

FigS1 Regional association plot for colocalization analysis of PRCP protein with SAH risk. The lead SNP is shown as a purple diamond. SNPs within ±100 kb of the expression quantitative trait locus were included; p12=1e-5, prior probability a SNP is associated with both gene and SAH.



FigS2 Regional association plot for colocalization analysis of PSMA4 protein with IA risk. The lead SNP is shown as a purple diamond. SNPs within ±100 kb of the expression quantitative trait locus were included; p12=1e-5, prior probability a SNP is associated with both gene and IA.



FigS3 Regional association plot for colocalization analysis of PSMA4 protein with SAH risk. The lead SNP is shown as a purple diamond. SNPs within ±100 kb of the expression quantitative trait locus were included; p12=1e-5, prior probability a SNP is associated with both gene and SAH.



FigS4 The summary-data-based Mendelian randomization(SMR) result of PRCP with SAH risk. (A)The SMR locusplot.Top plot, graydots represent the Pvalues for SNPs from the SAH GWASs, diamond represents the Pvalue for PRCP from the SMR test and the dashed line indicates the Bonferroni-corrected P-value threshold.Bottom plot represent the eQTL P-values of SNPs associated with expression PRCP in the blood. (B)The SMR effect plot.The horizontal axis represents the effect sizes of SNPs on PRCP, While the vertical axis represents the effect sizes of SNPs on SAH risk.



FigS5 The summary-data-based Mendelian randomization(SMR) result of PSMA4 with IA risk. (A)The SMR locusplot.Top plot, graydots represent the Pvalues for SNPs from the IA GWASs, diamond represents the Pvalue for PSMA4 from the SMR test and the dashed line indicates the Bonferroni-corrected P-value threshold.Bottom plot represent the eQTL P-values of SNPs associated with expression PSMA4 in the blood. (B)The SMR effect plot.The horizontal axis represents the effect sizes of SNPs on PSMA4, While the vertical axis represents the effect sizes of SNPs on IA risk.



FigS6 The summary-data-based Mendelian randomization(SMR) result of PSMA4 with SAH risk. (A)The SMR locusplot.Top plot, graydots represent the Pvalues for SNPs from the SAH GWASs,diamond represents the Pvalue for PSMA4 from the SMR test and the dashed line indicates the Bonferroni-corrected P-value threshold.Bottom plot represent the eQTL P-values of SNPs associated with expression PSMA4 in the blood. (B)The SMR effect plot.The horizontal axis represents the effect sizes of SNPs on PSMA4,While the vertical axis represents the effect sizes of SNPs on SAH risk.



FigS7 Differential Expression Analysis and Enrichment Profiling of PRCP-Associated Genes (A) Box plots delineate the differential gene expression profiles of PRCP and PSMA4 genes within distinct cohorts of the GSE15629 dataset, with statistical significance denoted as * p < 0.05, ** p < 0.01, *** p < 0.001. (B) Volcano plots portraying the distribution of differentially expressed genes (DEG) upon stratification of PRCP according to gene expression levels. (C) Gene Ontology (GO) enrichment analysis of DEG is presented in a circular format. Each layer represents enriched term annotations within specific pathways, the total gene count, counts of enriched and unenriched DEGs, the numbers of upregulated and downregulated genes, the -Log10(p.adjust) values, and enrichment indices. (D) Kyoto Encyclopedia of Genes and Genomes (KEGG) enrichment analysis of DEG. (E) Reactome pathway enrichment analysis of DEG. (F) Functional Gene Set Enrichment Analysis (fgsea) of DEG. Statistical significance is established at a p-value < 0.05.



FigS8 (A) Heatmap analysis depicting the correlation between immune cell infiltration scores generated by five algorithms (CIBERSORT, EPIC, ImmuneCellAI, MCPcounter, and Xcell) and the expression patterns of PRCP genes. (B) Heatmap representation of the correlation analysis between immune-related genes and pathways and the expression of PRCP genes. (C) Heatmap visualization of the correlation analysis between genes related to metabolism and relevant metabolic pathways and the expression of PRCP genes.



FigS9 (A) Construction of a gene-gene interaction network for PRCP via the GeneMANIA database. (B) Generation of a protein-protein interaction (PPI) network for PRCP genes using STRING. (C) Conducting GO enrichment analysis on the genes within the established PRCP network. (D) Faceted violin plots visually elucidate the differential expression patterns of PRCP network genes in patients with ruptured intracranial aneurysms relative to healthy controls, with statistical significance indicated as * p < 0.05, ** p < 0.01, *** p < 0.001.



FigS10 Construction of a drug-gene interaction network for PRCP and PSMA4.Orange color represents the names of the target genes. Blue represent drugs that regulate the expression of this gene.