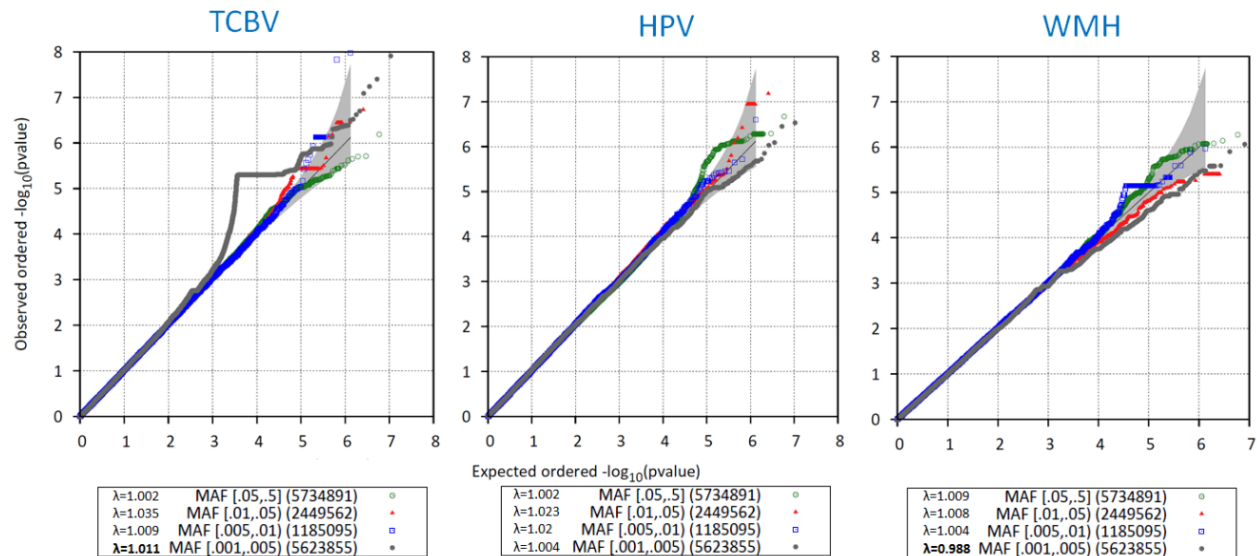


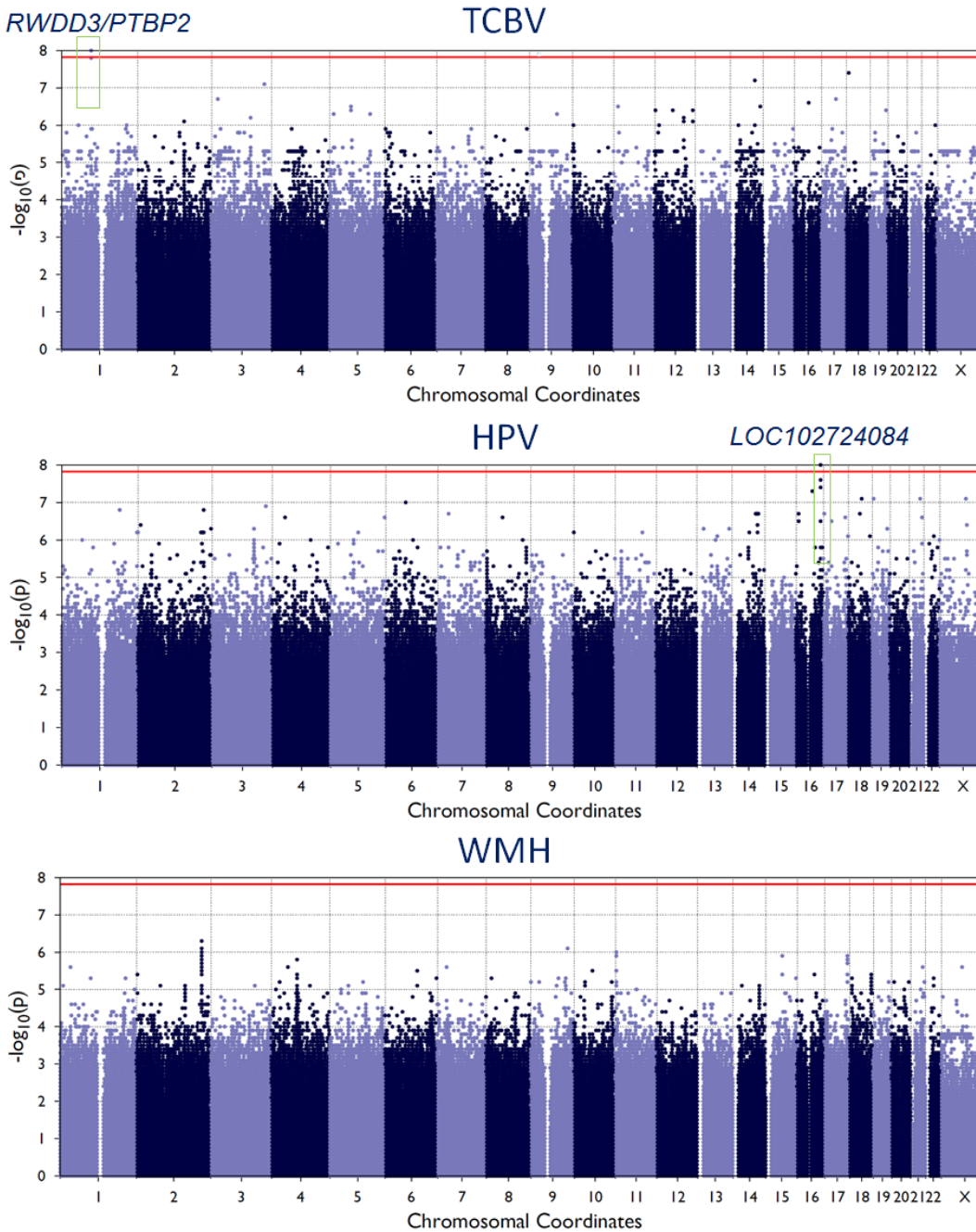
**Figure e-1:** Quantile-Quantile plots of association Pvalues of the WGS association

analyses of TCBV, HPV &amp; WMH.



The dots represent the distribution of observed ordered  $-\log_{10}(\text{Pvalues})$  against the theoretical model distribution of expected ordered  $-\log_{10}(\text{Pvalues})$ . The solid black line represents the theoretical model distribution of expected  $-\log_{10}(\text{Pvalues})$  under the null distribution.

**Figure e-2:** Manhattan plots showing association Pvalues of the WGS association analyses of TCBV, HPV & WMH.



The  $-\log_{10}(P\text{value})$  for each SNV on the y-axis is plotted against the genomic position on the x-axis. The solid red line indicates the genome-wide significance threshold of  $P = 1.5 \times 10^{-8}$ .

**Figure e-3:** Regional association plots for the 10 top gene-based test results.

