

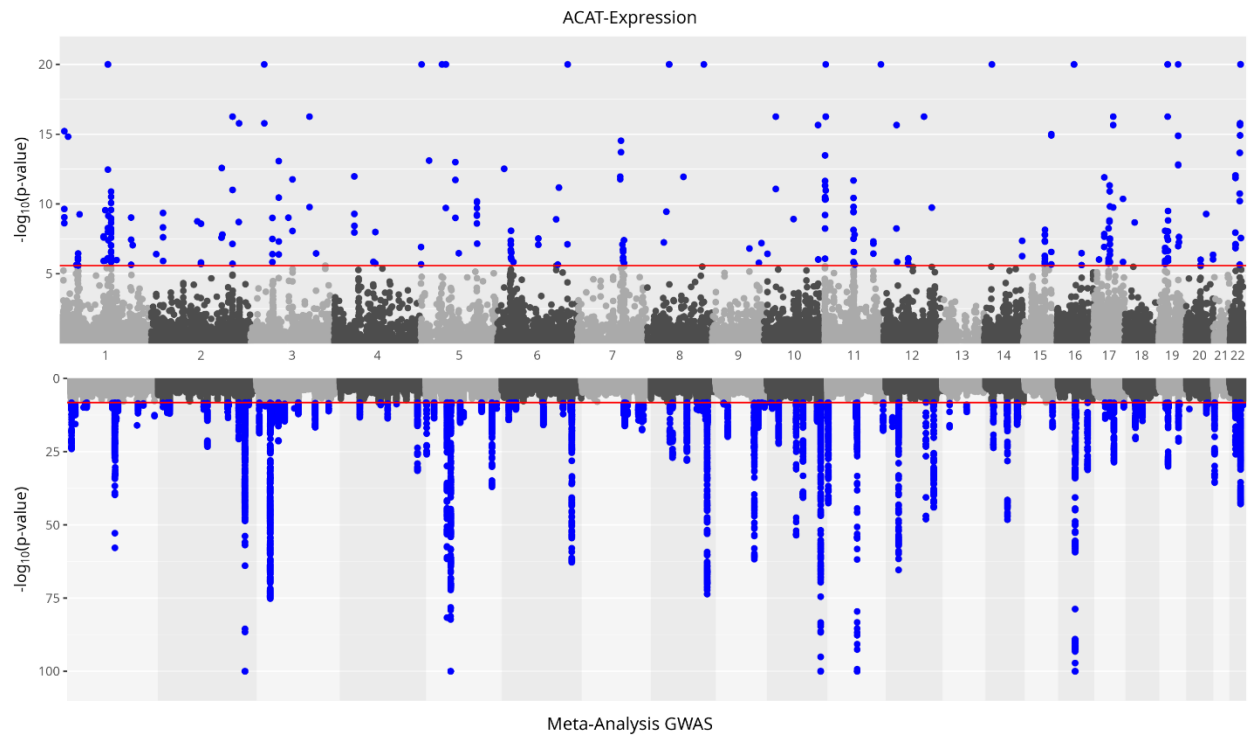
The American Journal of Human Genetics, Volume 110

Supplemental information

**A joint transcriptome-wide association study
across multiple tissues identifies candidate
breast cancer susceptibility genes**

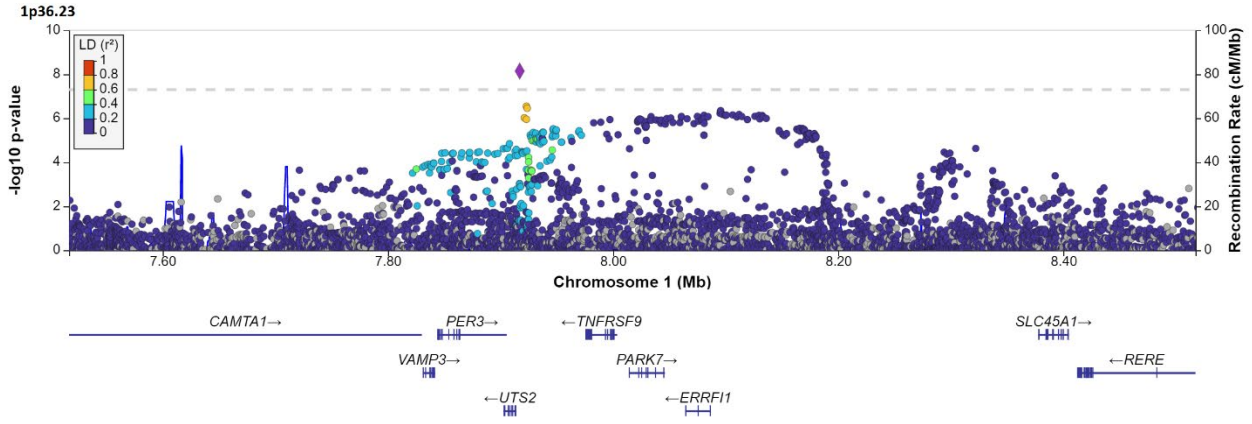
Guimin Gao, Peter N. Fiorica, Julian McClellan, Alvaro N. Barbeira, James L. Li, Olufunmilayo I. Olopade, Hae Kyung Im, and Dezheng Huo

Supplementary Figure S1. Manhattan plots of joint transcriptome-wide association study (TWAS) and genome-wide association study (GWAS). The dots in the top panel show $-\log_{10} p$ values for genes calculated using the aggregated Cauchy association test. The dots in the bottom panel show $-\log_{10} p$ values for variants calculated using logistic regressions. $-\log_{10} p$ values were capped at 20 and 100 for the TWAS and GWAS, respectively.

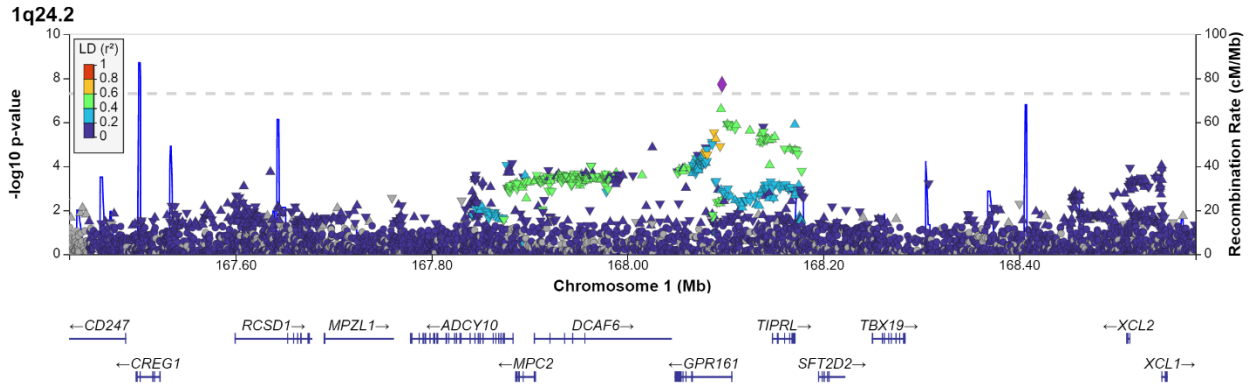


Supplementary Figure S2. LocusZoom plots of eight novel GWAS loci

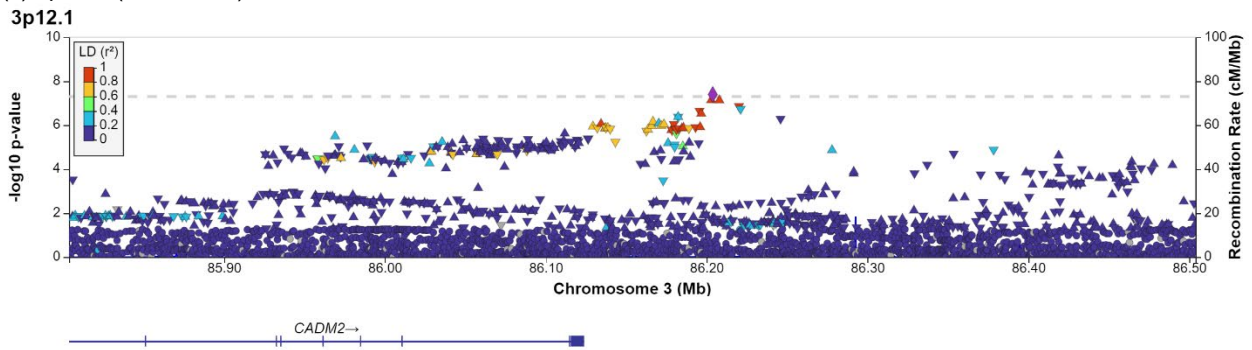
(a) 1p36.23 (rs707475)



(b) 1q24.2 (rs60504827)

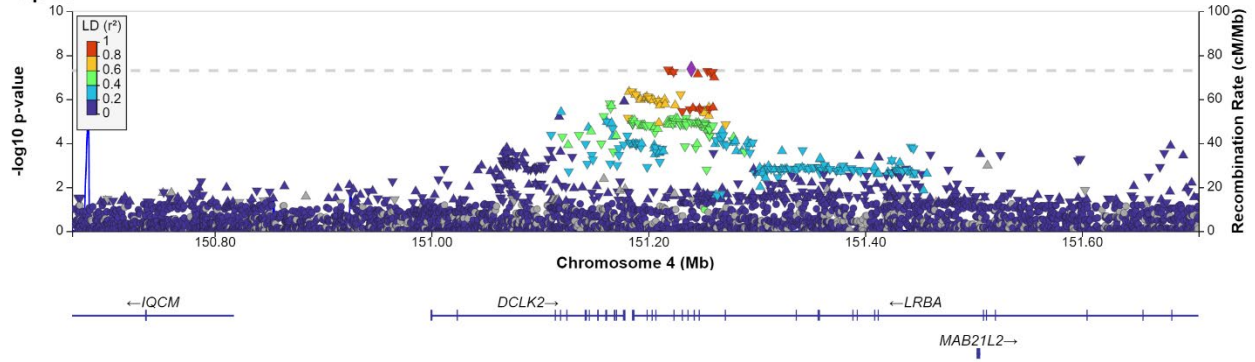


(c) 3p12.1 (rs9833726)



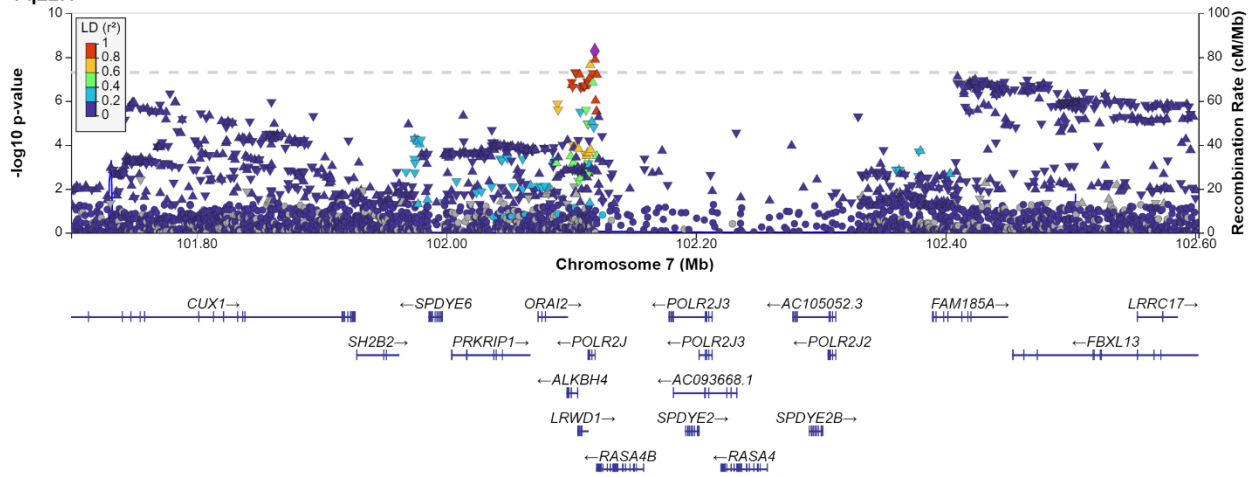
(d) 4q31.3 (rs35016840)

4q31.3



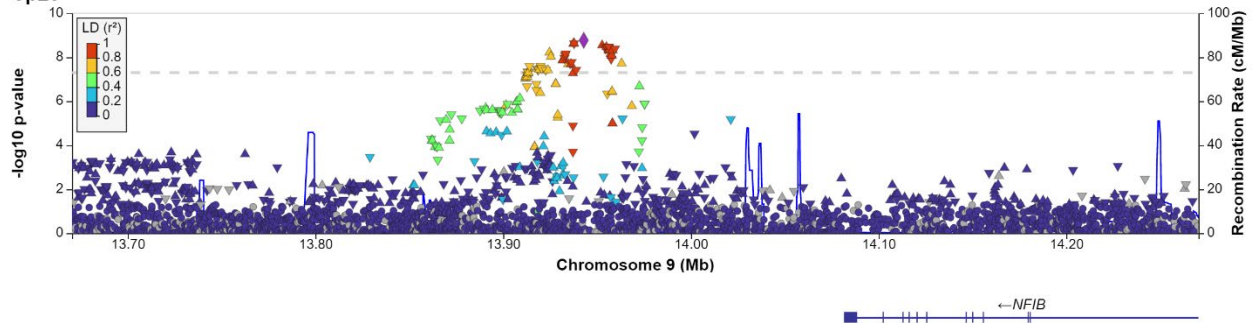
(e) 7q22.1 (rs62483813)

7q22.1



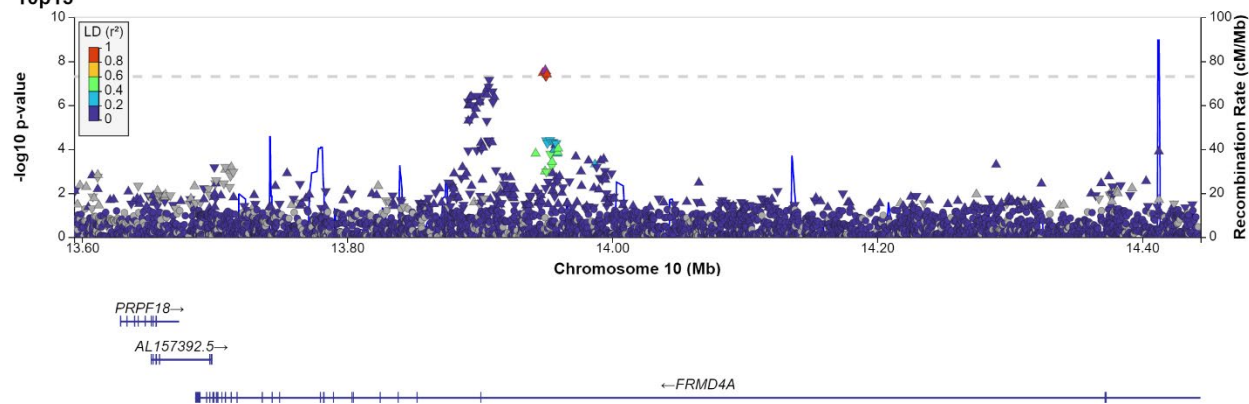
(f) 9p23 (rs77457752)

9p23



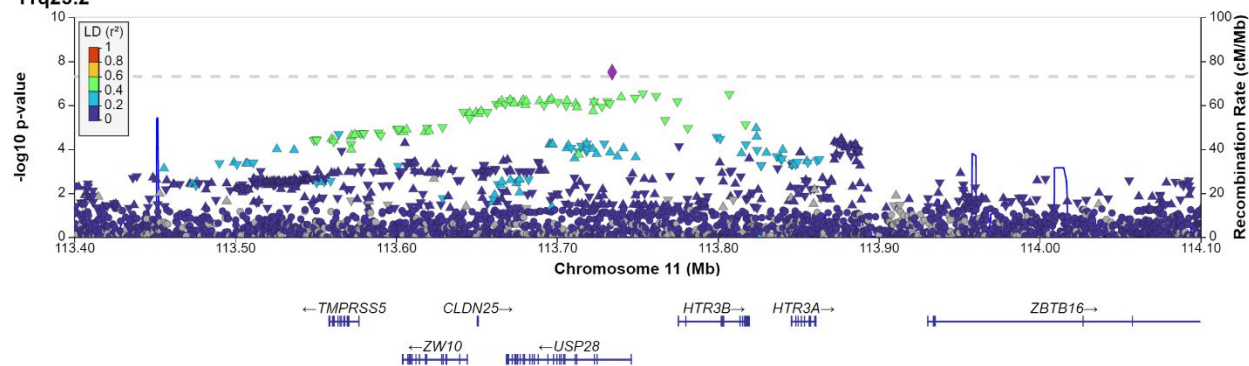
(g) 10p13 (rs3235)

10p13

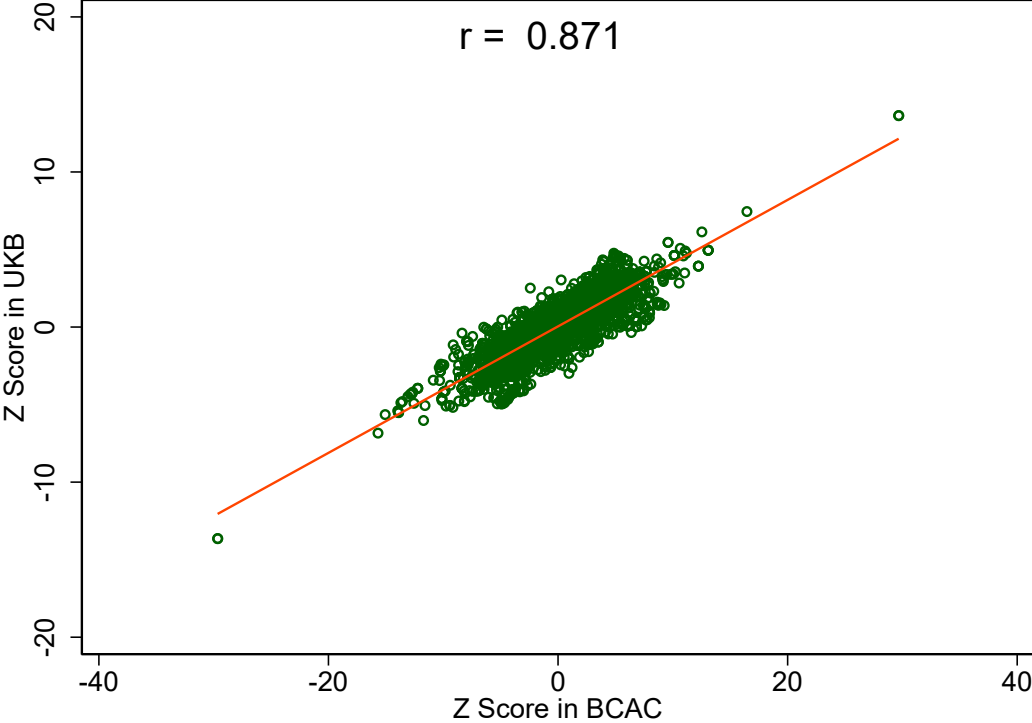


(h) 11q23.2 (rs71063528)

11q23.2



Supplementary Figure S3. Scatter plot of Z scores from tissue-specific TWAS in Breast Cancer Association Consortium (BCAC) and UK Biobank (UKB) datasets



Supplementary Figure S4. Differential analysis of expression of the joint TWAS-identified genes in GTEx v8 shows tissue specificity. Significantly enriched differentially expressed gene sets (Bonferoni adjusted $p < 0.05$) are highlighted in red.

