

Supplementary Table S9. Regulation of *B. napus* seed genes by ABA. The ABA data is taken from Huang et al (2007).

Systematic Name	Locus	ABA 6h	ABA 24h	PBI425 6h	PBI425 24h	Function
Genes commonly upregulated in PEG treated DH and ACE seeds >2.0 fold						
A021938_01	At1g26880	0.717	0.941	0.873	0.729	60S ribosomal protein L34 (RPL34A)
A020774_01	At5g14060	1.099	1.044	1.11	0.713	"aspartate kinase, lysine-sensitive ((CARAB-AK-LYS))"
A020560_01	At3g47340	1.116	1.421	1.034	1.606	asparagine synthetase 1 (glutamine-hydrolyzing) / glutamine-dependent asparagine synthetase 1 (ASN1) ((ASN1))
A019604_01	At3g60600	1.075	0.876	1.105	1.248	"vesicle-associated membrane protein, putative / VAMP, putative ((VAP27-1))"
A015134_01	At4g22710	0.511	0.707	0.535	0.659	cytochrome P450 family protein ((CYP706A2))
A011763_01	At3g14990	1.342	1.298	1.256	1.485	"4-methyl-5(b-hydroxyethyl)-thiazole monophosphate biosynthesis protein, putative"
A007132_01	At2g21240	1.174	1.231	1.068	1.281	expressed protein
A005727_01	At3g47340	1.277	1.353	1.096	1.936	asparagine synthetase 1 (glutamine-hydrolyzing) / glutamine-dependent asparagine synthetase 1 (ASN1) ((ASN1))
A002901_01	At1g32790	1.134	0.948	1.212	1.254	"RNA-binding protein, putative"
A000059_01	At1g12110	0.767	0.701	0.731	0.462	nitrate/chlorate transporter (NRT1.1) (CHL1) ((NRT1.1))
Genes commonly downregulated in PEG treated DH and ACE seeds < 0.5 fold						
A024522_01	At3g09390	1.223	1.635	1.177	1.978	"metallothionein protein, putative (MT2A) ((MT2A))"
A020179_01	At5g66400	1.118	1.706	1.179	9.84	dehydrin (RAB18) ((RAB18))
A017979_01	At5g02380	0.992	1.124	1.081	1.445	metallothionein protein 2B (MT-2B) ((MT2B))
A009107_01	At3g57520	1.301	1.452	0.969	2.945	"alkaline alpha galactosidase, putative"

A008532_01	At2g33150	1.175	1.409	1.101	1.401	"acetyl-CoA C-acyltransferase, putative / 3-ketoacyl-CoA thiolase, putative ((PED1))"
A003411_01	At1g47710	1.001	0.982	1.105	1.259	"serpin, putative / serine protease inhibitor, putative"
Genes upregulated in PEG treated DH seeds > 2.0 fold						
A024584_01	At2g24200	1.074	1.491	1.047	1.256	cytosol aminopeptidase
A024528_01	At3g22440	1.286	0.913	1.533	1.874	hydroxyproline-rich glycoprotein family protein
A022030_01	At2g02930	0.897	0.945	0.569	1.394	"glutathione S-transferase, putative ((ATGSTF3))"
A011822_01	At3g58610	0.942	0.525	0.905	0.721	ketol-acid reductoisomerase
Genes downregulated in PEG treated DH seeds < 0.5 fold						
A021811_01	At1g80920	1.269	2.955	1.369	3.174	DNAJ heat shock N-terminal domain-containing protein ((J8))
A021219_01	At5g03240	1.215	1.089	1.1	1.715	polyubiquitin (UBQ3) ((UBQ3))
A021057_01	At1g07890	1.263	0.58	1.252	1.01	"L-ascorbate peroxidase 1, cytosolic (APX1) ((APX1))"
A020560_01	At3g47340	1.116	1.421	1.034	1.606	asparagine synthetase 1 (glutamine-hydrolyzing) / glutamine-dependent asparagine synthetase 1 (ASN1) ((ASN1))
A019491_01	At3g59970	0.853	0.914	0.861	0.739	methylenetetrahydrofolate reductase 1 (MTHFR1) ((MTHFR1))
A018818_01	At5g41700	1.058	1.656	0.973	1.715	"ubiquitin-conjugating enzyme 8 (UBC8) ((E2-17, UBC8))"
A018069_01	At5g65220	0.93	0.761	0.967	0.59	ribosomal protein L29 family protein
A016275_01	At5g22000	1.106	1.218	1.113	1.423	"zinc finger (C3HC4-type RING finger) family protein ((CIC7E11, RHF2A))"
A015892_01	At5g58070	1.222	0.954	1.086	1.593	"lipocalin, putative"
A014534_01	At4g34000	2.886	1.245	2.784	3.57	"ABA-responsive element-binding protein / abscisic acid responsive elements-binding factor (ABRE) / ABA-responsive elements-binding factor (ABF3) ((ABF3, DPBF5))"
A012747_01	At3g15450	1.35	2.21	0.906	3.179	expressed protein
A010690_01	At3g04240	1.265	1.284	1.172	1.53	"O-linked N-acetyl glucosamine transferase, putative ((SEC))"
A010028_01	At3g07560	1.021	0.955	1.042	1.36	glycine-rich protein
A009139_01	At3g51600	0.704	0.72	0.577	0.751	nonspecific lipid transfer protein 5 (LTP5)

						((LTP5))
A008720_01	At2g47390	0.972	0.929	0.865	0.822	expressed protein
A008056_01	At2g38540	1.108	1.118	1.232	1.357	"nonspecific lipid transfer protein 1 (LTP1) ((LP1, LTP1))"
A006063_01	At2g38530	0.996	1.514	1.225	3.211	nonspecific lipid transfer protein 2 (LTP2) ((LTP2))
A006056_01	At2g37970	1.139	0.762	0.871	1.26	SOUL heme-binding family protein
A005959_01	At5g03240	1.129	1.095	1.123	1.139	polyubiquitin (UBQ3) ((UBQ3))
A005952_01	At3g59970	0.943	1.075	0.97	1.013	methylenetetrahydrofolate reductase 1 (MTHFR1) ((MTHFR1))
A005727_01	At3g47340	1.277	1.353	1.096	1.936	asparagine synthetase 1 (glutamine-hydrolyzing) / glutamine-dependent asparagine synthetase 1 (ASN1) ((ASN1))
A005714_01	At5g25460	0.582	1.01	0.627	0.679	expressed protein
A005219_01	At1g12090	1.024	0.979	0.987	0.904	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein ((ELP))
A003475_01	At1g80920	2.035	1.778	1.318	2.868	DNAJ heat shock N-terminal domain-containing protein ((J8))
A001229_01	At1g12090	1.473	0.528	1.533	1.093	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein ((ELP))
Genes upregulated in PEG treated ACE seeds > 2.0 fold						
A016209_01	At5g64260	2.054	1.781	2.641	4.696	"phosphate-responsive protein, putative ((MSJ1.10))"
A014789_01	At4g23670	1.709	3.131	2.152	4.225	major latex protein-related / MLP-related
A006063_01	At2g38530	0.996	1.514	1.225	3.211	nonspecific lipid transfer protein 2 (LTP2) ((LTP2))
A025765_01	At1g78850	1.134	0.99	1.072	2.75	curculin-like (mannose-binding) lectin family protein
A013714_01	At4g01610	1.104	2.253	0.986	2.216	"cathepsin B-like cysteine protease, putative"
A014636_01	At4g35790	1.443	1.572	1.362	2.154	phospholipase D delta / PLD delta (PLDDELTA) ((ATPLDDELTA))
A002120_01	At1g48300	2.146	1.819	1.209	1.936	expressed protein
A018066_01	At5g61820	2.271	1.268	1.656	1.918	expressed protein
A017110_01	At5g14920	1.046	0.927	1.427	1.897	gibberellin-regulated family protein
A006796_01	At2g43590	0.937	1.056	1.052	1.815	"chitinase, putative"
A014769_01	At4g02380	1.192	1.37	0.611	1.763	late embryogenesis abundant 3 family protein / LEA3 family protein ((SAG21))
A016148_01	At5g49360	1.416	1.615	1.131	1.752	glycosyl hydrolase family 3 protein ((BXL1))

A017098_01	At5g10860	1.333	1.353	1.207	1.745	CBS domain-containing protein
A018818_01	At5g41700	1.058	1.656	0.973	1.715	"ubiquitin-conjugating enzyme 8 (UBC8) ((E2-17, UBC8))"
A013095_01	At4g02520	0.752	1.239	0.532	1.644	"glutathione S-transferase, putative ((ATGSTF2))"
A001234_01	At1g64230	1.034	1.734	1.044	1.613	"ubiquitin-conjugating enzyme, putative"
A020795_01	At1g72150	1.241	1.401	1.065	1.446	SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein
A003144_01	At1g56300	0.935	1.078	0.879	1.432	DNAJ heat shock N-terminal domain-containing protein
A006260_01	At2g28840	1.107	0.853	1.115	1.403	ankyrin repeat family protein
A008056_01	At2g38540	1.108	1.118	1.232	1.357	"nonspecific lipid transfer protein 1 (LTP1) ((LP1, LTP1))"
A021207_01	At5g04740	1.282	1.22	1.071	1.338	ACT domain-containing protein
A016399_01	At5g04740	0.99	1.255	1.072	1.32	ACT domain-containing protein
A015185_01	At4g08980	1.114	0.94	1.179	1.319	F-box family protein (FBW2)
A012214_01	At3g61470	1.004	1.017	1.114	1.311	chlorophyll A-B binding protein (LHCA2) ((LHCA2))
A008081_01	At2g33340	1.016	1.08	1.041	1.257	transducin family protein / WD-40 repeat family protein
A022020_01	At1g30230	0.985	0.735	1.053	1.189	elongation factor 1-beta / EF-1-beta
A014725_01	At4g35100	1.504	0.556	1.642	1.177	plasma membrane intrinsic protein (SIMIP) ((PIP3))
A016359_01	At5g09440	1.378	1.116	1.089	1.15	"phosphate-responsive protein, putative"
A020880_01	At4g34050	1.22	0.97	1.008	1.121	"caffeoyl-CoA 3-O-methyltransferase, putative"
A013408_01	At4g37880	1.079	1.298	1.009	1.057	expressed protein
A025675_01	At1g77510	1.21	0.934	0.952	1.048	"protein disulfide isomerase, putative"
A020574_01	At5g45950	1.318	0.769	1.299	1.04	GDSL-motif lipase/hydrolase family protein
A005037_01	At1g78850	0.939	1.035	0.991	1.022	curculin-like (mannose-binding) lectin family protein
A004454_01	At1g57720	0.802	0.935	0.873	1.015	"elongation factor 1B-gamma, putative / eEF-1B gamma, putative"
A003360_01	At1g70600	0.74	0.962	0.896	0.994	60S ribosomal protein L27A (RPL27aC)
A021129_01	At1g59870	0.787	1.088	0.518	0.982	ABC transporter family protein
A007844_01	At2g36320	1.052	1.192	0.817	0.908	zinc finger (AN1-like) family protein
A005653_01	At1g70600	0.964	0.938	1.073	0.906	60S ribosomal protein L27A (RPL27aC)
A021994_01	At1g74060	0.746	1.167	0.936	0.885	60S ribosomal protein L6 (RPL6B)
A021034_01	At4g27440	1.081	1.228	1.392	0.878	"protochlorophyllide reductase B, chloroplast / PCR B / NADPH-protochlorophyllide oxidoreductase B (PORB) ((PORB))"
A020928_01	At4g15560	1.249	0.932	1.04	0.868	"1-deoxy-D-xylulose 5-phosphate synthase,

						putative / 1-deoxyxylulose-5-phosphate synthase, putative / DXP-synthase, putative (DEF) (CLA1) ((CLA1))"
A003176_01	At1g49600	0.736	0.852	0.841	0.843	"RNA-binding protein 47 (RBP47), putative"
A002102_01	At1g02640	0.674	1.01	0.78	0.839	glycosyl hydrolase family 3 protein ((BXL2))
A020291_01	At3g12780	1.01	0.883	0.965	0.802	"phosphoglycerate kinase, putative ((PGK1))"
A025868_01	At5g17920	0.845	0.902	0.918	0.792	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase / vitamin-B12-independent methionine synthase / cobalamin-independent methionine synthase (CIMS) ((ATCIMS))
A010670_01	At3g08030	0.747	0.849	0.806	0.792	expressed protein
A007438_01	At2g30970	0.797	0.92	0.911	0.792	"aspartate aminotransferase, mitochondrial / transaminase A (ASP1) ((ASP1))"
A025862_01	At1g79920	1.118	0.662	0.948	0.777	"heat shock protein 70, putative / HSP70, putative"
A014473_01	At4g16410	0.851	1.118	0.869	0.747	expressed protein
A012331_01	At3g16240	1.013	1.02	1.163	0.728	delta tonoplast integral protein (delta-TIP) ((DELTA-TIP))
A024441_01	At1g61740	1.181	0.584	1.078	0.722	expressed protein
A011822_01	At3g58610	0.942	0.525	0.905	0.721	ketol-acid reductoisomerase
A018047_01	At5g23060	1.001	0.581	1.082	0.705	expressed protein
A009579_01	At3g56940	0.95	0.785	1.046	0.652	"dicarboxylate diiron protein, putative (Crd1) ((AT103, AT103-1A))"
A019219_01	At5g05740	0.988	0.601	0.987	0.639	peptidase M50 family protein / sterol-regulatory element binding protein (SREBP) site 2 protease family protein
A018069_01	At5g65220	0.93	0.761	0.967	0.59	ribosomal protein L29 family protein
A004669_01	At1g52230	1.179	0.573	1.098	0.579	"photosystem I reaction center subunit VI, chloroplast, putative / PSI-H, putative (PSAH2)"
A024612_01	At5g53160	1.01	0.917	0.818	0.575	expressed protein
A004722_01	At1g62180	0.571	0.656	0.493	0.541	"5'-adenylylsulfate reductase 2, chloroplast (APR2) (APSR) / adenosine 5'-phosphosulfate 5'-adenylylsulfate (APS) sulfotransferase 2 / 3'-phosphoadenosine-5'-phosphosulfate (PAPS) reductase homolog 43 (PRH-43) ((APR2, APSR, PRH, PRH43))"
A001186_01	At1g30380	1.027	0.572	1.079	0.509	"photosystem I reaction center subunit psaK, chloroplast, putative / photosystem I subunit X, putative / PSI-K, putative (PSAK)"
A020873_01	At3g21670	1.02	0.512	1.002	0.425	nitrate transporter (NTP3)

A003207_01	At1g37130	1.18	0.618	0.935	0.3	nitrate reductase 2 (NR2) ((NIA2))
Genes downregulated in PEG treated ACE seeds < 0.5 fold						
A024670_01	At2g37220	0.882	0.759	0.944	0.843	"29 kDa ribonucleoprotein, chloroplast, putative / RNA-binding protein cp29, putative"
A024421_01	At5g02020	1.367	1.011	0.962	1.086	expressed protein
A016226_01	At5g01820	0.782	1.092	0.9	1.089	"CBL-interacting protein kinase 14 (CIPK14) ((ATSR1, CIPK14))"
A014954_01	At4g26850	0.79	0.816	0.825	0.703	expressed protein ((VTC2))
A014720_01	At4g38740	1.094	1.411	1.14	1.391	peptidyl-prolyl cis-trans isomerase / cyclophilin / rotamase / cyclosporin A-binding protein (ROC1) ((ROC1))
A014634_01	At4g39730	1.587	1.355	1.477	1.901	lipid-associated family protein
A012747_01	At3g15450	1.35	2.21	0.906	3.179	expressed protein
A005851_01	At5g02020	0.998	1.025	1.038	1.079	expressed protein
A005606_01	At1g19835	0.939	0.88	1.006	1.089	expressed protein
A003395_01	At1g19835	1.188	1.233	1.284	1.911	expressed protein
A002513_01	At1g19370	1.183	1.069	1.213	1.361	expressed protein
A001242_01	At1g52400	0.889	1.418	1.66	1.541	"glycosyl hydrolase family 1 protein / beta-glucosidase, putative (BG1) ((BG1, BGL1))"