Figure S1 GO and KEGG pathway enrichment analysis of DEGs in BCBM after removing the outliers. (A) GO CC of DEGs. (B) GO BP of DEGs. (C) GO MF of DEGs. (D) KEGG of DEGs. ICERM, integral component of endoplasmic reticulum membrane; ER-GIC, endoplasmic reticulum-Golgi intermediate compartment; PRPCP, positive regulation of protein catabolic process; NRTCRSP, negative regulation of T cell receptor signaling pathway; PRPCA, positive regulation of protein complex assembly; NRGE, negative regulation of gene expression; NRPMTRP2P, negative regulation of pri-miRNA transcription from RNA polymerase II promoter; miRNA, microRNA; PROD, positive regulation of osteoclast differentiation; RACR, regulation of actin cytoskeleton reorganization; NRTDT, negative regulation of transcription; DNA-templated; PRBM, positive regulation of bone mineralization; RSGMST, regulation of small GTPase mediated signal transduction; CRTMF, cellular response to tumor necrosis factor; C-MSP, chemokine-mediated signaling pathway; PRCM, positive regulation of cell migration; PRAP, positive regulation of apoptotic process; EASP, extrinsic apoptotic signaling pathway; NRSA-DCP, negative regulation of substrate adhesion-dependent cell spreading; PRNTFA, positive regulation of NF-kappaB transcription factor activity; PRTCA, positive regulation of T cell activation; PDGFB, platelet-derived growth factor binding; EMSC, extracellular matrix structural constituent; PSTPA, protein serine/threonine phosphatase activity; G-N EFA, guanyl-nucleotide exchange factor activity; EMSCCTS, extracellular matrix structural constituent conferring tensile strength; ETTA, efflux transmembrane transporter activity; PNMD, pathways of neurodegeneration-multiple diseases; A-G SPDC, AGE-RAGE signaling pathway in diabetic complications; AGE, advanced glycation end product; RAGE, receptor for AGE; GO, gene ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes; DEGs, differentially expressed genes; BCBM, breast cancer with brain metastases; CC, cellular component; BP, biological process; MF, molecular function.

Figure S2 PPI network and the most significant module of DEGs after removing the outliers. (A) PPI network of DEGs. (B) Most significant modules obtained from PPI network. PPI, protein-protein interaction; DEGs, differentially expressed genes.
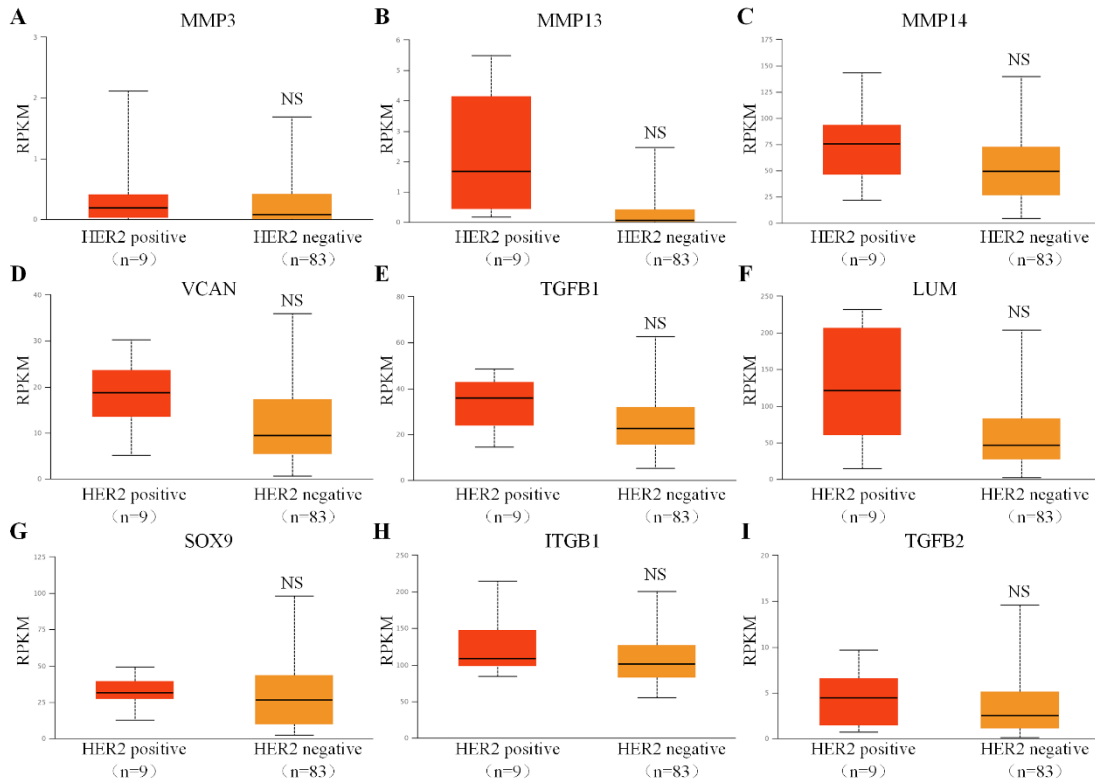

Figure S3 Comparison of 9 candidate hub genes expression between HER2-positive and negative MBC via UALCAN. (A) *MMP3* expression level. (B) *MMP13* expression level. (C) *MMP14* expression level. (D) *VCAN* expression level. (E) *TGFB1* expression level. (F) *LUM* expression level. (G) *SOX9* expression level. (H) *ITGB1* expression level. (I) *TGFB2* expression level. RPKM, reads per kilobase per million mapped reads; HER2, human epidermal growth factor receptor 2; NS, no significance; MBC, metastatic breast cancer.