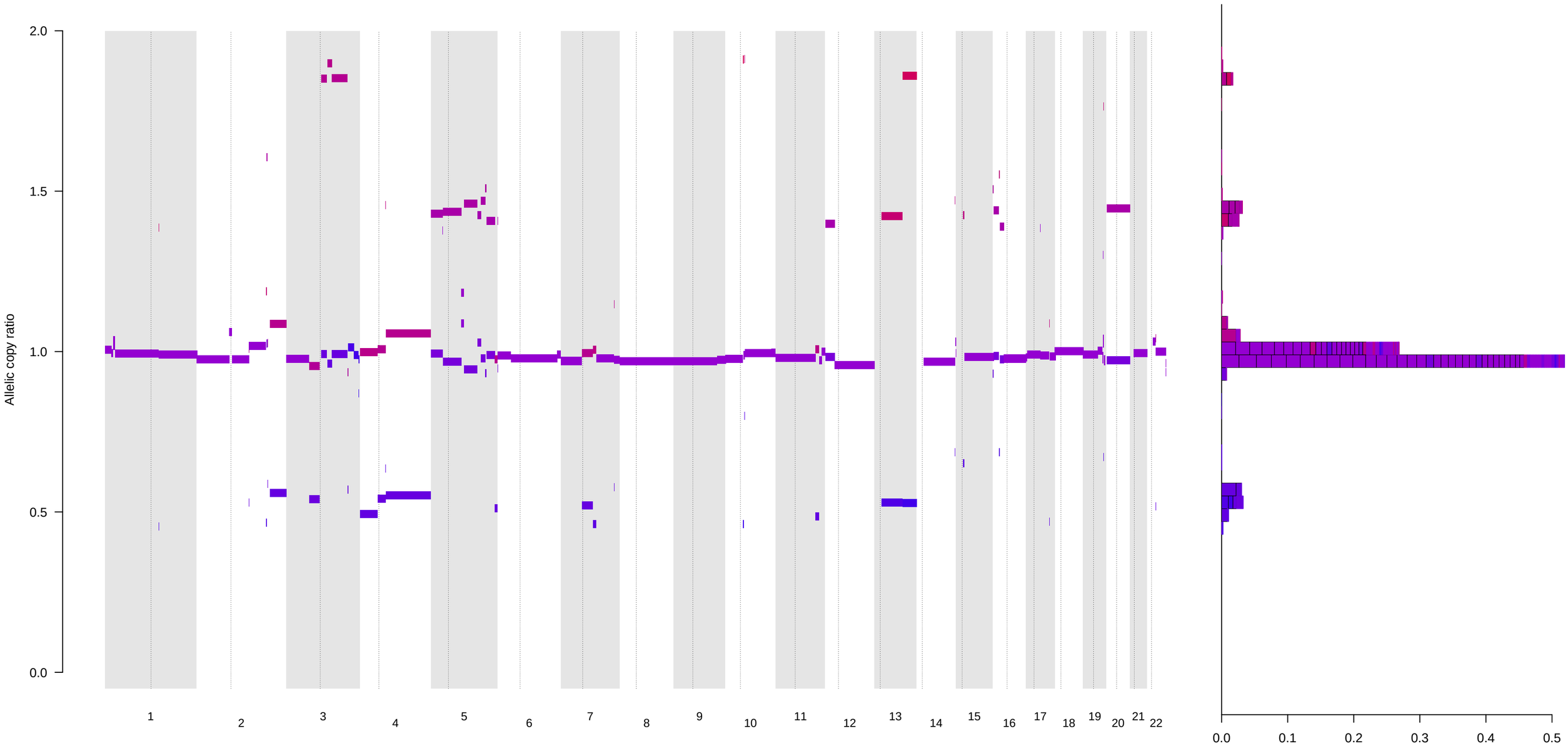
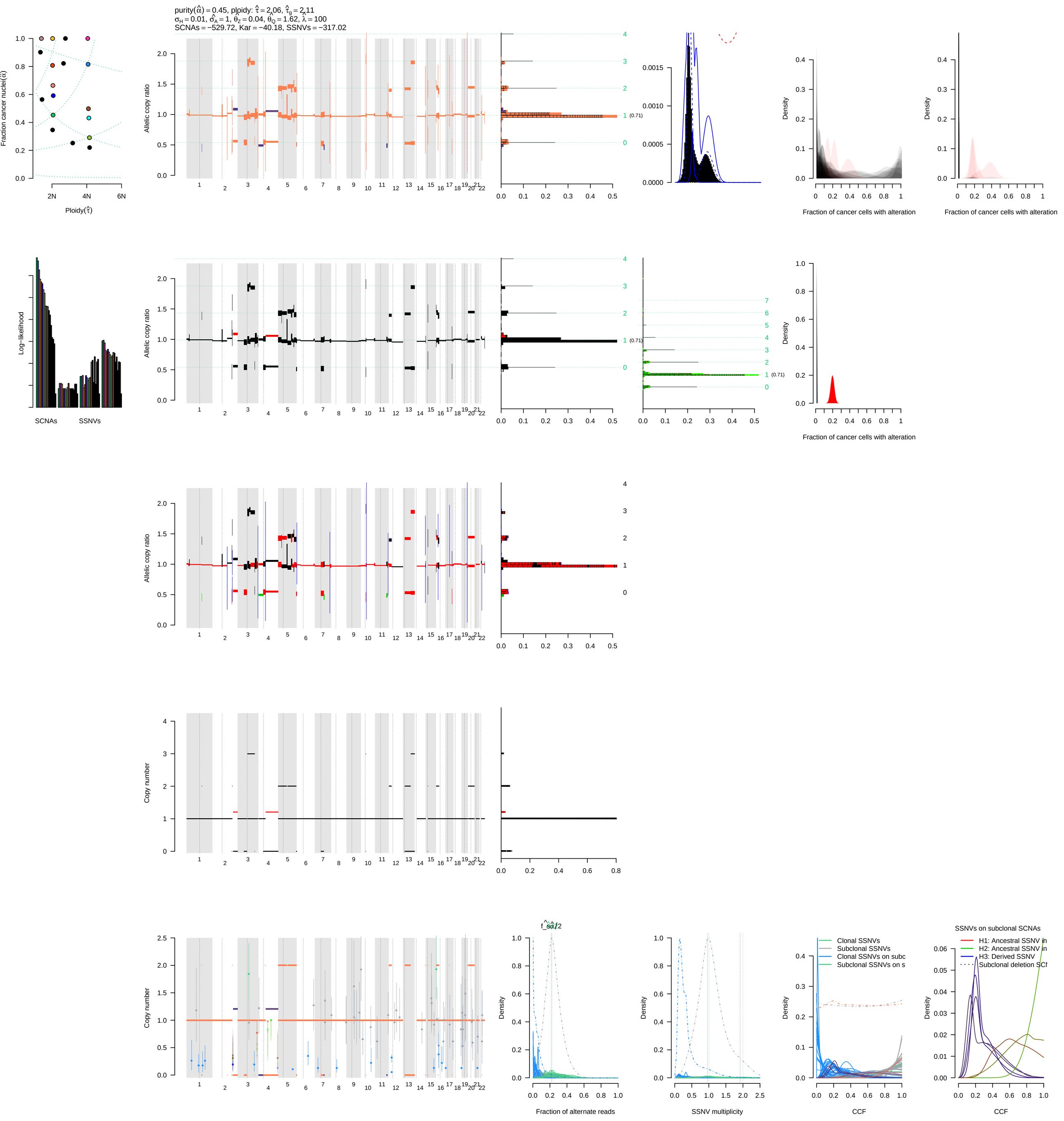
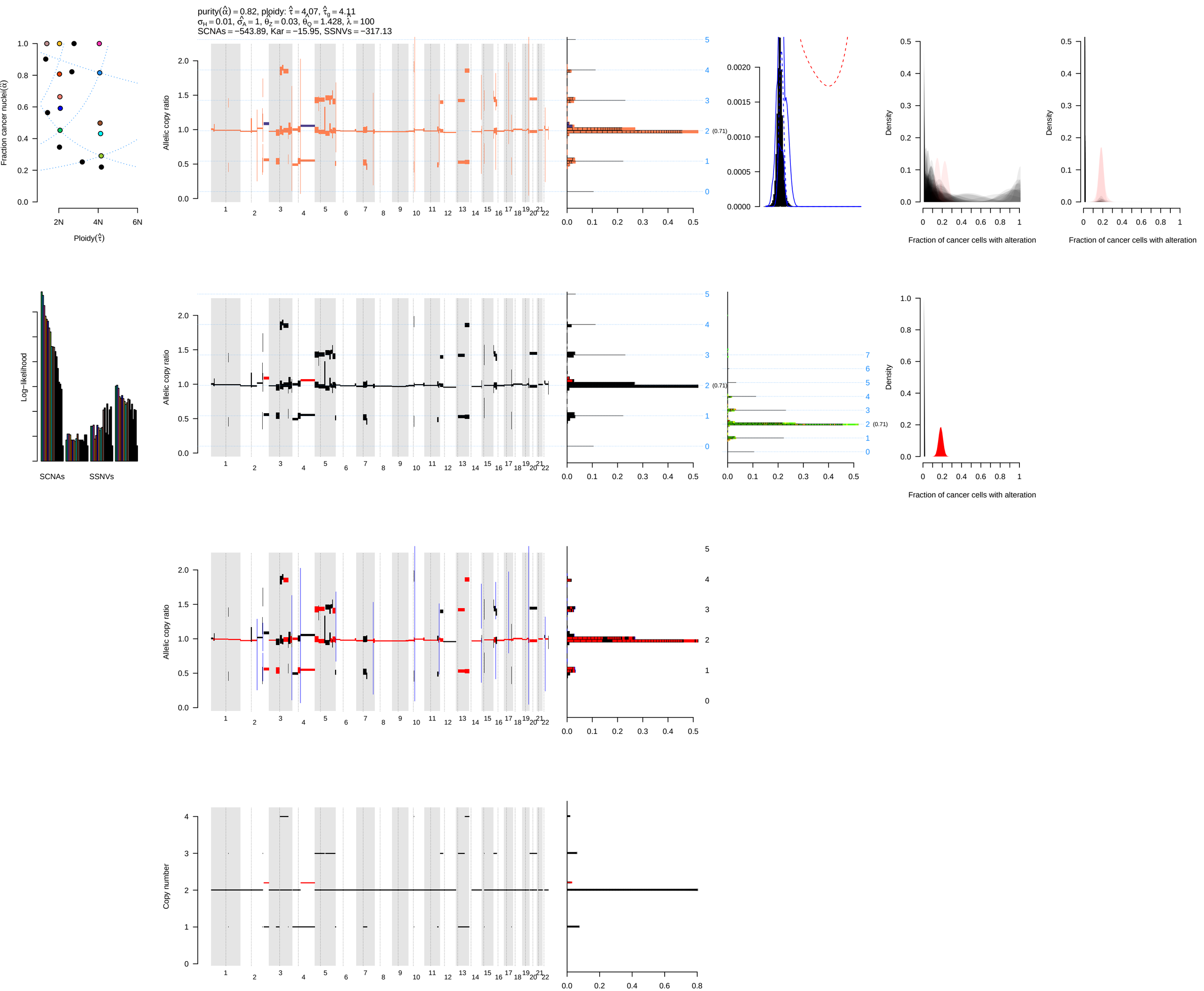
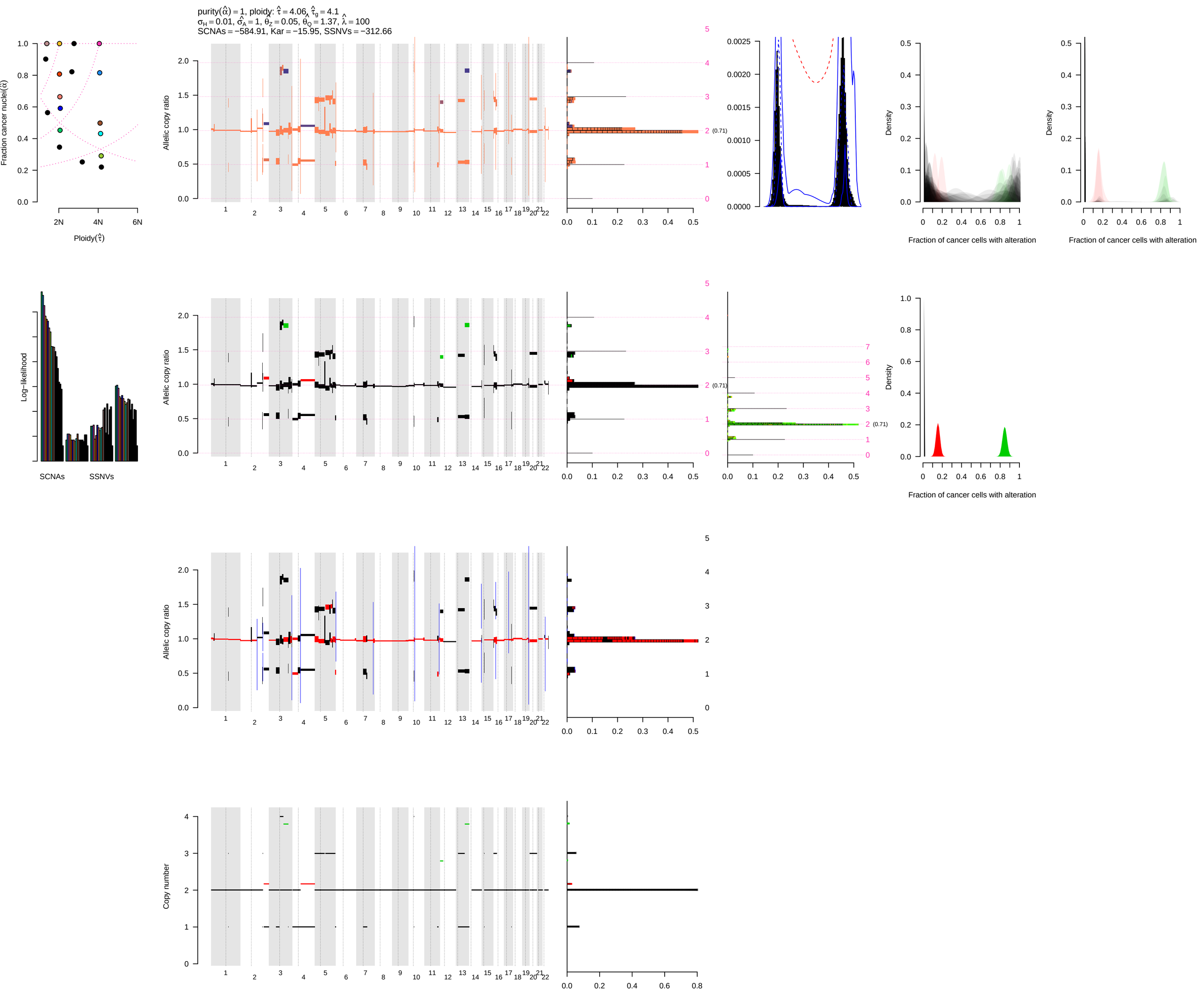
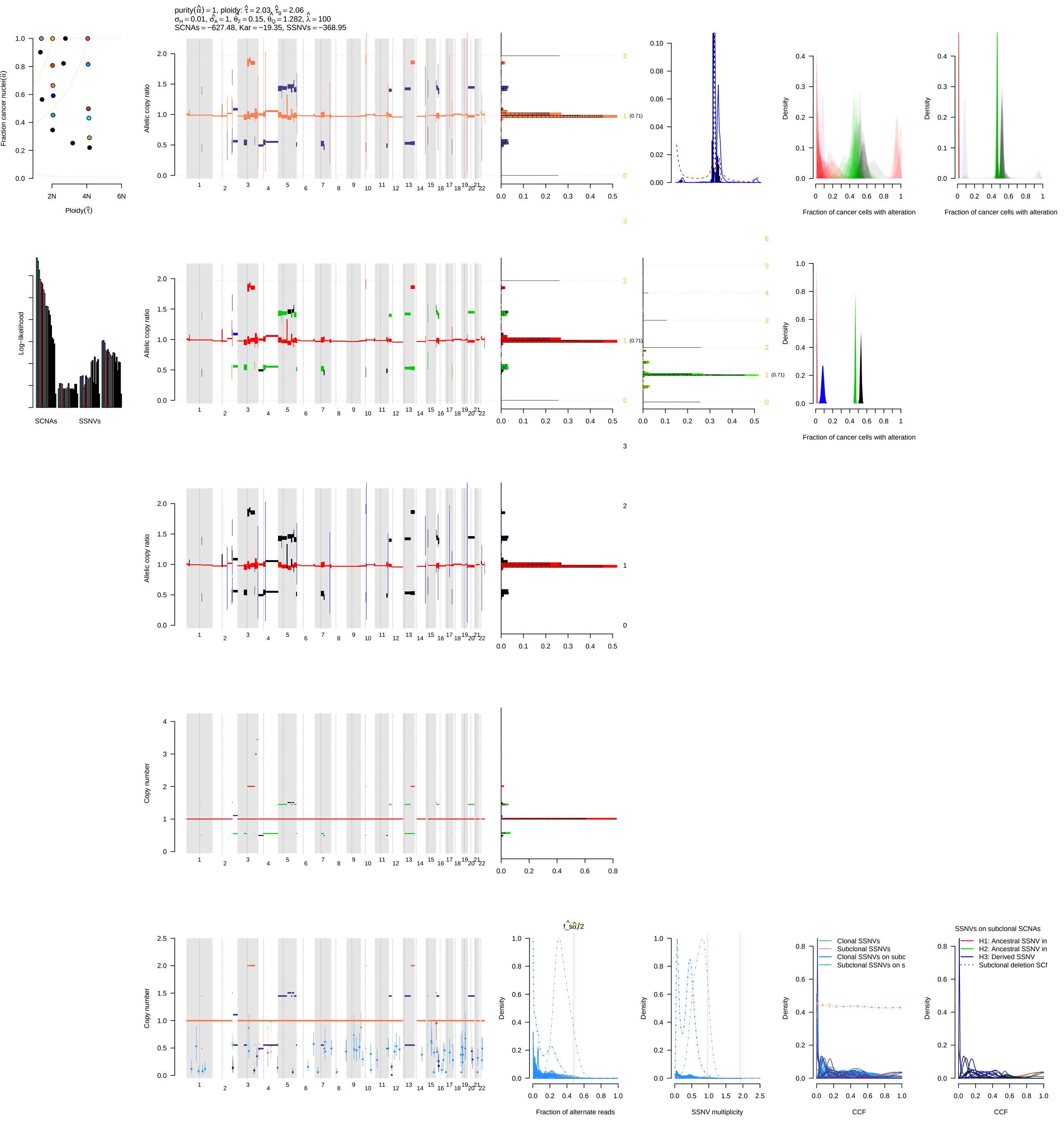
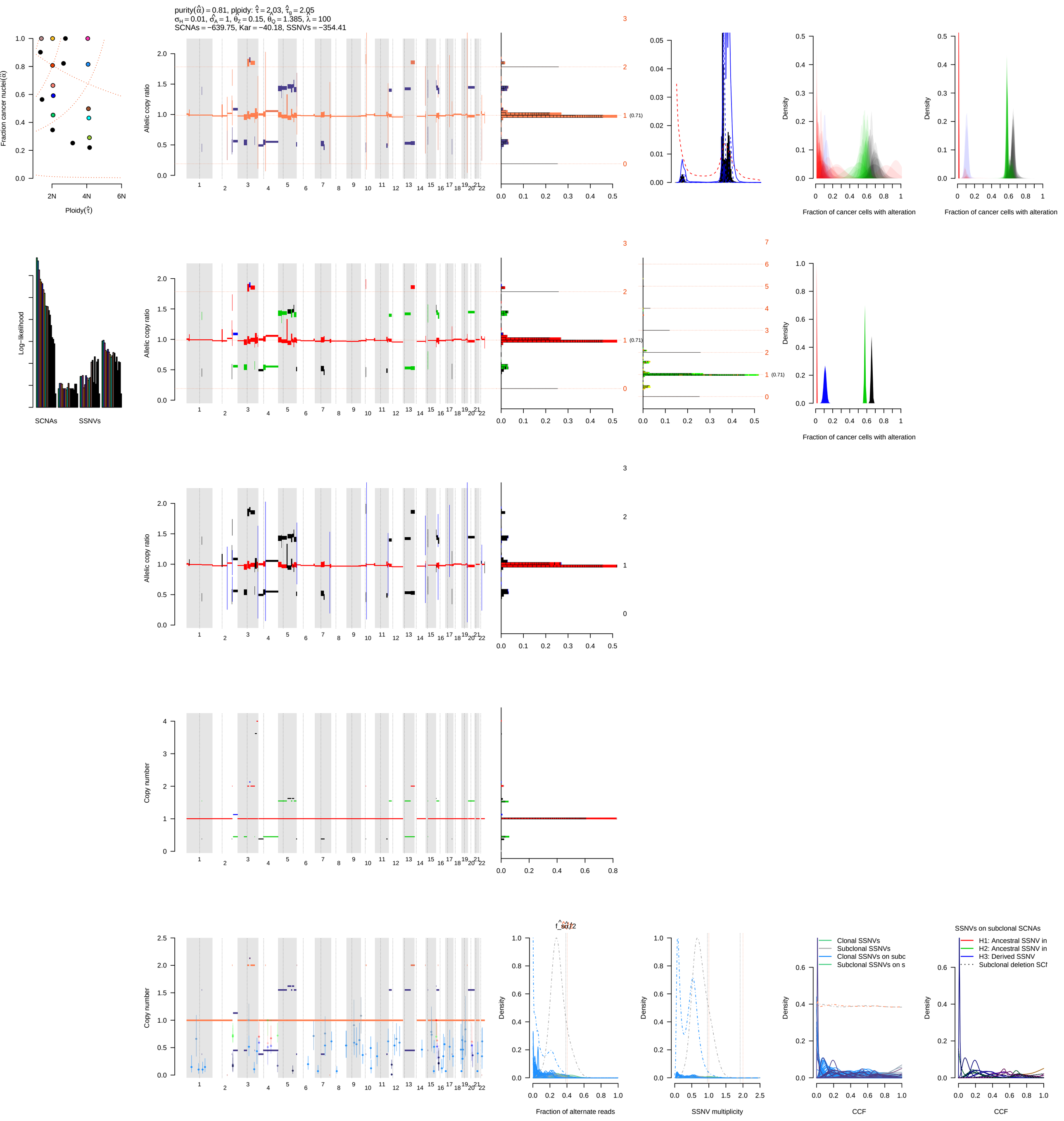

Allelic copy ratio
2.0
1.5
1.0
0.5
0.0
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
0.0
0.1
0.2
0.3
0.4
0.5

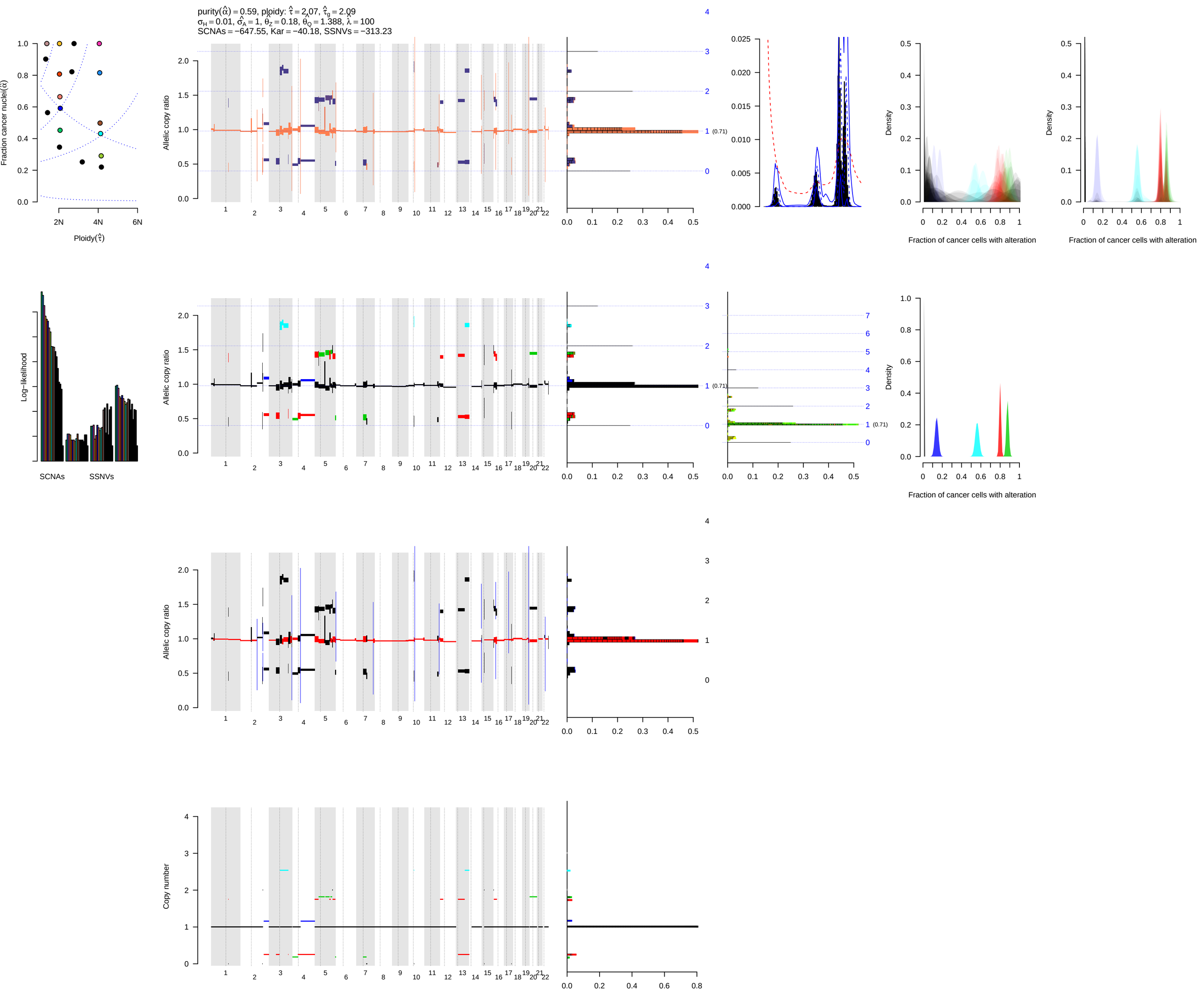

purity($\hat{\alpha}$) = 0.45, ploidy: $\hat{\tau}$ = 2.06, $\hat{\tau}_g$ = 2.11
$\sigma_H$ = 0.01, $\hat{\sigma}_A$ = 1, $\theta_Z$ = 0.04, $\theta_Q$ = 1.62, $\hat{\lambda}$ = 100
SCNAs = −529.72, Kar = −40.18, SSNVs = −317.02
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
Allelic copy ratio
Density
Fraction of cancer cells with alteration
Log−likelihood
SCNAs
SSNVs
Copy number
f_sol/2
Fraction of alternate reads
SSNV multiplicity
CCF
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

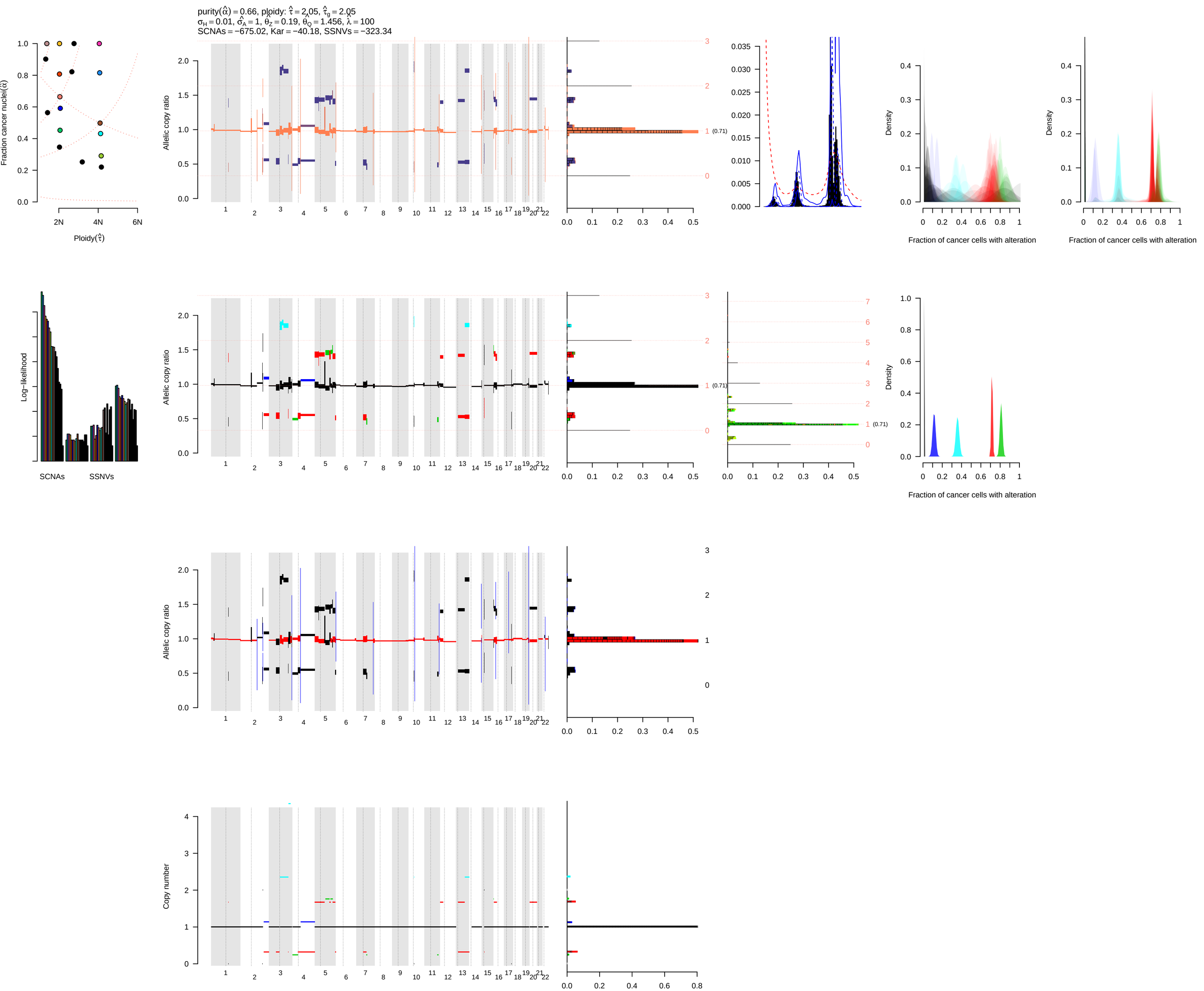

purity($\hat{\alpha}$) = 0.82, ploidy: $\hat{\tau}$ = 4.07, $\hat{\tau}_g$ = 4.11
$\sigma_H$ = 0.01, $\hat{\sigma}_A$ = 1, $\theta_Z$ = 0.03, $\theta_Q$ = 1.428, $\hat{\lambda}$ = 100
SCNAs = −543.89, Kar = −15.95, SSNVs = −317.13
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
Allelic copy ratio
Density
Fraction of cancer cells with alteration
Log−likelihood
SCNAs
SSNVs
Copy number
f_sc/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

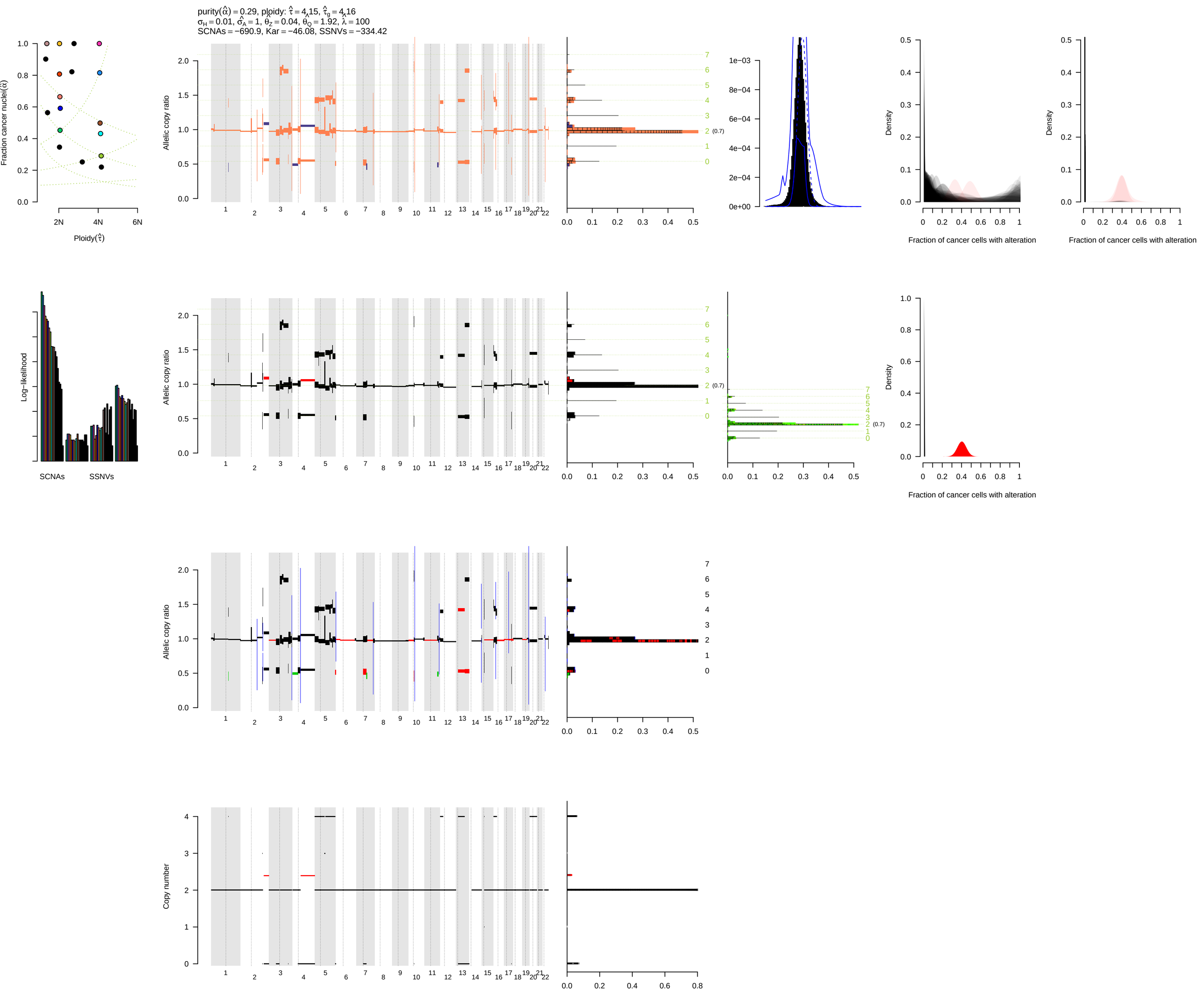

purity($\hat{\alpha}$) = 1, ploidy: $\hat{\tau}$ = 4.06, $\hat{\tau}_g$ = 4.1
$\sigma_H$ = 0.01, $\hat{\sigma}_A$ = 1, $\theta_Z$ = 0.05, $\theta_Q$ = 1.37, $\hat{\lambda}$ = 100
SCNAs = −584.91, Kar = −15.95, SSNVs = −312.66
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
Allelic copy ratio
(0.71)
Density
Fraction of cancer cells with alteration
Log−likelihood
SCNAs
SSNVs
Copy number
f_s
CCF
Fraction of alternate reads
SSNV multiplicity
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

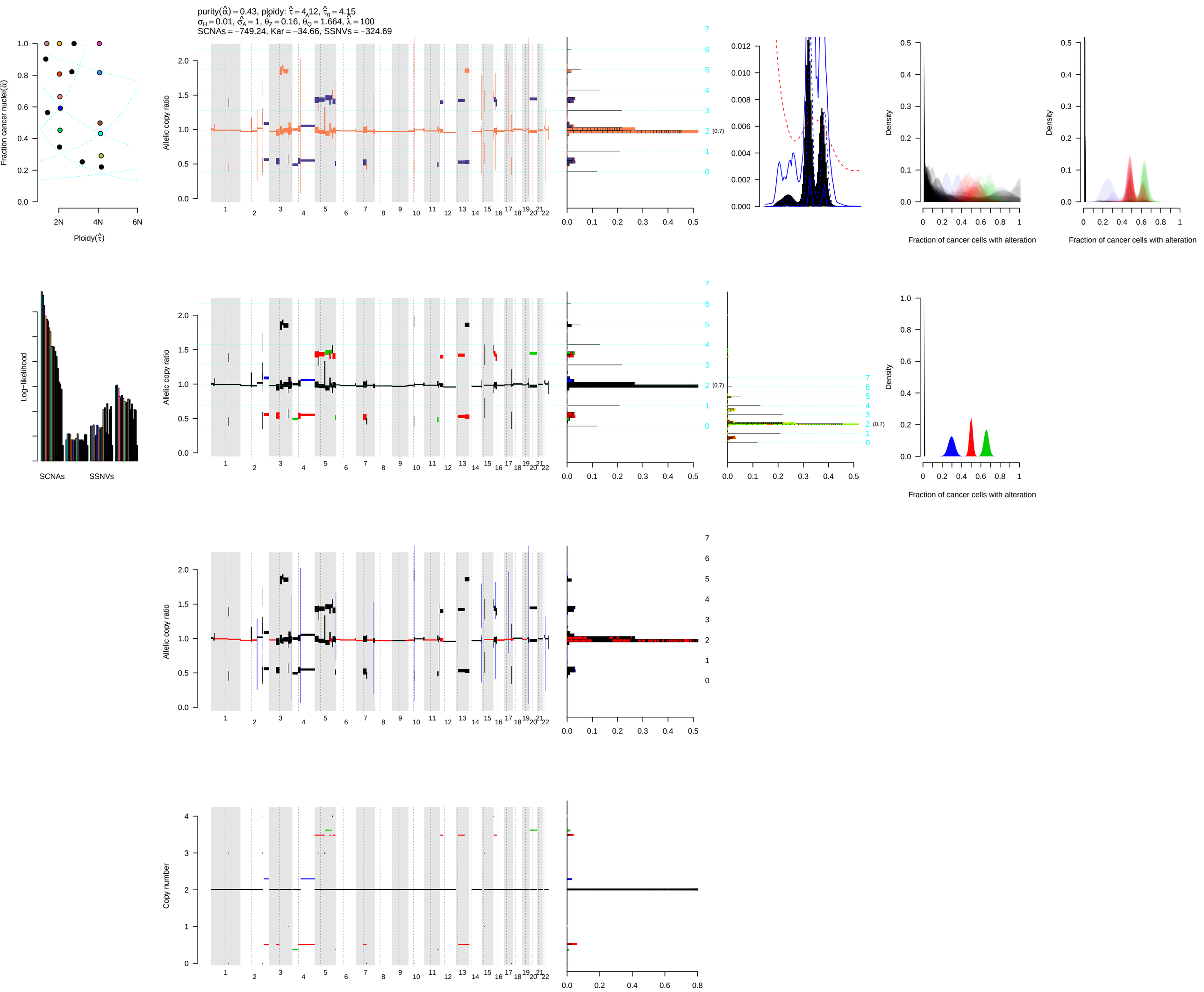

purity($\hat{\alpha}$) = 1, ploidy: $\hat{\tau}$ = 2.03, $\hat{\tau}_g$ = 2.06
$\sigma_H$ = 0.01, $\hat{\sigma}_A$ = 1, $\theta_Z$ = 0.15, $\theta_Q$ = 1.282, $\hat{\lambda}$ = 100
SCNAs = −627.48, Kar = −19.35, SSNVs = −368.95
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
Allelic copy 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

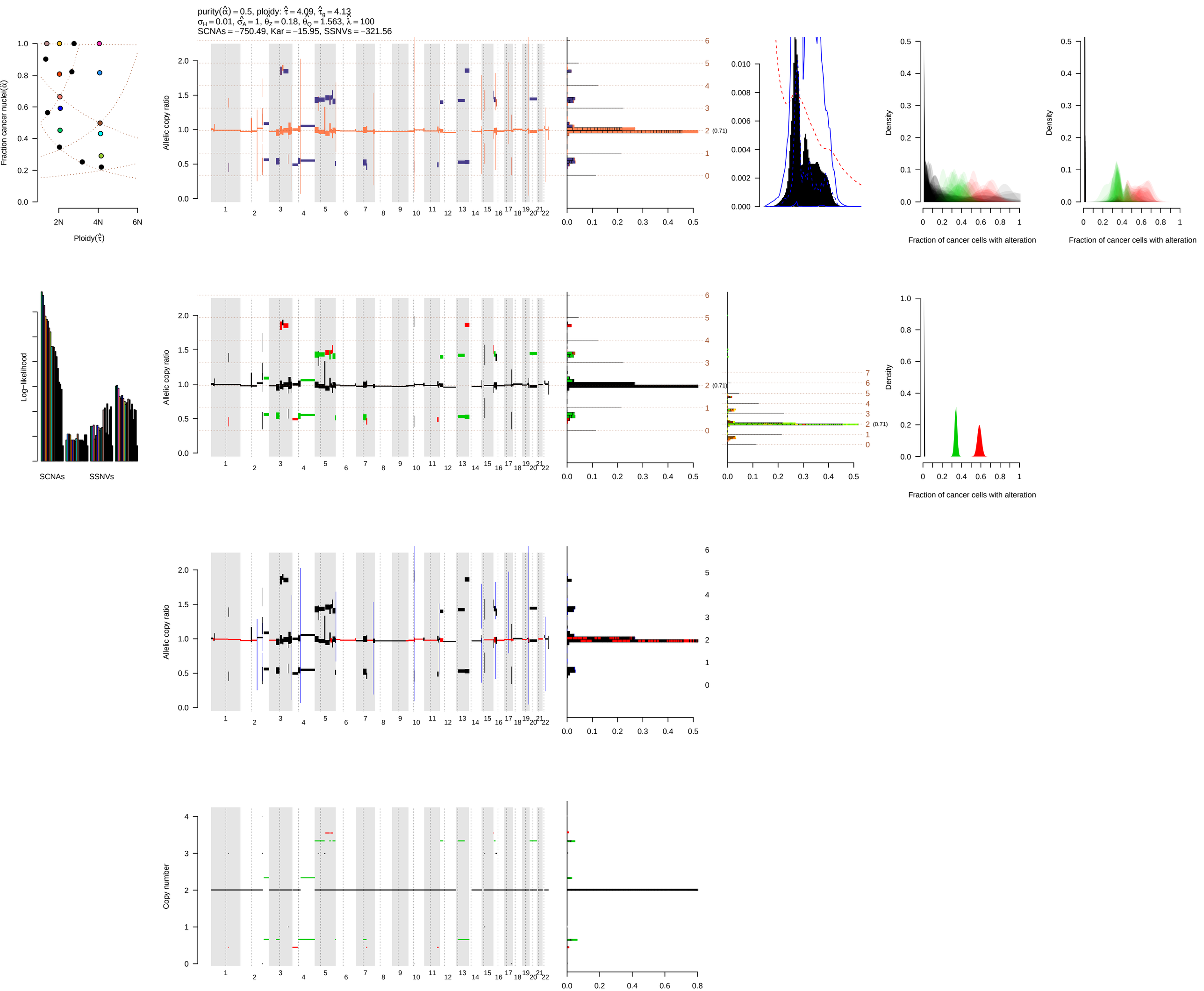

purity($\hat{\alpha}$) = 0.81, ploidy: $\hat{\tau}$ = 2.03, $\hat{\tau}_g$ = 2.05
$\sigma_H$ = 0.01, $\hat{\sigma}_A$ = 1, $\theta_Z$ = 0.15, $\theta_Q$ = 1.385, $\hat{\lambda}$ = 100
SCNAs = −639.75, Kar = −40.18, SSNVs = −354.41
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
Allelic copy ratio
Density
Fraction of cancer cells with alteration
Log−likelihood
SCNAs
SSNVs
Copy number
f_sc/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

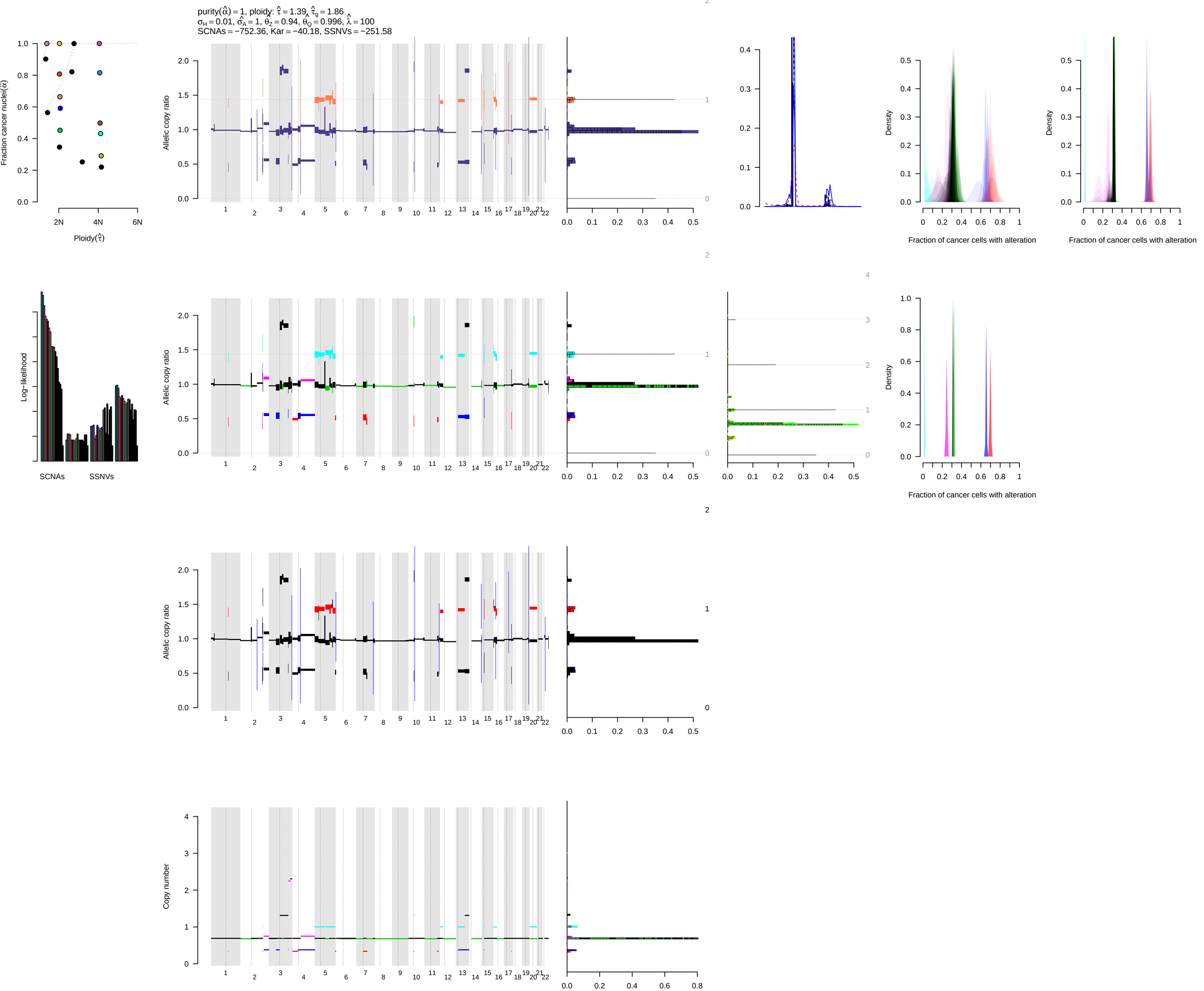

purity($\hat{\alpha}$) = 0.59, ploidy: $\hat{\tau}$ = 2.07, $\hat{\tau}_g$ = 2.09
$\sigma_H$ = 0.01, $\hat{\sigma}_A$ = 1, $\theta_Z$ = 0.18, $\theta_Q$ = 1.388, $\hat{\lambda}$ = 100
SCNAs = −647.55, Kar = −40.18, SSNVs = −313.23
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
Allelic copy 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

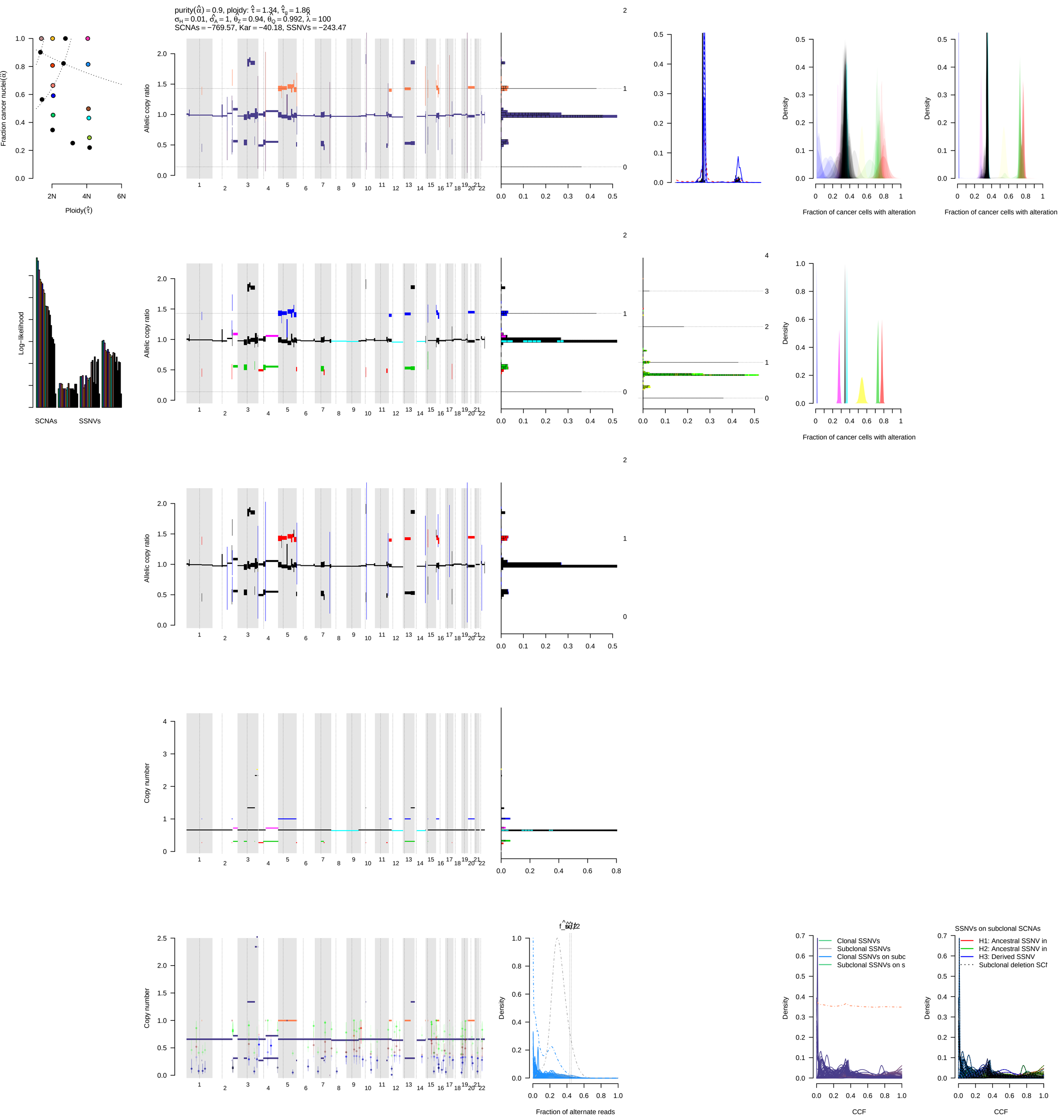

purity($\hat{\alpha}$) = 0.66, ploidy: $\hat{\tau}$ = 2.05, $\hat{\tau}_g$ = 2.05
$\sigma_H$ = 0.01, $\hat{\sigma}_A$ = 1, $\hat{\theta}_Z$ = 0.19, $\hat{\theta}_Q$ = 1.456, $\hat{\lambda}$ = 100
SCNAs = −675.02, Kar = −40.18, SSNVs = −323.34
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
Allelic copy ratio
Density
Fraction of cancer cells with alteration
Log−likelihood
SCNAs
SSNVs
Copy number
f_sc/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

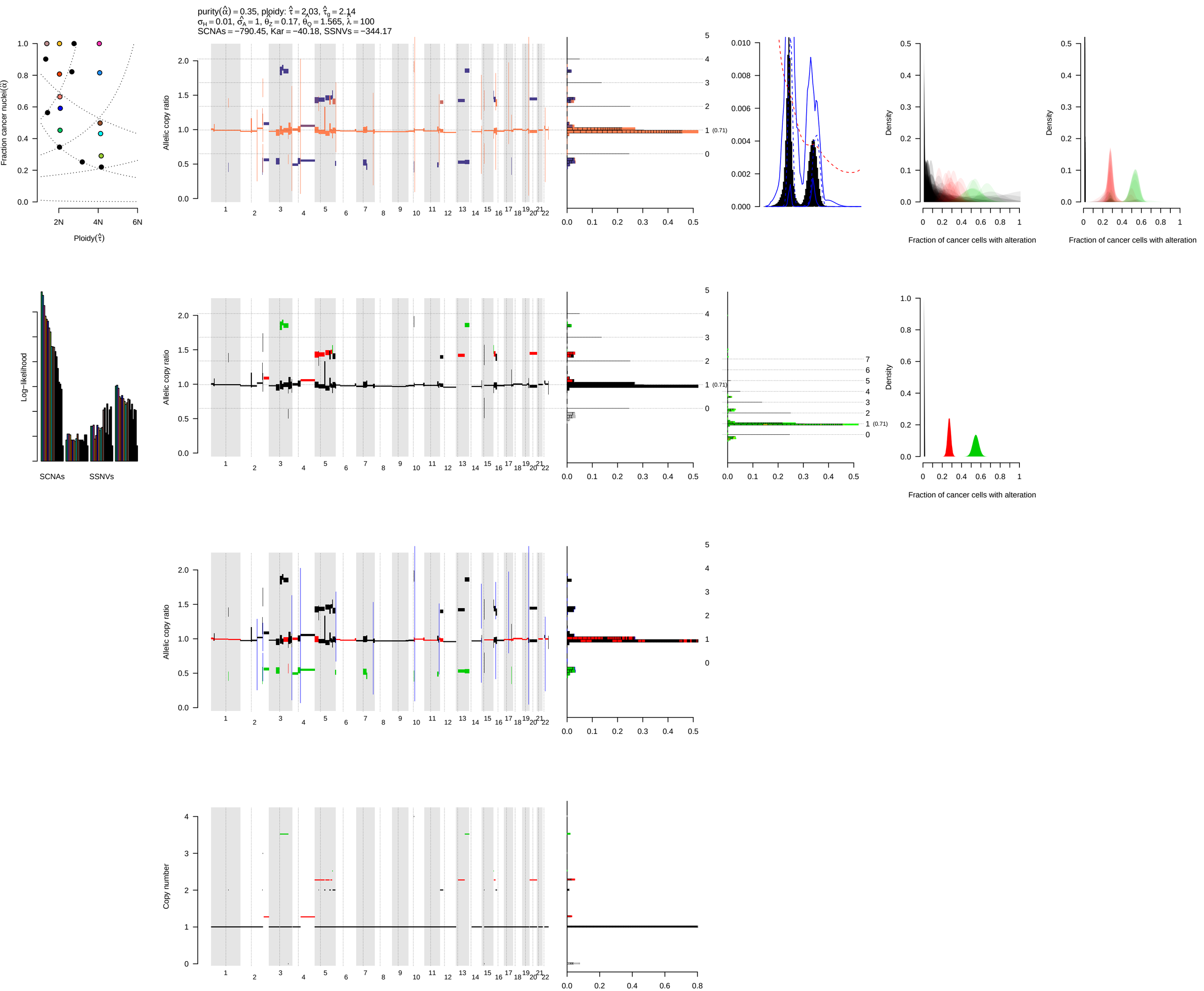

purity($\hat{\alpha}$) = 0.29, ploidy: $\hat{\tau}$ = 4.15, $\hat{\tau}_g$ = 4.16
$\sigma_H$ = 0.01, $\hat{\sigma}_A$ = 1, $\theta_Z$ = 0.04, $\theta_Q$ = 1.92, $\hat{\lambda}$ = 100
SCNAs = −690.9, Kar = −46.08, SSNVs = −334.42
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
Allelic copy 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

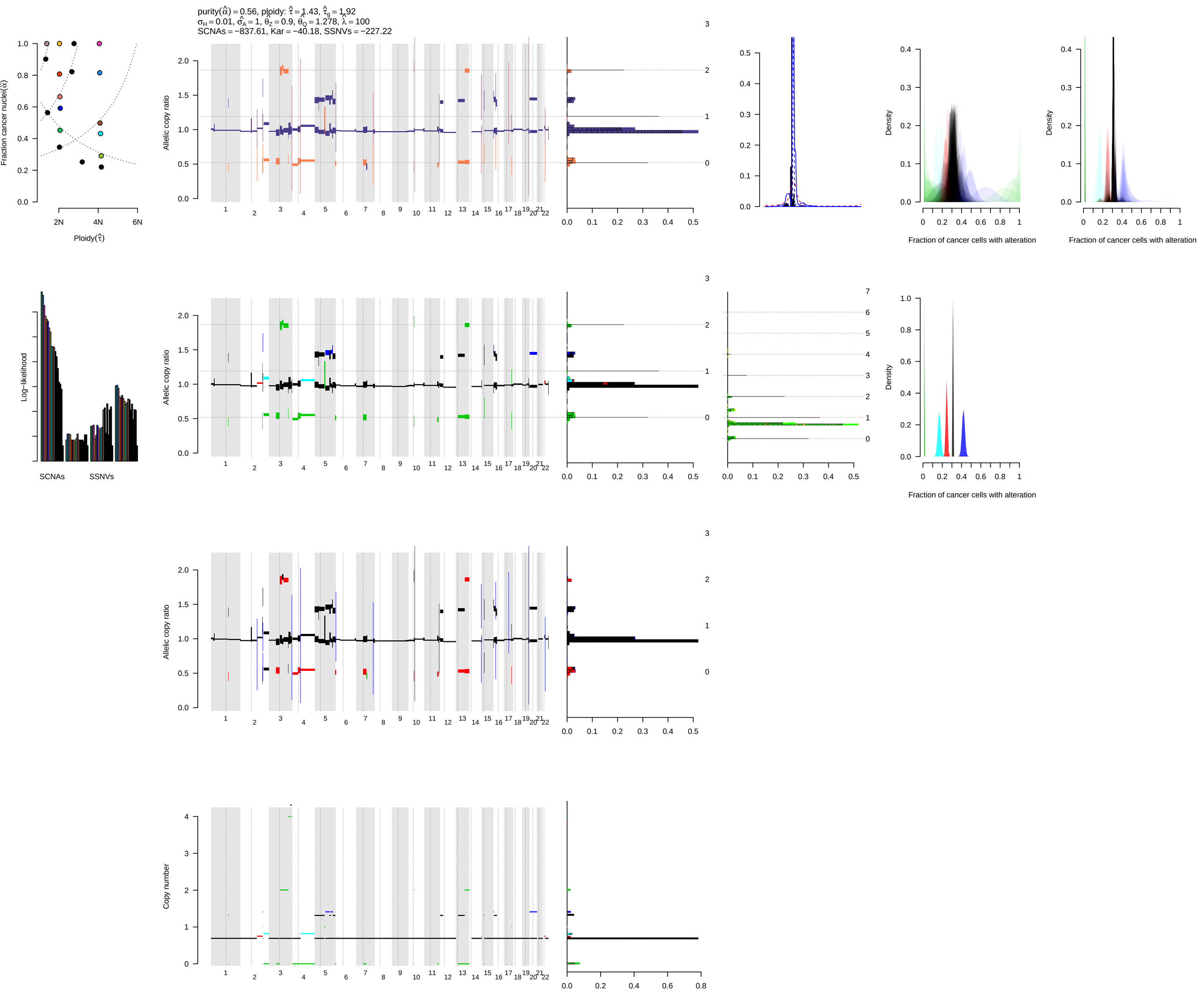

purity($\hat{\alpha}$) = 0.43, ploidy: $\hat{\tau}$ = 4.12, $\hat{\tau}_g$ = 4.15
$\sigma_H$ = 0.01, $\hat{\sigma}_A$ = 1, $\theta_Z$ = 0.16, $\theta_Q$ = 1.664, $\hat{\lambda}$ = 100
SCNAs = −749.24, Kar = −34.66, SSNVs = −324.69
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
Allelic copy ratio
Density
Fraction of cancer cells with alteration
Log−likelihood
SCNAs
SSNVs
Copy number
f_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

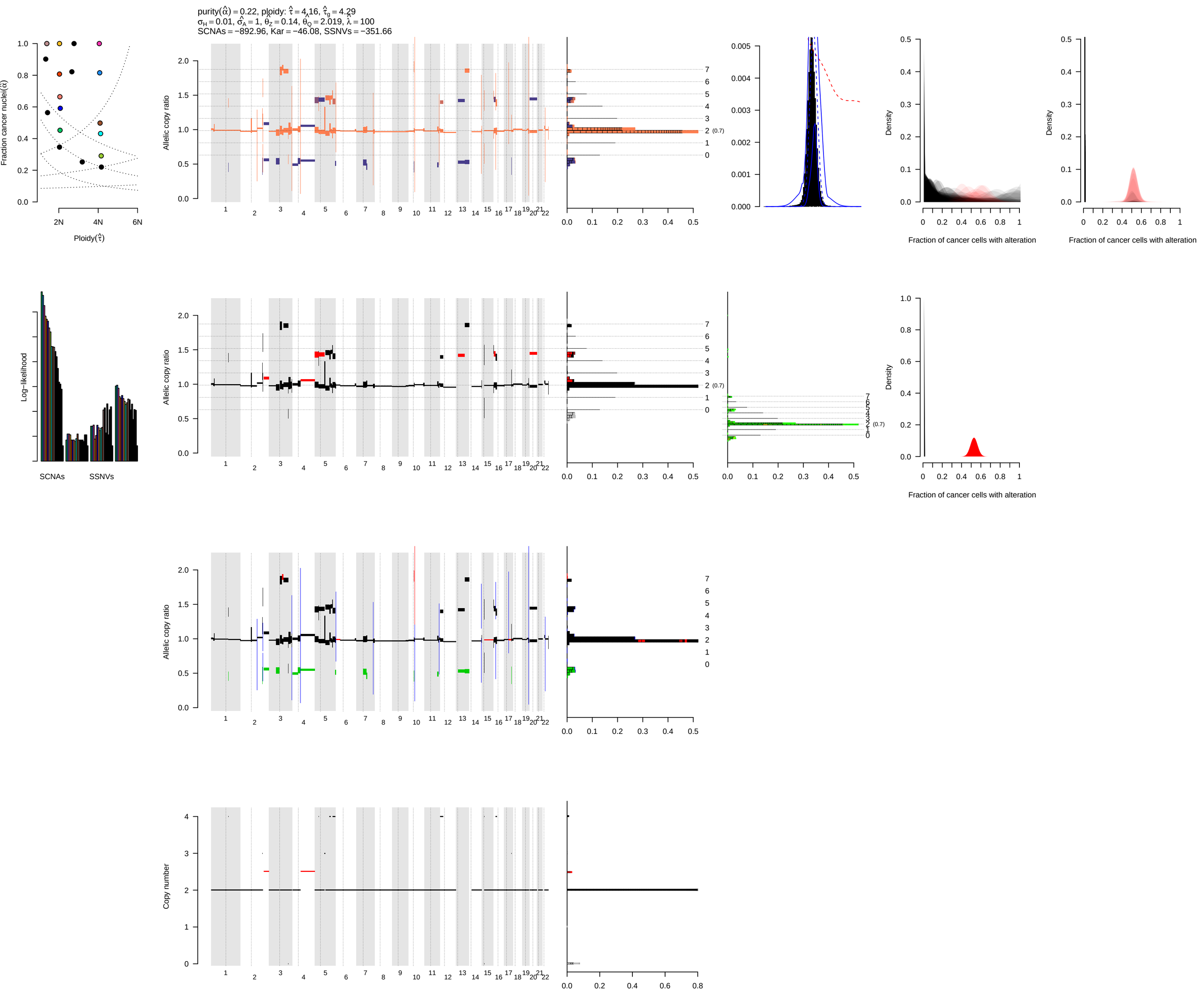

purity($\hat{\alpha}$) = 0.5, ploidy: $\hat{\tau}$ = 4.09, $\hat{\tau}_g$ = 4.13
$\sigma_H$ = 0.01, $\hat{\sigma}_A$ = 1, $\theta_Z$ = 0.18, $\theta_Q$ = 1.563, $\hat{\lambda}$ = 100
SCNAs = −750.49, Kar = −15.95, SSNVs = −321.56
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
Allelic copy ratio
Density
Fraction of cancer cells with alteration
Log−likelihood
SCNAs
SSNVs
Copy number
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

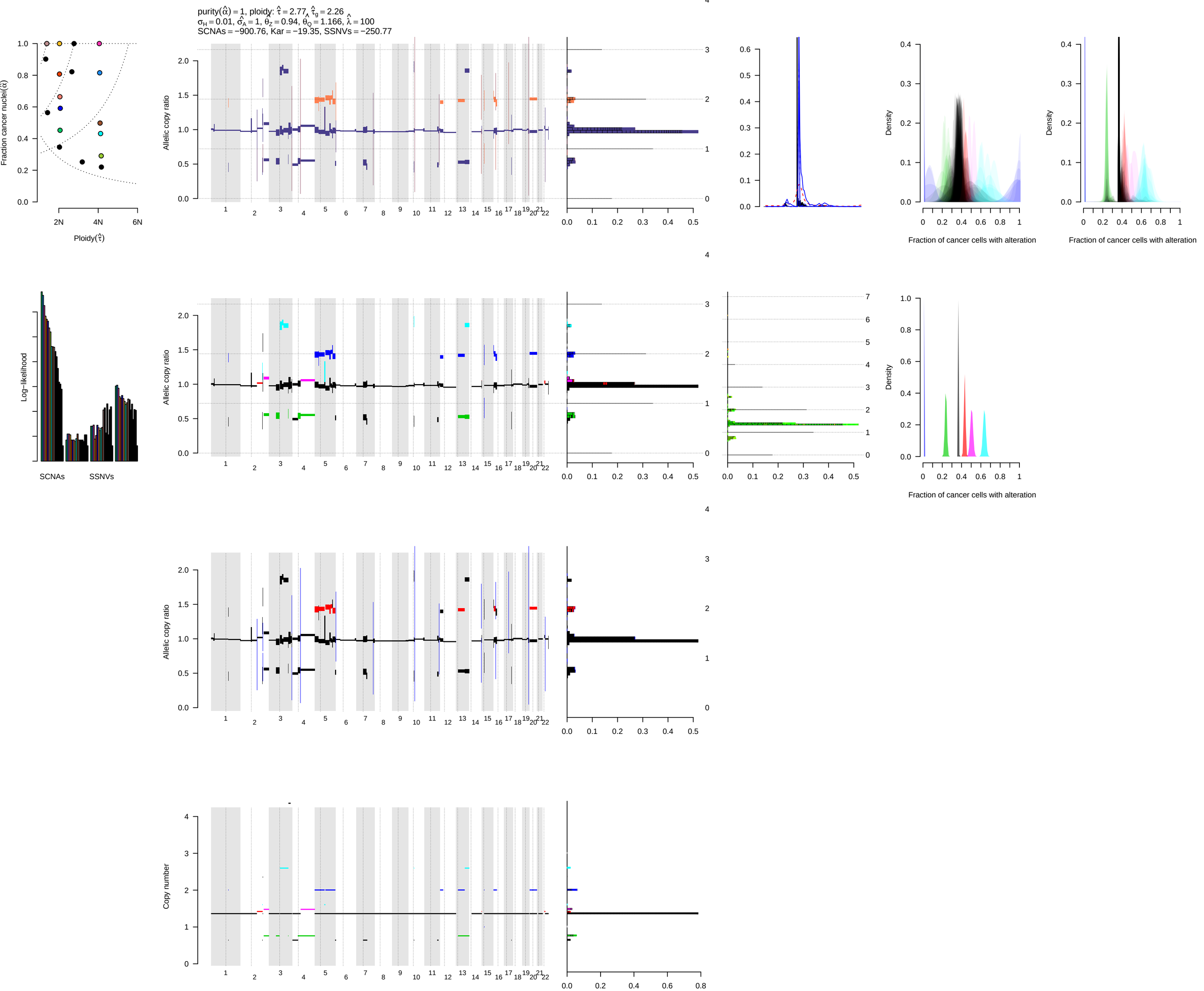

purity($\hat{\alpha}$) = 1, ploidy: $\hat{\tau}$ = 1.39, $\hat{\tau}_g$ = 1.86
$\sigma_H$ = 0.01, $\hat{\sigma}_A$ = 1, $\theta_Z$ = 0.94, $\theta_Q$ = 0.996, $\hat{\lambda}$ = 100
SCNAs = −752.36, Kar = −40.18, SSNVs = −251.58
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
Allelic copy ratio
Density
Fraction of cancer cells with alteration
Log−likelihood
SCNAs
SSNVs
Copy number
f_s$\hat{\alpha}$/2
Fraction of alternate reads
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

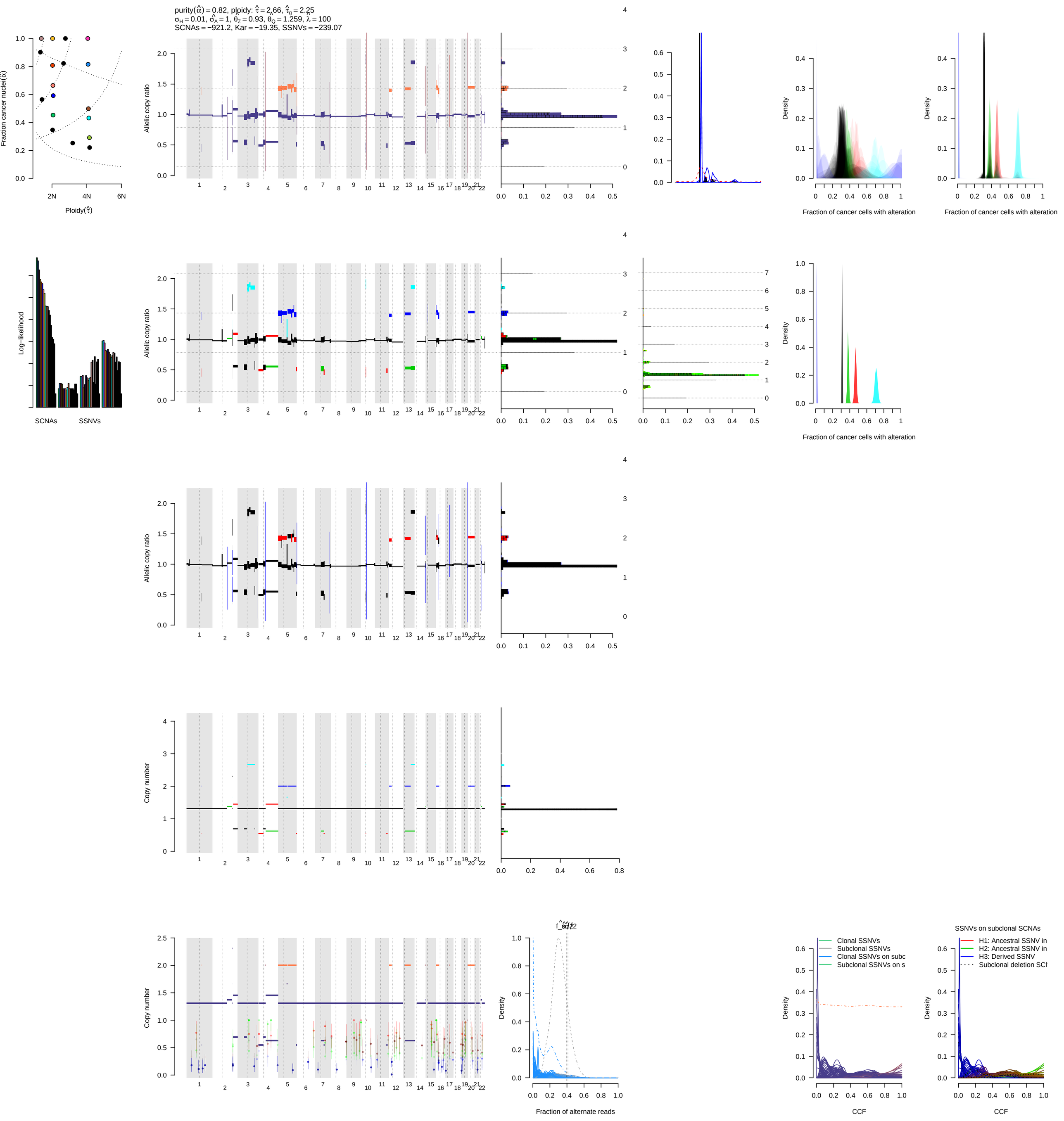

purity($\hat{\alpha}$) = 0.9, ploidy: $\hat{\tau}$ = 1.34, $\hat{\tau}_g$ = 1.86
$\sigma_H$ = 0.01, $\hat{\sigma}_A$ = 1, $\theta_Z$ = 0.94, $\theta_Q$ = 0.992, $\hat{\lambda}$ = 100
SCNAs = −769.57, Kar = −40.18, SSNVs = −243.47
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
2N
4N
6N
Allelic copy ratio
Density
Fraction of cancer cells with alteration
Log−likelihood
SCNAs
SSNVs
Copy number
f_sol
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

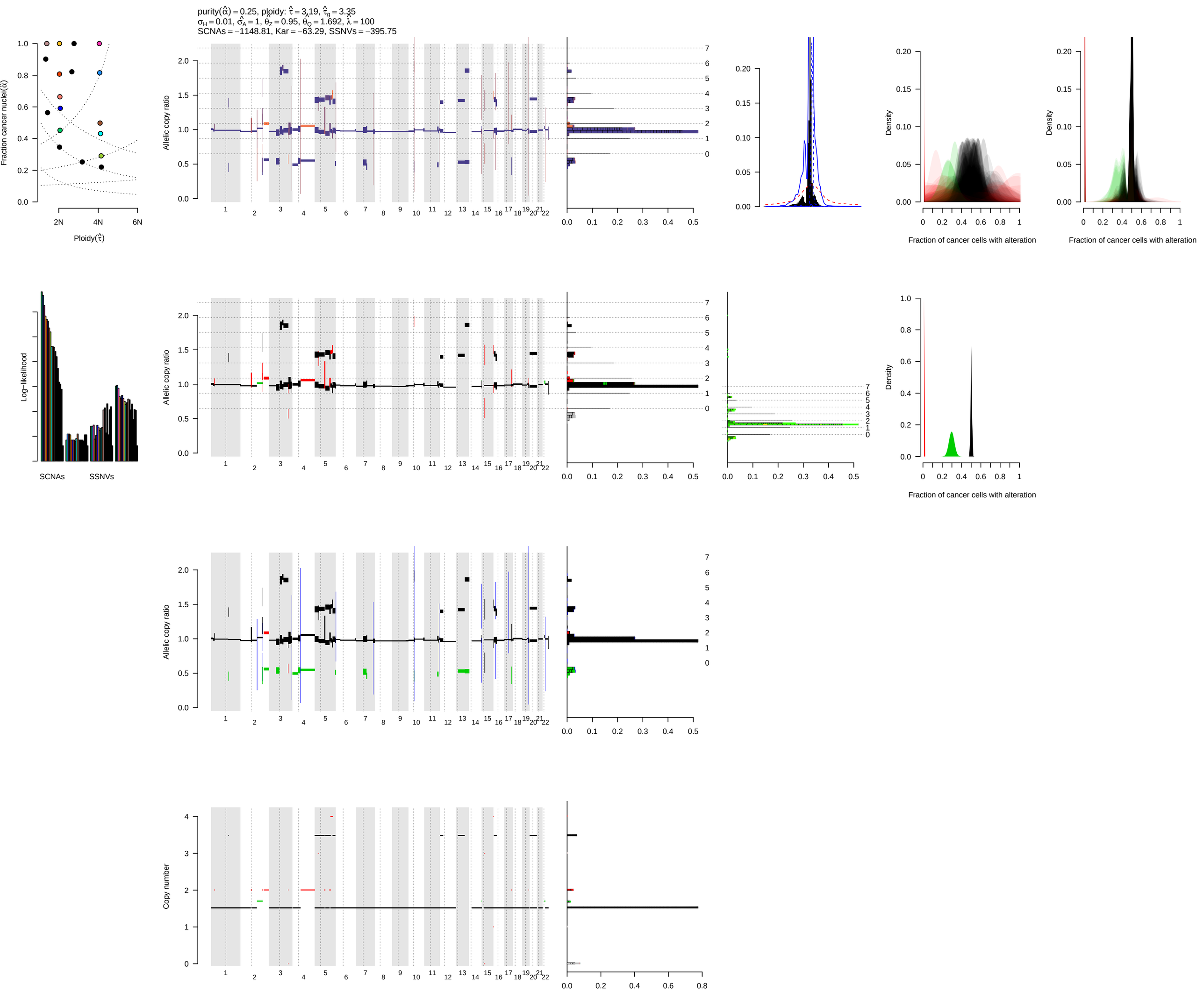

purity($\hat{\alpha}$) = 0.35, ploidy: $\hat{\tau}$ = 2.03, $\hat{\tau}_g$ = 2.14
$\sigma_H$ = 0.01, $\hat{\sigma}_A$ = 1, $\theta_Z$ = 0.17, $\theta_Q$ = 1.565, $\hat{\lambda}$ = 100
SCNAs = −790.45, Kar = −40.18, SSNVs = −344.17
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
Allelic copy 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: $\hat{\tau}$ = 1.43, $\hat{\tau}_g$ = 1.92
$\sigma_H$ = 0.01, $\hat{\sigma}_A$ = 1, $\theta_Z$ = 0.9, $\theta_Q$ = 1.278, $\hat{\lambda}$ = 100
SCNAs = −837.61, Kar = −40.18, SSNVs = −227.22
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_6472
Fraction of alternate reads
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($\hat{\alpha}$) = 0.22, ploidy: $\hat{\tau}$ = 4.16, $\hat{\tau}_g$ = 4.29
$\sigma_H$ = 0.01, $\hat{\sigma}_A$ = 1, $\theta_Z$ = 0.14, $\theta_Q$ = 2.019, $\hat{\lambda}$ = 100
SCNAs = −892.96, Kar = −46.08, SSNVs = −351.66
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: $\hat{\tau}$ = 2.77, $\hat{\tau}_g$ = 2.26
$\sigma_H$ = 0.01, $\hat{\sigma}_A$ = 1, $\theta_Z$ = 0.94, $\theta_Q$ = 1.166, $\hat{\lambda}$ = 100
SCNAs = −900.76, Kar = −19.35, SSNVs = −250.77
Fraction cancer nuclei($\hat{\alpha}$)
Ploidy($\hat{\tau}$)
Allelic copy ratio
Density
Fraction of cancer cells with alteration
Log−likelihood
SCNAs
SSNVs
Copy number
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


purity($\hat{\alpha}$) = 0.82, ploidy: $\hat{\tau}$ = 2.66, $\hat{\tau}_g$ = 2.25
$\sigma_H$ = 0.01, $\hat{\sigma}_A$ = 1, $\theta_Z$ = 0.93, $\theta_Q$ = 1.259, $\hat{\lambda}$ = 100
SCNAs = −921.2, Kar = −19.35, SSNVs = −239.07
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($\hat{\alpha}$) = 0.25, ploidy: $\hat{\tau}$ = 3.19, $\hat{\tau}_g$ = 3.35
$\sigma_H$ = 0.01, $\hat{\sigma}_A$ = 1, $\theta_Z$ = 0.95, $\theta_Q$ = 1.692, $\hat{\lambda}$ = 100
SCNAs = −1148.81, Kar = −63.29, SSNVs = −395.75
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