

Table 12. Expression characteristics of the genes in cluster I during different oxidative stress experiments

Affymetrix Probe set name	AGI code	Description	hpAtPARP2				CAT2HP1		H ₂ O ₂ spray	Ozone fumigation	Syringolin treatment
			0h HL	2h HL	4h HL	6h HL	3h HL	8h HL			
248486_at	At5g1060	NADPH respiratory burst oxidase protein C (RbohC)	1.049	1.059	-3.310	-24.637	A	A	-2.755	2.556	1.133
263210_at	At1g10585	bHLH transcription factor	-2.401	-2.610	-6.801	-17.494	85.124	16.028	3.421	102.651	-2.151
262518_at	At1g17170	Glutathione S-transferase AtGSTU24	-2.489	-1.391	-10.029	-16.197	78.533	107.716	31.63	6.09	22.347
253316_s_at	At4g34300	Glycine-rich protein	1.090	1.050	-1.660	-12.473	A	A	1.291	1.33	25.618
263403_at	At2g04040	MATE efflux family protein	-1.612	-1.543	-3.363	-11.448	2.302	9.569	2.554	9.288	5.57
260522_x_at	At2g41730	Expressed protein	1.004	-2.688	-12.441	-11.393	27.265	32.931	2.496	10.655	25.239
263823_s_at	At2g40350	DREB2-like transcription factor	1.104	1.078	-1.962	-10.577	4.035	6.547	10.228	8.249	22.915
266752_at	At2g47000	ATP-binding cassette (ABC) transport protein	-1.181	-1.747	-3.674	-8.858	5.188	14.169	1.326	3.074	72.205
245392_at	At4g15680	Glutaredoxin family protein	-1.026	-1.225	-1.825	-6.632	1.342	3.138	-1.433	-1.232	1.05
263231_at	At1g05680	UDP-glucuronosyl/UDP-glucosyl transferase	-1.570	-2.347	-18.220	-5.381	338.785	195.798	8.644	13.274	7.799
263402_at	At2g04050	MATE efflux family protein	-1.334	-1.404	-4.226	-5.207	2.761	5.422	1.762	29.41	14.709
259297_at	At3g05360	Disease resistance family protein / LRR family protein	-1.188	-1.471	-2.871	-4.920	A	A	12.314	8.335	20.827
257840_at	At3g25250	Protein kinase family protein	-1.053	1.095	-10.487	-4.792	11.596	7.662	2.362	8.425	32.75
266290_at	At2g29490	Glutathione S-transferase AtGSTU1	-2.747	-3.335	-12.101	-4.772	37.866	49.600	3.781	4.977	14.231
247287_at	At5g64230	Expressed protein	-1.276	-1.584	-3.851	-4.634	8.065	15.053	1.844	1.606	7.748
261240_at	At1g32940	Subtilase family protein	-1.497	-1.615	-1.714	-4.437	4.765	15.286	2.772	8.659	25.794
263515_at	At2g21640	Expressed protein	-1.147	-1.693	-2.445	-4.323	4.855	11.150	1.037	3.205	63.571
250182_at	At5g14470	GHMP kinase-related protein	1.033	-1.011	-10.950	-4.292	A	A	1.487	-2.203	1.569
249494_at	At5g39050	Transferase family protein	1.068	-2.722	-5.056	-4.011	8.451	6.143	10.372	9.689	4.259
254549_at	At4g19880	Glutathione S-transferase-related protein	-1.167	-1.601	-3.465	-3.695	6.002	4.220	3.9	2.217	-1.222
246584_at	At5g14730	Expressed protein	-1.247	-1.152	-9.599	-3.630	23.175	13.350	9.8	2.222	3.554
245506_at	At4g15700	Glutaredoxin family protein	-1.267	-1.149	-2.562	-3.559	-1.719	1.885	-1.393	1.931	1.074
262118_at	At1g02850	Glycosyl hydrolase family 1 protein	-1.308	-1.397	-2.379	-3.477	3.184	2.823	1.396	4.838	-4.082
250094_at	At5g17380	Pyruvate decarboxylase family protein	-1.582	-1.172	-2.129	-3.344	3.769	3.895	2.086	3.836	1.74
258815_at	At3g04000	Short-chain dehydrogenase/reductase	-1.209	-1.059	-2.480	-3.342	6.003	2.045	1.374	9.645	-4.386
262251_at	At1g53760	Expressed protein	-1.653	-1.554	-1.591	-3.308	2.944	2.657	1.546	1.739	2.316
248381_at	At5g51830	PKB-type carbohydrate kinase family protein	-1.361	-1.919	-2.911	-3.299	5.470	5.414	11.127	6.559	8.183
255230_at	At4g05390	Ferredoxin-NADP ⁺ reductase, putative	-1.244	-1.095	-1.698	-3.292	2.173	4.385	1.583	2.582	1.021
246744_at	At5g27760	Hypoxia-responsive family protein	-1.267	-1.195	-2.266	-3.224	3.177	3.159	5.847	5.476	2.998
253268_s_at	At4g34135	UDP-glucuronosyl/UDP-glucosyl transferase	-1.587	-2.448	-10.773	-3.034	11.307	6.565	10.301	5.439	2.262
263073_at	At2g17500	Auxin efflux carrier protein	-1.934	-1.868	-1.920	-3.008	8.880	4.405	1.194	2.472	-1.684
255462_at	At4g02940	Oxidoreductase, 2OG-Fe(II) oxygenase	-1.197	-1.293	-3.269	-2.909	4.300	3.215	1.517	2.702	-1.230
255543_at	At4g01870	Expressed protein	-1.246	-1.825	-4.566	-2.840	43.379	42.777	30.639	8.608	19.701
257216_at	At3g14990	DJ-1 family protein	-1.068	-1.024	-2.401	-2.778	5.924	7.011	2.577	2.19	-2.079
250252_at	At5g13750	Transporter-related protein	-1.194	-1.308	-4.929	-2.675	2.212	1.176	3.235	4.713	-5.051
251503_at	At3g59140	ATP-binding cassette (ABC) transport protein	-1.160	1.057	-2.356	-2.656	2.941	2.292	1.164	2.202	-2.793
252671_at	At3g44190	Pyridine nucleotide-disulphide oxidoreductase	-1.300	-1.478	-5.232	-2.548	9.876	6.479	3.89	2.873	2.679
259911_at	At1g72680	Cinnamyl-alcohol dehydrogenase, putative	-1.313	-2.093	-1.821	-2.539	3.179	3.989	1.956	4.874	-1.445
248330_at	At5g52810	Ornithine cyclodeaminase family protein	-1.149	-1.138	-1.485	-2.530	2.184	1.933	2.116	6.614	1.558
251971_at	At3g53160	UDP-glucuronosyl/UDP-glucosyl transferase	1.058	1.041	-1.004	-2.436	A	A	1.935	7.969	1.228
250449_at	At5g10830	Embryo-abundant protein-related	-1.364	-1.294	-5.575	-2.410	A	A	6.237	1.159	1.231
259980_at	At1g76520	Auxin efflux carrier family protein	1.069	-1.414	-1.829	-2.285	2.593	1.427	1.417	3.13	-3.356
249984_at	At5g18400	Expressed protein	-1.747	-1.189	-1.826	-2.269	2.441	2.888	2.307	3.101	5.783
259875_s_at	At1g76690	12-oxophytodienoate reductase (OPR2)	-1.459	-1.585	-4.624	-2.243	9.316	5.346	25.012	4.215	2.637
263904_at	At2g36380	ATP-binding cassette (ABC) transport protein	-1.166	-1.929	-3.612	-2.223	-1.111	-1.077	-1.328	1.473	1.267
266756_at	At2g46950	Cytochrome P450 family protein	1.123	-1.131	-4.512	-2.200	A	A	1.277	-1.366	1.015
262291_at	At1g70790	C2 domain-containing protein	-1.187	-1.003	-1.247	-2.194	1.091	-1.215	-1.570	1.316	-2.890
254204_at	At4g24160	Hydrolase, alpha/beta fold family protein	-1.033	-1.695	-5.233	-2.164	6.312	5.536	10.816	3.214	4.398
256308_s_at	At1g30410	ATP-binding cassette (ABC) transport protein	1.045	-1.373	-2.189	-2.113	3.539	5.861	1.291	3.417	1.168
266296_at	At2g29420	Glutathione S-transferase, putative	-1.333	-1.909	-5.764	-2.100	7.406	2.761	11.353	4.146	1.676
262653_at	At1g14130	2-oxoglutarate-dependent dioxygenase, putative	-1.162	-1.255	-3.044	-2.079	2.141	-1.961	1.343	2.394	-1.548
256589_at	At3g28730	High mobility group protein (HMG)	1.175	-3.948	-6.996	-2.076	90.461	29.895	9.668	4.666	-1.205
249319_s_at	At5g40880	WD-40 repeat family protein	1.262	-1.106	-1.795	-2.038	1.905	3.789	1.021	-1.032	5.196
256385_at	At1g14320	60S ribosomal protein L10 (RPL10A)	-1.124	-1.237	-1.625	-2.008	2.877	1.830	1.39	1.448	1.199
265061_at	At1g61640	ATP-binding cassette (ABC) transport protein	-1.662	-1.096	-1.782	-1.997	1.110	1.671	1.455	1.656	2.163
263015_at	At1g23440	Pyroglutamate-carboxylate peptidase family protein	-1.148	-1.238	-1.449	-1.941	1.724	2.042	1.224	2.893	-1.312
256453_at	At1g75270	Dehydroascorbate reductase	-1.566	-1.870	-3.359	-1.915	6.626	3.109	3.582	1.769	1.626
248101_at	At5g55200	Co-chaperone grpE protein, putative	-1.562	-1.041	-1.276	-1.858	2.025	2.919	1.276	2.306	9.722
261664_s_at	At1g18320	Mitochondrial import inner membrane translocase Tim17	-1.990	-1.433	-1.556	-1.854	-1.020	1.018	1.006	-1.653	1.135
262262_at	At1g70780	Expressed protein	-1.365	-1.656	-1.923	-1.834	1.330	1.045	-1.024	1.295	-2.283
257037_at	At3g19130	RNA-binding protein, putative	-1.137	-1.224	-1.781	-1.795	1.551	1.447	1.24	1.279	1.424
260592_at	At1g55850	Cellulose synthase family protein	-1.366	-2.089	-3.866	-1.760	3.422	1.389	4.581	2.261	-5.102
247272_at	At5g64300	GTP cyclohydrolase II	-1.065	-1.278	-2.127	-1.757	1.636	1.515	2.824	1.42	-1.279
246042_at	At5g19440	Cinnamyl-alcohol dehydrogenase (CAD)	-1.104	-1.111	-1.456	-1.750	1.947	2.224	2.177	3.083	-1.072
261344_at	At1g79710	Integral membrane transporter family protein	-1.065	-1.421	-4.991	-1.705	4.102	2.060	2.77	1.102	1.36
262422_at	At1g23440	Pyroglutamate-carboxylate peptidase family protein	-1.042	-1.084	-1.368	-1.705	1.731	1.494	1.189	2.277	1.266
263184_at	At1g05560	UDP-glucose transferase (UGT75B2)	-1.187	-2.336	-5.986	-1.698	22.399	9.744	10.381	4.4	-2.591
247989_at	At5g56350	Pyruvate kinase, putative	-1.183	-1.037	-1.213	-1.697	2.149	3.906	-1.116	2.478	9.377
267565_at	At2g30750	Cytochrome P450 71A12	1.006	1.118	1.049	-1.685	A	A	-1.942	3.408	6.378
253890_s_at	At5g54100	Expressed protein	-1.678	1.045	-1.358	-1.669	2.048	3.231	1.041	1.909	12.978
247283_at	At5g64250	2-nitropropane dioxygenase	-1.038	-1.051	-1.852	-1.660	2.457	2.023	3.022	3.46	1.297
265662_at	At2g24500	Zinc finger (C2H2 type) family protein	-1.250	-1.115	-2.003	-1.650	2.950	2.963	2.722	1.352	3.293
265147_at	At1g51380	Eukaryotic translation initiation factor 4A (eIF-4A)	-1.456	-1.224	-2.001	-1.632	1.004	1.218	1.646	-2.058	4.765
262611_at	At1g14060	Expressed protein	-1.617	-1.030	-1.562	-1.618	1.479	1.614	1.583	1.323	1.862
257708_at	At3g13330	Expressed protein	-1.009	-1.142	-1.473	-1.605	1.435	3.107	-1.005	2.527	12.896
249515_at	At5g38530	Tryptophan synthase-related protein	-1.653	-1.191	-1.738	-1.552	1.476	2.668	1.281	1.972	-3.215
262745_at	At1g28600	Lipase, putative	-1.753	-1.363	-1.997	-1.540	-1.092	-1.772	1.253	1.113	-3.322
248139_at	At5g54970	Expressed protein	-1.510	-1.267	-1.314	-1.533	1.403	1.369	-1.021	-1.106	-2.985
256055_at	At1g07030	Mitochondrial substrate carrier family protein	-1.295	-1.072	-1.470	-1.525	1.976	2.351	2.02	1.898	1.191
246463_at	At5g16970	NADP-dependent oxidoreductase, putative	-1.055	-1.249	-2.076	-1.517	4.832	3.161	6.403	3.282	-2.427
254343_at	At4g21990	5'-adenylylsulfate reductase (APR3)	-1.160	-1.158	-2.234	-1.503	6.645	3.413	21.703	2.052	-7.519
245937_at	At5g19750	Peroxisomal membrane 22 kDa family protein	-1.273	-1.172	-1.418	-1.481	1.301	-1.175	1.139	-1.309	-1.661
267162_s_at	At2g37690	Phosphoribosylamino									

258588_s_at	At3g04120	NAD-dependent glyceraldehyde-3-P dehydrogenase	-1.109	-1.067	-1.140	-1.393	1.465	1.490	1.128	1.188	2.002
246594_at	At1g13440										
258208_at	At5g14800	Pyrraline-5-carboxylate reductase	1.032	1.062	-1.469	-1.389	1.222	1.904	-1.218	-1.181	2.742
259056_at	At3g13930	Dihydrolipoamide S-acetyltransferase, putative	-1.085	-1.067	-1.341	-1.385	1.313	1.080	1.263	-1.277	-1.064
267095_at	At3g03420	Ku70-binding family protein	-1.127	-1.392	-1.423	-1.385	1.138	1.269	-1.036	1.215	1.753
247679_at	At2g38280	AMP deaminase, putative	-1.396	1.038	-1.304	-1.376	1.196	1.489	-1.083	-1.063	1.302
246303_at	At5g59540	Oxidoreductase, 2OG-Fe(II) oxygenase family protein	-1.142	-1.088	-1.310	-1.363	1.738	2.062	2.856	1.365	-1.087
253281_at	At3g51870	Mitochondrial substrate carrier protein	-1.522	-1.242	-1.931	-1.286	1.151	1.205	-1.139	-1.957	-1.344
253213_at	At4g34138	UDP-glucuronosyl/UDP-glucosyl transferase	2.512	-2.729	-4.544	-1.278	9.225	6.820	3.223	1.606	-2.475
247580_at	At4g34910	DEAD/DEAH box helicase, putative	-1.293	1.051	-1.352	-1.262	1.118	1.674	-1.160	-1.297	1.734
255455_at	At5g61330	rRNA processing protein-related	-1.376	1.044	-1.178	-1.256	-1.036	1.468	-1.116	-1.605	-1.100
249830_at	At4g02930	Elongation factor Tu, putative	-1.459	1.051	-1.304	-1.256	1.643	1.114	-1.133	1.001	2.121
258114_at	At5g23300	Mitochondrial dihydroorotate dehydrogenase	-1.659	1.063	-1.482	-1.221	1.206	-1.006	1.1	-1.832	1.448
246465_at	At3g14650	Cytochrome P450, putative	1.112	-1.244	-2.198	-1.214	1.620	1.375	1.856	1.624	-1.335
256628_at	At3g14660										
262117_at	At5g17000	NADP-dependent oxidoreductase, putative	1.053	-1.085	-2.784	-1.205	2.027	1.654	5.018	6.948	1.073
250909_at	At3g20000	Mitochondrial outer membrane protein - TOM40	-1.281	-1.114	-1.350	-1.202	1.302	1.073	1.024	-1.087	1.537
250192_at	At1g02780	60S ribosomal protein L19 (RPL19A)	-1.138	-1.004	-1.093	-1.117	1.151	-1.008	1.014	-1.081	1.041
265389_at	At5g03700	PAN domain-containing protein	-1.055	-1.170	-1.716	-1.101	A	A	1.245	1.199	-2.278
254981_at	At5g14520	Pescadillo-related protein	-1.302	-1.113	-1.445	-1.090	1.169	1.699	-1.248	-1.148	2.44
	At2g20690	Lumazine-binding family protein	-1.677	1.051	-1.182	-1.065	1.373	-1.417	-1.326	-1.399	-1.961
	At4g10480	Nascent polypeptide associated complex protein	-1.375	-1.064	-1.506	-1.026	1.098	1.223	-1.164	-1.695	1.959

Number of genes showing at least threefold induction during the respective treatment

38 40 28 38 28

Relative expression data (transgenic to wild type or treatment to control) for all genes in cluster I are presented. Affymetrix probe set names, AGI codes, and descriptions are given. The induction/suppression of each gene by HL treatment in the hpAtPARP2 plants or catalase-deficient plants (CAT2HP1), or by the different oxidative stress causing treatments (H₂O₂ spray, ozone fumigation, or syringolin treatment) is indicated. Yellow, orange, and red indicate transcript levels between three- and fourfold, four- and fivefold, and above fivefold, respectively. Expression data of transcripts with absent calls in both control and transgenic are indicated with A. For each oxidative stress experiment, the number of genes with at least threefold induction are indicated.