Supplementary Table

Putative disease resistance genes	Accession	Ch1	SD1	Ch2	SD2	NNDiff	Ratio	Ttest	Previously reported			
Putative disease resistance protein	T04362	0.071	0.00	0.261	0.10	-1.14	**3.68**	0.06	Loc	SA		Eth
Similar to flax rust resistance protein	R29891	0.448	0.20	1.010	0.54	-0.77	**2.26**	0.08	Loc			
Disease resistance protein	T43968	3.694	0.90	1.532	0.79	0.83	**-2.41**	0.06	Loc	SA	MJ	
Putative regulatory genes												
MYB-related protein	Z46510	0.186	0.06	0.562	0.35	-1.01	**3.03**	0.07	Loc	SA	MJ	
Putative SNF2 subfamily transcriptional activator	W43888	0.202	0.04	0.567	0.25	-0.95	**2.80**	0.09	Loc			
Salt-tolerance zinc finger protein (At1g27730)	R29923	0.438	0.29	1.472	1.04	-1.08	**3.36**	0.09			MJ	Eth
Putative CCCH zinc finger protein (At2g40140)	Z34649	0.285	0.19	0.952	0.69	-1.08	**3.34**	0.09		SA	MJ	
H-protein promoter binding factor 2a	F14111	0.069	0.04	0.294	0.17	-1.24	**4.26**	0.11		SA		
MEKK1 MAP kinase kinase kinase	T04696	0.093	0.01	0.261	0.14	-0.95	**2.79**	0.12		SA	MJ	
Calmodulin-domain protein kinase	R90026	0.066	0.03	0.155	0.08	-0.81	**2.36**	0.13				Eth
Putative protein phophatase regulatory subunit	Z47392	0.370	0.17	0.861	0.66	-0.80	**2.32**	0.14	Loc			
Putative leucine rich repeat protein	Z34571	0.063	0.05	0.141	0.06	-0.77	**2.25**	0.15		SA	MJ	
Putative response regulator	Z34204	0.564	0.32	1.127	0.75	-0.67	**2.00**	0.15	Loc	SA		
Transcription initiation factor II B	Z37605	0.130	0.08	0.298	0.26	-0.79	**2.29**	0.17	Loc	SA	MJ	Eth
Zinc finger protein	T41722	0.118	0.09	0.403	0.36	-1.10	**3.43**	0.20	Loc		MJ	
Cell wall modification												
Putative endo 1,4 beta glucanase	T43127	0.070	0.01	0.189	0.10	-0.92	**2.70**	0.06				
Cellulose synthase catalytic subunit	T45414	0.096	0.03	0.262	0.08	-0.93	**2.74**	0.06				
Xyloglucan endo 1,4 beta D glucanase	Z17989	0.073	0.00	0.146	0.04	-0.67	**2.00**	0.06				
Cellulose synthase catalytic subunit	N96707	0.444	0.19	1.181	0.72	-0.91	**2.66**	0.08	Loc			
Putative cellulase	T76139	0.060	0.02	0.186	0.10	-1.02	**3.07**	0.11		SA	MJ	Eth
Cellulase homolog (16 pep precursor)	N96850	0.991	0.52	1.996	1.35	-0.67	**2.01**	0.15	Loc	SA		
Extensin (from tomato, *L. esculentum*)	Z18787	0.036	0.03	0.101	0.06	-0.94	**2.78**	0.15				
Secondary metabolism												
Peroxidase ATP1a	T22814	2.056	0.52	5.376	1.69	-0.89	**2.61**	0.06				
Peroxidase	T76760	0.091	0.02	0.239	0.08	-0.89	**2.62**	0.06		SA		
Putative cytochrome P450 CYP76C2	N65907	0.655	0.49	2.585	1.66	-1.19	**3.95**	0.06	Loc		MJ	Eth
Tryptophan decarboxylase-like protein	H76002	0.045	0.02	0.090	0.02	-0.65	**2.00**	0.07				
Brassinosteroid insensitive 1	F13577	0.036	0.00	0.134	0.06	-1.16	**3.77**	0.08				
Putative cytochrome P450	T04016	0.062	0.04	0.162	0.06	-0.89	**2.60**	0.10			MJ	Eth
Peroxidase 8	T88162	0.072	0.08	0.191	0.11	-0.90	**2.65**	0.18				
Putative acetylglucosamine transferase	T88627	15.769	7.66	5.864	4.20	0.92	**-2.69**	0.12		SA	MJ	
Stress-associated												
DNA-damage-repair/toleration (DRT100) precursor	T75662	0.024	0.00	0.132	0.06	-1.38	**5.49**	0.06				
Blue copper binding protein	T44253	0.057	0.05	0.349	0.19	-1.44	**6.11**	0.09			MJ	
Polyubiquitin	T42370	0.853	0.52	1.943	1.23	-0.78	**2.28**	0.12	Loc			
Monodehydroascorbate reductase-like protein	H36099	0.022	0.00	0.114	0.08	-1.35	**5.15**	0.12				
Cysteine protease (AALP)	T04773	0.390	0.19	0.842	0.57	-0.73	**2.16**	0.13	Loc	SA		
Dehydrin ERD14	AA042534	1.107	0.74	2.641	2.05	-0.82	**2.38**	0.15	Loc		MJ	
Glutathione S-transferase	R30007	5.400	2.46	1.613	0.13	1.08	**-3.35**	0.08		SA		
Cell maintenance/development/other												
Gamma-glutamyl cysteine synthetase	R90472	0.498	0.08	1.086	0.51	-0.74	**2.18**	0.06	Loc		MJ	Eth
Hexokinase 2	E1C7T7	0.077	0.07	0.209	0.02	-0.92	**2.71**	0.06				
Unknown protein	T44615	0.062	0.04	0.153	0.04	-0.85	**2.47**	0.07		SA	MJ	
nuclear ribonucleoprotein	T88454	0.114	0.10	0.286	0.13	-0.86	**2.50**	0.07				
Protodermal factor PDF1	R29920	0.487	0.18	1.059	0.52	-0.74	**2.18**	0.07		SA		
Unknown protein	H36431	1.941	0.72	4.597	2.52	-0.81	**2.37**	0.08				
Unknown protein	T76703	0.721	0.28	1.499	0.71	-0.70	**2.08**	0.08	Loc	SA	MJ	Eth
Putative aldehyde dehydrogenase homolog	T20704	0.189	0.09	0.411	0.11	-0.74	**2.17**	0.08	Loc		MJ	
Adenylate translocator	T21051	0.753	0.34	1.844	1.05	-0.84	**2.45**	0.08	Loc			
Putative isocitrate lyase	N96226	0.029	0.04	0.110	0.04	-1.17	**3.84**	0.09			MJ	
Myrosinase	N38380	4.541	1.07	9.086	4.68	-0.67	**2.00**	0.09				
Unknown protein	N96773	0.180	0.04	0.452	0.30	-0.86	**2.51**	0.10		SA		
Unknown protein	H76266	0.268	0.16	0.535	0.31	-0.66	**2.00**	0.13	Loc		MJ	Eth
ATPase beta subunit	R30628	0.610	0.33	1.498	1.13	-0.84	**2.46**	0.13	Loc			
Plasma membrane ATPase 2 (proton pump)	AA042396	0.064	0.02	0.181	0.11	-0.96	**2.84**	0.13		SA		
Glucose-6-phosphate 1-dehydrogenase	H37123	0.197	0.15	0.398	0.24	-0.68	**2.03**	0.14	Loc			
Chlorophyll a/b-binding protein	N65380	0.447	0.01	1.006	0.80	-0.77	**2.25**	0.15		SA		
Unknown protein (At2g23120)	T21007	0.303	0.11	0.774	0.47	-0.87	**2.55**	0.15				
Unknown protein	T75756	0.035	0.00	0.091	0.06	-0.89	**2.61**	0.15				
Putative glucosyltransferase	B28707	0.063	0.02	0.149	0.11	-0.81	**2.37**	0.19		SA	MJ	
Senescence-associated protein sen1 (AT4g35770)	T04509	0.056	0.01	0.108	0.08	-0.63	**2.98**	0.22		SA	MJ	
GAST1-like protein	T76916	6.256	2.97	2.825	0.67	0.76	**-2.21**	0.06	Loc		MJ	Eth
Plasma membrane intrinsic protein SF3	T42925	1.861	0.61	0.651	0.36	0.96	**-2.86**	0.07	Loc	SA	MJ	
Glycolate oxidase-like protein	T88637	4.260	1.56	1.438	0.91	0.99	**-2.96**	0.08	Loc	SA		
ChloroplastpsbA	CI0018	0.977	0.76	0.363	0.19	0.92	**-2.69**	0.12	Loc			