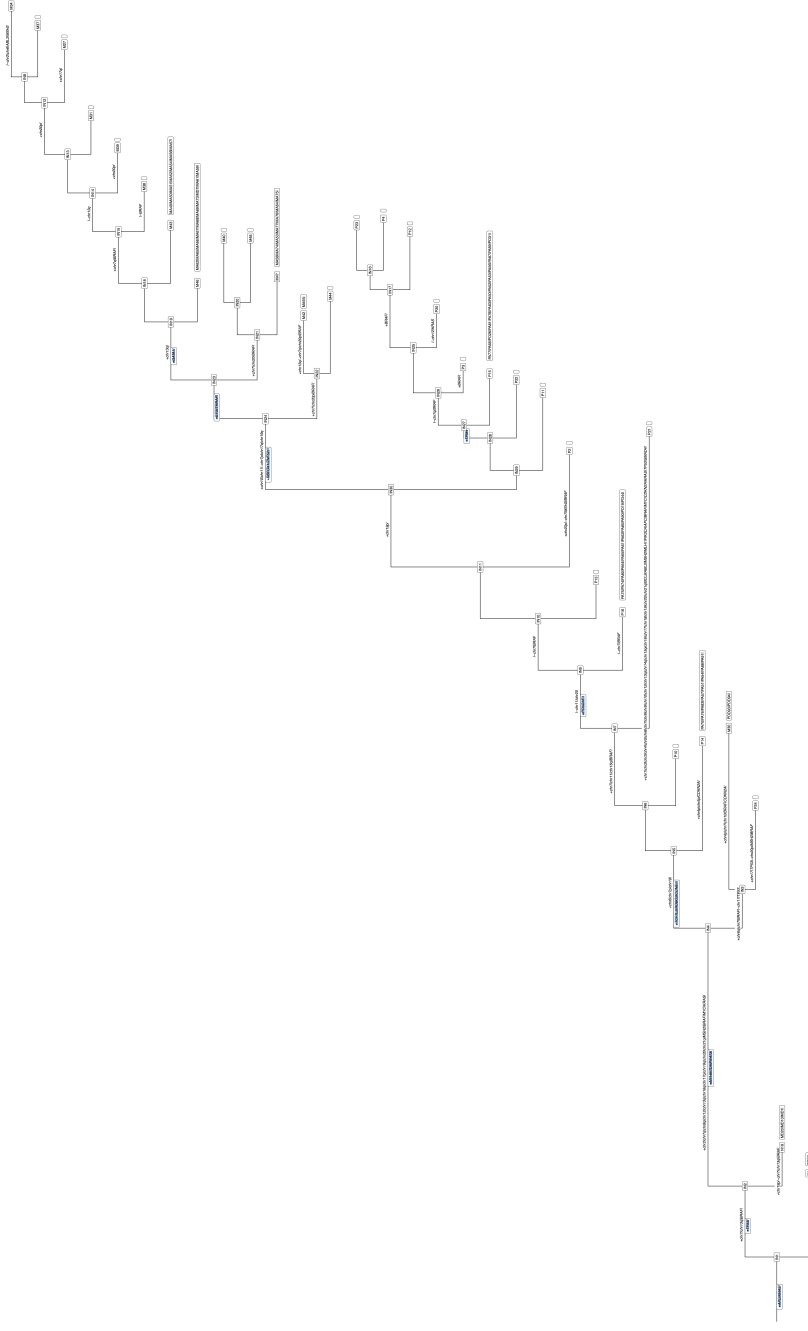




Supplemental Fig. S6 SCsnvcna-inferred phylogentic tree on CRC1 patient tumor dataset that has the placements of both SNVs and CNAs, and both SNV cells and CNA cells for CRC1 sample. Each internal node in the tree represents a subclone denoted by "IN" followed by an index. Each leaf of the tree represents a CNA cell. SCsnvcna placed SNV cells on the leaves of the CNA tree. The SNV cell IDs are placed next to the CNA cells' IDs. The SNV cells whose IDs start with "PA" and "MA" are from primary and metastasis resection position, respectively. SCsnvcna also placed SNVs on the edges of the CNA tree, the genes of which are in boxes in blue background. Also shown on the edges of the tree are the genes or chromosomes where CNAs were inferred to occur for the study of the interplay between CNAs and SNVs on the same sample. For CNAs, copy number gains and losses are denoted by "+" and "-" before the gene name, respectively. Large CNAs covering multiple genes are denoted by chromosomes instead of individual genes.