

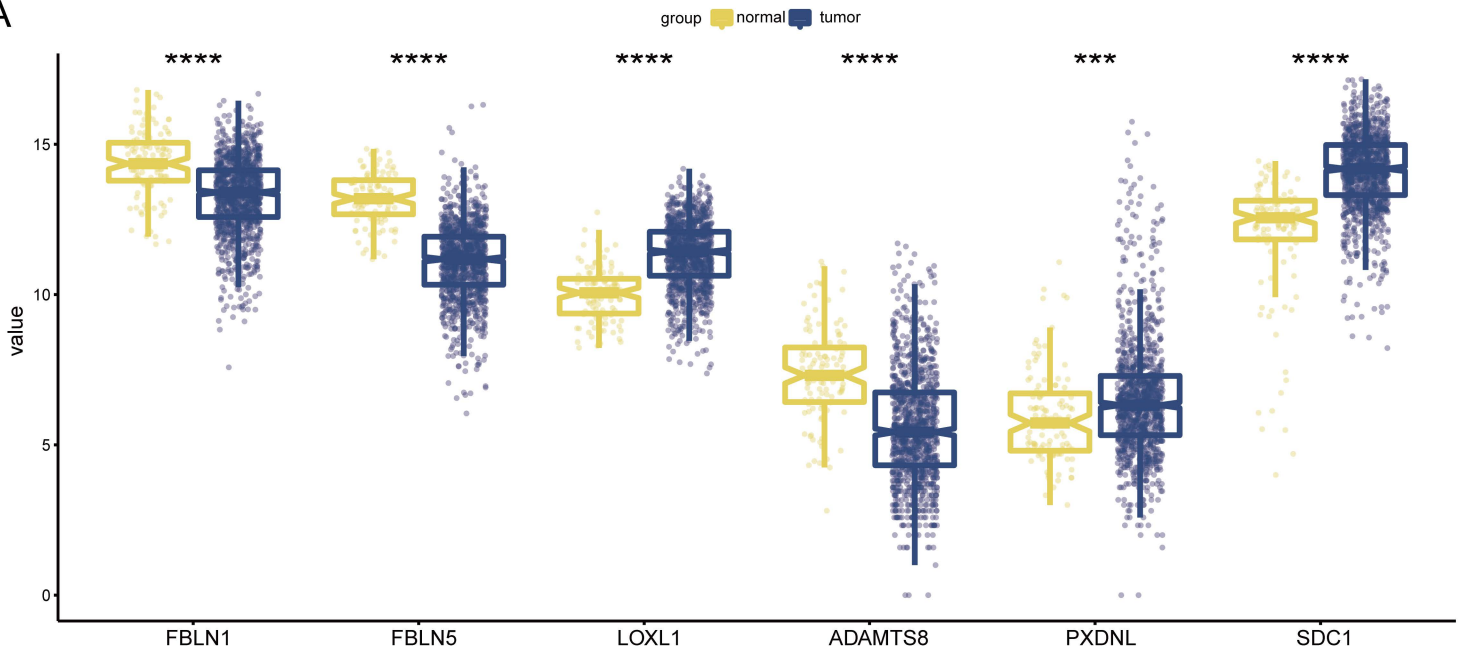
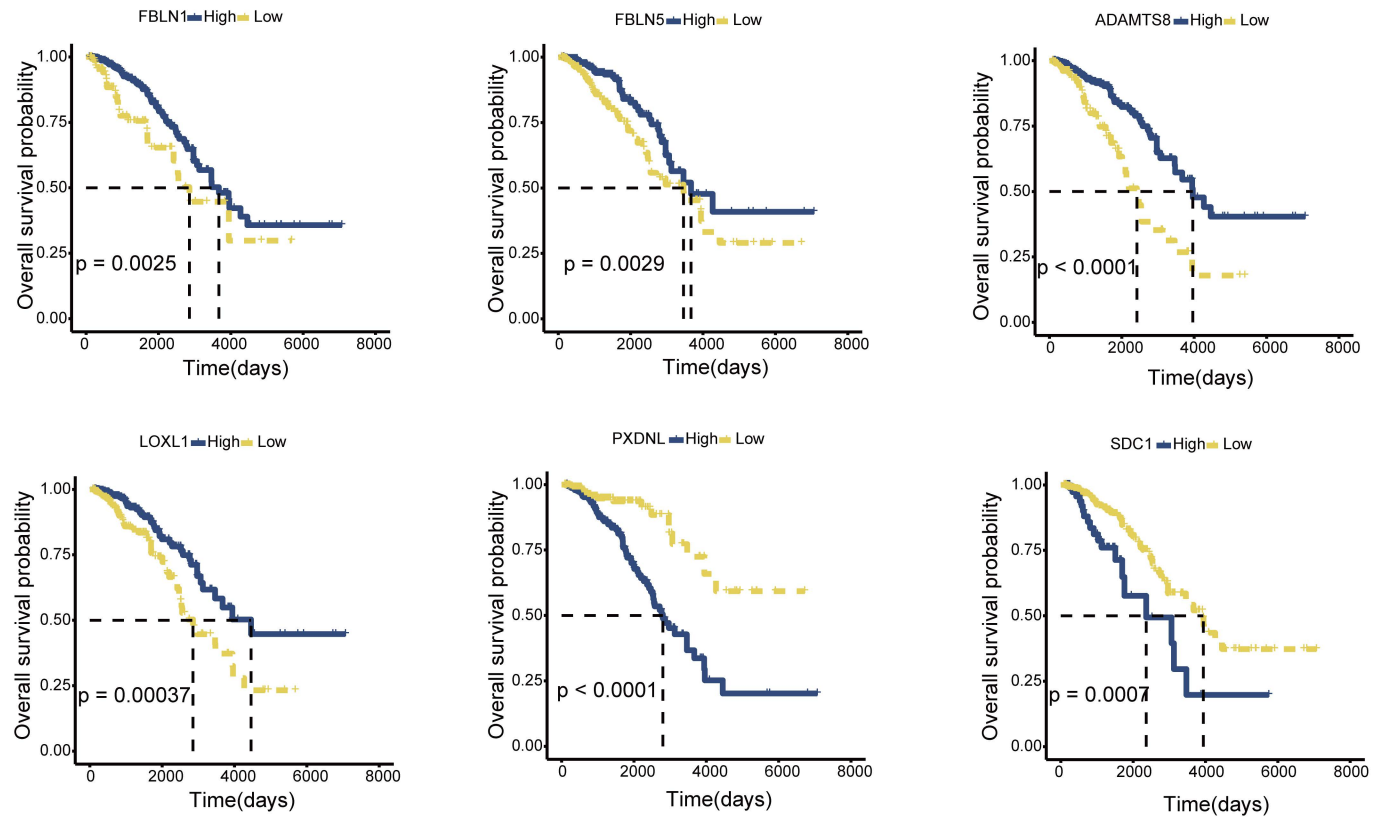
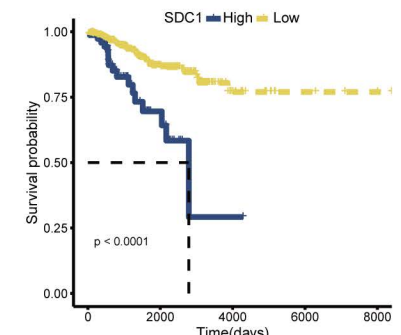
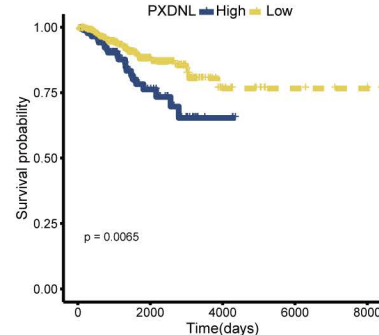
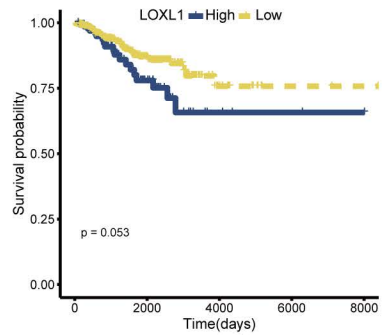
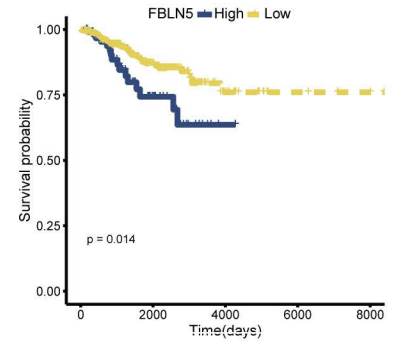
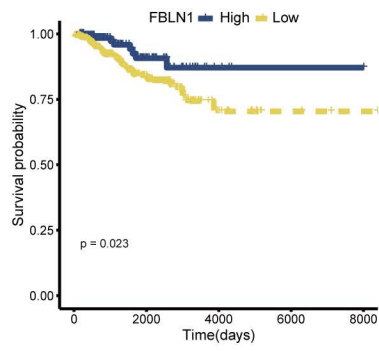
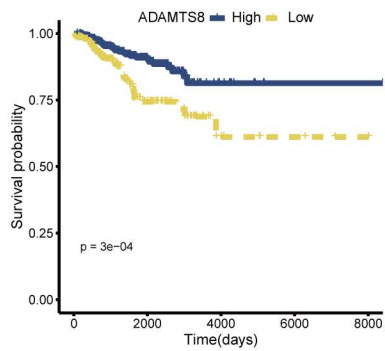
A**B**

Figure S1

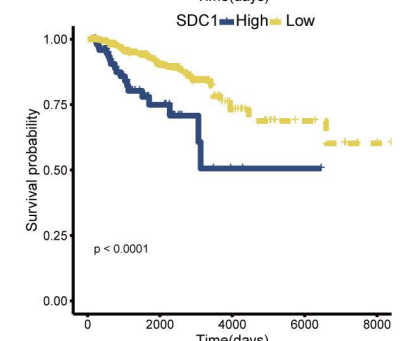
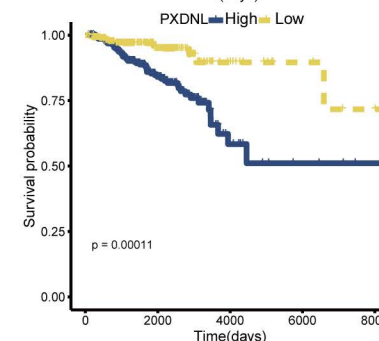
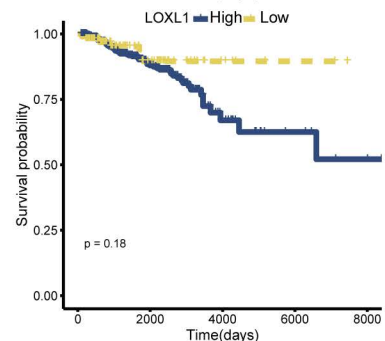
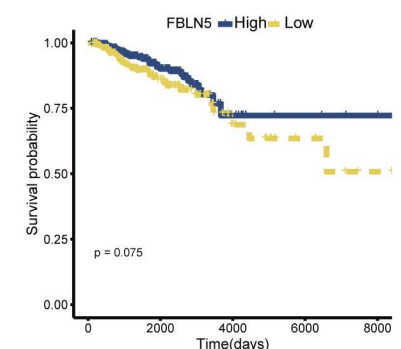
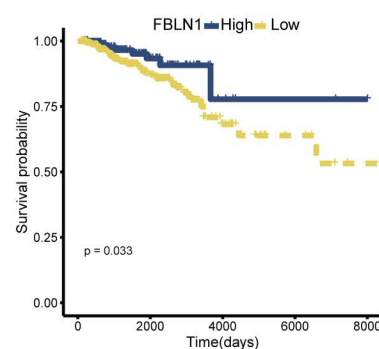
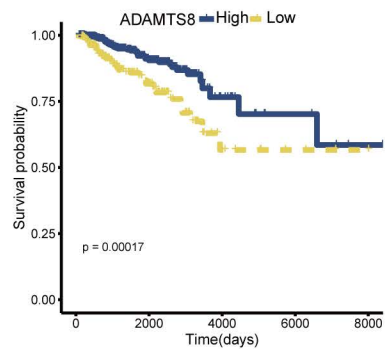
A

Disease-free Survival



B

Disease-specific Survival



C

Progression-free Survival

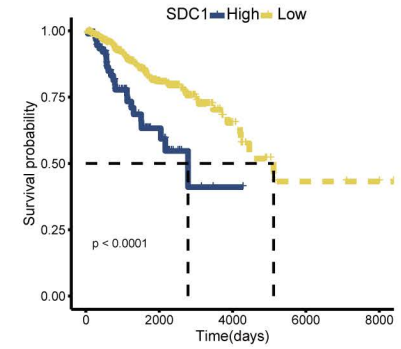
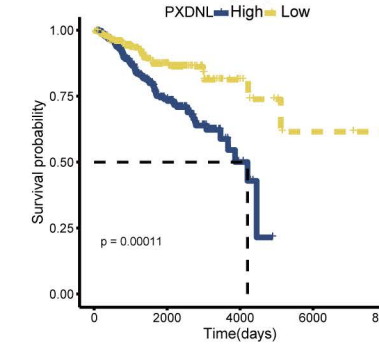
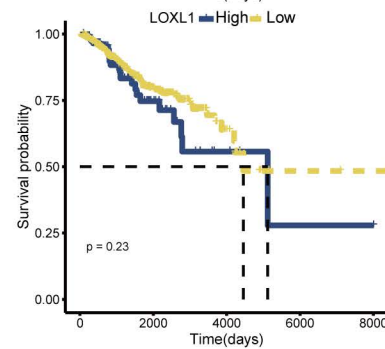
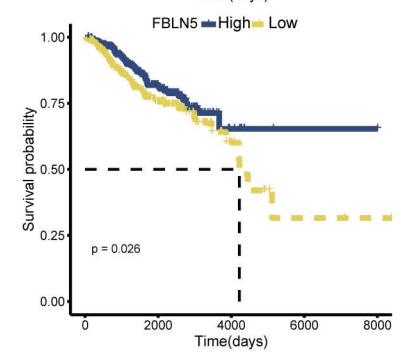
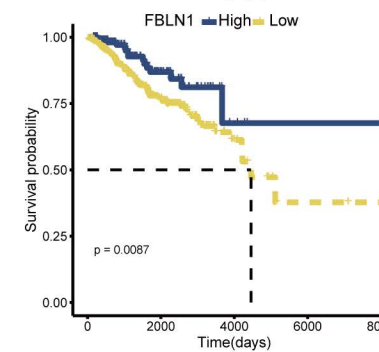
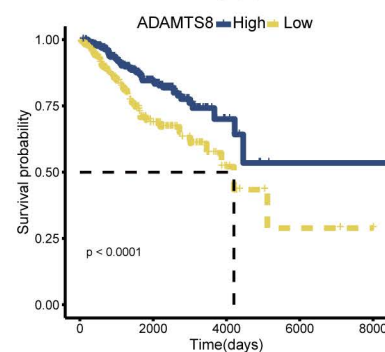
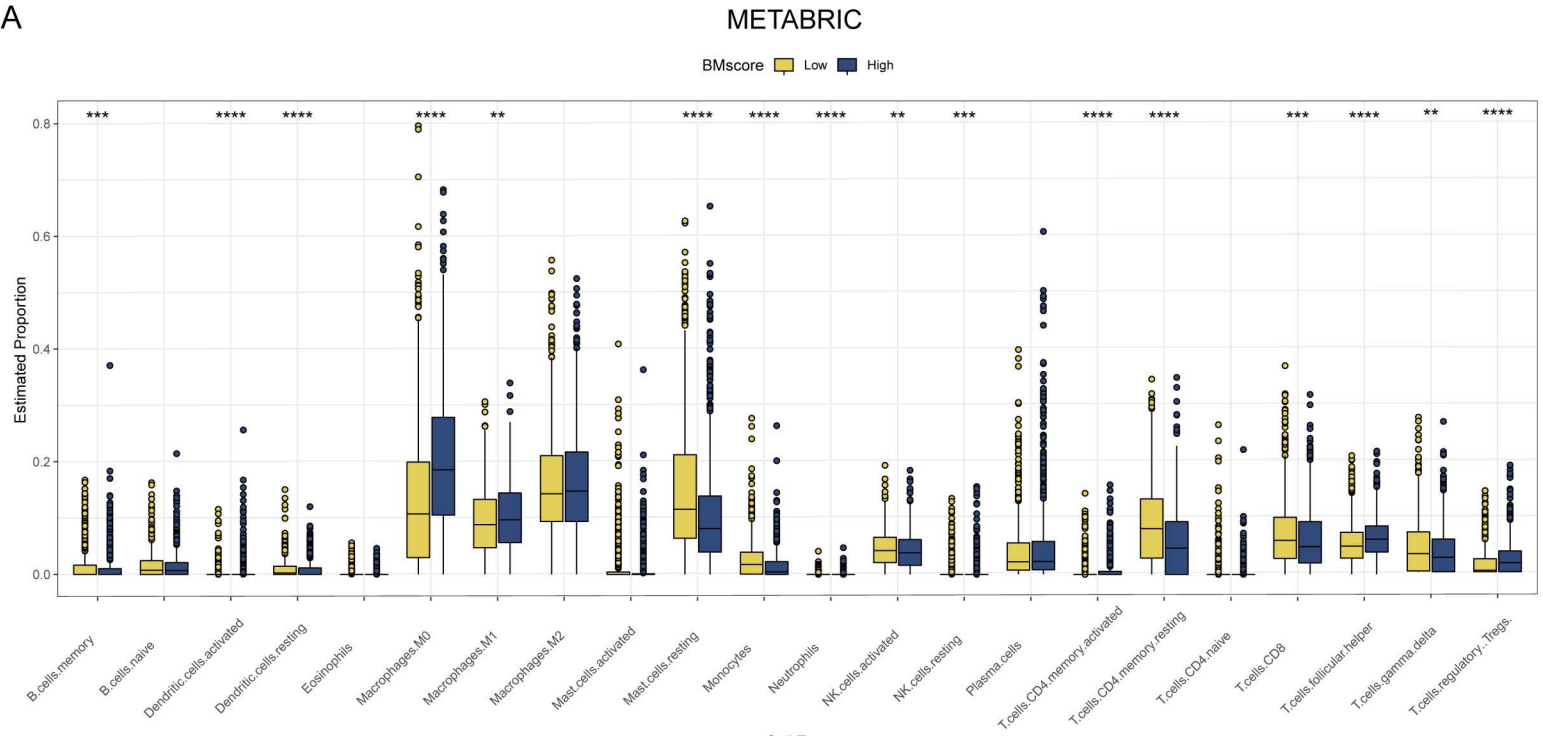
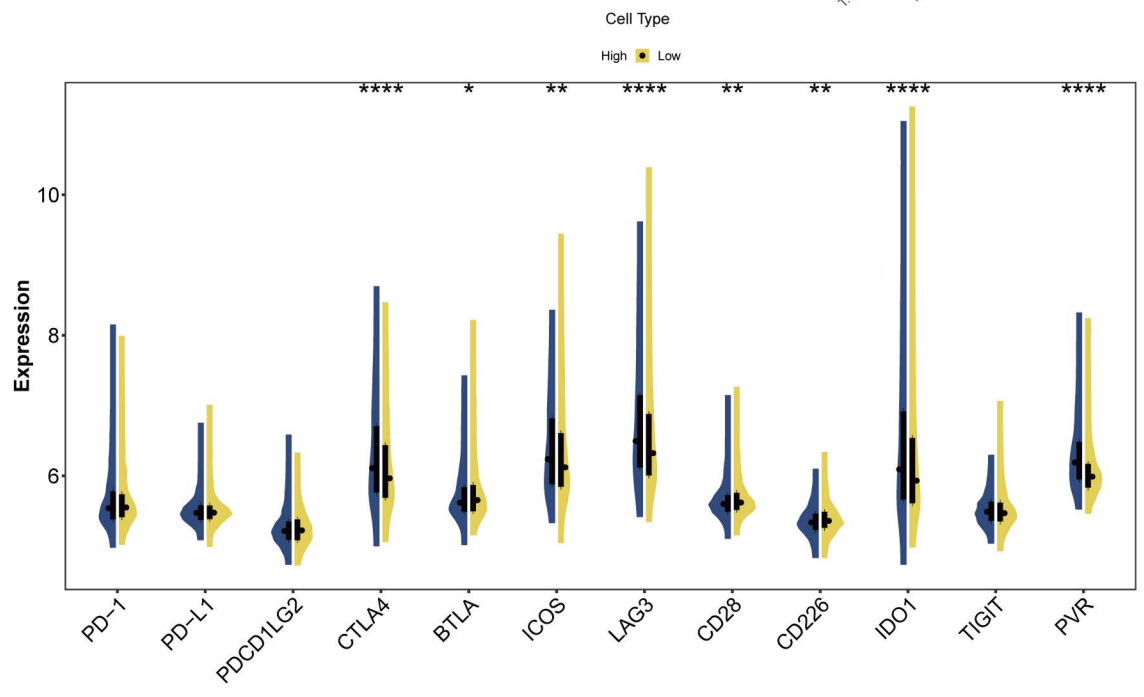
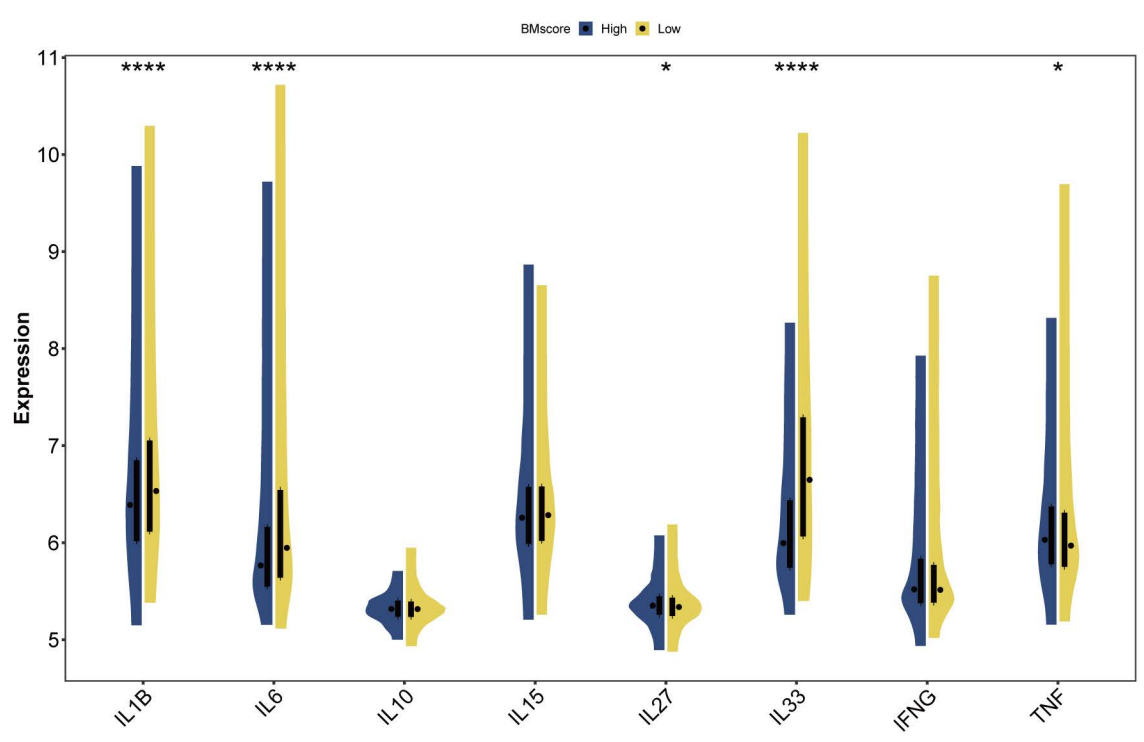


Figure S2

A**B****C****Figure S3**

Supplementary figure legends:

Figure S1. Description of the prognosis-related BM genes in breast cancer. (A) Estimation over the expression levels of six signature-contained BM genes in TCGA cohort. (B) The KM survival curves of six signature-contained BM genes based on expression levels and OS.

Figure S2. The KM survival curves of six signature-contained BM genes based on the mRNA expression levels for disease-free survival (A), disease-specific survival (B) and progression-free survival (C).

Figure S3. Tumor microenvironment assessment in METABRIC cohort. (A) Infiltrating degree of 22 immune cells between high and low BMscore groups. (B) Expression changes of immune checkpoint markers within different BMscore levels. (C) Changes of the cytokine mRNA expression levels based on BMscore levels.

Figure S4. The TME landscapes between high- and low-BMscore groups were estimated in GSE96058 cohort. (A) Infiltrating degree of 22 immune cells between high and low BMscore groups. (B) Expression changes of immune checkpoint markers within different BMscore levels. (C) Changes of the cytokine mRNA expression levels based on BMscore levels.