

Table S3a. All screened mutants from S-RNAi library

	Number	Chromosome	Mapping position	Knockdown genes	Mapping range	Identity	Description
1	S5	chr9	193130 to 192941	NO09G00440	Exon	190/190 (100%)	Light-harvesting protein
			195503 to 195692	NO09G00450	Exon	190/190 (100%)	VCP1
		chr25	241154 to 240969	NO25G00860	Exon	157/186 (84.41%)	VCP1
2	S19	chr14	157627 to 157778	IG region	IG region		
3	S20	chr4	1184210 to 1184444			234/235 (99.57%)	
			1184203 to 1184340			121/138 (87.68%)	
			1184244 to 1184373			114/130 (87.69%)	
			1184203 to 1184307			91/105 (86.67%)	
			1184276 to 1184373			84/98 (85.71%)	
			1184203 to 1184303	NO04G04380	Exon	83/101 (82.18%)	unknown protein
4	S27	chr18	140768 to 140847			76/79 (96.2%)	
			141072 to 141114	NO18G00330	Exon	43/43 (100%)	light harvesting complex protein
5	S32	chr14	123813 to 123963	NO14G00310	Exon	150/151 (99.34%)	Unknown protein
			118115 to 118264			149/150 (99.33%)	
			118975 to 119124	NO14G00290		149/150 (99.33%)	Circumsporozoite protein
			122353 to 122502			149/150 (99.33%)	
			123453 to 123602			149/150 (99.33%)	
			123693 to 123842			149/150 (99.33%)	
			124673 to 124822			149/150 (99.33%)	
			125773 to 125922			149/150 (99.33%)	
			126993 to 127142			149/150 (99.33%)	
			127233 to 127382			149/150 (99.33%)	
			129329 to 129478	NO14G00310	Exon	149/150 (99.33%)	Unknown protein
							
6	S33	chr3	552095 to 551916	NO03G01760	Exon		Dihydrolipoyl dehydrogenase 1, mitochondrial
7	S38	chr20	564421 to 564573			152/153 (99.35%)	
			568224 to 568376	NO20G01880	Exon	152/153 (99.35%)	Unknown protein
8	S47	chr25	254437 to 254274	NO25G00900	Exon	164/164 (100%)	beta glucosidase 42
		chr11	407978 to 408055	NO11G01120	Exon	70/78 (89.74%)	Unknown protein
9	S58	chr27	312261 to 312487	NO27G00920	Exon	227/227 (100%)	Glyceraldehyde-3-phosphate dehydrogenase
			309778 to 309654	NO27G00910	Exon	96/125 (76.8%)	Glyceraldehyde-3-phosphate dehydrogenase
		chr3	113075 to 112901	NO03G00350	Exon	158/175 (90.29%)	DNA-directed RNA polymerase II subunit rpb3
		chr8	488714 to 488589	NO08G01560	Exon	102/126 (80.95%)	Glyceraldehyde-3-phosphate dehydrogenase
		chr9	968027 to 968194	NO09G03360	Exon	127/168 (75.6%)	glyceraldehyde-3-phosphate dehydrogenase of plastid 1
10	S59	chr3	841091 to 840985	NO03G02800	Exon	106/107 (99.07%)	small subunit of nuclear cap-binding protein complex
11	S63	chr7	671667 to 671517	NO07G02250	Exon	150/151 (99.34%)	unknown protein
12	S93	chr13	126052 to 126245	NO13G00380	Exon	192/194 (98.97%)	Unknown protein
			132889 to 133082	NO13G00400	Exon	191/194 (98.45%)	Unknown protein
			142495 to 142680		Exon	169/186 (90.86%)	Unknown protein
			142063 to 142160		Exon	83/98 (84.69%)	
			141942 to 142031		Exon	77/90 (85.56%)	
			142254 to 142352		Exon	83/99 (83.84%)	
			142123 to 142211		Exon	76/89 (85.39%)	
			142315 to 142379		Exon	59/65 (90.77%)	
			142326 to 142391		Exon	59/66 (89.39%)	
			142435 to 142532		Exon	80/98 (81.63%)	
			142002 to 142100		Exon	80/99 (80.81%)	
			142170 to 142262		Exon	76/93 (81.72%)	
			142242 to 142334		Exon	76/93 (81.72%)	Unknown protein
			141978 to 142070		Exon	75/93 (80.65%)	
				NO13G00420			
		chr1	558402 to 558455	NO01G02190	3'UTR	54/54 (100%)	Serine hydroxymethyltransferase

13	S103	chr6	449244 to 448831			414/414 (100%)	
			449262 to 448831	NO06G01400	Exon	432/432 (100%)	Amine oxidase
14	S112	chr16	846121 to 846006		Exon	116/116 (100%)	
			845284 to 845195		Exon	90/90 (100%)	
			845522 to 845437		Exon	86/86 (100%)	Dolichyl-diphosphooligosaccharide--protein
			845854 to 845774	NO16G02910	Exon	81/81 (100%)	glycosyltransferase
15	S114	chr18	432339 to 431926	NO18G01260	5'UTR	413/414 (99.76%)	TPR domain protein
			538644 to 538274	NO18G01680	Exon+3'UTR	344/372 (92.47%)	Unknown protein
			753805 to 753669	NO18G02310	5'UTR	134/138 (97.1%)	Unknown protein
			249219 to 249159	NO18G00590	IG region+5'UTR	53/61 (86.89%)	Unknown protein
			252824 to 252890		IG region	56/67 (83.58%)	
		chr6	428748 to 428335		IG region	410/414 (99.03%)	
			539247 to 539617	NO06G01750	Exon+3'UTR	347/372 (93.28%)	Unknown protein
			428829 to 429082		IG region	253/254 (99.61%)	
			956823 to 957181	NO06G03460	5'UTR+Exon	322/361 (89.2%)	Unknown protein
			266375 to 266209		IG region	130/169 (76.92%)	
			586335 to 586262		IG region	61/74 (82.43%)	
			384200 to 384134	NO06G01200	Intron	56/67 (83.58%)	Atlastin-like protein
		chr4	1443313 to 1442900	NO04G05170	Exon+Intron	404/414 (97.58%)	Unknown protein
			389865 to 389498	NO04G01240	Exon+3'UTR	359/368 (97.55%)	Unknown protein
			673510 to 673845	NO04G02510	Intron	306/339 (90.27%)	Unknown protein
			555837 to 556189	NO04G01910	IG region+3'UTR	297/355 (83.66%)	Agc (Camp-cgmp-dependent and protein kinase c) kinase family protein
			812979 to 813248	NO04G03030	5'UTR+Exon	236/283 (83.39%)	Unknown protein
			671659 to 671837		IG region	155/188 (82.45%)	
			1436276 to 1436197	NO04G05150	Intron	79/80 (98.75%)	Unknown protein
			196873 to 197066	NO04G00540	3'UTR	150/195 (76.92%)	Transmembrane protein
				NO04G00550	Exon+Intron		SET domain protein
			902108 to 902060		IG region	46/49 (93.88%)	
			1406593 to 1406659		IG region	56/67 (83.58%)	
			1406672 to 1406722		IG region	45/51 (88.24%)	
		chr12	196820 to 197232	NO12G00530	3'UTR	403/414 (97.34%)	Unknown protein
			620203 to 619837	NO12G02160	Exon+Intron	357/368 (97.01%)	Ph-response regulator protein pala rim20
			592551 to 592901	NO12G02090	5'UTR	322/352 (91.48%)	Pre-mrna splicing factor prp38
			639629 to 639263	NO12G02230+NO12G02240	Exon+IG region+Exon	335/373 (89.81%)	Cell cycle arrest protein BUB3
			180493 to 180322		IG region	142/173 (82.08%)	
			1070731 to 1070790		IG region	54/60 (90%)	
		chr5	567866 to 568278	NO05G02110	3'UTR	397/414 (95.89%)	Unknown protein
			578488 to 578123	NO05G02150	Exon+3'UTR	350/367 (95.37%)	Unknown protein
			1417000 to 1417365	NO05G05320	Exon+3'UTR	348/368 (94.57%)	Zinc finger bed domain-containing 1-like protein
			899020 to 898657	NO05G03400	Exon+3'UTR	339/365 (92.88%)	Unknown protein
			1090651 to 1090296	NO05G04230	Exon+3'UTR	331/357 (92.72%)	Unknown protein
			1055004 to 1055326	NO05G04080	3'UTR	298/324 (91.98%)	Unknown protein
			1410494 to 1410766		IG region	238/276 (86.23%)	
			1295721 to 1295924		IG region	179/206 (86.89%)	
			629900 to 630087	NO05G02370	Exon+3'UTR	153/188 (81.38%)	Unknown protein
			154841 to 154693		IG region	127/150 (84.67%)	
			621786 to 621852	NO05G02340	5'UTR	59/67 (88.06%)	Unknown protein
				NO05G02350	5'UTR+Exon		Ferredoxin (2fe-2s)
			1446253 to 1446285	NO05G05390	Intron	31/33 (93.94%)	Major facilitator superfamily mfs_1
		chr3	1113026 to 1112613	NO03G03770	Exon+3'UTR	393/414 (94.93%)	Unknown protein
				NO03G03780	3'UTR		Elongation of fatty acids protein
			165520 to 165749		IG region	205/231 (88.74%)	
			1570046 to 1569890		IG region	139/157 (88.54%)	
			674304 to 674461		IG region	138/160 (86.25%)	
			872227 to 872408	NO03G02890	Exon+3'UTR	148/185 (80%)	Ania-6a type cyclin
			150084 to 150203		IG region	105/122 (86.07%)	
			1096353 to 1096418		IG region	60/66 (90.91%)	
			787093 to 787028		IG region	58/66 (87.88%)	

		chr20	871891 to 871988		IG region	84/100 (84%)	
			556057 to 555665	NO20G01850	3'UTR	377/394 (95.69%)	DNA-directed RNA polymerase I subunit RPA2,putative
			488920 to 488587		IG region	323/335 (96.42%)	
			504774 to 505072	NO20G01660	Exon+3'UTR	284/301 (94.35%)	anaphase promoting complex protein
			259083 to 259338	NO20G00760	5'UTR	242/256 (94.53%)	Phosphoglycerate mutase
				NO20G00770	5'UTR+Exon		Vacuolar protein sorting-associated protein 45
			429536 to 429174		IG region	311/370 (84.05%)	
			258991 to 259056		IG region	57/66 (86.36%)	
			423734 to 423663		IG region	62/74 (83.78%)	
16	S115	chr12	556248 to 556437	NO12G01960	Exon	190/190 (100%)	Protein of unknown function (DUF726)
17	S125	chr2	400084 to 400282	NO02G01300	Exon	198/199 (99.5%)	Nicotinamide nucleotide transhydrogenase
18	S129	chr15	274938 to 275098	NO15G00890	Exon	161/161 (100%)	Ribosomal rna large subunit methyltransferase h
19	S133	chr24	451995 to 451680	NO24G01680	Exon+3'UTR	315/316 (99.68%)	Photosystem II oxygen-evolving enhancer protein 1
		chr27	463911 to 463876	NO27G01420	Intron	33/36 (91.67%)	Omp85
20	S136	chr2	1556906 to 1557166	NO02G05820	Exon	261/261 (100%)	Erythromycin esterase
21	S140	chr29	239926 to 239744		Exon	183/183 (100%)	
			239466 to 239403	NO29G00620	Exon	64/64 (100%)	Unknown protein
22	S145	chr3	1244792 to 1245066	NO03G04310	Exon	274/275 (99.64%)	Homocysteine s-methyltransferase
23	S146	chr2	1450431 to 1450590			159/160 (99.38%)	
			1450226 to 1450307	NO02G05440	Exon	80/82 (97.56%)	Unknown protein
			1452727 to 1452568			160/160 (100%)	
			1452933 to 1452851	NO02G05450	Exon	82/83 (98.8%)	Unknown protein
			1455302 to 1455461			160/160 (100%)	
			1455096 to 1455178	NO02G05460	Exon	82/83 (98.8%)	Unknown protein
			1458152 to 1458070			82/83 (98.8%)	
			1457946 to 1457787	NO02G05470	Exon	160/160 (100%)	Unknown protein
			1460315 to 1460397			82/83 (98.8%)	
			1460521 to 1460680	NO02G05480	Exon	160/160 (100%)	Unknown protein
24	S148	chr2	1454486 to 1454815	NO02G05460	Exon+3'UTR	329/330 (99.7%)	Unknown protein
			1459705 to 1460034	NO02G05480	Exon+3'UTR	329/330 (99.7%)	Unknown protein
			1453543 to 1453214	NO02G05450	Exon+3'UTR	328/330 (99.39%)	Unknown protein
			1458762 to 1458433	NO02G05470	Exon+3'UTR	328/330 (99.39%)	Unknown protein
			1449616 to 1449944	NO02G05440	Exon+3'UTR	314/329 (95.44%)	Unknown protein
25	S149	chr5	720059 to 720203	NO05G02730	Exon	144/145 (99.31%)	Nad-dependent epimerase dehydratase
26	S156	chr22	216995 to 217338	NO22G00640	Exon	343/344 (99.71%)	lysine-ketoglutarate reductase/saccharopine dehydrogenase bifunctional enzyme
27	S161	chr1	638297 to 638121	NO01G02450	Exon	176/177 (99.44%)	Unknown protein
28	S162	chr2	1346486 to 1346668	NO02G05020	Exon	183/183 (100%)	Serine/threonine-protein phosphatase
		chr11	407736 to 407633	NO11G01120	3'UTR	103/104 (99.04%)	Unknown protein
29	S167	chr11	540571 to 540827	NO11G01630	Exon	257/257 (100%)	Acyl dehydratase
30	S169	chr23	256714 to 256873			160/160 (100%)	
			256491 to 256567	NO23G00640	Exon	77/78 (98.72%)	Heat shock protein 70
		chr15	421894 to 421984	NO15G01500	Exon	72/91 (79.12%)	Luminal binding protein
		chr8	246085 to 245996	NO08G00730	Exon	69/90 (76.67%)	Mediator of RNA polymerase II transcription subunit 37a
31	S170	chr29	166330 to 166227	NO29G00410	3'UTR	104/104 (100%)	Unknown protein
		chr18	484525 to 484565	NO18G01460	3'UTR	41/41 (100%)	Asparagine synthetase
32	S175	chr1	1371395 to 1371452			58/58 (100%)	
			1371202 to 1371247			45/46 (97.83%)	
			1371661 to 1371694	NO01G05160	Exon	33/34 (97.06%)	Histone H5
		chr3	599794 to 599825	NO03G01940	Exon		Histone h1
				NO03G01950	3'UTR	30/32 (93.75%)	Nucleolar mif4g domain-containing protein 1
33	S185	chr28	76489 to 76639		Exon+3'UTR	151/151 (100%)	
			76894 to 76944	NO28G00190	Exon	51/51 (100%)	ubiquitin 8
34	S194	chr4	614126 to 613963	NO04G02130	Exon	164/164 (100%)	pas-domain protein
35	S198	chr12	438420 to 438672	NO12G01410	Exon	253/253 (100%)	Adaptor protein complex AP-1, gamma subunit
		chr22	26238 to 26340			98/103 (95.15%)	
			25862 to 25922	NO22G00060	Exon	61/61 (100%)	Trypsin family
36	S199	chr21	627284 to 627169			116/116 (100%)	
			627088 to 626994	NO21G02120	Exon	95/95 (100%)	Unknown protein

37	S201	chr7	1177576 to 1177704 1177328 to 1177434 1177853 to 1177928 1178078 to 1178145	NO07G04210	Exon	129/129 (100%)	
38	S207	chr15 chr23 chr8	421459 to 421780 255769 to 255890 248078 to 248002	NO15G01500	Exon Exon Exon	107/107 (100%) 76/76 (100%) 68/68 (100%)	tRNA-dihydrouridine(47) synthase [NAD(P)()]-like
39	S208	chr3 chr14	752626 to 752856 671473 to 671572	NO03G02620	3'UTR	322/322 (100%) 102/122 (83.61%) 61/77 (79.22%)	Luminal binding protein Heat shock protein 70 Mediator of RNA polymerase II transcription subunit 37a
40	S209	chr22	217010 to 217338 216995 to 217338	NO14G02230 NO22G00640	Exon Exon	230/231 (99.57%) 100/100 (100%) 33/34 (97.06%)	Phosphoribosylpyrophosphate synthetase
41	S211	chr22	26238 to 26359 25862 to 25922 26544 to 26589			327/329 (99.39%) 342/344 (99.42%) 122/122 (100%)	lysine-ketoglutarate reductase/saccharopine dehydratase
42	S212	chr12	747123 to 746839	NO22G00060	Exon	61/61 (100%) 46/46 (100%)	Trypsin family
43	S213	chr9	195570 to 195692 193063 to 192941 241087 to 240969	NO12G02640 NO09G00450 NO09G00440 NO25G00860	Exon Exon Exon Exon	284/285 (99.65%) 123/123 (100%) 123/123 (100%) 104/119 (87.39%)	Light-harvesting protein VCP1 Light-harvesting protein Fucoxanthin-chlorophyll a-c binding protein A, chloroplastic
44	S216-1	chr11	59466 to 59281 67776 to 67591 71973 to 71788 74686 to 74871 143398 to 143213 126938 to 126778 133775 to 133615 1162734 to 1162893 902429 to 902571 906964 to 907106 498321 to 498445 314 to 236 84264 to 84344 84489 to 84557	NO11G00130 NO11G00150 NO11G00160 NO15G00260 NO13G00420 NO13G00380 NO13G00400 NO12G04010 NO16G03050 NO16G03070 NO28G00010 NO26G00240	Exon Exon Exon Exon Exon Exon Exon+5'UTR Exon Exon Exon IG region Exon+3'UTR Exon	186/186 (100%) 186/186 (100%) 185/186 (99.46%) 181/186 (97.31%) 161/186 (86.56%) 144/161 (89.44%) 144/161 (89.44%) 138/160 (86.25%) 126/143 (88.11%) 126/143 (88.11%) 111/127 (87.4%) 66/79 (83.54%) 81/81 (100%) 69/69 (100%)	Unknown protein Unknown protein Unknown protein Unknown protein Unknown protein Unknown protein Unknown protein Unknown protein Viral protein TPX Viral protein TPX Unknown protein Acyl-coenzyme A oxidase
45	S218	chr6	809024 to 808810	NO06G02810	Exon	214/215 (99.53%)	Polyketide synthase
46	S220	chr26	573861 to 573804 573618 to 573574	NO26G01720	Exon	58/58 (100%) 45/45 (100%)	
47	S224	chr10	367991 to 368362	NO10G01240	Exon+Intron	371/372 (99.73%)	Light-harvesting protein
48	S240	chr8	927051 to 926925	NO08G03350	Exon	126/127 (99.21%)	Ribokinase
49	S241-1	chr11	59492 to 59281 67802 to 67591 71999 to 71788 74660 to 74871 143423 to 143213 126988 to 126778 133825 to 133615 1162681 to 1162893 902363 to 902571 906898 to 907106 498321 to 498445 340 to 236 84264 to 84344 84489 to 84557	NO11G00130 NO11G00150 NO11G00160 NO15G00260 NO13G00420 NO13G00380 NO13G00400 NO12G04010 NO16G03050 NO16G03070 NO28G00010 NO26G00240	Exon Exon Exon Exon Exon Exon Exon+5'UTR Exon Exon Exon IG region Exon+3'UTR Exon	212/212 (100%) 212/212 (100%) 211/212 (99.53%) 206/212 (97.17%) 185/211 (87.68%) 184/211 (87.2%) 183/211 (86.73%) 181/213 (84.98%) 175/209 (83.73%) 175/209 (83.73%) 111/127 (87.4%) 91/105 (86.67%) 80/81 (98.77%) 69/69 (100%)	Unknown protein Unknown protein Unknown protein Unknown protein Unknown protein Unknown protein Unknown protein Unknown protein Viral protein TPX Viral protein TPX Unknown protein Acyl-coenzyme A oxidase
50	S242	chr11	961085 to 960892	NO11G03060	Exon	194/194 (100%)	Nadh:ubiquinone oxidoreductase complex i intermediate-associated protein 30
51	S244	chr9	944534 to 944389	NO09G03270 NO09G03280	5'UTR Exon	146/146 (100%)	Unknown protein
52	S245	chr9	195396 to 195692 193237 to 192941 241211 to 240969	NO09G00450 NO09G00440	Exon Exon Exon	297/297 (100%) 297/297 (100%) 209/243 (86.01%)	Unknown protein VCP1 Light-harvesting protein

			241413 to 241368	NO25G00860	Exon	42/46 (91.3%)	Fucoxanthin-chlorophyll a-c binding protein A, chloropl
		chr20	173221 to 173185		Exon	34/37 (91.89%)	Light-harvesting protein
		chr3	1043766 to 1043800		Exon	32/35 (91.43%)	Light-harvesting protein
53	S247	chr26	146367 to 146252		Exon	116/116 (100%)	
			146698 to 146652	NO26G00450	Exon	47/47 (100%)	DNA polymerase I
54	S249	chr27	380243 to 380139		Exon	105/105 (100%)	
			380018 to 379957	NO27G01200	Exon	62/62 (100%)	Peroxin-5
55	S250	chr13	505060 to 504925	NO13G01700	Exon	136/136 (100%)	GTP-binding protein
56	S253	chr20	524165 to 524416	NO20G01730	Exon	252/252 (100%)	Fgd6 protein
				NO20G01720	3'UTR		Sigma 54 modulation protein ribosomal protein s30ea
57	S258	chr8	852496 to 852732	NO08G03070	Exon	237/237 (100%)	
58	S260	chr11	105140 to 105259		Exon	120/120 (100%)	
			105465 to 105568	NO11G00250	Exon+3'UTR	104/104 (100%)	Histone h3
		chr14	414961 to 414754	NO14G01290	Exon	164/208 (78.85%)	Histone H3
		chr3	607530 to 607323	NO03G01990	Exon	164/208 (78.85%)	Histone H3
59	S262	chr7	526012 to 525869	NO07G01750	Exon	144/144 (100%)	5-3 exoribonuclease 2
60	S265	chr11	1072160 to 1072339	NO11G03360	Exon	180/180 (100%)	Nitric oxide dioxygenase
61	S266	chr16	435283 to 435110		Exon+3'UTR	174/174 (100%)	
			435595 to 435492	NO16G01410	Exon	104/104 (100%)	Glutathione peroxidase
62	S268	chr25	241210 to 240977		Exon	234/234 (100%)	
			241382 to 241346	NO25G00860	Exon	37/37 (100%)	violaxanthin/chlorophyll a binding protein precursor
		chr9	195407 to 195671	NO09G00450	Exon	225/265 (84.91%)	VCP1
			193226 to 192962	NO09G00440	Exon	225/265 (84.91%)	Light-harvesting protein
63	S275	chr20	51511 to 51379	NO20G00140	Exon+3'UTR	133/133 (100%)	Arsenate reductase
64	S279	chr4	1185473 to 1185327	NO04G04380	Exon	147/147 (100%)	Unknown protein
65	S280	chr9	195692 to 195554	NO09G00450	Exon	139/139 (100%)	VCP1
			192941 to 193079	NO09G00440	Exon	139/139 (100%)	Light-harvesting protein
		chr25	240969 to 241089	NO25G00860	Exon	106/121 (87.6%)	violaxanthin/chlorophyll a binding protein precursor
66	S283	chr9	944534 to 944389	NO09G03270	5'UTR	146/146 (100%)	Unknown protein
				NO09G03280	Exon	134/137 (97.81%)	Unknown protein
67	S287-1	chr18	845362 to 845658	NO18G02590	3'UTR	296/297 (99.66%)	Unknown protein
	S287-2	chr9	195692 to 195453	NO09G00450	Exon	240/240 (100%)	VCP1
			192941 to 193180	NO09G00440	Exon	240/240 (100%)	Light-harvesting protein
		chr25	240969 to 241204	NO25G00860	Exon	203/236 (86.02%)	violaxanthin/chlorophyll a binding protein precursor
68	S288	chr17	45481 to 45570		Exon	90/90 (100%)	
			45777 to 45844		Exon	68/68 (100%)	
			45300 to 45353	NO17G00130	Exon	54/54 (100%)	Sulfotransferase
69	S290-1	chr21	377551 to 377181	NO21G01240	5'UTR+Exon	371/371 (100%)	Unknown protein
		chr7	138128 to 138297	NO07G00350	Exon+3'UTR	170/170 (100%)	Late embryogenesis abundant protein (LEA) family protein
	S290-2	chr25	241210 to 240951		Exon	260/260 (100%)	
			241413 to 241346	NO25G00860	Exon	68/68 (100%)	violaxanthin/chlorophyll a binding protein precursor
		chr9	195396 to 195706	NO09G00450	Exon	260/311 (83.6%)	VCP1
			193237 to 192927	NO09G00440	Exon	260/311 (83.6%)	Light-harvesting protein
70	S291	chr20	629330 to 629091	NO20G02120	Exon+3'UTR	239/240 (99.58%)	heat shock protein 101
71	S292	chr11	1150617 to 1150432	NO11G03570	3'UTR		heat shock protein 70(Hsp 70) family protein
				NO11G03580	Exon	185/186 (99.46%)	Phosphoesterase pa-phosphatase related protein
72	S293	chr14	707661 to 707380	NO14G02380	Exon	282/282 (100%)	ATP-sulfurylase
73	S297	chr10	972000 to 971826		Exon	174/175 (99.43%)	
			972166 to 972101	NO10G03430	Exon	66/66 (100%)	Unknown protein
			980970 to 980797	NO10G03450+NO10G03460	Exon+IG+Exon	174/175 (99.43%)	Unknown protein
			981137 to 981072	NO10G03460	Exon	66/66 (100%)	Unknown protein
			990339 to 990165		Exon	174/175 (99.43%)	
			990505 to 990440	NO10G03480	Exon	66/66 (100%)	Unknown protein
			999322 to 999148		Exon	174/175 (99.43%)	
			999488 to 999423	NO10G03500	Exon	66/66 (100%)	Unknown protein
			1008264 to 1008091	NO10G03540+NO10G03550	Exon+IG+Exon	173/175 (98.86%)	Unknown protein
			1008429 to 1008364	NO10G03550	Exon	66/66 (100%)	Unknown protein
			1017235 to 1017061		Exon	174/175 (99.43%)	

			1017401 to 1017336	NO10G03570	Exon	66/66 (100%)	Unknown protein
			1026218 to 1026044		Exon	174/175 (99.43%)	
			1026384 to 1026319	NO10G03590	Exon	66/66 (100%)	Unknown protein
			1035202 to 1035028		Exon	174/175 (99.43%)	
			1035368 to 1035303	NO10G03610	Exon	66/66 (100%)	Unknown protein
			1044575 to 1044401		Exon	174/175 (99.43%)	
			1044741 to 1044676	NO10G03630	Exon	66/66 (100%)	Unknown protein
74	S300	chr27	572972 to 573076		Exon	105/105 (100%)	
			573219 to 573295		Exon	77/77 (100%)	
			572779 to 572849		Exon	71/71 (100%)	
			572478 to 572537	NO27G01710	Exon	60/60 (100%)	Unknown protein
75	S304	chr18	140413 to 140738	NO18G00330	Exon+3'UTR	326/326 (100%)	beta-Ig-H3/fasciclin
76	S306	chr25	240683 to 240811		Exon+3'UTR	129/129 (100%)	
			240950 to 240991	NO25G00860	Exon	42/42 (100%)	violaxanthin/chlorophyll a binding protein precursor
		chr9	192914 to 192954	NO09G00440	Exon	37/41 (90.24%)	Light-harvesting protein
			195719 to 195679	NO09G00450	Exon	37/41 (90.24%)	VCP1
77	S307	chr11	1138896 to 1138677		5'UTR+Exon	220/220 (100%)	
			1139068 to 1139006	NO11G03540	Exon	62/63 (98.41%)	Unknown protein
78	S311	chr4	363433 to 363078	NO04G01140	3'UTR	356/356 (100%)	Unknown protein
		chr18	841390 to 841205	NO18G02580	Exon	152/186 (81.72%)	Unknown protein
			846487 to 846634	NO18G02610	3'UTR	126/148 (85.14%)	Methyltransferase type 11
79	S312	chr19	526967 to 526736	NO19G01750	Exon+3'UTR	232/232 (100%)	Fructose-bisphosphate aldolase 6, cytosolic
80	S316	chr13	959942 to 959691	NO13G03270	Exon+3'UTR	252/252 (100%)	Haloacid dehalogenase-like hydrolase
		chr5	1415576 to 1415778	NO05G05310	Exon	203/203 (100%)	Unknown protein
81	S317	chr19	592975 to 593157	NO19G02010	5'UTR	183/183 (100%)	hydroxylamine reductase
82	S320	chr2	473526 to 473353	NO02G01600	Exon+3'UTR	174/174 (100%)	predicted protein
83	S322	chr9	192941 to 193106	NO09G00440	Exon	166/166 (100%)	Light-harvesting protein
			195692 to 195527	NO09G00450	Exon	166/166 (100%)	VCP1
		chr25	240969 to 241130	NO25G00860	Exon	136/162 (83.95%)	violaxanthin/chlorophyll a binding protein precursor
84	S324	chr5	674299 to 673981	NO05G02550	Exon	319/319 (100%)	Heat shock protein 90
85	S325-1	chr11	6118 to 6311	NO11G00010	5'UTR	194/194 (100%)	Unknown protein
				NO11G00030	5'UTR+Exon	194/194 (100%)	Isonitrile hydratase
		chr20	33213 to 33125		Exon	89/89 (100%)	
			33012 to 32981	NO20G00090	Exon	32/32 (100%)	DTW domain-containing protein 2
	S325-2	chr9	195130 to 195202		Exon	73/73 (100%)	
			195002 to 195051	NO09G00450	Exon	50/50 (100%)	VCP1
			193503 to 193431		Exon	71/73 (97.26%)	
			193648 to 193599	NO09G00440	Exon	48/50 (96%)	Light-harvesting protein
86	S328	chr18	845359 to 844960	NO18G02590	Exon+3'UTR	400/400 (100%)	Unknown protein
		chr7	1197822 to 1197520	NO07G04250	Exon	237/303 (78.22%)	Unknown protein
		chr6	125829 to 125512	NO06G00290	Exon	240/318 (75.47%)	Unknown protein
			158117 to 157802	NO06G00370	Exon	238/316 (75.32%)	Unknown protein
			110026 to 109709	NO06G00250	Exon	239/318 (75.16%)	Unknown protein
			113977 to 113660	NO06G00260	Exon	239/318 (75.16%)	Unknown protein
			117928 to 117611	NO06G00270	Exon	239/318 (75.16%)	Unknown protein
			121879 to 121562	NO06G00280	Exon	239/318 (75.16%)	Unknown protein
		chr19	997 to 1208	NO19G00010	Exon	161/212 (75.94%)	Unknown protein
		chr5	41720 to 41890	NO05G00090	3'UTR	129/174 (74.14%)	Cellulase 2;endo-1,4-beta-glucanase
		chr21	51802 to 51601	NO21G00160	Exon	147/202 (72.77%)	Unknown protein
			56063 to 55862	NO21G00170	Exon	147/202 (72.77%)	Unknown protein
87	S329	chr6	698826 to 698208	NO06G02470	Exon+3'UTR	619/619 (100%) ,	Unknown protein
88	S330	chr4	151643 to 151480	NO04G00360	Exon	164/164 (100%)	Abc transporter family protein
89	S332	chr15	295080 to 295435	NO15G00980	Exon+3'UTR	356/356 (100%)	T-complex protein 1 delta subunit
90	S336	chr11	361600 to 361790	IG region	IG region	191/191 (100%)	
91	S339-1	chr3	1043941 to 1043724	NO03G03480	Exon	218/218 (100%)	Light harvesting complex protein
	S339-2	chr8	1173413 to 1173258	NO08G04120	Exon	154/156 (98.72%)	Unknown protein
92	S340	chr3	304996 to 305128		Exon	132/133 (99.25%)	
			304808 to 304873		Exon	66/66 (100%)	

			305280 to 305334	NO03G00920	Exon	55/55 (100%)	Beta-lactamase/transpeptidase-like protein
93	S350	chr4	363433 to 363078	NO04G01140	3'UTR	356/356 (100%)	Unknown protein
		chr18	841390 to 841205	NO18G02580	Exon	152/186 (81.72%)	Unknown protein
			846487 to 846634	NO18G02610	3'UTR	126/148 (85.14%)	Unknown protein
94	S352	chr4	363433 to 363078	NO04G01140	3'UTR	356/356 (100%)	Unknown protein
		chr18	841390 to 841205	NO18G02580	Exon	152/186 (81.72%)	Unknown protein
			846487 to 846634	NO18G02610	3'UTR	126/148 (85.14%)	Unknown protein
95	S360	chr11	71999 to 71788	NO11G00160	Exon	212/212 (100%)	Unknown protein
			59492 to 59281	NO11G00130	Exon	211/212 (99.53%)	Unknown protein
			67802 to 67591	NO11G00150	Exon	211/212 (99.53%)	Unknown protein
		chr15	74660 to 74871	NO15G00260	Exon	205/212 (96.7%)	Unknown protein
		chr13	143423 to 143213	NO13G00420	Exon	184/211 (87.2%)	Unknown protein
			126988 to 126778	NO13G00380	Exon	183/211 (86.73%)	Unknown protein
			133825 to 133615	NO13G00400	5'UTR+Exon	182/211 (86.26%)	Unknown protein
		chr12	1162681 to 1162893	NO12G04010	Exon	180/213 (84.51%)	Unknown protein
		chr16	902363 to 902571	NO16G03050	Exon	174/209 (83.25%)	Viral protein TPX
			906898 to 907106	NO16G03070	Exon	174/209 (83.25%)	Viral protein TPX
		chr29	498321 to 498445	IG region	IG region	112/127 (88.19%)	
		chr28	340 to 236	NO28G00010	Exon+3'UTR	91/105 (86.67%)	Unknown protein
96	S361	chr14	386173 to 386019	NO14G01170	Exon	155/155 (100%)	Photosystem ii 12 kDa extrinsic protein
97	S364	chr22	4628 to 4851	NO22G00010	3'UTR	223/224 (99.55%)	myo-inositol dehydrogenase
98	S366	chr11	59278 to 58949	NO11G00130	Exon	330/330 (100%)	Unknown protein
			63813 to 63484	NO11G00140	Exon	330/330 (100%)	Unknown protein
			67588 to 67259	NO11G00150	Exon	330/330 (100%)	Unknown protein
			71785 to 71456	NO11G00160	Exon	330/330 (100%)	Unknown protein
		chr15	74877 to 75188	NO15G00260	Exon	289/312 (92.63%)	Unknown protein
		chr16	902577 to 902895	NO16G03050	Exon	279/322 (86.65%)	Viral protein TPX
			907112 to 907430	NO16G03070	Exon	278/322 (86.34%)	Viral protein TPX
		chr13	126772 to 126475	NO13G00380	Exon	260/298 (87.25%)	Unknown protein
			143207 to 142910	NO13G00420	Exon	260/298 (87.25%)	Unknown protein
			133609 to 133312	NO13G00400	Exon	259/298 (86.91%)	Unknown protein
		chr12	1162895 to 1163206	NO12G04010	Exon	272/315 (86.35%)	Unknown protein
		chr29	498462 to 498597	IG region	IG region	123/136 (90.44%)	
99	S367	chr4	1185327 to 1185473	NO04G04380	Exon	147/147 (100%)	Unknown protein
100	S373	chr22	4628 to 4851	NO22G00010	3'UTR	223/224 (99.55%)	myo-inositol dehydrogenase
101	S376	chr12	746817 to 747021	NO12G02640	Exon	205/205 (100%)	Light harvesting complex protein
102	S378-1	chr8	412874 to 413275	NO08G01370	Exon	402/402 (100%)	L-aspartate oxidase
	S378-2	chr17	858854 to 858603	NO17G02930	Exon	252/252 (100%)	Unknown protein
103	S380-1	chr1	1648280 to 1648364		Exon	85/85 (100%)	
			1647575 to 1647658		Exon	84/84 (100%)	
			1647835 to 1647901		Exon	67/67 (100%)	
			1647997 to 1648053	NO01G05860	Exon	57/57 (100%)	ribose-phosphate pyrophosphokinase
	S380-2	chr9	195692 to 195542	NO09G00450	Exon	151/151 (100%)	VCP1
			192941 to 193091	NO09G00440	Exon	151/151 (100%)	Light-harvesting protein
		chr25	240969 to 241089	NO25G00860	Exon	106/121 (87.6%)	violaxanthin/chlorophyll a binding protein precursor
104	S382	chr24	451680 to 451953	NO24G01680	Exon+3'UTR	274/274 (100%)	oxygen-evolving enhancer protein
105	S391	chr20	638087 to 638276		Exon	190/190 (100%)	
			638403 to 638430		Exon	28/28 (100%)	
			637900 to 637964	NO20G02130	Exon	65/65 (100%)	heat shock protein Hsp20
			640915 to 641104		Exon	190/190 (100%)	
			641231 to 641258		Exon	28/28 (100%)	
			640728 to 640792	NO20G02140	Exon	65/65 (100%)	Heat shock protein hsp20
			643607 to 643671		Exon	64/65 (98.46%)	
			643794 to 643983		Exon	190/190 (100%)	
			644110 to 644137	NO20G02150	Exon	28/28 (100%)	Heat shock protein hsp20
106	S394	chr11	59278 to 58949	NO11G00130	Exon	330/330 (100%)	Unknown protein
			63813 to 63484	NO11G00140	Exon	330/330 (100%)	Unknown protein
			67588 to 67259	NO11G00150	Exon	330/330 (100%)	Unknown protein

		71785 to 71456	NO11G00160	Exon	330/330 (100%)	Unknown protein
	chr15	74877 to 75188	NO15G00260	Exon	289/312 (92.63%)	Unknown protein
	chr16	902577 to 902895	NO16G03050	Exon	279/322 (86.65%)	Viral protein TPX
		907112 to 907430	NO16G03070	Exon	278/322 (86.34%)	Viral protein TPX
	chr13	126772 to 126475	NO13G00380	Exon	260/298 (87.25%)	Unknown protein
		143207 to 142910	NO13G00420	Exon	260/298 (87.25%)	Unknown protein
		133609 to 133312	NO13G00400	Exon	259/298 (86.91%)	Unknown protein
	chr12	1162895 to 1163206	NO12G04010	Exon	272/315 (86.35%)	Unknown protein
	chr29	498462 to 498597	IG region	IG region	123/136 (90.44%)	
107	S395	chr26	248319 to 248048	Exon	268/272 (98.53%)	
			248609 to 248532	Exon	76/78 (97.44%)	
			247837 to 247797	Exon	40/41 (97.56%)	ferredoxin nitrite reductase
108	S397	chr6	602180 to 601870	Exon	310/311 (99.68%)	Unknown protein
109	S398	chr6	240413 to 240260	Exon	154/154 (100%)	long chain acyl-coA synthetase
110	S404	chr19	27640 to 27476	Intron	159/165 (96.36%)	
			37126 to 36962	Exon	159/165 (96.36%)	Unknown protein
111	S412	chr22	626129 to 626231	Exon	103/103 (100%)	
			626370 to 626405	Exon	36/36 (100%)	oligopeptidase
112	S413	chr3	1178775 to 1179072	Exon	298/298 (100%)	Glyoxylase(ISS)
113	S415	chr11	1072551 to 1072800	Exon	250/250 (100%)	Nitric oxide dioxygenase
114	S417	chr8	904245 to 904123	Exon	123/123 (100%)	
			904474 to 904400	Exon	75/75 (100%)	Arf1,ARF family GTPase
115	S418-1	chr17	857317 to 857740	3'UTR	424/424 (100%)	Unknown protein
	S418-2	chr16	376312 to 376431	Exon	120/120 (100%)	ferredoxin component
116	S419	chr2	1346668 to 1346486	Exon	183/183 (100%)	serine threonine phosphatase
		chr11	407633 to 407758	3'UTR	126/126 (100%)	Unknown protein
117	S425	chr18	458595 to 458284	Exon+3'UTR	312/312 (100%)	PREDICTED: phosphatidylinositide phosphatase SAC1-like
118	S428	chr8	975165 to 975367	Exon+3'UTR	203/203 (100%)	Light harvesting complex protein
		chr26	574056 to 574022	Exon	32/35 (91.43%)	Unknown protein
		chr10	435741 to 435802	Exon	50/62 (80.65%)	Light harvesting complex protein
119	S430	chr26	573220 to 573111	Exon	110/110 (100%)	
			573571 to 573508	Intron+Exon	64/64 (100%)	Unknown protein
120	S431	chr3	1043941 to 1043810	Exon	131/132 (99.24%)	Light harvesting complex protein
121	S435	chr2	1346668 to 1346486	Exon	183/183 (100%)	serine threonine phosphatase
		chr11	407633 to 407758	3'UTR	126/126 (100%)	Unknown protein
122	S437	chr18	458595 to 458284	Exon+3'UTR	312/312 (100%)	Phosphatidylinositide phosphatase sac1
123	S438	chr1	560150 to 559939	Exon	212/212 (100%)	Beta-ketoacyl synthase
124	S439	chr2	21920 to 21853	Exon	68/68 (100%)	
			22114 to 22051	Exon	64/64 (100%)	
			21749 to 21702	Exon	48/48 (100%)	Unknown protein
125	S441	chr1	786775 to 787079	Exon	304/305 (99.67%)	Glu leu phe val dehydrogenase
126	S442	chr4	905242 to 905570	Exon	329/329 (100%)	Pseudouridine synthase 1-like protein
127	S448	chr3	1178553 to 1178422	Exon	132/132 (100%)	Ethylmalonic encephalopathy 1
128	S453	chr6	234572 to 234379	Exon	194/194 (100%)	
			234870 to 234782	Exon	86/89 (96.63%)	Farnesyltransferase beta subunit
129	S456	chr5	386180 to 386084	Exon+3'UTR	97/97 (100%)	Brix domain protein
130	S462	chr15	906689 to 906437	Exon	242/253 (95.65%)	Unknown protein
			913835 to 913583	Exon	242/253 (95.65%)	Unknown protein
			923153 to 922901	Exon	242/253 (95.65%)	Unknown protein
			930299 to 930047	Exon	242/253 (95.65%)	Unknown protein
		chr4	146852 to 146782	Exon	62/71 (87.32%)	Unknown protein
		chr27	532001 to 532056	Exon	50/56 (89.29%)	Unknown protein
		chr18	92549 to 92605	Exon	50/57 (87.72%)	Unknown protein
			97820 to 97876	Exon	50/57 (87.72%)	Unknown protein
		chr9	1234190 to 1234135	IG region	46/56 (82.14%)	
131	S464-1	chr3	609152 to 608961	Exon	191/192 (99.48%)	Histone H2A
		chr10	571891 to 572082	Exon	172/192 (89.58%)	Histone H2A

	S464-2	chr22	399854 to 399906	NO22G01340	Exon	47/53 (88.68%)	Histone H2A
		chr10	636259 to 636407	NO10G02300	Exon	146/149 (97.99%)	Unknown protein
			638196 to 638048	NO10G02310	Exon	146/149 (97.99%)	Unknown protein
132	S465	chr18	845107 to 845359	NO18G02590	Exon+3'UTR	253/253 (100%)	Unknown protein
		chr6	125652 to 125829	NO06G00290	Exon	138/178 (77.53%)	Unknown protein
			157940 to 158117	NO06G00370	Exon	138/178 (77.53%)	Unknown protein
			109849 to 110026	NO06G00250	Exon	137/178 (76.97%)	Unknown protein
			113800 to 113977	NO06G00260	Exon	137/178 (76.97%)	Unknown protein
			117751 to 117928	NO06G00270	Exon	137/178 (76.97%)	Unknown protein
			121702 to 121879	NO06G00280	Exon	137/178 (76.97%)	Unknown protein
			1197665 to 1197822	NO07G04250	Exon	124/158 (78.48%)	Unknown protein
		chr21	51745 to 51802	NO21G00160	Exon	48/58 (82.76%)	Unknown protein
			56006 to 56063	NO21G00170	Exon	48/58 (82.76%)	Unknown protein
		chr1	4917 to 4864	NO01G00030	Exon	45/54 (83.33%)	Unknown protein
			16726 to 16673	NO01G00100	Exon	45/54 (83.33%)	Unknown protein
			28527 to 28474	NO01G00170	Exon	45/54 (83.33%)	Unknown protein
			40332 to 40279	NO01G00240	Exon	45/54 (83.33%)	Unknown protein
133	S478	chr9	192941 to 193078	NO09G00440	Exon	138/138 (100%)	Light-harvesting protein
			195692 to 195555	NO09G00450	Exon	138/138 (100%)	VCP1
		chr25	240969 to 241089	NO25G00860	Exon	106/121 (87.6%)	violaxanthin/chlorophyll a binding protein precursor
134	S480	chr28	532786 to 532498	Exon+3'UTR	289/289 (100%)		
			532300 to 532101	NO28G01700	Exon	200/200 (100%)	CoA-disulfide reductase
		chr12	649109 to 648755	NO12G02270	Exon	355/355 (100%)	26S proteasome regulatory subunit N2
135	S481	chr10	540364 to 540146	NO10G01940	Exon	177/219 (80.82%)	pantothenate kinase,putative
136	S482	chr25	663403 to 663788	NO25G02100	Exon	386/386 (100%)	PREDICTED: similar to PI-3-kinase-related kinase SMG-1
137	S485	chr13	1018197 to 1018350		Exon	154/154 (100%)	
			1018539 to 1018692	NO13G03420	Exon	154/154 (100%)	heat shock protein
		chr8	215782 to 215618	NO08G00590	Exon	165/165 (100%)	cell division protein
		chr2	22051 to 22147		Exon	97/97 (100%)	
			21853 to 21920		Exon	68/68 (100%)	
138	S488		21702 to 21749	NO02G00080	Exon	48/48 (100%)	Unknown protein

□ The red box represents the mutant produced by multiple cassette insertions

Table S3b. All screened mutants from M-RNAi library

Number	Chromosome	Mapping position	Knockdown genes	Mapping range	Identity	Description
1 M3	chr9	64916 to 64565		Intron	342/342 (100%)	
		55139 to 54788	NO09G00090	Exon	351/352 (99.72%)	Unknown protein
2 M12	chr16	913928 to 913513	NO16G03080	Exon+3'UTR	415/416 (99.76%)	Unknown protein
3 M14	chr16	410208 to 409751	NO16G01340	Exon+3'UTR	458/458 (100%)	putative type 2C P-type ATPase
4 M25	chr29	459507 to 459616			101/110 (91.82%)	
		459579 to 459694			103/116 (88.79%)	
		459567 to 459655			77/89 (86.52%)	
		459905 to 459973			61/69 (88.41%)	
		459636 to 459718			69/83 (83.13%)	
		459486 to 459598			87/113 (76.99%)	
		459927 to 460033			83/107 (77.57%)	
		459480 to 459556			62/77 (80.52%)	
		459564 to 459643			64/80 (80%)	
		459492 to 459568			61/77 (79.22%)	
		459549 to 459652			79/104 (75.96%)	
		459633 to 459733			77/101 (76.24%)	
		459927 to 459997			57/71 (80.28%)	
		459954 to 460018			53/65 (81.54%)	
		459963 to 460054			71/92 (77.17%)	
		459975 to 460078			79/104 (75.96%)	
		459480 to 459526	NO29G01440	Exon	40/47 (85.11%)	Filamentous hemagglutinin family N-terminal domain prote
		463231 to 463346			116/116 (100%)	
		463330 to 463390			54/61 (88.52%)	
		463609 to 463688			65/80 (81.25%)	
		463204 to 463280			62/77 (80.52%)	
		463297 to 463370			60/74 (81.08%)	
		463630 to 463739			84/110 (76.36%)	
		463608 to 463676			56/69 (81.16%)	
		463608 to 463664			48/57 (84.21%)	
		463216 to 463292			61/77 (79.22%)	
		463654 to 463749			73/96 (76.04%)	
		463204 to 463250			40/47 (85.11%)	
		463645 to 463715			56/71 (78.87%)	
		463645 to 463709	NO29G01450	Exon	52/65 (80%)	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S
	chr4	1447777 to 1447896			120/120 (100%)	
		1447580 to 1447667			88/88 (100%)	
		1448056 to 1448120	NO04G05190	Exon	65/65 (100%)	Unknown protein
	chr16	464740 to 464859			89/120 (74.17%)	
		464822 to 464871	NO16G01530	Exon	42/50 (84%)	Filamentous hemagglutinin family N-terminal domain prote
		462255 to 462322	NO16G01520	Exon	54/68 (79.41%)	Filamentous hemagglutinin family N-terminal domain protein
5 M26	chr17	859372 to 858906	NO17G02930	Exon	466/466 (100%)	Unknown protein
6 M27	chr3	1177345 to 1177770	NO03G04040	Exon+ Intron+5'UTR	186/251 (74.1%)	Ethylmalonic encephalopathy 1
7 M29	chr27	621686 to 621931	NO27G01840	Exon	215/246 (87.4%)	Unknown protein
8 M32	chr27	312261 to 312506		Exon	212/288 (73.61%)	
		311781 to 311869		Exon	89/89 (100%)	
		312611 to 312692	NO27G00920	Exon	82/82 (100%)	carbohydrate metabolic process. catabolic process. catalytic
		309778 to 309654	NO27G00910	Exon	96/125 (76.8%)	Glyceraldehyde-3-phosphate dehydrogenase
	chr8	488714 to 488496	NO08G01560	Exon	175/225 (77.78%)	Glyceraldehyde-3-phosphate dehydrogenase
	chr7	63803 to 63706	NO07G00170	5'UTR	88/98 (89.8%)	Multidrug resistance-associated protein 1
	chr9	968027 to 968308			212/288 (73.61%)	
		967675 to 967713	NO09G03360	Exon	35/39 (89.74%)	glyceraldehyde-3-phosphate dehydrogenase of plastid 1
9 M34	chr18	297521 to 297127		Exon+3'UTR	393/395 (99.49%)	
		296690 to 296639		Exon	52/52 (100%)	
		296907 to 296861	NO18G00770	Exon	47/47 (100%)	Photosystem II subunit
10 M36	chr15	772725 to 772397	NO15G02820	Exon	329/329 (100%)	Conserved uncharacterized protein
11 M37	chr16	566878 to 567295	NO16G01940	Exon	418/418 (100%)	phosphate transporter 2
	chr3	414002 to 414054	NO03G01310	Exon	45/53 (84.91%)	phosphate transporter 2
12 M43	chr30	220965 to 220562	NO30G00560	IG region+5'UTR+Exon+Intr	402/404 (99.5%)	CoA ester lyase
13 M44	chr4	412867 to 413289	NO04G01330	Exon	423/423 (100%)	Regulator of chromosome condensation-like protein

14	M45	chr9	55171 to 55517		Exon	347/347 (100%)	
			64948 to 65294	NO09G00090	Intron	347/347 (100%)	Unknown protein
15	M47	chr16	530008 to 529742	NO16G01790	Exon	267/267 (100%)	Katanin p80 wd40 repeat-containing subunit b1-like protein
		chr3	113075 to 112901	NO03G00350	Exon	175/175 (100%)	DNA-directed RNA polymerase II subunit rpb3
16	M48	chr25	210011 to 209781			231/231 (100%)	
			210950 to 210814	NO25G00760	Exon	137/137 (100%)	Ribosomal protein L6 family protein
17	M49	chr7	556127 to 556314	NO07G01880	Exon	165/188 (87.77%)	Unknown protein
18	M58	chr21	302212 to 301760	NO21G00920	Exon	449/453 (99.12%)	Phosphatidylinositol 3-and 4-kinase family protein
19	M60	chr19	172751 to 172875			125/125 (100%)	
			173282 to 173389			108/108 (100%)	
			173030 to 173128			99/99 (100%)	
			172540 to 172591			52/52 (100%)	
			172285 to 172325			41/41 (100%)	
			173502 to 173541	NO19G00450	Exon	40/40 (100%)	Fad-dependent pyridine nucleotide-disulfide oxidoreductase
20	M61	chr15	797330 to 796876	NO15G02920	Exon	455/455 (100%)	unknown protein
		chr8	1286191 to 1286223	NO08G04390	Intron	30/32 (93.75%)	ubiquitin-like domain-containing ctd phosphatase 1
		chr27	497609 to 497640		IG region	30/32 (93.75%)	
		chr1	66684 to 66718	NO01G00320	Intron	32/35 (91.43%)	ATP-sensitive inward rectifier potassium channel 8
21	M66	chr5	811339 to 810990	NO05G03120	Exon	350/350 (100%)	DNA polymerase theta
22	M68	chr11	310617 to 310236	NO11G00760	Exon+3'UTR	381/382 (99.74%)	Phosphoenolpyruvate carboxylase
23	M69	chr19	28181 to 28320		Intron	139/140 (99.29%)	
			37667 to 37806		Exon	139/140 (99.29%)	
			27954 to 28041		Intron	88/88 (100%)	
			28445 to 28532		Intron	88/88 (100%)	
			37440 to 37527		Exon	88/88 (100%)	
			37931 to 38018		Exon	88/88 (100%)	
			27718 to 27804		Intron	87/87 (100%)	
			37204 to 37290	NO19G00110	Exon	87/87 (100%)	Unknown protein
24	M71	chr7	1037636 to 1038158	NO07G03720	3'UTR	522/523 (99.81%)	Cellulose synthase
25	M72	chr8	911491 to 910957	NO08G03300	Exon	532/535 (99.44%)	predicted protein
26	M74	chr29	55965 to 55742		Exon+3'UTR	224/224 (100%)	
			56163 to 56096		Exon	68/68 (100%)	
			56303 to 56263	NO29G00140	Exon	41/41 (100%)	Beta-lactamase
27	M75	chr12	718063 to 718196		Exon+3'UTR	134/134 (100%)	
			717280 to 717381		Exon	102/102 (100%)	
			717621 to 717700		Exon	80/80 (100%)	
			717107 to 717178		Exon	72/72 (100%)	
			717808 to 717872	NO12G02510	Exon	64/64 (100%)	Pentatricopeptide repeat containing protein
28	M78	chr21	517239 to 517649		Exon+3'UTR	409/411 (99.51%)	
			517059 to 517129	NO21G01720	Exon	71/71 (100%)	Receptor expression-enhancing protein 6
29	M83	chr25	240953 to 241210			258/258 (100%)	
			241346 to 241395	NO25G00860	Exon	50/50 (100%)	Fucoxanthin-chlorophyll a-c binding protein A, chloroplastic
		chr9	192929 to 193224	NO09G00440	Exon	249/296 (84.12%)	Light-harvesting protein
			195704 to 195409	NO09G00450	Exon	249/296 (84.12%)	VCP1
30	M84	chr6	558565 to 559110	NO06G01850	Exon	546/546 (100%)	Succinate fumarate mitochondrial transporter
31	M85	chr12	999476 to 999116	NO12G03640	Exon	361/361 (100%)	Peptidase m50
32	M86	chr16	579358 to 579756	NO16G01970	Exon	399/399 (100%)	Amine oxidase
33	M87	chr23	280837 to 281012	NO23G00730	Exon	176/176 (100%)	Serine threonine protein kinase
34	M89	chr23	68599 to 68750		Exon	151/152 (99.34%)	
			68300 to 68408		Exon	109/109 (100%)	
			69628 to 69717		Exon	90/90 (100%)	
			68898 to 68978		Exon	81/81 (100%)	
			69222 to 69287		Exon	66/66 (100%)	
			68075 to 68131	NO23G00130	Exon	57/57 (100%)	1,4-beta-D-glucan cellobiohydrolase C
35	M90	chr10	708950 to 708731	NO10G02590	3'UTR	220/220 (100%)	Geranylgeranyl reductase
36	M91	chr3	551930 to 552325	NO03G01760	Exon	396/396 (100%)	Dihydrolipoyl dehydrogenase 1, mitochondrial
37	M92	chr1	1665712 to 1665352		Exon	361/361 (100%)	
			1665144 to 1665074	NO01G05900	Exon	71/71 (100%)	Unknown protein
			1676289 to 1675929		Exon	361/361 (100%)	
			1675721 to 1675651	NO01G05920	Exon	71/71 (100%)	Unknown protein
		chr23	9343 to 9674	NO23G00020	Exon	262/338 (77.51%)	Unknown protein
38	M94	chr2	856741 to 857181	NO02G03180	Exon+5'UTR	441/441 (100%)	Arogenate dehydrogenase
39	M96	chr10	368125 to 367973			153/153 (100%)	

40	M97	chr7	368796 to 368651	NO10G01240	Exon	146/146 (100%)	Ribokinase
			368575 to 368460			116/116 (100%)	
			502444 to 502631			188/188 (100%)	
			502152 to 502280			129/129 (100%)	
41	M99	chr16	913910 to 913513	NO16G03080	Exon+3'UTR	397/398 (99.75%)	Unknown protein
42	M100	chr5	552972 to 552695	NO05G02030	Exon	277/278 (99.64%)	Cytochrome b6-f complex iron-sulfur subunit
			553130 to 553079		Exon+3'UTR	52/52 (100%)	
			555472 to 555195		Exon	277/278 (99.64%)	
			555630 to 555579		Exon+3'UTR	52/52 (100%)	
			557972 to 557695		Exon	277/278 (99.64%)	
			558130 to 558079		Exon+3'UTR	52/52 (100%)	
			560408 to 560141		Exon	242/268 (90.3%)	
43	M102	chr1	1413877 to 1413501	NO01G05300	Exon+3'UTR	376/377 (99.73%)	Unknown protein
44	M103	chr27	371840 to 371563	NO27G01160	Exon	278/278 (100%)	Gamma-glutamyltranspeptidase
			372122 to 372081		Exon	42/42 (100%)	
45	M104	chr23	68599 to 68750	NO23G00130	Exon	151/152 (99.34%)	1,4-beta-D-glucan cellobiohydrolase C
			68300 to 68408		Exon	109/109 (100%)	
			69628 to 69717		Exon	90/90 (100%)	
			68898 to 68978		Exon	81/81 (100%)	
			68050 to 68131		Exon	81/82 (98.78%)	
			69222 to 69287		Exon	66/66 (100%)	
			240811 to 240539		Exon+3'UTR	273/273 (100%)	
			241063 to 240950		Exon	114/114 (100%)	
46	M105	chr25	193039 to 192914	NO25G00860	Exon	107/126 (84.92%)	Fucoxanthin-chlorophyll a-c binding protein A, chloroplastic
			195594 to 195719		Exon	107/126 (84.92%)	
			110235 to 109840		Exon	395/396 (99.75%)	
			114186 to 113791		Exon	395/396 (99.75%)	
			118137 to 117742		Exon	395/396 (99.75%)	
			122088 to 121693		Exon	395/396 (99.75%)	
			125863 to 125643		Exon	219/221 (99.1%)	
			126003 to 125846		Exon	133/169 (78.7%)	
47	M106	chr6	158176 to 157931	NO06G00290	Exon+3'UTR	233/246 (94.72%)	Unknown protein
			158297 to 158213		3'UTR	79/85 (92.94%)	
			1197829 to 1197636		Exon	152/194 (78.35%)	
			845284 to 845098		Exon	146/187 (78.07%)	
			965877 to 966298		Exon	422/422 (100%)	
			974859 to 975280		Exon	422/422 (100%)	
			993199 to 993620		Exon	422/422 (100%)	
			1020095 to 1020516		Exon	422/422 (100%)	
			1029078 to 1029499		Exon	422/422 (100%)	
			1002173 to 1002593		Exon	422/422 (100%)	
			1011116 to 1011536		Exon+Intron	421/422 (99.76%)	
			1011116 to 1011536		Exon	421/422 (99.76%)	
			983826 to 984241		Exon	395/416 (94.95%)	
			1038062 to 1038477		Exon	395/416 (94.95%)	
			1047435 to 1047850		Exon	395/416 (94.95%)	
					Exon	381/382 (99.74%)	
48	M107	chr7	767362 to 767743	NO15G02800	Exon	171/171 (100%)	Carbonyl reductase
			767880 to 768050		Exon		
49	M108	chr15	288803 to 288295	NO26G01010	IG region	509/509 (100%)	pyruvate orthophosphate dikinase
			334372 to 334614		Exon	243/243 (100%)	
50	M110-1	chr22	333968 to 334107	NO22G01280	Exon	139/140 (99.29%)	Calcium-dependent protein
			389706 to 389251		Exon	455/456 (99.78%)	
			146132 to 146018		Exon	115/115 (100%)	
			144947 to 144856		Exon	92/92 (100%)	
			145742 to 145661		Exon	82/82 (100%)	
			145435 to 145376		Exon	59/60 (98.33%)	
			146399 to 146349		Exon	51/51 (100%)	
51	M111-1	chr22	529778 to 529268	NO18G00340	Exon	511/511 (100%)	Peptidylprolyl isomerase
52	M112	chr17	455262 to 455667	NO17G01840	Exon	511/511 (100%)	glutamate:glyoxylate aminotransferase
53	M113	chr4	236847 to 236638	NO04G01460	5'UTR+Exon+3'UTR	386/406 (95.07%)	Ribosomal protein
54	M115	chr8	702042 to 702356	NO08G00680	5'UTR+Exon	210/210 (100%)	Unknown protein,
55	M117	chr18	687292 to 686979		IG region	315/315 (100%)	
			688010 to 687903		IG region	314/315 (99.68%)	
			701310 to 701417		IG region	108/108 (100%)	
					IG region	108/108 (100%)	

		701591 to 701647		IG region	57/57 (100%)	
		687729 to 687673		IG region	56/57 (98.25%)	
56 M118	chr14	574758 to 574332	NO14G01860	Exon+3'UTR	427/427 (100%)	2-oxoglutarate dehydrogenase e1 component
57 M119	chr2	992615 to 992178	NO02G03670	Exon+3'UTR	438/438 (100%)	Pentatricopeptide repeat containing protein
58 M120	chr19	29974 to 29802		Intron	173/173 (100%)	
		39460 to 39288		Exon	173/173 (100%)	
		29453 to 29325		Intron	129/129 (100%)	
		38939 to 38811		Exon	129/129 (100%)	
		29689 to 29620		Intron	70/70 (100%)	
		39175 to 39106		Exon	70/70 (100%)	
		30230 to 30177		Intron	54/54 (100%)	
		39716 to 39663		Exon	54/54 (100%)	
		29127 to 29102		Intron	26/26 (100%)	
		38613 to 38588	NO19G00110	Exon	26/26 (100%)	Unknown protein
59 M123-1	chr13	10551 to 11138	NO13G00030	Exon+3'UTR	580/588 (98.64%)	RNA binding protein
M123-2	chr26	401890 to 402321	NO26G01250	Exon	432/432 (100%)	Beta-1,3-glucan-binding protein
60 M124	chr3	865266 to 865515	NO03G02860	Exon+3'UTR	248/250 (99.2%)	Nuclear receptor corepressor 1-like protein
	chr29	244442 to 244550	NO29G00640	Intron+Exon	109/109 (100%)	TatA-like sec-independent protein translocator subunit
61 M126	chr27	312506 to 312261		Exon	246/246 (100%)	
		312762 to 312611	NO27G00920	Exon	152/152 (100%)	Glyceraldehyde-3-phosphate dehydrogenase
		309489 to 309778	NO27G00910	Exon	217/296 (73.31%)	Glyceraldehyde-3-phosphate dehydrogenase
	chr8	488433 to 488714	NO08G01560	Exon	223/288 (77.43%)	Glyceraldehyde-3-phosphate dehydrogenase
	chr9	968378 to 968027		Exon	268/358 (74.86%)	
		967713 to 967675	NO09G03360	Exon	35/39 (89.74%)	glyceraldehyde-3-phosphate dehydrogenase of plastid 1
62 M127	chr7	434485 to 433976	NO07G01400	Exon+3'UTR	509/510 (99.8%)	Unknown protein
63 M129	chr10	966302 to 965852	NO10G03420	Exon	451/451 (100%)	Unknown protein
		975284 to 974834	NO10G03440	Exon	451/451 (100%)	Unknown protein
		993624 to 993174	NO10G03490	Exon	451/451 (100%)	Unknown protein
		1020520 to 1020070	NO10G03580	Exon	451/451 (100%)	Unknown protein
		1029503 to 1029053	NO10G03600	Exon	451/451 (100%)	Unknown protein
		1011540 to 1011091	NO10G03560	Exon	450/451 (99.78%)	Unknown protein
		1002597 to 1002153	NO10G03510	Exon+Intron	445/446 (99.78%)	Unknown protein
		984251 to 983801	NO10G03470	Exon	428/451 (94.9%)	Unknown protein
		1038487 to 1038037	NO10G03620	Exon	428/451 (94.9%)	Unknown protein
		1047860 to 1047410	NO10G03640	Exon	428/451 (94.9%)	Unknown protein
64 M133	chr3	1644017 to 1644423	NO03G05720	Exon+3'UTR	405/407 (99.51%)	Unknown protein
65 M134	chr24	109451 to 109777	NO24G00320	Exon+3'UTR	327/328 (99.7%)	Unknown protein
66 M136	chr10	965565 to 965256	NO10G03420	Exon+3'UTR	309/310 (99.68%)	Unknown protein
		974547 to 974238	NO10G03440	Exon+3'UTR	309/310 (99.68%)	Unknown protein
		983514 to 983205	NO10G03470	Exon+3'UTR	309/310 (99.68%)	Unknown protein
		992887 to 992578	NO10G03490	Exon+3'UTR	309/310 (99.68%)	Unknown protein
		1001866 to 1001557	NO10G03510	Exon+3'UTR	309/310 (99.68%)	Unknown protein
		1019783 to 1019474	NO10G03580	Exon+3'UTR	309/310 (99.68%)	Unknown protein
		1028766 to 1028457	NO10G03600	Exon+3'UTR	309/310 (99.68%)	Unknown protein
		1037750 to 1037441	NO10G03620	Exon+3'UTR	309/310 (99.68%)	Unknown protein
		1047123 to 1046814	NO10G03640	Exon+3'UTR	309/310 (99.68%)	Unknown protein
		1010804 to 1010496	NO10G03560	Exon+3'UTR	308/310 (99.35%)	Unknown protein
67 M137	chr10	965573 to 965200	NO10G03420	Exon+3'UTR	371/374 (99.2%)	Unknown protein
		974555 to 974182	NO10G03440	Exon+3'UTR	371/374 (99.2%)	Unknown protein
		992895 to 992522	NO10G03490	Exon+3'UTR	371/374 (99.2%)	Unknown protein
		1019791 to 1019418	NO10G03580	Exon+3'UTR	371/374 (99.2%)	Unknown protein
		1028774 to 1028401	NO10G03600	Exon+3'UTR	371/374 (99.2%)	Unknown protein
		1037758 to 1037385	NO10G03620	Exon+3'UTR	371/374 (99.2%)	Unknown protein
		1047131 to 1046758	NO10G03640	Exon+3'UTR	371/374 (99.2%)	Unknown protein
		983522 to 983150	NO10G03470	Exon+3'UTR	370/374 (98.93%)	Unknown protein
		1010812 to 1010440	NO10G03560	Exon+3'UTR	370/374 (98.93%)	Unknown protein
		1001874 to 1001510	NO10G03510	Exon+3'UTR	362/366 (98.91%)	Unknown protein
68 M138	chr1	558498 to 558047	NO01G02190	Exon+3'UTR	452/452 (100%)	Serine hydroxymethyltransferase
69 M139	chr9	193237 to 192941			297/297 (100%)	
		193456 to 193424	NO09G00440	Exon	32/33 (96.97%)	Light-harvesting protein
		195396 to 195692			297/297 (100%)	
		195177 to 195209	NO09G00450	Exon	33/33 (100%)	VCP1
	chr25	241211 to 240969			209/243 (86.01%)	
		241413 to 241368	NO25G00860	Exon	42/46 (91.3%)	Fucoxanthin-chlorophyll a-c binding protein A, chloroplastic
	chr20	173221 to 173185	NO20G00500	Exon	34/37 (91.89%)	Light-harvesting protein

70	M140	chr3	1043766 to 1043800	NO03G03480	Exon	32/35 (91.43%)	Light-harvesting protein
		chr5	461464 to 460984	NO05G01680	Exon	480/481 (99.79%)	methionine aminopeptidase 2B
71	M141	chr8	645781 to 645847	NO08G02190	Exon	67/67 (100%)	Leucyl-trna synthetase
		chr4	1184664 to 1184303		Exon	362/362 (100%)	
			1184340 to 1184270		Exon	65/71 (91.55%)	
			1184303 to 1184204		Exon	82/100 (82%)	
72	M142	chr5	1184307 to 1184237	NO04G04380	Exon	62/71 (87.32%)	Unknown protein
73	M143	chr19	1208379 to 1208011	NO05G04630	Exon	369/369 (100%)	Unknown protein
			28692 to 28876		Intron	185/185 (100%)	
			38178 to 38362		Exon	185/185 (100%)	
			29020 to 29127		Intron	108/108 (100%)	
			38506 to 38613		Exon	108/108 (100%)	
			28445 to 28532		Intron	88/88 (100%)	
			37931 to 38018		Exon	88/88 (100%)	
			28274 to 28320		Intron	47/47 (100%)	
			37760 to 37806		Exon	47/47 (100%)	
			29325 to 29363		Intron	39/39 (100%)	
			38811 to 38849		Exon	39/39 (100%)	Unknown protein
74	M145	chr6	770800 to 770204	NO19G00110	Exon	597/597 (100%)	C-1-tetrahydrofolate cytoplasmic
				NO06G02740	Exon+3'UTR		Indoleamine-dioxygenase subfamily
				NO06G02730	3'UTR		Prefoldin
75	M146	chr3	1158658 to 1158257	NO03G03960	Exon	415/418 (99.28%)	Unknown protein
		chr13	203034 to 202999	NO13G00590	Exon	35/36 (97.22%)	Phosphatidylinositol phosphatase sac1
		chr18	459321 to 459285	NO18G01360	Exon	35/37 (94.59%)	Nadp-dependent glyceraldehyde-3-phosphate dehydrogenase
76	M147	chr1	1308054 to 1308555	NO01G04930	Exon+3'UTR	501/502 (99.8%)	Long-chain acyl-coenzyme A synthetase
77	M148	chr6	239877 to 240263	NO06G00640	Exon	387/387 (100%)	
78	M151	chr1	236257 to 236661	IG region	IG region	405/405 (100%)	
79	M152	chr16	389303 to 388717		Exon	584/587 (99.49%)	
			389503 to 389461		Exon	43/43 (100%)	
			389641 to 389611	NO16G01260	Exon	31/31 (100%)	Atp-dependent chaperone
80	M153	chr3	865266 to 865515	NO03G02860	Exon+3'UTR	248/250 (99.2%)	Nuclear receptor corepressor 1-like protein
		chr29	244450 to 244550	NO29G00640	Exon+Intron	101/101 (100%)	TatA-like sec-independent protein translocator subunit
81	M154	chr7	138423 to 138089		Exon+3'UTR	335/335 (100%)	
			138573 to 138489	NO07G00350	3'UTR	73/91 (80.22%)	Late embryogenesis abundant protein (LEA) family protein
82	M155	chr1	1075893 to 1075762		Exon	131/132 (99.24%)	
			1076125 to 1076034	NO01G04020	Exon	84/92 (91.3%)	Acylaminoacyl peptidase
		chr30	129389 to 129457		IG region	66/69 (95.65%)	
83	M163	chr7	719624 to 719939		Exon	303/316 (95.89%)	
			719999 to 720197		Exon	199/199 (100%)	
			720257 to 720455		Exon	199/199 (100%)	
			720515 to 720713	NO07G02490	Exon	199/199 (100%)	peptidase S8 and S53
		chr6	634742 to 634674		Exon	69/69 (100%)	
			634529 to 634479	NO06G02170	5'UTR+Exon	51/51 (100%)	Cytochrome c oxidase subunit VIa
84	M167-1	chr1	560104 to 560524	NO01G02200	Exon	420/421 (99.76%)	Beta-ketoacyl synthase
	M167-2	chr25	240963 to 241210		Exon	248/248 (100%)	
			241346 to 241402	NO25G00860	Exon	57/57 (100%)	violaxanthin/chlorophyll a binding protein precursor
		chr9	192945 to 193237	NO09G00440	Exon	245/293 (83.62%)	Light-harvesting protein
			195688 to 195396	NO09G00450	Exon	245/293 (83.62%)	VCP1
85	M168	chr13	381592 to 382051	NO13G01250	Exon	460/460 (100%)	inorganic pyrophosphatase
86	M169	chr10	966331 to 965852	NO10G03420	Exon	480/480 (100%)	Unknown protein
			975313 to 974834	NO10G03440	Exon	480/480 (100%)	Unknown protein
			993653 to 993174	NO10G03490	Exon	480/480 (100%)	Unknown protein
			1020549 to 1020070	NO10G03580	Exon	480/480 (100%)	Unknown protein
			1029532 to 1029053	NO10G03600	Exon	480/480 (100%)	Unknown protein
			1011569 to 1011091	NO10G03560	Exon	479/480 (99.79%)	Unknown protein
			1002625 to 1002153	NO10G03510	Intron+Exon	473/475 (99.58%)	Unknown protein
			984280 to 983801	NO10G03470	Exon	456/480 (95%)	Unknown protein
			1038516 to 1038037	NO10G03620	Exon	456/480 (95%)	Unknown protein
			1047889 to 1047410	NO10G03640	Exon	456/480 (95%)	Unknown protein
87	M170-1	chr25	240811 to 240539		Exon+3'UTR	272/273 (99.63%)	
			241204 to 240950	NO25G00860	Exon	255/255 (100%)	Violaxanthin/chlorophyll a binding protein precursor
		chr9	193180 to 192914	NO09G00440	Exon	230/267 (86.14%)	Light-harvesting protein
			195453 to 195719	NO09G00450	Exon	230/267 (86.14%)	VCP1
	M170-2	chr10	1060465 to 1060296		Exon	170/170 (100%)	
			1061084 to 1060974		Exon	111/111 (100%)	
			1060142 to 1060068	NO10G03670	Exon	75/75 (100%)	Acid sphingomyelinase-like phosphodiesterase 3b

88	M172	chr4	854415 to 853911	NO04G03110	Exon+IG+Exon	505/505 (100%)	aminophospholipid-transporting P-type ATPase
		chr21	434811 to 434861	NO21G01440	Exon	43/51 (84.31%)	Phospholipid-transporting ATPase
89	M173	chr5	483802 to 483342	NO05G01760	Exon+3'UTR	461/461 (100%)	Lipid droplet surface protein
90	M176	chr11	624721 to 625246	NO11G01900	Exon	526/526 (100%)	Chloroplast sedoheptulose--bisphosphatase
91	M177	chr6	448831 to 449352	NO06G01400	Exon	520/522 (99.62%)	Amine oxidase
92	M179	chr5	552972 to 552695		Exon	277/278 (99.64%)	
			553144 to 553079	NO05G02030	Exon+3'UTR	66/66 (100%)	Cytochrome b6-f complex iron-sulfur subunit
			555472 to 555195		Exon	277/278 (99.64%)	
			555644 to 555579	NO05G02050	Exon+3'UTR	66/66 (100%)	Cytochrome b6-f complex iron-sulfur subunit
			557972 to 557695		Exon	277/278 (99.64%)	
			558144 to 558079	NO05G02060	Exon+3'UTR	66/66 (100%)	Cytochrome b6-f complex iron-sulfur subunit
			560408 to 560141	NO05G02070	Exon	242/268 (90.3%)	Cytochrome b6-f complex iron-sulfur subunit
93	M180	chr11	808578 to 808952	NO11G02560	3'UTR	375/375 (100%)	conserved unknown protein
				NO11G02570	Exon		proteasome subunit beta type2 putative
94	M182	chr1	305938 to 305624	NO01G01170	Exon	314/315 (99.68%)	predicted protein
		chr9	847265 to 847168	NO09G02870	Exon	84/98 (85.71%)	PREDICTED: OTU domain-containing protein 7B
		chr23	174494 to 174395	NO23G00380	Exon	82/100 (82%)	Unknown protein
		chr19	166380 to 166300	NO19G00430	Exon	70/84 (83.33%)	Unknown protein
			345358 to 345286	NO19G01010	Exon	60/73 (82.19%)	Unknown protein
		chr30	302981 to 303052		Exon	61/72 (84.72%)	
			302981 to 303046		Exon	56/66 (84.85%)	
			302982 to 303055	NO30G00830	Exon	61/74 (82.43%)	Unknown protein
95	M186	chr25	52118 to 51784	IG region	IG region	334/335 (99.7%)	
			46682 to 46593	IG region	IG region	78/90 (86.67%)	
96	M187	chr29	516215 to 516014		Exon+Intron	201/202 (99.5%)	
			517226 to 517090		Exon	137/137 (100%)	
			516637 to 516549		Exon	89/89 (100%)	
			516889 to 516801	NO29G01640	Exon	89/89 (100%)	beta-glucosidase
97	M189	chr16	933983 to 934151		Exon	169/169 (100%)	
			933608 to 933761		Exon	154/154 (100%)	
			933404 to 933468		Exon	65/65 (100%)	
			934306 to 934356	NO16G03140	Exon	51/51 (100%)	Unknown protein
		chr30	74387 to 74467		Exon	69/81 (85.19%)	
			73929 to 74038		Exon	88/110 (80%)	
			73735 to 73792		Exon	52/58 (89.66%)	
			74615 to 74662	NO30G00160	Exon	42/48 (87.5%)	Unknown protein
			77899 to 77979		Exon	69/81 (85.19%)	
			77444 to 77550		Intron+Exon	85/107 (79.44%)	
			77250 to 77307		Exon	52/58 (89.66%)	
			78127 to 78174	NO30G00170	Exon	42/48 (87.5%)	Unknown protein
			81391 to 81495		Exon	91/111 (81.98%)	
			80956 to 81065		Exon	88/110 (80%)	
			80762 to 80819		Exon	52/58 (89.66%)	
			81643 to 81690	NO30G00180	Exon	42/48 (87.5%)	Unknown protein
		chr27	553465 to 553521		Exon	53/57 (92.98%)	
			552983 to 553092		Exon	86/110 (78.18%)	
			552799 to 552849		Exon	46/51 (90.2%)	
			553693 to 553740	NO27G01660	Exon	43/48 (89.58%)	Unknown protein
			584124 to 584046		Exon	67/79 (84.81%)	
			584781 to 584724		Exon	53/58 (91.38%)	
			583883 to 583835	NO27G01730	Exon	44/49 (89.8%)	Unknown protein
		chr9	1234859 to 1234954	IG region	IG region	78/96 (81.25%)	
98	M194-1	chr29	516215 to 516014		Exon+Intron	198/202 (98.02%)	
			517226 to 517090		Exon	136/137 (99.27%)	
			516889 to 516801		Exon	89/89 (100%)	
			516637 to 516551	NO29G01640	Exon	84/87 (96.55%)	beta-glucosidase
	M194-2	chr16	933983 to 934151		Exon	169/169 (100%)	
			933608 to 933761		Exon	154/154 (100%)	
			934306 to 934356		Exon	51/51 (100%)	
			933427 to 933468	NO16G03140	Exon	42/43 (97.67%)	Unknown protein
		chr30	74387 to 74467		Exon	69/81 (85.19%)	
			74615 to 74662		Exon	42/48 (87.5%)	
			73929 to 74038	NO30G00160	Exon	88/110 (80%)	Unknown protein
			77899 to 77979		Exon	69/81 (85.19%)	
			77444 to 77550		Intron+Exon	85/107 (79.44%)	

		chr27	78127 to 78174	NO30G00170	Exon	42/48 (87.5%)	Unknown protein
			80956 to 81065		Exon	88/110 (80%)	
			81643 to 81690		Exon	42/48 (87.5%)	
			81391 to 81495	NO30G00180	Exon	91/111 (81.98%)	Unknown protein
			553465 to 553521		Exon	53/57 (92.98%)	
			552983 to 553092		Exon	86/110 (78.18%)	
			553693 to 553740	NO27G01660	Exon	43/48 (89.58%)	Unknown protein
			584124 to 584046		Exon	67/79 (84.81%)	
			583883 to 583835		Exon	44/49 (89.8%)	
			584765 to 584724	NO27G01730	Exon	40/43 (93.02%)	Unknown protein
M194-3	chr9 chr26		1234859 to 1234954	IG region	IG region	78/96 (81.25%)	
			248319 to 248048		Exon	271/272 (99.63%)	
			248612 to 248532		Exon	81/81 (100%)	
			247837 to 247797	NO26G00710	Exon	41/41 (100%)	ferredoxin nitrite reductase
M194-4	chr25		52118 to 51784	IG region	IG region	334/335 (99.7%)	
			46682 to 46593	IG region	IG region	78/90 (86.67%)	
99	M195	chr10	925123 to 925573	NO10G03290	Exon	449/451 (99.56%)	ATP-binding cassette transporter
100	M196	chr26	248319 to 248048		Exon	272/272 (100%)	
101	M199	chr22	248612 to 248532		Exon	81/81 (100%)	
			247837 to 247797	NO26G00710	Exon	41/41 (100%)	ferredoxin nitrite reductase
			1563 to 1694		Exon	132/132 (100%)	
			1298 to 1420		Exon	122/123 (99.19%)	
			2009 to 2038	NO22G00010	Exon	30/30 (100%)	Oxidoreductase domain protein
102	M202-1	chr26	229183 to 229043	NO26G00650	Exon	112/141 (79.43%)	Myo-inositol 2-dehydrogenase
		chr10	653859 to 653360	NO10G02380	5'UTR	500/500 (100%)	S-adenosylmethionine carrier 1
M202-2	chr12			NO10G02390	Exon		Rna family
			854535 to 854322		Exon	214/214 (100%)	
			854679 to 854499		Exon	170/181 (93.92%)	
			854607 to 854439		Exon	160/169 (94.67%)	
			854571 to 854399		Exon	161/173 (93.06%)	
			854643 to 854471		Exon	161/173 (93.06%)	
			854747 to 854583		Exon	154/165 (93.33%)	
			854715 to 854547		Exon	155/169 (91.72%)	
			854499 to 854363		Exon	128/137 (93.43%)	
			854782 to 854619		Exon	146/164 (89.02%)	
			854463 to 854367		Exon	92/97 (94.85%)	
			854793 to 854655		Exon	116/139 (83.45%)	
			854793 to 854697		Exon	84/97 (86.6%)	
			854857 to 854715		Exon	113/143 (79.02%)	
			854427 to 854363		Exon	60/65 (92.31%)	
			854857 to 854745		Exon	88/113 (77.88%)	
			854793 to 854723	NO12G03110	Exon	57/71 (80.28%)	Viral protein TPX
		chr13	142450 to 142309	NO13G00420	Exon	105/142 (73.94%)	Unknown protein
		chr16	462199 to 462123	NO16G01520	Exon	60/77 (77.92%)	Filamentous hemagglutinin family N-terminal domain protein
			464487 to 464411	NO16G01530	Exon	60/77 (77.92%)	Filamentous hemagglutinin family N-terminal domain protein
103	M206	chr5	82937 to 83425		Exon+3'UTR	489/489 (100%)	
104	M207	chr20	83537 to 83621		Exon	85/85 (100%)	
			83862 to 83937	NO05G00180	Exon	76/76 (100%)	Barwin-related endoglucanase
			638276 to 638087		Exon	190/190 (100%)	
			637964 to 637807		Exon	158/158 (100%)	
			637624 to 637573		Exon	52/52 (100%)	
105	M208	chr2	638430 to 638403	NO20G02130	Exon	28/28 (100%)	Heat shock protein hsp20
			641104 to 640915		Exon	190/190 (100%)	
			641258 to 641231		Exon	28/28 (100%)	
			640452 to 640401		Exon	52/52 (100%)	
			640792 to 640635	NO20G02140	Exon	158/158 (100%)	Heat shock protein hsp20
			643983 to 643794		Exon	190/190 (100%)	
			643671 to 643514		Exon	157/158 (99.37%)	
			643331 to 643280		Exon	52/52 (100%)	
			644137 to 644110	NO20G02150	Exon	28/28 (100%)	Heat shock protein hsp20
			1453449 to 1452991	NO02G05450	Exon+3'UTR	459/459 (100%)	
			1454580 to 1455038	NO02G05460	Exon	458/459 (99.78%)	
			1458668 to 1458210	NO02G05470	Exon+3'UTR	458/459 (99.78%)	
			1459799 to 1460257	NO02G05480	Exon+3'UTR	458/459 (99.78%)	
			1449709 to 1450167	NO02G05440	Exon+3'UTR	437/459 (95.21%)	Unknown protein

 The red box represents the mutant produced by multiple cassette insertions

Table S3c. All screened mutants from L-RNAi library

Number	Chromosome	Mapping position	Knockdown genes	Mapping range	Identity	Description
1 L3	chr27	381423 to 381512		Exon	90/90 (100%)	
		381667 to 381737		Exon	70/71 (98.59%)	
		381987 to 382062		Exon	76/76 (100%)	
		382209 to 382249	NO27G01200	Exon	41/41 (100%)	Peroxin-5
2 L6	chr7	1107137 to 1107312	NO07G03980	Exon	178/178 (100%)	Unknown protein
3 L38	chr29	459342 to 459223	NO29G01440	3'UTR	120/120 (100%)	Filamentous hemagglutinin family N-terminal domain protein
	chr5	1280050 to 1280181	NO05G04920	Exon	132/132 (100%)	Glutathione reductase
	chr1	1221925 to 1221854	NO01G04630	Exon	62/72 (86.11%)	Glutathione reductase
4 L43	chr9	193000 to 193139	NO09G00440	Exon	140/140 (100%)	Light-harvesting protein
		195633 to 195494	NO09G00450	Exon	140/140 (100%)	VCP1
	chr25	241028 to 241163	NO25G00860	Exon	121/136 (88.97%)	Fucoxanthin-chlorophyll a-c binding protein A, chloroplastic
	chr6	72724 to 72634		Exon	86/91 (94.51%)	
		73091 to 72990	NO06G00160	Exon	86/102 (84.31%)	Peptidoglycan-binding lysin domain containing protein
5 L48	chr6	73268 to 72974		Exon+3'UTR	295/295 (100%)	
		72724 to 72634	NO06G00160	Exon	91/91 (100%)	Peptidoglycan-binding lysin domain containing protein
6 L50	chr6	240399 to 240260	NO06G00640	Exon	139/140 (99.29%)	Long-chain acyl-coenzyme A synthetase
	chr11	407940 to 408053	NO11G01120	Exon	93/114 (81.58%)	Unknown protein
7 L54	chr11	407911 to 408059	NO11G01120	Exon	148/149 (99.33%)	Unknown protein
	chr10	1200015 to 1199937		Exon	79/79 (100%)	
		1199751 to 1199680	NO10G04020	Exon	71/72 (98.61%)	Rubisco methyltransferase family protein
8 L66-1	chr3	305478 to 305280		Exon	198/199 (99.5%)	
		305128 to 304996		Exon	133/133 (100%)	Beta-lactamase/transpeptidase-like protein
		304873 to 304808	NO03G00920	Exon	66/66 (100%)	
L66-2	chr16	765468 to 765315		Exon	154/154 (100%)	
		765153 to 765112	NO16G02650	Exon	42/42 (100%)	GTPase Obg
	chr22	329968 to 330041	NO22G01050	Exon	74/74 (100%)	Sit4 phosphatase-associated family protein
9 L67	chr23	652006 to 652442	NO23G01810	Exon	437/437 (100%)	Diaminopimelate decarboxylase
			NO23G01800	3'UTR	437/437 (100%)	cell division cycle 48
10 L68	chr7	894488 to 894675		Exon	188/188 (100%)	
		894401 to 894440	NO07G03230	Exon	40/40 (100%)	Glutamine synthetase 2
11 L70	chr22	452546 to 452678	NO22G01530	Exon+3'UTR	133/133 (100%)	Glycerophosphoryl diester phosphodiesterase
12 L78	chr4	788339 to 788444	NO04G02960	Exon	106/106 (100%)	DNA-directed RNA polymerase subunit photosynthesis, light harvesting
13 L92	chr20	569481 to 569351	NO20G01890	Exon	130/130 (100%)	Unknown protein
		565678 to 565548	NO20G01880	Exon	130/130 (100%)	Unknown protein
14 L99	chr12	870058 to 870311	NO12G03140	Exon	254/254 (100%)	Fructose-bisphosphate aldolase
15 L102	chr26	573220 to 573111		Exon	110/110 (100%)	
		573562 to 573508	NO26G01720	Exon	55/55 (100%)	Light-harvesting protein
	chr3	1097600 to 1097537	NO03G03690	Exon	53/64 (82.81%)	Light-harvesting protein
16 L103-1	chr3	1497955 to 1498239		Exon	283/285 (99.3%)	
		1497670 to 1497858	NO03G05250	Exon	188/189 (99.47%)	zeta-carotene desaturase
L103-2	chr17	252026 to 252298	NO17G00700	Exon	266/273 (97.44%)	mitochondrial carrier family protein
		663667 to 663708	NO17G02270	Exon	37/42 (88.1%)	dolichol kinase
	chr8	776452 to 776413	NO08G02740	Exon	36/40 (90%)	Unknown protein
	chr30	278565 to 278603	NO30G00750	Exon	35/39 (89.74%)	Protein kinase family protein
	chr13	908589 to 908549	NO13G03150	Exon	36/41 (87.8%)	VPS15 protein kinase /phosphoinositide 3-kinase regulatory subunit
	chr12	619411 to 619368	NO12G02160	Exon	38/44 (86.36%)	ph-response regulator protein pala rim20
	chr9	107247 to 107204	NO09G00190	Exon	38/44 (86.36%)	BEACH domain protein
	chr5	156062 to 156016	NO05G00410	Exon	40/47 (85.11%)	Unknown protein
	chr2	1338494 to 1338549	NO02G04980	Exon	46/56 (82.14%)	Unknown protein
17 L104	chr2	1329957 to 1330122			157/166 (94.58%)	Unknown protein
		1329920 to 1330122	NO02G04960	Exon	203/203 (100%)	Unknown protein
18 L112	chr25	241210 to 240950		Exon	261/261 (100%)	
		241395 to 241346	NO25G00860	Exon	50/50 (100%)	Fucoxanthin-chlorophyll a-c binding protein A, chloroplastic
	chr9	193224 to 192917	NO09G00440	Exon	260/308 (84.42%)	Light-harvesting protein
		195409 to 195716	NO09G00450	Exon	260/308 (84.42%)	VCP1
19 L117-1	chr2	1452345 to 1451844	NO02G05450	5'UTR+Exon	502/502 (100%)	Unknown protein
		1456108 to 1456486	NO02G05460	5'UTR	374/379 (98.68%)	Unknown protein

		1460903 to 1461184	NO02G05480	5'UTR+Exon	279/282 (98.94%)	Unknown protein
		1457564 to 1457281	NO02G05470	5'UTR+Exon	279/284 (98.24%)	Unknown protein
		1455684 to 1455967	NO02G05460	5'UTR+Exon	279/284 (98.24%)	Unknown protein
		1457332 to 1457149	NO02G05470	5'UTR	178/186 (95.7%)	Unknown protein
		1455916 to 1456099	NO02G05460	5'UTR	177/186 (95.16%)	Unknown protein
		1450813 to 1450956	NO02G05440	5'UTR+Exon	143/144 (99.31%)	Unknown protein
		1451025 to 1451093		IG region	61/71 (85.92%)	
		1461135 to 1461195	NO02G05480	5'UTR	55/63 (87.3%)	Unknown protein
			NO02G05490	5'UTR		50s ribosomal protein l28
		1451025 to 1451073		IG region	42/49 (85.71%)	
	chr10	624019 to 623638	NO10G02260	Exon	382/382 (100%)	Cytochrome p450
L117-2	chr16	223819 to 223926	NO16G00630	Exon	108/108 (100%)	Gdp-mannose-epimerase
		229068 to 229175	NO16G00650	Exon	108/108 (100%)	Gdp-mannose-epimerase
20 L118	chr1	1648770 to 1648882		Exon	113/113 (100%)	
		1648583 to 1648632	NO01G05860	Exon	50/50 (100%)	Ribose-phosphate pyrophosphokinase
21 L121	chr16	709409 to 709101	NO16G02460	Exon	308/309 (99.68%)	Tyrosine kinase
22 L123	chr5	1002057 to 1002460		Exon	404/404 (100%)	
		1002523 to 1002654		Exon	132/132 (100%)	
		1002820 to 1002872	NO05G03850	Exon	53/53 (100%)	Peptidyl-prolyl cis-trans isomerase
23 L130-1	chr18	503941 to 504145	NO18G01550	Exon+3'UTR	205/205 (100%)	Triacylglycerol lipase
L130-2	chr18	503986 to 503933	NO18G01550	Exon	51/54 (94.44%)	Triacylglycerol lipase
24 L134	chr7	894488 to 894675		Exon	188/188 (100%)	
		894395 to 894440	NO07G03230	Exon	46/46 (100%)	glutamine synthetase 2
25 L138	chr20	526890 to 526574		Exon+3'UTR	317/317 (100%)	
		526229 to 526020	NO20G01720	Exon	210/210 (100%)	Sigma 54 modulation protein ribosomal protein s30ea
26 L153	chr26	248048 to 248319		Exon	272/272 (100%)	
		248532 to 248612		Exon	81/81 (100%)	
		247797 to 247837	NO26G00710	Exon	41/42 (97.62%)	Nitrite reductase
27 L155	chr18	504140 to 503933	NO18G01550	Exon+3'UTR	208/208 (100%)	Triacylglycerol lipase
28 L157	chr9	481644 to 481467	NO09G01520	Exon	178/178 (100%)	Receptor for activated C kinase 1C
29 L160	chr12	1126938 to 1127306	NO12G03920	Exon	369/369 (100%)	Transformation transcription domain-associated protein
	chr4	1464856 to 1465014		Exon+3'UTR	158/159 (99.37%)	
		1465163 to 1465299		Exon	137/137 (100%)	
		1465488 to 1465585		Exon	98/98 (100%)	
		1465857 to 1465938		Exon	82/82 (100%)	
		1466057 to 1466098	NO04G05220	Exon	42/42 (100%)	Glucose 6-phosphate/phosphate translocator 1
30 L164	chr3	1043889 to 1043710	NO03G03480	Exon	180/180 (100%)	Light-harvesting protein
	chr20	173187 to 173225	NO20G00500	Exon	35/39 (89.74%)	Light-harvesting protein
31 L167	chr19	27476 to 27640		Intron	165/165 (100%)	
		36962 to 37126	NO19G00110	Exon	165/165 (100%)	Unknown protein
32 L168	chr8	83081 to 83187		Exon	107/107 (100%)	
		83405 to 83456	NO08G00210	Exon	52/52 (100%)	Ascorbate peroxidase
33 L174	chr20	603537 to 603735		Exon	199/199 (100%)	
		603840 to 603933	NO20G02030	3'UTR	93/94 (98.94%)	Cmhc dyrk yak protein kinase
34 L175	chr26	573220 to 573111		Exon	110/110 (100%)	
		573557 to 573508	NO26G01720	Exon	50/50 (100%)	Light-harvesting protein
	chr3	1097600 to 1097537	NO03G03690	Exon	53/64 (82.81%)	Light-harvesting protein
35 L176	chr23	385199 to 384867		Exon	333/333 (100%)	
		384724 to 384568	NO23G01030	Exon+3'UTR	157/157 (100%)	3-isopropylmalate dehydrogenase
36 L177	chr12	695419 to 695276	NO12G02410	Exon	144/144 (100%)	Tubulin alpha chain
37 L178-1	chr7	894386 to 894670	NO07G03230	Exon	285/285 (100%)	Glutamine synthetase 2
L178-2	chr17	180230 to 180121	NO17G00500	Exon	109/110 (99.09%)	Kinesin-like protein
38 L179	chr8	1101028 to 1100873	NO08G03910	Exon	155/157 (98.73%)	Vacuolar protein sorting-associated protein 16
39 L180	chr5	1002460 to 1002036		Exon	425/425 (100%)	
		1002654 to 1002523		Exon	132/132 (100%)	
		1002872 to 1002820	NO05G03850	Exon	53/53 (100%)	Peptidyl-prolyl cis-trans isomerase
40 L187	chr20	82901 to 82727	NO20G00240	Exon	175/175 (100%)	TDP-4-oxo-6-deoxy-D-glucose aminotransferase
41 L189	chr9	192941 to 193100	NO09G00450	Exon	160/160 (100%)	VCP1
		195692 to 195533	NO09G00440	Exon	160/160 (100%)	Light-harvesting protein
	chr25	240969 to 241122	NO25G00860	Exon	129/154 (83.77%)	Fucoxanthin-chlorophyll a-c binding protein A, chloroplastic
42 L194	chr9	192941 to 193053	NO09G00450	Exon	113/113 (100%)	VCP1
		195692 to 195580	NO09G00440	Exon	113/113 (100%)	Light-harvesting protein
	chr25	240969 to 241077	NO25G00860	Exon	94/109 (86.24%)	Fucoxanthin-chlorophyll a-c binding protein A, chloroplastic
43 L195	chr7	894392 to 894630	NO07G03230	Exon	239/239 (100%)	Glutamine synthetase 2

44	L196	chr12	138278 to 138189	NO12G00380	Exon	90/90 (100%)	Plasma membrane ATPase
			133079 to 133168	NO12G00370	Exon	90/90 (100%)	H-transporting ATPase
			143360 to 143279	NO12G00390	Exon	81/82 (98.78%)	Plasma membrane ATPase
		chr17	165434 to 165350	NO17G00440	Exon	69/85 (81.18%)	Plasma membrane ATPase
45	L200	chr13	768692 to 768404	NO13G02770	Exon	288/289 (99.65%)	SNF2 domain-containing protein / helicase domain-containing protein
46	L202	chr2	1326615 to 1326390		Exon	226/226 (100%)	
			1327221 to 1326999	NO02G04940	Exon	223/223 (100%)	Unknown protein
		chr27	161885 to 161839	NO27G00430	Exon	40/47 (85.11%)	Protein kinase
		chr19	340661 to 340636	NO19G01000	Exon	26/26 (100%)	Unknown protein
		chr23	479307 to 479350	NO23G01320	Exon	38/44 (86.36%)	Cyclin B2;2
47	L205	chr7	894391 to 894675	NO07G03230	Exon	285/285 (100%)	Glutamine synthetase 2
48	L206	chr8	654317 to 653767	NO08G02220	Exon	550/551 (99.82%)	Transketolase
		chr14	624640 to 624695	NO14G02050	Exon	48/56 (85.71%)	Transketolase
49	L209	chr2	1124058 to 1123763	NO02G04110	Exon+3'UTR	294/296 (99.32%)	Aconitate hydratase, mitochondrial
			24559 to 24528	NO02G00090	Intron	30/32 (93.75%)	Peptidase m1 membrane alanine aminopeptidase
			87585 to 87542	NO02G00240	Exon+Intron	38/44 (86.36%)	Alpha-mannosidase
			1299755 to 1299724	NO02G04810	Intron	30/32 (93.75%)	Calcium-independent phospholipase a2-gamma
50	L210-1	chr11	59278 to 58761	NO11G00130	Exon	518/518 (100%)	Unknown protein
			63813 to 63296	NO11G00140	Exon	518/518 (100%)	Unknown protein
			67588 to 67071	NO11G00150	Exon	518/518 (100%)	Unknown protein
			71785 to 71268	NO11G00160	Exon	518/518 (100%)	Unknown protein
			81984 to 82043		IG region	56/60 (93.33%)	
		chr15	74877 to 75394	NO15G00260	Exon	467/518 (90.15%)	Unknown protein
		chr12	1162895 to 1163418	NO12G04010	Exon	442/527 (83.87%)	Unknown protein
		chr16	902577 to 903085	NO16G03050	Exon	428/512 (83.59%)	Viral protein TPX
			907112 to 907620	NO16G03070	Exon	428/512 (83.59%)	Viral protein TPX
		chr13	126772 to 126267	NO13G00380	Exon	425/512 (83.01%)	Unknown protein
			143207 to 142702	NO13G00420	Exon	425/512 (83.01%)	Unknown protein
			133609 to 133104	NO13G00400	Exon	424/512 (82.81%)	Unknown protein
		chr19	323635 to 323856	NO19G00960	Exon+5'UTR	221/222 (99.55%)	Unknown protein
		chr4	1419905 to 1419809	NO04G05090	3'UTR	97/97 (100%)	Unknown protein
		chr29	498462 to 498597		IG region	123/136 (90.44%)	
	L210-2	chr2	1124050 to 1123763		Exon+3'UTR	287/288 (99.65%)	
			24559 to 24528		Intron	30/32 (93.75%)	
			87585 to 87542		Exon+Intron	38/44 (86.36%)	
			1299755 to 1299724	NO02G04110	Intron	30/32 (93.75%)	Aconitate hydratase, mitochondrial
51	L211	chr14	670609 to 669862	NO14G02230	Exon+3'UTR	748/748 (100%)	Helix-loop-helix DNA-binding protein
52	L220	chr19	588944 to 588729		Exon	216/216 (100%)	
			589251 to 589129		Exon	122/123 (99.19%)	
			589392 to 589359	NO19G02010	Exon	33/34 (97.06%)	Hybrid cluster protein
53	L222	chr16	223975 to 223819	NO16G00630	5'UTR+Exon	157/157 (100%)	Gdp-mannose-epimerase
			229224 to 229068	NO16G00650	5'UTR+Exon	157/157 (100%)	Gdp-mannose-epimerase
54	L224	chr6	852597 to 852990	NO06G02980	Exon	393/394 (99.75%)	CCR4-NOT transcription complex subunit 11
55	L228	chr17	569308 to 569485	NO17G01990	5'UTR+Exon	178/178 (100%)	Importin-like protein
		chr1	282351 to 282528	NO01G01110	Exon+Intron	178/178 (100%)	Importin-like protein
56	L229	chr20	638087 to 638276		Exon	190/190 (100%)	
			638403 to 638430		Exon	28/28 (100%)	
			637863 to 637964	NO20G02130	Exon	102/102 (100%)	Heat shock protein hsp20
			640915 to 641104		Exon	190/190 (100%)	
			640691 to 640792		Exon	102/102 (100%)	
			641231 to 641258	NO20G02140	Exon	28/28 (100%)	Heat shock protein hsp20
			643794 to 643983		Exon	190/190 (100%)	
			643570 to 643671		Exon	101/102 (99.02%)	
			644110 to 644137	NO20G02150	Exon	28/28 (100%)	Heat shock protein hsp20
57	L231	chr11	1137629 to 1137562	NO11G03530	Exon	68/68 (100%)	Unknown protein
58	L232	chr10	993162 to 992217	NO10G03490	Exon+3'UTR	944/946 (99.79%)	Unknown protein
			1038025 to 1037080	NO10G03620	Exon+3'UTR	944/946 (99.79%)	Unknown protein
			983789 to 982845	NO10G03470	Exon+3'UTR	943/946 (99.68%)	Unknown protein
			974822 to 973877	NO10G03440	Exon+3'UTR	940/946 (99.37%)	Unknown protein
			1020058 to 1019113	NO10G03580	Exon+3'UTR	940/946 (99.37%)	Unknown protein
			1029041 to 1028096	NO10G03600	Exon+3'UTR	940/946 (99.37%)	Unknown protein
			1047398 to 1046453	NO10G03640	Exon+3'UTR	940/946 (99.37%)	Unknown protein
			965840 to 964895	NO10G03420	Exon+3'UTR	939/946 (99.26%)	Unknown protein
			1011079 to 1010138	NO10G03560	Exon+3'UTR	936/946 (98.94%)	Unknown protein

59	L235	chr18	1002134 to 1001200	NO10G03510	Intron+Exon+3'UTR	930/941 (98.83%)	Unknown protein
			140761 to 140847		Exon	87/87 (100%)	
60	L236	chr18	141072 to 141114	NO18G00330	Exon	43/43 (100%)	Light harvesting complex protein
			140760 to 140847		Exon	88/88 (100%)	
			141072 to 141114	NO18G00330	Exon	43/43 (100%)	Light harvesting complex protein
61	L239-1	chr3	1577442 to 1577139			303/304 (99.67%)	
	L239-2	chr9	1577713 to 1577673	NO03G05490	Exon	41/41 (100%)	Zinc finger ccch domain-containing protein 63
			195446 to 195692	NO09G00450	Exon	247/247 (100%)	VCP1
			193187 to 192941	NO09G00440	Exon	247/247 (100%)	Light-harvesting protein
		chr25	241211 to 240969	NO25G00860	Exon	209/243 (86.01%)	Fucoxanthin-chlorophyll a-c binding protein A, chloroplastic
62	L241	chr2	438846 to 439034	NO02G01470	Exon	189/189 (100%)	Serine arginine-rich splicing factor 4
63	L242	chr11	1152202 to 1152049	NO11G03580	Exon	154/154 (100%)	Phosphoesterase pa-phosphatase related protein
64	L243	chr7	114132 to 114363		Exon	231/232 (99.57%)	
			114512 to 114634		Exon	123/123 (100%)	
			114744 to 114826		Exon	83/83 (100%)	
			115027 to 115105		Exon	79/79 (100%)	
			115324 to 115351	NO07G00290	Exon	28/28 (100%)	Protein of unknown function (DUF962)
65	L265	chr7	1036534 to 1036657	NO07G03720		124/124 (100%)	Cellulose synthase
66	L266	chr6	507351 to 507872	NO06G01620	3'UTR	521/522 (99.81%)	Pheophorbide a oxygenase
				NO06G01630	Exon		Pyruvate kinase
67	L267	chr2	1035532 to 1036260	NO02G03810	Exon	728/729 (99.86%)	Unknown protein
68	L271-1	chr19	589679 to 589427	NO19G02010	Exon	253/253 (100%)	Hybrid cluster protein
	L271-2	chr7	894675 to 894520	NO07G03230	Exon	156/156 (100%)	glutamine synthetase 2
69	L280	chr6	240263 to 240413	NO06G00640	Exon	149/151 (98.68%)	Long-chain acyl-coenzyme A synthetase
70	L284	chr3	1659855 to 1660021	NO03G05790	5'UTR	167/167 (100%)	Unknown protein
		chr20	417 to 339		IG region	66/79 (83.54%)	
71	L287	chr12	870147 to 870043	NO12G03140	Exon	105/105 (100%)	Fructose-bisphosphate aldolase
72	L288	chr9	919379 to 919120	NO09G03160	Exon	259/260 (99.62%)	Unknown protein
73	L296	chr25	76224 to 76122			103/103 (100%)	
			76002 to 75914	NO25G00250	Exon	88/89 (98.88%)	Thiamine pyrophosphate dependent pyruvate decarboxylase family protein
74	L300	chr14	720563 to 720342	NO14G02420	3'UTR	222/222 (100%)	Cation-transporting ATPase
				NO14G02430	Exon		Elongation factor tu
75	L301	chr12	451751 to 452360	NO12G01450	5'UTR+Exon+Intron	609/610 (99.84%)	Mitochondrial-processing peptidase subunit beta
		chr2	1453006 to 1453338	NO02G05450	Exon+3'UTR	332/333 (99.7%)	Unknown protein
			1458225 to 1458557	NO02G05470	Exon+3'UTR	331/333 (99.4%)	Unknown protein
			1455023 to 1454691	NO02G05460	Exon+3'UTR	331/333 (99.4%)	Unknown protein
			1460242 to 1459910	NO02G05480	Exon+3'UTR	331/333 (99.4%)	Unknown protein
			1450152 to 1449820	NO02G05440	Exon+3'UTR	313/333 (93.99%)	Unknown protein
76	L302	chr13	655844 to 655761	NO13G02350	Exon	83/84 (98.81%)	Abc1 family protein
77	L307	chr4	571914 to 571772	NO04G01930	3'UTR	143/143 (100%)	60s acidic ribosomal protein p0
78	L312	chr20	638156 to 638276			121/121 (100%)	
			638403 to 638430	NO20G02130	Exon	28/28 (100%)	Heat shock protein hsp20
			640984 to 641104			121/121 (100%)	
			641231 to 641258	NO20G02140	Exon	28/28 (100%)	Heat shock protein hsp20
			643863 to 643983			28/28 (100%)	
			644110 to 644137	NO20G02150	Exon	28/28 (100%)	Heat shock protein hsp20
79	L313	chr2	1538322 to 1538200	NO02G05760	Exon	122/123 (99.19%)	Unknown protein
80	L316	chr22	217022 to 217338	NO22G00640	Exon	317/317 (100%)	lysine-ketoglutarate reductase/saccharopine dehydrogenase bifunctional enzyme
81	L319	chr11	937258 to 937125	NO11G02980	Exon	134/134 (100%)	Unknown protein
82	L320	chr28	76541 to 76639		Exon+3'UTR	99/99 (100%)	
			76894 to 76944	NO28G00190	Exon	51/51 (100%)	ubiquitin 8
83	L321	chr5	288080 to 287849		Exon	232/232 (100%)	
			288383 to 288224		Exon	160/160 (100%)	
			288525 to 288490	NO05G00940	Exon	36/36 (100%)	Soul heme-binding protein
84	L322	chr3	919906 to 920222		Exon+3'UTR	317/317 (100%)	
			920395 to 920512	NO03G03070	Exon	118/118 (100%)	Enolase
		chr4	534649 to 534312	NO04G01820	Exon	265/338 (78.4%)	Enolase
85	L323	chr6	1153860 to 1154042	NO06G04120	Exon	183/183 (100%)	Phosphoglycerate kinase
			342624 to 342477	NO06G01060	Exon	114/148 (77.03%)	Phosphoglycerate kinase
86	L325	chr13	216904 to 216822	NO13G00630	Exon	83/83 (100%)	Cysteine protease
87	L329	chr9	332831 to 332551	NO09G00980	Exon	281/281 (100%)	26s proteasome subunit 4
		chr15	303398 to 303354		Exon	40/45 (88.89%)	26s protease regulatory subunit 8
		chr2	1137975 to 1137925		Exon	44/51 (86.27%)	26s protease regulatory subunit 6a-a
		chr28	233212 to 233166		Exon	41/47 (87.23%)	26s proteasome regulatory atpase rpt4
		chr11	984039 to 983990		Exon	42/50 (84%)	26S proteasome regulatory subunit T3

88	L331-1	chr1	1664584 to 1665144 1665352 to 1665540	NO01G05900	Exon+3'UTR Exon	561/561 (100%) 189/189 (100%)	Unknown protein
			1675929 to 1676117 1675539 to 1675721	NO01G05920	Exon Exon+3'UTR	189/189 (100%) 183/183 (100%)	Unknown protein
		chr23	9674 to 9508		Exon	137/167 (82.04%)	
			10003 to 9937	NO23G00020	Exon	54/67 (80.6%)	Unknown protein
	L331-2	chr8	669467 to 669237	NO08G02290	Exon+3'UTR	231/231 (100%)	Unknown protein
89	L332	chr16	843213 to 843041	NO16G02900	Exon	173/173 (100%)	Pentatricopeptide repeat-containing protein
90	L342	chr23	385061 to 385199	NO23G01030	Exon	139/139 (100%)	3-isopropylmalate dehydrogenase
91	L344	chr6	227236 to 227435	NO06G00580	Exon	200/200 (100%)	mitochondrial DNA-directed RNA polymerase
92	L346	chr7	645278 to 644962	NO07G02160	Exon	317/317 (100%)	Ribonuclease III, putative
93	L348	chr29	482507 to 482803 498842 to 499056	NO29G01530 IG region	Exon IG region	297/297 (100%) 203/222 (91.44%)	predicted protein
94	L350	chr15	368007 to 368258	NO15G01300	Exon+3'UTR	220/253 (86.96%)	putative zinc finger protein(ISS)
95	L352	chr1	421436 to 421331	NO01G01660	Exon	105/106 (99.06%)	X-Pro dipeptidyl-peptidase domain-containing protein
96	L355	chr17	865902 to 865630 864607 to 864471 865509 to 865393 864352 to 864240 864955 to 864850 864150 to 864079 865278 to 865227		Exon+3'UTR Exon Exon Exon Exon Exon Exon	273/273 (100%) 137/137 (100%) 117/117 (100%) 113/113 (100%) 106/106 (100%) 72/74 (97.3%) 52/52 (100%)	
97	L366	chr19	29453 to 29325 38939 to 38811 29127 to 29024 38613 to 38510 29889 to 29802 39375 to 39288 29689 to 29620 39175 to 39106	NO17G02940	Intron Exon Intron Exon Intron Exon Intron	129/129 (100%) 129/129 (100%) 104/104 (100%) 104/104 (100%) 88/88 (100%) 88/88 (100%) 70/70 (100%)	Unknown protein
98	L368	chr1	992229 to 992460	NO19G00110	Exon	70/70 (100%)	Unknown protein
99	L369	chr7	894675 to 894488 894440 to 894375	NO01G03700 NO07G03230	Exon Exon	230/232 (99.14%) 188/188 (100%)	conserved hypothetical protein
100	L337	chr23	256714 to 256873 256438 to 256567 256092 to 256187 255829 to 255896		Exon Exon Exon Exon	66/66 (100%) 160/160 (100%) 130/130 (100%) 96/96 (100%)	Glutamate ammonia ligase
		chr15	421545 to 421602 421894 to 421984	NO23G00640	Exon Exon	68/68 (100%) 51/58 (87.93%)	Molecular chaperones HSP70/HSC70,HSP70 superfamily
101	L343	chr9	192941 to 193177 195692 to 195456	NO15G01500 NO09G00440 NO09G00450	Exon Exon Exon	72/91 (79.12%) 236/237 (99.58%) 236/237 (99.58%)	Molecular chaperones GRP78/BiP/KAR2,HSP70 superfamily Light-harvesting protein VCP1
102	L345	chr25	240969 to 241201	NO25G00860	Exon	199/233 (85.41%)	violaxanthin/chlorophyll a binding protein precursor
		chr25	240539 to 240811 240950 to 240985		Exon+3'UTR Exon	273/273 (100%) 36/36 (100%)	
		chr9	192914 to 192954 195719 to 195679	NO09G00440 NO09G00450	Exon Exon	37/41 (90.24%) 37/41 (90.24%)	Light-harvesting protein VCP1
103	L351	chr11	59278 to 59149 63813 to 63684 67588 to 67459 71785 to 71656	NO11G00130 NO11G00140 NO11G00150 NO11G00160	Exon Exon Exon Exon	130/130 (100%) 130/130 (100%) 130/130 (100%) 130/130 (100%)	Unknown protein Unknown protein Unknown protein Unknown protein
		chr15	74877 to 75003	NO15G00260	Exon	122/127 (96.06%)	Unknown protein
		chr13	126772 to 126648 133609 to 133485 143207 to 143083	NO13G00380 NO13G00400 NO13G00420	Exon Exon Exon	112/125 (89.6%) 112/125 (89.6%) 112/125 (89.6%)	Unknown protein Unknown protein Unknown protein
		chr29	498462 to 498576	IG region	IG region	104/115 (90.43%)	
		chr16	902577 to 902706 907112 to 907241 1162895 to 1163024	NO16G03050 NO16G03070 NO12G04010	Exon Exon Exon	113/130 (86.92%) 112/130 (86.15%) 111/130 (85.38%)	Viral protein TPX Viral protein TPX Unknown protein
104	L354	chr18	508259 to 508496 515176 to 515413 526956 to 526719 511054 to 511118 520512 to 520448 524161 to 524097 415950 to 415846	NO18G01570 NO18G01600 NO18G01630 IG region NO18G01610 NO18G01620 NO11G01140	Exon Exon Exon IG region 3'UTR 3'UTR 3'UTR	234/238 (98.32%) 234/238 (98.32%) 234/238 (98.32%) 54/65 (83.08%) 54/65 (83.08%) 54/65 (83.08%) 105/105 (100%)	Dynamin-like protein Dynamin-like protein DRP,dynamin-related protein Dynamin-like protein Dynamin-like protein F-type H-ATPase beta subunit

105	L364	chr9	192941 to 193121	NO09G00440	Exon	181/181 (100%)	Light-harvesting protein
			195692 to 195512	NO09G00450	Exon	181/181 (100%)	VCP1
		chr25	240969 to 241145	NO25G00860	Exon	150/177 (84.75%)	violaxanthin/chlorophyll a binding protein precursor
106	L370	chr3	1097464 to 1097620	NO03G03690	Exon	156/157 (99.36%)	Light harvesting complex protein
		chr2	510801 to 510665	NO02G01740	Exon	110/137 (80.29%)	light harvesting complex protein 3
107	L375	chr18	140768 to 140847			80/80 (100%)	
			141072 to 141114	NO18G00330	Exon	43/43 (100%)	Light harvesting complex protein
108	L389	chr16	76598 to 76518			81/81 (100%)	
			76836 to 76780			57/57 (100%)	
			76327 to 76278	NO16G00200	Exon	50/50 (100%)	Mg-protoporphyrin IX chelatase
109	L394	chr27	257321 to 257485	NO27G00680	Exon+3'UTR	165/165 (100%)	Unknown protein
		chr21	306720 to 306641	NO21G00930	Exon+3'UTR	74/80 (92.5%)	Aminotransferase class i and ii
		chr9	19527 to 19484	NO09G00050	Intron	38/44 (86.36%)	E3 ubiquitin-protein ligase UPL1
110	L401-1	chr1	1370461 to 1370707		Exon+3'UTR	245/247 (99.19%)	
			1371661 to 1371843		Exon	183/183 (100%)	
			1370817 to 1370900		Exon	84/84 (100%)	
			1371179 to 1371247		Exon	69/69 (100%)	
			1372044 to 1372102		5'UTR+Exon	59/59 (100%)	
			1371012 to 1371069		Exon	58/58 (100%)	
			1371395 to 1371452		Exon	58/58 (100%)	
			1370832 to 1370870		Exon	37/39 (94.87%)	
			1370853 to 1370891	NO01G05160	Exon	37/39 (94.87%)	Histone H5
		chr27	90045 to 90085			41/41 (100%)	
			90377 to 90417		IG region	41/41 (100%)	
		chr23	47330 to 64293		IG region		
		chr5	1055775 to 1055735	NO05G04080	3'UTR	38/41 (92.68%)	Unknown protein
		chr3	599794 to 599825	NO03G01940	3'UTR	31/32 (96.88%)	Nucleolar mif4g domain-containing protein 1
				NO03G01950	Exon		Histone h1
	L401-2	chr12	855548 to 855276	NO12G03110	Exon	273/273 (100%)	Viral protein TPX
111	L402	chr16	612399 to 612185	NO16G02080	Exon	215/215 (100%)	ferredoxin oxidoreductase
112	L407	chr6	968923 to 969242	NO06G03510	Exon	320/320 (100%)	pyrophosphate-dependent phosphofructose kinase
113	L414	chr22	5164 to 5031	NO22G00020	Exon+3'UTR	134/134 (100%)	Ycil-like protein

The red box represents the mutant produced by multiple cassette insertions