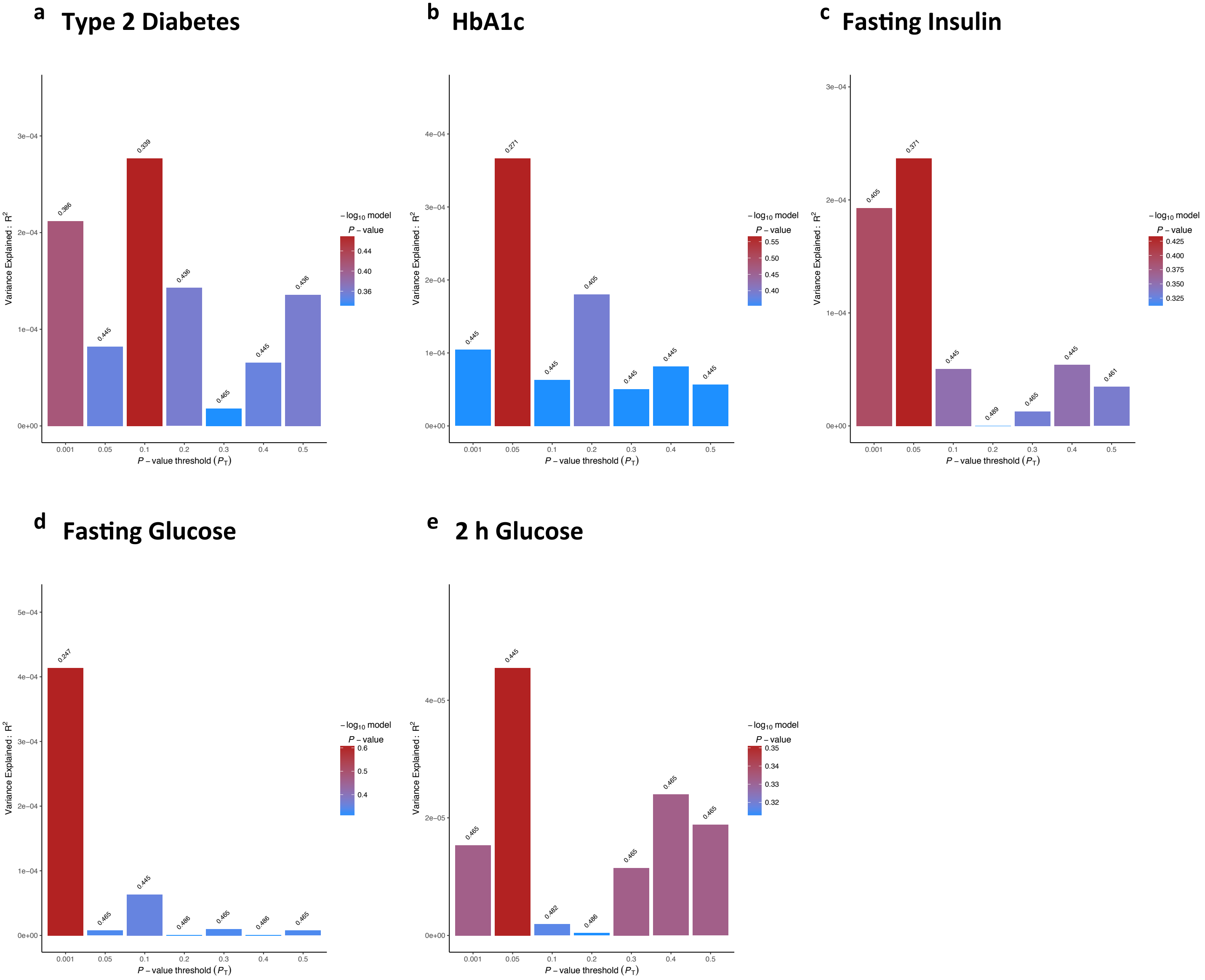

Supplementary Figure 5B. Bar plots from PRSice showing results at seven broad P-value thresholds (P_T) for shared genetic etiology between five peripheral insulin signaling-related traits (Type 2 Diabetes, HbA1C blood levels and blood levels of fasting insulin, fasting glucose and 2h Glucose) and TOCS factor 'symmetry/counting/ordering' (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.