

# **Analysing the genetic architecture of clubroot resistance variation in *Brassica napus* by Associative Transcriptomics**

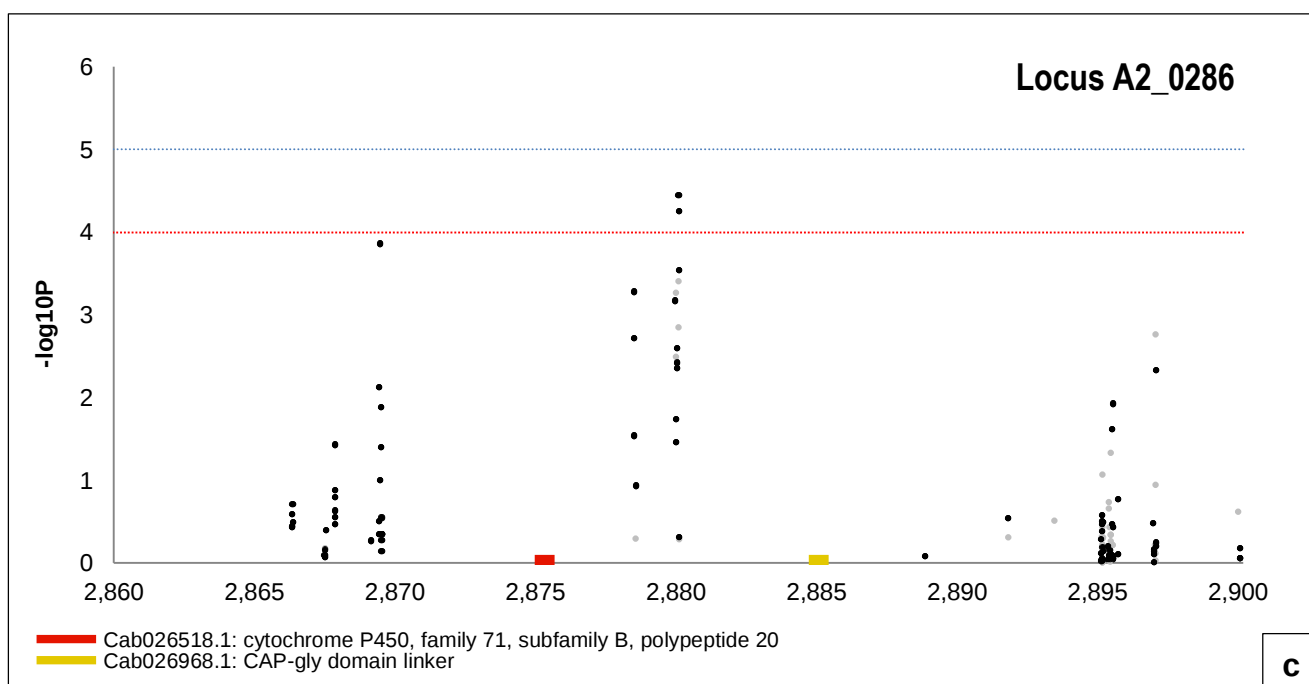
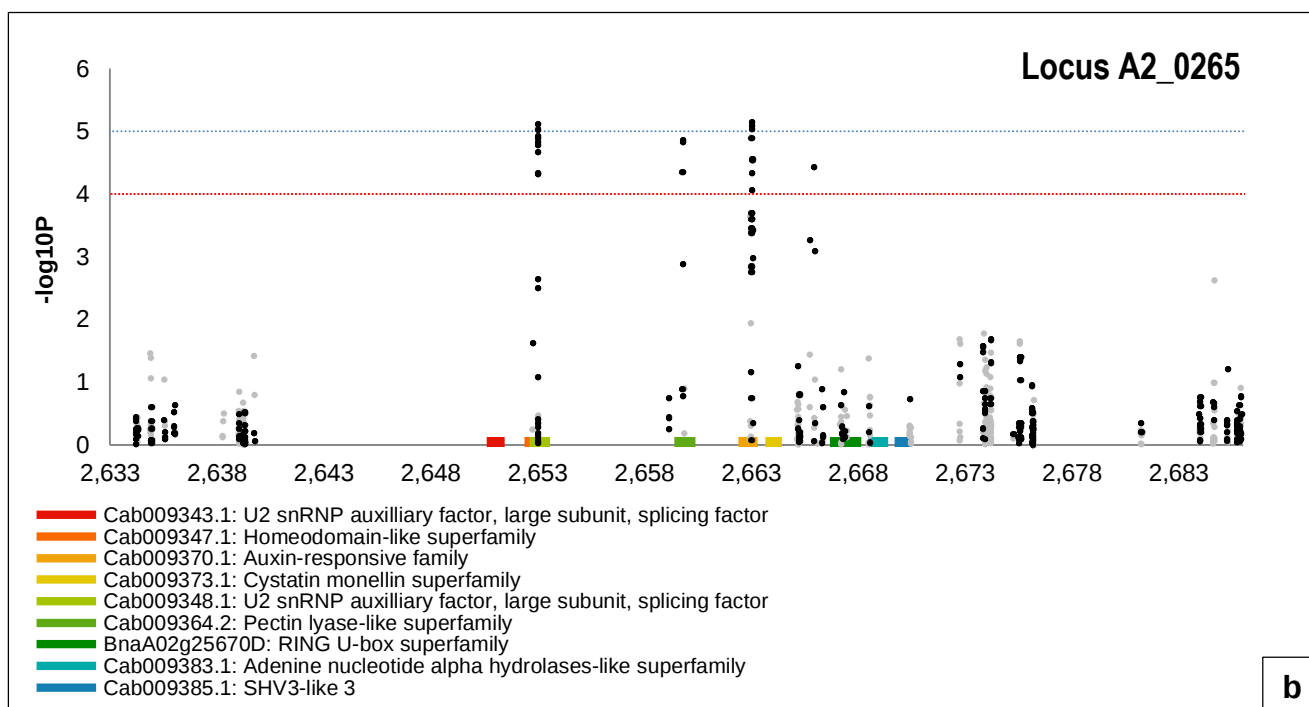
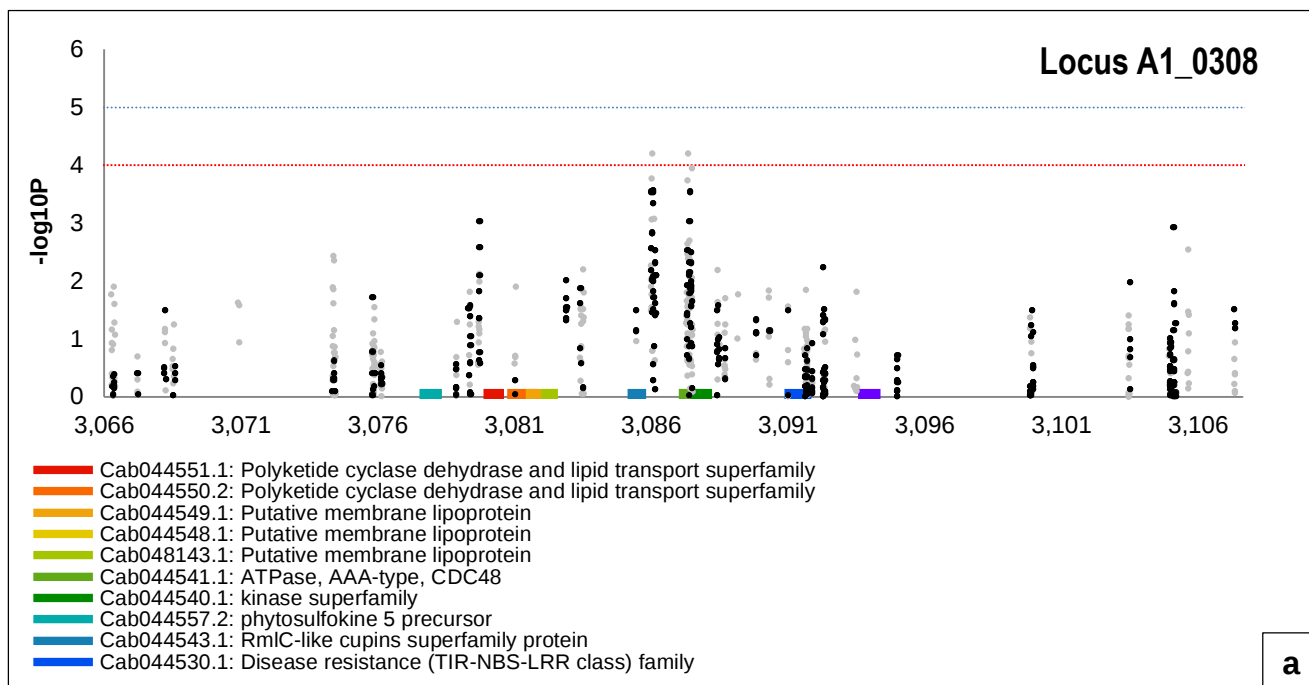
Molecular Breeding

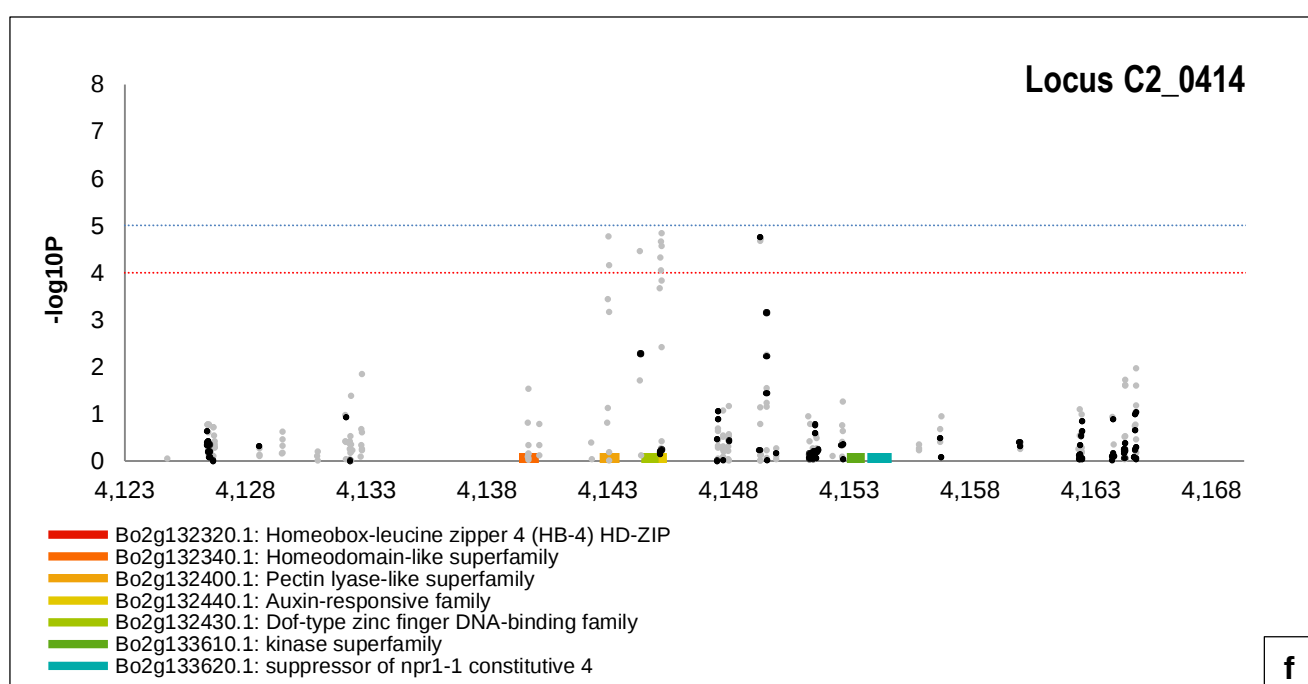
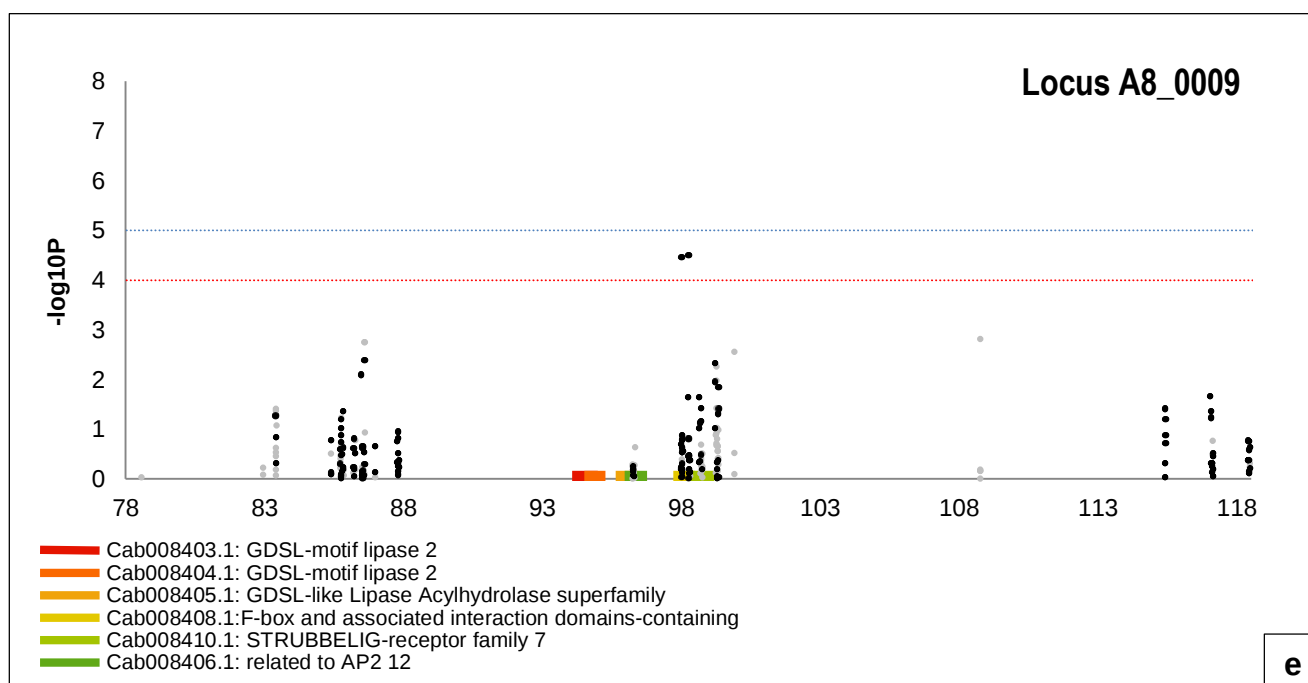
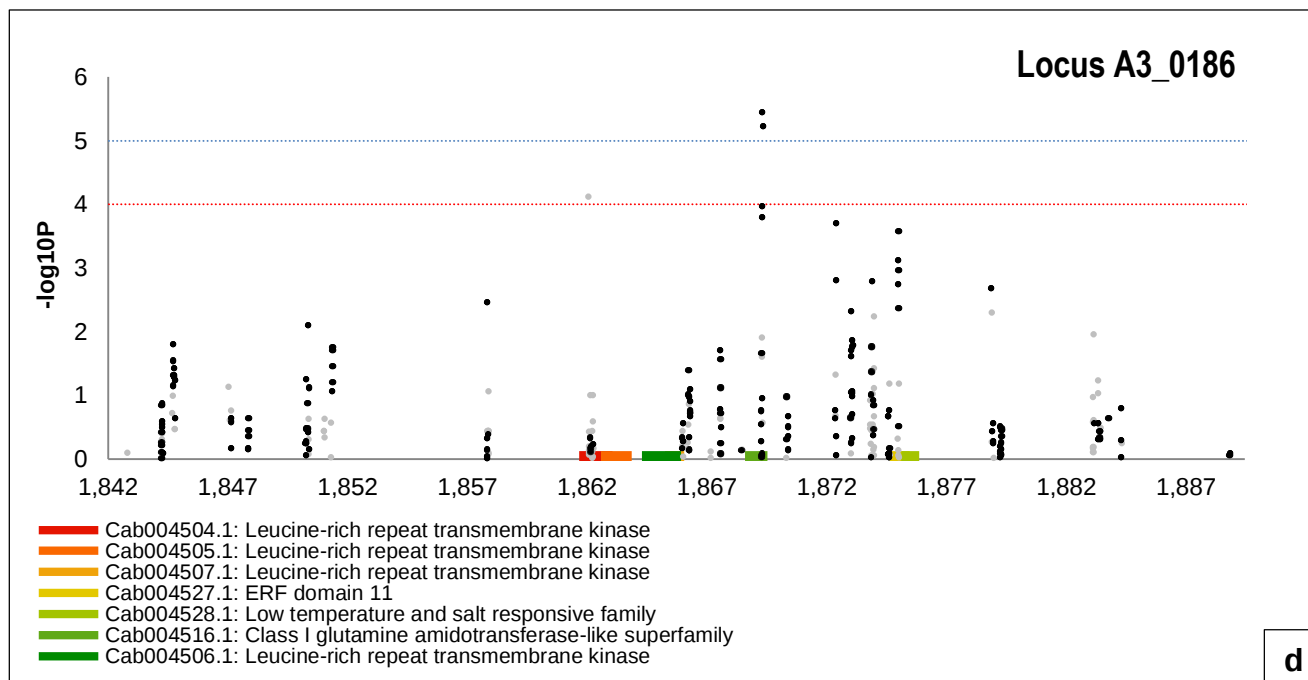
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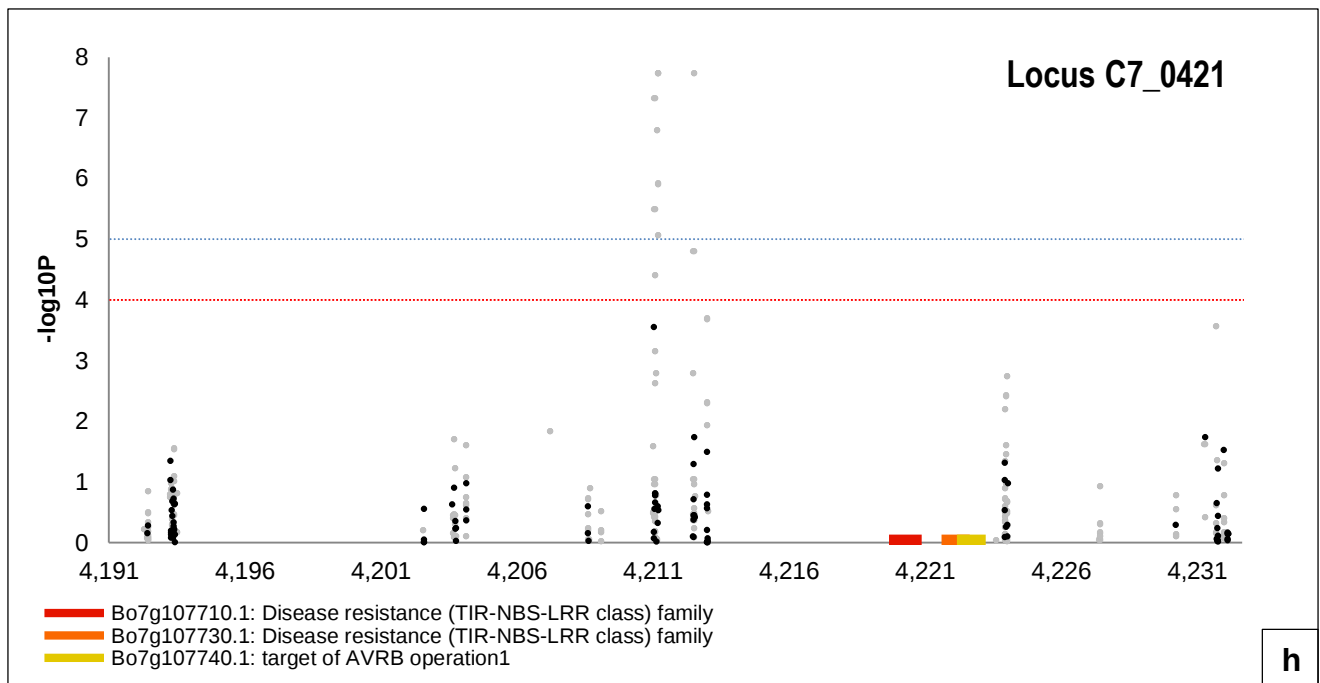
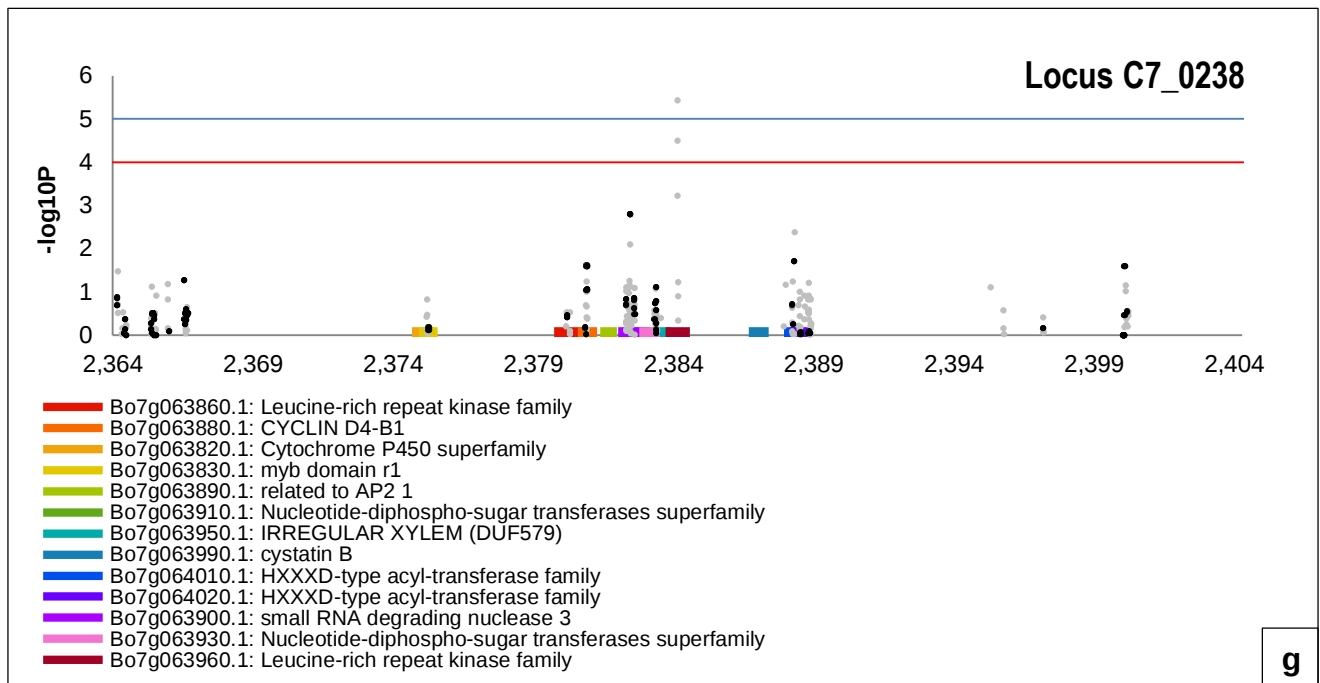
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Supplemental Figure 3. SNP association analysis for clubroot resistance focus on the parts of pseudomolecule with clubroot protentional loci ( $5 > -\log_{10}P > 4$ ) **a** - BnA01\_0308, **c** - BnA02\_0286, **e** - BnA08\_0009, **f** - BnC02\_0414 and significant loci ( $-\log_{10}P > 5$ ) **b** - BnA02\_0265, **d** - BnA03\_0186, **g** - BnC07\_0238, **h** - BnC07\_0421. The SNPs are positioned on the x-axis based on their location (units  $10^5$ ), the positions of the candidate genes for this locus are further indicated on x-axis for each loci. On the y-axis are values of the trait association significance ( $-\log_{10}P$ ). The black signs represent simple SNPs and grey hemi-SNPs. The dashed blue and red lines mark significance  $-\log_{10}P = 5$  and  $-\log_{10}P = 4$ , respectively.