (Strubbelig receptor family 2) - Arabidopsis thaliana (Mouse-ear cress)
chr4.CM0558.440.nd	119	comp.	(Q67XD6) Hypothetical protein At2g32500 - Arabidopsis thaliana (Mouse-ear cress)
chr4.CM1616.340.nc	94	comp.	(Q94K72) Hypothetical protein At1g16170 (Hypothetical protein) - Arabidopsis thaliana (Mouse-ear cress)
chr4.LjT06I07.110.nd	121	comp.	(Q9SA55) F10O3.3 protein (Hypothetical protein At1g03140) - Arabidopsis thaliana (Mouse-ear cress)
chr5.CM0096.380.nc	223	comp.	(Q9STX1) Hypothetical protein T22A6.60 (Hypothetical protein At4g24230) - Arabidopsis thaliana (Mouse-ear cress)
chr5.CM0200.710.nd	111	comp.	(Q9FPH4) AT4g33900 - Arabidopsis thaliana (Mouse-ear cress)
chr5.CM0200.820.nc	112	comp.	(Q8LEN7) Hypothetical protein (Hypothetical protein At3g19550) - Arabidopsis thaliana (Mouse-ear cress)

chr5.CM0200.980.nc	98	comp.	(Q3E6W8) Protein At2g15000 (Hypothetical protein At2g15000) - Arabidopsis thaliana (Mouse-ear cress)
chr5.CM0211.130.nc	505	comp.	(Q9LSG4) Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MJL12 - Arabidopsis thaliana (Mouse-ear cress)
chr5.CM0239.320.nc	112	comp.	(Q8LCV8) Hypothetical protein - Arabidopsis thaliana (Mouse-ear cress)
chr5.CM0911.140.nd	123	comp.	(Q9FK76) Subtilisin-like protease (Putative subtilisin) - Arabidopsis thaliana (Mouse-ear cress)
chr5.CM1125.670.nd	79	comp.	(Q9SY09) Small nuclear riboprotein Sm-D1 (At4g02840) - Arabidopsis thaliana (Mouse-ear cress)
chr5.CM1813.200.nc	198	comp.	(Q94BS1) Hypothetical protein At3g21290 - Arabidopsis thaliana (Mouse-ear cress)
chr5.LjT10N02.110.nd	189	comp.	(Q9M2P8) Hypothetical protein T10K17.210 - Arabidopsis thaliana (Mouse-ear cress)
chr5.LjT32I14.270.nd	56	comp.	(Q9T0K6) Hypothetical protein AT4g13350 - Arabidopsis thaliana (Mouse-ear cress)
chr6.CM0037.1150.nc	181	comp.	(O04248) Hypothetical protein T10M13.5 (At4g02040) (Hypothetical protein AT4g02040) - Arabidopsis thaliana (Mouse-ear cress)
chr6.CM0037.860.nc	214	comp.	(Q9LZW0) Putative zinc finger protein - Arabidopsis thaliana (Mouse-ear cress)
chr6.CM0137.220.nc	186	comp.	(Q9C7Y8) Hypothetical protein T2J15.13 (At1g47960/T2J15_13) (Hypothetical protein) - Arabidopsis thaliana (Mouse-ear cress)
chr6.LjT18B08.90.nd	135	comp.	(Q94CB6) Hypothetical protein At3g47070 - Arabidopsis thaliana (Mouse-ear cress)
CM0584.180.nd	68	comp.	(Q93Z49) AT5g64130/MHJ24_11 (Hypothetical protein) - Arabidopsis thaliana (Mouse-ear cress)
CM0601.240.nd	103	comp.	(Q9FIX3) Gb|AAD30619.1 - Arabidopsis thaliana (Mouse-ear cress)
LjB10M19.30.nd	55	comp.	(Q9LYG2) Hypothetical protein T22P22_70 (Hypothetical protein At5g11680) (Hypothetical protein) (Hypothetical protein At5g11680; T22P22_70) - Arabidopsis thaliana (Mouse-ear cress)
LjT03L21.100.nd	142	comp.	(Q9SK37) Hypothetical protein At2g24960 - Arabidopsis thaliana (Mouse-ear cress)
LjT09I09.130.nd	49	comp.	(Q9LDY7) Hypothetical protein AT4g11410 - Arabidopsis thaliana (Mouse-ear cress)
LjT13N04.20.nd	80	comp.	(Q9LT14) Genomic DNA, chromosome 3, P1 clone: MPN9 - Arabidopsis thaliana (Mouse-ear cress)

LjT27E22.120.nd	107	comp.	(Q94AT2) Hypothetical protein At5g58570 (Hypothetical protein) - Arabidopsis thaliana (Mouse-ear cress)
LjT30N18.310.nd	101	comp.	(Q9SJD5) Expressed protein (At2g04340) (Hypothetical protein At2g04340) - Arabidopsis thaliana (Mouse-ear cress)
LjT31F05.40.nd	136	comp.	(Q9SYM4) Trehalose-6-phosphate synthase - Arabidopsis thaliana (Mouse-ear cress)
LjT31N05.40.nd	69	comp.	(Q9LRR8) Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:MOA2 (Hypothetical protein At3g14430) (At3g14430) (Hypothetical protein) - Arabidopsis thaliana (Mouse-ear cress)
LjT32E09.180.nd	82	comp.	(Q9SN67) Hypothetical protein F25I24.20 (Hypothetical protein At4g10810) (Hypothetical protein) - Arabidopsis thaliana (Mouse-ear cress)
LjT35J12.200.nd	114	comp.	(A3KPG0) At4g10380 - Arabidopsis thaliana (Mouse-ear cress)
LjT37D10.220.nd	99	comp.	(Q2V2X9) Protein At5g56610 - Arabidopsis thaliana (Mouse-ear cress)
LjT38E08.190.nd	71	comp.	(Q4V3C1) At2g03070 (Hypothetical protein At2g03070) - Arabidopsis thaliana (Mouse-ear cress)
LjT40E15.90.nc	503	comp.	(Q9LPP9) F15H18.21 - Arabidopsis thaliana (Mouse-ear cress)
LjT40J14.20.nc	189	comp.	(Q9FMY7) Genomic DNA, chromosome 5, P1 clone:MJB21 (Hypothetical protein At5g42780) - Arabidopsis thaliana (Mouse-ear cress)
LjT42G13.70.nd	447	comp.	(Q08AA0) At3g52680 - Arabidopsis thaliana (Mouse-ear cress)
LjT45M09.30.nd	67	comp.	(A0JPT0) At1g80830 - Arabidopsis thaliana (Mouse-ear cress)
LjT45M09.70.nd	80	comp.	(Q8GXZ7) Hypothetical protein (At1g52821) - Arabidopsis thaliana (Mouse-ear cress)
LjT46I09.150.nd	78	comp.	(Q9M9T3) F14L17.5 protein - Arabidopsis thaliana (Mouse-ear cress)
LjSGA_002919.1.1	88	comp.	(Q8VYF1) Putative 60S ribosomal protein L15-like protein
LjSGA_002920.1	88	comp.	(Q8VYF1) Putative 60S ribosomal protein L15-like protein
LjSGA_006955.2	99	comp.	(Q9M1S6) Hypothetical protein T5N23_100
LjSGA_007637.1	189	comp.	(Q9SUL8) Hypothetical protein F9N11.110 (Hypothetical protein AT4g30260)
LjSGA_007871.1	45	comp.	(Q9LSW6) 1-aminocyclopropane-1-carboxylate oxidase (At5g43450)
LjSGA_008407.1	62	comp.	(Q8RWX2) Hypothetical protein At2g32170

LjSGA_008523.1	139	comp.	(Q8L9N1) Hypothetical protein (Hypothetical protein At3g02120) (Hypothetical protein At3g02120/F1C9_9)
LjSGA_008743.1.1	101	comp.	(Q8LG57) Dihydroxypolyprenylbenzoate methyltransferase
LjSGA_009551.2	66	comp.	(Q9M341) Hypothetical protein F5K20_150
LjSGA_010575.1	113	comp.	(Q9LZC9) Hypothetical protein F12E4_360
LjSGA_010666.2	146	comp.	(Q9ASW3) AT3g49260/F2K15_120 (Guard cell associated protein) (SF16-like protein)
LjSGA_011120.3	77	comp.	(Q9C8T3) Putative D-ribulose-5-phosphate; 35237-36732 (At1g63290/F9N12_9) (Putative D-ribulose-5-phosphate)
LjSGA_012155.2	99	comp.	(O49671) Replication A protein-like
LjSGA_013183.1	61	comp.	(Q9SKX3) Hypothetical protein At2g43040
LjSGA_014065.1	202	comp.	(O81315) F6N15.19 protein (Hypothetical protein AT4g00140)
LjSGA_014273.2.1	98	comp.	(Q8GW57) Hypothetical protein At1g80150/F18B13_23 (At1g80150)
LjSGA_014593.1	111	comp.	(Q9FJW1) Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K9I9 (At5g67620)
LjSGA_014633.1	34	comp.	(Q9LZE4) Hypothetical protein F12E4_190
LjSGA_015002.2	131	comp.	(Q9FYB1) Splicing factor SC35
LjSGA_015205.1	156	comp.	(Q9LFG8) ABC transporter-like protein
LjSGA_015289.3	61	comp.	(Q8L8N3) Hypothetical protein (At2g17350) (Hypothetical protein At2g17350)
LjSGA_015452.1	173	comp.	(Q9LZS0) GT2-like protein
LjSGA_015493.2.1	62	comp.	(Q9C5C1) Hypothetical protein At4g31330
LjSGA_015526.2	65	comp.	(Q9SCX9) Putative dihydroxyacetone 3-phosphate reductase dhaprd
LjSGA_016178.2	67	comp.	(Q9FGS2) Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K6A12
LjSGA_016333.3	126	comp.	(Q9LW53) Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLM24
LjSGA_016910.1	94	comp.	(P93051) ORFc protein (Fragment)
LjSGA_017288.2	44	comp.	(Q8L7R5) Ethylene responsive element binding protein, putative (At3g23220)
LjSGA_018239.1	119	comp.	(Q9SVZ6) Putative acidic ribosomal protein

LjSGA_018534.1	36	comp.	(Q9FRR8) F22O13.15 (Hypothetical protein At1g08670)
LjSGA_018783.1.1	142	comp.	(Q9LQ65) T30E16.6 (G-box binding factor, putative) (Transcription factor-like protein bZIP4)
LjSGA_020022.2	63	comp.	(Q9ZVN2) T22H22.2 protein (At1g54570) (Hypothetical protein) (Hypothetical protein At1g54570/T22H22_2)
LjSGA_021263.2	52	comp.	(Q8VYB5) Hypothetical protein At1g48790
LjSGA_021513.1	379	comp.	(Q9ZUN0) Hypothetical protein At2g19630
LjSGA_021693.1.1	124	comp.	(Q9LZX9) Hypothetical protein T4C21_260 (Hypothetical protein At3g60850)
LjSGA_021934.2	46	comp.	(Q3EB84) Protein At3g11540
LjSGA_023473.2	79	comp.	(Q3E7U8) Protein At5g26620
LjSGA_023523.2	81	comp.	(Q6IDL4) At1g09580
LjSGA_023990.1	54	comp.	(O48822) Expressed protein (Hypothetical protein)
LjSGA_024222.1	62	comp.	(P93048) GAG1At protein (Hypothetical protein At1g16000) (Hypothetical protein) (Hypothetical protein At1g16000/T24D18_10) (T24D18.10 protein)
LjSGA_024445.1	80	comp.	(Q94JU2) AT3g28050/MMG15_6
LjSGA_025453.1.1	84	comp.	(Q8LFQ6) Glutaredoxin
LjSGA_026270.1	76	comp.	(Q9SN67) Hypothetical protein F25I24.20 (Hypothetical protein At4g10810) (Hypothetical protein)
LjSGA_027137.1	195	comp.	(Q67XK7) Peroxidase ATP17a like protein (Fragment)
LjSGA_027260.2	173	comp.	(Q9LZS6) Cucumisin-like protein
LjSGA_027419.1	116	comp.	(Q9M899) F16B3.4 protein
LjSGA_027634.3	152	comp.	(Q9FGZ6) Protein kinase
LjSGA_028078.1	120	comp.	(Q9C9M8) MATE efflux family protein, putative
LjSGA_028296.1	68	comp.	(O49286) F22K20.10 protein (At1g77000) (F-box protein family, AtFBL5)
LjSGA_028456.1	147	comp.	(Q9FK26) Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K18G13
LjSGA_029221.1	108	comp.	(Q9FJ30) Similarity to heat shock transcription factor HSF30
LjSGA_029354.2	85	comp.	(Q6NKS1) At5g01700

LjSGA_029362.1	107	comp.	(Q9ZQA5) Putative giberellin beta-hydroxylase
LjSGA_030182.1	80	comp.	(Q8RWV5) Putative cell differentiation protein
LjSGA_030272.1	49	comp.	(Q8VZ42) Hypothetical protein At2g41835
LjSGA_030321.2	111	comp.	(Q6NPM5) Hypothetical protein At5g62200
LjSGA_030863.1	78	comp.	(Q9LRQ0) Emb|CAB39684.1
LjSGA_031645.1	43	comp.	(Q9M2S7) Peptidyl-prolyl cis-trans isomerase
LjSGA_031979.1	120	comp.	(Q9ZPU2) Putative MYB family transcription factor (MYB transcription factor)
LjSGA_033206.1	57	comp.	(Q9LQN3) F5D14.2 protein (Hypothetical protein F27G20_13) (At1g32260)
LjSGA_033907.1	157	comp.	(Q9SRQ0) T21P5.12 protein (Hypothetical protein)
LjSGA_034505.1	92	comp.	(Q8VY85) Hypothetical protein At2g06010
LjSGA_034653.1	165	comp.	(Q8GY42) Hypothetical protein At1g61110/F11P17_16 (At1g61110)
LjSGA_036244.1.1	65	comp.	(Q9M011) Light-inducible protein ATLS1
LjSGA_036541.1	160	comp.	(Q3E862) Protein At5g64360
LjSGA_037158.1	70	comp.	(Q93Z17) AT5g46160/MCL19_22 (HUELLENLOS PARALOG)
LjSGA_037585.1	101	comp.	(Q8W4M2) Hypothetical protein F5K20.24
LjSGA_039497.1	59	comp.	(Q8LE14) Hypothetical protein
LjSGA_039562.1	70	comp.	(Q9LTT5) Similarity to unknown protein
LjSGA_040171.1	121	comp.	(Q9LQR4) T4O12.25
LjSGA_040277.1	75	comp.	(Q8L8B8) Hypothetical protein At2g37210/T2N18.3
LjSGA_040638.1	66	comp.	(Q9FY93) NAM-like protein (AT5g13180/T19L5_140)
LjSGA_041144.2	53	comp.	(Q9XGR4) Protein phosphatase 2A 62 kDa B'' regulatory subunit (Protein phosphatase 2A 62 kDa B regulatory subunit) (Protein phosphatase 2A alpha)
LjSGA_042787.1	50	comp.	(Q8VXX3) Hypothetical protein At5g58740
LjSGA_043084.1	102	comp.	(Q9FY93) NAM-like protein (AT5g13180/T19L5_140)
LjSGA_045043.1	134	comp.	(O23637) Argininosuccinate lyase (EC 4.3.2.1)

LjSGA_045407.1	61	comp.	(Q9SFE9) T26F17.9 (GONST5 Golgi Nucleotide sugar transporter)
LjSGA_047860.1	107	comp.	(Q9SSG1) F25A4.26 protein
LjSGA_048292.1	116	comp.	(Q3EA10) Protein At4g16195
LjSGA_048464.1	89	comp.	(Q9LUI2) Centromere protein
LjSGA_048568.1	49	comp.	(Q4TYZ7) Ubiquitinating enzyme
LjSGA_048658.2	60	comp.	(Q9SRX9) F22D16.14 protein (RING finger family protein)
LjSGA_048822.1	66	comp.	(Q9M338) Reductase-like protein
LjSGA_051219.1	143	comp.	(O23120) F10G19.2 protein (T26J12.18 protein)
LjSGA_052201.1	83	comp.	(Q3E8B1) Protein At5g55100
LjSGA_052510.2	80	comp.	(Q9FKK2) MADS-box protein-like
LjSGA_053543.1	154	comp.	(Q9SVT5) Hypothetical protein F17L22.80 (Hypothetical protein) (AT4g21620/F17L22_80) (Hypothetical protein At4g21620)
LjSGA_054462.1	74	comp.	(Q8W4Q1) Hypothetical protein (At4g35360/F23E12_80)
LjSGA_054884.1	122	comp.	(Q9LZW0) Putative zinc finger protein
LjSGA_055358.1	102	comp.	(Q9C8Y6) Hypothetical protein T27F4.6 (F-box family protein)
LjSGA_056007.1	116	comp.	(Q9FIR9) Emb|CAB62461.1 (At5g24660) (Hypothetical protein) (Hypothetical protein At5g24660/MXC17_2)
LjSGA_056309.1	85	comp.	(Q9SCK6) Putative NAC2 protein
LjSGA_056636.1	101	comp.	(Q9FNB1) Gb|AAD43168.1
LjSGA_058572.1	59	comp.	(O80632) Hypothetical protein At2g39450
LjSGA_058637.1	92	comp.	(Q9LSH0) Gb|AAF26109.1 (Hypothetical protein At3g17780)
LjSGA_059230.1	49	comp.	(Q53YT9) TFIIB2 (Fragment)
LjSGA_059377.1.1	89	comp.	(Q8LFY6) Hypothetical protein
LjSGA_060115.1	124	comp.	(Q84MB5) At5g25752
LjSGA_060805.1	153	comp.	(Q8VYZ8) Hypothetical protein At1g64430

LjSGA_064251.1	51	comp.	(Q9FM58) Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MDF20
LjSGA_065721.1	50	comp.	(Q9LPP3) F18K10.11 protein (Hypothetical protein At3g10530)
LjSGA_065857.1	60	comp.	(Q9LSQ5) 1,4-benzoquinone reductase-like; Trp repressor binding protein-like (1,4-benzoquinone reductase-like protein)
LjSGA_066816.1	93	comp.	(Q9LJW5) Gb|AAF15936.1 (At3g28917) (Hypothetical protein)
LjSGA_066967.1	93	comp.	(Q9LJW5) Gb|AAF15936.1 (At3g28917) (Hypothetical protein)
LjSGA_067389.1	98	comp.	(Q9C6Y7) Aldehyde dehydrogenase, putative
LjSGA_067452.1	82	comp.	(Q9LFR7) Hypothetical protein F1N13_220 (Hypothetical protein At5g16080)
LjSGA_068625.1	50	comp.	(Q3EBJ1) Protein At2g40110
LjSGA_070010.1	64	comp.	(Q9LS90) Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MXC7 (Hypothetical protein At3g22990)
LjSGA_070125.1	105	comp.	(Q3EB61) Protein At3g14850
LjSGA_072650.2	45	comp.	(Q94BX4) AT3g45100/T14D3_40
LjSGA_074044.1	57	comp.	(Q9FE17) Transcription regulator Sir2-like protein
LjSGA_075950.2	67	comp.	(Q8GW63) Hypothetical protein At1g64600/F1N19_16 (At1g64600)
LjSGA_076490.1	145	comp.	(Q2V4E4) Protein At1g67490
LjSGA_076760.1.1	140	comp.	(Q9FMQ4) Similarity to S1 self-incompatibility protein (Self-incompatibility protein-related)
LjSGA_076936.1	127	comp.	(Q9ZS85) T4B21.1 protein
LjSGA_077182.1	94	comp.	(Q2V363) Protein At5g19473
LjSGA_078266.1	66	comp.	(Q9FY93) NAM-like protein (AT5g13180/T19L5_140)
LjSGA_078852.1	91	comp.	(Q53YQ5) Peroxidase ATP13A
LjSGA_078984.1	112	comp.	(Q8GX25) Hypothetical protein At1g76250/T23E18_34 (At1g76250)
LjSGA_079465.1	43	comp.	(Q9C8H5) Hypothetical protein F19C24.14
LjSGA_081114.1	95	comp.	(Q9FIS3) Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MTG10 (At5g62150)
LjSGA_081363.1	75	comp.	(Q8LG56) Hypothetical protein (At1g05205)

LjSGA_082634.2	61	comp.	(Q8RXY1) Hypothetical protein At4g26965
LjSGA_083147.1	116	comp.	(Q9FT50) Hypothetical protein T25B15_90
LjSGA_083280.1	75	comp.	(Q94BR1) Putative topoisomerase
LjSGA_083855.1	94	comp.	(Q2QB51) Fused
LjSGA_084155.1	68	comp.	(Q9SR79) T22K18.2 protein
LjSGA_084620.2	110	comp.	(Q8VYM4) Hypothetical protein At3g52150
LjSGA_085236.2	58	comp.	(Q9MA90) T12H1.26 protein (AT3g05290/T12H1_26)
LjSGA_086655.1	67	comp.	(Q3EDJ2) Protein At1g03780
LjSGA_088036.1	153	comp.	(Q8VYZ8) Hypothetical protein At1g64430
LjSGA_088784.2	48	comp.	(Q8GXU5) Hypothetical protein At5g48850/K24G6_19 (At5g48850)
LjSGA_088974.1	136	comp.	(Q3EA10) Protein At4g16195
LjSGA_089367.1	91	comp.	(Q9LPQ9) F15H18.8
LjSGA_089728.1	52	comp.	(Q6NKW8) Hypothetical protein At2g22620
LjSGA_090310.1	130	comp.	(Q9M280) Hypothetical protein T22K7_130 (At3g44450)
LjSGA_092537.1	94	comp.	(Q8VY59) Blue copper protein, putative (At3g27200)
LjSGA_097198.1.1	64	comp.	(Q3EAF2) Protein At3g63400
LjSGA_097619.2	90	comp.	(Q8VYP5) Hypothetical protein At3g60800
LjSGA_098555.1	56	comp.	(Q9FMS3) Emb|CAB88996.1 (At5g22280) (Hypothetical protein) (Hypothetical protein At5g22280; MWD9.6)
LjSGA_099976.2	57	comp.	(Q8RWU7) Putative membrane trafficking factor (CDC48-interacting UBX-domain protein)
LjSGA_101271.1	153	comp.	(Q94BY8) AT5g40660/MNF13_180
LjSGA_103898.1	44	comp.	(Q9T083) Hypothetical protein AT4g27590
LjSGA_104509.1	129	comp.	(Q3E8T5) Protein At5g31412
LjSGA_105453.1	59	comp.	(Q9S9Q9) F26G16.2 protein
LjSGA_106850.1	73	comp.	(Q9FKE9) GTP-binding protein-like; root hair defective 3 protein-like

LjSGA_107162.1	54	comp.	(Q9C6A5) Hypothetical protein F9E11.1
LjSGA_108363.1	126	comp.	(Q9LKT9) Hypothetical protein T32B20.c
LjSGA_111111.1	49	comp.	(O22283) Expressed protein (At2g39720/T5I7.2) (Hypothetical protein) (RING-H2 finger protein RHC2a)
LjSGA_113929.1	79	comp.	(Q9FNJ1) Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MDJ22
LjSGA_115867.1	51	comp.	(Q9FJJ5) Microtubule-associated protein EB1-like protein
LjSGA_117470.2	114	comp.	(Q9C5C8) Hypothetical protein At4g21860
LjSGA_118638.1	92	comp.	(Q9C920) Putative deoxyoctulonosic acid synthetase; 116195-114393 (Putative CMP-KDO synthetase) (EC 2.7.7.38)
LjSGA_120459.1	106	comp.	(Q3ED77) Protein At1g21610
LjSGA_121784.1	67	comp.	(Q9XI46) F9L1.17 protein (At1g15220/F9L1_17) (Hypothetical protein)
LjSGA_121922.1	62	comp.	(Q56YF5) Hypothetical protein
LjSGA_128393.0.1	56	comp.	(Q9LNX7) F22G5.8
LjSGA_131300.1	55	comp.	(Q9LTJ9) Arabidopsis thaliana genomic DNA, chromosome 5, BAC clone:F17P19
LjSGA_135560.1.1	96	comp.	(Q9LS09) Anti-silencing protein-like (Anti-silencing factor 1-like protein) (Anti-silencing function 1b)
LjSGA_138952.1	78	comp.	(Q3E7R7) Protein At5g10580
LjSGA_141014.1	60	comp.	(Q2HIF8) At2g45200
LjSGA_142103.1	36	comp.	(Q9FMA3) Peroxisomal targeting signal type 1 receptor
LjSGA_145184.2	77	comp.	(Q9C7N2) Hypothetical protein F15D2.24 (At1g29690/F15D2_24)
chr1.CM0171.470.nc	127	comp.	(A0A3A0) Putative ribosomal protein (Fragment) - Artemisia annua (Sweet wormwood)
LjSGA_060753.1	259	comp.	(Q752C9) AFR646Wp
LjSGA_076074.1.1	118	comp.	(Q9AXF3) Lipid transfer protein
LjSGA_104925.1	118	comp.	(Q9AXF3) Lipid transfer protein
LjSGA_051491.2	165	comp.	(Q29RT0) Hypothetical protein
chr3.CM0574.200.nd	93	comp.	(A1YN04) Hydrogen-transporting ATP synthase - Brassica campestris (Field mustard)

LjT13N04.50.nd	96	comp.	(Q2PQL8) Putative aldehyde dehydrogenase - Brassica campestris (Field mustard)
LjSGA_000444.1	74	comp.	(Q6YSP5) ATPase subunit 9
LjSGA_078671.1.1	91	comp.	(Q8RX50) PSR9 (Fragment)
chr1.CM0668.170.nd	64	comp.	(Q43408) Putative imbibition protein - Brassica oleracea (Wild cabbage)
chr1.CM0248.470.nd	311	comp.	(Q566W6) Zgc:112425 - Brachydanio rerio (Zebrafish) (Danio rerio)
chr3.LjT34H24.110.nd	160	comp.	(Q6P3H0) Zgc:77882 (Novel protein) - Brachydanio rerio (Zebrafish) (Danio rerio)
LjT13F18.40.nd	176	comp.	(Q566W6) Zgc:112425 - Brachydanio rerio (Zebrafish) (Danio rerio)
LjSGA_004944.1	131	comp.	(Q566W6) Hypothetical protein zgc:112425
LjSGA_106373.2	81	comp.	(Q6PGX7) Hypothetical protein zff9
LjSGA_016401.1	68	comp.	(Q7XAW7) Putative lipase (Fragment)
LjSGA_065424.1.1	94	comp.	(Q4ABV6) 52O08_1 (Fragment)
LjSGA_030619.1	80	comp.	(Q621R2) Hypothetical protein CBG02383
chr2.CM0099.160.nc	291	comp.	(Q23330) Hypothetical protein - Caenorhabditis elegans
chr5.CM0040.490.nc	147	comp.	(O45577) Hypothetical protein cpf-2 - Caenorhabditis elegans
chr2.LjT41F02.40.nc	64	comp.	(Q8S344) Hypothetical protein upa9 - Capsicum annuum (Bell pepper)
chr1.LjT41E18.190.nc	169	comp.	(A1DR82) AT-hook DNA-binding protein - Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle)
LjSGA_034638.1	80	comp.	(Q9ZRV5) Basic blue copper protein
LjSGA_046118.1	118	comp.	(Q949L4) Putative polyprotein (Fragment)
LjSGA_127044.1	154	comp.	(Q949L4) Putative polyprotein (Fragment)
LjSGA_140739.1	43	comp.	(Q8L5F9) Microtubule associated protein
LjSGA_140929.1	64	comp.	(Q949L4) Putative polyprotein (Fragment)
LjSGA_074658.1.1	70	comp.	(Q84V02) Vacuolar membrane ATPase subunit c''
LjSGA_102653.1.1	70	comp.	(Q84V02) Vacuolar membrane ATPase subunit c''
LjSGA_018510.1	108	comp.	(Q3HM93) Glutathione S-transferase

chr2.CM0018.280.nd	59	comp.	(Q2TM26) STO-1 - Coffea canephora (Robusta coffee)
LjSGA_024451.2	104	comp.	(Q8VXQ2) Aldehyde dehydrogenase (EC 1.2.1.3)
chr4.CM0025.20.nd	63	comp.	(Q96403) Stellacyanin - Cucumis sativus (Cucumber)
LjSGA_012718.2	694	comp.	(Q6BRX6) Similar to CA1766|CaNOP4 Candida albicans CaNOP4 Nucleolar protein
LjSGA_036483.1	184	comp.	(Q6BYF3) Debaryomyces hansenii chromosome A of strain CBS767 of Debaryomyces hansenii
chr1.CM0122.800.nd	310	comp.	(Q55GV8) Hypothetical protein - Dictyostelium discoideum AX4
chr2.CM0002.430.nc	268	comp.	(Q869R0) Similar to Entamoeba histolytica. Myosin heavy chain - Dictyostelium discoideum (Slime mold)
LjSGA_005100.1	103	comp.	(Q9V3T8) SR family splicing factor SC35 (CG5442-PB, isoform B) (LD32469p)
chr2.LjT16L14.100.nc	398	comp.	(O96063) Myosin heavy chain (Fragment) - Dugesia japonica (Planarian)
chr1.LjT45O14.120.nd	151	comp.	(Q71E52) Cytochrome f (Fragment) - Fagus sylvatica (Beechnut)
LjSGA_012361.1	66	comp.	(Q9ZPA7) ABA-inducible protein
LjSGA_019294.2	74	comp.	(Q9ZRV0) Metallothionein-like protein class II
LjSGA_027307.1	136	comp.	(Q70DJ9) Calcium binding protein
LjSGA_037289.1	105	comp.	(Q5Y381) Aldo/keto reductase
chr2.CM0346.240.nc	462	comp.	(Q4ICJ3) Hypothetical protein - Gibberella zeae (Fusarium graminearum)
chr3.CM0634.680.nc	188	comp.	(Q7X9S1) Fiber protein Fb19 (Fragment) - Gossypium barbadense (Sea-island cotton) (Egyptian cotton)
chr3.CM0282.820.nc	163	comp.	(Q5U8L5) AP2/EREBP transcription factor ERF-1 - Gossypium hirsutum (Upland cotton)
chr3.CM0112.30.nc	386	comp.	(Q9ZSP8) Latex-abundant protein - Hevea brasiliensis (Para rubber tree)
LjSGA_033388.1	66	comp.	(Q40068) Peroxidase
LjSGA_078340.1	50	comp.	(Q6FGU4) HIST3H3 protein (H3 histone family, member T) (Histone 3, H3) (Fragment)
LjSGA_040049.2	87	comp.	(Q6JJ39) Putative adapitin protein
LjSGA_143911.1.1	36	comp.	(Q7XJB0) Eukaryotic translation initiation factor iso4E
LjSGA_096416.1	192	comp.	(Q4Q1R0) Universal minicircle sequence binding protein (UMSBP), putative

LjSGA_117099.1	182	comp.	(Q4Q1R0) Universal minicircle sequence binding protein (UMSBP), putative
LjSGA_080830.1	45	comp.	(Q93YH3) ATP citrate lyase b-subunit (EC 4.1.3.8)
LjSGA_019213.1.1	58	comp.	(Q96569) L-lactate dehydrogenase (EC 1.1.1.27)
LjSGA_076667.1	98	comp.	(Q6V7U8) Putative anthocyanin permease
chr1.CM0393.250.nd	80	comp.	(Q5GAR2) Hypothetical protein - Zea mays (Maize)
chr5.CM0096.730.nd	90	comp.	(Q8S532) Cytosolic aldehyde dehydrogenase RF2C - Zea mays (Maize)
chr4.CM0044.290.nd	126	comp.	(Q84XY6) Cystatin - Malus domestica (Apple) (Malus sylvestris)
LjSGA_022997.1.1	64	comp.	(Q9XGY3) Small zinc finger-like protein (Fragment)
LjSGA_062048.1	92	comp.	(Q2LME7) MYB14
LjSGA_028575.2	68	comp.	(Q9AYN0) Inhibitor against trypsin (Fragment)
chr4.CM0288.490.nc	134	comp.	(Q1ENZ8) Hypothetical protein - Musa acuminata (Banana)
chr4.CM0429.30.nd	268	comp.	(A1YUL9) Impa2 - Nicotiana benthamiana
chr6.CM0539.340.nd	57	comp.	(Q2LFC3) AGO1-2 (Fragment) - Nicotiana benthamiana
LjSGA_114393.2	78	comp.	(Q5YLB4) DNA gyrase B subunit
LjSGA_032157.0.1	57	comp.	(Q3C1M8) Ribosomal protein S7
chr4.CM0061.290.nc	700	comp.	(Q8JIN6) Transformer-2b - Oryzias latipes (Medaka fish) (Japanese ricefish)
chr1.CM0017.460.nc	227	comp.	(A3B432) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr1.CM0064.540.nc	387	comp.	(Q84SZ0) Hypothetical protein OSJNBa0087C10.17 - Oryza sativa (japonica cultivar-group)
chr1.CM0094.790.nd	185	comp.	(Q8LHL0) Putative splicing factor, arginine/serine-rich 2 (Splicing factor SC35) (Os07g0623300 protein) - Oryza sativa (japonica cultivar-group)
chr1.CM0141.440.nd	90	comp.	(A3BLD9) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr1.CM0206.80.nd	72	comp.	(A3AH61) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr1.LjT04O21.90.nd	63	comp.	(A3AHR1) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr1.LjT32B13.70.nd	146	comp.	(A2ZFV9) Hypothetical protein - Oryza sativa (indica cultivar-group)
chr2.CM0065.190.nc	134	comp.	(Q6F303) Hypothetical protein P0483D07.18 - Oryza sativa (japonica cultivar-group)

chr2.CM0826.330.nd	126	comp.	(A2WVA2) Hypothetical protein - Oryza sativa (indica cultivar-group)
chr2.CM0903.360.nd	525	comp.	(A3BXI6) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr2.LjT02E02.170.nd	104	comp.	(Q7X902) P0076O17.1 protein (Hypothetical protein) (OJ000114_01.19 protein) - Oryza sativa (japonica cultivar-group)
chr2.LjT16L14.70.nc	316	comp.	(Q6ZDR7) Putative splicing factor, arginine/serine-rich (Os08g0486200 protein) - Oryza sativa (japonica cultivar-group)
chr2.LjT41F02.30.nc	64	comp.	(Q6I5W4) Hypothetical protein OJ1076_H08.11 (Hypothetical protein) (Os05g0217000 protein) - Oryza sativa (japonica cultivar-group)
chr2.LjT44L24.20.nd	77	comp.	(A3C8H5) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr3.CM0160.790.nd	93	comp.	(Q5W707) Hypothetical protein OSJNBa0037H06.2 (Hypothetical protein) (Os05g0244600 protein) - Oryza sativa (japonica cultivar-group)
chr3.LjT04G21.130.nd	91	comp.	(Q7X902) P0076O17.1 protein (Hypothetical protein) (OJ000114_01.19 protein) - Oryza sativa (japonica cultivar-group)
chr3.LjT15F18.170.nd	86	comp.	(Q8H065) Hypothetical protein OSJNBa0014O06.7 (Hypothetical protein) (Mitochondrial ribosomal protein L51/S25/CI-B8 family protein, putative, expressed) - Oryza sativa (japonica cultivar-group)
chr4.CM0175.610.nd	115	comp.	(Q5JKG8) Hypothetical protein B1033B05.21 - Oryza sativa (japonica cultivar-group)
chr4.CM0256.410.nc	112	comp.	(A2XXE6) Hypothetical protein - Oryza sativa (indica cultivar-group)
chr4.CM0297.180.nc	175	comp.	(Q6Z6S6) Hypothetical protein P0705A04.5 - Oryza sativa (japonica cultivar-group)
chr4.CM0429.340.nc	151	comp.	(Q2QWQ9) GRF zinc finger family protein (Hypothetical protein) - Oryza sativa (japonica cultivar-group)
chr4.CM0432.270.nd	43	comp.	(A3CBH1) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr4.CM0432.310.nd	43	comp.	(A3CBH1) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr4.CM0692.420.nd	165	comp.	(A2WRN1) Hypothetical protein - Oryza sativa (indica cultivar-group)
chr6.CM0045.280.nd	267	comp.	(Q6YUR8) Putative Glycine-rich protein 2 (Hypothetical protein) (Os02g0121100 protein) - Oryza sativa (japonica cultivar-group)

chr6.CM0314.350.nc	173	comp.	(Q6H5M3) Hypothetical protein OJ1759_F09.16 (Hypothetical protein P0564H06.22) - Oryza sativa (japonica cultivar-group)
chr6.LjT15B19.150.nd	209	comp.	(A3BPS7) Hypothetical protein - Oryza sativa (japonica cultivar-group)
CM0385.330.nd	170	comp.	(A3BZC5) Hypothetical protein - Oryza sativa (japonica cultivar-group)
LjT01F24.50.nd	173	comp.	(Q7XK11) OSJNBa0044K18.33 protein - Oryza sativa (japonica cultivar-group)
LjT03L21.140.nd	62	comp.	(A3BYJ5) Hypothetical protein - Oryza sativa (japonica cultivar-group)
LjT06N06.330.nd	62	comp.	(Q5N9R6) Transducin family protein / WD-40 repeat family protein-like (Os01g0702400 protein) - Oryza sativa (japonica cultivar-group)
LjT06N06.340.nd	60	comp.	(Q65XE1) Hypothetical protein OJ1504_G04.13 - Oryza sativa (japonica cultivar-group)
LjT34L14.70.nc	515	comp.	(Q6ZKI2) Putative RNA recognition motif (RRM)-containing protein (Os08g0139000 protein) - Oryza sativa (japonica cultivar-group)
LjT39F13.110.nc	904	comp.	(Q8LNH8) Putative glycine-rich protein (Hypothetical protein) - Oryza sativa (japonica cultivar-group)
LjT46I09.40.nd	166	comp.	(A2XWZ2) Hypothetical protein - Oryza sativa (indica cultivar-group)
LjSGA_004896.2.1	78	comp.	(Q7X877) P0076O17.3 protein
LjSGA_005817.3	58	comp.	(Q6K4A7) Hypothetical protein OJ1595_D08.10 (Hypothetical protein P0676H02.28)
LjSGA_010360.2	68	comp.	(Q7XD75) Small ribonucleoprotein, putative
LjSGA_011834.2	81	comp.	(Q5ZBN9) Hypothetical protein P0704D04.8
LjSGA_013627.2	79	comp.	(Q6H886) Hypothetical protein OJ1572_F02.6
LjSGA_017875.2	135	comp.	(Q7XDF4) Hypothetical protein
LjSGA_018270.1	78	comp.	(Q852B4) Ras-related GTP-binding protein
LjSGA_019231.1	92	comp.	(Q5VS25) Putative beta 1,3 glucan synthase
LjSGA_022399.1	113	comp.	(Q7EYZ3) Putative placental protein 6
LjSGA_023015.1	63	comp.	(Q6YU88) Putative kinesin
LjSGA_025069.1	47	comp.	(Q7XQ14) OSJNBb0065L13.5 protein
LjSGA_026483.1	123	comp.	(Q6ZHC0) Putative GAMM1 protein

LjSGA_029764.1	117	comp.	(Q5QLP6) Putative ionotropic glutamate receptor homolog GLR4
LjSGA_030848.1	168	comp.	(Q67UR6) Methyladenine glycosylase protein-like
LjSGA_031607.1	44	comp.	(Q8RV84) Putative 5-3 exoribonuclease
LjSGA_032372.1	72	comp.	(Q658H0) Hypothetical protein P0538C01.24
LjSGA_032836.1	117	comp.	(Q7XC13) Expressed protein
LjSGA_036478.1	196	comp.	(Q94DH7) Putative cysteine protease CP1
LjSGA_039113.1	130	comp.	(Q5WA77) MYB transcription factor-like
LjSGA_042391.1	77	comp.	(Q2QM65) Transparent testa 12 protein
LjSGA_043276.1	150	comp.	(Q5Z990) Putative transformer-SR ribonucleoprotein
LjSGA_047151.2	50	comp.	(Q259B2) H0901F07.8 protein
LjSGA_048570.2	76	comp.	(Q851R1) Hypothetical protein OSJNBa0052F07.12
LjSGA_049098.1.1	69	comp.	(Q5NBM8) Putative transcription factor
LjSGA_049792.1	99	comp.	(Q7X7M2) OSJNBb0003A12.5 protein
LjSGA_051587.2	57	comp.	(Q6H805) Putative response regulator 9
LjSGA_053671.1	170	comp.	(Q6YY34) Hypothetical protein OSJNBb0056I22.9 (Hypothetical protein OSJNBa0016D04.44)
LjSGA_058499.1	136	comp.	(Q8LHL0) Putative splicing factor, arginine/serine-rich 2 (Splicing factor SC35)
LjSGA_059154.1	117	comp.	(Q9AV46) Hypothetical protein OSJNBa0093B11.3 (Expressed protein)
LjSGA_060687.2	93	comp.	(Q6K456) Putative plastid protein
LjSGA_062884.1	80	comp.	(Q7XSQ7) OSJNBa0084K11.5 protein
LjSGA_064507.1	101	comp.	(Q5U1I2) Class III peroxidase 111 precursor (EC 1.11.1.7)
LjSGA_067521.2.1	78	comp.	(Q7F8I8) Calmodulin
LjSGA_077028.1	56	comp.	(Q948F9) Putative PAP-specific phosphatase
LjSGA_079557.0.1	48	comp.	(Q6K225) Phosphate translocator-like
LjSGA_085750.1	68	comp.	(Q8H4Q9) GTP-binding protein Rab6
LjSGA_093272.1	117	comp.	(Q7XEY9) SPX domain, putative

LjSGA_095761.1	67	comp.	(Q6K7U1) Putative pentatricopeptide (PPR) repeat-containing protein
LjSGA_096059.1	66	comp.	(Q2QNJ8) Prefoldin subunit 3, putative
LjSGA_101824.1	36	comp.	(Q84QA5) Hypothetical protein OJ1012B02.16
LjSGA_108567.1	111	comp.	(Q651J5) Putative xenotropic and polytropic murine retrovirus receptor
LjSGA_119225.1.1	106	comp.	(Q7XQ30) OSJNBb0005B05.11 protein
LjSGA_122485.1	93	comp.	(Q5JMM6) Putative NOGO-interacting mitochondrial protein
LjSGA_133676.2.1	91	comp.	(Q6EUS1) Putative bacterial-induced peroxidase (Class III peroxidase 27 precursor) (EC 1.11.1.7)
LjSGA_139108.1	66	comp.	(Q7XM92) OSJNBb0060E08.7 protein
chr1.CM0101.30.nc	376	comp.	(Q01FQ9) Chromosome 01 contig 1, DNA sequence. (Fragment) - Ostreococcus tauri
LjSGA_079149.1.1	54	comp.	(Q9MAW6) 60S ribosomal protein L27a
chr1.LjT34H22.210.nd	86	comp.	(Q9FZ10) Serine threonine kinase homolog COK-4 - Phaseolus vulgaris (Kidney bean) (French bean)
LjT03D05.210.nd	64	comp.	(A4GGF7) Ribosomal protein L23 - Phaseolus vulgaris (Kidney bean) (French bean)
LjT22M20.140.nd	92	comp.	(Q9XFL4) Peroxidase 3 - Phaseolus vulgaris (Kidney bean) (French bean)
LjT22M20.150.nd	93	comp.	(Q9XFL4) Peroxidase 3 - Phaseolus vulgaris (Kidney bean) (French bean)
chr2.LjT04L10.120.nc	225	comp.	(Q3ZDI8) SCF ubiquitin ligase - Picea abies (Norway spruce) (Picea excelsa)
chr2.LjT04L10.130.nc	217	comp.	(Q3ZDI8) SCF ubiquitin ligase - Picea abies (Norway spruce) (Picea excelsa)
chr2.LjT13P17.60.nd	85	comp.	(Q5ZF84) Hypothetical protein - Plantago major (Common plantain)
chr3.CM0005.460.nc	346	comp.	(Q8H6Q7) CTV.22 - Poncirus trifoliata (Hardy orange)
chr3.CM0160.590.nd	261	comp.	(Q41255) Arabinogalactan-protein - Pyrus communis (Pear)
chr6.LjT04E21.220.nc	336	comp.	(A2V756) PpSFBB5-alpha protein - Pyrus pyrifolia (Japanese pear) (Pyrus serotina)
LjT10A21.80.nd	124	comp.	(Q5ZGH7) Hypothetical protein - Ricinus communis (Castor bean)
LjT19F24.100.nd	49	comp.	(O24327) Orf protein - Ricinus communis (Castor bean)
LjSGA_080171.1	79	comp.	(Q9ZPL4) Pulvinus inward-rectifying channel for potassium SPICK1
LjSGA_034221.1	184	comp.	(O04925) 15.5 kDa oleosin

chr2.LjB15M17.20.nc	349	comp.	(Q2PH52) SKP1-like protein - Silene latifolia (White campion) (Bladder campion)
chr1.LjT14I13.260.nd	191	comp.	(Q5MAC2) Putative transcription regulator CPL1 - Solanum lycopersicum (Tomato) (Lycopersicon esculentum)
chr2.CM0262.130.nd	74	comp.	(A0ZS62) Cytochrome P450 - Solanum lycopersicum (Tomato) (Lycopersicon esculentum)
chr3.CM0216.410.nc	209	comp.	(Q8H272) Metacaspase 1 (Fragment) - Solanum lycopersicum (Tomato) (Lycopersicon esculentum)
chr3.CM0216.710.nc	210	comp.	(Q8H272) Metacaspase 1 (Fragment) - Solanum lycopersicum (Tomato) (Lycopersicon esculentum)
LjT30I08.110.nc	271	comp.	(Q8GSM4) Ovate protein - Solanum lycopersicum (Tomato) (Lycopersicon esculentum)
chr2.CM0225.280.nd	69	comp.	(Q5XWR4) Hypothetical protein - Solanum tuberosum (Potato)
LjSGA_026057.1	50	comp.	(Q3HRX9) RUB1 conjugating enzyme-like
LjSGA_050210.1	63	comp.	(Q43180) Fumarase (EC 4.2.1.2)
LjSGA_060719.2	81	comp.	(Q3HRY8) Hypothetical protein
chr1.CM0113.140.nc	153	comp.	(O23957) Dehydrin - Glycine max (Soybean)
chr1.CM0150.200.nd	86	comp.	(Q9S7N8) Seed maturation protein PM21 (Seed maturation protein PM35) - Glycine max (Soybean)
chr1.CM0150.210.nd	86	comp.	(Q9S7N8) Seed maturation protein PM21 (Seed maturation protein PM35) - Glycine max (Soybean)
chr2.CM0011.300.nc	119	comp.	(Q9SEW3) Receptor-like protein kinase (Fragment) - Glycine max (Soybean)
chr5.CM0359.80.nc	92	comp.	(Q7PCB2) Putative phytosulfokine peptide precursor - Glycine max (Soybean)
LjT36B24.260.nd	44	comp.	(Q949H4) Leaf ubiquitous urease (EC 3.5.1.5) - Glycine max (Soybean)
LjSGA_008055.0.1	100	comp.	(O24422) Desiccation protective protein LEA5
LjSGA_018071.1	83	comp.	(Q9FQD6) Glutathione S-transferase GST 22 (EC 2.5.1.18) (Fragment)
LjSGA_028469.2	117	comp.	(Q5IR71) Zinc finger homeodomain protein SZF-HD2
LjSGA_031056.1	93	comp.	(Q9FUJ4) Ribulose-1,5-bisphosphate carboxylase small subunit rbcS3
LjSGA_071345.1.1	69	comp.	(Q2PMR3) 50S ribosomal protein L33

LjSGA_098553.1	42	comp.	(Q6T301) Cyclin H (Fragment)
LjSGA_140901.1	53	comp.	(Q9SPB9) Ubiquitin carrier protein 4
chr5.CM0345.430.nc	362	comp.	(Q8NZA4) Streptococcal protective antigen - Streptococcus pyogenes serotype M18
LjSGA_086868.1	93	comp.	(Q4RJS7) Chromosome 9 SCAF15033, whole genome shotgun sequence. (Fragment)
chr5.CM1125.600.nd	110	comp.	(Q41251) Calmodulin-binding heat-shock protein - Nicotiana tabacum (Common tobacco)
LjT31M07.170.nd	137	comp.	(Q84QE6) Photosystem I reaction center subunit X psaK - Nicotiana tabacum (Common tobacco)
LjT41B04.200.nd	51	comp.	(A1KYB2) S-adenosyl-L-homocysteine hydrolase (EC 3.3.1.1) - Nicotiana tabacum (Common tobacco)
LjSGA_037274.2.1	84	comp.	(Q84KS0) Auxin-repressed protein-like protein
LjSGA_043736.1	104	comp.	(Q76DX9) AG-motif binding protein-5
LjSGA_059247.1	80	comp.	(Q6R0J1) Heat shock protein 90
LjSGA_060220.1	33	comp.	(Q45FL8) Ubiquitin extension protein
LjSGA_063791.1	71	comp.	(Q9FR00) Avr9/Cf-9 rapidly elicited protein 31
chr1.CM0284.230.nc	120	comp.	(Q95VT2) Histone H2B variant 1 - Toxoplasma gondii
LjT44L11.120.nd	72	comp.	(Q8KTP5) Elongation factor G - Tremblaya princeps
LjSGA_049956.1.1	48	comp.	(Q2PEQ8) Putative mitochondrial dicarboxylate carrier protein
LjSGA_063161.1	56	comp.	(Q2PET8) Putative eukaryotic translation initiation factor 6
LjSGA_065523.1	78	comp.	(Q2PEQ5) Hypothetical protein
LjSGA_107151.1	68	comp.	(Q2PEU8) Hypothetical protein
LjSGA_143436.1	36	comp.	(Q2PEV4) Putative 60S ribosomal protein L1
chr1.CM0231.280.nc	209	comp.	(Q8MTN7) Glutamic acid-rich protein cNBL1700 - Trichinella spiralis (Trichina worm)
chr2.CM0312.190.nc	204	comp.	(Q4CY01) Hypothetical protein (Fragment) - Trypanosoma cruzi
LjSGA_014215.1.1	46	comp.	(Q4FG34) Ribosomal protein S12 (Fragment)
LjSGA_053374.2	46	comp.	(Q4FG34) Ribosomal protein S12 (Fragment)
LjSGA_076651.0.1	46	comp.	(Q4FG34) Ribosomal protein S12 (Fragment)

LjSGA_078903.0.1	46	comp.	(Q4FG34) Ribosomal protein S12 (Fragment)
LjSGA_080671.2.1	46	comp.	(Q4FG34) Ribosomal protein S12 (Fragment)
LjSGA_080693.1	46	comp.	(Q4FG34) Ribosomal protein S12 (Fragment)
LjSGA_084172.0.1	46	comp.	(Q4FG34) Ribosomal protein S12 (Fragment)
LjSGA_086298.0.1	46	comp.	(Q4FG34) Ribosomal protein S12 (Fragment)
LjSGA_096029.1	46	comp.	(Q4FG34) Ribosomal protein S12 (Fragment)
LjSGA_101632.0.1	46	comp.	(Q4FG34) Ribosomal protein S12 (Fragment)
LjSGA_128850.0.1	46	comp.	(Q4FG34) Ribosomal protein S12 (Fragment)
LjSGA_132937.1	46	comp.	(Q4FG34) Ribosomal protein S12 (Fragment)
LjSGA_138106.1	46	comp.	(Q4FG34) Ribosomal protein S12 (Fragment)
LjSGA_013055.2	126	comp.	(Q43235) NADPH-ferrihemoprotein reductase (EC 1.6.2.4)
LjSGA_065697.1	71	comp.	(Q9AYM5) CPRD49 protein
chr3.CM0282.840.nc	201	comp.	(Q6TKQ3) Putative ethylene response factor ERF3b - Vitis aestivalis (Grape)
LjSGA_010097.2	85	comp.	(Q6YCG3) Wound induced protein-like (Fragment)
LjSGA_029069.2	56	comp.	(Q9SQK5) Putative sucrose transporter
LjSGA_035818.1	54	comp.	(Q6BDD4) Hexose transporter HT2
LjSGA_061233.1	110	comp.	(Q2MZW1) Brassinosteroid-6-oxidase
LjSGA_106860.1	58	comp.	(Q6BDD4) Hexose transporter HT2
chr3.CM0996.200.nc	158	comp.	(Q5DM35) NAC domain transcription factor - Triticum aestivum (Wheat)
LjSGA_132986.1	158	comp.	(Q91594) Cellular nucleic acid binding protein
chr1.LjT36G06.70.nc	457	comp.	(Q6GLB5) ELAV (Embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R) - Xenopus tropicalis (Western clawed frog) (Silurana tropicalis)
chr2.CM0074.100.nc	351	comp.	(Q6CG61) Similar to sp|P31209 Schizosaccharomyces pombe Polyadenylate-binding protein - Yarrowia lipolytica (Candida lipolytica)
chr1.CM0113.690.nd	135	comp.	unknown protein

chr2.CM0338.140.nc	59	comp.	unknown protein
chr3.CM0070.80.nc	97	comp.	unknown protein
chr5.LjT45G21.130.nc	474	comp.	unknown protein
LjT01P07.190.nd	28	comp.	unknown protein
LjT11A15.10.nc	110	comp.	unknown protein
LjSGA_017611.1	65	comp.	unknown protein
LjSGA_049240.1	111	comp.	unknown protein
LjSGA_055952.1	111	comp.	unknown protein
LjSGA_056861.1	82	comp.	unknown protein
LjSGA_074189.1	192	comp.	unknown protein
LjSGA_120458.1	73	comp.	unknown protein
LjSGA_142753.1	44	comp.	unknown protein
chr1.CM0001.10.nd	58	partial	(Q8GYP3) Hypothetical protein At2g30280 - Arabidopsis thaliana (Mouse-ear cress)
chr1.CM0001.50.nd	138	partial	(Q8GYP3) Hypothetical protein At2g30280 - Arabidopsis thaliana (Mouse-ear cress)
chr1.CM0001.600.nc	89	partial	(Q9SN79) Hypothetical protein F1P2.140 (Hypothetical protein At3g47590) (At3g47590) - Arabidopsis thaliana (Mouse-ear cress)
chr1.CM0012.160.nd	86	partial	(Q93VB1) Putative heme oxygenase 1 precursor - Pisum sativum (Garden pea)
chr1.CM0012.230.nd	90	partial	(Q9FFS1) Gb|AAC67354.1 (Hypothetical protein) - Arabidopsis thaliana (Mouse-ear cress)
chr1.CM0012.660.nd	74	partial	(Q9ZQ93) Hypothetical protein At2g36810 - Arabidopsis thaliana (Mouse-ear cress)
chr1.CM0016.270.nc	47	partial	(Q8LJS7) Homeodomain protein GhHOX2 - Gossypium hirsutum (Upland cotton)
chr1.CM0016.90.nd	56	partial	(Q6YTT3) Putative 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase (Hypothetical protein) (Os08g0484500 protein) - Oryza sativa (japonica cultivar-group)
chr1.CM0023.370.nd	82	partial	(Q69JW2) Putative nucleosome/chromatin assembly factor A (Os02g0576700 protein) - Oryza sativa (japonica cultivar-group)
chr1.CM0029.270.nd	43	partial	(A3AKX7) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr1.CM0032.380.nd	60	partial	(Q1SQT1) TPR repeat - Medicago truncatula (Barrel medic)

chr1.CM0033.1020.nc	46	partial	(Q9FI52) Nucleotide-binding protein - Arabidopsis thaliana (Mouse-ear cress)
chr1.CM0033.840.nc	88	partial	(Q9CB01) Ara6 (Putative Rab family GTP-binding protein) - Arabidopsis thaliana (Mouse-ear cress)
chr1.CM0039.40.nd	119	partial	(A3RCC8) Plant U box protein 8 - Arabidopsis thaliana (Mouse-ear cress)
chr1.CM0050.30.nc	120	partial	(Q71E52) Cytochrome f (Fragment) - Fagus sylvatica (Beechnut)
chr1.CM0051.130.nc	62	partial	(Q8GZT3) Thioredoxin h - Brassica campestris (Field mustard)
chr1.CM0088.140.nd	60	partial	(Q9LK47) Similarity to 30s ribosomal protein s1 (At3g23700/MYM9_3) - Arabidopsis thaliana (Mouse-ear cress)
chr1.CM0088.200.nd	43	partial	(A3ABL5) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr1.CM0088.490.nd	37	partial	(Q1T3K3) Phytochelatin synthetase-like conserved region; Carbohydrate-binding - Medicago truncatula (Barrel medic)
chr1.CM0094.160.nc	58	partial	(Q9FP19) Putative nucleolar protein family A member 2 (Os06g0274200 protein) - Oryza sativa (japonica cultivar-group)
chr1.CM0094.320.nc	44	partial	(Q4W5U7) Calnexin-like protein - Solanum lycopersicum (Tomato) (Lycopersicon esculentum)
chr1.CM0104.280.nc	65	partial	(Q8LCM4) Trehalose-phosphatase, putative - Arabidopsis thaliana (Mouse-ear cress)
chr1.CM0104.390.nd	98	partial	(A2Q5Q7) Not CCR4-Not complex component, N-terminal; tRNA-binding arm - Medicago truncatula (Barrel medic)
chr1.CM0104.50.nd	41	partial	(Q9LEA9) Lipoxygenase (EC 1.13.11.12) - Prunus dulcis (Almond) (Prunus amygdalus)
chr1.CM0109.210.nd	47	partial	(Q9LIF1) Glutaredoxin-like protein (Hypothetical protein) - Arabidopsis thaliana (Mouse-ear cress)
chr1.CM0121.110.nd	95	partial	(Q70SZ7) Aldehyde dehydrogenase - Crocus sativus (Saffron)
chr1.CM0121.180.nd	40	partial	(A3AV07) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr1.CM0122.10.nc	32	partial	(Q0PJD4) MYB transcription factor MYB64 (Fragment) - Glycine max (Soybean)
chr1.CM0122.720.nd	85	partial	(A0ZAN2) ATPase - Nodularia spumigena CCY9414
chr1.CM0122.790.nd	112	partial	(Q3ECB4) Protein At1g77860 - Arabidopsis thaliana (Mouse-ear cress)
chr1.CM0133.790.nd	88	partial	(A3ATU9) Hypothetical protein - Oryza sativa (japonica cultivar-group)

chr1.CM0133.830.nd	125	partial	(Q1SQK6) Helicase, C-terminal; Argonaute and Dicer protein, PAZ; Type III restriction enzyme, res subunit; Ribonuclease III, bacterial - Medicago truncatula (Barrel medic)
chr1.CM0141.500.nd	49	partial	(Q1T6P9) Vesicle transport v-SNARE - Medicago truncatula (Barrel medic)
chr1.CM0147.140.nd	86	partial	(Q5ZD06) Putative Mal d 1-associated protein (Hypothetical protein) (Os01g0771200 protein) - Oryza sativa (japonica cultivar-group)
chr1.CM0147.600.nd	46	partial	(Q9LZ94) Eceriferum3 (CER3) - Arabidopsis thaliana (Mouse-ear cress)
chr1.CM0147.720.nc	156	partial	(Q9LND3) T21E18.20 protein - Arabidopsis thaliana (Mouse-ear cress)
chr1.CM0163.200.nd	76	partial	(A3BGZ2) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr1.CM0163.260.nd	87	partial	(A2YW68) Hypothetical protein - Oryza sativa (indica cultivar-group)
chr1.CM0166.450.nd	126	partial	(Q2A9R7) Hypothetical protein - Brassica oleracea (Wild cabbage)
chr1.CM0171.60.nc	41	partial	(A3UE89) Fumarate hydratase (EC 4.2.1.2) - Oceanicaulis alexandrii HTCC2633
chr1.CM0171.620.nd	81	partial	(Q2HSK3) Cyclin-like F-box - Medicago truncatula (Barrel medic)
chr1.CM0171.800.nd	51	partial	(Q1RSH3) GroEL-like chaperone, ATPase - Medicago truncatula (Barrel medic)
chr1.CM0171.810.nd	62	partial	(Q1T3I2) AAA ATPase - Medicago truncatula (Barrel medic)
chr1.CM0171.860.nd	76	partial	(Q1SIS5) Immunoglobulin/major histocompatibility complex; Zinc finger, BED-type predicted; Zinc finger, C2H2-type - Medicago truncatula (Barrel medic)
chr1.CM0174.160.nc	55	partial	(Q0GPF1) BZIP transcription factor bZIP41 - Glycine max (Soybean)
chr1.CM0178.20.nd	138	partial	(Q9SWA8) Glycine-rich RNA-binding protein - Glycine max (Soybean)
chr1.CM0192.30.nd	44	partial	unknown protein
chr1.CM0195.200.nc	40	partial	(Q1RX21) Fibrillarin - Medicago truncatula (Barrel medic)
chr1.CM0195.70.nd	32	partial	(Q1S1H1) Hypothetical protein - Medicago truncatula (Barrel medic)
chr1.CM0206.980.nd	44	partial	(Q84W73) Putative cell division-related protein - Arabidopsis thaliana (Mouse-ear cress)
chr1.CM0231.380.nd	46	partial	(Q645N1) Mitochondrial malate dehydrogenase - Solanum lycopersicum (Tomato) (Lycopersicon esculentum)
chr1.CM0231.470.nd	81	partial	(A3AKX7) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr1.CM0231.580.nd	64	partial	(O24078) Protein phosphatase 2C - Medicago sativa (Alfalfa)

chr1.CM0233.160.nc	115	partial	(Q2V3Q7) Protein At3g45310 - Arabidopsis thaliana (Mouse-ear cress)
chr1.CM0248.380.nd	129	partial	(Q2HUN6) RNA-directed DNA polymerase (Reverse transcriptase); Ribonuclease H - Medicago truncatula (Barrel medic)
chr1.CM0269.340.nc	44	partial	(Q6EM96) Ribosomal protein S7 - Euptelea polyandra
chr1.CM0269.370.nd	54	partial	(Q5SMZ1) Aldose 1-epimerase-like (Hypothetical protein) - Oryza sativa (japonica cultivar-group)
chr1.CM0275.180.nd	384	partial	(Q9FX45) RNA-binding glycine-rich protein, putative (At1g73530) - Arabidopsis thaliana (Mouse-ear cress)
chr1.CM0284.330.nd	43	partial	(A2Y368) Hypothetical protein - Oryza sativa (indica cultivar-group)
chr1.CM0289.130.nd	95	partial	(Q0JDM5) Os04g0393300 protein - Oryza sativa (japonica cultivar-group)
chr1.CM0289.210.nc	107	partial	(A3AM99) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr1.CM0289.410.nc	35	partial	(Q9LTR4) Similarity to EH domain containing proteins - Arabidopsis thaliana (Mouse-ear cress)
chr1.CM0295.670.nc	57	partial	(A3ACJ3) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr1.CM0295.740.nd	73	partial	(Q337L2) TPR Domain containing protein, expressed (Os10g0471400 protein) - Oryza sativa (japonica cultivar-group)
chr1.CM0295.950.nc	49	partial	(Q4A185) Beclin 1 protein - Medicago truncatula (Barrel medic)
chr1.CM0295.990.nc	185	partial	(A3AA74) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr1.CM0315.390.nc	70	partial	(Q1SD50) Semialdehyde dehydrogenase, NAD-binding - Medicago truncatula (Barrel medic)
chr1.CM0318.460.nc	62	partial	(O04521) F20P5.3 protein - Arabidopsis thaliana (Mouse-ear cress)
chr1.CM0318.610.nd	47	partial	(Q570J3) Adenylosuccinate synthetase (Fragment) - Arabidopsis thaliana (Mouse-ear cress)
chr1.CM0320.290.nd	84	partial	(Q9T0I3) Hypothetical protein AT4g38750 - Arabidopsis thaliana (Mouse-ear cress)
chr1.CM0361.280.nd	57	partial	(Q0JGZ1) Os01g0895100 protein (Hypothetical protein) - Oryza sativa (japonica cultivar-group)
chr1.CM0375.150.nd	90	partial	(A2XLW4) Hypothetical protein - Oryza sativa (indica cultivar-group)
chr1.CM0375.30.nd	79	partial	unknown protein
chr1.CM0375.320.nd	341	partial	(Q9AT21) Histone H1 (Fragment) - Lathyrus sativus (Chickling vetch)
chr1.CM0375.410.nc	37	partial	(Q2PES9) Putative tetrahydrofolate synthase - Trifolium pratense (Red clover)

chr1.CM0375.420.nc	68	partial	(Q2HVK9) Tetrahydrofolate dehydrogenase/cyclohydrolase - Medicago truncatula (Barrel medic)
chr1.CM0393.270.nd	106	partial	(Q9SIW2) Hypothetical protein At2g16390 - Arabidopsis thaliana (Mouse-ear cress)
chr1.CM0393.370.nd	61	partial	(Q9LPF6) T12C22.2 protein (Hypothetical protein At1g44750) (Hypothetical protein At1g44750; T12C22.2) - Arabidopsis thaliana (Mouse-ear cress)
chr1.CM0393.400.nd	55	partial	(Q9SLR7) Thiamin biosynthetic enzyme - Glycine max (Soybean)
chr1.CM0476.310.nd	104	partial	(Q1RT77) Zinc finger, CCCH-type - Medicago truncatula (Barrel medic)
chr1.CM0476.60.nd	36	partial	(A3B6B9) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr1.CM0544.260.nc	47	partial	(Q8L833) Putative carbonic anhydrase - Arabidopsis thaliana (Mouse-ear cress)
chr1.CM0579.110.nd	81	partial	(Q53YG9) At3g51130/F24M12_170 - Arabidopsis thaliana (Mouse-ear cress)
chr1.CM0591.490.nd	66	partial	(Q0VJB4) Putative zinc-binding protein - Platanus acerifolia (London plane tree)
chr1.CM0591.500.nd	90	partial	(A2XLW4) Hypothetical protein - Oryza sativa (indica cultivar-group)
chr1.CM0593.510.nd	43	partial	(Q1SMQ9) Calcium-binding EF-hand; Adenine nucleotide translocator 1 - Medicago truncatula (Barrel medic)
chr1.CM0600.20.nd	46	partial	(Q9M838) T27C4.14 protein - Arabidopsis thaliana (Mouse-ear cress)
chr1.CM0600.220.nd	41	partial	(A3BBX0) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr1.CM0600.390.nd	42	partial	(Q9C4Z6) Guanine nucleotide-binding protein, putative (Putative guanine nucleotide-binding protein) - Arabidopsis thaliana (Mouse-ear cress)
chr1.CM0668.20.nd	42	partial	(A0IIU4) Catalase-like (EC 1.11.1.6) - Serratia proteamaculans 568
chr1.CM0668.220.nd	122	partial	(A2XPE5) Hypothetical protein - Oryza sativa (indica cultivar-group)
chr1.CM0794.170.nd	94	partial	(A3BR06) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr1.CM0800.100.nd	58	partial	(Q06XS4) Putative calcium-dependent protein kinase 2 - Isatis tinctoria (Dyer's woad) (Isatis indigotica)
chr1.CM0800.540.nd	87	partial	(Q6TK49) RNA polymerase beta subunit (Fragment) - Ecballium elaterium (Jumping cucumber)
chr1.CM0982.240.nd	160	partial	(Q9P127) Leucine zipper protein 4 - Homo sapiens (Human)
chr1.CM0982.360.nd	45	partial	(Q75ZE1) 14-3-3 d-2-AS protein - Nicotiana tabacum (Common tobacco)

chr1.CM0982.40.nd	63	partial	(Q9LTA2) Similarity to AT-hook DNA-binding protein (AT-hook motif nuclear localized protein 17) - Arabidopsis thaliana (Mouse-ear cress)
chr1.CM1413.170.nd	49	partial	(O82341) Eukaryotic translation initiation factor 3 delta subunit - Arabidopsis thaliana (Mouse-ear cress)
chr1.CM1875.40.nc	43	partial	(Q5K3W0) Monosaccharide transporter - Populus tremula x Populus tremuloides
chr1.LjT01D01.50.nd	164	partial	(Q6NME0) At1g79140 - Arabidopsis thaliana (Mouse-ear cress)
chr1.LjT01M20.40.nc	28	partial	(Q1SG03) Zinc finger, RING-type; Zinc finger, PHD-type - Medicago truncatula (Barrel medic)
chr1.LjT04O21.80.nd	190	partial	(A3CIU0) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr1.LjT06I14.100.nc	71	partial	(O23944) Cystathionine gamma synthase - Fragaria vesca (Woodland strawberry)
chr1.LjT08H21.110.nd	62	partial	(Q6RIB7) Enolase (EC 2.3.1.16) - Glycine max (Soybean)
chr1.LjT08H21.130.nd	43	partial	unknown protein
chr1.LjT14B18.210.nc	104	partial	(Q1SZG7) Zinc finger, B-box; CCT - Medicago truncatula (Barrel medic)
chr1.LjT14I13.100.nd	49	partial	(Q7X6U9) OSJNBb0034G17.1 protein (Hypothetical protein) - Oryza sativa (japonica cultivar-group)
chr1.LjT14I13.200.nd	45	partial	(Q9M461) Plasma membrane H+ ATPase (EC 3.6.1.3) - Prunus persica (Peach)
chr1.LjT14I13.50.nd	72	partial	(Q1RSQ9) Phosphotransferase KptA/Tpt1 - Medicago truncatula (Barrel medic)
chr1.LjT16B05.160.nd	41	partial	(O04326) T02O04.20 protein (Hypothetical protein At3g16310) (Hypothetical protein) (Gb|AAB63646.1) - Arabidopsis thaliana (Mouse-ear cress)
chr1.LjT16O03.110.nd	24	partial	(Q7XUP4) OSJNBb0011N17.19 protein (Os04g0482700 protein) - Oryza sativa (japonica cultivar-group)
chr1.LjT23O20.20.nd	100	partial	(Q45NK3) Hypothetical protein (Fragment) - Medicago sativa (Alfalfa)
chr1.LjT27C19.180.nd	51	partial	(Q9SCV6) Putative beta-galactosidase precursor (EC 3.2.1.23) - Arabidopsis thaliana (Mouse-ear cress)
chr1.LjT29L06.230.nd	31	partial	(Q1RSS0) Universal stress protein (Usp) - Medicago truncatula (Barrel medic)
chr1.LjT32B13.20.nd	68	partial	unknown protein
chr1.LjT34C24.10.nc	88	partial	(Q2HTR2) Cyclin-like F-box - Medicago truncatula (Barrel medic)

chr1.LjT34H22.110.nd	84	partial	(Q9FZ10) Serine threonine kinase homolog COK-4 - Phaseolus vulgaris (Kidney bean) (French bean)
chr1.LjT34H22.140.nd	82	partial	(A2XHZ3) Hypothetical protein - Oryza sativa (indica cultivar-group)
chr1.LjT34H22.200.nd	153	partial	(Q69F86) Serine-threonine kinase - Phaseolus vulgaris (Kidney bean) (French bean)
chr1.LjT34H22.80.nd	71	partial	(Q9LLC9) Fen kinase - Solanum lycopersicum (Tomato) (Lycopersicon esculentum)
chr1.LjT35H06.100.nc	471	partial	(Q0YGL9) Hypothetical protein - Geobacter sp. FRC-32
chr1.LjT36F23.140.nd	159	partial	(Q9LRX7) Phosphatidylinositol/phosphatidylcholine transfer protein-like - Arabidopsis thaliana (Mouse-ear cress)
chr1.LjT36G06.120.nc	26	partial	(Q5EE13) Calcineurin B-like protein (Calcineurin B-like protein 1) - Ammopiptanthus mongolicus
chr1.LjT36I17.10.nd	73	partial	(A1L4U4) At5g64300 - Arabidopsis thaliana (Mouse-ear cress)
chr1.LjT36P09.110.nd	58	partial	(Q1RSC2) Pentatricopeptide repeat - Medicago truncatula (Barrel medic)
chr1.LjT36P09.140.nd	65	partial	(A3BER2) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr1.LjT37A17.80.nc	53	partial	(Q0PY49) CCR4 associated factor 1-related protein - Capsicum annuum (Bell pepper)
chr1.LjT38A19.170.nc	20	partial	(Q9SPI7) Actin - Picea rubens (Red spruce)
chr1.LjT38A19.20.nc	34	partial	(A3BXM3) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr1.LjT38G13.70.nd	71	partial	(Q9SLG8) Putative strictosidine synthase - Arabidopsis thaliana (Mouse-ear cress)
chr1.LjT41E18.120.nc	45	partial	(A2ZQ76) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr1.LjT41J07.140.nd	38	partial	(Q1SGV7) Transcriptional factor B3; Auxin response factor; Aux/IAA_ARF_dimerisation - Medicago truncatula (Barrel medic)
chr1.LjT43D18.50.nd	85	partial	(Q1S126) Hypothetical protein - Medicago truncatula (Barrel medic)
chr1.LjT43O05.230.nd	65	partial	(Q43016) Alcohol dehydrogenase-1F (EC 1.1.1.1) - Phaseolus acutifolius (Tepary bean)
chr1.LjT43O05.310.nd	45	partial	(A2ZR99) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr1.LjT44L17.120.nd	59	partial	(A2WX55) Hypothetical protein - Oryza sativa (indica cultivar-group)
chr1.LjT44L17.30.nd	56	partial	(Q547P9) Copper transporter COPT1 (Copper transport protein) - Arabidopsis thaliana (Mouse-ear cress)

chr1.LjT48M07.90.nc	29	partial	(Q1SVD9) Pyridoxal-5-phosphate-dependent enzyme, beta subunit - Medicago truncatula (Barrel medic)
chr2.CM0002.340.nd	59	partial	(Q9FFF9) Meiotic check point regulator-like protein - Arabidopsis thaliana (Mouse-ear cress)
chr2.CM0008.100.nd	53	partial	(Q1PG92) Carbonic anhydrase (Fragment) - Striga asiatica
chr2.CM0008.110.nd	37	partial	(A1XX45) Chloroplast carbonic anhydrase - Pachysandra terminalis
chr2.CM0008.30.nd	94	partial	(Q6NKP9) Hypothetical protein At1g10600 - Arabidopsis thaliana (Mouse-ear cress)
chr2.CM0008.490.nc	41	partial	(A0MWE6) Na+/Pi transporter - Thellungiella halophila (Salt cress)
chr2.CM0008.500.nc	71	partial	(Q1S106) Exostosin-like - Medicago truncatula (Barrel medic)
chr2.CM0008.520.nc	72	partial	(Q1RWY8) P-type trefoil - Medicago truncatula (Barrel medic)
chr2.CM0011.370.nd	89	partial	(Q9ZTT3) Subtilisin-like protease C1 - Glycine max (Soybean)
chr2.CM0018.210.nd	58	partial	(Q2TM26) STO-1 - Coffea canephora (Robusta coffee)
chr2.CM0018.420.nd	51	partial	(Q8S3S8) Putative histidinol phosphate aminotransferase - Oryza sativa (japonica cultivar-group)
chr2.CM0018.720.nc	68	partial	(Q6ZBP3) Putative Histone H2B.2 (Hypothetical protein) - Oryza sativa (japonica cultivar-group)
chr2.CM0021.1180.nd	61	partial	(Q9LPJ1) F6N18.11 (Hypothetical protein) - Arabidopsis thaliana (Mouse-ear cress)
chr2.CM0021.130.nd	88	partial	(Q9FHP1) Uridylyl transferases-like (ACR1) - Arabidopsis thaliana (Mouse-ear cress)
chr2.CM0021.480.nc	50	partial	(Q8H6V8) Urease JBURE-II - Canavalia ensiformis (Jack bean) (Horse bean)
chr2.CM0028.240.nd	81	partial	(A1A6I1) At1g69980 - Arabidopsis thaliana (Mouse-ear cress)
chr2.CM0031.250.nc	56	partial	(Q1SXM4) Leucine-rich repeat, plant specific - Medicago truncatula (Barrel medic)
chr2.CM0056.230.nd	73	partial	(Q9FL09) Nodulin-like protein - Arabidopsis thaliana (Mouse-ear cress)
chr2.CM0056.30.nd	93	partial	(Q9M381) DIPHOSPHOMEVALONATE DECARBOXYLASE-like protein - Arabidopsis thaliana (Mouse-ear cress)
chr2.CM0056.520.nd	58	partial	(Q9FLS5) Gb|AAC80624.1 (NpGUT1 homolog) - Arabidopsis thaliana (Mouse-ear cress)
chr2.CM0056.60.nd	104	partial	(Q9T0K5) Extensin-like protein - Arabidopsis thaliana (Mouse-ear cress)
chr2.CM0056.630.nd	46	partial	(Q6H975) STY-L protein - Antirrhinum majus (Garden snapdragon)
chr2.CM0056.70.nd	49	partial	(Q9FSF5) Cysteine synthase - Nicotiana tabacum (Common tobacco)

chr2.CM0056.740.nd	69	partial	(Q6K456) Putative plastid protein (Hypothetical protein) (Os09g0132600 protein) - Oryza sativa (japonica cultivar-group)
chr2.CM0058.160.nc	44	partial	(Q8GWL2) Hypothetical protein At2g30270 - Arabidopsis thaliana (Mouse-ear cress)
chr2.CM0065.50.nd	99	partial	(Q1SND5) Protein kinase - Medicago truncatula (Barrel medic)
chr2.CM0067.170.nc	48	partial	(Q2QME5) Eukaryotic translation initiation factor 2 gamma subunit, putative, expressed (Hypothetical protein) (Os12g0607100 protein) - Oryza sativa (japonica cultivar-group)
chr2.CM0102.290.nd	109	partial	(Q7XUB7) OSJNBb0078D11.11 protein - Oryza sativa (japonica cultivar-group)
chr2.CM0102.590.nd	77	partial	(Q9LHJ2) UDP-glucose glucosyltransferase-like protein - Arabidopsis thaliana (Mouse-ear cress)
chr2.CM0102.630.nd	175	partial	(O65503) Hypothetical protein F23E12.200 (Hypothetical protein AT4g35240) - Arabidopsis thaliana (Mouse-ear cress)
chr2.CM0120.60.nc	71	partial	(Q1SBM2) Putative methyltransferase, putative - Medicago truncatula (Barrel medic)
chr2.CM0120.70.nc	52	partial	(Q9S7D7) Putative RNA-binding protein; 24808-23340 (Putative RNA-binding protein; 16955-18423) - Arabidopsis thaliana (Mouse-ear cress)
chr2.CM0124.200.nd	60	partial	(A3B2W3) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr2.CM0124.650.nd	57	partial	(P93570) Chaperonin-60 beta subunit precursor - Solanum tuberosum (Potato)
chr2.CM0124.670.nd	65	partial	(A3BY78) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr2.CM0177.510.nc	76	partial	(Q09FY5) Hypothetical chloroplast RF2 - Platanus occidentalis (Sycamore)
chr2.CM0191.540.nc	42	partial	(Q9LKJ2) Cytosolic phosphoglycerate kinase - Pisum sativum (Garden pea)
chr2.CM0191.620.nc	79	partial	(Q84K92) Hypothetical protein (Fragment) - Arabidopsis lyrata (Lyre-leaved rock-cress)
chr2.CM0201.140.nd	76	partial	(Q8VYF9) Hypothetical protein At3g01720 - Arabidopsis thaliana (Mouse-ear cress)
chr2.CM0201.60.nd	79	partial	(A2Q532) Transcriptional factor B3; Auxin response factor - Medicago truncatula (Barrel medic)
chr2.CM0210.160.nc	95	partial	(Q70SZ7) Aldehyde dehydrogenase - Crocus sativus (Saffron)
chr2.CM0210.90.nc	66	partial	(A3BAZ3) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr2.CM0237.20.nd	65	partial	(Q9LKB9) Myosin heavy chain MYA2 - Arabidopsis thaliana (Mouse-ear cress)
chr2.CM0237.210.nd	51	partial	(Q84ND6) Cation diffusion facilitator 8 - Stylosanthes hamata (Caribbean stylo)
chr2.CM0237.250.nd	49	partial	(Q5EMN3) CRABS CLAW - Nicotiana tabacum (Common tobacco)

chr2.CM0237.50.nd	62	partial	(A3ACP3) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr2.CM0249.700.nd	37	partial	(Q9C7X9) Peptide chain release factor 2, putative - Arabidopsis thaliana (Mouse-ear cress)
chr2.CM0249.820.nd	71	partial	(Q9FJZ5) Genomic DNA, chromosome 5, TAC clone:K1F13 (Hypothetical protein At5g66440) - Arabidopsis thaliana (Mouse-ear cress)
chr2.CM0249.860.nd	57	partial	unknown protein
chr2.CM0249.900.nd	83	partial	(Q9FJZ5) Genomic DNA, chromosome 5, TAC clone:K1F13 (Hypothetical protein At5g66440) - Arabidopsis thaliana (Mouse-ear cress)
chr2.CM0272.10.nd	82	partial	(Q1SAF9) Mov34/MPN/PAD-1 (Mov34-1) - Medicago truncatula (Barrel medic)
chr2.CM0304.540.nd	81	partial	(Q1SB83) E-class P450, group I - Medicago truncatula (Barrel medic)
chr2.CM0310.230.nd	69	partial	(Q1T3I5) Hypothetical protein - Medicago truncatula (Barrel medic)
chr2.CM0310.250.nd	56	partial	(Q06QU5) Potential heme-binding protein - Menodora longiflora
chr2.CM0310.280.nd	42	partial	(A3BUD4) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr2.CM0360.200.nd	58	partial	(Q7XVT5) OSJNBa0041M21.1 protein - Oryza sativa (japonica cultivar-group)
chr2.CM0373.220.nd	65	partial	(A2Z485) Hypothetical protein - Oryza sativa (indica cultivar-group)
chr2.CM0373.40.nd	51	partial	(Q1S2V6) Mitochondrial carrier protein - Medicago truncatula (Barrel medic)
chr2.CM0373.410.nc	59	partial	(A3AGK1) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr2.CM0405.40.nd	119	partial	(Q1S9B3) Ribosomal protein L6E; Ribosomal protein L6, N-terminal - Medicago truncatula (Barrel medic)
chr2.CM0504.200.nd	67	partial	(Q1S4F9) Leucine-rich-associated - Medicago truncatula (Barrel medic)
chr2.CM0608.270.nd	45	partial	(Q6E6L3) 5-enol-pyruvylshikimate-phosphate synthase (Fragment) - Conyza canadensis (Canadian horseweed)
chr2.CM0608.280.nd	46	partial	(Q1T2M0) RNA polymerase subunit, RPB5; RNA polymerase Rpb5, N-terminal - Medicago truncatula (Barrel medic)
chr2.CM0641.10.nc	23	partial	(A1Z3W7) EIF5A - Rosa chinensis (China rose)
chr2.CM0749.210.nd	40	partial	(Q7PCB3) Putative phytosulfokine peptide (Fragment) - Glycine max (Soybean)
chr2.CM0783.170.nd	49	partial	(Q7Y228) At5g19740 - Arabidopsis thaliana (Mouse-ear cress)

chr2.CM0783.180.nd	31	partial	(Q2V3W8) Protein At3g12100 - Arabidopsis thaliana (Mouse-ear cress)
chr2.CM0788.100.nc	34	partial	(Q10PH1) Ubiquitin fusion protein, putative, expressed (Hypothetical protein) (Os03g0234200 protein) - Oryza sativa (japonica cultivar-group)
chr2.CM0788.180.nc	36	partial	(Q45NM7) Histidyl-tRNA synthetase (Fragment) - Medicago sativa (Alfalfa)
chr2.CM0788.190.nc	59	partial	(Q1S7R4) Protein kinase - Medicago truncatula (Barrel medic)
chr2.CM0788.340.nd	74	partial	(A2WWI1) Hypothetical protein - Oryza sativa (indica cultivar-group)
chr2.CM0803.530.nc	48	partial	(Q39852) Putative ATP synthase subunit - Glycine max (Soybean)
chr2.CM0803.880.nd	34	partial	(A3AWV1) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr2.CM0826.350.nd	72	partial	(Q1RTI3) Glycosyl transferase, family 20; Trehalose-phosphatase - Medicago truncatula (Barrel medic)
chr2.CM0826.40.nc	75	partial	(Q1SIP0) Ribose-phosphate pyrophosphokinase - Medicago truncatula (Barrel medic)
chr2.CM0904.270.nd	32	partial	(Q93WW2) Hypothetical protein (Fragment) - Musa acuminata (Banana)
chr2.CM0904.310.nd	33	partial	(Q1H386) ATP-dependent metalloprotease FtsH (EC 3.6.4.6) - Methylobacillus flagellatus (strain KT / ATCC 51484 / DSM 6875)
chr2.CM1032.360.nc	707	partial	(A2Q4W6) RNA-binding region RNP-1 (RNA recognition motif) - Medicago truncatula (Barrel medic)
chr2.CM1150.20.nd	59	partial	(Q9FNY4) DNA polymerase lambda - Arabidopsis thaliana (Mouse-ear cress)
chr2.CM1150.260.nd	54	partial	(A2Q5N5) Protein kinase (Fragment) - Medicago truncatula (Barrel medic)
chr2.LjB26H15.10.nc	172	partial	(Q197X9) Heterogeneous nuclear ribonucleoprotein G - Haplochromis burtoni (Burton's mouthbrooder)
chr2.LjT02E02.100.nd	53	partial	(Q647J9) Homogentisate phytylprenyltransferase - Medicago sativa (Alfalfa)
chr2.LjT02E02.120.nd	47	partial	(Q647J9) Homogentisate phytylprenyltransferase - Medicago sativa (Alfalfa)
chr2.LjT02E02.150.nd	45	partial	(Q58FG4) Homogentisate phytylprenyltransferase - Glycine max (Soybean)
chr2.LjT09A09.50.nd	33	partial	(Q9FRY6) Uricase - Lotus japonicus
chr2.LjT13M01.90.nd	51	partial	(Q9FIU5) Serine/threonine-specific protein kinase-like protein - Arabidopsis thaliana (Mouse-ear cress)

chr2.LjT13P17.40.nd	62	partial	(Q4FH87) Dehydration responsive element-binding protein 3 - Glycine max (Soybean)
chr2.LjT17A07.220.nd	24	partial	(A3BTD3) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr2.LjT24P12.180.nd	56	partial	(Q9LIN8) Similarity to alpha galactosidase - Arabidopsis thaliana (Mouse-ear cress)
chr2.LjT24P12.80.nd	51	partial	(Q5QLK3) Putative alpha-galactosidase (Os01g0518500 protein) - Oryza sativa (japonica cultivar-group)
chr2.LjT34P04.170.nd	69	partial	(A0D0A0) Chromosome undetermined scaffold_33, whole genome shotgun sequence - Paramecium tetraurelia
chr2.LjT34P04.60.nd	59	partial	(A2TKE7) Ubiquitin-like protein (Fragment) - Pisum sativum (Garden pea)
chr2.LjT36E17.30.nd	170	partial	(Q5XWM2) No apical meristem (NAM) family protein-like - Solanum tuberosum (Potato)
chr2.LjT40P05.100.nd	89	partial	(Q2HVU7) Sodium/hydrogen exchanger - Medicago truncatula (Barrel medic)
chr2.LjT41F02.100.nc	106	partial	(Q1S1H9) Hypothetical protein - Medicago truncatula (Barrel medic)
chr2.LjT42I05.130.nd	48	partial	(Q5ZJ35) Hypothetical protein - Gallus gallus (Chicken)
chr2.LjT42I05.40.nd	41	partial	(Q9M9H4) F14O23.10 protein - Arabidopsis thaliana (Mouse-ear cress)
chr2.LjT44M20.320.nd	46	partial	(Q84W73) Putative cell division-related protein - Arabidopsis thaliana (Mouse-ear cress)
chr2.LjT45I07.100.nd	68	partial	(Q0WR55) GPI-anchored protein (Fragment) - Arabidopsis thaliana (Mouse-ear cress)
chr2.LjT46G02.160.nd	24	partial	(Q9M5M5) 60S acidic ribosomal protein PO (Fragment) - Euphorbia esula (Leafy spurge)
chr2.LjT46G02.270.nd	27	partial	(Q9FQ21) Putative Hs1pro-1-like receptor - Glycine max (Soybean)
chr2.LjT46G02.40.nd	61	partial	(Q9M5M5) 60S acidic ribosomal protein PO (Fragment) - Euphorbia esula (Leafy spurge)
chr2.LjT48A12.150.nd	85	partial	(Q9SUA2) Sucrase-like protein - Arabidopsis thaliana (Mouse-ear cress)
chr3.CM0005.170.nd	84	partial	(A2WNG7) Hypothetical protein - Oryza sativa (indica cultivar-group)
chr3.CM0005.230.nd	52	partial	(Q1SPA4) SAM (And some other nucleotide) binding motif - Medicago truncatula (Barrel medic)
chr3.CM0005.240.nd	87	partial	(A2ZRU0) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr3.CM0047.260.nc	64	partial	(Q4FFZ4) Ribosomal protein S11 (Fragment) - Nuphar advena (Common spatterdock) (Nuphar lutea subsp. advena)
chr3.CM0047.520.nc	178	partial	(Q8RWD7) Hypothetical protein At1g58210 - Arabidopsis thaliana (Mouse-ear cress)

chr3.CM0059.330.nd	72	partial	(Q9XIQ7) F13O11.19 protein (Hypothetical protein At1g64890) - Arabidopsis thaliana (Mouse-ear cress)
chr3.CM0091.180.nc	48	partial	(A3CCC8) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr3.CM0106.20.nd	33	partial	(Q1SZL0) Leucine-rich repeat - Medicago truncatula (Barrel medic)
chr3.CM0106.520.nd	139	partial	(A4GYV4) Ycf2 - Populus trichocarpa (Western balsam poplar)
chr3.CM0106.530.nd	62	partial	(Q1SSB0) Adenine nucleotide translocator 1 - Medicago truncatula (Barrel medic)
chr3.CM0110.420.nd	90	partial	(Q8GXX0) Hypothetical protein At1g49880/F10F5_3 (Mitochondrial sulfhydryl oxidase Erv1p) (At1g49880) - Arabidopsis thaliana (Mouse-ear cress)
chr3.CM0111.10.nd	42	partial	(Q9SI32) Expressed protein (Hypothetical protein At2g04940) - Arabidopsis thaliana (Mouse-ear cress)
chr3.CM0112.320.nd	235	partial	(Q9ZSP8) Latex-abundant protein - Hevea brasiliensis (Para rubber tree)
chr3.CM0112.50.nc	248	partial	(Q1SSK7) Peptidase C14, caspase catalytic subunit p20 - Medicago truncatula (Barrel medic)
chr3.CM0116.400.nd	118	partial	(Q9FKA7) Similarity to nuclear protein 95 (Zinc finger-like protein) (At5g39550) - Arabidopsis thaliana (Mouse-ear cress)
chr3.CM0127.70.nc	83	partial	unknown protein
chr3.CM0135.40.nc	72	partial	unknown protein
chr3.CM0142.20.nd	116	partial	(Q9SCM9) Hypothetical protein T8H10.30 - Arabidopsis thaliana (Mouse-ear cress)
chr3.CM0160.940.nd	76	partial	(Q9ZWC2) F21M11.4 protein - Arabidopsis thaliana (Mouse-ear cress)
chr3.CM0164.10.nd	59	partial	(Q8H0D9) Alcohol dehydroge - Phaseolus lunatus (Lima bean) (Phaseolus limensis)
chr3.CM0176.240.nd	32	partial	(Q1S821) Zinc finger, RING-type - Medicago truncatula (Barrel medic)
chr3.CM0213.210.nd	95	partial	(Q43781) Aspartate aminotransferase (EC 2.6.1.1) - Lotus japonicus
chr3.CM0216.10.nd	96	partial	(Q8S532) Cytosolic aldehyde dehydrogenase RF2C - Zea mays (Maize)
chr3.CM0216.130.nd	45	partial	(O65750) 26S protease regulatory subunit 6 (Fragment) - Cicer arietinum (Chickpea) (Garbanzo)
chr3.CM0216.920.nd	62	partial	(Q9LV48) Protein kinase-like protein (At3g24550) (Hypothetical protein At3g24550) (AT3g24550/MOB24_8) - Arabidopsis thaliana (Mouse-ear cress)
chr3.CM0216.960.nd	81	partial	(A3AKX7) Hypothetical protein - Oryza sativa (japonica cultivar-group)

chr3.CM0246.90.nd	50	partial	(Q1RWA1) Multicatalytic endopeptidase complex, proteasome component, beta subunit-related - Medicago truncatula (Barrel medic)
chr3.CM0261.250.nc	38	partial	(Q6IM91) DVL10 - Arabidopsis thaliana (Mouse-ear cress)
chr3.CM0261.270.nc	53	partial	(Q1T343) DNA topoisomerase II; Serine/threonine-specific protein phosphatase and bis(5-nucleosyl)-tetraphosphatase - Medicago truncatula (Barrel medic)
chr3.CM0261.300.nd	46	partial	(Q43445) S-adenosyl-L-methionine:delta24-sterol-C-methyltransferase - Glycine max (Soybean)
chr3.CM0261.390.nd	57	partial	(Q9M1X8) Hypothetical protein F24G16.250 (Hypothetical protein At3g59980) (Hypothetical protein) - Arabidopsis thaliana (Mouse-ear cress)
chr3.CM0279.400.nc	61	partial	(Q94B52) Hypothetical protein T10C21.40 (Hypothetical protein At4g30690; T10C21.40) - Arabidopsis thaliana (Mouse-ear cress)
chr3.CM0282.1050.nc	45	partial	(Q3E951) Protein At5g25560 - Arabidopsis thaliana (Mouse-ear cress)
chr3.CM0282.110.nd	88	partial	(A2WUU8) Hypothetical protein - Oryza sativa (indica cultivar-group)
chr3.CM0282.440.nc	43	partial	(Q6F361) Putative malate dehydrogenase (Hypothetical protein) (Os05g0574400 protein) - Oryza sativa (japonica cultivar-group)
chr3.CM0282.780.nc	100	partial	unknown protein
chr3.CM0396.400.nd	49	partial	(Q9FEE2) Tonneau 2 (Hypothetical protein At5g18580) - Arabidopsis thaliana (Mouse-ear cress)
chr3.CM0396.520.nd	99	partial	(A3B348) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr3.CM0406.120.nd	70	partial	(Q0WV78) Hypothetical protein At1g30240 - Arabidopsis thaliana (Mouse-ear cress)
chr3.CM0406.160.nd	73	partial	(Q3ZDM4) Natural resistance-associated macrophage protein 5 (Fragment) - Arabis gemmifera
chr3.CM0406.200.nd	60	partial	(Q9C756) Hypothetical protein F12P21.4 - Arabidopsis thaliana (Mouse-ear cress)
chr3.CM0423.250.nd	91	partial	(Q7XMJ0) OSJNBb0006N15.9 protein (Hypothetical protein) (Os04g0376100 protein) - Oryza sativa (japonica cultivar-group)
chr3.CM0460.200.nd	141	partial	(Q2BFM4) Hypothetical protein - Bacillus sp. NRRL B-14911
chr3.CM0460.250.nd	54	partial	(Q1RXS8) Multicopper oxidase, type 1 - Medicago truncatula (Barrel medic)
chr3.CM0574.120.nc	31	partial	(Q9SHS2) Similar to glucose inhibited division protein A from prokaryotes - Arabidopsis thaliana (Mouse-ear cress)

chr3.CM0574.230.nd	26	partial	(A3APL3) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr3.CM0574.240.nd	70	partial	(Q40156) L.esculentum protein with leucine zipper - Solanum lycopersicum (Tomato) (Lycopersicon esculentum)
chr3.CM0590.140.nc	68	partial	(A2RVW1) At4g33480 - Arabidopsis thaliana (Mouse-ear cress)
chr3.CM0634.130.nc	70	partial	(Q9SCZ4) Receptor-protein kinase-like protein - Arabidopsis thaliana (Mouse-ear cress)
chr3.CM0634.300.nd	90	partial	(Q1STP8) Hypothetical protein - Medicago truncatula (Barrel medic)
chr3.CM0711.210.nd	77	partial	(A2YW68) Hypothetical protein - Oryza sativa (indica cultivar-group)
chr3.CM0724.290.nd	98	partial	(Q1SL99) Zinc finger, RING-type; RINGv - Medicago truncatula (Barrel medic)
chr3.CM0726.10.nd	50	partial	(O04083) Lysophospholipase isolog; 25331-24357 (At1g11090) (Putative lysophospholipase isolog) - Arabidopsis thaliana (Mouse-ear cress)
chr3.CM0996.160.nd	96	partial	(Q1S0R7) Protein kinase - Medicago truncatula (Barrel medic)
chr3.CM0996.80.nd	56	partial	(A2Q3K0) AAA ATPase; ABC transporter, transmembrane region, type 1 - Medicago truncatula (Barrel medic)
chr3.CM1220.10.nc	106	partial	(Q9SS77) Putative mRNA capping enzyme, RNA guanylyltransferase - Arabidopsis thaliana (Mouse-ear cress)
chr3.CM1220.80.nc	81	partial	(Q9FHT3) Emb|CAB69840.1 - Arabidopsis thaliana (Mouse-ear cress)
chr3.CM1570.60.nd	186	partial	(Q9FX45) RNA-binding glycine-rich protein, putative (At1g73530) - Arabidopsis thaliana (Mouse-ear cress)
chr3.LjB23H05.50.nd	89	partial	(Q9M9S4) F14L17.16 protein - Arabidopsis thaliana (Mouse-ear cress)
chr3.LjT02C24.80.nd	72	partial	(A2YN52) Hypothetical protein - Oryza sativa (indica cultivar-group)
chr3.LjT02L14.100.nd	42	partial	(Q1SCS9) Plant lipoxygenase; Lipase/lipooxygenase, PLAT/LH2 - Medicago truncatula (Barrel medic)
chr3.LjT04G21.90.nd	119	partial	(Q1SCK8) Protease-associated PA; Peptidase A22B, minor histocompatibility antigen H13 - Medicago truncatula (Barrel medic)
chr3.LjT07H20.280.nd	73	partial	(Q1SP70) Tetratricopeptide-like helical - Medicago truncatula (Barrel medic)
chr3.LjT09M07.210.nd	38	partial	(A3AMN7) Hypothetical protein - Oryza sativa (japonica cultivar-group)

chr3.LjT14J20.120.nc	96	partial	(Q8LB55) Putative aldolase - Arabidopsis thaliana (Mouse-ear cress)
chr3.LjT18H18.230.nd	82	partial	(Q1SB83) E-class P450, group I - Medicago truncatula (Barrel medic)
chr3.LjT18H18.30.nd	45	partial	(A3B5Q0) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr3.LjT26B16.100.nd	80	partial	(A3A7M6) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr3.LjT26B16.150.nd	207	partial	(Q9SB43) Hypothetical protein F24A6.30 (Hypothetical protein AT4g25190) - Arabidopsis thaliana (Mouse-ear cress)
chr3.LjT29G18.160.nd	55	partial	(O82343) Expressed protein (Hypothetical protein At2g46260) - Arabidopsis thaliana (Mouse-ear cress)
chr3.LjT33O20.180.nd	64	partial	(Q1S1X4) Hypothetical protein - Medicago truncatula (Barrel medic)
chr3.LjT34H24.210.nd	176	partial	(Q4I0Q4) Hypothetical protein - Gibberella zeae (Fusarium graminearum)
chr3.LjT34H24.220.nd	49	partial	(Q9M6R5) Meiotic asynaptic mutant 1 - Arabidopsis thaliana (Mouse-ear cress)
chr3.LjT36L08.20.nc	73	partial	(Q8W1S2) ABC transporter-like protein - Glycine max (Soybean)
chr3.LjT39G24.140.nd	115	partial	(Q9LJM0) Gb|AAD50048.1 - Arabidopsis thaliana (Mouse-ear cress)
chr3.LjT39G24.180.nd	55	partial	unknown protein
chr3.LjT39G24.40.nd	87	partial	(Q5JL21) Hypothetical protein P0459B04.11 - Oryza sativa (japonica cultivar-group)
chr3.LjT39G24.60.nd	70	partial	(Q1SS74) C2 - Medicago truncatula (Barrel medic)
chr3.LjT40O07.100.nc	63	partial	(Q9ZWJ0) DNA binding zinc finger protein (Pspzf) (Fragment) - Pisum sativum (Garden pea)
chr3.LjT42K05.60.nd	47	partial	(Q1H5B6) At5g42970 - Arabidopsis thaliana (Mouse-ear cress)
chr3.LjT46L11.130.nc	44	partial	(Q9LTX1) Similarity to poly(A)-binding protein - Arabidopsis thaliana (Mouse-ear cress)
chr3.LjT46L11.60.nc	169	partial	(Q66GR3) At2g42280 (Putative bHLH transcription factor) - Arabidopsis thaliana (Mouse-ear cress)
chr3.LjT47O18.160.nc	48	partial	(O48931) ClpC - Arabidopsis thaliana (Mouse-ear cress)
chr3.LjT48P15.10.nc	52	partial	(Q9FP19) Putative nucleolar protein family A member 2 (Os06g0274200 protein) - Oryza sativa (japonica cultivar-group)
chr4.CM0003.450.nd	58	partial	(Q7XTM4) OSJNBa0033G05.21 protein (Hypothetical protein) (OSJNBa0070O11.1 protein) - Oryza sativa (japonica cultivar-group)

chr4.CM0003.600.nd	95	partial	(Q0JED6) Os04g0289800 protein (Hypothetical protein) - Oryza sativa (japonica cultivar-group)
chr4.CM0004.100.nd	48	partial	(A0A3A0) Putative ribosomal protein (Fragment) - Artemisia annua (Sweet wormwood)
chr4.CM0004.40.nd	29	partial	(Q2WFL0) Caffeoyl-CoA-O-methyltransferase - Codonopsis lanceolata
chr4.CM0006.460.nc	99	partial	(Q8LFF9) Hypothetical protein - Arabidopsis thaliana (Mouse-ear cress)
chr4.CM0006.530.nc	60	partial	unknown protein
chr4.CM0006.650.nd	52	partial	(A2Q3Z1) Tac7077, putative - Medicago truncatula (Barrel medic)
chr4.CM0006.70.nd	64	partial	(Q1RTL8) IMP dehydrogenase/GMP reductase - Medicago truncatula (Barrel medic)
chr4.CM0007.390.nc	34	partial	(Q2QME5) Eukaryotic translation initiation factor 2 gamma subunit, putative, expressed (Hypothetical protein) (Os12g0607100 protein) - Oryza sativa (japonica cultivar-group)
chr4.CM0007.540.nc	78	partial	(Q2PYX9) Glycoprotein endopeptidase-like protein - Solanum tuberosum (Potato)
chr4.CM0007.850.nd	121	partial	(Q1EPA1) Paired amphipathic helix repeat-containing protein / transcription regulator-related - Musa acuminata (Banana)
chr4.CM0042.1200.nc	44	partial	(Q9ZTW6) Histidyl-tRNA synthetase (EC 6.1.1.21) (Fragment) - Triticum aestivum (Wheat)
chr4.CM0042.1730.nd	47	partial	(Q1SRY8) RNA-binding region RNP-1 (RNA recognition motif) - Medicago truncatula (Barrel medic)
chr4.CM0042.1770.nd	63	partial	(P93881) Ribulose 1,5-biphosphate carboxylase large subunit (Fragment) - Hippocrepis emerus (Scorpion senna) (Coronilla emerus)
chr4.CM0042.670.nd	125	partial	(Q9FHD2) Kinesin-like protein - Arabidopsis thaliana (Mouse-ear cress)
chr4.CM0042.720.nd	54	partial	(Q9LS54) Gb|AAF16598.1 (At3g18360) - Arabidopsis thaliana (Mouse-ear cress)
chr4.CM0046.340.nd	47	partial	(Q8S4X1) UOS1 - Pisum sativum (Garden pea)
chr4.CM0075.230.nd	36	partial	(Q8H1P5) Urease accessory protein UreD - Glycine max (Soybean)
chr4.CM0079.20.nd	74	partial	(Q3E8F9) Protein At5g46250 - Arabidopsis thaliana (Mouse-ear cress)
chr4.CM0087.1050.nc	81	partial	(Q94KD4) At1g09270/T12M4_2 (Fragment) - Arabidopsis thaliana (Mouse-ear cress)
chr4.CM0087.490.nd	75	partial	(Q9SR06) F7O18.15 protein (Hypothetical protein At3g04680) (Hypothetical protein At3g04680; F7O18.15) - Arabidopsis thaliana (Mouse-ear cress)
chr4.CM0087.90.nd	46	partial	unknown protein

chr4.CM0100.230.nd	102	partial	(Q1SCI7) AtHVA22a, 65476-64429 [imported]-Arabidopsis thaliana - Medicago truncatula (Barrel medic)
chr4.CM0100.270.nd	181	partial	(Q67UQ0) Hypothetical protein P0453H04.38 (Os06g0651300 protein) - Oryza sativa (japonica cultivar-group)
chr4.CM0126.340.nd	42	partial	(Q8VWG7) Tetratricoredoxin (Putative HSC70-interacting protein) - Arabidopsis thaliana (Mouse-ear cress)
chr4.CM0126.610.nc	120	partial	(O81662) Transcription activator - Pimpinella brachycarpa
chr4.CM0128.530.nd	95	partial	(Q7Y1B4) GAI2 (Fragment) - Glycine max (Soybean)
chr4.CM0128.610.nc	54	partial	(Q1SBL9) Beta-glucosidase, putative - Medicago truncatula (Barrel medic)
chr4.CM0131.310.nd	49	partial	(Q9LVU8) Gb|AAF27101.1 - Arabidopsis thaliana (Mouse-ear cress)
chr4.CM0131.450.nd	79	partial	(Q9MFG6) NADH dehydrogenase subunit 9 - Lupinus albus (White lupin)
chr4.CM0161.430.nd	92	partial	(Q6EM00) Beta-galactosidase (Fragment) - Sandersonia aurantiaca (Christmas-bells) (Chinese-lantern lily)
chr4.CM0170.100.nd	98	partial	(A2Q544) FAD linked oxidase, N-terminal - Medicago truncatula (Barrel medic)
chr4.CM0175.20.nd	113	partial	(Q38HS6) Transaldolase-like protein - Solanum tuberosum (Potato)
chr4.CM0175.320.nc	72	partial	(Q1RX96) Monogalactosyldiacylglycerol synthase - Medicago truncatula (Barrel medic)
chr4.CM0175.580.nd	65	partial	(Q7FAB7) OSJNBa0033H08.4 protein (Hypothetical protein) - Oryza sativa (japonica cultivar-group)
chr4.CM0175.660.nd	95	partial	(Q9STY7) Hypothetical protein T21L8.110 - Arabidopsis thaliana (Mouse-ear cress)
chr4.CM0182.580.nc	44	partial	(A3BU92) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr4.CM0227.140.nd	428	partial	(Q59UK6) Potential GRIP domain Golgi protein - Candida albicans (Yeast)
chr4.CM0227.460.nc	83	partial	(Q0WST4) Hypothetical protein At2g40550 - Arabidopsis thaliana (Mouse-ear cress)
chr4.CM0229.360.nc	413	partial	(Q1SUL5) IMP dehydrogenase/GMP reductase - Medicago truncatula (Barrel medic)
chr4.CM0229.450.nc	49	partial	(Q45FY8) Coronatine-insensitive 1 - Glycine max (Soybean)
chr4.CM0229.480.nc	332	partial	(Q4DKK2) RNA-binding protein, putative - Trypanosoma cruzi
chr4.CM0234.220.nd	168	partial	(Q8L7Q0) Hypothetical protein At1g68580 - Arabidopsis thaliana (Mouse-ear cress)

chr4.CM0234.290.nd	38	partial	(Q9FVD7) Ser/Thr specific protein phosphatase 2A A regulatory subunit alpha isoform - Medicago varia (Alfalfa)
chr4.CM0244.380.nd	67	partial	(Q84P31) Aldehyde dehydrogenase family 7 member A1 (EC 1.2.1.3) - Glycine max (Soybean)
chr4.CM0244.620.nd	101	partial	(Q9ZUN9) Hypothetical protein At2g19530 - Arabidopsis thaliana (Mouse-ear cress)
chr4.CM0244.760.nd	35	partial	(Q6EM01) Beta-galactosidase (Fragment) - Sandersonia aurantiaca (Christmas-bells) (Chinese-lantern lily)
chr4.CM0247.240.nc	79	partial	(Q9LJ87) Arabidopsis thaliana genomic DNA, chromosome 3, BAC clone:F16J14 (Hypothetical protein At3g22590) - Arabidopsis thaliana (Mouse-ear cress)
chr4.CM0247.60.nd	85	partial	(Q1SUY5) Zinc finger, CCHC-type - Medicago truncatula (Barrel medic)
chr4.CM0247.70.nd	62	partial	(Q9XEY7) Trehalase 1 GMTRE1 - Glycine max (Soybean)
chr4.CM0256.30.nd	63	partial	(Q852R1) Serine palmitoyltransferase - Lotus japonicus
chr4.CM0281.190.nc	147	partial	(Q9FF55) Protein disulphide isomerase-like protein (At5g60640) (Protein disulfide isomerase-like) - Arabidopsis thaliana (Mouse-ear cress)
chr4.CM0288.100.nd	81	partial	(O82518) Alternative oxidase - Glycine max (Soybean)
chr4.CM0288.210.nd	84	partial	unknown protein
chr4.CM0288.320.nd	94	partial	(O23485) Hypothetical protein dl4230w (Hypothetical protein AT4g16400) - Arabidopsis thaliana (Mouse-ear cress)
chr4.CM0297.30.nd	114	partial	(Q0J258) Os09g0376600 protein (Hypothetical protein) - Oryza sativa (japonica cultivar-group)
chr4.CM0297.330.nc	117	partial	(Q9SU15) Hypothetical protein T20K18.60 (At4g12710) (Hypothetical protein At4g12710) - Arabidopsis thaliana (Mouse-ear cress)
chr4.CM0307.100.nc	136	partial	(Q5Q0I8) Hypothetical protein - Arabidopsis thaliana (Mouse-ear cress)
chr4.CM0307.220.nd	96	partial	(Q8LAL0) Hypothetical protein (At4g39740) - Arabidopsis thaliana (Mouse-ear cress)
chr4.CM0387.230.nc	24	partial	(Q1SH78) K+ potassium transporter - Medicago truncatula (Barrel medic)
chr4.CM0399.300.nd	47	partial	(Q6J9S1) Putative AP2/EREBP transcription factor - Arabidopsis thaliana (Mouse-ear cress)
chr4.CM0432.80.nd	49	partial	(A3BAL6) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr4.CM0500.200.nd	168	partial	(Q84TJ9) Putative respiratory burst oxidase protein B - Arabidopsis thaliana (Mouse-ear cress)

chr4.CM0501.180.nd	35	partial	(A2XPL8) Hypothetical protein - Oryza sativa (indica cultivar-group)
chr4.CM0536.40.nd	40	partial	(Q69PH3) Putative transcription factor EREBP1 (Hypothetical protein) (Os09g0434500 protein) - Oryza sativa (japonica cultivar-group)
chr4.CM0536.50.nd	49	partial	(A2YGX9) Hypothetical protein - Oryza sativa (indica cultivar-group)
chr4.CM0558.50.nd	83	partial	(Q3ECJ3) Protein At1g63640 - Arabidopsis thaliana (Mouse-ear cress)
chr4.CM0617.150.nd	40	partial	unknown protein
chr4.CM0617.20.nd	83	partial	(Q9M0Y7) Hypothetical protein AT4g04920 - Arabidopsis thaliana (Mouse-ear cress)
chr4.CM0680.190.nc	36	partial	(Q9M0B2) Hypothetical protein AT4g30480 - Arabidopsis thaliana (Mouse-ear cress)
chr4.CM0692.470.nd	78	partial	(Q1T3I5) Hypothetical protein - Medicago truncatula (Barrel medic)
chr4.CM1334.230.nc	129	partial	(A3CJW2) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr4.CM1616.310.nc	40	partial	(Q8GWL1) Hypothetical protein At4g21320/T6K22_50 - Arabidopsis thaliana (Mouse-ear cress)
chr4.LjT06I07.10.nd	76	partial	(A2YW68) Hypothetical protein - Oryza sativa (indica cultivar-group)
chr4.LjT06I07.150.nd	102	partial	(Q1SDM6) Hypothetical protein - Medicago truncatula (Barrel medic)
chr4.LjT06I07.160.nd	54	partial	(A3A5U6) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr4.LjT16L01.150.nd	51	partial	(Q9LU88) Acetyltranferase-like protein - Arabidopsis thaliana (Mouse-ear cress)
chr4.LjT38A20.10.nd	51	partial	(Q9LP53) F28N24.7 protein (Hypothetical protein) (At1g29250/F28N24_8) - Arabidopsis thaliana (Mouse-ear cress)
chr4.LjT38A20.120.nd	95	partial	(Q7Y1B4) GAI2 (Fragment) - Glycine max (Soybean)
chr4.LjT38A20.130.nd	38	partial	(Q1SH78) K+ potassium transporter - Medicago truncatula (Barrel medic)
chr4.LjT38A20.20.nd	38	partial	(Q1SH78) K+ potassium transporter - Medicago truncatula (Barrel medic)
chr4.LjT38A20.240.nd	39	partial	(A3A380) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr5.CM0024.550.nc	140	partial	(Q5I285) Minichromosome maintenance protein - Zea mays (Maize)
chr5.CM0034.170.nd	75	partial	(Q1S4Q5) Hypothetical protein - Medicago truncatula (Barrel medic)
chr5.CM0048.480.nd	54	partial	(Q9M262) Hypothetical protein F21F14.210 (At3g62040) - Arabidopsis thaliana (Mouse-ear cress)

chr5.CM0048.50.nd	50	partial	(Q549W5) ASYMMETRIC LEAVES2-like gene 5 protein (Fragment) - Arabidopsis thaliana (Mouse-ear cress)
chr5.CM0062.10.nd	62	partial	(Q5SMZ1) Aldose 1-epimerase-like (Hypothetical protein) - Oryza sativa (japonica cultivar-group)
chr5.CM0071.280.nd	37	partial	(Q9AUZ4) Hypothetical protein OSJNBa0026O12.14 (Hypothetical protein) (Protein kinase domain containing protein, expressed) - Oryza sativa (japonica cultivar-group)
chr5.CM0071.630.nc	37	partial	(Q1RSH3) GroEL-like chaperone, ATPase - Medicago truncatula (Barrel medic)
chr5.CM0072.270.nd	50	partial	(Q9ZQ24) Expressed protein (Hypothetical protein) (Hypothetical protein At2g24440/T28I24.17) - Arabidopsis thaliana (Mouse-ear cress)
chr5.CM0077.300.nd	44	partial	(Q8LFY7) Hypothetical protein - Arabidopsis thaliana (Mouse-ear cress)
chr5.CM0077.320.nd	101	partial	(Q1SB58) At1g05960/T21E18_20 - Medicago truncatula (Barrel medic)
chr5.CM0077.410.nd	60	partial	(Q69MC9) Putative carbonic anhydrase (Os09g0464000 protein) - Oryza sativa (japonica cultivar-group)
chr5.CM0077.710.nc	38	partial	(Q403G8) Dihydroflavonol 4-reductase - Lotus japonicus
chr5.CM0089.40.nc	47	partial	(Q1RTK2) Like-Sm ribonucleoprotein-related, core - Medicago truncatula (Barrel medic)
chr5.CM0089.560.nd	76	partial	(Q9SX85) F16N3.18 protein - Arabidopsis thaliana (Mouse-ear cress)
chr5.CM0089.800.nd	54	partial	(Q1S2K6) Xanthine/uracil/vitamin C permease - Medicago truncatula (Barrel medic)
chr5.CM0096.150.nc	59	partial	(Q9SUQ2) Putative Ap2 domain protein (At4g23750) (AT4g23750/F9D16_220) - Arabidopsis thaliana (Mouse-ear cress)
chr5.CM0096.600.nd	57	partial	(Q1SQZ3) Hypothetical protein - Medicago truncatula (Barrel medic)
chr5.CM0148.450.nd	74	partial	(Q6J2K7) Protein tyrosine phosphatase - Phaseolus vulgaris (Kidney bean) (French bean)
chr5.CM0180.100.nc	56	partial	unknown protein
chr5.CM0200.1140.nc	91	partial	(Q65XE1) Hypothetical protein OJ1504_G04.13 - Oryza sativa (japonica cultivar-group)
chr5.CM0200.1510.nd	40	partial	(A3A3X7) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr5.CM0200.1610.nc	62	partial	(Q6J8W9) Cellulose synthase - Populus tremula x Populus tremuloides
chr5.CM0200.1680.nc	48	partial	(Q1SEG6) Heavy metal transport/detoxification protein - Medicago truncatula (Barrel medic)

chr5.CM0200.440.nc	112	partial	(Q9LJN4) Beta-1,4-xylosidase - Arabidopsis thaliana (Mouse-ear cress)
chr5.CM0200.460.nc	53	partial	(Q1A3R7) CASTOR protein (Fragment) - Glycine max (Soybean)
chr5.CM0200.750.nd	69	partial	(A2TLT1) BRI1-associated receptor kinase 1 - Hordeum vulgare var. distichum (Two-rowed barley)
chr5.CM0211.10.nc	108	partial	(Q9SJZ8) Putative non-LTR retroelement reverse transcriptase - Arabidopsis thaliana (Mouse-ear cress)
chr5.CM0239.300.nc	40	partial	(Q76HA7) Beta subunit of ATP synthase (Fragment) - Chlamydomonas chlorococcoides
chr5.CM0260.80.nd	63	partial	(Q8LFK0) Beta-N-acetylhexosaminidase-like protein - Arabidopsis thaliana (Mouse-ear cress)
chr5.CM0299.520.nd	49	partial	(Q8H8M5) Putative kinase - Oryza sativa (japonica cultivar-group)
chr5.CM0328.780.nd	65	partial	(Q2V3Z2) Protein At3g02510 (Hypothetical protein At3g02510) - Arabidopsis thaliana (Mouse-ear cress)
chr5.CM0344.230.nc	100	partial	(Q1RZZ2) Ribonuclease H - Medicago truncatula (Barrel medic)
chr5.CM0344.310.nc	181	partial	(A0MEQ4) Hypothetical protein (Fragment) - Arabidopsis thaliana (Mouse-ear cress)
chr5.CM0344.470.nd	42	partial	(Q9SCS2) CDPK-related protein kinase - Arabidopsis thaliana (Mouse-ear cress)
chr5.CM0344.70.nd	100	partial	(Q7XA53) Sucrose transporter - Glycine max (Soybean)
chr5.CM0345.1550.nc	68	partial	(Q84V02) Vacuolar membrane ATPase subunit c" - Citrus limon (Lemon)
chr5.CM0345.350.nd	84	partial	(A3A3D1) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr5.CM0345.480.nc	73	partial	(Q9AST4) AT4g31930/F10N7_260 - Arabidopsis thaliana (Mouse-ear cress)
chr5.CM0345.840.nc	61	partial	(Q9LXM2) CCR4-associated factor 1-like protein - Arabidopsis thaliana (Mouse-ear cress)
chr5.CM0345.850.nc	45	partial	(Q4LAW5) Putative ethylene response protein - Capsicum chinense (Scotch bonnet) (Bonnet pepper)
chr5.CM0345.900.nc	46	partial	(Q5XEZ1) At2g25300 - Arabidopsis thaliana (Mouse-ear cress)
chr5.CM0345.920.nc	22	partial	(Q94A05) Hypothetical protein At4g32120 - Arabidopsis thaliana (Mouse-ear cress)
chr5.CM0345.960.nc	31	partial	(Q6VEV1) 40S ribosomal protein S25 (Fragment) - Glycine max (Soybean)
chr5.CM0357.130.nd	50	partial	(Q1S0J0) Generic methyltransferase - Medicago truncatula (Barrel medic)
chr5.CM0456.140.nd	120	partial	(Q1SVM0) Cyclin-like F-box - Medicago truncatula (Barrel medic)

chr5.CM0456.170.nd	109	partial	(Q9FGZ3) Similarity to unknown protein - Arabidopsis thaliana (Mouse-ear cress)
chr5.CM0456.360.nd	35	partial	(Q1RYK6) Cyclic peptide transporter - Medicago truncatula (Barrel medic)
chr5.CM0456.380.nd	47	partial	(Q9FHX1) TMV resistance protein-like - Arabidopsis thaliana (Mouse-ear cress)
chr5.CM0494.90.nd	75	partial	(Q8S8Z6) Syringolide-induced protein 13-1-1 - Glycine max (Soybean)
chr5.CM0569.120.nd	48	partial	(Q4VYC7) Coiled-coil-helix-coiled-coil-helix domain containing protein - Medicago truncatula (Barrel medic)
chr5.CM0569.310.nc	57	partial	(Q6K701) Putative fibrillarin (Hypothetical protein) - Oryza sativa (japonica cultivar-group)
chr5.CM0571.50.nd	83	partial	(Q1SHX1) Oligopeptide transporter OPT superfamily - Medicago truncatula (Barrel medic)
chr5.CM0813.250.nc	46	partial	(Q0WRJ1) Predicted GPI-anchored protein - Arabidopsis thaliana (Mouse-ear cress)
chr5.CM0852.150.nd	40	partial	(A3BW27) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr5.CM0911.210.nd	139	partial	(Q9FK76) Subtilisin-like protease (Putative subtilisin) - Arabidopsis thaliana (Mouse-ear cress)
chr5.CM0911.80.nd	38	partial	unknown protein
chr5.CM0953.170.nc	47	partial	(Q9FLH8) Fructokinase 1 - Arabidopsis thaliana (Mouse-ear cress)
chr5.CM0956.180.nc	55	partial	(Q1G3Y0) Hypothetical protein - Arabidopsis thaliana (Mouse-ear cress)
chr5.CM0956.250.nd	79	partial	(Q3E9C2) Protein At5g19310 - Arabidopsis thaliana (Mouse-ear cress)
chr5.CM0956.60.nc	37	partial	unknown protein
chr5.CM1125.420.nc	78	partial	(Q9C540) Cytochrome b-561, putative (At1g26100) (Cytochrome b-561D) - Arabidopsis thaliana (Mouse-ear cress)
chr5.CM1125.460.nc	265	partial	(Q7XJE4) Metacaspase 4 - Arabidopsis thaliana (Mouse-ear cress)
chr5.CM1125.470.nc	42	partial	(A3CEV8) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr5.CM1574.20.nc	50	partial	(Q6DXR6) Putative permease - Gossypium hirsutum (Upland cotton)
chr5.LjT02I10.80.nd	65	partial	(Q8RXQ4) Hypothetical protein At1g71840 - Arabidopsis thaliana (Mouse-ear cress)
chr5.LjT08L18.140.nd	92	partial	(Q9C8N3) Hypothetical protein F7P12.4 - Arabidopsis thaliana (Mouse-ear cress)
chr5.LjT09B23.50.nd	38	partial	(Q1SH78) K+ potassium transporter - Medicago truncatula (Barrel medic)
chr5.LjT09C21.200.nd	60	partial	(Q304W7) Calcium sensing protein (Hypothetical protein) - Oryza sativa (indica cultivar-group)

chr5.LjT15D05.120.nd	88	partial	(Q0WQX8) ABC transporter-like protein - Arabidopsis thaliana (Mouse-ear cress)
chr5.LjT17D03.160.nd	43	partial	(Q1H5B6) At5g42970 - Arabidopsis thaliana (Mouse-ear cress)
chr5.LjT18P14.190.nd	44	partial	(A2YYA6) Hypothetical protein - Oryza sativa (indica cultivar-group)
chr5.LjT25B19.120.nd	102	partial	(Q9XED4) Receptor-like protein kinase homolog RK20-1 - Phaseolus vulgaris (Kidney bean) (French bean)
chr5.LjT29J15.70.nc	40	partial	(Q9LVW1) DNA mismatch repair protein MutS2-like - Arabidopsis thaliana (Mouse-ear cress)
chr5.LjT39E05.170.nd	58	partial	(Q9C6S5) Amino acid permease, putative (At1g31830) - Arabidopsis thaliana (Mouse-ear cress)
chr5.LjT41L03.40.nd	130	partial	(Q9ZSP8) Latex-abundant protein - Hevea brasiliensis (Para rubber tree)
chr5.LjT42D02.50.nd	59	partial	(Q9SL69) Expressed protein (Putative membrane protein COV) (Hypothetical protein) - Arabidopsis thaliana (Mouse-ear cress)
chr5.LjT43D06.90.nd	44	partial	(A3CAN3) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr5.LjT48O19.140.nd	54	partial	(Q9XIK0) T10O24.14 (Hypothetical protein) - Arabidopsis thaliana (Mouse-ear cress)
chr6.CM0013.530.nd	37	partial	(Q9C9P4) Putative 3-ketoacyl-ACP synthase; 47419-50803 (At1g74960/F9E10_19) (Beta-ketoacyl-ACP synthetase 2) - Arabidopsis thaliana (Mouse-ear cress)
chr6.CM0037.1140.nc	59	partial	(Q9FJA0) Gb|AAD21756.1 - Arabidopsis thaliana (Mouse-ear cress)
chr6.CM0041.400.nd	187	partial	(Q9FKJ9) Gb|AAF24606.1 - Arabidopsis thaliana (Mouse-ear cress)
chr6.CM0055.550.nd	69	partial	(Q1SZU4) Protein kinase PKN/PRK1, effector - Medicago truncatula (Barrel medic)
chr6.CM0055.570.nd	49	partial	(Q94AF2) AT5g19150/T24G5_50 - Arabidopsis thaliana (Mouse-ear cress)
chr6.CM0055.630.nd	36	partial	(Q9FMF7) 2-oxoglutarate/malate translocator (At5g64290) - Arabidopsis thaliana (Mouse-ear cress)
chr6.CM0066.300.nc	44	partial	(A3A3D1) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr6.CM0114.190.nc	67	partial	(Q2RAU6) Mpp10 protein, expressed (Hypothetical protein) (Os11g0137100 protein) - Oryza sativa (japonica cultivar-group)
chr6.CM0118.130.nd	45	partial	(Q1SGY6) Transcriptional factor B3; Auxin response factor; Aux/IAA_ARF_dimerisation - Medicago truncatula (Barrel medic)

chr6.CM0118.200.nd	52	partial	(Q9FP19) Putative nucleolar protein family A member 2 (Os06g0274200 protein) - Oryza sativa (japonica cultivar-group)
chr6.CM0139.220.nd	445	partial	(Q2PET4) Hypothetical protein - Trifolium pratense (Red clover)
chr6.CM0139.650.nd	124	partial	(A3KDM4) Multi antimicrobial extrusion family protein - Nicotiana tabacum (Common tobacco)
chr6.CM0139.720.nd	77	partial	(Q3HVK4) Ribosomal protein S6-like protein - Solanum tuberosum (Potato)
chr6.CM0314.740.nd	110	partial	unknown protein
chr6.CM0314.810.nd	82	partial	(Q1S7E5) MtN3 and saliva related transmembrane protein - Medicago truncatula (Barrel medic)
chr6.CM0420.190.nd	187	partial	(Q6KAC4) Putative X1 (Hypothetical protein) (Os02g0293300 protein) - Oryza sativa (japonica cultivar-group)
chr6.CM0472.60.nc	59	partial	(A3BKC2) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr6.CM0539.260.nd	44	partial	(A3AWH4) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr6.CM0539.470.nd	63	partial	(Q3E9D5) Protein At5g18930 (S-adenosylmethionine decarboxylase) - Arabidopsis thaliana (Mouse-ear cress)
chr6.CM0539.480.nd	130	partial	(Q1T2V3) Concanavalin A-like lectin/glucanase - Medicago truncatula (Barrel medic)
chr6.CM0686.30.nd	45	partial	(Q84WH9) Hypothetical protein At1g04780 (Fragment) - Arabidopsis thaliana (Mouse-ear cress)
chr6.CM0836.110.nd	158	partial	(Q6DT75) AT1G06530 (Fragment) - Arabidopsis lyrata subsp. petraea (Northern rock-cress) (Cardaminopsis petraea)
chr6.CM0836.150.nd	50	partial	(Q1RXX6) Ycf1 - Medicago truncatula (Barrel medic)
chr6.CM0836.70.nd	135	partial	(Q6CGV5) Similarity - Yarrowia lipolytica (Candida lipolytica)
chr6.CM0885.300.nc	59	partial	(Q9LM93) F2D10.6 (Hypothetical protein At1g20570) (At1g20575) - Arabidopsis thaliana (Mouse-ear cress)
chr6.CM1789.180.nd	59	partial	(Q1SDQ9) E-class P450, group I - Medicago truncatula (Barrel medic)
chr6.CM1789.80.nd	43	partial	(A3BSQ7) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr6.CM1829.70.nc	49	partial	(Q1S821) Zinc finger, RING-type - Medicago truncatula (Barrel medic)
chr6.LjB02K20.70.nd	92	partial	(Q94B70) Hypothetical protein F27K19_220 (Hypothetical protein At3g56040; F27K19_220) - Arabidopsis thaliana (Mouse-ear cress)

chr6.LjT02P05.160.nd	95	partial	(Q7Y1B4) GAI2 (Fragment) - Glycine max (Soybean)
chr6.LjT04E21.100.nc	114	partial	(A2X7Q0) Hypothetical protein - Oryza sativa (indica cultivar-group)
chr6.LjT04E21.130.nc	41	partial	(Q6S4R9) Allantoinase (EC 3.5.2.5) - Robinia pseudoacacia (Black locust)
chr6.LjT09E22.30.nd	346	partial	(Q1LWB7) Novel protein similar to vertebrate early endosome antigen 1, 162kD (EEA1) (Fragment) - Brachydanio rerio (Zebrafish) (Danio rerio)
chr6.LjT14A08.100.nd	44	partial	(Q1SJG9) Aminotransferase, class V - Medicago truncatula (Barrel medic)
chr6.LjT14A08.30.nd	71	partial	(Q1SKK0) Cellular retinaldehyde-binding/triple function, N-terminal - Medicago truncatula (Barrel medic)
chr6.LjT17I05.220.nd	49	partial	(Q6EP65) Hypothetical protein B1077E10.21 (Hypothetical protein) (Os09g0261400 protein) (Hypothetical protein P0638A12.10) - Oryza sativa (japonica cultivar-group)
chr6.LjT17I05.240.nd	70	partial	(Q93ZL4) At3g07700/F17A17.4 - Arabidopsis thaliana (Mouse-ear cress)
chr6.LjT17I05.60.nd	57	partial	(Q944G3) Acetyl Co-A acetyltransferase - Hevea brasiliensis (Para rubber tree)
chr6.LjT28D11.20.nc	35	partial	(Q1T0B7) Argininosuccinate synthase - Medicago truncatula (Barrel medic)
chr6.LjT30N23.20.nd	79	partial	(Q9FQ21) Putative Hs1pro-1-like receptor - Glycine max (Soybean)
chr6.LjT34E09.170.nc	136	partial	(Q9FVN2) Dual-specific kinase DSK1 - Nicotiana tabacum (Common tobacco)
chr6.LjT34N14.50.nd	115	partial	(Q1SLU2) Leucine-rich repeat, plant specific - Medicago truncatula (Barrel medic)
chr6.LjT34O10.10.nd	49	partial	(Q1SM53) Hypothetical protein - Medicago truncatula (Barrel medic)
chr6.LjT35H04.240.nd	72	partial	(O24422) Desiccation protective protein LEA5 - Glycine max (Soybean)
chr6.LjT35H04.50.nd	45	partial	(Q8S4X0) Embryo-abundant protein EMB - Pisum sativum (Garden pea)
chr6.LjT40F03.130.nd	96	partial	(O82023) N7 protein (Fragment) - Medicago truncatula (Barrel medic)
chr6.LjT45M04.10.nd	44	partial	(A3AM15) Hypothetical protein - Oryza sativa (japonica cultivar-group)
chr6.LjT45M04.30.nd	92	partial	(Q6UD75) LysM domain-containing receptor-like kinase 6 - Medicago truncatula (Barrel medic)
chr6.LjT45M04.90.nd	46	partial	(A2Q1L9) Protein kinase - Medicago truncatula (Barrel medic)
CM0325.20.nd	51	partial	(Q8LAE7) Hypothetical protein - Arabidopsis thaliana (Mouse-ear cress)
CM0385.220.nd	237	partial	(Q9FR07) P-like protein - Zea mays subsp. parviglumis (Balsas teosinte)
CM0457.110.nd	119	partial	(Q672H5) 5-alpha-reductase - Pisum sativum (Garden pea)

CM0528.10.nd	37	partial	(A3AMN7) Hypothetical protein - Oryza sativa (japonica cultivar-group)
CM0528.120.nd	66	partial	(Q94C32) AT4g37280/C7A10_80 - Arabidopsis thaliana (Mouse-ear cress)
CM0528.80.nd	83	partial	(Q5I190) Beta-galactosidase - Prunus persica (Peach)
CM0547.190.nd	47	partial	(Q6Q3H4) Fructokinase - Citrus unshiu (Satsuma orange)
CM0547.80.nc	53	partial	(Q2MGR2) SGS; HSP20-like chaperone - Medicago truncatula (Barrel medic)
CM0601.210.nd	246	partial	(Q9LU79) Gb|AAF21150.1 - Arabidopsis thaliana (Mouse-ear cress)
CM0905.150.nd	78	partial	(A2Q222) Tetratricopeptide-like helical - Medicago truncatula (Barrel medic)
CM1102.10.nd	59	partial	(A3AB26) Hypothetical protein - Oryza sativa (japonica cultivar-group)
CM1102.250.nd	90	partial	(Q1PG93) Antiporter (Fragment) - Striga asiatica
CM1102.50.nd	38	partial	(Q8RW11) Putative glycine rich protein - Rumex obtusifolius (Bitter dock)
CM1324.170.nd	64	partial	(Q1SGW8) T29M8.1/T29M8.1-related - Medicago truncatula (Barrel medic)
CM1489.80.nc	48	partial	(Q59IV6) Plastidic phosphate translocator-like protein1 - Mesembryanthemum crystallinum (Common ice plant)
CM1729.150.nc	117	partial	(Q2HUC6) ELM2; AT-rich interaction region; Homeodomain-related - Medicago truncatula (Barrel medic)
LjB10M19.50.nd	215	partial	(Q6L4C0) Putative zinc finger protein, identical - Solanum demissum (Wild potato)
LjB12O06.20.nc	65	partial	(Q1SKK0) Cellular retinaldehyde-binding/triple function, N-terminal - Medicago truncatula (Barrel medic)
LjB16I02.10.nc	38	partial	(Q8H0U0) T-complex polypeptide 1 homologue - Arabidopsis thaliana (Mouse-ear cress)
LjB16I02.30.nc	144	partial	(Q9S851) Hypothetical protein F14G6.2 (Cup-shaped cotyledon 3) (Hypothetical protein F15M4.8) - Arabidopsis thaliana (Mouse-ear cress)
LjB18I11.90.nd	115	partial	(Q7XZD0) Isoflavonoid glucosyltransferase - Glycyrrhiza echinata (Licorice)
LjB18O14.140.nd	112	partial	(Q6L3K4) Myosin heavy chain-like protein, putative - Solanum demissum (Wild potato)
LjB25I10.30.nd	59	partial	(Q1SDQ9) E-class P450, group I - Medicago truncatula (Barrel medic)
LjT01E03.40.nd	91	partial	(Q1SST9) ABC transporter, transmembrane region - Medicago truncatula (Barrel medic)
LjT01E03.70.nd	72	partial	(Q1SEN8) Cyclic peptide transporter - Medicago truncatula (Barrel medic)

LjT01G11.180.nd	29	partial	(Q6A196) Ferritin - Conyza canadensis (Canadian horseweed)
LjT01G11.50.nd	51	partial	(Q097J8) Alkyl hydroperoxide reductase/ Thiol specific antioxidant/ Mal allergen - Stigmatella aurantiaca DW4/3-1
LjT01K14.90.nd	42	partial	(Q9SI32) Expressed protein (Hypothetical protein At2g04940) - Arabidopsis thaliana (Mouse-ear cress)
LjT01P07.180.nd	34	partial	(Q8LK61) Nonphosphorylating glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.9) - Triticum aestivum (Wheat)
LjT01P07.50.nd	96	partial	(Q4ZH67) High mobility group protein - Cucumis sativus (Cucumber)
LjT01P07.60.nd	119	partial	(Q41026) HMG 1 protein - Pisum sativum (Garden pea)
LjT02K08.100.nd	37	partial	(Q40206) RAB1X - Lotus japonicus
LjT02K08.190.nd	48	partial	(Q1T104) Zinc finger, RING-type; Zinc finger, CHY-type - Medicago truncatula (Barrel medic)
LjT02N03.90.nd	47	partial	(Q8MGD2) Ribulose bisphosphate carboxylase large subunit (Fragment) - Colysis wrightii
LjT03D12.100.nd	107	partial	(Q6ZEZ2) Putative ribose-5-phosphate isomerase (Hypothetical protein) (Os07g0176900 protein) - Oryza sativa (japonica cultivar-group)
LjT03D14.170.nd	53	partial	(Q6R2J8) Strubbelig receptor family 8 - Arabidopsis thaliana (Mouse-ear cress)
LjT03E06.30.nd	49	partial	(A3BAL6) Hypothetical protein - Oryza sativa (japonica cultivar-group)
LjT03K24.160.nd	241	partial	(Q8GT65) Serpin-like protein (Fragment) - Citrus paradisi (Grapefruit)
LjT03L03.130.nd	48	partial	(Q9FKI9) Emb|CAB86085.1 - Arabidopsis thaliana (Mouse-ear cress)
LjT04C06.160.nd	60	partial	(Q1A3R7) CASTOR protein (Fragment) - Glycine max (Soybean)
LjT04C06.220.nd	101	partial	(Q9SZE4) Hypothetical protein F19B15.190 (Hypothetical protein At4g29160; F19B15.190) (Hypothetical protein AT4g29160) - Arabidopsis thaliana (Mouse-ear cress)
LjT04D09.210.nd	66	partial	(Q05JG2) ABA 8'-hydroxylase1 (Hypothetical protein) - Oryza sativa (japonica cultivar-group)
LjT04D09.50.nd	60	partial	(Q1A3R7) CASTOR protein (Fragment) - Glycine max (Soybean)
LjT04I16.50.nd	96	partial	(Q8S532) Cytosolic aldehyde dehydrogenase RF2C - Zea mays (Maize)
LjT05D15.230.nd	56	partial	(Q672Q7) Hypothetical protein precursor - Solanum lycopersicum (Tomato) (Lycopersicon esculentum)

LjT05D15.80.nd	62	partial	(Q7XV33) OSJNBa0086B14.26 protein (Hypothetical protein) - Oryza sativa (japonica cultivar-group)
LjT06C12.180.nd	50	partial	(Q8H856) Hypothetical protein OJ1626B05.1 (Hypothetical protein) (Os03g0226600 protein) (Expressed protein) - Oryza sativa (japonica cultivar-group)
LjT06M01.50.nd	83	partial	(Q9M0Y7) Hypothetical protein AT4g04920 - Arabidopsis thaliana (Mouse-ear cress)
LjT06N06.290.nd	131	partial	(Q1SSS7) Plastocyanin-like - Medicago truncatula (Barrel medic)
LjT06P13.140.nd	81	partial	(A2Y7K0) Hypothetical protein - Oryza sativa (indica cultivar-group)
LjT06P13.180.nd	104	partial	(Q9FM79) Similarity to pectin methylesterase (Quartet1) - Arabidopsis thaliana (Mouse-ear cress)
LjT07B02.10.nd	82	partial	unknown protein
LjT07B02.130.nd	41	partial	(Q5JNF3) Hypothetical protein P0435H01.26 (Os01g0730500 protein) - Oryza sativa (japonica cultivar-group)
LjT07C14.10.nd	69	partial	(Q9LZ77) Hypothetical protein T32M21_80 - Arabidopsis thaliana (Mouse-ear cress)
LjT07C14.130.nd	35	partial	(Q1SUS8) Copper-resistance protein CopA - Medicago truncatula (Barrel medic)
LjT07J01.140.nd	41	partial	(Q1SF66) C2 - Medicago truncatula (Barrel medic)
LjT07P16.210.nd	56	partial	(A1K601) Probable GTP-binding protein - Azoarcus sp. (strain BH72)
LjT07P16.80.nd	38	partial	(Q9FLQ8) Similarity to unknown protein - Arabidopsis thaliana (Mouse-ear cress)
LjT08D05.180.nd	26	partial	unknown protein
LjT09A12.40.nd	55	partial	(Q8LJJ8) Pentatricopeptide (PPR) repeat-containing protein-like (Hypothetical protein) - Oryza sativa (japonica cultivar-group)
LjT09C09.110.nd	53	partial	(Q9FHR5) Similarity to COP1-interacting protein 7 - Arabidopsis thaliana (Mouse-ear cress)
LjT09C09.70.nd	60	partial	(Q3EA29) Protein At4g14746 - Arabidopsis thaliana (Mouse-ear cress)
LjT09F05.90.nd	32	partial	(Q7XAS4) Transaldolase - Gossypium hirsutum (Upland cotton) (Gossypium mexicanum)
LjT09F21.10.nc	102	partial	(Q0JQC4) Os01g0170400 protein - Oryza sativa (japonica cultivar-group)
LjT09F21.40.nc	346	partial	(Q8NZA4) Streptococcal protective antigen - Streptococcus pyogenes serotype M18
LjT09I09.150.nd	66	partial	(Q8L9T6) Putativepod-specific dehydrogenase SAC25 - Arabidopsis thaliana (Mouse-ear cress)

LjT09K03.150.nd	44	partial	(Q84P31) Aldehyde dehydrogenase family 7 member A1 (EC 1.2.1.3) - Glycine max (Soybean)
LjT10B22.90.nd	51	partial	(Q8LD39) Ribsomal protein-like (At5g09770) - Arabidopsis thaliana (Mouse-ear cress)
LjT10D02.110.nd	70	partial	(Q4JF74) Topoisomerase II - Scutellaria baicalensis (Baical skullcap)
LjT10E17.160.nd	104	partial	(Q682R0) Hypothetical protein At2g06040 - Arabidopsis thaliana (Mouse-ear cress)
LjT10F13.70.nd	74	partial	(Q1T2A0) Hypothetical protein - Medicago truncatula (Barrel medic)
LjT10F13.80.nd	124	partial	(O80986) Hypothetical protein At2g26110 (At2g26110) - Arabidopsis thaliana (Mouse-ear cress)
LjT10I07.150.nd	104	partial	(Q30D01) Putative 3-dehydroquinate synthase - Fagus sylvatica (Beechnut)
LjT10J09.20.nd	89	partial	(A3BCR2) Hypothetical protein - Oryza sativa (japonica cultivar-group)
LjT10O10.120.nd	46	partial	(Q6UA11) Fiber NTGP1-related protein - Gossypium barbadense (Sea-island cotton) (Egyptian cotton)
LjT11A15.30.nc	146	partial	(Q40899) Zinc-finger protein - Petunia hybrida (Petunia)
LjT11K12.120.nc	46	partial	(Q0DKR7) Os05g0147500 protein - Oryza sativa (japonica cultivar-group)
LjT12E12.90.nd	45	partial	(A0NMN4) Ribose-5-phosphate isomerase A (EC 5.3.1.6) - Stappia aggregata IAM 12614
LjT13F18.100.nd	32	partial	(Q1RYZ9) Glycoside hydrolase, family 1 - Medicago truncatula (Barrel medic)
LjT13N04.130.nd	72	partial	(Q9C6Y5) Nucellin, putative - Arabidopsis thaliana (Mouse-ear cress)
LjT13N04.160.nd	87	partial	(Q1RWD2) Peptidase aspartic, active site - Medicago truncatula (Barrel medic)
LjT13N04.30.nd	100	partial	(Q19TV8) UDP-glucose pyrophosphorylase (EC 2.7.7.9) - Cucumis melo (Muskmelon)
LjT13N04.90.nd	104	partial	(Q9LT14) Genomic DNA, chromosome 3, P1 clone: MPN9 - Arabidopsis thaliana (Mouse-ear cress)
LjT14D09.30.nc	28	partial	(Q9FJL3) Peptidylprolyl isomerase - Arabidopsis thaliana (Mouse-ear cress)
LjT14H02.200.nd	51	partial	(A2ZXL0) Hypothetical protein - Oryza sativa (japonica cultivar-group)
LjT14H02.220.nd	49	partial	(Q9LZ63) 8-amino-7-oxononanoate synthase-like protein - Arabidopsis thaliana (Mouse-ear cress)
LjT15A10.120.nd	74	partial	(Q8LPF0) At1g73960/F2P9_17 - Arabidopsis thaliana (Mouse-ear cress)
LjT15B14.50.nd	38	partial	(Q1SH78) K+ potassium transporter - Medicago truncatula (Barrel medic)
LjT15N18.230.nd	46	partial	(Q84WP5) Hypothetical protein At2g36330 - Arabidopsis thaliana (Mouse-ear cress)

LjT15N18.290.nd	34	partial	(A2ZND1) Hypothetical protein - Oryza sativa (japonica cultivar-group)
LjT16E14.120.nc	30	partial	(Q93VQ6) At1g07080/F10K1_15 - Arabidopsis thaliana (Mouse-ear cress)
LjT17L12.210.nd	33	partial	(Q1T3E8) Helix-turn-helix, AraC type; NAD-binding site; Fumarate lyase - Medicago truncatula (Barrel medic)
LjT17L12.70.nd	81	partial	(Q1SEH9) Carotenoid oxygenase - Medicago truncatula (Barrel medic)
LjT18K22.10.nc	80	partial	(Q8GW29) Putative lysine decarboxylase (At5g06300) - Arabidopsis thaliana (Mouse-ear cress)
LjT18L24.160.nd	57	partial	(Q1RU64) Thioredoxin fold - Medicago truncatula (Barrel medic)
LjT18N19.100.nd	164	partial	(Q1SUG8) Hypothetical protein - Medicago truncatula (Barrel medic)
LjT19A14.40.nd	97	partial	(Q9AXU2) Chloroplast translational elongation factor Tu - Pelargonium graveolens (rose geranium)
LjT19A14.80.nd	45	partial	(Q43611) Hypothetical protein (Fragment) - Phoenix dactylifera (Date palm)
LjT19F24.10.nd	33	partial	(Q9SJI9) Expressed protein (At2g42670) - Arabidopsis thaliana (Mouse-ear cress)
LjT19N22.20.nd	79	partial	(Q94KU0) ATP8 - Arabidopsis thaliana (Mouse-ear cress)
LjT20A21.40.nc	45	partial	(Q9FGZ7) Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K5J14 - Arabidopsis thaliana (Mouse-ear cress)
LjT21I06.190.nd	44	partial	(A3A694) Hypothetical protein - Oryza sativa (japonica cultivar-group)
LjT23J20.50.nc	34	partial	(Q1T5S4) Cellular retinaldehyde-binding/triple function, N-terminal - Medicago truncatula (Barrel medic)
LjT24E04.20.nc	175	partial	(Q8L607) Hypothetical protein At2g41670 (Short integuments 2) - Arabidopsis thaliana (Mouse-ear cress)
LjT24M05.180.nc	55	partial	(Q40221) Protein containing C-terminal RING-finger (RING-finger protein) - Lotus japonicus
LjT28H08.20.nd	124	partial	(A0MFJ0) Hypothetical protein (Fragment) - Arabidopsis thaliana (Mouse-ear cress)
LjT28K11.110.nd	71	partial	(A3BBL1) Hypothetical protein - Oryza sativa (japonica cultivar-group)
LjT28K11.190.nd	49	partial	(A3AM99) Hypothetical protein - Oryza sativa (japonica cultivar-group)
LjT28K11.220.nd	72	partial	(Q0D810) Os07g0192300 protein (Fragment) - Oryza sativa (japonica cultivar-group)
LjT28K11.230.nd	29	partial	(A3AM99) Hypothetical protein - Oryza sativa (japonica cultivar-group)

LjT28K11.250.nd	34	partial	unknown protein
LjT28K11.40.nd	37	partial	(Q1SGN8) GMC oxidoreductase - Medicago truncatula (Barrel medic)
LjT29B06.110.nd	46	partial	(Q2V3T4) Protein At3g23600 - Arabidopsis thaliana (Mouse-ear cress)
LjT29P04.200.nd	38	partial	(Q39880) Mitotic cyclin b1-type - Glycine max (Soybean)
LjT29P04.310.nd	78	partial	(Q39880) Mitotic cyclin b1-type - Glycine max (Soybean)
LjT30M06.40.nd	54	partial	(A3CHF8) Hypothetical protein - Oryza sativa (japonica cultivar-group)
LjT30N04.260.nd	85	partial	(Q53NE3) Histone H3-maize - Oryza sativa (japonica cultivar-group)
LjT30N04.60.nd	70	partial	(Q1RVC0) Sterol desaturase - Medicago truncatula (Barrel medic)
LjT30N18.40.nd	100	partial	(O80798) T8F5.4 protein (At1g65270) (Expressed protein) - Arabidopsis thaliana (Mouse-ear cress)
LjT30N24.230.nd	62	partial	(Q8H6S9) Transcription factor TSRF1 - Solanum lycopersicum (Tomato) (Lycopersicon esculentum)
LjT30N24.60.nd	53	partial	(A3B132) Hypothetical protein - Oryza sativa (japonica cultivar-group)
LjT31F12.10.nd	40	partial	(Q1SUA2) Proteasome component region PCI - Medicago truncatula (Barrel medic)
LjT31F12.180.nd	95	partial	(Q1S230) Protease-associated PA; Proteinase inhibitor I9, subtilisin propeptide - Medicago truncatula (Barrel medic)
LjT31J09.90.nd	142	partial	(A0PGA1) Mitogen-activated protein kinase kinase kinase - Vitis vinifera (Grape)
LjT31M07.20.nd	152	partial	(A3A498) Hypothetical protein - Oryza sativa (japonica cultivar-group)
LjT32E09.70.nd	57	partial	(Q4L0H4) Membrane acyl-CoA binding protein - Agave americana (Century plant)
LjT32E09.90.nd	53	partial	(Q1T4J5) AT5g18400/F20L16_120 - Medicago truncatula (Barrel medic)
LjT33K05.100.nd	74	partial	(Q9LY31) Palmitoyl-protein thioesterase-like - Arabidopsis thaliana (Mouse-ear cress)
LjT34B08.20.nd	55	partial	(Q9FF29) Receptor serine/threonine kinase - Arabidopsis thaliana (Mouse-ear cress)
LjT34K24.210.nd	44	partial	(O49627) NifU-like protein (Fe-S scaffold protein 1) (AT4g22220/T10I14_50) - Arabidopsis thaliana (Mouse-ear cress)
LjT34L14.50.nc	189	partial	(Q9M551) Polyubiquitin - Populus tremula x Populus tremuloides
LjT35D08.150.nd	149	partial	(Q1EMR5) HMG-protein (Fragment) - Plantago major (Common plantain)

LjT35D08.70.nd	33	partial	(Q9M024) Hypothetical protein F7A7_20 (At5g01500/F7A7_20) - Arabidopsis thaliana (Mouse-ear cress)
LjT35G18.150.nd	57	partial	(Q41399) Chalcone reductase - Sesbania rostrata
LjT35M05.30.nd	61	partial	(A2WMQ2) Hypothetical protein - Oryza sativa (indica cultivar-group)
LjT35M05.40.nd	91	partial	(Q9SHG7) F20D23.22 protein (At1g17080/F6I1.24) (F6I1.24/F6I1.24) - Arabidopsis thaliana (Mouse-ear cress)
LjT36B17.170.nd	85	partial	(Q494P4) At2g40070 (En/Spm-like transposon protein) - Arabidopsis thaliana (Mouse-ear cress)
LjT36B17.180.nd	413	partial	(Q1SJP2) Hypothetical protein - Medicago truncatula (Barrel medic)
LjT36B17.190.nd	48	partial	(Q941F3) AT4g01710/T15B16_22 - Arabidopsis thaliana (Mouse-ear cress)
LjT36L22.80.nd	190	partial	(Q947E3) Resistance gene analog NBS5 (Fragment) - Helianthus annuus (Common sunflower)
LjT37C05.150.nd	42	partial	(Q6IDB3) At3g09860 (Hypothetical protein At3g09860) - Arabidopsis thaliana (Mouse-ear cress)
LjT37D10.290.nd	62	partial	(Q9ZQP1) Expressed protein (Hypothetical protein At2g35680) (Putative dual specificity phosphatase) - Arabidopsis thaliana (Mouse-ear cress)
LjT37O09.20.nd	54	partial	(Q8H1A2) Mini-chromosome maintenance protein MCM3 - Pisum sativum (Garden pea)
LjT37O09.50.nd	56	partial	(A3AVL1) Hypothetical protein - Oryza sativa (japonica cultivar-group)
LjT38B21.260.nc	78	partial	(Q9FY93) NAM-like protein (At5g13180/T19L5_140) - Arabidopsis thaliana (Mouse-ear cress)
LjT38L02.210.nd	83	partial	(Q10QN3) 1,4-dihydroxy-2-naphthoate phytyltransferase family protein, expressed (Os03g0190100 protein) - Oryza sativa (japonica cultivar-group)
LjT38P01.240.nd	65	partial	(Q8RWW3) Hypothetical protein At5g62030 - Arabidopsis thaliana (Mouse-ear cress)
LjT39F13.90.nc	89	partial	(Q94A12) AT5g47880/MCA23_22 - Arabidopsis thaliana (Mouse-ear cress)
LjT39M07.120.nd	177	partial	(Q9LZ24) Hypothetical protein T1E3_90 - Arabidopsis thaliana (Mouse-ear cress)
LjT39N06.90.nd	98	partial	(Q0WSR2) Putative peroxidase - Arabidopsis thaliana (Mouse-ear cress)
LjT40J14.130.nc	57	partial	(Q1S7V4) Ribosomal protein S3Ae - Medicago truncatula (Barrel medic)
LjT41B04.50.nd	242	partial	(Q0WU37) Trithorax 3 - Arabidopsis thaliana (Mouse-ear cress)
LjT41D10.10.nd	119	partial	(Q1S1V9) Heavy metal transport/detoxification protein - Medicago truncatula (Barrel medic)
LjT41H24.140.nd	46	partial	(Q9C805) RNA-binding protein; 68390-68829 - Arabidopsis thaliana (Mouse-ear cress)

LjT41H24.230.nd	38	partial	(Q9LPI5) F6N18.17 - Arabidopsis thaliana (Mouse-ear cress)
LjT41H24.40.nd	46	partial	(Q9C8M0) RNA-binding protein, putative; 40942-42923 (At1g53650) - Arabidopsis thaliana (Mouse-ear cress)
LjT41H24.50.nd	75	partial	(Q3MB78) Photosystem II reaction centre protein PsbA/D1 - Anabaena variabilis (strain ATCC 29413 / PCC 7937)
LjT41N19.100.nd	51	partial	(Q1SR63) Blue (Type 1) copper domain - Medicago truncatula (Barrel medic)
LjT42G13.110.nd	229	partial	(Q7XP86) OSJNBa0021F22.14 protein - Oryza sativa (japonica cultivar-group)
LjT42G13.60.nd	41	partial	(Q6RFM6) NADH dehydrogenase subunit F (Fragment) - Rhigozum madagascariense
LjT43F20.100.nd	51	partial	(Q40210) RAB5B - Lotus japonicus
LjT43K05.100.nd	46	partial	(Q659H9) Putative histidine-containing phosphotransfer protein 1 - Populus canadensis (Carolina poplar)
LjT43N20.80.nc	62	partial	(Q1S278) Proteinase inhibitor I13, potato inhibitor I - Medicago truncatula (Barrel medic)
LjT44F11.60.nd	53	partial	(O49653) Glycoprotein endopeptidase - like protein - Arabidopsis thaliana (Mouse-ear cress)
LjT44F13.200.nd	34	partial	(A3BJ19) Hypothetical protein - Oryza sativa (japonica cultivar-group)
LjT44J06.190.nd	80	partial	(A3BW27) Hypothetical protein - Oryza sativa (japonica cultivar-group)
LjT44J06.20.nd	110	partial	(Q7XTT6) OSJNBa0058K23.17 protein - Oryza sativa (japonica cultivar-group)
LjT44J06.200.nd	35	partial	(Q7XTT6) OSJNBa0058K23.17 protein - Oryza sativa (japonica cultivar-group)
LjT44J06.250.nd	54	partial	(A4GGE1) Hypothetical protein ycf2a - Phaseolus vulgaris (Kidney bean) (French bean)
LjT44J06.270.nd	50	partial	(Q9M8X2) T6K12.22 protein - Arabidopsis thaliana (Mouse-ear cress)
LjT44L11.100.nd	68	partial	(A0MEE7) Hypothetical protein (Fragment) - Arabidopsis thaliana (Mouse-ear cress)
LjT46A12.10.nd	50	partial	(A3C9G1) Hypothetical protein - Oryza sativa (japonica cultivar-group)
LjT46F23.150.nd	50	partial	(A2Q5T5) Longin-like - Medicago truncatula (Barrel medic)
LjT46I09.10.nd	54	partial	(Q9LKB1) Uroporphyrinogen decarboxylase (At3g14930) - Arabidopsis thaliana (Mouse-ear cress)
LjT47B05.130.nd	102	partial	(Q5U9E3) Stress kinase (Serine/threonine protein kinase, active site) - Medicago truncatula (Barrel medic)

LjT47D03.200.nd	131	partial	(Q9FL17) Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MSN9 - Arabidopsis thaliana (Mouse-ear cress)
LjT47D03.90.nd	45	partial	(Q9FLS5) Gb|AAC80624.1 (NpGUT1 homolog) - Arabidopsis thaliana (Mouse-ear cress)
LjT47I02.90.nd	71	partial	(A3ADZ9) Hypothetical protein - Oryza sativa (japonica cultivar-group)
LjT48C16.10.nd	91	partial	(Q94KU0) ATP8 - Arabidopsis thaliana (Mouse-ear cress)
LjT48C16.120.nd	45	partial	(Q8RXM5) Hypothetical protein At5g47420 - Arabidopsis thaliana (Mouse-ear cress)
LjSGA_003135.1	69	partial	(Q3EAF1) Protein At3g63460
LjSGA_003424.1.1	47	partial	(Q9M0L9) Hypothetical protein AT4g18640
LjSGA_003590.1.1	51	partial	(Q2HUA6) Pathogenesis-related transcriptional factor and ERF
LjSGA_004063.1	45	partial	(Q5YGP7) PLETHORA2 (At1g51190)
LjSGA_004764.2	147	partial	(Q500V5) At1g09320
LjSGA_004787.1	51	partial	(O04472) F5I14.8 protein
LjSGA_004788.2.1	43	partial	(Q9CA89) Hypothetical protein F19K16.18
LjSGA_004789.1.1	63	partial	(Q9CA89) Hypothetical protein F19K16.18
LjSGA_004790.1	74	partial	(Q9CA89) Hypothetical protein F19K16.18
LjSGA_004953.1	59	partial	(Q2Z1Y8) 1-acyl-sn-glycerol-3-phosphate acyltransferase
LjSGA_004972.2	79	partial	(Q3L0K1) Cysteine proteinase
LjSGA_005337.1.1	63	partial	(Q6TNI9) UDP-D-apiose/UDP-D-xylose synthase
LjSGA_005512.1.1	73	partial	(Q8LEI6) Receptor-like protein kinase
LjSGA_005728.1	46	partial	(Q3EB73) Protein At3g13080
LjSGA_005832.1	44	partial	(Q8RYM1) MRNA-associated protein mrnp41-like
LjSGA_006300.2	247	partial	(P93716) Tapetum-specific zinc finger protein 1
LjSGA_006682.1	47	partial	(Q9SYM4) Trehalose-6-phosphate synthase
LjSGA_006938.1	51	partial	(Q5VRW3) Hypothetical protein P0013F10.15
LjSGA_007069.1	58	partial	(Q9SSC0) F18B13.27 protein (At1g80190)

LjSGA_007278.2	35	partial	(Q8GXY6) Hypothetical protein At1g05270/YUP8H12_12 (Hypothetical protein At1g05270)
LjSGA_007491.1	66	partial	(Q9ASU9) At1g07930/T6D22_3
LjSGA_007535.2	61	partial	(Q6Z7F0) Putative ATP-dependent Clp protease ATP-binding subunit ClpX1 (CLPX)
LjSGA_007606.1	84	partial	(Q9M0Z3) Putative potassium transporter
LjSGA_007607.1	42	partial	(Q40541) Protein kinase
LjSGA_007607.1.1	45	partial	(Q9FG16) Selenium-binding protein-like
LjSGA_007638.2	39	partial	(Q4QWQ5) Calmodulin
LjSGA_007640.1	34	partial	(Q4QWQ5) Calmodulin
LjSGA_007643.1.1	76	partial	(Q30D01) Putative 3-dehydroquinate synthase
LjSGA_008276.1	84	partial	(Q84PE0) AKIN betagamma
LjSGA_008284.1	69	partial	(O23544) Hypothetical protein AT4g17000
LjSGA_008317.1	161	partial	(Q6PEA8) Rnf13 protein (Adult inner ear cDNA, RIKEN full-length enriched library, clone:F930021D16 product:ring finger protein 13, full insert sequence)
LjSGA_008438.2.1	26	partial	(Q3EB48) Protein At3g18040
LjSGA_008480.3	53	partial	(Q93XB9) Bax inhibitor 1
LjSGA_008858.1	135	partial	(Q8LPQ5) AT3g18290/MIE15_8
LjSGA_008862.1	51	partial	(Q8LDI1) Hypothetical protein (Hypothetical protein At3g19900)
LjSGA_008876.0.1	37	partial	(Q5VSC2) MutT/nudix protein-like
LjSGA_009362.2	150	partial	(Q9LXQ8) Hypothetical protein T20N10_290
LjSGA_009557.1	47	partial	(Q6H7N3) Putative DnaJ homolog, subfamily C, member 9
LjSGA_009597.2	83	partial	(Q336P4) Hypothetical protein
LjSGA_009597.2.1	54	partial	(Q3KN68) Isoflavone reductase-like protein 5
LjSGA_009600.2	211	partial	(Q67UQ0) Hypothetical protein P0453H04.38
LjSGA_009621.2.1	33	partial	(Q6AUN4) Hypothetical protein OSJNBa0040E06.6 (Hypothetical protein OJ1781_H11.24)
LjSGA_010300.1	153	partial	(Q41042) Pisum sativum L. (clone na-481-5)

LjSGA_010373.1.1	40	partial	(Q5M964) Fumarate hydratase 1
LjSGA_010569.0.1	57	partial	(O22443) Seed coat peroxidase precursor (EC 1.11.1.7)
LjSGA_010583.0.1	63	partial	(Q5M9Z8) NADH dehydrogenase subunit 4
LjSGA_010755.0.1	43	partial	(Q76JK0) Putative class I chitinase (Fragment)
LjSGA_010921.1	80	partial	(Q4PSZ0) Zinc finger (C3HC4-type RING finger) family protein
LjSGA_010927.3	34	partial	(Q43NY1) Lipoate-protein ligase B
LjSGA_010951.1	52	partial	(Q5U9D4) Plasma membrane proton ATPase 5
LjSGA_011138.2	45	partial	(Q8LDT5) Hypothetical protein
LjSGA_011167.1	95	partial	(Q9SW47) Amidase-like protein
LjSGA_011225.0.1	51	partial	(Q9FIU1) Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MRB17 (AT5g54630/MRB17_13)
LjSGA_011455.1	47	partial	(Q66GJ6) At1g05140
LjSGA_011461.1	70	partial	(Q9SVY1) Zinc finger-like protein (WIP2 protein) (At3g57670)
LjSGA_011474.1	69	partial	(Q8S369) GIA/RGA-like gibberellin response modulator (Fragment)
LjSGA_011486.1	257	partial	(Q9ZPR3) Hypothetical protein At2g03630
LjSGA_011617.2.1	56	partial	(Q9ZPW5) Putative AAA-type ATPase
LjSGA_011770.1	106	partial	(Q5VRJ9) Putative isp4 protein
LjSGA_011923.1.1	167	partial	(Q2HUI7) Cyclin-like F-box; FBD; Zinc finger, FYVE/PHD-type
LjSGA_011962.1	70	partial	(Q9FMJ6) Similarity to NOI protein
LjSGA_012015.2	37	partial	(Q5N9C8) SPP30-like
LjSGA_012020.3	43	partial	(Q9FSD7) Kdo-8-phosphate synthase (EC 4.1.2.16) (Fragment)
LjSGA_012039.1	37	partial	(Q208T5) Actin depolymerizing factor 2
LjSGA_012074.2	62	partial	(Q948F9) Putative PAP-specific phosphatase
LjSGA_012100.2	42	partial	(Q69L73) Phosphodiesterase/alkaline phosphatase D-like protein
LjSGA_012111.1.1	48	partial	(Q9ZQZ2) Putative LRR receptor-linked protein kinase (Putative LRR receptor-like protein kinase)

LjSGA_012179.1	98	partial	(Q9LPQ6) F15H18.11
LjSGA_012283.1.1	51	partial	(Q9LZA4) Hypothetical protein F8F6_270 (AT5g04060/F8F6_270)
LjSGA_012286.1	161	partial	(Q5WN03) Hypothetical protein P0001A07.6
LjSGA_012298.1	83	partial	(Q2A9K1) Hypothetical protein
LjSGA_012425.1	160	partial	(Q40366) Peroxidase precursor
LjSGA_012431.2.1	37	partial	(Q6UZD6) Plastidic alpha 1,4-glucan phosphorylase (Fragment)
LjSGA_012444.2	60	partial	(Q8W2G5) Putative alkaline alpha-galactosidase seed imbibition protein
LjSGA_012746.2.1	112	partial	unknown protein
LjSGA_012818.1	49	partial	(Q7XJS0) Putative SET-domain transcriptional regulator
LjSGA_012861.1	44	partial	(Q9FNZ1) Zfwd2 protein (Fragment)
LjSGA_012912.1	86	partial	(O65655) Hypothetical protein AT4g39680
LjSGA_012926.2	134	partial	(Q9AT32) Poly(A)-binding protein
LjSGA_013001.0.1	68	partial	(Q8L5A6) Putative mitochondrial NAD-dependent malate dehydrogenase
LjSGA_013090.3	40	partial	(Q8GTE2) Ribosomal protein RL5
LjSGA_013105.1	101	partial	(Q8GY67) Hypothetical protein At1g23340/F26F24_11 (At1g23340)
LjSGA_013134.1	66	partial	(Q6Z4N3) Putative thioredoxin
LjSGA_013141.2	62	partial	(Q6F369) Hypothetical protein OJ1268_B08.13
LjSGA_013159.3	74	partial	(Q9FVZ9) Steroid membrane binding protein, putative
LjSGA_013231.1.1	70	partial	(Q8LNT4) N-acetyl-gamma-glutamyl-phosphate reductase, putative
LjSGA_013239.2.1	58	partial	(Q8GYH7) Hypothetical protein At3g15150/F4B12_6
LjSGA_013322.0.1	73	partial	(Q94AA4) AT4g26270/T25K17_80
LjSGA_013430.1	44	partial	(Q9LDU3) Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MJK13 (MJK13.9 protein) (Hypothetical protein At3g15430)
LjSGA_013604.1	61	partial	(Q9LIP9) Glutamine-fructose-6-phosphate transaminase 2
LjSGA_013618.2	46	partial	(Q67YC0) Hypothetical protein At1g73010

LjSGA_013691.2	66	partial	(Q9FI59) Gb|AAD29063.1
LjSGA_013828.2	48	partial	(Q9SEW3) Receptor-like protein kinase (Fragment)
LjSGA_013942.0.1	55	partial	(Q49KT4) Ribosomal protein L2
LjSGA_013991.1	79	partial	(Q6K204) Hypothetical protein B1469H02.35
LjSGA_014090.1	66	partial	(Q9FIL1) Protein kinase-like protein (AT5g59010/k19m22_210)
LjSGA_014133.2	71	partial	(Q9MM55) Cytochrome oxidase subunit 2
LjSGA_014134.2	72	partial	(Q9FR27) Hexokinase (EC 2.7.1.1)
LjSGA_014307.2.1	40	partial	(Q45NN8) Hydroxyacylglutathione hydrolase (Fragment)
LjSGA_014494.1	56	partial	(Q2QLR6) Transposable element protein, putative
LjSGA_014557.1.2	38	partial	(Q6I664) HD-ZIP protein (Fragment)
LjSGA_014576.2	107	partial	(Q75LJ3) Putative flavoprotein alpha-subunit, having alternative splicing products
LjSGA_014664.1	34	partial	(Q6Z2M5) Putative small nuclear ribonucleoprotein polypeptide E
LjSGA_014812.1.1	54	partial	(Q5W915) UDP-sugar pyrophospharylase
LjSGA_014982.1.1	54	partial	(Q8LPN7) AT3g19950/MPN9_19
LjSGA_014994.0.2	54	partial	(Q9SLZ4) Retinoblastoma-related protein
LjSGA_015431.1	192	partial	(Q9FME7) Kinesin-like protein
LjSGA_015476.0.1	46	partial	(Q9XI87) F7A19.9 protein
LjSGA_015514.1	70	partial	(Q9SIV8) Putative CDC21 protein
LjSGA_015566.1.1	93	partial	(O49279) F22K20.2 protein (At1g76920) (F-box protein AtFBX3) (Hypothetical protein At1g76920; F22K20.2)
LjSGA_015629.0.1	46	partial	(Q84XA4) Aminoimidazolecarboximide ribonucleotide transformylase/inosine monophosphate cyclohydrolase
LjSGA_015674.0.1	48	partial	(Q9C584) Hypothetical protein At5g22040
LjSGA_015734.0.1	46	partial	(Q9FZJ7) F17L21.17 (Hypothetical protein) (Hypothetical protein At1g27385/F17L21.17)
LjSGA_015821.1	41	partial	(Q5JJI4) Putative TOM20

LjSGA_015831.1	44	partial	(Q9M4H0) Putative ripening-related protein
LjSGA_015880.1	231	partial	(Q9MAL4) F27F5.2
LjSGA_015963.1.1	80	partial	(Q84VX5) At4g02100
LjSGA_015981.2	157	partial	(Q27335) Poly(A)-binding protein, putative
LjSGA_016013.1	59	partial	(Q6Z6M5) Putative syntaxin-related protein(Knolle)
LjSGA_016030.0.1	50	partial	(Q2QLM1) Hypothetical protein
LjSGA_016062.0.1	35	partial	(Q5VPE9) Leucine carboxyl methyltransferase family protein-like
LjSGA_016117.1	70	partial	(Q6WB92) Enolase
LjSGA_016294.2	44	partial	(Q30CZ7) Putative chorismate synthase
LjSGA_016300.3	64	partial	(Q9LHW0) Putative esterase
LjSGA_016325.1	53	partial	(Q7F808) Similar to Arabidopsis thaliana hypothetical protein T16H5.200
LjSGA_016371.1.1	64	partial	(O82471) Protein phosphatase-2C
LjSGA_016392.3	55	partial	(Q84TV1) Nodulin-like protein
LjSGA_016393.2	73	partial	(Q9AYN8) NRK1 MAPK
LjSGA_016408.1.1	51	partial	(Q67VQ4) BolA-like
LjSGA_016410.2	140	partial	(Q940J7) Hypothetical protein
LjSGA_016412.2	54	partial	(Q6YTS7) Hypothetical protein P0419H09.23
LjSGA_016418.1	74	partial	(Q9SF45) Putative oxidoreductase
LjSGA_016443.1.1	59	partial	(Q5ZAM8) Putative prolylcarboxypeptidase, isoform 1
LjSGA_016474.1	58	partial	(Q9SIM4) 60S ribosomal protein L14
LjSGA_016533.2.1	124	partial	(Q9FWT4) F1B16.1 protein (Putative protease) (Protease, putative)
LjSGA_016550.1.1	88	partial	(Q9FIN6) GblAAD32909.1
LjSGA_016567.2	76	partial	(Q9SHG6) Similar to tuftelin-interacting protein
LjSGA_016645.1	72	partial	(Q9FFZ0) Similarity to unknown protein (Hypothetical protein) (AT5g13810/MAC12_24)
LjSGA_016749.1.1	131	partial	(O23020) T1G11.10 protein

LjSGA_016860.1.1	33	partial	(Q9C976) Hypothetical protein F5I6.3 (Hypothetical protein At1g80280)
LjSGA_016862.2	73	partial	(Q9LYD6) Hypothetical protein F15N18_150
LjSGA_016906.1.1	34	partial	(Q2MIJ5) DNA-directed RNA polymerase (EC 2.7.7.6)
LjSGA_016982.1	90	partial	(Q70CE8) Ankyrin-repeat protein (Fragment)
LjSGA_017021.1	37	partial	(Q7XWP1) OSJNBa0032B23.5 protein
LjSGA_017062.1	41	partial	(Q71G33) COP8-like protein
LjSGA_017166.1	49	partial	(Q69P78) Putative serine protease
LjSGA_017195.1	41	partial	(O23024) T1G11.14 protein (Flavin-containing monooxygenase YUCCA3) (At1g04610)
LjSGA_017266.0.1	47	partial	(Q8H0U0) T-complex polypeptide 1 homologue
LjSGA_017271.1.1	53	partial	(Q541Y5) Putative villin
LjSGA_017303.0.1	76	partial	(Q5JN27) Putative receptor-like protein kinase 1
LjSGA_017402.1	47	partial	(Q8H1T4) Putative cleavage and polyadenylation specificity factor 160 kDa subunit
LjSGA_017442.2	48	partial	(Q9SQK0) Aldehyde reductase
LjSGA_017510.1	101	partial	(Q43180) Fumarase (EC 4.2.1.2)
LjSGA_017551.1	38	partial	(Q5VS25) Putative beta 1,3 glucan synthase
LjSGA_017714.1.2	44	partial	(Q8LP18) Cullin-like protein1
LjSGA_017718.1	112	partial	(Q67XZ2) Hypothetical protein At1g48040
LjSGA_017774.1	92	partial	(Q2HW14) Zinc finger, CCCH-type; Sugar transporter superfamily
LjSGA_017795.0.1	42	partial	(Q8W4M2) Hypothetical protein F5K20.24
LjSGA_017812.1	57	partial	(Q8L5Q0) Putative invertase inhibitor (Fragment)
LjSGA_017968.1	61	partial	(Q42606) Urophorphyrin III methylase (EC 2.1.1.107) (AT5g40850/MHK7_8)
LjSGA_018018.1	41	partial	(Q9LIH7) Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:K24M9 (Hypothetical protein At3g18620)
LjSGA_018122.2	127	partial	(Q9FHC3) Genomic DNA, chromosome 5, TAC clone:K24M7 (Hypothetical protein At5g52370)
LjSGA_018152.1.1	47	partial	(Q94JV2) AT3g27050/MOJ10_14

LjSGA_018233.1	56	partial	(Q5Z6U5) Putative CCT chaperonin gamma subunit
LjSGA_018315.1	101	partial	(Q9SZP7) Disease resistance response like protein
LjSGA_018346.1	106	partial	(Q7XDY0) Transposon protein, putative, unclassified
LjSGA_018438.2	48	partial	(Q3N2E7) Ribosomal protein L18
LjSGA_018538.1	48	partial	(Q84Z07) Putative WD repeat protein
LjSGA_018653.1	63	partial	(Q9ZW93) F5A8.5 protein
LjSGA_018658.1	45	partial	(Q7XTK0) OSJNBa0020P07.4 protein
LjSGA_018818.1	387	partial	(Q6YUC5) Aminotransferase-like protein
LjSGA_018826.1	94	partial	(Q9LEP6) Hypothetical protein
LjSGA_019062.1.1	53	partial	(Q3SCM6) Cinnamoyl-CoA reductase
LjSGA_019205.1	40	partial	(Q94LX6) Putative FPPsynthase1 (Fragment)
LjSGA_019215.2	63	partial	(Q33B71) Lipase, putative
LjSGA_019347.0.1	61	partial	(Q9SAI6) F23A5.7
LjSGA_019361.3	68	partial	(Q9CAE3) Hypothetical protein F13M14.34 (Flowering locus D)
LjSGA_019537.1	47	partial	(Q9LJE4) GloEL protein; chaperonin, 60 kDa
LjSGA_019850.1	107	partial	(Q8GY73) Hypothetical protein At2g42950
LjSGA_019856.0.1	35	partial	(Q9SX85) F16N3.18 protein
LjSGA_019881.3	111	partial	(Q3E9E3) Protein At5g18700
LjSGA_019892.1.1	66	partial	(Q9SRP6) T21P5.16 protein (Hypothetical protein At3g03420)
LjSGA_019985.1	46	partial	(O65606) Hypothetical protein M7J2.80
LjSGA_020010.1	46	partial	(Q7XI67) Hypothetical protein P0034A04.101-1 (Hypothetical protein P0597G07.131-1)
LjSGA_020100.1.1	57	partial	(Q9ZR45) Alpha-N-acetylglucosaminidase
LjSGA_020183.1	52	partial	(Q9SY80) F14N23.26
LjSGA_020235.1	113	partial	(Q9XF99) Skp1 (Fragment)
LjSGA_020245.2	287	partial	(Q6H443) Putative plastid-specific ribosomal protein 2

LjSGA_020339.1	50	partial	(Q7XKV2) OSJNBa0022H21.5 protein
LjSGA_020422.1	113	partial	(Q2HUJ7) V-ATPase subunit C
LjSGA_020458.1	149	partial	(Q9LIV4) Hypothetical protein
LjSGA_020558.0.1	95	partial	(Q8VYN6) Putative pyrophosphate-fructose-6-phosphate 1-phosphotransferase
LjSGA_020559.2	75	partial	(Q7XW27) OSJNBb0062H02.4 protein
LjSGA_020560.1.1	57	partial	(Q7XJM5) Putative transcription factor IIIB 70 KD subunit (TFIIIB)
LjSGA_020568.1	81	partial	(Q6UD74) LysM domain-containing receptor-like kinase 7
LjSGA_020642.2	47	partial	(Q7X864) OSJNba0093F12.4 protein (OSJNBa0006A01.22 protein)
LjSGA_020705.1	79	partial	(Q5N909) AT hook motif-containing protein-like
LjSGA_020800.1	85	partial	(Q8LK24) SOS2-like protein kinase
LjSGA_020832.1	78	partial	(Q5YLB4) DNA gyrase B subunit
LjSGA_020853.1	46	partial	(Q9FFZ0) Similarity to unknown protein (Hypothetical protein) (AT5g13810/MAC12_24)
LjSGA_020950.1.1	67	partial	(Q9ZTA8) Homeodomain protein (Fragment)
LjSGA_020964.1	71	partial	(Q9LVU6) RNA-binding protein-like
LjSGA_021085.2	102	partial	(Q621R2) Hypothetical protein CBG02383
LjSGA_021212.1	82	partial	(Q9LJQ5) Seed maturation protein-like (At3g18260)
LjSGA_021298.1	78	partial	(Q851E0) Hypothetical protein OSJNBb0021P10.2
LjSGA_021328.2	74	partial	(Q9LNC6) F9P14.7 protein (At1g06210/F9P14_4)
LjSGA_021348.1	41	partial	(Q2QNB5) Suppressor of forked protein
LjSGA_021514.2	71	partial	(Q84TV1) Nodulin-like protein
LjSGA_021615.1.1	47	partial	(Q3E9V2) Protein At4g28088
LjSGA_021635.2	53	partial	(Q9LIR8) Gb|AAF30317.1 (Hypothetical protein At3g23880/F14O13_7) (At3g23880)
LjSGA_021669.1	90	partial	(Q9C5K6) Hypothetical protein At1g34150
LjSGA_021767.1	65	partial	(Q75G50) Hypothetical protein B1003C08.7 (Hypothetical protein OSJNBb0043H23.5)
LjSGA_021794.1	310	partial	(O97767) RBM1

LjSGA_021834.1	69	partial	(Q9FMP7) Genomic DNA, chromosome 5, P1 clone:MXC9 (At5g12160)
LjSGA_021891.1	61	partial	(Q8H1A3) Mini-chromosome maintenance protein MCM6
LjSGA_021906.1	88	partial	(O64587) Hypothetical protein At2g34690
LjSGA_022139.1	108	partial	(Q8RWE2) Trehalose-6-phosphate phosphatase (At5g51460)
LjSGA_022279.1.1	38	partial	(Q9ZVT4) F15K9.7 protein
LjSGA_022684.1	122	partial	(Q70YP7) Leafy cotyledon protein (Fragment)
LjSGA_022708.1	45	partial	(Q6L8U1) Auxin response factor 3
LjSGA_022732.1.1	69	partial	(Q8VYN8) Hypothetical protein At4g25170 (Hypothetical protein)
LjSGA_022836.1	58	partial	(Q8H808) Hypothetical protein OJ1743A09.20
LjSGA_022989.1	49	partial	(Q9SGE3) T23G18.3 (T6D22.26) (Histone H2B family protein)
LjSGA_023044.2	38	partial	(Q8RW11) Putative glycine rich protein
LjSGA_023080.1	88	partial	(Q541V7) Hypothetical protein At2g24330
LjSGA_023272.1.1	71	partial	(Q9ZTA8) Homeodomain protein (Fragment)
LjSGA_023290.1	93	partial	(Q8L4G8) C4-dicarboxylate transporter-like protein
LjSGA_023309.1	114	partial	(Q6WB92) Enolase
LjSGA_023481.1	119	partial	(Q5N7S6) Receptor serine/threonine kinase PR5K-like
LjSGA_023506.1.1	134	partial	(Q2HS67) F-box associated, putative
LjSGA_023559.1	64	partial	(Q9FGH9) Leucine zipper protein (AT5g58430/mqj2_20)
LjSGA_023585.2	70	partial	(Q7X7E9) OSJNBa0035M09.8 protein
LjSGA_023624.0.1	44	partial	(Q39890) Calmodulin
LjSGA_023686.2	119	partial	(Q8L8M4) Hypothetical protein (At5g20935)
LjSGA_023844.1	45	partial	(Q2V2T2) Protein AtMg01320 (Protein AtMg00285)
LjSGA_023881.1	71	partial	(Q9SKD8) Expressed protein (At2g46420/F11C10.11)
LjSGA_023897.2	154	partial	(Q9FPL0) Magnesium transporter protein
LjSGA_023913.2	100	partial	(Q2HSF1) WD40-like

LjSGA_024064.1	36	partial	(Q652F0) Putative ribonucleotide reductase R2
LjSGA_024208.2	262	partial	(Q9LEU3) Zinc finger-like protein
LjSGA_024216.1	60	partial	(Q8LCM8) Transcription factor TINY, putative
LjSGA_024359.1	81	partial	(Q9S9Q4) F26G16.7 protein
LjSGA_024362.1	35	partial	(Q69SU8) Putative tetratricopeptide repeat (TPR)-containing protein
LjSGA_024636.2	35	partial	(Q3EAG1) Protein At3g61870
LjSGA_024708.0.1	35	partial	(Q20CB3) Geranyl diphosphate synthase (Fragment)
LjSGA_024712.1	155	partial	(Q9LTZ4) Gb|AAF01554.1 (Hypothetical protein At3g27350)
LjSGA_024759.1	88	partial	(Q6K8D7) DNAJ heat shock N-terminal domain-containing protein-like
LjSGA_024943.0.1	49	partial	(Q6DUX2) Regulator of gene silencing
LjSGA_025019.2	48	partial	(Q6T7C9) Fiber dTDP-glucose 4-6-dehydratase (Fragment)
LjSGA_025102.1	142	partial	(Q6K7P0) Putative DNA-binding protein PD3, chloroplast
LjSGA_025173.0.1	37	partial	(Q5DW42) Phototropin
LjSGA_025273.1	68	partial	(Q9FNK3) Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MCL19 (Hypothetical protein At5g46190)
LjSGA_025310.1	153	partial	(Q9MBD3) Sa-RNase precursor
LjSGA_025379.2	51	partial	(Q84N01) Putative sucrose-H+ symporter (Fragment)
LjSGA_025597.1.1	92	partial	(Q9FPM4) Myosin subfamily VIII heavy chain
LjSGA_025670.1	42	partial	(Q75GV0) Putative leucine-rich repeat receptor kinase (Leucine Rich Repeat, putative)
LjSGA_025698.1.1	56	partial	(Q8H811) Putative leucine-rich repeat transmembrane protein kinase
LjSGA_025699.1	35	partial	(Q75KW5) Expressed protein
LjSGA_025787.0.1	114	partial	(Q3ECK2) Protein At1g62680
LjSGA_025933.1.1	124	partial	(Q9CA80) Hypothetical protein F1M20.1
LjSGA_025957.1	54	partial	(Q9M6R8) MAP kinase PsMAPK2
LjSGA_026008.1	407	partial	(Q2HUJ3) Hypothetical protein

LjSGA_026043.1	69	partial	(Q3E9C1) Protein At5g19330
LjSGA_026044.1	81	partial	(Q6Z8U6) Putative glutathione transporter
LjSGA_026072.2	98	partial	(Q9MAI7) F12M16.4
LjSGA_026097.1	38	partial	(Q8LJS0) Hypothetical protein
LjSGA_026117.0.1	52	partial	(Q6S4J3) Endo-beta-1,3-glucanase (Fragment)
LjSGA_026117.1.1	84	partial	(Q9ZP12) Glucan endo-1,3-beta-d-glucosidase precursor (EC 3.2.1.39)
LjSGA_026166.2	91	partial	(Q6XQM5) Nicotinate phosphoribosyltransferase-like protein
LjSGA_026169.1	89	partial	(Q9LJW5) Gb|AAF15936.1 (At3g28917) (Hypothetical protein)
LjSGA_026241.3	73	partial	(Q9XH70) Hypothetical protein p69RF (Fragment)
LjSGA_026248.2	48	partial	(Q8W0W5) Repressor protein
LjSGA_026304.1	42	partial	(Q6F2T2) Hypothetical protein OSJNBa0027N19.10
LjSGA_026466.1	61	partial	(Q9XFL3) Peroxidase 1 (Fragment)
LjSGA_026521.1	70	partial	(Q94BZ0) At1g50450/F11F12_20
LjSGA_026592.1	68	partial	(Q3E6T0) Protein At5g25400
LjSGA_026636.2	124	partial	(Q5ZD87) HcrVf2 protein-like
LjSGA_026697.1.1	37	partial	(Q9C9B9) Hypothetical protein F2P9.15 (At1g73980/F2P9_15)
LjSGA_026891.2	128	partial	(Q501C5) At4g38110
LjSGA_027034.1	44	partial	(Q9SRZ5) F12P19.11
LjSGA_027040.1	272	partial	(Q9LF31) Hypothetical protein T20K14_120
LjSGA_027083.1	61	partial	(Q8LA45) Hypothetical protein
LjSGA_027102.1	40	partial	(Q2R0W7) Phosphoserine phosphatase SerB, putative
LjSGA_027116.1	91	partial	(Q8GXY6) Hypothetical protein At1g05270/YUP8H12_12 (Hypothetical protein At1g05270)
LjSGA_027170.1	59	partial	(Q94EA5) Hypothetical protein P0435H01.32
LjSGA_027265.1	60	partial	(Q69WR1) Putative IDN3 protein isoform A
LjSGA_027354.2	135	partial	(Q8LM38) Putative nucleosid phosphatase (GDA1/CD39 family, putative)

LjSGA_027409.1	60	partial	(Q2PEQ5) Hypothetical protein
LjSGA_027473.1	51	partial	(Q8W0W5) Repressor protein
LjSGA_027581.0.1	40	partial	(Q9ZST9) Tic22
LjSGA_027601.1	56	partial	(O24430) Calmodulin-like domain protein kinase isoenzyme beta
LjSGA_027615.2	93	partial	(Q9SF44) Putative pathogenesis-related protein
LjSGA_027695.1.1	42	partial	(Q9FNK3) Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MCL19 (Hypothetical protein At5g46190)
LjSGA_027780.2	58	partial	(Q5DVT3) Tonoplast intrinsic protein 1;2
LjSGA_027843.1	45	partial	(O24297) Phospholipase C
LjSGA_027862.2.1	53	partial	(Q9ZU41) Predicted by genscan and genefinder (At2g01260)
LjSGA_027907.1	64	partial	(Q9XGC6) Adenosine kinase (Fragment)
LjSGA_027919.1	42	partial	(Q2QPD4) Phenylalanyl-tRNA synthetase
LjSGA_027929.1	52	partial	(Q9SXL4) Histidine kinase 1
LjSGA_028013.1	56	partial	(Q6ZB67) Hypothetical protein OJ1119_B10.8
LjSGA_028028.1	57	partial	(Q8GS60) Hypothetical protein At1g04620 (Hypothetical protein At1g04620/T1G11_12)
LjSGA_028199.2	47	partial	(Q93WX4) Suppressor of K+ transport growth defect-like protein (Fragment)
LjSGA_028201.1	134	partial	(Q9FUB4) PRLI-interacting factor A (Fragment)
LjSGA_028272.1.1	54	partial	(Q9M9E5) F3F9.21
LjSGA_028307.1	59	partial	(Q7X7H3) OSJNBa0084K20.14 protein (OSJNBa0076N16.12 protein)
LjSGA_028314.2	50	partial	(Q9SRT9) Reversibly glycosylated polypeptide-1 (At3g02230)
LjSGA_028328.2.1	35	partial	(Q8S350) Auxin-induced SAUR-like protein (Fragment)
LjSGA_028437.1	36	partial	(Q5XLE1) Immunophilin
LjSGA_028439.0.2	48	partial	(Q2V2T2) Protein AtMg01320 (Protein AtMg00285)
LjSGA_028446.1	82	partial	(O23297) Hypothetical protein dl3245w (Hypothetical protein AT4g14410) (Putative bHLH transcription factor)

LjSGA_028458.1.1	109	partial	(Q7X9H7) MADS-box protein AGL62
LjSGA_028460.1	77	partial	(Q9AQZ5) Putative heat shock protein
LjSGA_028569.1	107	partial	(Q8S7I7) Putative NAM (No apical meristem) protein (Putative NAC domain protein)
LjSGA_028691.2	95	partial	(Q84LE6) RelA-SpoT like protein RSH4 (Fragment)
LjSGA_028784.2	85	partial	(Q9SK32) Expressed protein
LjSGA_028862.1	62	partial	(Q9SR92) T16O11.14 protein (Putative rhodanese family protein)
LjSGA_028958.2	47	partial	(Q5Q0I8) Hypothetical protein
LjSGA_028975.1	85	partial	(Q7X9A9) Beta-primeverosidase (EC 3.2.1.149)
LjSGA_029024.1	67	partial	(Q9SI58) Putative nonsense-mediated mRNA decay protein
LjSGA_029050.1	67	partial	(Q9XFI7) Peroxidase (Fragment)
LjSGA_029066.1.1	44	partial	(Q6XQM5) Nicotinate phosphoribosyltransferase-like protein
LjSGA_029102.2	82	partial	(Q9S7I5) Ribosomal RNA apurinic site specific lyase
LjSGA_029164.1.1	51	partial	(Q7XPL1) OSJNBa0085I10.15 protein
LjSGA_029293.0.1	40	partial	(O63067) Aspartokinase-homoserine dehydrogenase (EC 2.7.2.4) (EC 1.1.1.3)
LjSGA_029340.2	136	partial	(Q9FG61) Protein phosphatase-2C PP2C-like
LjSGA_029412.0.1	46	partial	(Q42606) Urophorphyrin III methylase (EC 2.1.1.107) (AT5g40850/MHK7_8)
LjSGA_029417.1	138	partial	(Q9S7P3) Kinesin-like protein
LjSGA_029429.1	68	partial	(Q69TX8) Putative transmembrane protein Tmp21
LjSGA_029436.1	158	partial	(Q2MJS0) MYB transcription factor
LjSGA_029471.0.1	50	partial	(Q8VYG2) Putative galactokinase
LjSGA_029748.1	102	partial	(Q93XA7) NAC domain protein NAC1
LjSGA_029940.1	72	partial	(Q653N8) ThiF family protein-like
LjSGA_029943.1.1	30	partial	(Q5DW42) Phototropin
LjSGA_029979.1	49	partial	(Q2HTW0) Myb, DNA-binding
LjSGA_030102.1	66	partial	(Q9LFT2) Hypothetical protein F1N13_20 (Hypothetical protein At5g15880)

LjSGA_030122.2	146	partial	(Q7M4Q5) Basic proline-rich peptide IB-8a (Fragments)
LjSGA_030315.1	52	partial	(Q5D875) Calcium-dependent protein kinase CDPK1444
LjSGA_030331.1	262	partial	(Q5VME8) Putative ring finger protein 126 isoform 1
LjSGA_030437.1	73	partial	(Q2V3E1) Protein At4g27745
LjSGA_030457.1	103	partial	(Q9C662) Hypothetical protein F28B23.15
LjSGA_030458.1	395	partial	(Q6K6E5) Aminotransferase-like protein
LjSGA_030577.1	71	partial	(Q7XR01) OSJNBa0015K02.12 protein
LjSGA_030660.1.1	97	partial	(Q9LYP2) Hypothetical protein T28J14_180 (Hypothetical protein At5g07240)
LjSGA_030675.2	95	partial	(Q7XUB3) OSJNBb0032E06.7 protein
LjSGA_030819.1	99	partial	(Q84LQ3) Putative FtsH protease
LjSGA_030914.1	48	partial	(Q8RYX0) Pentatricopeptide (PPR) repeat-containing protein-like
LjSGA_030934.1	94	partial	(Q8SUM5) Hypothetical protein ECU08_1410
LjSGA_030963.2	59	partial	(Q9SU03) Hydrolase-like protein
LjSGA_030994.1	92	partial	(Q8H1F1) Hypothetical protein At3g15160
LjSGA_031018.2	43	partial	(Q3E6X2) Protein At2g01260
LjSGA_031063.0.1	52	partial	(Q5ZDI8) Hypothetical protein P0686E09.31
LjSGA_031097.1	51	partial	(Q8RZK9) Putative ARF GAP-like zinc finger-containing protein ZiGA4
LjSGA_031101.0.1	25	partial	(Q2Z2G4) AINTEGUMENTA-like protein
LjSGA_031147.1	50	partial	(Q4TYZ7) Ubiquitinating enzyme
LjSGA_031181.1	60	partial	(Q3LHL0) TATA binding protein associated factor
LjSGA_031270.1	56	partial	(Q8S8N6) Expressed protein (Hypothetical protein At2g06925) (Phospholipase A2 alpha) (Hypothetical protein)
LjSGA_031412.1	34	partial	(Q9SF20) F26K24.7 protein (Hypothetical protein At3g11780)
LjSGA_031481.1	82	partial	(Q7XMI6) OSJNBb0006N15.13 protein
LjSGA_031521.1.1	106	partial	(Q9FL41) MtN21 nodulin protein-like

LjSGA_031564.1	107	partial	(Q9NHW2) Flagelliform silk protein (Fragment)
LjSGA_031586.0.1	81	partial	(Q2PMM8) Hypothetical chloroplast RF1
LjSGA_031654.1	190	partial	(Q7XUR1) OSJNBa0084K11.3 protein
LjSGA_031711.1	55	partial	(Q2HUX9) Esterase/lipase/thioesterase
LjSGA_031729.0.1	64	partial	(Q9LPV4) F13K23.21 protein (At1g12950)
LjSGA_031826.1	115	partial	(Q9AVQ2) Cytochrome P450
LjSGA_031923.1	85	partial	(O23124) F19G10.6 protein
LjSGA_032094.1	42	partial	(Q2PS27) Translationally controlled tumor protein
LjSGA_032215.1	61	partial	(Q9SUQ2) Putative Ap2 domain protein (AT4g23750/F9D16_220) (At4g23750)
LjSGA_032263.1.1	56	partial	(Q8LC53) Hypothetical protein
LjSGA_032273.1.1	70	partial	(Q58A50) Embryonic flower 2
LjSGA_032322.1.1	43	partial	(Q5JN27) Putative receptor-like protein kinase 1
LjSGA_032337.1	53	partial	(Q8VZK6) Hypothetical protein At5g49220
LjSGA_032422.1	65	partial	(Q9M6E6) Poly(A)-binding protein
LjSGA_032471.1.1	84	partial	(Q2QD76) Cytochrome f
LjSGA_032505.1	42	partial	(Q8RXR3) Hypothetical protein At5g52070
LjSGA_032663.1	103	partial	(Q8S9U1) Hypothetical protein B1064G04.8 (Hypothetical protein B1144D11.30)
LjSGA_032692.1	110	partial	(Q4DKK2) RNA-binding protein, putative
LjSGA_032756.2	78	partial	(Q9M6R3) Constitutive photomorphogenic 11
LjSGA_032814.1	77	partial	(Q8S8I4) Predicted protein
LjSGA_032829.1	80	partial	(Q8VYX3) Sucrose transporter SUC2
LjSGA_032846.1	149	partial	(Q9FZH6) F1O19.11 protein (Hypothetical protein At1g67050) (Hypothetical protein)
LjSGA_032869.1	46	partial	(Q5D1M5) Class III HD-Zip protein 2
LjSGA_032914.1	68	partial	(Q9LXB8) Periaxin-like protein
LjSGA_033058.1.1	37	partial	(Q332W3) Photosystem II protein L (Fragment)

LjSGA_033138.1	28	partial	(Q9LPV4) F13K23.21 protein (At1g12950)
LjSGA_033176.1	91	partial	(Q546G6) Homeodomain-leucine zipper protein HAT22
LjSGA_033188.1.1	44	partial	(Q52QH3) Phenylalanine ammonia-lyase
LjSGA_033209.1	186	partial	(Q39949) Hydroxyproline-rich protein
LjSGA_033297.1.1	33	partial	(O64876) Expressed protein (Hypothetical protein At2g44420)
LjSGA_033315.1.2	88	partial	(Q9ASP8) AT3g55400/T22E16_60
LjSGA_033328.1	57	partial	(Q9ZUS4) Putative kinesin heavy chain
LjSGA_033438.1.2	45	partial	(Q6ZKB0) Hypothetical protein OJ1124_B05.23 (Hypothetical protein OJ1111_B08.14)
LjSGA_033444.1	58	partial	(Q2V2T1) Protein At4g24810
LjSGA_033642.0.1	60	partial	(Q2A9R7) Hypothetical protein
LjSGA_033665.0.1	36	partial	(Q8W515) SGT1a
LjSGA_033698.1	65	partial	(Q9SR79) T22K18.2 protein
LjSGA_033703.2	53	partial	(Q7X9B3) 9/13 hydroperoxide lyase
LjSGA_033705.1	41	partial	(Q287W1) PHD finger/nucleic acid binding protein
LjSGA_033750.1	195	partial	(Q9C977) Hypothetical protein F5I6.2 (Hypothetical protein At1g80270; F5I6.2) (Hypothetical protein At1g80270)
LjSGA_033809.0.1	76	partial	(Q9ZT82) Putative glucan synthase component
LjSGA_033950.1	57	partial	(Q5NBD8) Hypothetical protein P0434D08.16
LjSGA_033999.1.1	61	partial	(Q6QP53) Hypothetical protein
LjSGA_034059.1.1	117	partial	(O82354) Hypothetical protein At2g46150 (Hypothetical protein At2g46150/T3F17.20)
LjSGA_034093.2	57	partial	(Q7XAU8) Phosphoenolpyruvate carboxykinase
LjSGA_034095.1	55	partial	(Q2HRG5) TIR
LjSGA_034292.1	75	partial	(Q9FQ45) Disrupted meiotic cDNA 1 protein (Fragment)
LjSGA_034324.1	56	partial	(Q69S29) Putative equilibrative nucleoside transporter ENT8 splice variant
LjSGA_034327.1	36	partial	(Q8L821) SET domain-containing protein SET118

LjSGA_034536.1	107	partial	(Q6YYB8) Putative OCL5 protein
LjSGA_034583.3	54	partial	(Q76H08) Hypothetical protein 1D11 (Fragment)
LjSGA_034608.1	54	partial	(Q8L784) Cytoplasmic aconitate hydratase (At2g05710)
LjSGA_034648.1.1	91	partial	(Q5JKW7) Hypothetical protein B1147A04.42
LjSGA_034732.1	88	partial	(Q9S7Y1) Putative DNA-binding protein; 36199-34606 (Putative DNA-binding protein)
LjSGA_035057.2.1	75	partial	(Q2V991) ArcA2 protein-like
LjSGA_035080.1	65	partial	(Q84TM8) Polygalactorunase PG11 precursor (EC 3.2.1.15)
LjSGA_035222.1	72	partial	(Q9FRR2) F22O13.25 (Hypothetical protein At1g08760)
LjSGA_035223.1	206	partial	(Q8TGW9) Putative transcriptional repressor
LjSGA_035295.1	63	partial	(Q2HVI3) Peptidase, cysteine peptidase active site; Ribosomal protein L30
LjSGA_035359.1.1	62	partial	(Q93X16) Spermidine synthase (EC 2.5.1.16)
LjSGA_035484.1	65	partial	(Q6DBN5) At5g05230
LjSGA_035519.1	49	partial	(Q9FMY8) Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MJB21
LjSGA_035565.2	72	partial	(O04532) F20P5.14 protein
LjSGA_035567.1	382	partial	(Q8IIX7) Hypothetical protein
LjSGA_035708.0.1	90	partial	(Q7X7N2) OSJNBb0085F13.5 protein (OSJNBb0004G23.10 protein)
LjSGA_035786.1.1	35	partial	(Q9ZPK0) Thiosulfate sulfurtransferase
LjSGA_035814.1.1	112	partial	unknown protein
LjSGA_036005.1	148	partial	(Q9FIX3) Gb|AAD30619.1
LjSGA_036015.1.1	40	partial	(Q5ZP80) Galactokinase (EC 2.7.1.6)
LjSGA_036016.1.1	36	partial	(Q9LV40) Emb|CAB41934.1
LjSGA_036101.1	89	partial	(Q8GTM4) Chlorophyllase 1 (EC 3.1.1.14)
LjSGA_036127.1	41	partial	(Q8L7P1) SF2/ASF-like splicing modulator Srp30, putative (At1g02840)
LjSGA_036171.1	49	partial	(Q9XIE0) F23H11.22 protein (At1g59910)
LjSGA_036191.2	45	partial	(Q5VNP3) Peptide deformylase-like

LjSGA_036257.1.1	61	partial	(Q947E7) Resistance gene analog NBS1 (Fragment)
LjSGA_036263.1	81	partial	(Q9C7B2) Hypothetical protein T2E22.10
LjSGA_036343.1.1	35	partial	(Q93X58) Beta-galactosidase (EC 3.2.1.23)
LjSGA_036365.1	55	partial	(Q9STC7) Plastidic glucose-6-phosphate dehydrogenase (EC 1.1.1.49)
LjSGA_036477.2	31	partial	(Q9LJP4) Glucosyltransferase-like protein (Hypothetical protein At3g28180)
LjSGA_036481.2.1	44	partial	(Q7EZJ3) Putative valyl-tRNA synthetase
LjSGA_036491.1	54	partial	(Q9C9B7) Hypothetical protein F2P9.17
LjSGA_036526.1	42	partial	(O64496) F20D22.14 protein
LjSGA_036615.1	37	partial	(Q9LF14) Peptidyl-tRNA hydrolase (EC 3.1.1.29) (PTH)
LjSGA_036620.1.1	110	partial	(Q9LMI5) T2D23.4 protein
LjSGA_036686.1	80	partial	(Q2HVI3) Peptidase, cysteine peptidase active site; Ribosomal protein L30
LjSGA_036692.1	118	partial	(Q7XUL6) OSJNBa0010H02.10 protein
LjSGA_036699.1	72	partial	(Q8GYR2) Hypothetical protein At1g15215
LjSGA_036764.2.1	51	partial	(O23143) Putative Ckc2
LjSGA_036766.2	136	partial	(Q9LEU3) Zinc finger-like protein
LjSGA_036768.1	60	partial	unknown protein
LjSGA_036817.1	114	partial	(Q9FJJ6) Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K19B1 (AT5g62460/K19B1_7)
LjSGA_036857.1	62	partial	(Q5TKF1) Hypothetical protein OSJNBa0030I14.15 (Hypothetical protein OSJNBb0086G17.6)
LjSGA_036917.1	47	partial	(O22778) Putative tyrosine-specific transport protein (Tryptophan/tyrosine permease family protein)
LjSGA_036969.1	133	partial	(Q9SC41) Translocon Tic40 precursor
LjSGA_037118.1	62	partial	(Q9FHB6) Genomic DNA, chromosome 5, TAC clone:K24M7 (Hypothetical protein At5g52450)
LjSGA_037161.1	65	partial	(Q8S3B9) Putative glucosyltransferase
LjSGA_037166.0.1	47	partial	(Q2V341) Protein At5g27640
LjSGA_037238.1	58	partial	(Q9M2E4) Hypothetical protein T20K12.100 (AT3g61200/T20K12_100)

LjSGA_037261.0.1	40	partial	(Q69MC9) Putative carbonic anhydrase
LjSGA_037277.1	44	partial	(Q9SV43) Hypothetical protein F28P10.70
LjSGA_037348.0.1	33	partial	(Q94KC7) Putative potassium transporter HAK1p
LjSGA_037354.0.1	71	partial	(Q6DUM8) Probable phytochelatin synthetase (Fragment)
LjSGA_037515.2	61	partial	(Q4U319) Cys2/His2 zinc-finger transcription factor
LjSGA_037582.1	66	partial	(Q8LAE1) Subtilisin-like serine protease
LjSGA_037624.1.1	50	partial	(Q9SB46) Rab geranylgeranyl transferase like protein (Fragment)
LjSGA_037651.1.1	52	partial	(Q9SDM5) P-glycoprotein
LjSGA_037702.1	78	partial	(Q5SNM6) Hypothetical protein P0675A05.15
LjSGA_037917.1	125	partial	(Q9FY93) NAM-like protein (AT5g13180/T19L5_140)
LjSGA_037966.0.1	54	partial	(Q75KW8) Putative CorA-like Mg2+ transporter protein
LjSGA_038011.1	175	partial	(O65430) Glu-rich protein
LjSGA_038036.1.1	41	partial	(Q8VZ78) Hypothetical protein At3g60260; F27H5_50 (Hypothetical protein) (Hypothetical protein At3g60260)
LjSGA_038271.1	286	partial	(Q84J88) Hypothetical protein At5g27690
LjSGA_038321.1	34	partial	(Q6AV34) Putative Semialdehyde dehydrogenase
LjSGA_038384.2	75	partial	(Q9XI97) F13F21.27 protein
LjSGA_038403.2	74	partial	(Q9LU66) Similarity to RNase H
LjSGA_038431.2	38	partial	(Q9SZQ6) Hypothetical protein F27B13.90 (At4g29850) (Hypothetical protein AT4g29850)
LjSGA_038511.1	82	partial	(Q2QUQ9) MIF4G domain, putative
LjSGA_038586.2	217	partial	(Q3E9C1) Protein At5g19330
LjSGA_038603.1	66	partial	(Q6YUH7) Putative target of myb1 (TOM1 protein)
LjSGA_038609.1.1	41	partial	(Q9SKN4) Hypothetical protein At2g28360
LjSGA_038656.1	158	partial	(Q7F1V0) Putative heme binding protein cemA
LjSGA_038711.1	98	partial	(Q8S4X3) TIR-similar-domain-containing protein TSDC

LjSGA_038719.1.1	38	partial	(Q8S5V1) Putative potassium/proton antiporter-like protein
LjSGA_038840.1	60	partial	(Q9LZR1) Myb-like protein (MYB transcription factor)
LjSGA_038876.1	58	partial	(Q7XK24) OSJNBa0044K18.21 protein
LjSGA_039006.1	75	partial	(O64634) Hypothetical protein At2g45540
LjSGA_039025.1	99	partial	(Q9LHE3) Nucleoid chloroplast DNA-binding protein-like (Hypothetical protein At3g20015)
LjSGA_039121.1	62	partial	(Q9ZVF8) Hypothetical protein At2g01460
LjSGA_039125.1	97	partial	(Q9C5J5) Hypothetical protein At1g19010
LjSGA_039163.1	87	partial	(Q8L7M0) Hypothetical protein At1g16570
LjSGA_039187.1	54	partial	(Q9FJY3) Photoreceptor-interacting protein-like
LjSGA_039253.2	101	partial	(Q7XP86) OSJNBa0021F22.14 protein
LjSGA_039331.1	216	partial	(Q84KA9) RING/C3HC4/PHD zinc finger-like protein
LjSGA_039334.1	165	partial	(Q49I32) 120 kDa pistil extensin-like protein (Fragment)
LjSGA_039344.2.1	88	partial	(Q3E6Q7) Protein At2g44980
LjSGA_039363.0.1	46	partial	(Q9TMS3) ATP synthase beta subunit (Fragment)
LjSGA_039409.0.1	50	partial	(Q94A05) Hypothetical protein At4g32120
LjSGA_039413.1	28	partial	(Q940I2) Hypothetical protein MED24.18
LjSGA_039467.1	53	partial	(Q94CF8) Branched-chain amino acid aminotransferase
LjSGA_039661.1.1	58	partial	(Q8LC13) Remorin
LjSGA_039743.1	94	partial	(Q2A9H0) GATA zinc finger containing protein
LjSGA_039786.1	39	partial	(P92952) HAPp48,5 protein (Fragment)
LjSGA_039790.2	134	partial	unknown protein
LjSGA_039795.1	89	partial	(Q25CI0) Hypothetical protein osysl6
LjSGA_039891.0.1	68	partial	(Q6UD72) LysM domain-containing receptor-like kinase 4 (Fragment)
LjSGA_040014.2	58	partial	(Q5BPG9) Hypothetical protein
LjSGA_040047.1.1	49	partial	(Q6DNI8) Tau class glutathione S-transferase

LjSGA_040105.1	64	partial	(Q7SY63) Cg9836-prov protein
LjSGA_040109.1	47	partial	(Q6Z2H7) Putative calcium binding protein
LjSGA_040160.1	108	partial	(Q9LYA8) Rac-GTP binding protein-like
LjSGA_040270.2	133	partial	(Q9FS17) OsIre1p
LjSGA_040287.1	59	partial	(Q2R135) Expressed protein
LjSGA_040320.1	148	partial	(Q6F2S9) Hypothetical protein OSJNBa0027N19.13
LjSGA_040347.1	100	partial	(Q9FL03) SCARECROW gene regulator
LjSGA_040398.1	155	partial	(Q9LLM3) MTD1
LjSGA_040424.2	59	partial	(Q84TM8) Polygalactorunase PG11 precursor (EC 3.2.1.15)
LjSGA_040572.1	51	partial	(Q3EDC4) Protein At1g14820
LjSGA_040684.1	76	partial	(Q9FFJ3) Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MJJ3 (At5g05850) (Plant intracellular Ras-group-related LRR protein 1)
LjSGA_040884.1	153	partial	(Q5XWN7) Hypothetical protein
LjSGA_040891.1	58	partial	(Q2HU24) Hypothetical protein
LjSGA_040947.1	111	partial	(Q9XEE6) Hypothetical Cys-3-His zinc finger protein (Putative CCCH-type zinc finger protein)
LjSGA_040967.1	38	partial	(Q9FYD1) Hypothetical protein F22J12_30 (Hypothetical protein At3g43590)
LjSGA_040993.1.2	37	partial	(Q332W3) Photosystem II protein L (Fragment)
LjSGA_041202.1	57	partial	(Q5DQ95) 4-amino-4-deoxychorismate lyase
LjSGA_041322.1.1	60	partial	unknown protein
LjSGA_041396.1	179	partial	(O18161) Hypothetical protein sig-7
LjSGA_041397.1	58	partial	(Q9FHX0) Similarity to glutathione-S-transferase/glutaredoxin (Hypothetical protein At5g42150) (Hypothetical protein)
LjSGA_041397.2	44	partial	(Q705X3) Rho GDP dissociation inhibitor 2 (RHO protein GDP dissociation inhibitor)
LjSGA_041421.1.1	40	partial	(Q3HVP5) Hypothetical protein
LjSGA_041467.1.1	46	partial	(O65152) Putative cinnamyl alcohol dehydrogenase

LjSGA_041524.1	82	partial	(Q9FPS7) Ubiquitin-specific protease 20
LjSGA_041724.1	35	partial	(Q2QX12) Growth regulator, putative
LjSGA_041869.1	55	partial	(Q84VS2) Potyviral helper component protease-interacting protein 2
LjSGA_041906.1	43	partial	(Q40213) RAB7C
LjSGA_041960.1	67	partial	(Q5Y381) Aldo/keto reductase
LjSGA_042040.0.1	75	partial	(Q6ZD98) Putative vesicle-associated membrane protein-associated protein
LjSGA_042173.1.1	46	partial	(Q506M2) Cinnamyl alcohol dehydrogenase
LjSGA_042176.1	61	partial	(Q9LIM5) Arabidopsis thaliana genomic DNA, chromosome 3, BAC clone:F4B12 (Hypothetical protein At3g15095)
LjSGA_042198.1	69	partial	(Q8W4B1) RNA-binding protein-like (At5g53060)
LjSGA_042433.1.1	66	partial	(Q93X58) Beta-galactosidase (EC 3.2.1.23)
LjSGA_042483.1.1	76	partial	(Q40868) Heat shock-like protein
LjSGA_042495.1	91	partial	(Q38B00) Universal minicircle sequence binding protein (UMSBP), putative
LjSGA_042513.1	43	partial	(Q9SRP6) T21P5.16 protein (Hypothetical protein At3g03420)
LjSGA_042537.1	107	partial	(Q3C251) Glutamate N-acetyltransferase
LjSGA_042540.1.1	64	partial	(Q6YWF9) Nucleoporin-like protein
LjSGA_042581.1.1	39	partial	(Q9LPZ4) T23J18.7 (Hypothetical protein At1g11400)
LjSGA_042622.1	53	partial	(Q8GZ75) Hypothetical protein At2g03780/F19B11.23 (At2g03780)
LjSGA_042627.2	42	partial	(Q84VQ7) Alpha-galactosidase
LjSGA_042650.1.1	61	partial	unknown protein
LjSGA_042668.1	25	partial	(Q2XSM3) NADH dehydrogenase subunit 6
LjSGA_042720.1	71	partial	(Q2HZ34) Plamsma membrane-associated AAA-ATPase
LjSGA_042754.2	147	partial	(Q9LW36) Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDJ14
LjSGA_042766.1	103	partial	(Q5XM22) Resistance-like protein HAAS-2 (Fragment)
LjSGA_042770.1	92	partial	(Q93XA7) NAC domain protein NAC1

LjSGA_042774.1	128	partial	(Q2HS00) TIR
LjSGA_042791.1	46	partial	(Q2V3X8) Protein At3g07110
LjSGA_042870.1.1	38	partial	(Q67Z55) Hypothetical protein At1g19710
LjSGA_042984.0.1	39	partial	(Q8LER0) Hypothetical protein
LjSGA_043018.2	71	partial	(Q67UL5) Putative fructokinase
LjSGA_043053.1.1	40	partial	(Q9LV06) Similarity to zinc finger protein
LjSGA_043098.1.1	47	partial	(Q3HRP5) Calcineurin B-like protein 2
LjSGA_043414.0.1	34	partial	(Q8LAC4) Hypothetical protein (At1g05620) (Expressed protein)
LjSGA_043451.1	145	partial	(Q67YE8) Protease HhoA like
LjSGA_043497.1.1	46	partial	(Q9M0K5) Hypothetical protein AT4g25550 (Fragment)
LjSGA_043629.1	107	partial	(Q8LHG0) Membrane protein-like
LjSGA_043731.1	118	partial	(Q6ZB67) Hypothetical protein OJ1119_B10.8
LjSGA_043904.2	37	partial	(Q3E9B0) Protein At5g19950
LjSGA_044148.1	60	partial	(Q9FG25) Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MPH15
LjSGA_044234.1.1	39	partial	(Q3ECD7) Protein At1g72550
LjSGA_044252.0.1	58	partial	(Q2HU54) SAM (And some other nucleotide) binding motif; WW/Rsp5/WWP
LjSGA_044281.1	67	partial	(Q7XIM1) Hypothetical protein OJ1714_H10.131
LjSGA_044329.1	77	partial	unknown protein
LjSGA_044437.1.1	37	partial	(Q332W3) Photosystem II protein L (Fragment)
LjSGA_044439.1	49	partial	(Q6K701) Putative fibrillarin
LjSGA_044448.1	43	partial	(Q2TUV6) Glutathione S-transferase 2
LjSGA_044484.1	58	partial	(Q2HV57) Hypothetical protein
LjSGA_044551.1.1	36	partial	(Q2QMY2) Protein kinase-like protein
LjSGA_044649.1	160	partial	(Q9M1L9) Hypothetical protein F18P9_20 (Hypothetical protein At3g42860)
LjSGA_044664.1	27	partial	(O23164) Cold acclimation protein homolog

LjSGA_044670.1.1	100	partial	(Q9LXM2) Putative CCR4-associated factor 1
LjSGA_044868.0.1	160	partial	(Q6Z553) Hypothetical protein OSJNBa0007M04.36
LjSGA_044878.1.1	38	partial	(Q9ZRV6) Hypothetical protein
LjSGA_044963.2	46	partial	(Q2HUG6) Peptidase C14, caspase catalytic subunit p20
LjSGA_044978.1	52	partial	(Q93X02) Putative ammonium transporter AMT2
LjSGA_045060.1	79	partial	(Q9ZSR1) Cytoplasmic glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49)
LjSGA_045123.1	43	partial	unknown protein
LjSGA_045180.1	64	partial	(Q9LXQ2) Hypothetical protein F26G5_50 (At3g44100) (Hypothetical protein)
LjSGA_045300.1	60	partial	(Q67YE7) Protein-tyrosine-phosphatase-like protein
LjSGA_045459.1	49	partial	unknown protein
LjSGA_045485.2	143	partial	(Q7S753) Hypothetical protein
LjSGA_045517.1	40	partial	(Q8S9M8) P53 binding protein (Fragment)
LjSGA_045564.1	57	partial	(Q9LZW2) Hypothetical protein T20L15_110
LjSGA_045623.1	122	partial	(Q4Q1R0) Universal minicircle sequence binding protein (UMSBP), putative
LjSGA_045720.1	121	partial	(Q9FY93) NAM-like protein (AT5g13180/T19L5_140)
LjSGA_045779.1.1	104	partial	(Q9ZWS2) Flavonoid 3-O-galactosyl transferase
LjSGA_046043.1	54	partial	(Q5TKP5) Hypothetical protein OJ1362_G11.13
LjSGA_046249.1	141	partial	(Q9LZS6) Cucumisin-like protein
LjSGA_046560.1	47	partial	(Q9SFE9) T26F17.9 (GONST5 Golgi Nucleotide sugar transporter)
LjSGA_046612.0.1	39	partial	(Q332T6) Ribosomal protein S19
LjSGA_046631.0.1	44	partial	(Q8LPM5) Starch phosphorylase type L (Fragment)
LjSGA_046842.1.1	35	partial	(Q41668) Guanine nucleotide regulatory protein
LjSGA_046895.1	51	partial	(Q94B52) Hypothetical protein T10C21.40 (Hypothetical protein At4g30690; T10C21.40)
LjSGA_046936.1	38	partial	(Q67YN9) Imidazoleglycerolphosphate dehydratase
LjSGA_047018.1.1	40	partial	(Q9C9R6) Putative RNA-binding protein; 42664-44784

LjSGA_047166.1	42	partial	(Q5I4I4) Calcium-dependent/calmodulin-independent protein kinase isoform 3 (Fragment)
LjSGA_047292.1.1	42	partial	(Q9FI35) DnaJ protein-like
LjSGA_047343.1.1	47	partial	(Q6W6R6) Putative serine carboxypeptidase
LjSGA_047414.1	44	partial	(Q9FHY3) Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MJC20 (Hypothetical protein At5g42000)
LjSGA_047461.1	35	partial	(Q9LN44) F18O14.26
LjSGA_047625.2	102	partial	(Q9FZH6) F1O19.11 protein (Hypothetical protein At1g67050) (Hypothetical protein)
LjSGA_047660.1	50	partial	(Q60EZ7) Hypothetical protein OJ1111_A10.16
LjSGA_047894.1.1	73	partial	(Q2VA65) Glucosyltransferase
LjSGA_047916.1	52	partial	(Q709Q5) Cytokinin oxidase 2
LjSGA_047985.2	52	partial	(Q94G04) Diphosphonucleotide phosphatase 1
LjSGA_047986.1	147	partial	unknown protein
LjSGA_048078.1	71	partial	(Q6X0N8) Putative spermine/spermidine synthase
LjSGA_048191.0.1	34	partial	(Q2V4H1) Protein At1g53580
LjSGA_048269.1	74	partial	(Q68UW2) Expansin
LjSGA_048344.2	53	partial	(O04512) F21M12.30 protein
LjSGA_048348.1	118	partial	(Q7S753) Hypothetical protein
LjSGA_048360.1.1	32	partial	(Q9FR28) Transcription factor WRKY5
LjSGA_048385.1	127	partial	(Q8L7M7) Hypothetical protein At1g17820
LjSGA_048388.1	33	partial	(Q9SL05) Expressed protein (At2g05620/T20G20.3)
LjSGA_048441.1.1	55	partial	(Q8LC13) Remorin
LjSGA_048461.1	183	partial	(Q8H1N0) Hypothetical protein At2g33400/F4P9.17
LjSGA_048503.1.1	53	partial	(Q9SJB4) Putative GDSL-motif lipase/hydrolase
LjSGA_048592.1	84	partial	(Q2V3C9) Protein At4g32180
LjSGA_048666.1	128	partial	(O48579) Mi-2 autoantigen-like protein (Helicase-like protein)

LjSGA_048701.1	36	partial	(Q8LNH8) Glycine-rich protein, putative
LjSGA_048716.1.1	82	partial	(Q9ASU6) At1g42440/F7F22_7 (Hypothetical protein At1g42440)
LjSGA_048818.1	55	partial	(Q8LE46) Zinc finger protein-like
LjSGA_049165.1.1	45	partial	(Q8LMQ4) Hypothetical protein OSJNBa0011L14.7
LjSGA_049190.1	51	partial	(Q9LP92) T32E20.28 (Hypothetical protein At1g36990)
LjSGA_049296.1.1	28	partial	(Q93W00) Putative CRK1 protein (Putative cyclin dependent kinase C)
LjSGA_049313.1	33	partial	(Q3HRY6) Hypothetical protein
LjSGA_049329.1	41	partial	(Q3EDE9) Protein At1g10820
LjSGA_049433.0.1	47	partial	(Q5XET5) At2g39740
LjSGA_049510.2	190	partial	(Q8RWG3) Hypothetical protein At3g56140
LjSGA_049529.1	80	partial	(Q42433) S3 self-incompatibility protein precursor
LjSGA_049549.2.1	210	partial	(Q5N967) Putative terbinafine resistance locus protein
LjSGA_049567.1	88	partial	(Q6ATK0) Hypothetical protein OSJNBa0015G13.14
LjSGA_049635.1.1	42	partial	(Q8LCU5) Transmembrane transport protein-like protein
LjSGA_049711.1	67	partial	(Q8SB36) Putative senescence-associated protein
LjSGA_049823.1	89	partial	(Q6A1K9) Anaerobic basic leucine zipper protein
LjSGA_049856.1	65	partial	(Q6Z553) Hypothetical protein OSJNBa0007M04.36
LjSGA_049858.1	54	partial	(Q5E919) At3g27300
LjSGA_050066.2	56	partial	(Q9M995) F27J15.28 (Putative glycosyl hydrolase family 9 (Endo-1,4-beta-glucanase) protein)
LjSGA_050101.1	59	partial	(Q2HUL1) Initiation factor eIF-4 gamma, middle
LjSGA_050199.0.1	48	partial	(Q2VEJ1) ATP synthase CF1 alpha chain
LjSGA_050239.1	57	partial	(Q2A9Q5) Acyl carrier protein, putative
LjSGA_050254.1.1	76	partial	(Q3EBQ5) Protein At2g32090
LjSGA_050288.1	53	partial	(Q67TV0) GPI inositol-deacylase PGAP1-like protein
LjSGA_050595.1	45	partial	(Q69MX4) Pentatricopeptide (PPR) repeat-containing protein-like

LjSGA_050671.1	49	partial	(Q8L947) Putative DNA-directed RNA polymerase 23kD subunit
LjSGA_050730.0.1	38	partial	(Q7G152) Hypothetical protein Sb07 (Fragment)
LjSGA_050778.1	112	partial	unknown protein
LjSGA_050879.1	71	partial	(Q9SMX5) GCN4-complementing protein (GCP1)
LjSGA_050890.1.1	86	partial	(Q9FNL1) Phosphate/triose-phosphate translocator
LjSGA_050999.1	51	partial	(Q8LGT9) Phosphoglycerate mutase-like protein
LjSGA_051098.0.1	68	partial	(Q9FJ81) Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MSG15
LjSGA_051100.2	69	partial	(Q9LYD6) Hypothetical protein F15N18_150
LjSGA_051142.1	65	partial	(Q8L9F9) Hypothetical protein
LjSGA_051338.1	67	partial	(Q9C7J0) Hypothetical protein T9I1.1
LjSGA_051364.1	36	partial	(Q9ZRU5) Protein phosphatase (Fragment)
LjSGA_051417.1	68	partial	(Q84K84) Hypothetical protein At5g63000
LjSGA_051569.1	78	partial	(Q6YU88) Putative kinesin
LjSGA_051593.1.1	65	partial	(Q6I681) Cytochrome b561
LjSGA_051710.1	43	partial	(Q9SXU4) Plastoquinol-plastocyanin reductase (Fragment)
LjSGA_051773.3	93	partial	(Q6ZGU0) Putative NAC domain protein NAM
LjSGA_051909.1	87	partial	(Q9T0I3) Hypothetical protein AT4g38750
LjSGA_051927.2	61	partial	(Q8L601) Hypothetical protein At2g22400
LjSGA_052340.1	68	partial	(Q8LSP1) Putative clathrin coat assembly protein
LjSGA_052385.1	254	partial	(Q752C9) AFR646Wp
LjSGA_052544.2	44	partial	(Q94L30) Receptor-like protein kinase (Fragment)
LjSGA_052580.1.1	68	partial	(Q9SIW6) Expressed protein (Hypothetical protein At2g16350; F16F14.15) (At2g16350)
LjSGA_052743.1	45	partial	(Q9ZQ41) Hypothetical protein At2g22730
LjSGA_052885.1	101	partial	(Q9M4A3) Putative cytochrome B 561 (Fragment)
LjSGA_052897.1	91	partial	(Q9C548) Myb-family transcription factor, putative (Hypothetical protein T18I24.13)

LjSGA_052899.1	59	partial	unknown protein
LjSGA_052926.1.1	129	partial	(Q9LS96) Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MVE11 (At3g18800) (Hypothetical protein)
LjSGA_052934.2	48	partial	(Q9LP15) F9C16.3
LjSGA_052948.1	86	partial	(Q2V3S3) Protein At3g26744
LjSGA_053000.1	59	partial	(Q7XKR2) OSJNBa0053B21.9 protein
LjSGA_053010.1	200	partial	(Q8S8Z9) Syringolide-induced protein 1-3-1B
LjSGA_053114.0.1	75	partial	(Q6J8W9) Cellulose synthase
LjSGA_053158.1.1	52	partial	(O22649) Alcohol dehydrogenase (Fragment)
LjSGA_053320.1	135	partial	(O23020) T1G11.10 protein
LjSGA_053536.1	35	partial	(Q56WW3) Putative mitochondrial translation elongation factor G
LjSGA_053748.1	52	partial	(Q8S8F8) Expressed protein
LjSGA_053826.1	159	partial	(Q9DGK5) Splicing factor arginine/serine rich 2 (Fragment)
LjSGA_054125.2	88	partial	(Q6K2Y3) Putative guanylate binding protein
LjSGA_054188.1.1	67	partial	(Q9LFR7) Hypothetical protein F1N13_220 (Hypothetical protein At5g16080)
LjSGA_054482.1	128	partial	(Q9C864) Chloroplast nucleoid DNA binding protein, putative (Aspartyl protease family protein)
LjSGA_054507.1	45	partial	(Q8GSD7) MRNA capping enzyme-like protein
LjSGA_054553.2.1	45	partial	(Q6W2J3) VDAC1.3
LjSGA_054565.1	47	partial	(Q570G5) Hypothetical protein At1g01540
LjSGA_054664.1	118	partial	(Q94B55) Putative RING zinc finger ankyrin protein (At2g28840)
LjSGA_054734.1	71	partial	(Q3E6Q7) Protein At2g44980
LjSGA_054886.2	109	partial	(Q9FF48) Gb|AAB97123.1
LjSGA_054957.1	205	partial	(Q42673) Papaya proteinase omega (EC 3.4.22.6)
LjSGA_055038.1	67	partial	(Q8VXZ5) Hypothetical protein At2g35610
LjSGA_055079.1	159	partial	(Q5N7S6) Receptor serine/threonine kinase PR5K-like

LjSGA_055157.1	155	partial	(Q9ZPE4) T3H13.1 protein (At4g08980) (F-box protein family, AtFBW2) (Hypothetical protein AT4g08980)
LjSGA_055214.1	48	partial	(Q9CAR6) Putative alpha-amylase; 60344-64829
LjSGA_055413.0.1	53	partial	(O23455) Hypothetical protein dl4070w (Hypothetical protein AT4g16060)
LjSGA_055806.1	62	partial	unknown protein
LjSGA_055829.1	46	partial	(Q84R59) Hypothetical protein OSJNBb0113I20.17
LjSGA_055979.1	84	partial	(Q8VZI8) At1g07510/F22G5_9
LjSGA_056024.1	42	partial	(Q3E9B7) Protein At5g19420
LjSGA_056101.2	58	partial	(Q84U30) Photosystem I-N subunit
LjSGA_056125.1.1	80	partial	(Q6JJ55) Putative PHD zinc finger protein
LjSGA_056127.1.1	147	partial	(Q9SB40) Hypothetical protein F24A6.70 (Hypothetical protein AT4g25230)
LjSGA_056278.1	53	partial	(Q2PEQ3) Hypothetical protein
LjSGA_056374.1	97	partial	(Q9ZQI2) Hypothetical protein At2g27370
LjSGA_056411.1	78	partial	(Q9LMD9) F14D16.3
LjSGA_056427.1	32	partial	(Q8LA67) Hypothetical protein
LjSGA_056473.2	57	partial	(Q5VSC2) MutT/nudix protein-like
LjSGA_056482.2	132	partial	(Q2WM17) Chitinase II
LjSGA_056536.1	40	partial	(Q9LL56) Receptor-like kinase
LjSGA_056543.1	35	partial	(Q4U3E9) Putative L24 ribosomal protein
LjSGA_056716.1	68	partial	(Q9LXB8) Periaxin-like protein
LjSGA_056743.1	61	partial	(Q94B71) Hypothetical protein F10B6.14 (Hypothetical protein At1g14740)
LjSGA_056803.1	173	partial	(Q84Q47) Hypothetical protein P0456B03.121-1
LjSGA_056888.1	63	partial	(Q657P0) Putative SecA
LjSGA_057054.1	75	partial	(Q9FQ45) Disrupted meiotic cDNA 1 protein (Fragment)
LjSGA_057169.1	48	partial	(Q2HUE7) PSP, proline-rich

LjSGA_057486.1	55	partial	(Q949V7) Hypothetical protein At3g59300
LjSGA_057487.1	62	partial	(Q6ASR0) Putative DegP2 protease
LjSGA_057634.1	35	partial	(Q653N8) ThiF family protein-like
LjSGA_057635.1	52	partial	(Q940R2) At1g04130/F20D22_10
LjSGA_057708.1	28	partial	(Q9FX34) Hypothetical protein T9L24.40 (Hypothetical protein At1g73390)
LjSGA_057886.2	90	partial	(Q852A6) Putative Hsp70 binding protein
LjSGA_058119.1	66	partial	(Q69S79) Putative ABC transporter
LjSGA_058176.1.1	64	partial	(Q9LDD4) Hypothetical protein AT4g11400
LjSGA_058250.1	62	partial	(Q8H1T4) Putative cleavage and polyadenylation specificity factor 160 kDa subunit
LjSGA_058256.1	39	partial	(O49607) Subtilisin proteinase-like (Putative subtilisin serine protease) (Putative subtilisin serine proteinase)
LjSGA_058352.1	79	partial	(Q8LI34) Putative histone acetyltransferase
LjSGA_058404.1	59	partial	(Q6Z9Y1) Putative high affinity sulfate transporter
LjSGA_058414.1	46	partial	(Q7XI54) Putative transmembrane protein
LjSGA_058496.1	153	partial	(Q2QYK7) RING zinc finger protein, putative
LjSGA_058518.1.1	37	partial	(Q8L4N2) Cell-wall invertase
LjSGA_058594.1	91	partial	(Q5ZC52) Hypothetical protein P0443D08.44
LjSGA_058664.1	71	partial	(Q9SY29) T17H7.15 (Hypothetical protein At1g30840) (Hypothetical protein)
LjSGA_058746.1	48	partial	(Q2V410) Protein At2g41700
LjSGA_058801.1	280	partial	(Q94FL7) Putative transcription factor MYB120
LjSGA_058803.1	71	partial	(Q5MJV5) Avr9/Cf-9 rapidly elicited protein 256 (Fragment)
LjSGA_058827.1	36	partial	(O22505) Cytosolic glutamine synthetase (EC 6.3.1.2) (Fragment)
LjSGA_058960.1	59	partial	(Q7EY41) Hypothetical protein OSJNBa0075N02.126
LjSGA_059015.2	146	partial	(Q3EDF8) Protein At1g09900
LjSGA_059053.1	211	partial	(Q4Q1R0) Universal minicircle sequence binding protein (UMSBP), putative

LjSGA_059083.1	55	partial	(Q67U28) Hypothetical protein B1047G05.17 (Hypothetical protein P0677B10.32)
LjSGA_059088.1	53	partial	(Q9CA89) Hypothetical protein F19K16.18
LjSGA_059232.1	181	partial	(Q949J9) Hypothetical protein
LjSGA_059320.1	53	partial	(Q41325) Cationic peroxidase
LjSGA_059324.0.1	35	partial	(Q8H6J1) Putative cytidine deaminase
LjSGA_059379.1	36	partial	(Q3C1M8) Ribosomal protein S7
LjSGA_059387.1	52	partial	(Q9FKW8) Senescence-associated protein sen1-like protein (AT5g66170/K2A18_25)
LjSGA_059431.1.2	37	partial	(Q332W3) Photosystem II protein L (Fragment)
LjSGA_059671.1.1	132	partial	(Q7XV50) OSJNBa0086B14.5 protein
LjSGA_059862.1	192	partial	(Q9LSB0) Emb|CAB70981.1
LjSGA_059909.1	61	partial	(Q9FF90) 60S ribosomal protein L13 (AT5g23900/MRO11_6)
LjSGA_059945.1.1	47	partial	(Q2PET1) Putative PSII-P protein (Fragment)
LjSGA_059954.2	49	partial	(Q4U0E3) Plasma membrane intrinsic protein (Fragment)
LjSGA_060025.1	56	partial	(Q9LD28) Histone H2A
LjSGA_060031.1.1	41	partial	(Q70Z23) Protein kinase 2 beta chain
LjSGA_060228.1	38	partial	(Q2HIW2) At4g14965
LjSGA_060249.1	43	partial	(Q6ENK8) Splicing factor 4-like protein
LjSGA_060318.0.1	42	partial	(Q2QYQ3) Hypothetical protein
LjSGA_060444.2	205	partial	(Q65XI3) Hypothetical protein OSJNBb0035J08.10
LjSGA_060504.1	45	partial	(Q9C5N4) Hypothetical protein At1g55680
LjSGA_060511.1	40	partial	(Q56ZY3) Putative pattern formation protein EMB30
LjSGA_060581.1	84	partial	(O80910) Hypothetical protein At2g38410
LjSGA_060663.1	203	partial	(Q27341) Trichosia pubescens puff C4B protein
LjSGA_060686.1	160	partial	(Q9FFL9) Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MIK22
LjSGA_060694.1	206	partial	(Q2HVE5) Cyclin-like F-box

LjSGA_060721.1.1	55	partial	(Q7EZT2) Hypothetical protein P0625E02.128
LjSGA_060749.1	55	partial	(Q8LKN3) SUMO activating enzyme 1b
LjSGA_060803.0.1	46	partial	(Q94AI6) Hypothetical protein At1g71820
LjSGA_060941.1	72	partial	(Q9SYL6) Putative gamma-glutamyl hydrolase
LjSGA_060952.1	46	partial	(Q2HXK3) Carotenoid isomerase
LjSGA_060988.1.1	65	partial	(Q6R311) Alcohol acyl transferase
LjSGA_061049.1	34	partial	(Q29PX1) At5g08565
LjSGA_061121.1	113	partial	(Q9FS17) OsIre1p
LjSGA_061247.0.1	34	partial	(Q94BQ9) Hypothetical protein At1g30890 (Hypothetical protein)
LjSGA_061554.1	79	partial	(Q6K7P0) Putative DNA-binding protein PD3, chloroplast
LjSGA_061608.2	64	partial	(Q9C9K5) Hypothetical protein F14G6.12 (Hypothetical protein At1g76520)
LjSGA_061650.1	75	partial	(Q5N9U6) Hypothetical protein P0408C03.31-1
LjSGA_061864.1	48	partial	(Q9SXG0) F1F0-ATPase inhibitor protein
LjSGA_061940.1	49	partial	(Q8RXT0) Putative phosphoesterase
LjSGA_061946.1	49	partial	(O82762) Hypothetical protein At2g25970 (F17H15.1/F17H15.1)
LjSGA_062028.1	115	partial	(Q8VXD2) P70 protein
LjSGA_062199.1.1	44	partial	(Q8L9B0) Pathogenesis-related protein-like protein
LjSGA_062215.1	71	partial	(Q6YSZ2) Hypothetical protein OSJNBa0003K21.26
LjSGA_062219.1	41	partial	(Q7XHI5) Putative bHLH133 transcription factor
LjSGA_062290.2	47	partial	(Q8W0W5) Repressor protein
LjSGA_062471.1	110	partial	(O22948) Putative salt-inducible protein
LjSGA_062507.1.1	99	partial	(Q549W5) ASYMMETRIC LEAVES2-like gene 5 protein (Fragment)
LjSGA_062634.1	61	partial	(Q59IN6) Alcohol dehydrogenase (Fragment)
LjSGA_062793.1.1	57	partial	(Q8H6U1) Cyclic nucleotide-gated channel C (Fragment)
LjSGA_062795.1	59	partial	(Q7XVK2) OSJNBa0069D17.4 protein

LjSGA_062796.0.1	60	partial	(Q2HVV5) Glyoxalase/bleomycin resistance protein/dioxygenase
LjSGA_062867.1	51	partial	(Q6AVB5) Hypothetical protein OJ1212_C10.15
LjSGA_062988.1.1	135	partial	(Q53Q77) Hypothetical protein
LjSGA_063048.1	83	partial	(Q7S5P3) Hypothetical protein
LjSGA_063081.1.1	50	partial	(Q94EK6) Ferric-chelate reductase (Iron reductase)
LjSGA_063118.0.1	65	partial	(Q9FXK9) Microsomal omega-3 fatty acid desaturase
LjSGA_063170.1.1	90	partial	(Q45NK3) Hypothetical protein (Fragment)
LjSGA_063197.1	85	partial	(Q947L4) Glutathione reductase (Fragment)
LjSGA_063224.1	40	partial	(Q6H7Q8) Tubulin-specific chaperone C-like protein
LjSGA_063231.1	77	partial	(Q5XF11) At4g35930
LjSGA_063379.1	66	partial	(Q2R178) Expressed protein
LjSGA_063463.1	61	partial	(Q9XIG1) Putative UDP-glucose:sterol glucosyltransferase (At1g43620)
LjSGA_063781.1	98	partial	(Q2HWB4) Cyclin-like F-box; F-box protein interaction domain
LjSGA_063914.1	45	partial	(Q6E6L5) 5-enol-pyruvylshikimate-phosphate synthase
LjSGA_063967.1.2	37	partial	(Q332W3) Photosystem II protein L (Fragment)
LjSGA_064042.1	81	partial	(Q39224) SRG1 protein (F6I1.30/F6I1.30) (At1g17020/F6I1.30)
LjSGA_064080.1.1	86	partial	(Q7XTT6) OSJNBa0058K23.17 protein
LjSGA_064081.0.1	40	partial	(Q24AV8) Ser/Thr protein phosphatase family protein
LjSGA_064123.1.1	47	partial	(Q3ED75) Protein At1g21750
LjSGA_064146.1.1	77	partial	(Q2HSV0) TGF-beta receptor, type I/II extracellular region
LjSGA_064162.1	95	partial	(Q850Z5) Putative zinc finger protein (Putative GATA-type zinc finger protein)
LjSGA_064371.1	70	partial	(Q6YW27) Putative ADP-ribosylation factor 3
LjSGA_064374.1	48	partial	(Q6H704) Hypothetical protein P0030G02.24-1 (Hypothetical protein OJ1116_A06.34-1)
LjSGA_064466.1	77	partial	(Q84PX1) Putative F-box protein (SKP1 interacting partner 3-related)
LjSGA_064478.1.1	55	partial	(Q45FY8) Coronatine-insensitive 1

LjSGA_064493.0.1	45	partial	(Q9LU67) Phosphatidylserine decarboxylase
LjSGA_064695.1	61	partial	unknown protein
LjSGA_064771.0.1	37	partial	(Q9FZ97) F3H9.11 protein
LjSGA_064782.1.1	103	partial	(Q9FJ30) Similarity to heat shock transcription factor HSF30
LjSGA_064890.1.1	70	partial	(Q6K1S6) Putative myb protein
LjSGA_065099.1.1	66	partial	(Q84TL4) At5g04570
LjSGA_065206.1	61	partial	(Q9SUE9) Hypothetical protein AT4g08310
LjSGA_065337.1	76	partial	(Q9FVD3) Hexokinase
LjSGA_065440.1.1	55	partial	(Q6EUQ8) Hypothetical protein OJ1077_E05.12
LjSGA_065543.1	117	partial	(Q9LIM5) Arabidopsis thaliana genomic DNA, chromosome 3, BAC clone:F4B12 (Hypothetical protein At3g15095)
LjSGA_065566.2	96	partial	unknown protein
LjSGA_065570.0.1	65	partial	(Q9LXC9) Chloroplast inorganic pyrophosphatase (EC 3.6.1.1)
LjSGA_065606.1	43	partial	(Q93VW9) AT5g53330/K19E1_13
LjSGA_065652.1	43	partial	(O81097) RNA polymerase I, II and III 16.5 kDa subunit (At1g54250) (RNA polymerase II subunit, putative)
LjSGA_065722.1	81	partial	(Q8GWB1) Hypothetical protein At3g19895
LjSGA_065797.1	59	partial	(Q9MB26) Type 1 protein phosphatase-1
LjSGA_065856.1.1	70	partial	(Q9SGS2) T23E18.4 (Hypothetical protein At1g76110)
LjSGA_065924.1	46	partial	(Q2W6C8) Acetylglutamate semialdehyde dehydrogenase
LjSGA_066050.2	63	partial	(Q9FR42) Anther-specific myb-related protein 1
LjSGA_066052.1	98	partial	(Q9M3I0) Putative glucosyltransferase (Fragment)
LjSGA_066171.1.1	64	partial	(O49607) Subtilisin proteinase-like (Putative subtilisin serine protease) (Putative subtilisin serine proteinase)
LjSGA_066227.1	53	partial	(Q6URA2) TIR-NBS-LRR type R protein 7
LjSGA_066344.1	117	partial	(Q9FY93) NAM-like protein (AT5g13180/T19L5_140)

LjSGA_066436.1	91	partial	(Q9FFC3) Protease-like protein
LjSGA_066495.1	84	partial	(Q9T0I3) Hypothetical protein AT4g38750
LjSGA_066699.1	50	partial	(Q651M0) Putative membrane protein
LjSGA_066793.1	52	partial	(Q2R9P0) C2 domain, putative
LjSGA_066906.1	82	partial	(Q9FUJ4) Ribulose-1,5-bisphosphate carboxylase small subunit rbcS3
LjSGA_067014.1	74	partial	(Q53M53) Hemolysin A, putative
LjSGA_067208.1	54	partial	(Q4A3I7) Myb-like protein
LjSGA_067265.1	105	partial	(Q2HS67) F-box associated, putative
LjSGA_067275.2	100	partial	(Q84XT8) Hypothetical protein
LjSGA_067327.1	62	partial	(Q76I95) PHCLF2
LjSGA_067334.1	61	partial	(Q5QT25) Putative proline synthetase associated protein (Fragment)
LjSGA_067396.1	58	partial	(Q8RY60) At1g47330/T3F24_2
LjSGA_067631.1	55	partial	(Q5JKR0) Hypothetical protein B1064G04.19 (Hypothetical protein B1144D11.41)
LjSGA_067657.1.1	43	partial	(Q6DBF1) At4g05000
LjSGA_067664.1	89	partial	(Q9SFD7) T26F17.21
LjSGA_068072.1.1	44	partial	(Q8LPV6) Pyruvate kinase-like (Fragment)
LjSGA_068288.1	45	partial	(Q6I5B9) Hypothetical protein OSJNBb0067H15.12
LjSGA_068530.1	50	partial	(O49285) F22K20.9 protein (Hypothetical protein At1g76990) (ACR3)
LjSGA_068643.1	53	partial	(Q9MA61) F22F7.7 protein (Rad9 protein)
LjSGA_068744.1	54	partial	(Q5VMA7) Putative CPRD49
LjSGA_068754.2	38	partial	(Q75GR5) Expressed protein
LjSGA_068816.1	225	partial	(Q5R1K4) Hypothetical protein
LjSGA_068839.1.1	29	partial	(Q2TM92) Hypothetical protein (Fragment)
LjSGA_068863.1	111	partial	(Q3EDH9) Protein At1g06210
LjSGA_068939.1.1	102	partial	(Q8WHM9) NADH dehydrogenase (Fragment)

LjSGA_069132.1	174	partial	(Q8RW95) AT5g38690/MBB18_24
LjSGA_069480.1	96	partial	(Q9LIH4) Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:MFD22
LjSGA_069502.1	49	partial	(Q9FVD0) Diacylglycerol kinase variant A
LjSGA_069670.1.1	45	partial	(Q5XWE3) Monodehydroascorbate reductase II (EC 1.6.5.4) (Fragment)
LjSGA_069701.1	244	partial	(Q949L3) Putative polyprotein (Fragment)
LjSGA_069846.2	92	partial	(Q94C32) AT4g37280/C7A10_80
LjSGA_070102.1	64	partial	(Q9LFE9) Hypothetical protein F5E19_20
LjSGA_070133.1	60	partial	(O80763) T13D8.29 protein (Hypothetical protein At1g60420)
LjSGA_070253.1	91	partial	(Q9LZR3) Hypothetical protein F17C15_180 (Glucosyltransferase-like protein) (AT5g03760/F17C15_180)
LjSGA_070260.1	77	partial	(Q8GRY6) Hypothetical protein At3g21710
LjSGA_070266.1	38	partial	unknown protein
LjSGA_070303.1	53	partial	(Q27JE5) Stress-induced transcription factor NAC1
LjSGA_070352.1	65	partial	(Q9SUN6) Putative serine proteinase
LjSGA_070371.2	93	partial	(Q9FVQ0) Flavin-containing monooxygenase, putative (Flavin-containing monooxygenase family protein)
LjSGA_070700.1	81	partial	(Q8W0Y5) Enod8.1
LjSGA_070713.1	161	partial	(Q2LMD5) MYBR6
LjSGA_071014.1.1	47	partial	(Q5BN14) Pyruvate decarboxylase 1 (EC 4.1.1.1) (Fragment)
LjSGA_071025.1	70	partial	(Q9C8A3) Acetyl-CoA synthetase, putative; 45051-31547
LjSGA_071042.1.1	82	partial	(Q683D2) Hypothetical protein At5g55060
LjSGA_071140.1	51	partial	(Q5XVE4) Hypothetical protein
LjSGA_071141.1	55	partial	(Q6YUS6) Putative serine/threonine protein kinase
LjSGA_071172.1.1	47	partial	(Q9LYX7) Hypothetical protein F15A17_110
LjSGA_071220.1	42	partial	(O49436) Membrane-associated salt-inducible-like protein (Embryo-defective 1025)

LjSGA_071289.1	97	partial	(Q45GJ7) Expressed protein
LjSGA_071437.1.1	55	partial	(Q8GT65) Serpin-like protein (Fragment)
LjSGA_071506.1	51	partial	(Q84J37) Putative laccase (Diphenol oxidase) family protein
LjSGA_071515.1	73	partial	(Q84VB4) WD repeat protein (Fragment)
LjSGA_071685.1.1	56	partial	(Q2HVT8) PDZ/DHR/GLGF
LjSGA_071700.1	41	partial	(Q6KC46) Rme-8 homologue (Fragment)
LjSGA_071738.1	45	partial	(Q5YJN3) Diadenosine tetraphosphate hydrolase
LjSGA_071832.1	60	partial	(Q8LE50) Putative splicing factor
LjSGA_071950.1	60	partial	(Q40556) Protein phosphatase 2A
LjSGA_072204.2	87	partial	(Q7XAM5) Putative developmental protein sina
LjSGA_072426.1	47	partial	(Q940P8) AT5g20890/F22D1_60 (Hypothetical protein At5g20890) (T-complex protein 1, beta subunit) (Hypothetical protein)
LjSGA_072654.2	164	partial	(Q8VWX5) Ribosome-like protein (Fragment)
LjSGA_072918.1	71	partial	(Q2HJ50) Hypothetical protein
LjSGA_072963.1	48	partial	(Q53HZ4) Putative mitochondrial carrier protein (Fragment)
LjSGA_072997.0.1	58	partial	(Q332T6) Ribosomal protein S19
LjSGA_073131.1	69	partial	(Q6Z3N3) Putative villin
LjSGA_073263.1.1	32	partial	(O22266) Hypothetical protein At2g47440
LjSGA_073276.1	61	partial	(Q6NMJ6) At1g03260
LjSGA_073332.1	87	partial	(Q9FIV4) Gb|AAF23842.1
LjSGA_073367.1	84	partial	(Q7EXZ2) Putative SBP-domain protein
LjSGA_073478.1	32	partial	(Q56ZV6) Hypothetical protein At5g14660
LjSGA_073481.1	98	partial	(Q9FFB5) Emb|CAB89309.1
LjSGA_073591.1	48	partial	(Q9SL97) Hypothetical protein At2g25660
LjSGA_073599.1	46	partial	(Q9FS26) Plastidic cysteine synthase 1

LjSGA_073818.2	43	partial	(Q5ZDS6) Putative leucyl-tRNA synthetase
LjSGA_073862.1	86	partial	(Q2TQ36) Transcription factor AP2D14 (Fragment)
LjSGA_073909.1.1	54	partial	(Q2QSW7) M36658 histone H3
LjSGA_073955.1	42	partial	(Q9LUQ2) Leucine-rich repeat protein; contains similarity to elicitor-inducible receptor EIR
LjSGA_073999.0.1	82	partial	(Q8W228) Cytochrome P450
LjSGA_074226.1	90	partial	(Q3L234) Zinc finger protein
LjSGA_074289.1.1	68	partial	(Q2V4H1) Protein At1g53580
LjSGA_074400.1	56	partial	(Q75L11) Putative histone H2A
LjSGA_074404.1	62	partial	(Q8L9F9) Hypothetical protein
LjSGA_074426.1	75	partial	(Q6DBN1) At4g08455
LjSGA_074697.1	66	partial	(Q2HUB1) Glycoside hydrolase, family 28
LjSGA_074858.1	54	partial	(Q5PNY9) At1g48460
LjSGA_074957.1.1	48	partial	(Q403H0) Dihydroflavonol 4-reductase
LjSGA_074964.1	88	partial	(Q9FNN6) Similarity to I-box binding factor (Hypothetical protein At5g08520) (MYB transcription factor)
LjSGA_074970.2	103	partial	(Q9LKA1) Emb|CAA17164.1 (At3g15040)
LjSGA_075199.2	85	partial	(Q6Z8E3) Putative ADP-ribosylation factor
LjSGA_075489.1	36	partial	(Q4U3E9) Putative L24 ribosomal protein
LjSGA_075692.1.1	73	partial	(Q9C7N4) Lipase/hydrolase, putative; 118270-120144 (At1g29670/F15D2_22)
LjSGA_075716.1	34	partial	(Q6ID84) At2g46100
LjSGA_075719.1	78	partial	(Q9MAT6) F13M7.13 protein (At1g04880)
LjSGA_075722.1	43	partial	(Q9SRP6) T21P5.16 protein (Hypothetical protein At3g03420)
LjSGA_075756.0.1	61	partial	(Q9SAI6) F23A5.7
LjSGA_075814.2	42	partial	(Q8H6S5) CTV.2
LjSGA_075864.1	34	partial	(Q6Z9U7) Putative mRNA cap methyltransferase

LjSGA_076003.2	68	partial	(Q9SB69) Hypothetical protein F22K18.50 (Hypothetical protein AT4g24750)
LjSGA_076010.1.1	47	partial	(Q8RWX6) Hypothetical protein At2g46060
LjSGA_076227.1.1	61	partial	(Q9FFC6) GDSL-motif lipase/hydrolase-like protein
LjSGA_076256.1	64	partial	(Q9CAC3) Hypothetical protein F5A18.8
LjSGA_076328.1.1	50	partial	(Q7F1Y6) Putative ATP synthase mitochondrial F1 complex assembly factor2
LjSGA_076349.1	60	partial	(Q67ZZ1) Hypothetical protein At2g41020
LjSGA_076367.1	70	partial	(Q30CZ6) Putative chorismate mutase
LjSGA_076399.1	64	partial	(Q9FXI9) F6F9.1 protein (At1g19940/F6F9_1)
LjSGA_076743.1.1	46	partial	(Q7XSA2) OSJNBa0005N02.3 protein
LjSGA_076807.1	74	partial	(O04043) F7G19.26
LjSGA_076935.1	79	partial	(Q9M8M9) Hypothetical protein T21F11.5
LjSGA_077184.1	43	partial	(Q9SMQ5) Proliferating-cell nucleolar antigen-like protein
LjSGA_077361.1	91	partial	(Q6K7M5) Putative monooxygenase
LjSGA_077456.1.1	80	partial	(Q2HUI7) Cyclin-like F-box; FBD; Zinc finger, FYVE/PHD-type
LjSGA_077583.1	60	partial	(Q9LFI5) Hypothetical protein F4P12_20 (Hypothetical protein At3g53320/F4P12_20) (At3g53320)
LjSGA_077751.1.1	43	partial	(Q9ZPK0) Thiosulfate sulfurtransferase
LjSGA_077803.1	52	partial	(Q9SS49) F14P13.2 protein
LjSGA_077893.1	40	partial	(Q9FNA2) Polyamine oxidase
LjSGA_078041.1	63	partial	(Q8VYM4) Hypothetical protein At3g52150
LjSGA_078084.1	134	partial	(Q7XDY0) Transposon protein, putative, unclassified
LjSGA_078148.1.1	46	partial	(Q6Z1G4) Hypothetical protein OSJNBa0033D24.31-3 (Hypothetical protein P0665C04.12-3)
LjSGA_078279.1.1	56	partial	(Q880P8) Lactoylglutathione lyase
LjSGA_078390.1.1	42	partial	(Q6YXJ6) Hypothetical protein B1029H08.25
LjSGA_078473.1	176	partial	(Q4Q1R0) Universal minicircle sequence binding protein (UMSBP), putative

LjSGA_078537.1	94	partial	(Q45W75) Disease resistance-responsive family protein
LjSGA_078619.1	164	partial	(Q9M0K9) Splicing factor At-SRp40 (Fragment)
LjSGA_079032.1	85	partial	(Q4FFY5) RNA polymerase beta" chain (Fragment)
LjSGA_079055.1	105	partial	(Q2LMD7) MYBR2
LjSGA_079344.1	110	partial	(Q9C6R0) Hypothetical protein T18I24.11
LjSGA_079421.0.1	47	partial	(Q9SNK4) EST AU068209(C12438) corresponds to a region of the predicted gene
LjSGA_079423.1.1	57	partial	(Q9FLH1) Lysosomal Pro-X carboxypeptidase
LjSGA_079576.1	63	partial	(Q93YF5) SET-domain-containing protein
LjSGA_079580.1.1	101	partial	(Q6DBF5) At1g31320
LjSGA_079583.1	58	partial	(Q84VC8) Gamma hydroxybutyrate dehydrogenase-like protein (Hypothetical protein)
LjSGA_079640.1	64	partial	(Q2V3W6) Protein At3g12530
LjSGA_079715.1	37	partial	(Q75M66) Putative capping protein beta subunit
LjSGA_079720.1	41	partial	(Q9LUD7) Glucan synthase-like protein
LjSGA_079831.1	100	partial	(Q3EA57) Protein At4g10840
LjSGA_080081.1	51	partial	(Q9LMT6) F2H15.16 (At1g17940)
LjSGA_080150.1	61	partial	(Q43757) Ferritin precursor
LjSGA_080154.1.1	35	partial	(Q588B7) Vacuolar Na+/H+ antiporter
LjSGA_080231.2	53	partial	(Q42606) Urophorphyrin III methylase (EC 2.1.1.107) (AT5g40850/MHK7_8)
LjSGA_080251.1.2	81	partial	(Q9SGA5) F1C9.14 protein (At3g02070)
LjSGA_080274.2	51	partial	(Q9M090) Kinase binding protein-like
LjSGA_080430.1	80	partial	(Q2V9A9) RabGAP/TBC domain-containing protein-like
LjSGA_080541.1	87	partial	(Q6SRZ9) YABBY-like transcription factor PROLONGATA
LjSGA_080551.1	54	partial	(Q30CZ6) Putative chorismate mutase
LjSGA_080559.1	84	partial	(Q6Z8A6) Zinc finger (C3HC4-type RING finger)-like
LjSGA_080760.1	63	partial	(Q38M62) Hypothetical protein

LjSGA_080839.1	193	partial	(Q6DBE6) At1g30960
LjSGA_081129.2	61	partial	(Q25AN2) H0212B02.1 protein
LjSGA_081141.0.1	46	partial	(Q7XTA4) OSJNBa0008A08.6 protein
LjSGA_081515.1	36	partial	(Q9M899) F16B3.4 protein
LjSGA_081518.1	63	partial	(Q336P9) AT-Hook DNA-binding protein, putative
LjSGA_081571.1.1	81	partial	(Q9LZX9) Hypothetical protein T4C21_260 (Hypothetical protein At3g60850)
LjSGA_081773.1	34	partial	(Q9FYA3) Hypothetical protein T19L5_30 (At5g13070)
LjSGA_081950.1	44	partial	(Q7XU45) OSJNBa0088I22.8 protein
LjSGA_082085.1.1	69	partial	(Q67UW7) Putative pentatricopeptide (PPR) repeat-containing protein
LjSGA_082151.2	33	partial	(Q2WEJ5) Polyubiquitin homolog (Fragment)
LjSGA_082156.1	68	partial	(Q67Z52) Tubulin folding cofactor B
LjSGA_082188.1	96	partial	(Q45W75) Disease resistance-responsive family protein
LjSGA_082280.1.1	75	partial	(Q9FQ45) Disrupted meiotic cDNA 1 protein (Fragment)
LjSGA_082431.1.1	93	partial	(Q9SXB5) T28P6.5 protein
LjSGA_082615.1	91	partial	(O49553) G10-like protein (AT4g21110/F7J7_50)
LjSGA_082669.1	129	partial	(Q5ZBJ9) Pentatricopeptide (PPR) repeat-containing protein-like
LjSGA_082902.1.1	67	partial	(Q6E0J4) Hypothetical protein (Fragment)
LjSGA_083111.1	86	partial	(Q2RBP8) Mitochondrial carrier protein, putative
LjSGA_083270.1	37	partial	(Q3E6Q7) Protein At2g44980
LjSGA_083297.1	34	partial	(Q2HW42) Phospholipase D/Transphosphatidylase; Pleckstrin-like
LjSGA_083317.1	27	partial	(Q682I4) Hypothetical protein At3g60150
LjSGA_083468.1	37	partial	(Q6TYR6) Beta-tubulin 2
LjSGA_083752.1	38	partial	(P93115) Monogalactosyldiacylglycerol synthase (EC 2.4.1.46)
LjSGA_083826.2	122	partial	(Q9SU15) Hypothetical protein T20K18.60 (Hypothetical protein AT4g12710)
LjSGA_083942.2	82	partial	(Q8LAY3) Inhibitor of apoptosis-like protein

LjSGA_084078.2	95	partial	(Q9SUE7) Hypothetical protein T13J8.20 (Hypothetical protein AT4g27910)
LjSGA_084218.1	47	partial	(Q8RWZ0) Hypothetical protein At1g69060
LjSGA_084225.1	79	partial	(Q84VT8) APS-AA2 protein (Fragment)
LjSGA_084236.1	47	partial	(Q9C7B4) Hypothetical protein T2E22.5
LjSGA_084398.1	49	partial	(Q49KT5) Ribosomal protein L23
LjSGA_084448.0.1	32	partial	(Q8L4D9) Oxygen evolving complex protein, putative
LjSGA_084477.0.1	36	partial	(Q259R9) H0403D02.15 protein
LjSGA_084703.1.1	77	partial	(Q2HS79) Cyclin-like F-box; Agenet
LjSGA_084730.1.1	65	partial	(Q9LS09) Anti-silencing protein-like (Anti-silencing factor 1-like protein) (Anti-silencing function 1b)
LjSGA_084734.1	212	partial	(Q5B8Z1) Hypothetical protein
LjSGA_084749.1	66	partial	(Q84WD0) Putative leucine-rich repeat transmembrane protein kinase (Fragment)
LjSGA_084760.1	56	partial	(Q9M3N2) Putative kinetochore protein (Fragment)
LjSGA_084767.1	59	partial	(Q2PJR6) WRKY54
LjSGA_084959.1.1	49	partial	(Q6H734) Putative DNA-damage inducible protein
LjSGA_085104.1	120	partial	(Q94AH1) Hypothetical protein At3g05010
LjSGA_085239.1	99	partial	(O64703) MADS-box protein (AGL29)
LjSGA_085241.1	118	partial	(Q3EA42) Protein At4g13730
LjSGA_085345.1	42	partial	(Q6E6S6) FUL-like protein
LjSGA_085402.1	66	partial	(Q9FVU8) Putative UDP-glucose:glycoprotein glucosyltransferase; 101200-91134
LjSGA_085552.1	79	partial	(Q58G16) Hypothetical protein
LjSGA_085603.1	30	partial	(Q9T088) Hypothetical protein AT4g27640
LjSGA_085943.1	60	partial	(Q69S57) Glucose/sorbosone dehydrogenases-like protein
LjSGA_085944.1	53	partial	(Q6XGX9) Putative oxalyl-CoA decarboxylase (Fragment)
LjSGA_086118.1	60	partial	(Q9M8Z0) T6K12.4 protein
LjSGA_086121.1	155	partial	(Q9SW48) Invertase-like protein (AT4g34860/F11I11_100)

LjSGA_086166.1	38	partial	(Q9LKJ2) Cytosolic phosphoglycerate kinase
LjSGA_086267.1	43	partial	(Q42681) Histone H3
LjSGA_086309.1	102	partial	(Q9SGH2) T13O15.10 protein
LjSGA_086310.1	97	partial	(Q5Z8A9) Putative wall-associated kinase 4
LjSGA_086355.0.1	74	partial	(Q9FKU9) Berberine bridge enzyme-like protein
LjSGA_086455.1	63	partial	(Q8L6V6) Putative ripening related protein
LjSGA_086579.1	99	partial	(Q2HS67) F-box associated, putative
LjSGA_086637.1	80	partial	(Q7XTA3) OSJNBa0008A08.7 protein
LjSGA_086690.1	63	partial	(Q9FIJ5) Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MCA23 (AT5g47860/MCA23_20)
LjSGA_086809.1	91	partial	(Q94IB4) WRKY DNA-binding protein (Fragment)
LjSGA_086825.1	58	partial	(Q6K8Z1) Hypothetical protein OJ1695_H09.11
LjSGA_086966.1	70	partial	(Q6EEW1) Cyclin T1
LjSGA_087152.1	59	partial	(O48791) Hypothetical protein At2g26770
LjSGA_087318.1	51	partial	(Q8H0W0) Hypothetical protein At1g73060
LjSGA_087334.1	108	partial	(Q9C986) Hypothetical protein F23O10.3
LjSGA_087354.1	65	partial	unknown protein
LjSGA_087563.1	43	partial	(Q8VY97) Hypothetical protein At4g32130; F10N7.60 (Hypothetical protein At4g32130)
LjSGA_087574.0.1	71	partial	(Q2V991) ArcA2 protein-like
LjSGA_087740.1.1	63	partial	(Q9ASV4) AT3g06720/F3E22_14
LjSGA_087765.1	93	partial	(Q949L4) Putative polyprotein (Fragment)
LjSGA_087807.1	33	partial	(Q5NDD2) Putative MYB transcription factor
LjSGA_087867.1	37	partial	(Q6Z748) RING zinc finger protein-like
LjSGA_087889.1	36	partial	(Q9C5H6) Putative transporter protein
LjSGA_088063.1	88	partial	(Q69IN4) Ribonucleoprotein antigen-like

LjSGA_088187.1	43	partial	unknown protein
LjSGA_088362.1	155	partial	(Q9FG26) Non-LTR retroelement reverse transcriptase-like
LjSGA_088433.1	94	partial	(Q2XTB4) Hypothetical protein
LjSGA_088449.1	69	partial	(Q7XU07) OSJNBb0012E24.3 protein
LjSGA_088467.1	54	partial	(Q501D0) At3g47010
LjSGA_088656.1	53	partial	(Q9AUK5) Putative exostoses
LjSGA_088723.1	109	partial	(Q9SCZ0) Nonspecific lipid-transfer protein (LTP)
LjSGA_088914.2	127	partial	(O82343) Expressed protein (Hypothetical protein At2g46260)
LjSGA_089374.1	62	partial	(Q8H1E1) Hypothetical protein At4g08540
LjSGA_089725.1	52	partial	(Q7X8B5) Cation-transporting ATPase
LjSGA_089796.1	47	partial	(Q6ZDG9) Putative SEC23
LjSGA_089888.1.1	58	partial	(Q58FG4) Homogentisate phytylprenyltransferase
LjSGA_089915.0.1	72	partial	(Q9ZVY8) T25N20.15
LjSGA_090311.1	106	partial	(Q2MJ18) Cytochrome P450 monooxygenase CYP72B
LjSGA_090331.1	37	partial	(O22791) Putative RNA-binding protein
LjSGA_090334.1	49	partial	(Q2MIZ8) Cytochrome P450 monooxygenase CYP711A
LjSGA_090516.1	94	partial	(Q3HVP0) 60s acidic ribosomal protein-like protein
LjSGA_090522.1	79	partial	(Q5FAL6) Putative Expressed protein
LjSGA_090585.1	57	partial	(Q6Z553) Hypothetical protein OSJNBa0007M04.36
LjSGA_090586.1	75	partial	(Q93XA7) NAC domain protein NAC1
LjSGA_090591.1.1	24	partial	(Q9CAR6) Putative alpha-amylase; 60344-64829
LjSGA_090701.1.1	53	partial	(Q69UH7) Putative SERK1 protein
LjSGA_090897.2	40	partial	(Q570P1) Hypothetical protein At3g20300
LjSGA_090900.1	46	partial	(Q9MAV9) Cytoplasmic ribosomal protein S13
LjSGA_091066.1	73	partial	(Q9FIL1) Protein kinase-like protein (AT5g59010/k19m22_210)

LjSGA_091069.2	68	partial	(Q5Y836) ERF transcription factor 5
LjSGA_091092.1	66	partial	(Q3EDI9) Protein At1g03960
LjSGA_091177.2	44	partial	(Q4FG34) Ribosomal protein S12 (Fragment)
LjSGA_091178.0.1	39	partial	(Q3C1N5) Ribosomal protein L23
LjSGA_091222.1.1	47	partial	(Q9XGC0) Starch synthase isoform SS III (EC 2.4.1.21)
LjSGA_091245.1	53	partial	(Q3E9E3) Protein At5g18700
LjSGA_091309.1.1	41	partial	(Q9FLD7) Glycosylation enzyme-like protein (At5g39990)
LjSGA_091385.2	225	partial	(Q4A185) Beclin 1 protein
LjSGA_091481.1	152	partial	(Q5IY47) DNA binding protein WRKY2
LjSGA_091516.1	161	partial	(Q5DJU1) Fas-associated factor 1-like protein
LjSGA_091700.1	39	partial	(Q2PF88) KANADI-like transcription factor FEATHERED
LjSGA_091734.1	95	partial	(Q84QZ3) Hypothetical protein OSJNBa0093I13.23
LjSGA_091763.1	41	partial	(Q8LG57) Dihydroxypolyprenylbenzoate methyltransferase
LjSGA_091946.2	78	partial	(Q6XBF8) CDR1
LjSGA_092077.2	62	partial	(Q9FV39) 1-deoxy-D-xylulose-5-phosphate synthase
LjSGA_092108.1	54	partial	(Q9STY4) Hypothetical protein T21L8.140
LjSGA_092110.2	73	partial	(Q6ET26) Putative MFAP1 protein
LjSGA_092168.2	56	partial	(Q94CA0) Hypothetical protein At1g77220
LjSGA_092238.1.1	73	partial	(Q9LIE7) Selenium-binding protein-like
LjSGA_092281.1	65	partial	(Q6ZDG9) Putative SEC23
LjSGA_092289.1	39	partial	(Q84TS1) Hypothetical protein OSJNBb0097F01.10
LjSGA_092400.2	88	partial	(Q949L3) Putative polyprotein (Fragment)
LjSGA_092415.1	55	partial	(Q6RUF6) Fructose-bisphosphate aldolase (EC 4.1.2.13)
LjSGA_092549.1	50	partial	(Q8S9Z2) Putative dTDP-glucose 4,6-dehydratase
LjSGA_092672.1.1	200	partial	(Q5QMN8) Hypothetical protein P0419B01.2

LjSGA_093087.1.1	56	partial	(Q6NL19) At1g20890
LjSGA_093090.1	26	partial	(Q2V603) Hypothetical protein
LjSGA_093273.1.1	78	partial	(Q8L733) Hypothetical protein At4g12130
LjSGA_093466.1.1	39	partial	(Q8GYJ1) Hypothetical protein
LjSGA_093476.1	106	partial	(Q8GUH2) Expressed protein (At1g01500)
LjSGA_093583.1	121	partial	(O65281) Arabidopsis thaliana homeodomain protein AHDP (SP:P93041)
LjSGA_093663.1	84	partial	(Q9FY93) NAM-like protein (AT5g13180/T19L5_140)
LjSGA_093673.1	30	partial	(Q9FNK4) Ornithine aminotransferase (At5g46180)
LjSGA_093680.1	39	partial	(Q7XKL1) OSJNBb0061C13.8 protein
LjSGA_093726.1	63	partial	(Q9FR42) Anther-specific myb-related protein 1
LjSGA_093918.1	325	partial	(Q41805) Extensin-like protein precursor
LjSGA_093919.1.1	35	partial	(Q4U3E9) Putative L24 ribosomal protein
LjSGA_094037.1.1	50	partial	(Q45W70) Isomerase-like protein
LjSGA_094296.1	96	partial	(Q5Z7T6) Hypothetical protein OJ1136_F03.14
LjSGA_094332.0.2	37	partial	(Q332W3) Photosystem II protein L (Fragment)
LjSGA_094364.1	41	partial	(Q9LZK5) Hypothetical protein F26K9_30 (At3g62600/F26K9_30) (Hypothetical protein)
LjSGA_094376.0.1	103	partial	(Q2L922) Chloroplast envelope membrane protein
LjSGA_094495.1	71	partial	(Q2HJ50) Hypothetical protein
LjSGA_094496.1	27	partial	(Q2V3A6) Protein At5g02840
LjSGA_094729.1.1	72	partial	(Q9C660) Pto kinase interactor, putative
LjSGA_094936.1	102	partial	(Q6ZDR7) Putative splicing factor, arginine/serine-rich
LjSGA_094942.1	68	partial	(Q9XFL4) Peroxidase 3
LjSGA_094977.2	89	partial	(Q3ED88) Protein At1g20510
LjSGA_095214.1	73	partial	(Q6IVK7) Putative UDP-glucose dehydrogenase 1 (EC 1.1.1.22)
LjSGA_095234.1	56	partial	(Q6K4Q2) Hypothetical protein OSJNBa0054K20.7 (Hypothetical protein OJ1316_E06.21)

LjSGA_095318.1	60	partial	(Q2MGR5) Glycoside hydrolase, family 28
LjSGA_095386.1	44	partial	(Q2QX53) N-acylethanolamine amidohydrolase
LjSGA_095451.1	219	partial	(Q9FFV8) Similarity to guanine nucleotide exchange factor (Hypothetical protein At5g38640; MBB18.19) (At5g38640)
LjSGA_095591.1.1	51	partial	(Q9LK77) Similarity to acyl-CoA thioesterase (At5g48370)
LjSGA_095600.1	64	partial	(Q6H7M7) Putative outer envelope membrane protein OEP75
LjSGA_095834.1	34	partial	(Q8RWW6) Putative isoamylase
LjSGA_095900.1.1	71	partial	(Q5VRL4) Putative syntaxin of plants 41
LjSGA_095971.2.1	55	partial	(Q9M3Y5) 25.7 kDa protein
LjSGA_096037.1	62	partial	(Q8VZB8) Hypothetical protein At5g55810; MDF20.25 (Hypothetical protein At5g55810)
LjSGA_096057.1	34	partial	(Q94AG4) AT5g52920/MXC20_15
LjSGA_096058.1	43	partial	(Q8LEW9) Hypothetical protein
LjSGA_096121.1	62	partial	(Q9SJI1) Expressed protein (At2g42750/F7D19.25) (Hypothetical protein)
LjSGA_096269.1	83	partial	(Q8GWF9) Hypothetical protein At5g57700/MRI1_6
LjSGA_096306.0.1	39	partial	(Q332X9) Photosystem I P700 chlorophyll A apoprotein A2
LjSGA_096314.1	122	partial	(Q8W468) Hypothetical protein At1g65430; T8F5.21 (Hypothetical protein At1g65430) (ARIADNE-like protein ARI8)
LjSGA_096344.0.1	47	partial	(Q8H0U0) T-complex polypeptide 1 homologue
LjSGA_096465.1	60	partial	(Q9SUQ2) Putative Ap2 domain protein (AT4g23750/F9D16_220) (At4g23750)
LjSGA_096648.2.1	114	partial	(Q9MBE8) Cytochrome P450
LjSGA_096670.1.1	49	partial	(Q9LXQ8) Hypothetical protein T20N10_290
LjSGA_096678.1	83	partial	(Q949Q7) Putative serine carboxypeptidase II
LjSGA_096750.1	67	partial	(Q94JS1) AT4g26860/F10M23_200 (Putative proline synthetase associated protein)
LjSGA_096761.1.1	50	partial	(Q2R227) RING-H2 zinc finger protein, putative
LjSGA_096940.1	46	partial	(Q38RG6) Chorismate synthase

LjSGA_097197.1.1	36	partial	(O48785) Putative second messenger-dependent protein kinase
LjSGA_097321.1	83	partial	(Q3EA36) Protein At4g14160
LjSGA_097379.1	66	partial	(Q9M9H4) F14O23.10 protein
LjSGA_097535.1	181	partial	(Q6FY25) Similar to sp|P32380 Saccharomyces cerevisiae YDR356w NUF1
LjSGA_097657.1	84	partial	(Q3MGX0) ATPase
LjSGA_097839.1	60	partial	(Q9CAU8) Hypothetical protein T9J14.23
LjSGA_098057.1	41	partial	(Q6ZGD1) DENN (AEX-3) domain-containing protein-like
LjSGA_098110.1	60	partial	(Q9LRV9) Probable selenium-binding protein
LjSGA_098267.1	55	partial	(Q6EN40) Tetratricopeptide repeat (TPR)-containing protein-like
LjSGA_098323.1.1	85	partial	(Q2HUA0) Hypothetical protein
LjSGA_098539.1.2	37	partial	(Q332W3) Photosystem II protein L (Fragment)
LjSGA_098542.1	46	partial	(Q7GB12) Mitochondrial F1-ATPase, gamma subunit (ATP3_ARATH)
LjSGA_098551.1	68	partial	(Q258Y8) H0624F09.10 protein
LjSGA_098774.1.1	37	partial	(Q9MAI7) F12M16.4
LjSGA_098973.1	66	partial	(Q8GT65) Serpin-like protein (Fragment)
LjSGA_098999.1.1	58	partial	(Q9LIE7) Selenium-binding protein-like
LjSGA_098999.2	63	partial	(Q945B8) Growth-on protein GRO10
LjSGA_099264.1	41	partial	(Q8LAY7) Hypothetical protein
LjSGA_099424.2	51	partial	(Q9ZS31) NL27
LjSGA_099517.1	347	partial	(Q9SU33) PEARLI 1-like protein (At4g12500)
LjSGA_099700.1	54	partial	(Q69SU8) Putative tetratricopeptide repeat (TPR)-containing protein
LjSGA_099719.2	64	partial	(O49396) Putative cytochrome P450
LjSGA_099741.1	61	partial	(Q5XF05) At1g56440
LjSGA_099748.1	61	partial	(Q9AV77) 60S ribosomal protein L17
LjSGA_099753.1	149	partial	(Q949L4) Putative polyprotein (Fragment)

LjSGA_099898.1	107	partial	(Q3EC95) Protein At1g80960
LjSGA_099955.1	50	partial	(Q9SU03) Hydrolase-like protein
LjSGA_099985.1	36	partial	(Q4PKE6) Calcium-dependent protein kinase (Fragment)
LjSGA_100030.1	47	partial	(Q9ATR0) Brassinosteroid biosynthetic protein LKB
LjSGA_100037.1	86	partial	(Q6GL15) MGC69190 protein
LjSGA_100072.1	82	partial	(Q9M8N0) Hypothetical protein T21F11.4 (Hypothetical protein)
LjSGA_100216.1	70	partial	(O49012) Beta-1,3-glucanase 3 (Fragment)
LjSGA_100314.1	88	partial	(Q9FKK2) MADS-box protein-like
LjSGA_100455.2.1	37	partial	(Q2WGL6) Cycloartenol synthase
LjSGA_100683.2.1	104	partial	(Q9LYD3) Putative AP2/EREBP transcription factor (DREB3)
LjSGA_100733.1	44	partial	(Q39755) FSGTP1
LjSGA_100828.2	56	partial	(Q4ACU9) Thioredoxin h
LjSGA_101389.1	47	partial	(Q948P0) Aspartic proteinase 2
LjSGA_102284.1	70	partial	(Q53LH8) Dna-directed rna polymerase ii 8.2 kDa polypeptide (Ec 2.7.7.6)(Rpb10) (Rp10) (Abc10)
LjSGA_102334.1	57	partial	(Q9M075) Putative poly(A) polymerase
LjSGA_102491.1	226	partial	(Q3L234) Zinc finger protein
LjSGA_102681.1.1	76	partial	(Q67ZF6) Putative cytochrome B561
LjSGA_102939.1	81	partial	(Q8L4W8) P0696G06.27 protein
LjSGA_102946.1	145	partial	(Q8GXI5) Hypothetical protein At1g79070/YUP8H12R_17 (Hypothetical protein At1g79070)
LjSGA_102957.1	287	partial	(Q6UUN6) Putative poly(A)-binding protein
LjSGA_103070.2	92	partial	(Q9FT50) Hypothetical protein T25B15_90
LjSGA_103158.1	37	partial	(Q6DBN5) At5g05230
LjSGA_103351.1	189	partial	(Q6Z9C8) Putative heat shock factor RHSF2
LjSGA_103572.0.1	39	partial	(Q6ASS7) MSI type nucleosome/chromatin assembly factor C, putative

LjSGA_103592.1	20	partial	(Q9MD76) NADH dehydrogenase subunit 9
LjSGA_103603.1	97	partial	(Q9FRS3) F22O13.10
LjSGA_103614.0.1	34	partial	(Q84NP4) Hypothetical protein P0034A04.133
LjSGA_103661.1.1	86	partial	(Q8GT65) Serpin-like protein (Fragment)
LjSGA_103672.1	88	partial	(Q541V7) Hypothetical protein At2g24330
LjSGA_103903.1.1	102	partial	(Q3EB63) Protein At3g14350
LjSGA_104179.1	66	partial	(O81976) 14-3-3 Protein (Fragment)
LjSGA_104188.1	95	partial	(Q9LF17) Hypothetical protein T21H19_30
LjSGA_104392.2	52	partial	(Q9C817) Hypothetical protein F19K6.19 (Fragment)
LjSGA_104812.1	68	partial	(Q84L44) Putative histone H2A
LjSGA_105186.1	29	partial	(Q6IEP2) WRKY transcription factor 39
LjSGA_105195.1	73	partial	(Q69SH7) Putative pantothenate kinase 4
LjSGA_105402.1	282	partial	(Q38B00) Universal minicircle sequence binding protein (UMSBP), putative
LjSGA_105731.1	57	partial	(Q8RXS4) Putative N2,N2-dimethylguanine tRNA methyltransferase (Fragment)
LjSGA_105787.1	221	partial	(Q517D6) Latent nuclear antigen, putative
LjSGA_106026.1	88	partial	(Q9M033) Hypothetical protein T10O8_110
LjSGA_106027.1	76	partial	(Q8GVF5) Putative eukaryotic translation initiation factor 6
LjSGA_106087.2	41	partial	(Q2Z1Y8) 1-acyl-sn-glycerol-3-phosphate acyltransferase
LjSGA_106147.1	66	partial	(O65750) 26S protease regulatory subunit 6 (Fragment)
LjSGA_106280.1.1	61	partial	(Q84ZV2) Hypothetical protein
LjSGA_106299.1	41	partial	(Q9SCV9) Putative beta-galactosidase (EC 3.2.1.23)
LjSGA_106313.1.1	81	partial	unknown protein
LjSGA_106315.1	62	partial	(Q6TAS3) Aminodeoxychorismate synthase/glutamine amidotransferase
LjSGA_106674.1	46	partial	(Q6H7N3) Putative DnaJ homolog, subfamily C, member 9
LjSGA_107216.2.1	59	partial	(Q67IN9) Ribosomal protein S7

LjSGA_107581.1	50	partial	(Q4PSM7) Putative LOB domain protein
LjSGA_107886.1.1	63	partial	unknown protein
LjSGA_107958.1	53	partial	(Q6EPP4) EL5-like
LjSGA_107962.1	59	partial	(Q8VYU5) At1g18700/F6A14_19
LjSGA_107973.1	65	partial	(Q6NMR9) At5g45920
LjSGA_108231.1.1	43	partial	(Q5E916) At2g25740
LjSGA_108333.0.1	35	partial	(Q7XSB8) OJ990528_30.5 protein
LjSGA_108573.1	49	partial	(Q9LF57) Farnesylated protein ATFP6-like protein
LjSGA_110000.1.1	86	partial	(Q656N0) Putative STH1 protein
LjSGA_110024.1	179	partial	(Q2JWX2) Putative RNA-binding protein
LjSGA_110307.1	52	partial	(Q93YQ1) Hypothetical protein T16O11.22 (Raptor1B) (At3g08850)
LjSGA_110980.1	268	partial	(Q4FX62) Proteophosphoglycan 5
LjSGA_111083.1	50	partial	(O23551) Hypothetical protein AT4g17070
LjSGA_111560.1	71	partial	(O22733) F11P17.15 protein
LjSGA_111572.2	35	partial	(Q945N9) Prunasin hydrolase isoform PH B (EC 3.2.1.118) (Fragment)
LjSGA_111734.1	45	partial	(Q941I0) Putative quinone oxidoreductase (Fragment)
LjSGA_112262.1	55	partial	(Q9FK05) Pectinesterase
LjSGA_112271.1	99	partial	(O81834) Hypothetical protein AT4g27310
LjSGA_112406.1	29	partial	(Q9SZW8) Hypothetical protein F6G3.180 (Hypothetical protein AT4g30150)
LjSGA_112428.1	56	partial	(Q5VPG9) DNA-binding bromodomain-containing protein-like
LjSGA_112675.1	41	partial	(Q9M9H4) F14O23.10 protein
LjSGA_112923.1	40	partial	(Q2A0N7) COP9 signalosome subunit 6
LjSGA_113067.1	58	partial	(Q5NBI1) Putative cysteine proteinase inhibitor
LjSGA_113232.1	48	partial	(Q9LFA1) Hypothetical protein F8J2_70
LjSGA_113358.1	63	partial	(Q9ZW93) F5A8.5 protein

LjSGA_113468.1	50	partial	(Q3EBU0) Protein At2g25850
LjSGA_113657.0.1	39	partial	(Q49KT4) Ribosomal protein L2
LjSGA_113687.2	65	partial	(Q2L962) Cytochrome c heme attachment protein
LjSGA_113699.1	76	partial	(Q9XH70) Hypothetical protein p69RF (Fragment)
LjSGA_113851.1.1	50	partial	(Q9ZV85) F9K20.29 protein (At1g78670/F9K20_29)
LjSGA_113853.1	43	partial	(Q40464) NTGB3 (Fragment)
LjSGA_114084.1	244	partial	(Q7S753) Hypothetical protein
LjSGA_114657.1	44	partial	(Q39890) Calmodulin
LjSGA_114954.1	48	partial	(Q9M305) Hypothetical protein T21J18_40
LjSGA_115011.1	52	partial	(Q9C9W6) Putative trehalose-6-phosphate synthase; 46897-44149
LjSGA_115052.1	46	partial	(Q94JS1) AT4g26860/F10M23_200 (Putative proline synthetase associated protein)
LjSGA_115232.1	78	partial	(Q9GV13) Vasa-related protein CnVAS1
LjSGA_115298.1	45	partial	(Q6E6L5) 5-enol-pyruvylshikimate-phosphate synthase
LjSGA_115646.1	74	partial	(Q56W60) Hypothetical protein At5g12370
LjSGA_115723.1	146	partial	(Q949L3) Putative polyprotein (Fragment)
LjSGA_116165.1.1	78	partial	(Q5KQN4) Putative LIM domain containing protein
LjSGA_116239.1	212	partial	(Q8LJR7) Hypothetical protein
LjSGA_116240.1	60	partial	(Q7XPH4) OSJNBb0003B01.9 protein
LjSGA_116402.1	36	partial	(Q84YG5) Isoamylase isoform 3
LjSGA_116551.1	26	partial	(Q3E6Q7) Protein At2g44980
LjSGA_116558.0.1	47	partial	(Q7F0Q2) Putative 3-oxo-5-alpha-steroid 4-dehydrogenase
LjSGA_116672.1	245	partial	(Q84J64) WRKY transcription factor 22
LjSGA_116907.1	78	partial	(Q3EB44) Protein At3g19000
LjSGA_117171.1	48	partial	(Q6Z1G7) Putative pyruvate dehydrogenase E1 beta subunit isoform 1 protein
LjSGA_117427.1	94	partial	(Q6TY49) Reductase 1

LjSGA_117586.1	40	partial	(Q7XAF0) Tocopherol cyclase
LjSGA_117992.1.1	76	partial	(Q9FFU2) Genomic DNA, chromosome 5, P1 clone:MBG8 (AT5g54880/MBG8_15)
LjSGA_117996.1	331	partial	(Q7XP86) OSJNBa0021F22.14 protein
LjSGA_118021.1	93	partial	(Q94CH3) Seven transmembrane protein Mlo2
LjSGA_118130.1	96	partial	(Q9FJ30) Similarity to heat shock transcription factor HSF30
LjSGA_118133.1	74	partial	(Q3LHL0) TATA binding protein associated factor
LjSGA_118572.2	61	partial	(Q9SUQ2) Putative Ap2 domain protein (AT4g23750/F9D16_220) (At4g23750)
LjSGA_118984.2	48	partial	(Q8LEG7) Protein kinase-like protein
LjSGA_118993.1.1	31	partial	(Q9SD20) MS5-like protein (At3g51280)
LjSGA_119042.1	102	partial	(Q6FNZ3) Similar to sp|P53849 Saccharomyces cerevisiae YNL255c GIS2
LjSGA_119211.1	35	partial	(Q4U3E9) Putative L24 ribosomal protein
LjSGA_119220.1	39	partial	(Q6QP53) Hypothetical protein
LjSGA_119280.1	29	partial	(Q8GYR4) Hypothetical protein At3g08620/F17O14_9
LjSGA_119354.1.1	42	partial	(Q8L586) Hypothetical protein At4g09580
LjSGA_119414.1	66	partial	(Q9ZW93) F5A8.5 protein
LjSGA_119616.1	91	partial	(Q3E8M1) Protein At5g37340
LjSGA_119745.1.1	49	partial	(Q84R15) Hypothetical protein At2g07370 (Hypothetical protein At2g07360)
LjSGA_119896.1	70	partial	(Q8VXZ9) Putative DNA binding protein ACBF
LjSGA_119934.1	89	partial	(Q8W214) Single-stranded DNA binding protein precursor
LjSGA_119962.1	208	partial	(Q4Q1R0) Universal minicircle sequence binding protein (UMSBP), putative
LjSGA_120242.1	63	partial	(Q9FX78) F19K19.6 protein
LjSGA_120858.1.1	37	partial	(Q332W3) Photosystem II protein L (Fragment)
LjSGA_121266.1	76	partial	(Q3ED88) Protein At1g20510
LjSGA_121474.1	97	partial	(Q6VWJ5) Fructokinase 3
LjSGA_121507.0.1	56	partial	(Q8L625) Hypothetical protein At1g73660

LjSGA_121531.1.1	32	partial	(Q9SGR8) T23E18.8
LjSGA_121649.1	84	partial	(Q9SYQ0) F9H16.15 protein
LjSGA_121900.1	49	partial	(Q9FEE2) Tonneau 2 (Hypothetical protein At5g18580)
LjSGA_122090.1	70	partial	(Q9LK22) Gb|AAF57656.1 (At3g27310) (Hypothetical protein At3g27310) (CDC48-interacting UBX-domain protein) (Hypothetical protein)
LjSGA_122223.1	30	partial	(Q43611) Hypothetical protein (Fragment)
LjSGA_122339.1	43	partial	(Q3E951) Protein At5g25560
LjSGA_122466.1.1	163	partial	(Q7XAC5) Embryo-specific urease (EC 3.5.1.5)
LjSGA_122686.1	64	partial	(Q9SU03) Hydrolase-like protein
LjSGA_122833.1	36	partial	unknown protein
LjSGA_122875.1	127	partial	(Q7S753) Hypothetical protein
LjSGA_123575.1	64	partial	(Q7X7E9) OSJNBa0035M09.8 protein
LjSGA_123604.1	37	partial	(Q332W3) Photosystem II protein L (Fragment)
LjSGA_123715.1	84	partial	(Q45NP0) Methylesterase (Fragment)
LjSGA_123843.1	124	partial	(Q9XIR3) F13O11.12 protein
LjSGA_124169.1	99	partial	(Q41695) Pectinacetylesterase precursor
LjSGA_124223.0.1	74	partial	(Q9FKU9) Berberine bridge enzyme-like protein
LjSGA_124245.1	152	partial	(Q6IWH2) Lipid transfer protein
LjSGA_124586.1	40	partial	(Q5UNS1) Arginase 2
LjSGA_124834.1	77	partial	(Q75WU3) Leucine-rich repeat receptor-like protein kinase 1
LjSGA_124886.1	68	partial	(Q8L8S5) Putative heat shock protein
LjSGA_124992.1	117	partial	(Q9LE86) Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:MJM20 (MJM20.4 protein)
LjSGA_125102.1	234	partial	(Q8DGQ9) RNA-binding protein
LjSGA_125121.1	93	partial	(Q9LTK3) Homeodomain transcription factor-like

LjSGA_125354.1.1	49	partial	(Q2PMM9) NADH-plastoquinone oxidoreductase subunit 5
LjSGA_125357.1	168	partial	(Q6VG41) Gag protein
LjSGA_125395.1	80	partial	(Q67YE7) Protein-tyrosine-phosphatase-like protein
LjSGA_125460.1	43	partial	(Q7XAF0) Tocopherol cyclase
LjSGA_125516.1	44	partial	(Q2HIG1) At3g17590
LjSGA_126126.1	49	partial	(Q541X2) Putative alpha subunit of F-actin capping protein
LjSGA_126143.1.1	91	partial	(Q5RFI2) Hypothetical protein DKFZp469D0532
LjSGA_126291.1	43	partial	(Q2PMM9) NADH-plastoquinone oxidoreductase subunit 5
LjSGA_126402.1	33	partial	(Q5JN42) Phosphatidylserine decarboxylase-like
LjSGA_126822.1	53	partial	(Q9XEY7) Trehalase 1 GMTRE1
LjSGA_126977.1	46	partial	(Q9FS08) UV-damaged DNA binding protein
LjSGA_126992.1	77	partial	(P93042) Root hair defective 3 (Hypothetical protein At3g13870)
LjSGA_127589.1	41	partial	(O04539) F20P5.21 protein
LjSGA_128021.2	110	partial	(Q9FF48) Gb|AAB97123.1
LjSGA_128169.1.1	57	partial	(Q8GU88) PDR-like ABC transporter
LjSGA_128550.0.1	74	partial	(Q9SJZ8) Putative non-LTR retroelement reverse transcriptase
LjSGA_128696.1	156	partial	(Q9LEX1) CaLB protein (At3g61050)
LjSGA_128883.1	34	partial	(Q9AST9) Hypothetical protein At1g73110/F3N23_39
LjSGA_129152.1	53	partial	(Q8RWU7) Putative membrane trafficking factor (CDC48-interacting UBX-domain protein)
LjSGA_129390.1	58	partial	(Q9SXU6) Pyruvate kinase (Fragment)
LjSGA_129394.1	52	partial	(O80564) Hypothetical protein At2g43940
LjSGA_129402.1.1	50	partial	(Q9LXT9) Callose synthase catalytic subunit-like protein
LjSGA_129492.1	80	partial	(Q9SVK5) Putative mitochondrial protein
LjSGA_129501.1	36	partial	(Q4U3E9) Putative L24 ribosomal protein
LjSGA_129556.1	135	partial	(O96063) Myosin heavy chain (Fragment)

LjSGA_129661.1	78	partial	(O82343) Expressed protein (Hypothetical protein At2g46260)
LjSGA_129887.1	138	partial	(Q3L234) Zinc finger protein
LjSGA_130110.1	67	partial	(Q9M7P3) GTP-binding protein
LjSGA_130169.1.1	83	partial	(Q9LZS7) Hypothetical protein F17C15_30 (Putative lipase/acylhydrolase) (Hypothetical protein At5g03610)
LjSGA_130244.1.1	48	partial	(Q9FJ30) Similarity to heat shock transcription factor HSF30
LjSGA_130403.0.2	30	partial	(Q9ZRH5) NADP-malic enzyme
LjSGA_130664.1	46	partial	(Q58FG4) Homogentisate phytylprenyltransferase
LjSGA_130728.1	61	partial	unknown protein
LjSGA_130806.1	121	partial	(Q2V4H0) Protein At1g53800
LjSGA_130848.1	60	partial	(Q9LQ19) F16P17.2 protein
LjSGA_131100.1	62	partial	(Q6V8R1) Putative GATA-type zinc finger protein (Fragment)
LjSGA_131380.1	97	partial	unknown protein
LjSGA_131627.1	108	partial	(Q949L4) Putative polyprotein (Fragment)
LjSGA_131903.1	58	partial	(Q9SEX4) Ornithine carbamoyltransferase OOCT1 (EC 2.1.3.3)
LjSGA_131922.1	208	partial	(Q512P7) Hypothetical protein
LjSGA_131991.0.1	46	partial	(Q8GYG0) Hypothetical protein At5g08139/At5g08140 (Hypothetical protein At5g08139)
LjSGA_132006.1	67	partial	(Q9SB69) Hypothetical protein F22K18.50 (Hypothetical protein AT4g24750)
LjSGA_132088.0.1	31	partial	(Q49KZ8) Photosystem I P700 apoprotein A1
LjSGA_132096.1	102	partial	(Q8LPQ5) AT3g18290/MIE15_8
LjSGA_132222.1	184	partial	(Q4Q1R0) Universal minicircle sequence binding protein (UMSBP), putative
LjSGA_132253.1	89	partial	(Q84WW3) Hypothetical protein At5g15070
LjSGA_132312.1	44	partial	(Q851E2) Putative P-type ATPase
LjSGA_132387.1	33	partial	(Q9LFR8) TCP-1 chaperonin-like protein
LjSGA_132576.0.1	46	partial	(Q84P29) Seed calcium dependent protein kinase a

LjSGA_133188.1	75	partial	(Q6NLQ0) At3g20475
LjSGA_133220.1	95	partial	(Q8GZ49) Hypothetical protein At1g58190/T15M6_19 (Hypothetical protein At1g58190)
LjSGA_133295.1	91	partial	(Q9LN45) F18O14.25
LjSGA_133315.1	34	partial	(Q6L8U0) Auxin response factor 4
LjSGA_133441.0.1	69	partial	(Q2PMR3) 50S ribosomal protein L33
LjSGA_133460.1	95	partial	unknown protein
LjSGA_133505.1	80	partial	(Q8LNH8) Glycine-rich protein, putative
LjSGA_133629.1	37	partial	(Q9FHR5) Similarity to COP1-interacting protein 7
LjSGA_133694.1	123	partial	(Q2QQS5) Cyclin, N-terminal domain, putative
LjSGA_133709.1	38	partial	(Q6ZIR2) DegP protease-like
LjSGA_133740.1.1	66	partial	(Q9LN49) F18O14.21
LjSGA_133805.1	71	partial	(Q84K72) Hypothetical protein At1g06510
LjSGA_133806.1	71	partial	(Q9LPZ4) T23J18.7 (Hypothetical protein At1g11400)
LjSGA_134343.1.1	54	partial	(Q5N7S1) 24 kDa seed maturation protein-like
LjSGA_134354.1	273	partial	(Q7XP86) OSJNBa0021F22.14 protein
LjSGA_134392.2	71	partial	(Q9FR42) Anther-specific myb-related protein 1
LjSGA_134451.1	50	partial	(Q6R3K8) Metal-nicotianamine transporter YSL4
LjSGA_134614.1.1	65	partial	(Q6Z0W7) Hypothetical protein OSJNBb0026D20.9
LjSGA_134779.1	103	partial	(O64815) Similar to hookless1 (HLS1)
LjSGA_134987.1	107	partial	(Q8W2C0) Functional candidate resistance protein KR1
LjSGA_135269.1	179	partial	(Q8LP36) PlCYC4 protein (Fragment)
LjSGA_135452.1	48	partial	(Q9SX86) F16N3.17 protein
LjSGA_135715.1	122	partial	(Q8W553) AT5g35180/T25C13_60
LjSGA_136660.1	64	partial	(Q9ARU3) Putative xylosyltransferase I
LjSGA_136793.1	37	partial	(Q9LKG4) Putative DNA binding protein

LjSGA_136836.1	48	partial	(Q8W040) Dihydrofolate synthetase /folylpolyglutamate synthetase
LjSGA_136899.1	51	partial	(Q259X8) B0811B10.8 protein
LjSGA_136900.1	38	partial	(Q6Z4T7) Hypothetical protein OSJNBa0054L03.38 (Hypothetical protein OJ1134_B10.7)
LjSGA_137333.1.1	56	partial	(Q9FHB6) Genomic DNA, chromosome 5, TAC clone:K24M7 (Hypothetical protein At5g52450)
LjSGA_137437.1	70	partial	(O22733) F11P17.15 protein
LjSGA_137526.0.1	44	partial	(Q3EAR7) Protein At3g42180
LjSGA_137600.1	55	partial	(Q949L3) Putative polyprotein (Fragment)
LjSGA_137731.1	195	partial	(Q949L4) Putative polyprotein (Fragment)
LjSGA_138013.1	46	partial	(Q9LR06) F10A5.14
LjSGA_138311.1	69	partial	(Q9FN15) Gb|AAC18972.1 (Hypothetical protein At5g67370)
LjSGA_138441.1	39	partial	(Q93ZN3) AT4g17070/dl4565c
LjSGA_138917.1	128	partial	(Q9AXF3) Lipid transfer protein
LjSGA_139204.1	77	partial	(Q9FRK9) Hypothetical protein F22H5.9 (Hypothetical protein At1g75180)
LjSGA_139237.2	46	partial	(Q8L845) Hypothetical protein At2g01220:At2g01230 (Hypothetical protein At2g01220)
LjSGA_139526.1.1	23	partial	(Q8GYJ1) Hypothetical protein
LjSGA_139590.1	44	partial	(Q6ZIE6) Putative permease
LjSGA_139591.1.2	37	partial	(Q332W3) Photosystem II protein L (Fragment)
LjSGA_139607.1.1	29	partial	(Q9FK38) DNA repair protein-like
LjSGA_139675.1	96	partial	(Q9XGC0) Starch synthase isoform SS III (EC 2.4.1.21)
LjSGA_139711.1	144	partial	(Q7S753) Hypothetical protein
LjSGA_139724.1	52	partial	(O49896) Hypothetical protein
LjSGA_139826.1	43	partial	(Q9LVD9) Gb|AAC28507.1 (At3g21690)
LjSGA_140053.0.1	49	partial	(Q84R15) Hypothetical protein At2g07370 (Hypothetical protein At2g07360)
LjSGA_140321.1	71	partial	(Q71G33) COP8-like protein
LjSGA_140700.1	128	partial	(Q8LEM2) Hypothetical protein

LjSGA_140758.1.1	118	partial	(Q2HUK0) Cyclin-like F-box
LjSGA_140767.0.1	55	partial	unknown protein
LjSGA_140894.2	46	partial	(Q7PSE2) ENSANGP00000015076
LjSGA_140961.1	73	partial	(O65519) Hypothetical protein F23E13.170 (Hypothetical protein AT4g36280)
LjSGA_141113.1	73	partial	(O65519) Hypothetical protein F23E13.170 (Hypothetical protein AT4g36280)
LjSGA_141248.1	68	partial	(Q24BQ3) Zinc knuckle family protein
LjSGA_141276.1	51	partial	(Q8H1E6) Putative growth regulator
LjSGA_141425.0.1	44	partial	(Q56SE1) Methyl jasmonate esterase
LjSGA_141855.1	42	partial	(Q9XFE8) Chloroplast envelope calcium ATPase (Fragment)
LjSGA_141883.1	106	partial	(Q91594) Cellular nucleic acid binding protein
LjSGA_141893.0.1	37	partial	(Q2VWB7) Prf interactor 30137
LjSGA_142272.1	38	partial	(Q2PMN3) Photosystem I subunit VII
LjSGA_142772.2	115	partial	(Q2PF19) Cytochrome P450
LjSGA_143243.1	62	partial	(Q9ASU6) At1g42440/F7F22_7 (Hypothetical protein At1g42440)
LjSGA_143331.1	59	partial	(Q9FFU2) Genomic DNA, chromosome 5, P1 clone:MBG8 (AT5g54880/MBG8_15)
LjSGA_143408.1	64	partial	(Q75LC8) Putative exoribonuclease
LjSGA_143464.1	48	partial	(Q941I6) DNA mismatch repair protein
LjSGA_143513.1	46	partial	(Q8LBE2) Hypothetical protein
LjSGA_143582.1	45	partial	(Q8VZB8) Hypothetical protein At5g55810; MDF20.25 (Hypothetical protein At5g55810)
LjSGA_143738.1	39	partial	(Q9S834) ATP-dependent Clp protease subunit ClpP (At1g02560) (ATP-dependent Clp protease proteolytic subunit ClpP5) (NClpP1)
LjSGA_143950.1	37	partial	(Q940D1) At1g64110/F22C12_22
LjSGA_144105.1	51	partial	(Q9LHE9) Putative myosin
LjSGA_144139.1.1	47	partial	(Q7A559) Pyruvate kinase
LjSGA_144154.2	45	partial	(Q8S8Z6) Syringolide-induced protein 13-1-1

LjSGA_144259.1	66	partial	(Q9SV17) Hypothetical protein F3L17.100 (Hypothetical protein AT4g31530)
LjSGA_144769.1	47	partial	(Q3ECD7) Protein At1g72550
LjSGA_144821.1	44	partial	(Q53JD1) ATPase, calcium-transporting-related (Fragment)
LjSGA_144865.1	41	partial	(Q5IRX9) ARF6
LjSGA_144922.1	47	partial	(Q93X14) Amino acid permease AAP3
LjSGA_145042.1	44	partial	(Q9FVE9) Cytosolic aconitase
LjSGA_145133.1	78	partial	(Q39873) Lea protein precursor
LjSGA_145144.0.1	47	partial	(Q2V341) Protein At5g27640
LjSGA_145237.1	59	partial	(Q9SY90) T25B24.5 protein
LjSGA_145263.1	53	partial	(Q8RY18) AT5g43560/K9D7_6
LjSGA_145265.1	220	partial	(O82388) Expressed protein (Hypothetical protein At2g29670) (At2g29670/T27A16.23)
LjSGA_145530.1	89	partial	(Q9M1V9) Hypothetical protein F16M2_160 (At3g63310)
LjSGA_145568.1	37	partial	(Q2QQX3) Expressed protein
LjSGA_145689.1	46	partial	(Q9ZQF1) Putative salt-inducible protein
LjSGA_145848.1	44	partial	(Q53M53) Hemolysin A, putative
LjSGA_145871.1	98	partial	(Q9FSX3) Hypothetical protein ORF1
LjSGA_145902.1.1	84	partial	(Q506K3) Squalene monooxygenase
LjSGA_146013.2	55	partial	(Q84P29) Seed calcium dependent protein kinase a
LjSGA_146047.1	34	partial	(Q9SV17) Hypothetical protein F3L17.100 (Hypothetical protein AT4g31530)
LjSGA_146164.1.1	42	partial	(Q66WR9) Sterol delta-7 reductase (Fragment)
LjSGA_146350.1	76	partial	(Q5K4L5) Villin 1 (Fragment)
LjSGA_146469.1	35	partial	(Q84N48) CRS2-associated factor 2
LjSGA_146478.1	116	partial	(Q9LMJ1) F10K1.31 protein
LjSGA_146485.1	58	partial	(Q9M3Y4) Germin-like protein
LjSGA_146629.1	62	partial	(Q6Z0P5) Putative sexual differentiation process protein isp4

LjSGA_146823.1	31	partial	(Q9XEI3) Beta-D-glucan exohydrolase isoenzyme ExoI
LjSGA_147112.1	28	partial	(Q49KT6) Hypothetical chloroplast RF2
LjSGA_147322.1	44	partial	unknown protein
LjSGA_147477.1.1	58	partial	(Q547H2) ARL2 G-protein
LjSGA_147531.1	143	partial	(O04180) Pge1 protein
LjSGA_147738.1	38	partial	(Q6H6L9) Root-specific protein RCc3
LjSGA_147748.1	135	partial	(Q8S9H4) Ethylene response factor 1
LjSGA_147920.1	57	partial	(Q8W0S8) Hypothetical protein
LjSGA_147935.1	91	partial	(Q9SFE4) T26F17.14 (At1g21910) (TINY like protein)
LjSGA_147985.1	36	partial	(Q9FJK3) Similarity to MADS-box DNA-binding protein (MADS-box family protein)
LjSGA_148098.0.1	36	partial	(Q5I7K6) Ribosomal protein L7
LjSGA_148099.1	41	partial	(Q2NVN7) Enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase)
LjSGA_148154.1	199	partial	(Q9LP76) T1N15.10
LjSGA_148425.1	36	partial	(Q6Z3T8) Auxin-regulated protein-like
LjSGA_148487.1	41	partial	(Q8H925) WD domain containing protein, putative
LjSGA_148519.1	36	partial	(Q9FLK9) Leucine-rich repeat disease resistance protein-like (Cf-5 disease resistance protein-like)
LjSGA_148703.1	164	partial	(Q98D39) Myo-inositol-1-monophosphotase
LjSGA_148720.1	167	partial	(Q6XGD7) VC0178-like protein
LjSGA_148942.1.1	53	partial	(Q9FN21) Similarity to unknown protein
LjSGA_149056.1	55	partial	unknown protein
LjSGA_149392.1	45	partial	(Q9LNT7) T20H2.10 protein
LjSGA_149766.1	65	partial	(Q9FJS0) Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MQD22
LjSGA_150180.1	54	partial	(Q9M390) Peptide transport-like protein
LjSGA_150256.1	59	partial	(Q651X6) Putative cellulose synthase-like protein OsCslE1
LjSGA_150405.1.1	48	partial	(Q9LQU6) F10B6.25

LjSGA_150780.1	51	partial	unknown protein
LjSGA_150782.2	63	partial	(Q9SML5) Knolle

Supplemental Table16. Tandem gene duplications in the *L. japonicus* HGS.

	chr1	chr2	chr3	chr4	chr5	chr6	unmapped	total
Number of predicted genes in HGS	**2376**	**1880**	**1680**	**1726**	**1464**	**783**	**1471**	**11380**
Number of tandem duplicated genes	**127**	**123**	**164**	**117**	**87**	**62**	**90**	**770**
Number of groups	46	52	68	47	36	24	37	310
Maximum copy numebr in a group	7	6	5	6	6	8	5	
Number of genes with homologs within 100kb range	177	180	213	166	114	107	110	1067