Supplemental information

Integrated analysis reveals

the molecular features of fibrosis

in triple-negative breast cancer

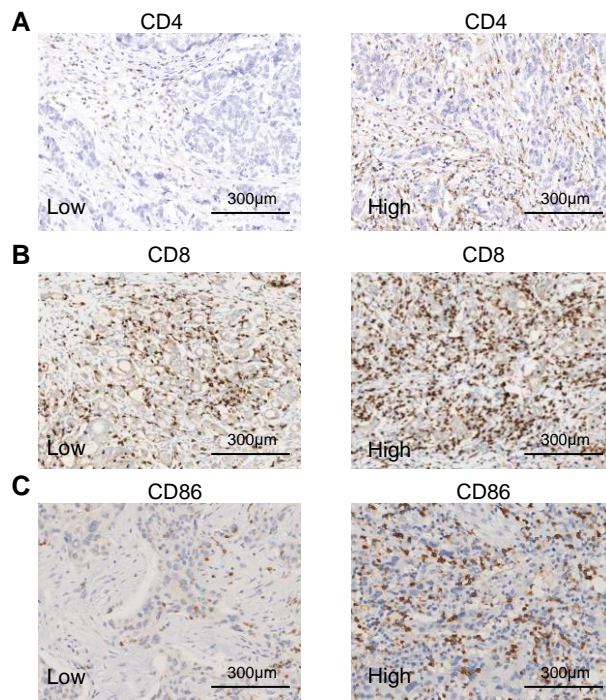Jia-Han Ding, Yi Xiao, Shen Zhao, Ying Xu, Yu-Ling Xiao, Zhi-Ming Shao, Yi-Zhou Jiang, and Gen-Hong Di

A CD4 — Low — 300μm ; CD4 — High — 300μm

B CD8 — Low — 300μm ; CD8 — High — 300μm

C CD86 — Low — 300μm ; CD86 — High — 300μm

Figure S1. Representative images of IHC staining for CD4, CD8 and CD86. (A) CD4 IHC staining. (B) CD8 IHC staining. (C) CD86 IHC staining.
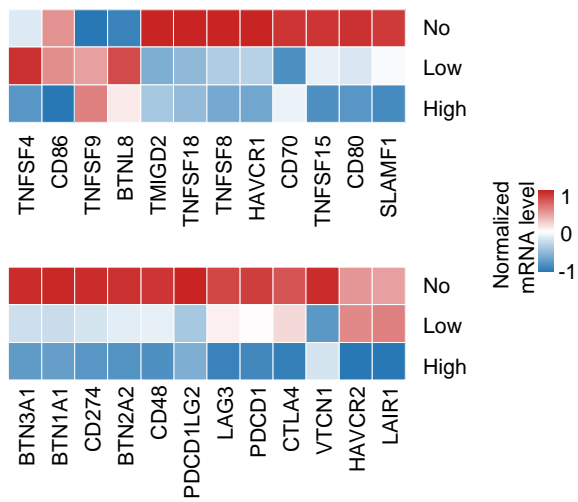
Figure S2. Expression of immunomodulators among three subgroups of fibrosis.

Expression of costimulatory molecules (upper) and coinhibitory molecules (lower) among three subgroups of fibrosis.

Supplementary Tables

Table S1. The clinicopathological information of all patients with the evaluation of fibrosis.

Table S2. Results of mutation frequency comparison between the high and no fibrosis group.

Table S3. Results of copy-number gain/amplification frequency comparison between the high and no fibrosis group.

Table S4. Results of copy-number loss/deletion frequency comparison between the high and no fibrosis group.

Table S5. Results of differentially expressed genes (DEGs) between the high and no fibrosis group.

Table S6. IHC data for CD4, CD8 and CD86.

Table S7. Abundance of pan-CAF subtypes calculated by CIBERSORTx.