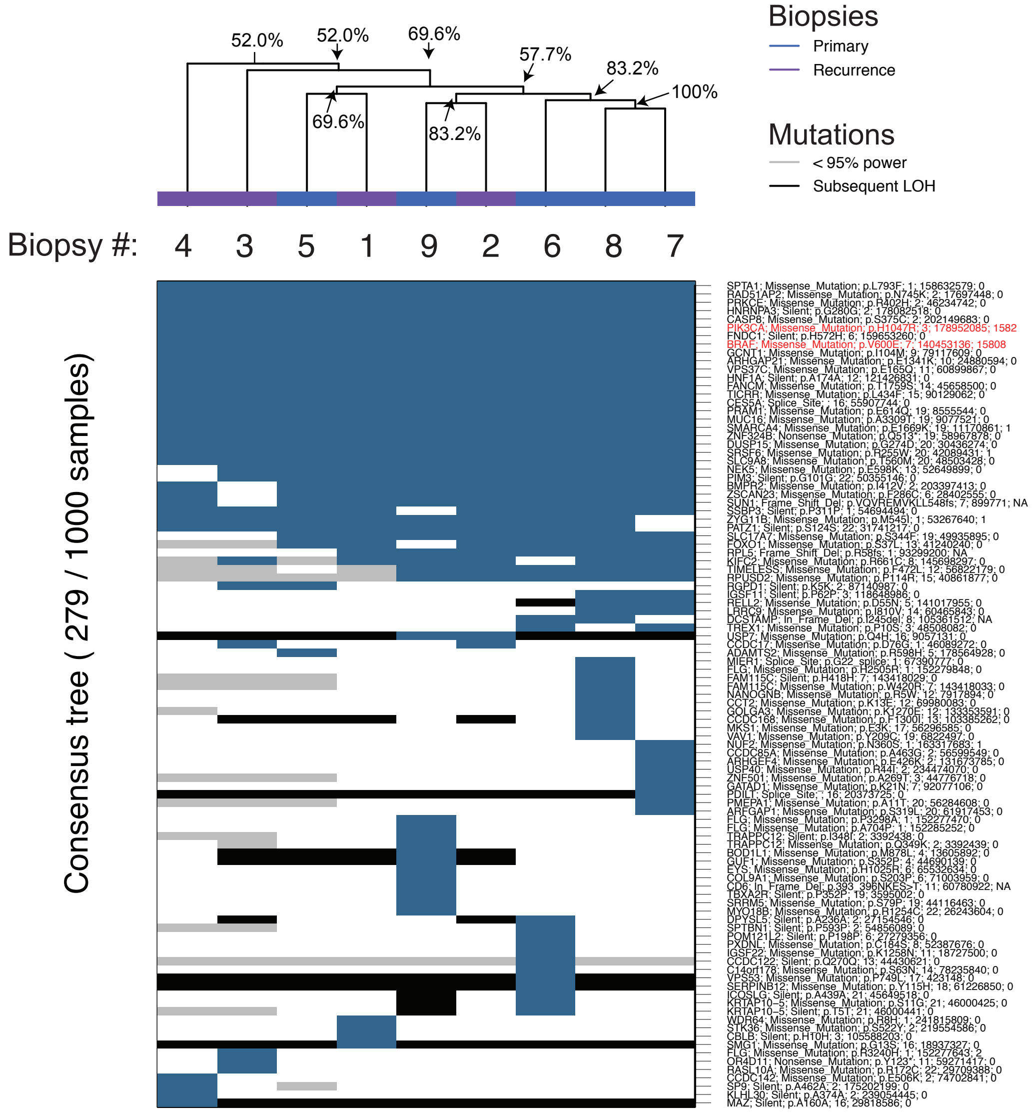
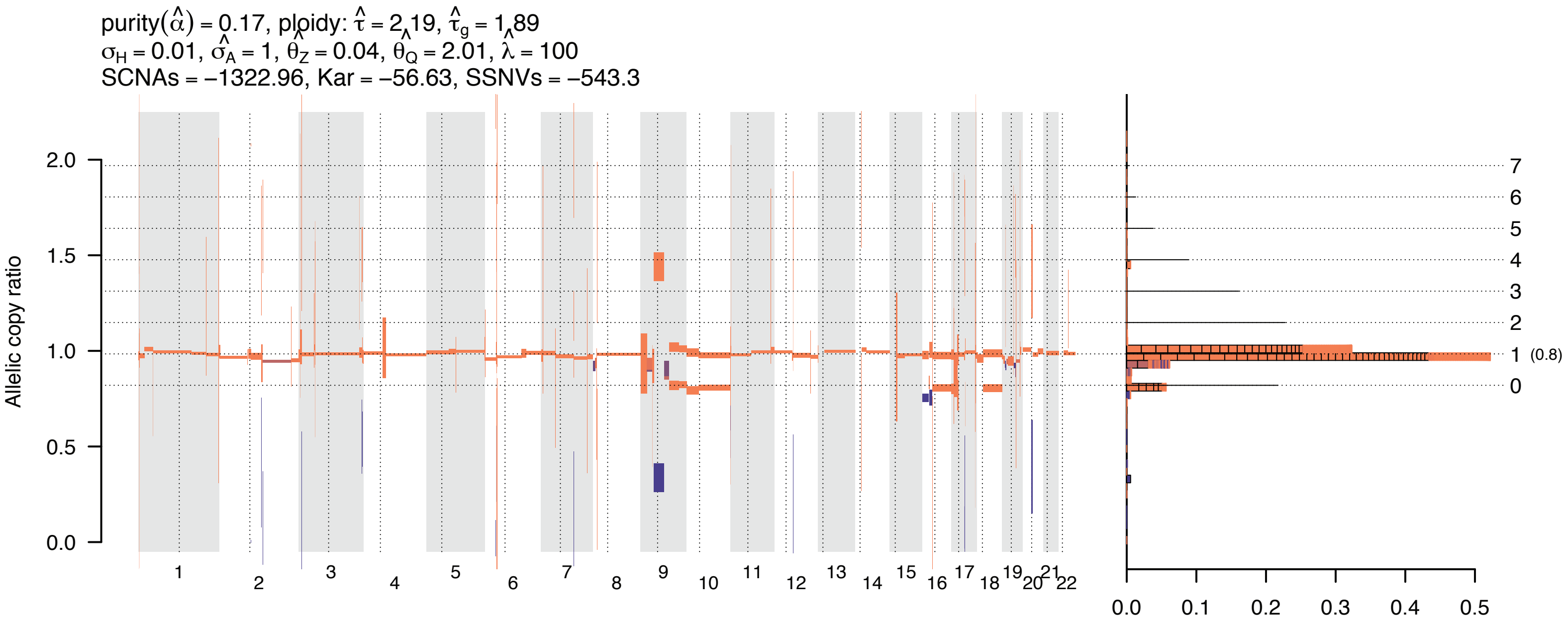


Supplementary Figure 1

The most frequent phylogenetic tree based on sampling mutations according to their detection power (276/1000 samples). At top is a dendrogram where each split is labeled with the fraction of sampled trees containing an equivalent split. Filled blue squares indicate the presence of a mutation in a given biopsy. Mutations are labeled on the right hand column.

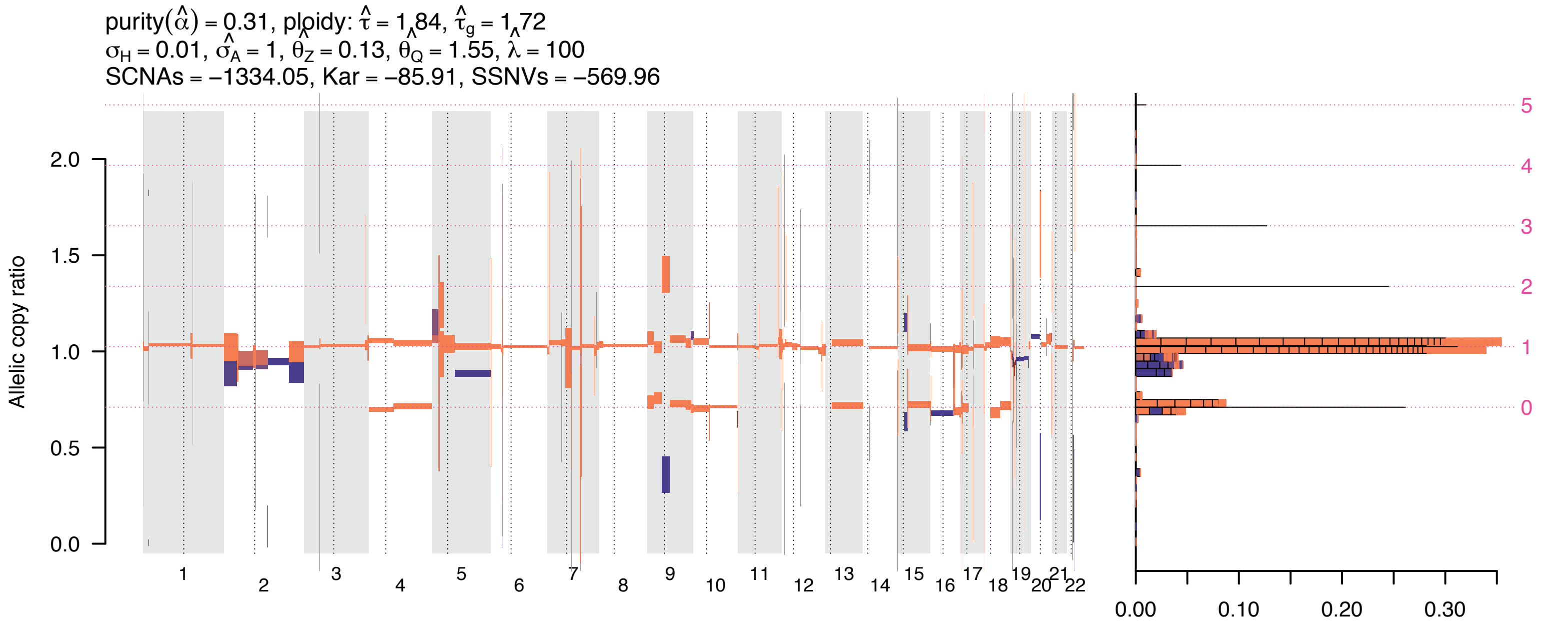
Biopsy 1



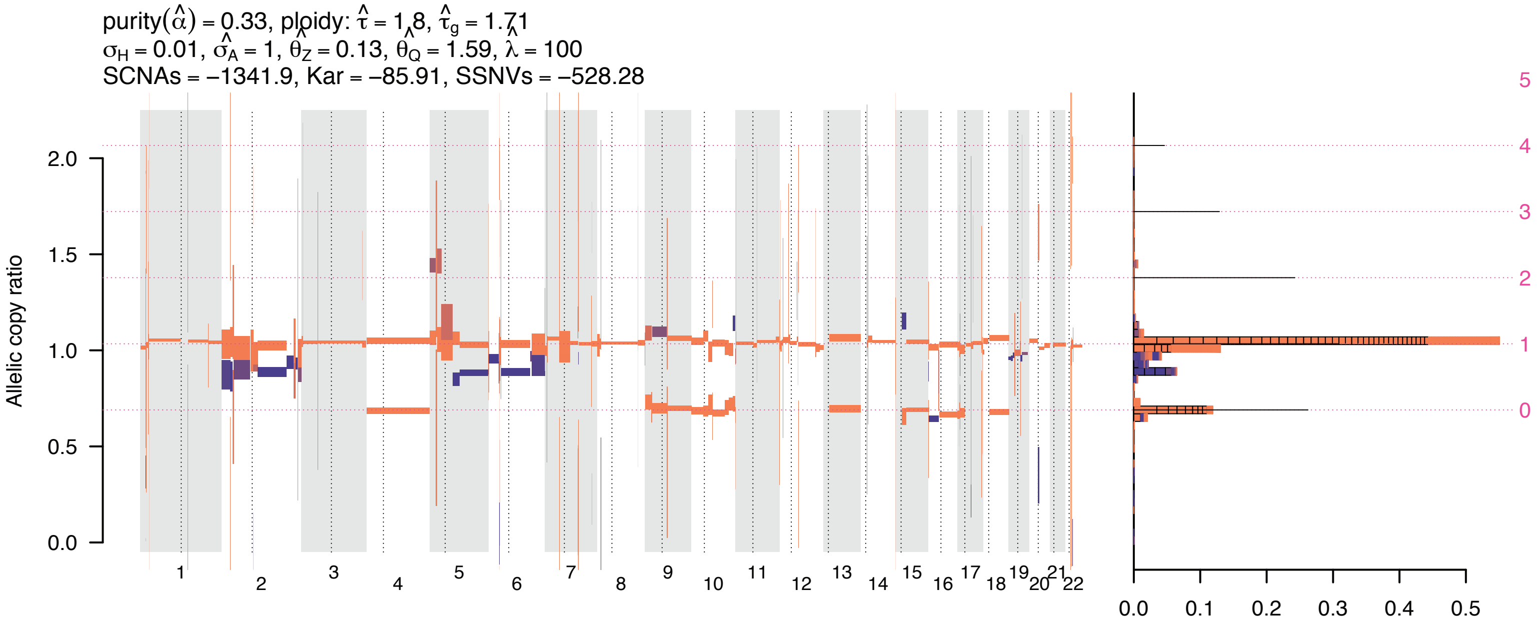
Supplementary Figure 2

Allelic copy number profiles generated by ABSOLUTE (see Methods).

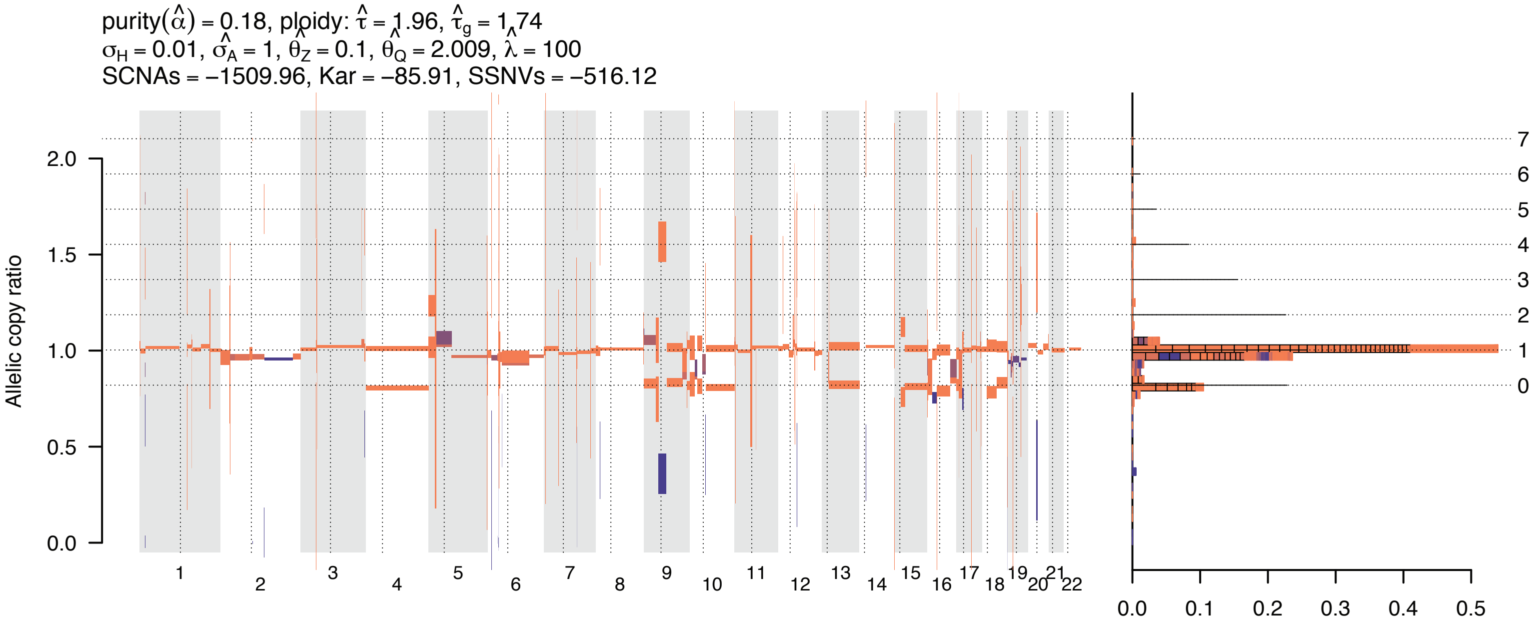
Biopsy 2


purity($\hat{\alpha}$) = 0.31, ploidy: $\hat{\tau}$ = 1.84, $\hat{\tau}_g$ = 1.72
σ_H = 0.01, $\hat{\sigma}_A$ = 1, $\hat{\theta}_Z$ = 0.13, $\hat{\theta}_Q$ = 1.55, $\hat{\lambda}$ = 100
SCNAs = −1334.05, Kar = −85.91, SSNVs = −569.96
Allelic copy ratio
0.0
0.5
1.0
1.5
2.0
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
0.00
0.10
0.20
0.30
0
1
2
3
4
5

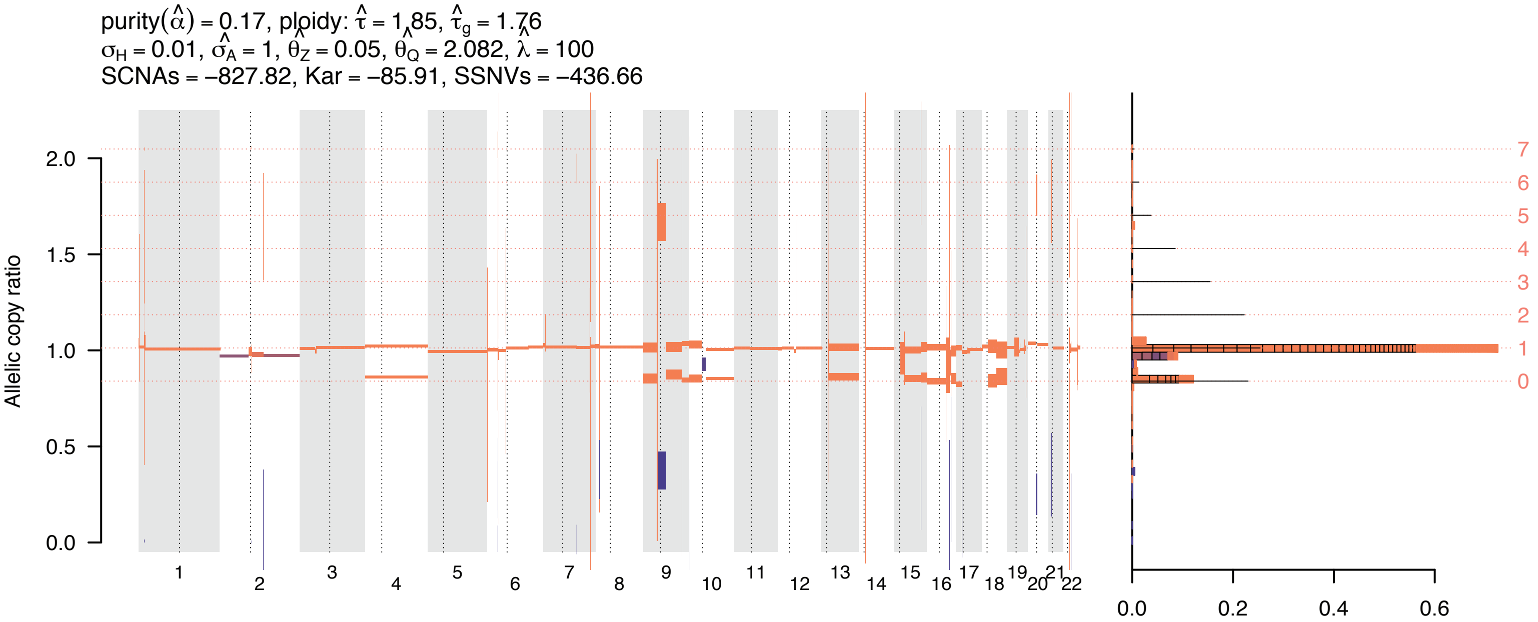
Biopsy 3


purity($\hat{\alpha}$) = 0.33, ploidy: $\hat{\tau}$ = 1.8, $\hat{\tau}_g$ = 1.71
σ_H = 0.01, $\hat{\sigma}_A$ = 1, $\hat{\theta}_Z$ = 0.13, $\hat{\theta}_Q$ = 1.59, $\hat{\lambda}$ = 100
SCNAs = −1341.9, Kar = −85.91, SSNVs = −528.28
Allelic copy ratio
0.0
0.5
1.0
1.5
2.0
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
0.0
0.1
0.2
0.3
0.4
0.5
0
1
2
3
4
5

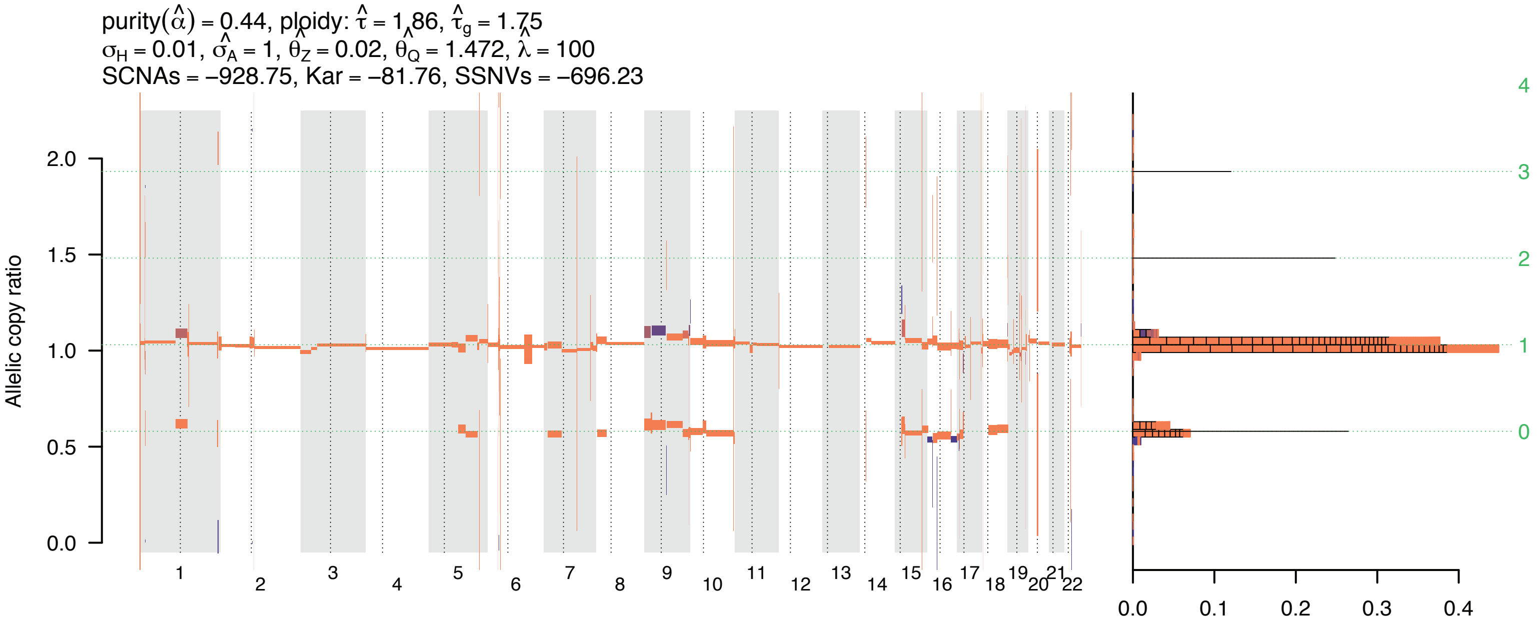
Biopsy 4


purity($\hat{\alpha}$) = 0.18, ploidy: $\hat{\tau}$ = 1.96, $\hat{\tau}_g$ = 1.74
σ_H = 0.01, $\hat{\sigma}_A$ = 1, $\hat{\theta}_Z$ = 0.1, $\hat{\theta}_Q$ = 2.009, $\hat{\lambda}$ = 100
SCNAs = −1509.96, Kar = −85.91, SSNVs = −516.12
Allelic copy ratio
2.0
1.5
1.0
0.5
0.0
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
7
6
5
4
3
2
1
0
0.0
0.1
0.2
0.3
0.4
0.5

Biopsy 5

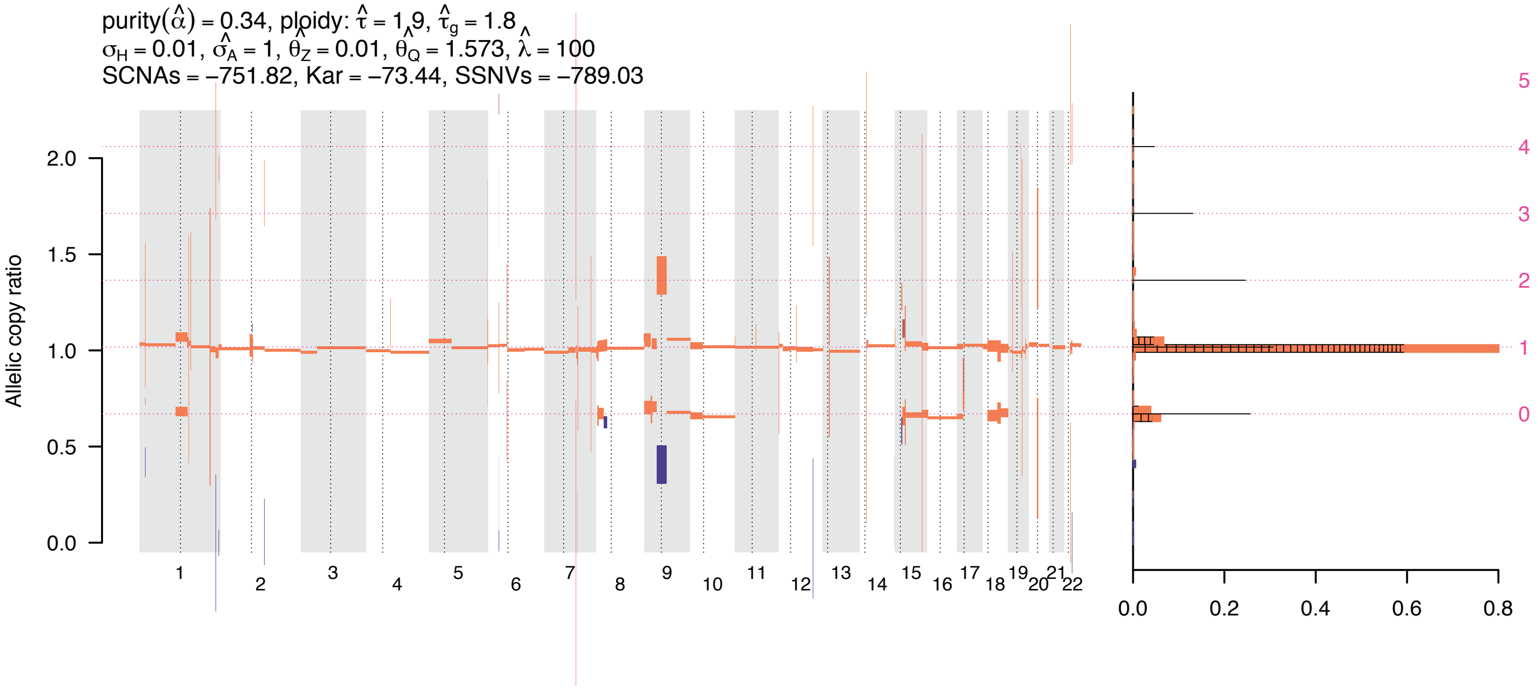

purity($\hat{\alpha}$) = 0.17, ploidy: $\hat{\tau}$ = 1.85, $\hat{\tau}_g$ = 1.76
σ_H = 0.01, $\hat{\sigma}_A$ = 1, $\hat{\theta}_Z$ = 0.05, $\hat{\theta}_Q$ = 2.082, $\hat{\lambda}$ = 100
SCNAs = −827.82, Kar = −85.91, SSNVs = −436.66
Allelic copy ratio
0.0
0.5
1.0
1.5
2.0
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
0.0
0.2
0.4
0.6
7
6
5
4
3
2
1
0

Biopsy 6

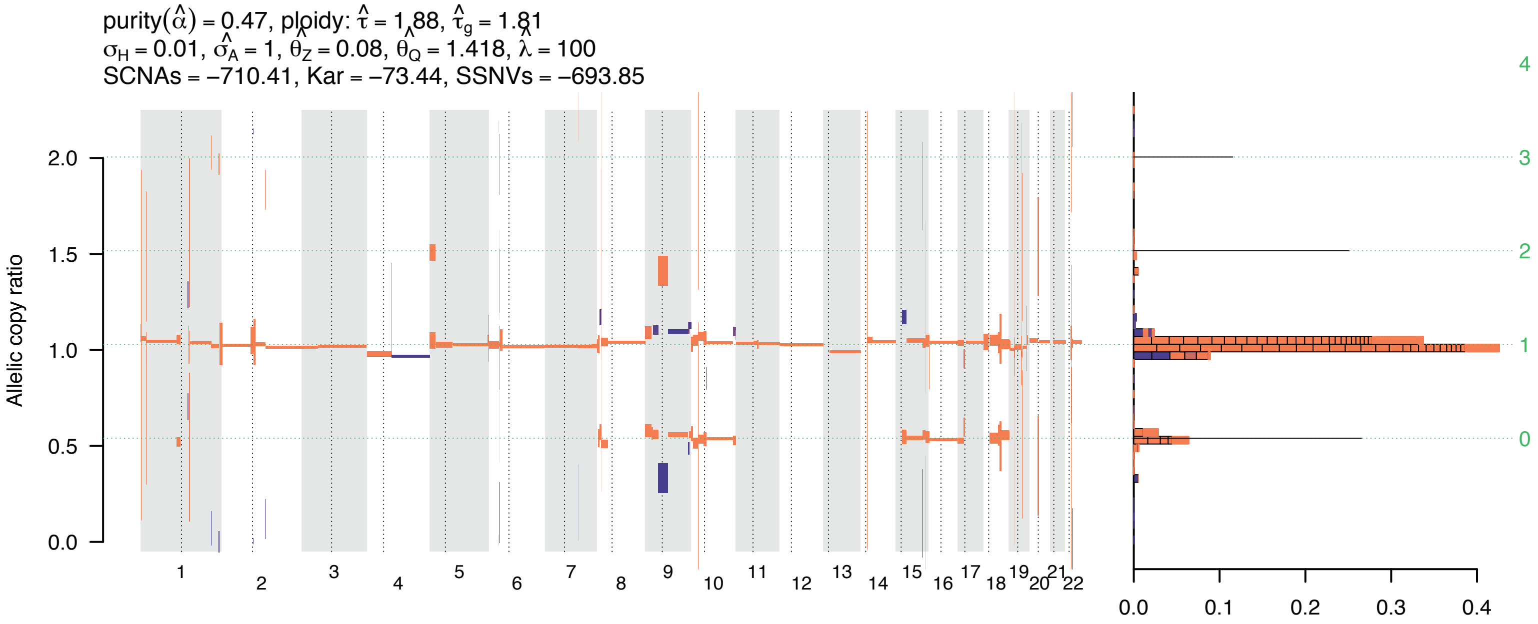


purity($\hat{\alpha}$) = 0.44, ploidy: $\hat{\tau}$ = 1.86, $\hat{\tau}_g$ = 1.75
σ_H = 0.01, $\hat{\sigma}_A$ = 1, $\hat{\theta}_Z$ = 0.02, $\hat{\theta}_Q$ = 1.472, $\hat{\lambda}$ = 100
SCNAs = −928.75, Kar = −81.76, SSNVs = −696.23
Allelic copy ratio
2.0
1.5
1.0
0.5
0.0
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
0.0
0.1
0.2
0.3
0.4
4
3
2
1
0

Biopsy 7

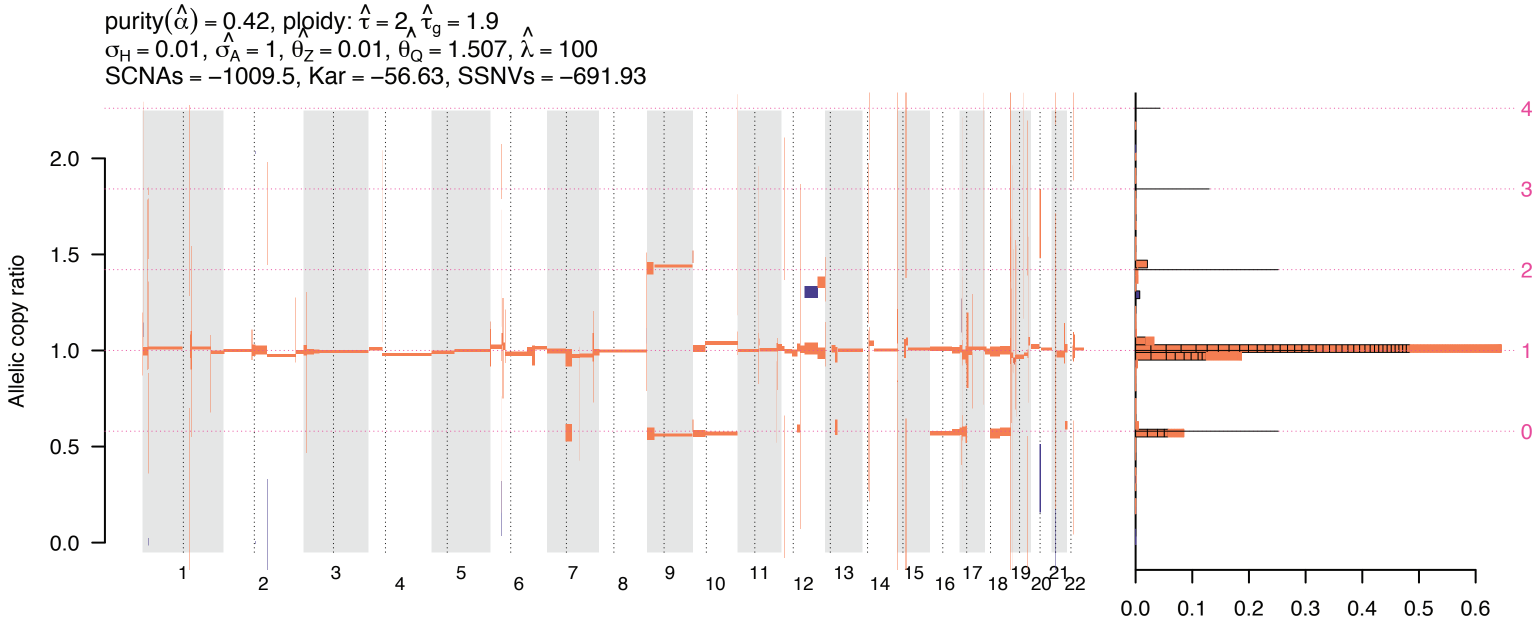

purity($\hat{\alpha}$) = 0.34, ploidy: $\hat{\tau}$ = 1.9, $\hat{\tau}_g$ = 1.8
σ_H = 0.01, $\hat{\sigma}_A$ = 1, $\hat{\theta}_Z$ = 0.01, $\hat{\theta}_Q$ = 1.573, $\hat{\lambda}$ = 100
SCNAs = −751.82, Kar = −73.44, SSNVs = −789.03
Allelic copy ratio
2.0
1.5
1.0
0.5
0.0
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
5
4
3
2
1
0
0.0
0.2
0.4
0.6
0.8

Biopsy 8



purity($\hat{\alpha}$) = 0.47, ploidy: $\hat{\tau}$ = 1.88, $\hat{\tau}_g$ = 1.81
σ_H = 0.01, $\hat{\sigma}_A$ = 1, $\hat{\theta}_Z$ = 0.08, $\hat{\theta}_Q$ = 1.418, $\hat{\lambda}$ = 100
SCNAs = −710.41, Kar = −73.44, SSNVs = −693.85
Allelic copy ratio
2.0
1.5
1.0
0.5
0.0
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
0.0
0.1
0.2
0.3
0.4
4
3
2
1
0

Biopsy 9


purity($\hat{\alpha}$) = 0.42, ploidy: $\hat{\tau}$ = 2, $\hat{\tau}_g$ = 1.9
σ_H = 0.01, $\hat{\sigma}_A$ = 1, $\hat{\theta}_Z$ = 0.01, $\hat{\theta}_Q$ = 1.507, $\hat{\lambda}$ = 100
SCNAs = −1009.5, Kar = −56.63, SSNVs = −691.93
Allelic copy ratio
2.0
1.5
1.0
0.5
0.0
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
0.0
0.1
0.2
0.3
0.4
0.5
0.6
4
3
2
1
0