

**Alternative Splicing in the *Anthocyanin fruit* Gene Encoding an R2R3 MYB
Transcription Factor Affects Anthocyanin Biosynthesis in Tomato Fruits**

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SUPPLEMENTAL INFORMATION

Supplemental Table 1. List of oligonucleotide primers used for gene cloning

Gene Name	Forward primer	Reverse primer
<i>SIAN2</i> (<i>Solyc10g086250</i>)	CACCATGAATACTCCTATGTGTGC	TTAATTAAGTAGATTCCATAAGTCAATATC
<i>SIANT1</i> (<i>Solyc10g086260</i>)	CACCATGAACAGTACATCTATGTC	TTAATCAAGTAGATTCCATAAGTCAA
<i>SIANT1like</i> (<i>Solyc10g086270</i>)	CACCATGAACAGTACATCTATGTCTTCT	TTAATTAAGTAAATCCCATATATCAATATCAAC
<i>SIAN2like</i> (<i>Solyc10g086290</i>)	CACCATGAATATTGCCAAGACA	CTAATTAATAGATTCCATAGGTCAATATC
<i>SIAN1</i> (<i>Solyc09g065100</i>)	CACCATGGAGATTATACAGCCTAATAG	TTAATTAACTCTAGGGATTATCTGATTATTG
<i>SIAN11</i> (<i>Solyc03g097340</i>)	CACCATGGAGAATTCAAGTCAAGAATC	TTATACTTTAAGCAGCTGCAACTTGTTAG
<i>SIJAF13</i> (<i>Solyc08g081140</i>)	CACCATGGCTATGGGACACCAAGATC	TCAAGATTTCCATACTACTCTCTGAAGTG
<i>SIAN2like</i> ^{WT} promoter	CACCGCTACTTCTATAATGATCAAATTA	GATATGTTAAGTCACAAATACTGCAAA
<i>SIAN2like</i> ^{Alt} promoter	CACCAAAATCACTATTTTCGCC	GATATGTTAAGTCACAAATACTGCAAA

Supplemental Table 2. List of oligonucleotide primers used for quantitative RT-PCR analysis

Gene Name	Forward primer	Reverse primer
<i>SIAN2</i> (<i>Solyc10g086250</i>)	TTCCAGGAAGGACAGCAAAC	AACGAGGACGAGAATGAGGA
<i>SIANT1</i> (<i>Solyc10g086260</i>)	ATAAGTCATGAAAATTGGGGTGAAT	AGATTCCATAAGTCAATTCAGCAG
<i>SIANT1like^{wt}</i> (<i>Solyc10g086270</i>)	GAGGAGGTGTAAGTACTGATTATGGAAA	TCATCCCAACCATCACTTTG
<i>SIANT1like^{alt}</i> (<i>Solyc10g086270</i>)	GAGGAGGTGTAAGTACTAATTATGAAAA	TCATCCCAACCATCACTTTG
<i>SIAN2like</i> (<i>Solyc10g086290</i>)	ATATTGCCAAGACATTGGGAGTG	CCATACTTGTCAATACATTTCTCA
<i>SIAN1</i> (<i>Solyc09g065100</i>)	CTAAGAGTGCCCCGCATACAGAC	ATCCGAAGTGGAGTGCTCAGATA
<i>SIJAF13</i> (<i>Solyc08g081140</i>)	TCAGGGGATCACTACCGAAC	TCCCATCAAGGTTGGAAGAC
<i>SIAN11</i> (<i>Solyc03g097340</i>)	ATGAAGTGGAGCCGAGAAGA	TCCATCAGCAGAAACAGA
<i>SIMYB-ATV</i> (<i>Solyc07g052490</i>)	GATTGGAATAGATCAAGCACATCA	TTCGTTGGTAGTCTCTAATGCAAC
<i>SIDFR</i> (<i>Solyc02g085020</i>) ^{**}	TCCGAAGACGACAACGGTTT	TGACAAGCCAAGAGCCGATAA
<i>SIANS</i> (<i>Solyc08g080040</i>) ^{**}	GAAGTAGCACTTGGCGTCGAA	TTGCAAGCCAGGCACCATA
<i>SIEF1a</i> (<i>Solyc06g005060</i>)	GCTGCTGTAACAAGATGGATGC	GGGGATTTTGTGAGGTTGTAA
<i>SIASR1</i> (<i>Solyc04g071610</i>)	CCTGTTCCACCACAAGGACAA	GTGCCAAGTTTACCGATTTC

*from Qiu et al. (2016)

**from Bovy et al. (2002)

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SLANT1      MNSTMSSSLGVRKGSWTEDEDFLLRKCIDKYEGEKWHLVPIRAGLNCRCKSCRLRWLNLYL
SLANT1like  MNSTMSSSLGVRKGSWTEDEDFLLRKCIDKYEGEKWHLVPIRAGLNCRCKSCRLRWLNLYL
SLAN2       MNTPMCASLGVRKGSWTEQEDSLLRKCIDKYEGEKWHLVPPARAGLNCRCKSCRLRWLNLYL
SLAN2like   --MNIAKTLGVRKGSWTEDEDFLLRKCIDKYEGEKWHLVPPARAGLNCRCKSCRLRWLNLYL
              :*****:* * * * :*****:
              :*****:* * * * :*****:

          R2
SLANT1      RPHIKRGDFQDEVDLILRLHLKLGNRWSLIAGRLPGRTANDVKNYWNTHLHKLLITPK-
SLANT1like  RPHIKRGDFASDEIDLILRLHLKLGNRWSLIAGRLPGRTANDVKNYWNTHLHKLLITPK-
SLAN2       RPHIKRGDFAPDEVDLILRLHLKLGNRWSLIAGRLPGRTANDVKNYWNTHFHKLLSI IAP
SLAN2like   RPHIKRGDFASDEIDLILRLHLKLGNRWSLIAGRLPGRTANDVKNYWNTHLHKLLITP-
              ***** * :*****:
              ***** * :*****:

          R3
SLANT1      -----IVPREKTNNKCGEISTKIEI IKPQPKYFSSTMKN-----ITNNIVILD
SLANT1like  -----IVPREKFKSKRGEISTKIEI IKPQARKFISNTEKN-----VTNNIVIVD
SLAN2       HLHPHPRPRSHPLRLQIKHKS IAVTKNEI IRPQPRNFSNVKKNDSHWCNKSMTINTSDKD
SLAN2like   -----OIOENKYNKTLKI ITESTILRPRPRPRPTFSSENNISWCTNNSMITNLDKD
              . . . . :*:* . . . . :* *

SLANT1      EEHCKEIKS-----EKQTPDASMDNVQWWINLLENCNDDEEED-----VINYE
SLANT1like  KEEECREIIS-----EKQTRDASIDNGDEWWANLLENCNDVVEEEEGAGGVNTNYE
SLAN2       DKRCN-EIVVNICKEKPIGENTSS--IDDGVEWWTNLENCNDEIEEETAN-----VINF
SLAN2like   DEQRNKEI AVNICEKPTRETPSSIDDGVKWWTNLENCNDEVEEEEGGGGVDTYDK
              . . . * . . . * : * * * * . . . *

SLANT1      KTLTSLHHEKSPPLNIGEGNSMQQGISHENWGEFSLNLQPMQGGVQNDDFS A EIDLWN
SLANT1like  KTLTSLHHEITPPLNGGG-----NFMQQGSDGWDFFVVDIDLWN
SLAN2       KTFPTMLLHEIISPPLINDED-----NSMQGPTNWNDDFSVDIDLWN
SLAN2like   ---FEENKLLPNLCEE-----HNSTTMQHGENDDFSVDIDLWN
              : . : * . . . . : . . . . * * * . : * * * :

SLANT1      LLD
SLANT1like  LLN
SLAN2       LLN
SLAN2like   LPN
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SLAN2       MNTPMCASLGVRKGSWTEQEDSLLRDCIDKYEGEKWHLVPPARAGLNCRCKSCRLRWLNLYL
SLAN2like   --MNIAKTLGVRKGSWTEDEDFLLRKCIDKYEGEKWHLVPPARAGLNCRCKSCRLRWLNLYL
SLANT1      MNSTMSSSLGVRKGSWTEDEDFLLRKCIDKYEGEKWHLVPIRAGLNCRCKSCRLRWLNLYL
SLANT1like  MNSTMSSSLGVRKGSWTEQEDSLLRKCIDKYEGEKWHLVPIRAGLNCRCKSCRLRWLNLYL
              :*****:* * * * :*****:
              :*****:* * * * :*****:

          R2
SLAN2       RPHIKRGDFAPDEVDLILRLHLKLGNRWSLIAGRLPGRTANDVKNYWNTHFHKLLSI IAP
SLAN2like  RPHIKRGDFALDEIDLILRLHLKLGNRWSLIAGRLPGRTANDVKNYWNTHLHKLLITPK-
SLANT1      RPHIKRGDFQDEVDLILRLHLKLGNRWSLIAGRLPGRTANDVKNYWNTHLHKLLITPK-
SLANT1like  RPHIKRGDFASDEIDLILRLHLKLGNRWSLIAGRLPGRTANDVKNYWNTHLHKLLITPK-
              ***** * :*****:
              ***** * :*****:

          R3
SLAN2       HLHPHPRPRSHPLRLQIKHKS IAVTKNEI IRPQPRNFSNVKKNDSHWCNKSMTINTLDKD
SLAN2like  QIQEN--KYNNTLKI ITESTILRPRPRPGPRTFS--SENNISWCTNNSMITINTLDKD
SLANT1      VPRESK-----INNKCGEISTKIEI IKPQPKYFSSTMKN-----VTNNIVILD
SLANT1like  VPRESK-----FKSKRGEISTKIEI IKPQARKFISNTEKN-----ITNNIVIVD
              : . . . . : * * . . . . : . . . . : * *

SLAN2       DKRCN-EIVVNICKEKPIGENTSS--IDDGVEWWTNLENCNDEIEEETAN-----TNFGK
SLAN2like  DEQHNKEI AVNICEKPTKTPSSIDDGVEWWTNLENCNDEVEEEEGAGGVNTNYE
SLANT1      EEHCKEIKS-----EKQTPDASMDNVQWWINLLENCNDDEEED-----VINYE
SLANT1like  KEEECREIIS-----EKQTRDASIDNGDEWWANLLENCNDVVEEEEGAGGVNTNYE
SLAN2       DKRCN-EIVVNICKEKPIGENTSS--IDDGVEWWTNLENCNDEIEEETAN-----VINF
SLAN2like   DEQRNKEI AVNICEKPTRETPSSIDDGVKWWTNLENCNDEVEEEEGGGGVDTYDK
              . . . * . . . * : * * * * . . . *

SLAN2       TPTMLLHEIISPPLVNGED-----NSMQGPTNWNDDFSVDIDLWN
SLAN2like  ---FEENKLLPNLLEE-----HNSTTMQHGENDDFSVDIDLWN
SLANT1      TLTSLHHEIISPPLNIGEGNSMQQGISHENWGEFSLNLQPMQGGVQNDDFS A EIDLWN
SLANT1like  TITSLHHEITPPLNGGG-----NIMQQESDQWDFFVVDIDLWN
              : . : * . . . . : . . . . * * * . : * * * :

SLAN2       LN
SLAN2like   FN
SLANT1      LD
SLANT1like  LN
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Supplemental Figure 1. Comparative analysis of the WT and the *Aft* sequences of the four R2R3 MYB proteins under study.

(A) ClustalW alignment of WT R2R3 MYB proteins codified from the four genes located in the distal part of the long arm of chromosome 10. (B) ClustalW alignment of *Aft* R2R3 MYB proteins codified from the four genes located in the distal part of the long arm of chromosome 10. R2 and R3 MYB domains are underlined. Symbols are as follows: “*” indicates perfect alignment; “:” indicates a site belonging to group exhibiting strong similarity; and “.” indicates a site belonging to a group exhibiting weak similarity.

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SIAN2_WT      MNTPMCASLGVKRGSWTEQEDSLLRDCIQKYGEGKWHLVPARAGLNRCRKSCLRWLNLYL
SIAN2_Aft    MNTPMCASLGVKRGSWTEQEDSLLRNCIQKYGEGKWHLVPARAGLNRCRKSCLRWLNLYL
*****
                R2
SIAN2_WT      RPHIKRGDFAPDEVLDLILRLHKLKLNRSWLIAGRLPGRTEANDVKNYWNTHFHKKLSIIAP
SIAN2_Aft    RPHIKRGDFAPDEVLDLILRLHKLKLNRSWLIAGRLPGRTEANDVKNYWNTHFHKKLSIIAP
*****
                R3
SIAN2_WT      HLHPHPRPRSHPRLQIKHKSIAVTKNEIIRPQPRNF#SNVKKNDSHWCNNKSMITNTLDKD
SIAN2_Aft    HLHPHPRPRSHPRLQIKHKSIAVTKNEIIRPQPRNF#SNVKKNDSHWCNNKSMITNTSDKD
*****

SIAN2_WT      DKRCNEIVVNICEKPIGENTSSIDGVEWWTNLENCIEIEEETANTNFGKTPTMLLHEE
SIAN2_Aft    DKRCNEIVVNICEKPIGENTSSIDGVEWWTNLENCIEIEEETANTNFGKTPTMLLHEE
*****

SIAN2_WT      ISPPLVNGEDNSMQQGPPTNNWDDFSTDIDLWNLLN
SIAN2_Aft    ISPPLINDEEDNSMQQGPPTNNWDDFSTDIDLWNLLN
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B

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SIANT1_WT     MNSTMSLGVKRGSWTDEEDFLLRKCIDKYGEGKWHLVPPIRAGLNRCRKSCLRWLNLYL
SIANT1_Aft   MNSTMSLGVKRGSWTDEEDFLLRKCIDKYGEGKWHLVPPIRAGLNRCRKSCLRWLNLYL
*****
                R2
SIANT1_WT     RPHIKRGDFEQDEVLDLILRLHKLKLNRSWLIAGRLPGRTEANDVKNYWNTNLLRKLNTTKI
SIANT1_Aft   RPHIKRGDFEQDEVLDLILRLHKLKLNRSWLIAGRLPGRTEANDVKNYWNTNLLRKLNTTKI
*****
                R3
SIANT1_WT     VPREKINNKCGEISTKIEIIRKQPRKY#SSTMKNVTNNVILDEEHCKEIISEKQTPDA
SIANT1_Aft   VPREKTNKCGEISTKIEIIRKQPRKY#SSTMKNVTNNVILDEEHCKEIISEKQTPDA
*****

SIANT1_WT     SMDNVDPWWINLLENCNDDIEEDEVVINYEKTLSLLHHEEISPPPLNIGEGNSMQQGQIS
SIANT1_Aft   SMDNVQVWINLLENCNDDIEEDEVVINYEKTLSLLHHEEKSPPLNIGEGNSMQQGQIS
*****

SIANT1_WT     HENWGEFSLNLPMPQQGVQNDDFSAEIDLWNLLD
SIANT1_Aft   HENWGEFSLNLQPMQQGVQNDDFSAEIDLWNLLD
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C

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SIANT1like_WT MNSTMSLGVKRGSWTEQEDLLLRKCIDKYGEGKWHLVPPIRAGLNRCRKSCLRWLNLYL
SIANT1like_Aft MNSTMSLGVKRGSWTEEDFLLRKCIDKYGEGKWHLVPPIRAGLNRCRKSCLRWLNLYL
*****
                R2
SIANT1like_WT RPHIKRGDFASDEIDLILRLHKLKLNRSWLIAGRLPGRTEANDVKNYWNTNLLRKNVITKI
SIANT1like_Aft RPHIKRGDFASDEIDLILRLHKLKLNRSWLIAGRLPGRTEANDVKNYWNTNLLRKNVITKI
*****
                R3
SIANT1like_WT VPREFKSKRGEISTKIEIIRKQARKFISNTEKNITNNVIVDKKEEKEIISEKQTRDA
SIANT1like_Aft VPREFKSKRGEISTKIEIIRKQARKFISNTEKNVTNNVIVDKKEEEREIISEKQTRDA
*****

SIANT1like_WT SIDNGDEWWANLLENCNDDVVEEEE-GGGGVTDYKGTITSLLHHEITPPLNGGGNIMQQ
SIANT1like_Aft SIDNGDEWWANLLENCNDDVVEEEEAGGGVTDYKGTITSLLHHEITPPLNGGGNFMQQ
*****

SIANT1like_WT EQSDGWDDFFVDIDIWDLN
SIANT1like_Aft GQSDGWDDFFVDIDIWDLN
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D

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SIAN2like_WT  MNIAKTLGVKRGSWTEDEDILLRKCIDKYGEGKWHLVPFRAGLNRCRKSCLRWLNLYL
SIAN2like_Aft MNIAKTLGVKRGSWTEDEDILLRKCIDKYGEGKWHLVPFRAGLNRCRKSCLRWLNLYL
*****
                R2
SIAN2like_WT  HIKRGDFALDEIDLILRLHKLKLNRSWLIAGRLPGRTEANDVKNYWNTLHKKLLITPQI
SIAN2like_Aft HIKRGDFALDEIDLILRLHKLKLNRSWLIAGRLPGRTEANDVKNYWNTLHKKLLITP-QI
*****
                R3
SIAN2like_WT  QENKYNLTKIITESTILRPRRPGQPRTF#SENNISWCTNNSMITNTLDKDEQHNKE
SIAN2like_Aft QENKYNLTKIITESTILRPRRPP--RPRTF#SENNISWCTNNSMITNTLDKDEQRNKE
*****

SIAN2like_WT  IAVNICEKPTKKTSSSIDDGVQWWTNLENWKEFEEEAVALNFEENKLLPNLLYEE
SIAN2like_Aft IAVNICEKPTRETPSSSIDDGVQWWTNLENWKEFEEEAVALNFEENKLLPNLLCEE
*****

SIAN2like_WT  HNSTTMQHGENDDFSVDIDLWNLFN
SIAN2like_Aft HNSTTMQHGENDDFSVDIDLWNLFN
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Supplemental Figure 2. Comparative analysis of the sequences of the R2R3 MYB proteins encoded by the WT and the *Aft* alleles of each gene. (A) ClustalW alignments of WT and *Aft* SIAN2 proteins. (B) ClustalW alignments of WT and *Aft* SIANT1 proteins. (C) ClustalW alignments of WT and *Aft* SIANT1like proteins. (D) ClustalW alignments of WT and *Aft*

SIAN2like proteins. R2 and R3 MYB domains are underlined. In each alignment the [DE]Lx2[RK]x3Lx6Lx3R motif containing the bHLH-binding site (Zimmermann et al., 2004) is boxed in grey, the aminoacidic signature [A/S/G]NDV typical of dicot R2R3 MYBs promoting anthocyanin (Lin-Wang et al., 2010; Heppel et al., 2013) is boxed in light purple and the KPRPR[ST]F motif, conserved in Arabidopsis MYBs involved in anthocyanin synthesis (Stracke et al., 2001), is boxed in green. Symbols are as follows: “*” indicates perfect alignment; “:” indicates a site belonging to group exhibiting strong similarity; and “.” indicates a site belonging to a group exhibiting weak similarity.

promSIAN2like ^{WT}	AAAATCAATATTTCGCCCATGAAATGCAACTGAACCTGTATTGAAAT.....AACTCT	54
promSIAN2like ^{Aft}	AAAATCAATATTTCGCCCATGAAATGCAACTGAACCTGTATTGAAATCTGAAAAACATCTAATAACTCT	70
promScAN2like	AAAATCAATATTTCGCCCATGAAATGCAACTGAACCTGTATTGAAATCTGAAAAACATCTAATAACTCT	70
consensus	aaaatca tatttcgcccat aaa gcaactgaactgtatt gaaat aactct	
promSIAN2like ^{WT}	TCCTTTTCCTTTTTATTTTTATCTTCTTTTTCAGAAAACCTTTTTTCCATTCAAATATATTTAATG	124
promSIAN2like ^{Aft}	TCCTTTTCCTTTTTATTTTTATCTTCTTTTTCAGAAAACCTTTTTTCCATTCAAATATATTTAATG	140
promScAN2like	TCCTTTTCCTTTTTATTTTTATCTTCTTTTTCAGAAAACCTTTTTTCCATTCAAATATATTTAATG	140
consensus	tctttttcctTTTTATTTTTATCTTCTTTTTCAGAAAACCTTTTTTCCATTCAAATATATTTAATG	
	Myb binding site	
promSIAN2like ^{WT}	TTTAAATATGCTTCAGCATAAGAAAAAGTATATTCAAACAGTTAAACATAAATTTGTTAAATATAATCA	194
promSIAN2like ^{Aft}	TTTAAATATGCTTCAGCATAAGAAAAAGTATATTCAAACAGTTAAACATAAATTTGTTAAATATAATCA	210
promScAN2like	TTTAAATATGCTTCAGCATAAGAAAAAGTATATTCAAACAGTTAAACATAAATTTGTTAAATATAATCA	210
consensus	tttaaataatgcttcagcataagaaaaagtataatcaaacagttaaacataaatttgtttaaataataatca	
promSIAN2like ^{WT}	TCGCCACTCCCGTCTCAACTTCAATTTTTTGAATTTTAAAAAAAATAAATAACATATAATAGCCC	263
promSIAN2like ^{Aft}	TCGCCACTCCCGTCTCAACTTCAATTTTTTGAATTTTAAAAAAAATAAATAACATATAATAGCCC	280
promScAN2like	TCGCCACTCCCGTCTCAACTTCAATTTTTTGAATTTTAAAAAAAATAAATAACATATAATAGCCC	279
consensus	tcgccac ctccgtcttcaacttcaatTTTTTGAATTTTAAAAAAAATAAATAACATATAATAGCCC	
promSIAN2like ^{WT}	ATATCTATGATCTAAATTTATGACATTATATTTAATTTTGCAAAATCAGAGGAACCATATGAAA	333
promSIAN2like ^{Aft}	ATATCTATGATCTAAATTTATGACATTATATTTAATTTTGCAAAATCAGAGGAACCATATGAAA	349
promScAN2like	ATATCTATGATCTAAATTTATGACATTATATTTAATTTTGCAAAATCAGAGGAACCATATGAAA	348
consensus	atatctatgatctaa tttatgacattatattttaatttttgcAAAATCAGAGGAACCATATGAAA	
	GATA	
promSIAN2like ^{WT}	CATTACGGCACATTTGGTTGATTACAATCCATCCAGTCCCTTCTATACTTTACTATTGTTCTTAATATC	403
promSIAN2like ^{Aft}	CATTACGGCACATTTGGTTGATTACAATCCATCCAGTCCCTTCTATACTTTACTATTGTTCTTAATATC	419
promScAN2like	CATTACGGCACATTTGGTTGATTACAATCCATCCAGTCCCTTCTATACTTTACTATTGTTCTTAATATC	418
consensus	cattacggcacatTTGGTTGATTACAATCCATCCAGTCCCTTCTATACTTTACTATTGTTCTTAATATC	
	bHLH binding site	
promSIAN2like ^{WT}	TATATAGATCGATAGATTTTCACTCATTTTGTATAACAATTTGTGGAAGAGCAAAGAAAAAAAACC	473
promSIAN2like ^{Aft}	TATATAGATCGATAGATTTTCACTCATTTTGTATAACAATTTGTGGAAGAGCAAAGAAAAAAAACC	489
promScAN2like	TATATAGATCGATAGATTTTCACTCATTTTGTATAACAATTTGTGGAAGAGCAAAGAAAAAAAACC	488
consensus	tatatagatcgatagatTTTCACTCATTTTGTATAACAATTTGTGGAAGAGCAAAGAAAAAAAACC	
	GATA Myb/SANT HD-ZIP	
promSIAN2like ^{WT}	ACCACCAAAGTACAAAAGGGTTTCTAAAAGGTCCTTTTTCTATATAGTTGTTGTTTTAGTATATTTCGT	543
promSIAN2like ^{Aft}	ACCACCAAAGTACAAAAGGGTTTCTAAAAGGTCCTTTTTCTATATAGTTGTTGTTTTAGTATATTTCGT	559
promScAN2like	ACCACCAAAGTACAAAAGGGTTTCTAAAAGGTCCTTTTTCTATATAGTTGTTGTTTTAGTATATTTCGT	558
consensus	accaccaaagtacaaaagggTTTTCTAAAAGGTCCTTTTTCTATATAGTTGTTGTTTTAGTATATTTCGT	
promSIAN2like ^{WT}	TATCATCCCCTTGTTTAACTTTACTTTCTTCCCTCTTTTATTCATTTTAAAAATTCACCTCACAATAT	613
promSIAN2like ^{Aft}	TATCATCCCCTTGTTTAACTTTACTTTCTTCCCTCTTTTATTCATTTTAAAAATTCACCTCACAATAT	629
promScAN2like	TATCATCCCCTTGTTTAACTTTACTTTCTTCCCTCTTTTATTCATTTTAAAAATTCACCTCACAATAT	627
consensus	tatcatccccttgTTTAACTTTACTTTCTTCCCTCTTTTATTCATTTTAAAAATTCACCTCACAATAT	
	Myb binding site	
promSIAN2like ^{WT}	TAAATCATA.....GTTTAAATATGTAAAGATTATAAAATTTGAAGTGTTTGAATT	664
promSIAN2like ^{Aft}	TAAATCATA.....GTTTAAATATGTAAAGATTATAAAATTTGAAGTGTTTGAATT	674
promScAN2like	TAAATCATA.....GTTTAAATATGTAAAGATTATAAAATTTGAAGTGTTTGAATT	697
consensus	ta tca tt a t gattataaaatTTGAAGTGTTTGAATT	
promSIAN2like ^{WT}	TAGGGGTAGAGTATTAGCATGTATACATGTTGATTGAATTCAAATACATTTATATAAATAATATATGT	734
promSIAN2like ^{Aft}	TAGGGGTAGAGTATTAGCATGTATACATGTTGATTGAATTCAAATACATTTATATAAATAATATATGT	744
promScAN2like	TAGGGGTAGAGTATTAGCATGTATACATGTTGATTGAATTCAAATACATTTATATAAATAATATATGT	767
consensus	taggggtagagTATTAGCATGTATACATGTTGATTGAATTCAAATACATTTATATAAATAATATATGT	
	Myb related	
promSIAN2like ^{WT}	ATGTTAATAAATTTATTAATATATACAATATTTATTTTACTTAAATCGTTATTGTAGGCCTTA	804
promSIAN2like ^{Aft}	ATGTTAATAAATTTATTAATATATACAATATTTATTTTACTTAAATCGTTATTGTAGGCCTTA	814
promScAN2like	ATGTTAATAAATTTATTAATATATACAATATTTATTTTACTTAAATCGTTATTGTAGGCCTTA	837
consensus	atgTTAATAAATTTATTAATATATACAATATTTATTTTACTTAAATCGTTATTGTAGGCCTTA	
promSIAN2like ^{WT}	AACTCAATAGTTGCTTTTGGTTTTGGATTTATTTGCAGTATTTGTGACTTAACATATC	862
promSIAN2like ^{Aft}	AACTCAATAGTTGCTTTTGGTTTTGGATTTATTTGCAGTATTTGTGACTTAACATATC	871
promScAN2like	AACTCAATAGTTGCTTTTGGTTTTGGATTTATTTGCAGTATTTGTGACTTAACATATC	894
consensus	aactcaatagttgctTTTGGTTTTGGATTTATTTGCAGTATTTGTGACTTAACATATC	
	WRKY	

Supplemental Figure 4. Alignment of 900 bp of *AN2like* promoter sequences of WT, *Aft* and *S. chilense* plants. WT and *Aft* sequences are from the present work. The sequence of the *S. chilense* promoter is from Stam et al. (2019). Major transcription factors binding sites are shown in red.

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Solyc10g086290.1.1 ATGAATATTGCCAAGACATTGGGAGTGAGAAAAGGTTTCATGGACTGAAGATGAAGATATTCTTTTGGAGAAAT
SIAN2like_Aft GTATTGACAAGTATGGAGAAGGAAAGTGGCATCTTGTTCCTTTTAGAGCTGTAAGCGAAATTAAGATTTTA
CTTTTATAAATTTTAAATTTTATGATAATAAATAGTCTCAAAATTTAGTAGATATTAAGTAATAATTTGTTA
ATGCAAAAATAATATTTAGGCAAAATCTATAGATATACATAAATTTCCCTTTTAAAGAAAAGAGAAACCTTAA
CTTTTGGTGTGATAGTGGGCTCCCAACCTATAACTAGCATGAATAGCAATTTTATGCTCCCTTTTATAC
CGAGTCAATAATCAATTTGTTAGGAGTTTACAATTAATATACACATATATTTAGTAAATTTTTTATGCTG
AATATAACACTACCAAAAAAATTTACTGGATTCGTTCAATCCCAAAATCCCACTTACTATTATTCATGTG
AAATATATGCTGCTCAATAGATGTCGAAGAGTTGTAGACTGAGGTGGTGAATATATCAAGGCCATATC
AAGAGAGGCTGCTTGTCTGGATGAATAGATCTCATTTTGGAGCTTCAAGACTTCTAGCAGCTTACGCAATAG
TCAAAAATTTGTTAAAAAATATTTAAAAATTTTGTACATATATATTCACGAAAAGTAATTTTGACATA
TAAATTTACGTACATACTAGTCTCTCGAATATATTTAGTAAGTTATCTTTGATGCCATTTTTTATATTTTT
TTGGTTTGAATGTCACCTTATTGCTGGGAGACTTCCGGAAGAACAGCAACAGATGTGAAAACATTTGGAAAC
ACACACCTACACAGAGTATTATAAATCTCCTCCTCAGATACAAGAGAAATAGTACAATAATACCCCTCAAGA
TTATCACTGAAAGCATACTACGACCACGACCAAGACCAGGACCTCAACCTCGAACCTTCTCAAGTGAAAA
TAATATTTCTTGTGTCATAACAATAGTATGATCACAACACATTTAGCAAAAGATGACGAACACACACAAAA
GAAATCGCAGTAATATTTGTGAGAAGCCAAACAAAAAACACCCGTCATCTATAGACGATGATGGATTC
AAATGTTGACAAATTTACTGGAAAAATTTGGAAGAATTTGAGGAAGAACCAACAGCAGTATGAACCTTGAGGA
AGAAAATAGTTGTGCCAAATTTGTTGATGAGGAACATAATTCACCAACCATGCAACATGGAGAAAATGAT
GACTTTTCAGTTGATATTGACCTATGGAATCTATTTAATTAG

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B

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ATGAATATTGCCAAGACATTGGGAGTGAGAAAAGGTTTCATGGACTGAAGATGAAGATATTCTTTTGGAGAAAT
GTATTGACAAGTATGGAGAAGGAAAGTGGCATCTTGTTCCTTTTAGAGCTGTAAGCGAAATTAAGATTTTA
ATTTTATGATTTTAAATTTTATGATAATAAATAGTCTCAAAATTTAGTAGATATTAAGTAATAATTTGTTA
TGCAAAAATACTATTAGGCAAAATCTATAGATATACATAAATTTCCCTTTTAAAGAAAAGAGAAACCTTAA
CTTTTGGTGTGATAGTGGGCTCCCAACCTATAACTAGCATGAATAGCAATTTTATGCTCCCTTTTATAC
AGTCTCAATAATTAATTTGTTAGGAGTTTACAATTAATATATATATATTTGATTAATTTTTTATGTTTATA
TACAATATCTATGAAAAAATTTACTAGGTTCTGTTCAACCCCAAAATCCCACTTACTATTATTCACGTTGATTA
TATGCTGCTCAATAGATGTCGAAGAGTTGTAGACTGAGGTGGTGAATATCTAAGGCCACATATCAAGA
GAGGTGACTTTGCTATGGAATAGATCTCATTTTGGAGCTTCAAGACTTCTAGGCAATAGCAAGTCAAGTCA
AAATATGTTTAAAGAAATTTAAAAATTTTGTACATATATTTTACGAAAAGAAATTTTGTACATCAAAAT
TGTGTACATATGCTTCCCGTATATATTTAAGTAGTTGTTCTTGTATGCCATATTTTATTTTCTTTTGGTT
TAGATGTCACCTTATTGCTGGGAGACTTCCGGGAAGAACGCAACAGATGTGAAAAACTATTGGAACACACAC
CTACACAGAGTATTATAAATCTCCTCAGATACAAGAGAAATAGTACAATAAACCCTCAAGATTTACCTG
AAAGCACTATCTACGACCACGACCAAGACTTCCGACTCCGAACTTCAAGTGAATAATATTTCTTGGTG
CACTAACAATAGTATGATCACAACACATTTAGCAAAAGATGACCAACACGCAACAGAAATCGCATTAAT
ATTTGTGAGAAGCCAAACAGAAACACCCGTCATCTGCTATAGACGATGATGGAGTTAAATGGTGGACAAAT
TACTGGAAAAATTTGGAAGAATTTGAGGAAGAAGCAACAGCAGTATGAACCTTTGAGGAAGAAAATTAAGTTGT
ACCAAAATTTGTTGTGAGGAACATAATTCACCAACCATGCAACATGGAGAAAATGATGACTTTTCAGTTGAT
ATTGACCTATGGAATCTATTTAATTAG

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Supplemental Figure 5. Alternative splicing of WT *SIAN2like* gene.

(A) ClustalW alignment of the cds of *SIAN2like*^{Att} with the sequence of the cds of *Solyc10g086290.1.1* (SOL Genomics Network). (B) Genomic sequence of *SIAN2like*^{Att}, showing the canonical splicing sites, represented in yellow, at the boundaries between exons (in green) and introns. (C) Genomic sequence of *Solyc10g086290.1* (SOL Genomics Network), corresponding to *SIAN2like*^{WT}, showing the canonical splicing sites, represented in yellow, at the boundaries between exons (in green) and introns. (D-E) Genomic sequence of *Solyc10g086290.1* (SOL Genomics Network), corresponding to *SIAN2like*^{WT}, showing the canonical (represented in yellow), and the alternative (represented in orange) splicing sites at the boundaries between exons (in green) and introns. In (D) and (E) the intro-exon structures of the WT pre-mRNAs of *SIAN2like* inferred from the sequences of the two transcripts cloned in WT fruit peel are shown. The premature stop codons are highlighted in red. Sequence D corresponds to the pre-mRNA of transcript 1. Sequence E corresponds to the pre-mRNA of transcript 2.

C

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ATGAATATTGCCAAGACATTGGGAGTGAGAAAAGGTTTCATGGACTGAAGATGAAGATATTCTTTTGGAGAAAT
GTATTGACAAGTATGGAGAAGGAAAGTGGCATCTTGTTCCTTTTAGAGCTGTAAGCGAAATTAAGATTTTA
CTTTTATAAATTTTAAATTTTATGATAATAAATAGTCTCAAAATTTAGTAGATATTAAGTAATAATTTGTTA
ATGCAAAAATAATATTTAGGCAAAATCTATAGATATACATAAATTTCCCTTTTAAAGAAAAGAGAAACCTTAA
CTTTTGGTGTGATAGTGGGCTCCCAACCTATAACTAGCATGAATAGCAATTTTATGCTCCCTTTTATAC
CGAGTCAATAATCAATTTGTTAGGAGTTTACAATTAATATACACATATATTTAGTAAATTTTTTATGCTG
AATATAACACTACCAAAAAAATTTACTGGATTCGTTCAATCCCAAAATCCCACTTACTATTATTCATGTG
AAATATATGCTGCTCAATAGATGTCGAAGAGTTGTAGACTGAGGTGGTGAATATCTAAGGCCATATC
AAGAGAGGCTGCTTGTCTGGATGAATAGATCTCATTTTGGAGCTTCAAGACTTCTAGCAGCTTACGCAATAG
TCAAAAATTTGTTAAAAAATATTTAAAAATTTTGTACATATATATTCACGAAAAGTAATTTTGACATA
TAAATTTACGTACATACTAGTCTCTCGAATATATTTAGTAAGTTATCTTTGATGCCATTTTTTATATTTTT
TTGGTTTGAATGTCACCTTATTGCTGGGAGACTTCCGGAAGAACAGCAACAGATGTGAAAACATTTGGAAAC
ACACACCTACACAGAGTATTATAAATCTCCTCCTCAGATACAAGAGAAATAGTACAATAATACCCCTCAAGA
TTATCACTGAAAGCATACTACGACCACGACCAAGACCAGGACCTCAACCTCGAACCTTCTCAAGTGAAAA
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AAATGTTGACAAATTTACTGGAAAAATTTGGAAGAATTTGAGGAAGAACCAACAGCAGTATGAACCTTGAGGA
AGAAAATAGTTGTGCCAAATTTGTTGATGAGGAACATAATTCACCAACCATGCAACATGGAGAAAATGAT
GACTTTTCAGTTGATATTGACCTATGGAATCTATTTAATTAG

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D

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ATGAATATTGCCAAGACATTGGGAGTGAGAAAAGGTTTCATGGACTGAAGATGAAGATATTCTTTTGGAGAAAT
GTATTGACAAGTATGGAGAAGGAAAGTGGCATCTTGTTCCTTTTAGAGCTGTAAGCGAAATTAAGATTTTA
CTTTTATAAATTTTAAATTTTATGATAATAAATAGTCTCAAAATTTAGTAGATATTAAGTAATAATTTGTTA
ATGCAAAAATAATATTTAGGCAAAATCTATAGATATACATAAATTTCCCTTTTAAAGAAAAGAGAAACCTTAA
CTTTTGGTGTGATAGTGGGCTCCCAACCTATAACTAGCATGAATAGCAATTTTATGCTCCCTTTTATAC
CGAGTCAATAATCAATTTGTTAGGAGTTTACAATTAATATACACATATATTTAGTAAATTTTTTATGCTG
AATATAACACTACCAAAAAAATTTACTGGATTCGTTCAATCCCAAAATCCCACTTACTATTATTCATGTG
AAATATATGCTGCTCAATAGATGTCGAAGAGTTGTAGACTGAGGTGGTGAATATCTAAGGCCATATC
AAGAGAGGCTGCTTGTCTGGATGAATAGATCTCATTTTGGAGCTTCAAGACTTCTAGCAGCTTACGCAATAG
TCAAAAATTTGTTAAAAAATATTTAAAAATTTTGTACATATATATTCACGAAAAGTAATTTTGACATA
TAAATTTACGTACATACTAGTCTCTCGAATATATTTAGTAAGTTATCTTTGATGCCATTTTTTATATTTTT
TTGGTTTGAATGTCACCTTATTGCTGGGAGACTTCCGGAAGAACAGCAACAGATGTGAAAACATTTGGAAAC
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TAATATTTCTTGTGTCATAACAATAGTATGATCACAACACATTTAGCAAAAGATGACGAACACACACAAAA
GAAATCGCAGTAATATTTGTGAGAAGCCAAACAAAAAACACCCGTCATCTATAGACGATGATGGATTC
AAATGTTGACAAATTTACTGGAAAAATTTGGAAGAATTTGAGGAAGAACCAACAGCAGTATGAACCTTGAGGA
AGAAAATAGTTGTGCCAAATTTGTTGATGAGGAACATAATTCACCAACCATGCAACATGGAGAAAATGAT
GACTTTTCAGTTGATATTGACCTATGGAATCTATTTAATTAG

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E

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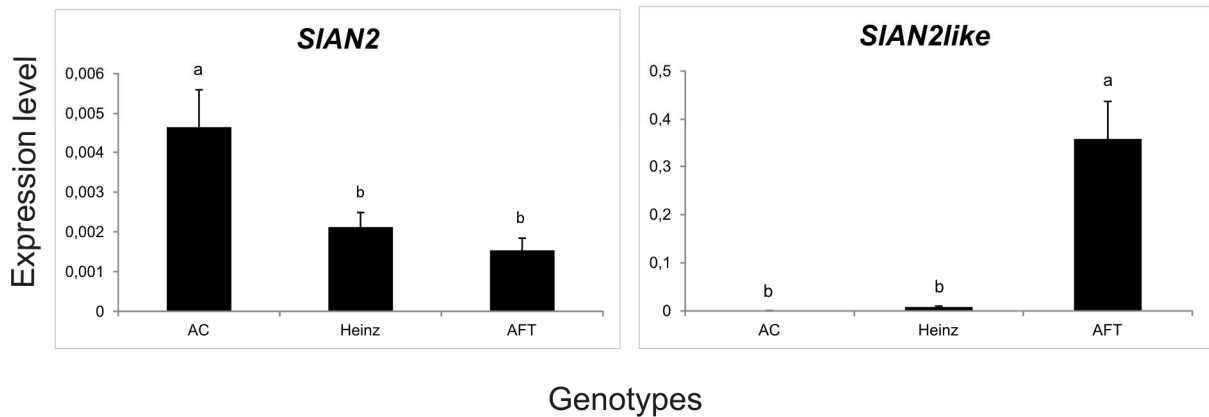
ATGAATATTGCCAAGACATTGGGAGTGAGAAAAGGTTTCATGGACTGAAGATGAAGATATTCTTTTGGAGAAAT
GTATTGACAAGTATGGAGAAGGAAAGTGGCATCTTGTTCCTTTTAGAGCTGTAAGCGAAATTAAGATTTTA
CTTTTATAAATTTTAAATTTTATGATAATAAATAGTCTCAAAATTTAGTAGATATTAAGTAATAATTTGTTA
ATGCAAAAATAATATTTAGGCAAAATCTATAGATATACATAAATTTCCCTTTTAAAGAAAAGAGAAACCTTAA
CTTTTGGTGTGATAGTGGGCTCCCAACCTATAACTAGCATGAATAGCAATTTTATGCTCCCTTTTATAC
CGAGTCAATAATCAATTTGTTAGGAGTTTACAATTAATATACACATATATTTAGTAAATTTTTTATGCTG
AATATAACACTACCAAAAAAATTTACTGGATTCGTTCAATCCCAAAATCCCACTTACTATTATTCATGTG
AAATATATGCTGCTCAATAGATGTCGAAGAGTTGTAGACTGAGGTGGTGAATATCTAAGGCCATATC
AAGAGAGGCTGCTTGTCTGGATGAATAGATCTCATTTTGGAGCTTCAAGACTTCTAGGCAATAGCAAGTCA
AAATATGTTTAAAGAAATTTAAAAATTTTGTACATATATTTTACGAAAAGAAATTTTGTACATCAAAAT
TGTGTACATATGCTTCCCGTATATATTTAAGTAGTTGTTCTTGTATGCCATATTTTATTTTCTTTTGGTT
TAGATGTCACCTTATTGCTGGGAGACTTCCGGGAAGAACGCAACAGATGTGAAAAACTATTGGAACACACAC
CTACACAGAGTATTATAAATCTCCTCAGATACAAGAGAAATAGTACAATAAACCCTCAAGATTTACCTG
AAAGCACTATCTACGACCACGACCAAGACTTCCGACTCCGAACTTCAAGTGAATAATATTTCTTGGTG
CACTAACAATAGTATGATCACAACACATTTAGCAAAAGATGACCAACACGCAACAGAAATCGCATTAAT
ATTTGTGAGAAGCCAAACAGAAACACCCGTCATCTGCTATAGACGATGATGGAGTTAAATGGTGGACAAAT
TACTGGAAAAATTTGGAAGAATTTGAGGAAGAAGCAACAGCAGTATGAACCTTTGAGGAAGAAAATTAAGTTGT
ACCAAAATTTGTTGTGAGGAACATAATTCACCAACCATGCAACATGGAGAAAATGATGACTTTTCAGTTGAT
ATTGACCTATGGAATCTATTTAATTAG

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A

<i>Solyc10g086290.1.1</i>	ATGAATATTGCCAAGACATGGGAGTGAGAAAAGTTTCATGGACTGAAGATGAAGATATCTTTTGAGGAAATGTATTGA	80
Heinz 1706 <i>SIAN2like</i> transcript	ATGAATATTGCCAAGACATGGGAGTGAGAAAAGTTTCATGGACTGAAGATGAAGATATCTTTTGAGGAAATGTATTGA	80
Ailsa Craig <i>SIAN2like</i> transcript1	ATGAATATTGCCAAGACATGGGAGTGAGAAAAGTTTCATGGACTGAAGATGAAGATATCTTTTGAGGAAATGTATTGA	80
Ailsa Craig <i>SIAN2like</i> transcript 2	ATGAATATTGCCAAGACATGGGAGTGAGAAAAGTTTCATGGACTGAAGATGAAGATATCTTTTGAGGAAATGTATTGA	80
consensus	atgaatattgccaaagacattgggagtgagaaaagtttcattggactgaagatgaagatattcttttgaggaatgtattga	
<i>Solyc10g086290.1.1</i>	CAAGTATGGAGAAGCAAGTGGCATCTTGTTCCTTTTAGAGCTGGTCTAAATAGATGTCGAAAGAGTTGTAGACTGAGGT	160
Heinz 1706 <i>SIAN2like</i> transcript	CAAGTATGGAGAAGCAAGTGGCATCTTGTTCCTTTTAGAGCTGGTCTAAATAGATGTCGAAAGAGTTGTAGACTGAGGT	160
Ailsa Craig <i>SIAN2like</i> transcript1	CAAGTATGGAGAAGCAAGTGGCATCTTGTTCCTTTTAGAGCTGGTCTAAATAGATGTCGAAAGAGTTGTAGACTGAGGT	160
Ailsa Craig <i>SIAN2like</i> transcript 2	CAAGTATGGAGAAGCAAGTGGCATCTTGTTCCTTTTAGAGCTGGTCTAAATAGATGTCGAAAGAGTTGTAGACTGAGGT	160
consensus	caagtatggagaagc.....tctaaatagatgtcgaaagagttgtagactgaggt	130
	caagtatggagaaggt.....tctaaatagatgtcgaaagagttgtagactgaggt	
<i>Solyc10g086290.1.1</i>	GGTTGAATTATCTAAGGCCACATATCAAGAGAGTGGACTTTGCTCTGGATGAAATAGATCTCATTTTGAGACTTCAAG	240
Heinz 1706 <i>SIAN2like</i> transcript	GGTTGAATTATCTAAGGCCACATATCAAGAGAGTGGACTTTGCTCTGGATGAAATAGATCTCATTTTGAGACTTCAAG	193
Ailsa Craig <i>SIAN2like</i> transcript1	GGTTGAATTATCTAAGGCCACATATCAAGAGAGTGGACTTTGCTCTGGATGAAATAGATCTCATTTTGAGACTTCAAG	193
Ailsa Craig <i>SIAN2like</i> transcript 2	GGTTGAATTATCTAAGGCCACATATCAAGAGAGTGGACTTTGCTCTGGATGAAATAGATCTCATTTTGAGACTTCAAG	163
consensus	ggttgaattatctaaaggccacatcaagagag.....tctaaatagatgtcgaaagagttgtagactgaggt	
	ggttgaattatctaaaggccacatcaagagag.....tctaaatagatgtcgaaagagttgtagactgaggt	
<i>Solyc10g086290.1.1</i>	CTTCTAGGCAATAGATGGTCACTTATTTGCTGGGAGACTTCTTGAAGAAGCAGCAACAGATGTGAAAACTATTGGAACAC	320
Heinz 1706 <i>SIAN2like</i> transcriptATGGTCACTTATTTGCTGGGAGACTTCTTGAAGAAGCAGCAACAGATGTGAAAACTATTGGAACAC	259
Ailsa Craig <i>SIAN2like</i> transcript1ATGGTCACTTATTTGCTGGGAGACTTCTTGAAGAAGCAGCAACAGATGTGAAAACTATTGGAACAC	259
Ailsa Craig <i>SIAN2like</i> transcript 2ATGGTCACTTATTTGCTGGGAGACTTCTTGAAGAAGCAGCAACAGATGTGAAAACTATTGGAACAC	229
consensus	atggtcacttattgctgggagacttcttgaagaagcagcaaacagatgtgaaaaactattggaacac	
	atggtcacttattgctgggagacttcttgaagaagcagcaaacagatgtgaaaaactattggaacac	
<i>Solyc10g086290.1.1</i>	ACACCTACACAAGAAAGTTATTAATAACTCCTCCTCAGATACAAGAGAATAAGTACAATAATACCCTCAAGATTATCACTG	400
Heinz 1706 <i>SIAN2like</i> transcript	ACACCTACACAAGAAAGTTATTAATAACTCCTCCTCAGATACAAGAGAATAAGTACAATAATACCCTCAAGATTATCACTG	339
Ailsa Craig <i>SIAN2like</i> transcript1	ACACCTACACAAGAAAGTTATTAATAACTCCTCCTCAGATACAAGAGAATAAGTACAATAATACCCTCAAGATTATCACTG	339
Ailsa Craig <i>SIAN2like</i> transcript 2	ACACCTACACAAGAAAGTTATTAATAACTCCTCCTCAGATACAAGAGAATAAGTACAATAATACCCTCAAGATTATCACTG	309
consensus	acacctacacaagaagtatttaataactcctcctcagatacaagagataaagtacaataataccctcaagattatcactg	
	acacctacacaagaagtatttaataactcctcctcagatacaagagataaagtacaataataccctcaagattatcactg	
<i>Solyc10g086290.1.1</i>	AAAGCACTATACTACGACCAGCAAGACAGCAGCTCAACCTCGAACCTTCTCAAGTGAATAAATATTTCTTGGTGC	480
Heinz 1706 <i>SIAN2like</i> transcript	AAAGCACTATACTACGACCAGCAAGACAGCAGCTCAACCTCGAACCTTCTCAAGTGAATAAATATTTCTTGGTGC	419
Ailsa Craig <i>SIAN2like</i> transcript1	AAAGCACTATACTACGACCAGCAAGACAGCAGCTCAACCTCGAACCTTCTCAAGTGAATAAATATTTCTTGGTGC	419
Ailsa Craig <i>SIAN2like</i> transcript 2	AAAGCACTATACTACGACCAGCAAGACAGCAGCTCAACCTCGAACCTTCTCAAGTGAATAAATATTTCTTGGTGC	389
consensus	aaagcactatactacgaccagcaagacagcagcctcaacctcgaaaccttctcaagtgaataaataatttcttgggtgc	
	aaagcactatactacgaccagcaagacagcagcctcaacctcgaaaccttctcaagtgaataaataatttcttgggtgc	
<i>Solyc10g086290.1.1</i>	ACTAACAAATAGTATGATCACAACACATTAGACAAGATGACGAACAACACAACAAGAAATCGCAGTAAATATTTGTGA	560
Heinz 1706 <i>SIAN2like</i> transcript	ACTAACAAATAGTATGATCACAACACATTAGACAAGATGACGAACAACACAACAAGAAATCGCAGTAAATATTTGTGA	499
Ailsa Craig <i>SIAN2like</i> transcript1	ACTAACAAATAGTATGATCACAACACATTAGACAAGATGACGAACAACACAACAAGAAATCGCAGTAAATATTTGTGA	499
Ailsa Craig <i>SIAN2like</i> transcript 2	ACTAACAAATAGTATGATCACAACACATTAGACAAGATGACGAACAACACAACAAGAAATCGCAGTAAATATTTGTGA	469
consensus	actaaacaatagatgatcacaacacattagacaagatgacgaacaacacaacaagaatcgagtaaatatttgtga	
	actaaacaatagatgatcacaacacattagacaagatgacgaacaacacaacaagaatcgagtaaatatttgtga	
<i>Solyc10g086290.1.1</i>	GAAGCCAAACAAAAAACACCGTCACTCGTCTATAGACGATGATGGAGTTCAATGGTGGACAAATTTACTGGAAAATTTGA	640
Heinz 1706 <i>SIAN2like</i> transcript	GAAGCCAAACAAAAAACACCGTCACTCGTCTATAGACGATGATGGAGTTCAATGGTGGACAAATTTACTGGAAAATTTGA	579
Ailsa Craig <i>SIAN2like</i> transcript1	GAAGCCAAACAAAAAACACCGTCACTCGTCTATAGACGATGATGGAGTTCAATGGTGGACAAATTTACTGGAAAATTTGA	579
Ailsa Craig <i>SIAN2like</i> transcript 2	GAAGCCAAACAAAAAACACCGTCACTCGTCTATAGACGATGATGGAGTTCAATGGTGGACAAATTTACTGGAAAATTTGA	549
consensus	gaagccaaacaaaaaacacccgtcactcgtctatagacgatgatggagttcaatggaggacaaatttactggaatattgga	
	gaagccaaacaaaaaacacccgtcactcgtctatagacgatgatggagttcaatggaggacaaatttactggaatattgga	
<i>Solyc10g086290.1.1</i>	AAGAATTTGAGGAAGAAGCAACAGCAGTATTGAACTTTGAGGAAGAAAATAAGTTGTGCCAAATTTGTTGATGAGGAA	720
Heinz 1706 <i>SIAN2like</i> transcript	AAGAATTTGAGGAAGAAGCAACAGCAGTATTGAACTTTGAGGAAGAAAATAAGTTGTGCCAAATTTGTTGATGAGGAA	659
Ailsa Craig <i>SIAN2like</i> transcript1	AAGAATTTGAGGAAGAAGCAACAGCAGTATTGAACTTTGAGGAAGAAAATAAGTTGTGCCAAATTTGTTGATGAGGAA	659
Ailsa Craig <i>SIAN2like</i> transcript 2	AAGAATTTGAGGAAGAAGCAACAGCAGTATTGAACTTTGAGGAAGAAAATAAGTTGTGCCAAATTTGTTGATGAGGAA	629
consensus	aagaatttgaggaagaagcaacagcagatttgaaactttgaggaagaaaataagttgtgccaatttgttattgagga	
	aagaatttgaggaagaagcaacagcagatttgaaactttgaggaagaaaataagttgttgcgaatttgttattgagga	
<i>Solyc10g086290.1.1</i>	CATAATTCACAACCACTGCAACATGGAGAAAATGATGACTTTTCAGTTGATATTGACCTATGGAATCTATTTAATTAG	798
Heinz 1706 <i>SIAN2like</i> transcript	CATAATTCACAACCACTGCAACATGGAGAAAATGATGACTTTTCAGTTGATATTGACCTATGGAATCTATTTAATTAG	737
Ailsa Craig <i>SIAN2like</i> transcript1	CATAATTCACAACCACTGCAACATGGAGAAAATGATGACTTTTCAGTTGATATTGACCTATGGAATCTATTTAATTAG	737
Ailsa Craig <i>SIAN2like</i> transcript 2	CATAATTCACAACCACTGCAACATGGAGAAAATGATGACTTTTCAGTTGATATTGACCTATGGAATCTATTTAATTAG	707
consensus	cataatccaacaacctgcaacatggagaaaatgatgacttttcagttgatattgacctatggaatctatttaattag	
	cataatccaacaacctgcaacatggagaaaatgatgacttttcagttgatattgacctatggaatctatttaattag	

B



Supplemental Figure 6. *SIAN2like* in Heinz fruits is spliced and expressed similarly to Ailsa Craig fruits.

(A) Clustal alignment of the *Solyc10g086290.1.1* cds (SolGenomics), the transcript sequence cloned from the Heinz 1706 fruit peel, and the two transcript sequences cloned from the Ailsa Craig fruit peel and. **(B)** qPCR analysis of the genes *SIAN2* and *SIAN2like* carried out in the peel of Ailsa Craig (AC), Heinz 1706 and *Aft* fruits at the mature green stage. Data are means of six biological replicates \pm SE. One-way ANOVA with Tukey's HSD post-hoc test was performed. Different letters indicate significant differences at $P \leq 0.05$.

A

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SIAN2like_WT_1      MNIARTLGVRKGSWTEDEDILLRKCIDRYGEGKWHLVFPFRAGLNRCKRSCLRWLNLYLRP
SIAN2like_WT_2      MNIARTLGVRKGSWTEDEDILLRKCIDRYGEG-----LNRCKRSCLRWLNLYLRP
Solyc10g086290.1.1  MNIARTLGVRKGSWTEDEDILLRKCIDRYGEGKWHLVFPFRAGLNRCKRSCLRWLNLYLRP
*****

SIAN2like_WT_1      HIKRD-----GHLLG-----
SIAN2like_WT_2      HIKRD-----GHLLG-----
Solyc10g086290.1.1  HIKRGDFALDEIDLILRLHLKLLGNRWSLIAGRLPGRANDVKNYWNLHLKLLITPPQI
*****
R2
*****

SIAN2like_WT_1      -----
SIAN2like_WT_2      -----
Solyc10g086290.1.1  QENRYNNTLKIITESTILRPRREGPQPRTESSENNISWCTNNSMTITNLDKDDQHNKE
*****

SIAN2like_WT_1      -----DFLEEQQTM-----
SIAN2like_WT_2      -----DFLEEQQTMKIGTHT-----
Solyc10g086290.1.1  IAVNICEKPTKTPSSSIDDDGVQWNLNLENWKEFEEETAVLNFEENKLLPNLLYEE
*****
:* **: :

SIAN2like_WT_1      -----
SIAN2like_WT_2      YTRSY-----
Solyc10g086290.1.1  HNSTTMQHGENDDFVSDIDLNLNLFN
*****

R3
*****

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B

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SIAN2like_WT      ATGAATATGCCAAGACATGGGAGTGAGAAAAGGTTCATGGACTGAAATGAAGATATT
SIAN2like_Aft     ATGAATATGCCAAGACATGGGAGTGAGAAAAGGTTCATGGACTGAAATGAAGATATT
*****

SIAN2like_WT      CTTTTCAGGAAATGATTGACACAGTATGGAGAAGGAAAGTGCATCTTCTCCTTTTAGA
SIAN2like_Aft     CTTTTCAGGAAATGATTGACACAGTATGGAGAAGGAAAGTGCATCTTCTCCTTTTAGA
*****

SIAN2like_WT      CCTGTAAAGCAGAAATTAAGATTTTATCTTTATTAATTTAAATTTTATGATAAATA
SIAN2like_Aft     CCTGTAAAGCAGAAATTAAGATTTTATCTTTATTAATTTAAATTTTATGATAAATA
*****

SIAN2like_WT      AGTTCTAAATTTATGTAGATTTAAGTAAATTTGTTAATGCAGAAATAATTTAGGC
SIAN2like_Aft     AGTTCTAAATTTATGTAGATTTAAGTAAATTTGTTAATGCAGAAATAATTTAGGC
*****

SIAN2like_WT      AAAATCTATTAGATTACTAAATTTCTCTTTTAAGAAAAGGAAACTTAACTTTTGT
SIAN2like_Aft     AAAATCTATTAGATTACTAAATTTCTCTTTTAAGAAAAGGAAACTTAACTTTTGT
*****

SIAN2like_WT      GTGATAGTGGCGTCCCAACCTATACTTAGCATGAATAGCATTTTCATGCCTCCTTTT
SIAN2like_Aft     GTGATAGTGGCGTCCCAACCTATACTTAGCATGAATAGCATTTTCATGCCTCCTTTT
*****

SIAN2like_WT      ATTACGAGTCATAAATCAATTTCTTAGGAGTTACAAATTAATATAAGATATATTA
SIAN2like_Aft     ATTACGAGTCATAAATCAATTTCTTAGGAGTTACAAATTAATATAAGATATATTA
*****

SIAN2like_WT      GTTAAATTTTTTGTAGTTATATATAAATCTACCAAAAAAATTAAGTCTCGTTCAATC
SIAN2like_Aft     GTTAAATTTTTTGTAGTTATATATAAATCTACCAAAAAAATTAAGTCTCGTTCAATC
*****

SIAN2like_WT      CACAAATCCCACTTACTATTATTCACTGATATATGCAGTCTAAATAGATGTCGAA
SIAN2like_Aft     CACAAATCCCACTTACTATTATTCACTGATATATGCAGTCTAAATAGATGTCGAA
*****

SIAN2like_WT      AGAGTTCTAGACTGAGGTGGTTGAAATTAATCTAAGGCCACATATCAAGAGAGGTGACTTG
SIAN2like_Aft     AGAGTTCTAGACTGAGGTGGTTGAAATTAATCTAAGGCCACATATCAAGAGAGGTGACTTG
*****

SIAN2like_WT      CTCTGGATGAAATAGATCTCATTTTGTAGACTTCACAAGCTTCAGGCAATAGGCAATCA
SIAN2like_Aft     CTCTGGATGAAATAGATCTCATTTTGTAGACTTCACAAGCTTCAGGCAATAGGCAATCA
*****

SIAN2like_WT      AAAATTTCTTAAATAATTTAAAAATTTATGTACATATATATTCACGAAAAGTAAT
SIAN2like_Aft     AAAATTTCTTAAATAATTTAAAAATTTATGTACATATATATTCACGAAAAGTAAT
*****

SIAN2like_WT      TTTTGACATAAAATTTCTACATACACTAGTCTCTCGAATATATTAGTAAGTTATCTT
SIAN2like_Aft     TTTTGACATAAAATTTCTACATACACTAGTCTCTCGAATATATTAGTAAGTTATCTT
*****

SIAN2like_WT      TGATGCCATATTTTATATTTTTGGTTTATGTTGTCATTAATGCTGGGAGACTTCC
SIAN2like_Aft     TGATGCCATATTTTATATTTTTGGTTTATGTTGTCATTAATGCTGGGAGACTTCC
*****

SIAN2like_WT      GGAAGAACACCAACGATGTGAAAAACTATTGGAACACACACCTACACAAAGATTATTA
SIAN2like_Aft     GGAAGAACACCAACGATGTGAAAAACTATTGGAACACACACCTACACAAAGATTATTA
*****

SIAN2like_WT      ATAACCTCTCTAGATACAAGAGAATAAGTACAATAATACCCTCAAGATTACTGAA
SIAN2like_Aft     ATAACCTCTCTAGATACAAGAGAATAAGTACAATAATACCCTCAAGATTACTGAA
*****

SIAN2like_WT      AGCACTACTACTAGACCACGACCAAGACCAGGACCTCAACCTCGAACCTTCTCAAGTGAA
SIAN2like_Aft     AGCACTACTACTAGACCACGACCAAGACCAGGACCTCAACCTCGAACCTTCTCAAGTGAA
*****

SIAN2like_WT      AATAATATTTCTTGGTGCATAACAATAGTATGATCACAACACATAGACAAAAGATGAC
SIAN2like_Aft     AATAATATTTCTTGGTGCATAACAATAGTATGATCACAACACATAGACAAAAGATGAC
*****

SIAN2like_WT      GAACAACAACAAGAAATCGCAGTAAATTTTGTGAGAAGCAACAACAAAAACCCG
SIAN2like_Aft     GAACAACAACAAGAAATCGCAGTAAATTTTGTGAGAAGCAACAACAAAAACCCG
*****

SIAN2like_WT      TCATCGTCTATAGACGATGATGGAGTTCAATGGTGGACAAATTTACTGAAAAATGGAAA
SIAN2like_Aft     TCATCGTCTATAGACGATGATGGAGTTCAATGGTGGACAAATTTACTGAAAAATGGAAA
*****

SIAN2like_WT      GAATTTGAGGAAGAAGCAACAGCAGTATTGAACCTTGAGGAAGAAAATAGTTGTTCCA
SIAN2like_Aft     GAATTTGAGGAAGAAGCAACAGCAGTATTGAACCTTGAGGAAGAAAATAGTTGTTCCA
*****

SIAN2like_WT      AATTTGTTGTGAGGAACATAAATCAACAACCATGCAACATGGAGAAAATGATGACTTT
SIAN2like_Aft     AATTTGTTGTGAGGAACATAAATCAACAACCATGCAACATGGAGAAAATGATGACTTT
*****

SIAN2like_WT      TCAGTTGATATTGACCTATGGAATCTATTTAATTAG
SIAN2like_Aft     TCAGTTGATATTGACCTATGGAATCTATTTAATTAG
*****

```

Supplemental Figure 7. Nucleotide and amino acid polymorphisms in different versions of SIAN2like.

(A) ClustalW alignment of the genomic sequences of *SIAN2like*^{WT}, with exon boundaries produced by the “canonical” splicing, and *SIAN2like*^{Aft}. Exons are boxed in green. The symbol “*” indicates a perfect alignment. Single nucleotide and other polymorphisms between WT and *Aft* sequences are highlighted in yellow. **(B)** ClustalW alignment of the protein sequence SIAN2like^{WT} from SOL Genomics Network database (Solyc10g086290.1.1) and the two shorter polypeptides SIAN2like_WT_1 and SIAN2like_WT_2 produced from the two transcripts cloned in WT fruit peel. R2 and R3 MYB domains are underlined. In the Solyc10g086290.1.1 sequence, the [DE]Lx2[RK]x3Lx6Lx3R motif containing the bHLH-binding site (Zimmermann et al., 2004) is boxed in grey, the aminoacidic signature [A/S/G]NDV typical of dicot R2R3 MYBs promoting anthocyanin (Lin-Wang et al., 2010; Heppel et al., 2013) is boxed in light purple and the KPRPR[ST]F motif, conserved in Arabidopsis MYBs involved in anthocyanin synthesis (Stracke et al., 2001), is boxed in green. Symbols are as follows: “*” indicates perfect alignment; “:” indicates a site belonging to group exhibiting strong similarity; and “.” indicates a site belonging to a group exhibiting weak similarity.

SLAN2like^{WT} ATGAATATGCGCAAGACATGGGAGTCAGAAAAGGCTTCATGGACTGAAGATCAAGATATCTTTTIGAGGAAATGTATTGA 80
 SpiAN2like ATGAATATGCGCAAGACATGGGAGTCAGAAAAGGCTTCATGGACTGAAGATCAAGATATCTTTTIGAGGAAATGTATTGA 80
 SLAN2like^{ΔTt} ATGAATATGCGCAAGACATGGGAGTCAGAAAAGGCTTCATGGACTGAAGATCAAGATATCTTTTIGAGGAAATGTATTGA 80
 SpeAN2like ATGAATATGCGCAAGACATGGGAGTCAGAAAAGGCTTCATGGACTGAAGATCAAGATATCTTTTIGAGGAAATGTATTGA 80
 ScAN2like ATGAATATGCGCAAGACATGGGAGTCAGAAAAGGCTTCATGGACTGAAGATCAAGATATCTTTTIGAGGAAATGTATTGA 80
 SlyAN2like ATGAATATGCGCAAGACATGGGAGTCAGAAAAGGCTTCATGGACTGAAGATCAAGATATCTTTTIGAGGAAATGTATTGA 80
 consensus atgaatat gc aagacattgggagt agaaaaggcttcattggactgaaga gaagat tcttttgaggaaatgtattga

SLAN2like^{WT} CAAGTATGCGAAGGAAAGTGGCATCTGTTCCTTTTACAGCIGGTAAGCCAAATTAAGATTTTACTTTTAAATTTT 160
 SpiAN2like CAAGTATGCGAAGGAAAGTGGCATCTGTTCCTTTTACAGCIGGTAAGCCAAATTAAGATTTTACTTTTAAATTTT 160
 SLAN2like^{ΔTt} CAAGTATGCGAAGGAAAGTGGCATCTGTTCCTTTTACAGCIGGTAAGCCAAATTAAGATTTTACTTTTAAATTTT 160
 SpeAN2like CAAGTATGCGAAGGAAAGTGGCATCTGTTCCTTTTACAGCIGGTAAGCCAAATTAAGATTTTACTTTTAAATTTT 160
 ScAN2like CAAGTATGCGAAGGAAAGTGGCATCTGTTCCTTTTACAGCIGGTAAGCCAAATTAAGATTTTACTTTTAAATTTT 160
 SlyAN2like CAAGTATGCGAAGGAAAGTGGCATCTGTTCCTTTTACAGCIGGTAAGCCAAATTAAGATTTTACTTTTAAATTTT 160
 consensus caagtatggagaaggaaagtggcatctgttctctt tagactggttaag aaatta gattt a ttttat atttt

SLAN2like^{WT} AAATTTTATGATAATAATAAAGTCTTAAATTTATCTAGATTAAGTATAAATTTCTTAAIGCAAAAATAATATTAGG 239
 SpiAN2like AAATTTTATGATAATAATAAAGTCTTAAATTTATCTAGATTAAGTATAAATTTCTTAAIGCAAAAATAATATTAGG 239
 SLAN2like^{ΔTt} AAATTTTATGATAATAATAAAGTCTTAAATTTATCTAGATTAAGTATAAATTTCTTAAIGCAAAAATAATATTAGG 238
 SpeAN2like AAATTTTATGATAATAATAAAGTCTTAAATTTATCTAGATTAAGTATAAATTTCTTAAIGCAAAAATAATATTAGG 239
 ScAN2like AAATTTTATGATAATAATAAAGTCTTAAATTTATCTAGATTAAGTATAAATTTCTTAAIGCAAAAATAATATTAGG 239
 SlyAN2like AAATTTTATGATAATAATAAAGTCTTAAATTTATCTAGATTAAGTATAAATTTCTTAAIGCAAAAATAATATTAGG 239
 consensus aaattttatgataataa taagt taaatttatctagat taagt a aatttgtaatgcaaaaa ta tat tag

SLAN2like^{WT} CAAAATCTTTAGATTTTACAAATTTCTTTTAAAGAAAAGAGAACTTAACTTTTCTTGTGATAGTGGCGTCCCAAC 319
 SpiAN2like CAAAATCTTTAGATTTTACAAATTTCTTTTAAAGAAAAGAGAACTTAACTTTTCTTGTGATAGTGGCGTCCCAAC 319
 SLAN2like^{ΔTt} CAAAATCTTTAGATTTTACAAATTTCTTTTAAAGAAAAGAGAACTTAACTTTTCTTGTGATAGTGGCGTCCCAAC 317
 SpeAN2like CAAAATCTTTAGATTTTACAAATTTCTTTTAAAGAAAAGAGAACTTAACTTTTCTTGTGATAGTGGCGTCCCAAC 319
 ScAN2like CAAAATCTTTAGATTTTACAAATTTCTTTTAAAGAAAAGAGAACTTAACTTTTCTTGTGATAGTGGCGTCCCAAC 319
 SlyAN2like CAAAATCTTTAGATTTTACAAATTTCTTTTAAAGAAAAGAGAACTTAACTTTTCTTGTGATAGTGGCGTCCCAAC 320
 consensus caaaaatct tttagatt tac aaatttctttttaaagaaaagagaaactta cctt tgtgtgatagtgccgt c aac

SLAN2like^{WT} CTATAACTCTAGCATGAATAGCATTTCATGCTCCTTTTATTATCCGACTGATTAATCAATTTTCTTAGGAGTTTACAA 399
 SpiAN2like CTATAACTCTAGCATGAATAGCATTTCATGCTCCTTTTATTATCCGACTGATTAATCAATTTTCTTAGGAGTTTACAA 399
 SLAN2like^{ΔTt} CTATAACTCTAGCATGAATAGCATTTCATGCTCCTTTTATTATCCGACTGATTAATCAATTTTCTTAGGAGTTTACAA 397
 SpeAN2like CTATAACTCTAGCATGAATAGCATTTCATGCTCCTTTTATTATCCGACTGATTAATCAATTTTCTTAGGAGTTTACAA 399
 ScAN2like CTATAACTCTAGCATGAATAGCATTTCATGCTCCTTTTATTATCCGACTGATTAATCAATTTTCTTAGGAGTTTACAA 399
 SlyAN2like CTATAACTCTAGCATGAATAGCATTTCATGCTCCTTTTATTATCCGACTGATTAATCAATTTTCTTAGGAGTTTACAA 400
 consensus tcaactctagcatgaatagcatttca g ctccttt ttatt ga tc t aat a ttt g taggagtttacaa

SLAN2like^{WT} ATTAATATGACATATATTTACTTAAATTTTATGTTTATATATGAAATCAATCCAAATAATTAAGGTTTCTTCAAT 479
 SpiAN2like ATTAATATGACATATATTTACTTAAATTTTATGTTTATATATGAAATCAATCCAAATAATTAAGGTTTCTTCAAT 479
 SLAN2like^{ΔTt} ATTAATATGACATATATTTACTTAAATTTTATGTTTATATATGAAATCAATCCAAATAATTAAGGTTTCTTCAAT 475
 SpeAN2like ATTAATATGACATATATTTGCTTAAATTTTATGTTTATATATGAAATCAATCCAAATAATTAAGGTTTCTTCAAT 477
 ScAN2like ATTAATATGACATATTTGCTTAAATTTTATGTTTATATATGAAATCAATCCAAATAATTAAGGTTTCTTCAAT 476
 SlyAN2like ATTAATATGACATATTTGCTTAAATTTTATGTTTATATATGAAATCAATCCAAATAATTAAGGTTTCTTCAAT 477
 consensus t aaata a a atatt ttaa ttttt agt atata aa at ta aa aaatta t t c ttcaa

SLAN2like^{WT} CCACAATCCCTACTTACATTAATTTCTATGTAATATGACAGGCTAAATAGATGTCGAAAGAGTTGTAGACTGAGGTG 559
 SpiAN2like CCACAATCCCTACTTACATTAATTTCTATGTAATATGACAGGCTAAATAGATGTCGAAAGAGTTGTAGACTGAGGTG 559
 SLAN2like^{ΔTt} CCACAATCCCTACTTACATTAATTTCTATGTAATATGACAGGCTAAATAGATGTCGAAAGAGTTGTAGACTGAGGTG 555
 SpeAN2like CCACAATCCCTACTTACATTT...ICATGCGAATATATGACAGGCTAAATAGATGTCGAAAGAGTTGTAGACTGAGGTG 554
 ScAN2like CCATAAATCCCTACTTACATTT...ICATGCGAATATATGACAGGCTAAATAGATGTCGAAAGAGTTGTAGACTGAGGTG 553
 SlyAN2like CCACAATCCCTACTTACATTT...ICATGCGAATATATGACAGGCTAAATAGATGTCGAAAGAGTTGTAGACTGAGGTG 554
 consensus cca aatcc acttac att tca a tatatgcaggctcaaatagatgtcgaaagagttgtagactgaggtg

SLAN2like^{WT} GTTGAATATCTAAGGCCACATATCAAGAGAGGTCACCTTTGCTTGGATGAAATAGATCTCTTTTGTAGACTTCAAGC 639
 SpiAN2like GTTGAATATCTAAGGCCACATATCAAGAGAGGTCACCTTTGCTTGGATGAAATAGATCTCTTTTGTAGACTTCAAGC 639
 SLAN2like^{ΔTt} GTTGAATATCTAAGGCCACATATCAAGAGAGGTCACCTTTGCTTGGATGAAATAGATCTCTTTTGTAGACTTCAAGC 635
 SpeAN2like GTTGAATATCTAAGGCCACATATCAAGAGAGGTCACCTTTGCTTGGATGAAATAGATCTCTTTTGTAGACTTCAAGC 634
 ScAN2like GTTGAATATCTAAGGCCACATATCAAGAGAGGTCACCTTTGCTTGGATGAAATAGATCTCTTTTGTAGACTTCAAGC 633
 SlyAN2like GTTGAATATCTAAGGCCACATATCAAGAGAGGTCACCTTTGCTTGGATGAAATAGATCTCTTTTGTAGACTTCAAGC 634
 consensus gttgaattatctaaggccacatatcaagagaggtcactttgctt g gatgaaatagatctc tttt agacttcacaagc

SLAN2like^{WT} TTCTAGGCAATAGGCAATCAAAATTTCTGTTAAAAAATTTAAAAATTATGTAATATATATTTCTGAAAAGTAA 719
 SpiAN2like TTCTAGGCAATAGGCAATCAAAATTTCTGTTAAAAAATTTAAAAATTATGTAATATATATTTCTGAAAAGTAA 719
 SLAN2like^{ΔTt} TTCTAGGCAATAGGCAATCAAAATTTCTGTTAAAAAATTTAAAAATTATGTAATATATATTTCTGAAAAGTAA 713
 SpeAN2like TTCTAGGCAATAGGCAATCAAAATTTCTGTTAAAAAATTTAAAAATTATGTAATATATATTTCTGAAAAGTAA 712
 ScAN2like TTCTAGGCAATAGGCAATCAAAATTTCTGTTAAAAAATTTAAAAATTATGTAATATATATTTCTGAAAAGTAA 711
 SlyAN2like TTCTAGGCAATAGGCAATCAAAATTTCTGTTAAAAAATTTAAAAATTATGTAATATATATTTCTGAAAAGTAA 712
 consensus ttctaggcaataggcaaa t a aaattt gttaaaa att aaaaattat a atatat t a gaaaag aa

SIAN2like ^{WT}	<u>T</u> TTTGACATATAAATCTGTACATACTACTCTCCGATATAATATACTAAGTATCTTTGATCCATATTTTATAT	799
SpiAN2like	<u>T</u> TTTGACATATAAATCTGTACATACTACTCTCCGATATAATATACTAAGTATCTTTGATCCATATTTTATAT	799
SIAN2like ^{Aft}	<u>C</u> TTTGACATACAATTTGTGTACATACTACTCTCCGATATAATATACTAAGTATCTTTGATCCATATTTTATAT	793
SpeAN2like	<u>T</u> TTTGACATATAAATCTGTACATACTACTCTCCGATATAATATACTAAGTATCTTTGATCCATATTTTATAT	792
ScAN2like	<u>C</u> TTTGACATATAAATCTGTGTACATACTACTCTCCGATATAATATACTAAGTATCTTTGATCCATATTTTATAT	791
SlyAN2like	<u>T</u> TTTGACATATAAATCTGTGTACATACTACTCTCCGATATAATATACTAAGTATCTTTGATCCATATTTTATAT	791
consensus	<u>t</u> tttgacata aaat t gtacatact tct cg atata tataagtaagt tctttgatgc atatttt t	
SIAN2like ^{WT}	<u>...</u> <u>T</u> TTTTCGTTTACGTGTCACCTTATTGCTGGGAGACTCCGGGAAGAACAGCAAACGATGTGAAAACTATGGAAC	876
SpiAN2like	<u>...</u> <u>T</u> TTTTCGTTTACGTGTCACCTTATTGCTGGGAGACTCCGGGAAGAACAGCAAACGATGTGAAAACTATGGAAC	876
SIAN2like ^{Aft}	<u>...</u> <u>T</u> TTTTCGTTTACGTGTCACCTTATTGCTGGGAGACTCCGGGAAGAACAGCAAACGATGTGAAAACTATGGAAC	870
SpeAN2like	<u>A</u> TTTTCGTTTACGTGTCACCTTATTGCTGGGAGACTCCGGGAAGAACAGCAAACGATGTGAAAACTATGGAAC	872
ScAN2like	<u>...</u> <u>T</u> TTTTCGTTTACGTGTCACCTTATTGCTGGGAGACTCCGGGAAGAACAGCAAACGATGTGAAAACTATGGAAC	867
SlyAN2like	<u>A</u> TTTTCGTTTACGTGTCACCTTATTGCTGGGAGACTCCGGGAAGAACAGCAAACGATGTGAAAACTATGGAAC	869
consensus	<u>t</u> ttt gtttag tggtcacttattgctgggagactcc ggaagaacagcaaacgatgtgaaaaactattggaac	
SIAN2like ^{WT}	<u>A</u> CACACCTACACAAGAAGTTATTAATAACCTCCCTCCGATACAAGAGAATAAGTACAATAATACCCCTCAAGATTATCAC	956
SpiAN2like	<u>A</u> CACACCTACACAAGAAGTTATTAATAACCTCCCTCCGATACAAGAGAATAAGTACAATAATACCCCTCAAGATTATCAC	956
SIAN2like ^{Aft}	<u>A</u> CACACCTACACAAGAAGTTATTAATAACCTCCCTCCGATACAAGAGAATAAGTACAATAATACCCCTCAAGATTATCAC	947
SpeAN2like	<u>A</u> CACACCTACACAAGAAGTTATTAATAACCTCCCTCCGATACAAGAGAATAAGTACAATAATACCCCTCAAGATTATCAC	952
ScAN2like	<u>A</u> CACACCTACACAAGAAGTTATTAATAACCTCCCTCCGATACAAGAGAATAAGTACAATAATACCCCTCAAGATTATCAC	947
SlyAN2like	<u>A</u> CACACCTACACAAGAAGTTATTAATAACCTCCCTCCGATACAAGAGAATAAGTACAATAATACCCCTCAAGATTATCAC	946
consensus	<u>c</u> acacctacacaagaagtta ataactcc c gatacaagagaataaagtacaataa accctcaagattatcac	
SIAN2like ^{WT}	<u>T</u> GAAAGCACTATCTACGACACGACCAACCCAGACCTCCACCTCGAACCTTCTCAAGTGAAAATAATATTTCTTGGT	1036
SpiAN2like	<u>T</u> GAAAGCACTATCTACGACACGACCAACCCAGACCTCCACCTCGAACCTTCTCAAGTGAAAATAATATTTCTTGGT	1036
SIAN2like ^{Aft}	<u>T</u> GAAAGCACTAT.....ACTACGACCAACCCAGACCTCCACCTCGAACCTTCTCAAGTGAAAATAATATTTCTTGGT	1021
SpeAN2like	<u>T</u> GAAAGCACTATCTACGACACGACCAACCCAGACCTCCACCTCGAACCTTCTCAAGTGAAAATAATATTTCTTGGT	1032
ScAN2like	<u>T</u> GAAAGCACTATCTACGACACGACCAACCCAGACCTCCACCTCGAACCTTCTCAAGTGAAAATAATATTTCTTGGT	1027
SlyAN2like	<u>T</u> GAAAGCACTATCTACGACACGACCAACCCAGACCTCCACCTCGAACCTTCTCAAGTGAAAATAATATTTCTTGGT	1026
consensus	<u>t</u> aaagcactat ac acgacca g cca gacctc acctcg ac tt tcaagtgaaaataatatttcttgggt	
SIAN2like ^{WT}	<u>GC</u> ACTAACAAATGATGATCACAAACACATTAGACAAAGATGACGAACAACCAACCAAGAAATCGAGTAAATATTTGT	1116
SpiAN2like	<u>GC</u> ACTAACAAATGATGATCACAAACACATTAGACAAAGATGACGAACAACCAACCAAGAAATCGAGTAAATATTTGT	1116
SIAN2like ^{Aft}	<u>GC</u> ACTAACAAATGATGATCACAAACACATTAGACAAAGATGACGAACAACCAACCAAGAAATCGAGTAAATATTTGT	1101
SpeAN2like	<u>GC</u> ACTAACAAATGATGATCACAAACACATTAGACAAAGATGACGAACAACCAACCAAGAAATCGAGTAAATATTTGT	1112
ScAN2like	<u>GC</u> ACTAACAAATGATGATCACAAACACATTAGACAAAGATGACGAACAACCAACCAAGAAATCGAGTAAATATTTGT	1107
SlyAN2like	<u>GC</u> ACTAACAAATGATGATCACAAACACATTAGACAAAGATGACGAACAACCAACCAAGAAATCGAGTAAATATTTGT	1106
consensus	<u>g</u> cactaacaat gtatgatcacaacacattagacaagaatgacgaacaa aac aagaatcg agtaaatattgtt	
SIAN2like ^{WT}	<u>G</u> AGAAGCCAACAAPAAAACCCGTCATCGTC...TATAGACGATGATGGACTTAATGGTGGACAAATTTACGGAAAA	1193
SpiAN2like	<u>G</u> AGAAGCCAACAAPAAAACCCGTCATCGTC...TATAGACGATGATGGACTTAATGGTGGACAAATTTACGGAAAA	1185
SIAN2like ^{Aft}	<u>G</u> AGAAGCCAACAAPAAAACCCGTCATCGTC...TATAGACGATGATGGACTTAATGGTGGACAAATTTACGGAAAA	1178
SpeAN2like	<u>G</u> AGAAGCCAACAAPAAAACCCGTCATCGTC...TATAGACGATGATGGACTTAATGGTGGACAAATTTACGGAAAA	1192
ScAN2like	<u>G</u> AGAAGCCAACAAPAAAACCCGTCATCGTC...TATAGACGATGATGGACTTAATGGTGGACAAATTTACGGAAAA	1184
SlyAN2like	<u>G</u> AGAAGCCAACAAPAAAACCCGTCATCGTC...TATAGACGATGATGGACTTAATGGTGGACAAATTTACGGAAAA	1183
consensus	<u>g</u> agaagccaacaa a aaac ccgtc agacgatga ggagt aatgggtggacaaatttac gaaaa	
SIAN2like ^{WT}	<u>T</u> TGGAAGAATTTGAGGAAGAAGCAACAGCAGTATGACCTTTCAGGAAGAAAATA...CTTCTCCAAATTTGTTCT	1270
SpiAN2like	<u>T</u> TGGAAGAATTTGAGGAAGAAGCAACAGCAGTATGACCTTTCAGGAAGAAAATA...CTTCTCCAAATTTGTTCT	1262
SIAN2like ^{Aft}	<u>T</u> TGGAAGAATTTGAGGAAGAAGCAACAGCAGTATGACCTTTCAGGAAGAAAATA...CTTCTCCAAATTTGTTCT	1255
SpeAN2like	<u>T</u> TGGAAGAATTTGAGGAAGAAGCAACAGCAGTATGACCTTTCAGGAAGAAAATA...CTTCTCCAAATTTGTTCT	1269
ScAN2like	<u>T</u> TGGAAGAATTTGAGGAAGAAGCAACAGCAGTATGACCTTTCAGGAAGAAAATA...CTTCTCCAAATTTGTTCT	1261
SlyAN2like	<u>T</u> TGGAAGAATTTGAGGAAGAAGCAACAGCAGTATGACCTTTCAGGAAGAAAATA...CTTCTCCAAATTTGTTCT	1263
consensus	<u>t</u> tggaaagaatttgaggaagaagca cagcagta tga ctttgaggaagaaaataa gttgtt ccaaattgtt t	
SIAN2like ^{WT}	<u>A</u> TGAGGACATAAATTC AACACCATGCAACATGGAGAAAATGATGACTTTTCAGTTGATATTGACCIATGGAATCTAATTT	1350
SpiAN2like	<u>A</u> TGAGGACATAAATTC AACACCATGCAACATGGAGAAAATGATGACTTTTCAGTTGATATTGACCIATGGAATCTAATTT	1342
SIAN2like ^{Aft}	<u>A</u> TGAGGACATAAATTC AACACCATGCAACATGGAGAAAATGATGACTTTTCAGTTGATATTGACCIATGGAATCTAATTT	1335
SpeAN2like	<u>A</u> TGAGGACATAAATTC AACACCATGCAACATGGAGAAAATGATGACTTTTCAGTTGATATTGACCIATGGAATCTAATTT	1349
ScAN2like	<u>A</u> TGAGGACATAAATTC AACACCATGCAACATGGAGAAAATGATGACTTTTCAGTTGATATTGACCIATGGAATCTAATTT	1341
SlyAN2like	<u>A</u> TGAGGACATAAATTC AACACCATGCAACATGGAGAAAATGATGACTTTTCAGTTGATATTGACCIATGGAATCTAATTT	1343
consensus	<u>t</u> gagg a ataattcaac accatgcaacatggagaaaatgatgacttttcagttgatattgacctatggaatctattt	
SIAN2like ^{WT}	<u>A</u> ATTAG	1356
SpiAN2like	<u>A</u> ATTAG	1348
SIAN2like ^{Aft}	<u>A</u> ATTAG	1341
SpeAN2like	<u>A</u> ATTAG	1355
ScAN2like	<u>A</u> ATTAG	1347
SlyAN2like	<u>A</u> ATTAG	1349
consensus	<u>a</u> attag	

Supplemental Figure 8. AN2like in different tomato species.

Alignment of AN2like gene sequences of *S. lycopersicum* (SIAN2like^{WT}), *Aft* (SIAN2like^{Aft}), *S. pimpinellifolium* (SpiAN2like), *S. pennellii* (SpeAN2like), *S. chilense* (ScAN2like) and *S. lycopersicoides* (SlyAN2like). Green lines underline exons.

Solyc10g086250 expression profile

ID	genotype	sample	normalized expression (RPKM)
S0584	Heinz	Heinz unopened flower buds	1.52
S0585	Heinz	Heinz fully opened flowers	1.59
S0586	Heinz	Heinz 1 cm fruits	0
S0587	Heinz	Heinz 2 cm fruits	0
S0588	Heinz	Heinz 3 cm fruits	0
S0589	Heinz	Heinz mature green fruits	0.15
S0590	Heinz	Heinz breaker fruits	0
S0591	Heinz	Heinz breaker+10 fruits	0
S0592	Heinz	Heinz roots	0.43
S0593	Heinz	Heinz leaves	9.92
S0594		pimpinellifolium immature green fruits	0.56
S0595		pimpinellifolium breaker fruits	0.06
S0596		pimpinellifolium breaker+5 fruits	0
S0597		pimpinellifolium leaves	4.08

Solyc10g086260 expression profile

ID	genotype	sample	normalized expression (RPKM)
S0584	Heinz	Heinz unopened flower buds	0
S0585	Heinz	Heinz fully opened flowers	0
S0586	Heinz	Heinz 1 cm fruits	0
S0587	Heinz	Heinz 2 cm fruits	0
S0588	Heinz	Heinz 3 cm fruits	0
S0589	Heinz	Heinz mature green fruits	0
S0590	Heinz	Heinz breaker fruits	0
S0591	Heinz	Heinz breaker+10 fruits	0
S0592	Heinz	Heinz roots	0
S0593	Heinz	Heinz leaves	0.24
S0594		pimpinellifolium immature green fruits	0
S0595		pimpinellifolium breaker fruits	0
S0596		pimpinellifolium breaker+5 fruits	0
S0597		pimpinellifolium leaves	0.44

Solyc10g086270 expression profile

ID	genotype	sample	normalized expression (RPKM)
S0584	Heinz	Heinz unopened flower buds	0.45
S0585	Heinz	Heinz fully opened flowers	0.13
S0586	Heinz	Heinz 1 cm fruits	0
S0587	Heinz	Heinz 2 cm fruits	0
S0588	Heinz	Heinz 3 cm fruits	0
S0589	Heinz	Heinz mature green fruits	0
S0590	Heinz	Heinz breaker fruits	0
S0591	Heinz	Heinz breaker+10 fruits	0
S0592	Heinz	Heinz roots	0
S0593	Heinz	Heinz leaves	6.06
S0594		pimpinellifolium immature green fruits	0
S0595		pimpinellifolium breaker fruits	0
S0596		pimpinellifolium breaker+5 fruits	0
S0597		pimpinellifolium leaves	5.75

Solyc10g086290 expression profile

ID	genotype	sample	normalized expression (RPKM)
S0584	Heinz	Heinz unopened flower buds	0
S0585	Heinz	Heinz fully opened flowers	0
S0586	Heinz	Heinz 1 cm fruits	1.2
S0587	Heinz	Heinz 2 cm fruits	1.13
S0588	Heinz	Heinz 3 cm fruits	0
S0589	Heinz	Heinz mature green fruits	0.15
S0590	Heinz	Heinz breaker fruits	0
S0591	Heinz	Heinz breaker+10 fruits	0
S0592	Heinz	Heinz roots	0
S0593	Heinz	Heinz leaves	0
S0594		pimpinellifolium immature green fruits	2.94
S0595		pimpinellifolium breaker fruits	0.68
S0596		pimpinellifolium breaker+5 fruits	0
S0597		pimpinellifolium leaves	0

Supplemental Figure 9. Expression of R2R3 MYB genes in *S. lycopersicum* var. Heinz and in the wild relative *S. pimpinellifolium*.

Data are from a transcriptome analysis of various tissues in tomato cultivar Heinz and *S. pimpinellifolium* (Tomato Functional Genomics Database, <http://ted.bti.cornell.edu/cgi-bin/TFGD/digital/experiment.cgi?ID=D004>; Tomato Genome Consortium, 2012). Data of *Solyc10g086250* (*SIAN2*), *Solyc10g086260* (*SIANT1*), *Solyc10g086270* (*SIANT1like*) and *Solyc10g086290* (*SIAN2like*) are shown.