Table S1: Quantitative analysis of root development in *xal1-2* and *xal1-3* strong alleles, and their respective wild-type plants.

| Plant line | Rate of root growth (µm h ⁻¹) | Meristem length (µm) | Elongation zone (µm) | Length of fully elongated cells (µm) | Cell cycle duration (h) | Cell production rate (cell h ⁻¹) |
|-----------------------------|---|----------------------------|----------------------------|--------------------------------------|-------------------------------|--|
| Col-0 <i>n</i> =17 | 394±11 | 249±10 | 1086±58 | 164±6 | 10.0±0.3 | 2.4±0.3 |
| xal1-2 n=20 | 134±7 | 139±5 | 548±25 | 120±3 | 12.6±0.9 | 1.1±0.1 |
| Statistics, P | <0.001 | <0.001 | <0.001 | <0.001 | 0.029 | <0.001 |
| | | | | | | |
| L <i>er</i> <i>n</i> =20 | 313±7 | 254±6 | 1231±29 | 169±3 | 14.2±0.5 | 1.9±0.04 |
| xal1-3 n=20 | 187±6 | 198±7 | 1312±33 | 160±3 | 16.9±0.8 | 1.2±0.04 |
| Statistics, P | <0.001 | <0.001 | 0.072 | 0.064 | 0.009 | <0.001 |

Mean±SE. As the number of replicates was unequal for Col-0 and *xal1-2*, the *P* was calculated using Mann-Whitney Rank Sum Test; statistical analysis of Ler and *xal1-3* was done using Student's independent *t* test; *n* indicates the number of plants analyzed of two independent experiments. Length of fully elongated cells was calculated as average of averages per each root; in each root 10 cortical cells were measured in young differentiated zone.