

**Supplementary Figure S1**| Genetic variation and expression of 15 FMGs in BRCA. (A) Genetic alteration of FMGs query. Only 21 out of 986 samples were mutated. (B)The location of CNV alterations in FMGs represents CNV amplification and green dots represent CNV deletion. (C)Compared with other FAM-related genes, ACSL1, ACSL5 and ALOX15B have a higher frequency of CNV deletion, while UBE2L6, HSPH1 and PSME1 have a higher frequency of CNV amplification.



**Supplementary Figure S2 |**Validation of the accuracy of FMGsScore. (A) Differences in expression of six immune checkpoint genes in the FMGsScore high and FMGsScore low groups in the GSE20685 dataset. (B) Kaplan-Meier curves of OS in the FMGsScore high and FMGsScore low groups in the GSE20685 dataset. (C) Proportion of patients with survival status in the high FMGsScore group and low FMGsScore group in the GSE20685 dataset and box plots. (D) Survival analysis of patients with high and low FMGsScore in the melanoma cohort. (E) Proportion of patients who responded or did not respond to PD-L1 blockade therapy in the FMGsScore high and FMGsScore low groups in the melanoma cohort and box plots. (F) Kaplan-Meier curves showing OS in the high FMGsScore and low FMGsScore groups in the IMvigor210 cohort. (G) Proportion of patients responding to immune checkpoint blockade treatment in the high FMGsScore and low FMGsScore groups in the IMvigor210 cohort and box plots.