

***The Plant Journal* Supporting Information**

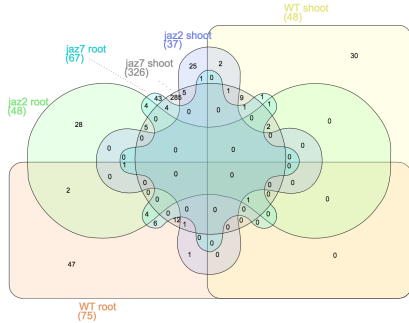
Article title: Jasmonate Induced Alternative Splicing Responses in Arabidopsis

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The following supporting information is available for this article:

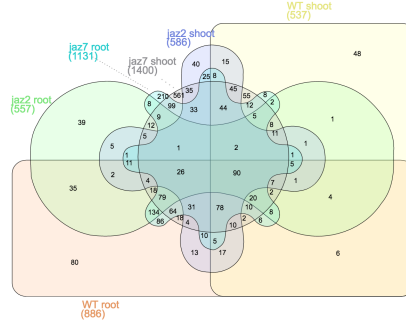
Differential AS

Treatment
no vs. 10 μ M MeJA

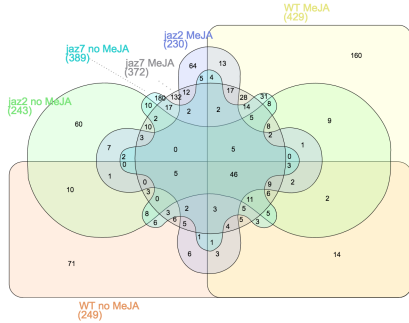


Differential exp.

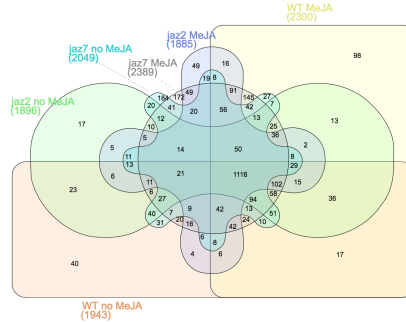
Treatment
no vs. 10 μ M MeJA



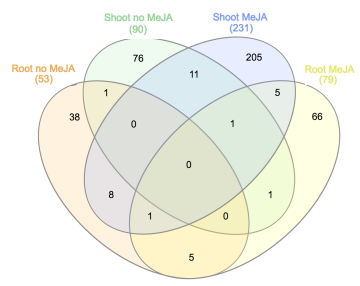
Tissue
root vs. shoot



Tissue
root vs. shoot



Genotype
WT vs. *jaz2* or
WT vs. *jaz7* or
jaz2 vs. *jaz7*



Genotype
WT vs. *jaz2* or
WT vs. *jaz7* or
jaz2 vs. *jaz7*

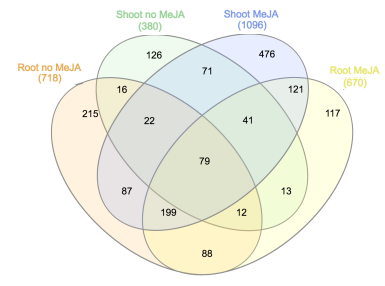


Figure S1. Venn diagram of genes that exhibit differential expression or differential AS in response to treatment (MeJA), between tissues (root and shoots) and between mutant backgrounds.

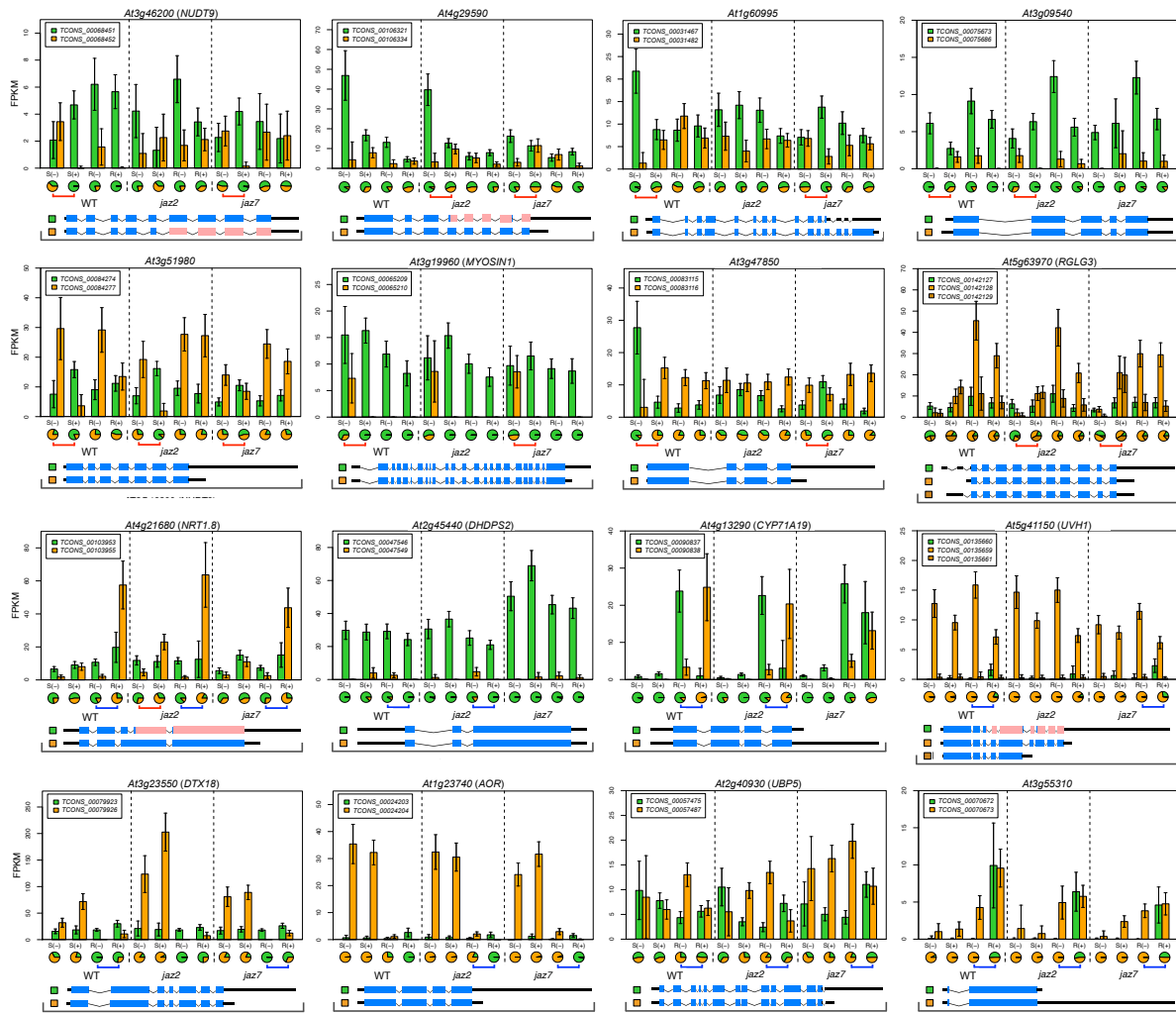


Figure S2. Example cases in which gene expression was regulated by AS in response to MeJA treatment. Pie charts under each condition indicate the proportion of each AS isoform present relative to the total expression from the locus. Red and blue lines under pies indicate significant differential AS in shoot and root, respectively. Under barplot are the isoform structures of the gene. Hat lines indicate introns; black thin boxes indicate UTR; blue boxes indicate CDS; pink boxes indicate regions which were turned to non-coding regions due to AS caused PTC.

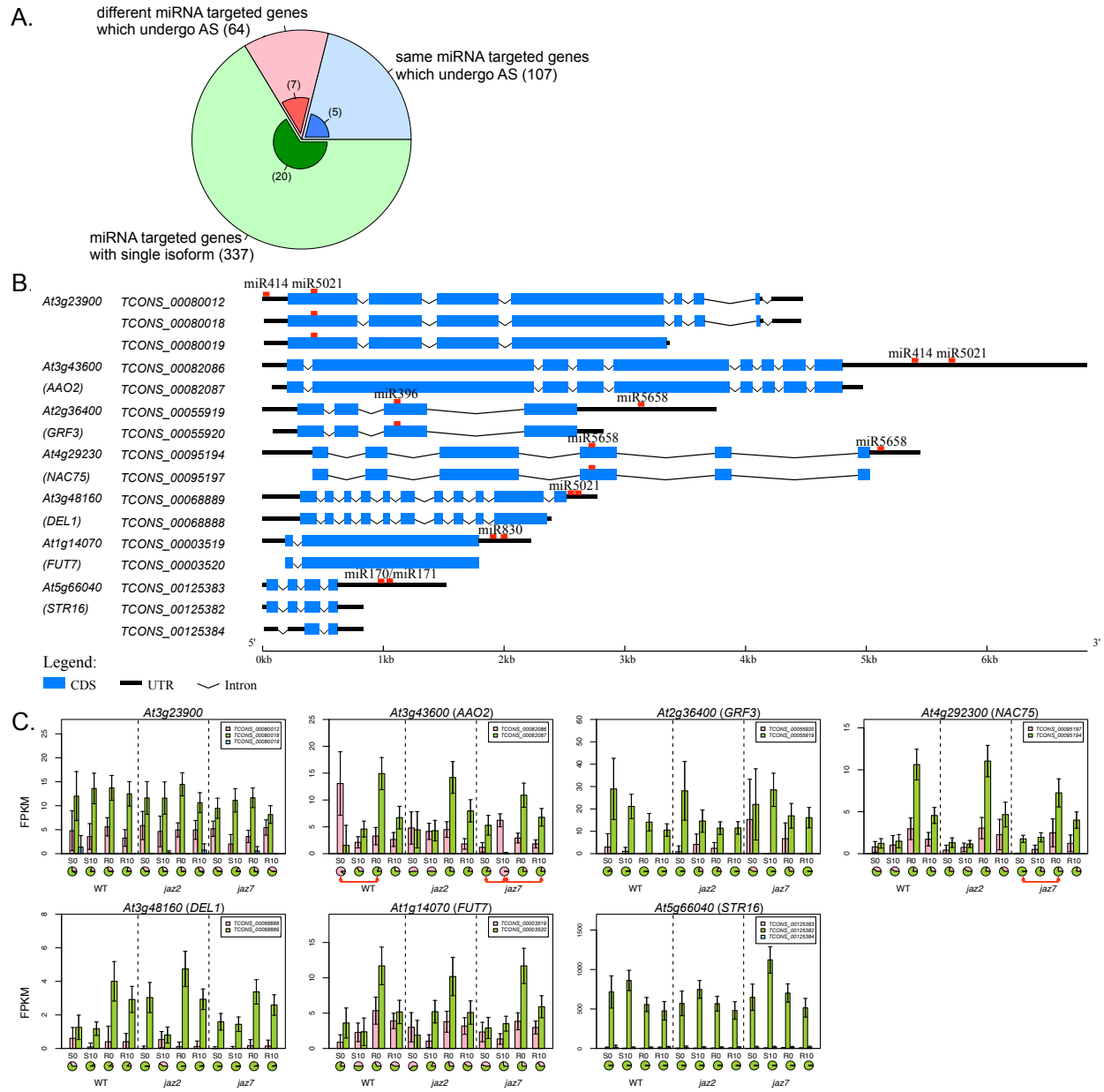


Figure S3. Genes undergoing AS that include miRNA binding sites that differ between isoforms.

A) Distribution of predicted miRNA target sites in genes that do not undergo AS, genes that undergo AS and AS isoforms of the gene contain different miRNA target sites and genes that undergo AS to produce isoforms with the same miRNA target sites. The darker shaded sections within each category indicate cases with multiple miRNA target sites. B) Gene structure of the seven cases (dark pink in A) with the predicted miRNA binding site indicated. C) Expression profiles of the seven genes shown in B. Pie charts under each condition indicate the proportion of

each AS isoform relative to the total expression from the locus. Significantly differential AS is indicated by red lines.

miRNA	No.	Gene	AS.diff												Transcript	Target	Target site										
			Treatment				Tissue				Genotype																
			a	b	c	d	e	f	a	b	c	d	e	f				a	b	c	d						
ath-miR156	1	AT1G35515 (MYB8/HOS10)																		TCONS_0008685	0						
																				TCONS_0008686	1	ath-miR156 [798-817: CUUCUCUCUCUCUCUCUCA]					
ath-miR172	2	AT3G54990 (SMZ)																		TCONS_00085221	1	ath-miR172 [965-985: UUGCAGCAUCAUCAGGAUUC]					
																				TCONS_00085222	0						
ath-miR414	3	AT3G43600 (AAC2)																			TCONS_00082086	2	ath-miR414 [4777-4797: UGAUGAUGAUGAUGAAGAUGC] ath-miR5021 [5090-5109: UUUUCUUCUCUCUCUCUCUCUC]				
																					TCONS_00082087	0					
																						TCONS_00051815	1	ath-miR414 [2818-2838: GGAUGAUGAUGAUGAUGAUGA]			
																						TCONS_00051822	1	ath-miR414 [2877-2897: GGAUGAUGAUGAUGAUGAUGA]			
																							TCONS_00051834	0			
	4	AT2G23140 (PUB4)																		TCONS_00137229	0						
	5	AT5G47040 (LON2/APEM10)																		TCONS_00137255	1	ath-miR414 [916-939: UGACAACGAUGAUGAUGAAGAUGA]					
ath-miR415	6	AT4G12560 (CPR1/CPR30)																			TCONS_00090637	1	ath-miR415 [1441-1461: CUUUUCUGUCUCUCUCUCUGUU]				
																					TCONS_00090640	0					
																						TCONS_00090641	1	ath-miR415 [1396-1416: CUUUUCUGUCUCUCUCUCUGUU]			
ath-miR472	7	AT5G43730 (RSG2)																			TCONS_00119400	0					
																						TCONS_00119402	1	ath-miR472 [1313-1334: GGU AUGGGGGGAAUAGGAAAA]			
																						TCONS_00119403	1	ath-miR472 [1313-1334: GGU AUGGGGGGAAUAGGAAAA]			
																							TCONS_00119404	0			
																							TCONS_00003955	0			
	8	AT1G15885																		TCONS_00003956	1	ath-miR472 [1191-1212: GGU AUGGGGGGAGUAGGUAAAA]					
ath-miR5021	9	AT4G19670																			TCONS_00103441	1	ath-miR5021 [47-67: UUCUUCUUCUUCUUCUUCUCU]				
																						TCONS_00103442	1	ath-miR5021 [47-67: UUCUUCUUCUUCUUCUUCUCU]			
																							TCONS_00103445	0			
																							TCONS_00103446	1	ath-miR5021 [44-64: UUCUUCUUCUUCUUCUUCUCU]		
																							TCONS_00042668	0			
																								TCONS_00042669	0		
																								TCONS_00042670	1	ath-miR5021 [24-44: UUCUUCUUCUUCUUCUUCUCU]	
																								TCONS_00059096	0		
																								TCONS_00059100	1	ath-miR5021 [128-147: CUUUCUUCUUCUUCUUCUCU]	
																								TCONS_00060511	1	ath-miR5021 [114-133: UUUUCUUCUUCUUCUUCUUU]	
ath-miR5021	12	AT3G02740																				TCONS_00060512	0				
																							TCONS_00074206	1	ath-miR5021 [1620-1640: UUCUUCUUCUUCUUCUUCUCU]		
																							TCONS_00074207	0			
																								TCONS_00082295	1	ath-miR5021 [18-38: UUCUUCUUCUUCUUCUUCUCU]	
																								TCONS_00082304	0		
																								TCONS_00101323	1	ath-miR5021 [2480-2500: UUUUAUCUUCUUCUUCUUCUC]	
																								TCONS_00101325	0		
																								TCONS_00124016	1	ath-miR5021 [57-76: UUUUUUUGUUCUUCUCUCA]	
ath-miR5641	17	AT5G55530																				TCONS_00124018	0				
																							TCONS_00122678	0			
																								TCONS_00122680	0		
																								TCONS_00122682	0		
																								TCONS_00122683	1	ath-miR5641 [60-80: UCUUUCUAUCAUCUUCUUA]	
																								TCONS_00119648	1	ath-miR5641 [1180-1200: UUAUUUAUCAUCUUCUUCU]	
																								TCONS_00119653	1	ath-miR5641 [1180-1200: UUAUUUAUCAUCUUCUUCU]	
																									TCONS_00119656	0	
																									TCONS_00124898	0	
																									TCONS_00124899	0	
ath-miR5658	19	AT5G64330 (NPH3/RPT3)																				TCONS_00124902	1	ath-miR5658 [3646-3666: AAUCAUCAUCAUAAUCAUCAU]			
																							TCONS_00095194	2	ath-miR5658 [1487-1507: GAUCAUCACCAUCAUCAUCAU] ath-miR5658 [1981-2001: GCUCAUCGUCAUCAUCAUCAU]		
ath-miR5658	20	AT4G29230 (NAC75)																				TCONS_00095197	1	ath-miR5658 [1078-1098: GAUCAUCACCAUCAUCAUCAU]			
																							TCONS_00004939	0			
ath-miR8177	21	AT1G18880 (NPF2.9)																			TCONS_00004941	1	ath-miR8177 [3771-3791: UA-GAGUGACACAUCAUCAACA]				

Figure S4. Twenty-one genes which contain miRNA binding sites potentially subjected to AS regulation. Blue, green and yellow shading indicate significantly changed isoform proportions identified in treatment, tissue or genotype comparisons, respectively. Targeted sequences within the transcript and their locations are presented within brackets [] in the “Target site” column.

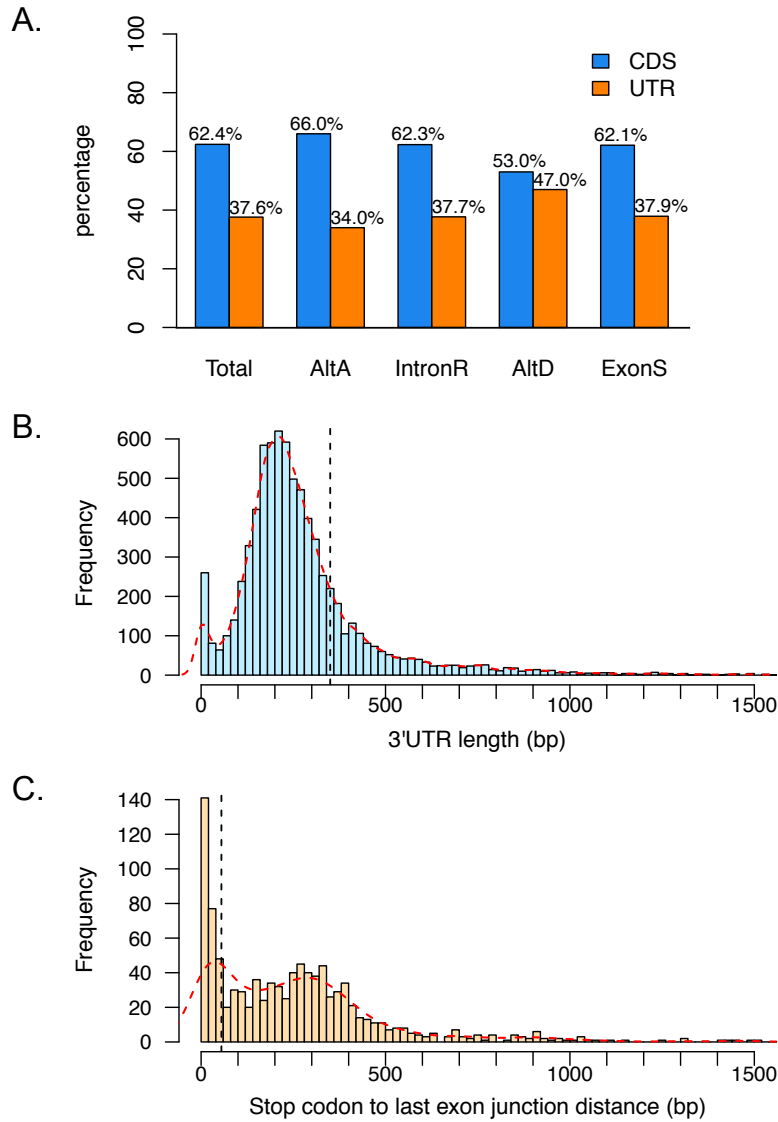


Figure S5. Cases in which AS won't generate multiple protein products. A) Distribution of AS events occurring within the CDS or UTRs. B) Distribution of 3'-UTR lengths of all identified transcripts. C) Distribution of the distance between the stop codon and the last exon junction when the stop codon is not within the last exon of the transcript.

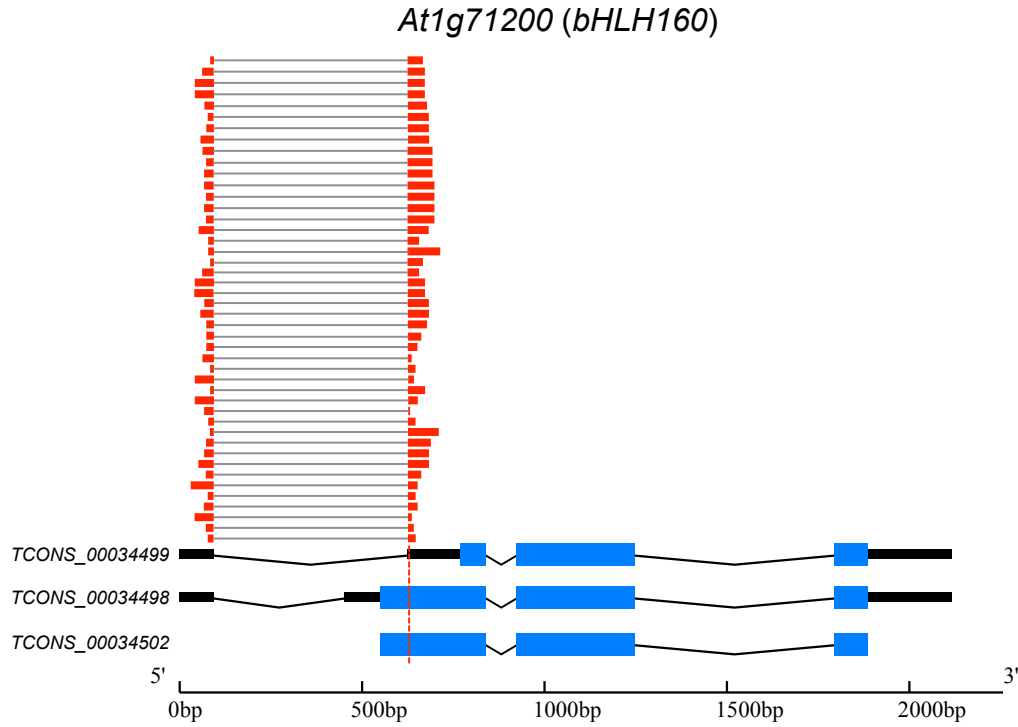
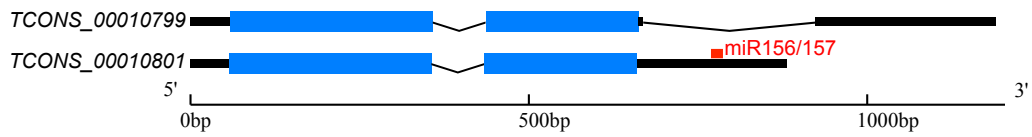


Figure S6. Mapped reads from the MeJA project supporting the AS junction in *Arabidopsis bHLH160^b*. Hat lines indicate introns; black thin boxes indicate UTR; blue boxes indicate CDS. Gray line connected red boxes indicate mapped reads supporting the novel junction in the alternative isoform *TCNS_00034499*.

A.

SPL4



B.

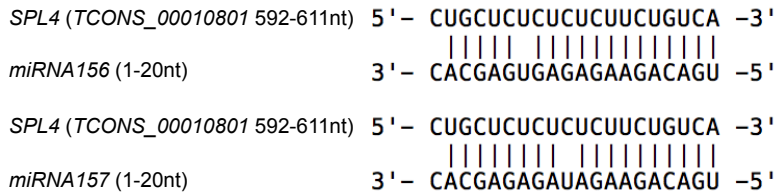


Figure S7. Differential miRNA regulation of *SPL4* splice variants. A) Gene structure of *SPL4* AS isoforms with the predicted miRNA binding site indicated. B) Complementarity of the miRNA with the predicted *SPL4* target site.

Table S1. RNA-seq library and mapping information.

Samples	# Raw reads	# Mapped reads	Percentage
WT_shoot_0_rep1	21,128,469	17,025,286	80.6%
WT_shoot_0_rep2	14,186,832	8,909,077	62.8%
WT_shoot_0_rep3	23,486,963	8,769,393	37.3%
WT_shoot_10_rep1	13,657,112	10,920,597	80.0%
WT_shoot_10_rep2	16,134,503	12,685,395	78.6%
WT_shoot_10_rep3	13,510,226	10,641,409	78.8%
WT_root_0_rep1	15,241,432	12,494,869	82.0%
WT_root_0_rep2	40,886,447	32,315,025	79.0%
WT_root_0_rep3	22,960,991	18,992,644	82.7%
WT_root_10_rep1	15,351,676	13,060,948	85.1%
WT_root_10_rep2	17,683,061	14,960,418	84.6%
WT_root_10_rep3	15,102,434	12,796,169	84.7%
jaz2_shoot_0_rep1	15,032,167	10,950,279	72.8%
jaz2_shoot_0_rep2	11,958,237	9,261,665	77.5%
jaz2_shoot_0_rep3	9,277,191	5,794,838	62.5%
jaz2_shoot_10_rep1	11,154,705	8,481,602	76.0%
jaz2_shoot_10_rep2	11,431,445	8,887,788	77.7%
jaz2_shoot_10_rep3	11,715,590	9,311,499	79.5%
jaz2_root_0_rep1	15,850,717	13,107,489	82.7%
jaz2_root_0_rep2	17,974,716	15,159,325	84.3%
jaz2_root_0_rep3	17,514,424	14,196,519	81.1%
jaz2_root_10_rep1	16,661,319	13,609,917	81.7%
jaz2_root_10_rep2	23,840,265	19,031,731	79.8%
jaz2_root_10_rep3	18,466,668	15,379,759	83.3%
jaz7_shoot_0_rep1	10,507,564	8,446,985	80.4%
jaz7_shoot_0_rep2	10,564,614	8,097,926	76.7%
jaz7_shoot_0_rep3	n.a.	n.a.	n.a.
jaz7_shoot_10_rep1	12,594,778	9,115,023	72.4%

To be continue

Samples	# Raw reads	# Mapped reads	Percentage
jaz7_shoot_10_rep2	17,867,067	13,564,544	75.9%
jaz7_shoot_10_rep3	15,161,488	11,884,760	78.4%
jaz7_root_0_rep1	17,388,880	14,375,611	82.7%
jaz7_root_0_rep2	17,181,387	14,247,505	82.9%
jaz7_root_0_rep3	15,300,499	13,159,910	86.0%
jaz7_root_10_rep1	16,636,604	13,859,228	83.3%
jaz7_root_10_rep2	13,528,403	11,442,447	84.6%
jaz7_root_10_rep3	20,662,422	17,233,780	83.4%
Total	577,601,296	452,171,360	78.3%