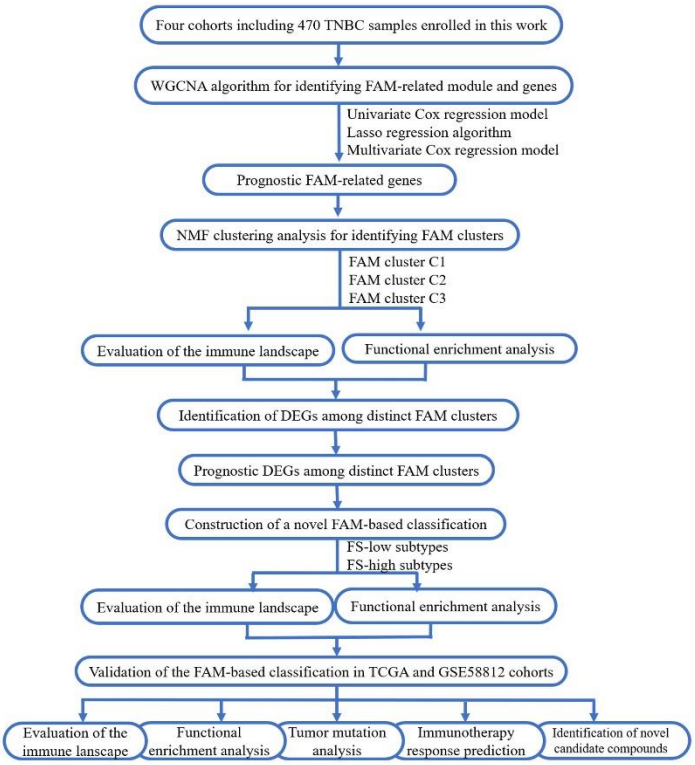

Fig. S1 The workflow of this study.

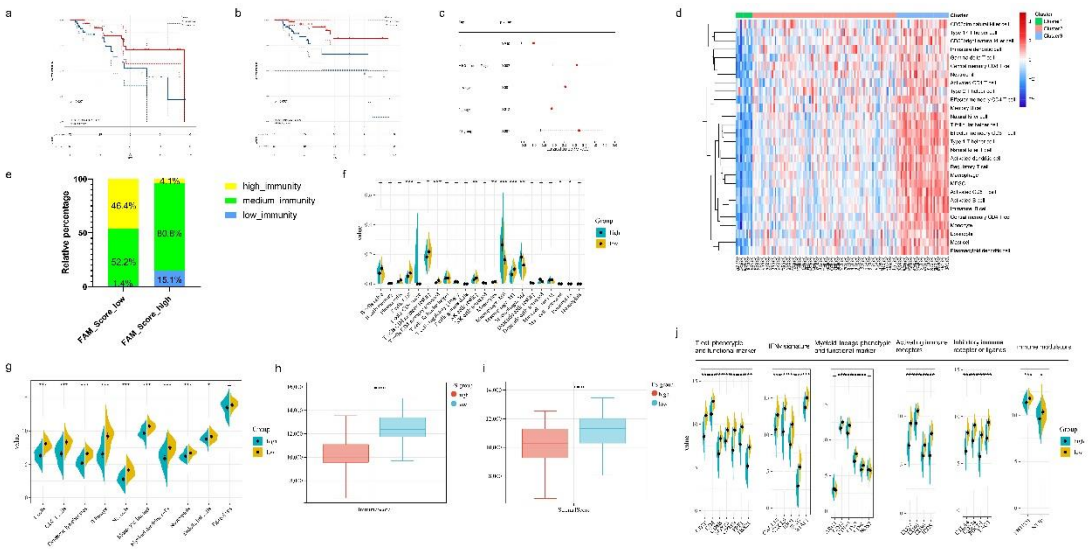

Fig. S2 a-b Survival analyses for DFS (a) and OS (b) between low- and high- FS groups in TCGA-TNBC cohort. c Multivariate Cox regression analysis confirmed that FS could serve as an independent prognostic biomarker for TCGA-TNBC samples. d ssGSEA showed three distinct immunity phenotypes were identified in TCGA cohort. e The rate of different immunity phenotypes between the low- and high FS groups. f Cibersort revealed the abundance of each TME infiltrating cells between the low- and high-FS groups. g MCPcounter revealed the abundance of each immune infiltrating cell types between the low- and high-FS groups. h-i ESTIMATE analysis exhibited the

diversity of the immune (h) and stromal score (i) between the low- and high-FS groups. j The expression of immune profiles between the low- and high-FS groups in TCGA cohort.

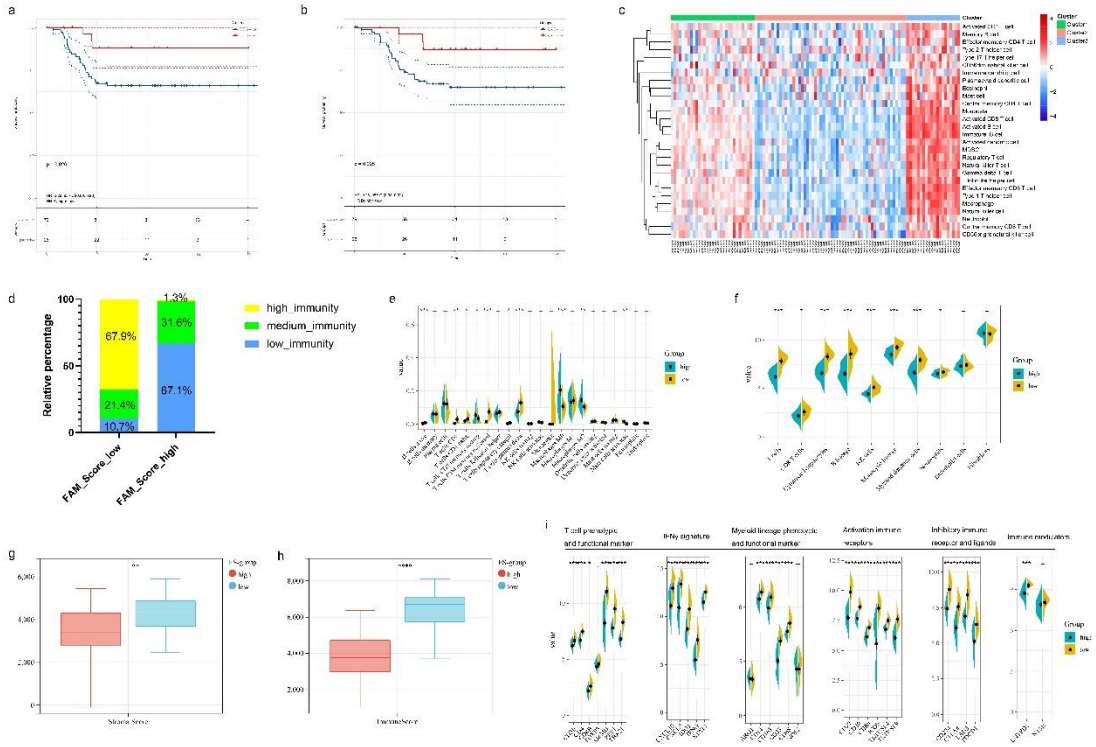

Fig. S3 a-b Survival analyses for MFS (a) and OS (b) between low- and high- FS groups in GSE58812 cohort. c ssGSEA showed three distinct immunity phenotypes were identified in GSE58812 cohort. d The rate of different immunity phenotypes between the low- and high FS groups. e Cibersort revealed the abundance of each TME infiltrating cells between the low- and high-FS groups. f MCPcounter revealed the abundance of each immune infiltrating cell types between the low- and high-FS groups. g-h ESTIMATE analysis exhibited the diversity of the immune (g) and stromal score (h) between the low- and high-FS groups. i The expression of immune profiles between the low- and high-FS groups in GSE58812 cohort.

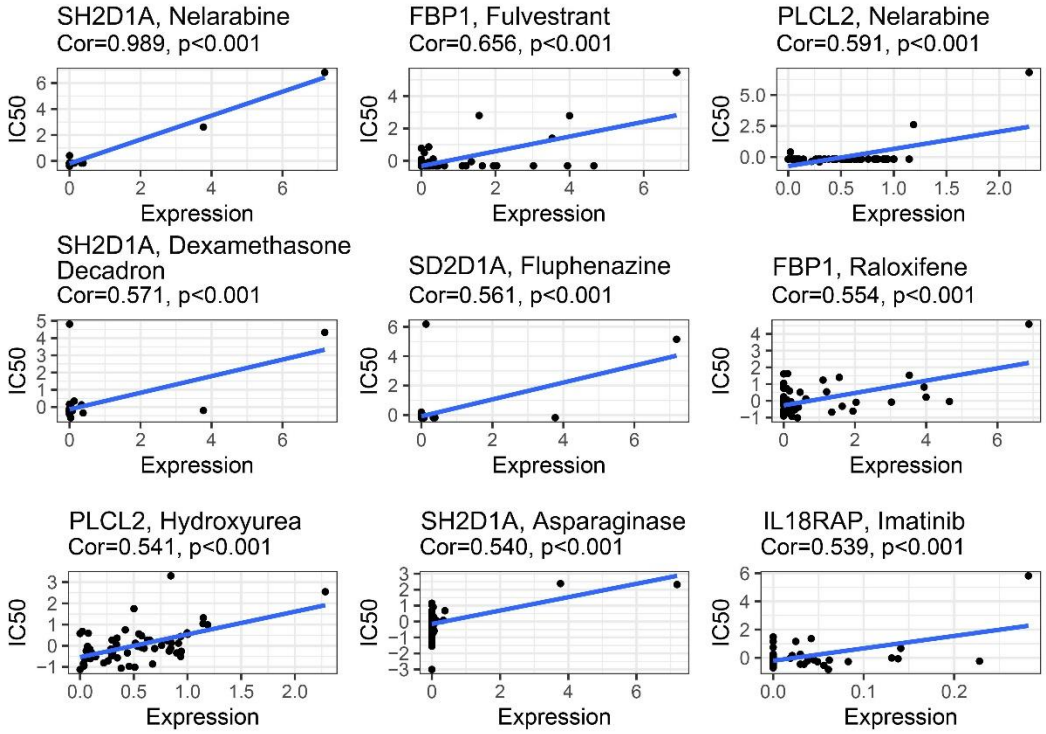

Figure S4. Identification of novel candidate compounds targeting the selected FS gene signatures.