



Figure S9 | Genomic alignment of accessions in relation to HopAM1-induced chlorosis near the most significant SNP. *A. thaliana* sequence differences are shown spanning a 30 kb region from 6140000 to 6170000, covering the area around the most significant SNP hit at 6150479 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 chlorosis (color code “0” = dark green/non-chlorotic, “1” = yellow/chlorotic). Statistical significance for correlation between phenotypic scores and haplotype structure (presence of multiple SNPs within At3g17970) was based on a type II ANOVA test (p -value = 0.015). High resolution image available as a supplemental file.