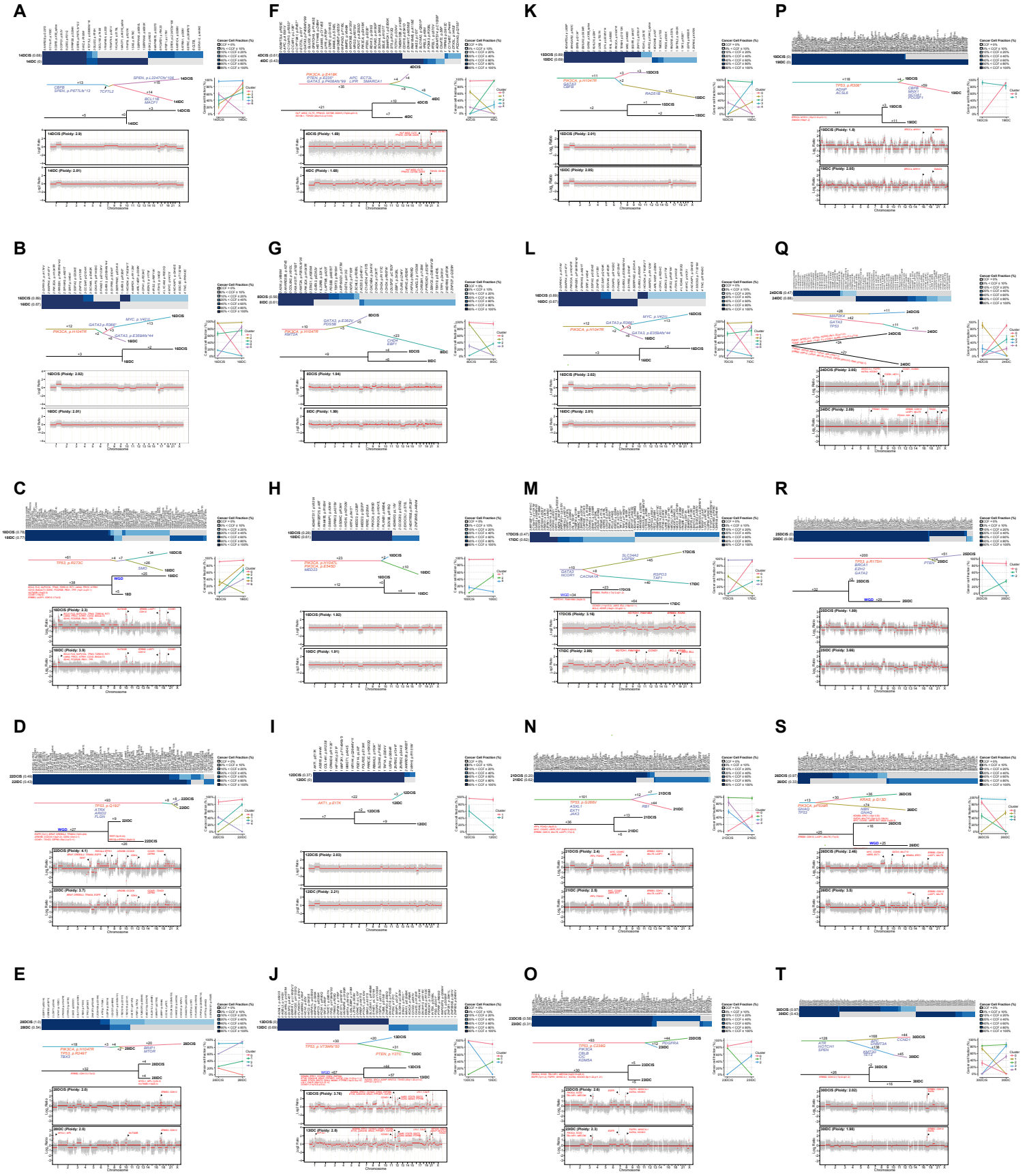
Supplementary Figure S4



Supplementary Figure S4. Clonal relatedness, clonal decomposition and phylogenetic analysis of synchronously diagnosed ductal carcinoma *in situ* and invasive breast cancers

(**A-T**) Clonal decomposition and phylogenetic analysis of (**A**) Case 14, (**B**) Case 16, (**C**) Case 18, (**D**) Case 22, (**E**) Case 28, (**F**) Case 4, (**G**) Case 8, (**H**) Case 10, (**I**) Case 12, (**J**) Case 13, (**K**) Case 15, (**L**) Case 16, (**M**) Case 17, (**N**) Case 21, (**O**) Case 23, (**P**) Case 19, (**Q**) Case 24, (**R**) Case 25, (**S**) Case 26 and (**T**) Case 30. Clonal frequency heatmaps of mutations in the DCIS and synchronous IDC-NST of a given case are shown (**top**), grouped by their clonal/subclonal structure (clusters) as inferred by PyClone. Cancer cell fractions are color-coded according to the legend. Shannon index of intratumor heterogeneity is shown in parentheses to the left. PyClone parallel coordinates plots are shown (**middle right**). Copy number plots depicting segmented Log2 ratios (*y*-axis) according to genomic position (*x*-axis) of DCIS and IDC-NSTs are depicted (**bottom**). Genes included in amplifications are shown in red. PyClone-derived phylogenetic trees of synchronous DCIS and IDC-NST (**middle center**) are shown. Trunk and branches are colored according to clusters as per PyClone, and the number of somatic mutations that result in the divergence of a clone/subclone from its ancestor are shown. Cancer genes (**blue**) and hotspot mutations (**orange**) that define a given clone are depicted. Phylogenetic trees based on copy number alterations is shown (**middle center**). The numbers alongside the branches represent the total number of copy number alterations. Genes included in amplifications are shown in red.