Table 13. Expression characteristics of the genes in cluster II during different oxidative stress experiments

Affymetrix Probe set name	AGI code	Description	hpAtPARP2				CAT2HP1		H_2O_2 spray	Ozone fumigation	Syringolin treatment
			0h HL	2h HL	4h HL	6h HL	3h HL	8h HL			
252334_at	At3g48850	Mitochondrial phosphate transporter, putative	-1.508	-1.355	-2.101	-9.940	6.392	14.784	1.209	7.943	13.924
248434_at	At5g51440	23.5 kDa mitochondrial small heat shock protein (HSP23.5-M)	-2.726	-2.677	-9.695	-8.460	12.825	53.640	20.297	9.291	117.442
250296_at	At5g12020	17.6 kDa class II heat shock protein (HSP17.6-CII)	1.732	-2.793	-9.584	-7.498	7.486	65.256	104.971	5.475	4.305
252908_at	At4g39670	Expressed protein	-1.977	-1.319	-4.536	-7.333	11.861	13.236	3.631	36.247	38.53
266267_at	At2g29460	Glutathione S-transferase, putative	-1.605	-1.573	-1.807	-7.104	8.476	9.316	3.623	47.061	11.038
258840_at	At3g04620	Expressed protein	1.088	-1.905	-3.357	-6.749	5.517	29.191	1.464	2.199	10.964
254059_at	At4g25200	23.6 kDa mitochondrial small heat shock protein (HSP23.6-M)	1.287	-1.022	-3.124	-6.512	3.258	194.968	7.157	11.487	26.969
253046_at	At4g37370	Cytochrome P450, putative	-1.145	-1.297	-5.753	-5.774	31.204	27.058	28.213	25.615	15.665
265221_s_at	At2g02010 At2g02000	Glutamate decarboxylase, putative	-2.598	1.050	-2.886	-5.120	12.440	11.863	95.405	86.891	21.106
259445_at	At1g02400	Gibberellin 2-oxidase, putative	-2.078	-1.678	-5.500	-4.555	5.946	4.937	6.252	2.279	-2.717
247279_at	At5g64310	Arabinogalactan-protein (AGP1)	-1.112	-2.212	-2.926	-4.328	4.504	2.368	3.431	2.382	3.553
248332_at	At5g52640	Heat shock protein 81-1 (HSP81-1)	-2.545	-1.558	-2.624	-4.095	6.486	24.891	11.91	30.3	53.181
265499_at	At2g15480	UDP-glucoronosyl/UDP-glucosyl transferase	-1.267	-1.052	-3.971	-4.039	30.902	16.608	223.416	16.3	22.112
266464_at	At2g47800	Glutathione-conjugate transporter (MRP4)	-2.169	-1.123	-2.529	-3.903	1.945	1.277	1.057	2.187	-1.953
251895_at	At3g54420	Class IV chitinase (CHIV)	-2.096	-1.016	-1.732	-3.751	4.413	12.880	-1.309	3.031	2.073
258975_at	At3g01970	WRKY family transcription factor 45	-2.523	-1.341	-2.171	-3.640	1.726	1.780	3.015	13.784	4.977
248551_at	At5g50200	Expressed protein	-1.178	-1.596	-1.687	-3.593	3.049	4.059	-1.451	2.026	1.577
250994_at	At5g02490	Heat shock cognate 70 kDa protein 2 (HSC70-2)	-1.667	-1.174	-1.718	-3.354	2.461	2.986	1.338	7.546	13.684
251282_at	At3g61630	AP2 domain-containing transcription factor	-1.580	-1.436	-1.854	-3.335	1.956	5.579	-2.114	9	25.244
245998_at	At5g20830	Sucrose synthase / sucrose-UDP glucosyltransferase (SUS1)	-1.468	-1.219	-1.273	-3.316	1.185	1.286	-1.245	4.275	1.724
254289_at	At4g22980	Expressed protein	-1.558	-1.071	-3.998	-3.199	3.166	2.146	2.203	4.935	1
259037_at	At3g09350	Armadillo/beta-catenin repeat family protein	-2.366	-2.054	-5.947	-3.057	15.208	18.458	6.865	6.924	16.706
248657_at	At5g48570	Peptidyl-prolyl cis-trans isomerase, putative	-1.856	-1.962	-3.241	-3.034	2.934	23.687	10.086	2.712	15.446
260248_at	At1g74310	Heat shock protein 101 (HSP101)	-1.990	-2.361	-12.066	-3.032	22.170	27.069	127.793	23.026	15.349
267559_at	At2g45570	Cytochrome P450 76C2, putative	-1.131	-2.031	-1.524	-2.891	6.379	38.919	2.373	55.778	-1.143
267168_at	At2g37770	Aldo/keto reductase family protein	-2.199	-1.899	-1.860	-2.819	8.493	5.367	1.292	9.153	-6.173
263150_at	At1g54050	17.4 kDa class III heat shock protein (HSP17.4-CIII)	-1.319	-1.576	-4.230	-2.812	8.584	12.186	10.343	-1.370	-2.667
266368_at	At2g41380	Embryo-abundant protein-related	-1.892	-1.361	-1.731	-2.697	4.181	10.090	52.879	3.812	10.876
255259_at	At4g05020	NADH dehydrogenase-related protein	-1.047	-1.182	-1.990	-2.644	2.398	3.054	1.497	8.816	5.69
262571_at	At1g15430	Expressed protein	1.085	-1.277	-2.232	-2.585	4.936	4.482	5.155	4.06	6.67
263374_at	At2g20560	DNAJ heat shock family protein	-3.954	-1.252	-3.222	-2.470	6.597	12.776	5.457	4.911	10.784
253453_at	At4g31860	Protein phosphatase 2C, putative	-1.112	-1.205	-1.802	-2.351	1.517	1.350	2.068	4.962	1.179
254839_at	At4g12400	Stress-inducible protein, putative	-1.270	-1.559	-3.158	-2.284	10.169	53.693	3.397	5.247	44.309
251975_at	At3g53230	Cell division cycle protein 48 (CDC48)	-1.792	-1.046	-1.338	-2.281	3.573	8.340	1.264	8.403	49.493
256245_at	At3g12580	Heat shock protein 70, putative	-4.193	1.085	-1.921	-2.241	4.985	9.506	14.257	22.415	73.192
257058_at	At3g15352	Cytochrome c oxidase copper chaperone-related	-1.550	-1.101	-1.514	-2.182	1.924	2.503	1.917	3.205	2.632
266461_at	At2g47730	Glutathione S-transferase 6 (GST6)	-1.217	-1.202	-1.905	-2.169	3.266	2.635	2.957	2.21	2.468
261618_at	At1g33110	MATE efflux family protein	-1.166	-1.109	-2.568	-2.168	1.874	1.400	2.329	5.825	-1.035
245977_at	At5g13110	Glucose-6-phosphate 1-dehydrogenase, putative	-1.498	-1.035	-1.831	-2.150	1.409	1.780	1.406	1.605	1.629
250934_at	At5g03030	DNAJ heat shock protein	-1.086	-1.273	-1.381	-2.136	2.219	2.147	1.603	2.028	2.952
254247_at	At4g23260	Protein kinase family protein	-1.319	-1.427	-1.582	-2.102	1.275	1.106	1.344	2.474	-2.174
254759_at	At4g13180	Short-chain dehydrogenase/reductase (SDR)	-1.308	-1.153	-2.522	-2.006	3.361	4.646	3.827	3.809	1.491
266841_at	At2g26150	Heat shock transcription factor AtHsfA2	-1.830	-2.228	-7.661	-1.992	27.644	112.818	55.233	43.64	14.579
259705_at	At1g77450	NAM transcription factor	-1.404	-1.296	-2.805	-1.942	5.027	3.390	4.663	8.88	-1.379
245854_at	At5g13490	Mitochondrial ADP/ATP carrier protein 2 (ANT2)	-1.328	-1.192	-1.362	-1.919	5.332	1.973	2.081	2.761	1.559
260025_at	At1g30070	SGS domain-containing protein	-1.381	-1.267	-2.125	-1.860	4.115	5.749	3.648	1.907	5.694
254108_at	At4g25230	C3HC4-type RING finger family protein	-1.618	-1.119	-1.600	-1.859	1.627	1.832	1.289	2.484	1.014
258794_at	At3g04710	Ankyrin repeat family protein	-1.888	-1.165	-1.951	-1.852	1.332	2.688	1.811	1.198	3.72
256787_at	At3g13790	Beta-fructosidase (BFRUCT1)	-1.600	-1.289	-1.275	-1.848	3.548	14.164	-1.342	2.873	-1.475
245686_at	At5g22060	DNAJ heat shock protein, putative	-1.548	-1.200	-1.589	-1.820	2.125	2.513	1.587	3.597	4.885
267300_at	At2g30140	UDP-glucoronosyl/UDP-glucosyl transferase	-1.627	-1.155	-1.788	-1.816	2.199	3.868	3.433	8.575	1.874
260327_at	At1g63840	C3HC4-type RING finger family protein	-1.956	-1.123	-1.780	-1.791	4.687	3.092	1.789	4.487	-1.064
255011_at	At4g10040	Cytochrome c, putative	-1.368	-1.176	-1.418	-1.763	1.876	2.070	1.232	2.889	4.433
265899_s_at	At2g25700	E3 ubiquitin ligase SCF complex subunit SKP1/ASK1	-1.479	-1.072	-1.170	-1.754	1.797	3.061	-1.321	1.137	12.208
246879_at	At5g26110	Expressed protein	-1.319	-1.183	-1.347	-1.738	1.379	2.224	-1.250	1.439	1.471
257713_at	At3g27380	Mitochondrial succinate dehydrogenase iron-sulphur subunit	-1.317	-1.296	-1.268	-1.714	2.064	1.946	-1.004	1.121	2.038
248607_at	At5g49480	Sodium-inducible calcium-binding protein (ACP1)	-4.668	-1.533	-2.247	-1.701	2.771	3.628	6.041	4.247	1.322
252421_at	At3g47540	Chitinase, putative	-1.533	-1.161	-1.341	-1.662	1.330	1.821	2.089	7.659	16.929
261717_at	At1g18400	Basic helix-loop-helix (bHLH) family protein	-1.134	-1.310	-1.366	-1.648	-1.264	-1.238	-1.178	-1.266	-1.499
265200_s_at	At2g36790	UDP-glucoronosyl/UDP-glucosyl transferase	-1.935	-1.668	-2.861	-1.634	5.608	4.382	6.839	6.449	4.211
266253_at	At2g27840	Histone deacetylase-related protein	-1.953	-1.119	-1.750	-1.627	1.822	1.321	-1.217	-2.105	-1.040
265730_at	At2g32220	60S ribosomal protein L27 (RPL27A)	-1.995	1.100	-1.651	-1.623	1.793	1.270	-1.135	-1.232	1.06
267181_at	At2g37760	Aldo/keto reductase family protein	-1.811	-1.167	-1.229	-1.602	2.547	1.568	1.115	5.122	-1.621
258452_at	At3g22370	Alternative oxidase 1a, mitochondrial (AOX1A)	-1.069	-1.064	-1.307	-1.594	2.351	3.286	2.116	4.205	8.89
248258_at	At5g53400	Nuclear movement family protein	-1.450	-1.111	-1.362	-1.572	2.396	3.286	1.014	1.769	6.714
258979_at	At3g09440	Heat shock cognate 70 kDa protein 3 (HSC70-3)	-3.433	-1.219	-1.947	-1.563	2.648	2.408	2.321	3.765	3.089
266934_at	At2g18900	Transducin/WD-40 repeat family protein	-2.735	-1.052	-1.543	-1.561	1.571	2.476	-1.016	-1.733	4.665
248045_at	At5g56030 At5g56000 At5g56010	Heat shock protein 81-2 (HSP81-2)	-2.968	-1.224	-1.934	-1.515	2.442	2.489	1.591	1.882	3.199
250866_at	At5g03905	HesB-like domain-containing protein	-1.469	-1.375	-1.188	-1.505	1.744	1.446	1.061	1.292	1.487
245365_at	At4g17720	RNA recognition motif (RRM)-containing protein	-1.186	-1.165	-1.143	-1.504	1.818	2.382	-1.052	3.754	4.697
264458_at	At1g10410	Expressed protein	-1.353	-1.110	-1.116	-1.483	-1.058	-1.086	1.133	1.842	2.169
248743_at	At5g48240	Expressed protein	-1.653	-1.011	-1.545	-1.472	1.462	2.204	-1.046	-1.100	3.82
245352_at	At4g15490	UDP-glucoronosyl/UDP-glucosyl transferase	-1.861	-1.015	-1.386	-1.437	-1.221	1.041	1.436	3.105	-1.597
257822_at	At3g25230	Peptidyl-prolyl cis-trans isomerase / FK506-binding protein (ROF1)	-1.833	-1.176	-1.786	-1.416	2.997	3.630	2.08	1.338	5.813
265649_at	At2g27510	Ferredoxin, putative	-1.444	1.053	-1.061	-1.414	1.038	2.289	1.111	-1.098	1
258678_at	At3g08690	Ubiquitin-conjugating enzyme 11 (UBC11)	-1.071	-1.058	-1.121	-1.401	1.936	2.418	1.255	2.167	6.353
253013_at	At4g37910	Mitochondrial heat shock protein 70	-1.698	-1.086	-1.442	-1.400	1.373	1.467	-1.064	1.253	3.938
245349_at	At4g16690	Esterase/lipase/thioesterase family	-1.830	-1.527	-1.335	-1.376	1.634	1.821	1.156	1.773	-2.203
246559_at	At5g15550	Transducin/WD-40 repeat family protein	-1.695	-1.073	-1.635	-1.358	1.181	1.629	-1.022	-1.076	1.959
263435_at	At2g28600	Expressed protein	-1.463	1.025	-1.677	-1.344	1.127	1.793	-1.233	-1.695	2.476
263251_at	At2g31410	Expressed protein	-1.337	-1.031	-1.205	-1.343	1.457	1.712	-1.681	1.208	1.475
253777_at	At4g28450	Transducin/WD-40 repeat family protein	-1.776	-1.014	-1.342	-1.342	1.185	1.751	-1.142	-1.170	2.866
252482_at	At3g46670	UDP-glucoronosyl/UDP-glucosyl transferase	-1.520	-1.521	-2.224	-1.338	2.905	1.702	1.546	2.123	-5.155
251538_at	At3g58660	60S ribosomal protein-related	-1.862	-1.061	-1.749	-1.334	1.203	2.047	-1.287	-1.245	2.211
264131_at	At1g79150	Expressed protein	-2.123	-1.147	-1.560	-1.334	1.004	1.516	1.046	-1.534	1.852
252625_at	At3g44750	Histone deacetylase, putative	-2.111	-1.092	-1.898	-1.326	1.169	1.340	-1.145	-2.033	2.288
247780_at	At5g58770	Dehydrodolichyl diphosphate synthase, putative	-4.758	-1.225	-1.279	-1.317	1.591	1.397	1.068	4.38	2.035

265850_at	At2g35720	DNAJ heat shock N-terminal domain-containing protein	-1.914	-1.168	-1.246	-1.314	1.162	1.450	1.117	1.602	4.931
247593_at	At5g60790	ATP-binding cassette (ABC) transport protein	-1.179	-1.225	-1.548	-1.313	1.460	1.734	1.051	1.454	1.45
263482_at	At2g03980	GDSL-motif lipase/hydrolase family protein	-1.224	-1.244	-1.172	-1.307	-1.102	-3.216	-1.613	1.473	-13.699
257658_at	At3g13230	Expressed protein	-1.783	-1.016	-1.515	-1.303	1.267	1.429	-1.063	-1.314	1.078
258104_at	At3g23620	Brix domain-containing protein	-1.621	1.022	-1.453	-1.302	1.033	1.613	-1.299	-1.070	1.717
258505_at	At3g06530	BAP28-related protein	-2.169	1.081	-1.793	-1.301	-1.118	1.904	-1.290	-1.475	2.153
248462_at	At5g50960	Nucleotide-binding family protein	-1.252	1.046	-1.300	-1.300	1.353	1.858	1.168	1.375	3.803
266299_at	At2g29450	Glutathione S-transferase (103-1A)	-1.615	-1.097	-1.497	-1.295	1.674	-1.343	2.219	2.879	-1.036
258996_at	At3g01800	Ribosome recycling/releasing factor protein	-1.617	-1.030	-1.328	-1.292	-1.073	1.216	1.108	-1.056	4.314
254076_at	At4g25340	Peptidyl-prolyl cis-trans isomerase-related immunophilin	-2.113	-1.110	-1.657	-1.292	1.050	2.045	1.087	-1.340	2.861
256905_at	At3g23990	Chaperonin (CPN60) (HSP60)	-1.890	-1.125	-1.630	-1.292	1.847	1.637	1.211	1.066	3.211
249344_at	At5g40770	Prohibitin	-1.634	-1.078	-1.308	-1.292	1.475	1.280	-1.255	-1.300	1.91
251787_at	At3g55410	2-oxoglutarate dehydrogenase E1 component, putative	-1.190	-1.059	-1.022	-1.285	1.179	1.448	1.05	1.754	2.236
248043_s_at	At5g56000	Heat shock protein 81-4 (HSP81-4)	-1.895	-1.160	-1.608	-1.264	1.506	1.440	1.192	1.349	2.226
263372_at	At2g20450	60S ribosomal protein L14 (RPL14A)	-1.503	-1.118	-1.580	-1.260	1.755	1.025	-1.297	-1.479	1.38
256797_at	At3g18600	DEAD/DEAH box helicase, putative	-1.967	-1.053	-1.683	-1.259	1.063	1.463	-1.381	-1.739	2.372
257652_at	At3g16810	Pumilio/Puf RNA-binding domain-containing protein	-2.035	1.045	-1.811	-1.258	-1.046	2.211	1.017	-1.247	2.031
258701_at	At3g09720	DEAD/DEAH box helicase, putative	-1.838	-1.075	-1.497	-1.254	1.043	2.195	-1.248	-1.538	2.872
262933_at	At1g65840	Amine oxidase family protein	-1.730	-1.017	-1.505	-1.249	1.602	1.619	-1.227	-1.107	1.363
262943_at	At1g79470	Inosine-5'-monophosphate dehydrogenase	-1.869	-1.014	-1.602	-1.246	-1.006	1.066	-1.524	-1.420	4.431
262956_at	At1g54270 At3g13920	Eukaryotic translation initiation factor 4A-2	-1.205	-1.006	-1.159	-1.246	1.423	1.285	1.256	1.276	1.524
261011_at	At1g26340	Cytochrome b5, putative	-1.573	-1.039	-1.265	-1.235	1.250	1.455	1.017	1.361	2.123
265340_at	At2g18330	AAA-type ATPase family protein	-1.781	-1.123	-1.309	-1.231	1.111	1.485	1.007	-1.224	3.403
264803_at	At1g08580	Expressed protein	-1.639	-1.018	-1.400	-1.230	1.229	1.092	-1.115	-1.658	1.017
245164_at	At2g33210	Chaperonin, putative	-1.642	-1.050	-1.407	-1.224	1.281	1.598	1.013	-1.368	2.48
246527_at	At5g15750	40S ribosomal protein	-1.566	1.113	-1.289	-1.224	1.067	1.550	-1.087	-1.185	1.999
251492_at	At3g59280	Signaling molecule-related protein	-1.187	-1.044	-1.212	-1.219	1.752	1.718	1	1.655	2.047
250995_at	At5g02500	Heat shock cognate 70 kDa protein 1 (HSC70-1)	-1.208	-1.047	-1.326	-1.209	1.458	1.187	1.013	1.069	1.488
260049_at	At1g29940	DNA-directed RNA polymerase	-1.682	1.095	-1.434	-1.205	1.047	1.662	-1.065	-1.008	1.395
261377_at	At1g18850	Expressed protein	-1.778	-1.157	-1.524	-1.203	-1.007	1.553	-1.314	-1.060	1.841
247453_at	At5g62440	Expressed protein	-1.477	-1.143	-1.330	-1.199	-1.072	1.607	-1.013	-1.282	3.544
264452_at	At1g10270	Pentatricopeptide (PPR) repeat-containing protein	-2.818	1.024	-1.056	-1.185	1.024	1.392	-1.157	-1.299	2.751
258532_at	At3g06700	60S ribosomal protein L29 (RPL29A)	-1.221	1.010	-1.319	-1.183	1.048	-1.179	-1.264	-1.309	-1.134
260481_at	At1g10960	Ferredoxin, chloroplast, putative	-1.717	1.022	-1.291	-1.183	1.310	-1.196	1.079	-1.721	-1.045
263474_at	At2g31725	Expressed protein	-2.189	1.052	-1.138	-1.178	6.379	38.919	1.997	-1.422	1.378
253867_at	At4g27490	3' exoribonuclease family	-1.204	1.024	-1.021	-1.171	1.803	1.311	1.161	-1.017	-1.030
256523_at	At1g66070	Eukaryotic translation initiation factor (eIF-3 alpha)	-1.210	-1.035	-1.278	-1.168	1.224	1.465	1.132	1.083	2.22
250502_at	At5g09590	Heat shock protein 70	-1.754	1.118	-1.417	-1.165	1.430	2.009	1.709	2.05	2.391
252952_at	At4g38710	Glycine-rich protein	-1.455	-1.082	-1.310	-1.163	1.823	1.624	1.362	1.257	1.965
247488_at	At5g61820	Expressed protein	-1.137	-1.074	-1.370	-1.163	2.339	2.088	3.607	2.78	-1.042
260157_at	At1g52930	Expressed protein	-2.182	-1.087	-1.528	-1.156	1.015	1.629	-1.340	-1.616	1.691
267044_at	At2g34357	Expressed protein	-1.864	1.093	-1.463	-1.148	-1.429	1.675	-1.724	-1.142	3.369
260585_at	At2g43650	Sas10/U3 ribonucleoprotein	-1.592	-1.197	-1.727	-1.147	-1.337	1.884	-4.348	-1.938	2.45
250825_at	At5g05210	Nucleolar matrix protein-related	-1.100	-1.130	-1.417	-1.133	1.920	1.914	-1.008	-1.164	2.663
263810_at	At2g04520	Eukaryotic translation initiation factor 1A (eIF1A)	-1.108	-1.014	-1.210	-1.112	1.707	1.152	-1.019	1.38	1.544
256661_at	At3g11964	S1 RNA-binding domain-containing protein	-1.646	1.030	-1.554	-1.106	-1.209	2.442	-1.456	-2.049	1.997
261296_at	At1g48460	Expressed protein	-1.952	1.095	-1.240	-1.101	1.007	1.145	1.069	-2.092	1.378
254654_at	At4g18040	Eukaryotic translation initiation factor 4E 1(eIF-4E1)	-1.313	-1.007	-1.238	-1.099	1.310	1.115	1.011	-1.091	1.655
264675_at	At1g09830	Phosphoribosylamine-glycine ligase (PUR2)	-1.339	1.022	-1.140	-1.094	1.075	-1.241	-1.276	-1.637	2.554
248582_at	At5g49910	Heat shock protein 70	-1.927	1.005	-1.320	-1.033	1.060	-1.198	-1.074	-1.121	1.424
252305_at	At3g49240	Pentatricopeptide (PPR) repeat-containing protein	-1.453	1.180	-1.278	-1.026	-1.001	1.746	-1.171	-1.546	2.74
Number of genes showing at least threefold induction during the respective treatment							**37**	**42**	**29**	**45**	**51**

Relative expression data (transgenic to wild type or treatment to control) for all genes in cluster II 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 (H_2O_2 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.