

Supplemental Table S1. Comparison of cotyledon vein patterns of wild type and *svr4-2*.

| Genotype | Total* | Cotyledon vein patterns | | | | | |
|---------------|--------|-------------------------|------------|--------------|----------------|---------------|--------------|
| | | Zero Areole | One Areole | Two Areoles | Three Areoles | Four Areoles | Five Areoles |
| WT | 290 | N.A. | N.A. | 113 (39%) | 127 (43.8%) | 50 (17.2%) | N.A. |
| <i>svr4-2</i> | 150 | N.A. | N.A. | 72 (48%) | 47 (31.3%) | 31 (20.7%) | N.A. |

*: Total number of cotyledons examined.

Supplemental Table S2. Primers used in this study.

| Primer Name | Primer sequence | Notes |
|-----------------------------|--|---------------------------------------|
| F26B6#1F | 5'-TGC ATT AGG GCT TTG AGA AC-3' | Indel 27/-27 |
| F26B6#1R | 5'-TTT CCG ATC CTC TTC AGA AG-3' | |
| F13B15#1F | 5'-TAA GTG TTG TCT TAG GCC TC-3' | Indel 23/-23 |
| F13B15#1R | 5'-GAC TTA CAC GTC TCT CTT TC-3' | |
| F27A10#1F | 5'-ACC AAT ATG TAT TGG GTC TG-3' | Indel 11/-11 |
| F27A10#1R | 5'-AAG TAC AGG TGA ATA ACT GG-3' | |
| F27D4#2F | 5'-AAG AAG CGT ACA AGG AGA TG-3' | Indel 30/-30 |
| F27D4#2R | 5'-GAG TGT CAT AGA ATC GCA AG-3' | |
| F27L4#1F | 5'-TGA TCT TGA GTA GCC AAG CT-3' | dCAPs w/ <i>HindIII</i> |
| F27L4#1R | 5'-TCT TGG TAA TCT TTC GTT TG-3' | cut <i>Ler</i> sequence |
| T28I24#1F | 5'-CTT GTG AAG CTG CAG GTC TA-3' | dCAPs w/ <i>XbaI</i> cut |
| T28I24#1R | 5'-TCG AGA GTG GAG AAA GTA TG-3' | <i>Col</i> sequence |
| 24060F | 5'-CAT GGA TCC TTC TGG ATA AGA GCT TCG TGA TG-3' | Amplifying <i>SVR9</i> |
| 24060R | 5'-CAT GGA TCC TTG GCT CTC TTG AGA CAT GGT AG-3' | cDNA |
| 24060F1 | 5'- CAT TGA CGT TTA GCT TCC AA-3' | |
| 24060R1 | 5'-CTG CAT CAG GCG ATA GTA TA-3' | |
| 24060F2 | 5'-CGT AGA GCA ATT GGT AGT AG-3' | |
| 24060R2 | 5'-TAG CTC TTG CTA AGC TCC TC-3' | Genotyping |
| 24060F3 | 5'-GAT ACG AAC AGC AAA AGA GG-3' | <i>svr9-1</i> and |
| 24060R3 | 5'-CTA GTT TCT GTC ATG GAA GC-3' | <i>svr9-2</i> |
| 24060F4 | 5'-TAT ACT ATC GCC TGA TGC AG-3' | |
| 24060R4 | 5'-CCT CTT TTG CTG TTC GTA TC-3' | |
| 24060PF-XbaI2 | 5'-CAT TCT AGA AAT CAG CAC AGG GGT AGG ACC AG-3' | Amplifying the promoter region |
| 24060PR-BamHI2 | 5'-CAT GGA TCC GGC GCT TCT TCT TCA CTC AGA GG -3' | of <i>SVR9</i> cDNA |
| At2g24060GFPR | 5'-CAT GGG ATC CAC CAC CAC CAC CAG AAT CGA TCT GTA GAG GCT C-3' | Generating <i>P35S:SVR9-GFP</i> |
| cTPF | 5'-CAT TCT AGA TTC TGG ATA AGA GCT TCG TGA TG-3' | Amplifying the cTP region of |
| cTPR | 5'-CAT GGA TCC TCG ATA ACC TCC ACC ACC ACC GC-3' | <i>SVR9</i> |
| GFP-F | 5'-CAT GGA TCC ATG GTG AGC AAG GGC GAG GAG-3' | Amplifying eGFP coding |
| GFP-R | 5'-CAT CTC GAG TTA CTT GTA CAG CTC GTC CAT-3' | sequences |
| <i>E. coli</i> IF3-F | 5'-CAT GGA TCC ATG AAA GGC GGA AAA CGA GTT CA-3' | Amplifying <i>E. coli</i> infC coding |

| | | |
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| <i>E. coli</i> IF3-R | 5'-CAT CTC GAG TTA CTG TTT CTT CTT AGG AGC GA -3' | sequences |
| 30690F | 5'-CAT GGA TCC CAT TCT AAT TGG TGG AGA GAC AG-3' | Amplifying |
| 30690R | 5'-CAT GGA TCC TTT ACA TCA GAC AAT TCC GCA TC-3' | <i>SVR9L1</i> cDNA |
| 30690F1 | 5'-TGG TCT TCG ACT CTG TGT AC-3' | Genotyping |
| 30690R1 | 5'-CAC CGT CTT GCA AGA ACT TC-3' | <i>svr9l1-1</i> |
| At4g30690GFPR | 5'-CATGCCATGGAACCACCACCACCACCAC CTATATCTTGTGTTGCAGTTAT-3' | Generating <i>P35S:SVR9L1-GFP</i> |
| CUC2F | 5'-CAT CTC GAG ATG GAC ATT CCG TAT TAC CAC-3' | Amplifying <i>CUC2</i> |
| CUC2R | 5'-CAT CTC GAG TCA GTA GTT CCA AAT ACA GTC-3' | cDNA |
| CUC2F1Z | 5'-GAC AGA GAG ATC TTT AGT TC-3' | Semi-quantitati |
| CUC2R1Z | 5'- AGA CGG CTG AAT GAG TTA AC-3' | ve RT-PCR analysis of <i>CUC2</i> transcripts |
| CUC2F(s) | 5'-GAG TAA TTG GGT TAT GCA TG-3' | Genotyping |
| CUC2R1 | 5'-TGC GTA GGA GCA ACT GCT G-3' | <i>cuc2-101</i> and |
| CUC2DF | 5'-TCT CCT GGA TCC GAC CAC TA -3' | <i>cuc2-1D</i> |
