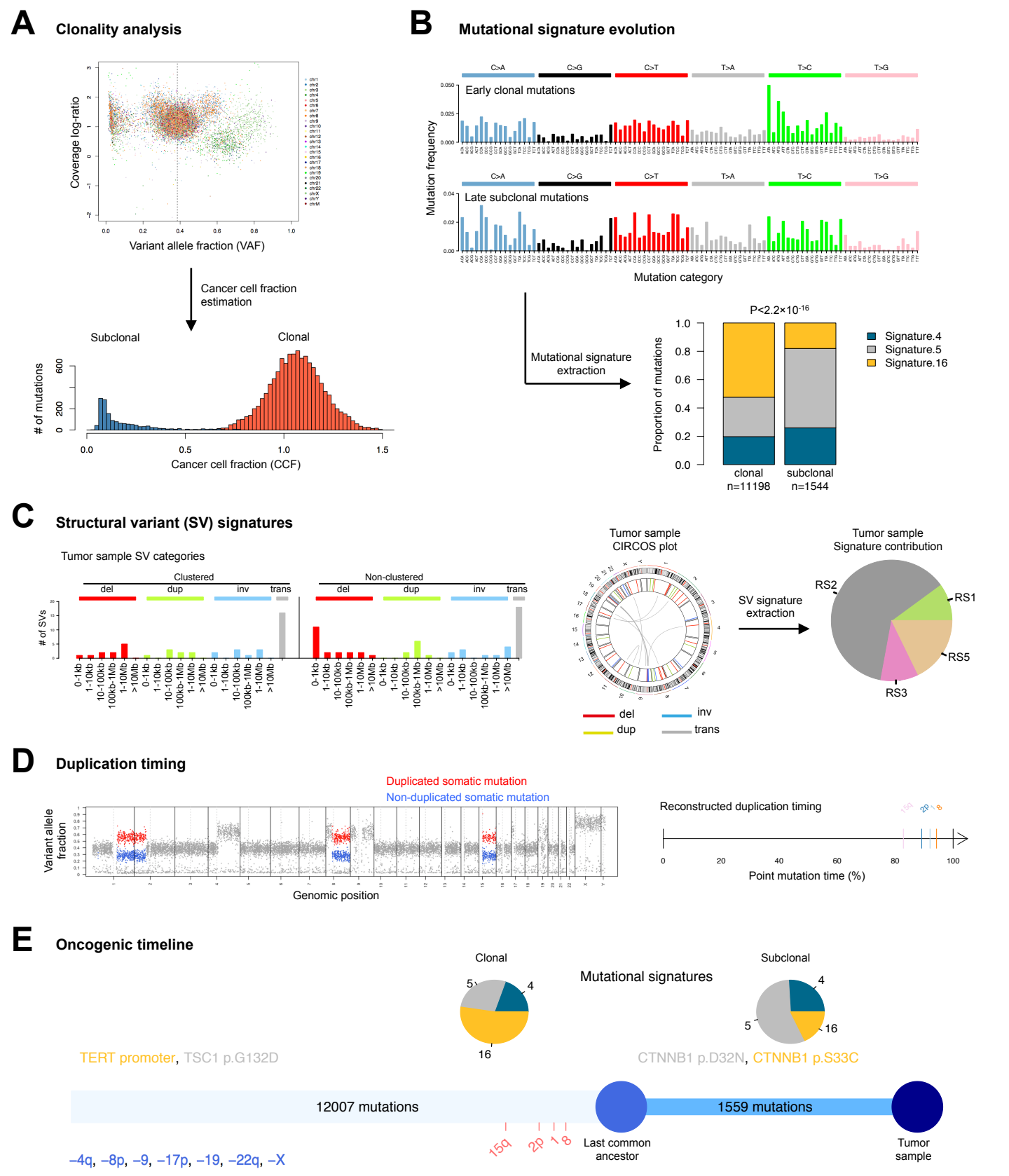

Supplementary Fig.1. Typical outputs of a *Palimpsest* analysis. (A) *Palimpsest* estimates the cancer cell fraction (proportion of tumor cells harboring a somatic variant) and classifies each variant as clonal or subclonal. **(B)** Mutational signatures analyzed separately in early clonal and late subclonal mutations highlight the evolution of mutational processes along tumorigenesis. **(C)** *Palimpsest* can also extract structural variant (SV) signatures considering the type and size of SVs identified in the tumor. Del: deletion; dup: duplication; inv: inversion; trans: translocation. **(D)** The ratio of duplicated/non-duplicated somatic mutations allows estimating the timing of each chromosome duplication in molecular time. **(E)** Finally, an oncogenic timeline of the tumor is generated, with the number of clonal and subclonal mutations, their distribution per mutation signature, the driver alterations (colored according to the most likely causal mutational process) and CNA timing. This example comes from a previously analyzed tumor (Letouzé *et al.*, 2017).