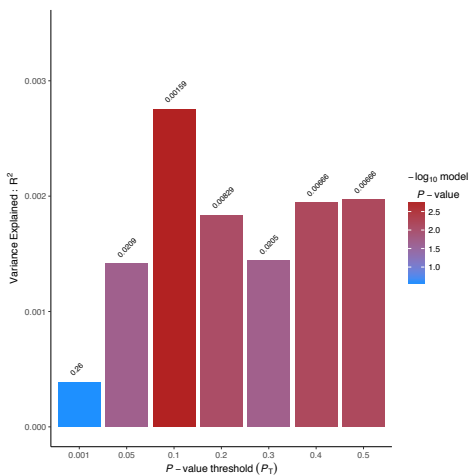
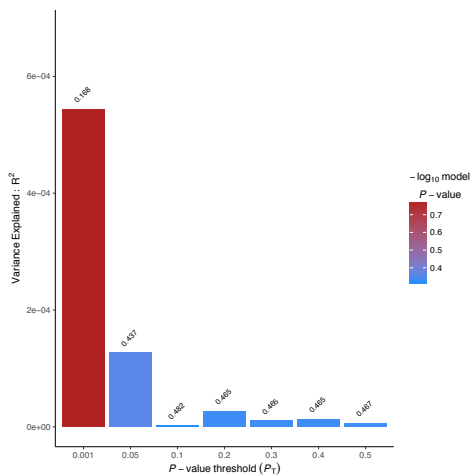
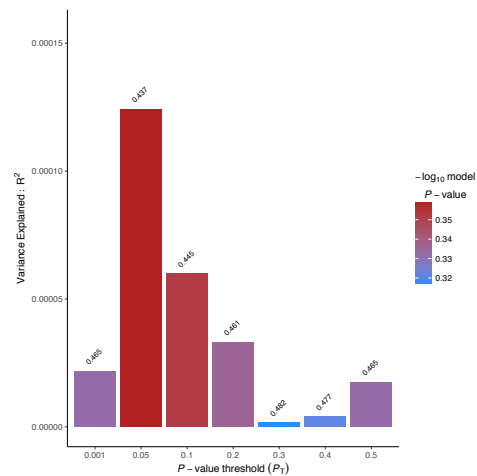
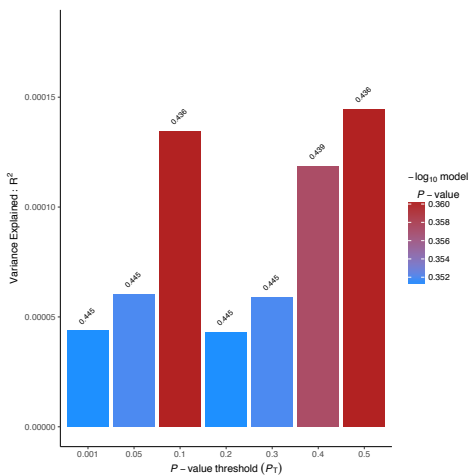
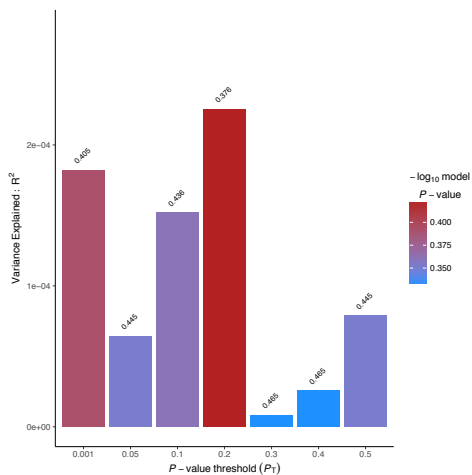


a Type 2 Diabetes**b HbA1c****c Fasting Insulin****d Fasting Glucose****e 2 h Glucose**

Supplementary Figure 5C. Bar plots from PRSice showing results at seven broad P -value thresholds (P_T) for shared genetic etiology between five peripheral insulin signaling-related traits (Type 2 Diabetes, HbA1c blood levels and blood levels of fasting insulin, fasting glucose and 2h Glucose) and TOCS factor 'contamination/cleaning' (a–e) (see Methods). The numbers above the bars indicate the P -values for shared genetic etiology, and these P -values were corrected using the Benjamini-Hochberg false discovery rate method.