

<b>Group 1: Sequencing errors</b>		
1	False positive rate	0.001, 0.01 (d), 0.05
2	False negative rate	0.1, 0.2 (d), 0.3
3	Missing rate	0.1, 0.2 (d), 0.3
<b>Group 2: Scalability</b>		
4	Number of subclones	8, 16 (d), 32
5	Number of SNV cells	50, 100 (d), 200, 500
6	Number of mutations	20, 100 (d), 200
<b>Group 3: Challenges from biology</b>		
7	Percentage of CNAs detectable by SNV cells	0, 0.1 (d), 0.2
8	Mutation loss rate	0.01, 0.1 (d), 0.2
9	Beta splitting variable	0.1, 0.3 (d), 0.5
<b>Group 4: CP difference between SNV cells and CNA cells</b>		
10	Standard deviation of CPs in a Gaussian distribution	0.01, 0.05 (d), 0.1
11	Mean of a Beta distribution imputed to CP difference	0 (d), 0.2, 0.5, 0.8
12	Both SNV/CNA cells' CPs are sampled from a multinomial distribution from true CPs	NA
<b>Group 5: Imperfect input CNA tree</b>		
13	Percentage of internal nodes which do not have CNAs on the outgoing edges on the true tree	0 (d), 0.1, 0.25, 0.5
14	Percentage of missing leaf nodes on the CNA tree	0 (d), 0.1, 0.25, 0.5
15	Number of bulk samples given a CNA bulk tree	4, 8, 16 (d)

**Supplemental Table S1** Summary of simulated datasets. Each row represents a simulated dataset with an index (first column) whose values of the varying variable (second column) are shown in the third column. The default value is denoted by “(d)” on its right. In total five groups of simulated datasets are shown, with the group tags on top of each group of datasets.