

Supplemental data

Transcriptome survey reveals increased complexity of the alternative splicing landscape in *Arabidopsis*

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Analysis of the normalized cDNA library

To test whether the normalization of the cDNA library was indeed reducing the representation of highly abundant genes we compared our results with previously published non-normalized cDNA libraries sequenced by different high-throughput technologies. Three data sets were used for such comparisons. The first one was a gene list and read coverage reported by Weber et al (2007) generated from an oligo-dT cDNA library of wild type 8 day old seedlings sequenced by 454 Sequencing. The second and the third data sets are short reads (36 nt single-end) generated by Solexa/Illumina sequencing of a full-length oligo_dT cDNA library from pooled tissues of 3 week old wild type plants and a random primed cDNA library of 12 day old wild type seedlings (referred further as oligo_dT and RP, respectively) (Filichkin et al. 2010). These two libraries were obtained from the Sequence Read Archive at NCBI (SRA files: SRX006704, SRX006692, SRX006192, SRX006191). To have a more direct comparison to the 36 nt single-end non-normalized libraries (oligo_dT and RP), we have truncated our original 75 nt paired-end reads to 36 nt and used only left-side reads. In addition, to exclude a possibility that the results obtained are due to the sequencing depth of the libraries we used about 40 Mio reads from our original set (two sequencing lanes).

The reads from the libraries were aligned as described in Methods. We used the alignment file to evaluate the expression profile of TAIR9 annotated genes using Cufflinks (Trapnell et al. 2010). Cufflinks uses RPKM (Reads Per Kilobase of exon model per Million mapped reads) as an expression value that is based on the number of reads that align to a particular gene model, as described by Mortazavi et al. (2008).

As depicted in the Supplemental Table 1, the proportion of reads that represent the 10 highest expressed genes is considerably lower in the 75 nt pair-end read normalized cDNA library (1.05%) in contrast to non-normalized libraries (25%, Weber et al. 2007; 26.8% and 7.8% in the oligo-dT and RP libraries, respectively). The results obtained with the 36 nt single-end read normalized cDNA library were very similar to those achieved with our original set of reads (1.03% vs 1.05%, Supplemental Table 1), so we can conclude that neither the

read length, nor the coverage have any influence on the expression profiles obtained. Additionally, we observed a difference in the distribution of the RPKM value between the different libraries. The normalized cDNA libraries have a wider distribution with higher RPKM values (Supplemental Fig. 2). This observation was reflected in an increase in the proportion of medium and high covered genes ($\text{RPKM} > 15$) compared to the non-normalized libraries (Supplemental Fig. 3). Altogether, these results indicate that the normalization procedure efficiently reduces the read representation of highly expressed genes compared to non-normalized libraries (Supplemental Table 1, Supplemental Fig. 2 and Supplemental Fig. 3).

Supplemental figures

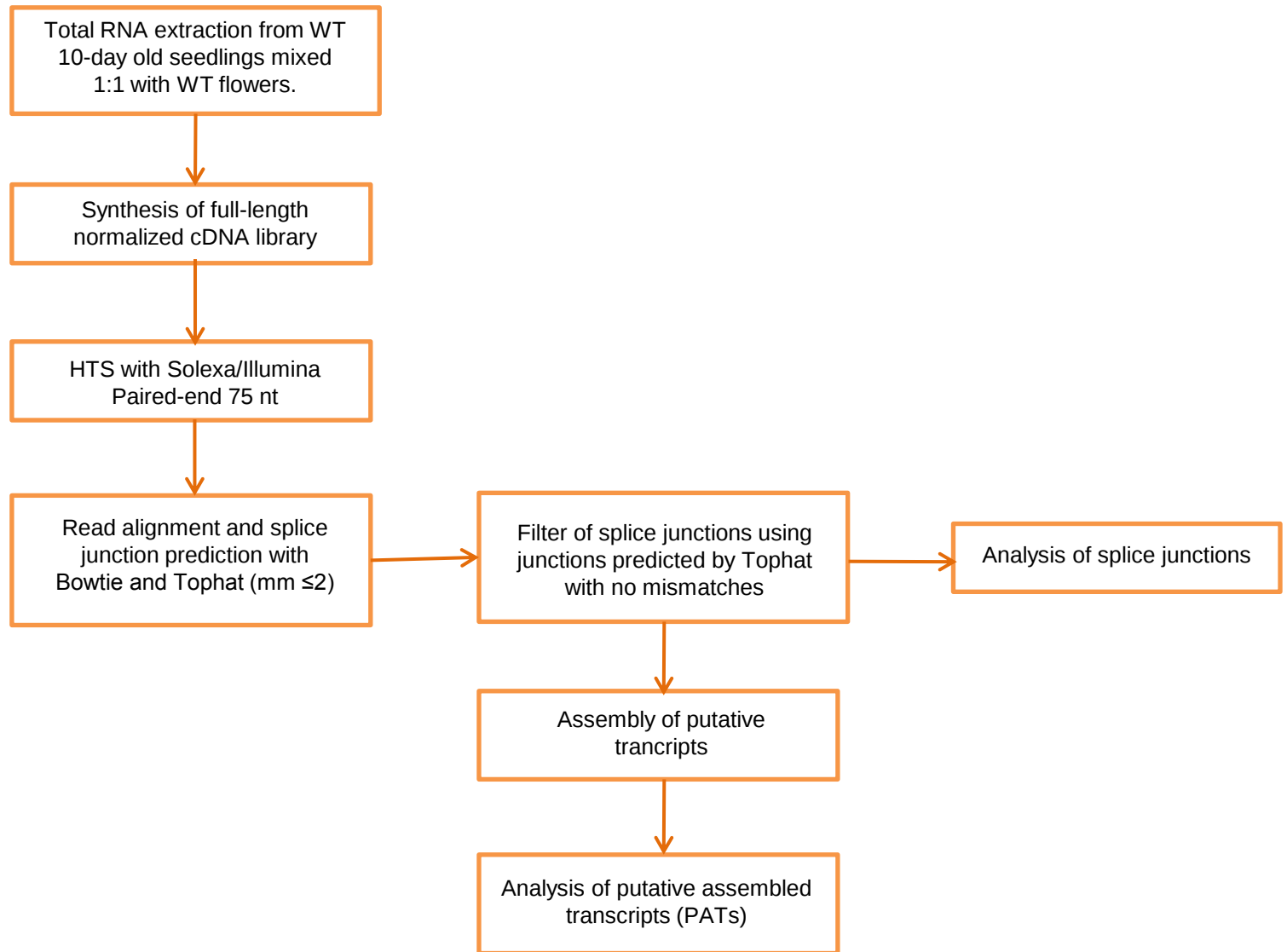


Figure S1. Workflow for the analysis of alternative splicing events in *Arabidopsis*. mm = mismatches.

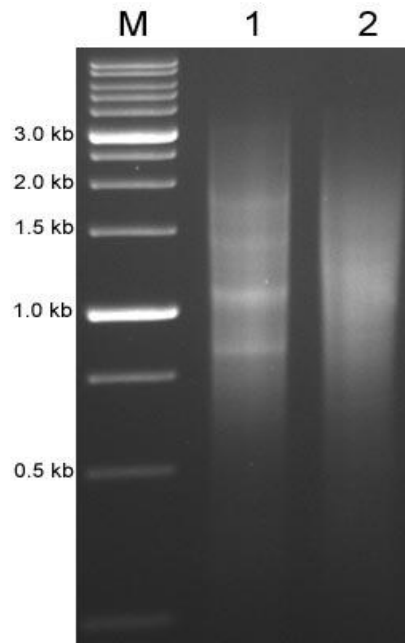
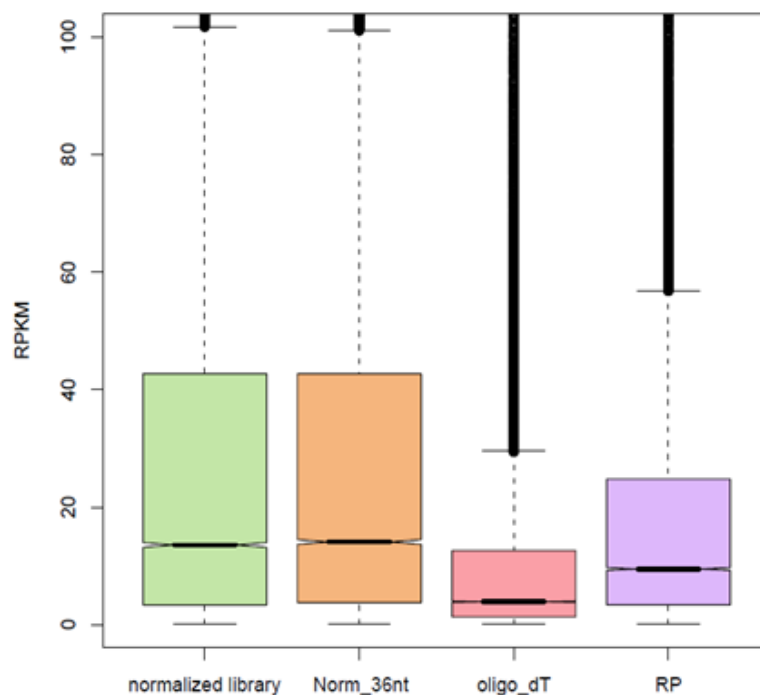


Figure S2. Normalized oligo-dT cDNA library. 2% agarose gel of cDNA obtained from total RNA of 10 day old wild type seedlings and flowers before (lane 1) and after (lane 2) the normalization procedure (see Methods).

A



B

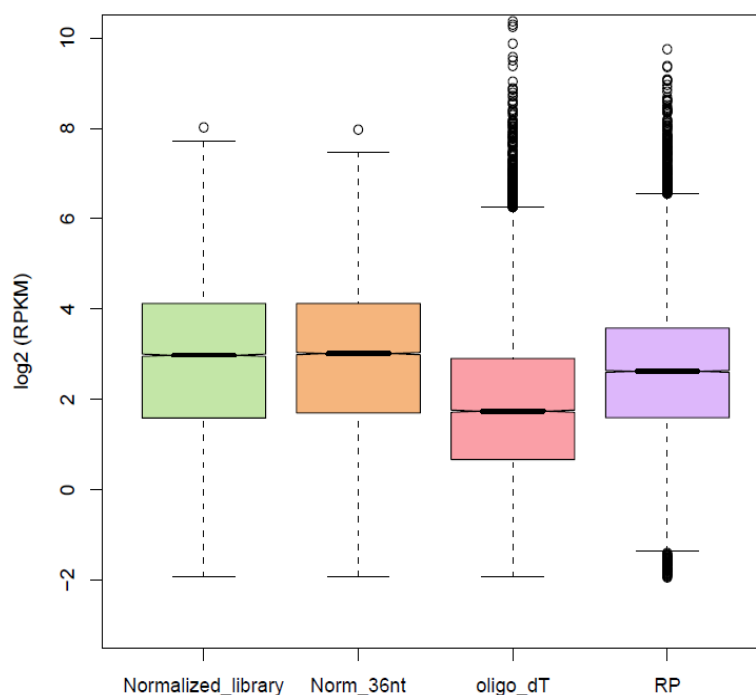


Figure S3. RPKM value distributions of TAIR9 annotated genes in the different libraries tested calculated by Cufflinks. (A) Distribution of RPKM (Reads Per Kilobase of exon model per Million mapped reads) absolute values. (B) Distribution of $\log_2$ RPKM values. The green and orange boxplots represent normalized cDNA library: green - 75 nt paired-end reads (5 sequencing lanes), orange - 36 nt single-end reads derived from the original 75 nt reads (2 sequencing lanes). The boxplots depicted in red and purple represent non-normalized cDNA libraries of 36 nt single-end reads (Filichkin et al. 2010) obtained using different priming methods (oligo-dT and random priming (RP), respectively).

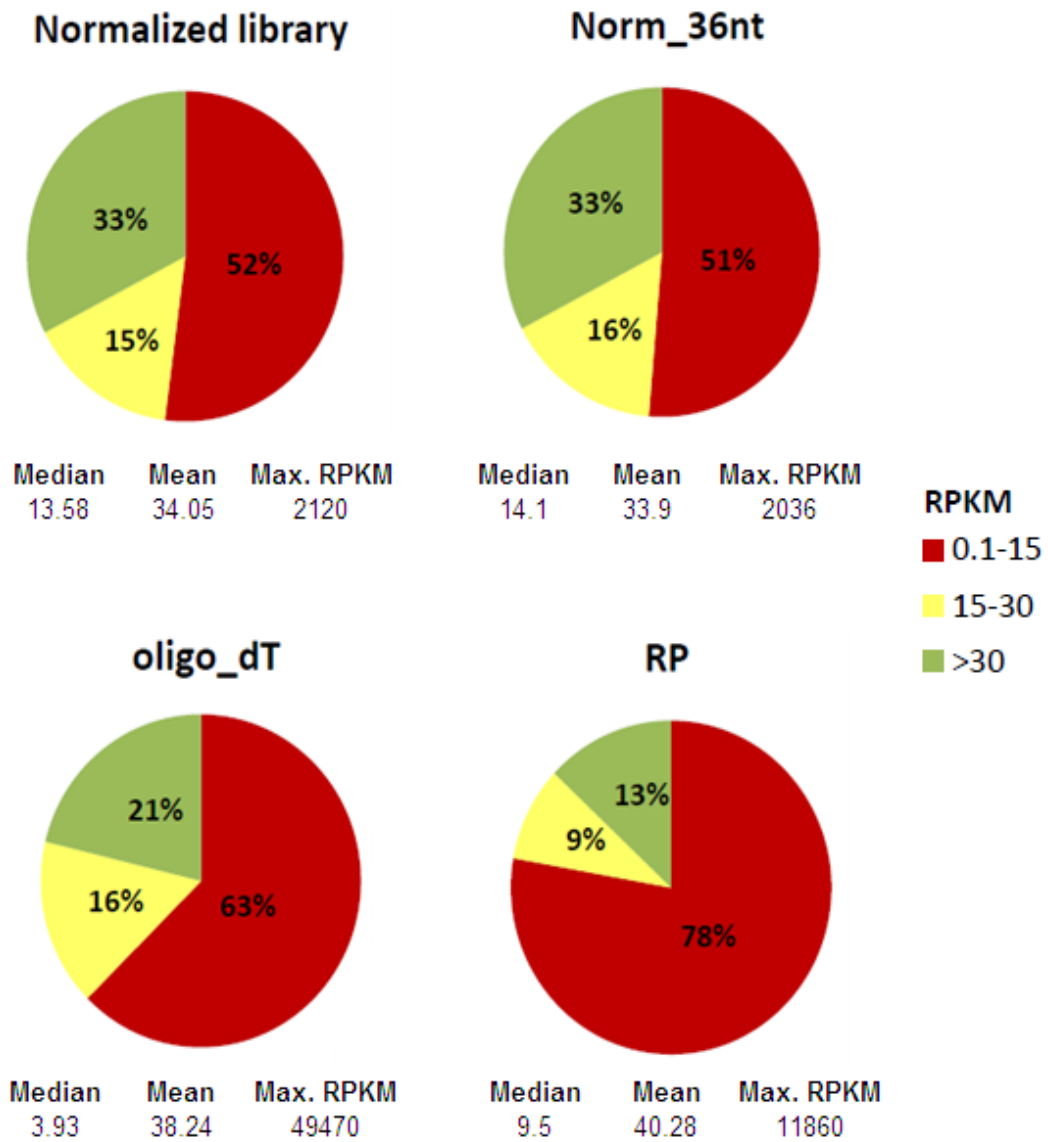


Figure S4. Proportion of TAIR9 genes in different RPKM categories in the different libraries tested. Libraries compared are normalized cDNA library of 75 nt paired-end reads, normalized cDNA library of 36 nt single-end reads derived from original 75 nt reads and non-normalized cDNA libraries (Filichkin et al. 2010) of 36 nt single-end reads obtained using different priming methods (oligo-dT and random priming (RP)). Genes with RPKM < 15 are considered to be expressed at low levels, genes with RPKM between 15 and 30 are considered to be moderately expressed and genes with values higher than 30 are considered to be highly expressed. As in our normalized data we are not measuring expression values *per se*, RPKM values reflect the coverage of the genes as this value is based on the number of reads that align to a gene model. The median, mean and maximum RPKM values for each library are depicted below each pie plot.

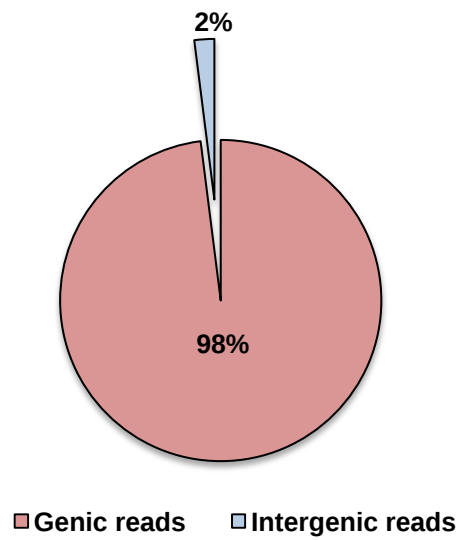
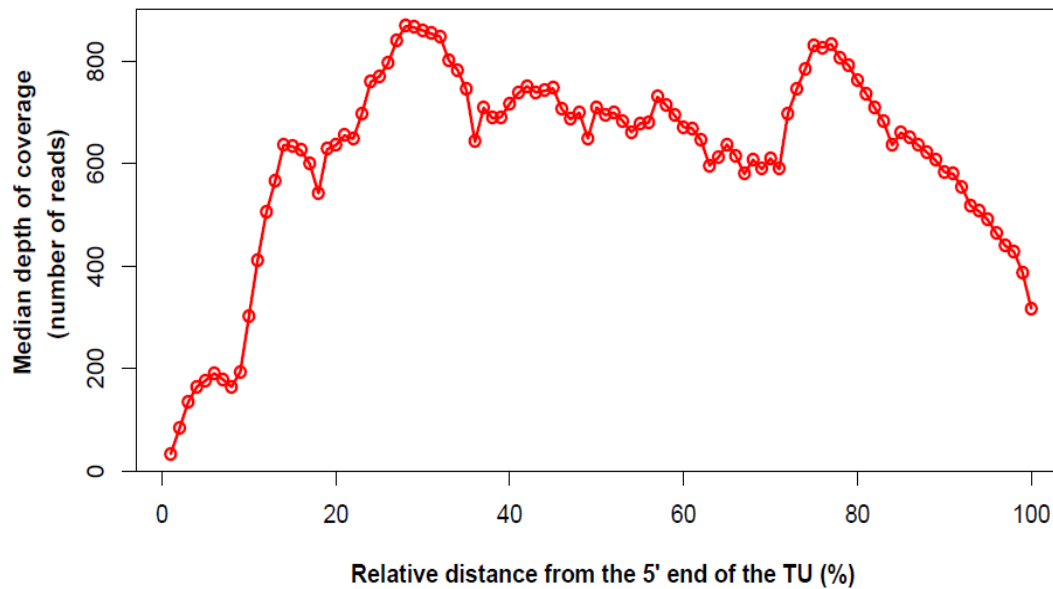
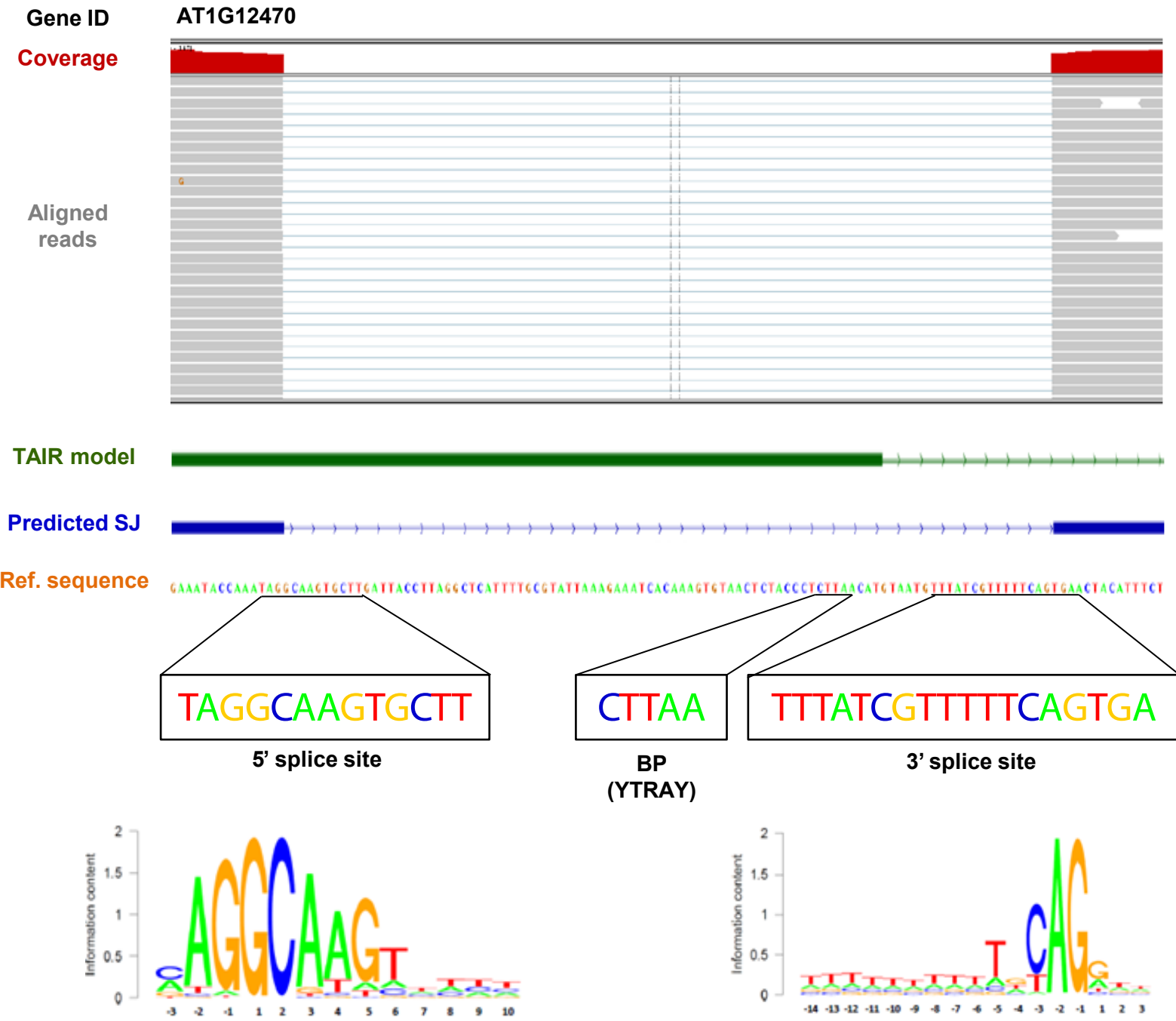
A**B**

Figure S5. Aligned reads by their genomic distribution and by coverage of transcriptional units. (A) Aligned reads by genomic region according to TAIR9 annotation. (B) Median depth of coverage along TAIR9 annotated transcriptional units (TU) (see Methods).

A



B

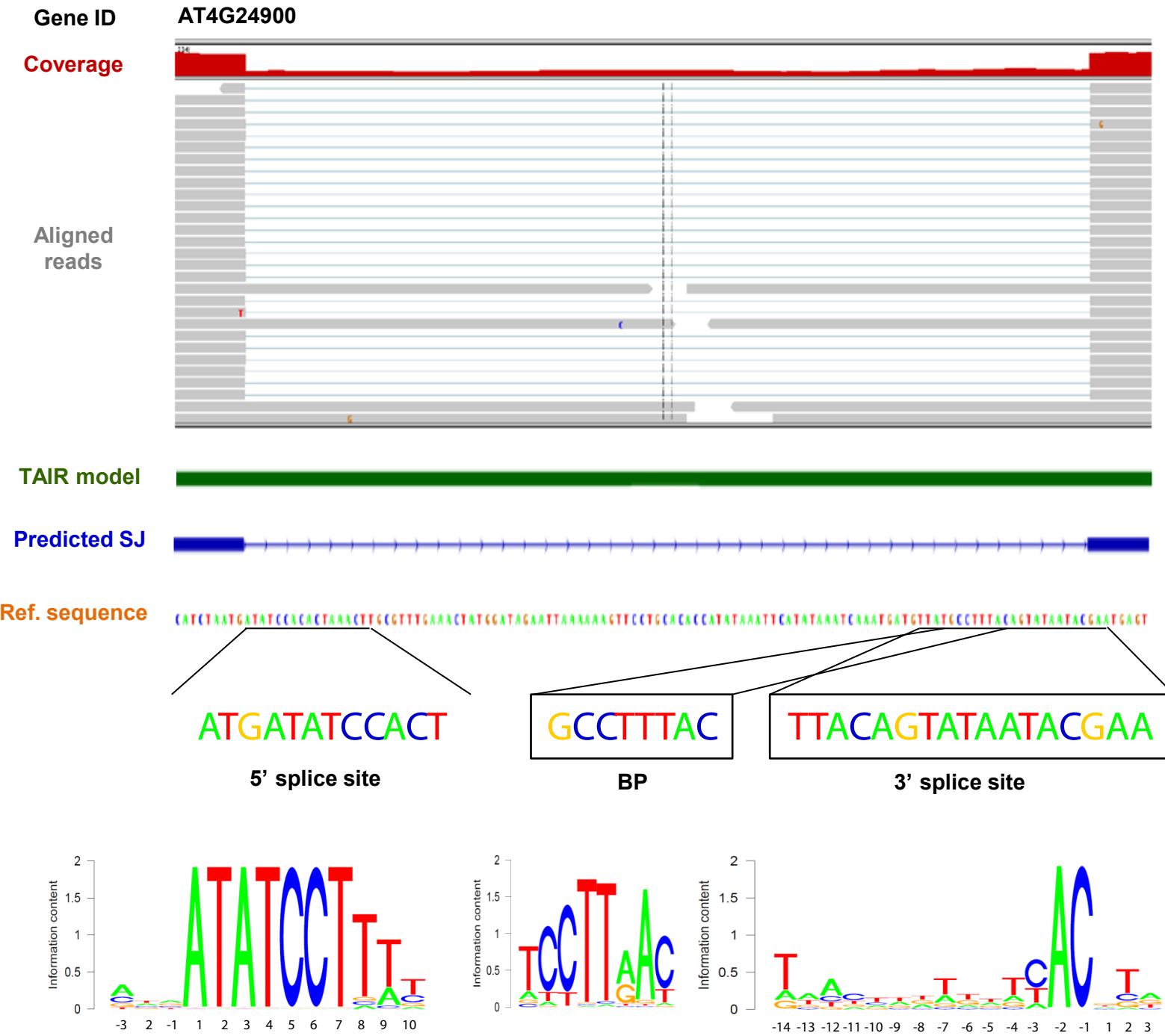
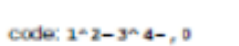
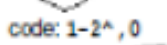
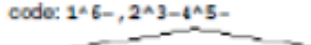
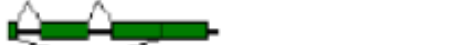
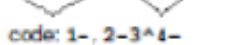
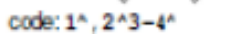
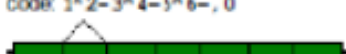
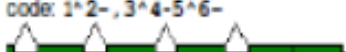
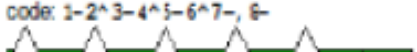
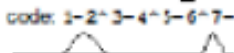
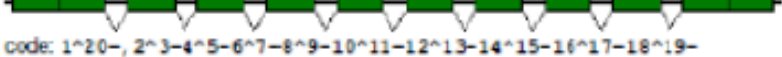
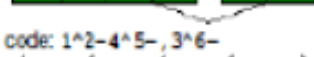
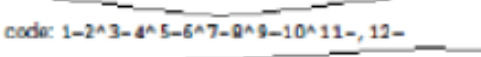
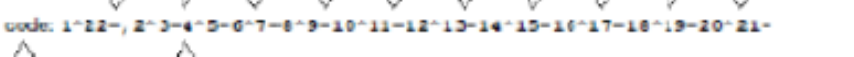
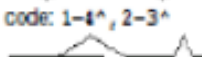


Figure S6. Splice site signatures in predicted splice junctions. Modified screenshots were done using IGV browser (Robinson et al. 2011). (A) Non-annotated splice junction (SJ) that possess U2 known signatures. (B) Non-annotated splice junction that has U12 known signatures. The 5' splice site, 3' splice site and branch point (BP) found in each intron are underlined and shown in boxes above the consensus sequence logo that corresponds to each signature. Sequence logos were obtained using R (seqLogo package). The reads covering the junctions are depicted in grey, while the coverage generated by the reads is shown in red. The annotated region in TAIR9 is displayed in green and the new splice junction predicted in this study is in blue.

Rank	Frequency	Number of events	IR	Intron-exon structure
1.1	24.21%	10622	+	 code: 1^2-, 0
2.1	15.46%	6784		 code: 1-, 2-
3.1	7.55%	3314		 code: 1^, 2^
4.1	5.17%	2271	+	 code: 1^4-, 2^3-
5.1	4.59%	2015		 code: 1^2-, 3^4-
6.1	3.09%	1359		 code: 1^2-3^4-, 0
7.1	2.74%	1204	+	 code: 1^3-, 2^4-
8.1	2.73%	1200		 code: 1-2^, 0
9.1	2.41%	1058		 code: 1^6-, 2^3-4^5-
10.1	1.75%	771	+	 code: 1^8-, 2^3-4^5-6^7-
11.1	1.21%	535		 code: 1^10-, 2^3-4^5-6^7-8^9-
12.1	1.10%	486		 code: 1-2^3-, 4-
13.1	0.95%	421	+	 code: 1^12-, 2^3-4^5-6^7-8^9-10^11-
14.1	0.94%	414		 code: 1-3^4-, 2-
15.1	0.93%	408		 code: 1-, 2-3^4-
16.1	0.82%	364		 code: 1^, 2^3-4^

Rank	Frequency	Number of events	IR	Intron-exon structure
17.1	0.67%	296		 code: 1^14-, 2^3-4^5-6^7-8^9-10^11-12^13-
18.1	0.57%	252		 code: 1^3-4^5-, 2^6-
19.1	0.56%	246		 code: 1-2^3-4^5-, 6-
20.1	0.54%	238		 code: 1^16-, 2^3-4^5-6^7-8^9-10^11-12^13-14^15-
21.1	0.51%	224		 code: 1-2^3-4^, 0
22.1	0.48%	212		 code: 1^, 2^3-4^5-6^
23.1	0.45%	201	+	 code: 1^2-3^4-, 5^6-
24.1	0.45%	199		 code: 1^18-, 2^3-4^5-6^7-8^9-10^11-12^13-14^15-16^17-
25.1	0.43%	193		 code: 1-2^4-, 3-
26.1	0.43%	192		 code: 1^5-, 2^3-4^6-
27.1	0.40%	176	+	 code: 1^2-3^, 4^
28.1	0.39%	175	+	 code: 1^2-3^4-5^6-, 0
29.1	0.38%	171	+	 code: 1^2-, 3^4-5^6-
30.1	0.36%	158		 code: 1-2^3-4^5-6^7-, 6-
31.1	0.35%	157		 code: 1-2^3-4^5-6^7-8^9-, 10-
32.1	0.34%	150	+	 code: 1^2-4^, 3^

Rank	Frequency	Number of events	IR	Intron-exon structure
33.1	0.33%	148	+	 code: 1^2-5^6-, 3^4-
34.1	0.31%	136		 code: 1^-, 2^3-4^5-6^7-8^
35.1	0.30%	135	+	 code: 1-3^, 2-4^
36.1	0.30%	132		 code: 1^3-4^, 2^
37.1	0.29%	130	+	 code: 1^20-, 2^3-4^5-6^7-8^9-10^11-12^13-14^15-16^17-18^19-
38.1	0.26%	116		 code: 1^2-4^5-, 3^6-
39.1	0.25%	113	+	 code: 1-2^3-4^5-6^7-8^9-10^11-, 12-
40.1	0.25%	112		 code: 1^22-, 2^3-4^5-6^7-8^9-10^11-12^13-14^15-16^17-18^19-20^21-
41.1	0.25%	110	+	 code: 1-4^, 2-3^
42.1	0.23%	102		 code: 1^3-4^5-6^7-, 2^8-
43.1	0.21%	93	+	 code: 1^5-6^7-, 2^3-4^8-
44.1	0.20%	90		 code: 1^-, 2^3-4^5-6^7-8^9-10^
45.1	0.18%	82	+	 code: 1-3^6-, 2-4^5-
46.1	0.17%	78		 code: 1^7-, 2^3-4^5-6^8-
47.1	0.17%	77	+	 code: 1-1^3-4^5-6^7-8^9-10^11-12^13-, 14-
48.1	0.17%	75		 code: 1^24-, 2^3-4^5-6^7-8^9-10^11-12^13-14^15-16^17-18^19-20^21-22^23-

Rank	Frequency	Number of events	IR	Intron-exon structure
52.1	0.14%	63		 code: 1-2^3-4^5-6^-, 0
53.1	0.14%	62		 code: 1-2^3-4^5-6^7-8^9-10^11-12^13-14^15-, 16-
54.1	0.13%	61		 code: 1^3-4^6-, 1^5-
55.1	0.13%	58		 code: 1^3-4^5-6^7-8^9-, 2^10-
56.1	0.12%	56		 code: 1-2^3-4^6-, 5-
56.2	0.12%	56	+	 code: 1^4-, 2^3-3^8-
56.3	0.12%	56	+	 code: 1^2-3^8-, 4^5-6^7-
57.1	0.12%	55	+	 code: 1^2-4^6-, 3^5-
58.1	0.12%	53	+	 code: 1^4-5^6-, 2^3-
59.1	0.11%	51		 code: 1^9-, 2^3-4^5-6^7-8^10-

Figure S7. Types of alternative splicing in the putative assembled transcripts according to ASTALAVISTA software (Foissac and Sammeth 2007). The first column indicates the alternative splicing event ranking considering the occurrence of the given event in the sample. The rank nomenclature is given by the place in the ranking followed by a number that indicates the number of events having such ranking. If two events have the same frequency, then the same rank is given and the number that follows the ranking will distinguish the distinct events. The second column indicates the proportion of the events found in the sample followed by the raw number of such events in the third column. The fourth column (IR) indicates splicing events involving intron retention. The last column illustrates the type of alternative splicing and the code of such event according to ASTALAVISTA output. Only those events occurring at least 50 times are shown.

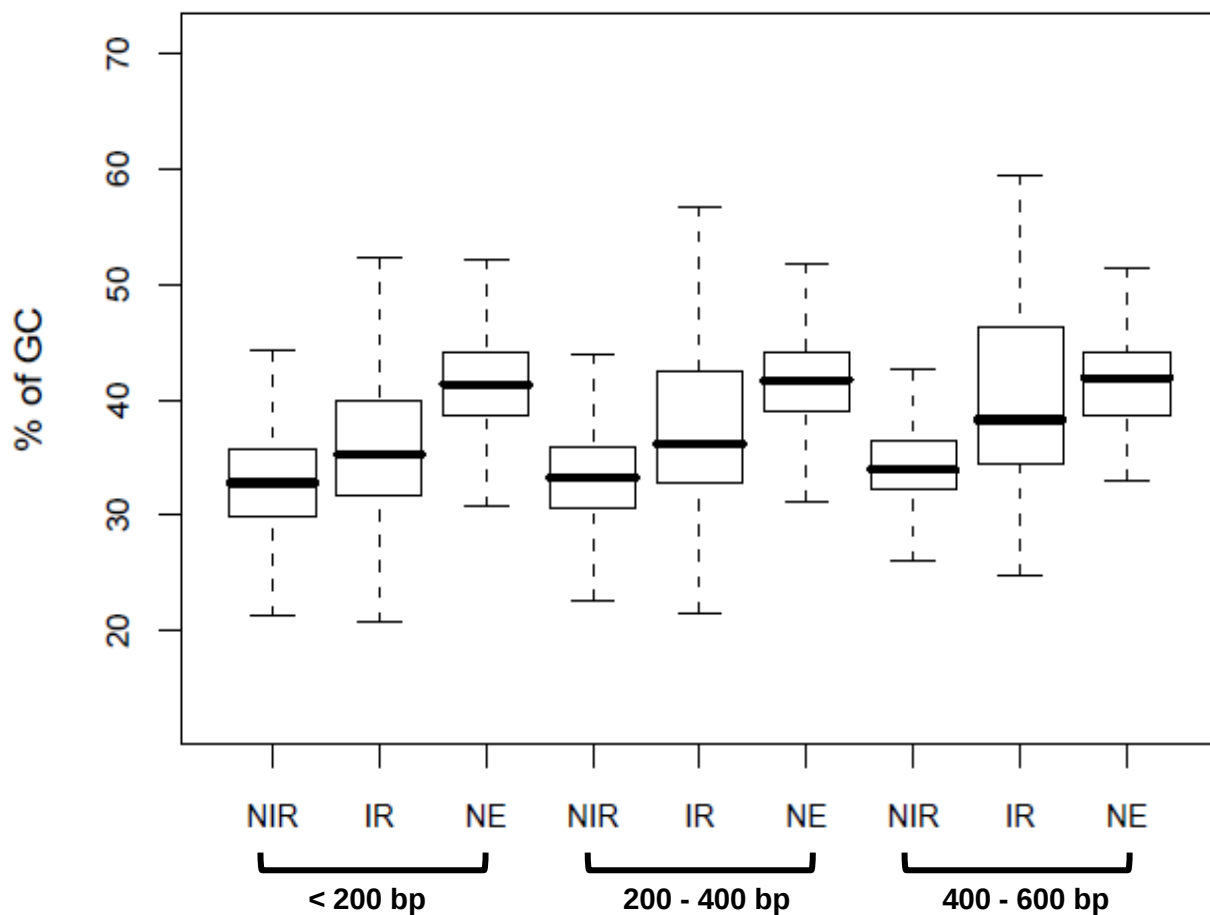


Figure S8. GC content distribution of retained introns with intron retention ratio higher than 0.3, neighboring exons and non-retained introns in three windows of intron size. The neighboring exon set (NE) corresponds to those exons that are flanking the retained introns (IR). For the GC content distribution of non-retained introns (NIR), the same number of randomly selected non-retained introns was used in the calculation.

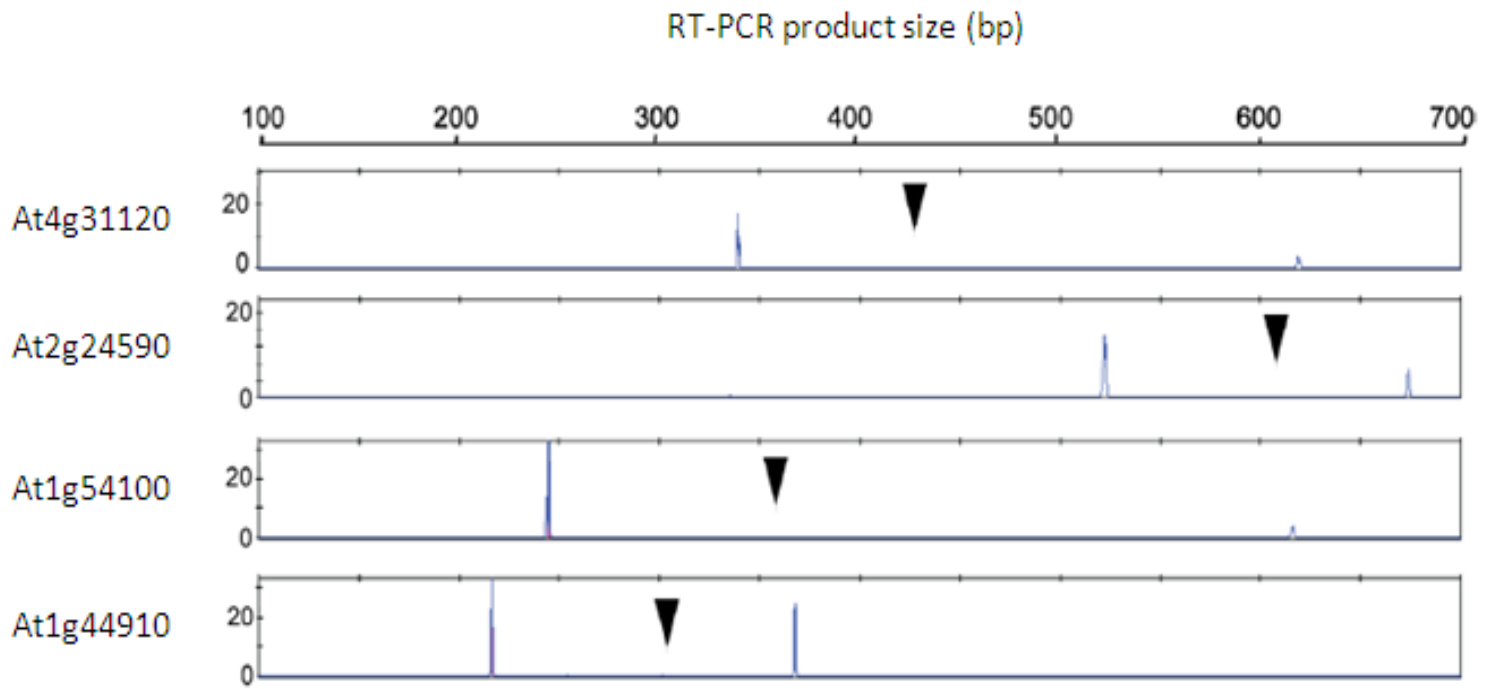


Figure S9. Intron retention events which are undetectable or $\leq 1\%$ of transcript abundance. AGI codes of the genes reported to have intron retention AS events are shown to the left of the corresponding electrophoregrams of RT-PCR products generated by GeneMapper. Numbers on the x-axis represent the size markers in bp; the y-axis is the abundance of the product in arbitrary units ($\times 10^3$). The position of the expected RT-PCR peak is indicated by an arrowhead.

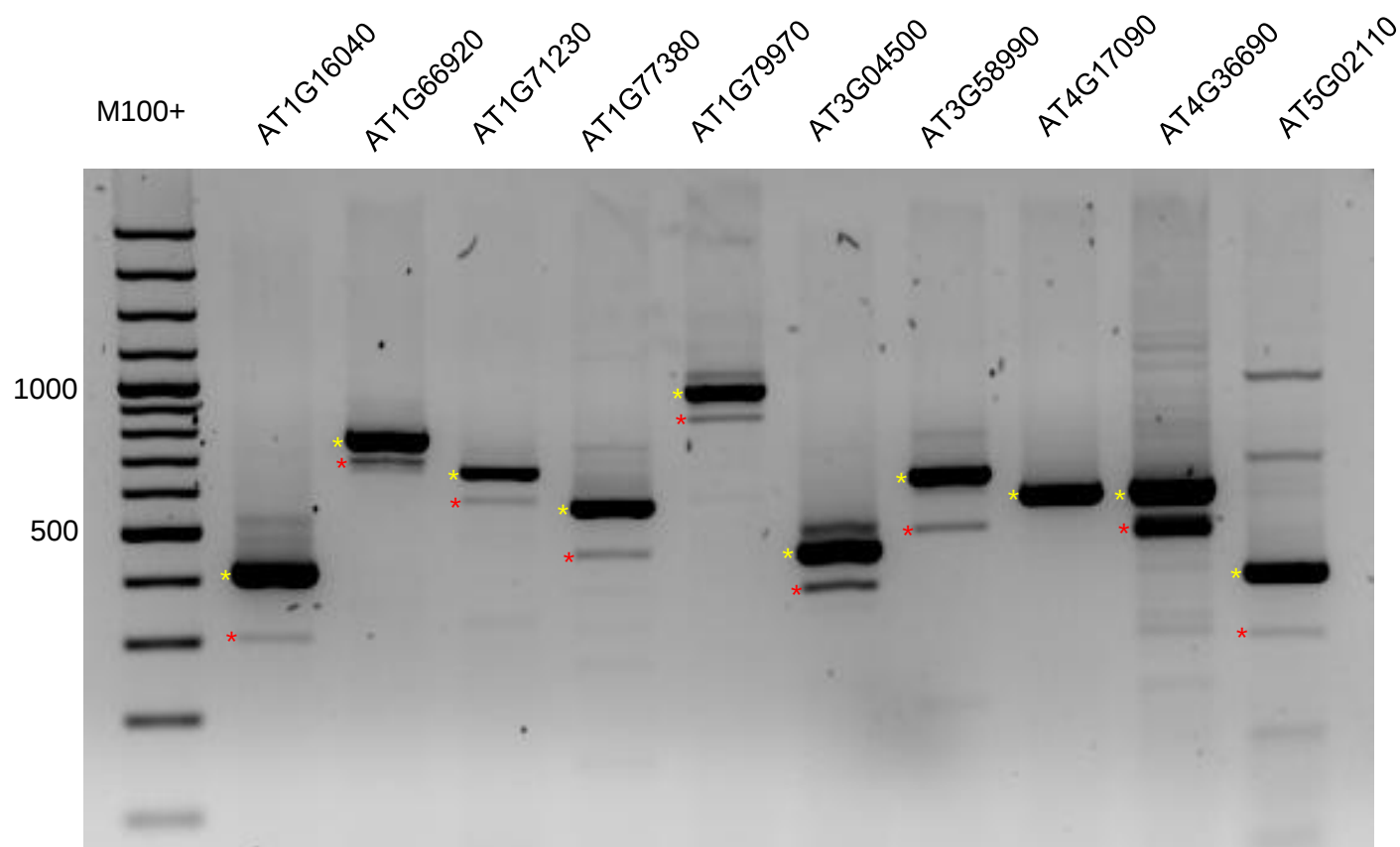


Figure S10. Verification of cryptic introns by RT-PCR. The primer sequences used to amplify regions containing 10 randomly selected cryptic introns are listed in the Supplemental Table 9. AGI codes of the genes tested are shown above each gel lane. The yellow asterisks mark the products containing a cryptic intron, while the red asterisks represent products generated by removal of the cryptic intron.

Supplemental Tables

Table S1. Top 10 genes with the highest expression values in different sequencing libraries											
1. Normalized library 75 nt paired-end (this study)				2. Normalized library 36 nt single-end (this study)							
GENE_ID	% DEPTH_COV	ABS_DEPTH _COV	RPKM	GENE_ID	% DEPTH_COV	ABS_DEPTH _COV	RPKM				
AT1G67090	0.26	27,303	2,120.38	AT1G67090	0.25	2,570	2,036.32				
AT1G29930	0.15	15,600	1,208.47	AT2G07786	0.13	1,351	1,070.00				
AT2G07671	0.13	14,347	1,112.11	AT1G29930	0.13	1,324	1,048.84				
AT2G07786	0.11	11,301	877.00	AT2G07671	0.10	963	762.54				
AT4G34050	0.08	8,501	660.28	AT4G34050	0.08	805	638.10				
AT2G34420	0.07	7,759	601.21	AT2G40060	0.07	708	560.62				
AT2G40060	0.07	7,157	555.46	AT5G38410	0.07	702	555.81				
AT5G38430	0.06	6,884	535.46	AT2G34420	0.07	675	534.53				
AT3G53020	0.06	6,843	533.01	AT3G53020	0.07	673	533.14				
AT4G16410	0.06	6,287	487.38	AT2G28000	0.06	586	464.57				
Total	1.05			Total	1.03						
3. Oligo_dT 36 nt single-end (Filichkin et al. 2010)				4. RP 36 nt single-end (Filichkin et al. 2010)							
GENE_ID	% DEPTH_COV	ABS_DEPTH _COV	RPKM	GENE_ID	% DEPTH_COV	ABS_DEPTH _COV	RPKM				
AT1G79040	6.19	38,260	49,465.40	AT1G29930	1.44	6,056	11,863.10				
AT4G00360	4.80	29,665	38,354.20	AT1G54410	1.01	4,215	8,257.33				
AT1G76810	4.79	29,613	38,286.40	AT2G45180	0.98	4,116	8,062.32				
AT1G67090	2.59	15,980	20,660.40	AT3G41768	0.75	3,162	6,194.75				
AT5G42800	2.48	15,343	19,836.20	AT1G08380	0.74	3,095	6,061.99				
AT5G38430	1.70	10,513	13,592.70	AT2G01010	0.66	2,785	5,455.72				
AT5G37770	1.26	7,791	10,073.40	AT2G36120	0.61	2,574	5,042.18				
AT2G16760	1.16	7,155	92,50.46	AT4G21960	0.57	2,397	4,696.07				
AT5G38410	1.05	6,466	8,360.03	AT5G02380	0.50	2,098	4,109.33				
AT5G38420	0.78	4,472	5,781.18	AT2G05380	0.48	2,023	3,963.03				
Total	26.76			Total	7.76						
5. 454 sequencing (Weber et al. 2007)											
GENE_ID	% DEPTH_COV	ABS_DEPTH_COV									
AT1G67090	7.50	56,357									
AT5G38410	5.39	40,476									
AT5G38420	2.44	18,353									
AT5G38430	2.20	16,518									
AT1G29930	2.11	15,818									
AT1G29910	1.38	10,360									
AT1G29920	1.25	9,395									
AT2G45180	1.04	7,852									
AT2G34420	0.92	6,902									
AT4G05320	0.83	6,220									
Total	25.05										

Table S1. Top 10 genes with the highest expression values in different sequencing libraries. The first and the second libraries are the normalized cDNA libraries generated in this study: 1 - original library of 75 nt paired-end reads; 2 – library of 36 nt single-end reads derived from original 75 nt paired-end read library (see Methods). The third and the fourth libraries (Filichkin et al. 2010) are the non-normalized cDNA 36 nt single-end read sequencing libraries generated using different priming methods (oligo_dT and random priming (RP)). The last library (5) represents data extracted from Weber et al. 2007 (non-normalized cDNA library, 454 Sequencing). Depth_cov is the percentage of read contribution of a gene to the total number of mapped reads. Abs_depth_cov represents an absolute number of reads mapped to a gene. RPKM stands for Reads Per Kilobase of exon model per Million mapped reads, as described by Mortazavi et al. 2008. Total is the sum of the %Depth coverage of the top 10 expressed genes.

Table S2. Alignment and splice junction statistics in different sequencing libraries		
Sequencing library	1. Normalized library 75 nt paired-end (this study)	
Starting reads	115,883,414	
Aligned reads	73.85%	
Unique reads	96.92%	
Predicted junctions	149,925	
Genes with junctions	19,505	
Genes with overlapping introns*	10,103	
Sequencing library	2. Normalized library 36nt single-end (this study)	3. Normalized library 75nt single-end (this study)
Starting reads	43,929,404	43,929,404
Aligned reads	84.27%	78.26%
Unique reads	94.09%	96.02%
Predicted junctions	85,297	111,427
Genes with junctions	16,435	17,804
Genes with overlapping introns*	1,320	6,570
Sequencing library	4. Normalized library 36nt paired-end (this study)	5. Normalized library 75nt paired-end (this study)
Starting reads	41,797,918	41,797,918
Aligned reads	82.36%	77.24%
Unique reads	96.32%	96.86%
Predicted junctions	84,557	109,949
Genes with junctions	16,289	17,725
Genes with overlapping introns*	1,463	6,191
Sequencing library	6. Oligo_dT 36 nt single-end (Filichkin et al. 2010)	7. RP 36 nt single-end (Filichkin et al. 2010)
Starting reads	80,412,263	43,124,211
Aligned reads	29.24%	39.47%
Unique reads	44.03%	78.54%
Predicted junctions	42,240	41,913
Genes with junctions	10,938	11,476
Genes with overlapping introns*	335	402

Table S2. Alignment and splice junction statistics in different sequencing libraries.

The sequencing library 1, is the original library of 75 nt pair-end read used in this study. Single-end reads were obtained from left-side reads of the original pair-end reads (libraries 2 and 3). The normalized sequencing libraries of 36 nt reads (libraries 2 and 4) were obtained by truncating our 75 nt reads of the original library. To allow better comparison, number of starting reads in the sequencing libraries 2, 3, 4 and 5 was reduced from ~115 Mio pair-end reads of our original library to ~40 Mio. The remaining two sequencing libraries (6 and 7) were obtained by analyzing the high-throughput sequencing data from non-normalized cDNA libraries already available (Filichkin et al., 2010) - an oligo_dT cDNA library from 3 week old wild type plants and a random primed (RP) cDNA library from 12 day old wild type seedlings. The alignment and splice junction prediction was done as described in Methods. All the splice junctions listed in the table have a score minimum of 3 (at least 3 alignments spanning the splice junction).

*Introns are defined by the predicted splice junctions (see text).

Table S3. Primer sequences used in the HR RT-PCR panel

GENE_ID	PRIMER_ID	FORWARD PRIMER	REVERSE PRIMER
AT1G01060	305	CCCGGTGAGATGATAAGTC	CCATCTTTGATCTCCCCAAC
AT1G02090	241	CAAAAAACATCGTAAGGAAGC	CCCATCTTCTTCGTAGTCC
AT1G02840	1	GGCCCCGCTCGAAGTCAAGG	GGTAGAGGAGATCTTGATCTTG
AT1G03457	268	CCGTTGCAAGTTAAGTATGC	CCCTCTTAGAATCTGTAGATCC
AT1G04400	2	GGAAGAAAGAAGAGTCAAG	GGATTATCCTCAATCCTTAGG
AT1G04950	236	GGATCTTCGTCGCTCAACG	GGAGCAAGCATAAGAGCAGCTCAGG
AT1G07350	193	CCTTGTCCTGGACCCATGGAC	CTCGAGCAGTTCTCAGCCCC
AT1G07830	237	CCATTCTCTGTGGCGTCACCGTCGCC	CCGAATCGTCGAGGCAGCTGCTGC
AT1G09000	358	CCGTACAGATAAATAACACC	CCATTACCAGGACTTTCGTC
AT1G09140	3	CCTGCTAGATCCATTTCCCC	GATCTTGATCTTGATTTTG
AT1G09230	208	CCGTCGGTTGTACTGTATATCAAAAACC	CTGCATTAGCCTCACACCAAGAC
AT1G09530	112	CCGTCTTGTCGTCGATTTG	CCTGTCTTGAGCAGATTCAAGC
AT1G11650	203	CCAGAGCTCTGCTGCAGGGGTAAC	CGAAACAACAAGCAGAGTGAC
AT1G15200	224	CAAAAGAAATTGGAATTGCTTTTCC	CCTCACTTGATCTTCTTCC
AT1G16610	217	CCTAAACCTGTCTCAGCTGCACC	CCTTCTAGGTGATAAGCCTCTCC
AT1G18660	116	GGATTCACCTTTAGTACTG	GAGACTCTTTGAATGATTGG
AT1G23970	68	CTTGACATGATCCCGATCC	CCATCGCCCAATGCGCCACC
AT1G27370	102	CCTCCTTCTACTCTCGCTC	CCCACGGGAACGAAGATACC
AT1G27770	353	CGAAGCACTTCAACTCTTTGCC	CTCACCAAAGTATGCTTATCC
AT1G30200	108	GGAACCGTTTGGGACTGTG	GCAGATTCATTTCGACGCAGG
AT1G30500	103	CCAACCACCAATCCCTTCTGC	CTTGCTCTTGATTGTCTGCGCC
AT1G31500	239	CTACAACTCTGCATCATCTTCC	CCTTCAACAGATTCAAATTTGC
AT1G31600	214	CTCGCTTCGACCTCTCTTTC	CTAACCAAGAGACTTTGTTC
AT1G31600	215	GACCATGTCTGACCTTAAAGG	GGTAACAAGAAAAGCCCTGG
AT1G33060	105	GGCTAATTTAAGTGCTCAGGGG	GCTACATTTTCGCATCACTTG
AT1G37150	251	GGACAAAGAGTGATTGCTGAAG	CCATCAGGATGAAGCTCATAC
AT1G44910	382	GCAAAATTCAAGATAGACTGG	GGCTGTAAGGATGCCTGCAG
AT1G48960	232	CCACGGCGGCGCGTCTCCTCCGCC	CCAACGAGAAGCATCGAAGCACC
AT1G49730	345	CTAAGCTGCATCACCGTAACC	CTTGATTTAATATCTCTATGAC
AT1G49950	106	CCTTGATTTCGCATTAACCC	CCAGGTCCATGCTTTATAACTCC
AT1G52500	6	CCCGTTGCAGACTGCTTCTAGCC	CCATCAACAAAGGCCCTTCC
AT1G53650	270	CCATGTTCAAGAACTCAATCC	CCTTAGAAGCTCTTCCAGGTAACC
AT1G54080	256	CCAGAGGTTACTGATGCAGC	CCATCAGAGCTATGTTGTCC
AT1G54100	357	CATTTCTTCGATACGATCAACC	CCATATTTTAGCTGCTTCCTC
AT1G54360	70	CCTTCCATTCCACAGAATTC	CCAGATTGAGTCAAAGCCCAC
AT1G55310	7	GGAAGTCGTTTGAGCAGTTTGG	GGTTTCTTTCTGTTCTCTTCTG
AT1G55870	234	CTACATCAATGGATTTTCTTGCC	CCAACTTTAACTCTTCAGTTTACC
AT1G59750	107	CCGTCTTCACAACCTCAGCC	CCCACCATGACCAAACGTAGC
AT1G60850	242	CTAAATTGCTCAATTCTCTCGGCC	CCGGCAGGGACGTCAGGGAGATC
AT1G61660	111	GGACATGGTCTATGTCTCGTCC	GCTTTAGAGTCTCCAAGCTG
AT1G64625	376	GGGAGAAGTAGCTTCATCCGG	GAGTAGATCCTAGCTGAACAACG
AT1G67210	286	GAACTCGATCCTCCTCCATGG	GAGGGCTAGCTTTTCCAAAG
AT1G67980	296	CACAAGATTAATTTTATCCATTCC	CCTTCAACCAATTTTAGAAGCC
AT1G69080	235	GGAGAAGACGAATCTTGTG	GGCATGTTGTTTCTTCTGG
AT1G69250	326	GGTCCTATCAAAGAAAACGGG	GGTCTGCAAGCATGAAGGGCG
AT1G71860	367	CCACCTAGTCTCGGCCCAATC	CCCTCTTAAGCAGACGAACC
AT1G72050	110	GGTTGATGAGGAGTCTTCAAG	GGACACTTAAAGAGCTTCCC

AT1G72320	12	CGTCAACTGTGTTTTGCATCC	CATCAAATCCACGGTTACCC
AT1G72560	249	GGCTTCAACAAAACGGGAGTCACG	GGATGGTGAAAGCGAACCTTG
AT1G72650	113	GGTTTATTGCATTCTGATAATG	GGTGGACTTGATCCTCCTC
AT1G76460	372	GGTCGATCCAAAGGATATGG	GGAAGTGGTTGCTGATACGG
AT1G76510	148	CCGTTTCTCGTCTCTTTTCTC	CCTCTACAACACCTTTGGTACC
AT1G76580	323	GGGTAACACGCGTCAATGG	GATTCAACTCTTTGCAATCGTGG
AT1G77080	109	GATCTTGAAGAAAAATTACAG	CCTAGCTCTACTTACGGACAG
AT1G77740	350	CAGCGGTGAGGCTAAGAAACC	CAGGATCCACCGTGAATAGCTCCC
AT1G79650	13	GGAGAACAAAGTTACGGAGG	GGAACAGGTGAAGACTGGG
AT1G79880	199	GGGAGATGGAGAGAGAGTTGTGG	GGCTCCTTTCCGGCCTTCTTGG
AT1G79880	200	GGCCTCCTCCTTCAACGAAG	GGCCATCTTTGCTCTTGGTG
AT2G02390	295	GGCTTGATTATGAGTATATACCAG	GGTAACAAAGGTGGCTCAGGG
AT2G02570	278	GGCAGCTTTTGTGAGGATCCTAGG	GGAGTTGCTTCAGCACTAACTCCGG
AT2G02960	118	GGGGAGCTTTCACCAATTAG	GCCTTATCATTAAACCACCGG
AT2G04790	72	CCCTGAAAGCATAGAAGCAGC	CCCATGACTTATTAACCTCC
AT2G15530	128	CCCAGAAATTGAACTACC	CCCTTGCAATTGGATTTCATACC
AT2G15970	341	CACTATCGCTGCTAAGAACC	CTACGAAAGCAATCCATTTACC
AT2G16940	209	GGAGTCAGGAAAGAGAAAAGCTTGG	GTTCTCTGATCTCTTTCAGG
AT2G18300	121	GGATGCAATAAGGTCACAGG	GGTCTAACGGAACAATGG
AT2G18960	351	CACTAGCAGAGCTATCTTCC	CGCTGAGAAGTCAAATTTCCC
AT2G21620	73	CCGGAACCTTGAGAGAGAGAGC	CCATGAGGGGCTTGGCTCGTC
AT2G21660	206	GGCGTCCGGTGATGTTGAGTATCGG	GGCTTTCTCATCCTTGAAGG
AT2G22670	117	GAAACTGAAGATCATGAAGGG	GAGACGAAATATCTTGAAGG
AT2G26150	393	GGAAATGGAGGAAGAAACGG	GCCTCAACCTAACTACCTCAG
AT2G28550	316	CGAAATTGGTAACTCCGGTTCC	CCAAGAGTAAAGTTGATATC
AT2G28550	317	CTTGGAATCTCTTTATCGACC	CCCCAGTTACTCATCATCCC
AT2G29210	223	GCAAATGAAATAATGAAGAAGAGGG	GTCAGCCCTTCTCCCATCCTCTGG
AT2G30260	218	CCACCGAATCAATCAATCTACATCC	CAGTGACTTCACTAAAAGTAACCC
AT2G31370	132	CCAACAGCAGCAGCAGCAAC	CCAAAAGGTTTCTTCTACGTACC
AT2G32250	133	CCCATCGATTCTTCCATCC	CTTCGATGTCATAGCAGCC
AT2G32320	19	CTTTTGAATGAGCACTCC	CCGTAGGCAAAGGCAATATCC
AT2G33120	413	CCTTCTCTAACAACAAGTTTACC	CCATATCTCTTGTTGAATCC
AT2G33480	322	CCGATGTTTGTAATCCGATCC	CTGTCTCTTCTCATTCTCC
AT2G33830	243	CCGGACCTAAACCGGAGCATGGCC	CCGATCCTGGCGTCGTCGGAGTTCC
AT2G36000	75	CTCGTTTAGTTTGGAGAATC	CTTCATCAGCATTTCATTAC
AT2G36010	122	CCAAAGATGGAATGCTGGACC	CTCAGGTCTCTTAATCTTTCC
AT2G37060	124	CCCTCTCTGCCTCCTCTCTTCC	CCCATTAGCAGGAAGACCTC
AT2G37340	21	GGACCCGAGACCTTGAACG	GGTAATGTCTTGATCATCAG
AT2G38170	359	GGAAATGCAGCTGAACATGCTGG	GGACCAGTCCCTTCATGTAG
AT2G38185	130	GCTTGATTACTCAGAACCAAGG	GAACCGCAGAACCTTGTGG
AT2G38880	131	GGCAACATTAGGATTTGAGG	GGAAACAATAAACCAACG
AT2G39730	23	CCTCCCGTGTTTCGAGCAACCC	CCGTTGGATCAAAGTTTTCAGCC
AT2G40830	129	CTAGGGTTTCTCATTCCGATCC	CCGTGAAGGCGGACAGCACGC
AT2G41710	120	GGCTGCTGCTAGAGCTTACG	GGTCCAGGCATACGACTGG
AT2G42240	267	CAGGGTACATATGGGACTCC	CCCTAATTAATCTTCTTACGC
AT2G42890	216	GTACACTTACAAGATGCTGGTGG	GGAAGGGAACGATGTGCAATGG
AT2G43010	127	CCGTTATGGATCAGTCTGC	CCGTGCGTGGTCTTCGTCGGC
AT2G43410	314	GGGCTGGCTCTTACGATAACAG	GATGGCCTCCTCCAGTTTGG
AT2G43640	383	CCTTTTACCAGAGAGACTCC	CCCTTCTCTTTGCTTTTCTC
AT2G43810	385	GGCTGCTTCATCGAGCGGAAG	GTTGAGCTTGACAACAACCTGG

AT2G46270	291	CTCATTTTCATTCTGTTTCTCC	CCTTAATCTTGACCTTCTAGC
AT2G46370	192	CCTTTTTTCTCTCTCTCTCTATCC	CCACAGTTTTGTAAAGTAAATGGC
AT2G46790	125	GGATTTGCCATCTATATCTGG	GCTTTGAGCATGAGCAGTAGG
AT2G46830	306	GGACTGAGGAAGAACATAATAG	GGTTTACGCTTAGGCCGTGG
AT2G47580	207	GGCGTTTAAGACCTTTAAGCACAAAGG	GGTTTTGGACAAAGAGAATATTATTGG
AT2G47890	325	CCACGGATGTTCTCTCTGCCC	CGAACCTTGCGTGATTCATACC
AT3G01090	342	CCGAATTTTCTCCTCCGCC	CCAATACCAAGAGTTCTCCC
AT3G01150	195	GGCCAAAGAAGCACTGGAAGG	GGGTTCTGCCAACCTGCTGGTGG
AT3G01150	196	CCATGAGATTGTTAACAATCAGAGTCC	CCAGCAGCTTTCTCAAATGTGGC
AT3G01540	283	CCAAGTACCACCACCTCTAATGTCC	CCTACCTTGCATAGCAATGGGCC
AT3G04030	139	GCACTGCAAATGCAAATAGAGG	GGCAGCTTCGATCCCAGCTG
AT3G06510	360	CTCTACCAATGGGTGATTCC	CCCGATTCACTGTATTCATC
AT3G07740	136	GGGAAGAAGTGCGAGCTTGG	GGTGAAATTGATGCCGCAG
AT3G07810	273	GCTAGAAGTTCATCTCCAGG	GGAAAAGAAGATAATCTAAAAG
AT3G08505	134	CTATCAGAGTTCCTTGGTGGCC	CATTGAGTTTCTCCTGTGTCC
AT3G10300	330	CTCCTTATGTATCTATTACC	CCGCTTCTGTCTTATCAAACC
AT3G10300	331	CTTCACTTTTCTTAGTCTTC	GGTAAACAGTGAGCATGAAG
AT3G10490	138	GGAATGGGCTGATGATGAAGG	GGTCCGATTGATATCCAGTGG
AT3G11540	307	GAGAAGGCTGCACTTGAGAGG	GAATCTGGATCTATCTTAAGG
AT3G12250	142	GGACAACCTTTTACTCAGACAGG	GGTATCAGCCATACTAGTTTCTG
AT3G12250	143	CCCTCTAGTGTGAACTCTGC	CCTTTGATCGATCACTGGAATC
AT3G12570	288	CCATGTGTTGTACTAGTGCC	CCATGGATAGCAGTGTGAC
AT3G12570	289	GGGATCATTTTGATAGGAGCG	GGTGATAGTTCTCCATAGACAGG
AT3G13224	373	GTTGGTGGTATACCCTCAACGG	GGGTGACTACCGTAAGAAGG
AT3G13570	202	GGAGGCCATTTGAGCAGTTTGG	GGTTTTCTTCAGCAAATACGACAG
AT3G14230	82	CCTTCGTCCTTACC GCAAC	CCAAGCCATTCTCGGGAGCC
AT3G14740	137	CCGGAAGTTTACTTTGAGGATCC	CAACAATCTTGTA CTTTCC
AT3G15030	140	GAAGAGGAGCAGCACGACGG	GGCCATTGACTACACAAACCG
AT3G16785	355	CTCTCTTTGTGGTCCGAACACC	CCCAAATCGATCGTTGTGTGCCC
AT3G16800	332	GAATATTCATATCAGAGAAG	GGCTATCACATGTCCCCATGG
AT3G16800	333	CCCGGTTCACTCTCGGTAGAC	CCTCTTACTATCTCCACTGCC
AT3G17090	259	GGGACTTTTGTTGGTGTTTACG	GGTATTTCTTGCCACAGCTCTG
AT3G17609	145	CCAACGACCCAATGGGAATC	CGTTTAGCTGTAGAGACTCC
AT3G19840	285	CCATATTCTGTTCTCATCC	CCAGGCATCTAACCGATTTC
AT3G20270	375	CTCAGGGATTACTTACTACC	CTCCGCGGAATAAATTAGCCC
AT3G23280	144	GCACAGTGATGCCTTTGTGG	GGCTGTCACCTTCAGTCGAAGG
AT3G23830	277	CCTCTTTTCTCACTCACTGTTAC	CCATTTGAGCTCTGAGAAACCCC
AT3G23900	272	GGATTATTCTTAAGTCATAGG	GGAGTGAAGGTGGTTCTTGG
AT3G24120	146	CCAAGTCACCGAAGCTCTAC	CCAGCAAAAGTAGCAGCTTGC
AT3G25840	279	GGAGAGATTTTAGAAGAAGATGGG	GTTAGACTGCCTGCTGTTTGACGG
AT3G26740	260	CCAATATTCTTCTCCTCTTCC	CCACTGATTACTTCGCATGC
AT3G26744	411	GGAGAAATAGTGACGGTGAG	GATCTTGTGGATGTGGTTGG
AT3G29160	343	CCTGACTCAGCTCTGCGTCACC	CCCAATTCCAAGAGTTTACC
AT3G29160	344	CCTGTTATTGGATAACCGTTCC	CCAAGAGCCCATTTTCGATCAAC
AT3G44300	297	GGTGATGTTTCGTATTGTCGG	GGTCAAGTGTA AACATCTGG
AT3G47550	151	CCTTCTTCGTGCTGCTGGTTTTC	CCTTAACGGAGAATCATTGCC
AT3G49430	194	CCTCCGAGTATTGTTGGCTTCAGACC	CCTAATGTCACCGGGCAAGTTACC
AT3G51530	377	CCGTCGTGCTATGTCTCTCTC	CCCATACTCCAACATAAACACC
AT3G51880	141	GGGAGTGATGAATCTGAAAAG	GGATCTGCAGTTAAGCTTGAG
AT3G53270	30	CCAACATCATCATCTTCTC	CCACA AACTCGTCTATCAGC

AT3G53500	204	GGAAACACTCGCCTCTATGTTGG	GCGTCATCAGCATCACGAGG
AT3G53570	225	CCGGCGATCAAATTACGACAGCGAC	CCGATGAGGGAATTCAACATTCC
AT3G54480	135	GGAGTTACATGAGATCTCAAAG	GATAAATCCTTGACAAAACGG
AT3G55460	220	CCCTTTGAGAGGTTTGGACC	CCTGTTTCATGCTTCTTTGAGCC
AT3G56860	356	CACTAAATGTATCATGTATCC	CGTTGAGAAGCTTGCAACCAC
AT3G58030	152	CCATCTCTATTCTGTAATTAGC	CCCAAGATTCAAATCCAGGTTT
AT3G59060	153	CCATCCCGGTTTAGTATGTC	CCTATTTTACCCATATGAAGACTGTC
AT3G61860	205	GGCAATTTGAGTATGAAACTCGCCAGTCGG	GGAAAATTGTCGAGTTTGCGAATAG
AT3G61860	97	GCGAATTAAGATAAAGATGAGG	GGAAAATTGTCGAGTTTGCG
AT3G62190	378	CCTGATGATCAGAAGCTTGTGGCC	CCGAGGAACCCAGTCTTGAC
AT4G01060	154	GGTGCCGTTTGACATGGATAACC	GTCACCGACAAGCTTATGCATT
AT4G01250	386	CCGGTAGCGTCACTAGCAAACCC	CTTGTTTACGGGCTAAACAACC
AT4G02200	384	GTGTCACCATATCGATGAGG	GACATCTCTATGCTGAGTGG
AT4G02430	210	CACATGCGTAAAGGAGGAGAAG	CCGAACATATTCATGAGAAAAC
AT4G02430	212	CCTGCAAAATCTACATCGAGATCTCC	CTGTCCTAGCTCGATGGGTCC
AT4G02560	66	CGCAAATTGATTTCGAGAGTC	CCACCATCTGTACTTTCTGTC
AT4G10100	261	CTCATGTGTGTGGTATTACC	CAGTGTTAGATCAGGCACACC
AT4G12790	36	GGTTTTGAGAGCAAAGAAAAACG	GGTTAACAACATGCATTGTTTCG
AT4G13020	339	GTAGATACTTGTCTTCAAGG	GGATGATTTAGCTTACGAAG
AT4G13850	361	CCTTAAGGGATGCTTTTGCTC	CCTCCTCTGTTTAGAAACCACC
AT4G14410	160	CCTTCTCTCGACGATGATTTTCG	CCAATACTAAAGACTTCATCTGG
AT4G16420	165	GCAGAACATGAAAGAAGAGTAC	GCTCAGCATCATTGTCATATTC
AT4G16845	86	GGATTGTTCTTGTCCATTTTG	GCAAGCTCTGTTGCCTCGGG
AT4G18020	167	CCGATCATTGCATCACTACTAC	CCTTATGAACAACATGCTGC
AT4G23260	346	GGGAAGTGTATCCCTTCTCTGG	GGAAAAGTTGCTTGTGCCCCG
AT4G24740	226	GGTGTGAAGAAATACCGTGAGG	GGAGACTAACAGAATATTTTCTGG
AT4G24740	227	CCTCATACTCACATGGATCGTCGTCC	CCATTTCTTCTCTCCCTATCCC
AT4G25500	219	GGTGACCTGGAACGACTATTCAGG	GCGGTCAAGTGCTCGGATGG
AT4G25990	166	GTTCCGAGAAAGTGGTATGAGAG	CGTAGACCACTTAAATTCCTTG
AT4G26070	362	CCTTCAAATCTGTAATCAATC	CCTGCGTCGGTGAAGTAAGCC
AT4G27050	155	GGTCTTTCTTTGTGAACAAC	GGGAAACTCCTTAGACAGCAG
AT4G27410	321	CGATCTCTACAAGTTCGATCC	CTTGTAATTCGACACAACACCC
AT4G28790	161	CCATGCTGGATGATGTTATAG	CCTAGGGAAAGGTATGAATGC
AT4G29810	412	GGATTGAGCAATAATCTCAAG	GCTCAGCTGATCATCAGCTGG
AT4G31120	315	CTCAACGAAAGTCAACAACC	CCAACCCAGTACGAACGGCC
AT4G31720	369	CGTCTCAGCTCAATTCTCTTCC	CTCTTAGCCAAGTAGTGCTCC
AT4G32660	228	GGGGTGCTGAGAAATATTTACAGG	GCTGTGAGACGCTCAGATGG
AT4G33060	284	GGAGAAGAAGCTGAAGAAGAGG	GAAAAGCTTTTATCTTTTGTAG
AT4G34000	365	GGTGCAAGTCTGGAGAAAGTG	GCATCCCATTCCCCATGGCTGG
AT4G34430	156	GGGCTTCCATTAAATCTCTTACAG	GGAGACCTCTTCTGCTTTTTTG
AT4G34460	347	CCAACCTCAGGTCTATCAGCC	CCTGTACACAAGGCACTTCC
AT4G34460	348	CGCCTCCAGCTCCTCGATACC	CTTGAGATGCACTGACAATCC
AT4G35450	87	CCACCACAACATTGTCTTTTC	CCAGCGTTAGGAATAGATCTC
AT4G35785	229	GGTGCATTAAATATCTCAACCAG	GGAGCTTTTCAAGCCAAGATAGTGG
AT4G36690	198	GGATGAGCTTAGAGATGATGAGG	GGCCTGCCACTGGCTGACCATTGG
AT4G36730	292	GATGAAAGTGTACAGCGGG	GGCTTCATGGGCACCGAACCTTGG
AT4G36960	374	GTTTAGGGCATCCTTGTGGG	GTAATCCTTAAGCCCCATCGG
AT4G37180	159	CGAGGATCAAAGACAATCATTCC	GGTTTTGCCCTTTCAACATC
AT4G38510	89	CCTCTACACAGATCTTTGATTTC	CTTGACCACGTGGGTAGTTCC
AT4G38900	157	GGGAACTCGGGTGCTGCTTTAG	GGTAGCCTCGGTCTGAAGAGTCTG

AT4G39260	90	GGTGCTTTGTGCGGCGCCTTG	GGCTTTCTCGTCCTTGAAGG
AT5G02470	187	CAGTTTGTTTGTGTTTATAG	CCAATTTCAGAATCATCATC
AT5G02840	188	GCTGTTGATGAGAAACCTCAC	GCTGGTAGAGAGTTGTTGCG
AT5G04275	379	GTTTGTTGTGTGTGAGACTTTGG	AGATGAGCTTTCTTCCATGG
AT5G04430	42	CCTTCGAGGAGCAGATGCGGGC	CCTCCAGAACC GTTGGGTGC
AT5G05550	181	GGAGAAGCAGAGAATGGAAG	GGATCCTCCAATTTCAATGAG
AT5G06160	222	GGAGCCACCGTCCAGCAAGG	GTCGCAGTCTGGCCACCAAGCGCTG
AT5G06960	176	CCACGTCTTTGCAGTTGTAG	CCATCTGTTGAGACTGATGTTT
AT5G08185	380	GTCCATTGGTTTCATAAGG	GCTTTCCAGAAAAGTAATCGG
AT5G09230	244	CATACAGTTCTGGTTTCAAACC	CCTGGTTGTGCTGCAGTGAACC
AT5G09230	43	CATCCGCCATTAACGACCTC	CTCACAACCGTCTGCATCC
AT5G09790	301	CCCATTGTTGTTGTCGTCCCC	CCGTTAATGCAGAAGCAAGTGTCC
AT5G09880	298	GGGATGTGCGATTGATCATGG	GGGCTTAACCATCACAGG
AT5G10140	308	GGAGGAACACCTTGAGACTG	GAGTCACCGGAAGATTGTCGG
AT5G11330	299	CCTCAGGCTCGGCAGATCATC	CCGAATCGAAGACAAACACCC
AT5G12840	186	GGATTGATGGGAGCATATGG	GGCACGTGCTTTTCTTCGCC
AT5G13220	174	CCCATCGCAAGGAGAAAGTC	CCAAATCCAAAACGAACATGG
AT5G13730	44	GGGTACCAAGGCAAAGTTTG	GCAATCTCTTCACAGCTTGG
AT5G13790	312	GGGTTACTTAAGAAAGCTCG	GTAGGATGGAACATAGTGGG
AT5G16820	182	GGAGAATAATGACTTGGTATTGG	GGTAAATCTTTTATGTTTCTTC
AT5G18240	168	CCCATAAGTGATGCCCTTCAAATG	CCCAGCTGCACCTAGGTTCTG
AT5G18620	171	CCATCAAACGACCTTCGGG	CCTTGTCTCTAAGGAGCTTC
AT5G18830	191	GGAGCCAGACAGTCTTGTTTAC	GGATCAGTCTCTTTTCCGCC
AT5G19030	274	GGTTTTCGGATTCAGTGAGTGAAGG	GGCTTCGACAGCCGACTGTG
AT5G19030	275	GGACTCGGCAGTCACTAGGATACGG	GGAAATCGGAATGTGGTCTCCGG
AT5G20040	262	CCGGAGTCTCTAAGAATGAGC	CCACGCATGAAGCTTCACTC
AT5G20250	47	CCATTCAAATCTCACATTCCC	CCCGTCGGAAATACGAACCGCC
AT5G22000	183	CCTGAAACAAACAATGAGCAC	CCTTCTTCTATGCTCCACAC
AT5G23090	184	GGAGAGAGAAAATCCCTCCG	GGAAGAGAAGCGTCTTCTTGG
AT5G23090	185	GGATCCAATGGATATAGTCG	GGAGCAATCGTCCGTTTATCC
AT5G23450	354	CTTTTGCTGATACACTTCTCTCC	CGTCTAAGCGACTGTTGTGCC
AT5G24270	363	GAGTTTGGTGAATTTGTCCGG	GGCAAAGTCATGTTCTTGATG
AT5G24520	169	GGTCTTCTTCGAGCCTGATTG	GGAGCGCAAACCAAACCTAC
AT5G24590	320	CCCTGAGGTTACAACCACC	CCACATCCTTTCGTATAGTTTCC
AT5G25610	366	CCTCTGATCTGTCTTCTTGGTTC	CCAACGTTACGCGCGTTC
AT5G28080	337	GTCAAGATTGGAGATCTTGG	GAGTCTAAGGGACACTGTGG
AT5G28770	170	GGTGTTCGCTCTCTCTCC	GGAAGAAGCAAGAGAGGCTTG
AT5G35410	370	CAGCAGAGTTTCTTGTCCACC	CCAAGGATCTTCTTGATTCC
AT5G35680	48	CCTAATCACTTCAACAACCTC	CCGTCAATGCACATAACGTC
AT5G37055	313	GGAAGAGATGTGGAACCGTCG	GCTGCTTTCAAGTAAGTCCG
AT5G37370	371	GGACGGATGACGACAATGGG	GGGCAGTGTCTTCTGAGCCACGGG
AT5G40280	349	CTTTAGGAGGTGACAAAGCCC	CCCTGGGTGAGTTCATCATCC
AT5G41150	49	CCATCCTGACATGGGTTTGTG	CCAGTTCCTTCTTCCGCTGC
AT5G43270	189	CCTCTGGGATCCATAAGTTTGTG	CCATCAATTTCCCACTCCATTG
AT5G43270	324	GGGATCCATAAGTTTGTGAG	GCTTGAAGAATACAGAGAGG
AT5G43910	50	GGTTGTGTGATGCTTGAGAG	GGTTGTGTCTATGAGTCCG
AT5G45510	51	GGAGAAAGTTGTTGTAGGAG	GGTGGAGGTACATCACTGTGG
AT5G46110	245	GGCGATCAACGGAGGAGAGAAAAG	GAAGAATCCAGTACTAGCCATGG
AT5G47210	281	CCAAAGTGTTGAGTCCATGCAAC	CCACCTCTCCCGTTGTACCTC
AT5G48150	179	CCTTGTCTCCGACAACCTTC	CCTAAGCTTCTCAACAGAGTTAG

AT5G48560	318	GGACGCTCTTGTGTCAAAGG	GTTGAGATTCATTGTTGGGG
AT5G50240	254	CCGCTACAATTCATCATCATC	CCTCTATCTAAAGCCTCCATAAC
AT5G53180	213	GGATGTTGTGGGAATGTTCTTCTGG	GGTATCCGGCTGTCTTCTCGAAAG
AT5G53450	381	GGGAAAGAATCAAACTTTTG	GGTTTCGTTTATAACCAATG
AT5G54430	233	GGTGGAGATGATGATGGAGATG	GGTGATATATTACTTAGATCCCACG
AT5G56370	190	GGGCAAAATGTCAAATTAGG	GGAAGCAATGACAGTATGCGC
AT5G57110	352	CTTACCGGAATTTTCTCTCC	CCCAGACTCCACATCGCTCC
AT5G57630	338	CAGATGCTAGAAAACTTTTCC	CCATACATCTACTGCTGCTCC
AT5G59440	246	GAAACGGATCTGCTCGGTTTCAAG	GGTCTGACACCAGAAGAAAAG
AT5G59780	177	GGACCGTGGACAGAACAGGAGG	GGCGTGAAGCTCAAGGACTAAAC
AT5G59950	327	CTGCTCCATACCAATCAGCC	CCACTTCTATCAAAATGAAC
AT5G60580	172	GGTACAGGTGCCATCGCTATATC	GGGCGAAGAGAACGACCAACGC
AT5G60670	64	GTCACCGGAGGTGAGGTCGG	GATGACTAGAGCCGCTGCGG
AT5G63120	282	GGTGACAAGACCCAATCGG	GGTTCGACCAATCCTATGG
AT5G63870	57	GGTCCAAGATCCAAGCTTTGG	GGGAAGGAGGTAGATTCCATG
AT5G63990	340	CGAGTTTCTTCGAGTCATACC	CTGCGTCGTAAACGACGATTCC
AT5G65050	58	CAAAGATCATTGATCGTTAC	CTTCACTTCCCCCATCATTAGTTC
AT5G65060	309	CAAGGAGTTACTAGAAATAGTCC	CCCGTGACATTCTCTGTCAACC
AT5G65070	310	CCGTCGCTCTTATCATCATCTC	CCGGTGACATTGCTCTTGCATCC
AT5G65080	311	GTCAACTCTCAATTCTCTGTGG	GTGGCCAGAGCTATTTTCCGG
AT5G65430	264	CCGATCAGGCTTGGTTTGGC	CCGTCTTTTCTTCCATTAGACC
AT5G65640	319	CCTCTGGTCAGAACTCACC	CATTGTTCAATCTCCAAGCC
AT5G66010	59	GGCGGCAGGTCATGTACGG	GGGAAGACCCCTGAGGCGAACG
AT5G66210	335	CAAAGACGGGTACATAACGCC	CCTCTTGCATCTAGTGCACC
AT5G67030	364	CCATCGATGCTTGACTGGGTCC	CCGAAACGCAACAATCGTCGCC
AT5G67580	178	GCGAATCACATTTGATCTATG	GCTTAAGAACTCCAGCTTTAAG

Table S3. Primer sequences used in the HR RT-PCR panel.

Table S4. Validation of the putative assembled transcripts.						
GENE_ID	PRIMER_ID	SIZE	TAIR9	AS PANEL	RNA_SEQ	SANGER_SEQ
AT1G01060	305	161	1	1	1	NA
AT1G01060	305	232	NA	1	NA	NA
AT1G01060	305	331	1	1	NA	NA
AT1G02090	241	119	1	1	1	NA
AT1G02090	241	138	1	1	1	NA
AT1G02840	1	421	1	1	NA	NA
AT1G02840	1	490	NA	1	NA	NA
AT1G02840	1	503	NA	1	1	NA
AT1G03457	268	109	NA	1	NA	NA
AT1G03457	268	148	1	1	1	NA
AT1G03457	268	158	NA	1	NA	NA
AT1G03457	268	175	1	1	1	NA
AT1G03457	268	287	NA	1	1	NA
AT1G04400	2	262	1	1	1	NA
AT1G04400	2	329	NA	1	1	NA
AT1G04950	236	134	NA	1	NA	NA
AT1G04950	236	152	1	1	1	NA
AT1G04950	236	267	1	1	NA	NA
AT1G04950	236	282	NA	1	NA	NA
AT1G04950	236	295	NA	1	NA	NA
AT1G04950	236	376	1	1	1	NA
AT1G07350	193	200	1	1	1	NA
AT1G07350	193	279	NA	1	NA	NA
AT1G07350	193	282	NA	1	NA	NA
AT1G07350	193	294	NA	1	NA	SANGER_SEQ
AT1G07350	193	297	1	1	1	SANGER_SEQ
AT1G07350	193	443	NA	1	1	NA
AT1G07350	193	452	NA	1	NA	NA
AT1G07830	237	121	NA	1	1	NA
AT1G07830	237	193	1	1	1	NA
AT1G07830	237	273	NA	1	NA	NA
AT1G07830	237	350	NA	1	NA	NA
AT1G09000	358	189	NA	1	NA	NA
AT1G09000	358	242	NA	1	NA	NA
AT1G09000	358	316	1	1	1	NA
AT1G09140	3	101	1	1	1	NA
AT1G09140	3	445	1	1	1	NA
AT1G09230	208	120	NA	1	1	NA
AT1G09230	208	128	1	1	1	NA
AT1G09230	208	139	NA	1	NA	NA
AT1G09530	112	230	1	1	1	NA
AT1G09530	112	291	1	1	1	NA
AT1G11650	203	135	NA	1	NA	NA
AT1G11650	203	420	NA	NA	1	NA
AT1G11650	203	532	2	1	1	NA
AT1G15200	224	130	1	1	1	NA
AT1G15200	224	148	NA	NA	NA	NA
AT1G15200	224	217	NA	1	NA	NA
AT1G15200	224	225	NA	1	NA	NA
AT1G15200	224	236	NA	1	1	NA
AT1G15200	224	274	NA	NA	NA	NA
AT1G15200	224	313	NA	1	1	NA
AT1G16610	217	154	1	1	1	NA
AT1G16610	217	169	NA	1	NA	NA
AT1G16610	217	175	1	1	1	NA
AT1G18660	116	322	1	1	1	NA
AT1G18660	116	338	NA	1	1	NA
AT1G18660	116	416	NA	NA	1	NA
AT1G23970	68	175	1	1	1	NA
AT1G23970	68	190	1	1	1	NA
AT1G27370	102	163	1	1	1	NA
AT1G27370	102	191	1	1	1	NA
AT1G27770	353	144	1	1	NA	NA
AT1G27770	353	365	1	1	1	NA

AT1G27770	353	440	NA	1	NA	NA
AT1G27770	353	446	NA	1	NA	NA
AT1G30200	108	248	1	1	1	NA
AT1G30200	108	259	1	1	1	NA
AT1G30200	108	600	NA	NA	1	NA
AT1G30500	103	274	1	1	1	NA
AT1G30500	103	288	1	1	1	SANGER_SEQ
AT1G31500	239	119	2	1	1	NA
AT1G31500	239	134	1	1	1	NA
AT1G31500	239	149	NA	1	NA	NA
AT1G31600	214	163	1	1	NA	NA
AT1G31600	214	170	1	1	1	NA
AT1G31600	214	645	NA	1	NA	NA
AT1G31600	215	135	1	1	1	NA
AT1G31600	215	142	1	1	1	NA
AT1G33060	105	271	1	1	1	NA
AT1G33060	105	283	1	1	1	NA
AT1G37150	251	106	1	1	1	NA
AT1G37150	251	135	1	1	1	NA
AT1G37150	251	220	NA	1	1	NA
AT1G44910	382	216	1	1	1	NA
AT1G44910	382	221	NA	1	NA	NA
AT1G44910	382	250	NA	1	NA	NA
AT1G44910	382	282	NA	1	NA	NA
AT1G44910	382	301	NA	1	NA	NA
AT1G48960	232	175	1	1	1	NA
AT1G48960	232	209	NA	1	NA	NA
AT1G48960	232	263	NA	1	1	NA
AT1G49730	345	237	1	1	1	SANGER_SEQ
AT1G49730	345	274	NA	1	1	NA
AT1G49730	345	342	1	1	1	NA
AT1G49950	106	191	1	1	1	SANGER_SEQ
AT1G49950	106	236	NA	1	1	NA
AT1G49950	106	285	NA	NA	1	NA
AT1G49950	106	311	NA	1	1	NA
AT1G49950	106	400	NA	1	1	NA
AT1G52500	6	171	1	1	1	NA
AT1G52500	6	188	NA	1	NA	NA
AT1G52500	6	329	1	NA	1	NA
AT1G52500	6	456	NA	1	NA	NA
AT1G53650	270	176	1	1	1	NA
AT1G53650	270	195	1	1	1	NA
AT1G54080	256	184	NA	1	NA	NA
AT1G54080	256	247	1	1	1	NA
AT1G54080	256	259	1	1	1	NA
AT1G54080	256	582	NA	1	NA	NA
AT1G54100	357	245	1	1	1	NA
AT1G54100	357	353	NA	1	1	NA
AT1G54360	70	129	1	1	1	NA
AT1G54360	70	152	1	1	1	NA
AT1G54360	70	231	NA	1	1	NA
AT1G55310	7	199	1	1	1	SANGER_SEQ
AT1G55310	7	235	NA	NA	NA	NA
AT1G55310	7	244	NA	1	NA	NA
AT1G55310	7	252	NA	1	NA	NA
AT1G55310	7	288	NA	1	NA	NA
AT1G55310	7	293	NA	1	NA	NA
AT1G55310	7	361	NA	1	1	SANGER_SEQ
AT1G55310	7	364	NA	1	NA	SANGER_SEQ
AT1G55310	7	523	NA	1	1	NA
AT1G55870	234	151	NA	1	NA	NA
AT1G55870	234	171	1	1	1	NA
AT1G59750	107	171	NA	1	1	NA
AT1G59750	107	176	1	1	1	NA
AT1G59750	107	185	1	1	1	NA
AT1G60850	242	107	1	1	1	NA
AT1G60850	242	118	1	1	1	NA

AT1G60850	242	150	NA	1	NA	NA
AT1G60850	242	227	1	1	1	NA
AT1G61660	111	177	1	1	1	SANGER_SEQ
AT1G61660	111	186	NA	1	1	SANGER_SEQ
AT1G61660	111	195	NA	1	NA	NA
AT1G61660	111	230	NA	1	NA	NA
AT1G64625	376	111	NA	1	NA	NA
AT1G64625	376	135	NA	1	NA	NA
AT1G64625	376	141	NA	1	NA	NA
AT1G64625	376	155	1	1	1	NA
AT1G64625	376	168	NA	NA	1	NA
AT1G64625	376	185	1	1	NA	NA
AT1G67210	286	175	1	1	NA	NA
AT1G67210	286	180	1	1	1	NA
AT1G67210	286	269	NA	1	1	NA
AT1G67980	296	145	1	1	1	NA
AT1G67980	296	157	NA	1	NA	NA
AT1G69080	235	163	1	1	1	NA
AT1G69080	235	195	NA	1	1	NA
AT1G69080	235	205	1	1	1	NA
AT1G69250	326	147	1	1	1	NA
AT1G69250	326	246	1	1	1	NA
AT1G71860	367	172	NA	1	NA	NA
AT1G71860	367	274	NA	1	NA	NA
AT1G71860	367	284	2	1	1	NA
AT1G71860	367	288	1	1	1	SANGER_SEQ
AT1G71860	367	363	NA	1	NA	SANGER_SEQ
AT1G71860	367	375	NA	1	NA	SANGER_SEQ
AT1G72050	110	207	1	1	1	NA
AT1G72050	110	380	1	1	2	NA
AT1G72320	12	141	1	1	1	NA
AT1G72320	12	150	1	1	1	NA
AT1G72320	12	215	1	1	1	SANGER_SEQ
AT1G72560	249	138	1	1	1	NA
AT1G72560	249	148	1	1	1	NA
AT1G72560	249	174	NA	1	NA	NA
AT1G72650	113	183	1	1	1	NA
AT1G72650	113	194	NA	NA	1	NA
AT1G72650	113	201	1	1	1	NA
AT1G72650	113	354	NA	1	1	NA
AT1G76460	372	259	1	1	1	NA
AT1G76460	372	268	NA	1	NA	NA
AT1G76460	372	314	NA	1	NA	NA
AT1G76460	372	483	NA	1	NA	NA
AT1G76510	148	190	1	1	1	NA
AT1G76510	148	212	1	1	1	NA
AT1G76580	323	156	NA	1	1	NA
AT1G76580	323	199	1	1	1	NA
AT1G76580	323	291	NA	1	1	NA
AT1G77080	109	118	NA	1	1	SANGER_SEQ
AT1G77080	109	158	1	1	1	SANGER_SEQ
AT1G77080	109	239	1	1	1	NA
AT1G77740	350	282	1	1	1	NA
AT1G79650	13	156	1	1	NA	NA
AT1G79650	13	174	1	1	1	SANGER_SEQ
AT1G79650	13	182	NA	1	NA	SANGER_SEQ
AT1G79880	199	131	NA	1	NA	NA
AT1G79880	199	136	1	NA	1	NA
AT1G79880	199	169	1	1	NA	NA
AT1G79880	200	104	1	1	1	NA
AT1G79880	200	122	1	1	1	NA
AT2G02390	295	181	1	1	1	NA
AT2G02390	295	202	1	1	1	NA
AT2G02390	295	368	NA	1	NA	NA
AT2G02570	278	153	1	1	1	NA
AT2G02570	278	221	NA	1	NA	NA
AT2G02570	278	310	NA	1	1	NA

AT2G02960	118	197	1	1	1	NA
AT2G02960	118	200	1	1	2	NA
AT2G02960	118	222	1	1	1	NA
AT2G02960	118	233	NA	1	1	NA
AT2G02960	118	237	NA	1	NA	NA
AT2G02960	118	240	NA	1	NA	NA
AT2G02960	118	289	NA	1	1	SANGER_SEQ
AT2G02960	118	449	1	1	1	NA
AT2G04790	72	167	1	1	1	NA
AT2G04790	72	190	1	1	1	NA
AT2G04790	72	252	NA	1	NA	NA
AT2G04790	72	294	NA	1	1	NA
AT2G15530	128	223	1	1	1	SANGER_SEQ
AT2G15530	128	242	NA	1	1	SANGER_SEQ
AT2G15530	128	251	1	1	1	NA
AT2G15530	128	363	NA	1	1	SANGER_SEQ
AT2G15530	128	381	1	1	1	SANGER_SEQ
AT2G15530	128	389	NA	1	1	SANGER_SEQ
AT2G15970	341	239	1	1	1	NA
AT2G15970	341	322	NA	1	NA	NA
AT2G15970	341	326	NA	1	NA	NA
AT2G16940	209	136	NA	1	NA	NA
AT2G16940	209	144	1	1	NA	NA
AT2G16940	209	209	NA	1	NA	NA
AT2G16940	209	227	NA	1	NA	NA
AT2G16940	209	289	NA	NA	NA	NA
AT2G16940	209	418	NA	1	NA	NA
AT2G16940	209	423	NA	1	NA	NA
AT2G16940	209	445	NA	1	NA	NA
AT2G16940	209	543	NA	NA	1	NA
AT2G18300	121	222	1	1	1	NA
AT2G18300	121	228	1	1	1	NA
AT2G18960	351	118	1	1	1	NA
AT2G18960	351	215	NA	1	NA	NA
AT2G21620	73	199	1	1	1	NA
AT2G21620	73	216	1	1	NA	NA
AT2G21620	73	307	NA	1	1	NA
AT2G21660	206	181	1	1	1	SANGER_SEQ
AT2G21660	206	349	NA	1	1	NA
AT2G22670	117	282	1	1	1	NA
AT2G22670	117	288	1	1	1	NA
AT2G26150	393	212	NA	1	NA	NA
AT2G26150	393	531	1	1	1	NA
AT2G26150	393	558	1	NA	1	SANGER_SEQ
AT2G26150	393	565	NA	1	NA	NA
AT2G26150	393	646	NA	1	NA	NA
AT2G28550	316	262	1	1	NA	NA
AT2G28550	316	332	NA	1	1	NA
AT2G28550	317	266	1	1	1	NA
AT2G28550	317	338	1	1	NA	NA
AT2G28550	317	341	NA	1	NA	NA
AT2G29210	223	151	1	1	1	NA
AT2G29210	223	202	NA	1	1	NA
AT2G30260	218	134	NA	1	NA	SANGER_SEQ
AT2G30260	218	171	1	1	1	SANGER_SEQ
AT2G31370	132	187	NA	1	NA	NA
AT2G31370	132	193	1	1	1	SANGER_SEQ
AT2G31370	132	204	1	1	NA	NA
AT2G31370	132	213	NA	1	NA	NA
AT2G31370	132	233	NA	1	NA	NA
AT2G31370	132	236	NA	1	NA	NA
AT2G31370	132	239	NA	1	NA	NA
AT2G31370	132	320	NA	1	1	NA
AT2G32250	133	178	1	1	1	NA
AT2G32250	133	184	1	1	1	NA
AT2G32250	133	307	NA	1	NA	NA
AT2G32250	133	341	NA	1	1	NA

AT2G32250	133	347	NA	1	NA	NA
AT2G32250	133	469	NA	1	1	NA
AT2G32320	19	202	NA	1	1	NA
AT2G32320	19	273	1	1	1	NA
AT2G32320	19	308	NA	1	1	NA
AT2G33120	413	124	NA	1	NA	NA
AT2G33120	413	155	NA	1	NA	NA
AT2G33120	413	164	1	1	1	NA
AT2G33120	413	188	1	1	NA	NA
AT2G33480	322	321	NA	1	1	SANGER_SEQ
AT2G33480	322	394	1	1	1	SANGER_SEQ
AT2G33480	322	399	1	1	1	SANGER_SEQ
AT2G33480	322	488	NA	1	1	NA
AT2G33830	243	140	NA	1	NA	NA
AT2G33830	243	147	2	1	1	NA
AT2G36000	75	151	1	1	1	NA
AT2G36000	75	255	1	1	1	SANGER_SEQ
AT2G36010	122	270	1	1	NA	SANGER_SEQ
AT2G36010	122	275	1	1	1	NA
AT2G37060	124	140	NA	1	NA	NA
AT2G37060	124	230	1	1	1	NA
AT2G37060	124	251	1	1	1	NA
AT2G37060	124	255	1	1	1	NA
AT2G37060	124	403	NA	NA	1	NA
AT2G37340	21	121	1	1	1	NA
AT2G37340	21	263	1	1	NA	NA
AT2G37340	21	341	1	1	NA	NA
AT2G37340	21	481	NA	1	NA	NA
AT2G38170	359	259	1	1	1	NA
AT2G38170	359	364	1	1	NA	NA
AT2G38170	359	368	NA	1	NA	NA
AT2G38185	130	172	1	1	1	NA
AT2G38185	130	195	1	1	1	NA
AT2G38880	131	312	1	1	1	SANGER_SEQ
AT2G38880	131	373	1	1	1	SANGER_SEQ
AT2G38880	131	377	NA	1	1	SANGER_SEQ
AT2G38880	131	443	NA	NA	NA	NA
AT2G38880	131	460	1	NA	NA	NA
AT2G38880	131	462	1	NA	NA	NA
AT2G39730	23	247	1	1	1	NA
AT2G39730	23	258	1	1	1	NA
AT2G39730	23	374	1	NA	NA	NA
AT2G40830	129	218	1	1	1	SANGER_SEQ
AT2G40830	129	230	1	1	NA	SANGER_SEQ
AT2G40830	129	329	1	1	NA	SANGER_SEQ
AT2G40830	129	363	NA	1	NA	NA
AT2G41710	120	230	1	1	1	NA
AT2G41710	120	245	1	1	1	NA
AT2G42240	267	165	1	1	1	NA
AT2G42240	267	174	1	1	1	SANGER_SEQ
AT2G42240	267	264	1	1	NA	NA
AT2G42890	216	147	1	1	1	NA
AT2G42890	216	176	NA	1	NA	NA
AT2G43010	127	213	1	1	1	NA
AT2G43010	127	219	1	1	1	NA
AT2G43010	127	358	NA	1	1	NA
AT2G43410	314	406	1	1	1	NA
AT2G43410	314	540	1	1	1	NA
AT2G43640	383	114	NA	1	NA	NA
AT2G43640	383	143	NA	1	NA	NA
AT2G43640	383	169	1	1	1	NA
AT2G43640	383	187	NA	1	1	NA
AT2G43640	383	215	1	1	1	NA
AT2G43640	383	377	NA	NA	1	NA
AT2G43810	385	119	NA	1	NA	NA
AT2G43810	385	160	NA	1	NA	NA
AT2G43810	385	167	NA	1	NA	NA

AT2G43810	385	177	1	1	1	NA
AT2G43810	385	213	NA	1	NA	NA
AT2G43810	385	237	1	1	NA	NA
AT2G43810	385	256	NA	1	NA	NA
AT2G43810	385	264	NA	1	NA	NA
AT2G46270	291	154	1	1	1	NA
AT2G46270	291	222	1	1	1	NA
AT2G46370	192	200	1	1	1	NA
AT2G46370	192	284	1	1	NA	NA
AT2G46370	192	598	NA	NA	NA	NA
AT2G46790	125	163	NA	1	NA	NA
AT2G46790	125	243	1	1	1	SANGER_SEQ
AT2G46790	125	251	1	1	1	SANGER_SEQ
AT2G46830	306	218	1	1	1	NA
AT2G46830	306	593	NA	1	NA	NA
AT2G47580	207	172	NA	1	NA	NA
AT2G47580	207	390	NA	1	NA	NA
AT2G47580	207	395	1	NA	1	NA
AT2G47890	325	497	1	1	1	NA
AT2G47890	325	575	NA	1	1	NA
AT2G47890	325	582	1	NA	NA	NA
AT3G01090	342	117	1	1	1	NA
AT3G01090	342	135	NA	1	NA	NA
AT3G01090	342	222	1	1	1	NA
AT3G01090	342	444	1	NA	NA	NA
AT3G01090	342	449	NA	1	NA	NA
AT3G01150	195	156	NA	1	NA	SANGER_SEQ
AT3G01150	195	203	1	1	1	SANGER_SEQ
AT3G01150	196	165	1	1	1	SANGER_SEQ
AT3G01150	196	268	NA	1	1	SANGER_SEQ
AT3G01540	283	135	1	1	1	NA
AT3G01540	283	349	NA	1	NA	NA
AT3G01540	283	387	NA	1	1	NA
AT3G01540	283	480	NA	1	NA	NA
AT3G04030	139	145	NA	1	NA	NA
AT3G04030	139	151	1	1	1	SANGER_SEQ
AT3G04030	139	164	NA	1	NA	NA
AT3G04030	139	170	1	1	1	SANGER_SEQ
AT3G04030	139	462	NA	1	NA	NA
AT3G06510	360	256	NA	1	NA	NA
AT3G06510	360	307	NA	1	NA	SANGER_SEQ
AT3G06510	360	314	1	1	1	SANGER_SEQ
AT3G06510	360	343	NA	1	NA	NA
AT3G06510	360	415	1	1	1	SANGER_SEQ
AT3G07740	136	136	1	1	1	SANGER_SEQ
AT3G07740	136	149	NA	1	1	NA
AT3G07740	136	240	NA	1	NA	SANGER_SEQ
AT3G07810	273	124	1	1	NA	NA
AT3G07810	273	173	1	1	1	NA
AT3G08505	134	197	1	1	NA	NA
AT3G08505	134	205	1	1	1	NA
AT3G10300	330	118	NA	1	NA	NA
AT3G10300	330	122	1	1	1	SANGER_SEQ
AT3G10300	330	128	NA	NA	NA	NA
AT3G10300	330	175	NA	1	NA	NA
AT3G10300	331	123	NA	1	NA	NA
AT3G10300	331	309	1	NA	NA	NA
AT3G10300	331	316	1	1	1	NA
AT3G10300	331	407	NA	NA	NA	NA
AT3G10300	331	439	NA	1	NA	NA
AT3G10300	331	529	1	1	NA	NA
AT3G10490	138	172	NA	1	1	NA
AT3G10490	138	181	1	1	1	SANGER_SEQ
AT3G10490	138	225	1	1	NA	NA
AT3G11540	307	116	1	1	NA	NA
AT3G11540	307	618	NA	1	NA	NA
AT3G12250	142	160	1	1	1	SANGER_SEQ

AT3G12250	142	203	1	1	NA	NA
AT3G12250	142	234	1	1	1	SANGER_SEQ
AT3G12250	143	220	1	1	1	SANGER_SEQ
AT3G12250	143	329	1	1	1	NA
AT3G12570	288	159	1	1	NA	NA
AT3G12570	288	175	NA	1	NA	NA
AT3G12570	288	189	1	1	1	NA
AT3G12570	288	279	1	1	1	NA
AT3G12570	289	141	1	1	1	SANGER_SEQ
AT3G12570	289	172	NA	1	NA	NA
AT3G12570	289	230	1	1	NA	SANGER_SEQ
AT3G12570	289	259	1	1	1	SANGER_SEQ
AT3G12570	289	351	1	1	1	SANGER_SEQ
AT3G12570	289	587	NA	1	NA	NA
AT3G13224	373	267	1	1	1	NA
AT3G13224	373	494	1	1	1	NA
AT3G13570	202	189	1	1	1	NA
AT3G13570	202	350	NA	1	NA	NA
AT3G13570	202	513	NA	NA	1	NA
AT3G14230	82	213	NA	1	NA	NA
AT3G14230	82	216	2	1	2	NA
AT3G14230	82	228	1	1	NA	NA
AT3G14740	137	288	1	1	1	SANGER_SEQ
AT3G14740	137	294	1	1	1	SANGER_SEQ
AT3G14740	137	384	NA	1	1	NA
AT3G15030	140	169	1	1	NA	NA
AT3G15030	140	180	1	1	1	NA
AT3G16785	355	225	NA	1	NA	NA
AT3G16785	355	234	1	1	NA	NA
AT3G16785	355	313	NA	1	NA	NA
AT3G16785	355	464	NA	NA	1	NA
AT3G16785	355	547	NA	1	1	NA
AT3G16800	332	327	NA	1	NA	NA
AT3G16800	332	367	1	1	1	NA
AT3G16800	332	385	1	1	1	NA
AT3G16800	332	399	NA	1	NA	NA
AT3G16800	333	313	1	1	1	NA
AT3G16800	333	408	1	1	NA	SANGER_SEQ
AT3G17090	259	197	1	1	1	SANGER_SEQ
AT3G17090	259	214	NA	1	NA	NA
AT3G17090	259	252	NA	1	NA	NA
AT3G17090	259	263	NA	1	NA	NA
AT3G17090	259	386	NA	1	NA	NA
AT3G17609	145	147	NA	1	NA	SANGER_SEQ
AT3G17609	145	151	2	1	2	SANGER_SEQ
AT3G17609	145	187	NA	1	NA	SANGER_SEQ
AT3G17609	145	193	1	1	1	SANGER_SEQ
AT3G17609	145	266	1	1	1	NA
AT3G19840	285	162	1	NA	NA	NA
AT3G19840	285	172	NA	1	1	NA
AT3G19840	285	207	NA	1	1	SANGER_SEQ
AT3G20270	375	195	1	1	1	NA
AT3G20270	375	217	NA	1	1	NA
AT3G20270	375	247	NA	1	1	NA
AT3G20270	375	265	NA	NA	1	NA
AT3G20270	375	475	NA	NA	1	NA
AT3G20270	375	625	NA	NA	1	NA
AT3G23280	144	128	NA	1	NA	NA
AT3G23280	144	132	1	1	1	NA
AT3G23280	144	201	1	1	1	SANGER_SEQ
AT3G23280	144	286	NA	1	NA	NA
AT3G23830	277	131	1	1	1	NA
AT3G23830	277	145	1	1	1	NA
AT3G23900	272	118	NA	1	1	NA
AT3G23900	272	125	1	1	1	NA
AT3G24120	146	170	1	1	1	NA
AT3G24120	146	179	1	1	NA	NA

AT3G25840	279	283	1	1	1	NA
AT3G25840	279	341	1	1	1	NA
AT3G25840	279	463	NA	NA	1	NA
AT3G25840	279	503	NA	1	1	NA
AT3G25840	279	623	NA	NA	1	NA
AT3G26740	260	207	1	1	1	NA
AT3G26740	260	290	NA	1	NA	NA
AT3G26744	411	294	1	1	NA	NA
AT3G26744	411	345	1	1	1	NA
AT3G26744	411	592	NA	NA	1	NA
AT3G29160	343	159	1	1	1	NA
AT3G29160	343	167	NA	1	1	NA
AT3G29160	343	188	NA	1	1	NA
AT3G29160	343	308	1	1	1	NA
AT3G29160	344	195	1	1	1	SANGER_SEQ
AT3G29160	344	200	1	1	1	SANGER_SEQ
AT3G44300	297	285	1	1	1	NA
AT3G47550	151	228	NA	1	NA	NA
AT3G47550	151	233	1	1	1	NA
AT3G47550	151	237	1	1	1	SANGER_SEQ
AT3G49430	194	141	1	1	1	NA
AT3G49430	194	366	NA	1	1	NA
AT3G49430	194	386	NA	NA	NA	NA
AT3G49430	194	535	NA	NA	1	NA
AT3G49430	194	544	NA	1	NA	NA
AT3G51530	377	442	NA	1	1	NA
AT3G51530	377	450	1	1	1	NA
AT3G51530	377	538	NA	1	1	NA
AT3G51880	141	153	NA	NA	1	NA
AT3G51880	141	202	1	1	1	SANGER_SEQ
AT3G51880	141	223	1	1	1	NA
AT3G53270	30	109	NA	1	1	NA
AT3G53270	30	212	1	1	NA	NA
AT3G53270	30	264	1	1	1	NA
AT3G53270	30	270	1	1	1	NA
AT3G53270	30	277	NA	1	NA	NA
AT3G53270	30	360	1	1	1	NA
AT3G53270	30	368	1	1	1	NA
AT3G53270	30	588	NA	NA	1	NA
AT3G53270	30	595	NA	1	NA	NA
AT3G53500	204	155	1	1	1	NA
AT3G53500	204	272	NA	1	NA	NA
AT3G53500	204	373	1	1	NA	NA
AT3G53500	204	414	NA	1	NA	NA
AT3G53500	204	493	NA	1	1	NA
AT3G53500	204	643	NA	NA	1	NA
AT3G53570	225	138	1	1	NA	NA
AT3G53570	225	179	1	1	1	NA
AT3G53570	225	300	NA	1	NA	NA
AT3G53570	225	388	1	1	1	NA
AT3G54480	135	227	NA	1	NA	NA
AT3G54480	135	258	1	1	1	SANGER_SEQ
AT3G55460	220	135	1	1	1	SANGER_SEQ
AT3G55460	220	590	NA	1	NA	NA
AT3G56860	356	330	NA	1	NA	NA
AT3G58030	152	246	1	1	1	NA
AT3G58030	152	252	1	1	1	SANGER_SEQ
AT3G59060	153	232	1	1	1	NA
AT3G59060	153	238	1	1	1	NA
AT3G61860	205	158	1	1	1	SANGER_SEQ
AT3G61860	205	556	NA	1	NA	NA
AT3G61860	97	192	1	1	1	SANGER_SEQ
AT3G61860	97	590	NA	1	NA	NA
AT3G62190	378	143	1	1	1	NA
AT3G62190	378	218	NA	1	1	NA
AT3G62190	378	335	NA	1	1	NA
AT4G01060	154	160	1	1	NA	SANGER_SEQ

AT4G01060	154	163	1	1	1	SANGER_SEQ
AT4G01060	154	169	NA	1	1	SANGER_SEQ
AT4G01060	154	266	NA	1	1	NA
AT4G01250	386	200	NA	NA	1	NA
AT4G01250	386	213	1	1	1	SANGER_SEQ
AT4G01250	386	397	NA	1	NA	NA
AT4G01250	386	423	NA	1	1	NA
AT4G02200	384	110	NA	1	NA	NA
AT4G02200	384	115	1	1	1	SANGER_SEQ
AT4G02200	384	134	NA	1	NA	NA
AT4G02200	384	149	NA	1	NA	SANGER_SEQ
AT4G02200	384	160	1	NA	NA	NA
AT4G02430	210	153	1	1	NA	NA
AT4G02430	210	162	1	1	1	NA
AT4G02430	212	131	NA	1	1	NA
AT4G02430	212	143	1	1	1	NA
AT4G02430	212	295	NA	1	NA	NA
AT4G02430	212	332	NA	1	NA	NA
AT4G02430	212	389	NA	1	NA	NA
AT4G02430	212	531	NA	NA	1	NA
AT4G02560	66	239	1	1	NA	NA
AT4G02560	66	314	NA	1	1	NA
AT4G10100	261	242	NA	1	NA	NA
AT4G10100	261	253	1	1	1	SANGER_SEQ
AT4G10100	261	269	NA	1	1	SANGER_SEQ
AT4G10100	261	287	1	NA	1	SANGER_SEQ
AT4G10100	261	425	NA	1	NA	NA
AT4G12790	36	168	NA	1	NA	NA
AT4G12790	36	170	1	1	NA	NA
AT4G12790	36	183	2	1	1	NA
AT4G12790	36	212	1	1	1	NA
AT4G12790	36	261	NA	1	1	NA
AT4G12790	36	341	1	1	1	NA
AT4G12790	36	494	NA	1	1	NA
AT4G13020	339	267	1	1	1	NA
AT4G13020	339	294	NA	NA	NA	NA
AT4G13020	339	359	1	1	NA	NA
AT4G13850	361	243	NA	1	1	NA
AT4G13850	361	252	1	1	1	NA
AT4G13850	361	262	NA	NA	1	NA
AT4G13850	361	273	NA	NA	1	NA
AT4G13850	361	276	NA	NA	1	NA
AT4G13850	361	297	1	NA	NA	NA
AT4G13850	361	324	1	NA	NA	NA
AT4G13850	361	341	1	1	1	NA
AT4G14410	160	182	1	1	1	NA
AT4G14410	160	341	1	1	1	NA
AT4G14410	160	505	NA	NA	1	NA
AT4G16420	165	183	1	1	1	NA
AT4G16420	165	195	1	1	1	NA
AT4G16420	165	448	NA	1	1	NA
AT4G16845	86	374	1	1	1	NA
AT4G16845	86	396	1	1	1	NA
AT4G18020	167	105	NA	1	NA	NA
AT4G18020	167	115	1	1	1	NA
AT4G23260	346	245	NA	1	NA	NA
AT4G23260	346	254	NA	NA	NA	NA
AT4G23260	346	285	1	1	1	NA
AT4G23260	346	317	NA	1	NA	NA
AT4G23260	346	401	NA	1	1	NA
AT4G24740	226	143	NA	1	1	SANGER_SEQ
AT4G24740	226	309	1	1	1	SANGER_SEQ
AT4G24740	226	407	NA	NA	1	NA
AT4G24740	226	418	NA	1	1	SANGER_SEQ
AT4G24740	226	460	NA	1	1	NA
AT4G24740	226	516	NA	NA	1	SANGER_SEQ
AT4G24740	227	152	1	1	1	NA

AT4G24740	227	278	NA	NA	1	NA
AT4G24740	227	343	1	1	1	NA
AT4G24740	227	525	NA	1	1	NA
AT4G25500	219	124	1	1	1	NA
AT4G25500	219	382	1	1	1	NA
AT4G25500	219	422	NA	1	NA	NA
AT4G25500	219	582	NA	NA	1	NA
AT4G25500	219	628	NA	1	NA	NA
AT4G25990	166	174	1	1	1	SANGER_SEQ
AT4G25990	166	220	1	1	1	SANGER_SEQ
AT4G26070	362	459	1	1	1	NA
AT4G26070	362	548	NA	1	NA	NA
AT4G26070	362	637	1	NA	NA	NA
AT4G27050	155	178	NA	1	1	SANGER_SEQ
AT4G27050	155	187	1	1	1	NA
AT4G27050	155	226	1	1	NA	NA
AT4G27050	155	233	NA	1	1	NA
AT4G27050	155	344	NA	1	1	NA
AT4G27050	155	352	1	1	1	NA
AT4G27050	155	434	NA	1	1	NA
AT4G27410	321	336	1	1	1	SANGER_SEQ
AT4G27410	321	348	NA	1	NA	NA
AT4G27410	321	388	1	NA	NA	NA
AT4G27410	321	418	NA	1	NA	NA
AT4G27410	321	446	NA	1	NA	NA
AT4G27410	321	539	NA	1	NA	NA
AT4G28790	161	176	1	1	1	NA
AT4G28790	161	243	1	1	NA	NA
AT4G29810	412	155	NA	1	1	NA
AT4G29810	412	185	1	1	1	NA
AT4G29810	412	212	1	1	NA	NA
AT4G29810	412	301	NA	1	NA	NA
AT4G31120	315	332	NA	NA	1	NA
AT4G31120	315	339	1	1	1	NA
AT4G31120	315	432	1	1	NA	NA
AT4G31720	369	134	NA	1	NA	NA
AT4G31720	369	189	1	1	1	SANGER_SEQ
AT4G31720	369	206	1	1	1	SANGER_SEQ
AT4G31720	369	220	NA	1	NA	NA
AT4G31720	369	286	NA	1	NA	NA
AT4G31720	369	303	NA	1	NA	SANGER_SEQ
AT4G31720	369	388	NA	1	NA	NA
AT4G31720	369	434	NA	1	NA	NA
AT4G32660	228	199	1	1	1	SANGER_SEQ
AT4G32660	228	220	1	1	NA	NA
AT4G33060	284	203	1	1	1	NA
AT4G33060	284	290	NA	1	NA	NA
AT4G33060	284	295	NA	1	1	NA
AT4G33060	284	300	NA	1	NA	NA
AT4G34000	365	186	NA	1	NA	NA
AT4G34000	365	228	1	1	1	NA
AT4G34000	365	320	1	1	1	NA
AT4G34430	156	192	1	1	1	NA
AT4G34430	156	197	1	1	1	NA
AT4G34460	347	172	NA	NA	1	NA
AT4G34460	347	221	NA	1	NA	NA
AT4G34460	347	233	1	1	1	NA
AT4G34460	347	245	1	1	NA	NA
AT4G34460	348	160	1	1	NA	NA
AT4G34460	348	167	NA	1	NA	NA
AT4G34460	348	172	NA	1	NA	NA
AT4G34460	348	175	1	1	1	NA
AT4G34460	348	185	NA	1	NA	NA
AT4G34460	348	247	NA	1	NA	NA
AT4G34460	348	416	1	1	NA	NA
AT4G35450	87	304	1	1	1	NA
AT4G35450	87	350	1	1	1	NA

AT4G35450	87	448	NA	1	1	NA
AT4G35785	229	115	1	1	1	NA
AT4G35785	229	153	NA	1	1	NA
AT4G35785	229	281	NA	1	NA	NA
AT4G35785	229	302	NA	1	2	NA
AT4G35785	229	364	NA	NA	1	NA
AT4G35785	229	414	1	1	1	NA
AT4G35785	229	493	NA	1	NA	NA
AT4G36690	198	129	1	1	1	SANGER_SEQ
AT4G36690	198	303	1	1	1	NA
AT4G36690	198	403	1	1	1	NA
AT4G36730	292	151	1	1	1	NA
AT4G36730	292	157	1	1	1	NA
AT4G36960	374	228	1	1	1	SANGER_SEQ
AT4G36960	374	328	NA	1	1	SANGER_SEQ
AT4G36960	374	399	1	1	1	NA
AT4G37180	159	216	1	1	1	SANGER_SEQ
AT4G37180	159	237	1	1	NA	NA
AT4G38510	89	216	1	1	1	SANGER_SEQ
AT4G38510	89	232	1	1	1	SANGER_SEQ
AT4G38510	89	289	1	1	1	SANGER_SEQ
AT4G38510	89	308	NA	1	NA	NA
AT4G38510	89	379	NA	1	1	NA
AT4G38510	89	395	NA	NA	1	NA
AT4G38900	157	229	1	1	1	NA
AT4G38900	157	249	1	1	NA	NA
AT4G39260	90	158	1	1	1	SANGER_SEQ
AT4G39260	90	316	NA	1	1	NA
AT4G39260	90	444	NA	1	1	NA
AT5G02470	187	165	1	1	1	NA
AT5G02470	187	293	NA	1	1	NA
AT5G02470	187	579	NA	NA	1	NA
AT5G02840	188	152	1	1	1	NA
AT5G02840	188	165	NA	1	NA	NA
AT5G02840	188	174	1	1	1	SANGER_SEQ
AT5G04275	379	141	NA	1	NA	NA
AT5G04275	379	162	NA	1	NA	NA
AT5G04275	379	254	NA	1	NA	NA
AT5G04275	379	278	NA	1	NA	NA
AT5G04275	379	482	NA	1	NA	NA
AT5G04430	42	140	1	1	1	NA
AT5G04430	42	205	1	1	1	NA
AT5G05550	181	208	1	1	1	SANGER_SEQ
AT5G05550	181	307	1	1	1	SANGER_SEQ
AT5G05550	181	580	NA	NA	1	SANGER_SEQ
AT5G05550	181	588	NA	1	NA	NA
AT5G06160	222	159	1	1	1	NA
AT5G06160	222	205	NA	1	NA	NA
AT5G06160	222	296	NA	1	NA	NA
AT5G06960	176	214	1	1	1	NA
AT5G06960	176	230	1	1	1	NA
AT5G08185	380	101	1	1	2	NA
AT5G08185	380	167	1	1	1	NA
AT5G08185	380	170	NA	1	1	NA
AT5G08185	380	252	NA	1	NA	NA
AT5G08185	380	260	NA	1	1	NA
AT5G08185	380	263	NA	1	1	NA
AT5G08185	380	269	NA	NA	1	NA
AT5G08185	380	361	NA	1	NA	NA
AT5G09230	244	119	1	1	1	NA
AT5G09230	244	131	1	1	1	NA
AT5G09230	244	230	NA	1	1	NA
AT5G09230	43	112	1	1	1	NA
AT5G09230	43	157	1	1	2	NA
AT5G09230	43	196	1	1	1	NA
AT5G09790	301	205	1	NA	NA	NA
AT5G09790	301	275	NA	1	NA	NA

AT5G09790	301	277	NA	1	NA	NA
AT5G09790	301	281	NA	1	NA	NA
AT5G09790	301	284	1	1	1	NA
AT5G09790	301	543	NA	NA	1	NA
AT5G09790	301	550	NA	NA	1	NA
AT5G09880	298	143	1	1	1	SANGER_SEQ
AT5G09880	298	219	NA	1	NA	SANGER_SEQ
AT5G09880	298	270	NA	1	NA	SANGER_SEQ
AT5G09880	298	281	NA	1	NA	NA
AT5G09880	298	299	NA	1	NA	SANGER_SEQ
AT5G09880	298	311	NA	1	NA	SANGER_SEQ
AT5G09880	298	341	NA	1	NA	SANGER_SEQ
AT5G09880	298	376	NA	1	1	SANGER_SEQ
AT5G09880	298	464	NA	1	NA	SANGER_SEQ
AT5G09880	298	508	NA	1	NA	NA
AT5G09880	298	561	NA	1	NA	NA
AT5G09880	298	634	NA	1	NA	NA
AT5G10140	308	173	NA	NA	NA	NA
AT5G10140	308	213	1	1	1	NA
AT5G10140	308	285	2	1	NA	NA
AT5G10140	308	293	NA	NA	1	NA
AT5G11330	299	189	NA	1	NA	NA
AT5G11330	299	253	NA	1	NA	NA
AT5G11330	299	289	NA	1	NA	NA
AT5G11330	299	354	NA	1	1	NA
AT5G11330	299	360	1	1	1	NA
AT5G12840	186	158	1	1	1	SANGER_SEQ
AT5G12840	186	221	NA	1	NA	SANGER_SEQ
AT5G12840	186	471	NA	1	1	NA
AT5G13220	174	172	1	1	1	NA
AT5G13220	174	194	NA	1	NA	NA
AT5G13220	174	224	1	1	1	NA
AT5G13220	174	245	NA	1	NA	NA
AT5G13220	174	643	1	1	1	NA
AT5G13730	44	201	NA	1	NA	NA
AT5G13730	44	273	1	1	1	SANGER_SEQ
AT5G13730	44	288	NA	1	1	SANGER_SEQ
AT5G13790	312	461	NA	1	NA	NA
AT5G13790	312	469	1	1	NA	NA
AT5G13790	312	544	NA	1	NA	NA
AT5G13790	312	575	NA	1	NA	NA
AT5G13790	312	584	NA	1	NA	NA
AT5G13790	312	648	NA	1	NA	NA
AT5G16820	182	236	1	1	1	NA
AT5G16820	182	241	1	1	1	NA
AT5G16820	182	323	NA	1	1	NA
AT5G18240	168	145	NA	1	NA	SANGER_SEQ
AT5G18240	168	151	1	1	1	SANGER_SEQ
AT5G18240	168	163	1	1	1	SANGER_SEQ
AT5G18240	168	169	1	1	1	SANGER_SEQ
AT5G18620	171	212	1	1	1	SANGER_SEQ
AT5G18620	171	221	1	1	1	SANGER_SEQ
AT5G18830	191	194	1	1	1	NA
AT5G18830	191	271	1	1	1	NA
AT5G19030	274	162	1	1	1	NA
AT5G19030	274	182	1	1	1	NA
AT5G19030	275	151	1	1	1	NA
AT5G19030	275	164	1	1	1	NA
AT5G20040	262	118	NA	1	NA	NA
AT5G20040	262	151	1	1	NA	NA
AT5G20040	262	163	1	1	1	NA
AT5G20250	47	203	1	1	NA	NA
AT5G20250	47	219	NA	1	NA	NA
AT5G20250	47	305	1	NA	NA	NA
AT5G20250	47	313	1	1	1	NA
AT5G20250	47	411	NA	1	1	NA
AT5G22000	183	195	1	1	NA	NA

AT5G22000	183	222	1	1	1	NA
AT5G23090	184	170	1	1	1	NA
AT5G23090	184	196	NA	1	1	NA
AT5G23090	184	205	NA	NA	1	NA
AT5G23090	184	211	1	1	1	NA
AT5G23090	185	169	NA	1	NA	NA
AT5G23090	185	174	1	NA	NA	NA
AT5G23090	185	212	1	1	1	NA
AT5G23450	354	218	1	1	1	NA
AT5G23450	354	254	NA	1	NA	NA
AT5G23450	354	278	NA	1	NA	NA
AT5G23450	354	354	1	1	1	NA
AT5G23450	354	381	NA	1	NA	NA
AT5G24270	363	299	NA	1	NA	SANGER_SEQ
AT5G24270	363	307	1	1	1	SANGER_SEQ
AT5G24270	363	330	NA	1	NA	SANGER_SEQ
AT5G24270	363	337	NA	1	NA	SANGER_SEQ
AT5G24270	363	415	NA	1	NA	SANGER_SEQ
AT5G24270	363	426	NA	1	NA	SANGER_SEQ
AT5G24270	363	445	NA	1	NA	NA
AT5G24270	363	540	NA	1	NA	NA
AT5G24520	169	146	1	1	1	SANGER_SEQ
AT5G24520	169	152	1	1	1	SANGER_SEQ
AT5G24520	169	201	1	NA	NA	NA
AT5G24590	320	521	1	1	1	NA
AT5G24590	320	602	NA	1	NA	NA
AT5G24590	320	609	NA	1	NA	NA
AT5G25610	366	232	1	1	1	NA
AT5G25610	366	607	NA	1	NA	NA
AT5G28080	337	312	1	1	1	NA
AT5G28770	170	174	1	1	1	NA
AT5G28770	170	195	1	1	1	NA
AT5G28770	170	258	NA	1	NA	NA
AT5G35410	370	115	NA	1	NA	NA
AT5G35410	370	120	1	1	3	NA
AT5G35680	48	112	NA	1	NA	NA
AT5G35680	48	191	NA	1	NA	NA
AT5G35680	48	199	1	1	1	SANGER_SEQ
AT5G35680	48	228	1	1	1	SANGER_SEQ
AT5G37055	313	346	NA	1	NA	NA
AT5G37055	313	355	1	1	1	SANGER_SEQ
AT5G37055	313	362	NA	1	NA	NA
AT5G37055	313	422	NA	1	NA	NA
AT5G37055	313	433	NA	1	1	NA
AT5G37055	313	442	NA	1	1	NA
AT5G37055	313	524	NA	1	NA	NA
AT5G37370	371	166	1	NA	NA	NA
AT5G37370	371	182	NA	1	NA	NA
AT5G37370	371	190	1	1	1	SANGER_SEQ
AT5G37370	371	285	NA	1	1	SANGER_SEQ
AT5G40280	349	187	1	1	1	NA
AT5G41150	49	292	1	1	1	SANGER_SEQ
AT5G41150	49	346	NA	1	NA	SANGER_SEQ
AT5G43270	189	161	1	1	1	NA
AT5G43270	189	244	1	1	NA	NA
AT5G43270	324	187	1	1	1	NA
AT5G43270	324	270	1	1	NA	NA
AT5G43270	324	503	NA	1	NA	NA
AT5G43910	50	190	1	1	1	SANGER_SEQ
AT5G43910	50	203	1	1	NA	SANGER_SEQ
AT5G43910	50	210	NA	1	1	NA
AT5G43910	50	221	1	1	1	SANGER_SEQ
AT5G43910	50	307	NA	1	1	NA
AT5G45510	51	114	1	1	1	NA
AT5G45510	51	200	1	1	1	NA
AT5G46110	245	124	NA	1	NA	NA
AT5G46110	245	130	1	1	1	SANGER_SEQ

AT5G46110	245	138	1	1	NA	SANGER_SEQ
AT5G46110	245	207	NA	1	NA	NA
AT5G47210	281	121	NA	1	NA	NA
AT5G47210	281	170	NA	1	NA	NA
AT5G47210	281	179	2	1	1	NA
AT5G48150	179	192	NA	1	1	NA
AT5G48150	179	203	1	1	1	NA
AT5G48150	179	272	NA	1	1	NA
AT5G48150	179	283	1	1	1	NA
AT5G48150	179	398	NA	1	1	NA
AT5G48560	318	336	1	1	1	NA
AT5G48560	318	409	NA	1	NA	NA
AT5G50240	254	193	1	1	1	NA
AT5G50240	254	198	NA	1	NA	NA
AT5G50240	254	201	1	1	1	NA
AT5G53180	213	140	1	1	1	NA
AT5G53180	213	198	1	1	1	NA
AT5G53180	213	201	NA	1	1	NA
AT5G53450	381	106	1	1	1	NA
AT5G53450	381	189	1	1	1	NA
AT5G54430	233	100	1	1	1	NA
AT5G54430	233	194	NA	1	1	NA
AT5G54430	233	198	NA	1	1	NA
AT5G56370	190	161	1	1	1	NA
AT5G56370	190	191	1	1	NA	NA
AT5G57110	352	121	1	1	NA	NA
AT5G57110	352	126	NA	1	NA	NA
AT5G57110	352	138	1	1	1	NA
AT5G57630	338	209	NA	1	1	NA
AT5G57630	338	253	1	1	1	NA
AT5G57630	338	351	NA	1	1	NA
AT5G59440	246	143	1	1	2	NA
AT5G59440	246	151	1	1	1	NA
AT5G59780	177	207	1	1	1	NA
AT5G59780	177	229	NA	NA	1	NA
AT5G59780	177	239	1	1	1	NA
AT5G59780	177	318	1	1	1	NA
AT5G59950	327	224	2	1	1	SANGER_SEQ
AT5G59950	327	322	NA	1	NA	NA
AT5G59950	327	421	1	1	NA	NA
AT5G60580	172	141	1	1	1	NA
AT5G60580	172	164	1	1	1	NA
AT5G60670	64	198	1	1	1	NA
AT5G63120	282	180	1	1	1	NA
AT5G63120	282	366	1	1	NA	NA
AT5G63120	282	471	NA	1	NA	NA
AT5G63870	57	131	NA	1	NA	NA
AT5G63870	57	174	1	1	1	NA
AT5G63870	57	185	1	1	1	NA
AT5G63870	57	190	NA	1	1	NA
AT5G63990	340	304	1	1	1	NA
AT5G63990	340	397	1	1	NA	NA
AT5G65050	58	174	NA	1	NA	NA
AT5G65050	58	178	NA	1	NA	NA
AT5G65050	58	205	NA	1	NA	NA
AT5G65050	58	208	NA	1	1	NA
AT5G65050	58	237	NA	1	NA	NA
AT5G65050	58	241	1	1	1	NA
AT5G65050	58	247	NA	1	NA	NA
AT5G65050	58	324	NA	1	1	NA
AT5G65050	58	328	NA	1	1	NA
AT5G65050	58	347	NA	1	NA	NA
AT5G65050	58	351	NA	1	NA	NA
AT5G65050	58	433	NA	1	NA	NA
AT5G65050	58	437	NA	1	NA	NA
AT5G65050	58	530	NA	NA	1	NA
AT5G65060	309	219	NA	1	NA	SANGER_SEQ

AT5G65060	309	223	NA	1	2	SANGER_SEQ
AT5G65060	309	228	1	1	NA	SANGER_SEQ
AT5G65060	309	257	NA	1	NA	NA
AT5G65060	309	261	NA	1	1	SANGER_SEQ
AT5G65060	309	263	1	1	1	SANGER_SEQ
AT5G65060	309	268	NA	1	NA	NA
AT5G65060	309	302	NA	1	NA	NA
AT5G65060	309	306	NA	1	NA	NA
AT5G65060	309	338	NA	1	1	NA
AT5G65060	309	342	NA	1	NA	NA
AT5G65060	309	344	NA	1	1	NA
AT5G65060	309	348	NA	1	NA	NA
AT5G65070	310	318	NA	1	NA	NA
AT5G65070	310	360	NA	1	NA	NA
AT5G65070	310	362	NA	1	NA	NA
AT5G65070	310	365	NA	1	NA	SANGER_SEQ
AT5G65070	310	368	NA	1	1	SANGER_SEQ
AT5G65070	310	375	NA	1	NA	NA
AT5G65070	310	416	NA	1	NA	NA
AT5G65070	310	419	NA	1	NA	SANGER_SEQ
AT5G65070	310	422	NA	1	NA	SANGER_SEQ
AT5G65070	310	426	1	1	NA	SANGER_SEQ
AT5G65070	310	501	NA	1	NA	NA
AT5G65070	310	509	NA	1	NA	NA
AT5G65070	310	518	NA	NA	1	NA
AT5G65070	310	522	1	NA	NA	NA
AT5G65070	310	525	NA	NA	NA	NA
AT5G65080	311	365	NA	1	NA	SANGER_SEQ
AT5G65080	311	405	NA	1	NA	NA
AT5G65080	311	421	NA	1	1	NA
AT5G65080	311	462	1	1	NA	SANGER_SEQ
AT5G65080	311	467	1	1	1	SANGER_SEQ
AT5G65430	264	245	1	1	1	NA
AT5G65430	264	251	1	1	1	NA
AT5G65430	264	371	NA	NA	NA	NA
AT5G65640	319	131	NA	1	NA	NA
AT5G65640	319	135	1	1	NA	NA
AT5G65640	319	143	1	1	1	NA
AT5G65640	319	274	NA	1	1	NA
AT5G66010	59	103	NA	1	1	NA
AT5G66010	59	182	1	1	1	NA
AT5G66010	59	556	NA	NA	1	NA
AT5G66210	335	113	NA	1	NA	NA
AT5G66210	335	119	1	1	NA	NA
AT5G66210	335	290	NA	1	NA	NA
AT5G66210	335	295	NA	1	NA	NA
AT5G66210	335	327	1	1	NA	NA
AT5G66210	335	430	1	1	1	NA
AT5G66210	335	530	NA	1	1	NA
AT5G67030	364	177	NA	1	NA	NA
AT5G67030	364	183	NA	1	NA	NA
AT5G67030	364	186	1	1	1	NA
AT5G67580	178	155	1	1	1	NA
AT5G67580	178	197	1	1	1	NA

Table S4. Validation of the putative assembled transcripts.

Validation of the putative assembled transcripts was performed by comparing TAIR9 annotated transcripts, fragment sizes reported by the HR RT-PCR panel (AS panel) and putative transcripts predicted using RNA-seq (see Methods). Columns 4, 5 and 6 - numbers of fragments found in each data set that corresponds to the fragment size in the column 3. If a Sanger sequence was obtained for the fragment, then in the column 7 it is indicated by "SANGER_SEQ". If there is no correspondence of size in the respective data set then it is denoted with NA (Not Available). PRIMER_ID corresponds to the primers in the Table S3.

Table S10. Primer sequences for cryptic intron validation						
Gene_ID	Intron size	Forward primer sequence	Reverse primer sequence	Unspl size	FS size	FS-CI
AT1G16040	113	TCACTGGTCCTTTCTAATGTCTGT	CCAAGCTAACAAAAACCTTTGCCC	721	419	306
AT1G66920	78	TCGCAGAAGTGGTGGGGCGA	GCCGGGCGATCTAATGGCCA	787	787	709
AT1G71230	83	ATGGTGGTTCACGCTCGCTC	TGGCACAACTCCTCCAAAGCG	963	678	595
AT1G77380	99	AGGTGAAGGGAAGTCTCACTGGGA	GCCCCGAGCAGACCCACAAC	768	580	481
AT1G79970	133	GAGCACCTGCATTTGGGGGCT	GGGATGAGCCGGGGCATCAG	1497	1009	876
AT3G04500	71	GCGATTGCGCGATTGCTTCTCC	CCCAAGATCACCACAGAACAGACG	920	459	388
AT3G58990	142	GCGACGAGTGCAAAACAGGG	TCAAACCACAAATTCAACTAACATTAC	645	645	503
AT4G17090	93	CGCTAGCGTTCCGGTGTTTCGT	CGGGGAATCTCCAGGTCCCGT	773	578	485
AT4G36690	100	TGCCAATTCAGGCTATGACACAGCAG	ATTTAGGGCAGCGCACGCGA	973	590	490
AT5G02110	103	TGAAACGGTATTTCCGCCGCT	GGCCACAACGCTTGGTGGGT	583	394	291

Table S10. Primer sequences for cryptic intron validation.

“Unspl size” is the size corresponding to the unspliced product (column 5) amplified by corresponding primer pair. “FS size” is the size of the product that corresponds to a splice variant with retention of a cryptic intron (column 6). “FS-CI” is the size of the expected product that results from the removal of a cryptic intron (column 7).

Table S5. Intron retention events which are undetectable or present $\leq 1\%$ of transcript abundance.							
PRIMER ID	GENE_ID	GENE_DESCRIPTION	NUMBER OF EXONS	PRIMER SITES	SPLICING PHENOTYPE	HR RT-PCR PANEL TRANSCRIPT RATIO	RNA-SEQ IRR
330	AT3G10300	Calcium-binding EF hand protein	5	Ex1-3	FS IR1	100% 0%	ND
331	AT3G10300	Calcium-binding EF hand protein	5	Ex2-5	FS IR3 and IR4	100% 0%	ND
340	AT5G63990	3'(2'),5'-bisphosphate nucleotidase	8	Ex6-8	FS IR7	100% 0%	ND
349	AT5G40280	ATFTB/ERA1 (Farnesyl transferase beta subunit/enhanced response to ABA 1)	14	Ex5-8	FS IR5 and IR6	100% 0%	ND
350	AT1G77740	PIP5K2 (Phosphatidylinositol-4-phosphate 5-kinase 2)	8	Ex1-3	FS IR1	100% 0%	ND
355	AT3G16785	PLDP1 (Phospholipase D P1)	20	EX17-20	FS IR18 and IR19	100% 0%	0.93
364	AT5G67030	ZEP (Zeaxanthin epoxidase)/ABA1 (ABA deficient 1)	16	Ex9-12	FS IR11	100% 0%	ND
351	AT2G18960	AHA1 (Arabidopsis H+ ATPase 1)/OST2 (Open stomata 2)	16	Ex9-11	FS IR10	100% 0%	ND
386	AT4G01250	ATWRKY22 (WRKY family transcription factor 22)	3	Ex1-3	FS IR2	100% 0%	ND
313	AT5G37055	SEF (Serrated leaves and early flowering)	4	Ex1-4	FS IR2	79% 1%	0.09
315	AT4G31120	PRMT5 (Protein arginine methyltransferase 5)/SKB1 (SHK1 binding protein 1)	23	Ex20-23	FS IR21	99 $\pm$ 0.1% 1 $\pm$ 0.1%	0.02
320	AT5G24590	ANAC091 (Arabidopsis NAC 091)/TIP (TCV interacting protein)	5	Ex3-5	FS IR4	99 $\pm$ 0.4% 1 $\pm$ 0.4%	0.03
341	AT2G15970	ATCYP19 (Cyclophilin 19)/ATCOR413-PM1 (Arabidopsis thaliana cold induced protein 1)	4	Ex1-3	FS IR1	99 $\pm$ 0.3% 1 $\pm$ 0.3%	0.008
348	AT4G34460	AGB1 (GTP binding protein 1)/ELK4 (Erecta-like 4)	6	Ex1-3	FS IR2	99 $\pm$ 0.3% 1 $\pm$ 0.3%	0.005
357	AT1G54100	ALDH7B4 (Aldehyde dehydrogenase 7B4)	14	Ex1-3	FS IR1	99 $\pm$ 0.3% 1 $\pm$ 0.3%	1.22
359	AT2G38170	CAX1 (cation exchanger 1) – calcium antiporter	10	Ex7-9	FS IR7	99 $\pm$ 0.4% 1 $\pm$ 0.4%	0.009
365	AT4G34000	ABF3 (ABA-responsive elements-binding factor 3)	6	Ex3-6	FS IR4	99 $\pm$ 0.1% 1 $\pm$ 0.1%	0.05
382	AT1G44910	PRP40A (Pre-mRNA processing protein)	27	Ex17-19	FS IR18	99 $\pm$ 0.1% 1 $\pm$ 0.1%	ND

Table S5. Intron retention events which are undetectable or present $\leq 1\%$ of transcript abundance. The intron retention events were identified from TAIR, ASIP and AceView databases. PRIMER_ID corresponds to the primers in the Table S3. Primers are positioned in the exons indicated (column 5) and amplify across at least two introns. FS – fully spliced; IRn - retention of intron, where n is an intron number. Transcript abundance (% of total) is the mean of three experiments with standard errors. IRR - the intron retention ratio was calculated using the median number of reads along the retained intron divided by the number of reads supporting the splice junction in question. ND – not detected.

Table S6. Distribution of the retained introns in different regions of transcripts.		
	Observed	Expected
5'UTR	897	447
5'UTR-CDS	110	65
CDS	8,576	9,373
CDS-3'UTR	49	30
3'UTR	400	117

Table S6. Distribution of the retained introns in different regions of transcripts. The number of retained introns observed in our data set in each of the transcript regions is shown in the column 2. The expected distribution of retained introns if they would follow the same distribution as all the introns (see Figure 2A) was calculated by multiplying the proportion of introns in a given region by the total of retained introns (column 3).

Table S7. Enrichment of PFAM domain hits in the set of retained introns.

DOMAIN_NAME	PFAM_ID	ATH_REP	EXP_HITS	SAMPLE_REP	FOLD_ENRICH	P-VALUE	CORR P-VALUE
p450	PF00067	255	5.77	17	2.94	0.0001	0.00
Pkinase_Tyr	PF07714	152	3.44	16	4.65	0.0000	0.00
Lipase_GDSL	PF00657	112	2.53	12	4.73	0.0000	0.00
GTP_EFTU	PF00009	30	0.68	8	11.78	0.0000	0.00
HSP70	PF00012	20	0.45	7	15.46	0.0000	0.00
MFS_1	PF07690	55	1.25	6	4.81	0.0013	0.02
SMC_N	PF02463	9	0.20	6	29.44	0.0000	0.00
GRAS	PF03514	34	0.77	5	6.50	0.0008	0.02
B_lectin	PF01453	47	1.06	5	4.70	0.0035	0.05
GRP	PF07172	7	0.16	4	25.24	0.0000	0.00
DJ-1_Pfpl	PF01965	12	0.27	3	11.04	0.0021	0.03
Miro	PF08477	10	0.23	3	13.25	0.0012	0.02
K_trans	PF02705	13	0.29	3	10.19	0.0026	0.04
GAF	PF01590	10	0.23	3	13.25	0.0012	0.02
DUF642	PF04862	10	0.23	3	13.25	0.0012	0.02
DUF300	PF03619	7	0.16	3	18.93	0.0004	0.01
Nramp	PF01566	7	0.16	3	18.93	0.0004	0.01
UAA	PF08449	8	0.18	3	16.56	0.0006	0.01
Pept_tRNA_hydro	PF01195	4	0.09	3	33.13	0.0000	0.00
HSP90	PF00183	7	0.16	3	18.93	0.0004	0.01
SecA_DEAD	PF07517	2	0.05	2	44.17	0.0005	0.01
UNC-93	PF05978	3	0.07	2	29.44	0.0015	0.02
PARG_cat	PF05028	2	0.05	2	44.17	0.0005	0.01
UPF0172	PF03665	2	0.05	2	44.17	0.0005	0.01
PAL	PF00221	4	0.09	2	22.08	0.0029	0.04
CK_II_beta	PF01214	4	0.09	2	22.08	0.0029	0.04
DER1	PF04511	3	0.07	2	29.44	0.0015	0.02

Table S7. Enrichment of PFAM domain hits in the set of retained introns.

ATH_REP (column 3) has the number of hits of the given domain in the *Arabidopsis* genome. EXP_HITS (column 4) represents the expected number of hits for a given domain according to the genome distribution. SAMPLE_REP (column 5) is the number of hits for the given domain found in the set of retained introns. FOLD_ENRICH (column 6) is the fold enrichment of the given PFAM domain in the set of retained introns. The p-value for the fold enrichment followed by the corrected p-value for multiple testing is shown the columns 7 and 8.

Table S8. Comparison of proportion of codons in the retained introns that contribute to protein domains.		
	Codons in domains (%)	P-value
Retained introns	10.4 %	<0.00001
Non-retained introns	2.6 %	<0.00001
UTRs	0.76 %	<0.00001
Exons	54.6 %	<0.00001

Table S8. Comparison of proportion of codons in the retained introns that contribute to protein domains. P-values of the comparisons between retained introns and non-retained introns, UTRs and exons were obtained using binomial test. Non-retained introns and UTRs were used as negative controls and exons as the positive control.

Table S9. Codon usage of retained introns		
IRR CATEGORY	CODON USAGE	
IRR <0.1	AVG_χ ²	STD
EXONS VS INTRONS	45143.27	39146.43
INTRONS VS TEOR.INTRONS	59.30	13.20
EXONS VS TEOR.EXONS	60.76	12.49
INTRONS VS IRS	319.45	32.20
EXONS VS IRS	48684.65	616.55
IRR 0.1-0.2	AVG_χ ²	STD
EXONS VS INTRONS	33626.16	29159.48
INTRONS VS TEOR.INTRONS	60.51	11.80
EXONS VS TEOR.EXONS	61.52	11.60
INTRONS VS IRS	276.13	32.82
EXONS VS IRS	36623.26	541.54
IRR 0.2-0.3	AVG_χ ²	STD
EXONS VS INTRONS	13728.07	10027.51
INTRONS VS TEOR.INTRONS	60.75	10.21
EXONS VS TEOR.EXONS	59.12	9.79
INTRONS VS IRS	173.50	26.03
EXONS VS IRS	14484.24	366.36
IRR 0.3-0.4	AVG_χ ²	STD
EXONS VS INTRONS	6772.93	1209.64
INTRONS VS TEOR.INTRONS	57.49	10.21
EXONS VS TEOR.EXONS	60.38	9.79
INTRONS VS IRS	125.70	19.93
EXONS VS IRS	6947.60	201.29
IRR 0.4-0.5	AVG_χ ²	STD
EXONS VS INTRONS	4689.50	312.31
INTRONS VS TEOR.INTRONS	61.07	10.68
EXONS VS TEOR.EXONS	59.71	11.69
INTRONS VS IRS	139.87	19.73
EXONS VS IRS	5325.24	229.52
IRR 0.5-0.6	AVG_χ ²	STD
EXONS VS INTRONS	2837.50	210.43
INTRONS VS TEOR.INTRONS	59.75	10.63
EXONS VS TEOR.EXONS	57.36	10.98
INTRONS VS IRS	137.03	21.03
EXONS VS IRS	2949.74	193.48
IRR 0.6-0.7	AVG_χ ²	STD
EXONS VS INTRONS	2309.53	219.58
INTRONS VS TEOR.INTRONS	60.67	10.98
EXONS VS TEOR.EXONS	58.25	12.17
INTRONS VS IRS	120.17	18.49
EXONS VS IRS	2350.55	142.34
IRR 0.7-0.8	AVG_χ ²	STD
EXONS VS INTRONS	1842.22	187.59
INTRONS VS TEOR.INTRONS	62.70	11.70
EXONS VS TEOR.EXONS	59.65	10.81
INTRONS VS IRS	119.04	18.13

EXONS VS IRS	1834.01	127.26
IRR 0.8-0.9	AVG_χ2	STD
EXONS VS INTRONS	1680.03	162.67
INTRONS VS TEOR.INTRONS	59.24	11.12
EXONS VS TEOR.EXONS	60.02	10.38
INTRONS VS IRS	155.29	27.42
EXONS VS IRS	2032.65	112.82
IRR 0.9-1	AVG_χ2	STD
EXONS VS INTRONS	1110.03	121.26
INTRONS VS TEOR.INTRONS	59.61	9.83
EXONS VS TEOR.EXONS	60.31	11.40
INTRONS VS IRS	140.56	29.76
EXONS VS IRS	1307.75	139.26
IRR 1-2	AVG_χ2	STD
EXONS VS INTRONS	6561.31	339.46
INTRONS VS TEOR.INTRONS	58.88	11.17
EXONS VS TEOR.EXONS	60.11	11.09
INTRONS VS IRS	299.68	34.34
EXONS VS IRS	4509.76	184.72
IRR 2-3	AVG_χ2	STD
EXONS VS INTRONS	3216.61	206.72
INTRONS VS TEOR.INTRONS	58.97	8.62
EXONS VS TEOR.EXONS	60.41	10.44
INTRONS VS IRS	407.10	32.37
EXONS VS IRS	1405.48	71.20
IRR 3-4	AVG_χ2	STD
EXONS VS INTRONS	3487.32	218.64
INTRONS VS TEOR.INTRONS	61.48	10.94
EXONS VS TEOR.EXONS	60.14	11.18
INTRONS VS IRS	1630.93	81.32
EXONS VS IRS	534.93	42.45
IRR 4-5	AVG_χ2	STD
EXONS VS INTRONS	2702.28	231.17
INTRONS VS TEOR.INTRONS	59.44	10.23
EXONS VS TEOR.EXONS	60.42	11.83
INTRONS VS IRS	1071.48	71.32
EXONS VS IRS	597.96	59.65
IRR 5-10	AVG_χ2	STD
EXONS VS INTRONS	7969.59	313.01
INTRONS VS TEOR.INTRONS	60.32	10.24
EXONS VS TEOR.EXONS	60.20	8.88
INTRONS VS IRS	5299.01	170.54
EXONS VS IRS	454.25	43.95
IRR 10-15	AVG_χ2	STD
EXONS VS INTRONS	6249.99	318.38
INTRONS VS TEOR.INTRONS	58.41	10.34
EXONS VS TEOR.EXONS	59.79	10.48
INTRONS VS IRS	5800.42	159.12
EXONS VS IRS	516.38	39.89
IRR 15-20	AVG_χ2	STD

EXONS VS INTRONS	4414.76	250.93
INTRONS VS TEOR.INTRONS	60.74	10.39
EXONS VS TEOR.EXONS	59.37	11.25
INTRONS VS IRS	4638.99	175.22
EXONS VS IRS	288.59	31.31
IRR 20-25	AVG_χ ²	STD
EXONS VS INTRONS	4206.71	247.58
INTRONS VS TEOR.INTRONS	60.12	11.04
EXONS VS TEOR.EXONS	59.42	10.70
INTRONS VS IRS	4918.22	169.27
EXONS VS IRS	268.33	31.05
IRR 25-30	AVG_χ ²	STD
EXONS VS INTRONS	2601.93	213.68
INTRONS VS TEOR.INTRONS	60.14	12.21
EXONS VS TEOR.EXONS	59.46	11.91
INTRONS VS IRS	2654.21	142.74
EXONS VS IRS	298.85	40.64
IRR >30	AVG_χ ²	STD
EXONS VS INTRONS	21105.78	548.33
INTRONS VS TEOR.INTRONS	61.19	10.82
EXONS VS TEOR.EXONS	57.99	9.59
INTRONS VS IRS	30489.33	490.88
EXONS VS IRS	1675.49	86.18

Table S9. Codon usage of retained introns.

The codon usage was calculated for each non-overlapping category of intron retention ratio (IRR) (see Figure 8) according to Galante et al. 2004. IRS - retained introns.

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