



Supplemental Fig. S2 Group 5: evaluation of methods given imperfect CNA trees. Genotype error, pairwise SNV error and pairwise SNV/CNA error are shown for SCsnvcna, SCARLET and COMPASS on A. percentage of internal nodes which do not have CNAs on the outgoing edges on the true tree. In B, genotype error, pairwise SNV error and pairwise SNV/CNA error are shown for SCsnvcna when there are missing leaf nodes on the CNA tree due to sampling bias. In C, genotype error, pairwise SNV error and pairwise SNV/CNA error are shown for SCsnvcna on the experiment of using CNA bulk tree as the input, in which the number of bulk samples varies between 4 and 8. Also shown as the reference in C is the results that take the CNA single-cell tree with 16 leaves as the input.