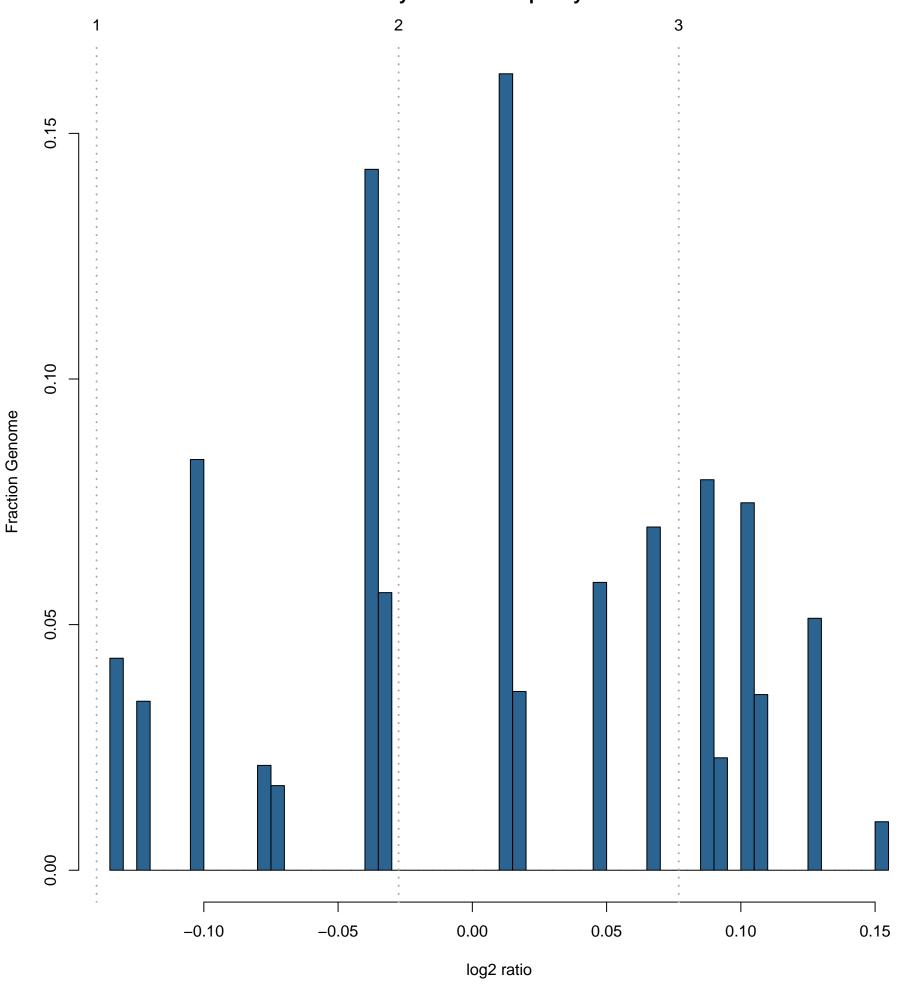
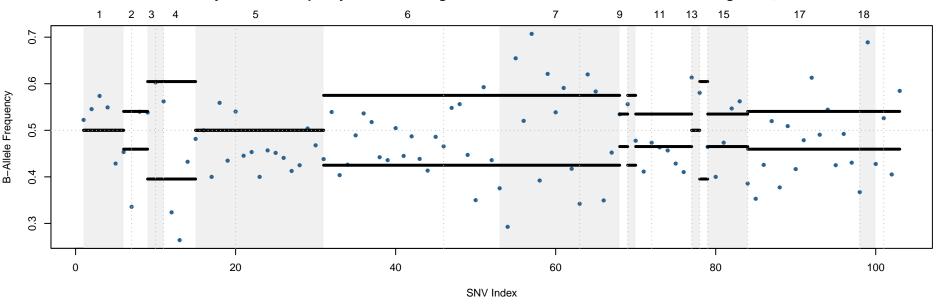
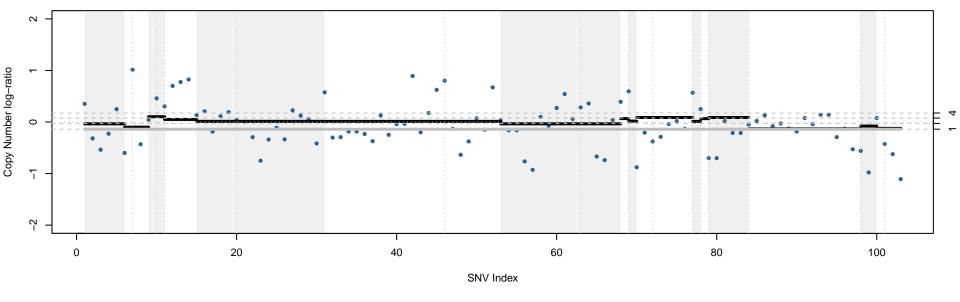
Purity: 0.15 Tumor ploidy: 2.256

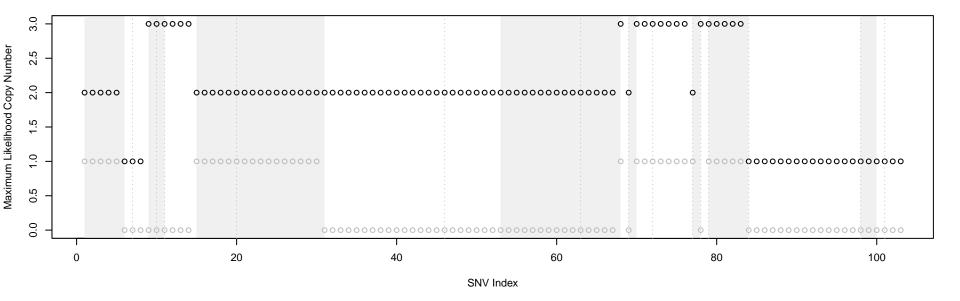


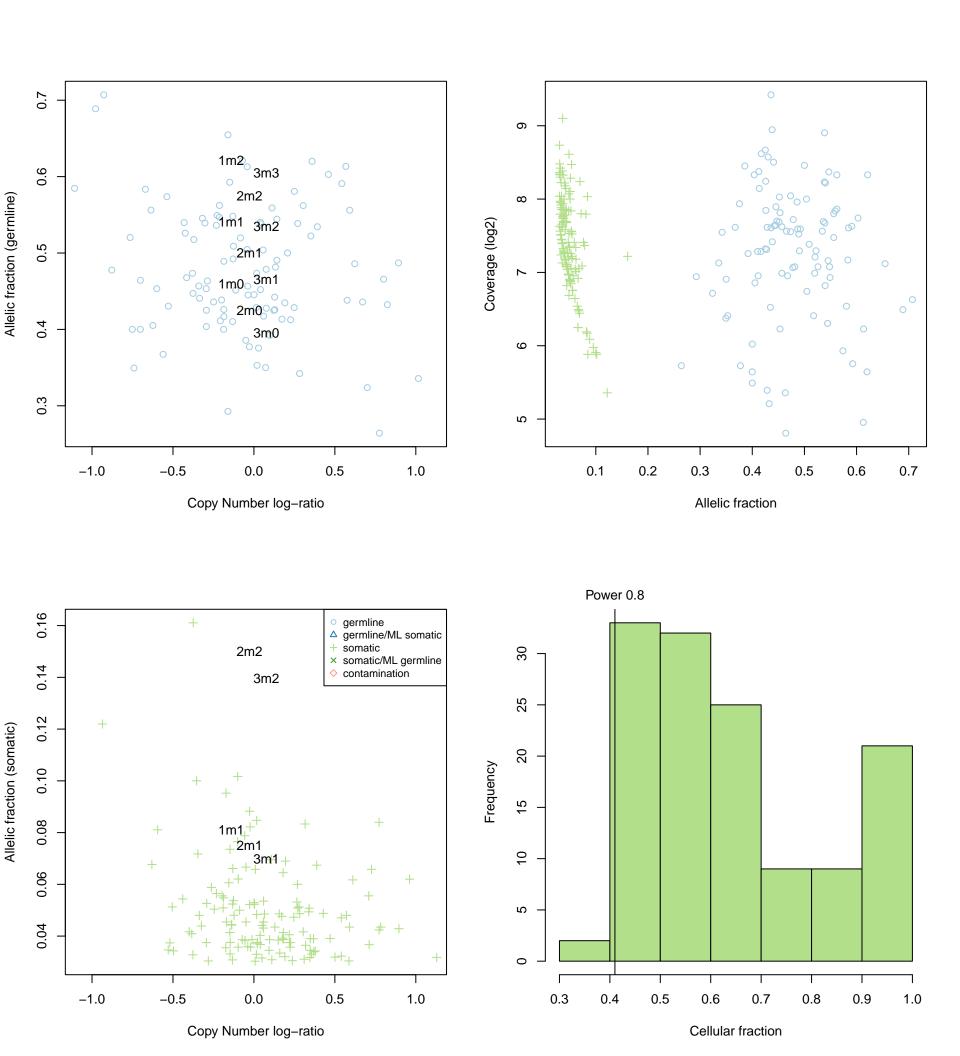
Purity: 0.15 Tumor ploidy: 2.256 SNV log-likelihood: 50.46 GoF: 95.6% Mean coverage: 187;674



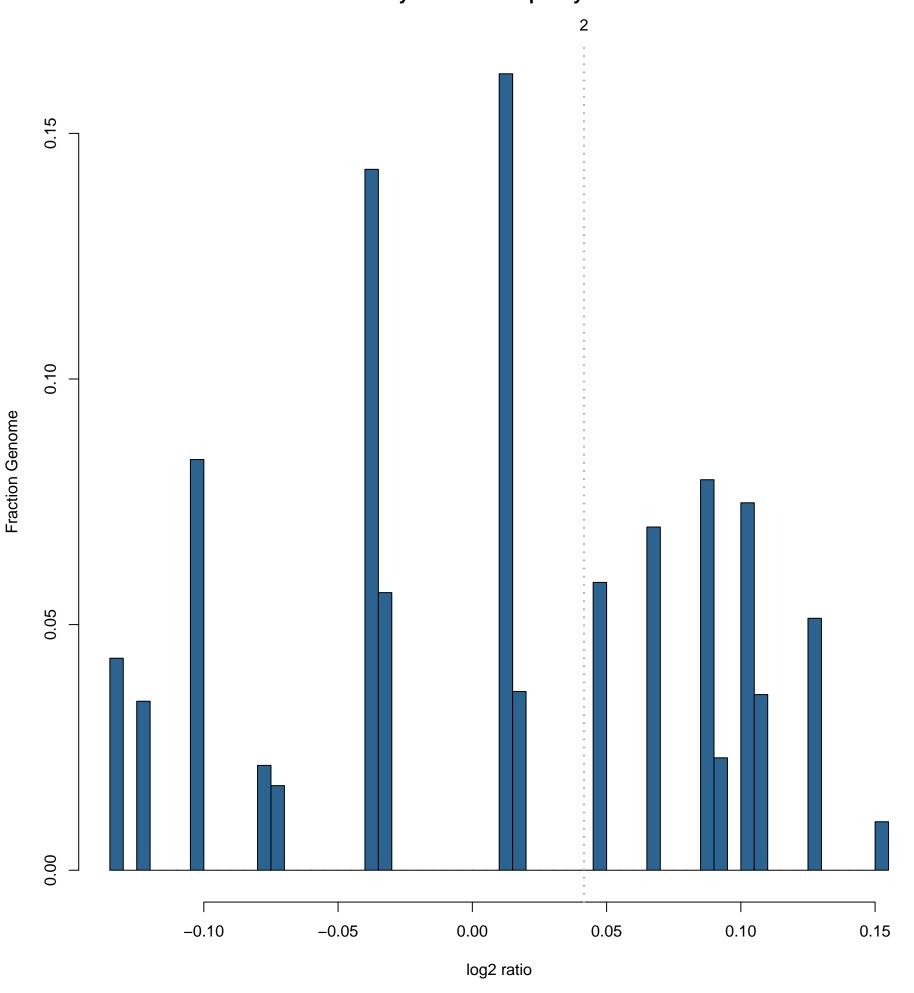
SCNA-fit log-likelihood: -23665.75



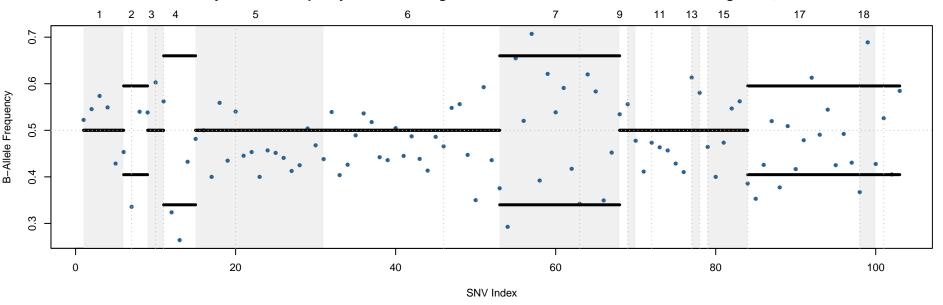




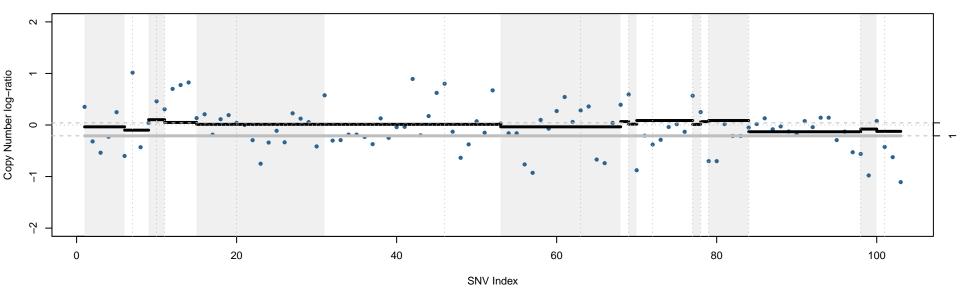
Purity: 0.32 Tumor ploidy: 1.822

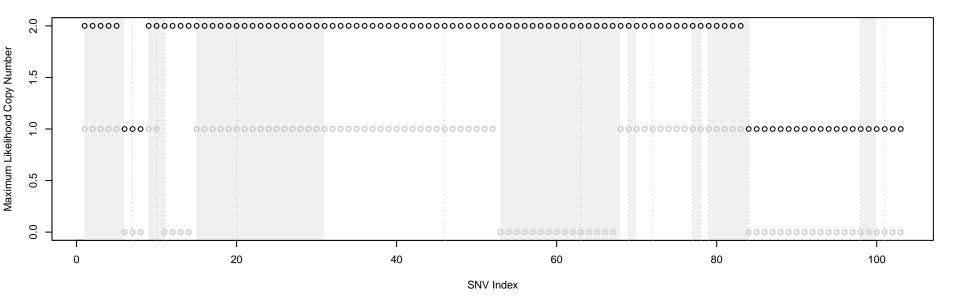


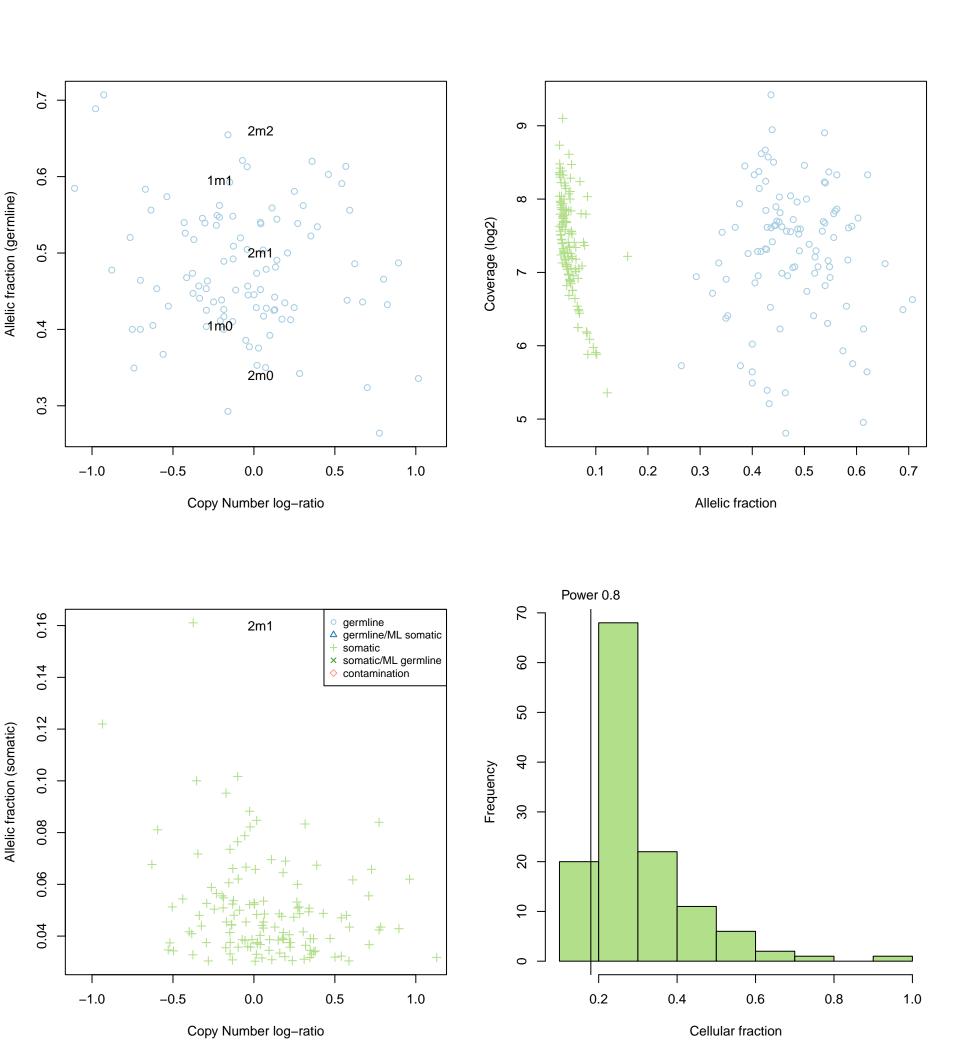
Purity: 0.32 Tumor ploidy: 1.822 SNV log-likelihood: 72.78 GoF: 76.5% Mean coverage: 187;674



SCNA-fit log-likelihood: -23728.57







Purity: 0.19 Tumor ploidy: 5.256 6 5 Fraction Genome 0.05 0.00 -0.10 -0.05 0.00 0.05 0.10 0.15 log2 ratio

Purity: 0.19 Tumor ploidy: 5.256 SNV log-likelihood: -116.26 GoF: 96.7% Mean coverage: 187;674

B-Allele Frequency

0.4

0.3

0

20

SCNA-fit log-likelihood: -23665.36

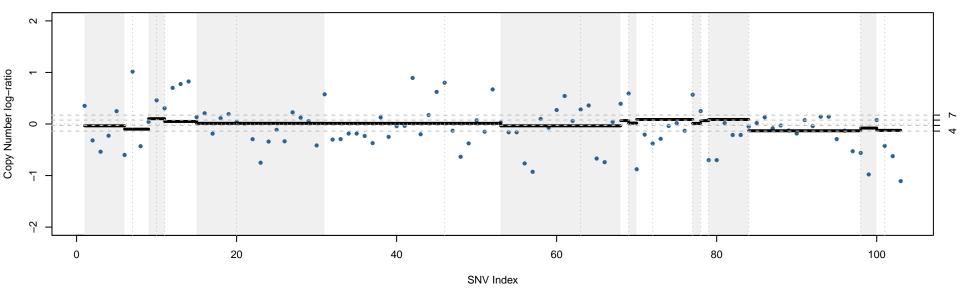
SNV Index

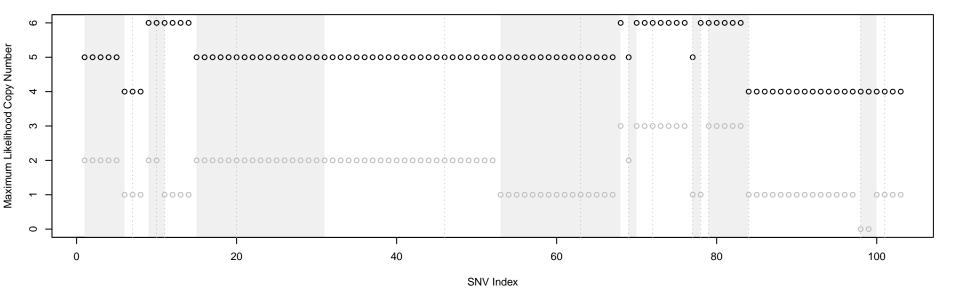
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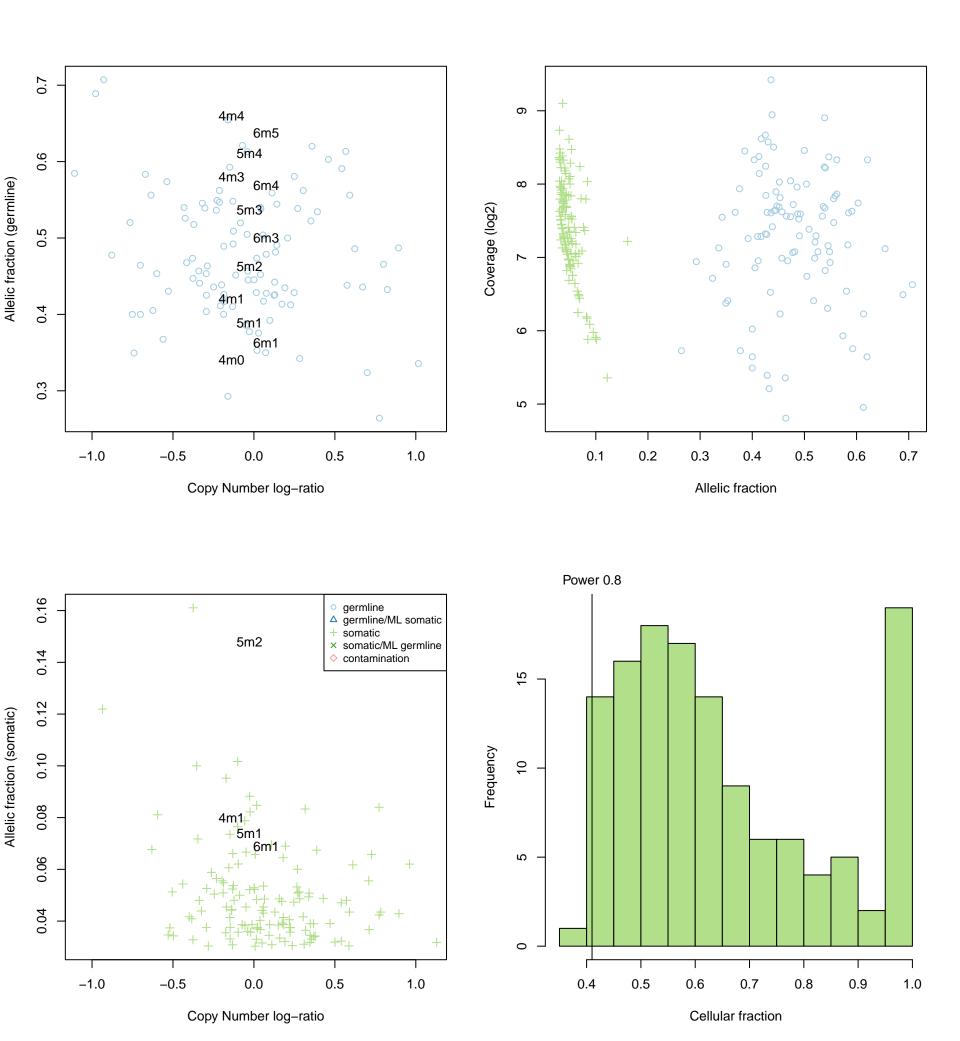
80

100

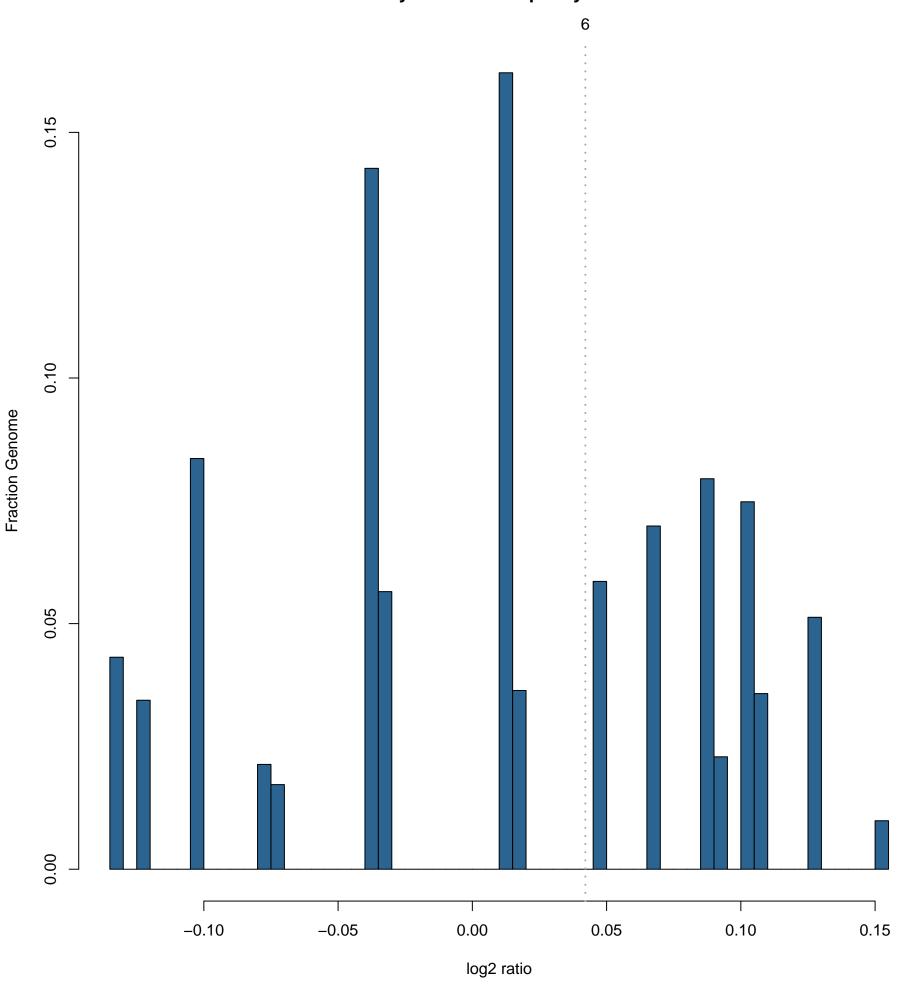
40

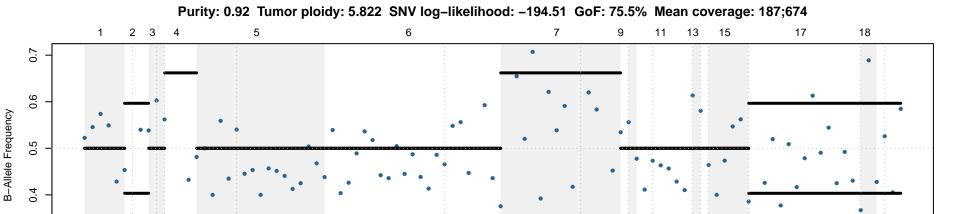






Purity: 0.92 Tumor ploidy: 5.822

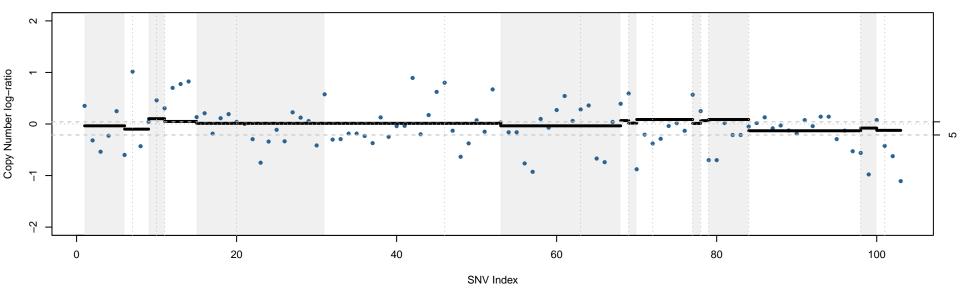


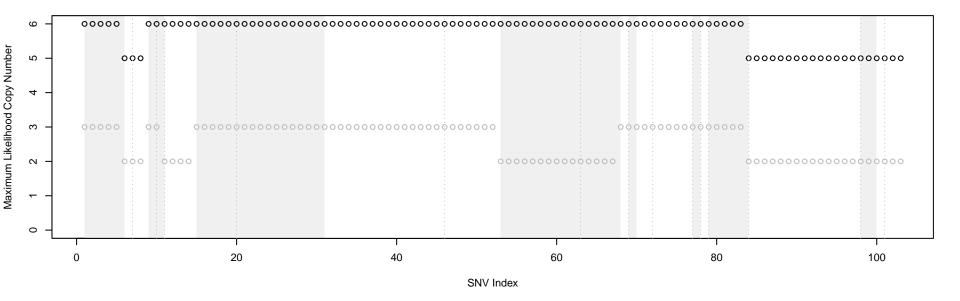


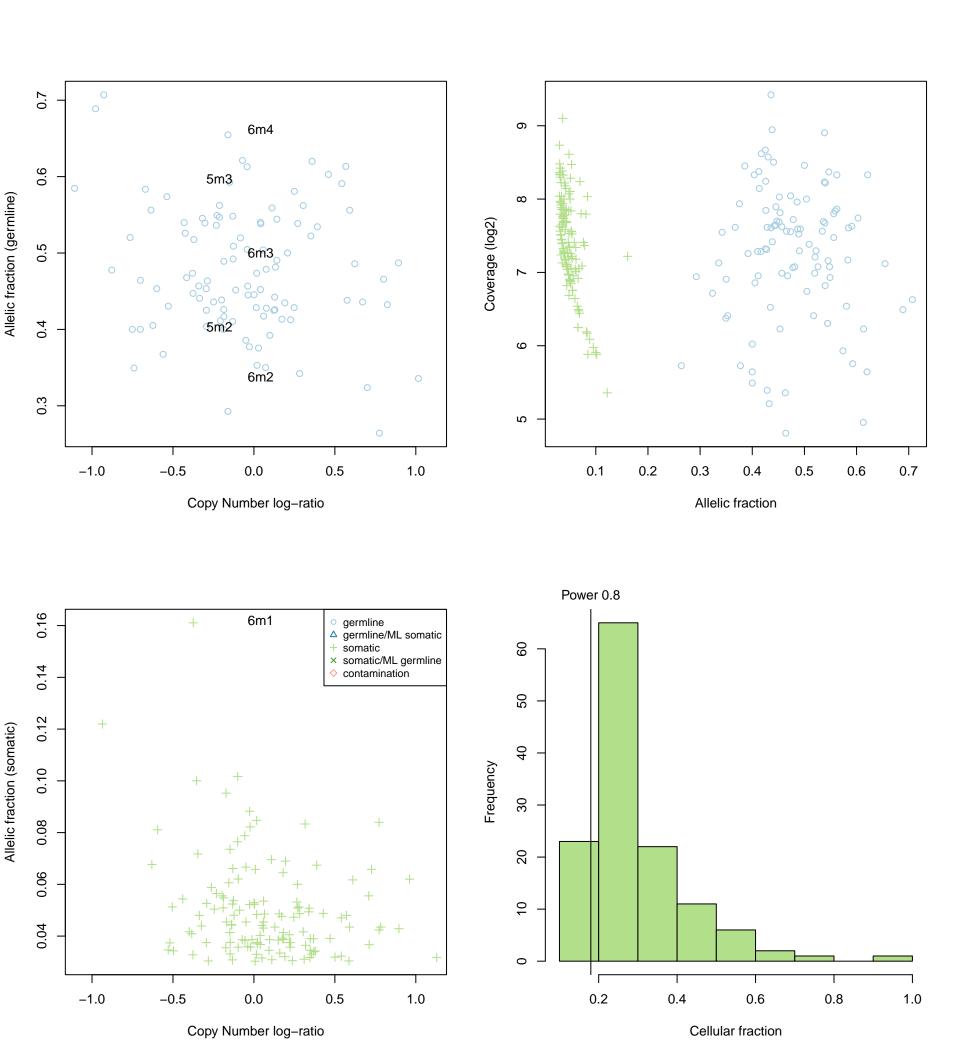
0.3

SCNA-fit log-likelihood: -23730.63

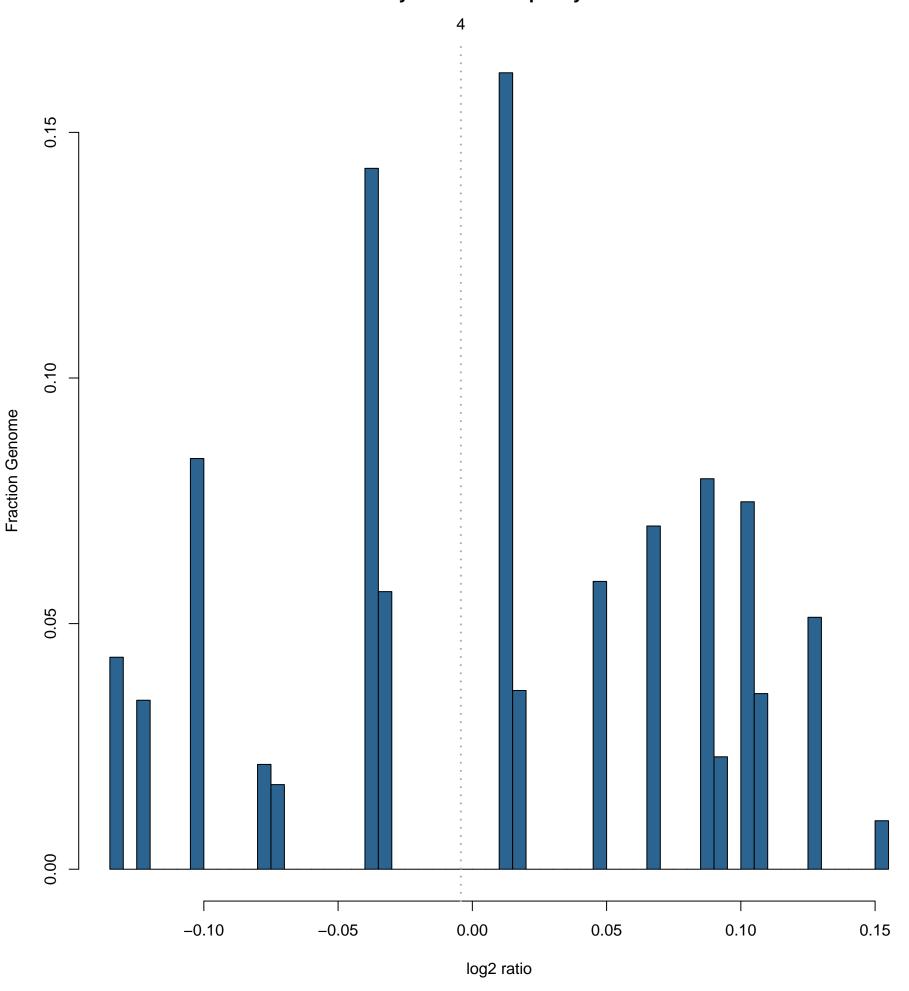
SNV Index



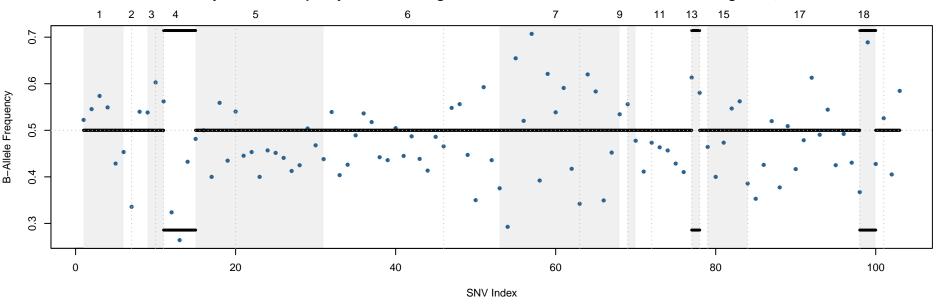




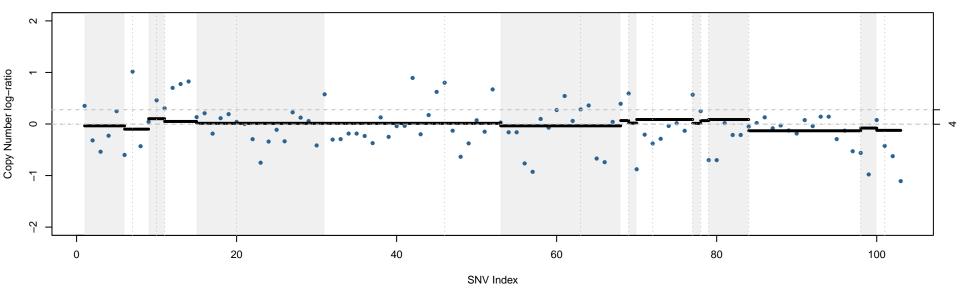
Purity: 0.75 Tumor ploidy: 4.014

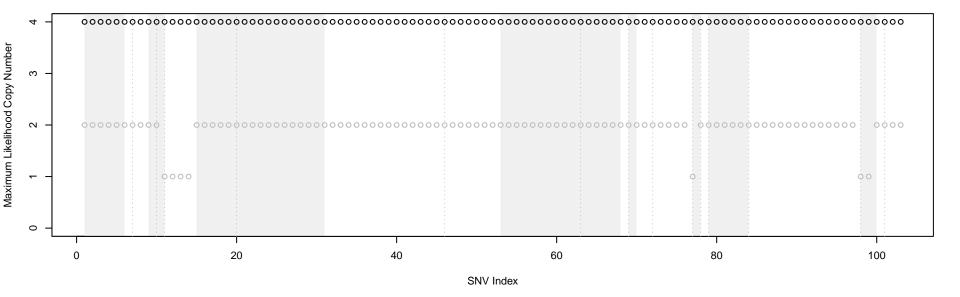


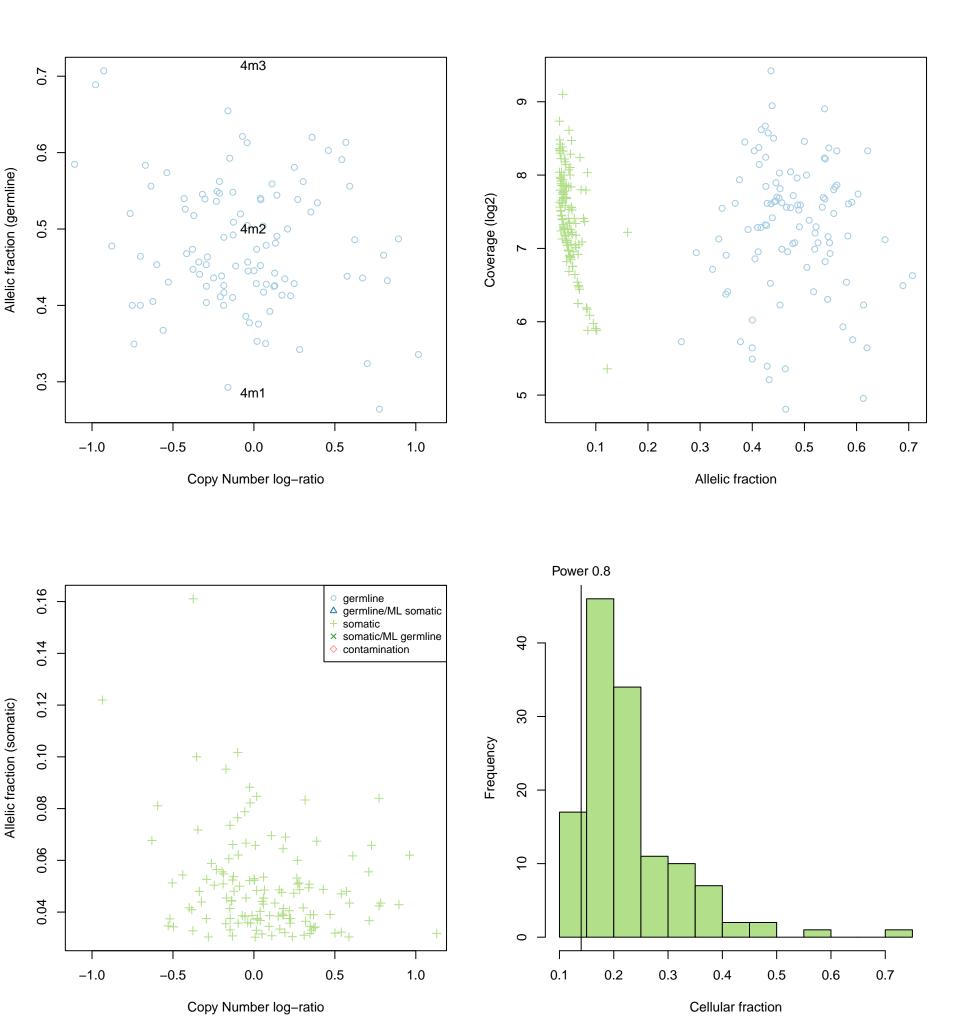
Purity: 0.75 Tumor ploidy: 4.014 SNV log-likelihood: -258.34 GoF: 56% Mean coverage: 187;674



SCNA-fit log-likelihood: -23759.9

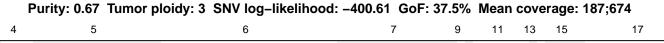


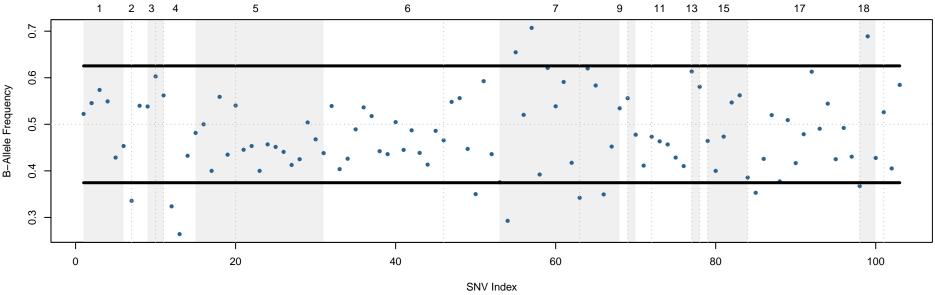




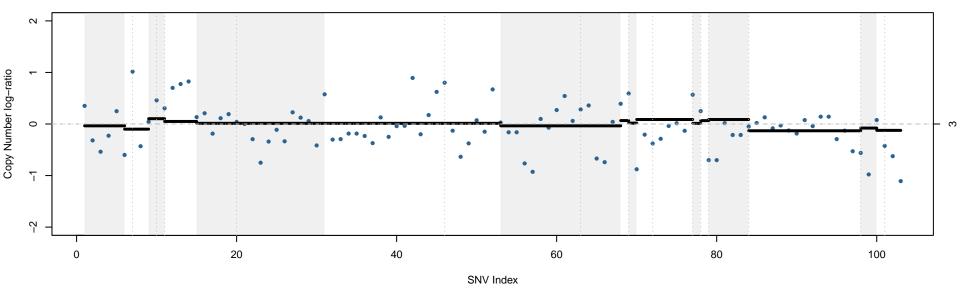
Purity: 0.67 Tumor ploidy: 3 3 Fraction Genome 0.05 0.00 -0.10 -0.05 0.00 0.05 0.10 0.15

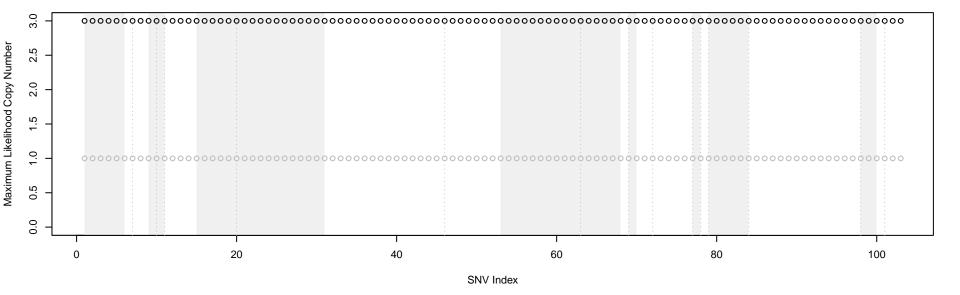
log2 ratio

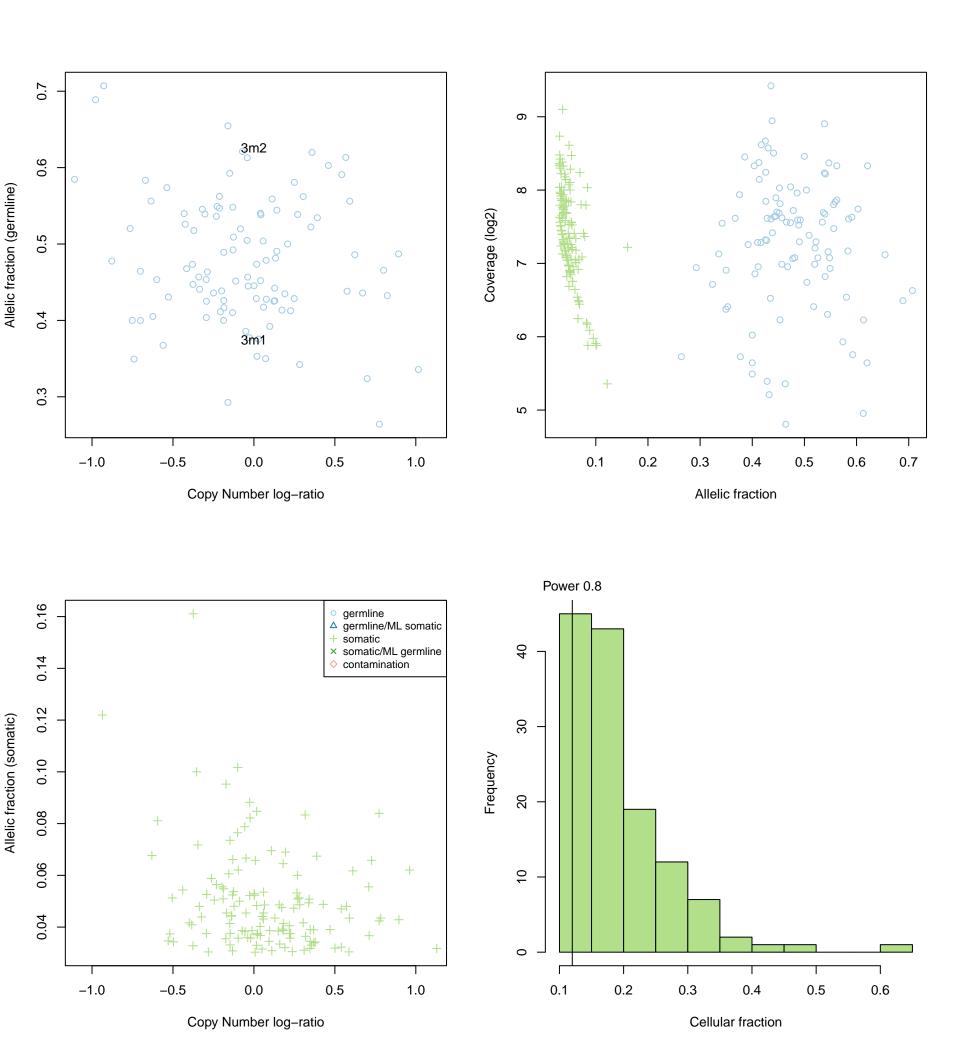




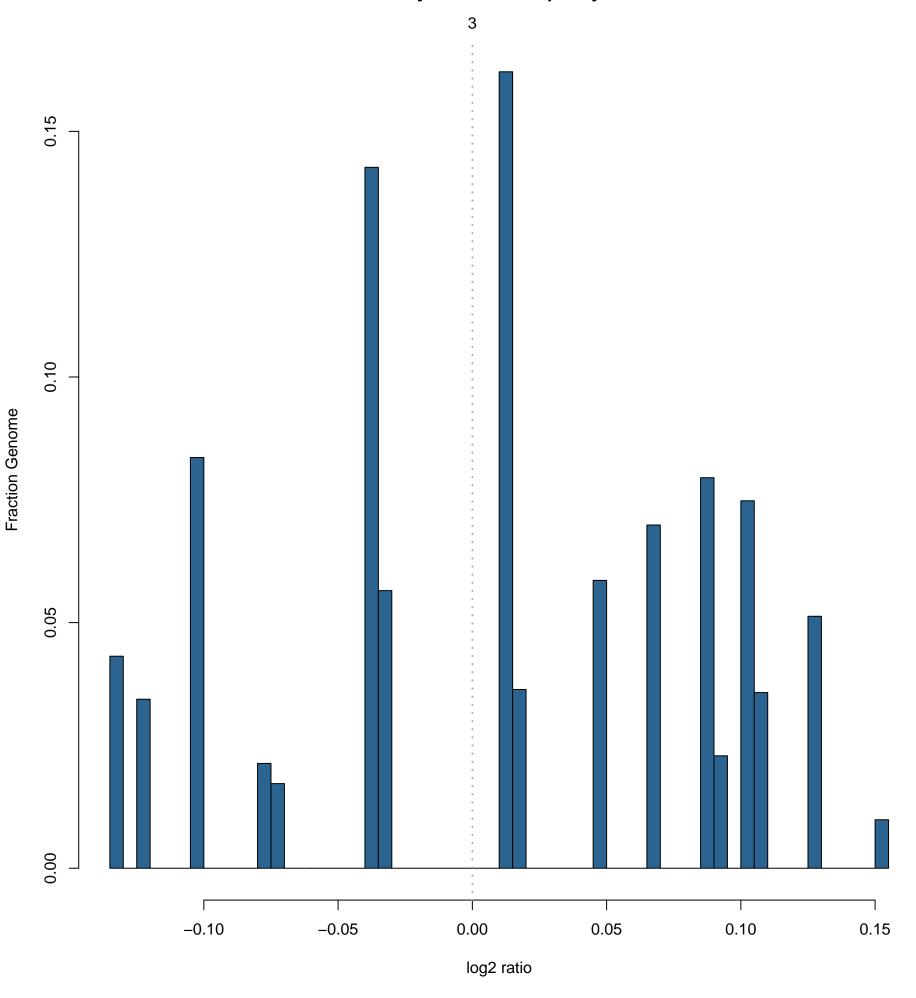
SCNA-fit log-likelihood: -23760.34

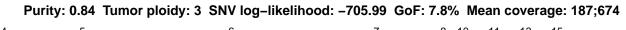


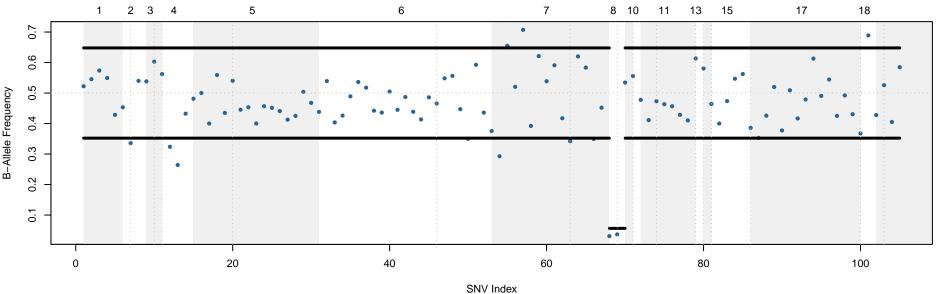




Purity: 0.84 Tumor ploidy: 3







SCNA-fit log-likelihood: -23760.29

