

Supplementary Material

Identifying Therapeutic Targets for Breast Cancer: Insights from Systematic Mendelian Randomization Analysis

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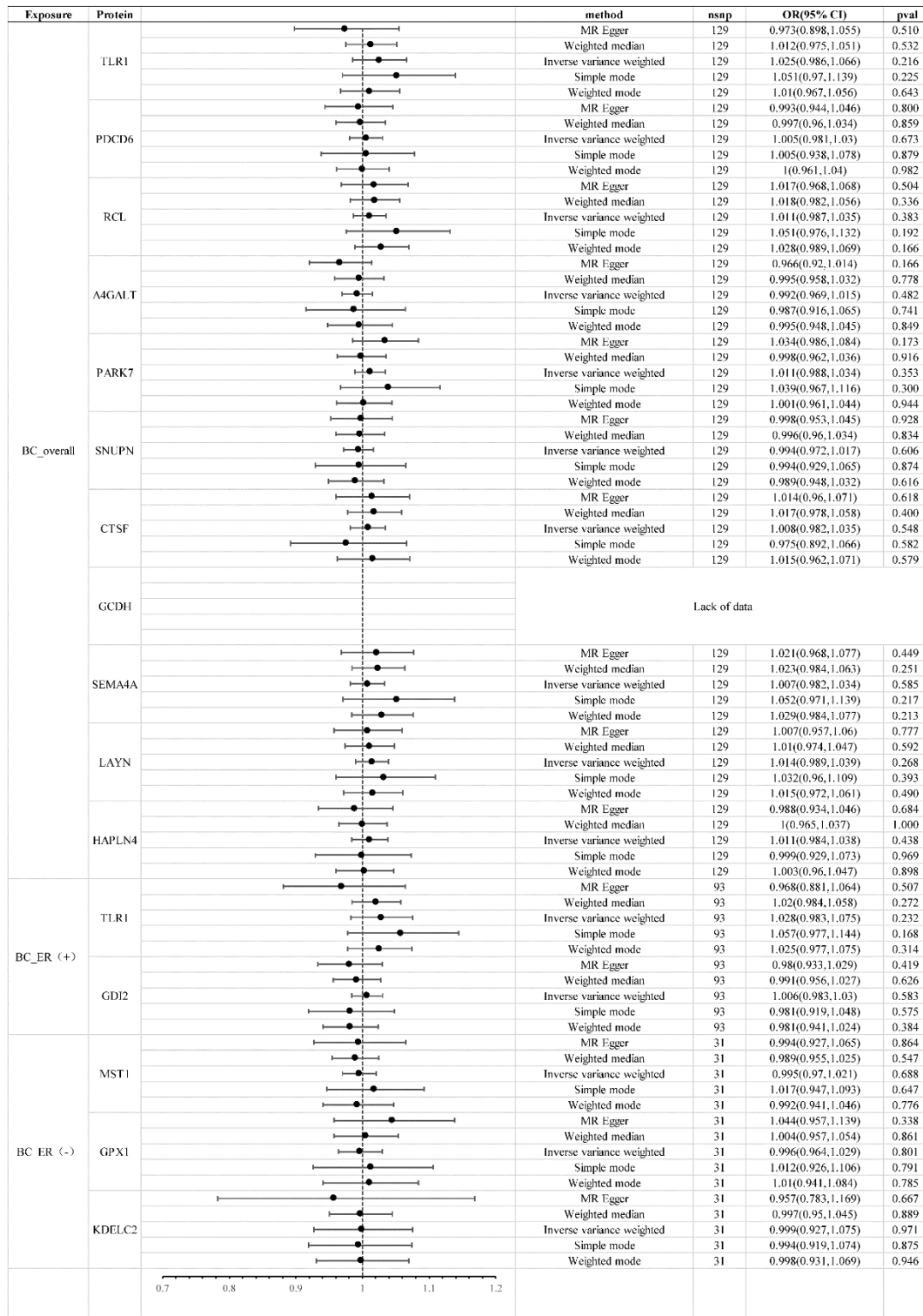


Figure S1 Bidirectional MR analysis for breast cancer on levels of prioritized proteins

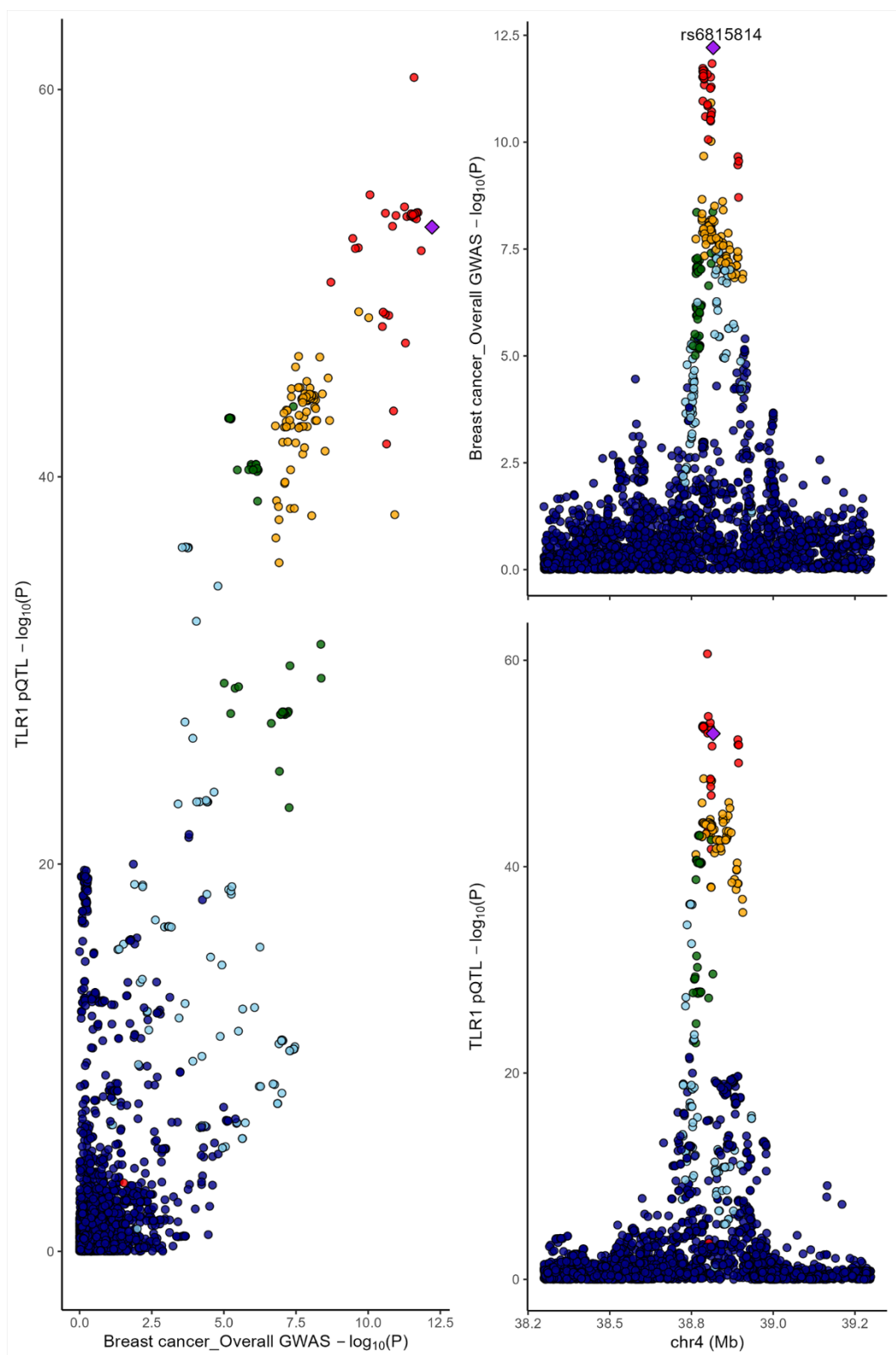


Figure S2 Bayesian colocalization analysis for TLR1 and BC_overall

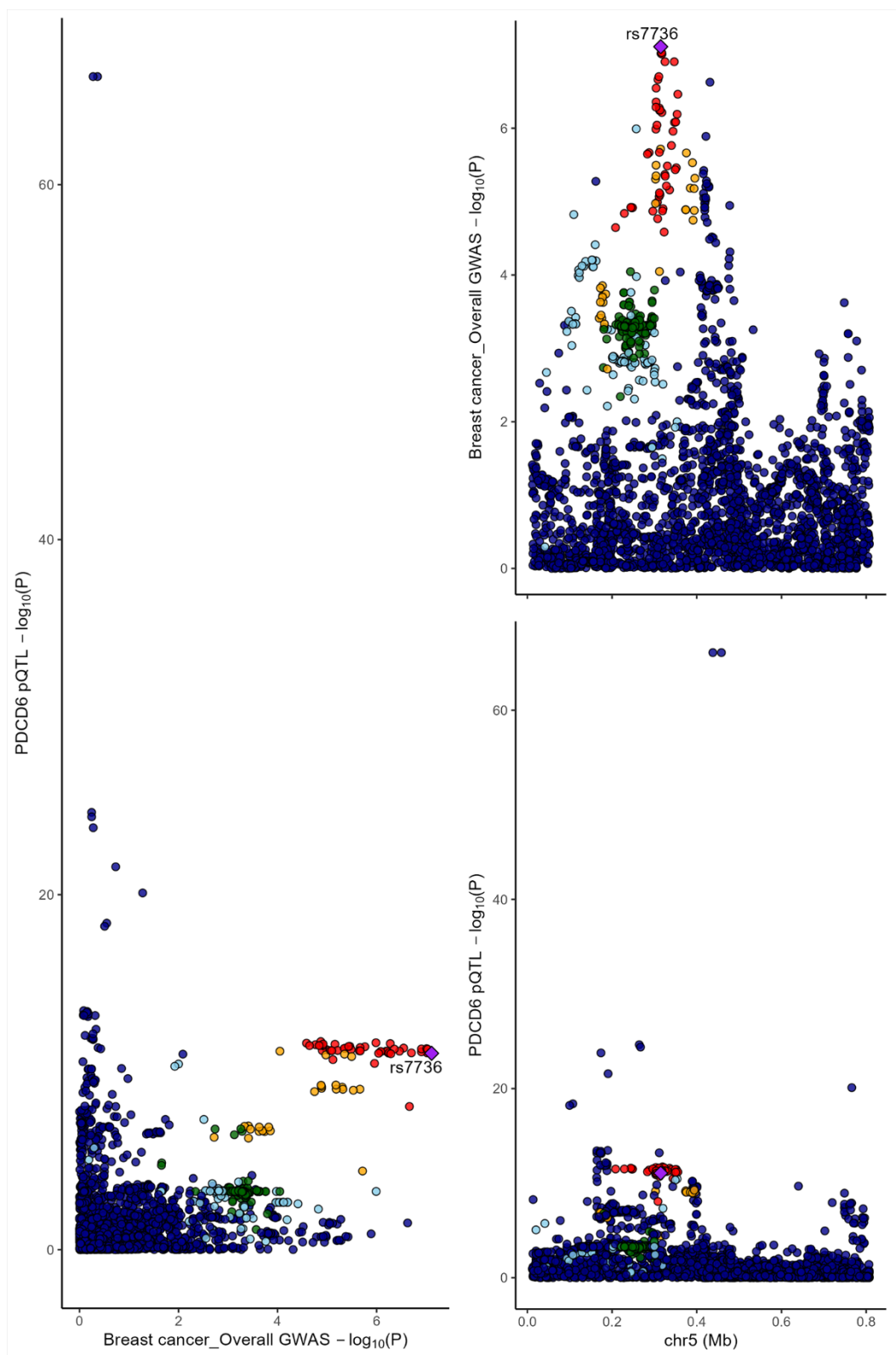


Figure S3 Bayesian colocalization analysis for PDCD6 and BC_overall

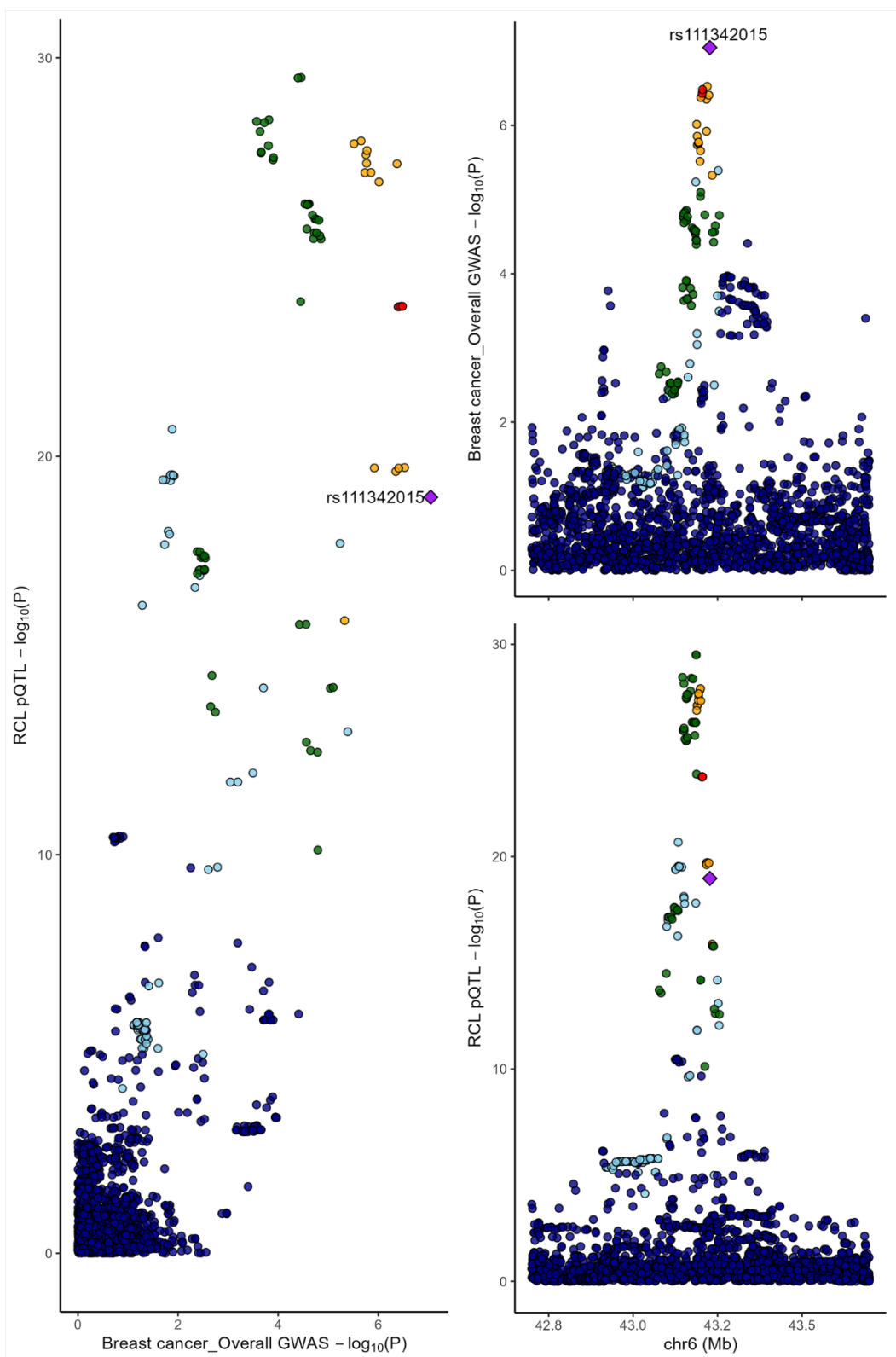


Figure S4 Bayesian colocalization analysis for RCL and BC_overall

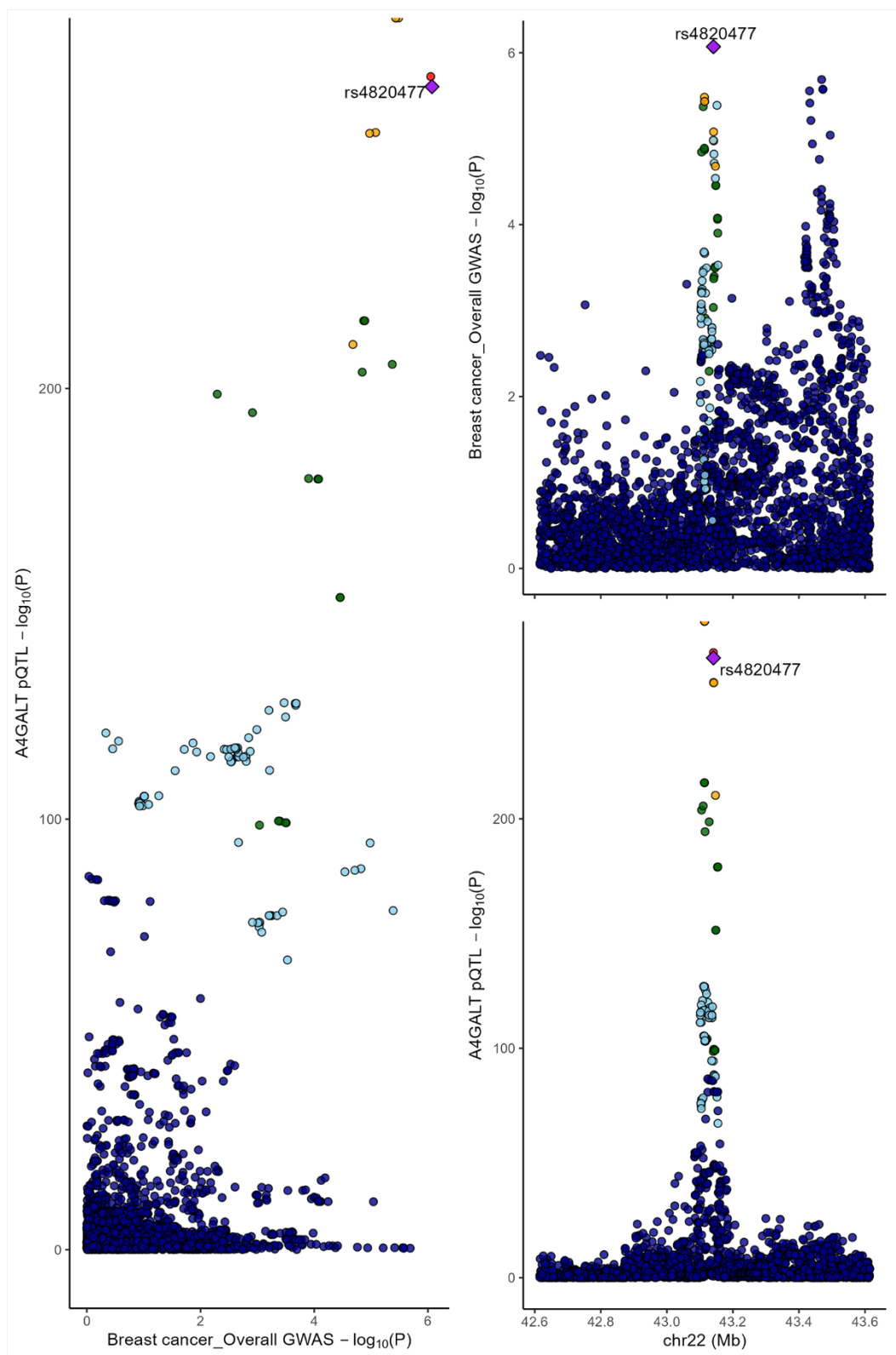


Figure S5 Bayesian colocalization analysis for A4GALT and BC_overall

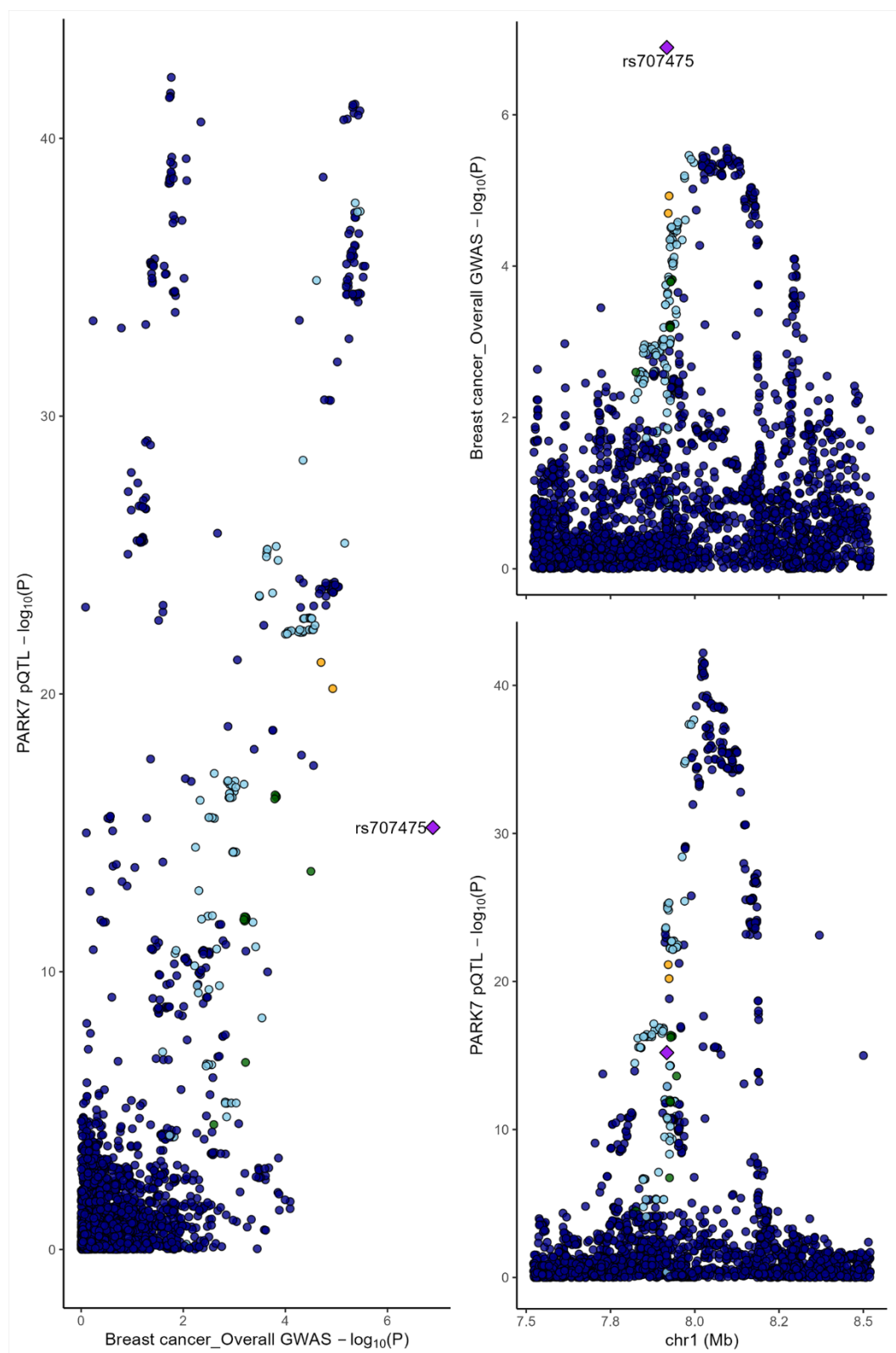


Figure S6 Bayesian colocalization analysis for PARK7 and BC_overall

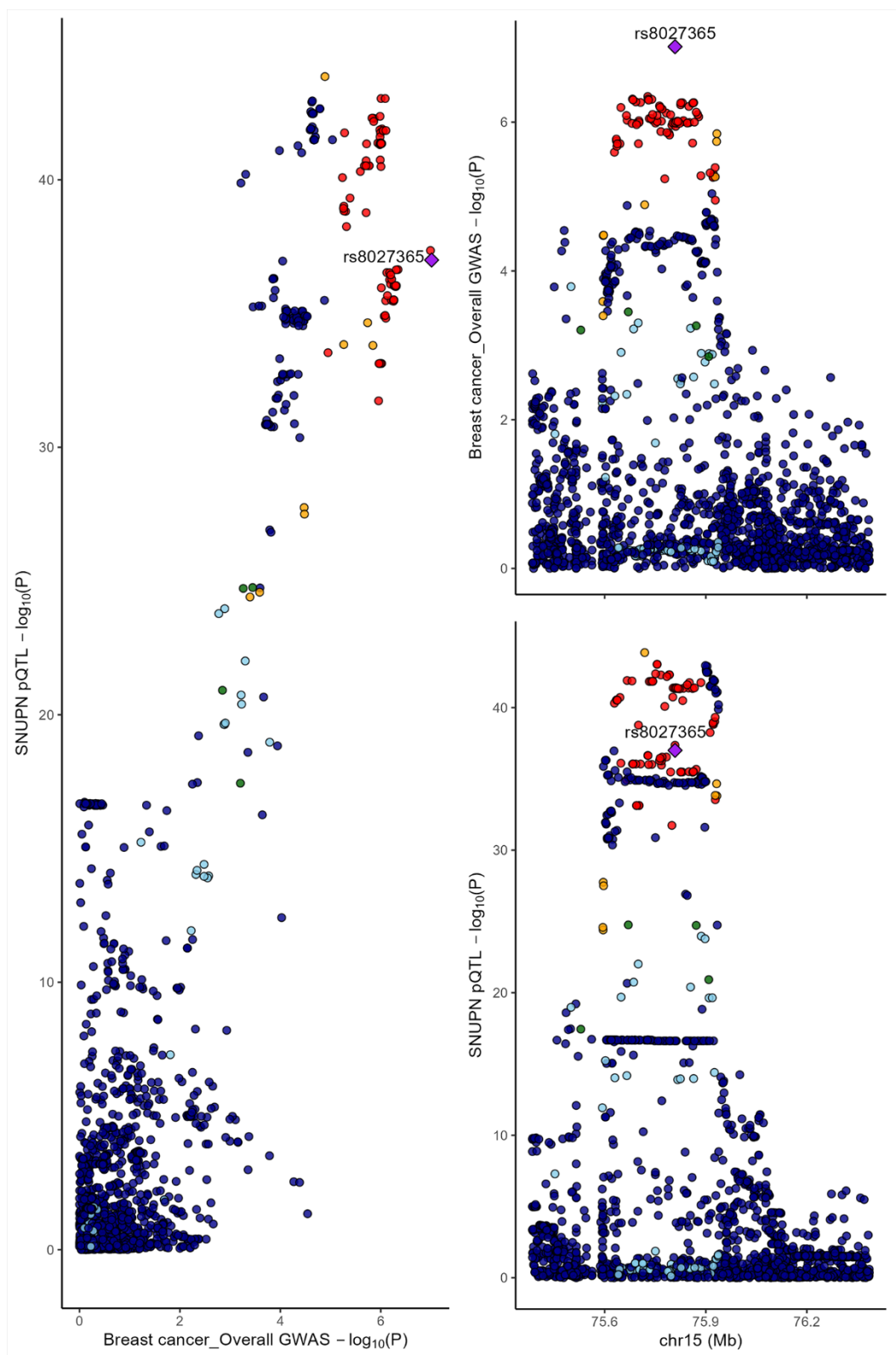


Figure S7 Bayesian colocalization analysis for SNUPN and BC_overall

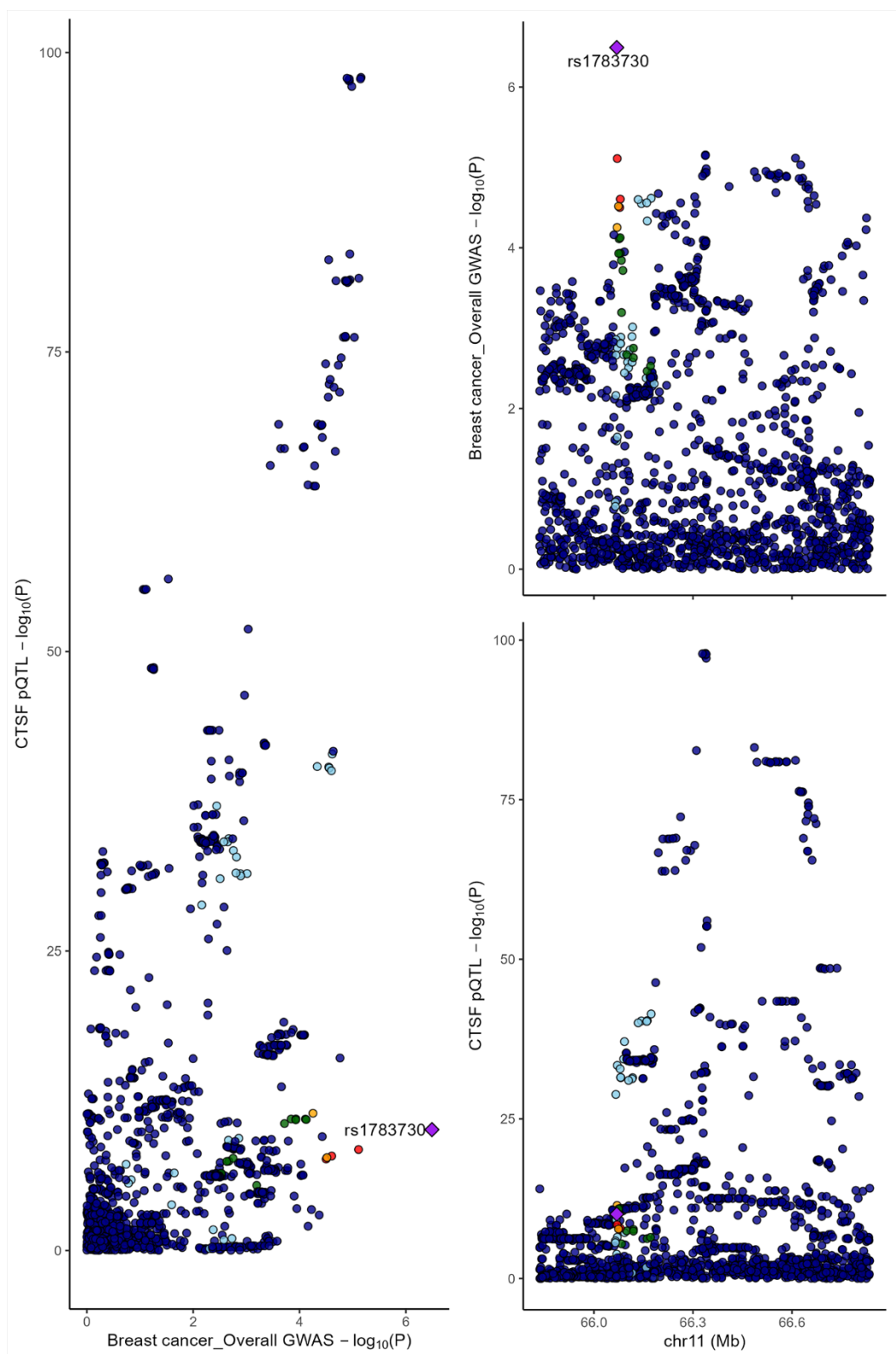


Figure S8 Bayesian colocalization analysis for CTSF and BC_overall

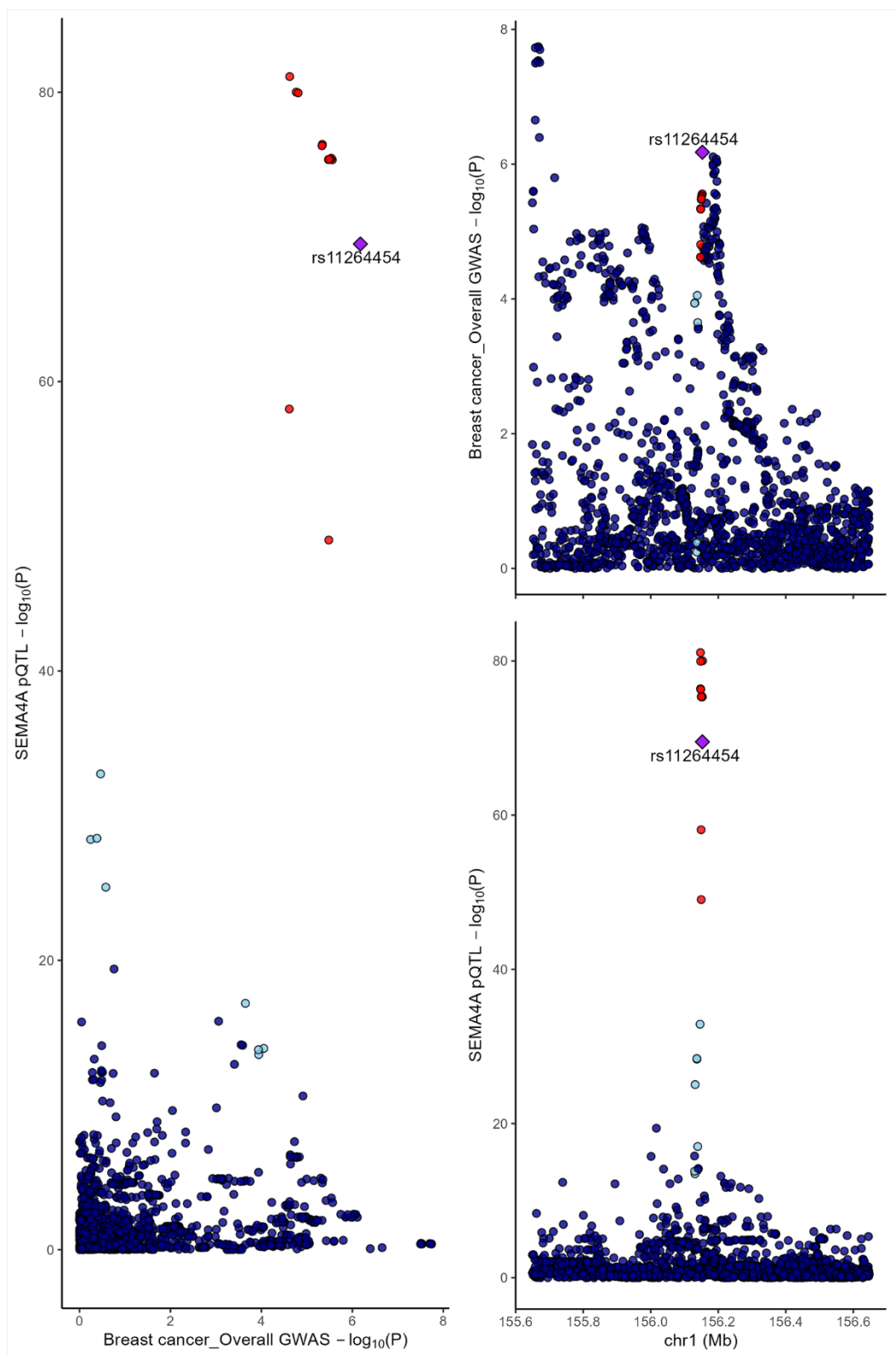


Figure S9 Bayesian colocalization analysis for SEMA4A and BC_overall

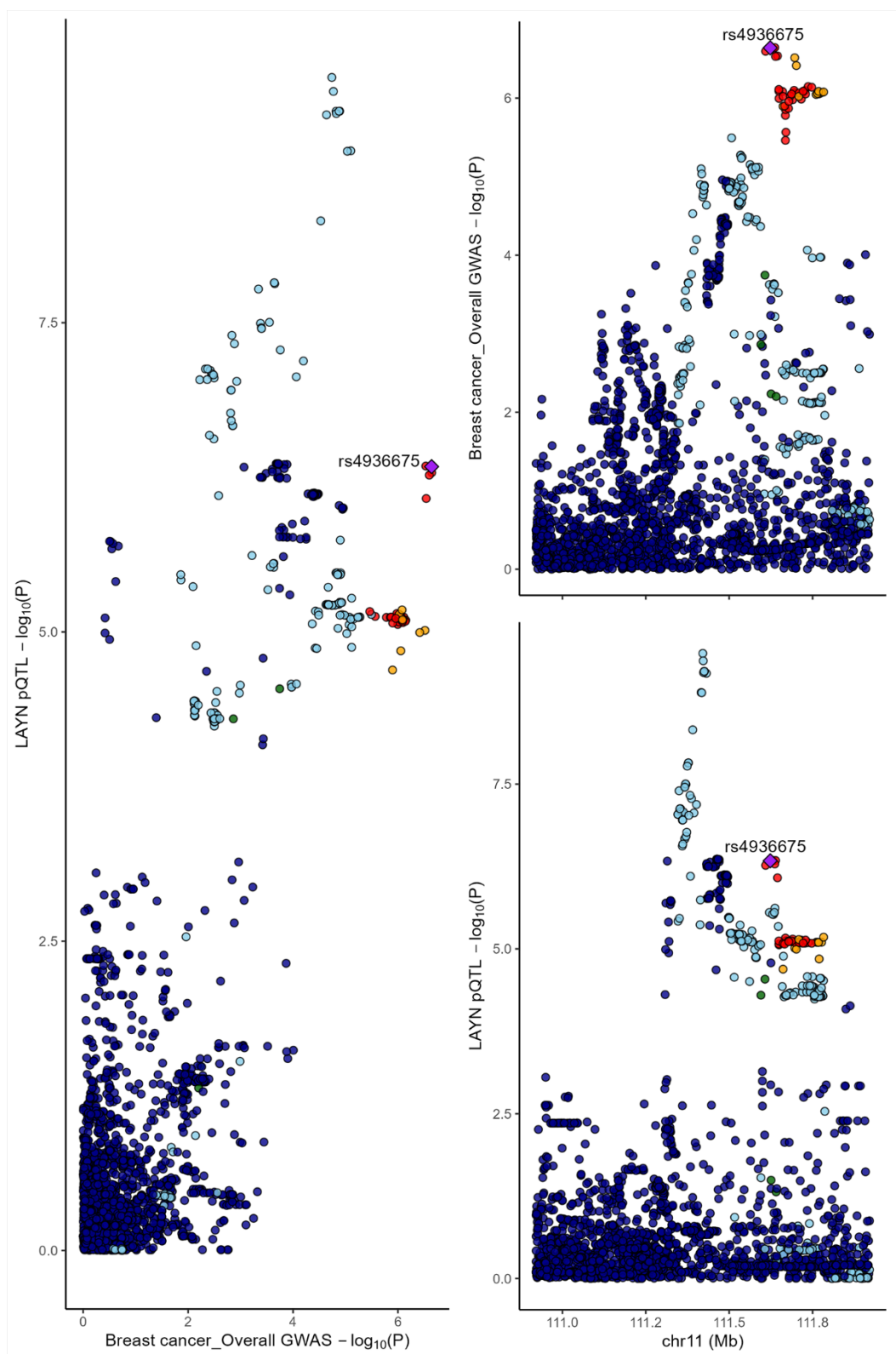


Figure S10 Bayesian colocalization analysis for LAYN and BC_overall

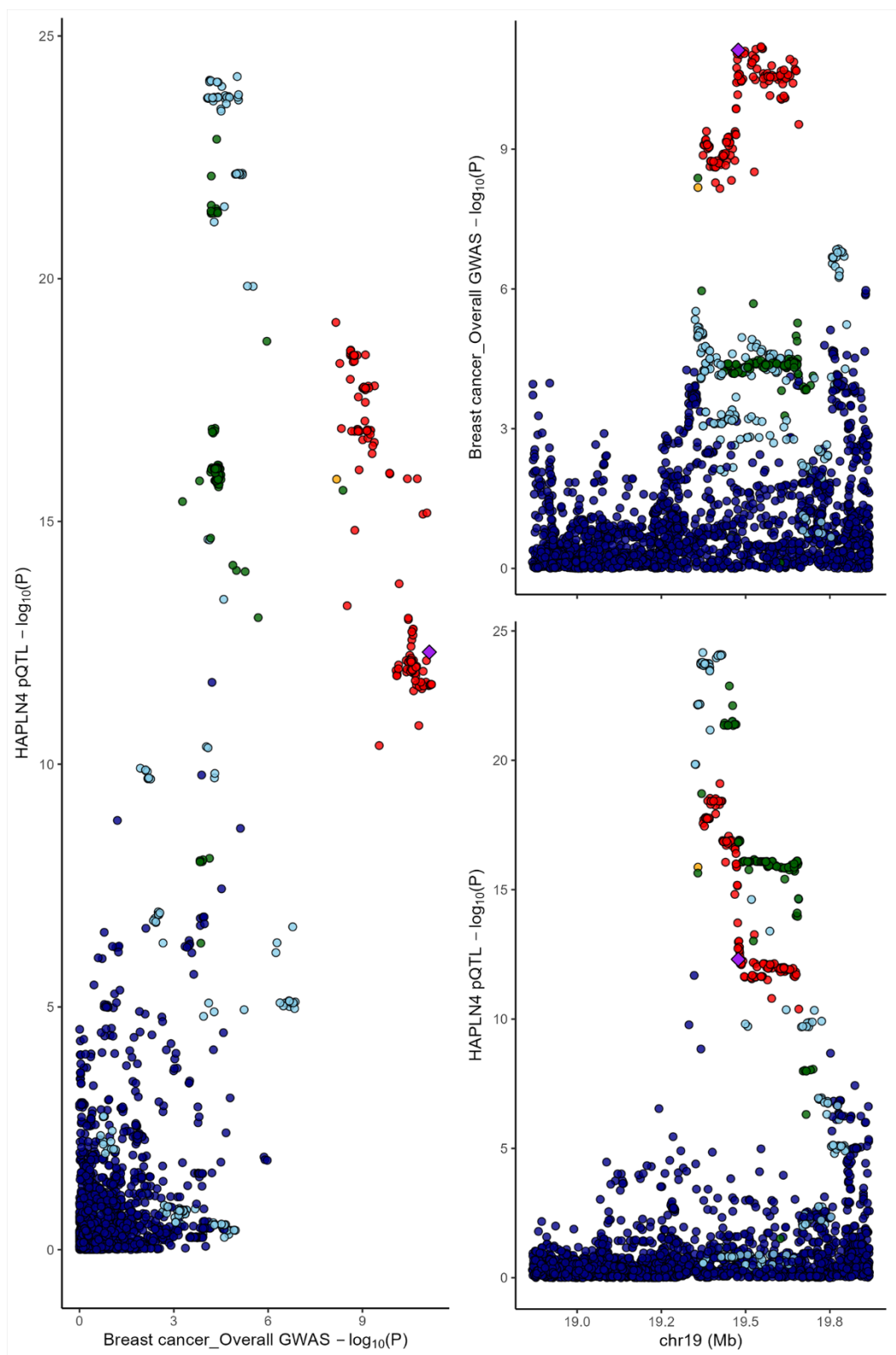


Figure S11 Bayesian colocalization analysis for HAPLN4 and BC_overall

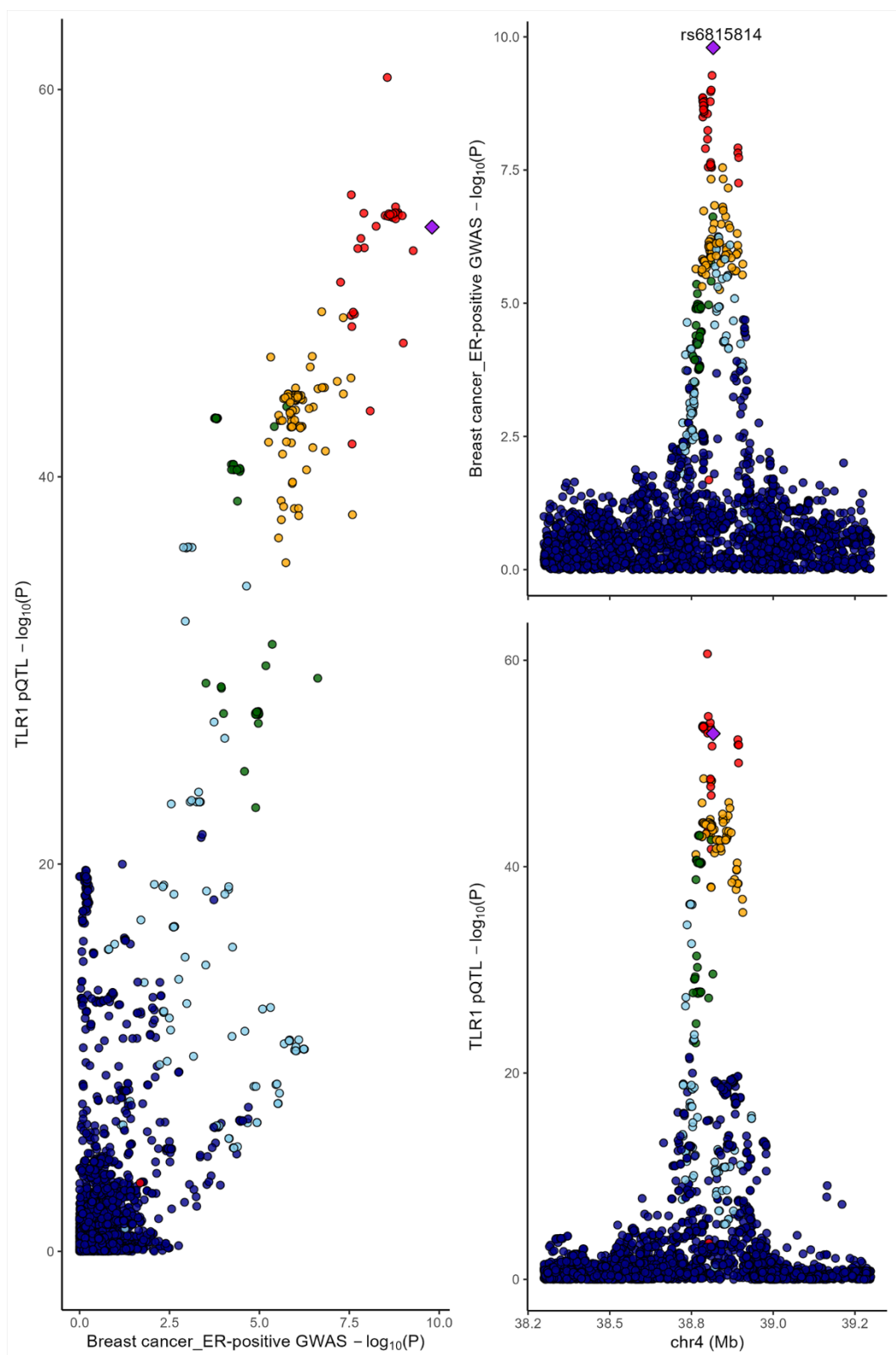


Figure S12 Bayesian colocalization analysis for TLR1 and BC_ER(+)

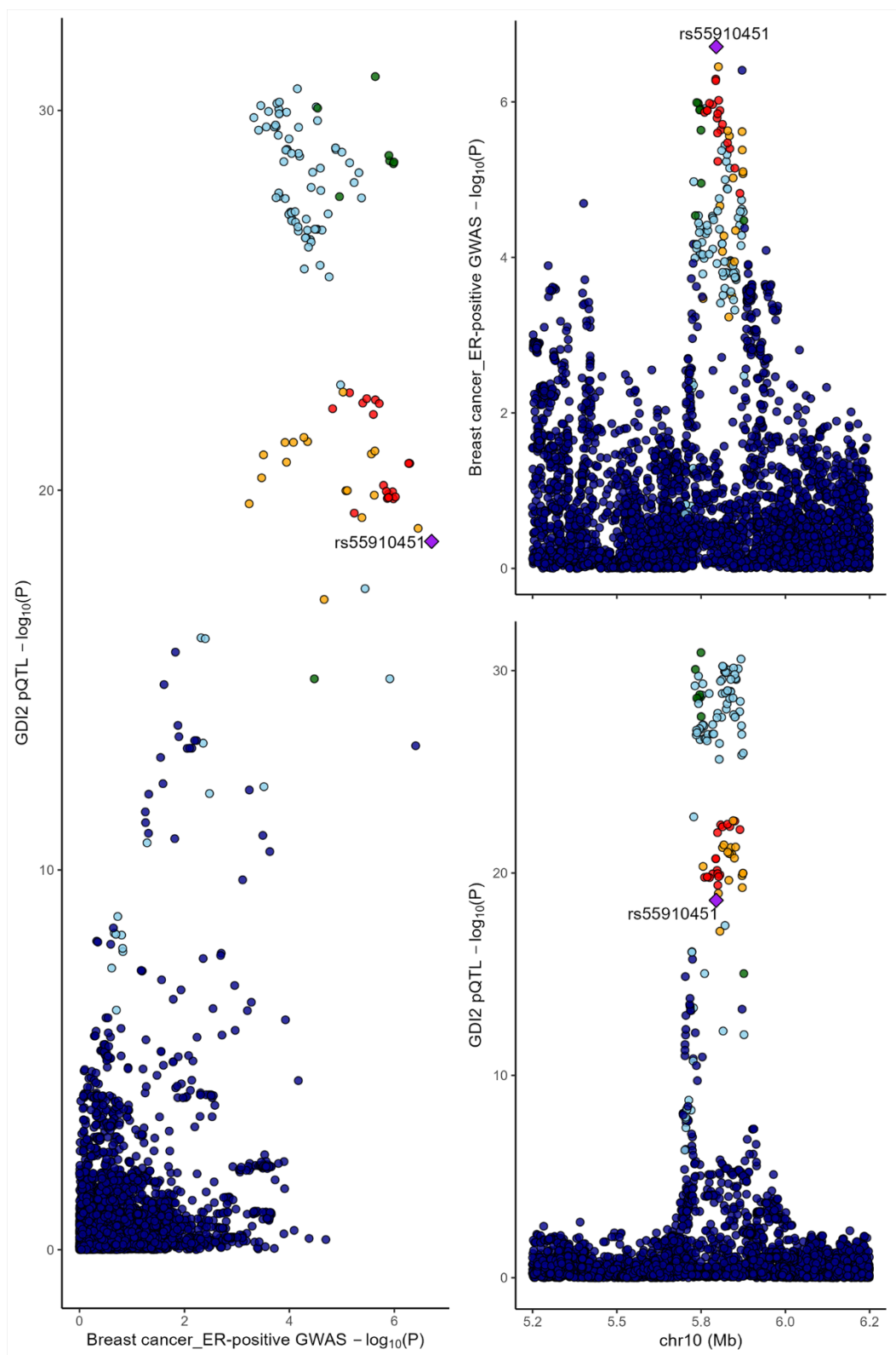


Figure S13 Bayesian colocalization analysis for GDI2 and BC_ER(+)

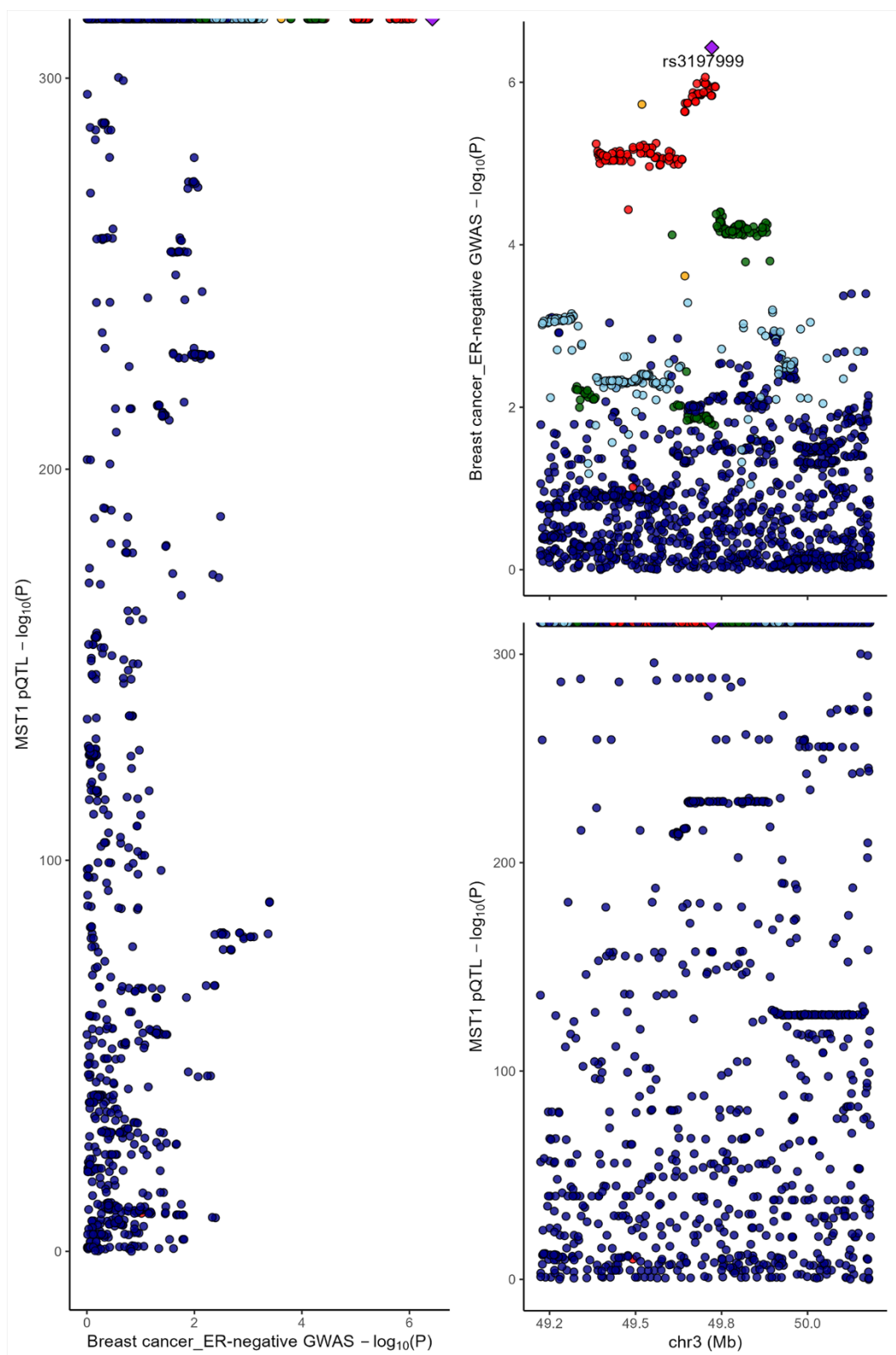


Figure S14 Bayesian colocalization analysis for MST1 and BC_ER(-)

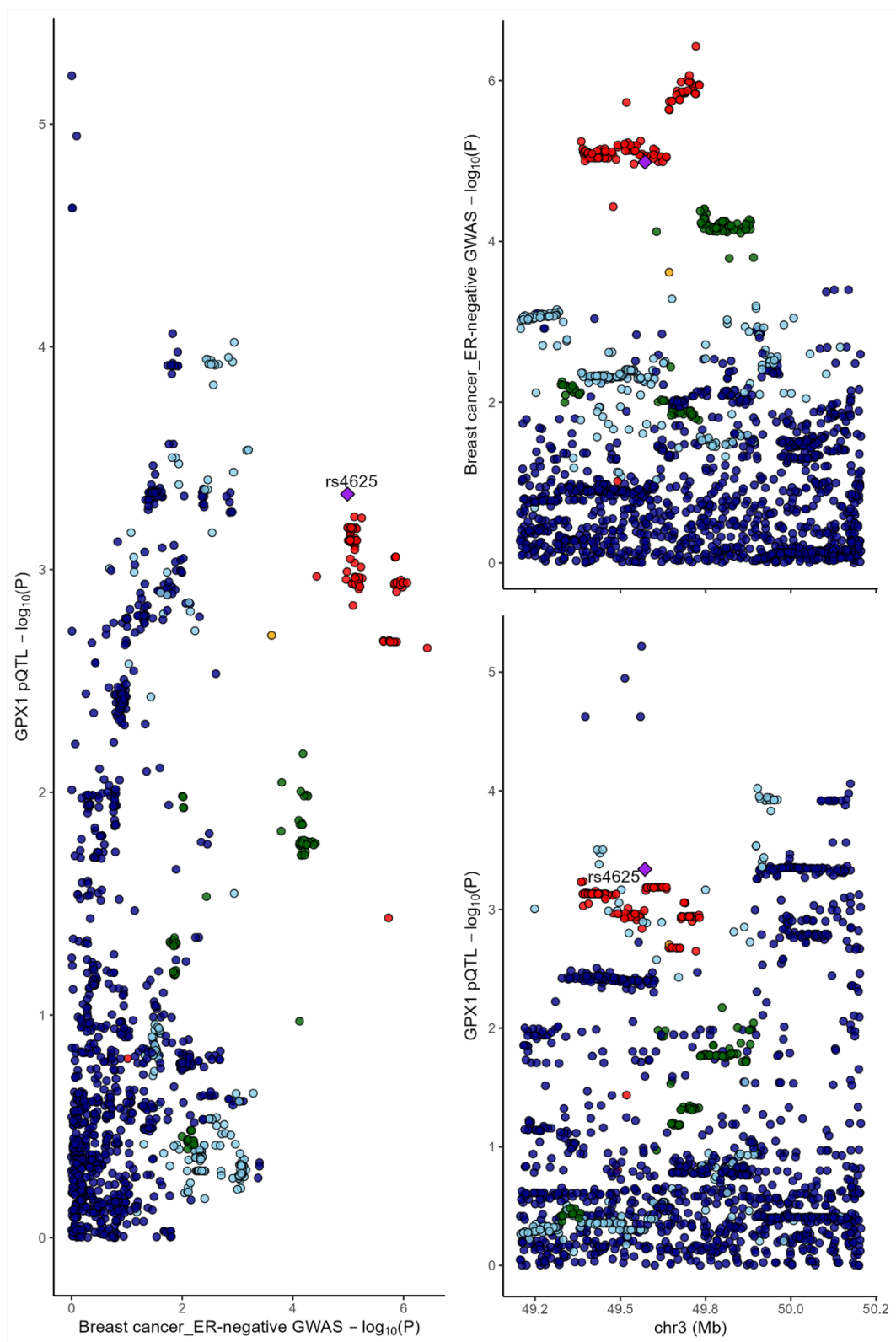


Figure S15 Bayesian colocalization analysis for GPX1 and BC_ER(-)

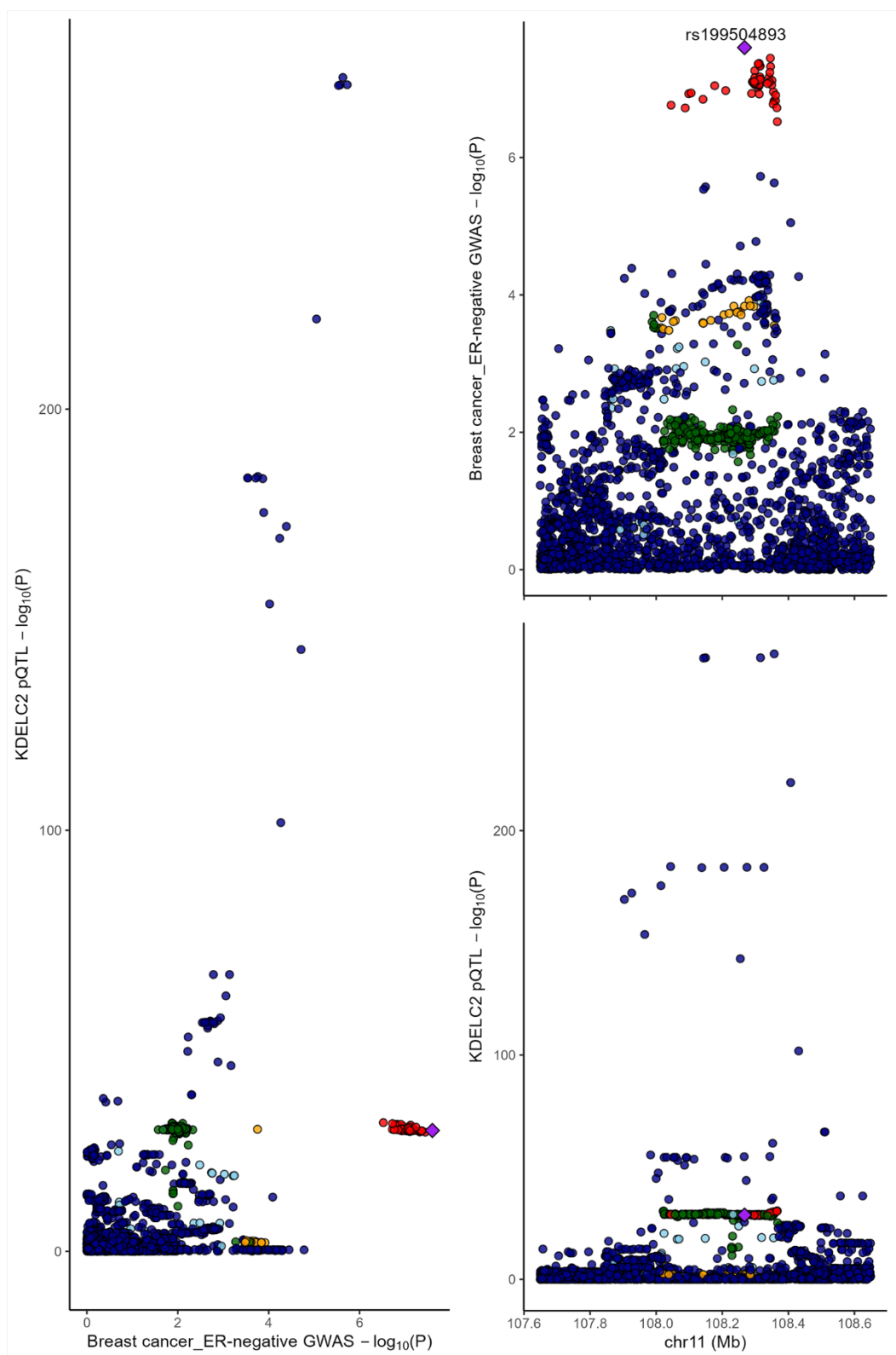


Figure S16 Bayesian colocalization analysis for KDELC2 and BC_ER(-)

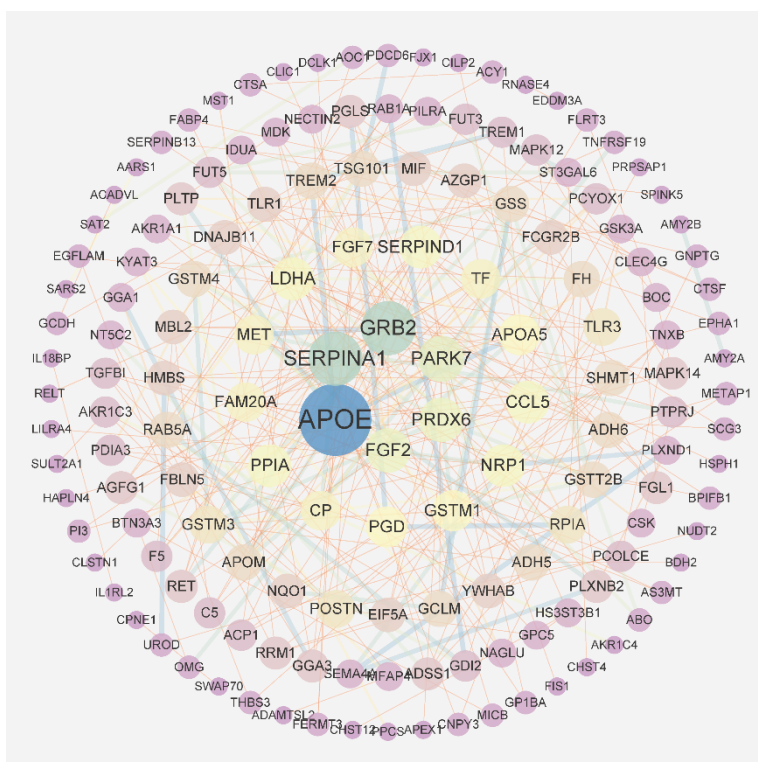


Figure S17 Protein-protein interaction network between suggestive BC_overall-related proteins ($P < 0.05$) from plasma

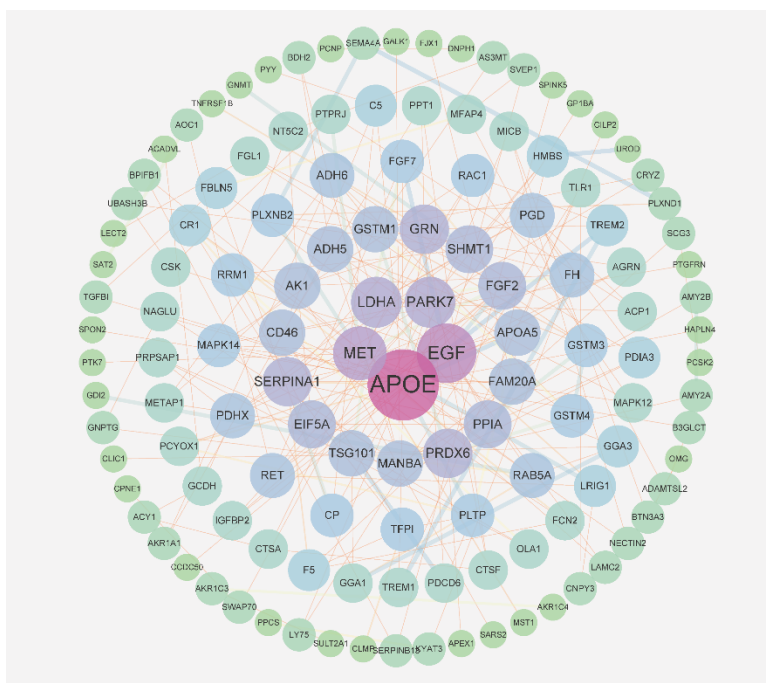


Figure S18 Protein-protein interaction network between suggestive BC_ER(+)-related proteins (P < 0.05) from plasma

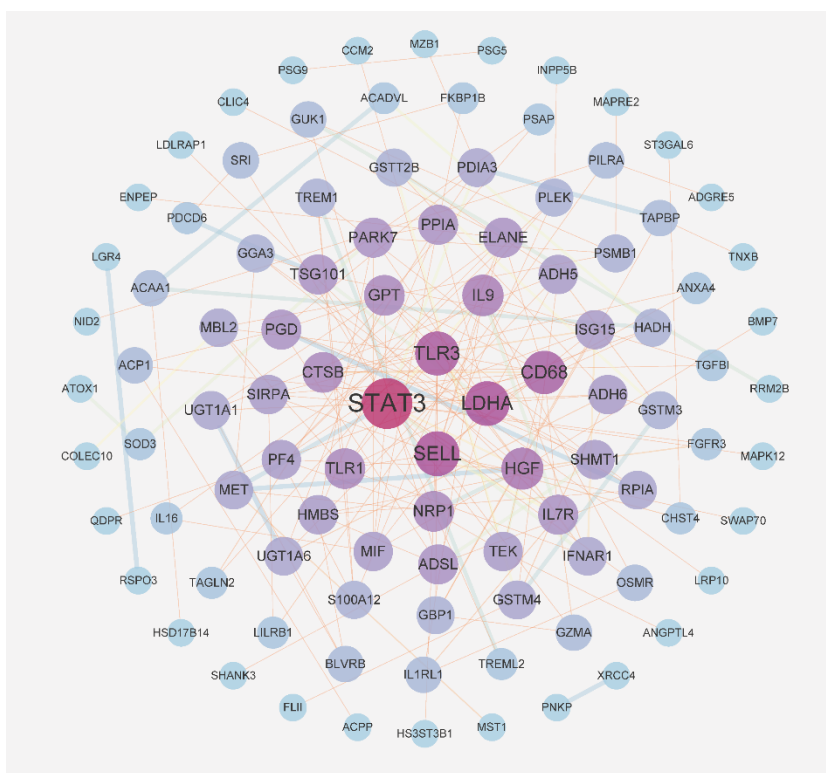


Figure S19 Protein-protein interaction network between suggestive BC_ER(-)-related proteins ($P < 0.05$) from plasma

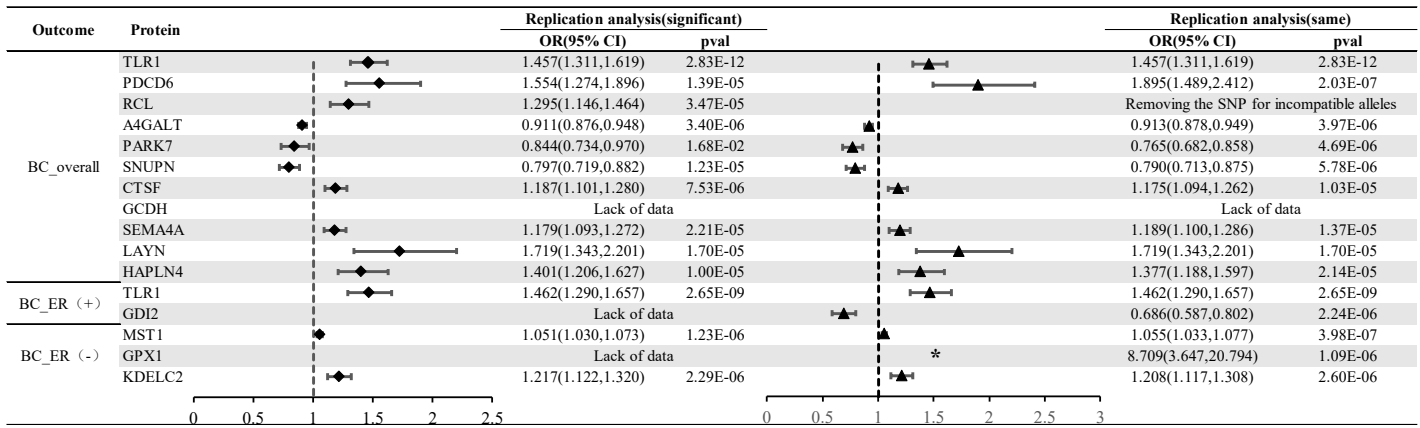


Figure S20 Replication of causal relationship between prioritized proteins and breast cancer

* symbolizes instances where exceptionally large numerical values disrupt the aesthetic appeal of the forest plot, necessitating its use to maintain visual clarity.

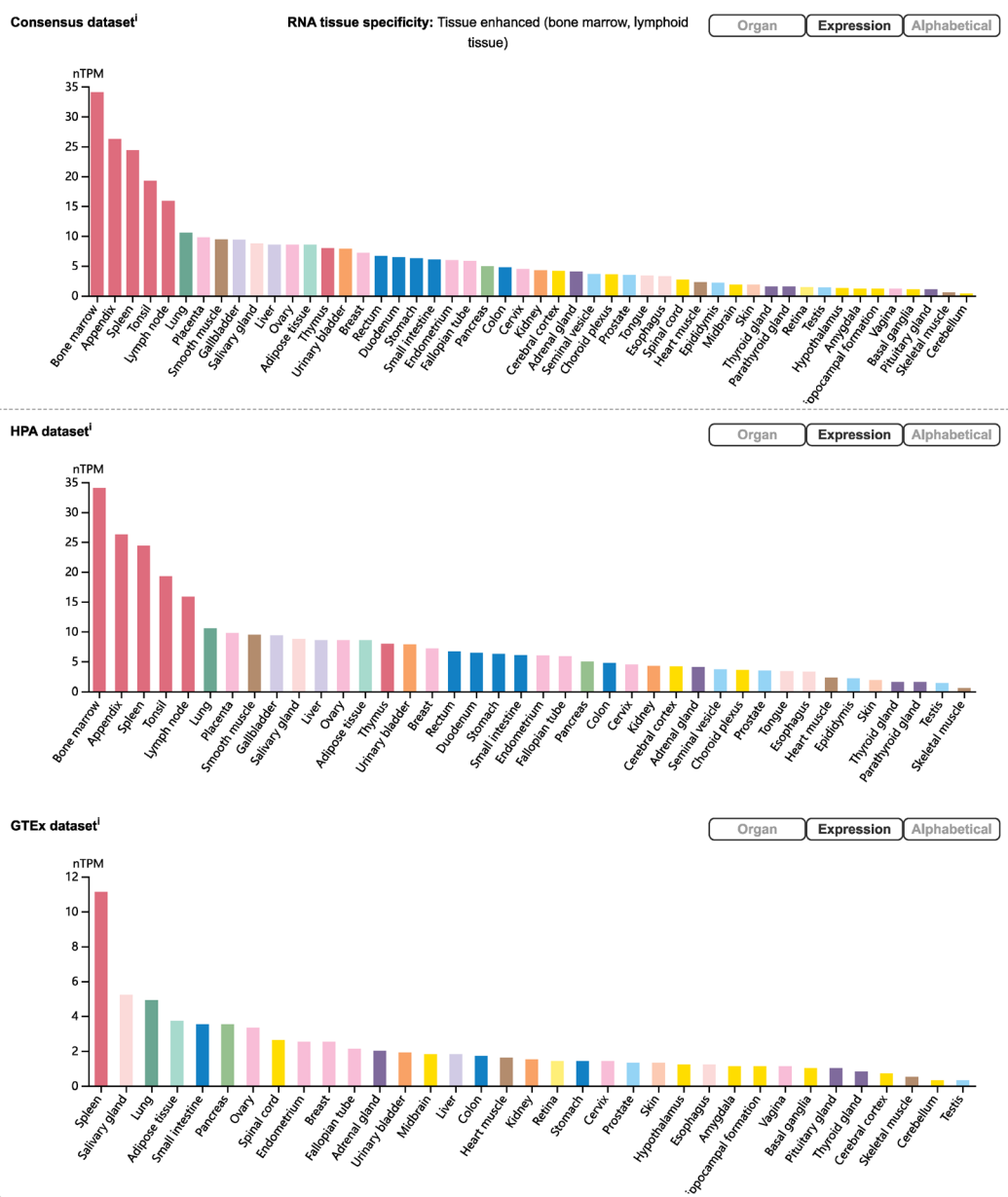


Figure S21 The mRNA expression profile of TLR1 across human tissues (The human protein atlas, <https://www.proteinatlas.org/>).

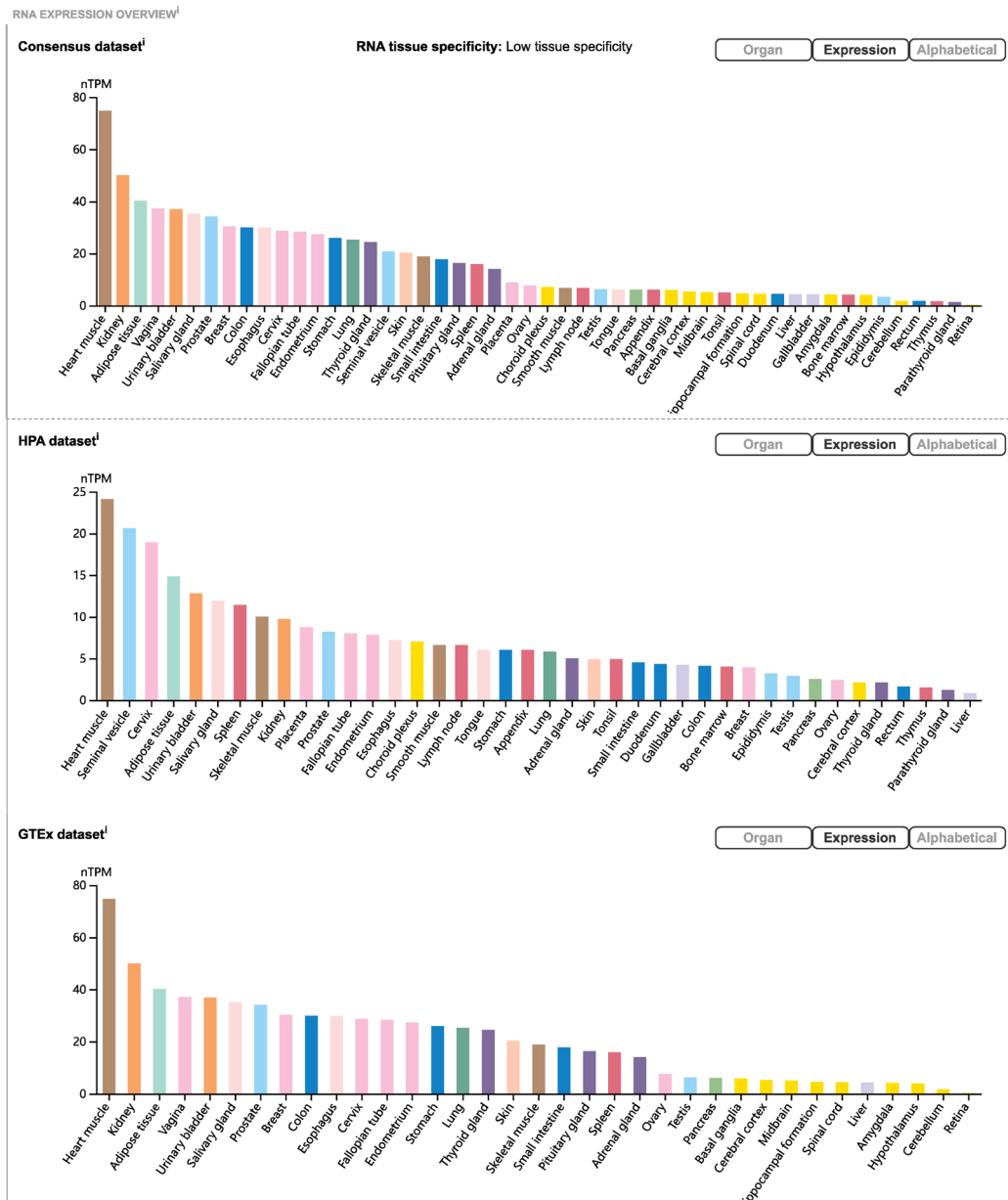


Figure S22 The mRNA expression profile of A4GALT across human tissues (The human protein atlas, <https://www.proteinatlas.org/>).

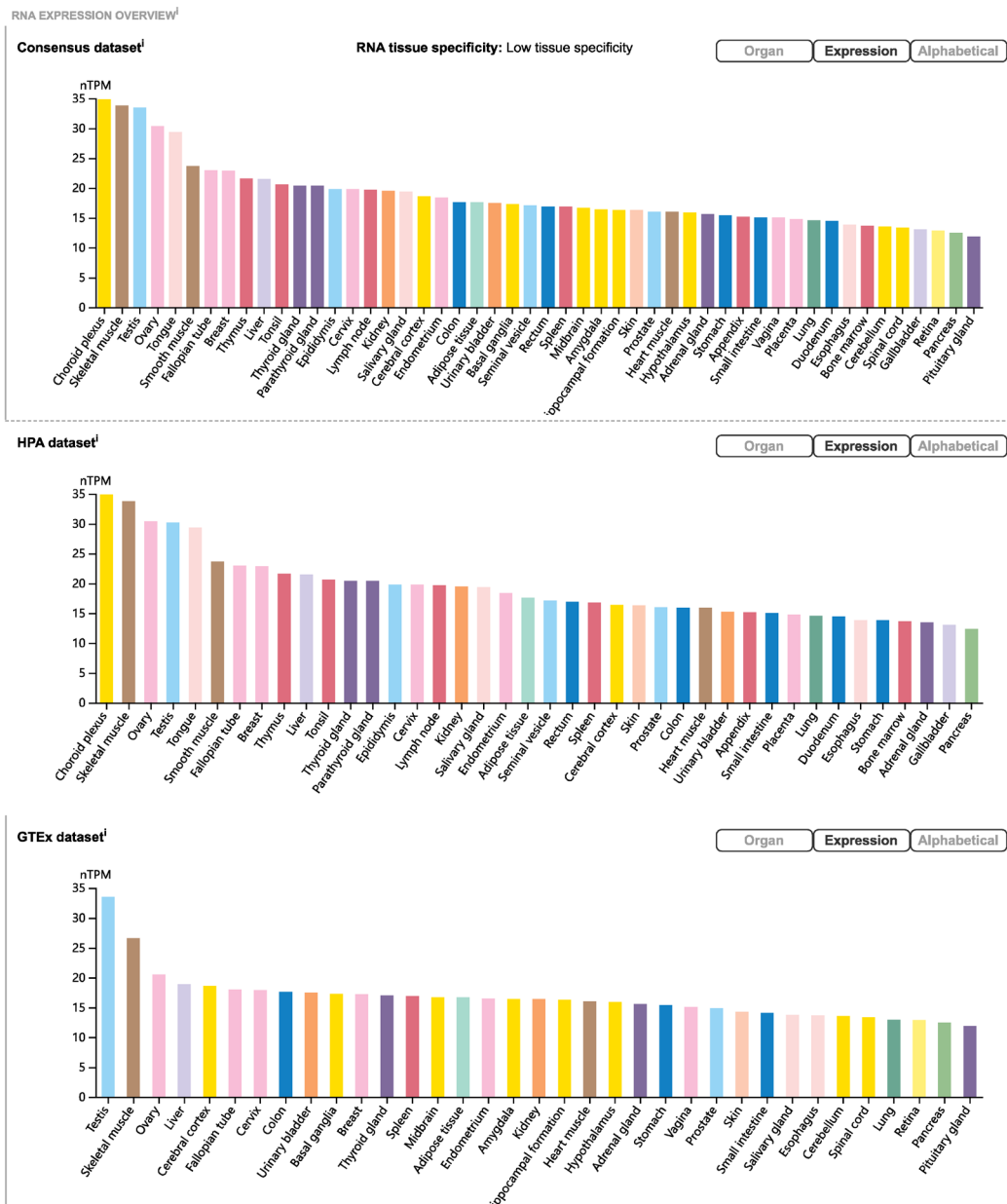


Figure S23 The mRNA expression profile of SNUPN across human tissues (The human protein atlas, <https://www.proteinatlas.org/>).

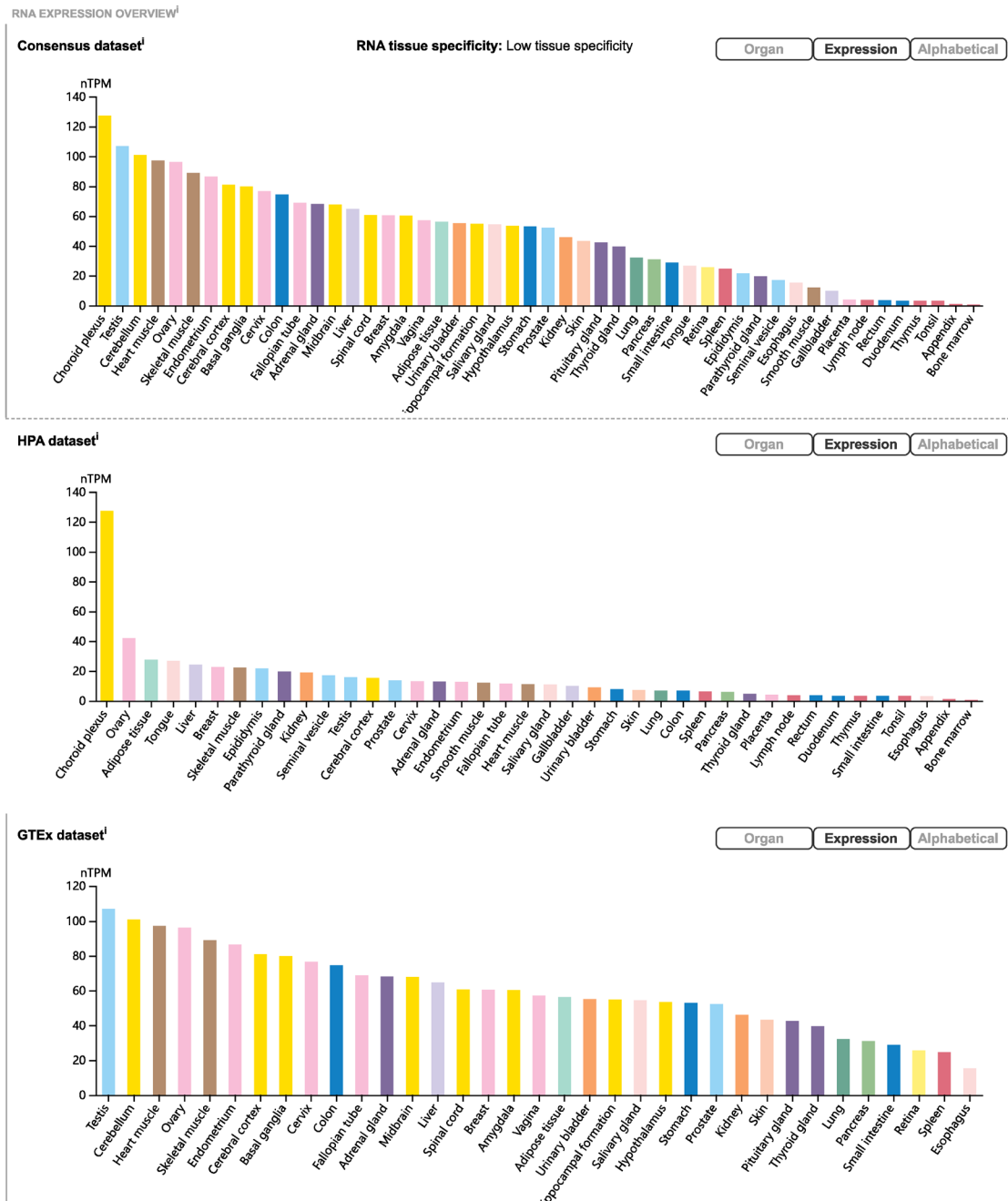


Figure S24 The mRNA expression profile of CTSF across human tissues (The human protein atlas, <https://www.proteinatlas.org/>).