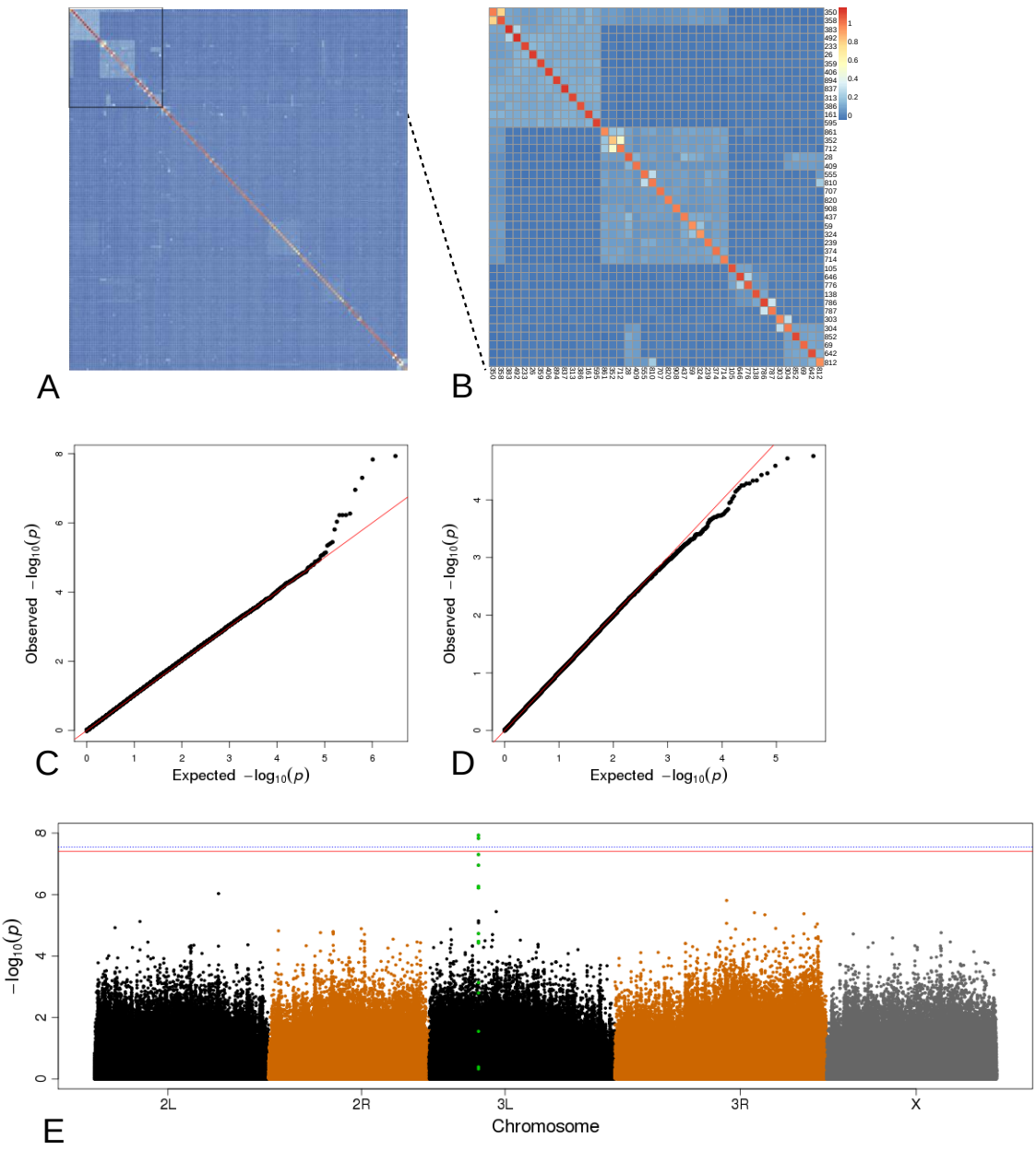

Figure S4 Mixed linear model regression accounting for cryptic relatedness. (A) The heat map shows a 154 x 154 matrix representing the centered genetic relatedness matrix (GRM) estimated using EMMAX. The boxed area is shown in detail in (B), with their line ID (RAL#) indicated on the right and bottom. The GRM was used in a mixed linear model to perform genome wide association in the 154 lines. And the resulting p-values for autosomal and X-linked variants are plotted as Q-Q plot in (C) and (D), with the red line indicating matches between the data and the null (uniform) p-value distribution. (E) Manhattan plot showing the –log10 p-values against the chromosomal coordinates. No association is expected on the X chromosome. The blue dotted line indicates a Bonferroni corrected $P < 0.05$, while the red solid line indicates a 5% genome-wide significant level based on 500 permutations.