

Diagram legends

Figure S1. Summary of snps and mapped genes for (a) SCZ_Breast cancer,(b) SCZ_ovarian cancer,(c) SCZ_thyroid cancer.

Figure S2. The expression of mapping genes (A) *AS3MT* (B) *SFXN2* (C) *IMMP2L* (D)*PCCB* were differentially expressed significantly in cancers and significantly correlated with the prognosis of (E) breast cancer and (F) thyroid cancer patients.

Figure S3. (A), Immunohistochemistry staining images from Human Protein Atlas showed the protein expression levels of *AS3MT* and *SFXN2* in breast or thyroid cancers. (B), Gene-gene interaction network among common genes (*AS3MT*, *SFXN2*, *PCCB*, *IMMP2L*) in the GeneMANIA dataset. (C), possible explanations for observed association in 2SMR analysis between SCZ and cancer risk.

Figure S4. Functional consequences of SNPs on genes for (a) SCZ_Breast cancer, (b) SCZ_ovarian cancer,(c) SCZ_thyroid cancer. tissue expression enrichment in GTEx tissue types for (D) SCZ_ovarian cancer,(E) SCZ_thyroid cancer.

Figure S5. Pathway enrichment for (a) SCZ_Breast cancer, (b) SCZ_ovarian cancer,(c) SCZ_thyroid cancer related genes.

Table S1. The information of 13 cancers data

Table S2. Summary statistics for all instrument variables after data harmonization.

Table S3. 2SMR results of all cancers and SCZ

Table S4. 2SMR results of SCZ and 2 subtypes breast

Table S5. 2SMR results of SCZ and different type cancers