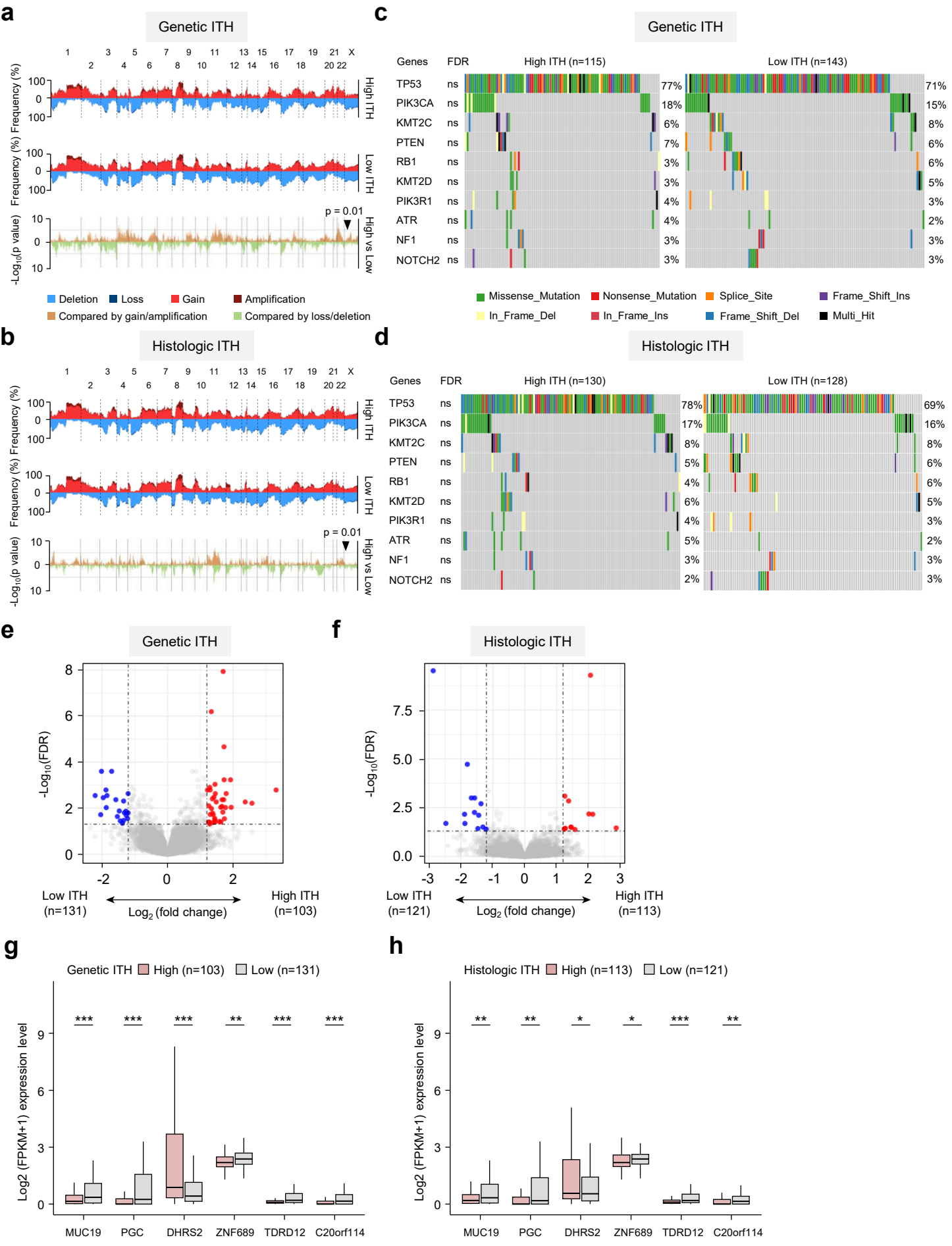


Supplementary information, Fig. S2



Supplementary information, Fig. S2 Genomic alterations in TNBC tumors with different levels of ITH.

a, b Comparison of the SCNVs between the high ITH group and the low ITH group at the genetic (**a**) and histologic (**b**) levels in the FUSCC cohort. The top plot illustrates the frequency of the amplification (dark red), gain (light red), loss (light blue), and deletion (dark blue) of each gene in each group, and the bottom plot illustrates the $-\text{Log}_{10}(\text{P value})$ of each gene when comparing the frequency of loss or deletion or gain or amplification between the two groups. **c, d** Oncoplots depicting the top 10 most frequently mutated genes and their mutation types per subgroup of genetic (**c**) and histologic (**d**) ITH in the FUSCC cohort. FDR, false discovery rate; ns, not significant. **e, f** Volcano plots of differentially expressed genes between the high ITH group and the low ITH group at the genetic (**e**) and histologic (**f**) levels in the FUSCC cohort. Red represents upregulated genes, and blue represents downregulated genes ($|\text{Log}_2(\text{fold change})| > 1.2$ and $\text{FDR} < 0.05$). **g, h** Box plots showing the differential expression of six genes between the high ITH group and the low ITH group at the genetic (**g**) and histologic (**h**) levels in the FUSCC cohort. P values were determined using Fisher's exact tests (**c, d**) and Wilcoxon tests (**g, h**). * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.