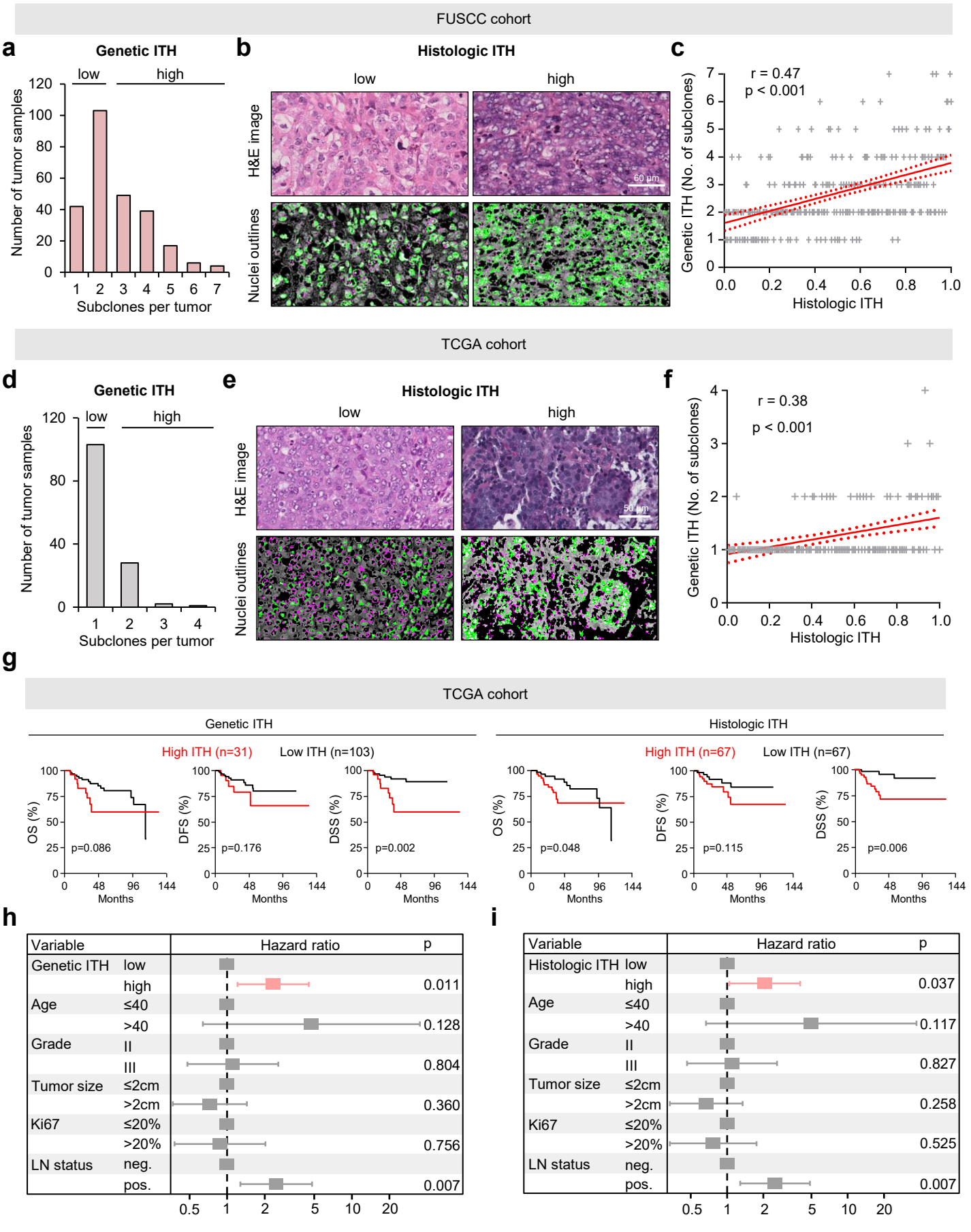
Supplementary information, Fig. S1



Supplementary information, Fig. S1 ITH levels correlate with TNBC patient survival.

a Subclone number distribution as predicted by PyClone in the FUSCC cohort. **b** Representative images of histologic ITH from H&E-stained tumor samples in the FUSCC cohort. Representative staining regions are shown for low and high levels of histologic ITH (top) with outlined nuclei (bottom) by CellProfiler software. Scale bar, 60 μm. **c** Spearman's rank analysis of correlations between levels of histologic ITH and genetic ITH in the FUSCC cohort (n = 260). **d** Subclone number distribution as predicted by PyClone in the TCGA cohort. **e** Representative images of histologic ITH in H&E-stained tumor samples in the TCGA cohort. Scale bar, 50 μm. **f** Spearman's rank analysis of correlations between levels of histologic ITH and genetic ITH in the TCGA cohort (n = 134). **g** Kaplan-Meier analyses of the OS, DFS and DSS of TCGA cohort patients grouped according to genetic ITH and histologic ITH. P values were determined using log-rank tests. **h, i** Multivariate analyses revealed that genetic ITH (**h**) and histologic ITH (**i**) are independent prognostic factors for DMFS in the FUSCC cohort.