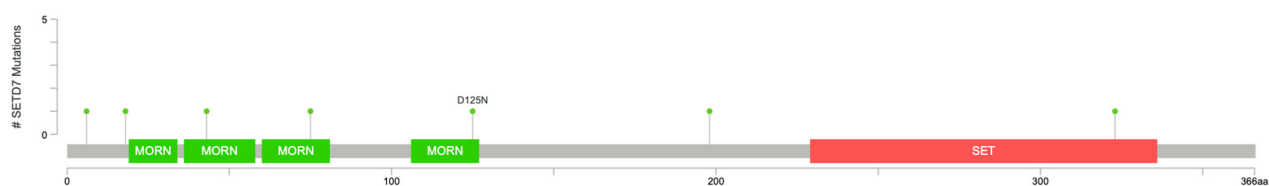
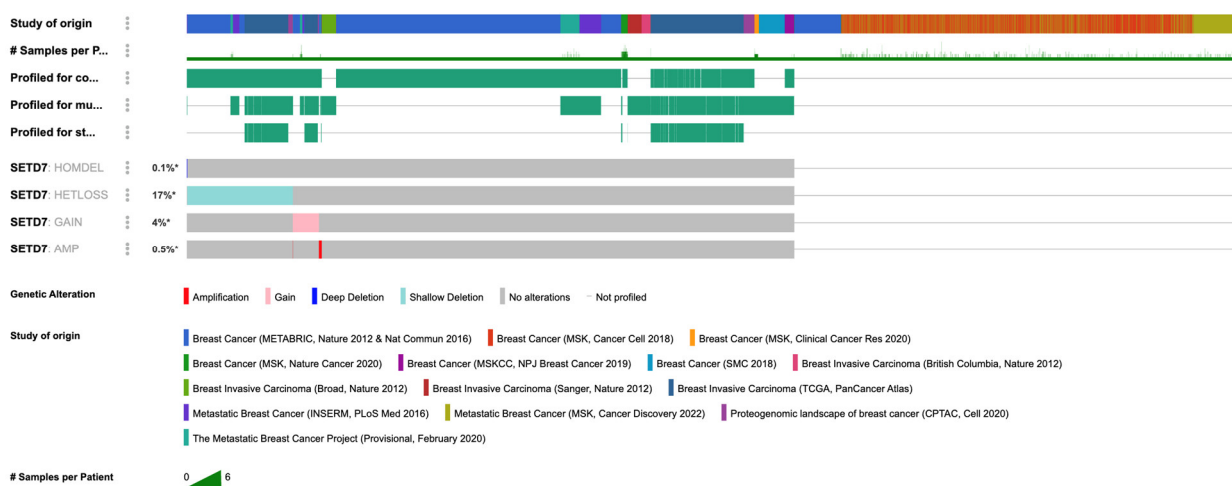


(a)

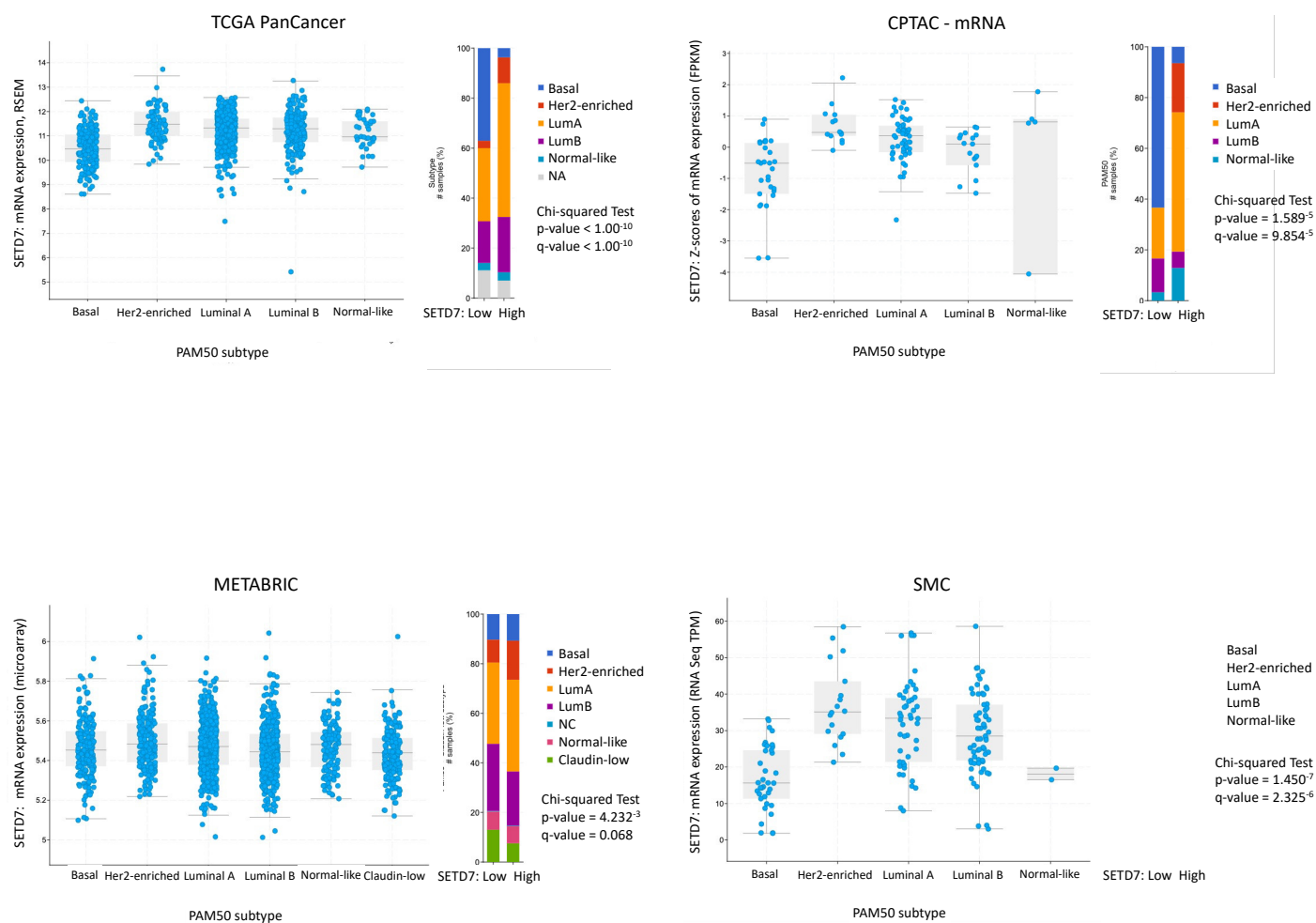


(b)

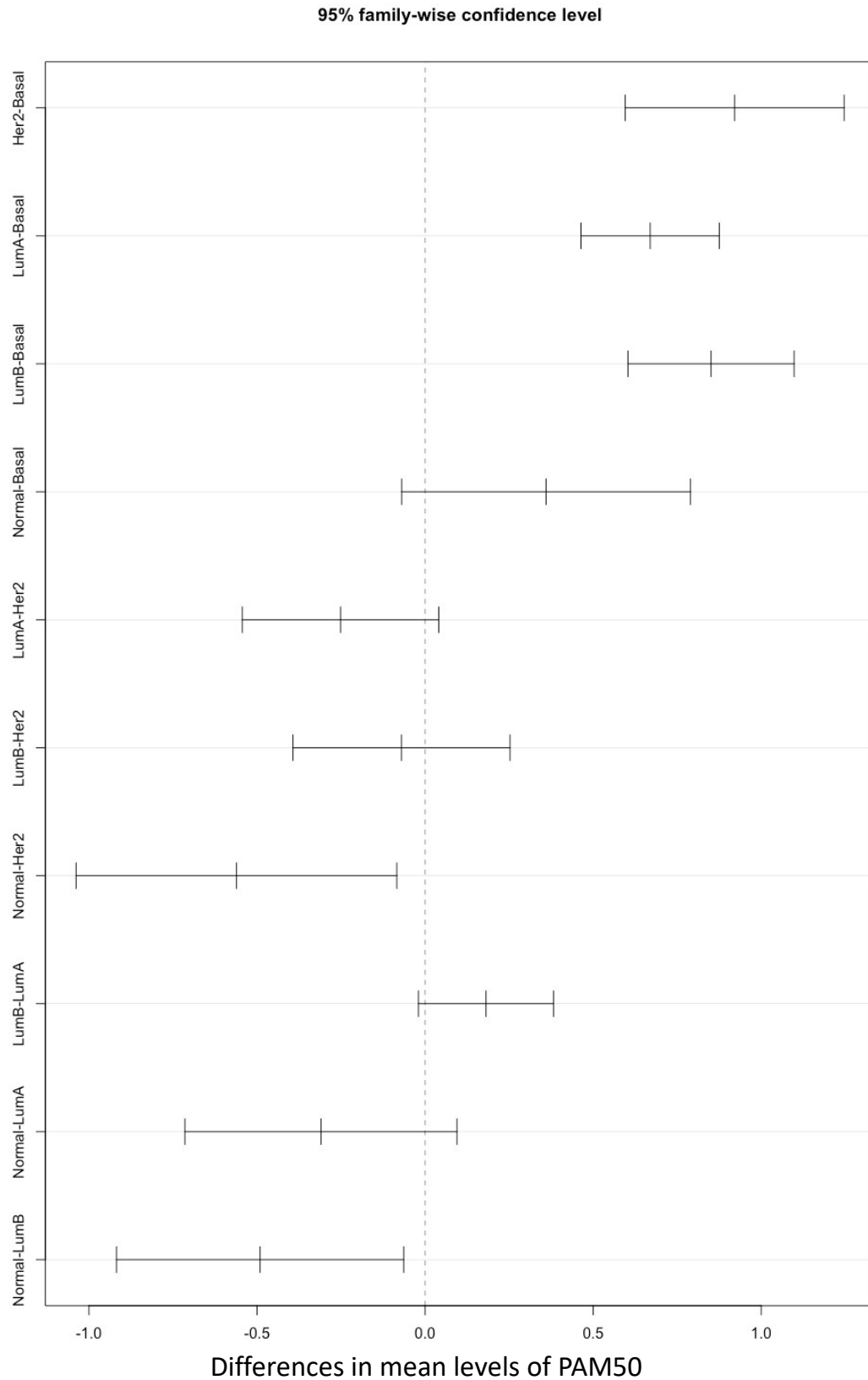


(c)

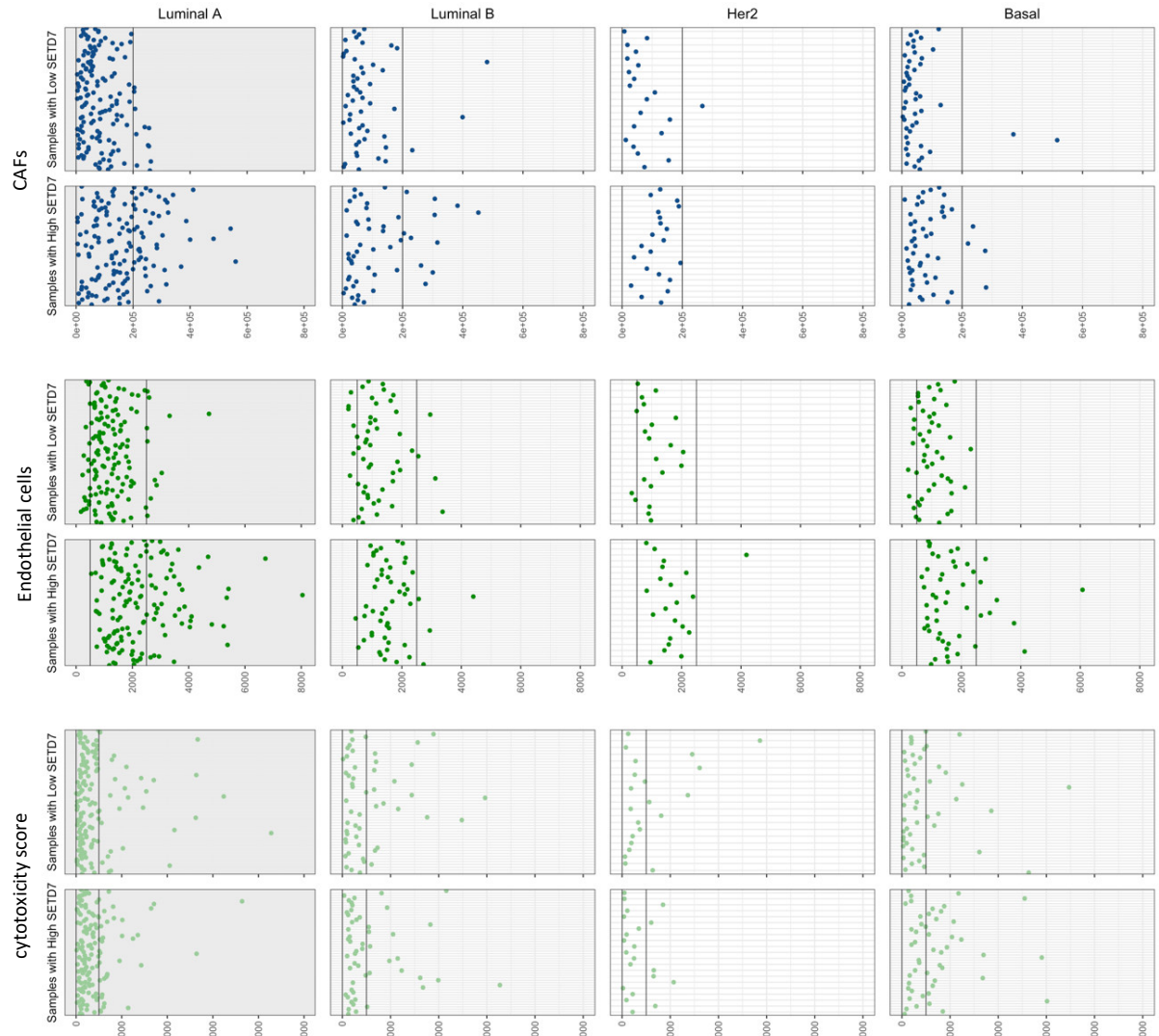
**Figure S1.** *SETD7* genomic alterations in breast cancer using cBioPortal. (a) Oncogrid for mutations; (b) *SETD7* mutation sites (lolipop) (c). Oncogrid for copy number alterations.



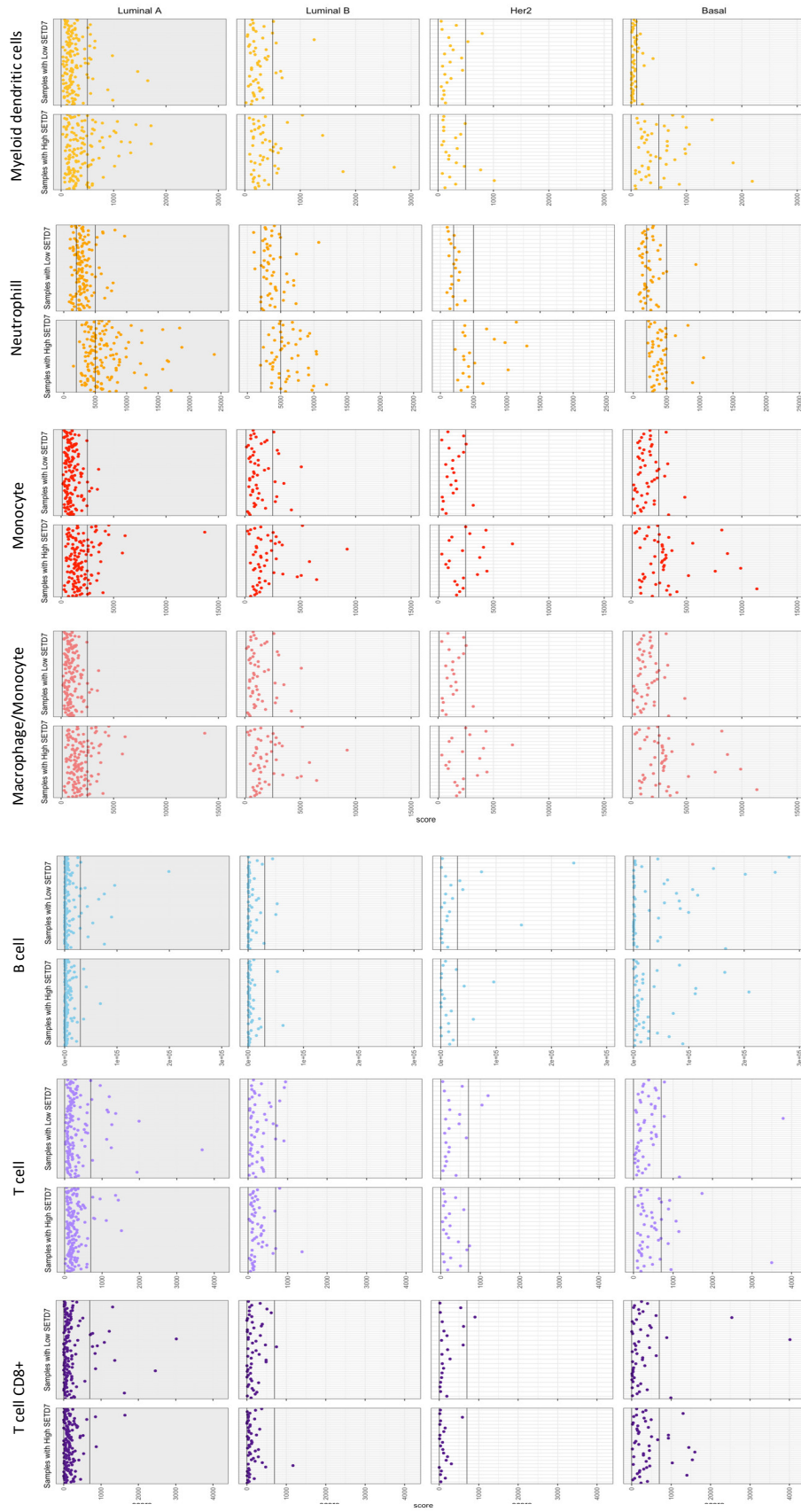
**Figure S2.** *SETD7* mRNA expression in breast cancer PAM50 subtypes using cBioPortal datasets.



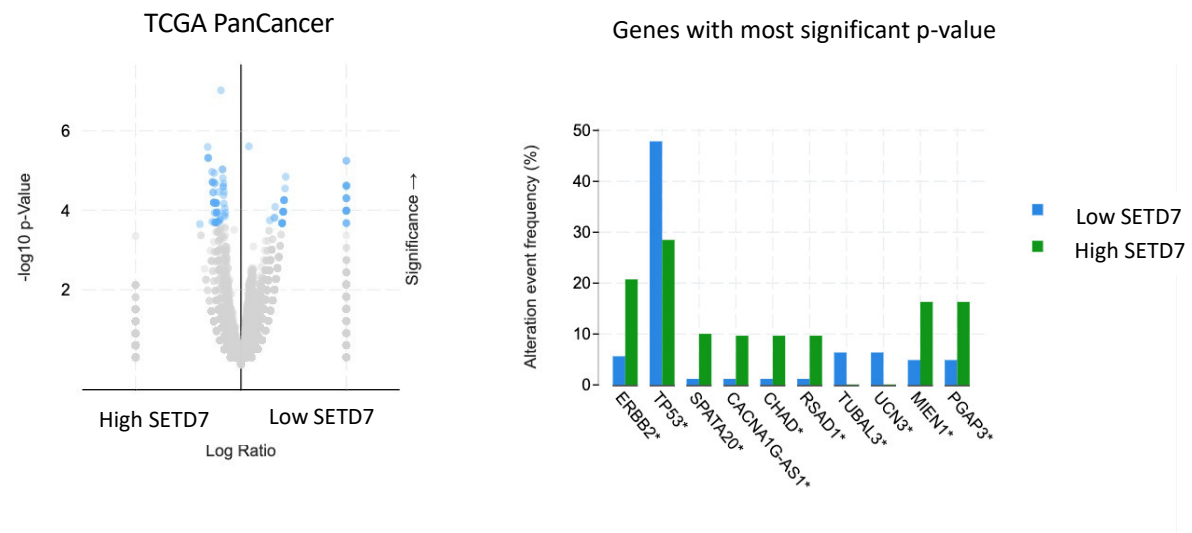
**Figure S3.** Mean differences of each comparison done in Figure 1B and the 95% confidence intervals associated with them.



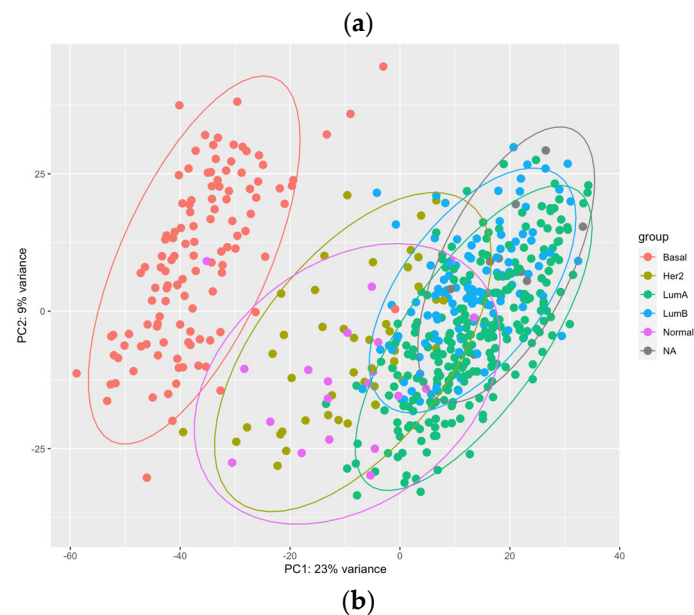
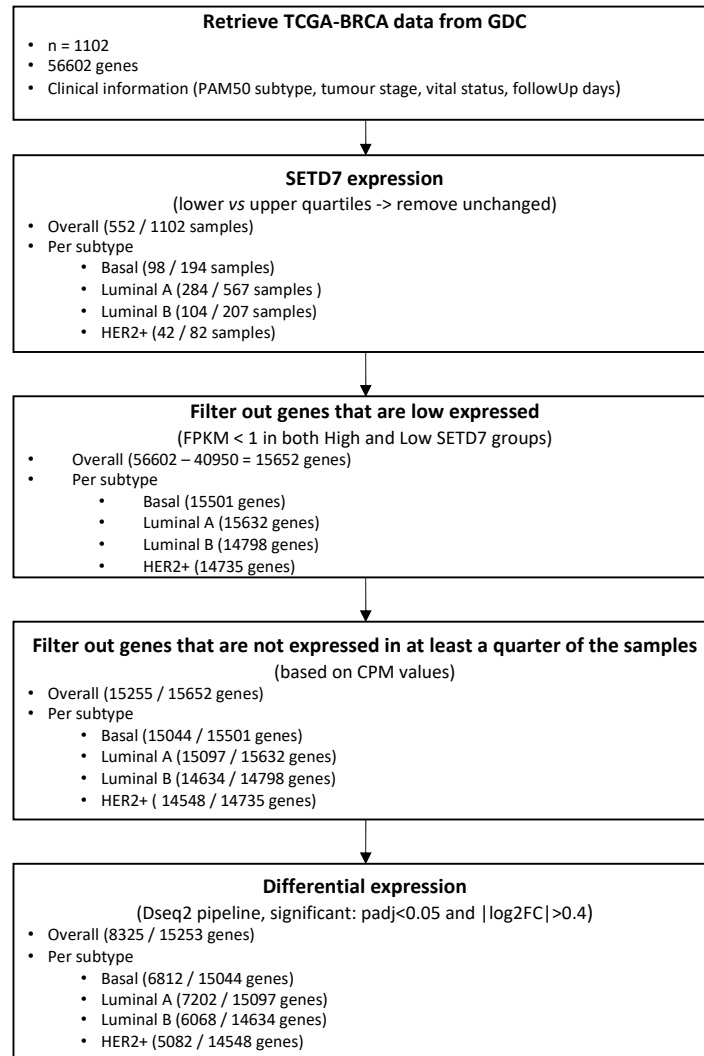
**Figure S4.** Predicted infiltration of cancer-associated fibroblasts (CAFs), endothelial cells and cytotoxicity score in samples with differential *SETD7* mRNA expression (high *vs* low) from different breast cancer PAM50 subtypes using *mcp\_count* method from *immunodeconv* package and TCGA-BRCA data overall.



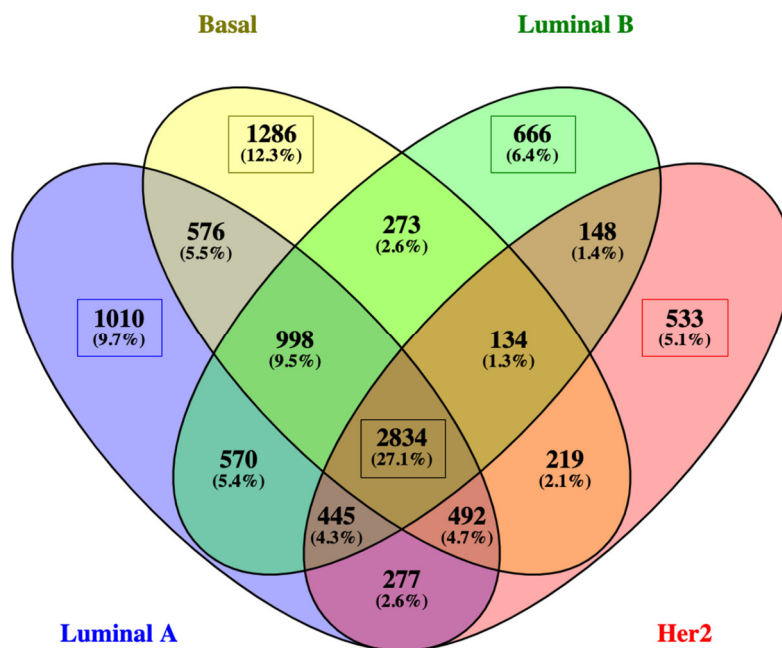
**Figure S5.** Predicted infiltration of immune cells in samples with differential *SETD7* mRNA expression (high *vs* low) from different breast cancer PAM50 subtypes, using *mcp\_count* method from *immunodeconv* package and TCGA-BRCA data overall.



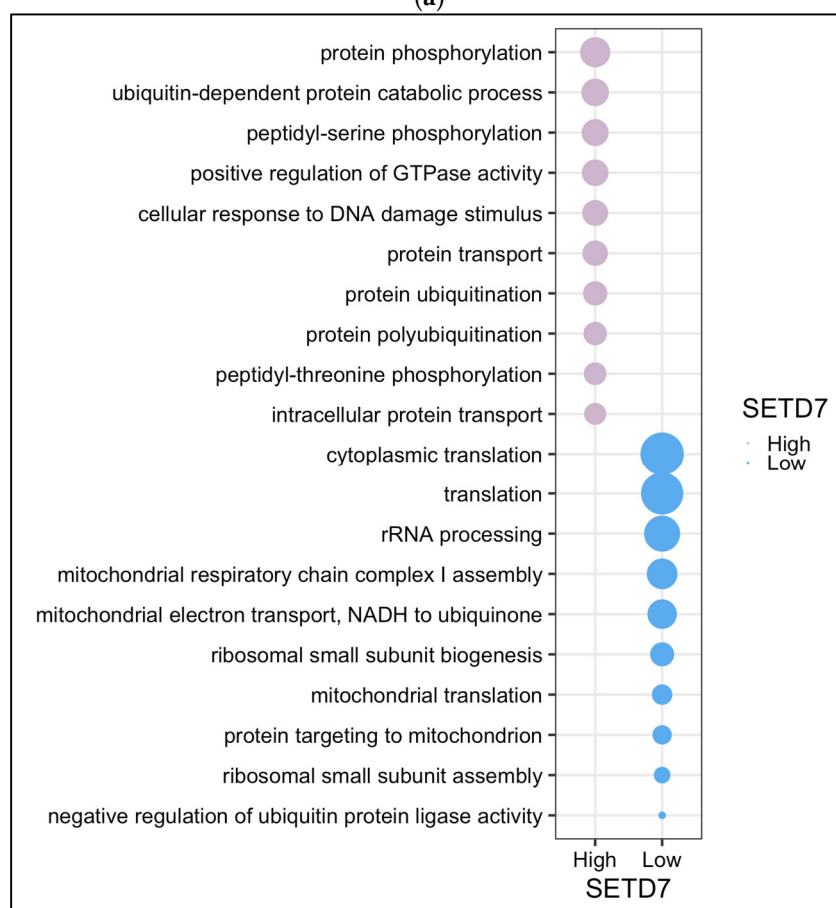
**Figure S6.** Genomic alterations associated *SETD7* mRNA differential expression from TCGA PanCancer Atlas in cBioPortal.



**Figure S7.** TCGA-BRCA data processing. (a) Scheme describing the TCGA-BRCA data processing; (b) PCA plot of TCGA-BRCA samples stratified by high- and low-SETD7.



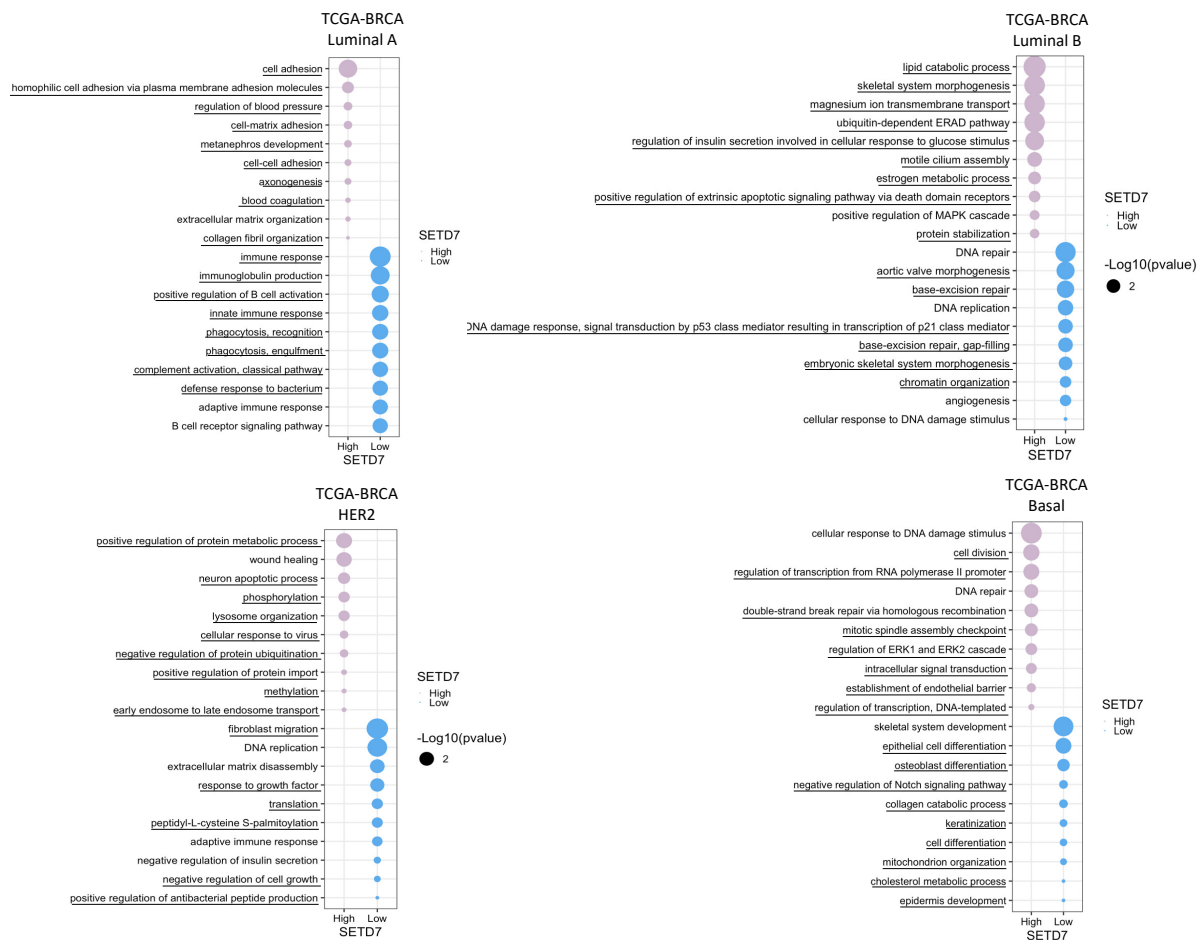
(a)



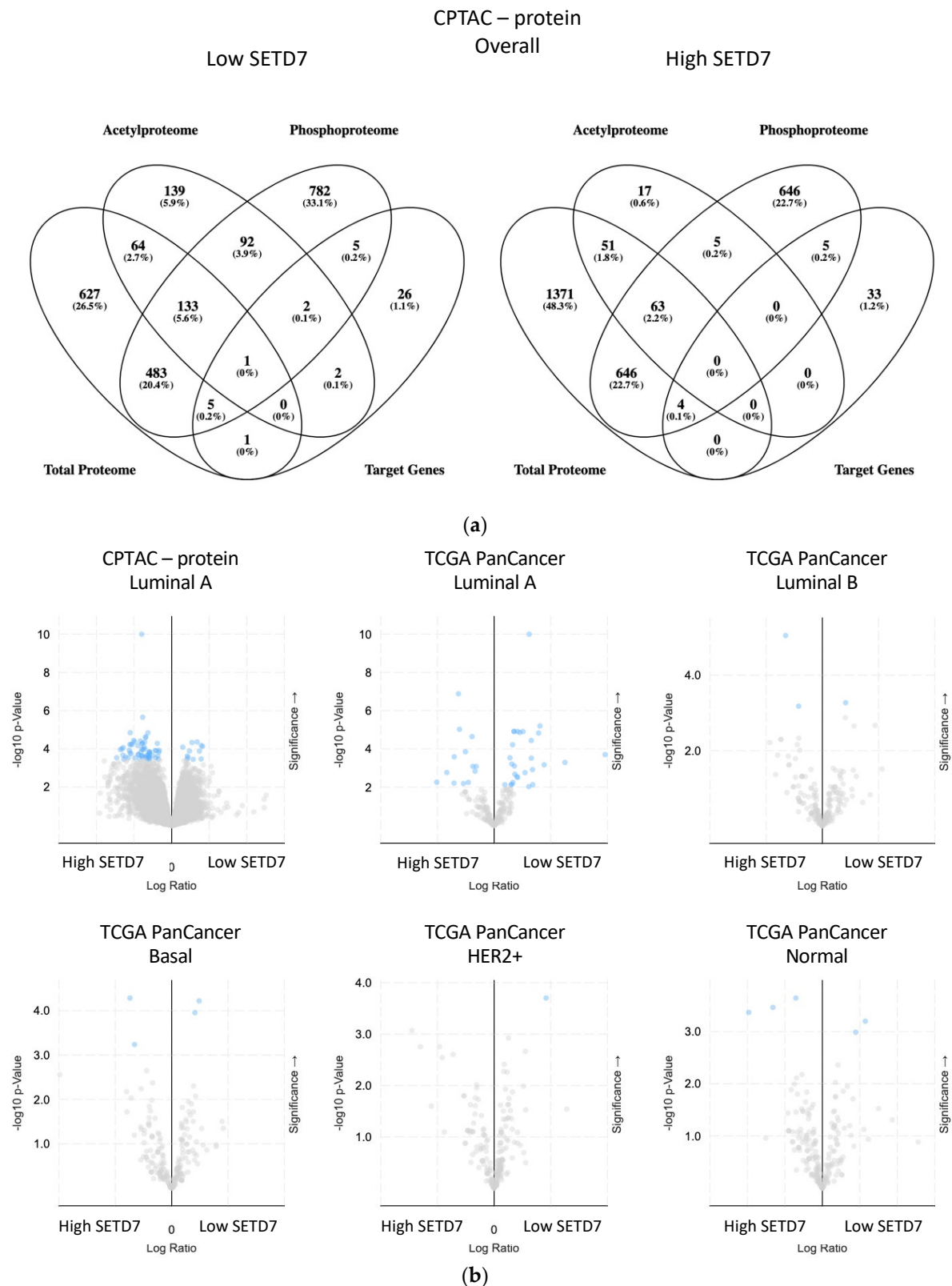
(b)

**Figure S8.** Analysis of genes associated with *SETD7* mRNA differential expression per subtype from TCGA-BRCA. (a) Venn diagram; (b) Top-10 Biological processes overrepresented by the genes common to all subtypes and significantly associates with *SETD7* differential expression (high and low distinctly).





**Figure S9.** Top-10 biological processes overrepresented by the genes associated with *SETD7* differential expression (high and low distinctly) and unique for each subtype. Biological processes unique to each subtype are underlined.



**Figure S10.** Analysis of proteins associated with SETD7 protein differential expression using CPTAC. **(a)** Venn diagrams showing the intersection of the results from total proteome, acetylproteome, phosphoproteome and target genes for high- and low-SETD7 groups distinctly. **(b)** Volcano plots of the total proteome analysed per subtype.