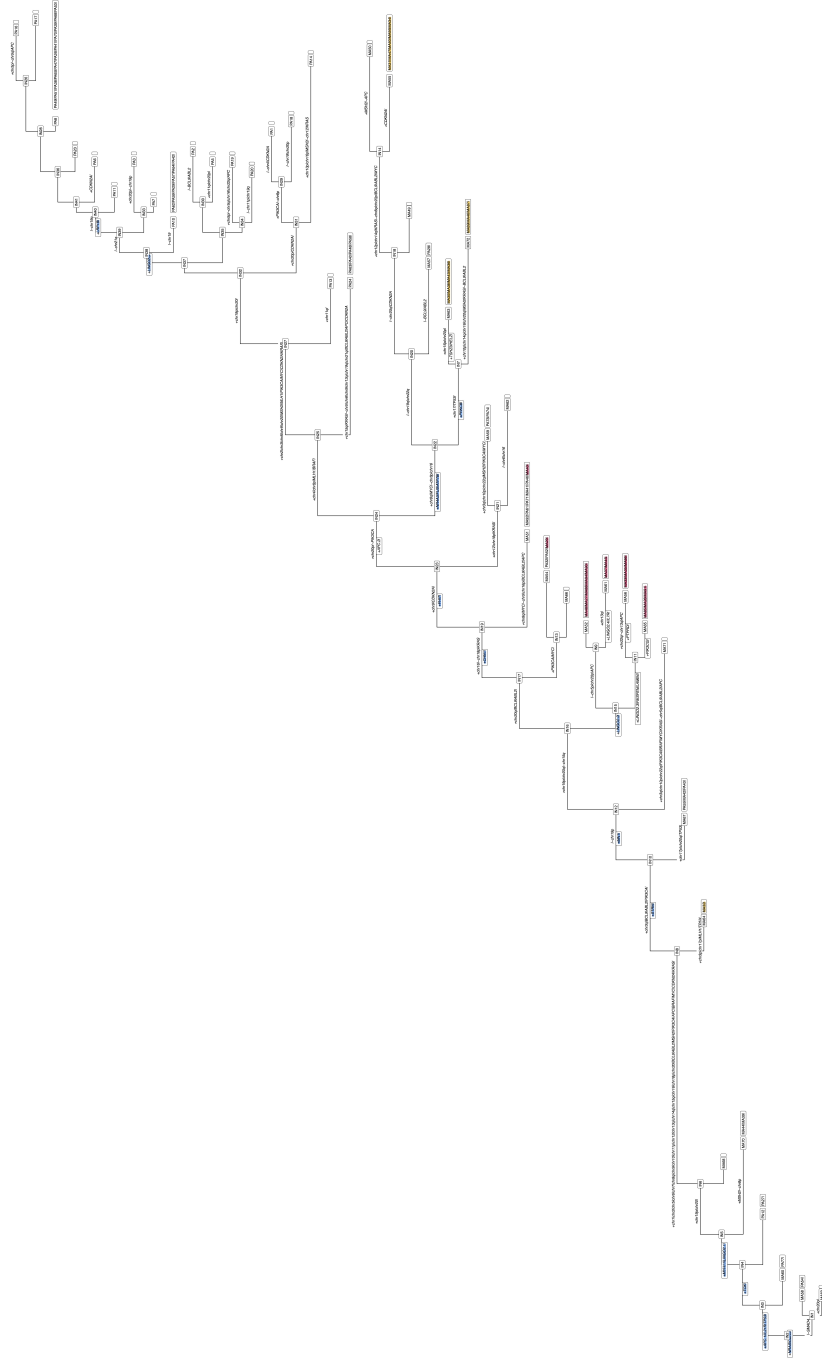




Supplemental Fig. S5 SCsnvcna-inferred phylogenetic tree on CRC2 patient tumor dataset that has the placements of both SNVs and CNAs, and both SNV cells and CNA cells for CRC2 sample. Each internal node in the tree represents a subclone denoted by "IN" followed by an index. Each leaf of the tree represents 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. SNV cells are colored by their known resection position, primary (white), M1 (red) and M2 (yellow). SCsnvcna also placed SNVs on the edges of the CNA tree, the genes of which are in blue background. Also shown on the edges of the tree are the genes where CNAs (no background color) 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.