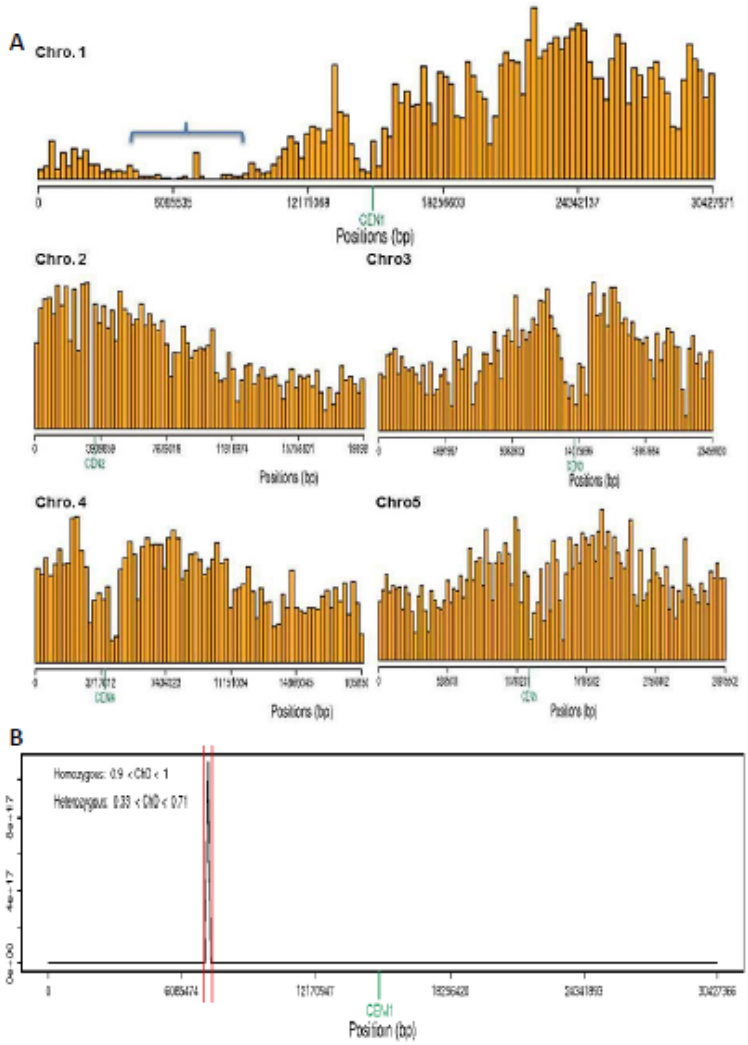

S2 Figure. Genome-wide SNP frequencies in a *cäö* F2 mapping population. (A) SNPs frequencies in sequencing reads were plotted along each chromosome using a bin size of 250 kb. SNPs are caused by reads from the L*er* accession, which was crossed with the *cäö* mutant in Col. A non-recombinant region on the left arm of chromosome 1 with very few L*er* reads is indicated by a brace. Chro., abbreviation for Chromosome. Histograms were generated by the Next-generation mapping tool (Austin et al., 2011). (B) SNP localization by the Next-Generation Mapping web application. Screenshot of the final stage of region selection and SNP annotation. The sharp delimited peak, at position 7307231 corresponds to the position of a mutation in *AT1G20960*.

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