

**SUPPLEMENTARY FIGURES OF THE MANUSCRIPT
“WAVELET-BASED GENETIC ASSOCIATION ANALYSIS
OF FUNCTIONAL PHENOTYPES ARISING FROM
HIGH-THROUGHPUT SEQUENCING ASSAYS”**

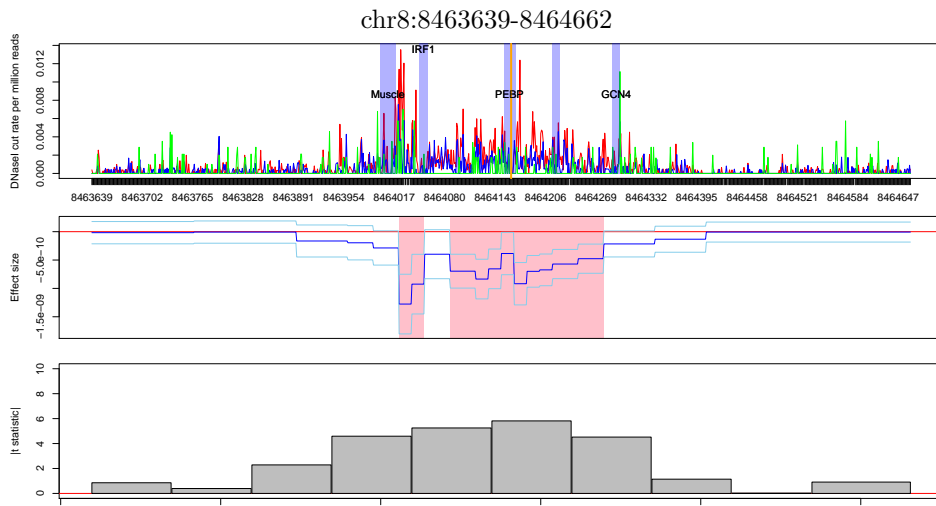


FIG 1. **Example of typical dsQTL found by both methods.** Labels and colors are as in Figure 2 of the main text. The most strongly associated SNP: chr8.8462948 with MAF of 0.29. For wavelet-based approach $\log \hat{\Lambda}_{max} = 39.89$; $p < 0.00001$. For window-based approach $p < 0.0001$. The orange line indicates the position of genetic variant that are in high linkage disequilibrium with chr8.8462948 ($r^2 > 0.99$).

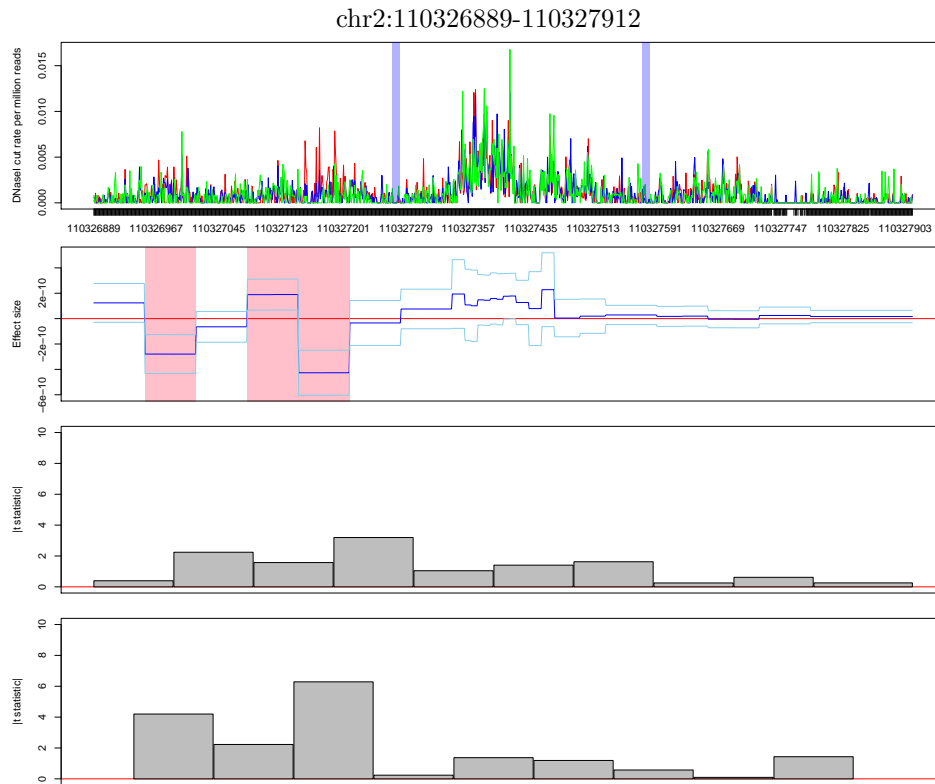


FIG 2. Example of dsQTL showing complex pattern of association with DNase I cut rates. Labels and colors are as in Figure 2 of the main text. The bottom figure shows absolute value of t -statistic for each 50bp-shifted 100bp window. $p < 0.00001$ (wavelet-based approach and 100bp window approach with 50bp shift) 0.23 (100bp window approach)