Supplemental material

Supplemental materials and methods - The construction of the microarray

Clustering and assembly pipeline

A dedicated pipeline was set up for clustering and assembling apple sequences for the construction of a 30k microarray (Figure S1). Different parameters were preliminary tested at each step of the clustering process to assess the specificity and reliability of the whole procedure. Only the best final setups are reported below along with a step-by-step description of the bioinformatic tools used to obtain the final temptative contigs.

Malus x *domestica* sequences were downloaded from NCBI Taxonomy database (http://www.ncbi.nlm.nih.gov/Taxonomy/taxonomyhome.html/index.cgi), in the nucleotide EST section, and included 539 mRNAs (complete or partial CDS), and 255,411 ESTs, for a total of 255,950 sequences (sequences were retrieved in January 2009). Database records were filtered for uninformative and/or spurious nucleotides (not ACGTN). In the following step sequences were further cleaned and validated. This process was performed with SeqClean (http://compbio.dfci.harvard.edu/tgi/software/) tool and consisted of i) low-quality and low-complexity sequences trimming, ii) polyA/T tails removal, and iii) vectors/adaptors contamination removal. UniVec_core (http://www.ncbi.nlm.nih.gov/VecScreen/UniVec.html) was used to recover vectors, adapters, linkers, and primers commonly used to isolate cDNAs. This lead to the selection of a dataset consisting of 252,300 sequences. RepeatMasker (http://www.repeatmasker.org/) tool was used to screen for interspersed repeats and low-complexity sequences. The screening was made using *Malus* x *domestica* libraries and the option '-small' returning repetitive regions in lowercase. A total of 1,445,369 bp were masked, including retroelements, small RNAs and simple repeats. Sequences with stretches of masked nucleotides near the ends (within 35 bp from the end) were trimmed. Only sequences longer than 100 bp were considered for the next steps.

The clustering and assembly phase was accomplished by TGIcl tool (http://compbio.dfci.harvard.edu/tgi/software/), a software using Megablast (Zhang et al., 2000) for the clustering step (not considering lowercase masked nucleotides) and Cap3 (http://dendrome.ucdavis.edu/resources/tooldocs/Cap3/readme.html) for the assembly step (Huang and Madan, 1999). To this end, the following three parameters were chosen: i) 95% of sequence identity between the overlapping region; ii) 60 bp minimum overlap between 2 sequences; iii) 30 bp maximum number of overhanging, unaligned bases. The assembly step produced 77,040 sequences (26,658 contigs and 50,382 singletons). An additional filtering phase was carried out by developing *ad hoc* Perl scripts to eliminate putative chimera or incorrect clusters, based upon ACE file and quality values produced by CAP3, leading to an increase of the dataset to a total 77,074 sequences, due to the breaking of some clusters. In order to reduce the number of unigenes and remove the redundancy caused by the high-level of stringency, CDhit (Li et al., 2001; Li et al., 2002; Li and Godzik, 2006; http://bioinformatics.ljcrf.edu/cd-hi/) tool was launched to group together different unigenes with a strong overlap (90% identity and 70% coverage of shorter sequence). The longest sequence for each group was considered. This process removed similar sequences, but did not affect the contig reliability, because discarded sequences did not contribute to the contig formation. The resulting dataset (48,045 seqs) was blasted against NCBI UniGene db for *Malus* x *domestica* and the best-hits were collected with high-stringency (90% identity and 80% coverage of UniGene ESTs). The sequences belonging to the same UniGene were grouped, and the longest representative considered, allowing to obtain 41,927 sequences. The transcription orientation was determined by using the relative orientation of the protein best-hit (UniProt). The best-hits were selected according to a minimum 30% identity, 60% similarity and 50% coverage.

Annotation of sequences

Tentative contigs and singletons obtained above were initially annotated with Gene Ontology (GO) terms recovered from the five Uniprot best-hits. Annotations were imported in Blast2GO v2.4.0 (Conesa et al., 2005; Conesa and Goetz, 2008) and further enriched using the built-in tools as described by Botton et al. (2008). In particular, the Annex function (Myhre et al., 2006) was used to increase the total number of annotations. Direct acyclic graphs were traced to recover father GO terms allowing to select the most suitable annotation level for comparisons with other species. Level 2 annotations were finally adopted and compared with those of *Arabidopsis thaliana*, *Vitis vinifera*, *Prunus persica*, and *Populus* publicly available in The Gene Index website (http://compbio.dfci.harvard.edu/tgi/plant.html). Pearson correlation coefficient was calculated separately for each GO subvocabulary (molecular function, biological process, and cellular component), in order to assess if the relative proportion of GO categories of apple sequences may resemble those of other dicot species.

Microarray design and preparation

A total of 30,419 oligos were designed with OligoArray 2.1 (Rouillard et al., 2002) by adopting parameters compatible with CombiMatrix protocols (http://www.combimatrix.com/support_docs.htm). Sequences for oligo design were chosen among the 41,927 obtained as described above, with priority given to those with annotation and orientation. Chip layout was planned using Layout Designer 4.2.1 CombiMatrix software

(CombiMatrix, Mulkiteo, USA) with each probe randomly spotted in triplicate. In addition to standard CombiMatrix negative and quality controls included by default in factory layouts, 21 negative controls were designed on bacterial and viral sequences (*Bacillus anthracis* phage Gamma genome, *Haemophilus ducreyi* genome, *Alteromonas* phage PM2 genome) using the same parameters adopted for apple oligos, and checked for cross-hybridization by BLAST searches against all available apple sequences. Microarrays were prepared on Blank 90K CustomArray chips using a 90K/12K CombiMatrix Synthesizer (CombiMatrix, Mulkiteo, USA) with the standard manufacturing and quality control protocols provided by CombiMatrix.

Supplemental references

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Table S1 – Globaltest statistics summarizing the associations between expression data in the cortex and fruitlet destiny.

Gene set	No. Genes	Response variable	T0		T2		T3		Overall	
			P-value	Sign.	P-value	Sign.	P-value	Sign.	P-value	Sign.
Spotted genes	30,419	Position[a]	0.66667	ns	0.17143	ns	0.17143	ns	0.05040	*
		Weight	0.12500	ns	0.36493	ns	0.49528	ns	0.21072	ns
		Treatment[b]	0.75000	ns	0.91429	ns	0.05714	*	0.06500	*
		Destiny[c]	0.25000	ns	0.02857	*	0.01190	*	0.00359	**
Variable	4,361	Position[a]	0.66667	ns	0.14286	ns	0.17143	ns	0.02371	*
		Weight	0.16667	ns	0.29722	ns	0.43178	ns	0.14749	ns
		Treatment[b]	0.75000	ns	0.62857	ns	0.05714	*	0.07296	*
		Destiny[c]	0.25000	ns	0.02143	*	0.00714	**	0.00117	**
ABA	190	Position[a]	0.66667	ns	0.11429	ns	0.08571	*	0.01061	*
		Weight	0.25000	ns	0.26541	ns	0.32293	ns	0.06722	*
		Treatment[b]	0.50000	ns	0.45714	ns	0.14286	ns	0.10849	ns
		Destiny[c]	0.25000	ns	0.00952	**	0.00476	**	0.00045	***
Auxin	313	Position[a]	0.66667	ns	0.11429	ns	0.28571	ns	0.03930	*
		Weight	0.12500	ns	0.39521	ns	0.54183	ns	0.18662	ns
		Treatment[b]	0.50000	ns	0.94286	ns	0.14286	ns	0.12741	ns
		Destiny[c]	0.25000	ns	0.06429	*	0.04048	*	0.00228	**
Cytokinin	70	Position[a]	0.66667	ns	0.14286	ns	0.11429	ns	0.01285	*
		Weight	0.29167	ns	0.19734	ns	0.26819	ns	0.13789	ns
		Treatment[b]	0.50000	ns	0.25714	ns	0.08571	*	0.06448	*
		Destiny[c]	0.25000	ns	0.01429	*	0.00238	**	0.00051	***
Ethylene	165	Position[a]	0.66667	ns	0.20000	ns	0.37143	ns	0.07157	*
		Weight	0.12500	ns	0.37615	ns	0.48997	ns	0.24528	ns
		Treatment[b]	0.75000	ns	0.82857	ns	0.14286	ns	0.14176	ns
		Destiny[c]	0.25000	ns	0.03333	*	0.07381	*	0.00524	**
Gibberellin	72	Position[a]	0.66667	ns	0.02857	*	0.08571	*	0.00504	**
		Weight	0.16667	ns	0.22502	ns	0.29211	ns	0.04685	*
		Treatment[b]	0.75000	ns	0.97143	ns	0.14286	ns	0.23505	ns
		Destiny[c]	0.25000	ns	0.05000	*	0.00238	**	0.00048	***
Minor hormones	152	Position[a]	0.66667	ns	0.34286	ns	0.14286	ns	0.07432	*
		Weight	0.12500	ns	0.56089	ns	0.45846	ns	0.19304	ns
		Treatment[b]	1.00000	ns	0.71429	ns	0.08571	*	0.17825	ns
		Destiny[c]	0.25000	ns	0.40000	ns	0.00714	**	0.01085	*
Transcription factors	977	Position[a]	1.00000	ns	0.17143	ns	0.11429	ns	0.04591	*
		Weight	0.25000	ns	0.34399	ns	0.35985	ns	0.19634	ns
		Treatment[b]	0.75000	ns	0.91429	ns	0.08571	*	0.12823	ns
		Destiny[c]	0.25000	ns	0.03095	*	0.00476	**	0.00191	**

a) Lateral vs central
b) Untreated vs treated with BA
c) Abscising vs persisting
ns=non-significant (P>=0.1)
*=significant (P<0.1)
**=highly significant (P<0.01)
***=extremely significant (P<0.001)

Table S2 – Globaltest statistics summarizing the associations between expression data in the seed and fruitlet destiny.

Gene set	No. Genes	Response variable	T0		T2		T3		Overall	
			P-value	Sign.	P-value	Sign.	P-value	Sign.	P-value	Sign.
Spotted genes	30,419	Position[a]	0.66667	ns	0.45714	ns	0.17143	ns	0.18350	ns
		Weight	0.08333	*	0.12233	ns	0.06858	*	0.00827	**
		Treatment[b]	1.00000	ns	0.11429	ns	0.37143	ns	0.20484	ns
		Destiny[c]	0.50000	ns	0.43571	ns	0.01667	*	0.01170	*
Variable	4,276	Position[a]	0.66667	ns	0.45714	ns	0.20000	ns	0.09562	*
		Weight	0.08333	*	0.08679	*	0.04510	*	0.00084	***
		Treatment[b]	1.00000	ns	0.05714	*	0.40000	ns	0.16630	ns
		Destiny[c]	0.25000	ns	0.36190	ns	0.03333	*	0.00478	**
ABA	190	Position[a]	0.66667	ns	0.42857	ns	0.22857	ns	0.03741	*
		Weight	0.08333	*	0.05896	*	0.07442	*	0.00424	**
		Treatment[b]	1.00000	ns	0.17143	ns	0.31429	ns	0.50632	ns
		Destiny[c]	0.25000	ns	0.69286	ns	0.01905	*	0.00355	**
Auxin	313	Position[a]	1.00000	ns	0.57143	ns	0.14286	ns	0.06846	*
		Weight	0.04167	*	0.07862	*	0.05381	*	0.00148	**
		Treatment[b]	1.00000	ns	0.05714	*	0.31429	ns	0.24623	ns
		Destiny[c]	0.50000	ns	0.47381	ns	0.00952	**	0.00971	**
Cytokinin	70	Position[a]	1.00000	ns	0.82857	ns	0.20000	ns	0.23853	ns
		Weight	0.04167	*	0.08257	*	0.08890	*	0.01813	*
		Treatment[b]	1.00000	ns	0.17143	ns	0.22857	ns	0.34261	ns
		Destiny[c]	0.50000	ns	0.74286	ns	0.01667	*	0.01162	*
Ethylene	165	Position[a]	0.66667	ns	0.51429	ns	0.20000	ns	0.10813	ns
		Weight	0.08333	*	0.07559	*	0.04037	*	0.00173	**
		Treatment[b]	1.00000	ns	0.11429	ns	0.42857	ns	0.43325	ns
		Destiny[c]	0.50000	ns	0.84048	ns	0.03095	*	0.01865	*
Gibberellin	72	Position[a]	1.00000	ns	0.74286	ns	0.20000	ns	0.05382	*
		Weight	0.37500	ns	0.06059	*	0.05542	*	0.00423	**
		Treatment[b]	1.00000	ns	0.11429	ns	0.48571	ns	0.40545	ns
		Destiny[c]	0.25000	ns	0.48095	ns	0.02143	*	0.00260	**
Minor hormones	152	Position[a]	0.66667	ns	0.48571	ns	0.14286	ns	0.05859	*
		Weight	0.08333	*	0.12111	ns	0.04041	*	0.00130	**
		Treatment[b]	1.00000	ns	0.08571	*	0.54286	ns	0.28445	ns
		Destiny[c]	0.25000	ns	0.60952	ns	0.04286	*	0.01077	*
Trans. factors	977	Position[a]	0.66667	ns	0.60000	ns	0.20000	ns	0.11529	ns
		Weight	0.16667	ns	0.12182	ns	0.05369	*	0.00457	**
		Treatment[b]	1.00000	ns	0.05714	*	0.34286	ns	0.27578	ns
		Destiny[c]	0.25000	ns	0.60238	ns	0.01905	*	0.00977	**

a) Lateral vs central
b) Untreated vs treated with BA
c) Abscising vs persisting
ns=non-significant (P>=0.1)
*=significant (P<0.1)
**=highly significant (P<0.01)
***=extremely significant (P<0.001)

Table S3 – Number of DE genes in all the sample combinations with a score ≥0.5 (see materials and methods section for a detailed description of the statistical analyses).

				Lateral fruits										Central fruits										
				CTRL						+BA				CTRL						+BA				
				L1			L3			LB1		LB3		C1			C3			CB1		CB3		
				T0	T2	T3	T0	T2	T3	T2	T3	T2	T3	T0	T2	T3	T0	T2	T3	T2	T3	T2	T3	
Lateral fruits	CTRL	L1	T0	■	188	198	203	456	222	51	32	219	31	492	373	225	242	255	238	225	146	340	192	Cortex
			T2	97	■	225	458	336	291	46	10	270	20	385	368	107	479	260	219	436	152	299	229	
			T3	181	78	■	334	282	360	527	13	458	12	267	321	139	383	359	179	242	450	337	326	
		L3	T0	116	141	264	■	65	352	130	40	303	19	62	258	78	77	165	120	111	169	132	115	
			T2	178	224	271	56	■	430	191	41	220	33	205	261	193	56	118	96	110	137	198	167	
			T3	514	359	480	38	104	■	215	35	598	54	193	274	97	305	226	315	293	207	267	379	
	+BA	LB1	T2	183	273	151	163	382	338	■	15	102	27	193	126	122	96	126	119	83	124	90	124	
			T3	269	185	299	283	378	547	319	■	17	783	50	30	59	21	48	93	39	60	29	18	
		LB3	T2	362	157	347	52	53	68	29	358	■	16	253	351	117	295	251	150	138	87	127	235	
			T3	278	302	536	31	56	83	428	532	79	■	30	24	41	8	32	76	38	13	26	1	
Central fruits	CTRL	C1	T0	312	579	474	59	136	200	185	432	118	132	■	170	78	50	105	74	183	98	211	197	
			T2	168	141	182	195	217	448	318	324	165	404	207	■	108	282	228	167	207	123	267	243	
			T3	563	322	525	31	62	125	249	643	116	146	151	412	■	53	94	84	173	55	297	57	
		C3	T0	203	204	320	40	123	48	283	493	54	100	84	368	47	■	107	94	62	44	138	93	
			T2	195	435	532	171	107	23	227	554	62	77	255	430	55	56	■	69	100	62	114	97	
			T3	445	485	516	57	184	171	642	605	96	212	259	559	91	145	63	■	183	80	114	67	
	+BA	CB1	T2	360	68	125	47	57	119	43	131	41	81	79	93	123	45	65	169	■	68	114	105	
			T3	188	80	112	400	232	366	293	73	114	306	218	178	299	248	381	466	87	■	47	16	
		CB3	T2	319	138	186	84	88	77	89	316	17	102	123	182	116	61	62	123	40	174	■	128	
			T3	367	345	469	238	155	171	344	641	86	238	238	672	165	142	46	248	152	845	102	■	
				Seed																				

Table S4 – Genes differentially expressed in the cortex of fruitlets that were induced to abscise upon BA treatment. A temptative annotation (with EC number when available), and the expression pattern is reported for each gene (up_J = up-regulated from T0 to T2; down_J = down-regulated from T0 to T2; up_K = up-regulated from T2 to T3; down_K = down-regulated from T2 to T3).

Gene ID	Temptative annotation (EC)	Molecular function	Exp.
Md_1:85:a	Extensin	Structural constituent of cell wall	up_J
Md_10757:1:a	Uncharacterized protein	Unknown molecular function	up_J
Md_10798:1:a	Amino acid permease	Substrate-specific transporter activity	up_J
Md_10973:1:a	Heat shock protein binding protein	Protein binding	down_J
Md_1109:1:a	WRKY53 transcription factor	Nucleic acid binding	up_J
Md_11157:1:a	3'-N-debenzoyl-2'-deoxytaxol N-benzoyltransferase (EC=2.3.1.15)	Transferase activity	up_J
Md_1122:1:a	NAC/NAM transcription factor	Nucleic acid binding	up_J
Md_1133:1:a	LEA/dehydrin	Unknown molecular function	up_J
Md_116911:s	No match found	Unknown molecular function	down_J
Md_117252:s	WRKY53 transcription factor	Nucleic acid binding	up_J
Md_118786:s	Cytochrome P450 (EC=1.14.13.88)	Ion binding, oxidoreductase activity	up_J
Md_11946:1:a	No match found	Unknown molecular function	down_J
Md_119754:s	MYC1 transcription factor	Nucleic acid binding	up_J
Md_12040:1:a	F-box family protein	Protein binding	up_J
Md_121294:s	Ethylene-responsive AP2/ERF transcription factor	Nucleic acid binding	up_J
Md_12188:1:a	Uncharacterized protein	Unknown molecular function	up_J

Md_12387:1:a	SNF1-related kinase 3.10 (EC=2.7.11.1)	Ion binding, transferase activity, nucleotide binding, protein binding	up_J
Md_12393:1:a	NAC/NAM transcription factor	Nucleic acid binding	up_J
Md_124:5:a	Repetitive proline-rich cell wall protein	Structural constituent of cell wall	down_K
Md_125:1:a	No match found	Unknown molecular function	up_J
Md_12505:1:a	Uncharacterized protein	Unknown molecular function	up_J
Md_1257:1:a	Polyphenol oxidase, chloroplastic (EC=1.10.3.1)	Ion binding, oxidoreductase activity	up_J
Md_126596:s	Ribulose bisphosphate carboxylase large chain (EC=4.1.1.39)	Oxidoreductase activity, lyase activity, transmembrane transporter activity	up_J
Md_128142:s	Aldehyde dehydrogenase family 2 member B7, mitochondrial (EC=1.2.1.3)	Oxidoreductase activity	up_J
Md_128177:s	Extensin	Structural constituent of cell wall	up_J
Md_131178:s	14-3-3-like protein	Protein binding	down_J
Md_132098:s	Pectate lyase (EC=4.2.2.2)	Ion binding, lyase activity, transmembrane transporter activity	up_J
Md_13311:1:a	Uncharacterized protein	Transferase activity	up_K
Md_135689:s	ADP-ribosylation factor, ARF	Nucleotide binding, signal transducer activity	down_J
Md_136185:s	Major allergen Mal d 1.03G	Unknown molecular function	up_J
Md_136858:s	No match found	Unknown molecular function	up_J
Md_137415:s	Amino acid permease	Substrate-specific transporter activity	up_J
Md_13801:s	No match found	Unknown molecular function	down_J
Md_13809:1:a	Uncharacterized protein	Unknown molecular function	down_J
Md_13835:1:a	Uncharacterized protein	Unknown molecular function	down_J
Md_14070:1:a	Gibberellin 2-oxidase (EC=1.14.11.-)	Ion binding, oxidoreductase activity	up_J

Md_140962:s	BRI1-associated receptor kinase 1 (BAK1) (EC=2.7.11.23)	Transferase activity, nucleotide binding	up_J
Md_1412:1:a	FERONIA receptor-like kinase	Transferase activity, nucleotide binding, signal transducer activity	up_J
Md_14276:1:a	No match found	Unknown molecular function	up_J
Md_14497:1:a	Xyloglucan-specific endoglucanase inhibitor protein	Hydrolase activity	up_J
Md_1457:2:a	Sieve element-occluding protein	Unknown molecular function	up_J
Md_153461:s	Uncharacterized protein	Unknown molecular function	up_J
Md_154937:s	Calmodulin binding protein	Protein binding	down_J
Md_15501:1:a	Uncharacterized protein	Unknown molecular function	up_J
Md_157343:s	Uncharacterized protein	Nucleotide binding, ligase activity	up_J
Md_160:4:a	Quinone oxidoreductase (EC=1.6.5.5)	Ion binding, oxidoreductase activity	down_K
Md_16050:1:a	Uncharacterized protein	Unknown molecular function	up_J
Md_16163:1:a	Protein transport protein Sec23	Ion binding, protein binding	up_J
Md_16256:1:a	Multidrug resistance protein 1, 2 (EC=3.6.3.27, EC=3.6.3.44)	Hydrolase activity, nucleotide binding	up_J
Md_16774:1:a	23S rRNA methyltransferase (EC=2.1.1.-)	Transferase activity, nucleic acid binding	up_J
Md_16774:1:a	23S rRNA methyltransferase (EC=2.1.1.48)	Transferase activity, nucleic acid binding	down_K
Md_167974:s	DNA-directed RNA polymerase subunit beta (EC=2.7.7.6)	Transferase activity, nucleic acid binding	up_J
Md_169133:s	ATPase subunit 8 (EC=3.6.3.14)	Hydrolase activity, substrate-specific transporter activity	up_J
Md_1709:2:a	EIL2 (EIN3-like)	Nucleotide binding, signal transducer activity	up_J
Md_171:2:a	Chloroplast envelope membrane protein	Substrate-specific transporter activity	up_J
Md_17245:1:a	Serine-threonine protein kinase (EC=1.3.1.74)	Transferase activity, nucleotide binding, protein binding	up_J

Md_1741:2:a	Senescence-associated protein	Unknown molecular function	up_J
Md_174442:s	Uncharacterized protein	Structural constituent of ribosome	up_J
Md_17792:1:a	Cytochrome C oxidase subunit (EC=1.9.3.1)	Oxidoreductase activity, substrate-specific transporter activity	up_J
Md_179063:s	Dynamin	Hydrolase activity, nucleotide binding, lipid binding	up_J
Md_1791:1:a	DNA-directed RNA polymerase subunit beta (EC=2.7.7.6)	Transferase activity, nucleic acid binding	up_J
Md_179488:s	Transcription factor	Hydrolase activity, protein binding, nucleic acid binding	up_J
Md_18018:1:a	No match found	Unknown molecular function	up_J
Md_182062:s	No match found	Unknown molecular function	up_J
Md_18337:1:a	NADH-ubiquinone oxidoreductase chain 1 (EC=1.6.5.3)	Oxidoreductase activity	up_J
Md_18421:1:a	Uncharacterized protein	Ion binding, hydrolase activity, nucleotide binding, substrate-specific transporter activity	down_J
Md_185136:s	Uracil phosphoribosyltransferase (EC=2.4.2.9)	Transferase activity, nucleotide binding	up_J
Md_18993:1:a	Disease resistance response protein	Unknown molecular function	down_J
Md_19496:1:a	Zinc finger DHHC domain-containing protein At3g22180	Ion binding, transferase activity	up_J
Md_19664:1:a	Uncharacterized protein	Unknown molecular function	up_J
Md_19747:1:a	Laccase (EC=1.10.3.3)	Ion binding, oxidoreductase activity	up_J
Md_19796:1:a	Uncharacterized protein	Signal transducer activity	up_J
Md_2007:2:a	Cytochrome P450 (EC=1.14.13.-)	Ion binding, oxidoreductase activity	up_J
Md_2007:4:a	Cytochrome P450 (EC=1.14.13.21)	Ion binding, oxidoreductase activity	up_J
Md_200958:s	Zinc-finger C2H2 protein SERRATE	Ion binding	up_J
Md_201734:s	Nucleic acid binding protein	Nucleotide binding, nucleic acid binding	up_J

Md_20223:1:a	Xylan endohydrolase (EC=3.2.1.8)	Ion binding, hydrolase activity	up_J
Md_203119:s	Ceramidase (EC=3.5.1.23)	Hydrolase activity	up_J
Md_20392:1:a	Anthocyanin 5-aromatic acyltransferase (EC=2.3.1.153)	Transferase activity	down_J
Md_20453:1:a	Aspartic proteinase nepenthesin (EC=3.4.23.12)	Hydrolase activity, nucleic acid binding	up_J
Md_20585:1:a	Cleavage and polyadenylation specificity factor, 73 kDa subunit	Hydrolase activity, protein binding	up_J
Md_207445:s	Peroxisomal membrane ABC transporter family	Hydrolase activity, nucleotide binding	up_J
Md_210798:s	No match found	Unknown molecular function	down_J
Md_2112:1:a	Nucleic acid binding protein	Nucleotide binding, nucleic acid binding	up_J
Md_212068:s	Uncharacterized protein	Unknown molecular function	down_J
Md_214104:s	Gibberellin 2-oxidase (EC=1.14.11.-)	Ion binding, oxidoreductase activity	up_J
Md_214706:s	Kinase (EC=2.7.10.2)	Ion binding, transferase activity, oxidoreductase activity, nucleotide binding	up_J
Md_219419:s	No match found	Unknown molecular function	up_J
Md_219650:s	No match found	Unknown molecular function	down_J
Md_22:8:a	Hydrolase, hydrolyzing O-glycosyl compounds (EC=2.4.1.67)	Hydrolase activity	up_J
Md_225721:s	ATP binding protein	Hydrolase activity, nucleotide binding	up_J
Md_2258:1:a	Uncharacterized protein	Unknown molecular function	up_J
Md_226587:s	TIP GROWTH DEFECTIVE 1	Ion binding, transferase activity, acyl binding	up_J
Md_2280:1:0:b	Leucoanthocyanidin dioxygenase (EC=1.14.11.19)	Ion binding, oxidoreductase activity	up_J
Md_232357:s	Uncharacterized protein	Ion binding, transferase activity, nucleotide binding, nucleic acid binding	up_K
Md_2328:2:a	ATP sulfurylase (EC=2.7.7.4)	Transferase activity	up_J

Md_2343:1:a	Carboxylesterase (EC=3.1.1.1)	Hydrolase activity	up_J
Md_235374:s	No match found	Unknown molecular function	up_J
Md_240669:s	Ubiquitin-protein ligase (EC=6.3.2.19)	Ligase activity	up_J
Md_241340:s	No match found	Unknown molecular function	down_J
Md_241578:s	Fructose-1,6-bisphosphatase, chloroplastic (EC=3.1.3.11)	Ion binding, hydrolase activity	down_J
Md_242520:s	Fimbrin	Protein binding	up_J
Md_246922:s	Terpene synthase	Ion binding, lyase activity, transmembrane transporter activity	up_J
Md_246936:s	Mitogen-activated protein kinase (MAPK) (EC=2.7.11.24)	Transferase activity, nucleotide binding, signal transducer activity	up_J
Md_249698:s	Ethylene-responsive AP2/ERF transcription factor	Nucleic acid binding	up_J
Md_25179:s	Gibberellin 2-oxidase (EC=1.14.11.-)	Ion binding, oxidoreductase activity	up_J
Md_253006:s	AMP-activated protein kinase, gamma regulatory subunit (EC=2.7.11.3)	Transferase activity	up_J
Md_255371:s	26S protease regulatory subunit 7	Hydrolase activity, nucleotide binding	down_J
Md_2556:1:a	GASA4-like protein	Unknown molecular function	down_J
Md_2568:2:a	Leucoanthocyanidin dioxygenase (EC=1.14.11.19)	Ion binding, oxidoreductase activity	up_J
Md_2575:1:a	MdMYB6 transcription factor	Nucleic acid binding	up_J
Md_2582:1:a	Lipoxygenase (EC=1.13.11.12)	Ion binding, oxidoreductase activity	up_J
Md_259:7:a	Uncharacterized protein	Hydrolase activity	up_J
Md_2594:1:0:b	Vacuolar acid invertase (EC=3.2.1.26)	Hydrolase activity	down_J
Md_2750:1:a	LEA/dehydrin	Unknown molecular function	up_J
Md_27611:s	Initiation factor eIF-4 gamma, middle	Protein binding, nucleic acid binding	up_J

Md_2788:1:a	No match found	Unknown molecular function	down_J
Md_2827:2:a	Cryptochrome 1	Lyase activity, transmembrane transporter activity	up_J
Md_288:2:a	Ferritin	Ion binding, oxidoreductase activity	up_J
Md_2896:1:0:b	Uncharacterized protein	Unknown molecular function	up_J
Md_294:2:a	NADH dehydrogenase ND 4 subunit (EC=1.6.5.3)	Oxidoreductase activity, cofactor binding, tetrapyrrole binding	up_J
Md_2976:1:a	E6-1 protein kinase (EC=2.7.1.-)	Transferase activity	down_J
Md_3129:1:a	No match found	Unknown molecular function	up_J
Md_3190:1:a	3-ketoacyl-CoA thiolase B (EC=2.3.1.16)	Transferase activity	up_J
Md_3203:1:a	ATP binding protein	Transferase activity, nucleotide binding, protein binding	up_J
Md_323:1:a	Ripening-induced protein 1	Structural constituent of cell wall	up_J
Md_323:2:a	Proline-rich cell wall protein	Structural constituent of cell wall	up_J
Md_33654:s	Endoglucanase (EC=3.2.1.4)	Hydrolase activity, carbohydrate binding	up_J
Md_34857:s	Uncharacterized protein	Nucleic acid binding	up_J
Md_3600:3:a	PsbP domain-containing protein 1, chloroplastic	Ion binding	down_J
Md_3669:1:a	Hydrolase, hydrolyzing O-glycosyl compounds (EC=2.4.1.67)	Hydrolase activity	up_J
Md_370:s	Glycosyl hydrolase (EC=3.2.1.-)	Hydrolase activity	up_J
Md_373:3:a	UDP-glucose glucosyltransferase (EC=2.4.1.11)	Transferase activity	up_J
Md_3747:1:a	Protein SSM1	Hydrolase activity	up_J
Md_382:1:a	Cysteine synthase (EC=2.5.1.47)	Transferase activity, lyase activity, transmembrane transporter activity, cofactor binding, tetrapyrrole binding, lipid binding, vitamin binding	up_K
Md_3836:1:a	Polyneuridine-aldehyde esterase (EC=3.1.1.78)	Hydrolase activity	up_J

Md_3896:1:0:b	WRKY4 transcription factor	Nucleic acid binding	up_J
Md_403:5:a	Glycine-rich protein	Structural constituent of cell wall	down_J
Md_4050:1:a	No match found	Unknown molecular function	up_J
Md_40605:s	Ethylene-responsive AP2/ERF transcription factor	Nucleic acid binding	up_J
Md_40927:s	NB-ARC domain-containing protein	Hydrolase activity, nucleotide binding, protein binding	up_J
Md_41108:s	bHLH transcription factor	Nucleotide binding, nucleic acid binding	up_J
Md_419:3:a	Cell wall-plasma membrane linker protein	Structural constituent of cell wall	up_J
Md_4328:1:a	Alpha-glucosidase (EC=3.2.1.20)	Hydrolase activity	up_J
Md_4363:1:a	Uncharacterized protein	Transferase activity, isomerase activity	up_J
Md_4451:1:a	Jasmonate induced protein	Unknown molecular function	down_K
Md_4451:1:a	Jasmonate induced protein	Unknown molecular function	up_J
Md_48:1:a	Aldehyde dehydrogenase, RF2 (EC=1.2.1.3)	Hydrolase activity, nucleotide binding	up_J
Md_4837:1:a	No match found	Unknown molecular function	down_J
Md_4900:1:a	Receptor protein kinase, CLAVATA1 (EC=1.3.1.74, EC=2.7.10.1)	Hydrolase activity, transferase activity, nucleotide binding, protein binding, signal transducer activity	up_J
Md_4972:1:a	Fructose-bisphosphate aldolase (EC=4.1.2.13)	Lyase activity, transmembrane transporter activity	up_J
Md_50213:s	Chromatin remodeling complex subunit	Hydrolase activity, nucleotide binding, nucleic acid binding	up_J
Md_5069:1:a	Uncharacterized protein	Ion binding, lyase activity, transmembrane transporter activity	down_K
Md_50991:s	Anthranilate N-hydroxycinnamoyl/benzoyltransferase (EC=2.3.1.144)	Transferase activity	up_J
Md_51:1:a	No match found	Unknown molecular function	up_J
Md_5321:1:a	Uncharacterized protein At5g11550	Protein binding	down_J

Md_5375:1:a	Respiratory burst NADPH-oxidase (EC=1.6.99.-)	Ion binding, oxidoreductase activity, nucleotide binding, cofactor binding, tetrapyrrole binding	up_J
Md_5413:2:a	Ankyrin repeat-containing protein	Unknown molecular function	up_J
Md_5550:1:a	IAA-amino acid hydrolase, ILR1 (EC=3.5.1.32)	Hydrolase activity, protein binding	up_J
Md_564:1:a	Cadmium induced protein CdI19	Ion binding	up_J
Md_5687:1:a	Uncharacterized protein	Hydrolase activity, protein binding	up_J
Md_5724:1:a	Zinc finger protein CONSTANS-LIKE 5	Ion binding	down_J
Md_57702:s	Uncharacterized protein At5g05840	Unknown molecular function	down_J
Md_5793:1:0:b	Mitogen-activated protein kinase kinase (MAPKK) (EC=2.7.11.25)	Transferase activity, nucleotide binding, protein binding, kinase regulator activity, enzyme activator activity	up_J
Md_6:53:a	Endonuclease/exonuclease/phosphatase	Hydrolase activity	up_J
Md_60011:s	No match found	Unknown molecular function	down_J
Md_60263:s	Metal ion binding protein	Ion binding	up_J
Md_6068:1:a	No match found	Unknown molecular function	up_J
Md_6098:1:a	No match found	Unknown molecular function	up_J
Md_612:1:a	Beta-galactosidase (EC=3.2.1.23)	Ion binding, hydrolase activity, carbohydrate binding	up_J
Md_6142:1:a	Subtilisin-like protease (EC=3.4.21)	Ion binding, hydrolase activity, protein binding	up_J
Md_6192:1:a	Omega-3 fatty acid desaturase (EC=1.14.99.-)	Oxidoreductase activity	up_J
Md_6231:1:a	Microtubule-associated protein, TORTIFOLIA1	Protein binding	up_J
Md_6240:1:a	Zinc finger homeodomain protein SZF-HD1	Nucleic acid binding	down_J
Md_6435:1:a	Uncharacterized protein	Signal transducer activity	up_J
Md_6531:1:a	MdMYB8 transcription factor	Nucleic acid binding	up_J

Md_66:2:a	Carbonic anhydrase, chloroplastic (EC=4.2.1.1)	Ion binding, lyase activity, transmembrane transporter activity	up_J
Md_66411:s	Ubiquitin-protein ligase (EC=6.3.2.19)	Protein binding, ligase activity	up_J
Md_6659:1:a	Synaptotagmin	Lipid binding	up_J
Md_6703:1:a	Uncharacterized protein	Unknown molecular function	up_J
Md_67394:s	Peroxidase (EC=1.11.1.7)	Ion binding, oxidoreductase activity	up_J
Md_674:s	Plasma membrane H+ ATPase (EC=3.6.1.3)	Ion binding, hydrolase activity, nucleotide binding, substrate-specific transporter activity	up_J
Md_6808:1:a	UDP-glucose glucosyltransferase (EC=2.4.1.11)	Transferase activity	up_J
Md_69440:s	SGT1-like protein	Protein binding	down_J
Md_6974:1:0:b	Uncharacterized protein	Unknown molecular function	up_J
Md_6997:1:0:b	Uncharacterized protein	Unknown molecular function	down_J
Md_7045:1:a	Gibberellin 2-oxidase (EC=1.14.11.-)	Ion binding, oxidoreductase activity	up_J
Md_7112:2:a	WRKY19 transcription factor	Hydrolase activity, protein binding, nucleic acid binding	up_J
Md_71285:s	Myo-inositol oxygenase (EC=1.13.99.1)	Ion binding, oxidoreductase activity	up_J
Md_7162:1:a	WD-repeat protein (EC=2.7.11.7)	Unknown molecular function	up_J
Md_7242:1:a	No match found	Unknown molecular function	up_J
Md_7330:1:a	Oligopeptide transporter	Substrate-specific transporter activity	up_J
Md_7412:1:a	Chloroplast-targeted copper chaperone	Ion binding	up_J
Md_74377:s	Cytokinin dehydrogenase (EC=1.5.99.12)	Oxidoreductase activity, nucleotide binding, cofactor binding, tetrapyrrole binding	up_J
Md_74434:s	Myo-inositol oxygenase (EC=1.13.99.1)	Ion binding, oxidoreductase activity	up_J
Md_75:5:a	Class III chitinase (EC=3.2.1.14)	Ion binding, hydrolase activity	up_J

Md_7571:1:a	Coatomer beta subunit (EC=2.7.11.7)	Protein binding	up_J
Md_7638:1:a	Uncharacterized protein At1g21390	Unknown molecular function	up_J
Md_770:2:a	Uncharacterized protein	Transferase activity, nucleotide binding, structural constituent of cell wall	down_J
Md_77189:s	Uncharacterized protein	Oxidoreductase activity	up_J
Md_77513:s	Uncharacterized protein	Unknown molecular function	up_J
Md_78298:s	L-aspartate oxidase (EC=1.4.3.16)	Oxidoreductase activity	up_J
Md_79388:s	Ribulose bisphosphate carboxylase small chain (EC=4.1.1.39)	Oxidoreductase activity, lyase activity, transmembrane transporter activity	up_J
Md_8:16:a	Polyphenol oxidase, chloroplastic (EC=1.10.3.1)	Ion binding, oxidoreductase activity	up_J
Md_81431:s	Uncharacterized protein At5g23890	Unknown molecular function	up_J
Md_8451:1:a	UDP-glucuronosyltransferase (EC=2.4.1.115)	Transferase activity	up_J
Md_8531:1:a	30S ribosomal protein S15, chloroplastic	Structural constituent of ribosome	up_J
Md_8558:1:a	Clathrin assembly protein At2g25430	Protein binding, lipid binding	up_J
Md_869:1:a	Malate dehydrogenase, malic enzyme (EC=1.1.1.40)	Ion binding, oxidoreductase activity, cofactor binding, tetrapyrrole binding	up_J
Md_8693:1:a	Chitin-inducible protein	Unknown molecular function	up_J
Md_8742:1:a	No match found	Unknown molecular function	up_J
Md_8837:1:a	Uncharacterized protein	Unknown molecular function	up_J
Md_8959:1:a	Uncharacterized protein	Unknown molecular function	up_J
Md_9063:1:a	Phosphoenolpyruvate carboxylase (EC=1.3.1.74)	Lyase activity, transmembrane transporter activity	up_J
Md_9130:1:a	Leucine-rich repeat receptor-like kinase	Transferase activity, nucleotide binding, protein binding, signal transducer activity	up_J
Md_9183:1:a	Uncharacterized protein	Unknown molecular function	up_J

Md_92075:s	Uncharacterized protein At1g09290	Unknown molecular function	up_J
Md_92669:s	Ribulose bisphosphate carboxylase small chain (EC=4.1.1.39)	Oxidoreductase activity, lyase activity, transmembrane transporter activity	down_J
Md_93:4:a	14-3-3-like protein	Protein binding	down_J
Md_93451:s	ATP-binding cassette transporter (EC=3.6.3.28)	Hydrolase activity, nucleotide binding	down_J
Md_9390:1:a	Auxin response factor 3 (ARF3)	Nucleic acid binding	up_J
Md_93992:s	Uncharacterized protein	Unknown molecular function	up_K
Md_94413:s	Arabidopsis Mei2-like 1, AML1	Nucleotide binding, nucleic acid binding	up_J
Md_9554:1:a	(-)-germacrene D synthase (EC=4.2.3.22)	Ion binding, lyase activity, transmembrane transporter activity	down_K
Md_9554:1:a	Sesquiterpene synthase (EC=4.2.3.22)	Ion binding, lyase activity, transmembrane transporter activity	up_J
Md_9662:1:a	Sucrose synthase (EC= 2.4.1.13)	Transferase activity	up_J
Md_9772:1:a	ATP binding protein	Transferase activity, nucleotide binding, protein binding	up_J
Md_9928:1:a	ANP32/acidic nuclear phosphoprotein	Protein binding	up_J

Table S5 – Genes differentially expressed in the seed of fruitlets that were induced to abscise upon BA treatment.

A temptative annotation (with EC number when available), and the expression pattern is reported for each gene (up_J = up-regulated from T0 to T2; down_J = down-regulated from T0 to T2; up_K = up-regulated from T2 to T3; down_K = down-regulated from T2 to T3).

Gene_ID	Temptative annotation (EC)	Molecular function	Exp.
Md_10154:1:a	1-acyl-sn-glycerol-3-phosphate acyltransferase (EC=2.3.1.51)	Transferase activity	down_K
Md_1024:1:a	Polyphenol oxidase, chloroplast (EC=1.10.3.1)	Ion binding, oxidoreductase activity	down_J
Md_102479:s	No match found	Unknown molecular function	up_K
Md_103049:s	Uncharacterized protein	Protein binding	up_K
Md_105836:s	Amino acid transporter	Transmembrane transporter activity, substrate-specific transporter activity	up_J
Md_10661:1:a	No match found	Unknown molecular function	up_J
Md_114537:s	Homeobox-leucine zipper protein ATHB-40	Nucleic acid binding	up_K
Md_11646:1:a	Protein synthesis inhibitor, DPH2	Unknown molecular function	up_J
Md_12112:1:a	No match found	Unknown molecular function	up_J
Md_1225:1:a	Glycerol-3-phosphate acyltransferase (EC=2.3.1.15)	Transferase activity	up_K
Md_124360:s	H+-translocating pyrophosphatase (EC=3.6.1.1)	Hydrolase activity, ion binding, transmembrane transporter activity, substrate-specific transporter activity	up_J
Md_125286:s	Heat shock protein 70-2	Nucleotide binding	down_J
Md_1263:1:a	Metal ion binding protein	Ion binding	down_J
Md_132121:s	Probable inositol transporter	Transmembrane transporter activity, substrate-specific transporter activity	down_K
Md_134601:s	Hydrolase, hydrolyzing O-glycosyl compounds (EC=3.1.1.-)	Hydrolase activity, ion binding	down_J

Md_13925:1:a	Subtilisin	Hydrolase activity, protein binding	up_K
Md_14561:s	Uncharacterized protein	Unknown molecular function	up_J
Md_150042:s	Septum site-determining protein minD	Hydrolase activity, protein binding	down_J
Md_150042:s	Septum site-determining protein minD	Hydrolase activity, protein binding	up_K
Md_15425:1:a	2-oxoglutarate/malate translocator	Transmembrane transporter activity, substrate-specific transporter activity	up_J
Md_15698:1:a	Uncharacterized protein	Ion binding, nucleic acid binding	up_J
Md_160835:s	Uncharacterized protein	Unknown molecular function	up_K
Md_176079:s	Nucleoid chloroplast DNA-binding protein	Hydrolase activity, nucleic acid binding	up_J
Md_176335:s	Uncharacterized protein	Ion binding	up_K
Md_177051:s	Uncharacterized protein	Transferase activity	up_K
Md_17879:1:a	Uncharacterized protein	Unknown molecular function	down_J
Md_17879:1:a	Uncharacterized protein	Unknown molecular function	up_K
Md_1844:2:a	ALG2-interacting protein	Protein binding	up_K
Md_1867:1:a	No match found	Unknown molecular function	up_K
Md_19486:1:a	Bel1 homeotic protein	Nucleic acid binding	up_K
Md_20016:1:a	Uncharacterized protein	Structural constituent of cell wall	up_J
Md_20453:1:a	Aspartic proteinase, nepenthesin-1 (EC=3.4.23.6)	Hydrolase activity, nucleic acid binding	up_K
Md_20513:1:a	DEAD-box ATP-dependent RNA helicase (EC=3.6.1.-)	Hydrolase activity, nucleotide binding, nucleic acid binding	up_K
Md_20585:1:a	Cleavage and polyadenylation specificity factor, 73 kDa subunit	Hydrolase activity, protein binding	up_J
Md_219638:s	Uncharacterized protein	Transferase activity, nucleotide binding	down_J

Md_219638:s	Uncharacterized protein	Transferase activity, nucleotide binding	up_K
Md_219708:s	No match found	Unknown molecular function	up_J
Md_220544:s	No match found	Unknown molecular function	up_K
Md_237503:s	One helix protein	Unknown molecular function	up_J
Md_238804:s	Uncharacterized protein	Hydrolase activity, transferase activity, nucleotide binding, structural constituent of cell wall, signal transducer activity, enzyme inhibitor activity	up_K
Md_241578:s	Fructose-1,6-bisphosphatase, chloroplastic (EC=3.1.3.11)	Hydrolase activity, ion binding	up_J
Md_248247:s	Serine/threonine-protein kinase (EC=2.7.11.17)	Hydrolase activity, transferase activity, nucleotide binding, protein binding	up_J
Md_288:2:a	Ferritin (EC=1.16.3.1)	Ion binding, oxidoreductase activity	up_K
Md_2943:1:a	Uncharacterized protein	Unknown molecular function	up_K
Md_3290:2:a	MADS-box transcription factor, STK/AGL11	Nucleic acid binding	down_J
Md_3329:1:a	Ethylene responsive AP2/ERF transcription factor	Nucleic acid binding	up_K
Md_4091:1:a	Uncharacterized protein	Transferase activity, ion binding	up_K
Md_4146:1:a	Dynein	Hydrolase activity	up_K
Md_4628:1:a	High affinity nitrate transporter	Transmembrane transporter activity, substrate-specific transporter activity	up_K
Md_4950:1:a	F-box family protein	Protein binding	up_K
Md_4981:1:a	No match found	Unknown molecular function	up_K
Md_5177:1:a	Purple acid phosphatase (EC=3.1.3.2)	Hydrolase activity	up_K
Md_5177:1:a	Purple acid phosphatase (EC=3.1.4.46)	Hydrolase activity	down_J
Md_5416:1:a	Probable glycerophosphoryl diester phosphodiesterase	Hydrolase activity, transferase activity, nucleotide binding	up_J

Md_556:2:a	Uncharacterized protein	Unknown molecular function	up_K
Md_570:2:a	Dehydrin, ABA responsive	Unknown molecular function	up_K
Md_59405:s	NADH-Monodehydroascorbate reductase (EC=1.6.5.4)	Nucleotide binding, oxidoreductase activity, cofactor binding	up_K
Md_60462:s	Inositol polyphosphate multikinase alpha (EC=2.7.1.140)	Transferase activity	up_J
Md_618:1:a	Hydrolase, hydrolyzing O-glycosyl compounds (EC=3.1.1.-)	Hydrolase activity, ion binding	down_J
Md_74377:s	Cytokinin dehydrogenase (EC=1.5.92.12)	Nucleotide binding, oxidoreductase activity, cofactor binding	up_K
Md_770:1:a	Proline-rich cell wall protein	Transferase activity, nucleotide binding, structural constituent of cell wall	up_K
Md_78200:s	CC-NBS-LRR resistance protein	Nucleotide binding, protein binding	up_K
Md_7948:1:a	Uncharacterized protein	Unknown molecular function	down_J
Md_7974:1:a	Uncharacterized protein	Transferase activity, nucleic acid binding	up_K
Md_82931:s	Laccase (EC=1.10.3.2)	Ion binding, oxidoreductase activity	up_K
Md_843:4:a	Ubiquitin carboxyl-terminal hydrolase (EC=3.1.2.15)	Hydrolase activity	down_J
Md_843:4:a	Ubiquitin carboxyl-terminal hydrolase (EC=3.1.2.15)	Hydrolase activity	up_K
Md_89293:s	Uncharacterized protein	Unknown molecular function	up_K
Md_9315:1:a	Galactinol synthase (EC=2.4.1.123)	Transferase activity	up_K
Md_9430:1:a	Uncharacterized protein	Unknown molecular function	up_K
Md_9597:1:a	ATP synthase subunit beta (EC=3.6.3.14)	Hydrolase activity, nucleotide binding, transmembrane transporter activity, substrate-specific transporter activity	down_J
Md_9597:1:a	ATP synthase subunit beta (EC=3.6.3.14)	Hydrolase activity, nucleotide binding, transmembrane transporter activity, substrate-specific transporter activity	up_K
Md_965:2:a	Uncharacterized protein	Hydrolase activity	up_K
Md_9712:1:a	No match found	Unknown molecular function	up_K

Md_97343:s	Ribosomal protein L19	Structural constituent of ribosome	up_K
Md_98050:s	Alpha/beta fold family protein hydrolase	Hydrolase activity	up_J

Table S6 – Primers used in qPCR experiments given in 5’-3’ orientation.

The last five genes were used as reference for qPCR normalization in the cortex (indicated by asterisks). As far as the seed, only *Md18S* was used as a reference (indicated by two asterisks).

Gene (Array ID)	**Forward primer**	**Reverse primer**	**Reference**
MdACO1	CAGTCGGATGGGACCAGAA	GCTTGGAATTTCAGGCCAGA	Dal Cin et al., 2005
MdACS5B	CACATGCGCTTCACAATG	CTTGAGCAGCCTACGCAA	Dal Cin et al., 2005
ERS2 (Md_247145:s)	ATTGCCTGTTCATCCAACTT	TTGTCGATACCCTCGCTTTC	-
HB40 (Md_114537:s)	AAGGGCTCGTTGGAAGAACA	GCCTCCGACAGTTGATCCTT	-
MADS10 (Md_3290:2:a)	TGGGTCAGAGATGAATGCAA	TGGCTAAAGAAATGGCGAGAA	-
AP2/ERF (Md_3329:1:a)	CAAAGTGTGGAGGTTTCGGTA	CCACCCTTTGGTCAACACG	-
ACTIN3 (Md_507:4:a)	ATCCCTCAGCACCTTCCAAC	AGAAGCATTTCCTGTGAACAA	-
TPS (Md_15339:1:a)	GCGAATGAGCCCGTAGTTGT	CGCATTCCCATTACCAATCA	-
MYB8 (Md_6531:1:a)	GGCATCTCCGAATCGACAC	GGCTGCGAAATGGTATGGTT	-
JAI (Md_4451:1:a)	CCACTTCAAACCGCAGCAC	CTGTTATTCCCGCCATGAGT	-
LEA/DEH2 (Md_570:2:a)	TGGCGGTGCTACTACAGGTG	CTGCCGTAATCGTGACCAGT	-
LEA/DEH (Md_425:1:a)	GACCCACACGTATTCCACGA	TGCGGACATCTGGTGAGTTC	-
*MdUBI**	CATCCCCCCAGACCAGCAGA	ACCACGGAGACGCAACACCAA	Dal Cin et al., 2005
*Md18S***	GTTACTTTTAGGACTCCGCC	TTCCTTTAAGTTTCAGCCTTG	Dal Cin et al., 2005
*MdACT**	TGACCGAATGAGCAAGGAAATTACT	TACTCAGCTTTGGCAATCCACATC	Li and Yuan, 2008
Md_8283:1:a*	CTCGTCGTCTTGTTCCCTGA	GCCTAAGGACAGGTGGTCTATG	-
Md_4592:1:a*	GTCGAAATGGTCAGCGGTAG	GCAATGGCAAACTCCACCTT	-

Supplemental figure legends

Figure S1 – The sequence clustering/assembling pipeline specifically set up for apple sequences. See materials and methods section for a detailed description.

Figure S2 – Schematic representation of the experimental plan for microarray experiments (**A** = small lateral fruitlets; **B** = big lateral fruitlets; **C** = small central fruitlets; **D** = big central fruitlets; +BA = treatment with BA; To= 15 days after petal fall; T2 = 17 days after petal fall; T3 = 19 days after petal fall). Each letter on the square brackets refers to a comparison between two samples.

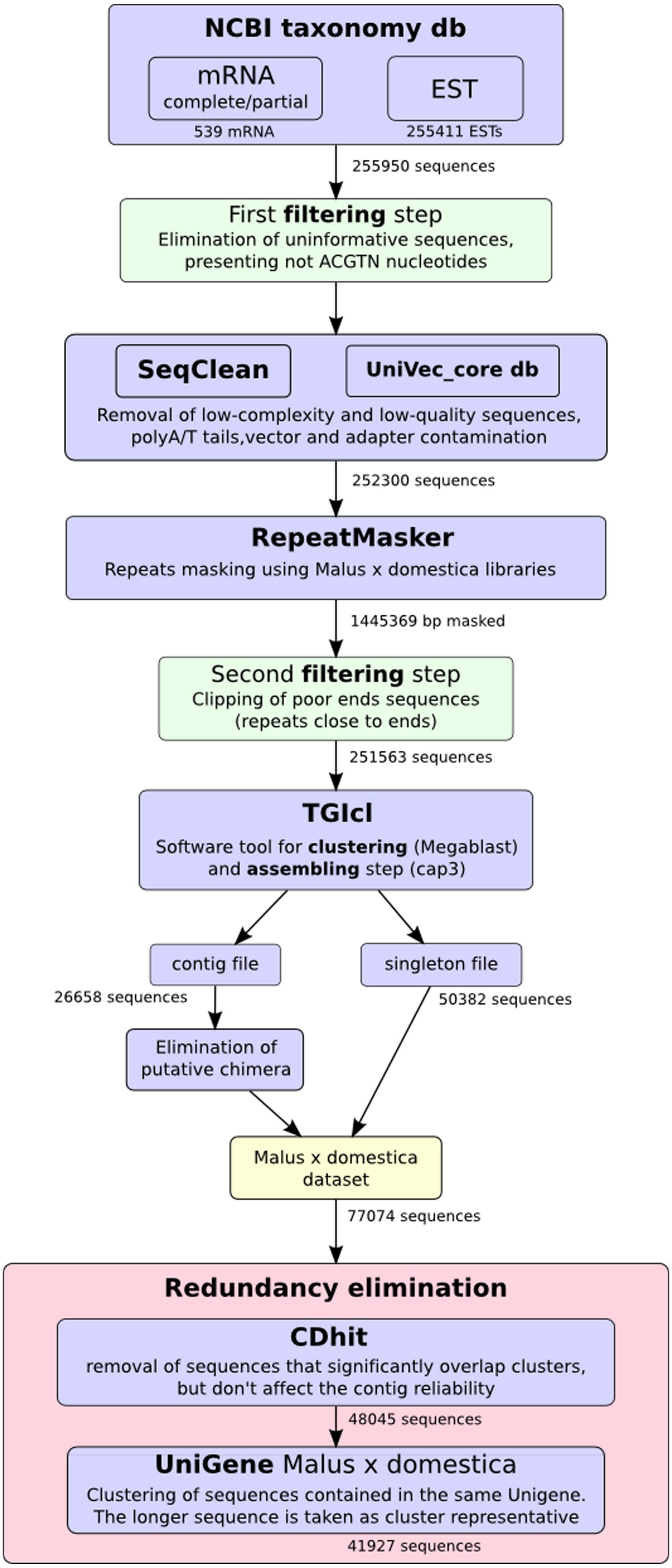
Figure S3 – Gene Ontology (GO) annotation of the 30,419 probes spotted on the apple microarray according to the molecular function (**A**), biological process (**B**), and cellular component (**C**) subvocabularies reported as percentage of the total sequences. In each chart, the Pearson correlation coefficients are reported with respect to the GO annotation pools of other important dicots for which a relevant number of genes have been annotated (*Arabidopsis thaliana*, *Vitis vinifera, Prunus persica*, and *Populus*).

Figure S4 – Concentration of glucose, fructose, sorbitol, and starch in small (**A**) and big (**B**) lateral fruitlets, and in small (**C**) and big (**D**) central fruitlets, either untreated (circles and continuous line) or treated with BA (squares and dot-line). Bars represent standard deviation. DAPF: days after petal fall.

Figure S5 – Flow-chart of the data processing. Laboratory work is evidenced by a green box, the Globaltest analysis by a yellow box, the differentially expressed (DE) genes discovery by a cyan box, the setting-up of the model by a pink box. The red boxes represent the two main statistical analyses carried out to obtain the candidate abscission-related genes. The number of biological replicates is indicated for the samples undergone Globaltest analysis (AP = abscission potential; NA = naturally abscising fruitlets; SA = strongly abscising fruitlets; PP = probably persisting fruitlets; SP = strongly persisting fruitlets).

Figure S6 – Hierarchical clustering of the significantly variable transcriptome (see materials and methods section) in all samples of cortex (**A**) and seed (**B**). Samples are reported on the right side of the heatmap with the following codes: c: cortex, s: seed; L: lateral, C: central, B: treated with BA; first number indicates fruit size category: 1: small fruitlets, 3: big fruitlets; second number indicates sampling time: 0: T0, 2:T2. 3:T3. SP: strongly persisting, PP: probably persisting, NA: naturally abscising, SA: strongly abscising.

Figure S7 – Quantitative real-time PCR (qPCR) validation of selected genes in seed (left) and cortex (right) of L3 and LB3 samples. Transcript levels are reported for five genes for each tissue as normalized intensities for microarray analyses (in red coloration), and as Mean Normalized Expression for qPCR (in black coloration), for both untreated (circles and continuous line) and treated samples (squares and dot-line). Selected genes are: *ERS2* (Md_247145:s), *HB40* (Md_114537:s), *MADS10* (Md_3290:2:a), *AP2/ERF* (Md_3329:1:a), *ACTIN* (Md_507:4:a), *TPS* (Md_15339:1:a), *MYB8* (Md_6531:1:a), *JAI* (Md_4451:1:a), *LEA/DEH2* (Md_570:2:a), *LEA/DEH* (Md_425:1:a). In the bottom charts, correlations are shown for the same genes along with Pearson coefficient, considering normalized expression values of microarrays and qPCRs in all samples analyzed. DAPF: days after petal fall.



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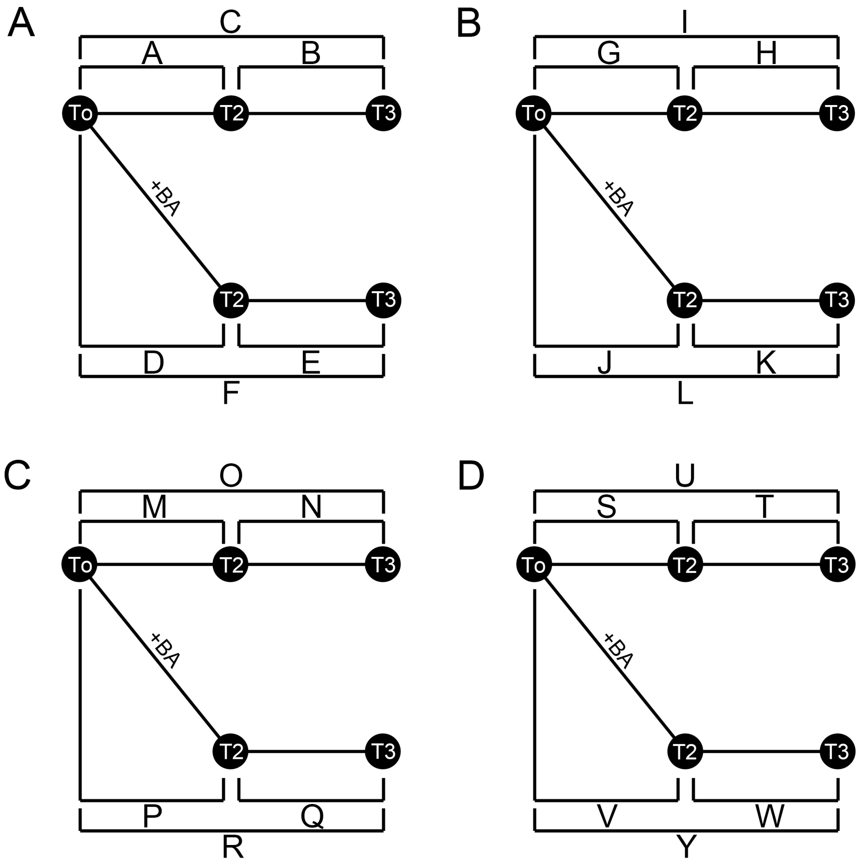

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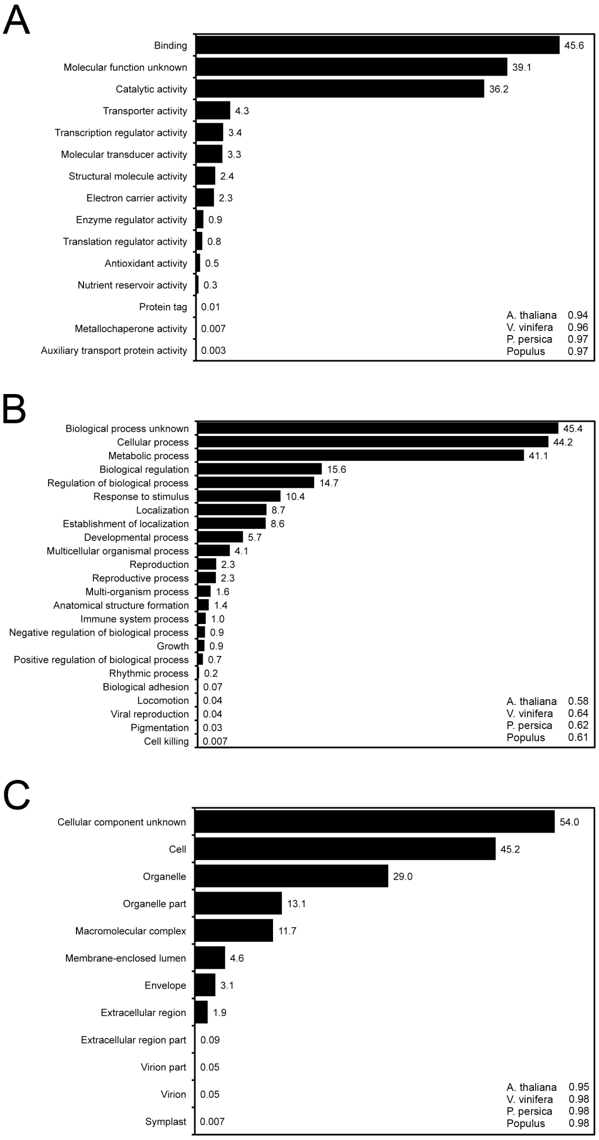

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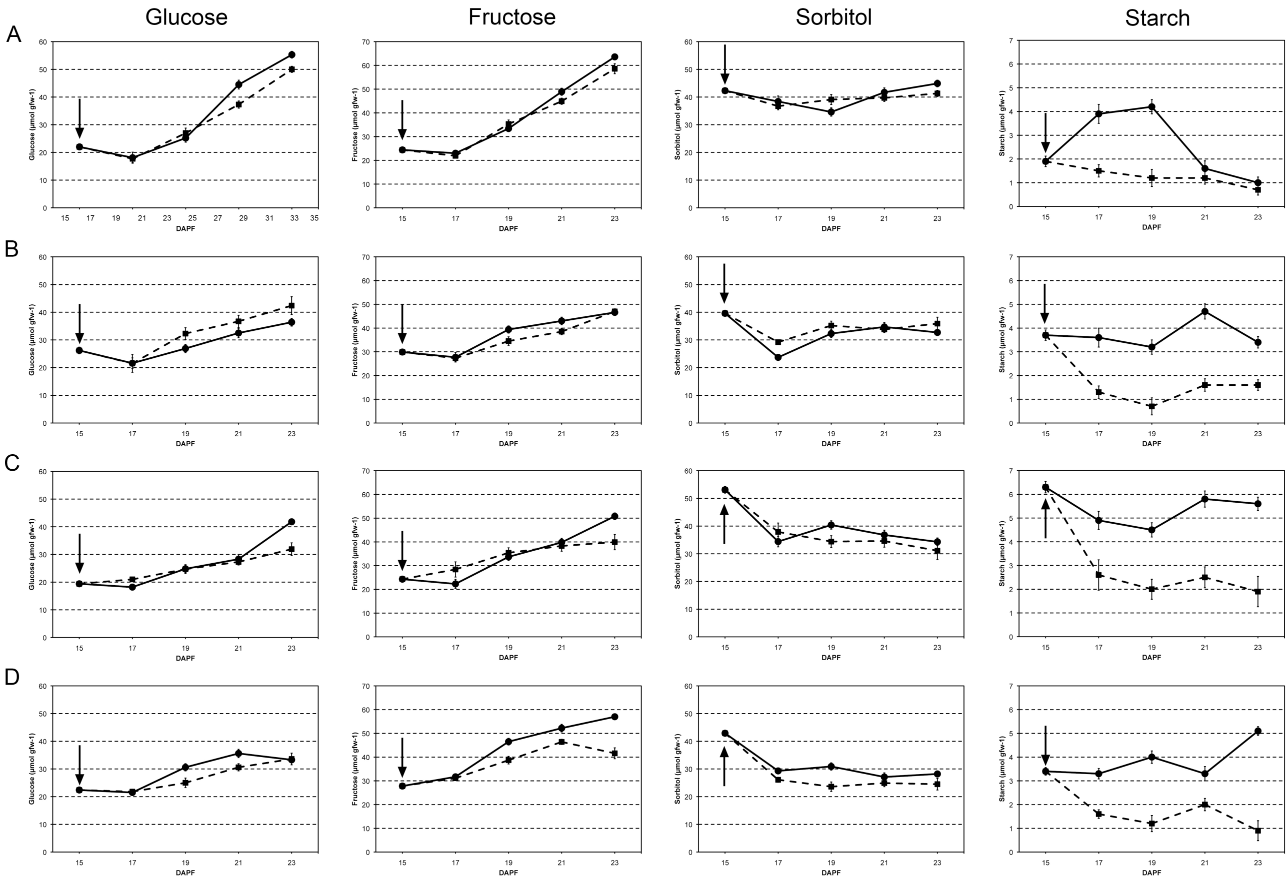

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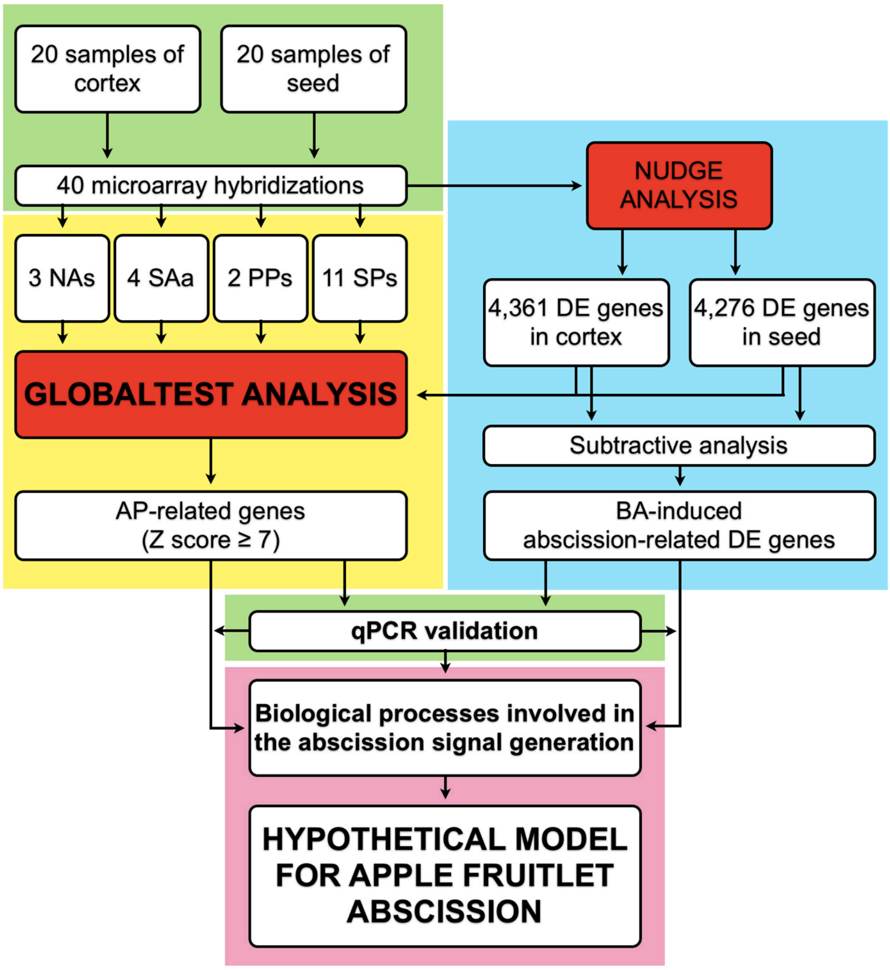

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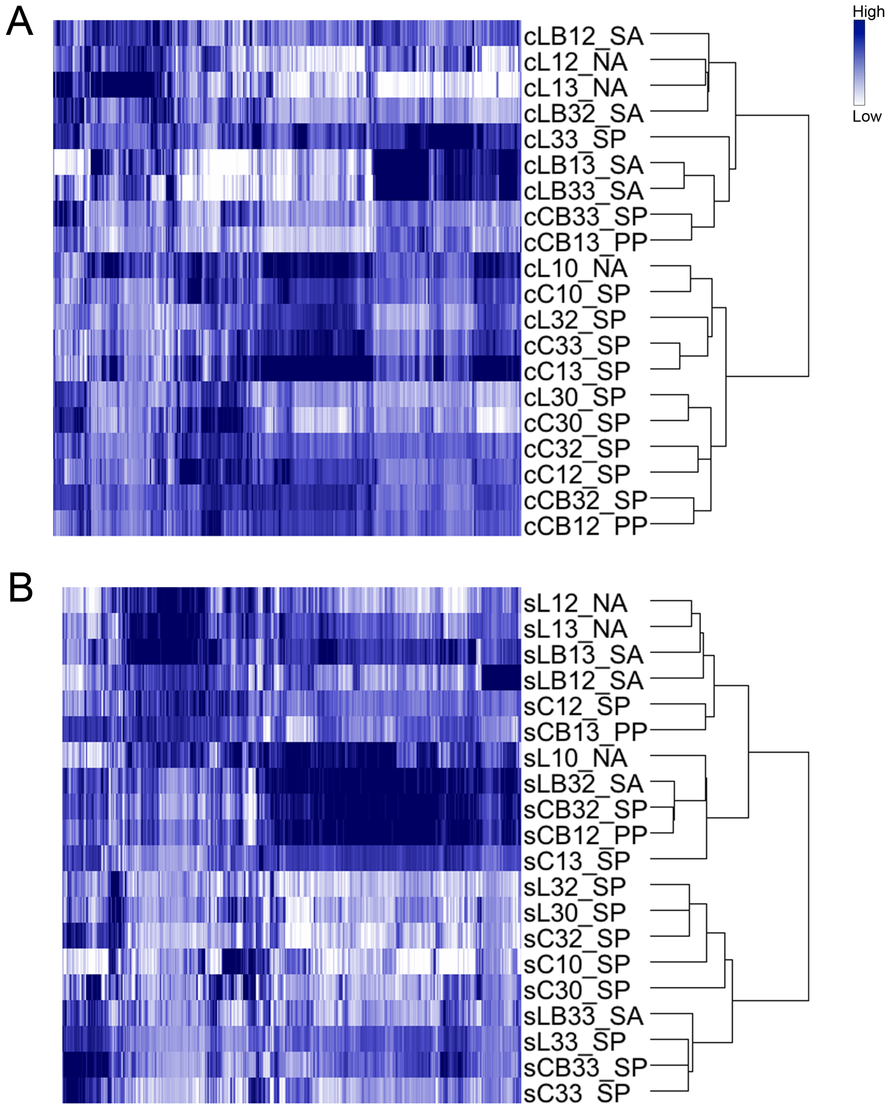

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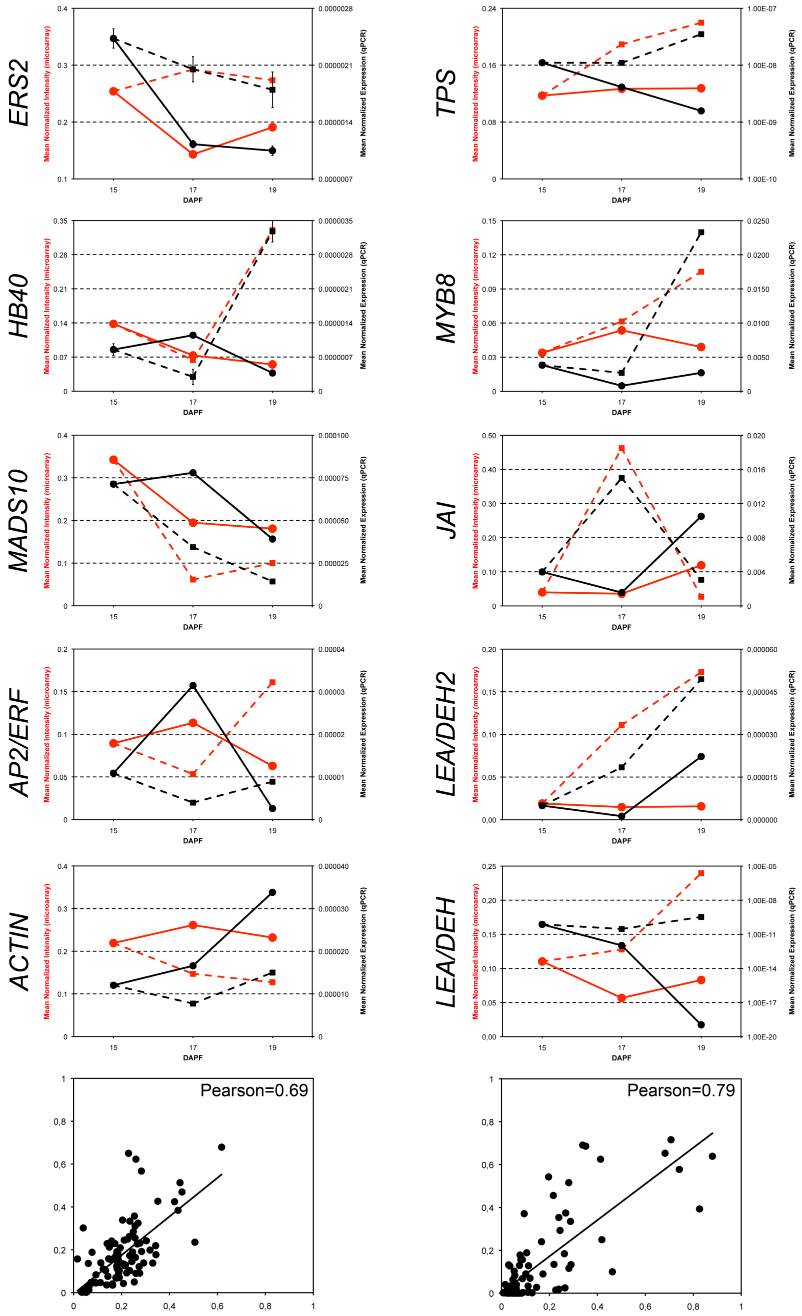

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