Supplementary information

Extraordinary transgressive phenotypes of hybrid tomato are influenced by epigenetics and small silencing RNAs

Padubidri V. Shivaprasad, Ruth M. Dunn, Bruno ACM Santos, Andrew Bassett, and David C. Baulcombe†

Department of Plant Sciences,
University of Cambridge, Downing Street, Cambridge CB2 3EA, United Kingdom

Supplementary Information contains Supplementary Methods (Section 1), Supplementary Figures S1-S12 (Section 2), Supplementary Tables SI-SV (Section 3) and Supplementary References (Section 4).

Section 1: Supplementary Methods

RT-PCR and quantitative (q)PCR

RPL2 was amplified using primers RPL2for 5’-ACACAAAGTTGTGA CCG TGG-3’ and RPL2rev 5’-ACCATGAGGATGCTCCACAGG-3’ with *Taq* DNA polymerase. Tomato GAPDH (238 bp amplicon) was amplified using GAPDHFor 5’-GGAGGAGGGAACAACAAGAGG-3’and GAPDHRev 5’-AGATGCCGTCAGTGCCGA-3’. A 543 bp fragment of *SlAPS1* was amplified using APS1For 5’- CGGGCTGATCGAGCCGGATG-3’ and APS1 Rev 5’-GCAGGGGAAAGCCGGAACCTG-3’. Locus H06 fragment (335 bp) was amplified using H06for 5’- GTTGTAGAAGGCGAGGTGG -3’ and H06rev 5’- GTCTCGTTTCCTCTCACACG -3’. PAL fragment (275 bp) was amplified using primers PALfor 5’-TCAGCAAGGAAAACCGCTGAGGC-3’ and PALRev 5’- GGGTAGGTGGAGCTGCAGGGA-3’. Error bars indicate standard deviation.

DNA Methylation assay

Primers used for amplification are H06F1 5’-GGAAACGAATTCAAAAGGAGAAGTATGA-3’ and H06R1 5’-CTAGAGACCGAAATGCAAAATCAAATTG-3’; 95˚C 2 min, then 40 cycles of 95˚C 20 s, 60˚C 30 s, 72˚C 30 s. Values are expressed as a percentage of the mock digested control. Three replicates were performed for each sample.

Phylogenetic analysis

Multiple alignment of PAL sequences was made using ClustalW2 (Larkin et al, 2007). The alignment was processed with Phylip (a maximum parsimony method, http://www.phylip.com/) package 3.69. Bootstrapping analysis was carried out using Phylip *seqboot* with 1000 replications. The output was processed with Phylip *protpars* program with randomized input order options and Phylip consensus was used to combine multiple trees. Tree was drawn using Dendroscope (Huson et al, 2007) program version 2.7.4.

Section 2: Supplementary Figures

Supplementary Figures S1-S12.

Section 3: Supplementary Tables

Supplementary Table titles-

Supplementary Table I. Primer sequences used for northern blot analysis.

Supplementary Table SII. Table showing 153 sRNA loci used for heatmap generation in Figure 2A. Values indicate transgressive index as described in text and Methods section.

Supplementary Table SIII. List of transgressive sRNA loci that are used for heatmap in Figure 3A. Unigenes and gene descriptions are given.

Supplementary Table SIV. Transgressive sRNA loci targeting cDNAs that are marked to show different transgressive features. MPV, mid parental value. Values are normalized sRNA counts.

Supplementary Table SV. Number of sRNA sequences matching four PALs identified from tomato Chromosome 9.

Section 4: Supplementary References

Huson DH, Richter DC, Rausch C, Dezulian T, Franz M, Rupp R (2007) Dendroscope: An interactive viewer for large phylogenetic trees. *BMC Bioinformatics* **8:** 460

Larkin MA, Blackshields G, Brown NP, Chenna R, McGettigan PA, McWilliam H, Valentin F, Wallace IM, Wilm A, Lopez R, Thompson JD, Gibson TJ, Higgins DG (2007) Clustal W and clustal X version 2.0. *Bioinformatics* **23**(21)**:** 2947-2948

Supplementary Figures (S1 to S12)

Extraordinary transgressive phenotypes of hybrid tomato are influenced by epigenetics and small silencing RNAs

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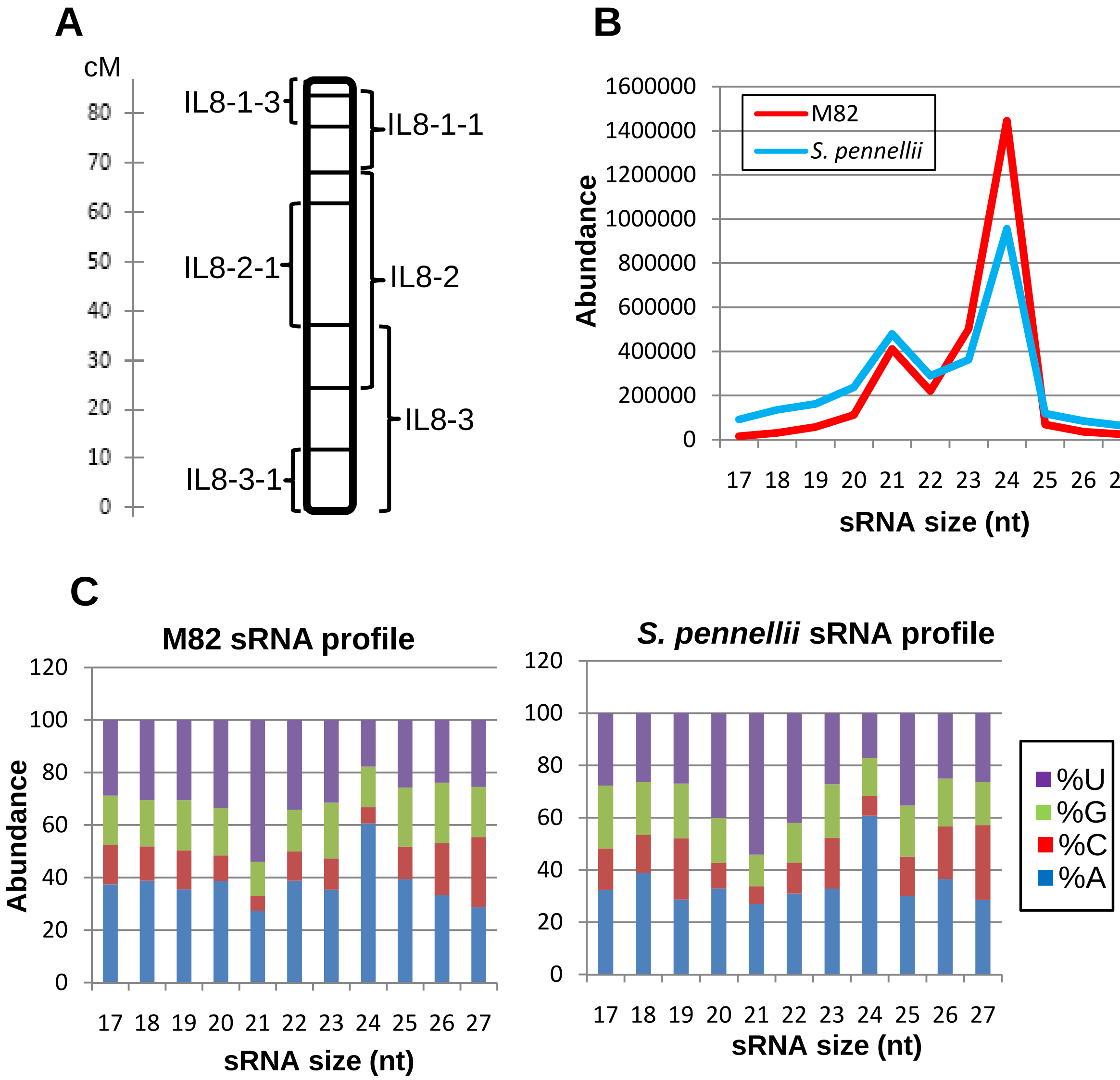
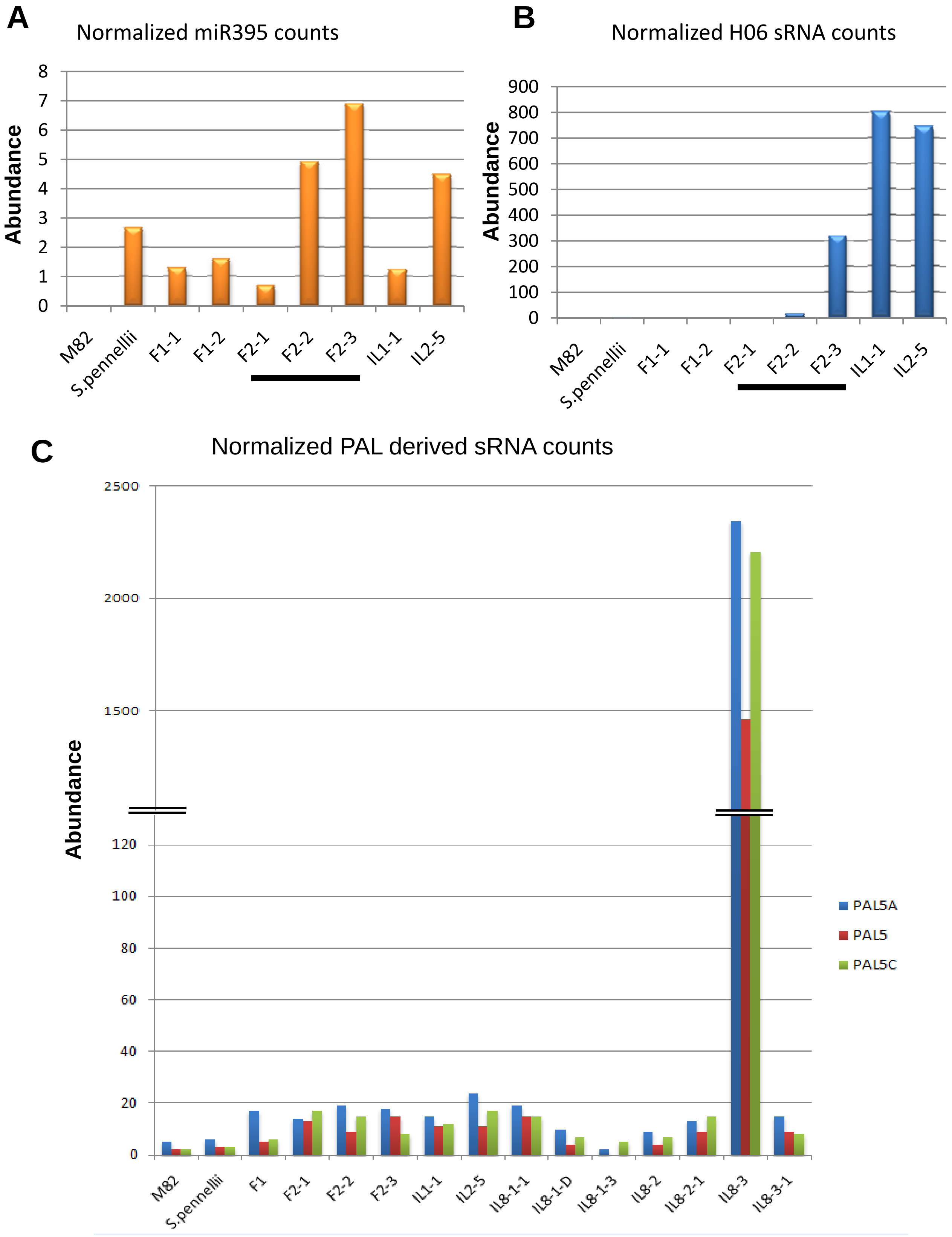


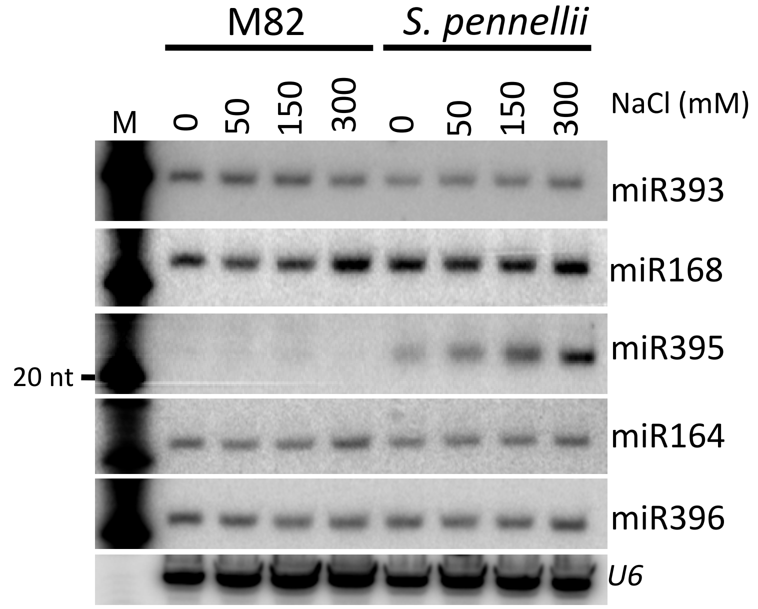
Supplementary Figure 1. (**A**)**.** Map of chromosome 8 showing the locations of the *S. pennellii* regions inserted in introgression lines (redrawn based on Lippman et al, 2007). cM, centimorgan. (**B**). Profile of small RNAs from M82 and *S. pennellii*, showing abundance of small RNAs by size (length in base pairs). Counts are per million reads of cloned small RNA. (**C**). Profile of the first 5' nucleotide of sRNAs of different sizes in sRNA libraries from M82 (left panel) and *S. pennellii* (right panel).

Variation in sRNA accumulation among F2 lines

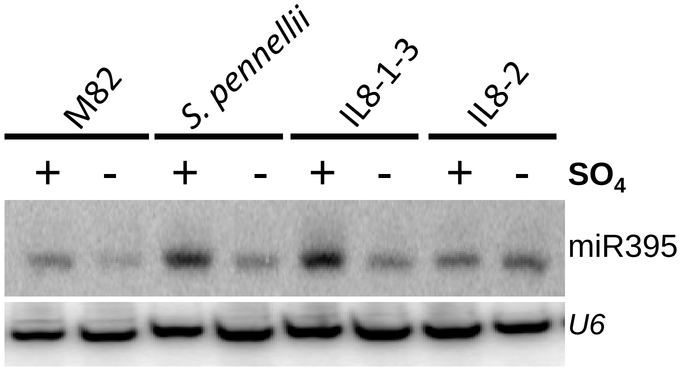


Supplementary Figure 2. (**A**). miR395 counts for tomato lines, normalised to library size. Three independent F2 lines are marked (black bar). (**B**). Counts of sRNAs aligning to genomic locus H06, counts normalised to library size. Three independent F2 lines are marked. (**C**). Counts of siRNAs aligning to three PALs (PAL5A: SGN-E235342, PAL5:SGN-E304219, PAL5C: SGN-E316424). Counts normalised to library size.

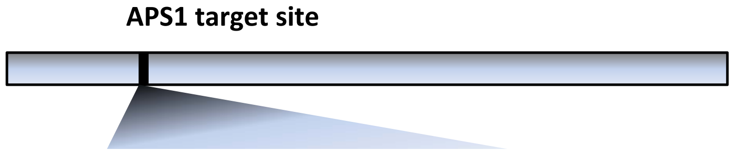
A. miR395 accumulation upon salt stress



B. miR395 accumulation upon sulphate stress



C. Conserved miR395 targets



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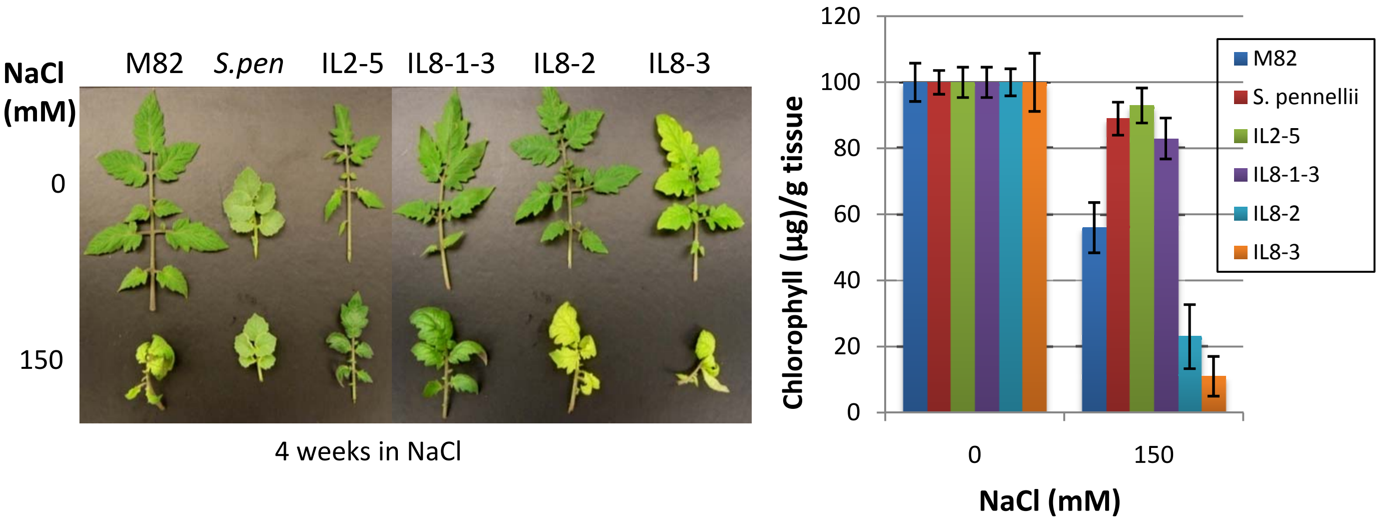
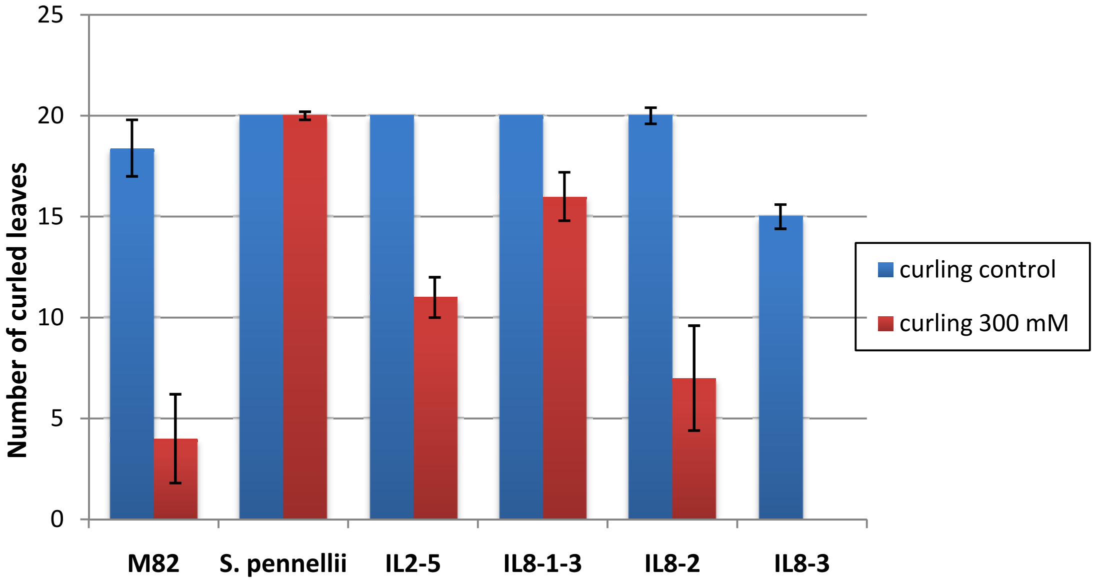
AtAPS1      5'-...GAGUUCCUCCAAACUCUUCAU...-3'
LeAPS1      5'-...GAGUUCCUCCAAACUCUUCAU...-3' SGN-U573424
                  ||||||| |||||| |||||
               3'-CUCAAGGGGGUUUGUGAAGUC-5'  miR395a
```

Supplementary Figure 3. (**A**). Accumulation of miR395 during salt stress in the two parental lines, M82 and *S. pennellii*. Primer sequences as in Supplementary Table SI. M, Size marker. (**B**). miR395 accumulation upon sulphate (SO_4) stress. 3 week-old plants were grown in normal (+) or medium without sulphates (medium had chlorides instead of sulphates). (**C**). Alignment of miR395 to target sequences in the *APS1* from *Arabidopsis* and tomato. Analysis was performed using the MultiAlin (http://bioinfo.genotoul.fr/multalin/multalin.html) tool.



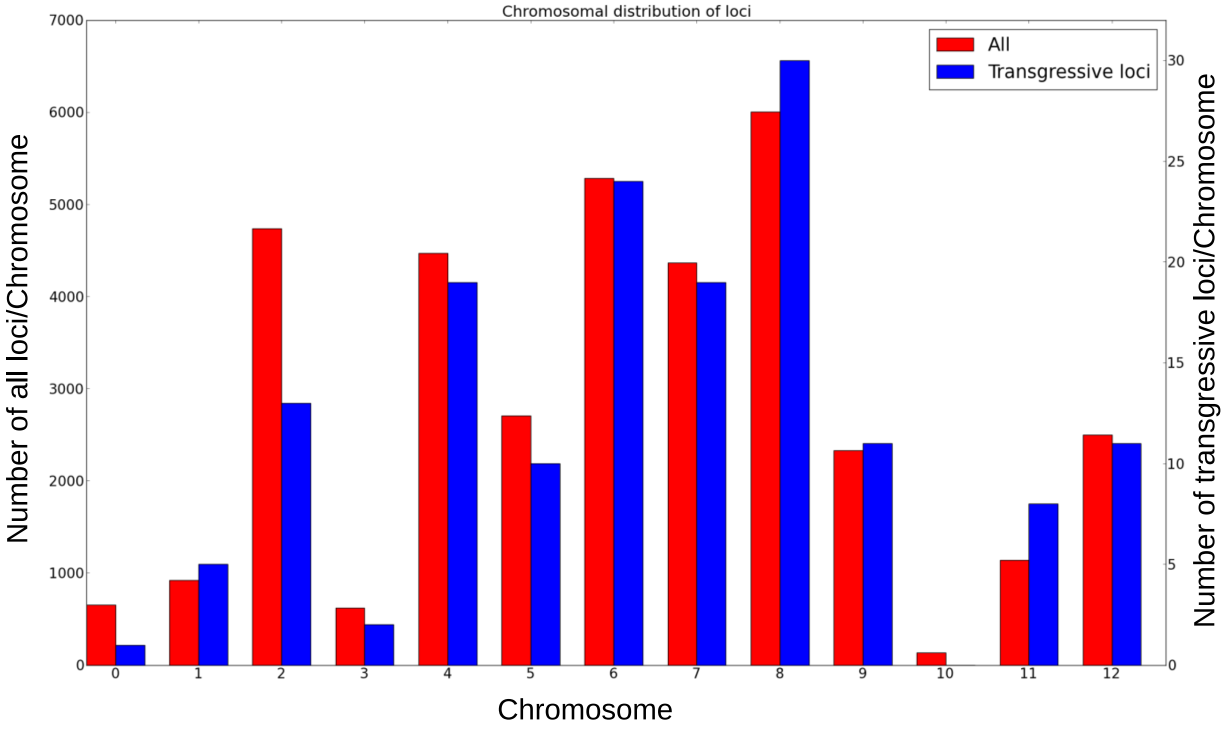
A. Leaf phenotypes upon prolonged salt stress



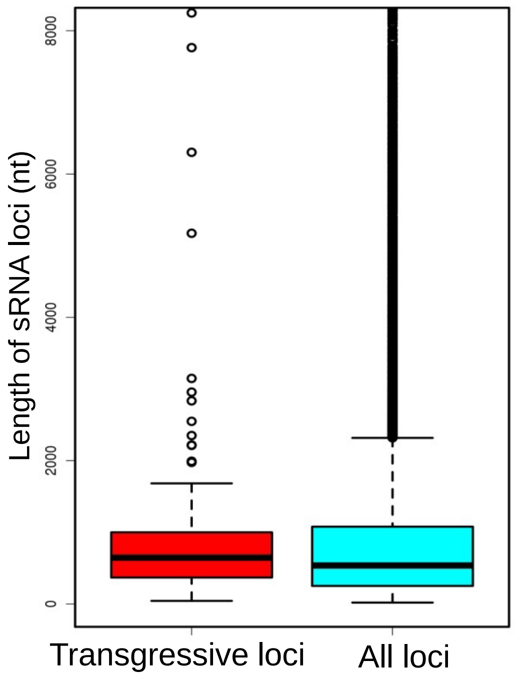
B. Leaf curling upon salt stress

Supplementary Figure 4. (**A**)**.** Phenotypes of leaves taken from salt treated tomato lines (left panel) and their chlorophyll content (right panel). Photograph taken 4 weeks upon treatment with salt. (**B**). Leaf curling phenotype upon salt stress. 20 leaves from 3 replicate experiments were scored for curling (terminal leaflet curled outwards more than 130^o) from water treated (blue bars) or salt treated (red bars) plants. Note that all leaves were curled in IL8-3 upon salt stress while *S. pennellii* did not show curling in control and stressed conditions.

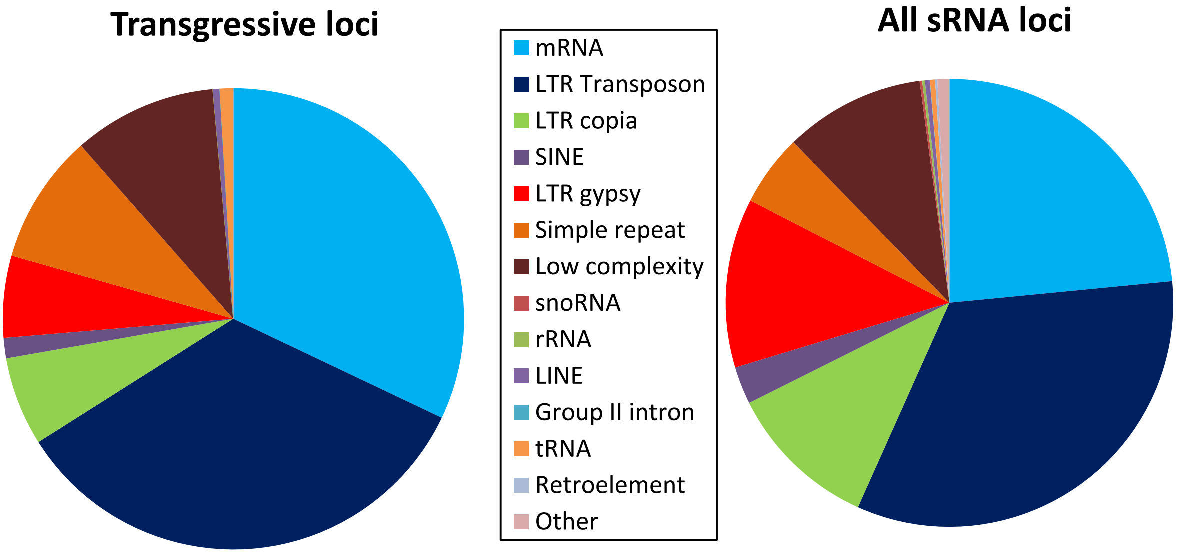
A. Distribution of transgressaive loci among tomato Chromosomes



B. Length of transgressive loci

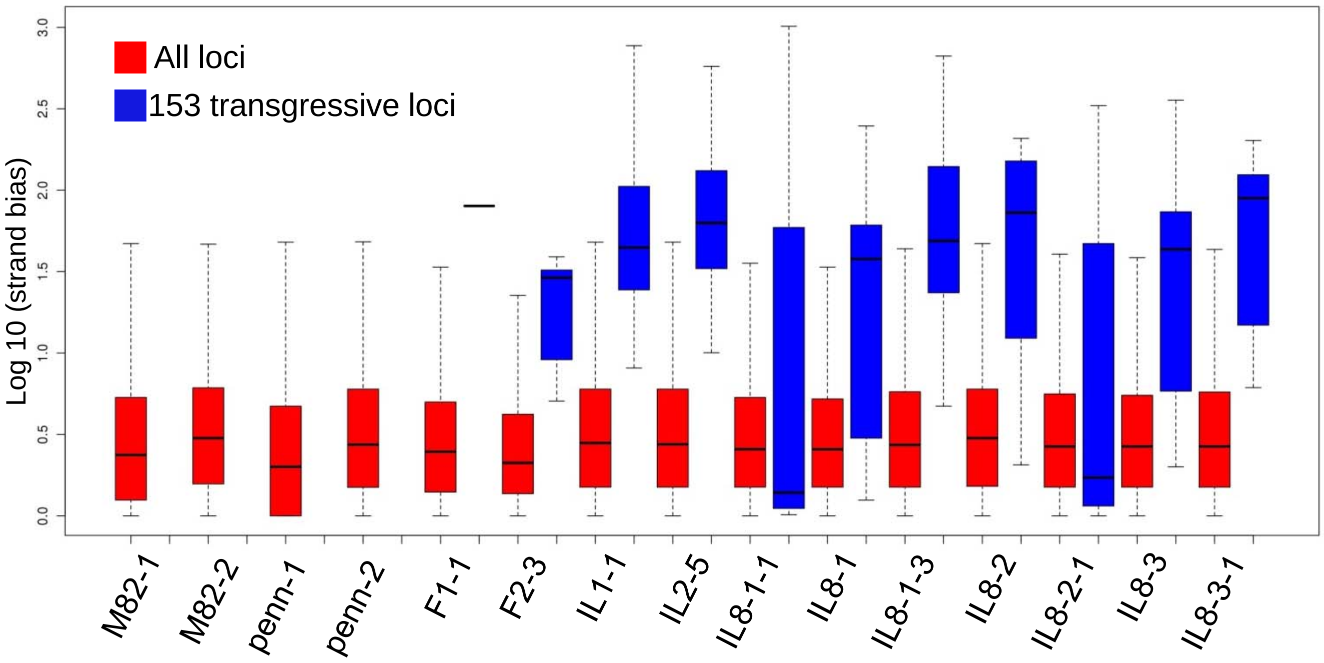


Supplementary Figure 5. Distribution and length of transgressive loci. **A.** Distribution of transgressive loci among 12 chromosomes of tomato. Chromosome 0 has sequences of unassigned Chromosomes. **B.** Boxplot showing average length of 153 transgressive loci in comparison to all sRNA loci.

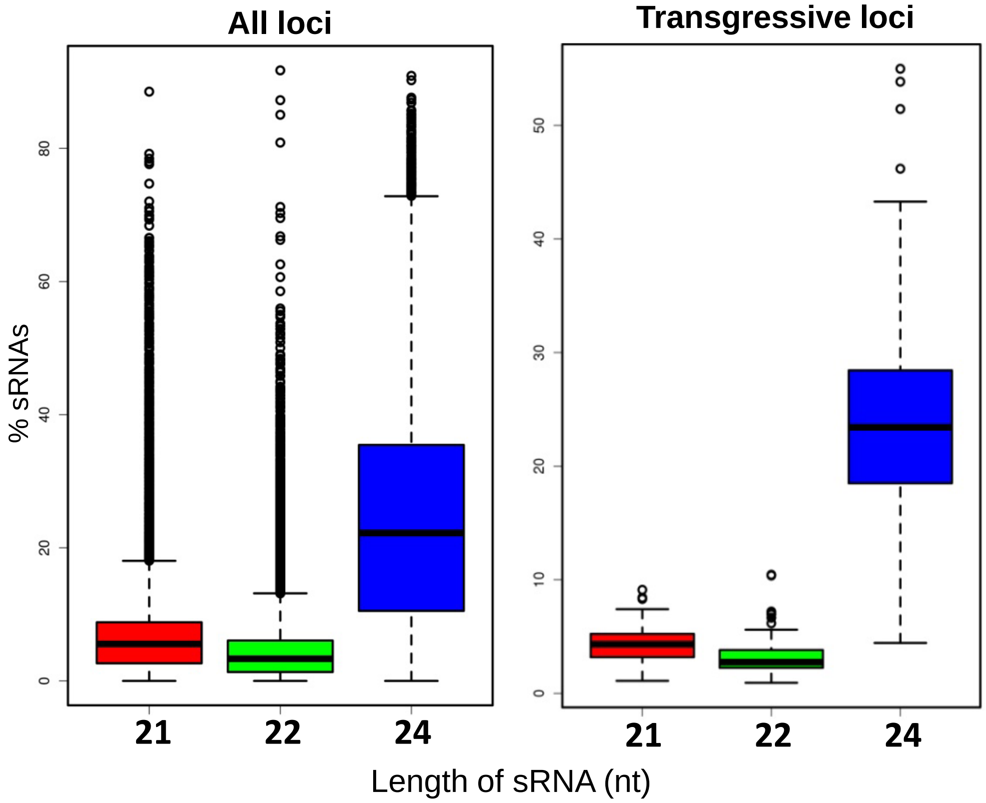


Supplementary Figure 6. Annotation of sRNA loci.

A. Strand bias

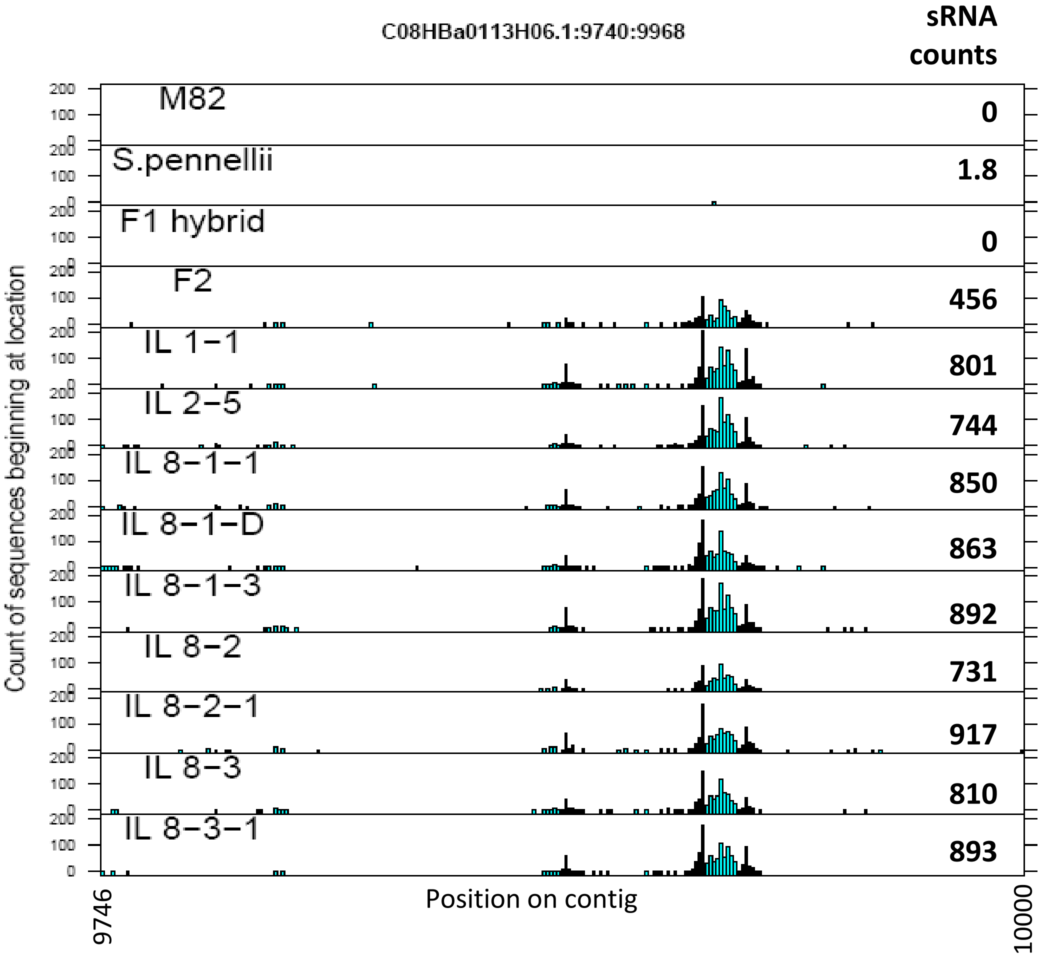


B. Size distribution of sRNAs among transgressive loci



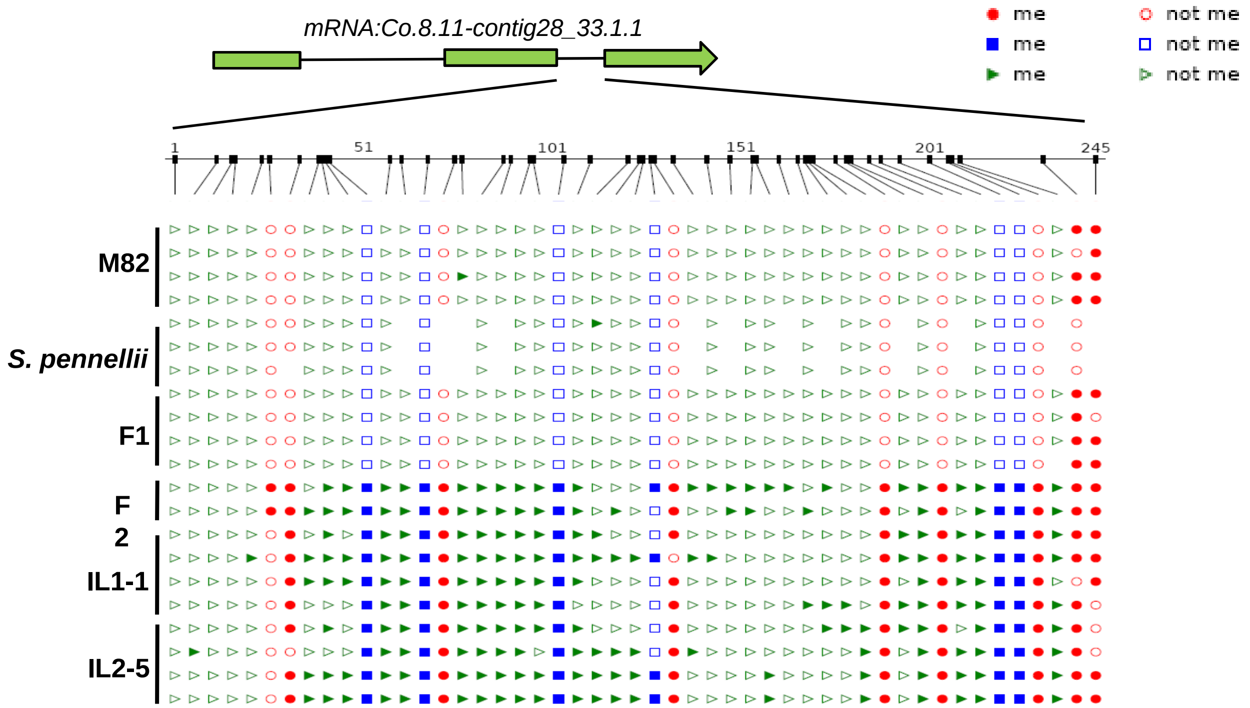
Supplementary Figure 7. Strand bias and sRNA length among transgressive sRNA loci. (**A**). Strand bias among transgressive loci. Transgressive loci are present only among ILs and F2-3 where they show slight strand bias. (**B**). Size distribution of sRNAs among transgressive loci.

Graph showing abundance and distribution of H06 sRNAs

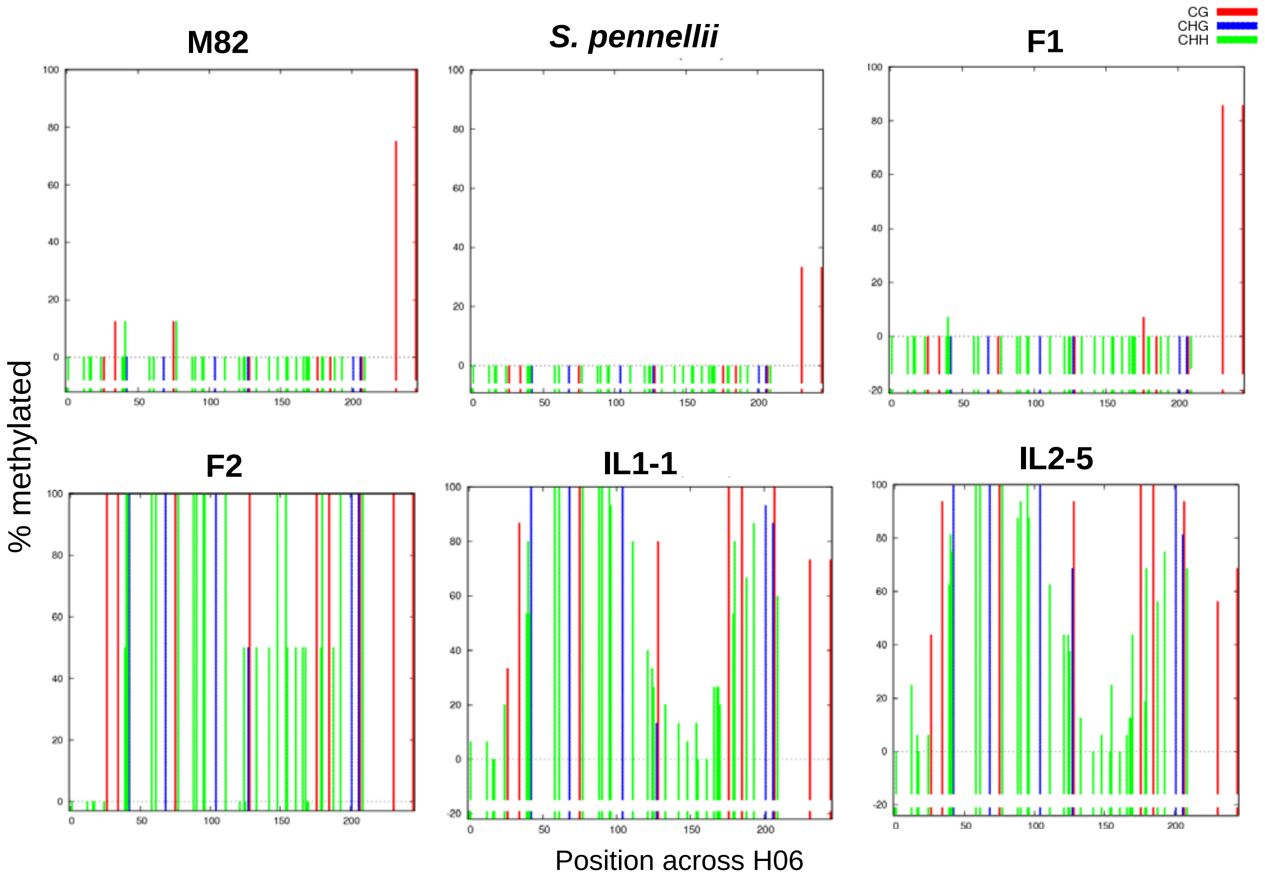


Supplementary Figure 8. Graph showing the number of sRNAs which have a first base pair mapping to each position across the H06 350 bp region of Chromosome 8. Reads matching sense strand (black bars) and antisense strand (green) are shown.

A. Bisulphite sequencing analysis of H06 locus

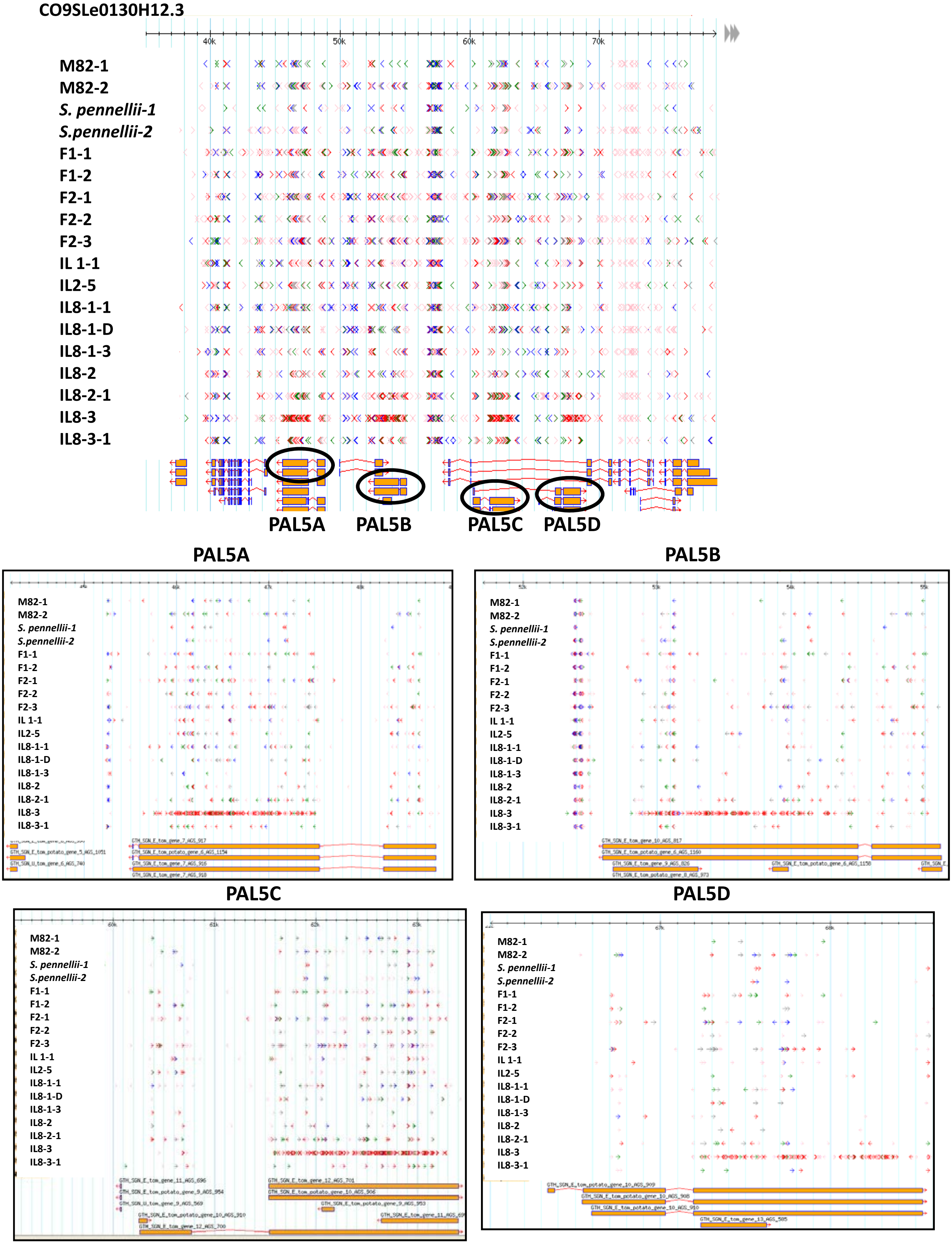


B. Methylation across H06 locus among parents and hybrids

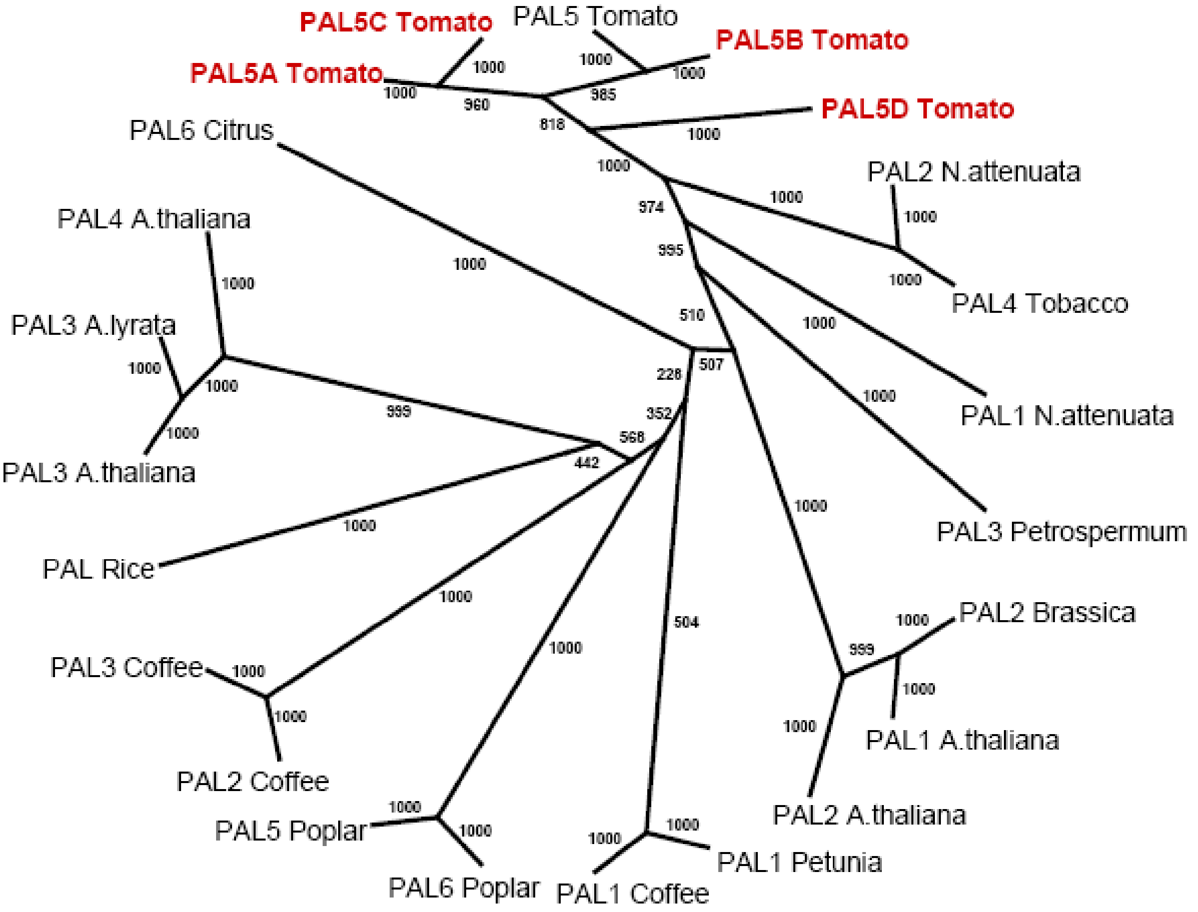


Supplementary Figure 9. Bisulphite sequencing analysis of H06 DNA in parental lines and hybrids. PCR products were cloned into pGEM-T easy and sequenced. Each sample had at least 10 independent clones. (**A**). Analysis of Bisulphite data by Cymate tool (red circles CG methylation; blue squares CHG methylation and Green arrows, CHH methylation). me, methylated (**B**). Distribution of methylation across H06 region.

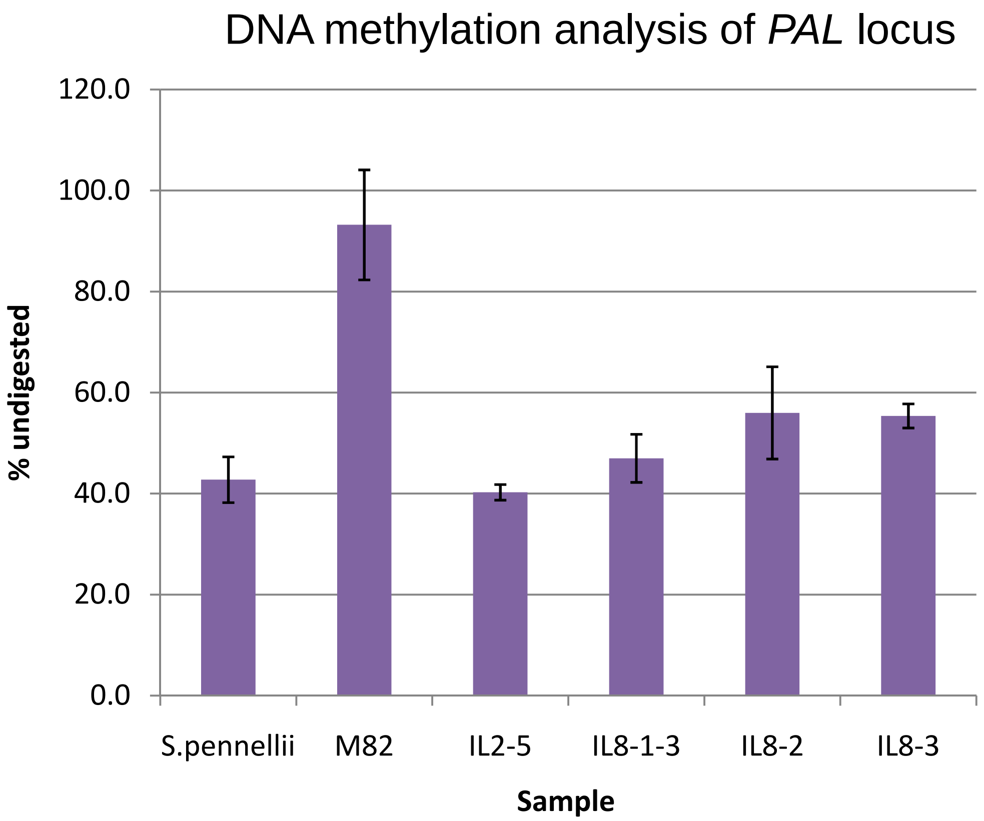
Browser views of 4 PAL sequences in Chromosome 9



Supplementary Figure 10. Genome Browser view of genomic locations of four *PAL* sequences. Four individual *PAL*s are named and alignment of sRNAs from small RNA datasets including IL8-3 for all four *PAL* sequences is shown in individual panels.



Supplementary Figure 11. An unrooted consensus phylogenetic tree to show relationships between some plant PAL family members and four new Tomato PAL sequences. Values at branches are bootstrapping values. Phylogenetic analysis is described in Supplementary Methods section. 4 PAL sequences from tomato Chromosome 9 are shown in red. Sequences used: PAL1 (*A. thaliana*) NP_181241.1; PAL1(*Petunia*) AAV98199.1; PAL1 (*Nicotiana attenuata*) ABG75910.1; PAL1 (Coffee)ABG75910.1; PAL2 (*A. thaliana*) NP_190894.1; PAL2 (Coffee) AAN32867.1; PAL2 (*Brassica*) ABY89691.1; PAL2 (*N. attenuata*) ABG75911.1; PAL3 (*A. thaliana*) NP_196043.2; PAL3 (Coffee) CAJ41418.1; PAL3 (*A. lyrata*) XP_002871081.1; PAL3 (*Petrospermum*) P45729.1; PAL4 (*A. thaliana*) NP_187645.1; PAL4 (Tobacco) ACJ66298.1; PAL5 (Tomato) AAA34176.1; PAL5 (Poplar) ACC63891.1; PAL5 (Citrus) AAB67733.1; PAL6 (Poplar) EEF01480.1.



Supplementary Figure 12. DNA methylation analysis of PAL locus. Analysis was performed as described in Methods Section. A 209 bp target region was amplified by quantitative PCR from 40 ng digested DNA using SYBR Green JumpStart *Taq* ReadyMix (Sigma S9194) (PAL For 5'-GACCCTTTGATGCAGAAGCTGAGACA-3', PALRev 5'- CCGCATTCTGTGATCCTGTTAGGAA-3'; 95˚C 2 min, then 40 cycles of 95˚C 20 s, 60˚C 30 s, 72˚C 30 s). Values are expressed as a percentage of the mock digested control. Three replicates were performed for each sample.

Supplementary Table I. Primer sequences used for northern blot analysis.

Probe name	**Probe sequence (5’ to 3’)**
miR164	TGCACGTGCCCTGCTTCTCCA
miR168	GTCCCGACCTGCACCAAGCGA
miR171	GATATTGGCGCGGCTCAATCA
miR319	AGGGAGCTCCCTTCAGTCCAA
U6	GGCCATGCTAATCTTCTCTGTATCGTT
miR395	GGAGTTCCCCCAAACACTTCAG
miR396	CAGTTCAAGAAAGCTGTGGAA
miR393	GGATCAATGCGATCCCTTTGGA
H06 a	GCGTCTTCAGACAATAGTAGATTT
H06 b	TCTTGTTGTGTCTTCCTCCGTAGC
PAL siRNA	AGGACTTGTCTCAGCTTCTGC

Supplementary Table SII. Table showing 153 sRNA loci used for heatmap generation in Fig. 3A. Values indicate transgressive Index as described in Methods section.

Genomic Locus	**M82-1**	**M82-2**	**S.penn-1**	**S.penn-2**	**F1-1**	**F2-3**	**IL1-1**	**IL2-5**	**IL8-1-1**	**IL8-1D**	**IL8-1-3**	**IL8-2**	**IL8-2-1**	**IL8-3**	**IL8-3-1**
C08HBa0113H06.1_9731	0.0	0.0	2.0	0.0	0.0	245.5	1407.7	1284.3	1097.4	1224.5	1490.8	724.9	1144.6	1012.7	1325.1
C06HBa0310B09.1_114490	-1.8	1.4	-269.5	-141.5	-6.6	-13.4	4.7	-1.5	-8.7	3.5	12.4	-1.4	-2.6	1.9	2.0
C06HBa0153G23.1_45626	-1.8	1.4	-269.5	-141.5	-6.6	-13.4	4.7	-1.5	-8.7	3.5	12.4	-1.4	-2.6	1.9	2.0
C05SLm0005B15.1_62823	0.0	2.0	0.0	0.0	1.1	1.4	54.4	56.0	34.7	55.1	79.0	70.1	71.6	3.2	-2.0
C07HBa0037F23.1_2254	0.0	1.7	0.0	2.0	1.9	11.4	44.0	23.8	42.2	44.7	23.3	58.8	70.5	54.0	22.8
C08SLe0082C24.1_62428	1.2	-1.3	0.0	-1.7	0.0	23.7	84.1	62.6	0.0	6.4	91.2	73.3	90.3	92.0	99.2
C02HBa0040B13.1_82475	1.2	-1.3	0.0	1.2	0.0	44.7	32.2	0.0	135.2	1.4	55.7	144.5	179.9	116.8	124.2
C07SLm0093E04.2_52824	0.0	2.0	0.0	1.6	0.0	68.6	1.7	0.0	0.0	5.6	1.8	1.9	0.0	0.0	237.1
C06HBa0307J13.1_20725	1.1	-2.2	-1.3	1.3	2.3	1.6	1.2	-1.3	20.3	1.7	1.5	-2.4	10.2	1.7	1.4
C06HBa0301C21.1_123626	1.1	-2.2	-1.3	1.3	2.3	1.6	1.2	-1.3	20.3	1.7	1.5	-2.4	10.2	1.7	1.4
C11HBa0054I23.2_2977	1.1	-1.1	0.0	1.6	1.0	1.6	-1.0	1.3	18.4	1.5	1.9	-1.2	9.9	-1.6	-1.1
C04HBa0128L09.1_55084	-3.6	1.2	0.0	2.0	1.3	1.2	1.3	2.4	20.1	2.1	1.1	1.6	11.2	1.9	1.5
C11HBa0027B05.1_160627	-2.1	1.5	-2.0	1.4	1.4	4.2	2.9	1.0	19.0	1.4	3.6	2.0	9.9	-1.2	2.1
C02HBa0329G05.3_43554	1.0	-1.0	-1.9	-1.6	-1.4	1.4	1.1	1.6	22.3	1.8	2.0	1.0	10.1	2.3	-1.3
C04HBa0204I09.1_44407	1.1	-1.1	-3.5	-1.0	1.4	-1.1	1.8	1.2	21.6	1.5	2.1	1.5	11.9	1.1	-2.9
C08SLm0066D16.1_50268	-1.1	1.1	-3.3	1.0	-1.6	-1.4	1.6	2.8	23.9	2.4	1.5	1.5	10.4	1.7	1.1
C08SLe0028K16.1_832	0.0	2.0	0.0	-2.9	1.3	-1.5	2.5	1.1	20.1	2.9	1.8	-2.4	8.9	2.0	-1.5
C08HBa0022O08.1_3499	0.0	2.0	0.0	-2.9	1.3	-1.5	2.5	1.1	20.1	2.9	1.8	-2.4	8.9	2.0	-1.5
C08SLe0008I14.1_76712	-1.0	1.0	-1.4	-4.3	1.5	-1.0	2.2	1.3	21.4	1.7	-1.1	-1.8	9.4	1.1	1.0
C02HBa0040B13.1_105145	1.2	-1.3	0.0	-2.8	0.0	-3.8	-1.1	-1.5	17.2	1.3	-1.8	-1.8	8.1	1.4	-1.1
C06SLe0045F21.1_42095	-1.2	-1.6	0.0	2.0	1.2	4.4	2.6	3.1	12.2	3.5	2.6	-1.2	8.7	1.5	1.1
C06SLe0039G15.1_78263	-1.2	-1.6	0.0	2.0	1.2	4.4	2.6	3.1	12.2	3.5	2.6	-1.2	8.7	1.5	1.1
C08HBa0197A05.1_72989	-1.3	1.2	-2.5	-1.8	-1.2	1.2	1.9	2.7	15.7	4.1	3.1	1.8	7.7	1.3	1.2
C11HBa0064J13.2_90570	1.1	-3.6	-1.1	1.1	-3.2	1.4	1.9	1.2	17.7	2.1	2.2	1.4	8.6	-1.6	1.7
C06HBa0066P09.1_49867	1.0	-1.0	-1.9	1.3	1.4	2.0	3.3	2.7	17.2	5.7	3.8	3.6	11.4	5.2	3.8
C02HBa0228I09.1_80757	-1.0	1.0	0.0	-12.6	1.3	-4.1	1.8	1.4	10.0	3.1	1.2	1.9	15.0	0.0	1.9
C02HBa0165K22.1_42119	-1.0	1.0	0.0	-12.6	1.3	-4.1	1.8	1.4	10.0	3.1	1.2	1.9	15.0	0.0	1.9
C04HBa0077O05.2_50931	-2.0	1.3	-1.3	1.2	2.5	1.1	1.1	1.5	12.0	2.6	2.3	1.2	6.1	2.3	1.1
C05SLm0118J18.1_1260	-1.7	1.3	-1.0	1.0	-1.1	-1.1	1.5	1.1	9.6	1.0	1.3	1.6	5.9	1.6	-1.4
C08HBa0058M16.1_17030	-1.0	1.0	-2.1	-1.2	-1.2	1.4	1.8	-1.3	12.8	2.5	2.7	2.5	5.0	2.3	-1.1
C06HBa0116O16.1_120641	-1.1	1.1	-4.1	-1.6	-2.0	-2.6	1.2	-1.0	10.6	1.5	1.1	-1.3	6.0	-1.4	-1.3
C01HBa0006K08.1_127343	-4.7	-1.5	-1.2	1.1	1.8	1.2	-1.8	-4.5	12.0	-1.0	-1.4	-1.2	6.4	-1.0	-2.6
C08SLe0068N03.1_131153	-3.9	-1.0	-3.8	1.7	0.0	-1.2	-3.7	-1.2	15.2	-1.3	-3.5	-1.4	6.8	-3.5	-1.1
C08SLe0114E15.1_38488	-1.1	-4.6	-1.4	1.3	-1.6	-2.7	-1.2	-1.8	9.2	-1.4	-2.5	-4.9	4.8	-2.5	-1.5
C07SLm0009N18.2_3030	-4.1	-1.1	-1.1	1.0	1.4	-2.1	2.6	-6.5	7.5	-1.2	9.7	3.1	5.2	-1.9	2.3
C08SLe0090D03.1_17474	-2.6	-2.5	1.4	-1.6	-1.5	-1.4	5.4	5.1	3.8	1.5	1.8	1.2	1.0	2.7	1.8
C12HBa0144B17.1_120378	-2.9	-2.7	1.4	-1.6	-1.4	-1.3	5.3	4.9	3.8	1.6	1.8	1.2	1.0	2.7	1.8
C04SLm0141K23.1_54841	-3.0	-2.5	1.3	-1.5	-1.6	-1.4	5.6	5.4	4.0	1.6	1.8	1.2	1.1	2.8	1.9
C08HBa0323O07.1_88692	-2.7	-1.7	1.3	-1.4	-1.0	-1.2	5.3	5.5	4.1	1.7	1.9	1.5	1.1	2.9	2.3
C06HBa0046P09.1_14651	-2.7	-3.3	1.5	-2.0	-1.6	-1.3	6.0	5.7	4.3	1.7	1.9	1.3	1.2	3.0	2.0
C06HBa0015I15.1_536	-2.7	-3.3	1.5	-2.0	-1.6	-1.3	6.0	5.7	4.3	1.7	1.9	1.3	1.2	3.0	2.0
C04HBa0067O19.1_6112	-5.5	-2.5	1.3	-1.4	-1.5	-1.4	5.4	5.1	3.8	1.4	1.6	1.2	-1.0	2.7	1.8

C05HBa0091D14.1_11542	-5.3	-3.8	1.7	-3.4	-1.2	-1.3	7.8	8.3	6.0	2.0	2.2	1.8	1.3	4.2	2.9
C04HBa0103J09.1_42370	-4.1	-2.1	1.7	-3.1	-1.5	-1.2	7.3	7.1	5.3	1.8	2.0	1.3	1.1	3.6	2.4
C03HBa0318C22.1_76957	-1.9	-1.5	1.4	-1.6	-1.0	1.2	6.2	6.1	4.6	1.7	2.0	-1.1	-1.7	2.0	2.1
C07HBa0325D07.1_62352	-2.5	-2.0	1.4	-1.6	-1.2	1.2	6.0	6.0	4.5	1.6	1.9	-1.2	-2.0	1.9	2.0
C04HBa0107N23.1_4597	-3.8	-2.5	1.4	-1.8	-1.3	1.2	6.7	6.8	5.0	1.6	1.9	-1.4	-2.5	2.0	2.1
C08HBa0323O07.1_24299	-2.9	-2.5	1.4	-1.7	-1.3	1.1	6.3	6.4	4.8	1.6	1.9	-1.3	-2.4	2.0	2.1
C09SLm0105D02.1_96970	-1.8	-1.2	1.4	-1.7	1.1	1.3	6.6	6.6	5.0	1.8	2.2	1.0	-1.5	2.2	2.4
C04HBa0158A08.1_22367	-3.3	-1.9	1.5	-1.8	1.2	1.2	7.4	8.4	5.9	1.8	2.0	-1.1	-1.9	2.4	2.6
C08HBa0033P21.1_102690	2.3	-1.5	1.5	-2.0	1.0	-4.8	0.0	1.6	2.2	1.3	1.6	3.7	-1.7	-1.2	-2.0
C06HBa0052N09.1_28071	-2.8	-9.1	-1.4	1.3	-8.1	-1.7	4.1	2.0	4.4	1.7	9.9	5.1	6.2	6.8	-2.3
C11HBa0323C14.1_139784	-1.4	1.3	-2.8	-5.9	-1.4	-6.7	1.3	1.9	1.3	14.9	1.5	1.3	2.2	1.2	-9.3
C08HBa0086C12.1_5634	-1.1	1.1	-5.0	1.3	1.5	1.4	3.8	4.1	10.7	5.8	2.9	3.1	6.7	5.1	2.6
C08SLm0019J03.1_96646	-1.1	1.1	-5.0	1.3	1.5	1.4	3.8	4.1	10.5	5.8	2.9	3.1	6.6	5.1	2.6
C06SLe0045F21.1_62802	-1.2	1.2	-1.8	-1.3	2.1	1.8	3.5	3.0	10.9	3.8	3.5	3.5	6.7	3.4	2.5
C06HBa0304P16.1_8244	-1.2	1.2	-1.8	-1.3	2.1	1.8	3.5	3.0	10.9	3.8	3.5	3.5	6.7	3.4	2.5
C07SLm0140K05.1_20295	-1.4	1.3	-3.3	-1.6	-1.2	-1.7	5.8	1.0	9.1	6.2	2.1	4.3	9.8	4.3	1.5
C04HBa0068N05.1_37863	-1.7	1.2	-2.0	1.5	1.4	-1.2	3.7	8.6	6.6	7.5	4.8	3.7	5.7	7.4	4.6
C09SLm0017K18.2_2329	1.4	-1.7	-2.1	-4.4	-1.5	3.8	6.0	4.9	4.4	7.9	7.4	3.5	12.5	9.5	1.2
C01HBa0155M04.1_41815	-1.0	1.0	-4.1	-1.4	2.0	1.4	15.8	3.0	5.6	3.2	5.7	3.5	7.0	2.8	-1.7
C09HBa0170H21.1_99572	-1.3	1.3	-1.8	1.3	1.0	1.5	8.7	4.4	7.6	7.7	6.1	13.3	13.7	9.6	6.0
C06HBa0225A15.1_5238	-1.6	1.4	-2.6	1.3	-1.0	1.4	7.6	3.9	6.6	6.6	5.3	11.4	11.6	8.3	5.2
C05SLm0115G01.3_111365	-1.8	1.5	-4.4	1.3	-1.2	-1.0	5.7	3.0	6.6	5.7	4.3	11.0	9.1	6.7	3.9
C01HBa0051C14.1_135746	-4.2	1.8	-2.1	-1.2	1.2	-1.0	10.7	6.9	9.2	7.7	8.0	14.2	14.0	10.5	7.2
C04SLm0098C07.1_84445	-5.8	1.8	0.0	0.0	-1.0	-3.2	5.0	13.4	13.7	6.7	6.5	14.4	1.9	5.2	-1.7
C02HBa0161P02.1_107887	-2.3	1.4	1.4	-1.5	0.0	-3.5	3.1	8.1	12.0	5.1	4.0	10.0	1.5	3.5	-3.7
C07SLm0046H06.1_19884	-10.7	1.7	-3.5	1.7	5.3	-1.3	4.2	12.1	10.1	13.4	11.4	7.8	5.2	-1.9	1.4
C01HBa0155M04.1_93171	-2.5	-4.0	1.2	-1.3	1.1	1.5	2.1	-2.4	34.1	2.6	1.6	1.4	17.2	1.8	-2.0
C12HBa0266F15.1_47176	1.0	-1.0	0.0	0.0	0.0	-9.1	1.7	6.2	3.2	56.7	1.5	11.9	2.0	-1.1	3.5
C02HBa0108N03.2_21605	1.7	-2.9	0.0	0.0	1.5	-8.5	0.0	28.3	-1.7	26.3	-1.6	-3.1	18.7	-3.2	-1.5
C06HBa0023D12.1_63482	1.3	-1.3	-63.5	-66.6	-1.1	-11.0	-1.7	8.2	-2.6	6.4	-3.2	-2.2	-3.1	-2.1	-1.4
C07SLm0096B05.1_61107	-2.5	1.6	2.2	1.2	-1.7	-35.8	-34.8	-27.5	-22.7	-10.2	-46.0	-11.8	-11.5	-10.5	0.0
C02HBa0090O01.2_49940	-2.4	1.6	2.4	1.1	-1.6	-34.9	-44.8	-28.4	-20.9	-10.8	-30.2	-11.5	-11.1	-9.7	0.0
C08SLm0064E10.1_10518	-2.4	1.6	2.4	1.1	-1.6	-33.1	-45.0	-28.6	-21.0	-10.9	-35.4	-13.0	-10.6	-9.7	0.0
C08SLm0031I10.1_121471	-3.2	1.7	2.3	1.2	-1.5	-19.2	-38.5	-26.1	-3.8	-10.1	-24.2	-7.9	-8.1	-7.3	0.0
C07HBa0049C13.2_44916	-2.9	1.7	2.2	1.1	-1.5	-17.6	-38.7	-26.2	-26.4	-10.1	-10.4	-10.2	-5.6	-9.2	0.0
C09HBa0113I06.1_18795	-2.6	1.6	2.2	1.2	-1.5	-24.6	-15.7	-40.0	-26.9	-9.0	-18.5	-6.6	-8.3	-7.5	0.0
C11HBa0303G16.1_63707	-2.8	1.6	2.1	1.1	-1.6	-28.6	-26.7	-40.7	-27.4	-12.2	-37.8	-12.3	-10.8	-7.6	0.0
C01HBa0130I12.1_40414	-1.8	1.4	1.7	-1.1	-1.8	-12.1	-9.2	-4.9	-6.5	-6.2	-6.0	-7.8	-5.3	-6.9	0.0
C06SLe0129O21.1_42844	-1.8	1.4	2.9	1.6	-1.4	-10.4	-12.6	-12.8	-11.6	-6.1	-11.8	-5.9	-5.9	-6.6	-18.8
C04HBa0223O22.1_11322	-2.5	1.6	2.3	1.1	-1.6	-23.6	-12.4	-17.1	-11.5	-8.7	-12.4	-8.7	-7.4	-6.4	-29.2
C07HBa0046G04.1_88999	-2.2	1.5	2.2	1.0	-1.6	-18.2	-16.6	-6.8	-8.8	-5.7	-10.2	-8.5	-7.8	-6.4	-30.8
C08HBa0216M19.1_80302	-1.8	1.4	2.3	1.0	-1.7	-16.6	-14.9	-11.6	-8.4	-6.0	-16.5	-8.7	-6.2	-5.6	-32.7
C07HBa0046G04.1_33876	-1.2	1.1	2.5	-1.4	-2.3	-23.5	-13.1	-9.8	-7.8	-7.2	-13.3	-6.9	-7.4	-7.4	-19.1
C06SLm0118M03.1_62516	-1.2	1.2	2.4	-1.5	-2.3	-29.5	-11.6	-9.8	-9.3	-8.6	-13.9	-9.6	-7.3	-8.9	-18.0
C11HBa0029C01.2_92878	-1.6	1.4	2.6	-1.1	-1.9	-27.4	-17.4	-11.6	-10.2	-7.8	-18.1	-7.3	-7.4	-8.4	-22.9
C05SLe0077B22.1_16612	-1.5	1.3	2.5	-1.1	-1.9	-26.3	-14.6	-10.6	-11.7	-7.1	-17.2	-8.8	-7.1	-8.3	-26.7
C06SLe0093P23.1_37922	-1.3	1.2	2.6	-1.0	-1.9	-30.2	-14.3	-11.8	-8.6	-7.7	-15.5	-10.6	-9.3	-9.2	-25.1

C06HBa0120H21.2_88031	-1.3	1.2	2.6	-1.0	-1.9	-30.2	-14.3	-11.8	-8.6	-7.7	-15.5	-10.6	-9.3	-9.2	-25.1
C07HBa0073N22.1_13459	-3.5	1.7	1.7	1.3	-1.8	-29.0	-8.7	-26.5	-10.7	-6.8	-49.2	-6.4	-9.9	-7.6	-18.1
C06HBa0054K13.2_13188	-2.4	1.6	2.3	1.1	-1.6	-18.9	-19.6	-10.4	-12.7	-7.0	-31.7	-7.5	-7.9	-7.7	-15.7
C09HBa0226D21.1_66486	-1.6	1.4	2.5	-1.1	-2.0	-32.3	-23.9	-15.1	-12.6	-9.2	-28.6	-9.8	-8.5	-9.5	-15.5
C09HBa0109D11.1_90498	-1.6	1.4	2.5	-1.1	-2.0	-32.3	-23.9	-15.1	-12.6	-9.2	-28.6	-9.8	-8.5	-9.5	-15.5
C11HBa0027B05.1_86941	-3.9	1.7	1.5	1.3	-1.6	-24.3	-8.3	-14.8	-10.9	-6.7	-12.2	-11.9	-6.1	-7.4	-50.5
C04HBa0114C15.1_59772	-1.8	1.5	2.5	-1.0	-1.8	-22.7	-18.9	-15.5	-6.8	-7.0	-15.4	-10.2	-7.7	-8.6	-51.3
C12HBa0133N05.1_1682	-1.3	1.2	2.6	-1.2	-2.0	-24.5	-14.7	-15.3	-10.4	-6.2	-15.4	-8.2	-6.3	-8.2	-41.9
C07SLm0075L20.1_13464	-1.6	1.4	2.5	-1.1	-1.9	-30.8	-13.4	-17.2	-9.1	-7.0	-13.8	-7.6	-7.2	-8.9	-44.9
C08SLe0129C18.1_30752	-1.8	1.5	2.4	1.1	-1.7	-18.1	-22.4	-18.4	-15.1	-9.6	-22.2	-11.4	-9.7	-8.3	-34.0
C12HBa0026C13.1_1924	-1.3	1.3	2.5	-1.2	-1.9	-22.7	-21.3	-12.2	-10.4	-8.0	-19.1	-9.6	-7.4	-8.6	-32.8
C12HBa0073O10.1_5791	-1.3	1.2	2.5	-1.2	-1.9	-25.0	-21.3	-12.9	-10.7	-8.7	-21.7	-10.0	-8.1	-8.8	-35.0
C04SLm0129D14.1_28153	-1.2	1.1	2.5	-1.3	-1.9	-29.5	-20.4	-19.1	-4.5	-9.8	-23.7	-10.4	-5.6	-8.2	-32.1
C05SLe0087C17.1_76921	-2.0	1.5	2.5	-1.0	-1.7	-28.4	-19.0	-17.2	-11.1	-8.0	-20.5	-9.3	-8.1	-9.0	-28.2
C05SLm0093K24.1_74997	-1.2	1.1	2.6	-1.4	-2.3	-31.9	-19.2	-16.5	-10.7	-8.6	-21.7	-9.3	-8.4	-9.7	-35.8
C07HBa0116M01.1_3736	-1.9	1.5	2.5	1.0	-1.8	-27.4	-32.9	-19.5	-12.4	-9.4	-20.7	-9.9	-8.5	-7.9	-44.3
C12HBa0026C13.1_85973	-2.5	1.6	2.4	1.1	-1.6	-22.7	-32.4	-16.5	-16.6	-9.5	-19.5	-11.6	-8.6	-6.7	-49.2
C04SLm0098C07.1_73026	-1.3	1.2	2.6	-1.2	-2.1	-28.5	-29.7	-19.1	-12.1	-9.6	-36.7	-10.2	-9.5	-9.2	-48.9
C09HBa0168F14.2_2148	-1.2	1.1	2.6	-1.3	-2.2	-25.8	-30.8	-20.0	-14.8	-10.2	-43.6	-12.4	-9.6	-10.6	-54.5
C05HBa0251J13.2_11022	-1.1	1.1	2.6	-1.5	-2.5	-52.8	-29.1	-23.4	-14.7	-10.8	-29.0	-13.2	-10.0	-11.0	-42.2
C03HBa0054O21.1_71801	-1.6	1.4	2.7	-1.1	-1.9	-40.2	-22.5	-15.3	-12.8	-8.3	-30.4	-8.7	-7.3	-7.1	-39.1
C06SLm0118M03.1_6691	-1.5	1.3	2.6	-1.1	-2.0	-39.6	-37.0	-22.6	-13.1	-9.5	-28.2	-10.4	-9.3	-9.6	-42.1
C12HBa0144B17.1_103446	-2.4	1.6	2.4	1.1	-1.5	-30.1	-32.7	-21.2	-18.0	-11.1	-30.8	-10.6	-9.4	-9.4	-39.7
C12HBa0062P09.1_68276	-2.4	1.6	2.4	1.1	-1.5	-30.1	-32.7	-21.2	-18.0	-11.1	-30.8	-10.6	-9.4	-9.4	-39.7
C07HBa0033E17.1_91927	-1.6	1.4	2.6	-1.1	-1.9	-46.3	-52.9	-31.4	-16.9	-12.1	-41.1	-12.0	-10.0	-10.8	-321.3
C07SLm0034N13.2_108337	-1.5	1.3	2.6	-1.1	-1.9	-49.9	-61.6	-26.9	-18.5	-12.3	-69.8	-13.1	-10.6	-11.3	-320.8
C07HBa0066M15.1_122349	-1.5	1.3	2.6	-1.1	-2.0	-51.2	-63.2	-28.5	-17.3	-12.2	-65.0	-13.4	-10.9	-11.4	-328.7
C09HBa0179M08.1_16283	-1.9	1.5	2.6	1.0	-1.7	-39.6	-34.2	-28.2	-19.0	-11.6	-46.6	-12.0	-10.5	-9.2	-385.1
C08HBa0017M21.1_70047	-1.9	1.5	2.5	1.0	-1.7	-41.3	-44.6	-25.2	-16.9	-11.4	-60.1	-12.9	-10.5	-9.6	-386.6
C02HBa0180C05.1_22479	-1.9	1.5	2.5	-1.0	-1.7	-43.0	-49.7	-28.4	-17.6	-11.7	-60.3	-12.9	-10.1	-10.1	-387.8
C07HBa0040A11.1_99938	1.1	-1.1	2.5	-1.7	-2.9	-96.8	-68.5	-39.8	-22.9	-18.2	-129.3	-17.7	-13.0	-16.9	-221.8
C12HBa0161H10.1_136368	1.2	-1.2	2.2	-2.2	-3.5	-118.4	-61.4	-43.9	-14.9	-20.8	-137.7	-20.9	-12.4	-18.5	-159.7
C00HBa0182E16.1_19272	1.2	-1.2	2.3	-2.1	-3.4	-124.4	-64.4	-43.9	-27.4	-21.0	-162.3	-20.4	-14.7	-18.7	-194.8
C06HBa0215M16.3_1732	-1.3	1.2	2.7	-1.2	-2.1	-59.5	-65.9	-33.5	-17.9	-13.5	-55.6	-13.8	-10.5	-12.5	-242.8
C12HBa0147G13.1_48727	-1.1	1.1	2.6	-1.4	-2.3	-67.6	-62.8	-33.3	-18.3	-14.3	-77.9	-14.6	-11.5	-13.8	-272.2
C06SLm0012J12.1_96058	-1.2	1.1	2.6	-1.3	-2.3	-63.6	-51.8	-32.9	-19.0	-14.3	-91.6	-13.6	-10.9	-13.1	-224.5
C04HBa0128L09.1_30711	-1.5	1.3	2.7	-1.1	-1.9	-50.0	-39.0	-27.9	-16.9	-11.9	-58.2	-12.2	-10.0	-11.5	-214.0
C02SLe0011K05.1_38769	-1.4	1.3	2.6	-1.1	-2.0	-53.3	-55.6	-29.3	-18.4	-12.4	-54.4	-12.2	-10.8	-11.5	-225.2
C08SLm0031I10.1_139625	-1.9	1.5	2.5	1.0	-1.7	-39.9	-49.7	-21.6	-17.6	-10.5	-38.3	-12.9	-10.3	-9.0	-96.9
C07HBa0033E17.1_117159	-1.5	1.4	2.6	-1.1	-1.9	-36.4	-29.8	-19.9	-13.6	-9.2	-36.9	-11.6	-9.0	-8.6	-107.5
C06HBa0302A23.1_71773	-1.5	1.4	2.6	-1.1	-1.9	-31.5	-37.2	-28.0	-15.9	-11.0	-50.2	-11.4	-8.5	-10.6	-107.6
C05SLm0118J18.1_57917	-1.1	1.1	2.6	-1.3	-2.3	-46.0	-38.2	-26.1	-15.7	-12.4	-43.4	-12.6	-10.3	-12.4	-113.1
C08HBa0270A17.1_73840	-2.4	1.6	2.4	1.1	-1.5	-14.4	-17.7	-10.2	-12.4	-7.0	-24.1	-10.1	-8.1	-8.1	-99.9
C02SLm0065M14.2_29554	-2.4	1.6	2.4	1.1	-1.6	-22.7	-20.6	-13.6	-13.7	-9.9	-23.8	-9.1	-7.9	-9.4	-98.3
C05SLe0028N03.1_53645	-2.4	1.6	2.4	1.1	-1.6	-24.8	-45.6	-23.2	-15.6	-10.5	-23.9	-11.1	-10.3	-7.5	-98.8
C08HBa0216M19.1_82592	-2.5	1.6	2.4	1.1	-1.6	-26.8	-33.3	-23.5	-19.2	-8.3	-23.6	-11.5	-9.1	-8.6	-86.7
C04HBa0075G11.1_42755	-1.5	1.3	2.6	-1.1	-1.9	-34.1	-41.7	-22.4	-15.4	-11.1	-25.3	-11.0	-10.3	-9.8	-81.4

C04HBa0178P03.1_12363	-3.1	1.7	2.2	1.2	-1.5	-17.0	-13.6	-41.4	-13.9	-7.5	-19.2	-7.5	-8.6	-6.4	-70.6
C09SLm0143I09.1_21120	-1.9	1.5	2.6	1.0	-1.7	-32.7	-34.3	-23.9	-16.9	-10.2	-42.0	-12.8	-10.0	-9.2	-77.3
C08HBa0239G21.1_113862	-2.5	1.6	2.2	1.2	-1.7	-16.5	-16.3	-15.6	-15.7	-8.3	-38.5	-9.8	-8.3	-9.7	-70.7
C08HBa0028C13.1_59559	-2.5	1.6	2.2	1.2	-1.7	-16.5	-16.3	-15.6	-15.7	-8.3	-38.5	-9.8	-8.3	-9.7	-70.7
C04HBa0078E04.1_60284	-2.4	1.6	2.3	1.1	-1.6	-26.4	-23.3	-16.9	-18.3	-8.2	-22.0	-10.2	-8.5	-7.9	-67.3
C08HBa0069E09.1_103230	-1.9	1.5	2.5	1.0	-1.7	-25.7	-22.6	-17.7	-8.9	-8.0	-26.7	-9.3	-8.4	-9.1	-78.4
C12HBa0161H10.1_74348	1.1	-1.1	2.4	-1.9	-3.1	-85.1	-34.9	-37.7	-14.0	-17.6	-89.9	-18.8	-10.9	-16.7	-121.0
C11HBa0323E19.1_90980	-1.3	1.2	2.7	-1.2	-2.1	-56.0	-53.3	-28.5	-15.7	-12.4	-48.0	-13.6	-10.6	-11.7	-107.9
C08HBa0060C12.1_158504	-1.0	1.0	2.5	-1.6	-2.6	-54.6	-57.5	-33.6	-18.6	-15.8	-65.7	-13.9	-11.2	-13.9	-109.2
C07SLm0046H06.1_12996	-1.1	1.1	2.6	-1.5	-2.4	-65.3	-48.0	-28.8	-17.8	-13.1	-60.9	-15.0	-10.4	-13.7	-137.7
C02HBa0044L14.1_40379	-1.1	1.1	2.6	-1.4	-2.5	-72.6	-56.6	-30.0	-16.6	-15.5	-54.8	-15.4	-11.5	-13.7	-143.4
C09HBa0135N15.1_83929	-1.9	1.5	2.6	1.0	-1.7	-41.2	-55.6	-26.6	-18.2	-10.8	-60.0	-11.7	-10.8	-10.1	-193.0
C09SLm0104L22.2_19673	-1.1	1.1	2.6	-1.3	-2.3	-48.9	-57.7	-31.0	-18.8	-14.8	-63.2	-14.4	-11.4	-13.8	-163.7
C08HBa0197O20.1_111612	-1.1	1.1	2.6	-1.5	-2.5	-77.3	-57.6	-32.9	-20.2	-15.8	-78.2	-15.7	-11.4	-14.2	-179.7
C08HBa0165B06.1_25820	-1.2	1.1	2.6	-1.3	-2.3	-68.3	-60.0	-33.7	-18.2	-14.6	-70.1	-14.2	-11.3	-13.6	-193.2
C04SLm0033N19.1_46625	-1.1	1.1	2.6	-1.4	-2.4	-59.3	-54.3	-33.3	-19.1	-14.6	-74.9	-14.8	-11.5	-14.1	-179.0
C02HBa0198A03.1_11003	-1.1	1.1	2.6	-1.4	-2.4	-59.3	-54.3	-33.3	-19.1	-14.6	-74.9	-14.8	-11.5	-14.1	-179.0

Supplementary Table SIII. List of transgressive sRNA loci that are used for heatmap in Fig. 5A. Unigenes and gene descriptions are given.

Locus	M82-1	M82-2	S.penn-1	S.penn-2	F1-1	F2-3	IL1-1	IL2-5	IL8-1-1	IL8-1D	IL8-1-3	IL8-2	IL8-2-1	IL8-3	IL8-3-1	Unigene	Gene (highest homology)
SGN-E539913	0.0	1.2	0.0	0.0	0.0	24.3	126.6	1.0	0.0	6.8	4.4	1.1	145.0	2.2	111.0	SGN-U571087	No gene description
SGN-E370639	2.0	0.0	0.0	0.0	1.4	1.5	4.3	3.1	4.7	7.0	9.0	4.0	5.1	2.2	1.8	SGN-U573010	UGE3 (UDP-D-GLUCOSE/UDP-D-GALACTOSE 4-EPIMERASE 3)
SGN-E353539	2.0	0.0	0.0	0.0	1.4	1.5	4.3	3.1	4.7	7.0	9.0	4.0	5.1	2.2	1.8	SGN-U573010	UGE3 (UDP-D-GLUCOSE/UDP-D-GALACTOSE 4-EPIMERASE 3)
SGN-E354550	2.0	0.0	0.0	0.0	1.4	1.5	3.7	3.1	4.7	7.0	8.5	4.0	5.1	2.2	1.8	SGN-U573010	UGE3 (UDP-D-GLUCOSE/UDP-D-GALACTOSE 4-EPIMERASE 3)
SGN-E204259	2.0	0.0	0.0	0.0	1.4	1.5	3.7	3.1	4.7	7.0	8.5	4.0	5.1	2.2	1.8	SGN-U573010	UGE3 (UDP-D-GLUCOSE/UDP-D-GALACTOSE 4-EPIMERASE 3)
SGN-E255091	2.0	0.0	0.0	0.0	-1.4	1.7	3.7	3.1	4.7	7.5	8.5	4.0	5.1	2.2	1.8	SGN-U573010	UGE3 (UDP-D-GLUCOSE/UDP-D-GALACTOSE 4-EPIMERASE 3)
SGN-E391208	2.0	0.0	0.0	0.0	-1.4	1.1	4.3	3.1	4.7	6.4	8.5	4.0	5.1	2.2	1.8	SGN-U573010	UGE3 (UDP-D-GLUCOSE/UDP-D-GALACTOSE 4-EPIMERASE 3)
SGN-E263047	-1.6	-1.0	-2.7	-2.7	-1.2	1.1	1.7	2.8	4.6	1.8	5.0	6.1	6.1	3.5	1.6	SGN-U579850	DCL1 (DICER-LIKE1)/ ATP-dependent helicase/ ribonuclease III
SGN-E299775	0.0	1.2	0.0	0.0	-6.5	-1.3	2.0	1.9	5.7	6.0	5.2	4.7	3.0	-2.7	2.1	SGN-U578638	EMB1075 (EMBRYO DEFECTIVE 1075)/ carboxy-lyase
SGN-E271269	0.0	1.2	0.0	0.0	-6.5	-1.3	1.9	1.8	5.6	6.0	5.1	4.5	3.0	-2.7	2.0	SGN-U578638	EMB1075 (EMBRYO DEFECTIVE 1075)/ carboxy-lyase
SGN-E299842	0.0	1.2	0.0	0.0	-6.5	-1.3	1.9	1.8	5.4	5.6	5.1	4.2	2.8	-2.7	2.0	SGN-U578638	EMB1075 (EMBRYO DEFECTIVE 1075)/ carboxy-lyase
SGN-E208774	0.0	1.2	0.0	0.0	-5.1	1.0	2.1	3.2	9.5	9.0	7.6	6.3	4.3	1.1	1.9	SGN-U577168	EMB1075 (EMBRYO DEFECTIVE 1075)/ carboxy-lyase
SGN-E214531	0.0	1.1	0.0	-7.8	-2.7	-1.0	2.1	3.0	8.9	8.1	7.1	5.5	3.8	1.0	1.8	SGN-U577168	No gene description
SGN-E212787	0.0	1.1	0.0	-7.8	-5.4	-1.0	2.1	3.0	8.9	8.4	7.1	5.9	4.0	1.0	1.8	SGN-U577168	EMB1075 (EMBRYO DEFECTIVE 1075)/ carboxy-lyase
SGN-E207866	-2.6	1.1	0.0	-5.7	-4.0	-1.5	1.7	1.7	4.9	5.0	4.3	4.0	2.4	-3.3	1.9	SGN-U578638	EMB1075 (EMBRYO DEFECTIVE 1075)/ carboxy-lyase
SGN-E746678	-1.5	-1.0	-1.9	-2.6	-3.6	1.4	-1.2	-1.0	1.2	7.8	-1.5	3.4	3.8	-1.3	6.1	SGN-U581284	GA2 (GA REQUIRING 2)/ ent-kaurene synthase
SGN-E719927	0.0	1.2	0.0	0.0	1.4	2.9	7.3	2.1	4.1	5.7	6.7	1.1	7.7	4.4	13.3	SGN-U580226	BETA-VPE (vacuolar processing enzyme beta)/ cysteine-type endopeptidase
SGN-E578363	2.0	-2.4	0.0	0.0	-2.1	1.4	3.2	2.1	4.2	2.3	9.0	1.2	3.8	5.2	8.6	SGN-U586753	SCPL33 (serine carboxypeptidase-like 33)/ serine carboxypeptidase
SGN-E333372	1.4	1.2	0.0	0.0	-1.0	-1.7	6.1	1.5	3.2	2.4	2.5	7.6	1.3	1.9	15.3	SGN-U574902	COBL8 (COBRA-LIKE PROTEIN 8 PRECURSOR)
SGN-E702789	2.0	1.6	0.0	0.0	1.4	2.3	3.2	2.1	2.6	4.1	0.0	1.7	1.1	-1.8	12.3	SGN-U588051	ATPPC2 (PHOSPHOENOLPYRUVATE CARBOXYLASE 2)
SGN-E320684	0.0	1.2	0.0	0.0	2.8	-1.2	0.0	-1.9	1.0	1.1	7.8	3.4	3.3	3.9	1.2	SGN-U568025	No gene description
SGN-E201045	0.0	1.2	0.0	0.0	2.8	-1.2	0.0	-1.9	1.0	1.1	7.8	3.4	3.3	3.3	1.2	SGN-U568025	No gene description
SGN-E307466	-1.5	1.2	0.0	0.0	0.0	1.4	1.7	2.4	2.7	2.3	7.4	1.5	1.5	1.1	-1.2	SGN-U569493	No gene description
SGN-E706583	-1.6	1.0	-3.6	-3.2	-1.1	-2.8	1.6	1.1	2.2	1.3	11.5	1.4	1.5	-1.4	1.9	SGN-U571553	DNA-binding storekeeper protein-related
SGN-E702932	-1.6	1.0	-3.6	-3.2	-1.1	-2.8	1.6	1.1	2.2	1.3	11.5	1.4	1.5	-1.4	1.9	SGN-U571553	DNA-binding storekeeper protein-related
SGN-E344306	-1.6	1.0	-3.6	-3.2	-1.1	-2.8	1.6	1.1	2.2	1.3	11.5	1.4	1.4	-1.4	1.8	SGN-U571553	DNA-binding storekeeper protein-related
SGN-E727290	-1.6	1.0	-3.6	-3.2	-1.1	-2.8	1.6	1.1	2.2	1.3	11.4	1.4	1.5	-1.4	1.9	SGN-U571553	DNA-binding storekeeper protein-related
SGN-E326822	-1.4	1.1	-4.8	-4.1	-1.1	-2.6	1.7	1.2	2.2	1.5	10.4	1.5	1.5	-1.3	1.8	SGN-U571553	transcription regulator
SGN-E328484	-1.4	1.1	-4.8	-4.1	-1.1	-2.6	1.7	1.1	2.2	1.5	10.4	1.5	1.5	-1.3	1.8	SGN-U571553	DNA-binding storekeeper protein-related
SGN-E347347	-1.4	1.1	-4.7	-5.0	-1.1	-2.5	1.7	1.2	2.2	1.4	10.3	1.5	1.6	-1.2	1.9	SGN-U571553	No gene description
SGN-E209175	-1.8	1.2	0.0	0.0	-1.3	-8.4	1.8	1.3	1.9	2.6	1.9	1.8	4.3	6.1	1.4	SGN-U579437	similar to unknown [A. thaliana] (TAIR:AT3G22850.1)/ similar to a Al-induced protein-like protein
SGN-E339921	-2.2	1.2	0.0	-8.9	-1.2	-6.7	1.9	1.6	2.0	2.7	1.6	1.5	4.4	6.4	1.9	SGN-U579437	similar to unknown [A. thaliana] (TAIR:AT4G27450.1)/ similar to unknown [P. trichocarpa] (GB:ABK93866.1)
SGN-E284094	-2.5	1.2	-2.5	0.0	4.4	1.6	3.1	1.9	3.7	-1.5	1.6	3.6	2.9	10.4	2.2	SGN-U577570	No gene description
SGN-E277847	1.3	1.2	0.0	0.0	1.4	1.3	2.4	1.0	2.7	-1.3	1.1	2.3	1.5	9.9	3.6	SGN-U577578	MI-1-P SYNTHASE (Myo-inositol-1-phosphate synthase)/ inositol-3-phosphate synthase
SGN-E322114	-2.5	-1.2	-3.7	-1.5	2.3	1.3	2.1	-1.3	1.3	-1.8	-1.2	1.2	3.6	7.9	3.9	SGN-U578125	fructose-bisphosphate aldolase/2C putative
SGN-E557117	-1.6	1.2	0.0	0.0	-1.7	-16.7	4.5	5.9	4.8	4.1	4.3	4.1	1.3	2.8	4.5	SGN-U579444	similar to unnamed protein product [Vitis vinifera] (GB:CAO63390.1)
SGN-E542800	-1.6	1.2	0.0	0.0	-1.7	-16.7	4.5	5.9	4.8	4.1	4.3	4.1	1.3	2.8	4.5	SGN-U579444	similar to unnamed protein product [Vitis vinifera] (GB:CAO63390.1)
SGN-E715854	-1.6	1.2	0.0	0.0	-1.7	-16.7	4.5	5.9	4.8	4.1	4.3	4.1	1.3	2.8	4.5	SGN-U579444	similar to unnamed protein product [Vitis vinifera] (GB:CAO63390.1)
SGN-E337031	-1.6	1.2	0.0	0.0	-1.7	-16.7	4.3	6.0	4.8	4.1	4.3	4.1	1.3	2.8	4.5	SGN-U579444	similar to unnamed protein product [Vitis vinifera] (GB:CAO63390.1)
SGN-E717822	-1.6	1.2	0.0	0.0	-1.7	-16.7	4.5	5.9	4.8	4.1	4.4	4.2	1.3	2.8	4.5	SGN-U579444	similar to unnamed protein product [Vitis vinifera] (GB:CAO63390.1)
SGN-E301331	-3.1	1.2	0.0	0.0	-2.2	-14.3	5.1	6.9	5.6	4.8	5.0	4.5	1.3	2.9	5.2	SGN-U579444	similar to unnamed protein product [Vitis vinifera] (GB:CAO63390.1)
SGN-E241663	-1.5	1.2	-1.5	0.0	-1.1	-1.4	0.0	1.0	6.8	0.0	0.0	1.1	-1.4	-2.7	13.3	SGN-U569795	HB53 (homeobox-8)/ DNA binding / transcription factor
SGN-E226990	-1.5	1.2	-1.5	0.0	-1.1	-1.4	0.0	1.0	6.8	0.0	0.0	1.1	-1.4	-2.7	13.3	SGN-U569795	HB53 (homeobox-8)/ DNA binding / transcription factor
SGN-E272075	-1.5	1.2	-1.5	0.0	-1.1	-1.4	0.0	1.0	6.8	0.0	0.0	1.1	-1.4	-2.7	13.3	SGN-U569795	HB53 (homeobox-8)/ DNA binding / transcription factor
SGN-E329464	-1.5	1.2	-1.5	0.0	-1.1	-1.2	0.0	1.0	6.8	0.0	0.0	1.1	-1.4	-2.7	13.3	SGN-U569795	ATHB22 (ARABIDOPSIS THALIANA HOMEOBOX PROTEIN 22)/ DNA binding / transcription factor
SGN-E317767	-1.5	1.2	-1.5	0.0	-1.1	-1.2	0.0	1.0	6.8	0.0	0.0	1.1	-1.4	-2.7	13.3	SGN-U569795	HB53 (homeobox-8)/ DNA binding / transcription factor
SGN-E241673	-1.5	1.2	-1.5	0.0	-1.1	-1.8	0.0	1.0	6.8	0.0	0.0	1.1	-1.4	-2.7	13.3	SGN-U569795	ATHB-3 (ARABIDOPSIS THALIANA HOMEOBOX 3)/ DNA binding / transcription factor
SGN-E237742	-1.5	1.2	-1.5	0.0	-1.1	-1.8	0.0	1.0	6.8	0.0	0.0	1.1	-1.4	-2.7	13.3	SGN-U569795	ATHB5 (ARABIDOPSIS THALIANA HOMEOBOX PROTEIN 5)/ transcription factor
SGN-E377988	-1.5	1.2	-1.5	0.0	-1.1	-1.0	0.0	1.0	6.8	-1.3	0.0	2.3	-1.4	-2.7	13.3	SGN-U569793	ATHB5 (ARABIDOPSIS THALIANA HOMEOBOX PROTEIN 5)/ transcription factor
SGN-E243547	-1.5	1.2	-1.5	0.0	-1.1	-1.0	0.0	1.0	6.8	-1.3	0.0	2.3	-1.4	-2.7	13.3	SGN-U569793	ATHB5 (ARABIDOPSIS THALIANA HOMEOBOX PROTEIN 5)/ transcription factor
SGN-E237947	-1.5	1.2	-1.5	0.0	-1.1	-1.2	0.0	1.0	6.8	-1.3	0.0	1.5	-1.4	-2.7	13.3	SGN-U569793	ATHB-16/ATHB16 (A. THALIANA HOMEOBOX PROTEIN 16)/ transcription activator/ transcription factor

SGN-E230980	-1.5	1.2	-1.5	0.0	-1.1	-1.4	0.0	1.0	6.5	-1.3	0.0	-1.3	-1.4	-2.7	13.3	SGN-U569793	HB53 (homeobox-8)/ DNA binding / transcription factor
SGN-E244618	-1.5	1.2	-1.5	0.0	-1.1	-1.8	0.0	1.0	6.5	0.0	0.0	-2.6	-1.4	-2.7	13.3	SGN-U569795	HB53 (homeobox-8)/ DNA binding / transcription factor
SGN-E236433	-1.8	1.1	-1.7	-3.6	-1.3	-1.4	-3.3	-1.1	5.6	-1.0	0.0	-1.5	-1.6	-3.2	11.8	SGN-U569793	HB53 (homeobox-8)/ DNA binding / transcription factor
SGN-E238378	-1.8	1.1	-1.7	-3.6	-1.3	-1.4	-3.3	-1.1	5.9	-3.0	0.0	-1.0	-1.6	-3.2	11.8	SGN-U569795	HB53 (homeobox-8)/ DNA binding / transcription factor
SGN-E231438	-2.0	1.2	-2.0	0.0	1.4	-1.9	0.0	-1.3	5.1	0.0	-3.6	1.1	-1.2	-3.6	10.3	SGN-U569795	ATHB23 (ARABIDOPSIS THALIANA HOMEOBOX PROTEIN 23)/ DNA binding / transcription factor
SGN-E204494	-2.0	1.2	-2.0	0.0	1.4	-1.9	0.0	-1.3	5.1	0.0	-3.6	1.1	-1.2	-3.6	10.3	SGN-U569795	ATHB5 (ARABIDOPSIS THALIANA HOMEOBOX PROTEIN 5)/ transcription factor
SGN-E398011	-2.0	1.2	-2.0	0.0	1.4	-1.9	0.0	-1.3	5.1	0.0	-3.6	1.1	-1.2	-3.6	10.3	SGN-U569795	ATHB40/HB-5 (ARABIDOPSIS THALIANA HOMEOBOX PROTEIN 40)/ DNA binding / transcription factor
SGN-E396656	-2.0	1.2	-2.0	0.0	1.4	-1.6	0.0	-1.3	5.1	0.0	-3.6	1.1	-1.2	-3.6	10.3	SGN-U569795	ATHB22 (ARABIDOPSIS THALIANA HOMEOBOX PROTEIN 22)/ DNA binding / transcription factor
SGN-E326542	-2.0	1.2	-2.0	0.0	1.4	-1.6	0.0	-1.3	5.1	0.0	-3.6	1.1	-1.2	-3.6	10.3	SGN-U569795	HB53 (homeobox-8)/ DNA binding / transcription factor
SGN-E322234	-2.0	-1.1	-2.0	-2.1	-1.4	-1.6	-3.8	-1.3	5.2	-3.5	0.0	-1.2	-1.8	-3.6	10.4	SGN-U569795	HB53 (homeobox-8)/ DNA binding / transcription factor
SGN-E241891	-2.5	-1.0	-2.5	-2.6	-1.2	-2.0	-4.7	-1.6	3.9	-1.4	0.0	-2.2	-2.2	-4.5	8.3	SGN-U569793	HB53 (homeobox-8)/ DNA binding / transcription factor
SGN-E377567	-2.8	-1.1	-2.7	-1.9	-1.3	-1.9	-5.2	-1.8	3.6	-4.8	0.0	-4.8	-2.5	-4.9	7.6	SGN-U569793	HB53 (homeobox-8)/ DNA binding / transcription factor
SGN-E396917	-2.8	-1.1	-2.7	-1.9	-1.3	-2.2	-5.2	-1.8	3.6	-4.8	0.0	-4.8	-2.5	-4.9	7.6	SGN-U569793	HB53 (homeobox-8)/ DNA binding / transcription factor
SGN-E254986	1.0	1.0	0.0	-3.3	2.0	0.0	-1.0	1.1	6.7	2.5	1.4	-1.2	-8.5	-1.2	-3.9	SGN-U583356	CBL5 (CALCINEURIN B-LIKE PROTEIN 5)
SGN-E252889	0.0	0.0	0.0	0.0	0.0	-8.1	-1.1	4.9	4.2	2.9	3.1	5.7	1.3	-2.1	0.0	SGN-U586401	similar to unknown [A. thaliana] (TAIR:AT4G24530.1)/ similar to unnamed [V. vinifera] (GB:CAO61608.1)
SGN-E544003	0.0	0.0	0.0	0.0	0.0	-8.1	-1.6	0.0	0.0	0.0	3.1	0.0	-6.1	-6.2	0.0	SGN-U582046	ATCHX27 (cation/hydrogen exchanger 27)/ monovalent cation:proton antiporter
SGN-E206578	0.0	0.0	0.0	0.0	0.0	-4.0	0.0	-6.6	0.0	0.0	0.0	0.0	0.0	7.0	0.0	SGN-U581452	PAL (PHENYL ALANINE AMMONIA-LYASE)/ phenylalanine ammonia-lyase
SGN-E341777	0.0	0.0	0.0	0.0	-2.5	-4.0	-3.2	-1.6	-1.3	-6.0	1.6	0.0	-3.1	1.1	1.1	SGN-U578285	similar to unknown protein [A.thaliana] (TAIR:AT1G72510.1)
SGN-E733270	-1.2	1.2	0.0	-17.3	1.2	-4.9	4.7	3.7	5.0	1.7	2.9	7.7	5.8	8.5	4.0	SGN-U579800	VTC5/ galactose-1-phosphate guanylyltransferase (GDP)
SGN-E288004	-1.2	1.2	0.0	-17.3	1.1	-4.9	4.6	3.7	5.0	1.7	2.9	7.7	5.8	8.5	4.0	SGN-U579800	VTC5/ galactose-1-phosphate guanylyltransferase (GDP)
SGN-E231778	-1.2	1.2	0.0	-17.3	1.1	-4.9	4.8	3.7	5.0	1.7	2.9	7.6	5.6	8.8	4.0	SGN-U579800	VTC5/ galactose-1-phosphate guanylyltransferase (GDP)
SGN-E338078	-1.2	1.2	0.0	-17.3	1.1	-4.9	4.8	3.7	5.0	1.7	2.9	7.6	5.6	8.7	4.0	SGN-U579800	VTC5/ galactose-1-phosphate guanylyltransferase (GDP)
SGN-E353609	-1.2	1.2	0.0	-17.3	1.0	-4.9	4.4	3.6	4.9	1.8	2.9	7.6	5.8	8.2	4.0	SGN-U579800	No gene description
SGN-E352537	-1.2	1.2	0.0	-17.3	1.0	-4.9	4.4	3.6	4.9	1.8	2.9	7.6	5.8	8.2	4.0	SGN-U579800	No gene description
SGN-E370454	-1.3	1.2	0.0	-18.3	1.1	-4.6	4.6	3.5	4.9	1.8	2.7	7.3	5.6	8.6	3.9	SGN-U579800	VTC2 (VITAMIN C DEFECTIVE 2)
SGN-E317957	-1.3	1.2	0.0	-18.3	1.1	-4.6	4.6	3.5	4.9	1.8	2.7	7.3	5.6	8.6	3.9	SGN-U579800	VTC2 (VITAMIN C DEFECTIVE 2)
SGN-E713361	-1.3	1.2	0.0	-18.3	1.1	-4.6	4.6	3.5	4.9	1.8	2.7	7.3	5.6	8.6	3.9	SGN-U579800	VTC2 (VITAMIN C DEFECTIVE 2)
SGN-E350235	-1.3	1.2	0.0	-18.3	1.1	-5.2	4.5	3.5	4.7	1.8	2.7	7.3	5.4	8.4	3.8	SGN-U579800	VTC5/ galactose-1-phosphate guanylyltransferase (GDP)
SGN-E206238	-1.2	1.2	0.0	-17.3	1.2	-4.4	4.8	3.7	5.1	1.9	2.9	7.6	5.8	9.0	4.0	SGN-U579800	VTC2 (VITAMIN C DEFECTIVE 2)
SGN-E288385	-1.2	1.2	0.0	-17.3	1.1	-4.4	4.5	3.7	5.0	1.9	2.9	7.6	5.8	8.6	4.0	SGN-U579800	VTC5/ galactose-1-phosphate guanylyltransferase (GDP)
SGN-E209658	-1.0	1.2	0.0	-17.3	1.0	-4.4	4.9	3.4	5.4	1.8	3.0	7.7	5.8	9.2	4.2	SGN-U579800	VTC2 (VITAMIN C DEFECTIVE 2)
SGN-E334284	-1.0	1.2	0.0	-17.3	1.1	-3.6	4.9	3.6	5.4	1.9	3.1	7.8	5.9	9.4	4.3	SGN-U579800	VTC2 (VITAMIN C DEFECTIVE 2)
SGN-E351643	-1.1	1.2	0.0	-16.2	1.1	-4.6	5.1	4.0	5.3	2.0	3.1	8.1	6.1	9.3	4.2	SGN-U579800	VTC5/ galactose-1-phosphate guanylyltransferase (GDP)
SGN-E219946	-1.1	1.2	0.0	-16.2	1.2	-4.6	5.0	3.9	5.2	1.8	3.1	8.1	6.0	9.0	4.3	SGN-U579800	VTC5/ galactose-1-phosphate guanylyltransferase (GDP)
SGN-E710048	1.0	1.2	0.0	-18.3	1.2	-3.5	4.7	3.4	5.2	1.8	2.9	7.4	5.6	8.8	4.1	SGN-U579800	VTC5/ galactose-1-phosphate guanylyltransferase (GDP)
SGN-E706831	1.0	1.2	0.0	-18.3	1.2	-3.5	4.7	3.5	5.3	1.8	2.9	7.3	5.5	8.8	4.1	SGN-U579800	VTC5/ galactose-1-phosphate guanylyltransferase (GDP)
SGN-E698153	1.0	1.2	0.0	-18.3	1.2	-3.8	4.7	3.4	5.2	1.8	2.9	7.3	5.5	8.7	4.0	SGN-U579800	VTC5/ galactose-1-phosphate guanylyltransferase (GDP)
SGN-E332718	-1.1	1.2	0.0	-18.3	1.0	-3.5	4.7	3.4	5.2	1.8	2.9	7.4	5.5	8.7	4.0	SGN-U579800	VTC5/ galactose-1-phosphate guanylyltransferase (GDP)
SGN-E334413	-1.1	1.2	0.0	-18.3	1.0	-3.8	4.6	3.5	5.1	1.8	3.0	7.3	5.6	8.8	4.1	SGN-U579800	VTC2 (VITAMIN C DEFECTIVE 2)
SGN-E728545	-1.0	1.2	0.0	-19.4	1.0	-3.2	4.4	3.5	4.9	1.8	2.8	7.0	5.3	8.3	3.9	SGN-U579800	VTC5/ galactose-1-phosphate guanylyltransferase (GDP)
SGN-E738314	-1.2	1.2	0.0	-20.4	1.1	-3.6	4.2	3.3	4.7	1.7	2.7	6.6	5.0	8.0	3.7	SGN-U579800	VTC5/ galactose-1-phosphate guanylyltransferase (GDP)
SGN-E735691	-1.2	1.2	0.0	-20.4	1.1	-3.6	4.2	3.3	4.7	1.7	2.7	6.6	5.0	8.0	3.7	SGN-U579800	VTC5/ galactose-1-phosphate guanylyltransferase (GDP)
SGN-E738531	-1.2	1.2	0.0	-20.4	1.1	-3.6	4.2	3.3	4.7	1.7	2.7	6.6	5.0	8.0	3.7	SGN-U579800	VTC5/ galactose-1-phosphate guanylyltransferase (GDP)
SGN-E740723	-1.2	1.2	0.0	-20.4	1.1	-4.2	4.1	3.2	4.6	1.7	2.7	6.6	5.1	8.0	3.7	SGN-U579800	VTC5/ galactose-1-phosphate guanylyltransferase (GDP)
SGN-E739612	-1.2	1.2	0.0	-20.4	-1.0	-4.2	4.1	3.3	4.6	1.6	2.7	6.5	5.0	7.8	3.7	SGN-U579800	VTC5/ galactose-1-phosphate guanylyltransferase (GDP)
SGN-E737197	-1.2	1.2	0.0	-20.4	-1.0	-4.2	4.1	3.2	4.6	1.6	2.7	6.5	5.0	7.8	3.7	SGN-U579800	VTC5/ galactose-1-phosphate guanylyltransferase (GDP)
SGN-E340803	-1.2	1.2	0.0	-19.4	-1.0	-4.4	4.4	3.3	4.8	1.7	2.6	6.8	5.3	8.2	3.9	SGN-U579800	VTC2 (VITAMIN C DEFECTIVE 2)
SGN-E734179	-1.2	1.2	-8.2	-17.3	1.0	-4.9	4.4	3.6	4.9	1.8	2.9	7.7	5.8	8.4	4.0	SGN-U579800	No gene description
SGN-E705284	-1.0	1.2	0.0	-9.4	1.2	-3.6	4.6	3.4	5.2	1.8	2.8	7.2	5.5	8.7	4.0	SGN-U579800	VTC5/ galactose-1-phosphate guanylyltransferase (GDP)
SGN-E703715	-1.0	1.2	0.0	-9.4	1.2	-3.6	4.6	3.4	5.2	1.8	2.8	7.2	5.5	8.7	4.0	SGN-U579800	VTC5/ galactose-1-phosphate guanylyltransferase (GDP)
SGN-E705085	-1.0	1.2	0.0	-9.4	1.2	-3.6	4.6	3.4	5.2	1.8	2.8	7.2	5.4	8.6	4.0	SGN-U579800	VTC5/ galactose-1-phosphate guanylyltransferase (GDP)
SGN-E733652	-1.2	1.2	0.0	-8.9	1.1	-4.5	4.7	3.6	5.0	1.8	2.8	7.4	5.7	8.7	3.9	SGN-U579800	VTC2 (VITAMIN C DEFECTIVE 2)
SGN-E739776	-1.3	1.2	0.0	-11.0	-1.0	-4.5	3.8	3.0	4.3	1.5	2.5	6.0	4.8	7.3	3.5	SGN-U579800	VTC5/ galactose-1-phosphate guanylyltransferase (GDP)
SGN-E219802	1.0	1.2	0.0	-14.1	-1.1	-4.0	5.4	4.0	5.9	2.0	3.5	9.3	6.9	9.8	4.7	SGN-U579800	No gene description
SGN-E268810	-1.1	1.2	0.0	-15.2	1.1	-3.8	5.6	4.0	6.0	2.1	3.2	8.7	6.7	10.1	4.5	SGN-U579800	VTC2 (VITAMIN C DEFECTIVE 2)

SGN-E254110	-1.1	1.2	0.0	-12.0	-1.8	-2.5	3.5	3.6	2.5	3.7	7.8	5.2	3.1	3.2	3.3	SGN-U578664	No gene description
SGN-E262182	-1.1	1.2	0.0	-12.1	-1.8	-2.5	3.5	3.6	2.5	3.7	7.7	5.1	3.1	3.2	3.2	SGN-U578664	No gene description
SGN-E244444	-4.8	1.2	0.0	-9.9	-3.4	-2.3	2.2	1.1	2.2	1.6	1.1	-2.8	2.6	6.6	2.4	SGN-U580215	DELTA-VPE (delta vacuolar processing enzyme)/ cysteine-type endopeptidase
SGN-E715887	-5.8	1.2	0.0	-12.0	-4.2	-2.1	1.8	-1.1	1.8	1.3	1.1	-2.0	2.6	6.0	2.0	SGN-U580215	DELTA-VPE (delta vacuolar processing enzyme)/ cysteine-type endopeptidase
SGN-E713189	0.0	1.2	0.0	-12.0	-4.2	-2.3	1.8	-1.0	1.9	1.3	-1.1	-3.4	2.4	5.9	1.9	SGN-U580215	DELTA-VPE (delta vacuolar processing enzyme)/ cysteine-type endopeptidase
SGN-E716212	0.0	1.2	0.0	-12.0	-4.2	-2.3	1.8	-1.0	1.9	1.2	-1.1	-3.4	2.4	5.9	1.9	SGN-U580215	DELTA-VPE (delta vacuolar processing enzyme)/ cysteine-type endopeptidase
SGN-E390928	2.0	-1.5	0.0	-7.7	-5.4	-3.5	-1.6	-3.6	-2.1	-1.3	-1.7	-1.4	-1.9	13.5	1.1	SGN-U577055	CYP79F1 (SUPERSHOOT 1)
SGN-E390927	2.0	-1.5	0.0	-7.7	-5.4	-3.5	-2.0	-3.6	-2.1	-1.4	-1.9	-1.6	-2.2	13.5	1.1	SGN-U577055	CYP705A27 (cytochrome P450/2C family 705/2C subfamily A/2C polypeptide 27)
SGN-E554047	0.0	1.2	0.0	0.0	1.4	2.9	16.7	2.1	3.1	11.4	7.8	1.1	18.8	6.6	14.5	SGN-U580226	BETA-VPE (vacuolar processing enzyme beta)/ cysteine-type endopeptidase
SGN-E539916	0.0	0.0	0.0	0.0	0.0	3.6	18.7	-6.6	0.0	1.0	-2.0	-6.0	21.5	-3.1	16.4	SGN-U571087	No gene description
SGN-E288193	0.0	0.0	0.0	0.0	0.0	3.6	18.7	-6.6	0.0	1.0	-2.0	-6.0	21.5	-3.1	16.4	SGN-U571087	No gene description
SGN-E346063	0.0	-1.2	0.0	-1.5	1.9	2.8	16.3	0.0	2.8	2.3	0.0	0.0	0.0	3.7	18.0	SGN-U567550	BAN (BANYULS)
SGN-E322420	-1.5	1.2	0.0	0.0	1.4	-1.8	6.3	6.9	7.8	8.4	9.6	5.7	5.5	8.1	2.8	SGN-U573856	CYP86C3 (cytochrome P450/2C family 86/2C subfamily C/2C polypeptide 3)/ oxygen binding
SGN-E321043	-1.5	1.2	0.0	0.0	1.4	-1.8	6.3	6.9	7.8	8.4	9.6	5.7	5.5	8.1	2.8	SGN-U573856	CYP96A11 (cytochrome P450/2C family 96/2C subfamily A/2C polypeptide 11)/ oxygen binding
SGN-E323332	-1.5	1.2	0.0	0.0	1.4	-1.8	6.3	6.9	7.8	8.4	9.6	5.7	5.5	8.1	2.8	SGN-U573856	CYP86C3 (cytochrome P450/2C family 86/2C subfamily C/2C polypeptide 3)/ oxygen binding
SGN-E325318	-1.5	1.2	0.0	0.0	1.4	-1.8	6.3	6.9	7.8	8.4	9.6	5.7	5.5	8.1	2.8	SGN-U573856	CYP86C3 (cytochrome P450/2C family 86/2C subfamily C/2C polypeptide 3)/ oxygen binding
SGN-E325837	-1.5	1.2	0.0	0.0	1.4	-1.8	5.9	6.9	7.5	8.7	9.6	5.7	5.5	8.1	2.8	SGN-U573856	CYP86C4 (cytochrome P450/2C family 86/2C subfamily C/2C polypeptide 4)/ oxygen binding
SGN-E323122	-1.5	1.2	0.0	0.0	1.4	-2.4	6.3	6.9	7.8	8.4	9.6	5.7	5.5	7.7	2.4	SGN-U573856	CYP86C3 (cytochrome P450/2C family 86/2C subfamily C/2C polypeptide 3)/ oxygen binding
SGN-E278518	0.0	1.2	0.0	0.0	4.1	1.7	8.4	9.3	3.1	12.5	14.4	5.7	6.6	6.6	1.2	SGN-U579752	No gene description
SGN-E334385	0.0	1.2	0.0	0.0	0.0	-2.4	1.6	2.6	6.6	19.4	5.5	4.0	3.3	3.3	1.2	SGN-U563291	No gene description
SGN-E311195	1.3	-1.2	0.0	-1.5	0.0	2.8	3.5	4.9	5.5	4.6	15.0	3.1	3.0	2.2	1.6	SGN-U569493	No gene description
SGN-E300181	1.3	-1.2	0.0	-1.5	0.0	2.8	3.5	4.9	5.5	4.6	15.0	3.1	3.0	2.2	1.6	SGN-U569493	No gene description
SGN-E311810	1.3	-1.2	0.0	-1.5	0.0	2.8	3.5	4.9	5.5	4.6	15.0	3.1	3.0	2.2	1.6	SGN-U569493	No gene description
SGN-E303822	2.0	1.2	0.0	0.0	0.0	-1.2	5.2	5.1	8.2	4.6	16.6	3.4	3.3	3.3	0.0	SGN-U569493	No gene description
SGN-E305856	2.0	0.0	0.0	-1.0	0.0	1.3	5.3	3.1	8.3	3.5	16.9	3.5	3.4	3.4	0.0	SGN-U569493	No gene description
SGN-E242734	0.0	-1.6	0.0	-1.0	0.0	1.7	0.0	0.0	1.6	5.8	19.3	0.0	0.0	-1.8	-1.6	SGN-U602836	tRNA-splicing endonuclease positive effector-related
SGN-E204785	2.0	0.0	0.0	0.0	1.4	3.0	7.5	6.3	9.3	15.1	16.9	8.1	10.1	4.5	3.7	SGN-U573010	UGE3 (UDP-D-GLUCOSE/UDP-D-GALACTOSE 4-EPIMERASE 3)
SGN-E355200	0.0	1.2	0.0	0.0	1.4	2.9	2.1	9.3	14.3	17.1	24.4	3.4	5.5	3.3	1.2	SGN-U577965	No gene description
SGN-E335305	0.0	1.2	0.0	0.0	1.8	-2.4	9.1	-2.9	0.0	28.9	1.1	1.5	-1.4	0.0	-1.2	SGN-U589947	No gene description
SGN-E706599	2.0	1.1	0.0	-14.4	-2.0	-16.4	9.7	9.3	17.4	9.4	10.2	18.4	1.6	1.9	-11.4	SGN-U577849	chloroplast outer membrane protein/2C putative
SGN-E351528	0.0	1.2	0.0	0.0	-2.5	3.4	15.4	15.1	13.0	7.0	12.7	10.4	12.3	10.1	9.7	SGN-U567805	Encodes a Wound-induced protein (WIP) family protein
SGN-E351377	0.0	1.2	0.0	0.0	-2.5	3.4	15.4	15.1	13.0	7.0	12.7	10.4	12.3	10.1	9.7	SGN-U567805	Encodes a Wound-induced protein (WIP) family protein
SGN-E357643	0.0	1.2	0.0	0.0	-2.5	3.4	15.4	15.1	13.0	7.0	12.5	10.4	12.3	10.1	9.7	SGN-U567805	Encodes a Wound-induced protein (WIP) family protein
SGN-E396950	0.0	1.2	0.0	0.0	-2.5	3.4	15.4	15.1	13.1	7.0	12.7	10.4	12.3	10.1	9.5	SGN-U567805	Encodes a Wound-induced protein (WIP) family protein
SGN-E356594	0.0	1.2	0.0	0.0	-2.5	3.4	15.3	15.1	13.1	7.0	12.5	10.4	12.3	10.1	9.5	SGN-U567805	Encodes a Wound-induced protein (WIP) family protein
SGN-E720573	0.0	1.2	0.0	0.0	-2.5	3.4	15.5	15.1	13.3	7.0	12.5	10.4	12.5	10.4	9.7	SGN-U567805	ATHCHIB (BASIC CHITINASE)/ chitinase
SGN-E717440	0.0	1.2	0.0	0.0	-2.5	3.4	15.4	15.1	13.3	7.0	12.5	10.4	12.5	10.1	9.7	SGN-U567805	ATHCHIB (BASIC CHITINASE)/ chitinase
SGN-E351410	0.0	0.0	0.0	0.0	0.0	3.5	14.2	15.2	12.2	7.2	11.9	9.4	11.6	9.1	8.9	SGN-U567805	Encodes a Wound-induced protein (WIP) family protein
SGN-E304228	0.0	1.2	0.0	0.0	-1.9	3.0	13.5	13.2	11.6	6.1	11.0	9.1	10.9	8.8	8.3	SGN-U567805	ATHCHIB (BASIC CHITINASE)/ chitinase
SGN-E353135	0.0	1.2	0.0	0.0	-3.3	2.7	12.8	12.5	10.7	6.1	10.4	8.2	10.1	8.3	7.5	SGN-U567805	Encodes a Wound-induced protein (WIP) family protein
SGN-E376537	0.0	1.1	0.0	-4.2	-1.9	3.0	13.4	13.3	11.6	6.2	11.0	9.3	10.9	9.0	8.3	SGN-U567805	Encodes a Wound-induced protein (WIP) family protein
SGN-E744742	-4.1	1.2	-4.0	0.0	-1.9	2.9	13.1	13.2	11.2	6.1	10.8	8.9	10.7	8.4	8.3	SGN-U567805	Encodes a Wound-induced protein (WIP) family protein
SGN-E297141	0.0	1.2	0.0	0.0	-2.2	4.0	18.0	17.7	15.5	8.2	14.6	12.1	14.6	11.8	11.1	SGN-U567805	ATHCHIB (BASIC CHITINASE)/ chitinase
SGN-E351482	0.0	1.2	0.0	0.0	-4.4	3.9	17.6	17.5	15.1	8.0	14.6	12.1	14.4	11.6	11.3	SGN-U567805	Encodes a Wound-induced protein (WIP) family protein
SGN-E744907	0.0	1.2	0.0	0.0	-1.8	4.8	20.9	21.0	18.4	9.8	17.5	14.5	17.0	13.9	13.3	SGN-U567805	Encodes a Wound-induced protein (WIP) family protein
SGN-E372004	2.0	-1.6	0.0	0.0	4.9	3.0	15.4	16.2	10.9	20.9	6.8	12.1	23.6	14.6	10.4	SGN-U568037	catalytic
SGN-E287121	2.0	-1.6	0.0	0.0	4.9	3.0	15.4	16.2	10.9	20.9	6.8	12.1	23.6	14.6	10.4	SGN-U568037	catalytic
SGN-E337845	2.0	0.0	0.0	1.9	4.2	-1.2	9.6	12.6	8.3	10.4	7.9	16.2	7.9	21.3	20.9	SGN-U577627	RHA1
SGN-E278955	2.0	0.0	0.0	1.9	4.2	-1.2	9.6	12.6	8.3	10.4	7.9	16.2	7.9	21.3	20.9	SGN-U577627	RHA1
SGN-E397078	2.0	0.0	0.0	1.9	4.2	-1.2	9.6	12.6	8.3	10.4	7.9	16.2	7.9	21.3	20.9	SGN-U577627	AtRABG3d (Arabidopsis Rab GTPase homolog G3d)/ GTP binding
SGN-E378032	1.4	0.0	0.0	2.0	2.9	-1.1	6.6	8.6	5.7	7.2	5.4	11.1	5.4	14.7	14.4	SGN-U577627	AtRABH1c (Arabidopsis Rab GTPase homolog H1c)/ GTP binding
SGN-E317484	0.0	0.0	0.0	0.0	0.0	-8.1	30.8	30.0	26.6	26.2	12.9	2.0	2.6	16.7	-5.6	SGN-U600578	No gene description
SGN-E709466	-1.2	-1.3	0.0	-1.3	1.1	1.2	-1.6	-2.4	-1.6	-4.3	-2.2	-4.3	0.0	34.8	-1.0	SGN-U580736	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E332099	-1.2	-1.3	0.0	-1.3	1.1	1.2	-1.6	-2.4	-1.6	-4.3	-2.2	-4.3	0.0	34.8	-1.0	SGN-U580736	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E703898	1.0	-1.6	0.0	-1.0	1.4	1.6	-1.2	-1.9	-1.3	-1.7	-1.8	-3.4	0.0	39.2	1.2	SGN-U580736	PAL (PHENYL ALANINE AMMONIA-LYASE)

SGN-E265134	-1.5	1.2	0.0	0.0	0.0	-1.0	-1.4	-1.5	-2.9	0.0	0.0	0.0	1.1	35.6	-1.2	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E280687	-2.0	1.2	0.0	0.0	0.0	1.9	-1.3	-1.3	-1.3	-3.5	0.0	0.0	2.2	42.1	1.2	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E354605	0.0	1.1	-8.7	-3.6	-2.1	-2.3	-1.5	-1.4	-1.7	-3.8	-3.1	-5.1	-2.0	39.7	-2.1	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E349491	0.0	1.1	-8.7	-3.6	-2.1	-2.3	-1.5	-1.4	-1.7	-3.8	-3.1	-5.1	-2.0	39.7	-2.1	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E286569	-8.8	1.1	-8.7	-3.6	-2.1	-2.3	-1.5	-1.4	-1.7	-3.8	-3.1	-5.1	-2.0	41.8	-2.1	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E304497	-8.8	1.1	-8.7	-3.6	-2.1	-2.4	-1.5	-1.5	-1.7	-3.8	-3.1	-5.1	-2.0	37.7	-2.1	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E205725	0.0	1.0	-3.0	-3.1	-1.1	1.3	-1.1	-1.9	-1.5	-5.2	0.0	-1.7	1.5	33.9	-1.6	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E207172	-1.6	1.1	0.0	-6.8	-2.4	1.0	-1.2	-1.6	-1.3	-5.7	0.0	0.0	1.5	34.9	-1.3	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E298063	-2.3	1.1	-4.5	-4.7	-3.3	-1.0	-1.4	-1.7	1.1	-7.9	0.0	-2.6	1.7	30.0	-2.5	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E305836	-3.8	1.1	0.0	-7.8	-2.7	1.1	-1.2	-1.8	-1.5	-6.6	0.0	-3.3	1.3	30.2	-1.5	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E205183	-4.3	1.2	-4.2	-8.9	-3.1	1.1	-1.2	-2.1	-1.4	-7.4	0.0	-2.5	1.4	29.5	-1.8	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E736096	-3.8	-1.2	0.0	-1.5	-1.8	-1.3	-1.8	-2.4	-3.6	0.0	-3.3	-1.1	-3.3	33.0	-2.0	SGN-U580050	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E736034	-3.8	-1.2	0.0	-1.5	-1.8	-1.3	-1.8	-2.4	-3.6	0.0	-3.3	-1.1	-6.7	32.5	-2.0	SGN-U580050	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E311991	-3.3	-1.1	0.0	-2.2	-2.3	-2.2	-2.0	-2.1	0.0	0.0	-2.9	-1.4	-5.8	27.6	-2.7	SGN-U580050	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E336129	0.0	-1.1	-4.0	-2.1	-5.7	-1.9	-1.5	-1.3	-1.5	-2.3	-1.8	-7.0	-1.4	35.4	-2.2	SGN-U577677	phenylalanine ammonia-lyase/2C putative
SGN-E323057	-3.4	-1.1	-6.7	-2.0	-3.2	-2.9	-1.4	-2.6	-1.6	-2.9	-2.4	-2.9	-3.0	32.1	-1.8	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E303178	2.0	1.2	0.0	0.0	2.8	5.0	4.2	1.0	2.0	5.7	2.2	2.3	6.6	37.5	4.8	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E228199	2.0	1.2	0.0	0.0	-1.5	2.1	1.0	-1.9	1.0	2.9	-1.8	1.7	1.7	26.4	1.2	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E376010	0.0	-1.1	0.0	-2.1	1.0	-1.2	1.9	-1.3	-3.9	1.4	0.0	1.4	2.5	25.4	-1.6	SGN-U580050	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E289786	1.1	1.1	0.0	-3.6	-1.3	1.7	1.5	-3.4	1.5	1.6	-1.6	1.3	2.2	17.1	1.4	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E206146	-1.6	-1.1	-1.1	-2.2	-2.3	1.4	1.1	-3.1	1.4	1.1	-1.9	1.2	2.1	20.1	-1.1	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E200349	0.0	1.2	-2.0	0.0	-2.9	-3.2	-1.9	-3.9	-2.0	-1.2	-3.6	0.0	-1.8	26.2	-1.1	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E308375	0.0	1.2	-2.5	0.0	-3.6	-3.0	-2.4	-4.9	-1.6	-1.5	-4.5	0.0	-1.5	24.0	-1.4	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E200348	-4.3	1.0	-1.1	-2.9	-1.5	1.1	-1.2	-2.7	-1.4	-3.7	-7.6	-1.9	1.3	26.4	-2.3	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E212120	-2.7	1.1	-1.7	-3.6	-3.8	-1.1	-1.4	-2.5	-1.0	-4.6	-9.4	-3.1	1.3	27.2	-2.2	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E241239	0.0	1.1	-1.5	-4.7	-3.3	1.0	-1.2	-2.2	-1.3	-3.9	-8.1	-2.6	1.2	24.5	-1.9	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E304081	0.0	1.1	-1.7	-3.6	-3.8	-1.1	-1.4	-2.5	-1.1	-4.6	-9.4	-3.1	1.2	21.6	-2.2	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E309768	-3.3	1.1	-3.2	-6.8	-2.4	-3.9	-3.1	-6.3	-2.1	-1.4	-5.8	0.0	-2.0	18.7	-1.8	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E349300	-3.3	1.1	-3.2	-6.8	-4.7	-5.2	-3.1	-6.3	-2.1	-1.4	-5.8	0.0	-2.0	18.0	-1.8	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E738936	-3.0	1.0	-1.5	-3.1	-1.4	1.2	-1.0	-2.9	-1.1	-1.5	-3.6	-1.3	1.7	21.8	-1.6	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E301501	-4.0	1.1	-1.3	-4.2	-2.9	1.3	-1.3	-1.5	1.2	-1.2	-3.6	-1.2	1.8	19.5	-1.6	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E298210	-2.1	1.0	-2.1	-2.9	-3.1	1.1	-1.3	-2.0	1.3	-1.1	-3.8	-1.2	1.4	17.5	-2.3	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E210268	-3.8	-1.0	-1.2	-2.6	-2.7	-1.3	-1.2	-2.4	1.2	-2.2	-6.7	-1.3	1.6	18.8	-3.1	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E291356	-5.3	1.1	-1.7	-3.6	-3.8	-1.1	-1.4	-2.5	-1.1	-4.6	-9.4	-3.1	1.2	21.6	-2.2	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E304260	-2.9	1.1	-1.9	-4.0	-4.2	-1.2	-1.4	-2.8	-1.1	-5.0	-10.3	-3.4	1.2	21.1	-2.4	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E210324	-5.3	1.1	-1.7	-3.6	-3.8	-1.2	-1.4	-2.5	-1.0	-1.5	-9.4	-1.5	1.5	16.4	-2.2	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E303794	-5.3	1.1	-1.7	-3.6	-3.8	-1.2	-1.4	-2.5	-1.0	-4.6	-9.4	-3.1	1.2	15.5	-2.9	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E204856	-2.0	-1.1	-2.0	-2.1	1.4	1.6	1.1	1.0	1.5	-3.5	0.0	-1.2	2.2	59.7	1.5	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E307792	-2.8	1.0	-5.5	-2.9	-1.6	-2.9	-2.1	-1.5	-2.7	-4.8	-3.3	-2.4	-2.0	64.4	-3.0	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E212083	-1.7	1.0	-2.2	-2.8	-3.2	-1.1	-1.4	-1.9	-1.1	-3.9	-12.1	-3.9	1.7	57.2	-2.2	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E378130	-3.4	-1.2	-1.7	-1.5	-1.9	-1.9	-2.1	-1.8	-1.9	-5.8	-6.0	-5.9	-2.0	54.0	-1.6	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E706559	-1.5	-1.1	-1.5	-2.1	-1.7	1.0	-1.1	-1.9	1.1	-2.1	-10.7	-1.5	2.0	47.8	-1.6	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E233499	-1.5	-1.2	2.0	-1.5	0.0	5.3	-2.8	2.8	2.4	36.3	-1.3	13.1	11.6	0.0	29.0	SGN-U581284	terpene synthase/cyclase family protein
SGN-E546080	-1.4	-2.2	1.7	1.3	0.0	3.6	-3.9	1.9	1.1	30.6	-2.5	11.0	12.1	-1.2	27.8	SGN-U581284	pseudogene/2C similar to vetispiradiene synthase
SGN-E389935	1.2	-1.0	1.2	-2.6	0.0	3.2	1.1	2.1	1.6	22.1	-1.5	8.2	6.9	1.1	17.3	SGN-U581284	terpene synthase/cyclase family protein
SGN-E688091	-7.5	0.0	1.2	2.0	-10.7	3.1	-14.1	1.5	-1.0	25.3	-2.7	8.7	9.9	-4.5	24.5	SGN-U579603	terpene synthase/cyclase family protein
SGN-E246031	-4.1	0.0	2.2	2.0	0.0	5.8	-3.9	2.3	1.0	47.3	-2.4	16.7	18.9	-3.7	48.1	SGN-U578127	terpene synthase/cyclase family protein
SGN-E391776	0.0	1.2	0.0	0.0	0.0	0.0	0.0	1.0	0.0	0.0	65.4	0.0	17.7	0.0	0.0	SGN-U584082	YUC10/ monooxygenase
SGN-E246737	0.0	1.2	0.0	0.0	0.0	0.0	0.0	1.0	0.0	0.0	65.4	0.0	17.7	0.0	0.0	SGN-U584082	YUC11/ monooxygenase
SGN-E396200	0.0	1.2	0.0	0.0	0.0	0.0	0.0	1.0	0.0	0.0	65.4	0.0	17.7	0.0	0.0	SGN-U584082	YUC11/ monooxygenase
SGN-E306646	1.2	-1.1	-1.3	-2.1	1.0	-9.4	67.5	56.2	1.2	59.3	2.1	61.1	29.7	63.1	2.7	SGN-U592085	LHCA2 (Photosystem I light harvesting complex gene 2)
SGN-E283674	1.4	-1.4	-2.1	-1.2	1.8	-1.8	-1.3	-1.0	1.1	1.5	-1.9	-1.2	1.9	96.3	-1.4	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E209052	1.4	-1.4	-2.1	-1.2	1.8	-1.8	-1.3	-1.0	1.1	1.5	-1.9	-1.2	1.9	93.5	-1.4	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E290404	1.5	-1.5	-1.3	-1.1	2.3	-1.4	-2.6	1.1	1.3	1.9	-1.2	-1.6	-1.6	97.3	-1.1	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E265996	1.5	-1.5	-1.3	-1.1	2.3	-1.8	-2.6	1.1	1.3	1.7	-4.9	-1.2	-2.4	92.6	-1.1	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)

SGN-E320183	1.1	-1.1	0.0	-2.2	-1.3	1.1	1.2	-1.1	1.2	-1.5	0.0	-1.3	2.7	95.0	-1.4	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E698861	1.2	-1.1	0.0	-2.1	-1.4	-1.4	-1.1	-1.3	-1.1	-1.0	-3.6	-2.6	2.4	99.3	-1.2	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E739096	-3.0	-1.0	-3.0	-2.5	-1.2	-2.2	-1.2	-1.0	-1.1	-1.6	-3.6	-2.3	-1.8	92.0	-1.6	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E711810	-3.0	-1.0	-2.9	-2.7	-1.2	-2.1	-1.2	-1.1	-1.1	-2.0	-3.5	-2.3	-1.8	91.6	-1.6	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E738005	-3.0	-1.0	-2.4	-2.5	-1.2	-2.2	-1.2	-1.2	-1.1	-2.1	-3.6	-2.3	-1.8	89.0	-1.8	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E214120	1.1	-1.1	-6.4	-2.2	-1.9	-1.5	-1.8	-1.4	-1.4	-1.1	-3.9	-2.8	2.2	91.4	-1.3	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E285103	-3.4	1.0	-3.4	-3.0	-1.6	-2.4	-1.1	-1.1	-1.1	-2.2	-3.7	-2.6	-1.5	98.6	-1.5	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E214681	-3.4	1.0	-3.4	-3.0	-1.8	-2.4	-1.1	-1.1	-1.1	-2.2	-3.7	-2.6	-1.5	98.3	-1.5	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E304372	-4.9	1.1	-3.2	-4.1	-2.0	-2.4	-1.1	-1.3	-1.1	-2.4	-3.5	-2.4	-1.8	98.4	-1.5	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E279008	-5.2	1.0	-3.4	-3.0	-1.3	-2.2	-1.1	-1.0	-1.2	-3.6	-3.7	-2.6	-1.7	101.3	-1.5	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E214126	-3.9	-1.1	-2.3	-2.0	-1.1	-2.2	-1.4	-1.1	-1.2	-2.0	-10.2	-2.5	-1.9	98.5	-1.6	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E241007	-4.9	1.0	-3.2	-2.9	-1.4	-2.1	-1.1	1.0	-1.2	-3.4	-3.5	-2.4	-1.6	106.1	-1.5	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E308905	-4.9	1.0	-3.2	-2.9	-1.3	-2.1	-1.1	1.0	-1.2	-2.4	-3.5	-2.4	-1.6	104.7	-1.5	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E286786	-2.8	-1.0	-2.2	-2.6	-1.1	-2.0	-1.1	-1.0	-1.1	-2.0	-3.3	-2.2	-1.5	104.1	-1.4	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E346721	-2.7	-1.0	-2.1	-2.5	-1.0	-1.9	-1.1	1.0	1.0	-1.9	-3.2	-2.1	-1.5	108.4	-1.4	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E304219	-3.7	1.1	-2.4	-5.0	-2.1	-2.6	-1.3	-1.3	1.1	-3.2	0.0	-3.2	-1.4	111.7	-1.3	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E281116	-1.1	-1.3	-1.6	-1.3	1.5	-2.2	-3.0	1.1	1.3	1.1	-5.8	-1.1	-1.9	111.9	-1.1	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E304522	1.3	-1.0	0.0	-2.3	-1.6	-1.2	-1.2	-1.2	-1.1	1.2	-2.7	-2.0	2.5	109.9	-1.2	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E301998	1.1	-1.4	-1.7	-1.2	-2.5	-2.0	-1.6	-3.3	-3.4	1.7	-1.0	-1.5	-1.0	108.9	-2.8	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E268405	1.1	-1.0	0.0	-2.6	-2.7	1.0	-1.0	-1.8	-1.5	-1.6	-2.2	-2.2	3.0	107.8	-1.5	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E316202	1.1	-1.0	0.0	-2.6	-2.7	-1.1	-1.0	-1.8	-1.2	-2.2	-2.2	-2.2	2.8	104.6	-1.2	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E238020	-5.0	-1.1	-2.5	-2.1	-1.8	-2.5	-1.5	-1.1	-1.4	-2.5	-17.8	-2.9	-1.6	105.8	-1.5	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E242040	-5.1	-1.1	-2.5	-1.9	-1.3	-2.3	-1.5	-1.0	-1.7	-3.6	-18.2	-3.0	-1.7	106.8	-1.5	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E201694	1.2	-1.4	-2.1	-1.2	1.3	-2.5	-1.3	-1.6	1.1	1.4	-1.9	-1.5	1.3	83.2	-1.7	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E302638	-1.0	-1.0	0.0	-2.6	-1.8	-1.2	1.1	-1.4	-1.2	-1.4	-3.0	-2.9	2.7	86.6	-1.6	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E323308	-1.0	-1.0	-6.9	-2.4	-1.7	-1.1	-1.1	-1.1	1.0	-1.1	-4.2	-1.7	2.2	79.8	-1.4	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E307128	-1.1	-1.2	-3.3	-1.5	1.6	-2.0	-1.6	1.1	-1.2	-1.2	-12.0	-2.0	1.5	74.6	-1.8	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E303368	-1.5	-1.1	-3.0	-2.1	1.5	-1.8	-2.3	1.0	-1.3	-1.3	-10.7	-2.1	-1.8	77.7	-1.6	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E319164	-5.0	-1.0	-5.0	-2.6	-1.0	-1.6	-2.4	-1.2	-4.9	-2.2	-8.9	-2.9	-1.3	79.5	-2.7	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E207605	-1.5	-1.1	-2.2	-2.0	1.2	-2.1	-1.4	1.1	1.0	-1.1	-3.9	-1.5	-1.4	135.0	-1.4	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E302639	-2.3	-1.0	-2.3	-2.4	-1.4	-2.1	1.1	1.1	1.2	-1.5	-2.5	-2.0	-1.3	134.9	-1.1	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E242042	-2.2	-1.2	-1.6	-1.7	1.3	-1.8	-1.1	1.3	1.0	-1.9	-5.8	-1.9	-1.4	138.3	-1.2	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E301663	1.8	-1.5	-3.7	-1.6	-1.1	-1.6	-1.2	1.1	1.2	1.5	-2.3	-1.7	3.0	139.4	-1.6	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E204184	2.0	1.2	0.0	0.0	0.0	2.1	1.0	0.0	0.0	0.0	0.0	0.0	1.1	139.9	2.4	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E303723	1.8	-1.1	0.0	-1.9	-2.0	1.0	1.5	-1.1	1.1	1.1	-1.6	-1.6	3.7	133.8	1.1	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E215107	1.6	-1.1	-4.2	-1.8	1.3	-1.3	-1.1	-1.0	1.3	1.5	-1.9	-1.2	2.6	130.4	-1.2	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E242924	-1.6	-1.2	-2.0	-1.7	1.4	-1.8	-1.3	1.4	1.1	-1.4	-14.2	-1.5	-1.4	146.3	-1.2	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E739118	-2.4	-1.2	-2.4	-1.7	1.3	-2.0	-1.2	1.2	1.0	-2.1	-12.9	-1.6	-1.6	133.1	-1.7	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E208908	1.7	-1.5	-2.3	-1.6	1.2	-1.5	-1.2	1.0	1.3	1.4	-2.0	-1.3	2.4	122.3	-1.3	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E325555	1.6	-1.2	-4.4	-1.5	1.1	-1.3	-1.1	-1.1	1.0	1.4	-2.0	-1.6	2.5	124.0	-1.2	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E214424	1.5	-1.1	0.0	-2.1	-1.4	-1.3	-1.1	-1.1	1.0	1.3	-2.4	-1.7	2.8	122.4	-1.1	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E266877	1.2	-1.1	0.0	-2.2	-2.3	-1.2	-1.0	-1.6	-1.3	-1.4	-1.9	-1.9	3.3	121.5	-1.8	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E240427	-2.3	-1.0	-2.3	-2.7	1.1	-1.9	1.1	1.1	1.1	-2.3	-3.3	-1.8	-1.5	118.5	-1.5	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E235452	-4.3	-1.2	-2.8	-1.5	-1.7	-2.5	-1.2	-1.0	-1.0	-1.8	0.0	-2.1	-1.1	120.4	-1.7	SGN-U578065	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E201367	-2.3	-1.1	-2.2	-1.9	1.1	-1.8	1.0	1.2	1.1	-2.2	-3.2	-1.6	-1.5	126.8	-1.5	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E209819	2.0	-1.6	0.0	-2.1	-1.4	-1.0	1.6	1.0	1.3	-1.7	0.0	-1.2	5.3	150.2	-1.6	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E304765	-1.3	-1.1	-1.9	-1.8	1.4	-1.8	-1.3	1.3	1.1	-1.0	-3.4	-1.5	-1.3	147.0	-1.3	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E207888	2.0	1.2	0.0	0.0	0.0	2.9	1.0	3.1	0.0	0.0	0.0	1.1	2.2	162.0	1.2	SGN-U581452	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E200633	1.6	-1.0	0.0	-2.6	-1.8	1.9	-1.2	1.2	1.2	-2.2	0.0	0.0	2.7	208.7	1.5	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)
SGN-E277402	-2.5	-1.0	-2.5	-2.6	-1.2	-2.1	1.1	1.4	1.1	-1.4	-3.0	-1.2	1.1	187.5	-1.4	SGN-U577677	PAL (PHENYL ALANINE AMMONIA-LYASE)

Supplementary Table SIV. Transgressive sRNA loci targeting cDNAs that are marked to show distinct transgressive features. Values are normalized sRNA abundance.

SGN-EST	Gene/High homology	M82-1	M82-2	S.penn-1	S.penn-2	F1	IL1-1	IL2-5	IL8-1-1	IL8-1D	IL8-1-3	IL8-2	IL8-2-1	IL8-3	IL8-3-1	Observations
SGN-E229629	Nascent polypeptide alpha chain protein, putativealpha-NAC	**66**	**102**	**76**	**134**	18	2	2	8	1	1	6	4	4	1	High in parents
SGN-E239386	Seven in absentia (SINA) family protein	**52**	**83**	**61**	**164**	18	2	1	6	0	0	7	4	4	1	High in parents
SGN-E552623	unknown	**85**	**155**	**95**	**193**	25	2	3	7	0	0	10	6	0	1	High in parents
SGN-E719396	ATEM1 (Early methionine labelled)	**33**	**124**	**48**	**164**	20	1	3	5	2	0	2	9	3	1	High in parents
SGN-E578128	Hydrolase, alpha/beta fold family protein	51	61	35	80	**105**	14	84	4	10	122	3	8	29	7	Activation in F1
SGN-E296258	LHCA2 (Photosystem I light harvesting complex gene 2)	37	150	96	213	**414**	50	40	85	52	80	65	74	260	71	Activation in F1
SGN-E389790	Unknown	61	77	114	275	**951**	35	44	46	69	74	17	23	37	63	Activation in F1
SGN-E744425	Unknown	2	0	395	616	**163**	5	3	0	2	3	1	2	2	627	MPV in F1
SGN-E324054	disease resistance protein (NBS-LRR class), putative	0	0	54	204	**76**	0	0	0	0	0	0	1	155	0	MPV in F1
SGN-E549037	AOX2 (alternative oxidase 2); alternative oxidase	205	174	0	0	**71**	290	241	261	301	0	1	2	206	289	MPV in F1
SGN-E214112	Unknown	1314	3276	1	10	**522**	9	2761	15	2157	40	16	16	154	**4467**	MPV in F1
SGN-E312996	S-adenosylmethionine-dependent methyltransferase	37	135	0	0	***5***	92	39	52	42	67	92	65	25	0	Reduction in F1
SGN-E697787	Transcriptional factor B3 family protein	408	613	4	4	**25**	**1086**	**1797**	**989**	**1489**	**1027**	**2373**	**2887**	**882**	**827**	Activating in one or manyILs
SGN-E304219	PAL (PHENYL ALANINE AMMONIA-LYASE)	2	13	3	3	5	11	11	15	4	0	4	9	**1463**	9	Activating in one IL
SGN-E739672	PAL (PHENYL ALANINE AMMONIA-LYASE)	10	18	4	13	17	23	25	27	16	8	13	29	**2769**	13	Activating in one IL
SGN-E373983	Pectinacetylesterase family protein	2	2	90	141	17	1	1	**442**	**356**	2	5	1	0	0	Activating in few ILs
SGN-E577553	Copper-binding family protein	11	36	8	22	96	37	109	73	137	**207**	14	20	110	13	Activating in few ILs
SGN-E246031	Terpene synthase/cyclase family protein	1	0	9	17	0	2	18	8	**336**	3	**119**	**138**	2	**323**	Activating in few ILs
SGN-E238040	Endonuclease/exonuclease/phosphatase family protein	0	0	0	0	0	1	0	**129**	0	0	0	58	0	0	Activating in few ILs
SGN-E390928	CYP79F1 (SUPERSHOOT 1)	15	8	0	2	2	9	4	7	10	8	9	7	**181**	14	Activating in few ILs
SGN-E555182	Unknown	2	1	1	0	1	**120**	0	0	5	3	0	**135**	3	**92**	Activating in few ILs
SGN-E315555	Zinc finger (C3HC4-type RING finger) family protein	1	2	0	0	0	2	1	**109**	2	0	1	**49**	0	0	Activating in few ILs
SGN-E577818	Unknown	7	9	20	50	24	33	15	25	12	20	9	18	**579**	8	Activating in few ILs
SGN-E306646	LHCA2 (Photosystem I light harvesting complex gene 2)-like	5	6	3	4	6	**510**	**432**	9	**411**	15	**426**	**212**	**453**	18	Activating in many ILs
SGN-E317484	Unknown	0	0	0	0	0	**200**	**198**	**177**	**156**	**79**	**12**	**16**	**103**	1	Activating in many ILs
SGN-E353135	Encodes a Wound-induced protein (WIP) family protein	0	9	0	0	2	**110**	**109**	**94**	**48**	**84**	**65**	**82**	**68**	**56**	Activating in many ILs

Supplementary Table SV. Number of sRNA sequences matching four *PAL* s identified from to

	PAL5A	**PAL5B**	**PAL5C**	**PAL5D**	**PAL5**
Total sRNAs matching	812	399	756	230	464
Number of unique sequences	**39**	**201**	**11**	**12**	**1**