



Figure S7 | Genomic alignment of accessions in relation to HopAM1-induced cell death response near the most significant SNP. A. *thaliana* sequence differences are shown spanning a 30 kb region on chromosome 3 from 6870000 to 6900000 bp, covering the area around the most significant SNP hit at 6879376 bp (shown by a yellow arrow). Sequence differences are based on comparison of each accession with the Col-0 reference genome. The accessions are aligned from top to bottom based on their phenotypic score for HopAM1-induced cell death (color code 5-4-3-2-1-0 = Red-Yellow-Green-Blue-White-Pink). Statistical significance for correlation between phenotypic scores and haplotype structure (absence of the three transposable elements: At2g15800, At2g15810 and At2g15815) was based on a type II ANOVA test (p -value = 0.002). High resolution image available as a supplemental file.