

Fig. S1

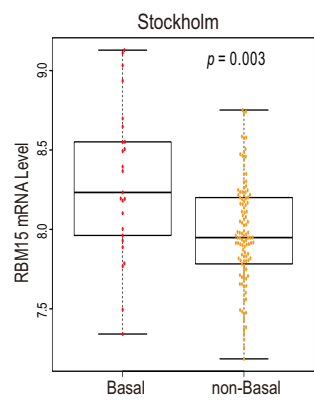


Fig. S1| RBM15 expression in human breast cancer.

RBM15 expression level from indicated BC patient cohorts. RBM15 expression between basal and non-basal from indicated BC patients. *p*-value indicates significance of analysis.

Fig. S2

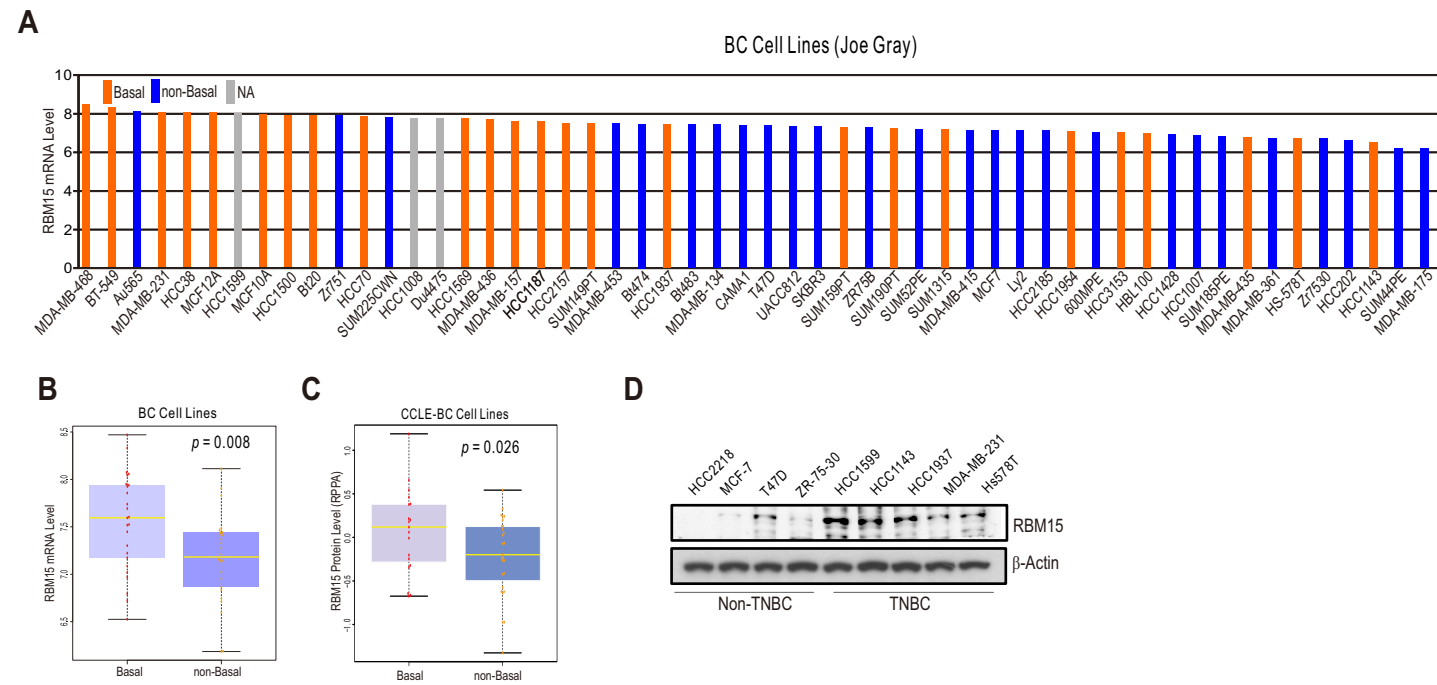


Fig. S2| RBM15 expression in human breast cancer cell lines.

A, RBM15 expression level from indicated BC cell lines, B and C, RBM15 expression between basal and non-basal from indicated BC cell lines gene expression data sets. D, western blot analysis with indicated cell and antibody. p -value indicates significance of analysis.

Fig. S3

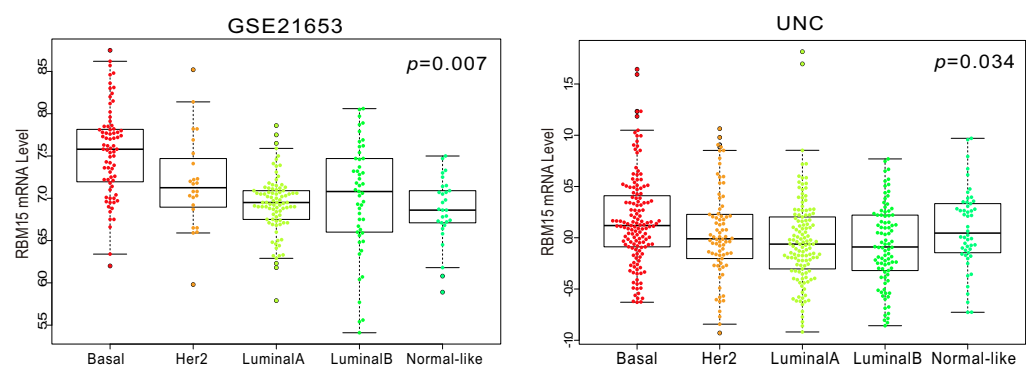


Fig. S3| RBM15 expression in human breast cancer patients.

RBM15 expression from indicated BC cohorts-depending on molecular subtypes. *p*-value indicates significance of analysis.

Fig. S4

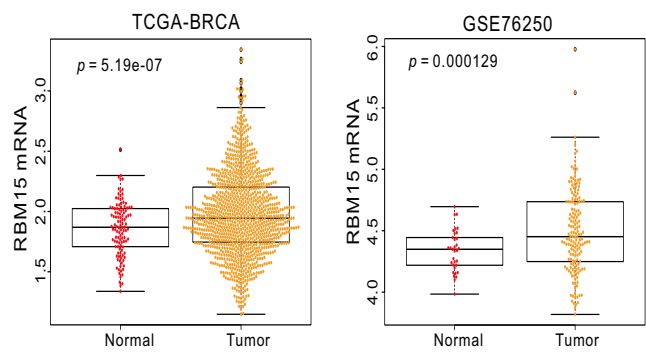


Fig. S4| RBM15 expression in human breast cancer.

RBM15 expression between normal and tumor from indicated BC patients. *p*-value indicates significance of analysis.

Fig. S5

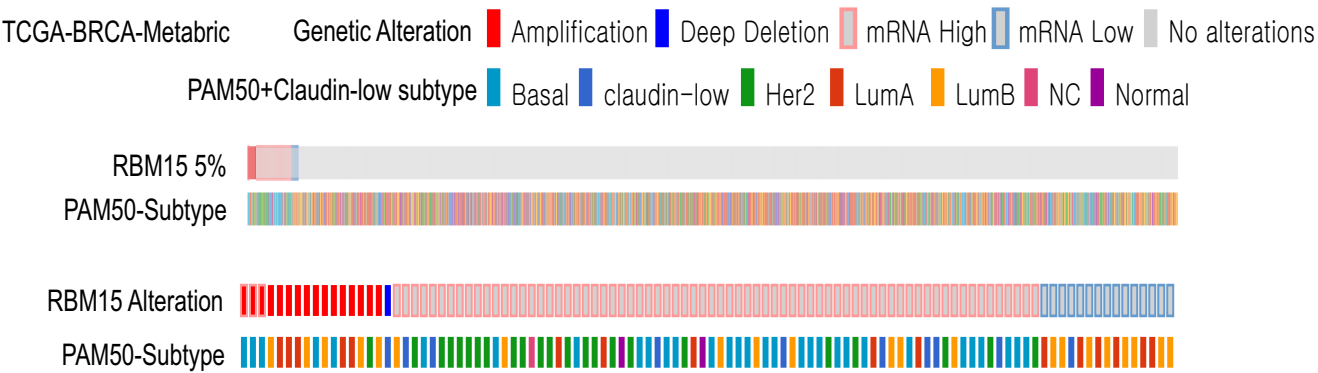


Fig. S5| Genetic alteration of RBM15 in breast cancer.

Genetic alteration of RBM15 from TCGA-BRCA cohorts. These analysis were done in cBioportal.

Fig. S6

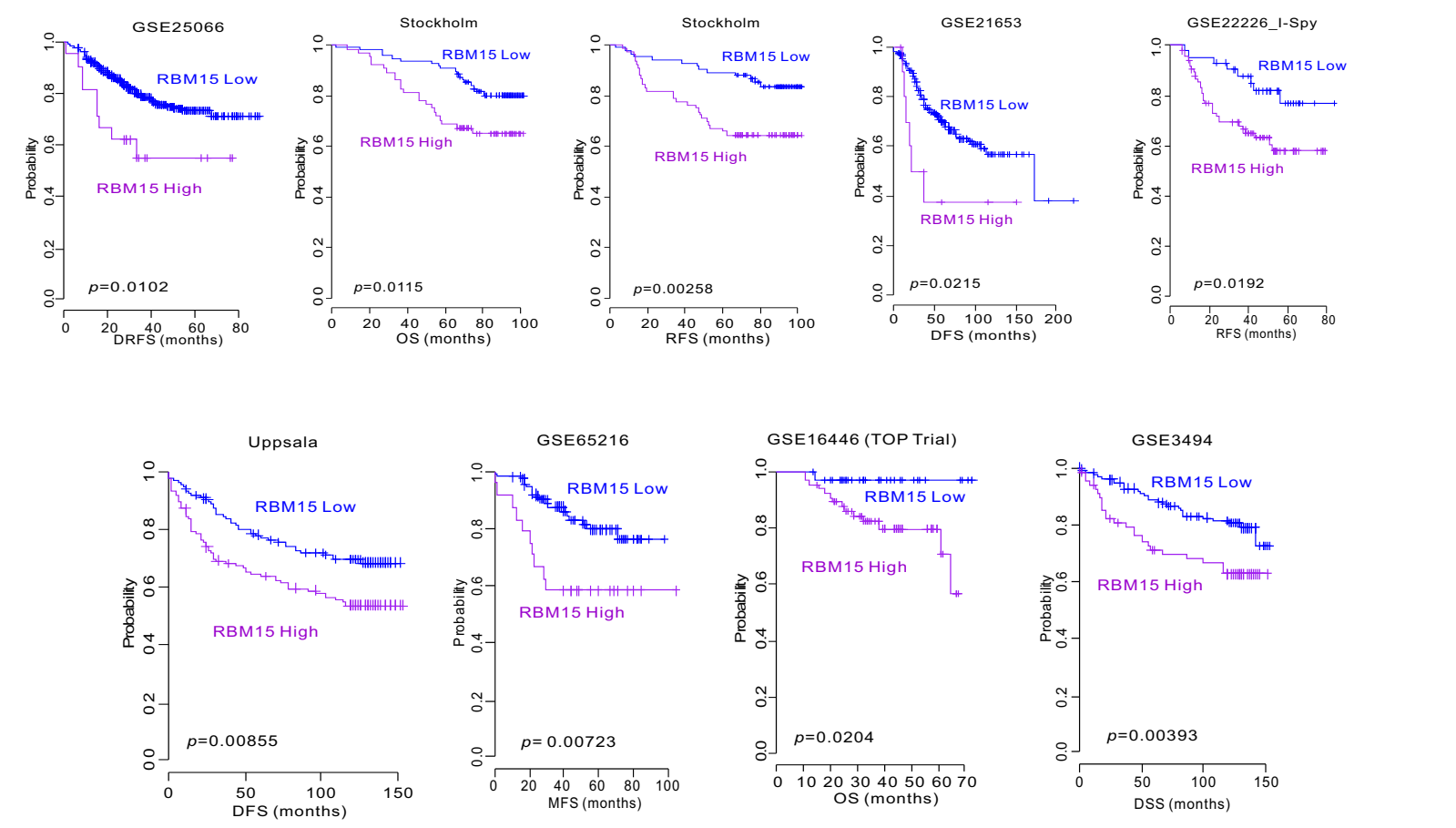


Fig. S6| Survival analysis of RBM15 in human breast cancer

Using indicated cohort, patients were classified according to the expression level of RBM15. Kaplan-Meier plots and the log-rank test were used to estimate patient prognosis. *p*-value indicates significance of analysis.

Fig. S7

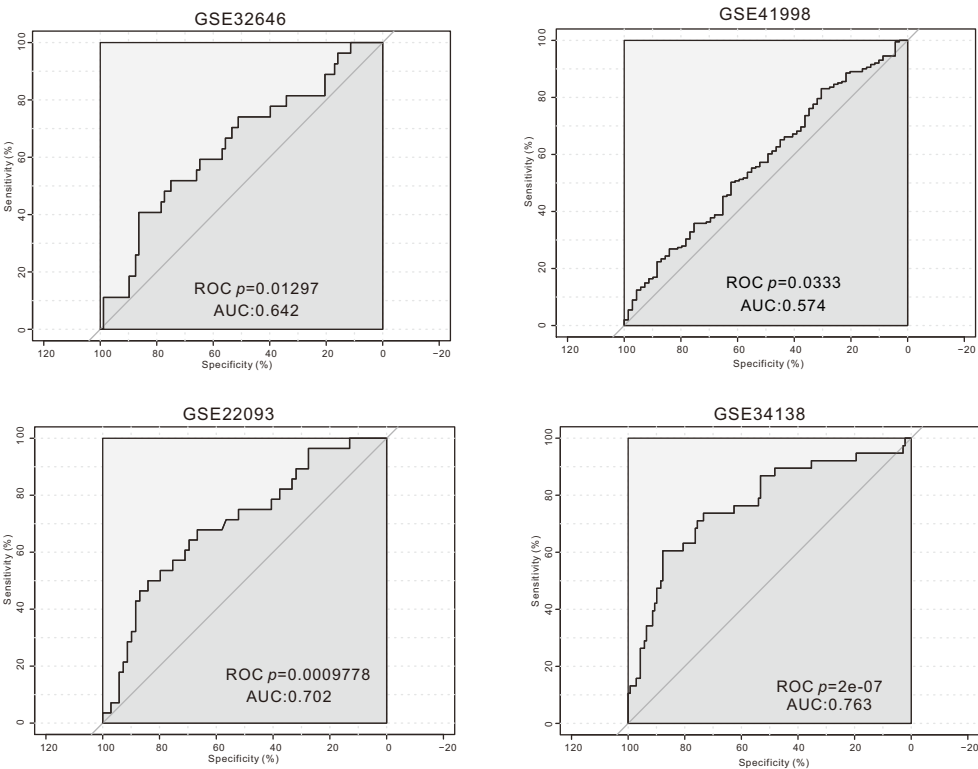


Fig. S7| Survival analysis of RBM15 in human breast cancer

ROC (Receiver operating characteristic) analysis with indicated cohorts. p -value indicates significance of analysis.

Fig. S8

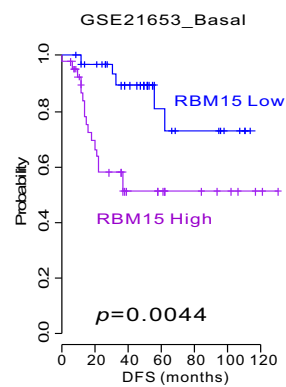


Fig. S8| Survival analysis of RBM15 in basal BC

Using indicated cohort, patients were classified according to the expression level of RBM15. Kaplan-Meier plots and the log-rank test were used to estimate patient prognosis. *p*-value indicates significance of analysis.

Fig. S9

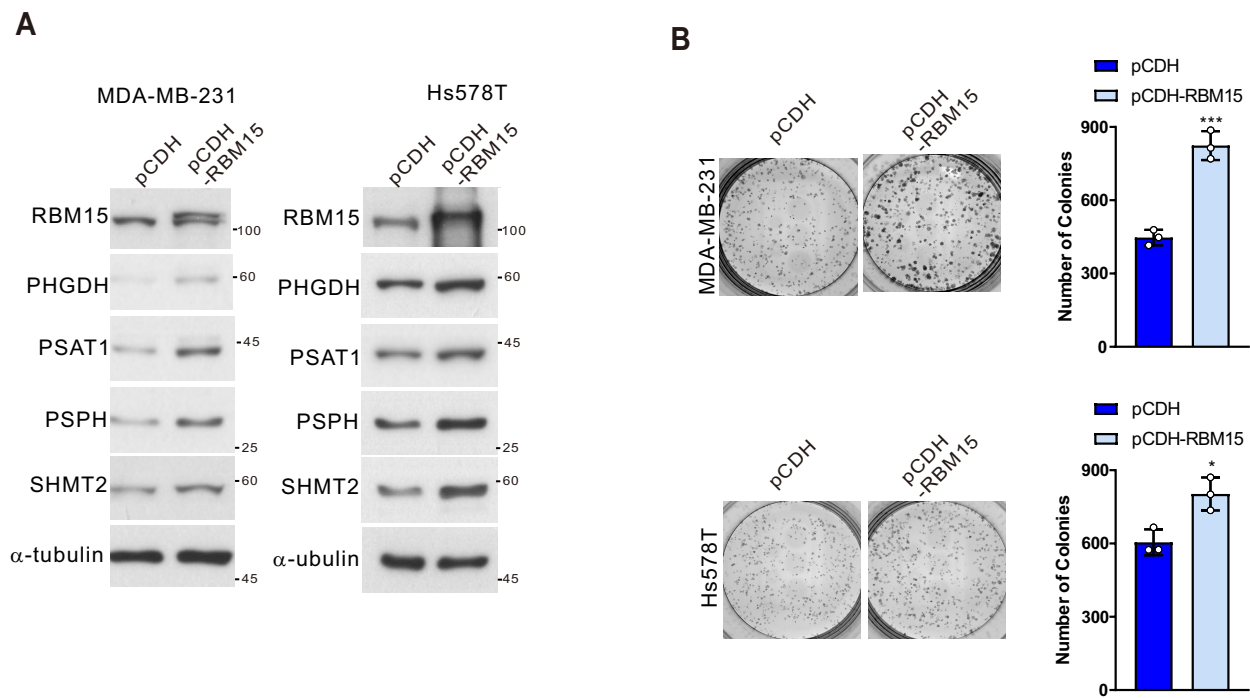


Fig. S9| Target gene expression of RBM15 in BC

A-B, MDA-MB-231 and Hs578T breast cells were infected with indicated cDNA pCDH or pCDH-RBM15). The cells were used for WB assay with indicated antibodies (A) and used for colony formation assay (B) (* $p<0.05$, ** $p<0.01$ and *** $p<0.005$).

Fig. S10

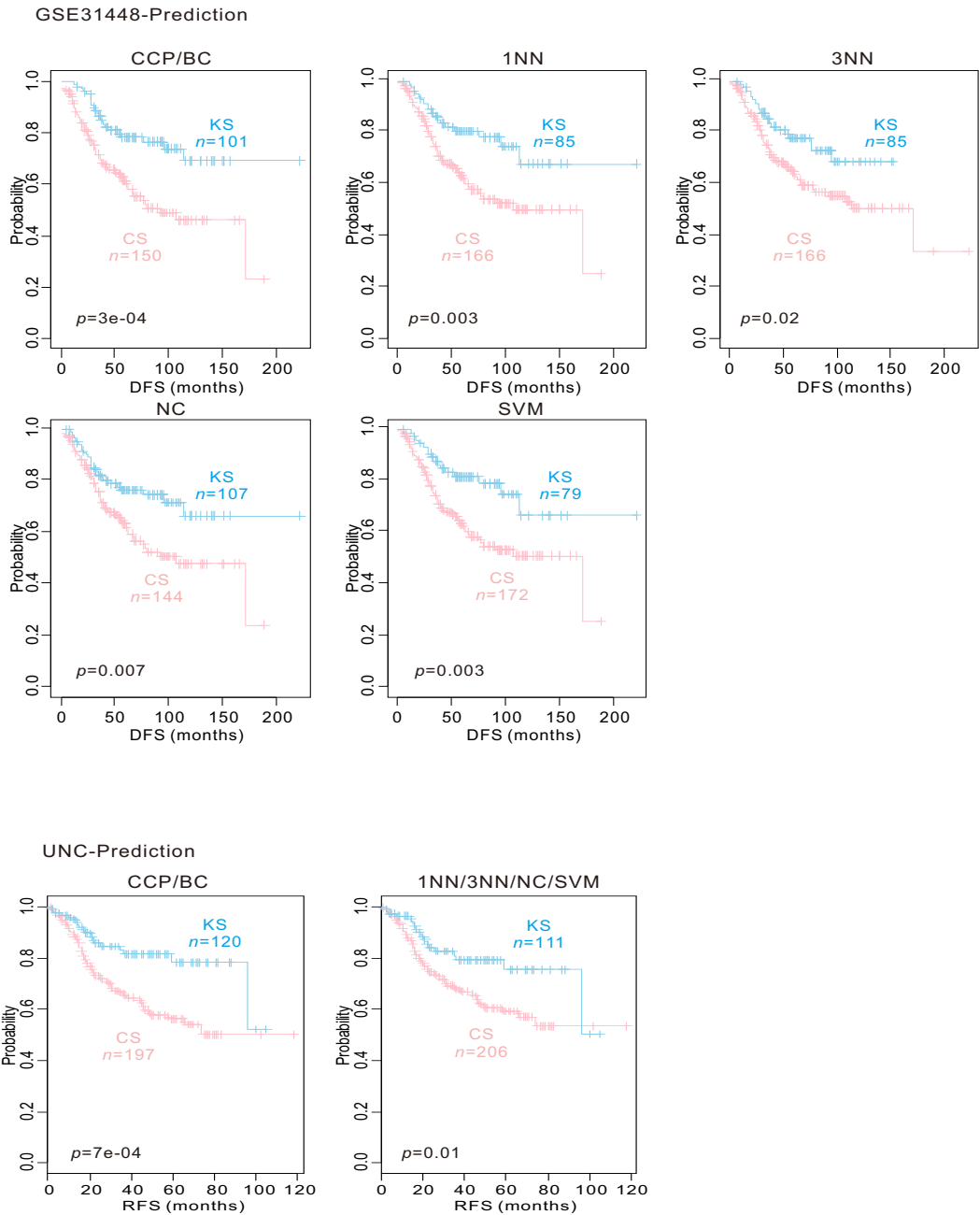


Fig. S10| Survival prediction with RBM15 gene signatures in BC

Kaplan-Meier plots of DFS and RFS (Relapse-free survival) of BC patients from GSE31448 and UNC cohorts predicted by using RBM15 gene expression signature with indicated classifiers (CS:Cotrol Signature; KS: Knock down Signature; SC:Compound covariate predictor (CCP), one nearest neighbor (1NN), three nearest neighbor (3NN), nearest centroid (NC), support vector machines (SVM) and bayesian analysis (BC). *p*-value indicates significance between groups-based on log-rank test.

Fig. S11

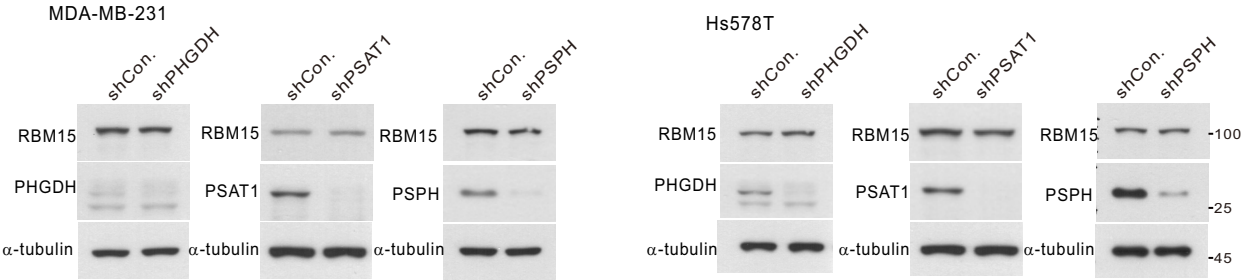


Fig. S11| SSP-silencing effect on RBM15 gene expression BC

MDA-MB-231 and Hs578T breast cells were infected with indicated shRNAs and the cells were used for WB assay with indicated antibodies (A) and used for colony formation assay (* $p<0.05$, ** $p<0.01$ and *** $p<0.005$).

Fig. S12

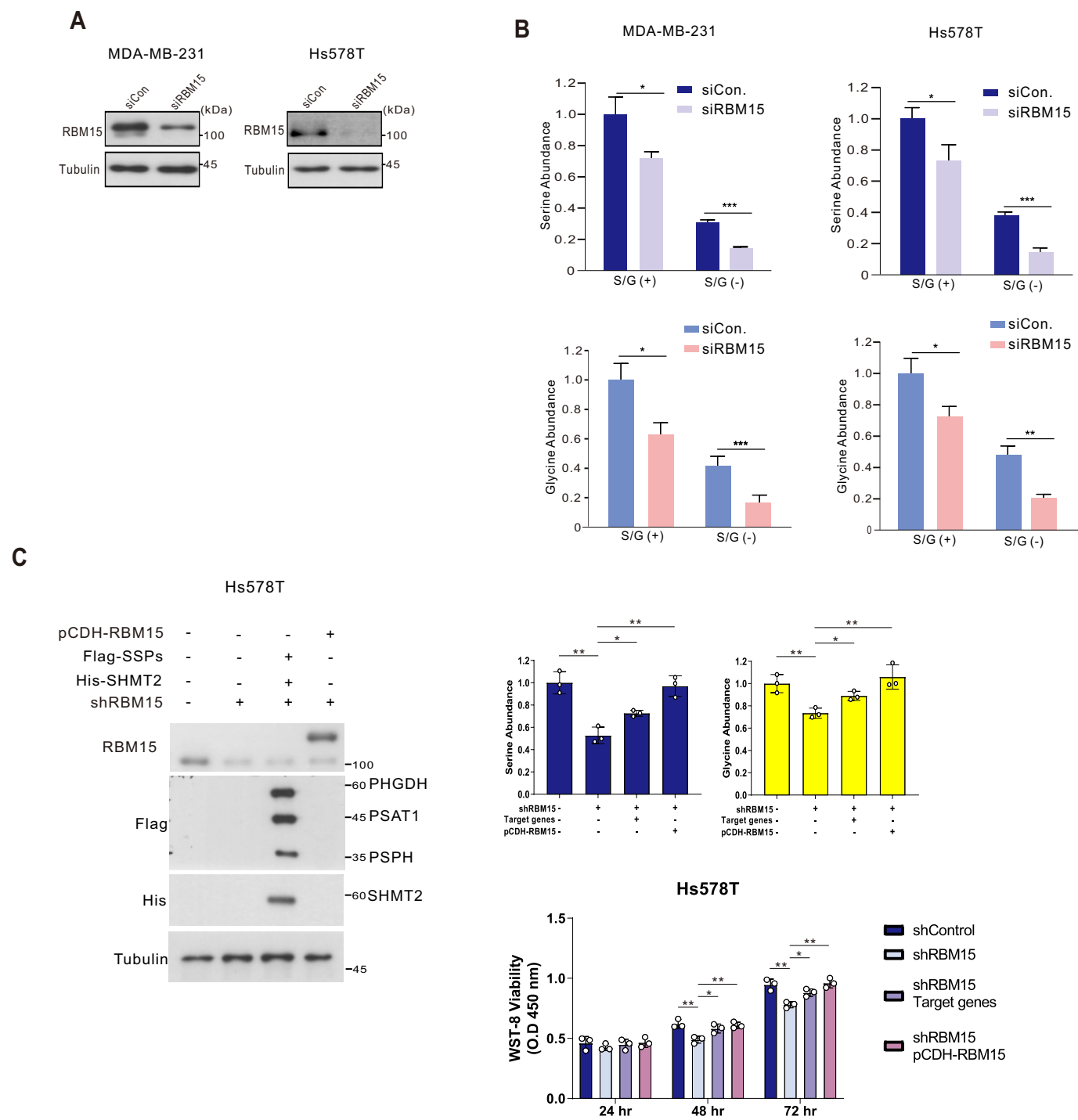


Fig. S12| Serine and glycine metabolite change by RBM15 in BC

A ~ B, Indicated breast cells were transfected with siRBM15 or siCon. The cells were used for WB with indicated antibodies (A), and for measuring serine and glycine metabolites (B). Student t-test (two-tailed) was applied to estimate the significance of assay (* $p<0.05$, ** $p<0.01$, and *** $p<0.005$).

Fig. S13

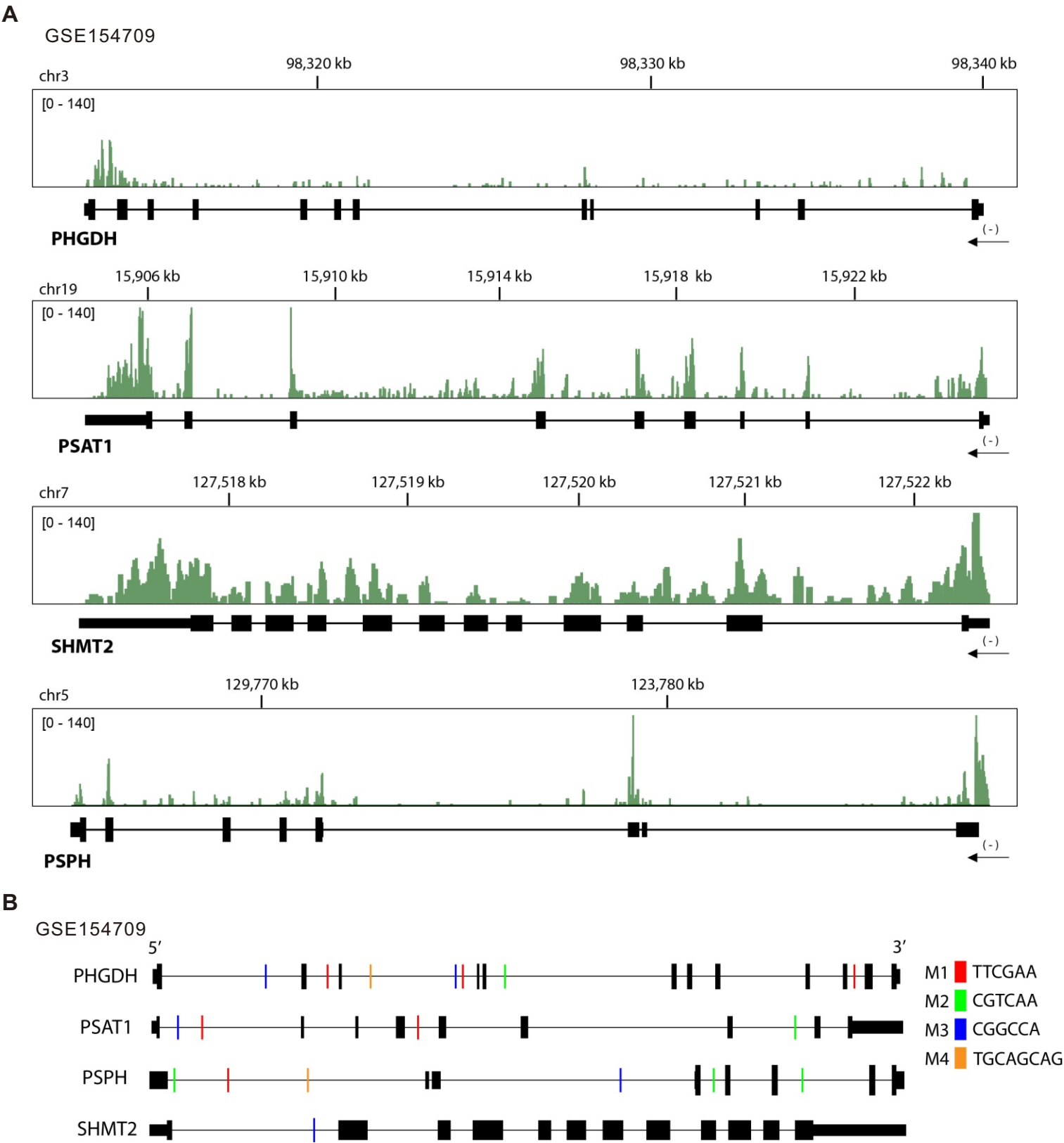


Fig. S13| RBM15 binding sites from sequence alignment.

A ~ B, Indicated genomic data were analyzed. (A) UCSC genome browser view of the RIP-seq reads mapping to PHGDH, PSAT1, PSPH, and SHMT2. (B) Sequencing alignment of PHGDH, PSAT1, PSPH, and SHMT2 genomic locus-based on RBM15-binding motif.

Fig. S14

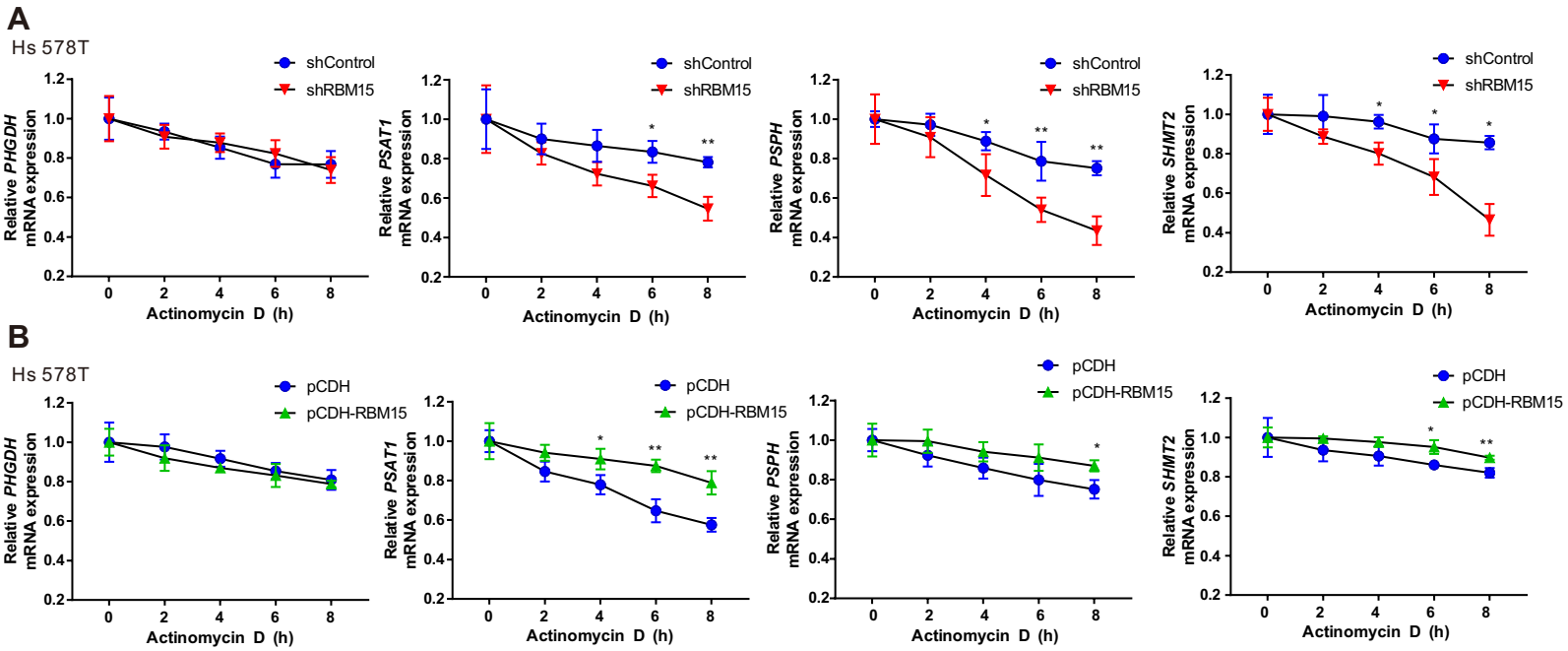


Fig. S14| Stability of RBM15 target gene by RBM15 in BC

Hs-578T breast cells were transfected with shRBM15 (or shCon; A) or pCDH-RBM15 (or pCDH; B) and treated with ActD. The cells were harvested at indicated time points and used for qRT-PCR with indicated probe. Student t-test (two-tailed) was applied to estimate the significance of assay (* $p<0.05$ and ** $p<0.01$).

Fig. S15

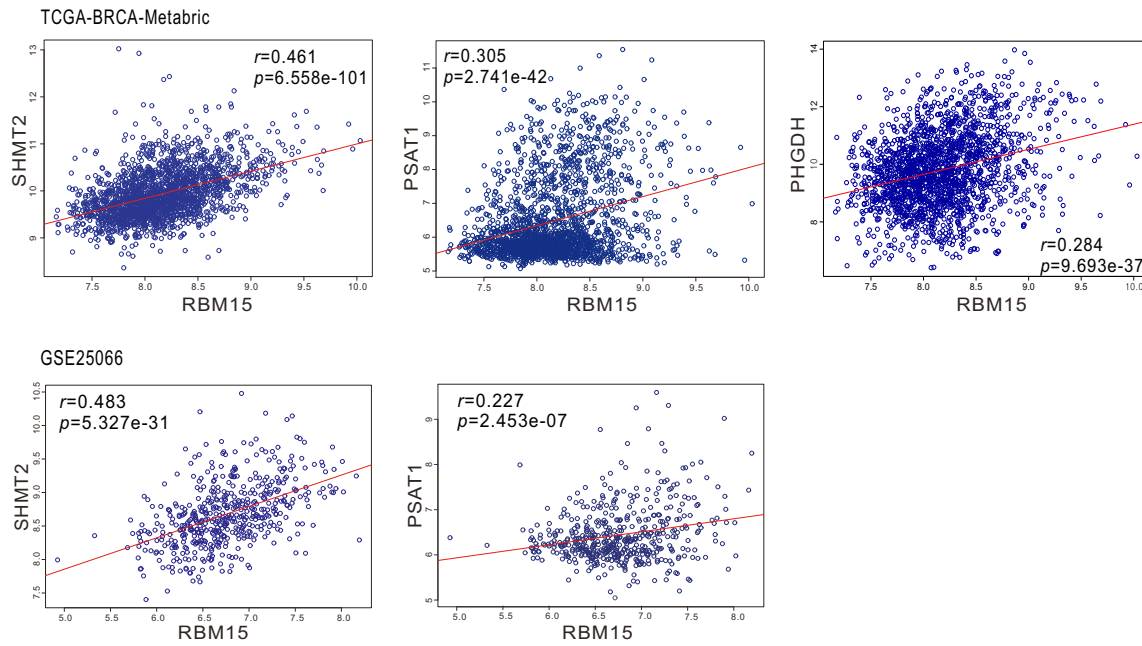
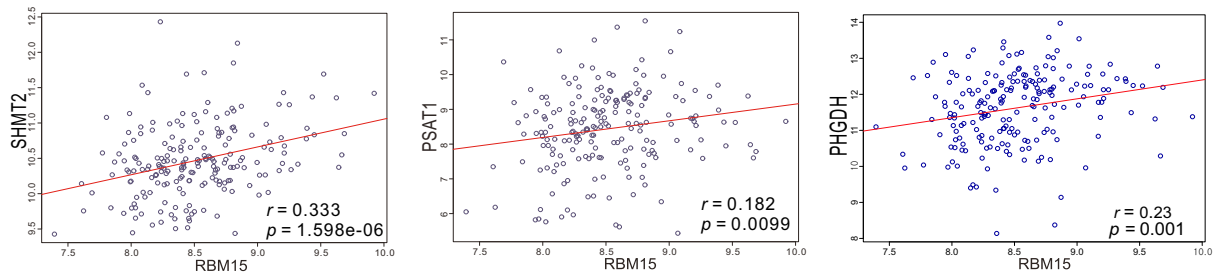


Fig. S15| Correlation of RBM15 and its target genes in BC

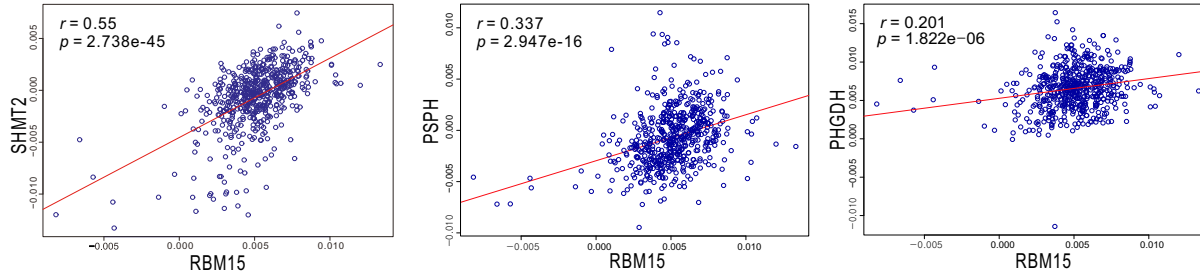
Correlation scatter plots between RBM15 and PSAT1, SHMT2, and PHGDH in indicated BC cohorts. p -value indicates significance of analysis (* $p < 0.05$, ** $p < 0.01$, *** $p < 0.005$, and **** $p < 0.001$).

Fig. S16

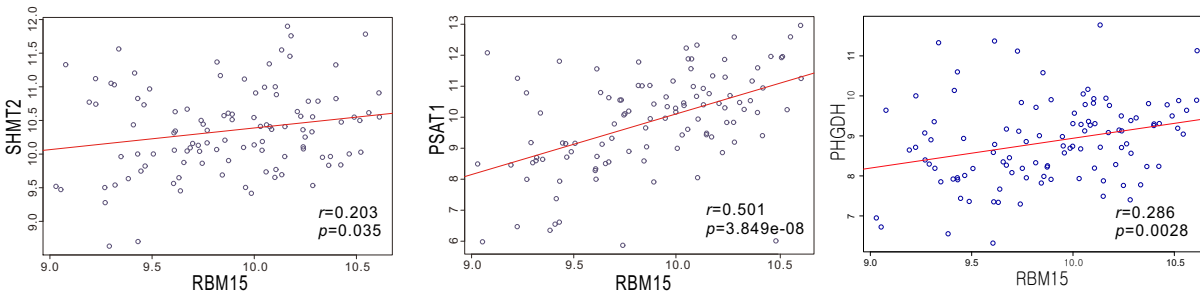
TCGA-BRCA-Metabric-Basal



GSE31519-TNBC



GSE58812-TNBC



GSE83937-TNBC

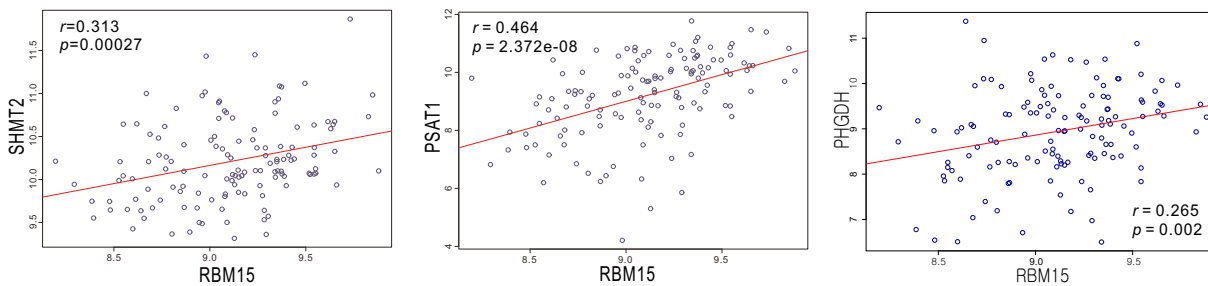


Fig. S16| Correlation of RBM15 and serine /glycine metabolism genes in TNBC/Basal BC

Correlation scatter plots between RBM15 and PHGDH, PSAT1, PSPH, and SHMT2 in indicated BC cohorts. p -value indicates significance of analysis (* $p < 0.05$, ** $p < 0.01$, *** $p < 0.005$, and **** $p < 0.001$).

Fig. S17

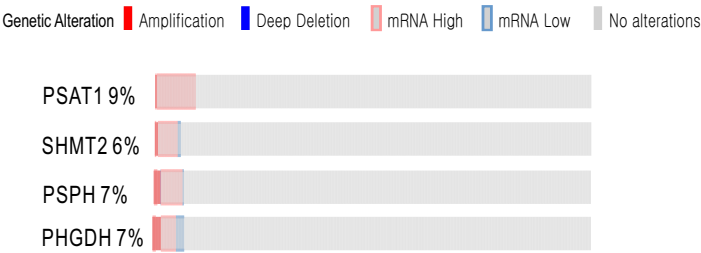
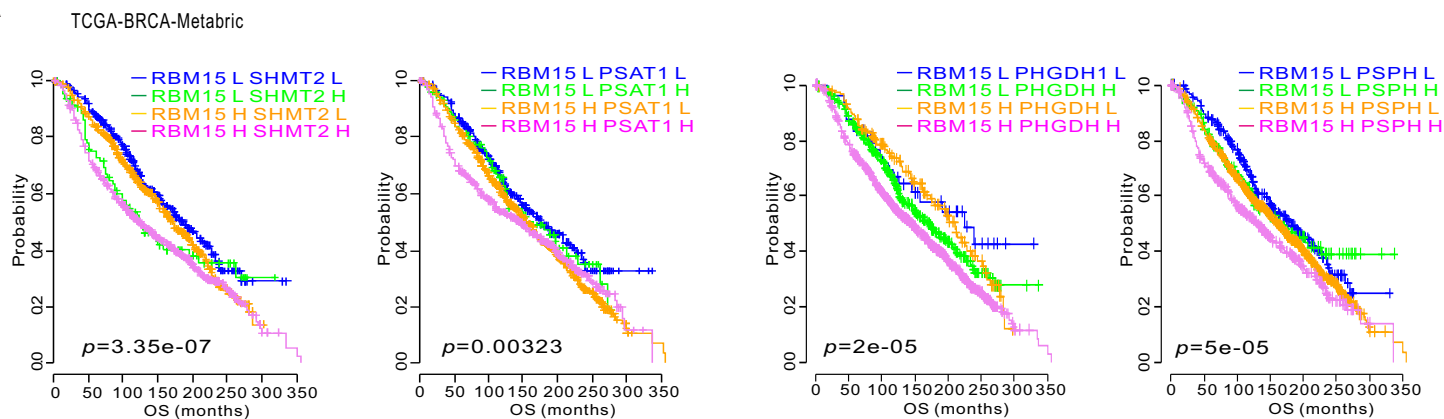


Fig. S17| Genetic alteration of serine and glycine metabolism genes in breast cancer.

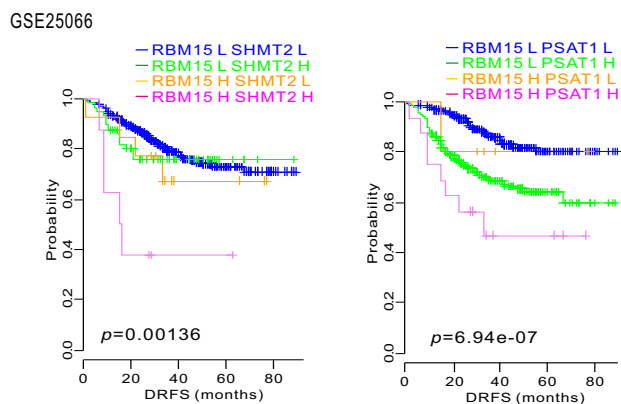
Genetic alteration of PHGDH, PSAT1, PSPH, and SHMT2 from TCGA-BRCA cohorts. These analysis were done in cBioportal.

Fig. S18

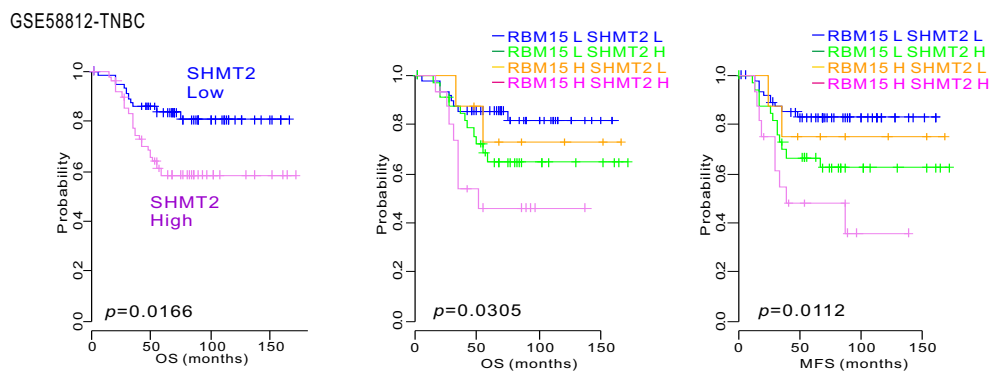
A



B



C



D

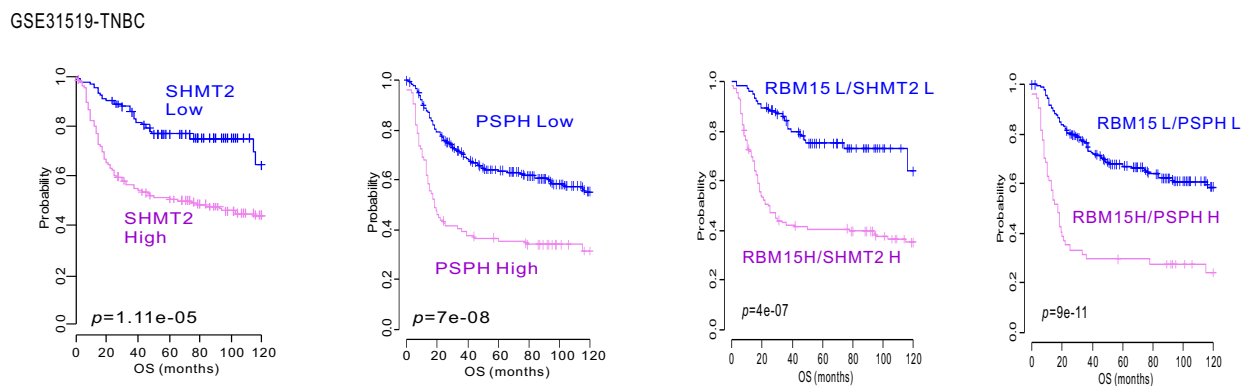


Fig. S18| Survival analysis of serine and glycine metabolism genes in BC

(A-D) Using indicated cohort, patients were classified according to the expression level of indicated genes. Kaplan-Meier plots and the log-rank test were used to estimate patient prognosis. p -value indicates significance of analysis.

Fig. S19

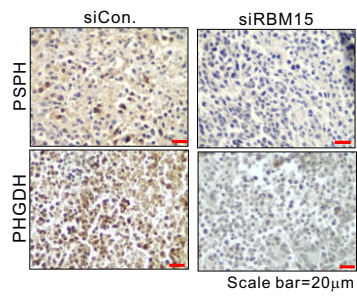


Fig. S19| RBM15-silencing reduced SSP gene expression in BC mouse model

After siRBM15 was injected to mice harboring MDA-MB-231 cells, tissues were used for IHC with indicated antibody.