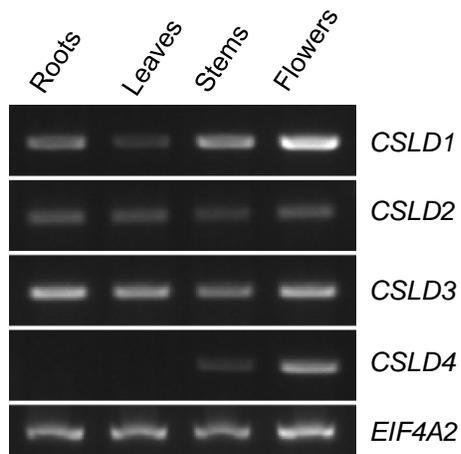
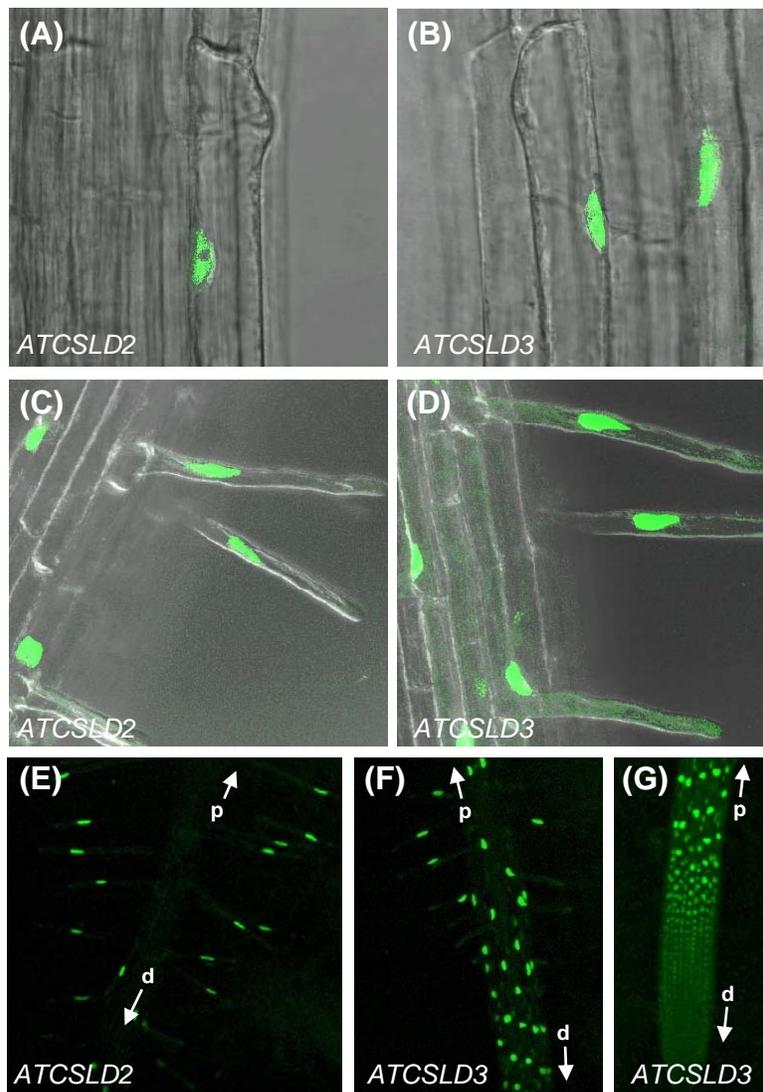


	CSLD1	CSLD2	CSLD3	CSLD4	CSLD5	CSLD6	
90	3184	2232	249	1255	13		> callus
94	2760	2506	301	1438	11		> cell suspension
63	1793	1988	262	1374	13		> seedling
63	1135	944	340	1368	16		• cotyledons
69	1438	2195	233	4300	15		• hypocotyl
104	2719	2850	264	1865	17		• radicle
853	1287	1185	513	3093	35		> inflorescence
2806	1102	1052	1265	2482	84		• flower
141	1047	1130	169	1871	17		• carpel
75	666	869	118	1231	8		• ovary
69	647	1347	134	383	8		• stigma
290	1346	1083	285	309	8		• petal
268	2024	844	323	220	9		• sepal
20472	615	519	7596	854	105		• stamen
105229	569	518	31852	301	38		• pollen
108	727	917	212	1502	15		• pedicel
280	1512	1144	322	1500	19		• silique
83	1789	1262	209	684	13		• seed
110	1161	1531	293	1675	21		• stem
19	1050	1700	158	1400	8		• node
62	1222	1204	139	7212	7		• shoot apex
59	1931	964	238	262	21		• cauline leaf
73	1578	1107	272	903	15		> rosette
66	1159	1104	263	2104	13		• juvenile leaf
73	2286	1282	291	435	15		• adult leaf
94	993	981	234	959	11		• petiole
100	2278	763	243	114	7		• senescent leaf
94	2375	1549	142	386	11		• hypocotyl
91	2106	1241	202	305	10		• xylem
86	1857	1292	137	521	11		• cork
82	3563	3324	250	1215	12		> roots
108	4184	4824	267	1164	15		• lateral root
146	1962	1611	224	2629	11		• root tip
80	4645	5136	235	1213	13		• elongation zone
108	8086	5357	165	550	19		• root hair zone
220	5776	8036	332	743	32		• endodermis
162	3869	5819	141	1563	13		• endodermis+cortex
388	2269	4937	194	1707	10		• epid. atrichoblasts
198	5278	10071	126	1913	16		• lateral root cap
230	2991	5170	76	1032	15		> 60 stele

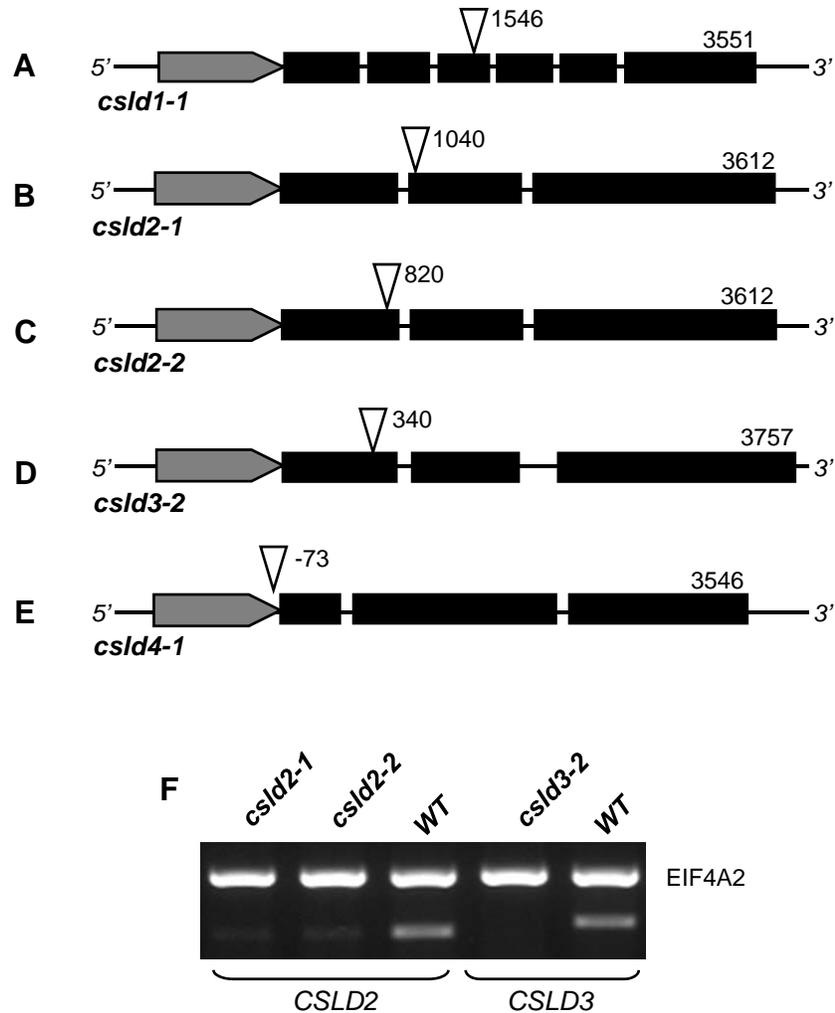
**Supplemental Figure 1. *In silico* Expression Profiling of the CSLD family.** The relative expression of *CSLD* genes in all major Arabidopsis organs/tissues was analyzed using the Geninvestigator Meta-Analyzer tool (<https://www.geneinvestigator.ethz.ch/>). Signal intensity values are arbitrary units.



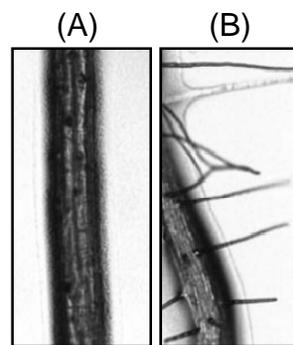
**Supplemental Figure 2. RT-PCR analysis of the CSLD family.** RT-PCR analysis was carried out on various organs of wild type (Col-0) plants using primers specific for each of the members of the CSLD family. Arabidopsis translation initiation factor EIF4A2 was used as a constitutive expression control.



**Supplemental Figure 3.** Analysis of promoter activity for CSLD2 and CSLD3. Confocal microscopic analysis of GFP expression in roots of 6 day old wild type seedlings carrying proCSLD2::GFP::GUS or proCSLD3::GFP::GUS fusion constructs. Expression of constructs was observed in some trichoblasts at early (A and B) and late (C and D) stages of root hair development. proCSLD2::GFP::GUS expression was generally sparse in the distal (d) portion of roots and stronger in proximal (p) portions (E). In contrast, proCSLD3::GFP::GUS expression was strong in distal portions (F and G).



**Supplemental Figure 4.** Generation of *CSLD* Knockout Lines. Schematic showing the gene structures of *CSLD1* (A), *CSLD2* (B and C) *CSLD3* (D) and *CSLD4* (E). Promoter regions are represented by grey boxes, black boxes are exons and connecting lines are introns. Insertional mutants were generated and the position of the T-DNA insertion in each gene is indicated by open triangles. *csld2-1*, *csld2-2*, and *csld3-2* are homozygous mutants whereas *csld1-1* and *csld4-1* are heterozygous. (F), Semi-quantitative RT-PCR of *CSLD2* and *CSLD3* in wild-type (WT), *csld2-1*, *csld2-2* and *csld3-2*. Total RNA was prepared from root tissue. *EIF4A2* primers were used as a control. Products obtained from primers for *CSLD2* and *CSLD3* are indicated at the bottom.



**Supplemental Figure 5.** Functional complementation of *csld3-2* with YFP-CSLD3. Phenotypes of the *csld3-2* mutant (A) and *csld3-2* complemented with the 35S::YFP::CSLD3 construct used in Figure 10 (B).