

**Supplemental Table 1. Confidence levels for statistical differences in genotype-dependent phenotypes**  
 Summary of *p*-values from statistical analyses

| Phenotype            | Non-tagged |             |        |             |                         |             |       |             | 10×Myc-tagged |             |        |             |                         |             |       |             |
|----------------------|------------|-------------|--------|-------------|-------------------------|-------------|-------|-------------|---------------|-------------|--------|-------------|-------------------------|-------------|-------|-------------|
|                      | R25D E248K |             | W109A  |             | Q120R<br>T188K<br>R235E |             | S129R |             | R25D E248K    |             | W109A  |             | Q120R<br>T188K<br>R235E |             | S129R |             |
|                      | WT         | <i>agb1</i> | WT     | <i>agb1</i> | WT                      | <i>agb1</i> | WT    | <i>agb1</i> | WT            | <i>agb1</i> | WT     | <i>agb1</i> | WT                      | <i>agb1</i> | WT    | <i>agb1</i> |
| Hypocotyl length     | <0.001     | 0.092       | 0.027  | 0.002       | <0.001                  | 0.103       | 0.016 | <0.001      | <0.001        | 0.784       | 0.002  | 0.005       | <0.001                  | 0.116       | 0.002 | 0.037       |
| Lateral root density | <0.001     | <0.001      | 0.035  | <0.001      | 0.008                   | 0.019       | 0.845 | <0.001      | 0.005         | <0.001      | <0.001 | <0.001      | <0.001                  | <0.001      | 0.679 | <0.001      |
| Stomatal index       | <0.001     | 0.715       | <0.001 | 0.021       | <0.001                  | 0.682       | 0.754 | <0.001      | <0.001        | 0.863       | <0.001 | 0.025       | <0.001                  | 0.880       | 0.542 | <0.001      |
| Glucose assay        | <0.001     | 0.632       | 0.009  | 0.291       | <0.001                  | 0.810       | 0.007 | 0.070       | <0.001        | 0.553       | 0.007  | 0.224       | <0.001                  | 0.523       | 0.098 | 0.028       |
| ABA Assay            | <0.001     | 0.681       | 0.004  | 0.378       | <0.001                  | 0.325       | 0.276 | 0.003       | 0.004         | 0.427       | 0.046  | 0.044       | 0.013                   | 0.040       | 0.136 | 0.014       |
| <i>F. ox</i> assay   | <0.001     | 0.222       | 0.308  | <0.001      | <0.001                  | 0.293       | 0.015 | <0.001      | <0.001        | 0.004       | 0.110  | <0.001      | <0.001                  | 0.675       | 0.688 | <0.001      |

Statistical analyses were performed as described in ‘Materials and Methods’. Phenotypic parameters of each transgenic line expressing the indicated variant AGB1 (R25D, E248; W109A; Q120R, T188K, R235E; S129R either tagged or not tagged to Myc) were compared to those of WT and *agb1*-2 plants to examine the extent to which a phenotype of *agb1* mutants was rescued. Student *t*-test was adopted for all the phenotypes except ABA responsiveness. The complementation of ABA phenotype was analysed using two-way ANOVA.