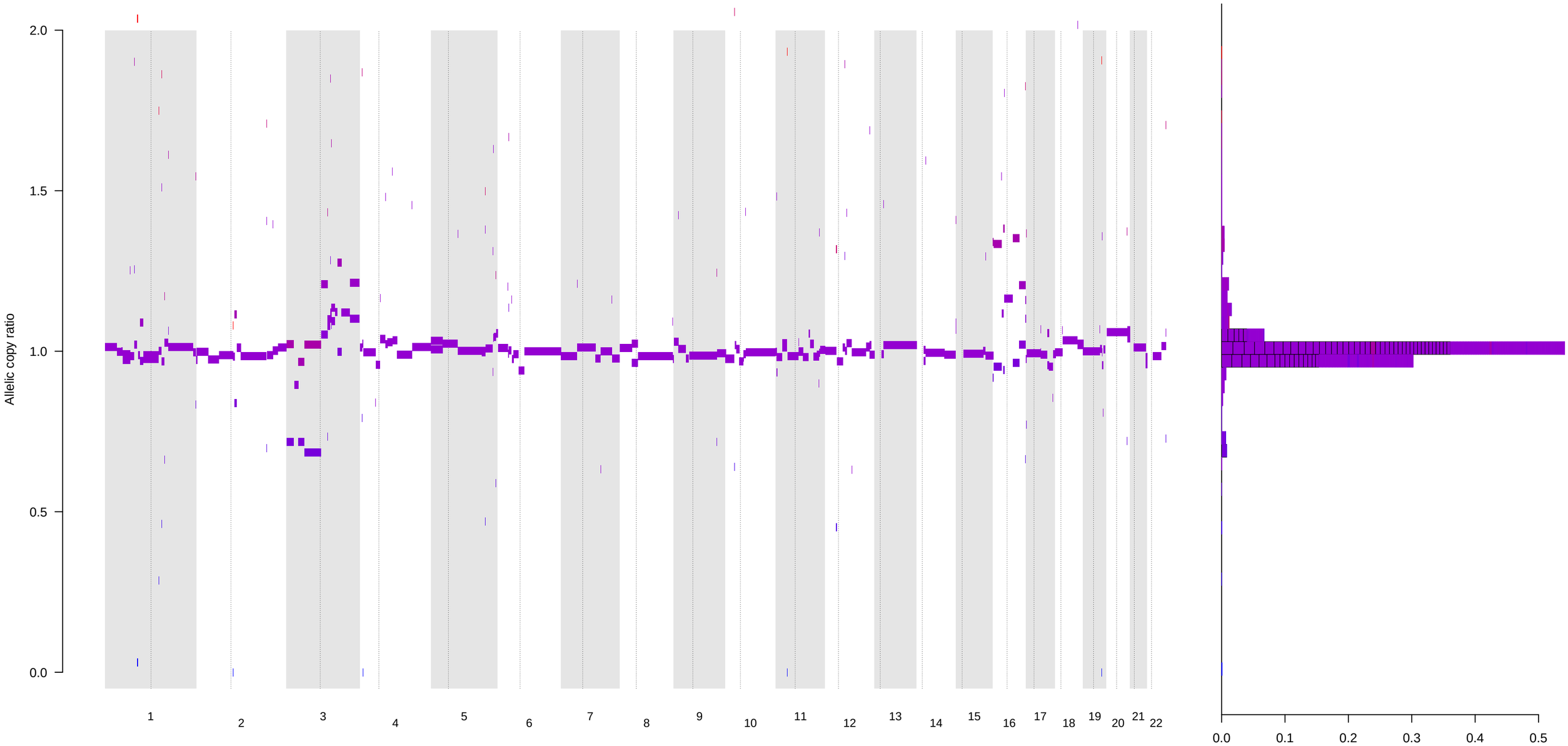
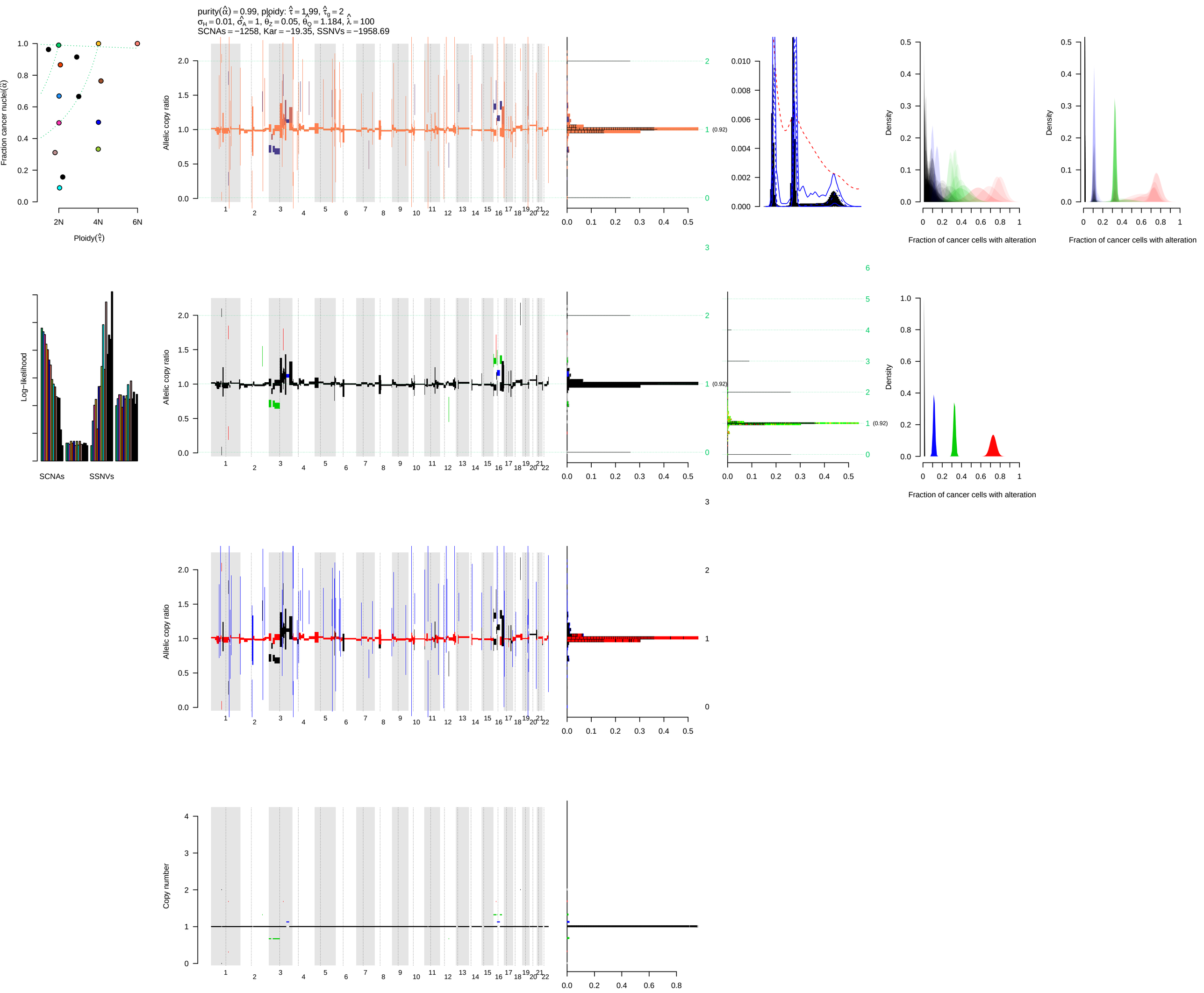
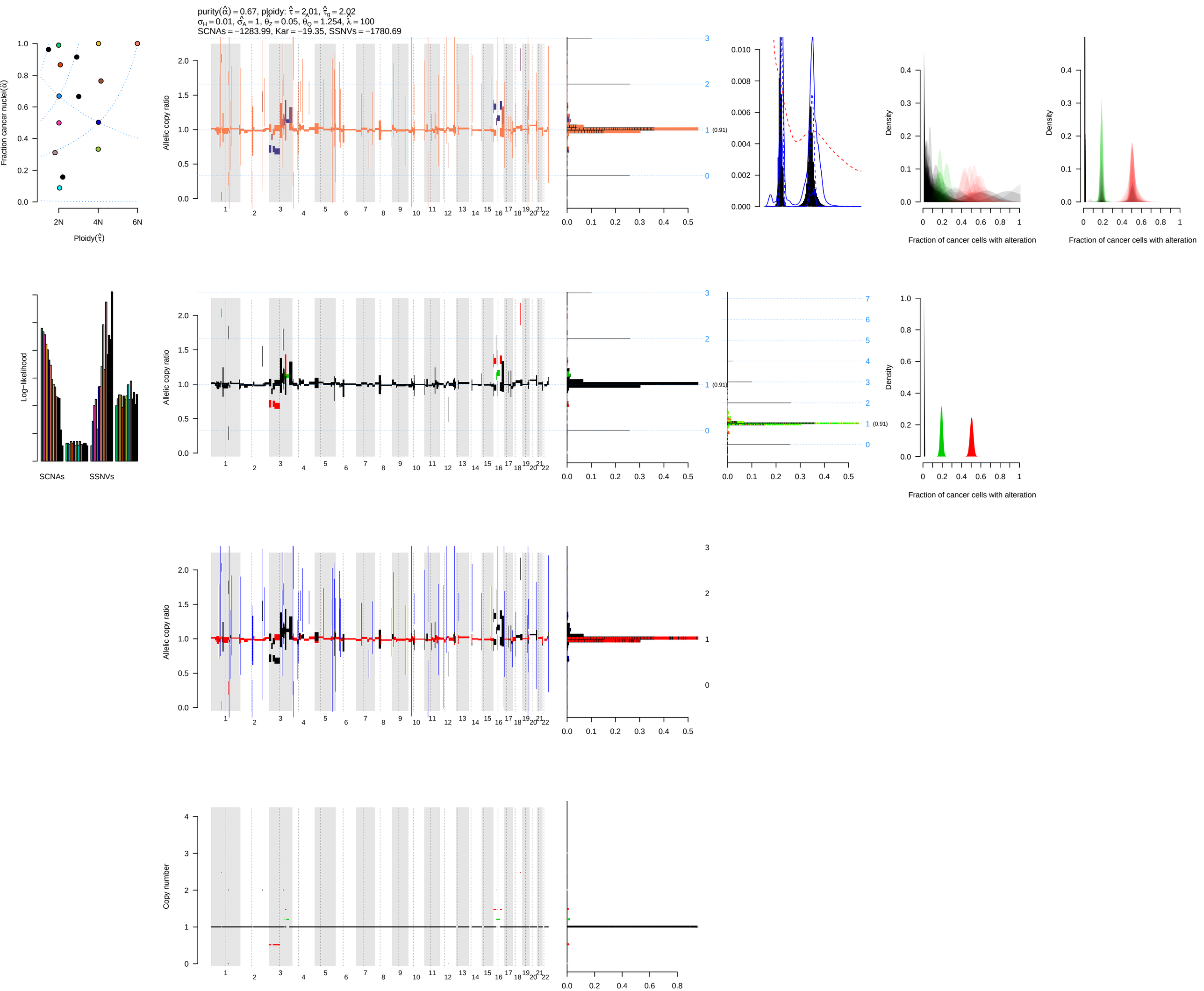
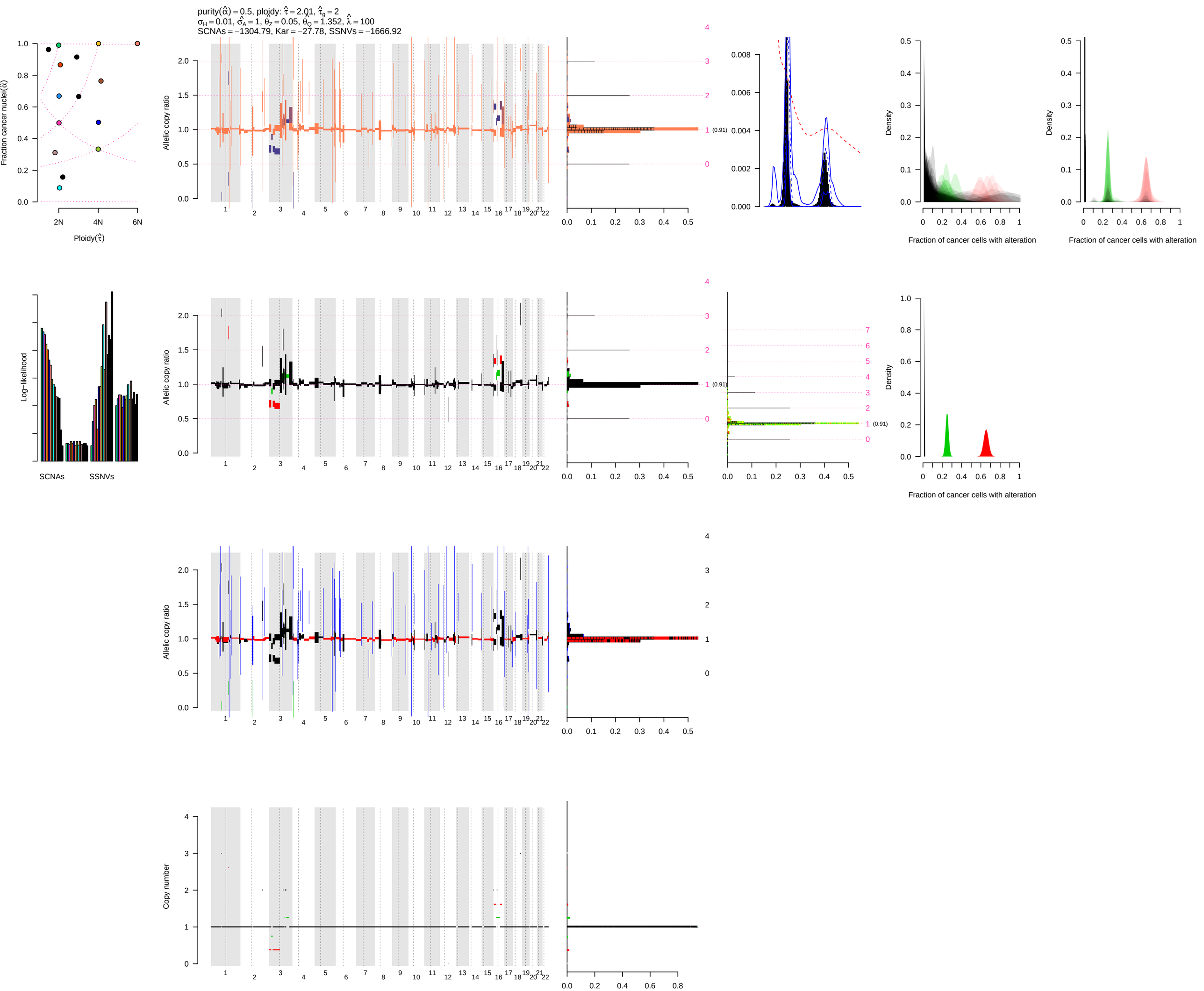
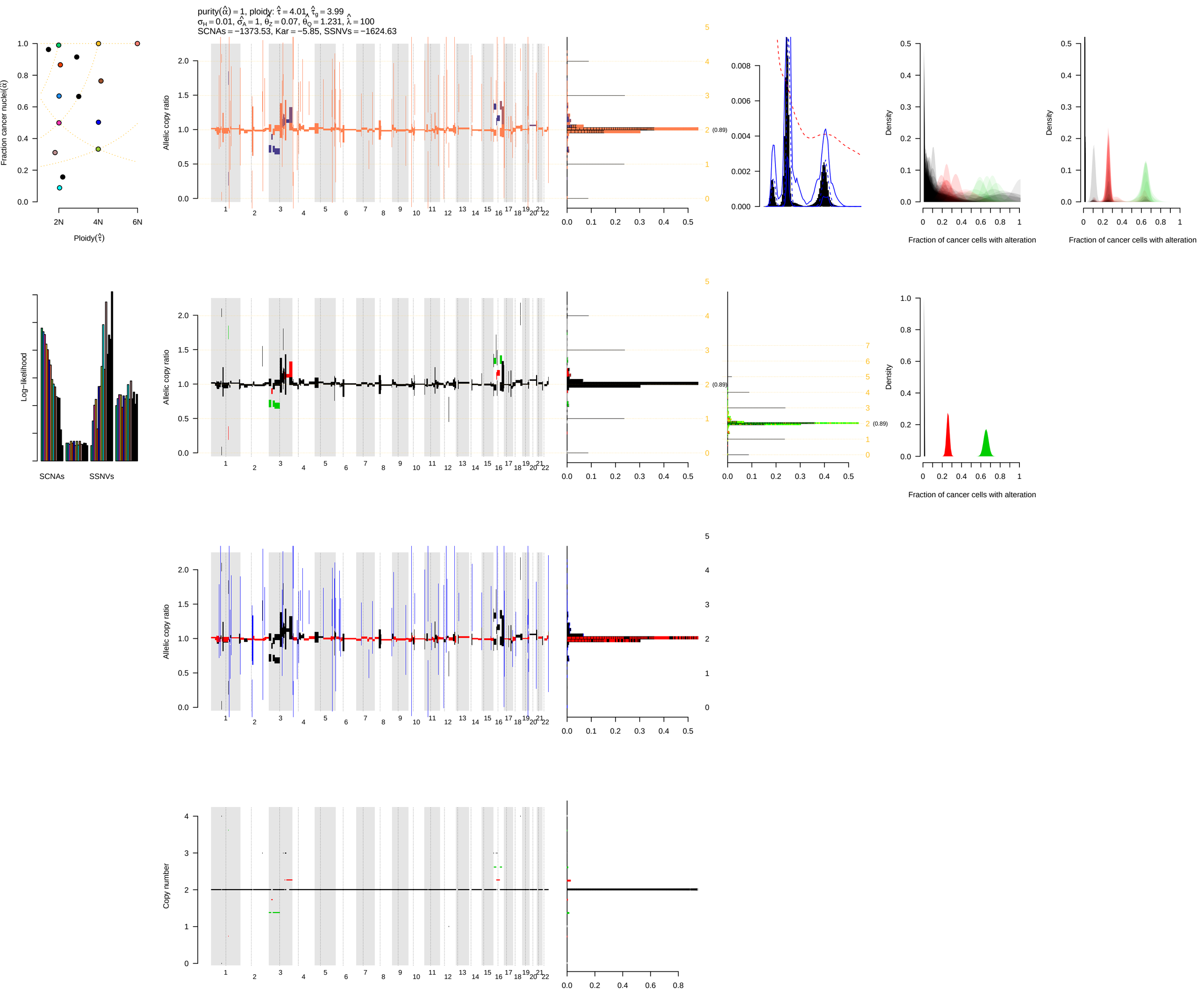
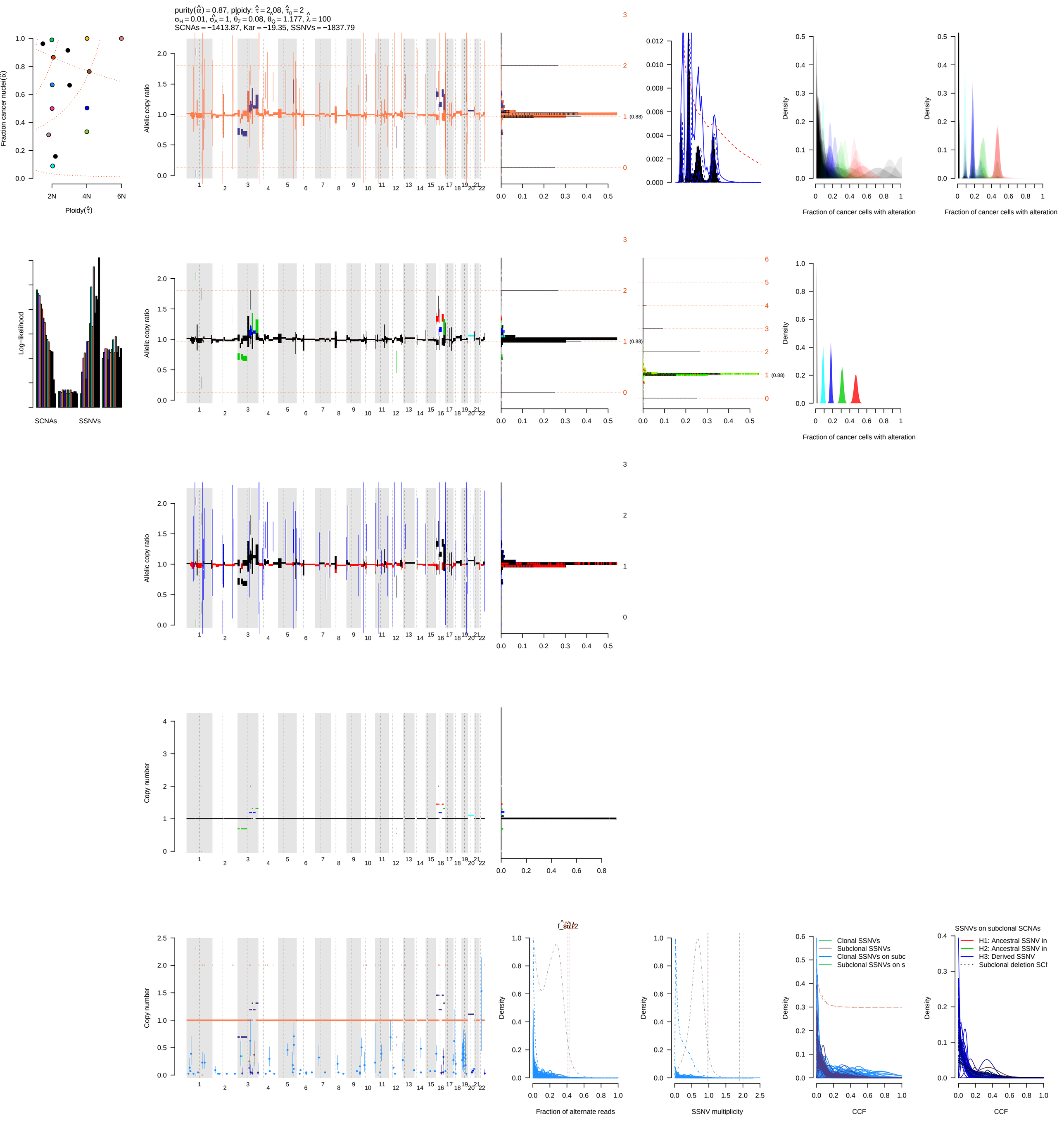

Allelic copy ratio
2.0
1.5
1.0
0.5
0.0
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
0.0
0.1
0.2
0.3
0.4
0.5

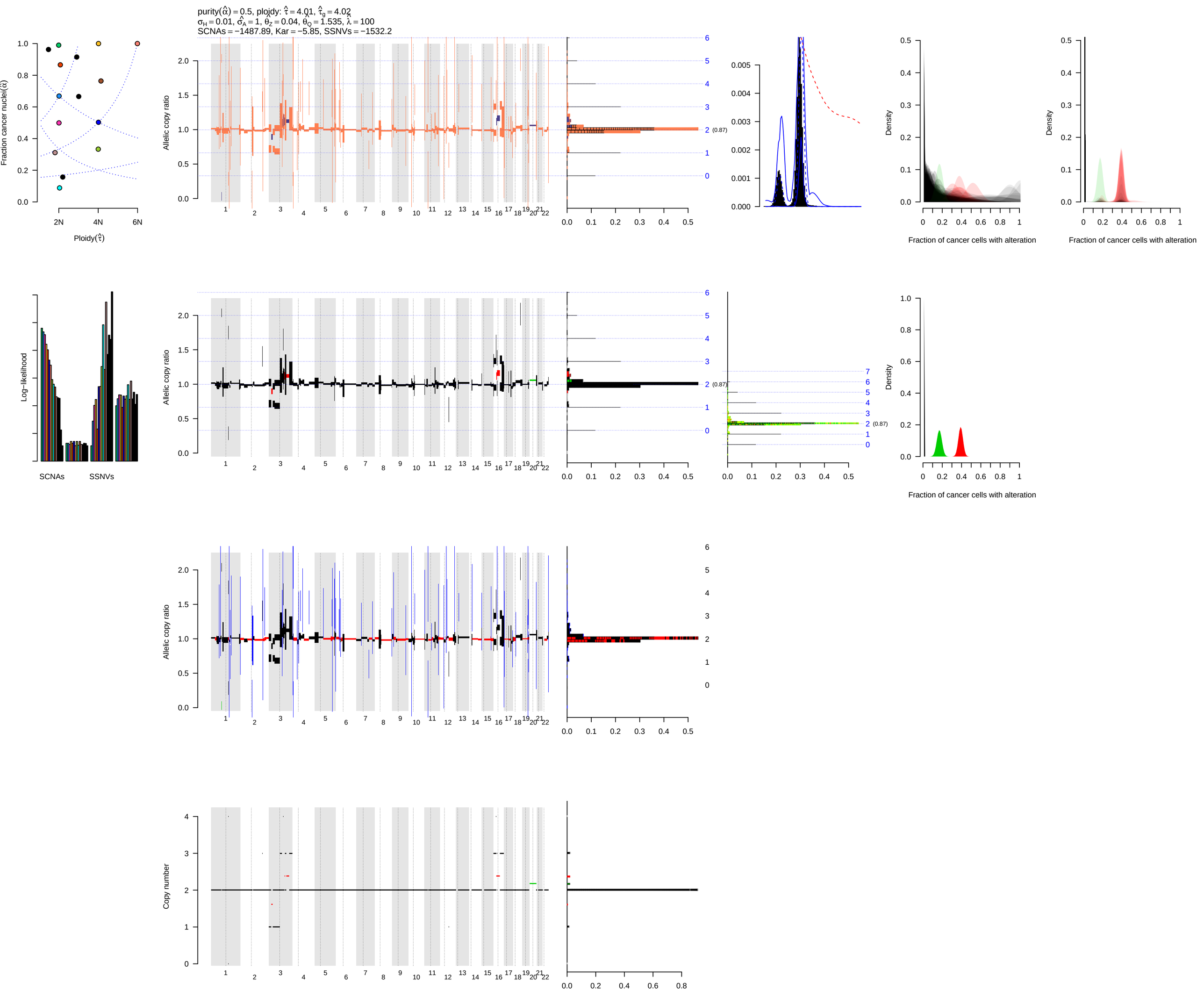

purity($\hat{\alpha}$) = 0.99, ploidy: $\hat{\tau}$ = 1.99, $\hat{\tau}_g$ = 2
$\sigma_H$ = 0.01, $\hat{\sigma}_A$ = 1, $\hat{\theta}_Z$ = 0.05, $\hat{\theta}_Q$ = 1.184, $\hat{\lambda}$ = 100
SCNAs = −1258, Kar = −19.35, SSNVs = −1958.69
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
Allelic copy ratio
Density
Fraction of cancer cells with alteration
Log−likelihood
SCNAs
SSNVs
Copy number
f_sa/2
Fraction of alternate reads
SSNV multiplicity
CCF
Clonal SSNVs
Subclonal SSNVs
Clonal SSNVs on subc
Subclonal SSNVs on s
SSNVs on subclonal SCNAs
H1: Ancestral SSNV in
H2: Ancestral SSNV in
H3: Derived SSNV
Subclonal deletion SCI

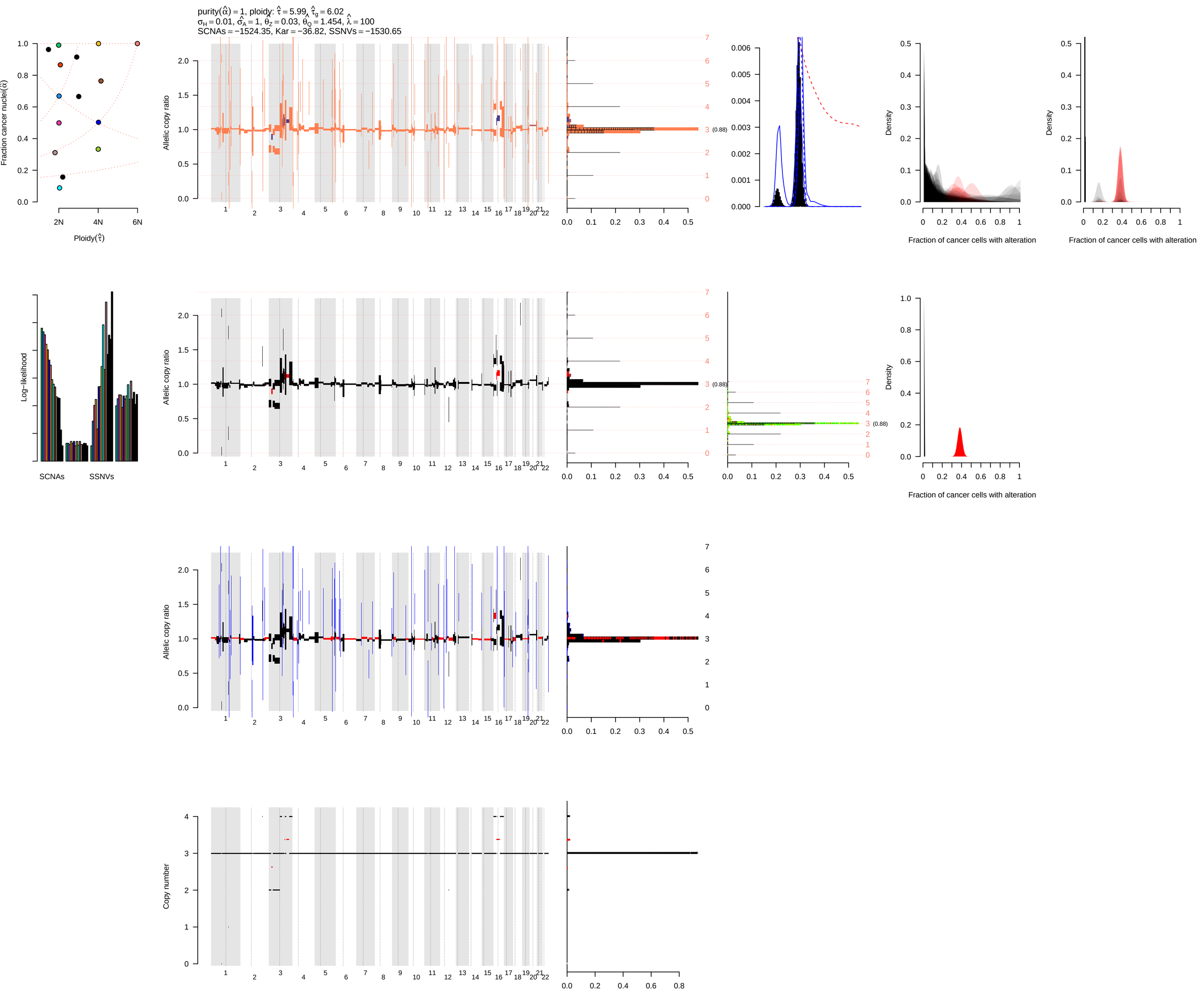

purity($\hat{\alpha}$) = 0.67, ploidy: $\hat{\tau}$ = 2.01, $\hat{\tau}_g$ = 2.02
$\sigma_H$ = 0.01, $\hat{\sigma}_A$ = 1, $\theta_Z$ = 0.05, $\theta_Q$ = 1.254, $\hat{\lambda}$ = 100
SCNAs = −1283.99, Kar = −19.35, SSNVs = −1780.69
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
Allelic copy ratio
Density
Fraction of cancer cells with alteration
Log−likelihood
SCNAs
SSNVs
Copy number
f_sc
Fraction of alternate reads
SSNV multiplicity
CCF
Clonal SSNVs
Subclonal SSNVs
Clonal SSNVs on subc
Subclonal SSNVs on s
SSNVs on subclonal SCNAs
H1: Ancestral SSNV in
H2: Ancestral SSNV in
H3: Derived SSNV
Subclonal deletion SCI

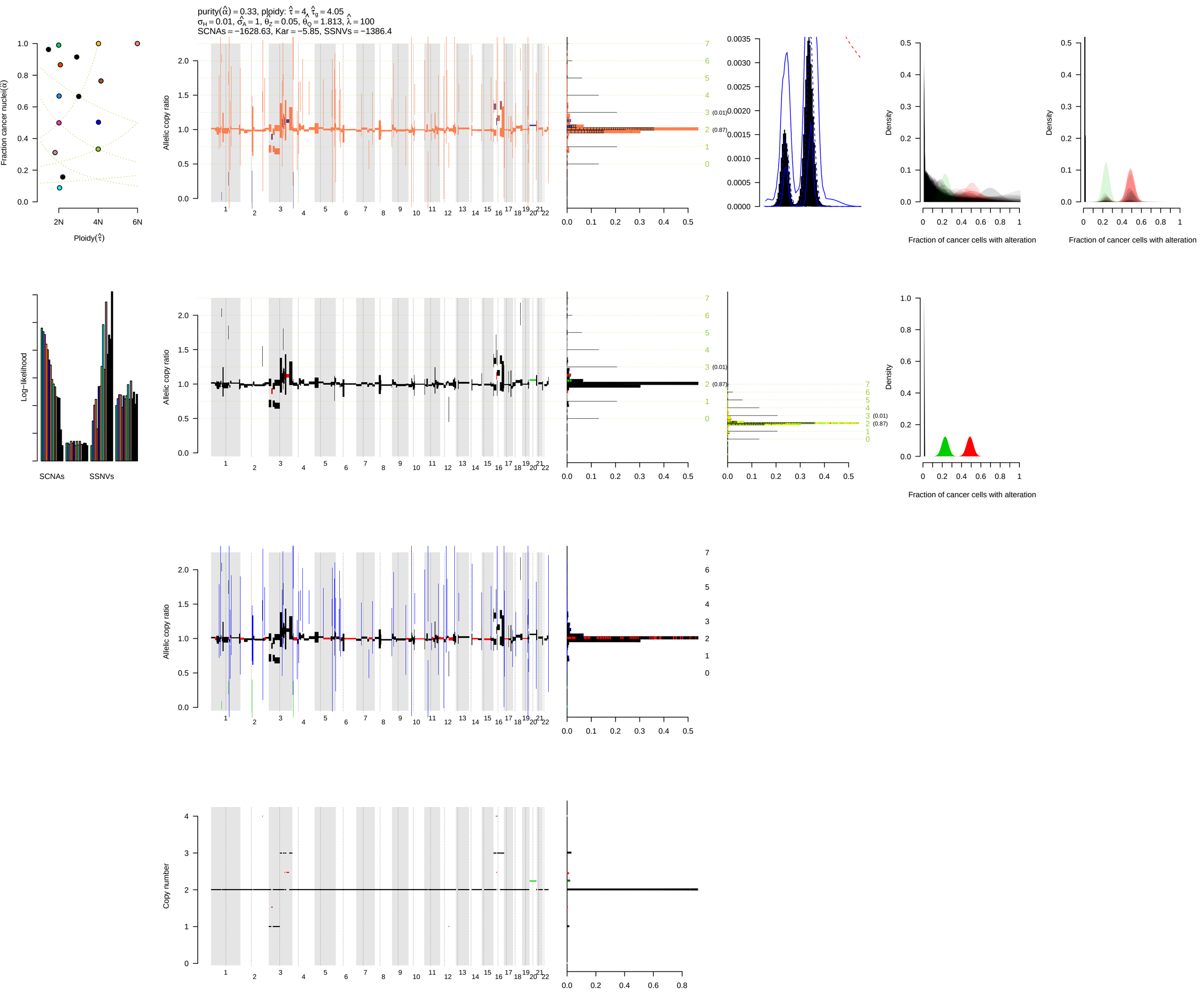

purity($\hat{\alpha}$) = 0.5, ploidy: $\hat{\tau}$ = 2.01, $\hat{\tau}_g$ = 2
$\sigma_H$ = 0.01, $\hat{\sigma}_A$ = 1, $\theta_Z$ = 0.05, $\theta_Q$ = 1.352, $\hat{\lambda}$ = 100
SCNAs = −1304.79, Kar = −27.78, SSNVs = −1666.92
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
Allelic copy ratio
Density
Fraction of cancer cells with alteration
Log−likelihood
SCNAs
SSNVs
Copy number
f_s
Fraction of alternate reads
SSNV multiplicity
CCF
Clonal SSNVs
Subclonal SSNVs
Clonal SSNVs on subc
Subclonal SSNVs on s
SSNVs on subclonal SCNAs
H1: Ancestral SSNV in
H2: Ancestral SSNV in
H3: Derived SSNV
Subclonal deletion SCI

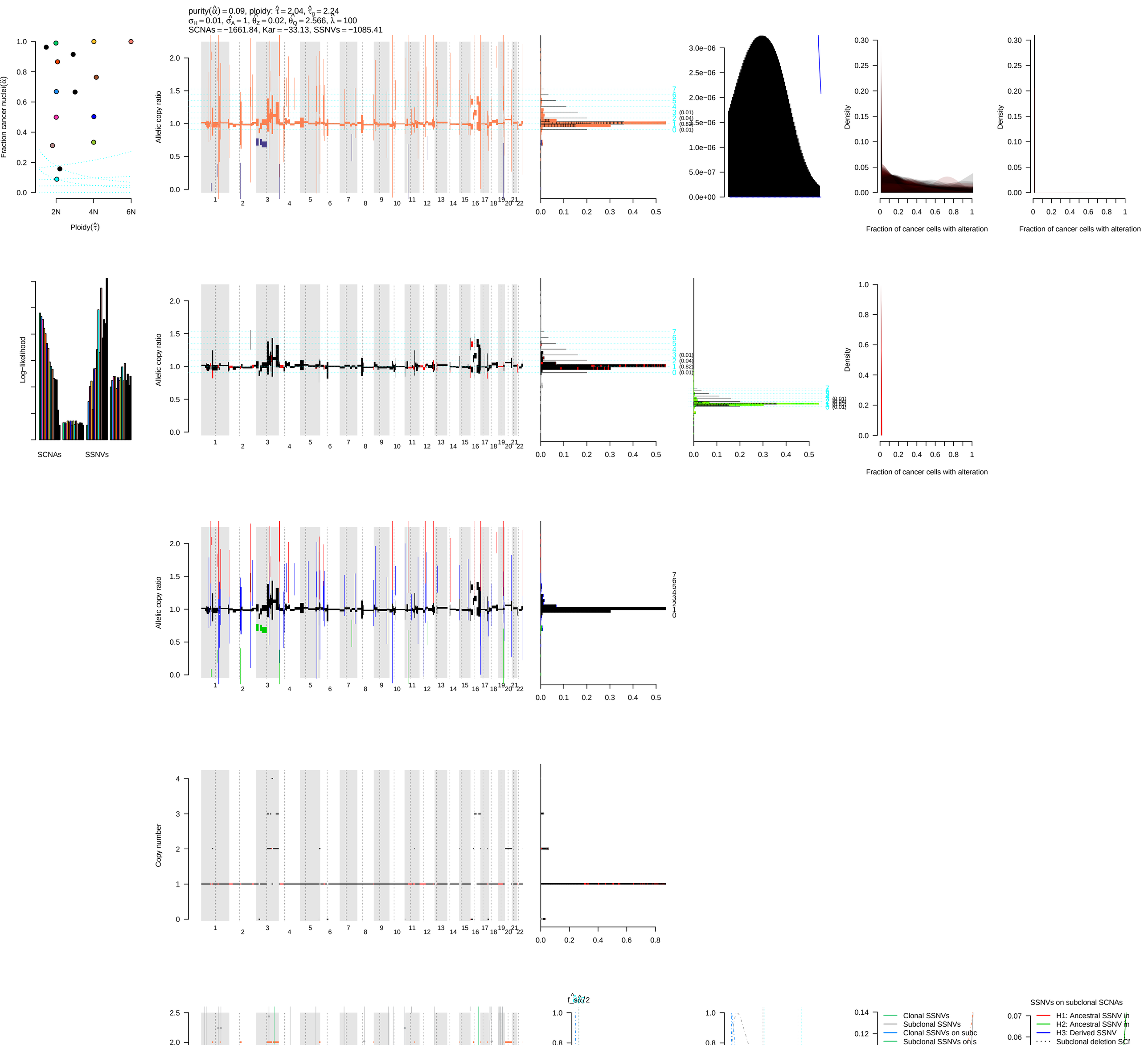

purity($\hat{\alpha}$) = 1, ploidy: $\hat{\tau}$ = 4.01, $\hat{\tau}_g$ = 3.99
$\sigma_H$ = 0.01, $\hat{\sigma}_A$ = 1, $\theta_Z$ = 0.07, $\theta_Q$ = 1.231, $\hat{\lambda}$ = 100
SCNAs = −1373.53, Kar = −5.85, SSNVs = −1624.63
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
Allelic copy ratio
Density
Fraction of cancer cells with alteration
Log−likelihood
SCNAs
SSNVs
Copy number
$\hat{f}_s\hat{\alpha}/2$
Fraction of alternate reads
SSNV multiplicity
CCF
Clonal SSNVs
Subclonal SSNVs
Clonal SSNVs on subc
Subclonal SSNVs on s
SSNVs on subclonal SCNAs
H1: Ancestral SSNV in
H2: Ancestral SSNV in
H3: Derived SSNV
Subclonal deletion SCI

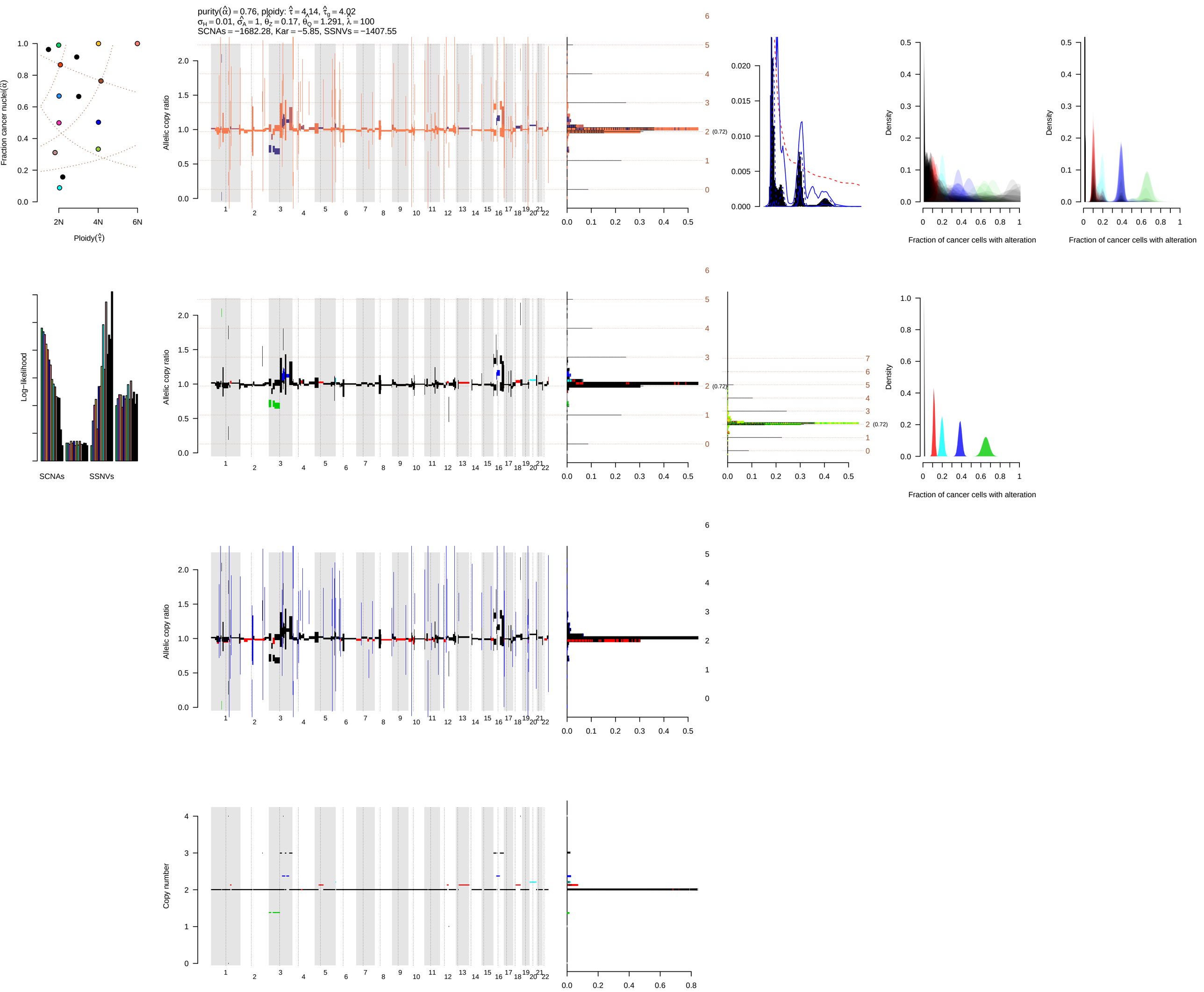

purity($\hat{\alpha}$) = 0.87, ploidy: $\hat{\tau}$ = 2.08, $\hat{\tau}_g$ = 2
$\sigma_H$ = 0.01, $\hat{\sigma}_A$ = 1, $\hat{\theta}_Z$ = 0.08, $\hat{\theta}_Q$ = 1.177, $\hat{\lambda}$ = 100
SCNAs = −1413.87, Kar = −19.35, SSNVs = −1837.79
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
Allelic copy ratio
Density
Fraction of cancer cells with alteration
Log−likelihood
SCNAs
SSNVs
Copy number
f_sol
Fraction of alternate reads
SSNV multiplicity
CCF
SSNVs on subclonal SCNAs
Clonal SSNVs
Subclonal SSNVs
Clonal SSNVs on subc
Subclonal SSNVs on s
H1: Ancestral SSNV in
H2: Ancestral SSNV in
H3: Derived SSNV
Subclonal deletion SCI

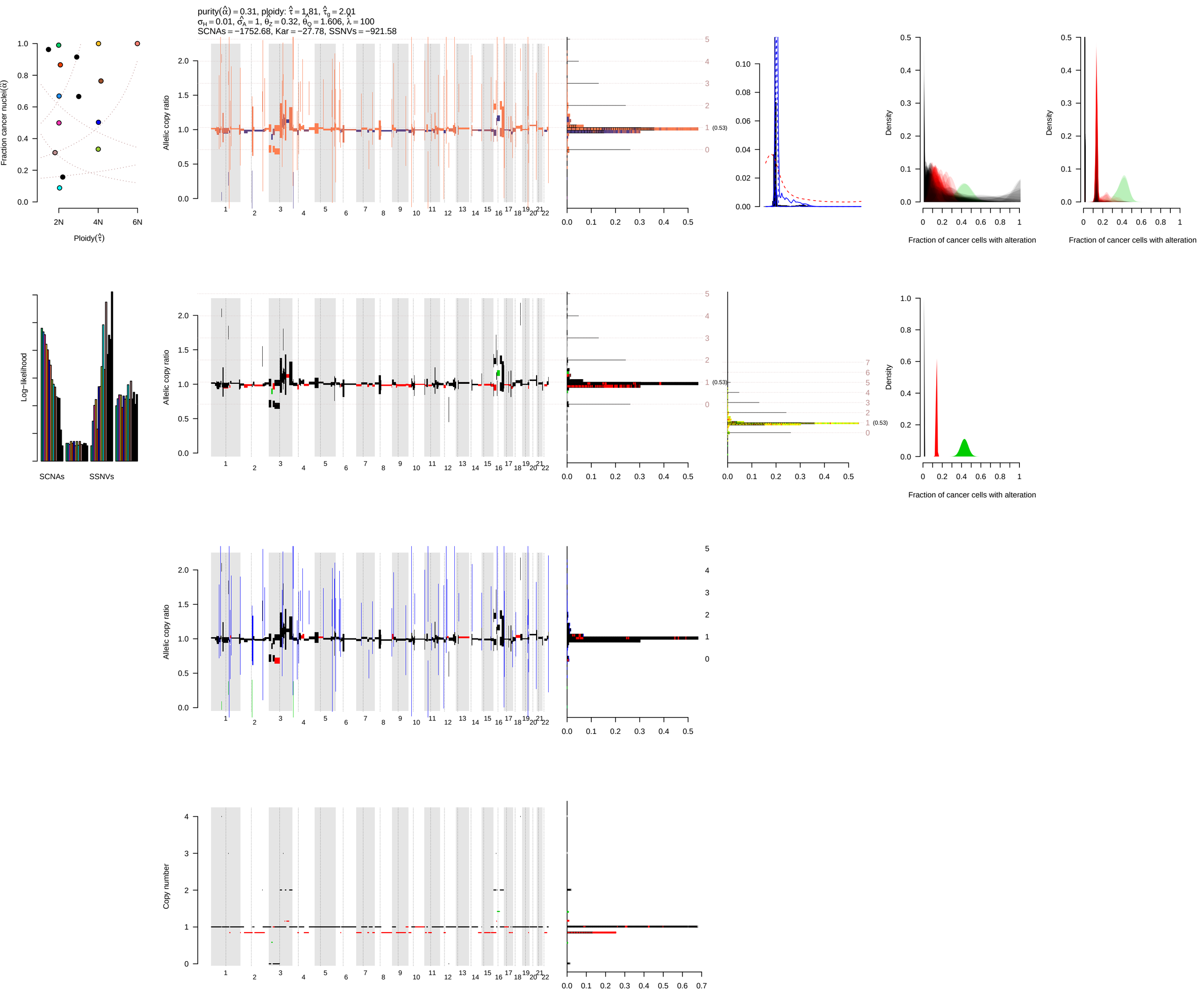

purity($\hat{\alpha}$) = 0.5, ploidy: $\hat{\tau}$ = 4.01, $\hat{\tau}_g$ = 4.02
$\sigma_H$ = 0.01, $\hat{\sigma}_A$ = 1, $\theta_Z$ = 0.04, $\theta_Q$ = 1.535, $\hat{\lambda}$ = 100
SCNAs = −1487.89, Kar = −5.85, SSNVs = −1532.2
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
Allelic copy ratio
Density
Fraction of cancer cells with alteration
Log−likelihood
SCNAs
SSNVs
Copy number
Fraction of alternate reads
SSNV multiplicity
CCF
Clonal SSNVs
Subclonal SSNVs
Clonal SSNVs on subc
Subclonal SSNVs on s
SSNVs on subclonal SCNAs
H1: Ancestral SSNV in
H2: Ancestral SSNV in
H3: Derived SSNV
Subclonal deletion SCI

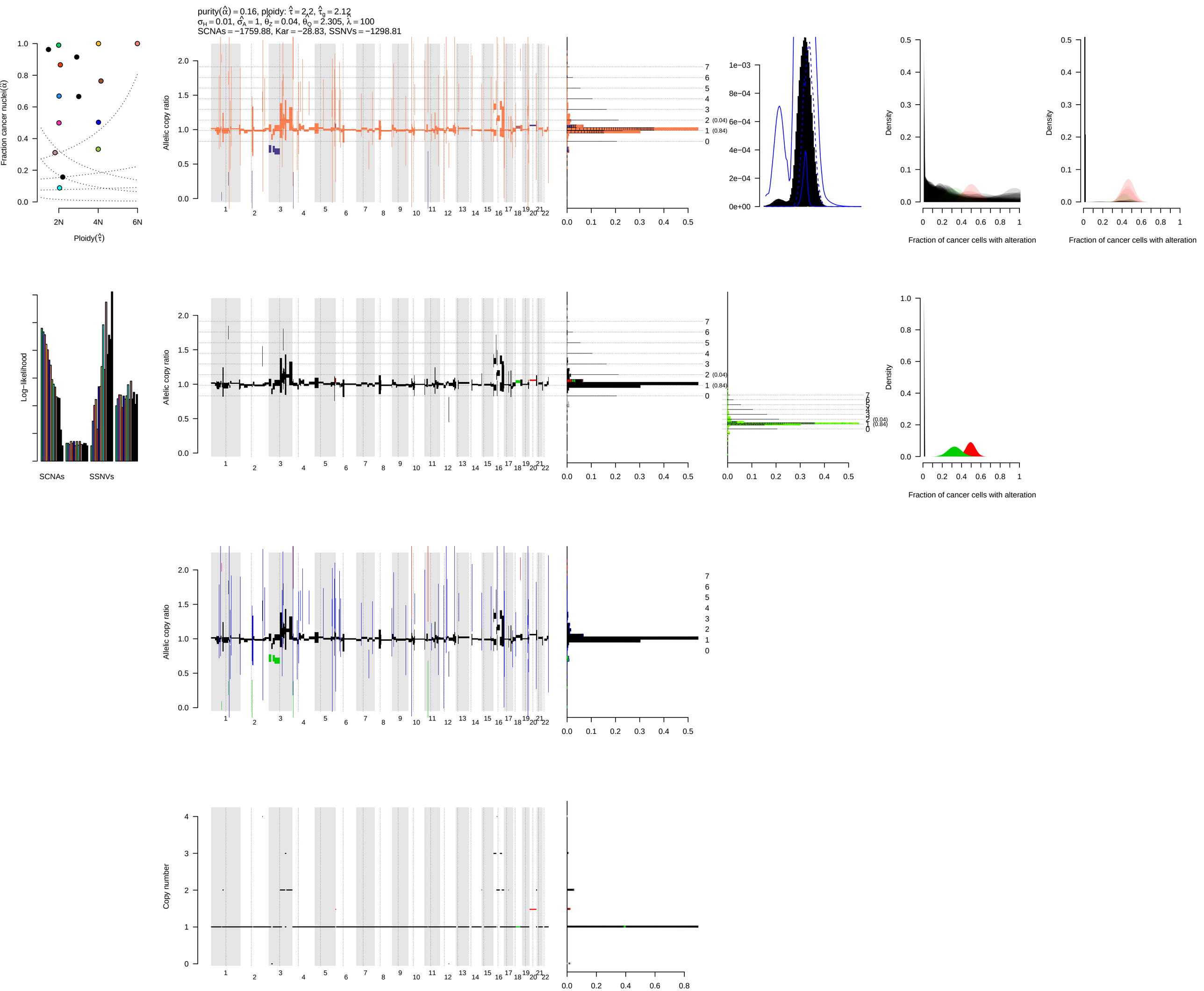

purity($\hat{\alpha}$) = 1, ploidy: $\hat{\tau}$ = 5.99, $\hat{\tau}_g$ = 6.02
$\sigma_H$ = 0.01, $\hat{\sigma}_A$ = 1, $\theta_Z$ = 0.03, $\theta_Q$ = 1.454, $\hat{\lambda}$ = 100
SCNAs = −1524.35, Kar = −36.82, SSNVs = −1530.65
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
Allelic copy ratio
(0.88)
Density
Fraction of cancer cells with alteration
Log−likelihood
SCNAs
SSNVs
Copy number
$\hat{f}_s\hat{\alpha}/2$
Fraction of alternate reads
SSNV multiplicity
Clonal SSNVs
Subclonal SSNVs
Clonal SSNVs on subc
Subclonal SSNVs on s
CCF
SSNVs on subclonal SCNAs
H1: Ancestral SSNV in
H2: Ancestral SSNV in
H3: Derived SSNV
Subclonal deletion SCI

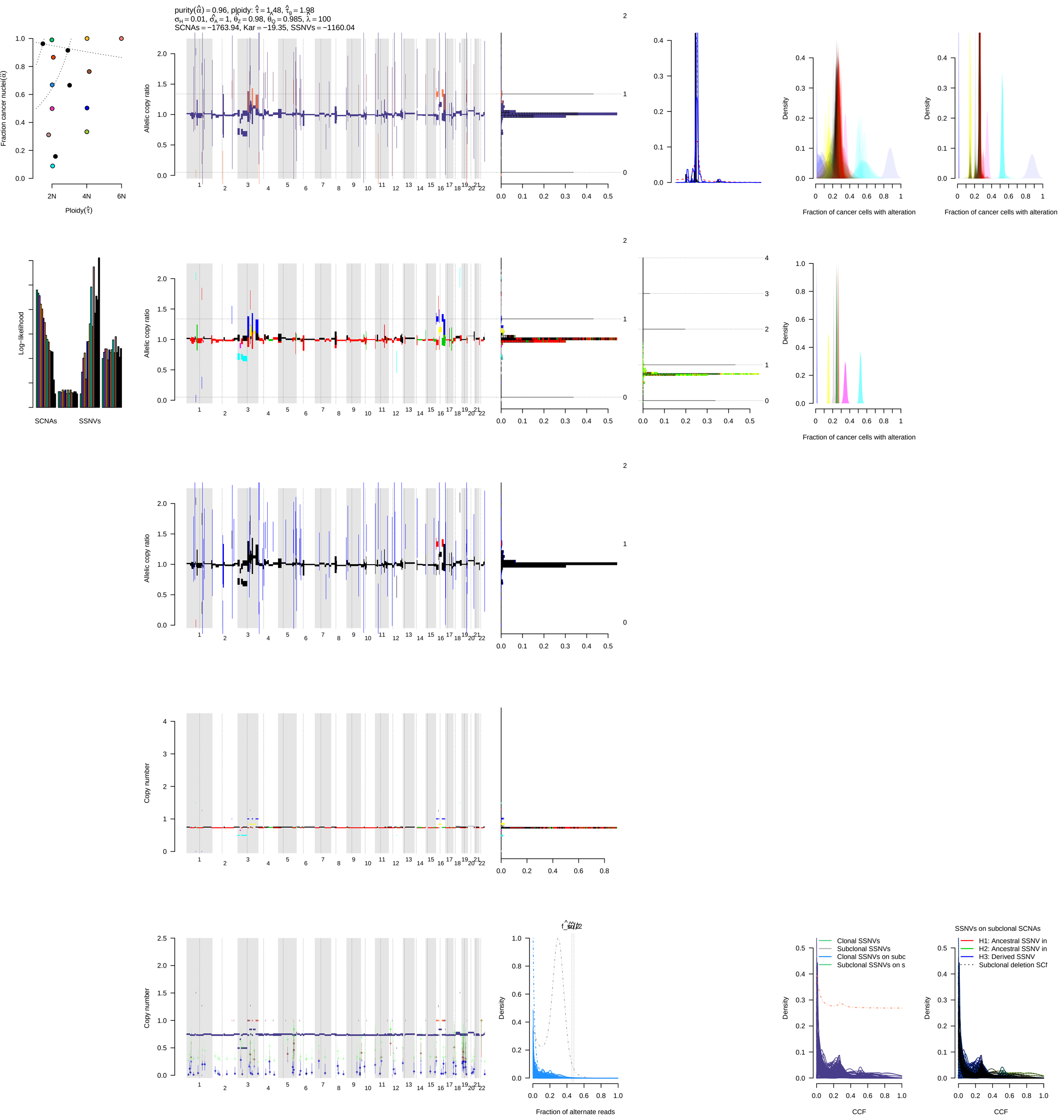

purity($\hat{\alpha}$) = 0.33, ploidy: $\hat{\tau}$ = 4, $\hat{\tau}_g$ = 4.05
$\sigma_H$ = 0.01, $\hat{\sigma}_A$ = 1, $\theta_Z$ = 0.05, $\theta_Q$ = 1.813, $\hat{\lambda}$ = 100
SCNAs = −1628.63, Kar = −5.85, SSNVs = −1386.4
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
Allelic copy ratio
Density
Fraction of cancer cells with alteration
Log−likelihood
SCNAs
SSNVs
Copy number
f_s
Fraction of alternate reads
SSNV multiplicity
CCF
Clonal SSNVs
Subclonal SSNVs
Clonal SSNVs on subc
Subclonal SSNVs on s
SSNVs on subclonal SCNAs
H1: Ancestral SSNV in
H2: Ancestral SSNV in
H3: Derived SSNV
Subclonal deletion SCI

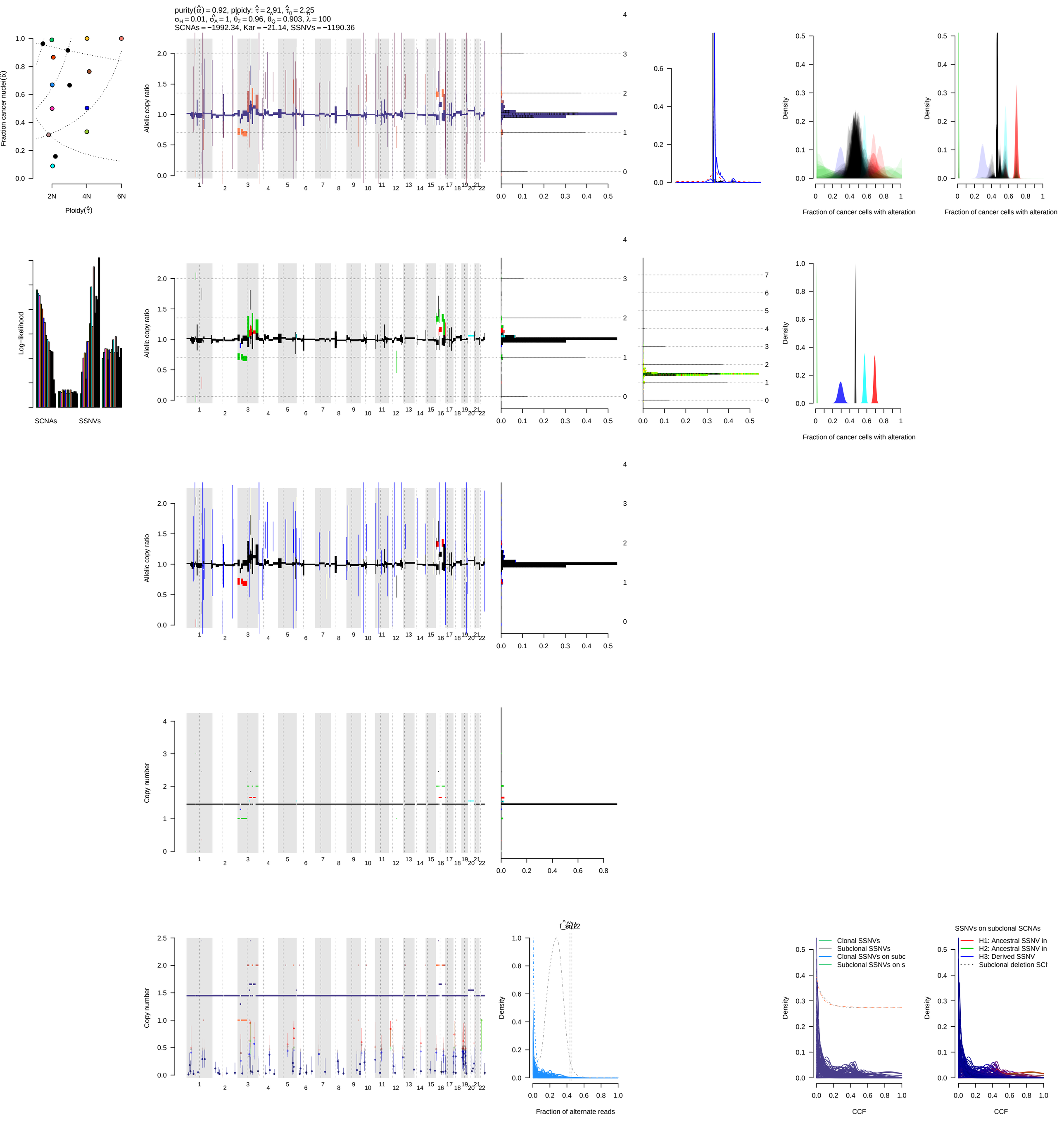

purity($\hat{\alpha}$) = 0.09, ploidy: $\hat{\tau}$ = 2.04, $\hat{\tau}_g$ = 2.24
$\sigma_H$ = 0.01, $\hat{\sigma}_A$ = 1, $\theta_Z$ = 0.02, $\theta_Q$ = 2.566, $\hat{\lambda}$ = 100
SCNAs = −1661.84, Kar = −33.13, SSNVs = −1085.41
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
Allelic copy ratio
Density
Fraction of cancer cells with alteration
Log−likelihood
SCNAs
SSNVs
Copy number
f_sol/2
Fraction of alternate reads
SSNV multiplicity
CCF
Clonal SSNVs
Subclonal SSNVs
Clonal SSNVs on subc
Subclonal SSNVs on s
SSNVs on subclonal SCNAs
H1: Ancestral SSNV in
H2: Ancestral SSNV in
H3: Derived SSNV
Subclonal deletion SCI

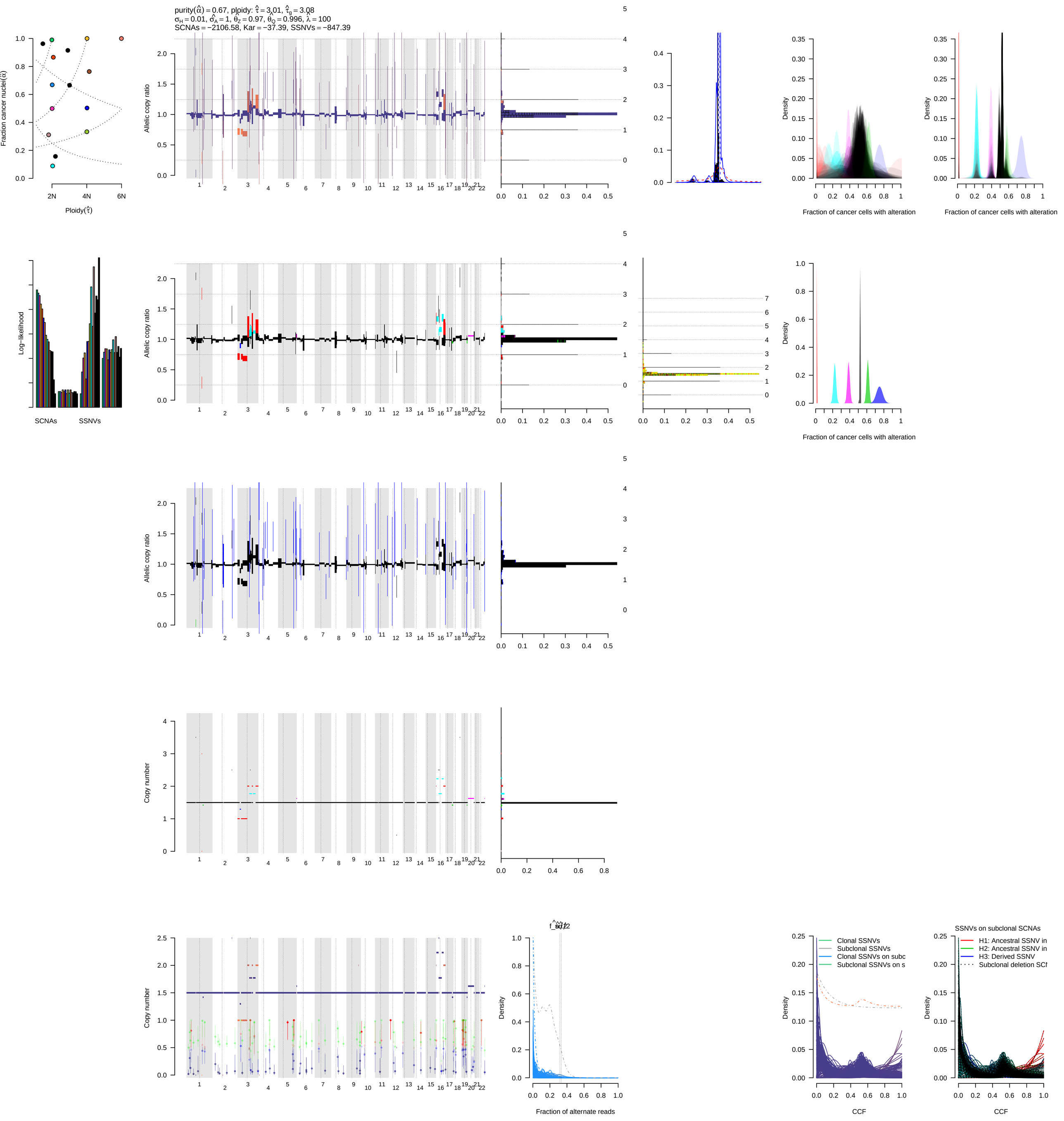

purity($\hat{\alpha}$) = 0.76, ploidy: $\hat{\tau}$ = 4.14, $\hat{\tau}_g$ = 4.02
$\sigma_H$ = 0.01, $\hat{\sigma}_A$ = 1, $\theta_Z$ = 0.17, $\theta_Q$ = 1.291, $\hat{\lambda}$ = 100
SCNAs = −1682.28, Kar = −5.85, SSNVs = −1407.55
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
Allelic copy ratio
Density
Fraction of cancer cells with alteration
Log−likelihood
SCNAs
SSNVs
Copy number
f_sq/2
Fraction of alternate reads
SSNV multiplicity
CCF
SSNVs on subclonal SCNAs
Clonal SSNVs
Subclonal SSNVs
Clonal SSNVs on subc
Subclonal SSNVs on s
H1: Ancestral SSNV in
H2: Ancestral SSNV in
H3: Derived SSNV
Subclonal deletion SCI


purity($\hat{\alpha}$) = 0.31, ploidy: $\hat{\tau}$ = 1.81, $\hat{\tau}_g$ = 2.01
$\sigma_H$ = 0.01, $\hat{\sigma}_A$ = 1, $\theta_Z$ = 0.32, $\theta_Q$ = 1.606, $\hat{\lambda}$ = 100
SCNAs = −1752.68, Kar = −27.78, SSNVs = −921.58
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
Allelic copy ratio
Density
Fraction of cancer cells with alteration
Log−likelihood
SCNAs
SSNVs
Copy number
f_s$\hat{\alpha}$/2
Fraction of alternate reads
SSNV multiplicity
CCF
Clonal SSNVs
Subclonal SSNVs
Clonal SSNVs on subc
Subclonal SSNVs on s
SSNVs on subclonal SCNAs
H1: Ancestral SSNV in
H2: Ancestral SSNV in
H3: Derived SSNV
Subclonal deletion SCI


purity($\hat{\alpha}$) = 0.16, ploidy: $\hat{\tau}$ = 2.2, $\hat{\tau}_g$ = 2.12
$\sigma_H$ = 0.01, $\hat{\sigma}_A$ = 1, $\theta_Z$ = 0.04, $\theta_Q$ = 2.305, $\hat{\lambda}$ = 100
SCNAs = −1759.88, Kar = −28.83, SSNVs = −1298.81
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
Allelic copy ratio
Density
Fraction of cancer cells with alteration
Log−likelihood
SCNAs
SSNVs
Copy number
Fraction of alternate reads
SSNV multiplicity
CCF
Clonal SSNVs
Subclonal SSNVs
SSNVs on subclonal SCNAs
H1: Ancestral SSNV in
H2: Ancestral SSNV in
H3: Derived SSNV
Subclonal deletion SCN


purity($\hat{\alpha}$) = 0.96, ploidy: $\hat{\tau}$ = 1.48, $\hat{\tau}_g$ = 1.98
$\sigma_H$ = 0.01, $\hat{\sigma}_A$ = 1, $\theta_Z$ = 0.98, $\theta_Q$ = 0.985, $\hat{\lambda}$ = 100
SCNAs = −1763.94, Kar = −19.35, SSNVs = −1160.04
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
Allelic copy ratio
Density
Fraction of cancer cells with alteration
Log−likelihood
SCNAs
SSNVs
Copy number
Fraction of alternate reads
SSNVs on subclonal SCNAs
Clonal SSNVs
Subclonal SSNVs
Clonal SSNVs on subc
Subclonal SSNVs on s
H1: Ancestral SSNV in
H2: Ancestral SSNV in
H3: Derived SSNV
Subclonal deletion SCI
CCF


purity($\hat{\alpha}$) = 0.92, ploidy: $\hat{\tau}$ = 2.91, $\hat{\tau}_g$ = 2.25
$\sigma_H$ = 0.01, $\hat{\sigma}_A$ = 1, $\theta_Z$ = 0.96, $\theta_Q$ = 0.903, $\hat{\lambda}$ = 100
SCNAs = −1992.34, Kar = −21.14, SSNVs = −1190.36
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
Allelic copy ratio
Density
Fraction of cancer cells with alteration
Log−likelihood
SCNAs
SSNVs
Copy number
Fraction of alternate reads
Clonal SSNVs
Subclonal SSNVs
Clonal SSNVs on subc
Subclonal SSNVs on s
SSNVs on subclonal SCNAs
H1: Ancestral SSNV in
H2: Ancestral SSNV in
H3: Derived SSNV
Subclonal deletion SCI
CCF


purity($\hat{\alpha}$) = 0.67, ploidy: $\hat{\tau}$ = 3.01, $\hat{\tau}_g$ = 3.08
$\sigma_H$ = 0.01, $\hat{\sigma}_A$ = 1, $\theta_Z$ = 0.97, $\theta_Q$ = 0.996, $\hat{\lambda}$ = 100
SCNAs = −2106.58, Kar = −37.39, SSNVs = −847.39
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
Allelic copy ratio
Density
Fraction of cancer cells with alteration
Log−likelihood
SCNAs
SSNVs
Copy number
Fraction of alternate reads
CCF
Clonal SSNVs
Subclonal SSNVs
Clonal SSNVs on subc
Subclonal SSNVs on s
SSNVs on subclonal SCNAs
H1: Ancestral SSNV in
H2: Ancestral SSNV in
H3: Derived SSNV
Subclonal deletion SCI