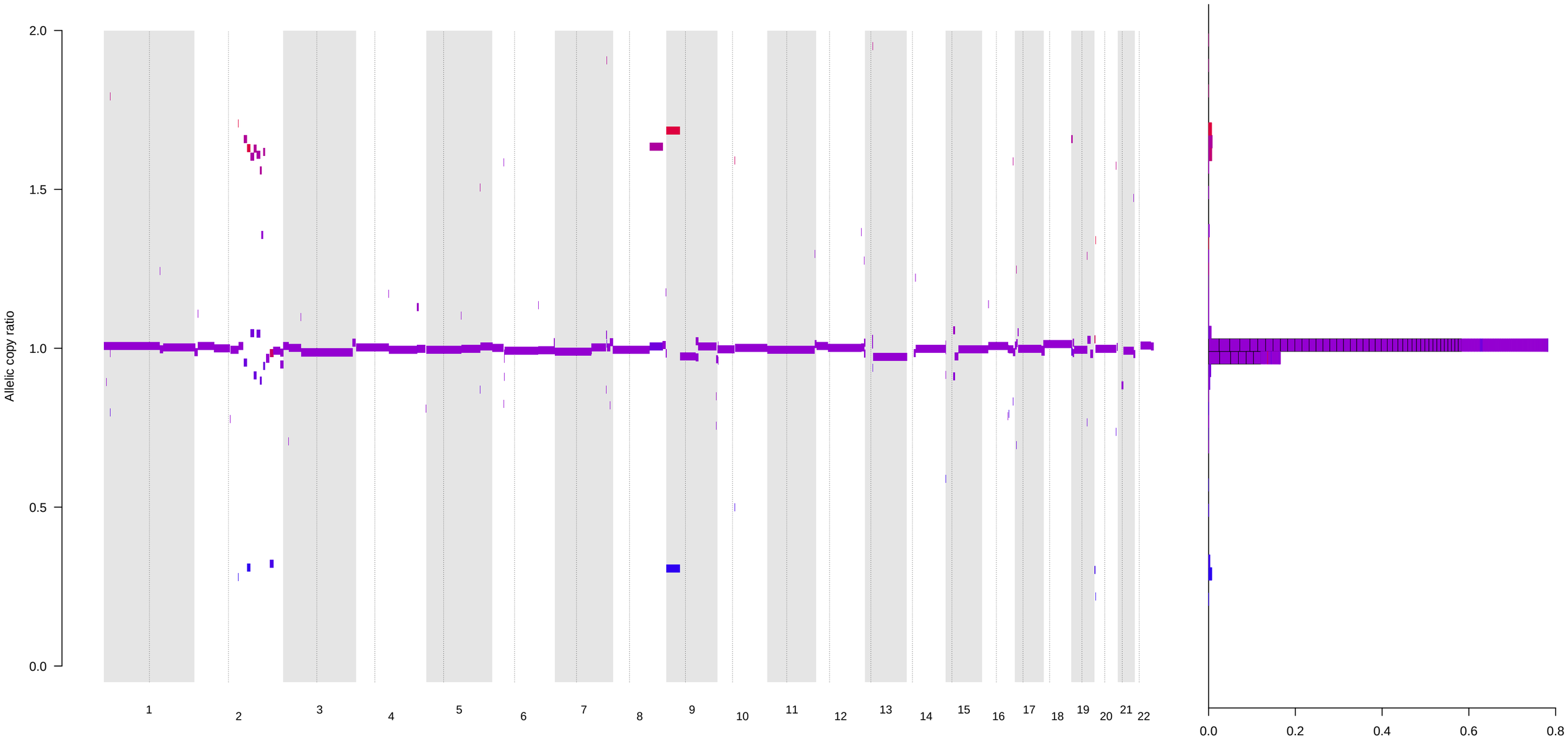
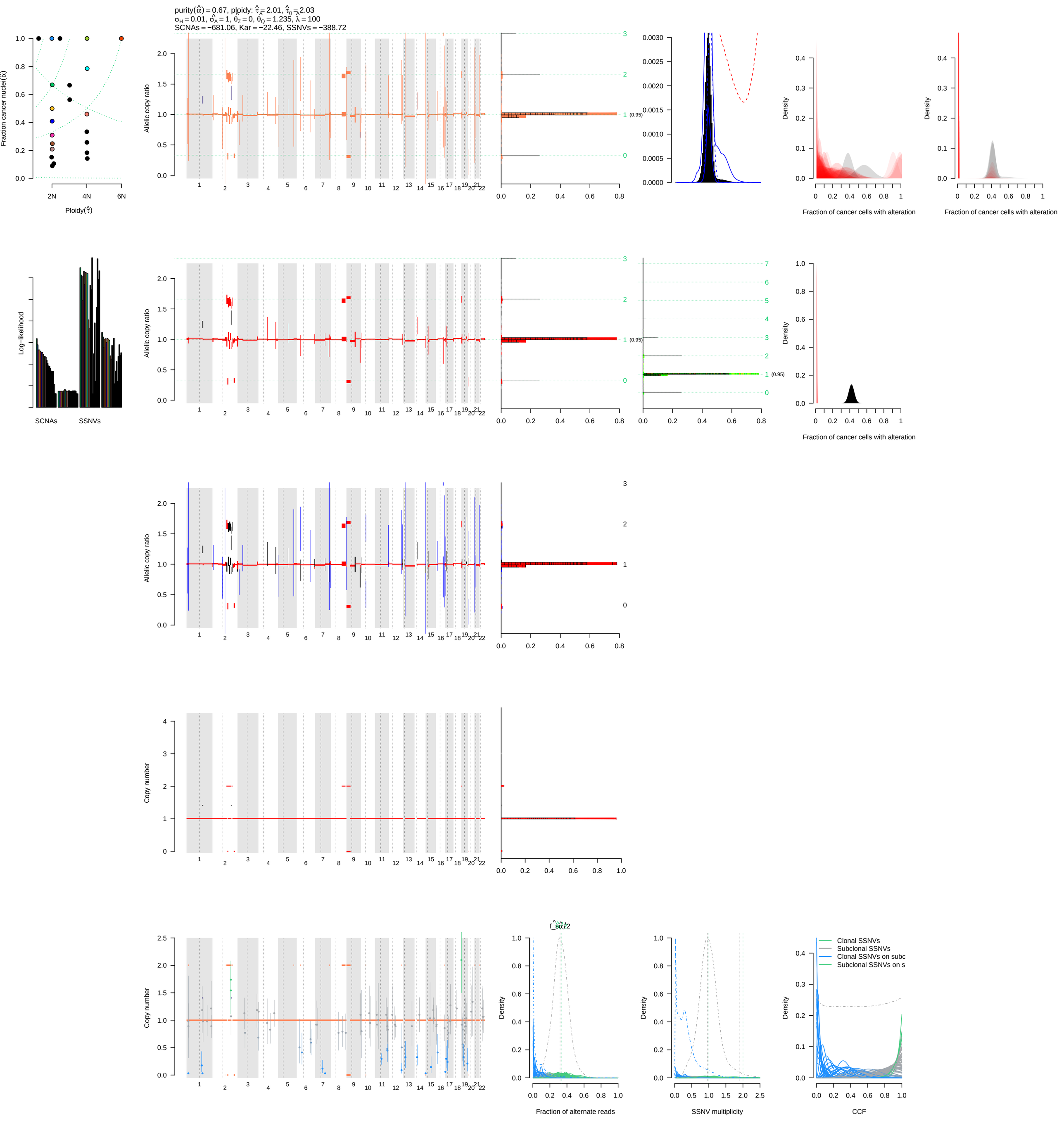
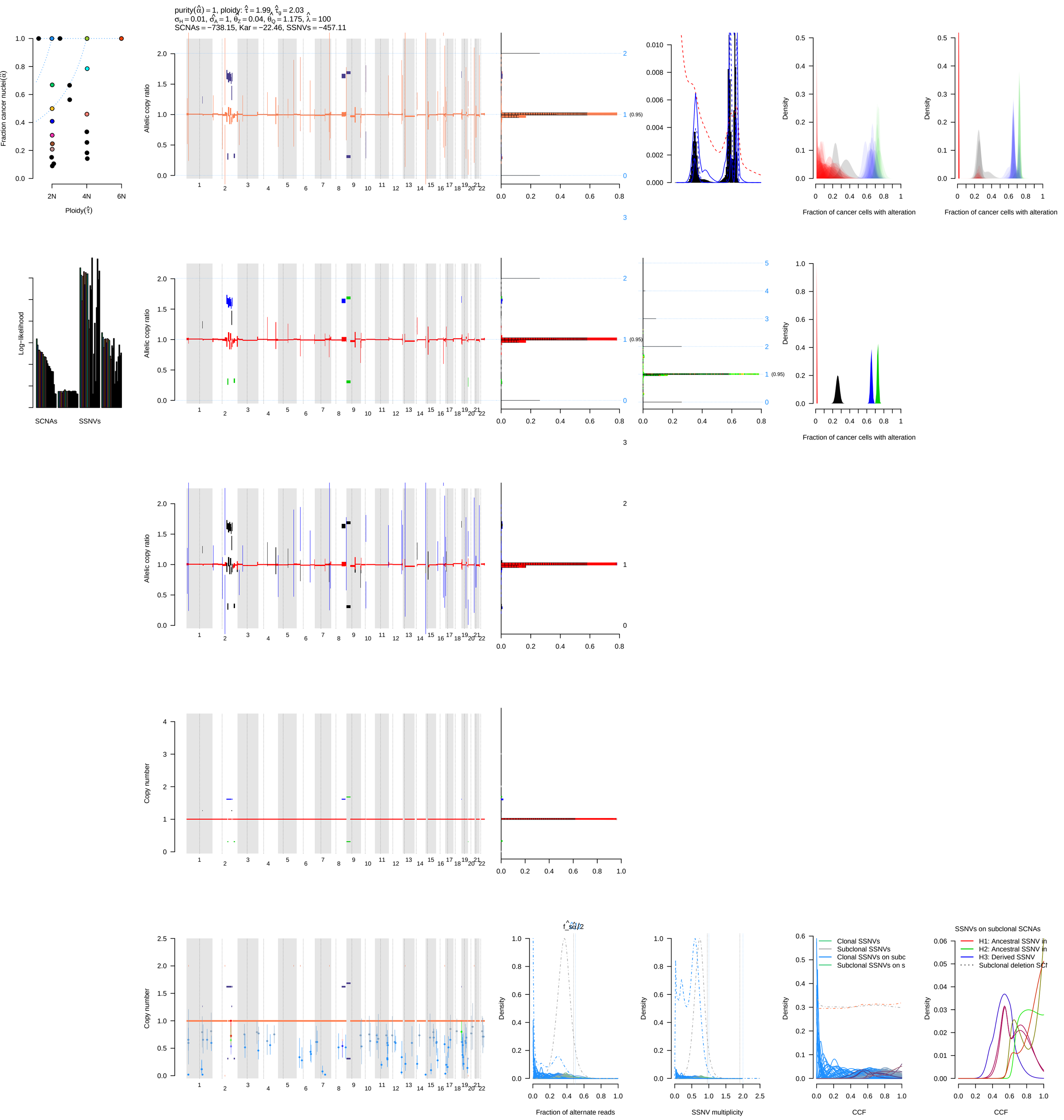
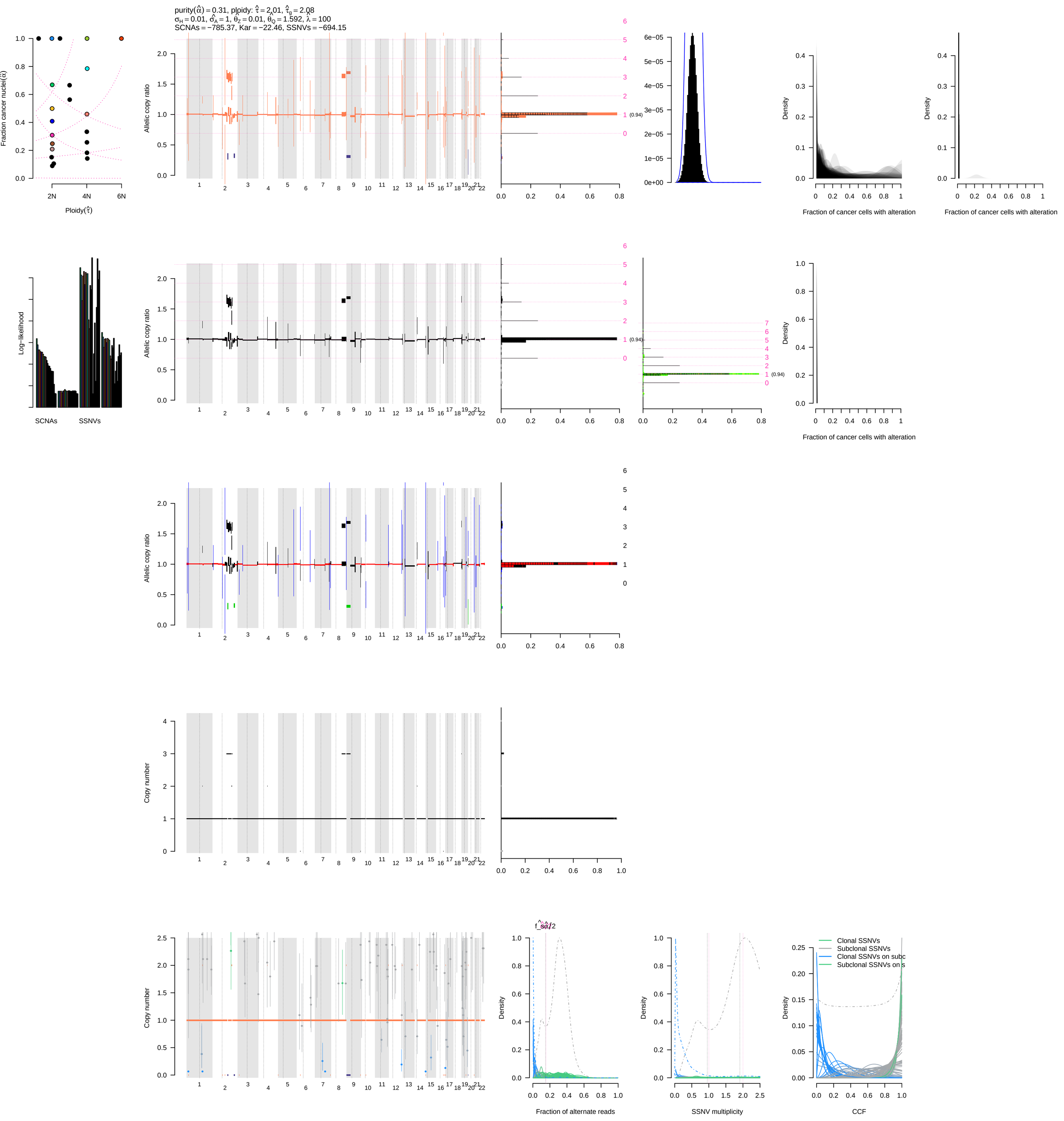
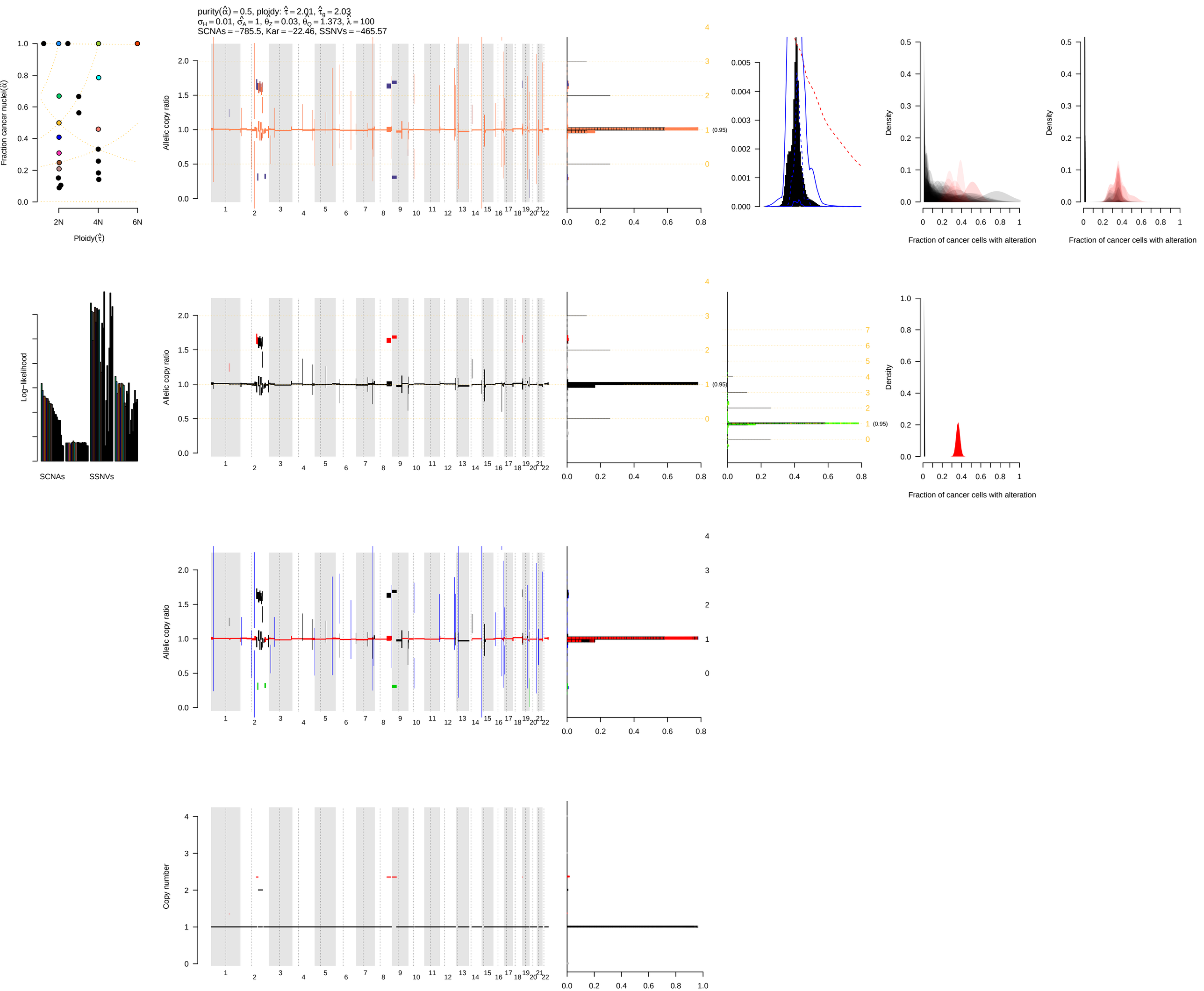
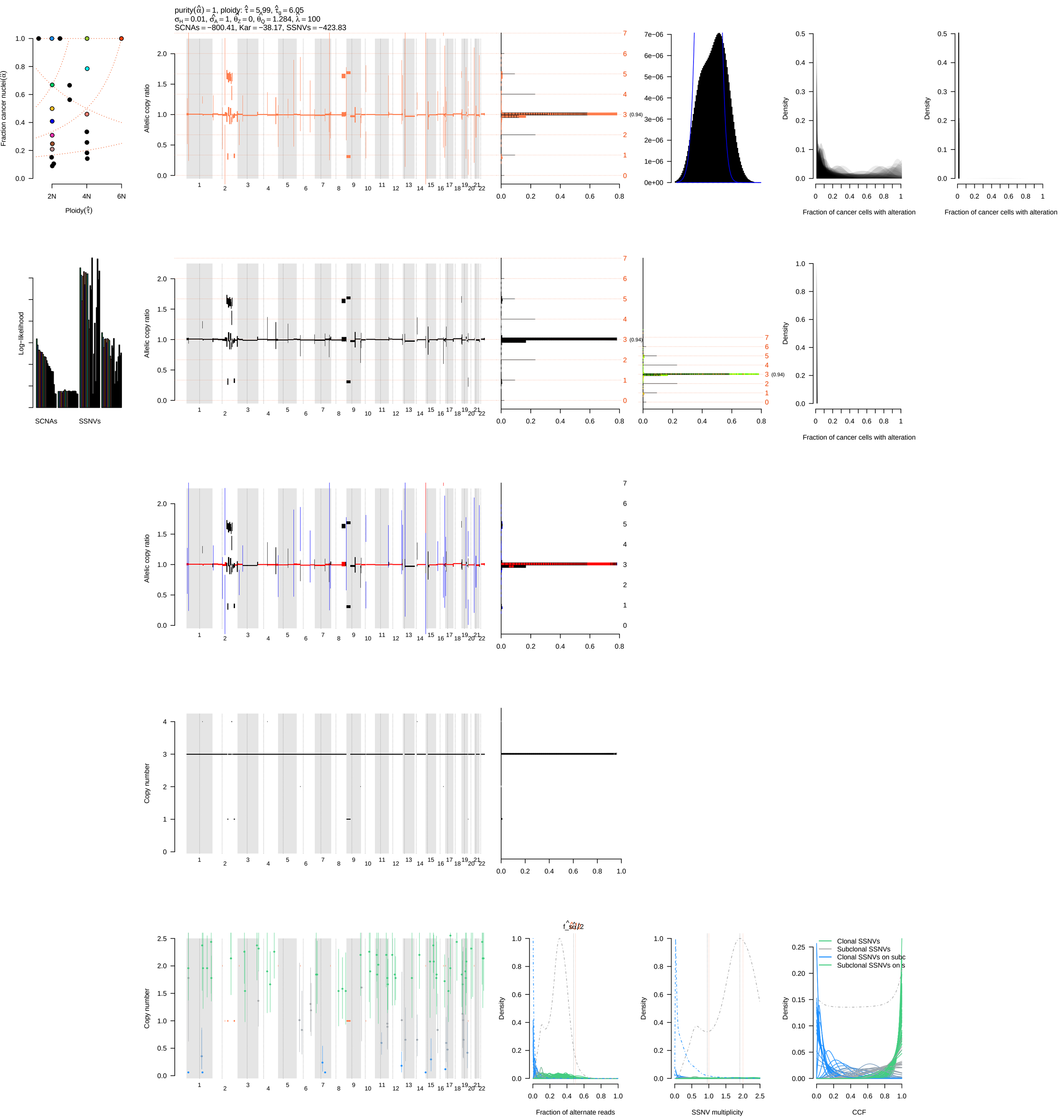

Allelic copy ratio
2.0
1.5
1.0
0.5
0.0
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
0.0
0.2
0.4
0.6
0.8

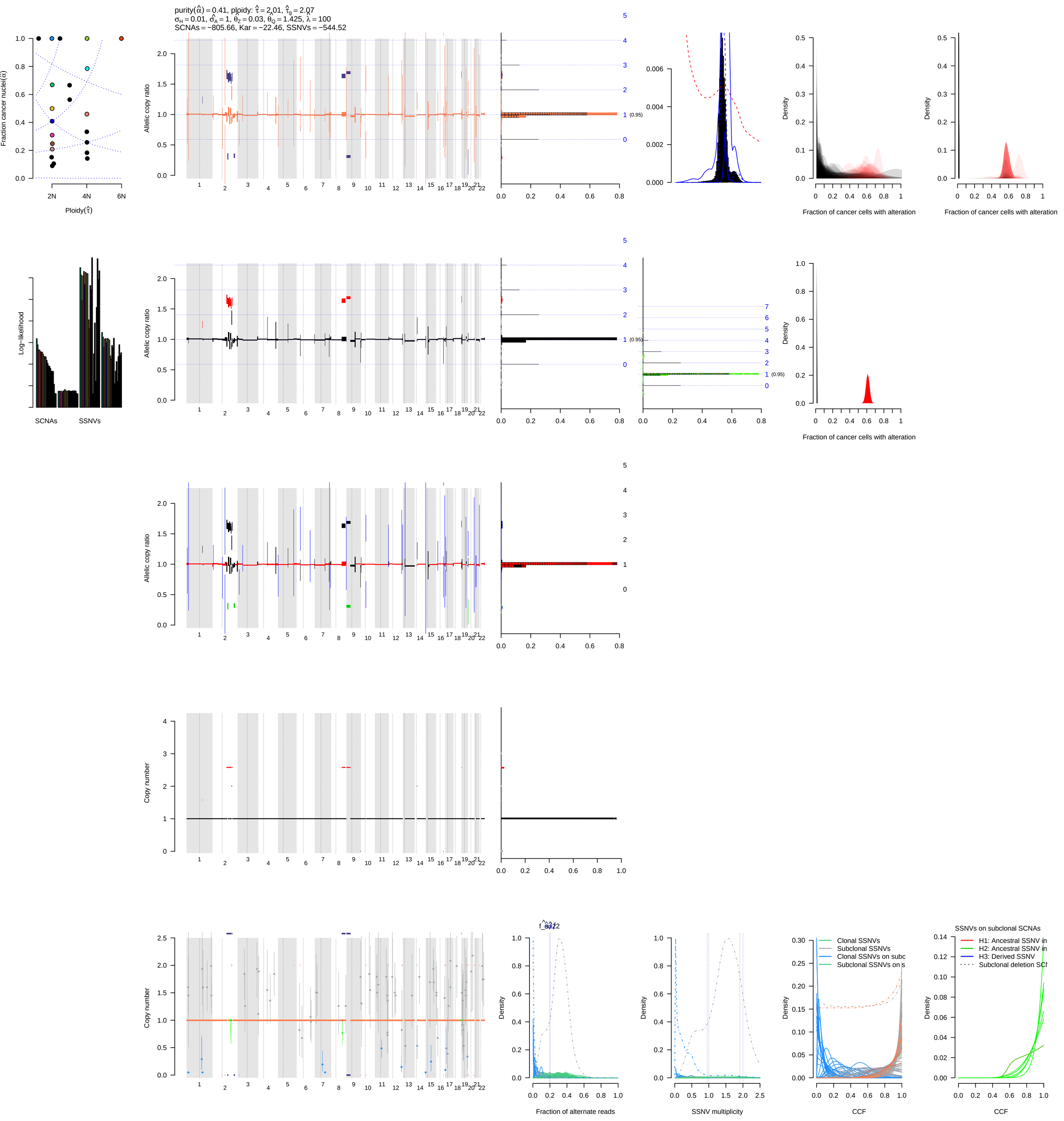

purity($\hat{\alpha}$) = 0.67, ploidy: $\hat{\tau}$ = 2.01, $\hat{\tau}_g$ = 2.03
σ_H = 0.01, $\hat{\sigma}_A$ = 1, θ_Z = 0, θ_Q = 1.235, $\hat{\lambda}$ = 100
SCNAs = −681.06, Kar = −22.46, SSNVs = −388.72
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
Allelic copy ratio
Density
Fraction 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

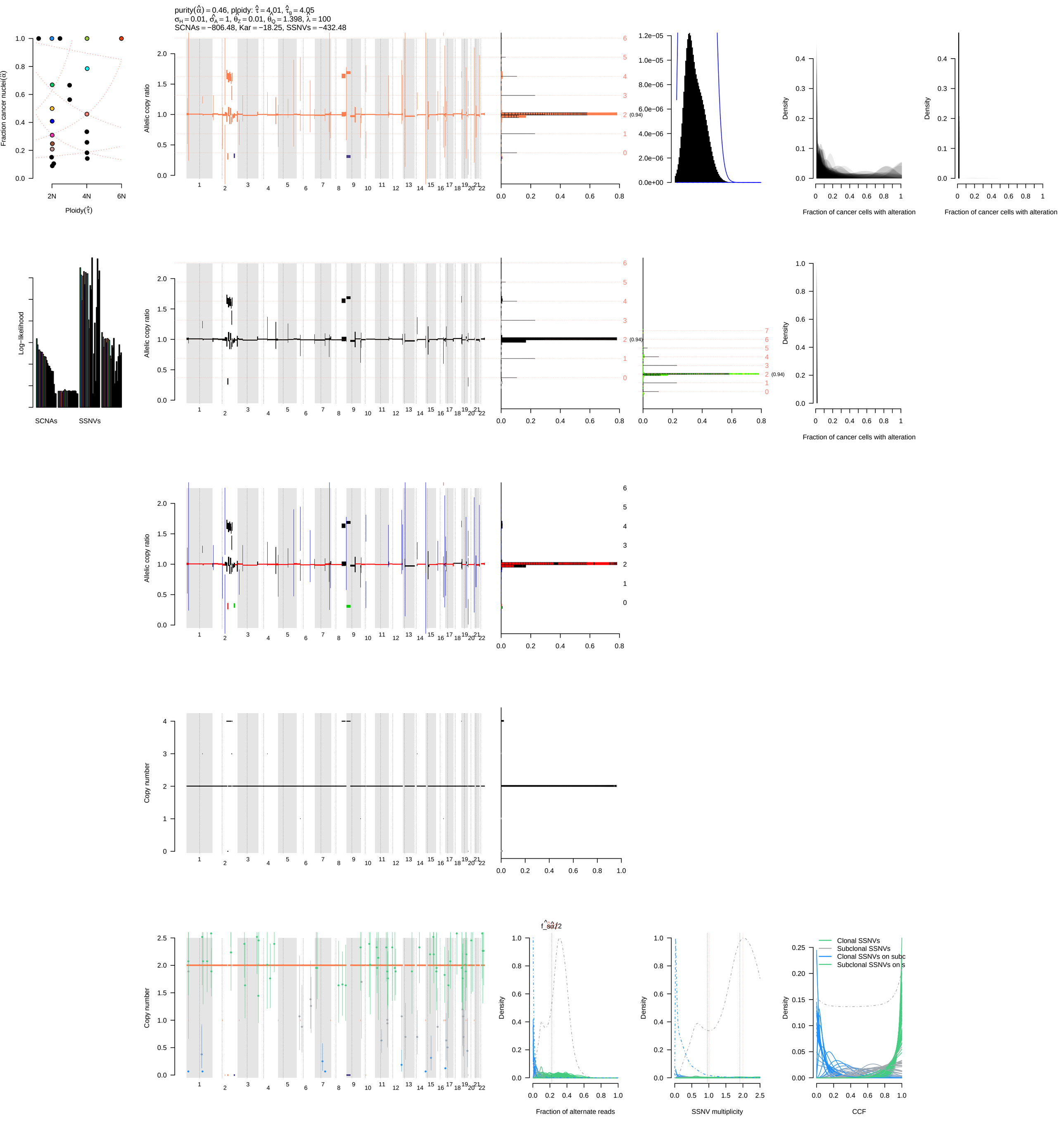

purity($\hat{\alpha}$) = 1, ploidy: $\hat{\tau}$ = 1.99, $\hat{\tau}_g$ = 2.03
σ_H = 0.01, $\hat{\sigma}_A$ = 1, θ_Z = 0.04, θ_Q = 1.175, $\hat{\lambda}$ = 100
SCNAs = −738.15, Kar = −22.46, SSNVs = −457.11
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
Allelic copy ratio
Density
Fraction 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

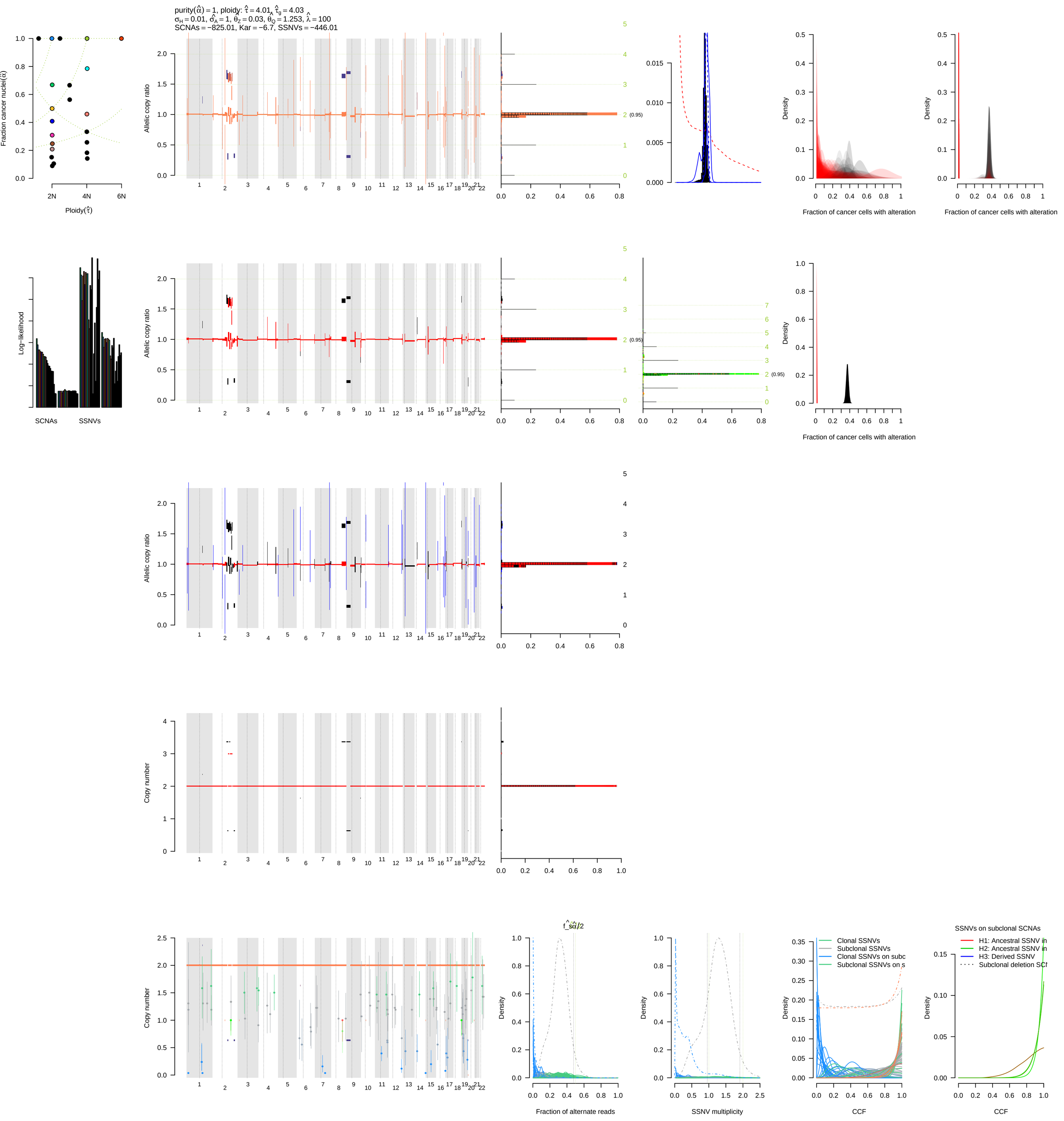

purity($\hat{\alpha}$) = 0.31, ploidy: $\hat{\tau}$ = 2.01, $\hat{\tau}_g$ = 2.08
σ_H = 0.01, $\hat{\sigma}_A$ = 1, θ_Z = 0.01, θ_Q = 1.592, $\hat{\lambda}$ = 100
SCNAs = −785.37, Kar = −22.46, SSNVs = −694.15
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
Allelic copy ratio
Density
Fraction 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

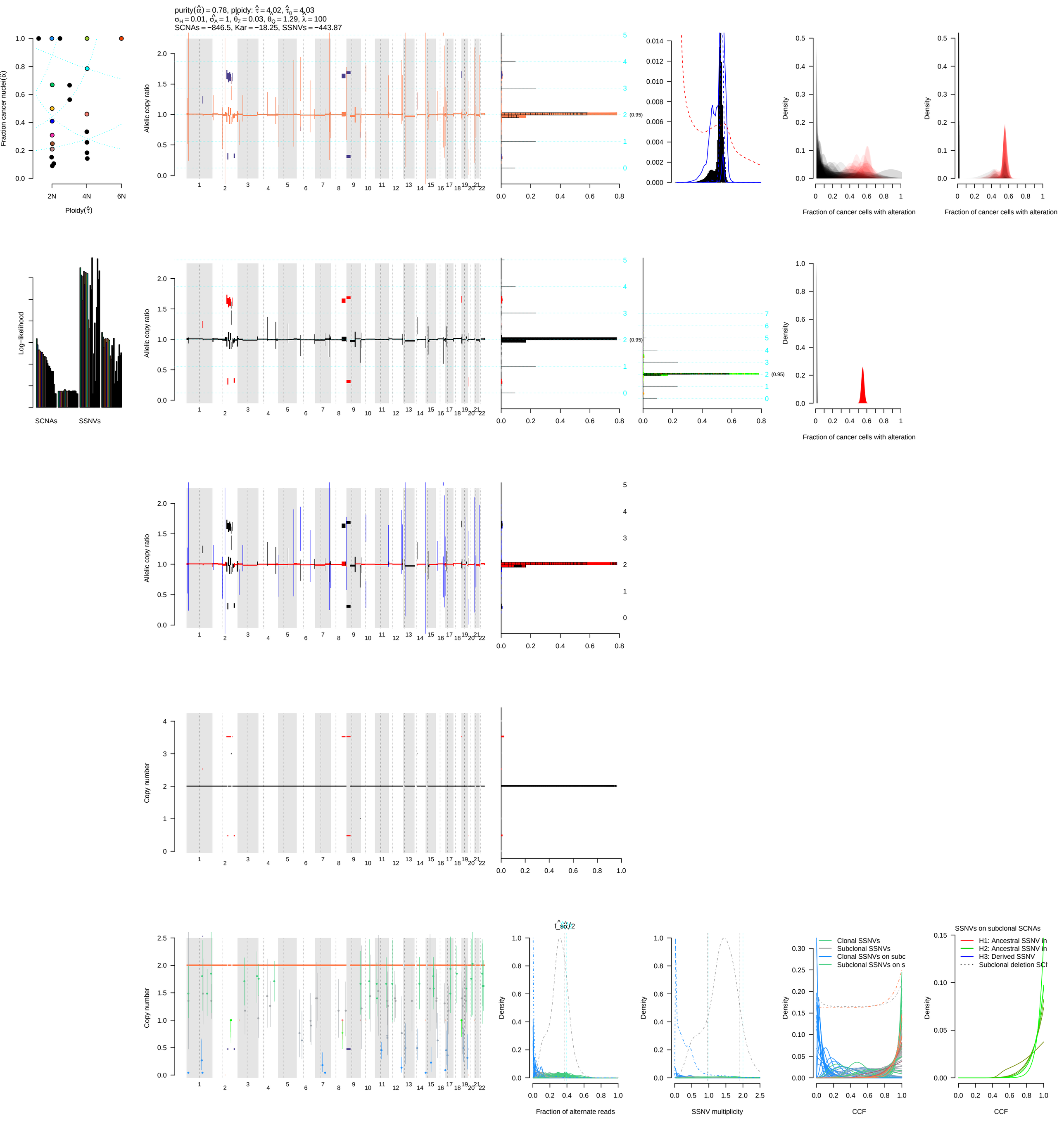

purity($\hat{\alpha}$) = 0.5, ploidy: $\hat{\tau}$ = 2.01, $\hat{\tau}_g$ = 2.03
σ_H = 0.01, $\hat{\sigma}_A$ = 1, θ_Z = 0.03, θ_Q = 1.373, $\hat{\lambda}$ = 100
SCNAs = −785.5, Kar = −22.46, SSNVs = −465.57
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
2N
4N
6N
Allelic copy ratio
(0.95)
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

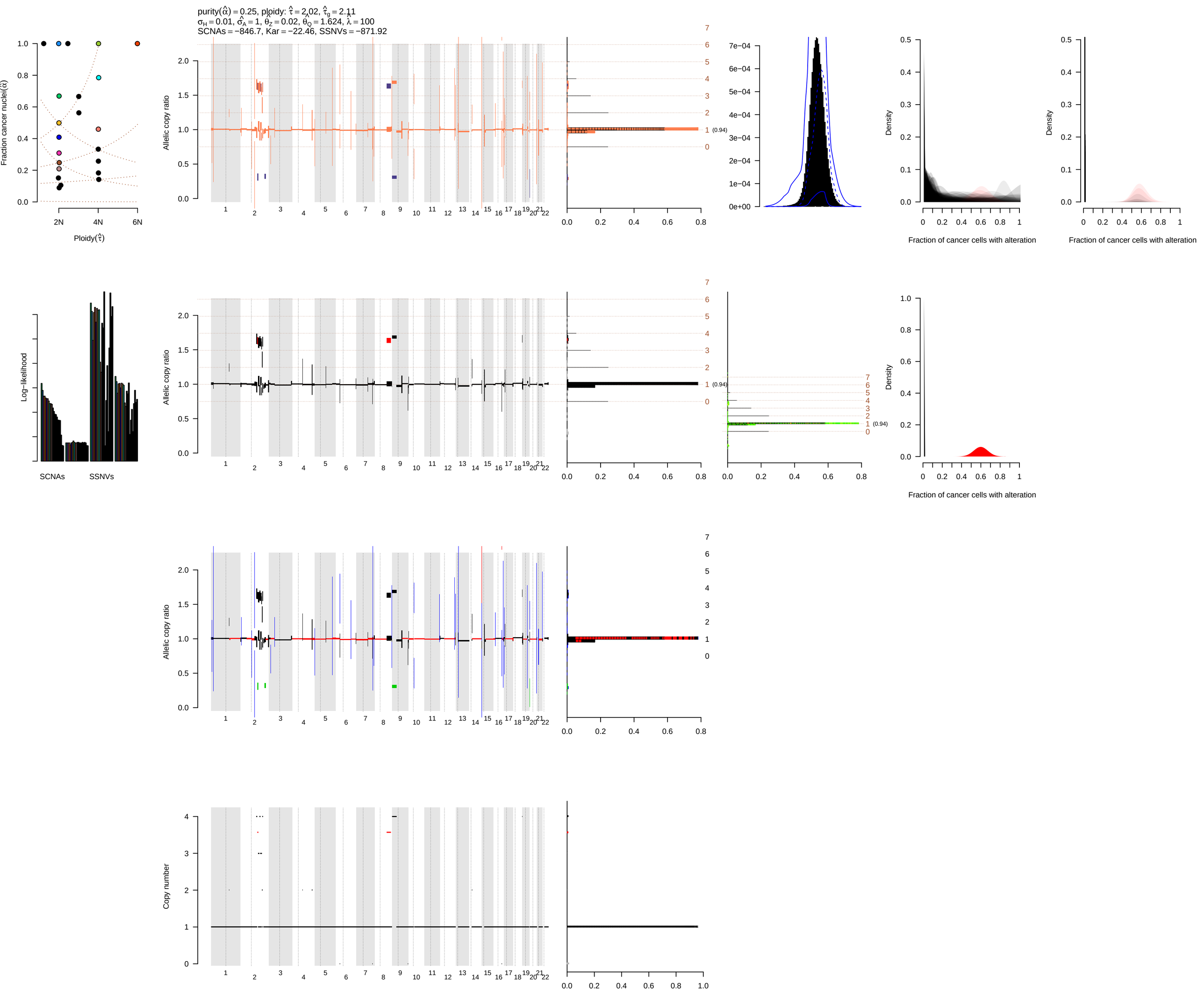

purity($\hat{\alpha}$) = 1, ploidy: $\hat{\tau}$ = 5.99, $\hat{\tau}_g$ = 6.05
σ_H = 0.01, $\hat{\sigma}_A$ = 1, θ_Z = 0, θ_Q = 1.284, λ = 100
SCNAs = −800.41, Kar = −38.17, SSNVs = −423.83
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
Allelic copy ratio
(0.94)
Density
Fraction of cancer 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

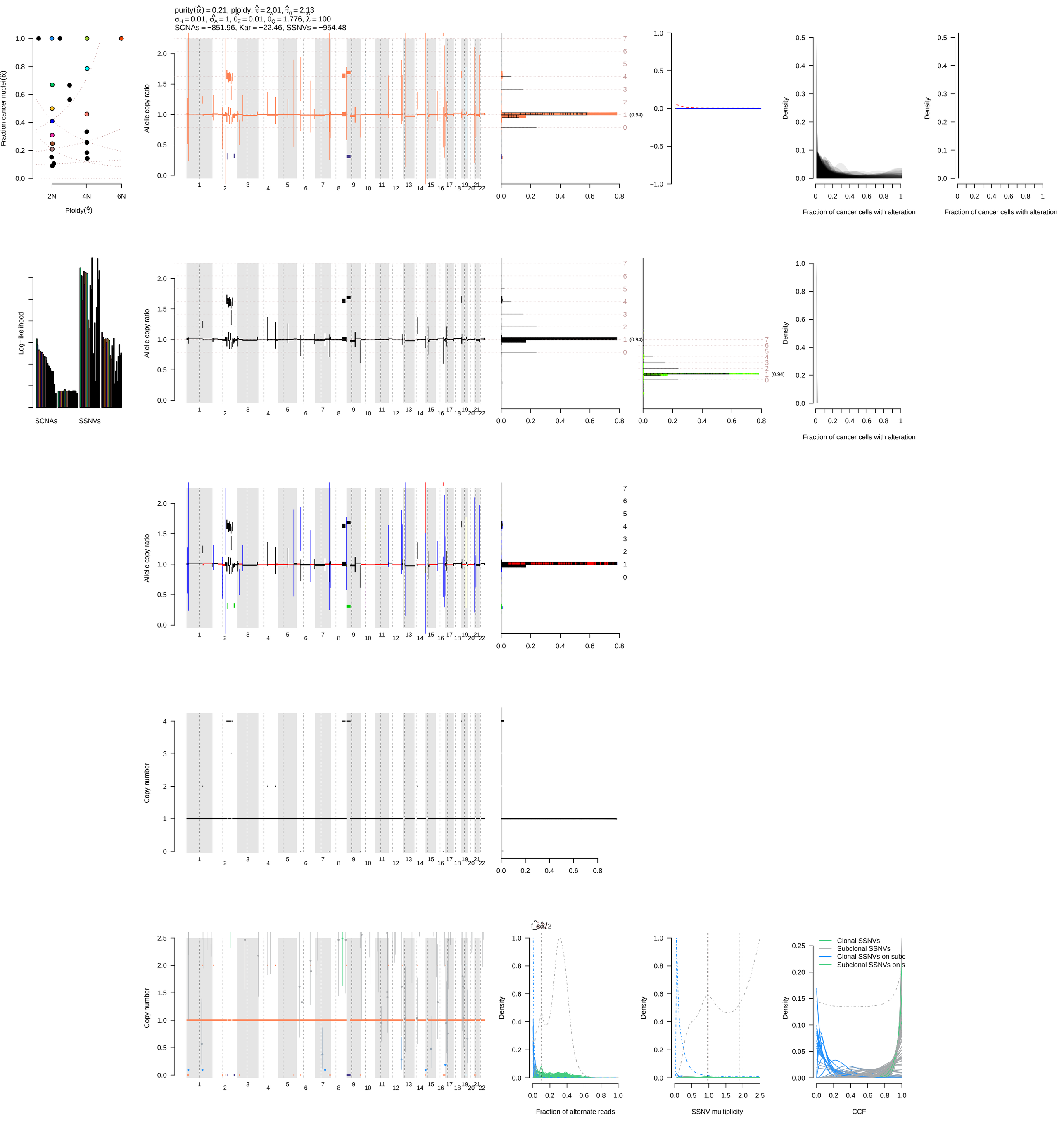

purity($\hat{\alpha}$) = 0.41, ploidy: $\hat{\tau}$ = 2.01, $\hat{\tau}_g$ = 2.07
σ_H = 0.01, $\hat{\sigma}_A$ = 1, θ_Z = 0.03, θ_Q = 1.425, $\hat{\lambda}$ = 100
SCNAs = −805.66, Kar = −22.46, SSNVs = −544.52
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
2N
4N
6N
Allelic copy ratio
(0.95)
Density
Fraction of cancer cells with alteration
Log−likelihood
SCNAs
SSNVs
Copy number
f_6012
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

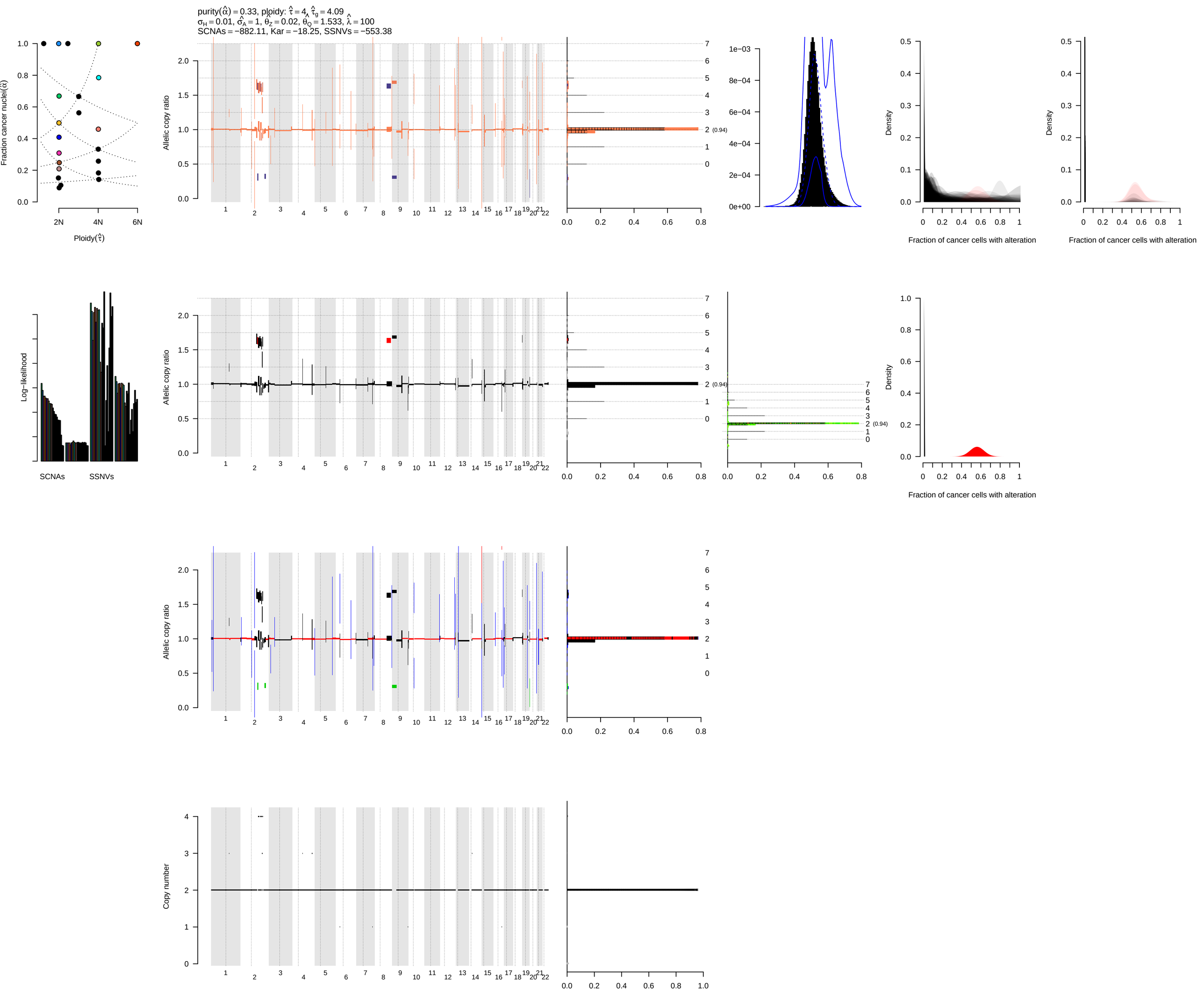

purity($\hat{\alpha}$) = 0.46, ploidy: $\hat{\tau}$ = 4.01, $\hat{\tau}_g$ = 4.05
σ_H = 0.01, $\hat{\sigma}_A$ = 1, θ_Z = 0.01, θ_Q = 1.398, $\hat{\lambda}$ = 100
SCNAs = −806.48, Kar = −18.25, SSNVs = −432.48
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
Allelic copy ratio
Density
Fraction 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

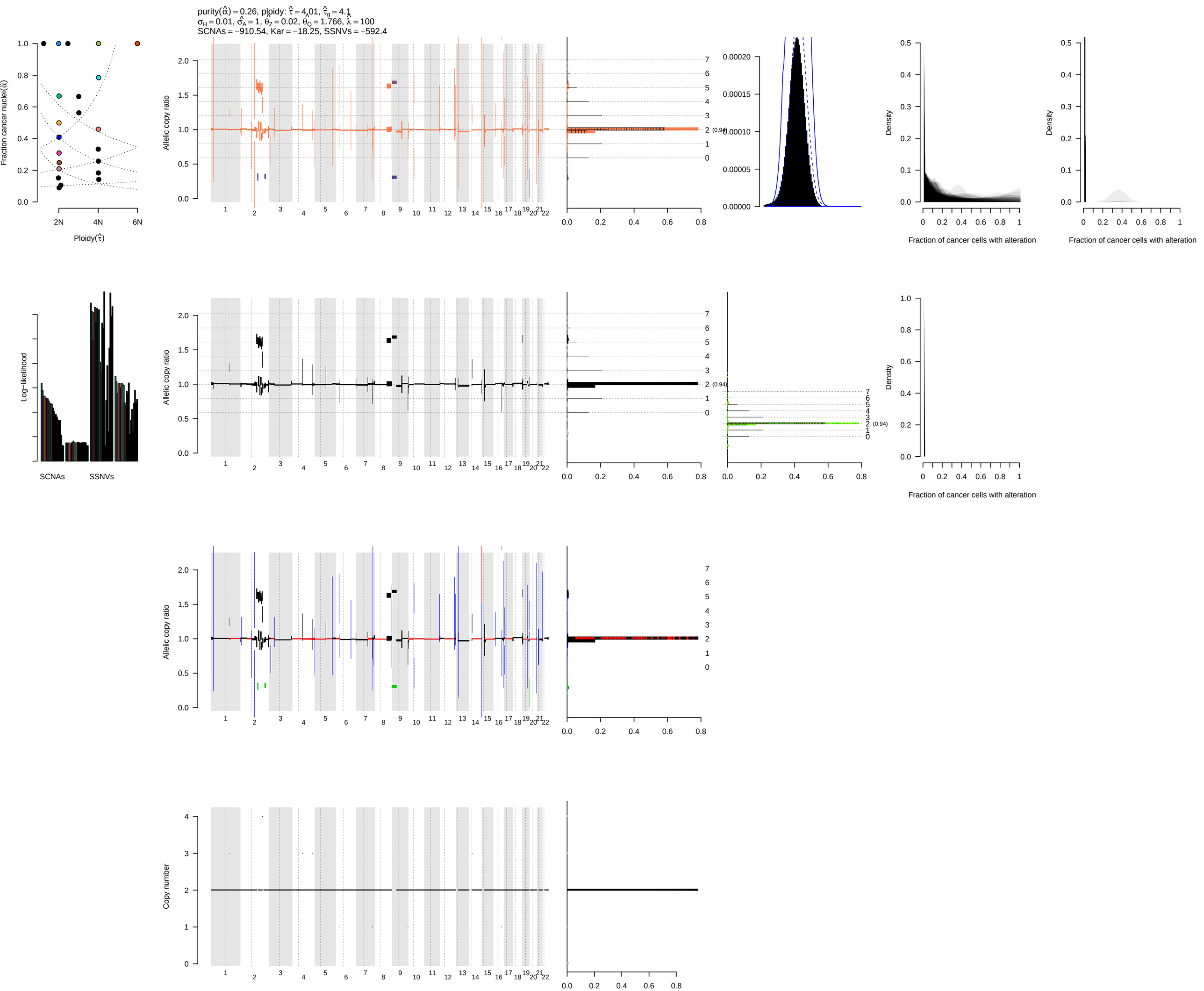

purity($\hat{\alpha}$) = 1, ploidy: $\hat{\tau}$ = 4.01, $\hat{\tau}_g$ = 4.03
σ_H = 0.01, $\hat{\sigma}_A$ = 1, θ_Z = 0.03, θ_Q = 1.253, $\hat{\lambda}$ = 100
SCNAs = −825.01, Kar = −6.7, SSNVs = −446.01
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
Allelic copy ratio
Density
Fraction of cancer cells with alteration
Log−likelihood
SCNAs
SSNVs
Copy number
f_s$\hat{\alpha}$/2
Fraction of alternate reads
SSNV multiplicity
CCF
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

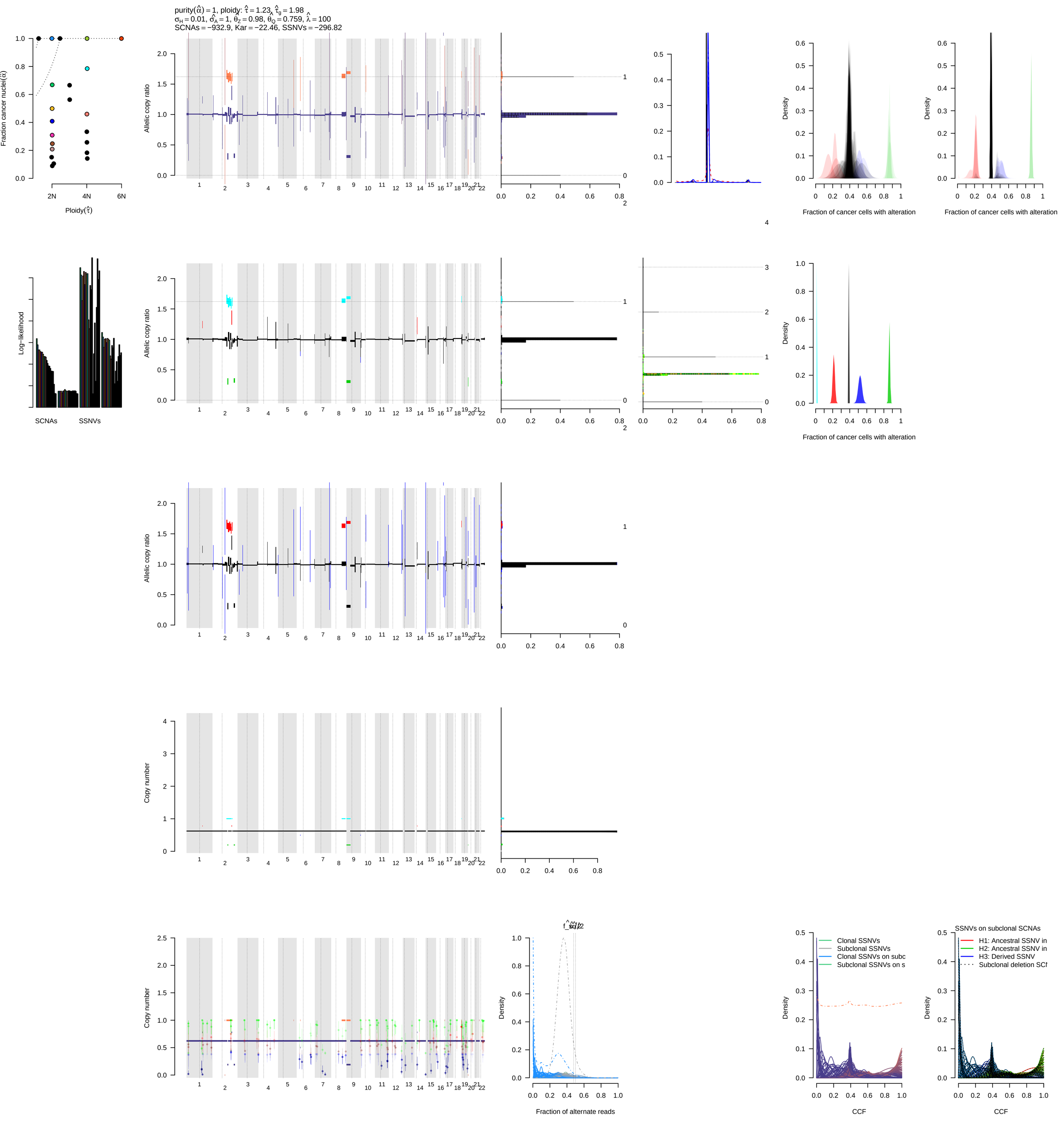

purity($\hat{\alpha}$) = 0.78, ploidy: $\hat{\tau}$ = 4.02, $\hat{\tau}_g$ = 4.03
σ_H = 0.01, $\hat{\sigma}_A$ = 1, θ_Z = 0.03, θ_Q = 1.29, $\hat{\lambda}$ = 100
SCNAs = −846.5, Kar = −18.25, SSNVs = −443.87
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
Allelic copy ratio
Density
Fraction 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

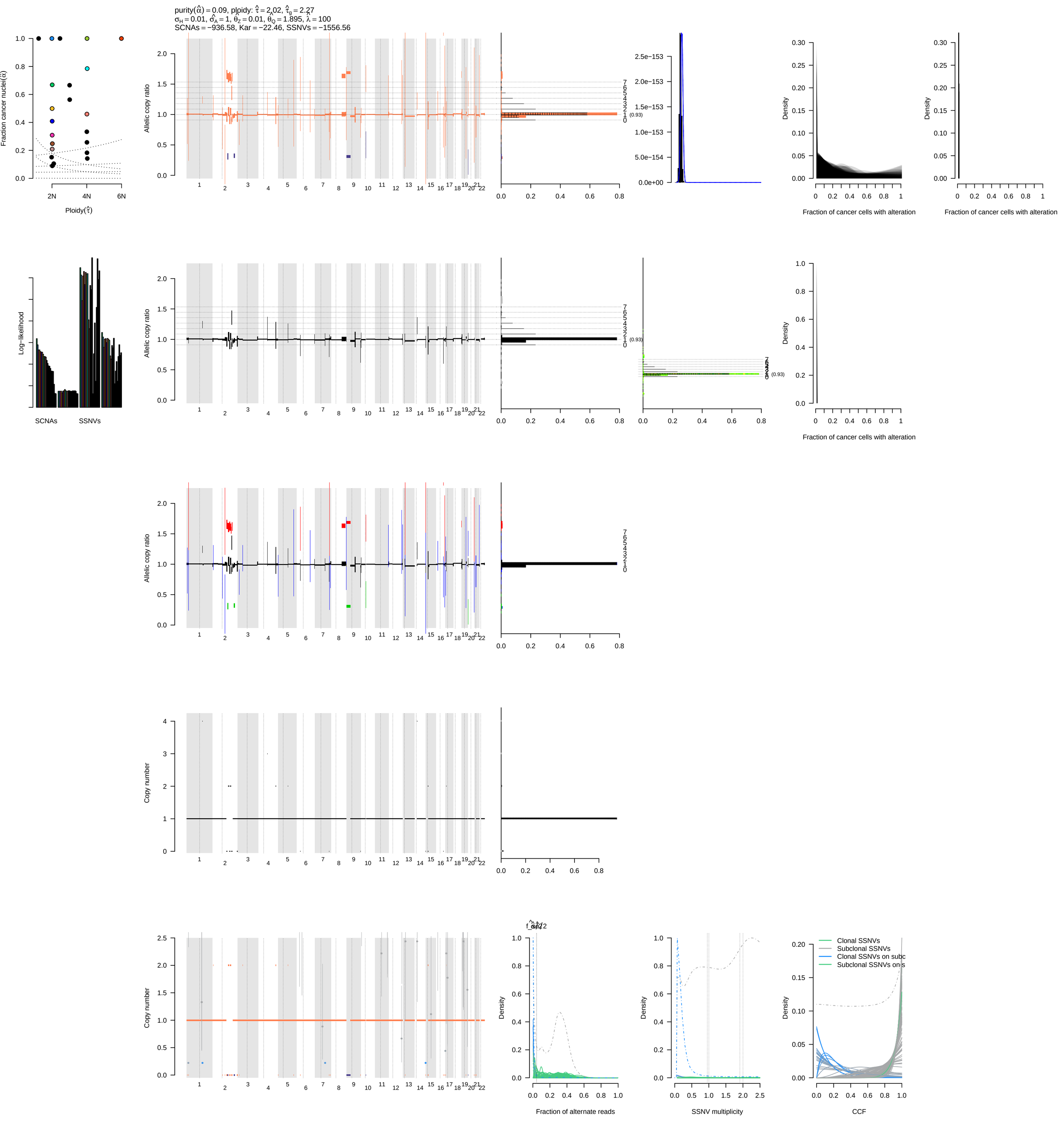

purity($\hat{\alpha}$) = 0.25, ploidy: $\hat{\tau}$ = 2.02, $\hat{\tau}_g$ = 2.11
σ_H = 0.01, $\hat{\sigma}_A$ = 1, θ_Z = 0.02, θ_Q = 1.624, $\hat{\lambda}$ = 100
SCNAs = −846.7, Kar = −22.46, SSNVs = −871.92
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
2N
4N
6N
Allelic copy ratio
(0.94)
Density
Fraction of cancer cells with alteration
Log−likelihood
SCNAs
SSNVs
Copy number
f_sol2
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

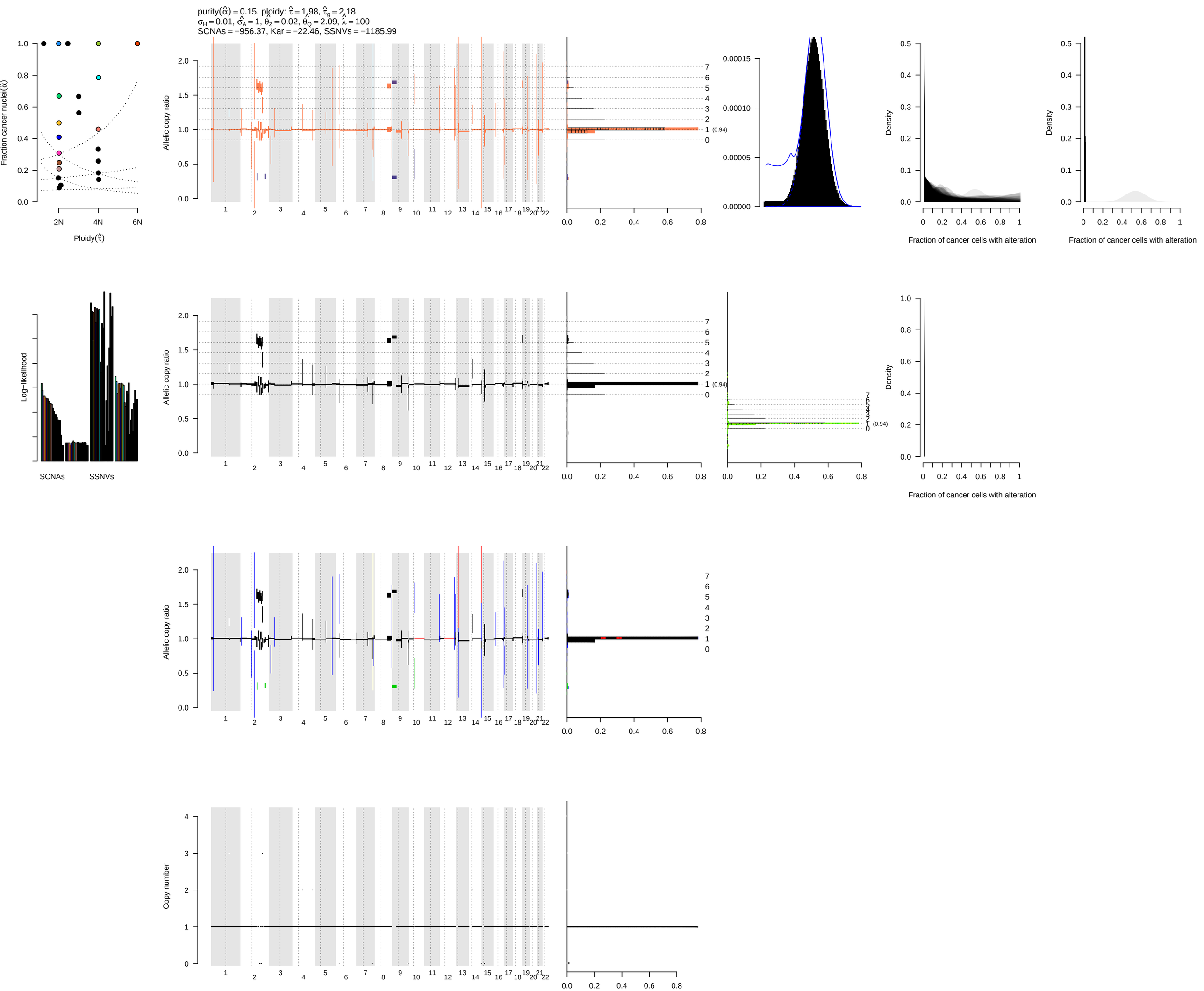

purity($\hat{\alpha}$) = 0.21, ploidy: $\hat{\tau}$ = 2.01, $\hat{\tau}_g$ = 2.13
σ_H = 0.01, $\hat{\sigma}_A$ = 1, θ_Z = 0.01, θ_Q = 1.776, $\hat{\lambda}$ = 100
SCNAs = −851.96, Kar = −22.46, SSNVs = −954.48
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
2N
4N
6N
Allelic copy ratio
(0.94)
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

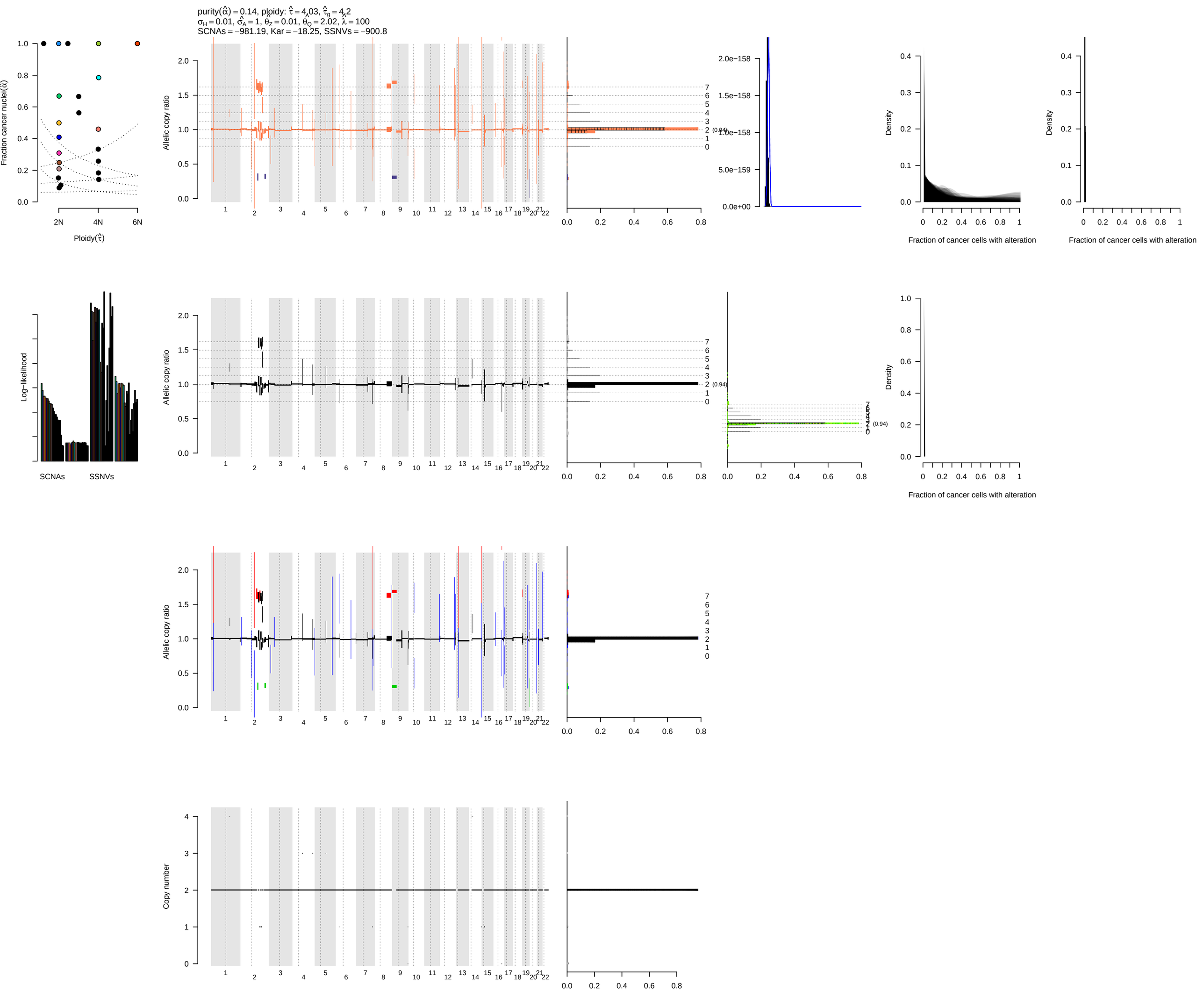

purity($\hat{\alpha}$) = 0.33, ploidy: $\hat{\tau}_A = 4$, $\hat{\tau}_g = 4.09$
$\sigma_H = 0.01$, $\hat{\sigma}_A = 1$, $\theta_Z = 0.02$, $\theta_Q = 1.533$, $\hat{\lambda} = 100$
SCNAs = −882.11, Kar = −18.25, SSNVs = −553.38
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
Allelic copy 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
H3: Derived SSNV

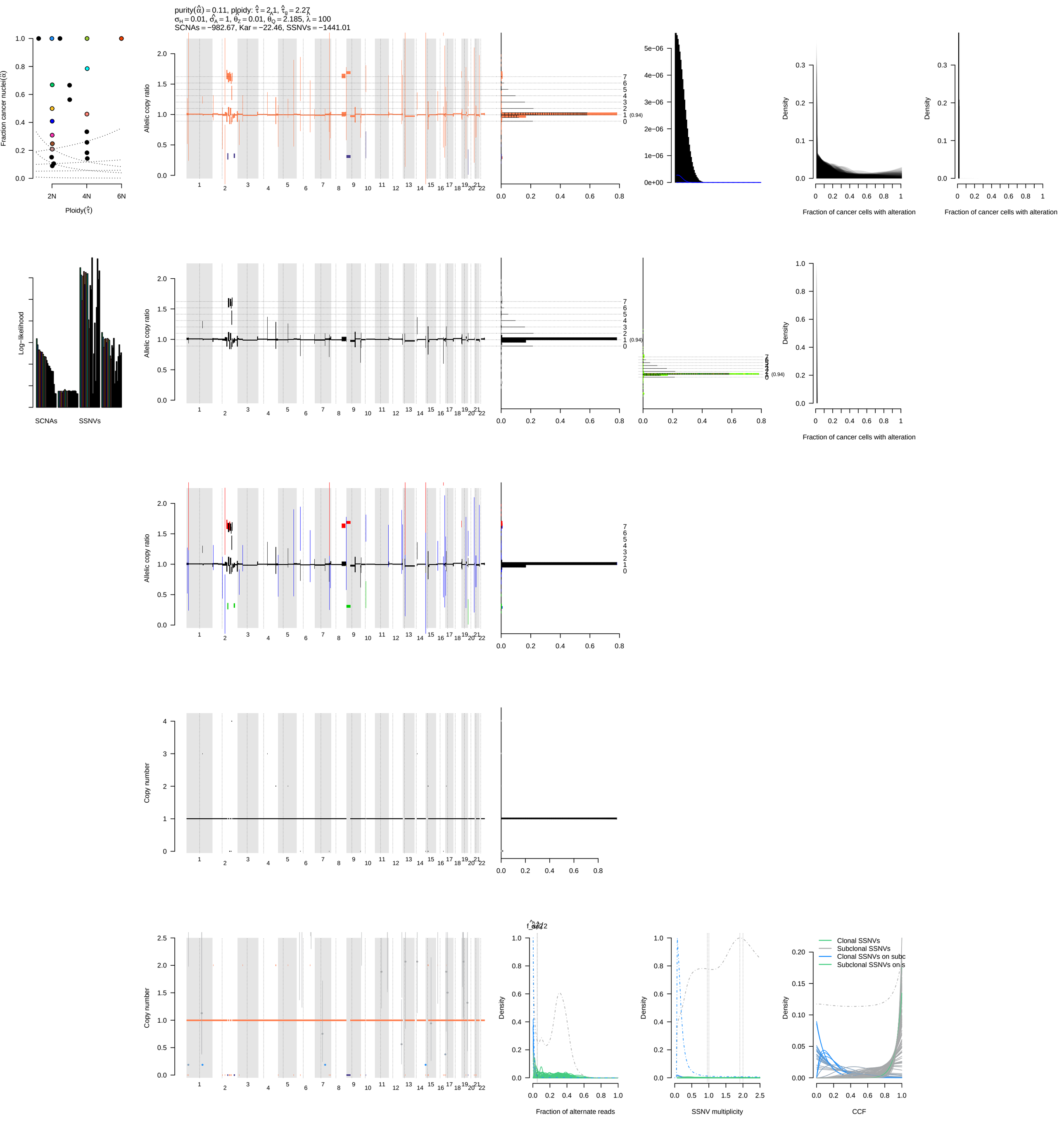

purity($\hat{\alpha}$) = 0.26, ploidy: $\hat{\tau}$ = 4.01, $\hat{\tau}_g$ = 4.1
σ_H = 0.01, $\hat{\sigma}_A$ = 1, θ_Z = 0.02, θ_Q = 1.766, $\hat{\lambda}$ = 100
SCNAs = −910.54, Kar = −18.25, SSNVs = −592.4
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
Allelic copy ratio
Density
Fraction of cancer cells with alteration
Log−likelihood
SCNAs
SSNVs
Copy number
Fraction of alternate reads
SSNV multiplicity
CCF
Clonal SSNVs
Subclonal SSNVs
Clonal SSNVs on subc
Subclonal SSNVs on s

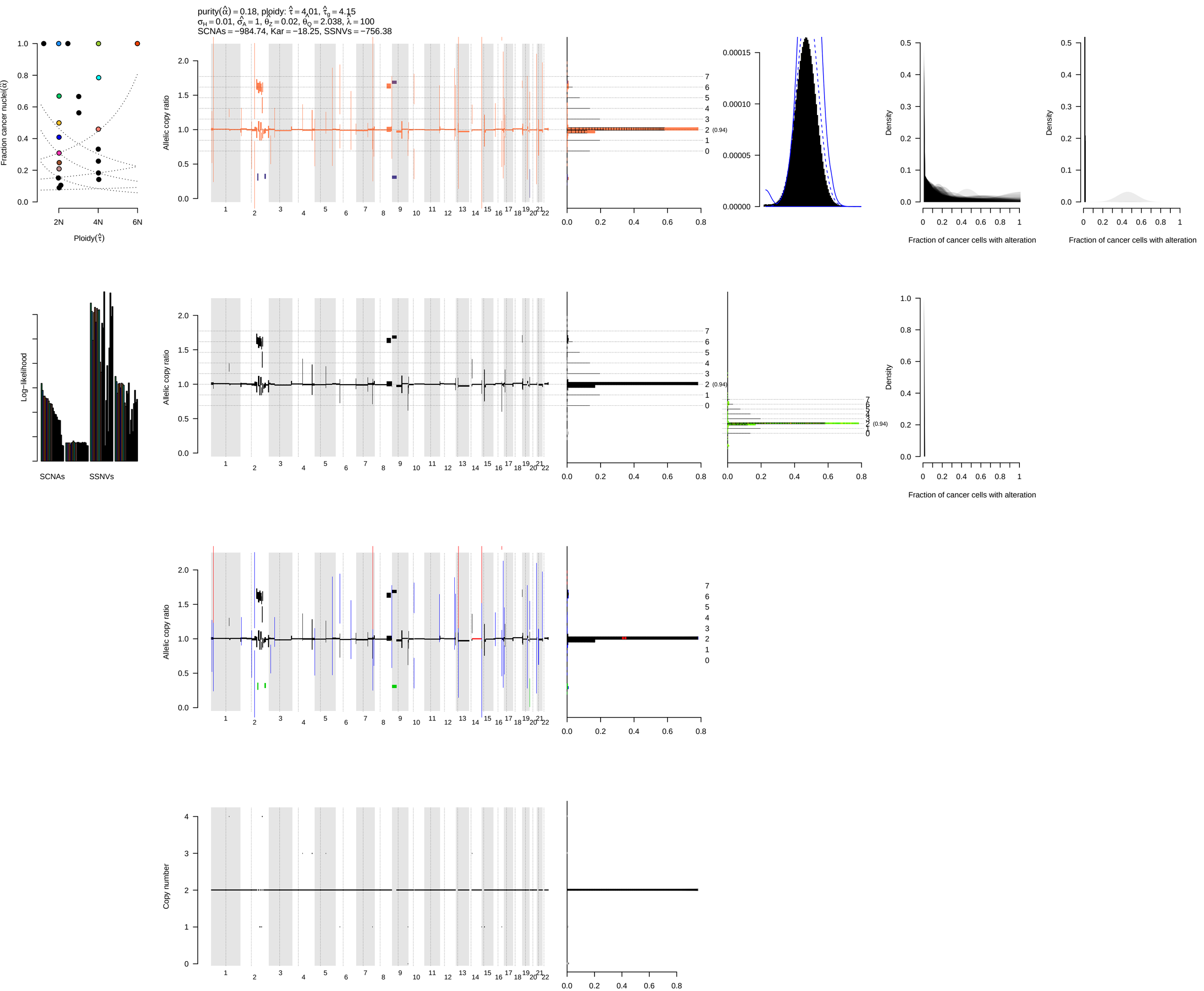

purity($\hat{\alpha}$) = 1, ploidy: $\hat{\tau}$ = 1.23, $\hat{\tau}_g$ = 1.98
σ_H = 0.01, $\hat{\sigma}_A$ = 1, θ_Z = 0.98, θ_Q = 0.759, $\hat{\lambda}$ = 100
SCNAs = −932.9, Kar = −22.46, SSNVs = −296.82
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
2N
4N
6N
Allelic copy ratio
Density
Fraction of cancer cells with alteration
Log−likelihood
SCNAs
SSNVs
Copy number
Fraction of alternate reads
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

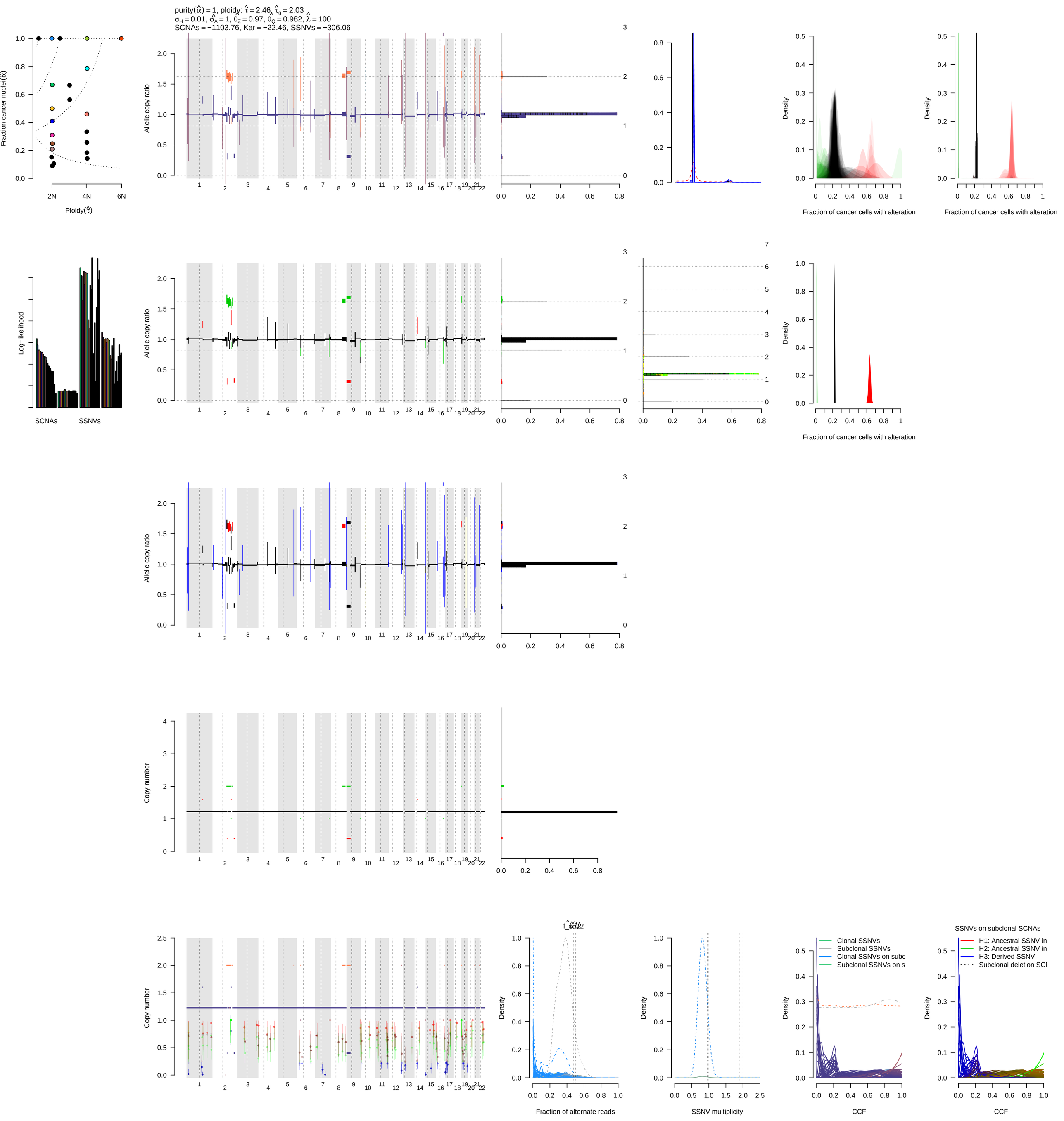

purity($\hat{\alpha}$) = 0.09, ploidy: $\hat{\tau}$ = 2.02, $\hat{\tau}_g$ = 2.27
σ_H = 0.01, $\hat{\sigma}_A$ = 1, θ_Z = 0.01, θ_Q = 1.895, $\hat{\lambda}$ = 100
SCNAs = −936.58, Kar = −22.46, SSNVs = −1556.56
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
Allelic copy ratio
Density
Fraction 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

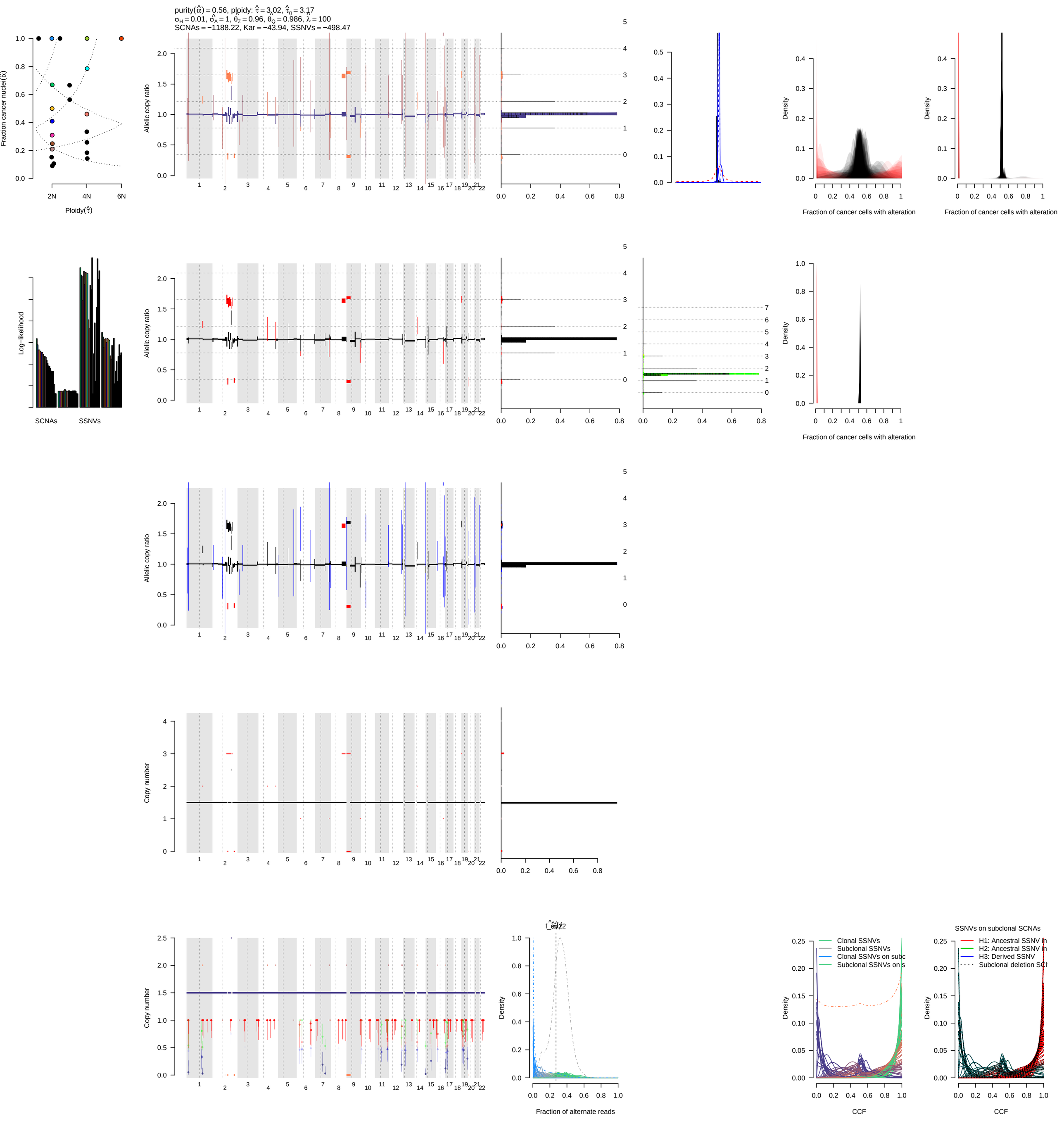

purity($\hat{\alpha}$) = 0.15, ploidy: $\hat{\tau}$ = 1.98, $\hat{\tau}_g$ = 2.18
σ_H = 0.01, $\hat{\sigma}_A$ = 1, θ_Z = 0.02, θ_Q = 2.09, $\hat{\lambda}$ = 100
SCNAs = −956.37, Kar = −22.46, SSNVs = −1185.99
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
Allelic copy ratio
(0.94)
Density
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

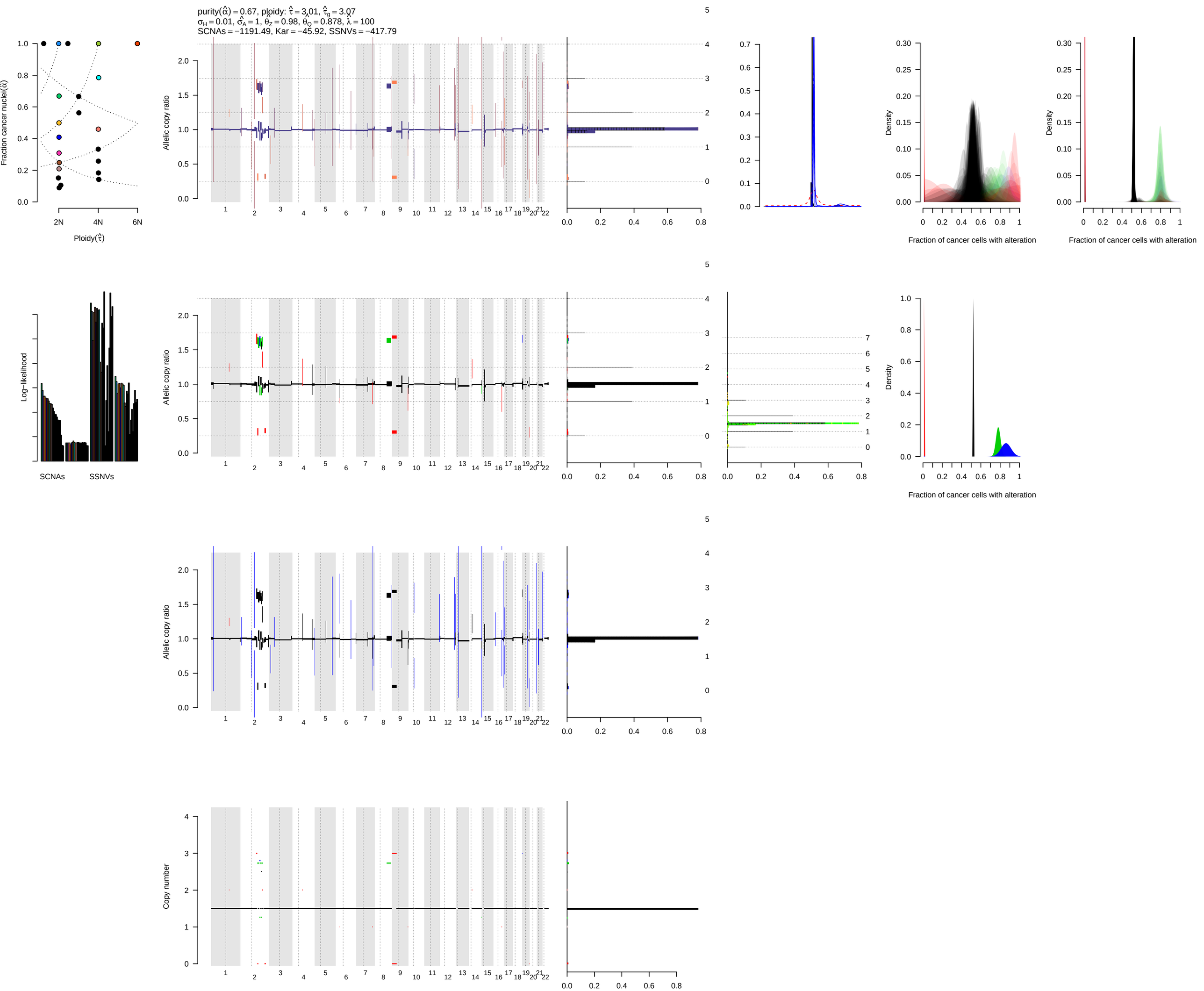

purity($\hat{\alpha}$) = 0.14, ploidy: $\hat{\tau}$ = 4.03, $\hat{\tau}_g$ = 4.2
σ_H = 0.01, $\hat{\sigma}_A$ = 1, θ_Z = 0.01, θ_Q = 2.02, $\hat{\lambda}$ = 100
SCNAs = −981.19, Kar = −18.25, SSNVs = −900.8
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
Allelic copy ratio
Density
Fraction 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


purity($\hat{\alpha}$) = 0.11, ploidy: $\hat{\tau}$ = 2.1, $\hat{\tau}_g$ = 2.27
σ_H = 0.01, $\hat{\sigma}_A$ = 1, θ_Z = 0.01, θ_Q = 2.185, $\hat{\lambda}$ = 100
SCNAs = −982.67, Kar = −22.46, SSNVs = −1441.01
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
2N
4N
6N
Allelic copy ratio
(0.94)
Density
Fraction of cancer cells with alteration
Log−likelihood
SCNAs
SSNVs
Copy number
f_cut
Fraction of alternate reads
SSNV multiplicity
CCF
Clonal SSNVs
Subclonal SSNVs
Clonal SSNVs on subc
Subclonal SSNVs on s


purity($\hat{\alpha}$) = 0.18, ploidy: $\hat{\tau}$ = 4.01, $\hat{\tau}_g$ = 4.15
σ_H = 0.01, $\hat{\sigma}_A$ = 1, θ_Z = 0.02, θ_Q = 2.038, $\hat{\lambda}$ = 100
SCNAs = −984.74, Kar = −18.25, SSNVs = −756.38
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
2N
4N
6N
Allelic copy ratio
(0.94)
Density
Fraction of cancer cells with alteration
Log−likelihood
SCNAs
SSNVs
Copy number
Clonal SSNVs
Subclonal SSNVs
Clonal SSNVs on subc
Subclonal SSNVs on s
Fraction of alternate reads
SSNV multiplicity
CCF


purity($\hat{\alpha}$) = 1, ploidy: $\hat{\tau}$ = 2.46, $\hat{\tau}_g$ = 2.03
σ_H = 0.01, $\hat{\sigma}_A$ = 1, θ_Z = 0.97, θ_Q = 0.982, $\hat{\lambda}$ = 100
SCNAs = −1103.76, Kar = −22.46, SSNVs = −306.06
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($\hat{\alpha}$) = 0.56, ploidy: $\hat{\tau}$ = 3.02, $\hat{\tau}_g$ = 3.17
σ_H = 0.01, $\hat{\sigma}_A$ = 1, θ_Z = 0.96, θ_Q = 0.986, $\hat{\lambda}$ = 100
SCNAs = −1188.22, Kar = −43.94, SSNVs = −498.47
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
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, $\hat{\tau}_g$ = 3.07
σ_H = 0.01, $\hat{\sigma}_A$ = 1, θ_Z = 0.98, θ_Q = 0.878, $\hat{\lambda}$ = 100
SCNAs = −1191.49, Kar = −45.92, SSNVs = −417.79
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
Allelic copy ratio
Density
Fraction of cancer cells with alteration
Log−likelihood
SCNAs
SSNVs
Copy number
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