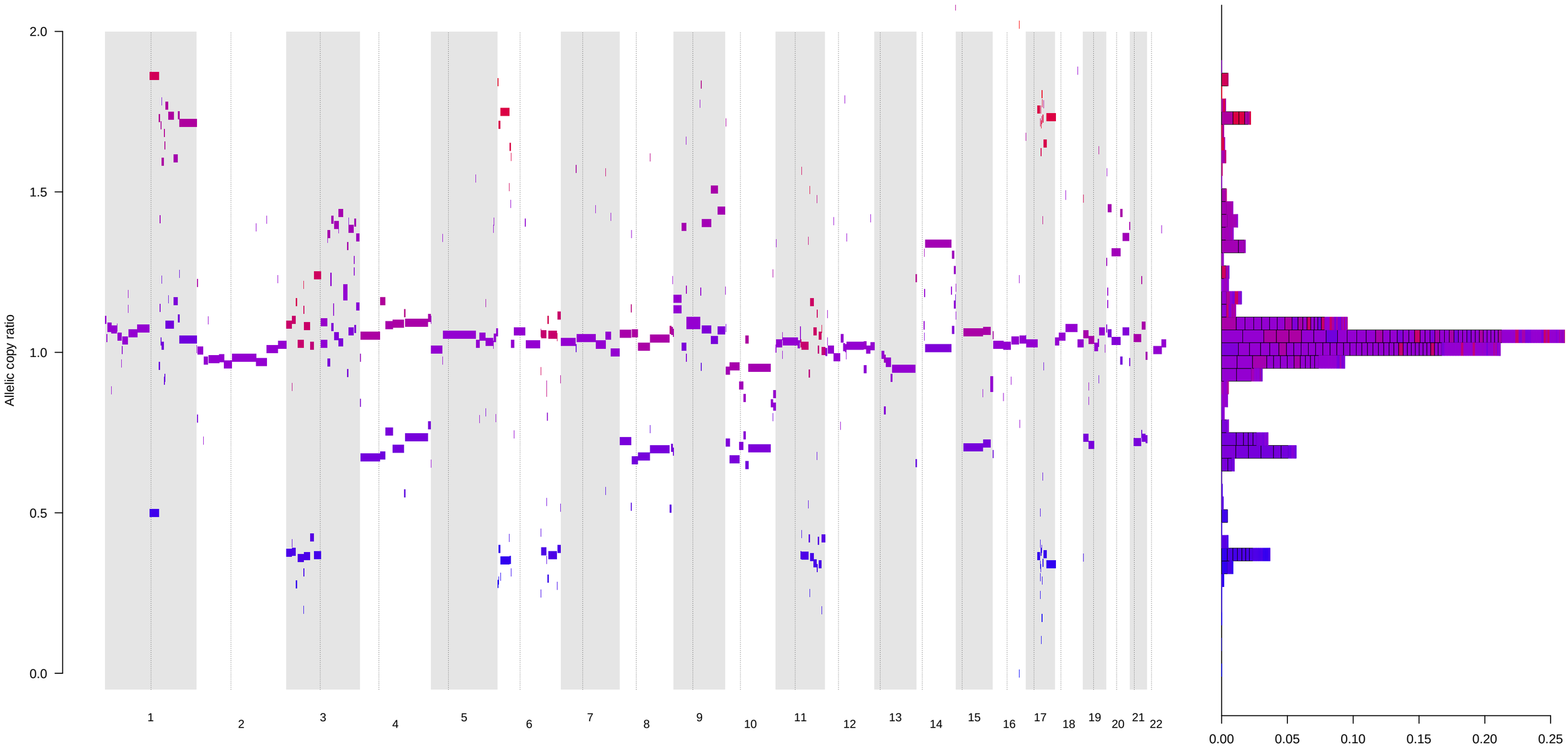
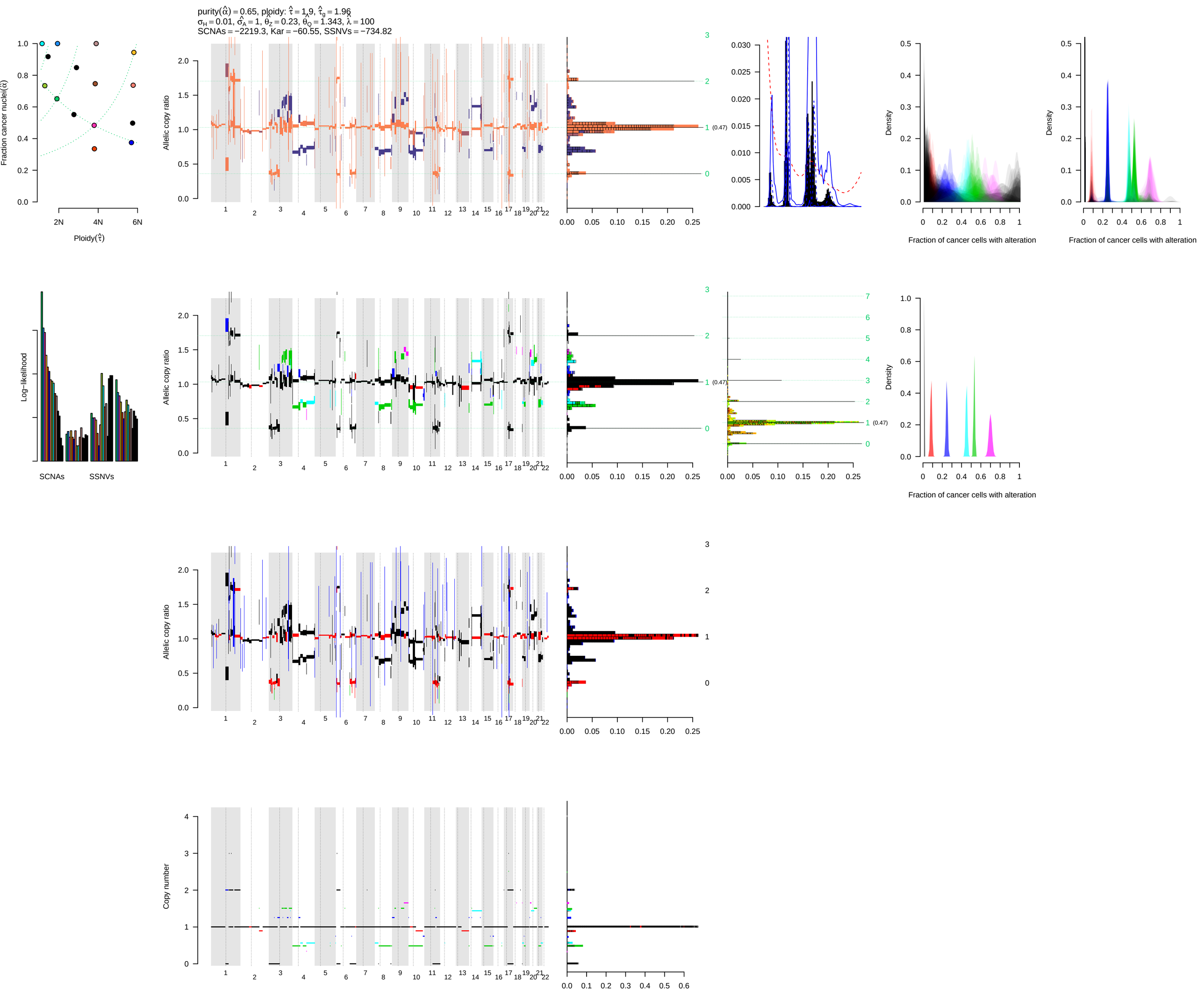
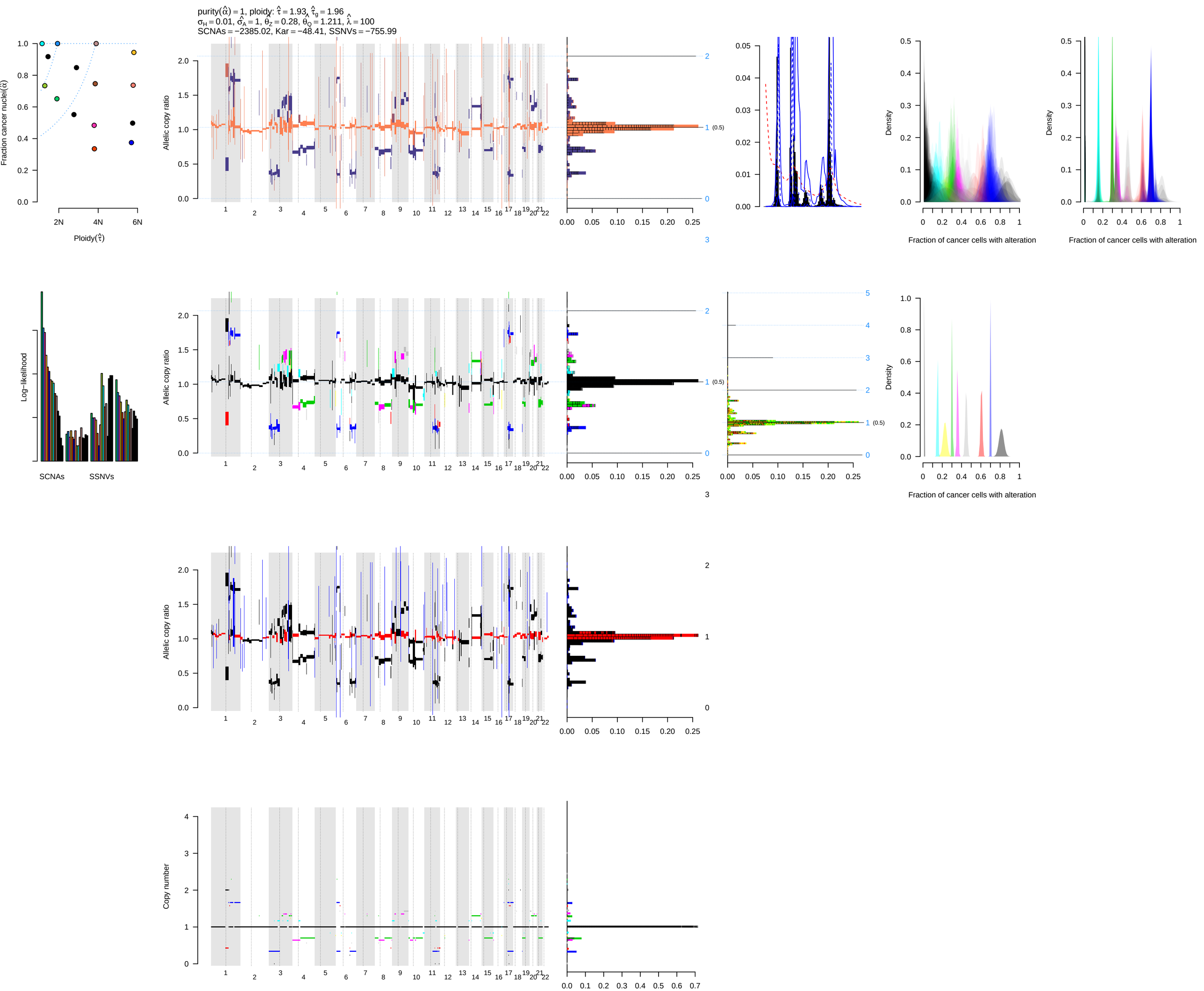
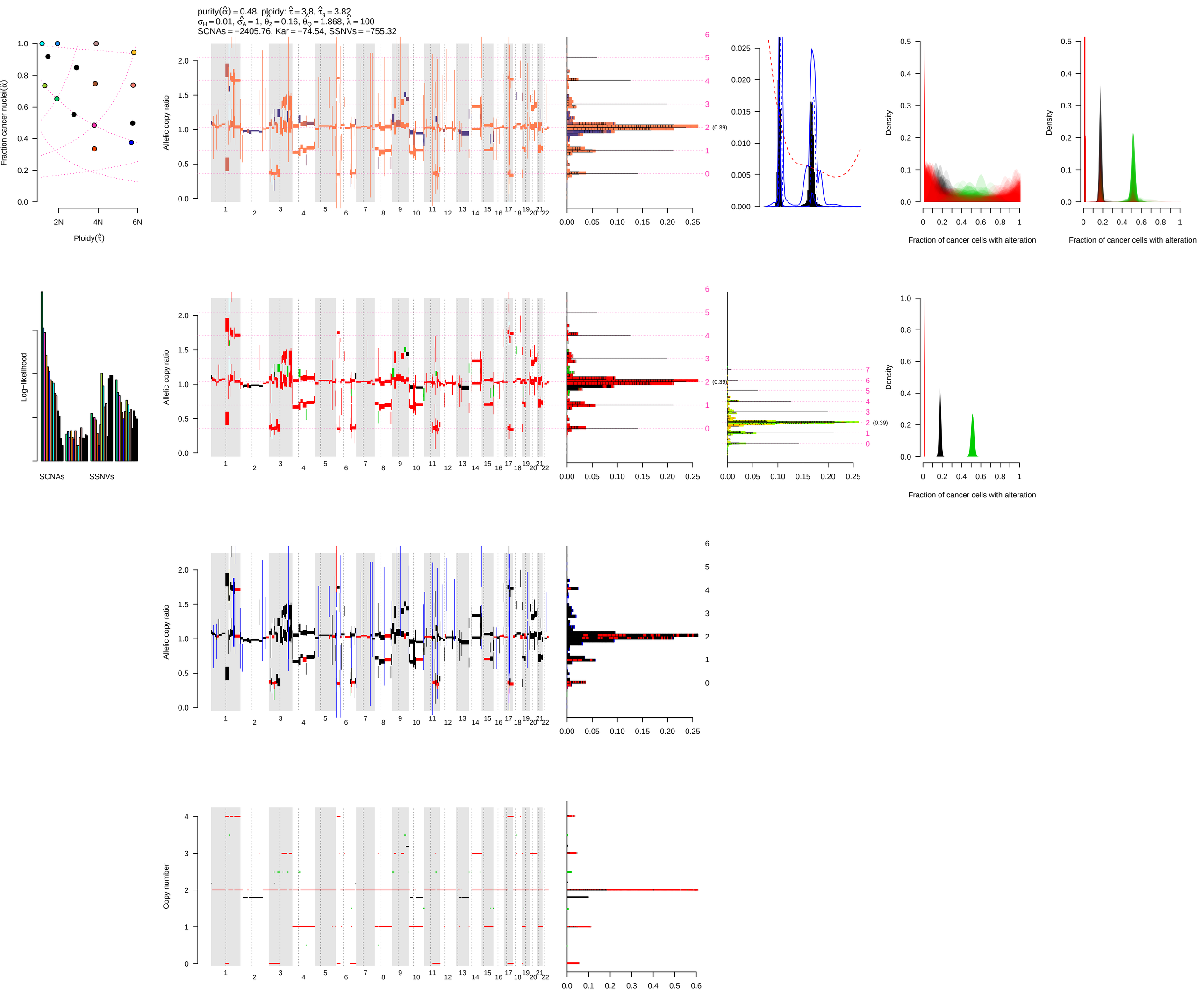
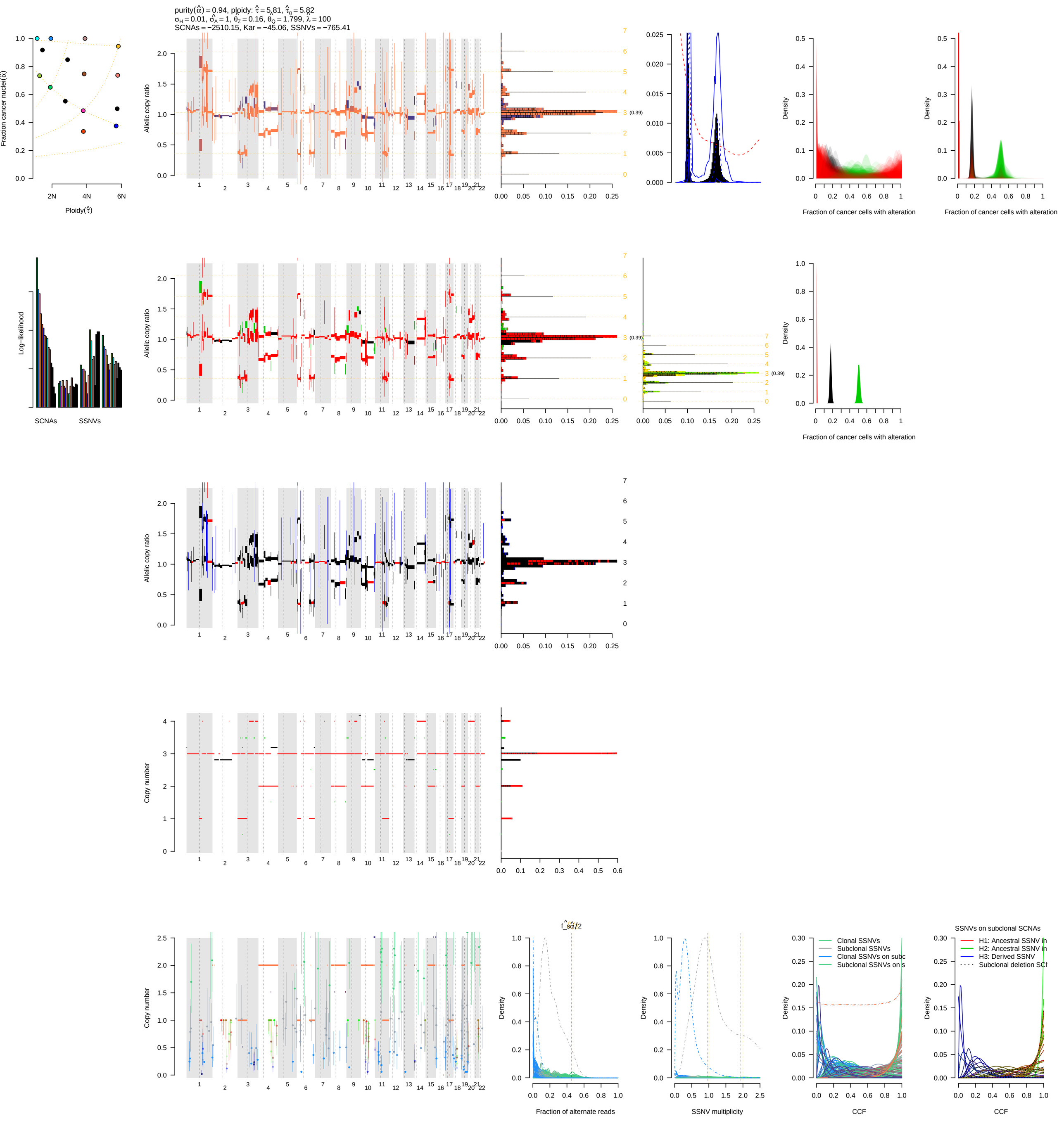
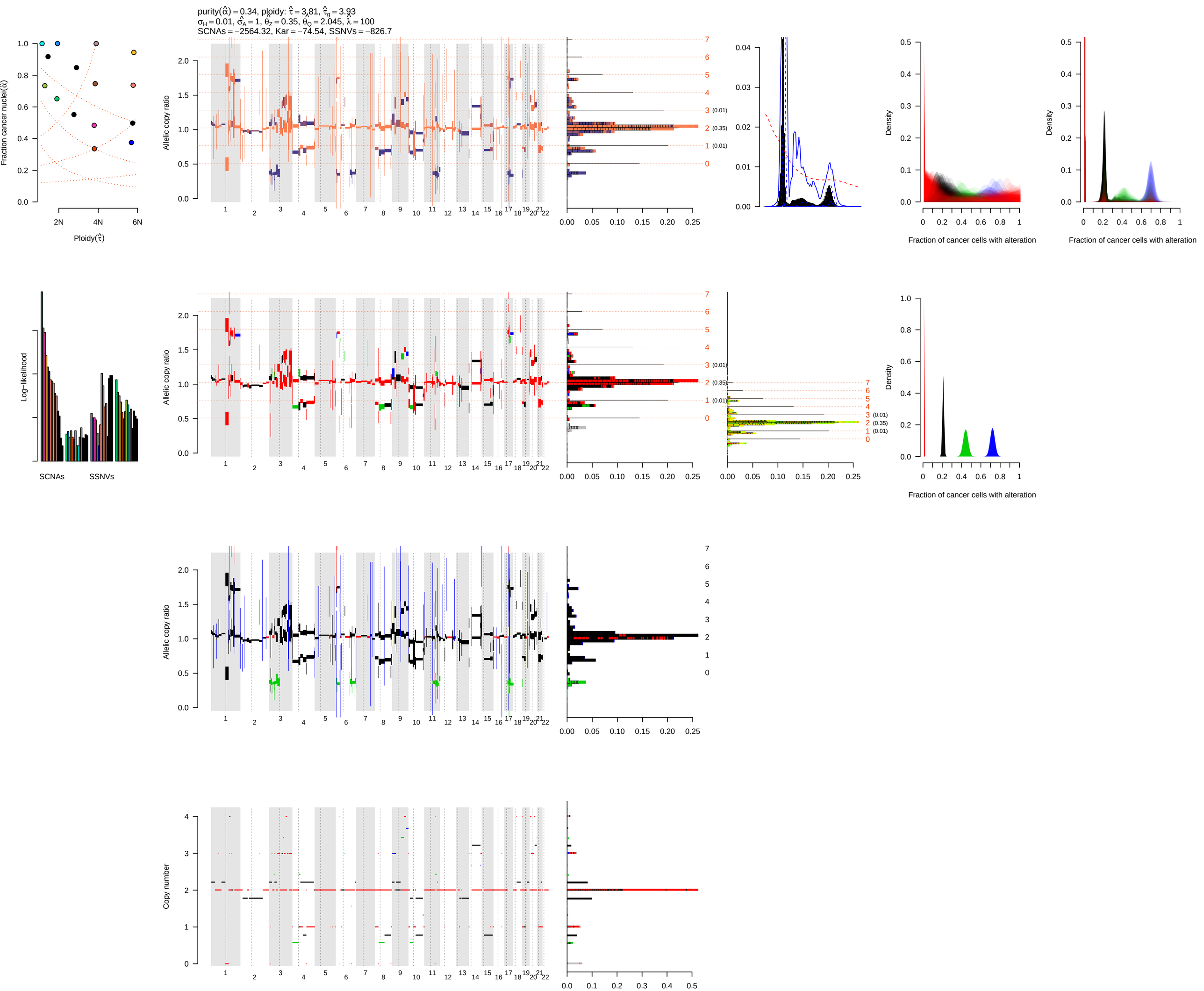

Allelic copy ratio
2.0
1.5
1.0
0.5
0.0
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
0.00
0.05
0.10
0.15
0.20
0.25

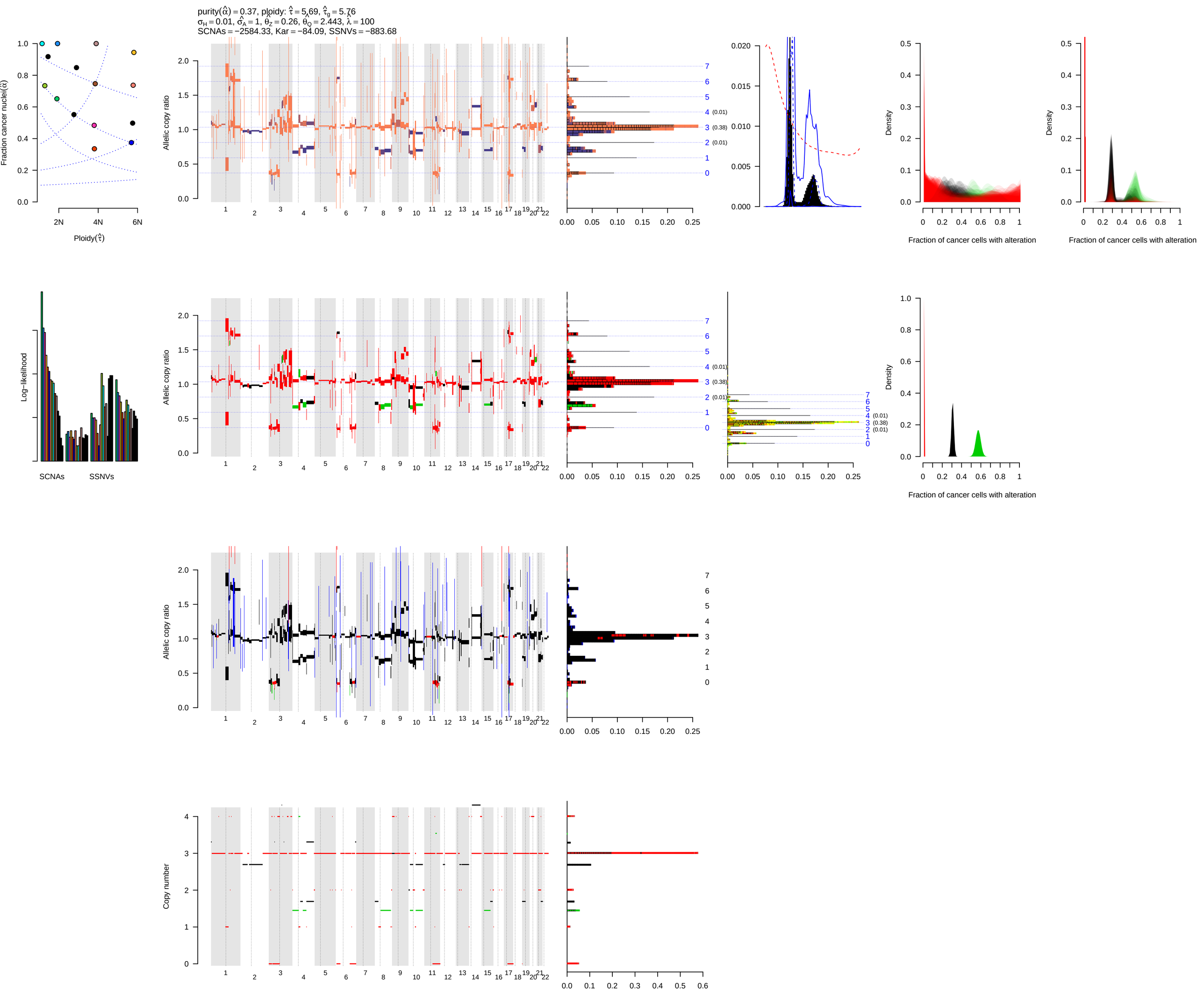

purity($\hat{\alpha}$) = 0.65, ploidy: $\hat{\tau}$ = 1.9, $\hat{\tau}_g$ = 1.96
$\sigma_H$ = 0.01, $\hat{\sigma}_A$ = 1, $\theta_Z$ = 0.23, $\theta_Q$ = 1.343, $\hat{\lambda}$ = 100
SCNAs = −2219.3, Kar = −60.55, SSNVs = −734.82
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
Allelic copy ratio
Density
Fraction of cancer cells with alteration
Log−likelihood
SCNAs
SSNVs
Copy number
f_sol
Fraction of alternate reads
SSNV multiplicity
CCF
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

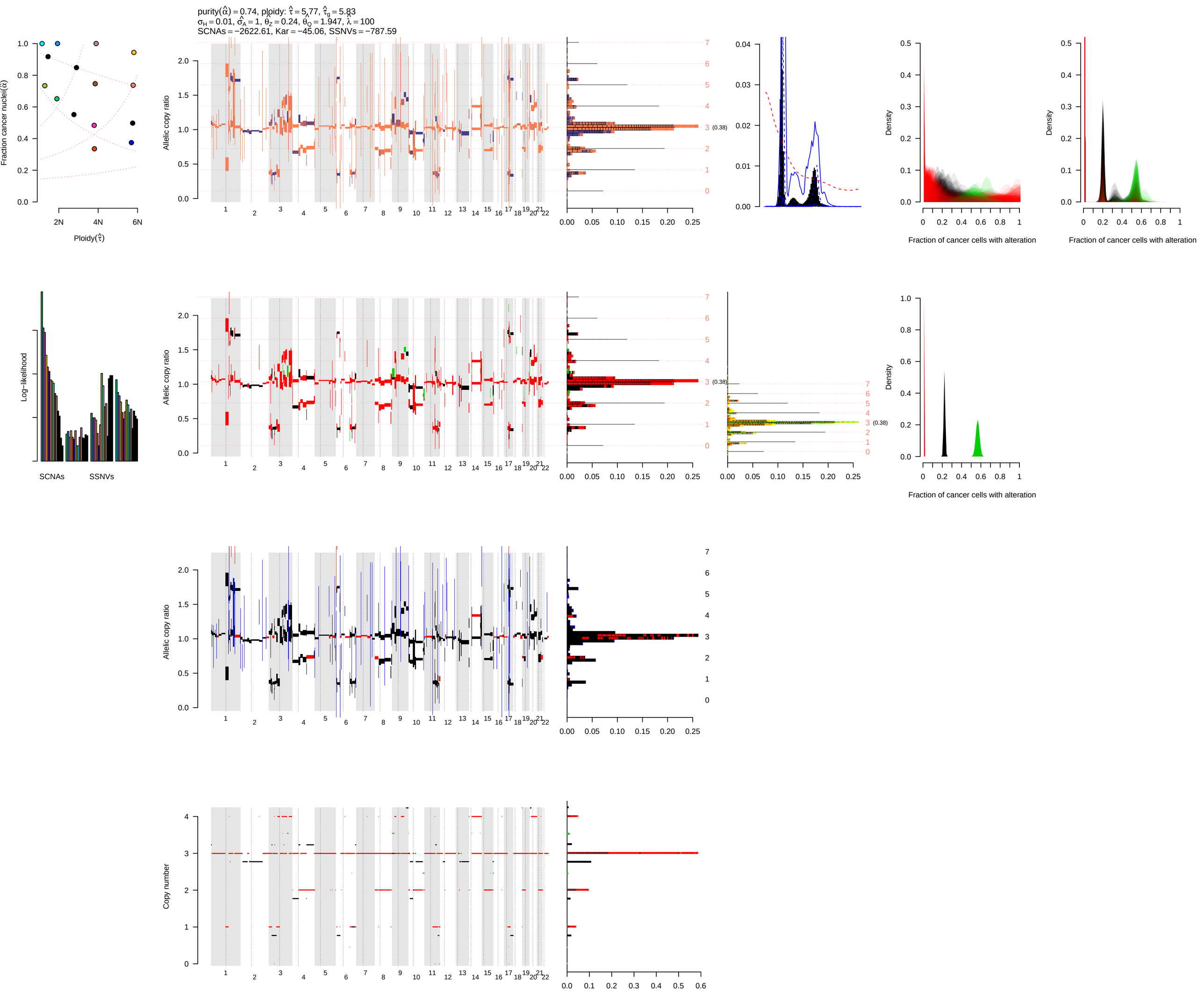

purity($\hat{\alpha}$) = 1, ploidy: $\hat{\tau}$ = 1.93, $\hat{\tau}_g$ = 1.96
$\sigma_H$ = 0.01, $\hat{\sigma}_A$ = 1, $\theta_Z$ = 0.28, $\theta_Q$ = 1.211, $\hat{\lambda}$ = 100
SCNAs = −2385.02, Kar = −48.41, SSNVs = −755.99
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
Allelic copy ratio
Density
Fraction of cancer cells with alteration
Log−likelihood
SCNAs
SSNVs
Copy number
f_sa/2
Fraction of alternate reads
SSNV multiplicity
CCF
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

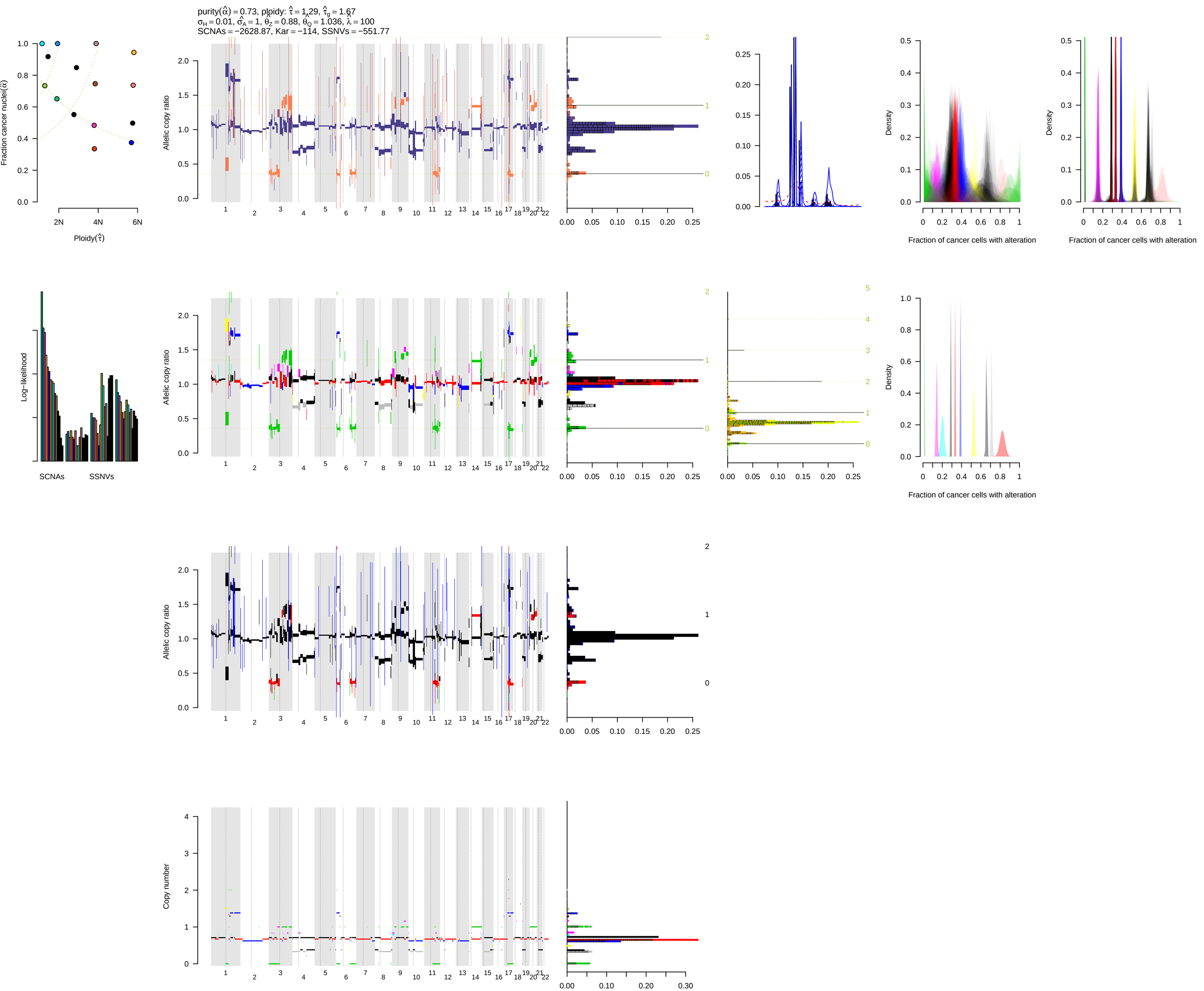

purity($\hat{\alpha}$) = 0.48, ploidy: $\hat{\tau}$ = 3.8, $\hat{\tau}_g$ = 3.82
$\sigma_H$ = 0.01, $\hat{\sigma}_A$ = 1, $\theta_Z$ = 0.16, $\theta_Q$ = 1.868, $\hat{\lambda}$ = 100
SCNAs = −2405.76, Kar = −74.54, SSNVs = −755.32
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
Allelic copy ratio
(0.39)
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

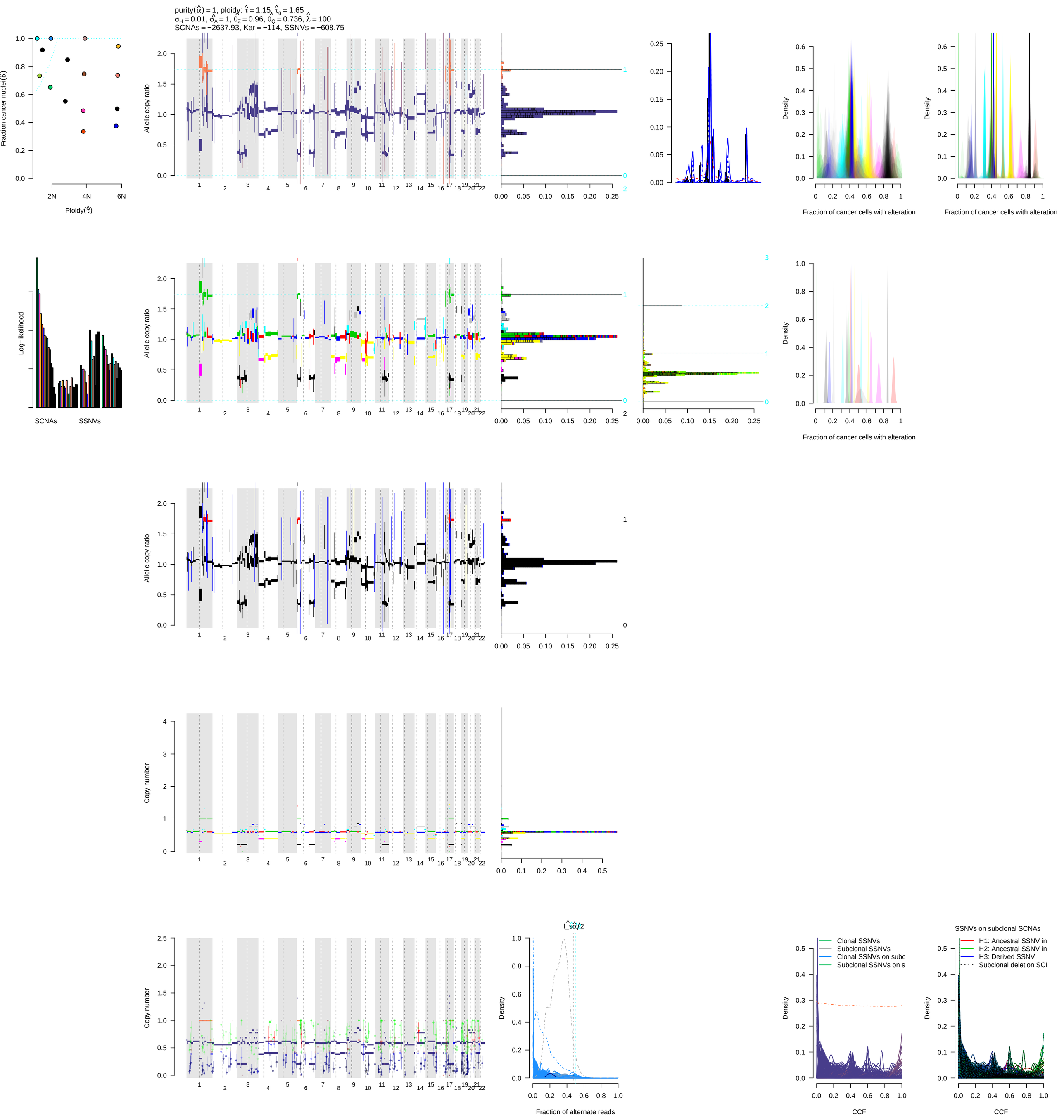

purity($\hat{\alpha}$) = 0.94, ploidy: $\hat{\tau}$ = 5.81, $\hat{\tau}_g$ = 5.82
$\sigma_H$ = 0.01, $\hat{\sigma}_A$ = 1, $\theta_Z$ = 0.16, $\theta_Q$ = 1.799, $\hat{\lambda}$ = 100
SCNAs = −2510.15, Kar = −45.06, SSNVs = −765.41
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
Allelic copy ratio
(0.39)
Density
Fraction of cancer cells with alteration
Log−likelihood
SCNAs
SSNVs
Copy number
f_$\hat{\sigma}$/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

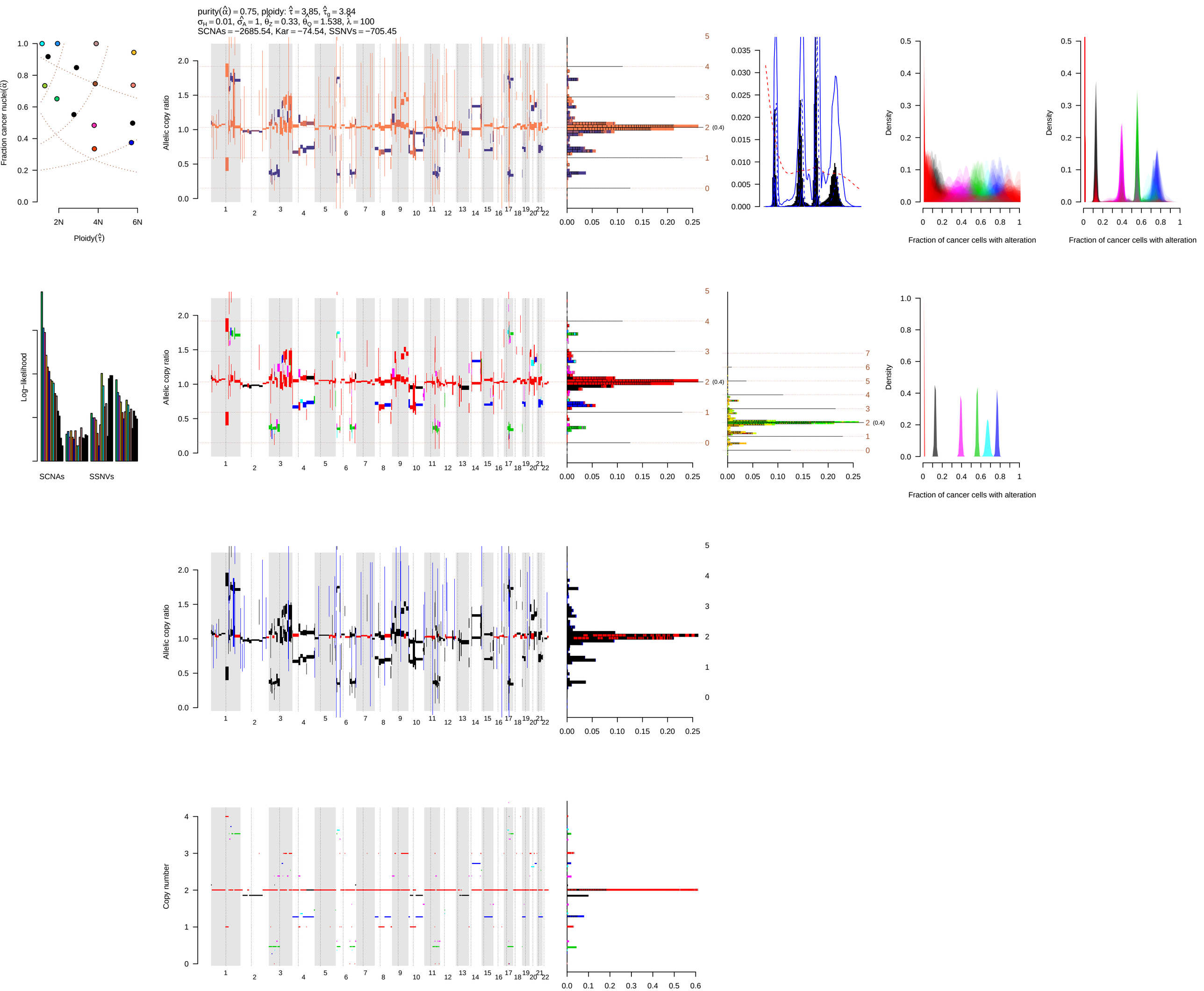

purity($\hat{\alpha}$) = 0.34, ploidy: $\hat{\tau}$ = 3.81, $\hat{\tau}_g$ = 3.93
$\sigma_H$ = 0.01, $\hat{\sigma}_A$ = 1, $\theta_Z$ = 0.35, $\theta_Q$ = 2.045, $\hat{\lambda}$ = 100
SCNAs = −2564.32, Kar = −74.54, SSNVs = −826.7
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
Allelic copy 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

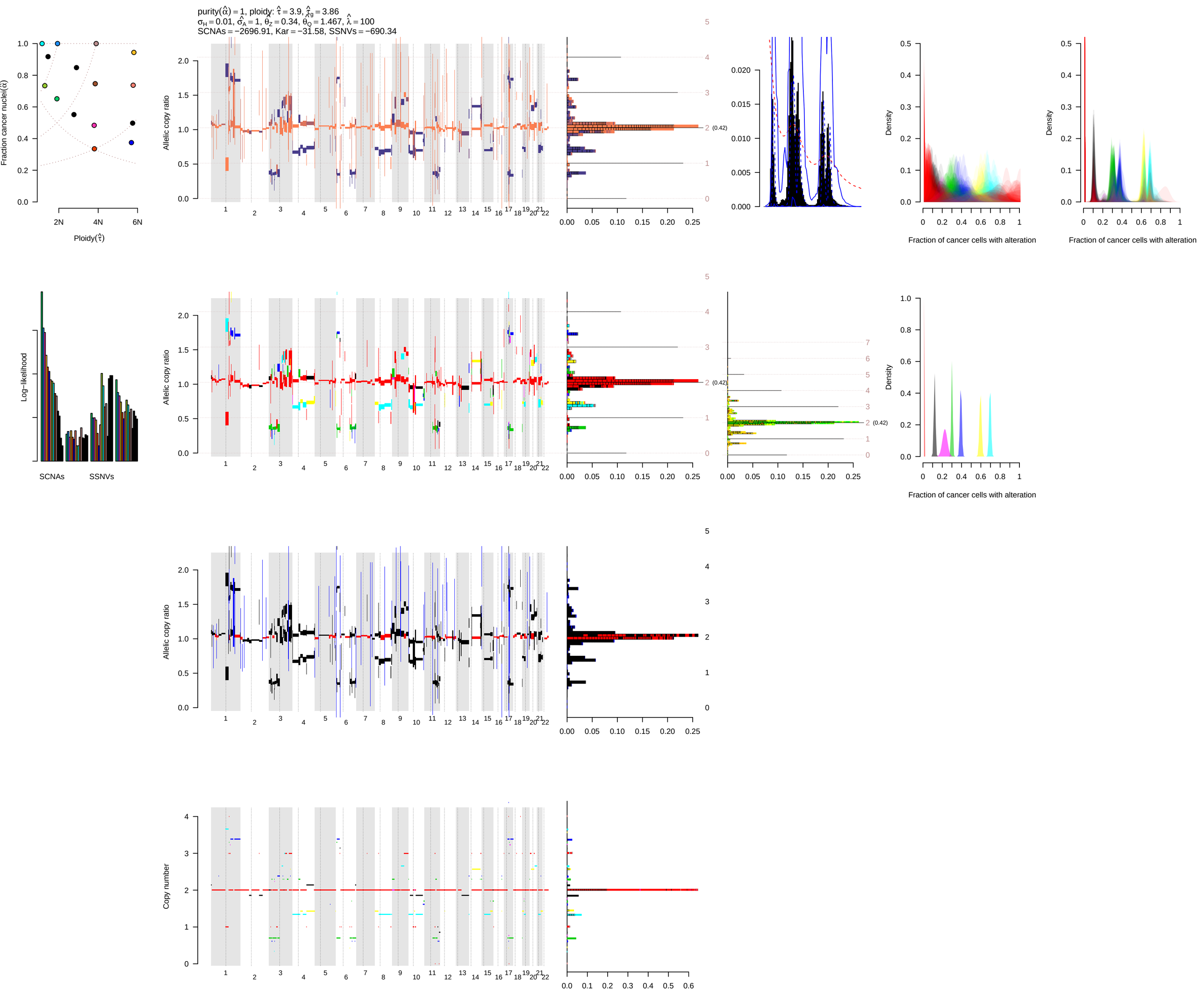

purity($\hat{\alpha}$) = 0.37, ploidy: $\hat{\tau}$ = 5.69, $\hat{\tau}_g$ = 5.76
$\sigma_H$ = 0.01, $\hat{\sigma}_A$ = 1, $\theta_Z$ = 0.26, $\theta_Q$ = 2.443, $\lambda$ = 100
SCNAs = −2584.33, Kar = −84.09, SSNVs = −883.68
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
2N
4N
6N
Allelic copy ratio
Density
Fraction of cancer cells with alteration
Log−likelihood
SCNAs
SSNVs
Copy number
f_sol
Fraction of alternate reads
SSNV multiplicity
CCF
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

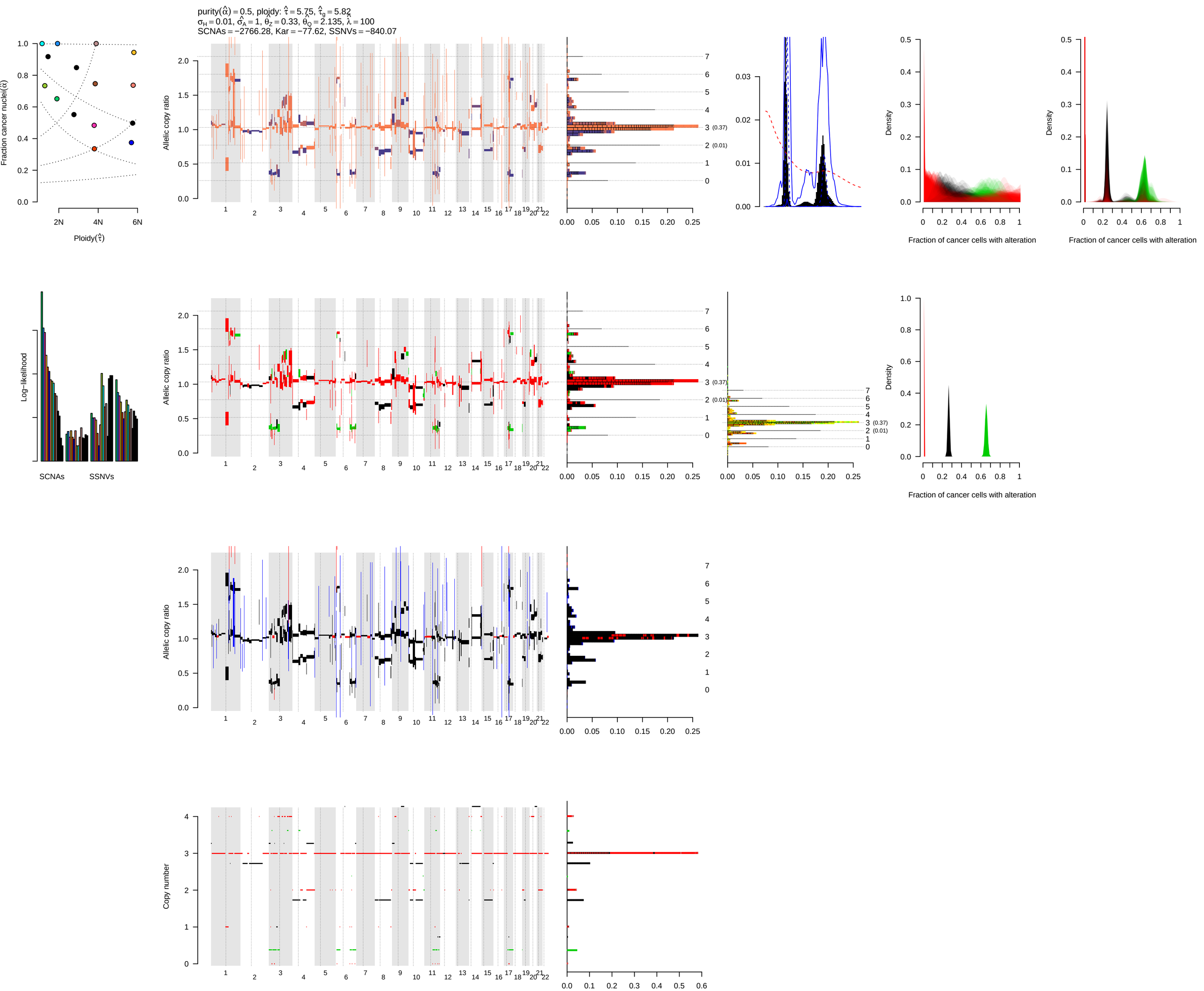

purity($\hat{\alpha}$) = 0.74, ploidy: $\hat{\tau}$ = 5.77, $\hat{\tau}_g$ = 5.83
$\sigma_H$ = 0.01, $\hat{\sigma}_A$ = 1, $\theta_Z$ = 0.24, $\theta_Q$ = 1.947, $\hat{\lambda}$ = 100
SCNAs = −2622.61, Kar = −45.06, SSNVs = −787.59
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
Allelic copy ratio
(0.38)
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

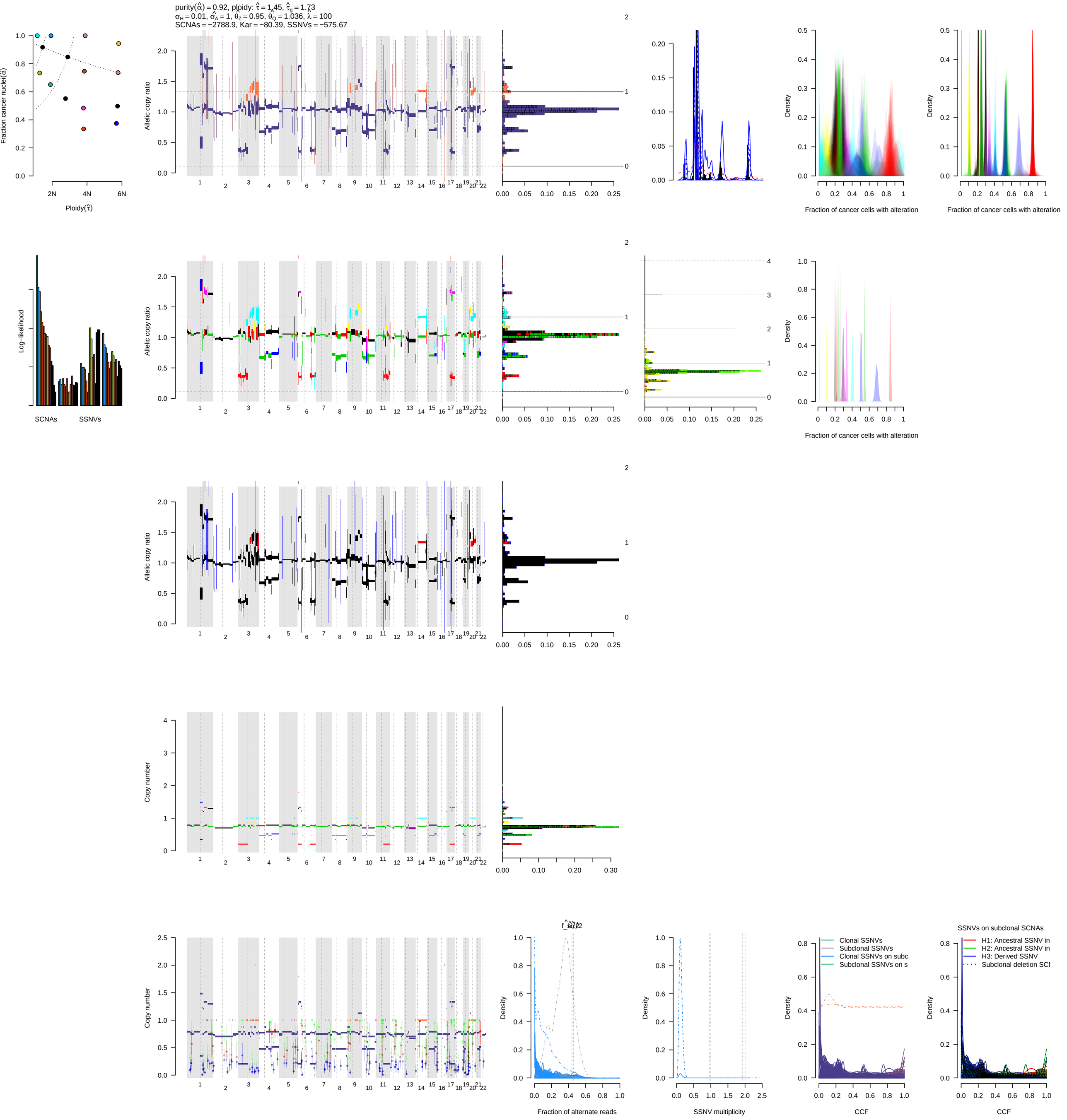

purity($\hat{\alpha}$) = 0.73, ploidy: $\hat{\tau}$ = 1.29, $\hat{\tau}_g$ = 1.67
$\sigma_H$ = 0.01, $\hat{\sigma}_A$ = 1, $\theta_Z$ = 0.88, $\theta_Q$ = 1.036, $\hat{\lambda}$ = 100
SCNAs = −2628.87, Kar = −114, SSNVs = −551.77
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
Allelic copy 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

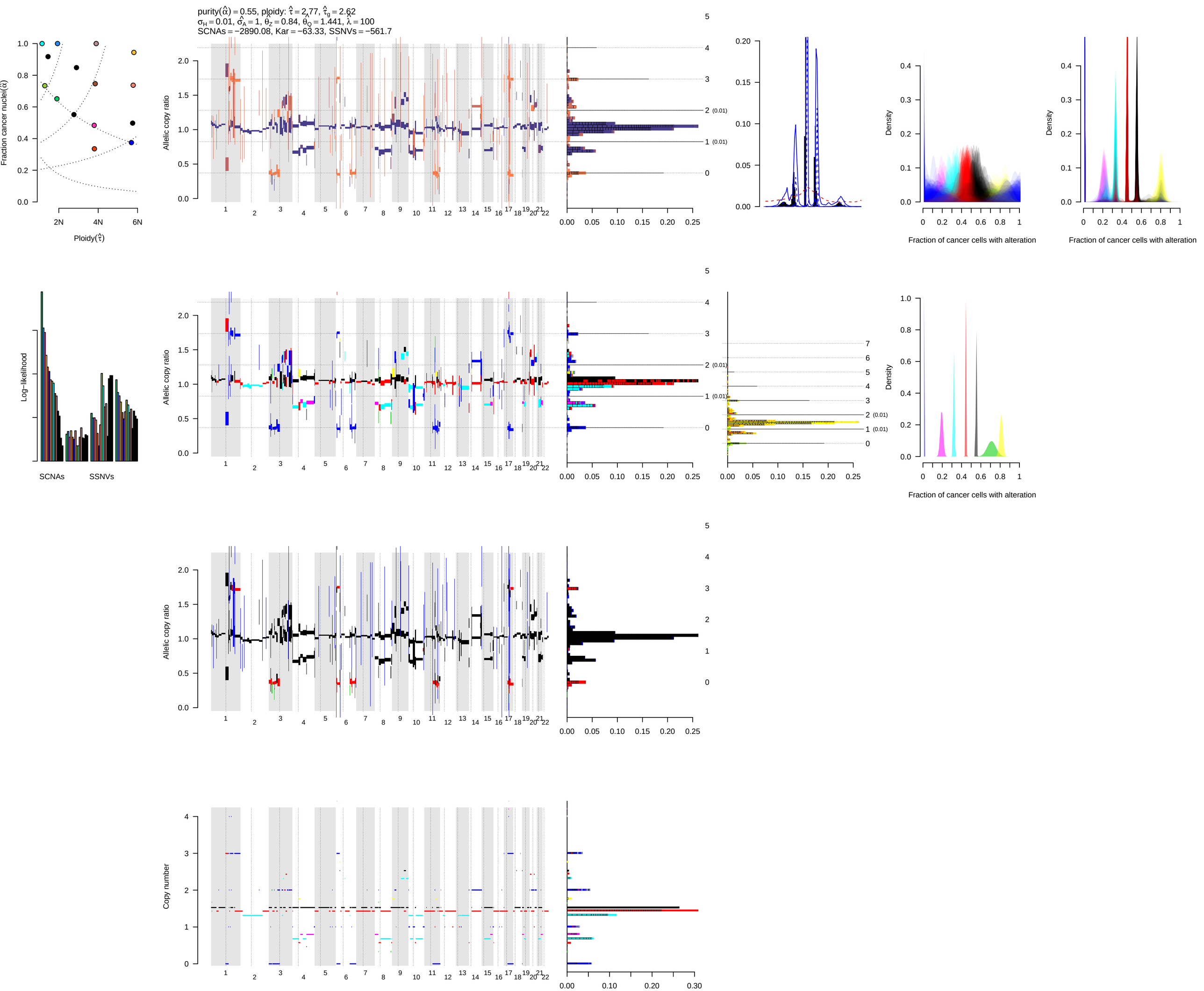

purity($\hat{\alpha}$) = 1, ploidy: $\hat{\tau}$ = 1.15, $\hat{\tau}_g$ = 1.65
$\sigma_H$ = 0.01, $\hat{\sigma}_A$ = 1, $\theta_Z$ = 0.96, $\theta_Q$ = 0.736, $\hat{\lambda}$ = 100
SCNAs = −2637.93, Kar = −114, SSNVs = −608.75
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
2N
4N
6N
Allelic copy ratio
Density
Fraction of cancer cells with alteration
Log−likelihood
SCNAs
SSNVs
Copy number
f_s$\hat{\alpha}$/2
Fraction of alternate reads
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

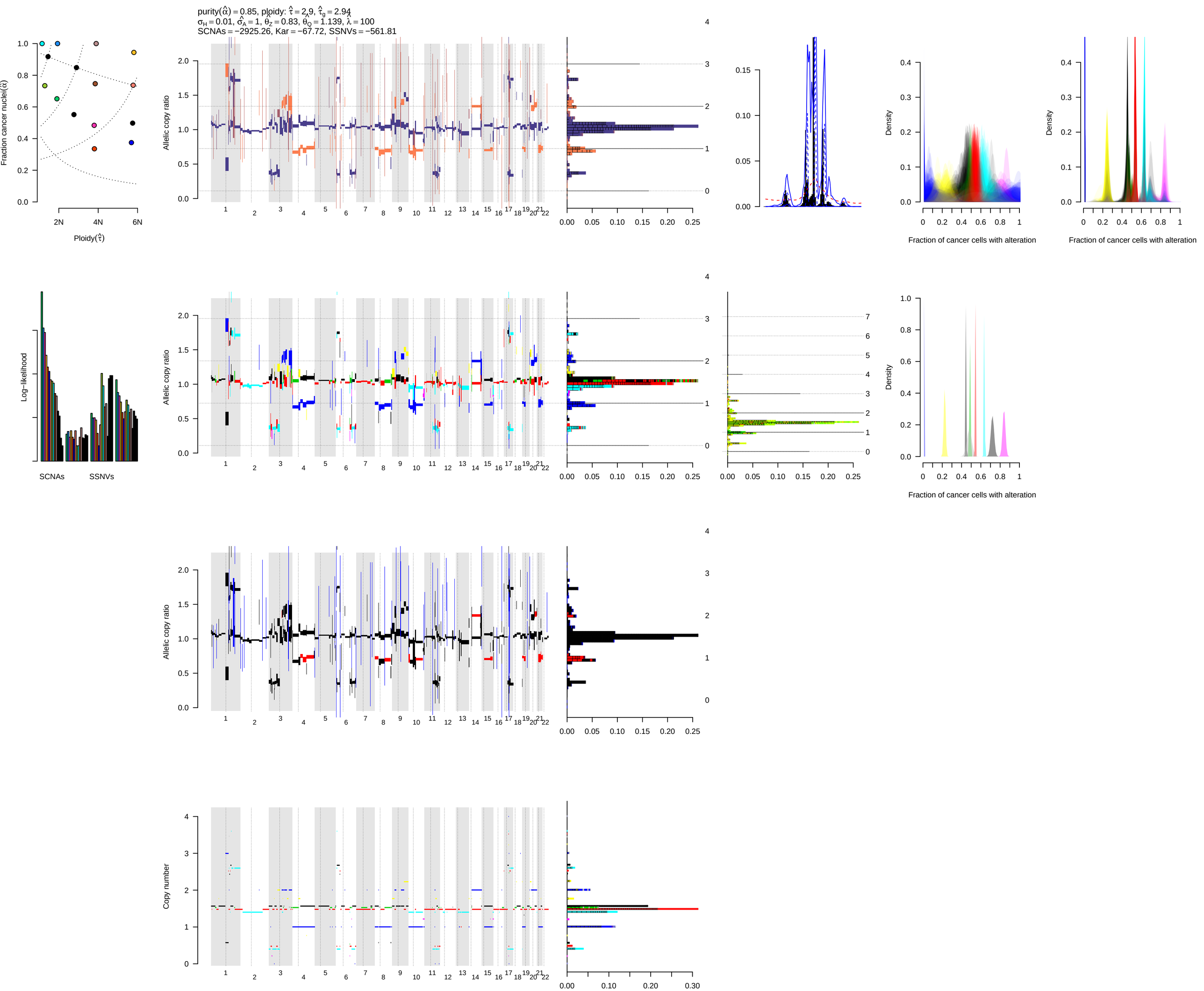

purity($\hat{\alpha}$) = 0.75, ploidy: $\hat{\tau}$ = 3.85, $\hat{\tau}_g$ = 3.84
$\sigma_H$ = 0.01, $\hat{\sigma}_A$ = 1, $\hat{\theta}_Z$ = 0.33, $\hat{\theta}_Q$ = 1.538, $\hat{\lambda}$ = 100
SCNAs = −2685.54, Kar = −74.54, SSNVs = −705.45
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
Allelic copy ratio
Density
Fraction of cancer cells with alteration
Log−likelihood
SCNAs
SSNVs
Copy number
$\hat{f}_{soft}$
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: $\hat{\tau}$ = 3.9, $\hat{\lambda}_g$ = 3.86
$\sigma_H$ = 0.01, $\hat{\sigma}_A$ = 1, $\theta_Z$ = 0.34, $\theta_Q$ = 1.467, $\hat{\lambda}$ = 100
SCNAs = −2696.91, Kar = −31.58, SSNVs = −690.34
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($\hat{\alpha}$) = 0.5, ploidy: $\hat{\tau}$ = 5.75, $\hat{\tau}_g$ = 5.82
$\sigma_H$ = 0.01, $\hat{\sigma}_A$ = 1, $\theta_Z$ = 0.33, $\theta_Q$ = 2.135, $\hat{\lambda}$ = 100
SCNAs = −2766.28, Kar = −77.62, SSNVs = −840.07
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
2N
4N
6N
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($\hat{\alpha}$) = 0.92, ploidy: $\hat{\tau}$ = 1.45, $\hat{\tau}_g$ = 1.73
$\sigma_H$ = 0.01, $\hat{\sigma}_A$ = 1, $\hat{\theta}_Z$ = 0.95, $\hat{\theta}_Q$ = 1.036, $\hat{\lambda}$ = 100
SCNAs = −2788.9, Kar = −80.39, SSNVs = −575.67
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($\hat{\alpha}$) = 0.55, ploidy: $\hat{\tau}_A$ = 2.77, $\hat{\tau}_g$ = 2.62
$\sigma_H$ = 0.01, $\hat{\sigma}_A$ = 1, $\theta_Z$ = 0.84, $\theta_Q$ = 1.441, $\hat{\lambda}$ = 100
SCNAs = −2890.08, Kar = −63.33, SSNVs = −561.7
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
2N
4N
6N
Allelic copy ratio
Density
Fraction of cancer cells with alteration
Log−likelihood
SCNAs
SSNVs
Copy number
f_ccf
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($\hat{\alpha}$) = 0.85, ploidy: $\hat{\tau}$ = 2.9, $\hat{\tau}_g$ = 2.94
$\sigma_H$ = 0.01, $\hat{\sigma}_A$ = 1, $\theta_Z$ = 0.83, $\theta_Q$ = 1.139, $\hat{\lambda}$ = 100
SCNAs = −2925.26, Kar = −67.72, SSNVs = −561.81
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
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