Rice *SLENDER LEAF 1* Gene Encodes Cellulose Synthase-like D4 and is Specifically Expressed in M-phase Cells to Regulate Cell Proliferation.

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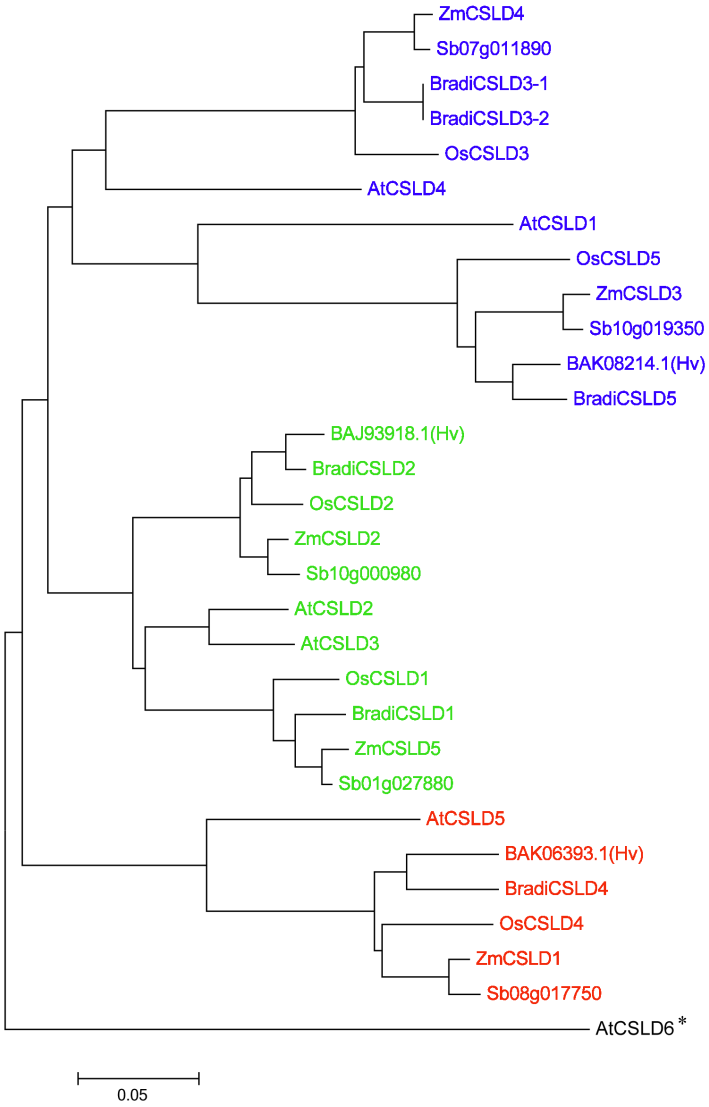

Fig. S1. Phylogenetic tree of CSLD proteins in rice (Os), maize (Zm), *Arabidopsis* (At), barley (Hv), sorghum (Sb), and purple false brome (Bradi). Nomenclature for proteins was due to Li *et al*. (2009) for rice, Hunter *et al*. (2011) for maize, Tair (http://www.arabidopsis.org) for *Arabidopsis*, NCBI (http://www.ncbi.nlm.nih.gov) for purple false brome. As for barley and sorghum, amino acid sequences showing the highest similarity to CSLD proteins in each clade were searched using the protein blast in NCBI. Obtained sequences were analyzed with MEGA ver. 5.1 (available at http://megasoftware.net/, Tamura *et al*. 2011) to create the phylogenetic tree. The proteins in blue are associated with pollen tube elongation, those in green with root hair development, and those in red with plant growth. The scale bar indicates genetic distance based on branch length. The accession numbers of CSLDs are Os10g42750 (OsCSLD1), Os06g02180 (OsCSLD2), Os08g25710 (OsCSLD3), Os12g36890 (OsCSLD4), Os06g22980 (OsCSLD5), GRMZM2G015886 (ZmCSLD1), GRMZM2G052149 (ZmCSLD2), GRMZM2G061764 (ZmCSLD3), GRMZM2G044269 (ZmCSLD4), GRMZM2G436299 (ZmCSLD5), At2g33100 (AtCSLD1), At5g16910 (AtCSLD2), At3g03050 (AtCSLD3), At4g38190 (AtCSLD4), At1g02730 (AtCSLD5), At1g32180 (AtCSLD6), XP_003572134.1 (BradiCSLD1), XP_003557145.1 (BradiCSLD2), XP_003573792.1 (BradiCSLD3-1), XP_003573793.1 (BradiCSLD3-2), XP_003575482.1 (BradiCSLD4), XP_003568676.1 (BradiCSLD5).

* *AtCSLD6* is likely a pseudogene.

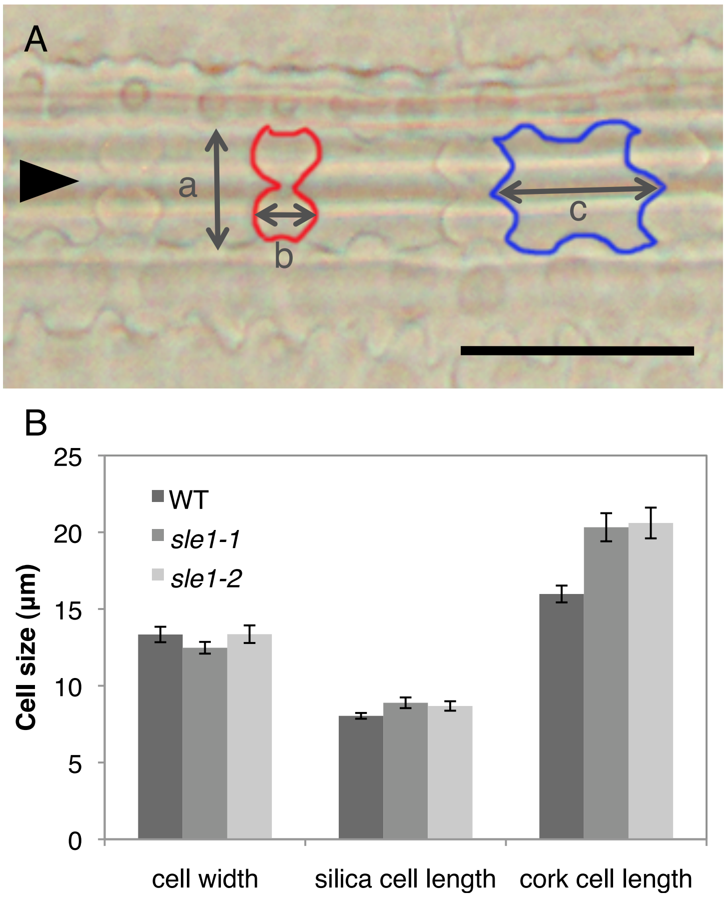

Fig. S2. Comparison of costal cell size in wild type and *sle1*. (A) Cleared image of abaxial surface of wild-type third leaf blade. An arrowhead indicates costal cell line. The representative silica cell and cork cell are outlined in red and blue, respectively. a, b, and c indicate cell width, silica cell length, and cork cell length, respectively. Bar = 25μm. (B) Comparison of costal cell sizes on the abxial surface of third leaf blade in wild type and *sle1-1* and *sle-2*. Vertical bar represent SE (n = 5).

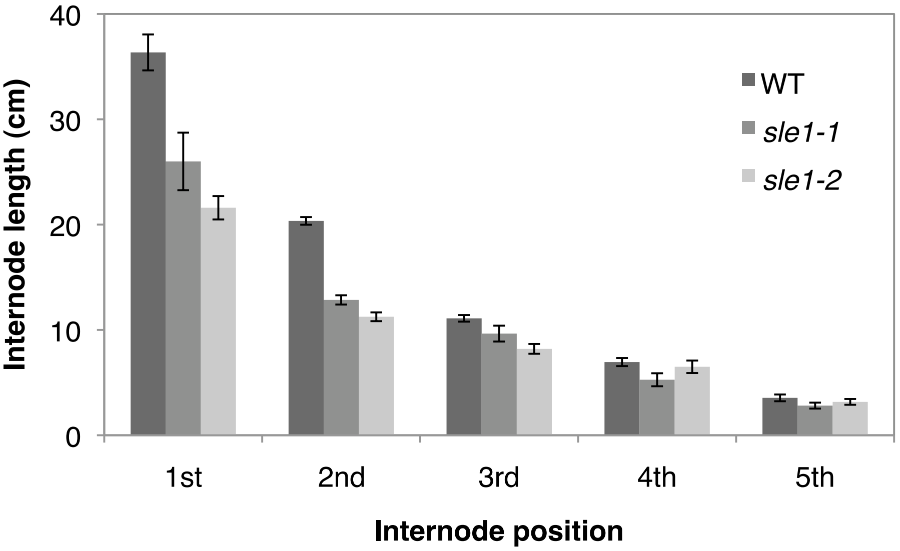

Fig. S3. Internode elongation pattern in wild type, *sle1-1* and *sle1-2* mature plants. Positions of internodes are indicated from the top. Vertical bars represent SE (n = 10).

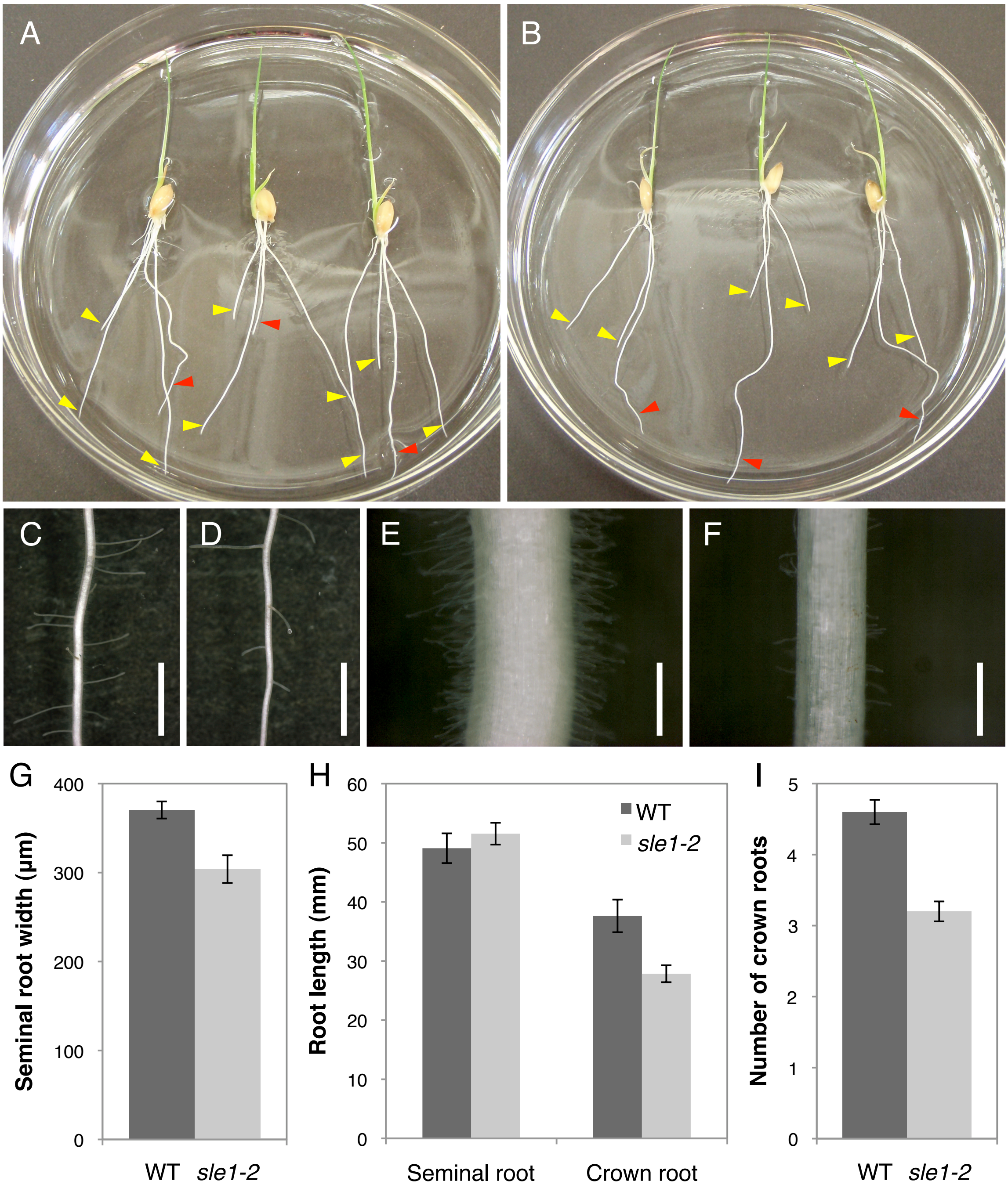

Fig. S4. Root phenotypes of wild type and *sle1* mutant. (A, B) Seven-day-old seedlings of wild type (A) and *sle1-2* (B). While three crown roots are present in wild type, only two crown roots are formed in *sle1-2*. Red and yellow arrowheads indicate seminal and crown roots, respectively. (C, D) Development of lateral roots on the seminal roots of wild type (C) and *sle1-2* (D). (E, F) Development of root hairs on the seminal roots of wild type (E) and *sle1-2* (F). Bars = 3mm (C, D), 300µm (E, F). (G-I) Comparison of seminal root width (G), root length (H), and number of crown roots (I) in 14-day-old seedlings between wild type and *sle1-2*. The length of seminal roots is comparable between wild type and *sle1-2*, but crown roots of sle1 are significantly shorter and fewer than those of wild type. Vertical bars represent SE (n = 10).

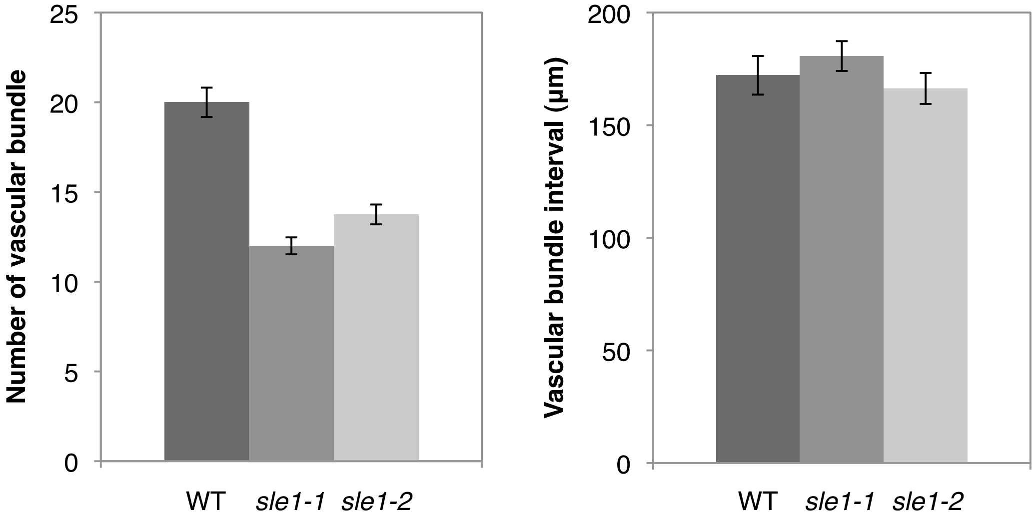

Fig. S5. Comparison of the number of vascular bundles and the vascular bundle interval in the third leaf blade among wild type, *sle1-1*, and *sle1-2*. Vertical bars represent SE (n = 4).

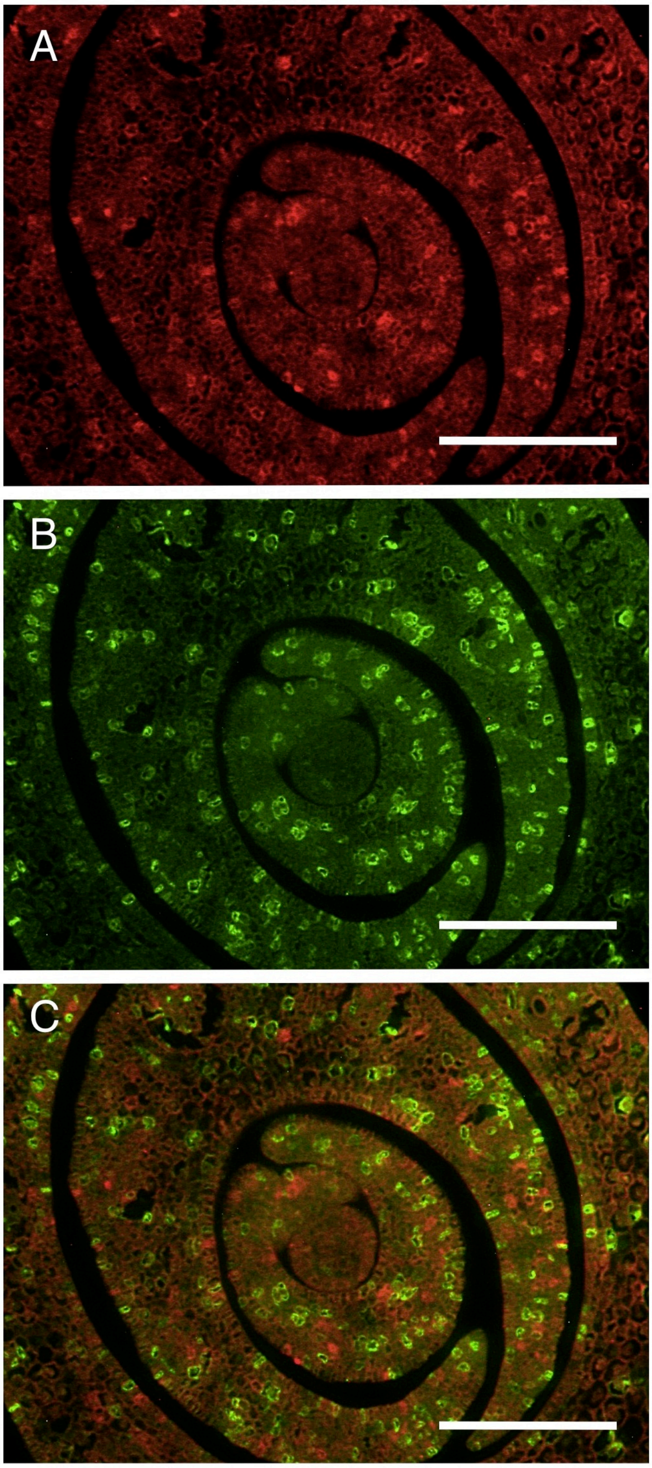

Fig. S6. Double-target *in situ* hybridization of *OsCLSD4/SLE1* counterstained with histone *H4* in a cross section of shoot apex in wild type. Ten-day-old seedling was used. (A) Expression pattern of *OsCSLD4*. (B) Expression pattern of histone *H4*. (C) A merged view of (A–B). Bars = 100µm.

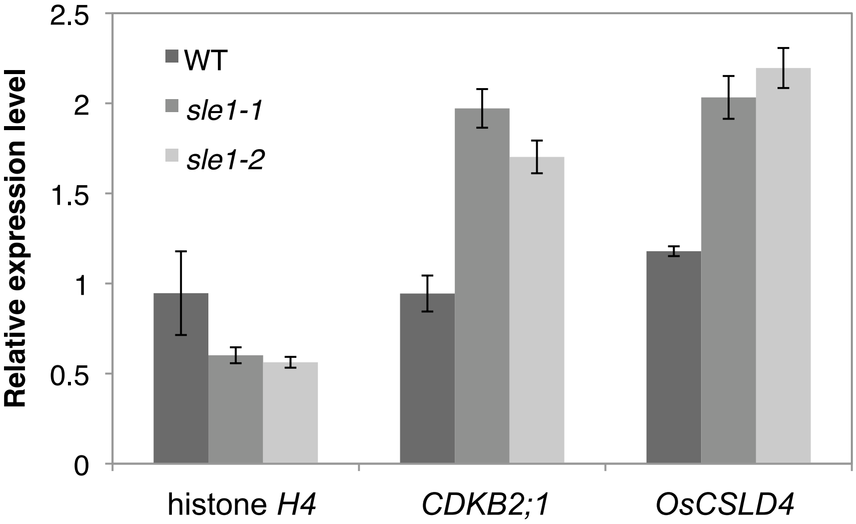

Fig. S7. Real-time PCR analysis of histone *H4*, *CDKB2;1*, and *OsCSLD4* expressions in wild type, *sle1-1* and *sle1-2*. Ten-day-old seedlings were used. The expression levels of histone *H4* and *CDKB2;1* were normalized by that of *UBQ5*, and the expression level of *OsCSLD4* was normalized by that of *eEF-1a*. Vertical bars represent SE (n = 3).

Fig. S8. Expression pattern of *AtCSLD5* in a cross section of *Arabidopsis* shoot apex. Asterisk indicates shoot apical meristem. Bar = 100μm.