



Fig. S1. The epidermal phenotype of *basl +/-* plants and quantification of absolute numbers of stomatal clusters in BASL variant lines.

(A) Confocal image of 5 dpf *BASL +/-* abaxial cotyledon epidermis. Cell outlines are visualized by pATML1::RC12A-mCherry. Braces indicate clustered small cells. This and similar images are the source data quantified in Figure 1 K-L. Scale bar, 10 μ m. (B) Counts of stomatal clusters from which Figure 3D was calculated. P-values are calculated by Student's *t*-test due to small sample sizes. Pairwise p-values comparing individual genotypes to *basl* are presented.

Table S1. Primers used in this study

| Primer name | Sequence (5'-3') |
|--|--|
| <i>Cloning of BASL CDS into pENTR R2-BASL Stop-L3</i> | |
| attB2r-BASL F | GTACAAAGTGGCTATGGCTTCACAGTGG |
| attB3-BASL Stop R | ATAATAAAGTTGTCAGAATCTACAAC |
| attB2r_adapter | GGGGACAACCTTGTATAATAAAGTTG |
| attB3_adapter | CTCTATCACTCACTAAAGAG |
| <i>Cloning of Venus-DBox into pENTR L1-Venus-DBox-L2</i> | |
| DBox part1 BamHI cacc F | CTCAACAATCCACGGATGATGTTGTTGTGG |
| DBox part2 F | CAGGTTTTTTGAGATTATCCTCC |
| DBox part2 R | AAAAAACCTGTAGTCAAGAGAAACGC |
| DBox part3 F | CTTCTCTCGAGCAGCAACTAAACC |
| DBox part3 R | GCUGGUGGATCCATGGTGAGCAAGGGCG |
| BamHI-Venus F | ACCAGCGGATCCCTTGTACAGCTCGTCCATGCC |
| BamHI-Venus w/o Stop R | GTACAAAGTGGCTGGTACCATGGTGAGCAAGGG |
| <i>Cloning of BASL promoter into pENTR L4-pBASL-R1</i> | |
| pBASL F | CCGCGGCCGCGGATATTCATCTTTGCTACACAAGAGTC |
| pBASL R | CGCGGCCGCGGCTGTTATGTTTGTGTTTCTTTGTCAC |
| <i>Cloning of KNOLLE promoter into pENTR L4-pKNOLLE-R1</i> | |
| pKNOLLE F | TGATGATTACCACAAGCTCC |
| pKNOLLE R | CTTTTTCACCTGAAAGTCAAC |
| <i>Direct mutagenesis of DBox into mDBox</i> | |
| Direct mut DBox F | GAAACGGTCAAGTTGTTGGTGA |
| Direct mut DBox R | TCACCAACAACCTTGACCGTTTC |