Figure S1. *S. sclerotiorum* **lesion size and** *AB3* **transcript abundance in individual T2 generation AT1703 lines.** A) Sample size of n = 15 leaves per line were measured using ImageJ software and normalized to wild-type Col-0 leaves for lesion measurements. B) Target transcript abundance calculated using the $\Delta\Delta CT$ method with Sac7 as a reference gene. Each line consists of 3 biological replicates, each containing three infected *A. thaliana* leaves. Error bars represent standard error and significance was determined using a student's t-test ($p < 0.05$). * = significance.