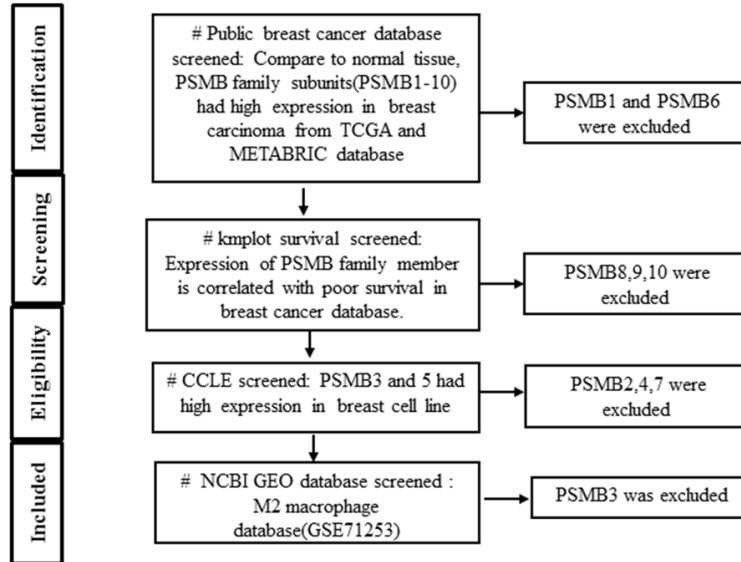
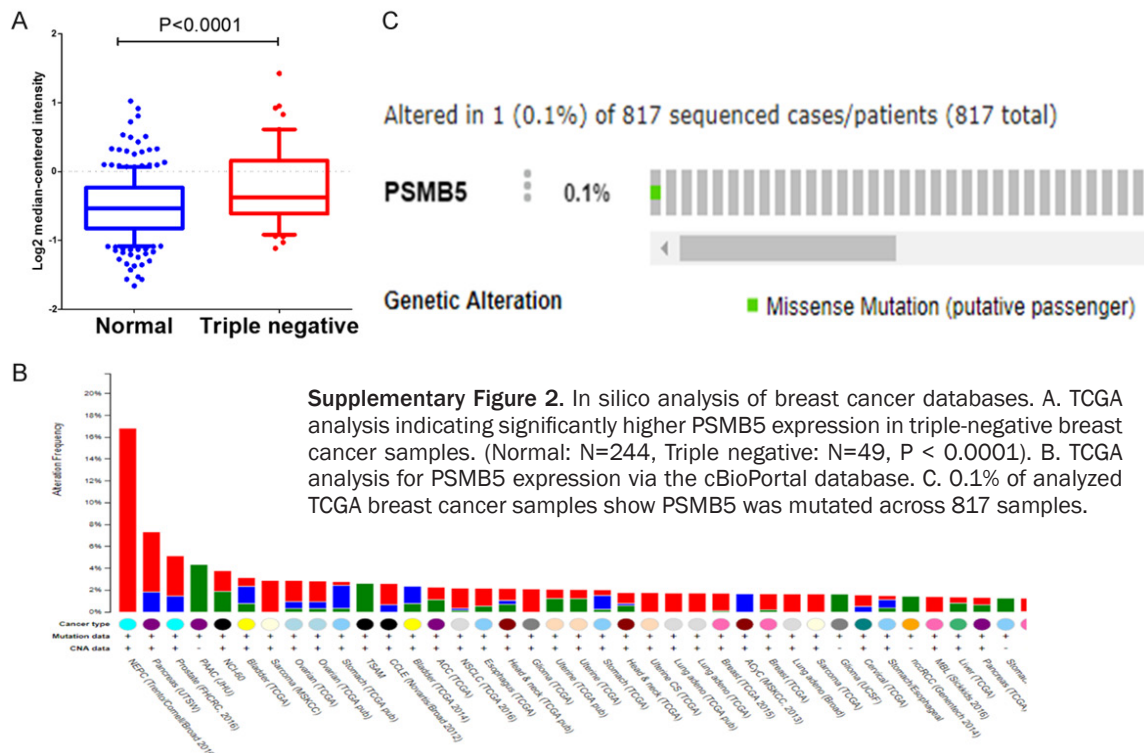


Dual role of PSMB5 in breast cancer



Supplementary Figure 1. Flowchart presenting the identification and collection of the studies for the statistical meta-analysis. A flow diagram, in accordance with the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) guidelines. Briefly, PSMB family contain 10 subunits, most PSMB subunits were found high expression in breast cancer tissue from TCGA as well as METABRIC database whereas PSMB1 and 6 were not, therefore PSMB1 and 6 were excluded in the first step screened. Of the remaining PSMB family subunits (PSMB2, 3, 4, 5, 7, 8, 9, 10), we found that high expression of PSMB2, 3, 4, 5, 7 were associated with poor survival, however, PSMB8, 9, 10 are not, thus they were excluded in the second step screened. Next, Of the remaining PSMB family subunits (PSMB2, 3, 4, 5, 7) we found that only PSMB3 and 5 had high expression in breast cancer cell line in CCLE database, therefore we excluded PSMB2, 4, 7, 10. Finally, Of the remaining PSMB family subunits (PSMB3, 5), we found that only PSMB5 had high expression in M2 macrophage dataset whereas PSMB3 were not. Therefore, only PSMB5 fulfilled all our inclusion criteria to do further study.



Supplementary Figure 2. In silico analysis of breast cancer databases. A. TCGA analysis indicating significantly higher PSMB5 expression in triple-negative breast cancer samples. (Normal: N=244, Triple negative: N=49, $P < 0.0001$). B. TCGA analysis for PSMB5 expression via the cBioPortal database. C. 0.1% of analyzed TCGA breast cancer samples show PSMB5 was mutated across 817 samples.