Table S1: **Alleles of *SEUSS-LIKE* transcriptional co-regulators in Arabidopsis**

Allele name	ABRC stock number	Insertion type	Last AA or noncoding insertion location	nucleotide change - mutant in red insertion site red *	selection
slk1-1	SALK*043166*	SALK	G242	cac cat gcg ctt ggc a*tg ttc cca cag gca gct	Kan sensitive
slk1-2	SALK*093829C*	SALK	D387	GTT TCT CAG CAG GAT *TTA CAG TCA AAT AGT AAC ATgtaagttaatgcacattattcttttattgtcg* atactctggcatttgtttct	nd
slk1-3	*CS852593*	WiscDsLox 3566.04	5'UTR	TGCACAAATCCCAAAA*atcagaaatttggaagaaac t	basta resistant
slk2-1	SALK*089954*	SALK	M278	caa caa gga atg caa atg c*aa cta acc ggt ggg	nd
slk2-2	SALK*038662*	SALK	L455 5th exon	GT CGA CAT GAA GAA CTA CTT *CC*T CGT CGC CTA GTA GCT CCA CAG	nd
slk3-1	SALK *090714*	SALK	intron 8	gag acc caa a*ac gag gtt gc	Kan resistant
slk3-2	SALK *117317*	SALK	intron 4	ttt ctt ttg c*cc tgc cta tt*t acc gaa aat	Kan partial (weak) resistance

Our qRT PCR analysis indicated that the *slk2-1* allele was a near null mutant, expressing only 0.4% of the wild type level of *SLK2* mRNA. The *slk1-1* allele is a strong loss-of-function allele that expresses *SLK1* mRNA at 30% of wild type levels and is predicted to encode a truncated protein product containing 242 of 748 amino acids.

Table S2: **Oligos used in this study**

Genotyping oligos

Allele or oligo name	**Type**	**oligo fwd**	**oligo rev**
slk1-1	SALK	TTGGCGTCTGTGCTCGGAAA	GTCTGGCAAGCACATCAAAC
slk1-2	SALK	AACTGGCCCATTTATAGCTCC	TGAAGAGCTTCTTCTTCGCAG
slk1-3	WiscDsLox	CGCTGGATCAACTGCTGTAA	TGACCGGTACAGTCGGTTATTA
slk2-1	SALK	GGTGGACCTACTGGTGGCTA	ATCAGCAATGACACGACTGG
slk2-2	SALK	GCACTTGGTGTTTCTCCTCAG	GAGCAAAAGACTTGGCATCAG
slk3-2	SALK	TGCTCTGTGTGTTTTGGTCTG	TACACTTCCCAAAACCATTGC
slk3-1	SALK	CTGCTGCTCCTGAGTGTTACC	TTTGGTGGATGCCAACTATTC
Wisc LB p745	WiscDsLox	AACGTCCGCAATGTGTTATTAAGTTGTC	
LBb1	SALK	GCGTGGACCGCTTGCTGCAACT	

qRT-PCR oligos

Name of oligos	**Gene**	**Oligo fwd**	**Oligo rev**
RTAPT3/4	*APT*	GTTGCAGGTGTTGAAGCTAGAGGT	TGGCACCAATAGCCAACGCAATAG
qETT5658f/5634r	*ETT*	CGAAGACACCACAGACACAGA	GAGGAAGACGAAACGCAAAC
MPqF2/R2	*MP*	CGAATGCATGTTTGGATTGGAAGG	ACGCATCCCACAAACTCTTCCC
RTIAA1-F/R	*IAA1*	AAAGATGGAGATTGGATGTTGG	CAGTAGGAGCTTCGGATCCTT
RTIAA17-F/R	*IAA17*	CCTAAAGATCCAGCCAAACC	TTGATTTTTGGCAGGAAACC
RTPHB1/2	*PHB*	TCATGCAACAGGGCTATGCT	AGAACTTTCCACACCGTTGC
RTREV1/2	*REV*	CGCCAAGCTAATGCAACAGGGATT	TGTCTTCCCATCGTTGACACACAG
RTSTM/1	*STM*	TCTCCGGTTATGGAGAGACAGCAA	TCGACTTCTTCCTCGGATGACCCA
RTYUC4-1/2	*YUC4*	GGACAAATTAAAGTGACGCAAG	GGACAAATTAAAGTGACGCAAG

Table S3) qRT PCR quantification in inflorescence meristem through stage 6 flowers.

early arising flowers - flowers 1-15 from apical meristem

INF to stage 6 flowers					**Stat. Sig. Y/N (p value)**
	col-0	***slk1***	***seu***	***seu slk1***	
YUC4	0.06 +/- 0.01	0.07 +/- 0.007	0.04 +/- 0.003	0.03 +/- 9.0 x10^{-4}	N (0.1)
MP	3.6 +/- 0.42	3.3 +/- 0.37	3.1 +/- 0.30	1.7 +/- 0.16	Y (0.006)
ETT	0.42 +/- 0.02	0.46 +/- 0.07	0.47 +/- 0.03	0.26 +/- 0.05	Y (0.02)
PHB	1.14 +/- 0.15	1.5 +/- 0.18	1.1 +/- 0.14	0.32 +/- 0.06	Y (0.0005)

+/- = Standard error of the mean

Table S4) qRT PCR quantification in stage 8-10 carpels.

early arising flowers - flowers 1-15 from apical meristem

stage 8-10 carpels					**Stat. Sig. Y/N (p value)**
	col-0	***slk1***	***seu***	***seu slk1***	
YUC4	.07 +/- 0.007	.06 +/- 0.007	.05 +/- 0.006	.04 +/- 0.01	N (0.2)
MP	3.9 +/- 0.33	4.0 +/- 0.93	3.2 +/- 0.34	2.8 +/- 0.39	N (0.14)
ETT	0.31 +/- 0.02	0.34 +/- 0.01	0.25 +/- 0.01	0.26 +/- 0.02	N (0.5)
PHB	1.3 +/- 0.26	1.4 +/- 0.18	1.1 +/- 0.14	0.57 +/- 0.03	Y (0.04)

+/- = Standard error of the mean

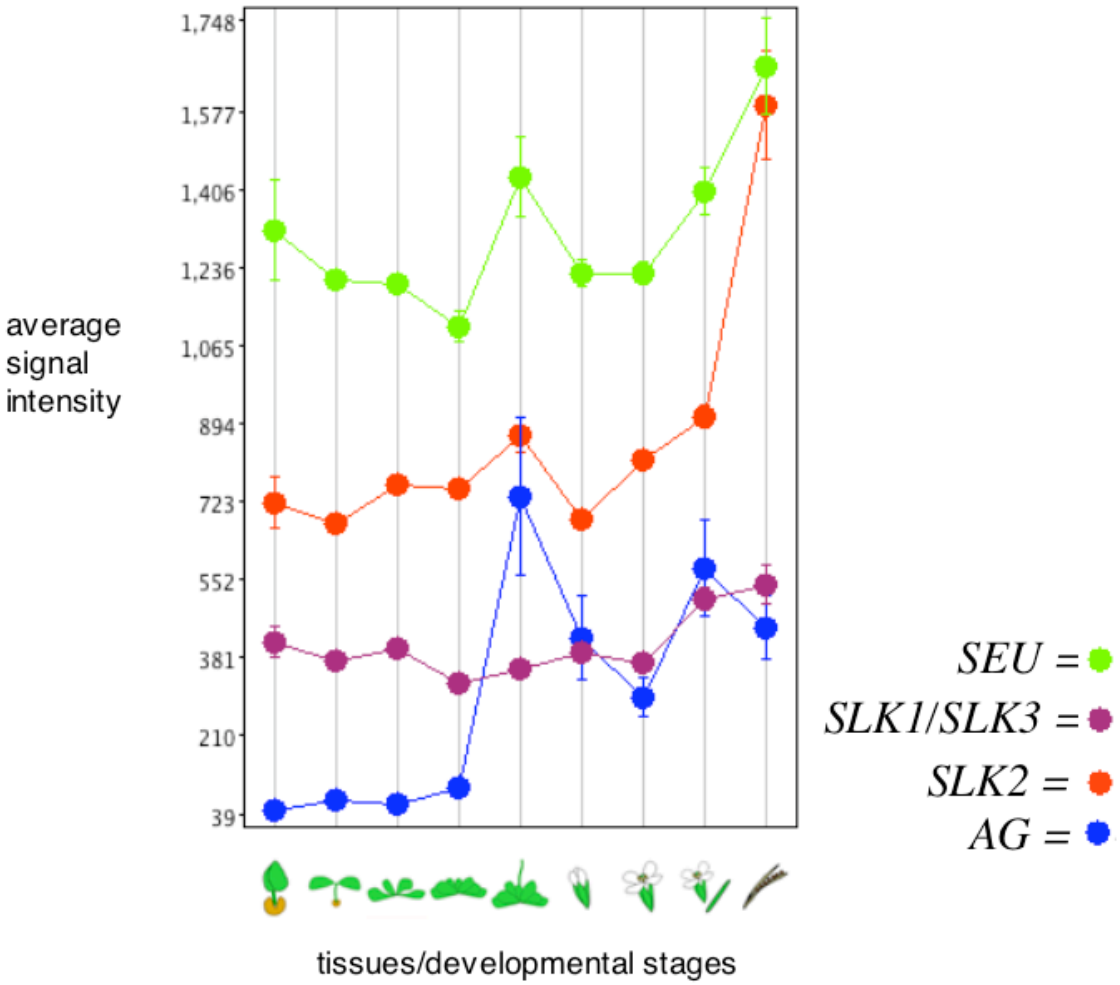

Figure S1) Genevestigator Expression Data for *SEU* and *SLK* genes

https://www.genevestigator.ethz.ch/gv/index.jsp

Developmental stages are pictured along the x-axis and average signal intensity of the indicated gene along the y-axis. *SLK1* and *SLK3* are shown together as the *SLK3* gene is not represented on the Affymetrix array and the signal reported for the *SLK1* gene may reflect expression of both *SLK1* and *SLK3* due to their high sequence similarity. Expression of *AG* is shown as a comparison and to indicate background (non-specific) level of signal as AG is not expected to be expressed in the early vegetative developmental stages.

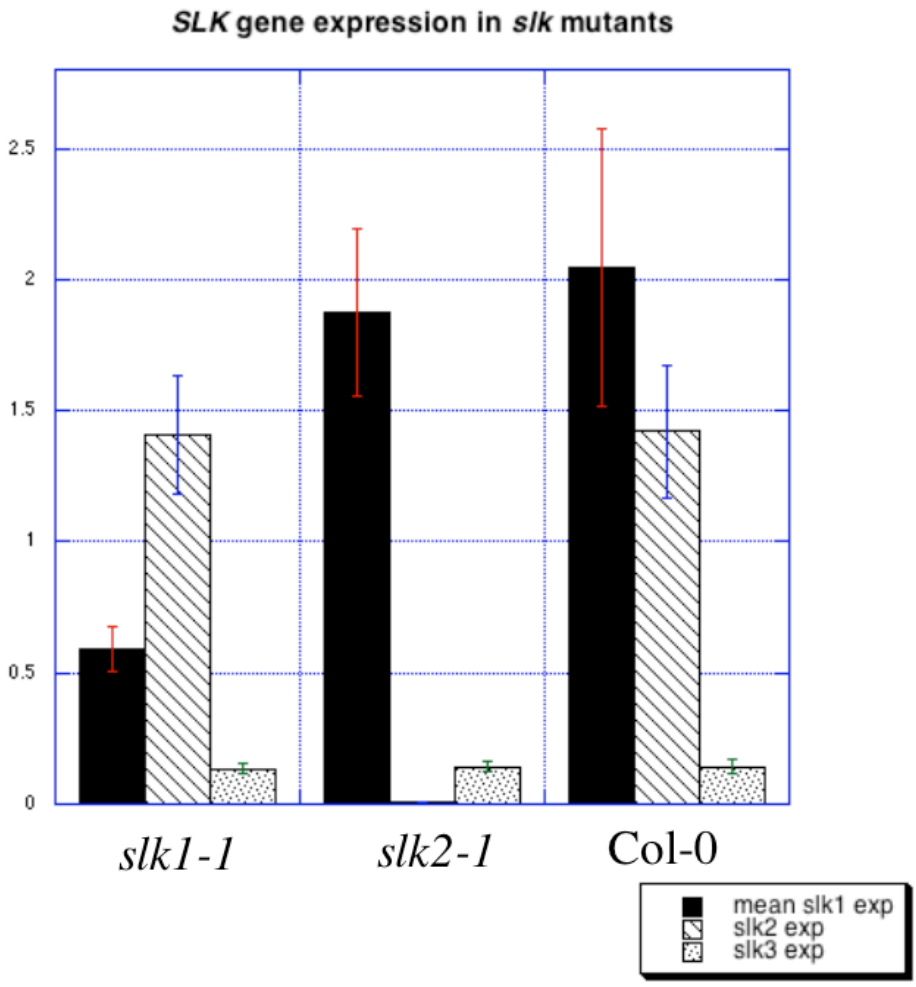

Figure S2) Quantitative Real-time PCR Expression Data for *SEU* and *SLK* genes
Mean expression of indicated *SLK* gene normalized relative to *ADENOSINE PHOSPHORIBOSYL TRANSFERASE* (*APT*) (At1g27450) as determined by quantitative real-time PCR. RNA prepared from whole inflorescence (inflorescence meristem plus floral stages 1-14). Results are averages and standard error of the mean for four biological replicates each in technical triplicate.Genotype of the tissues used is indicated along the X-axis. Results indicate the *slk2-1* allele is a near RNA null (0.4% of wild type levels of *SLK2* RNA). No significant reduction in the expression levels of relevant transcript were detected in the *slk2-2*, or *slk3-1* alleles (data not shown). Expression of relevant transcript was determined with PCR primers that are anneal to the mRNA at a location three prime from the site of T-DNA insertion (Table S2).

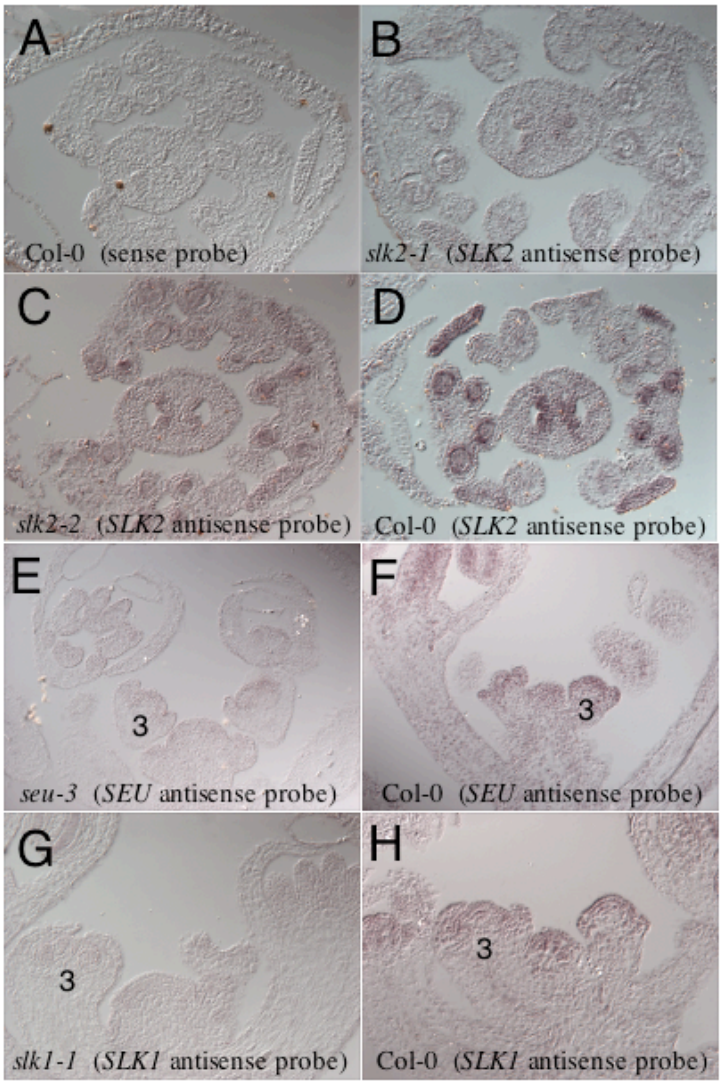

Figure S3 - Specificity of the *SEU*, *SLK1* and *SLK2* antisense in situ probes

In situ hybridization on floral sections. Probes and genotypes as indicated in panels. Floral stage 3 indicated (3).

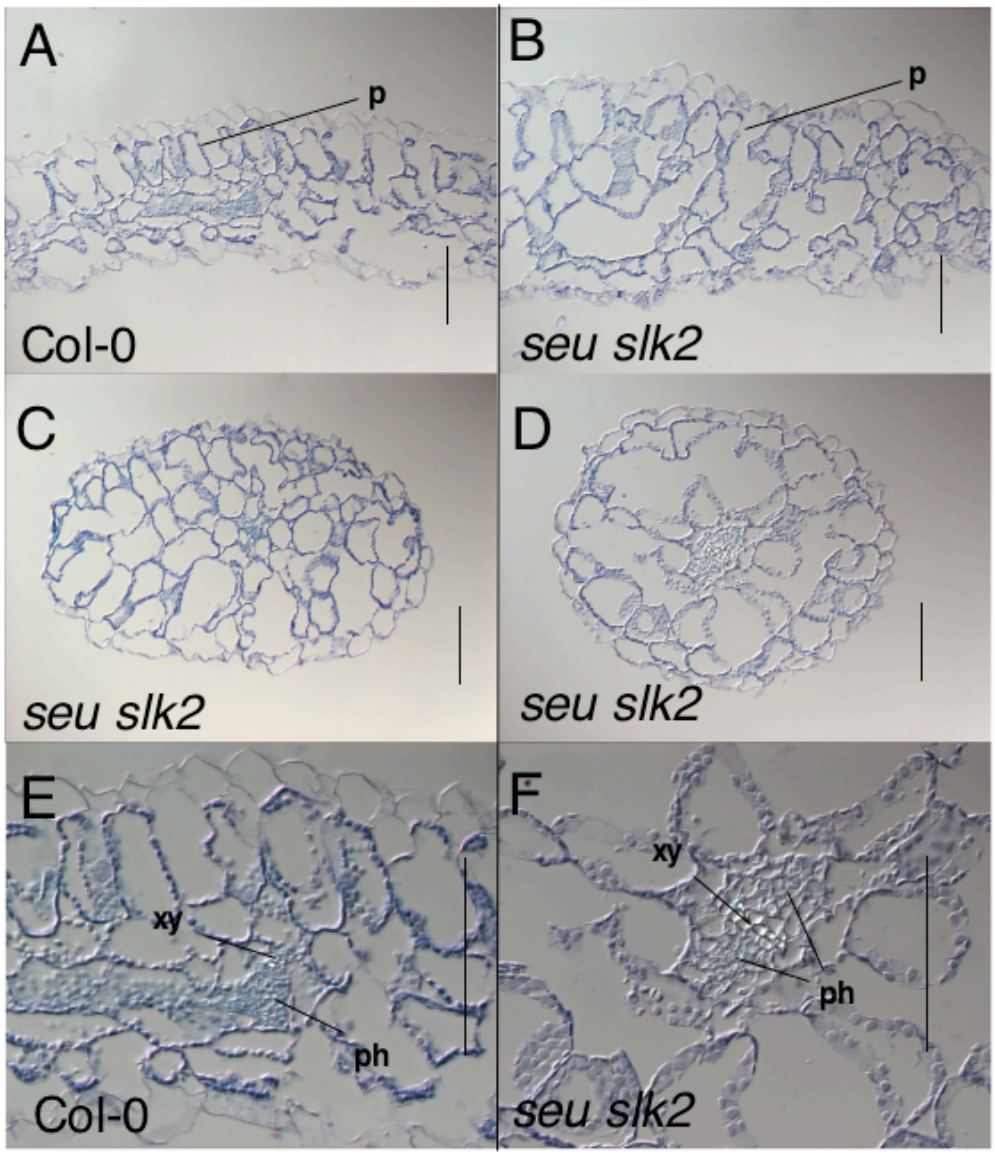

Figure S4.) Morphological alterations of cotyledon mesophyll cells and vascular elements in the *seu slk2* double mutant

Toluidine blue-stained cotyledon cross-sections from Col-0 and *seu slk2* double mutant seedlings at seven days post germination. Adaxial surface is orientated upwards in all images. A) Col-0 cotyledon shows closely-packed, cylindrical-shaped palisade mesophyll cells (p) positioned adaxially in the sub-epidermal cell layer. B) In the majority of *seu slk2* mutant cotyledons palisade-like cells were observed adaxially. The *seu slk2* mutant cells were slightly larger than the wild type palisade cells. C and D) In intermediate and severely radialized cotyledons the palisade cell layer could not be easily distinguished. E and F) Higher magnification images of panels A and D, respectively show alterations to arrangement of xylem (xy) and phloem (ph) in the radialized *seu slk2* mutant cotyledons. In this vascular element, phloem cells were observed on both sides of the xylem trace.