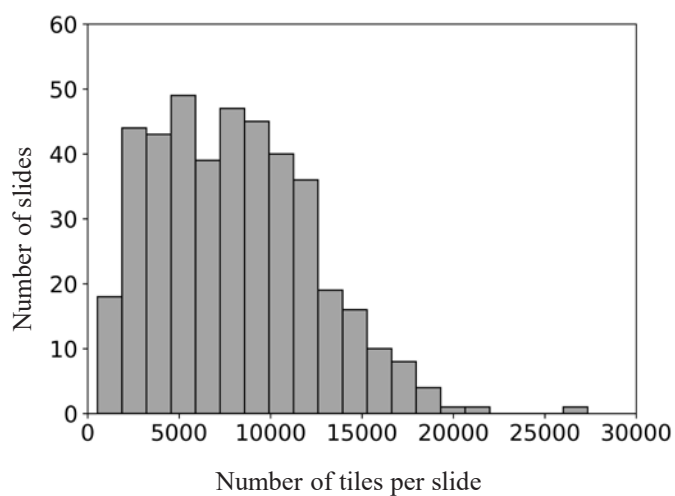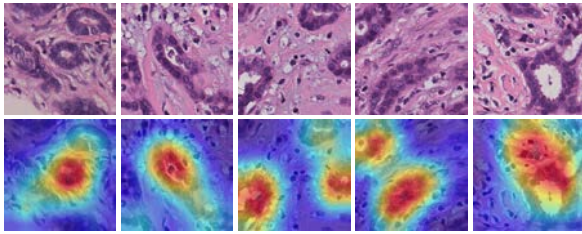**Figure S1** Patient inclusion procedure of the HR+/HER2− breast cancer cohort. FFPE, formalin-fixed, paraffin-embedded; WSIs, whole-slide images; WES, whole-exome sequencing; RNA seq, RNA-sequencing; CNV, copy number variation.
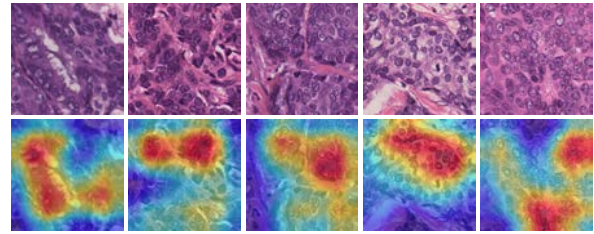

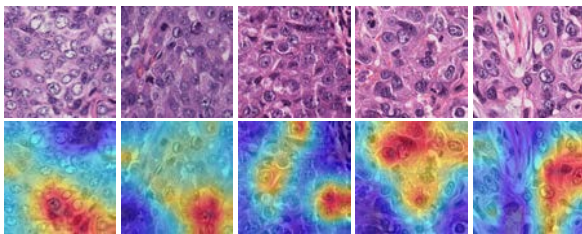**Figure S2** Histogram of the number of tiles per slide of the HR+/HER2− breast cancer cohort.
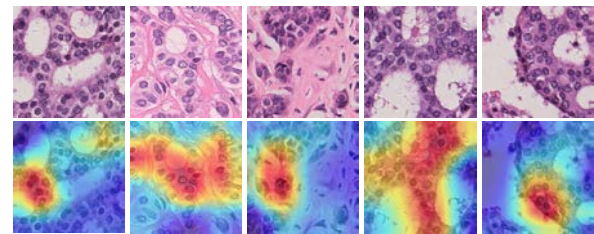
A   Tiles indicating grade Ⅰ

B   Tiles indicating grade Ⅱ
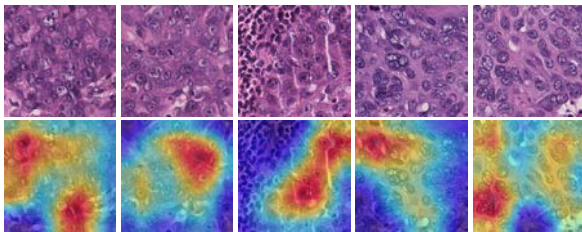

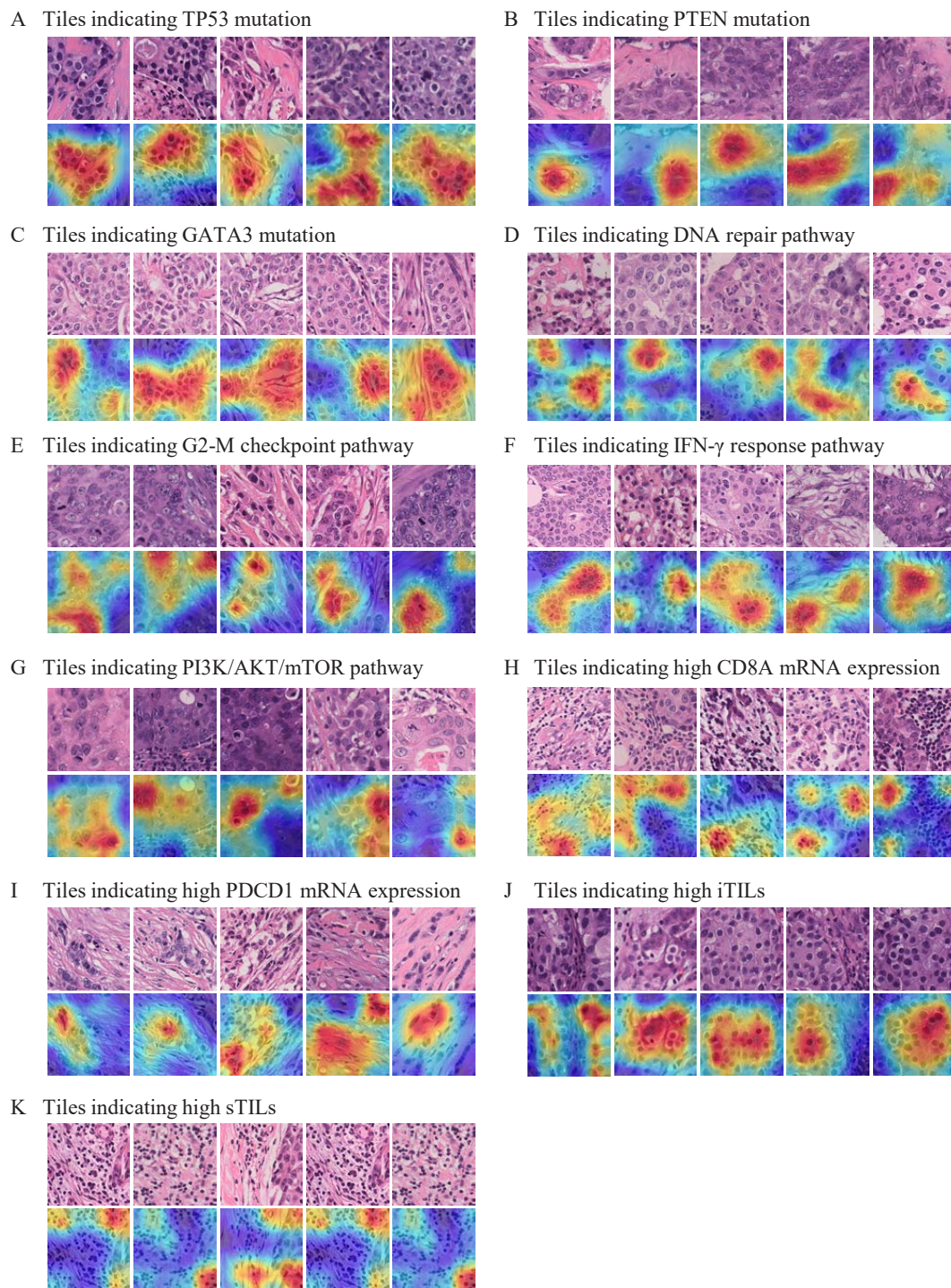C   Tiles indicating grade Ⅲ

D   Tiles indicating low Ki67

E   Tiles indicating high Ki67

Figure S3 Representative image tiles for the tumors of grade I (A), grade II (B), grade III (C), low Ki67 (D), and high Ki67 (E). Class activation maps highlight the regions contributing most to the prediction. Staining method: hematoxylin and eosin; scale bar: 128 μm.

Figure S4 Representative image tiles indicating certain molecular or pathological features. Representative image tiles for tumors with TP53 mutation (A), PTEN mutation (B) and GATA3 mutation (C). Representative image tiles for tumors with high GSEA scores of DNA repair pathway (D), G2-M checkpoint pathway (E) and IFN-γ response pathway (F). Representative image tiles for tumors with high CD8A mRNA expression (H), PDCD1 mRNA expression (I), high iTILs (J) and high sTILs (K). Staining method: hematoxylin and eosin; scale bar: 128 µm. iTILs, intratumoral tumor-infiltrating lymphocytes; sTILs, stromal tumor-infiltrating lymphocytes; GSEA, gene set enrichment analysis.