Figure S1: GWAS planting model. a) seven-day-old seedlings distribution from two different accessions after *R. solanacearum* infection. Twelve seeds per accession were sow, distributed between two MS medium (six seeds per MS- plate). **b)** BRAT software.
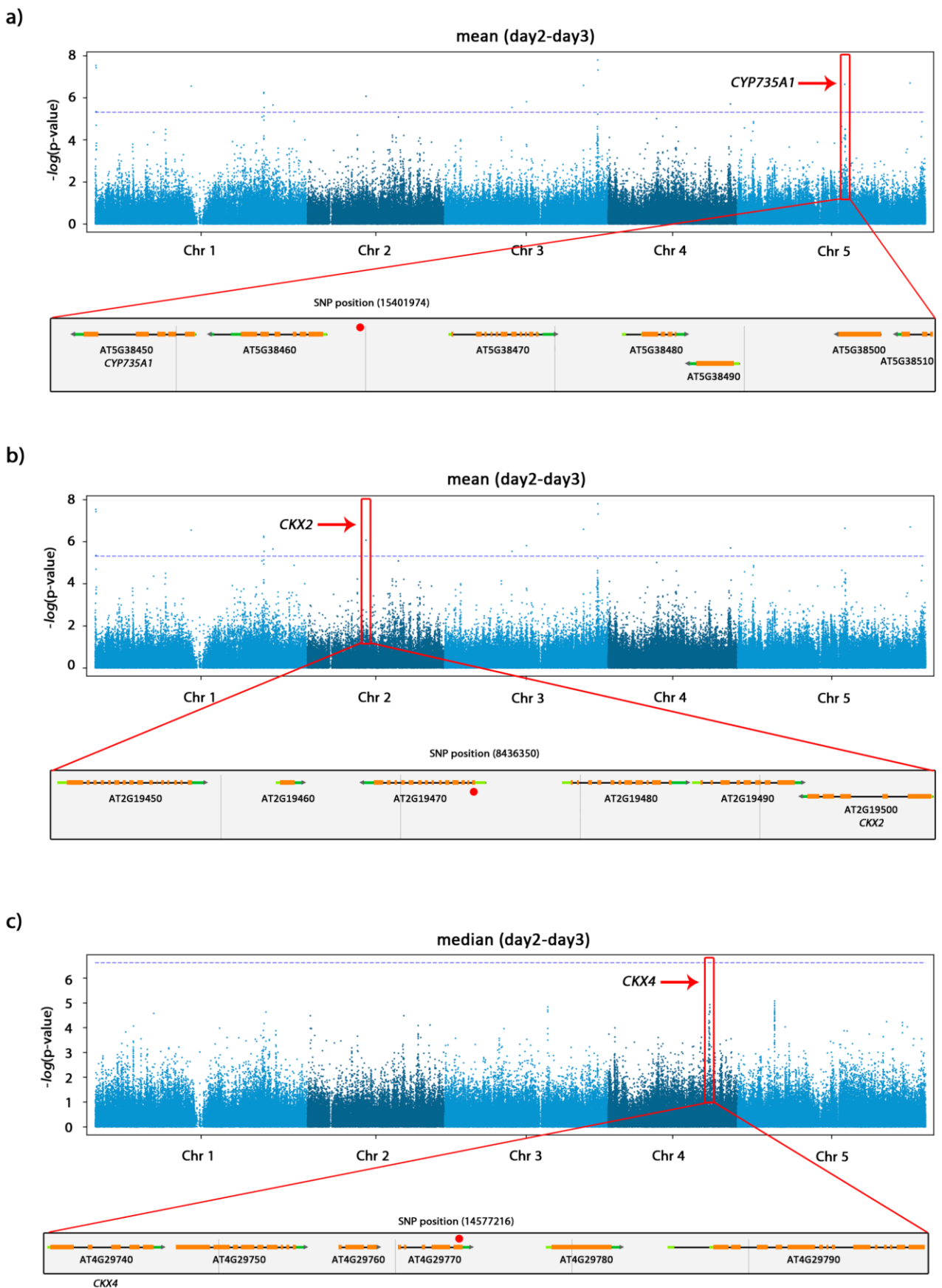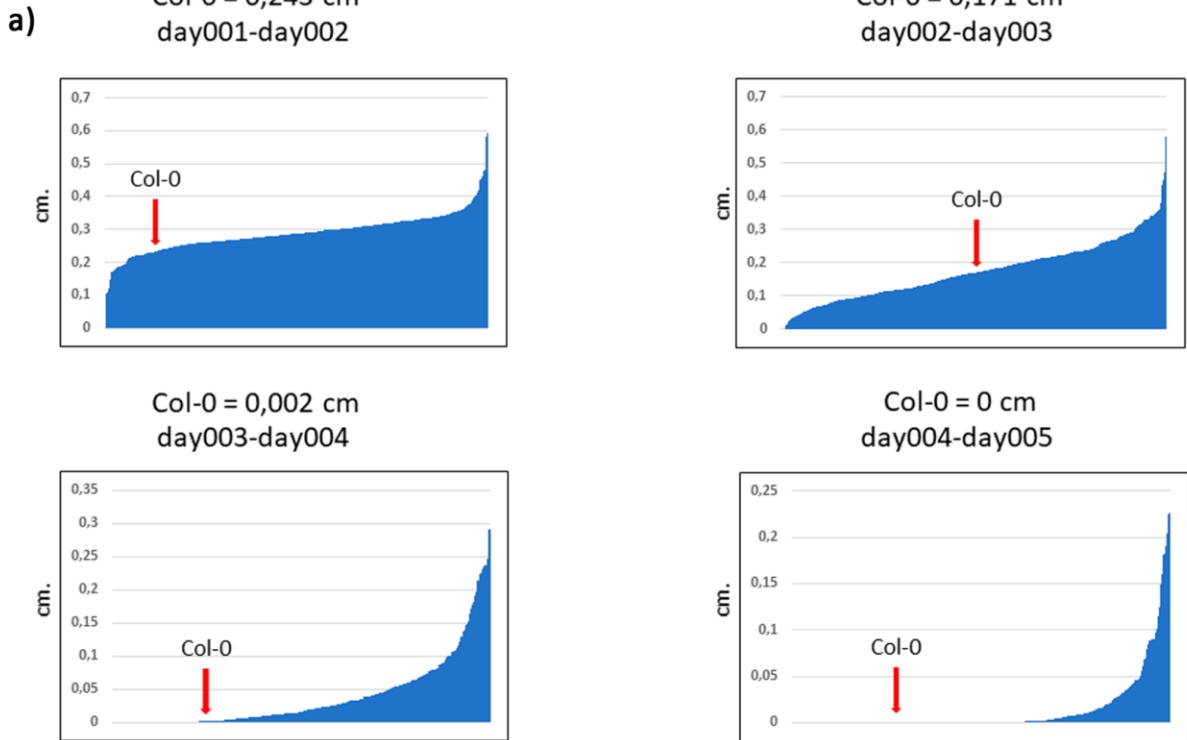
Figure S2: Zoom in SNP position. a) SNP 15401974 on mean relative root growth rate (day2-day3), and b) SNP 8436350 on mean relative root growth rate (day2-day3) and SNP 14577216 on median relative root growth rate (day2-day3).
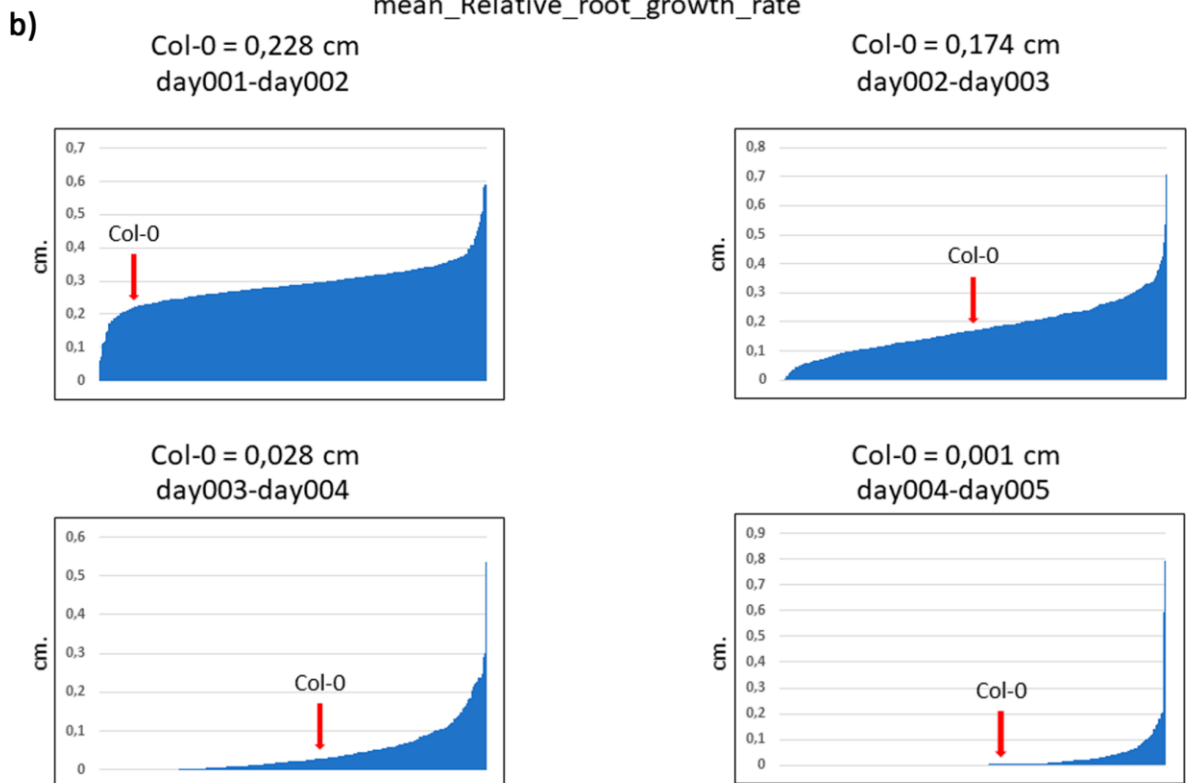
Figure S3: Col-0 ecotype distribution based on root growth after *Ralstonia sola-nacearum* infection. a) median relative root growth rate and b) mean relative root growth rate.
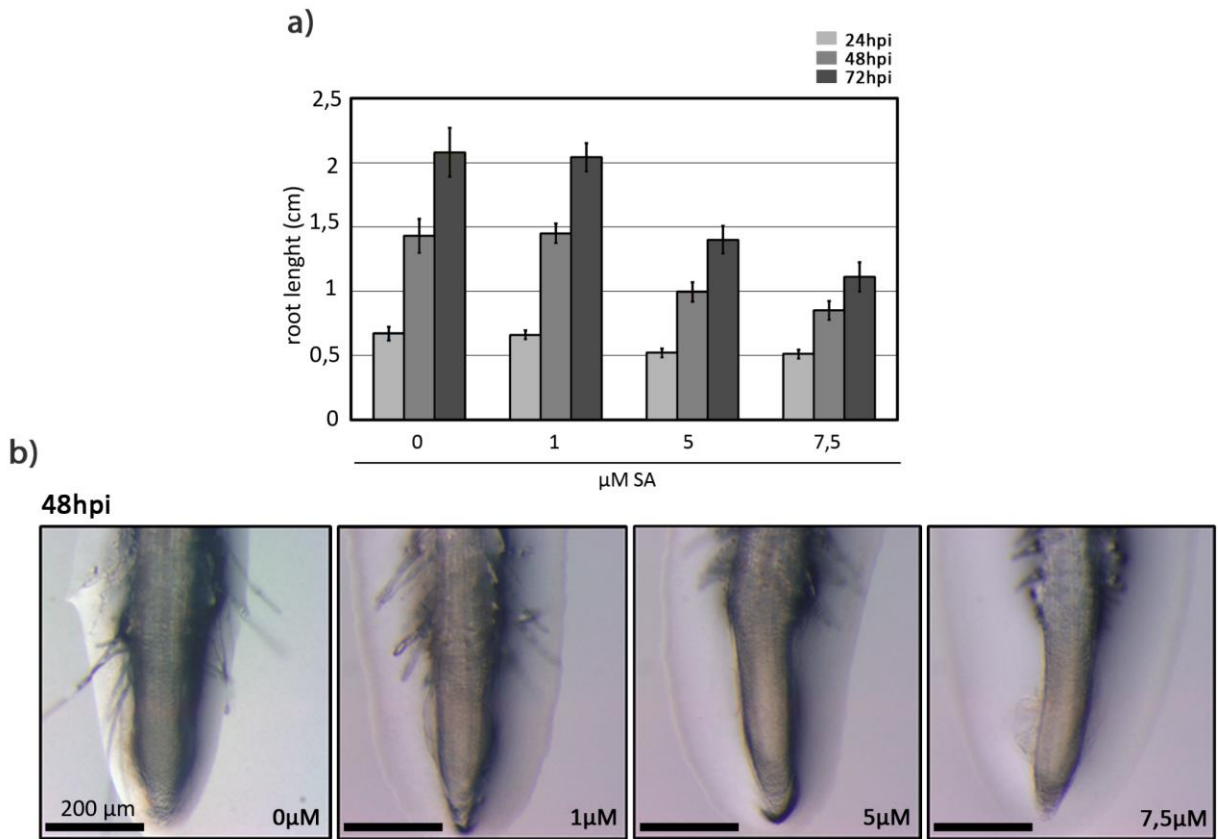
a)

Legend: 24hpi, 48hpi, 72hpi

Y-axis: root lenght (cm)

X-axis: µM SA — 0, 1, 5, 7,5

b)

48hpi

200 µm — 0µM — 1µM — 5µM — 7,5µM

Figure S4: Role of SA in *R. solanacearum* infection. Seven-day-old Col-0. Seedlings were grown for 24 hours in MS medium supplemented with SA (0, 1, 5 and 7,5µM) and were inoculated with *R. solanacearum* or water; a) root lenght was measured in water control and b) root hair production under *R. solanacearum* infection at 48hpi.

Figure S5: Disease index scale of Arabidopsis plants after *R. solanacearum* infection. A disease index scale was calculated based on symptoms ranging from 0 – 4, where 0 = no symptoms to 4 = completely wilted plant. Pictures were taken from the top (top) or side (bottom) of the jiffys at different d.p.i., when plants showed the specified symptoms showed on top.