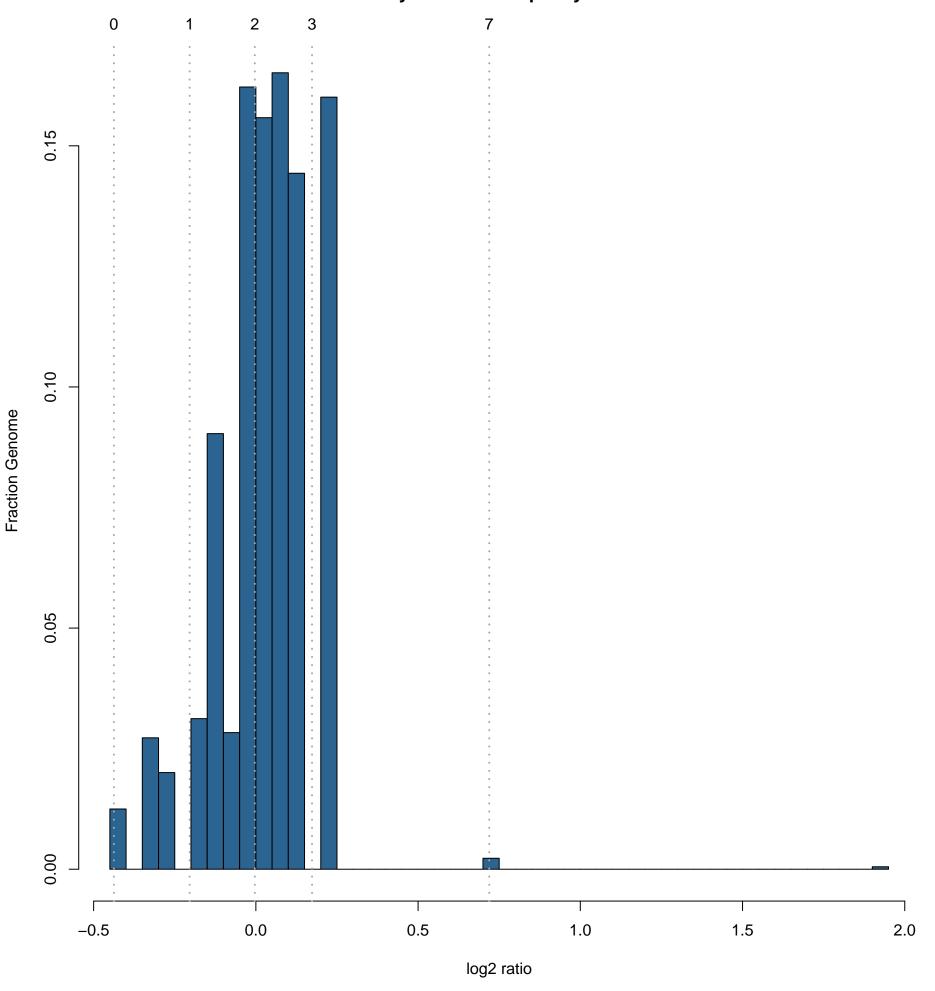
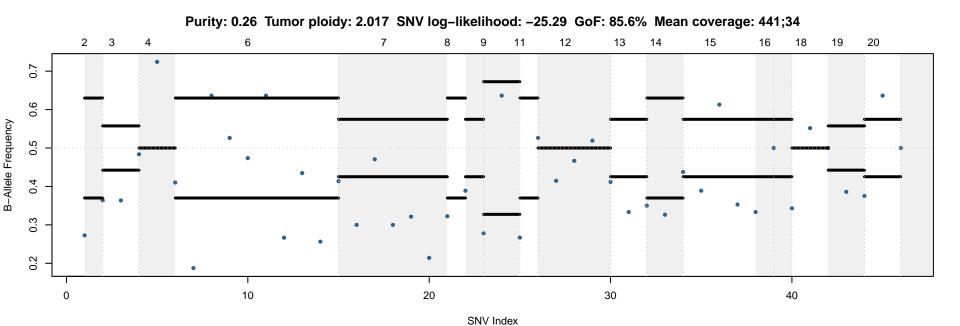
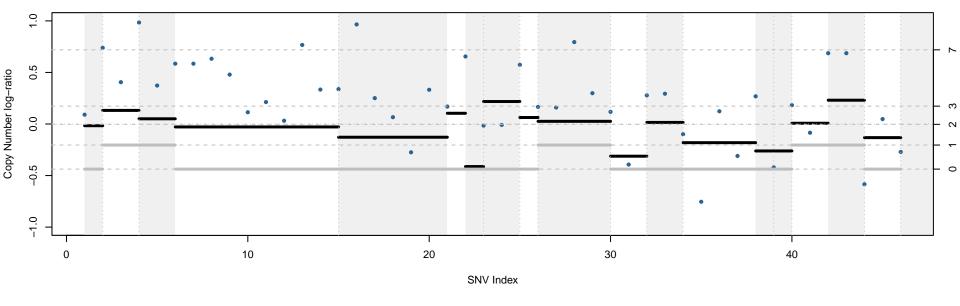
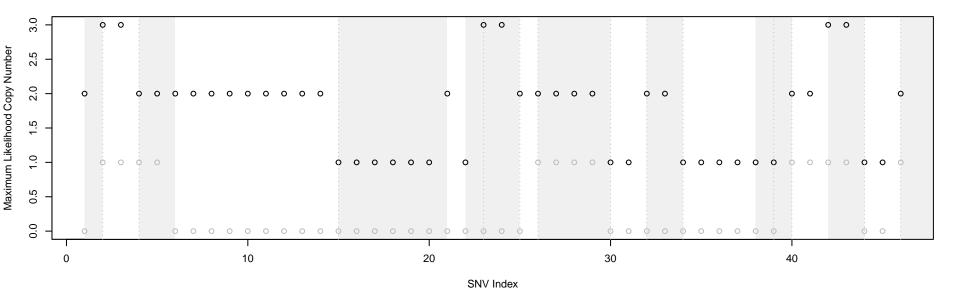
Purity: 0.26 Tumor ploidy: 2.017

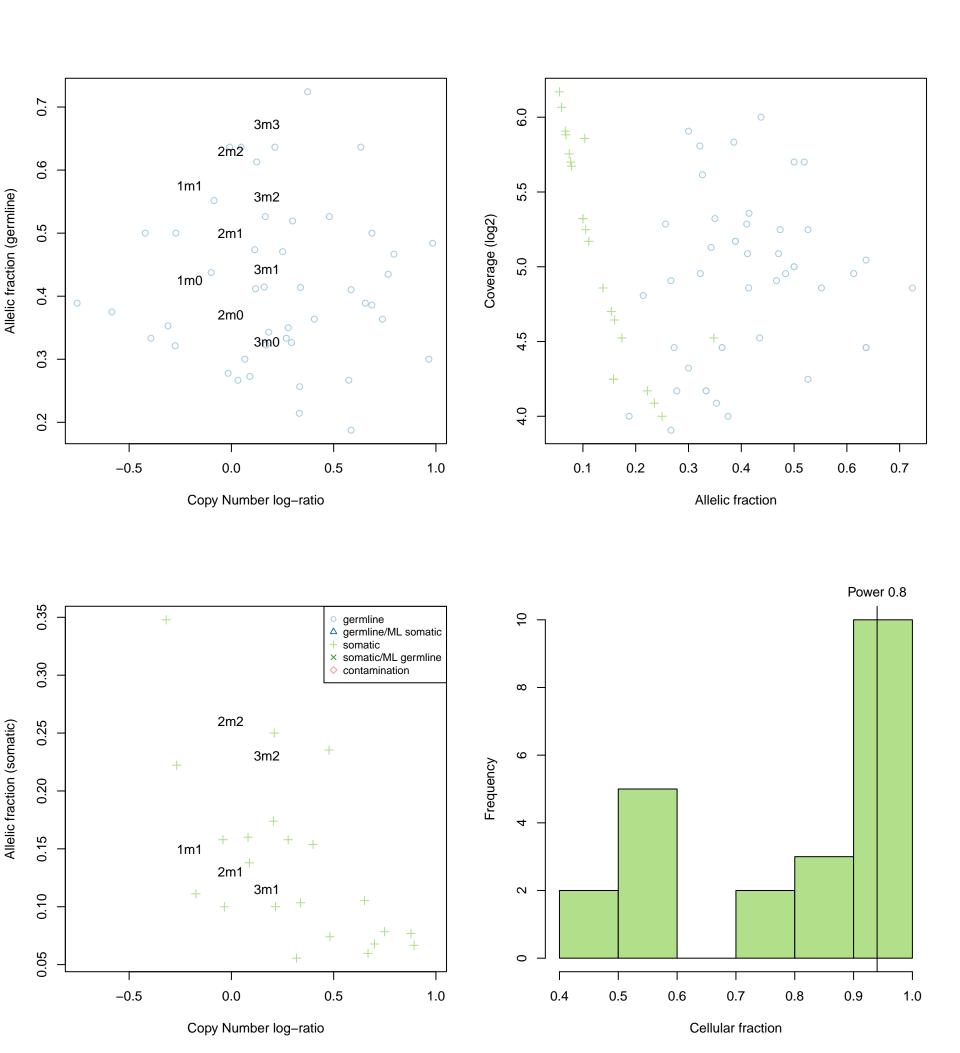




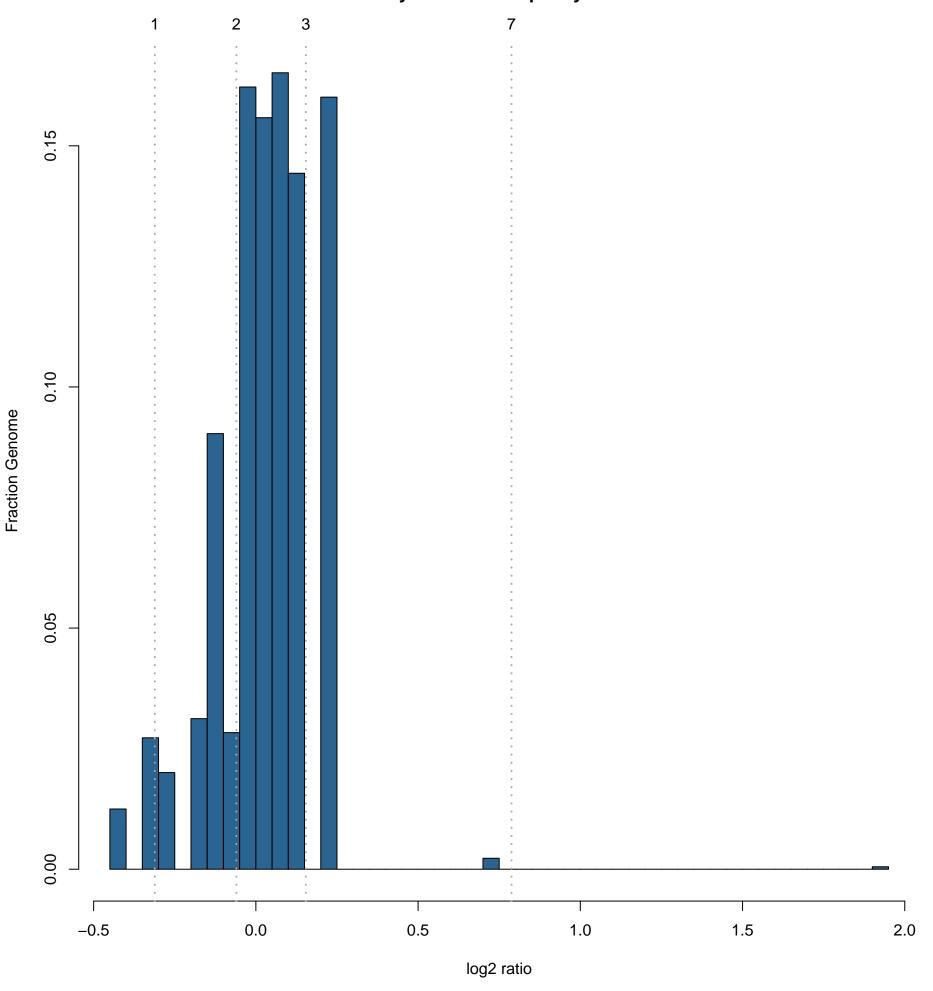
# SCNA-fit log-likelihood: -20161.93

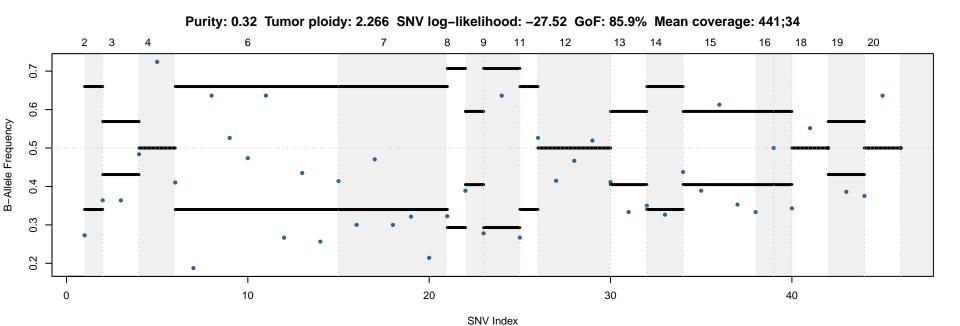




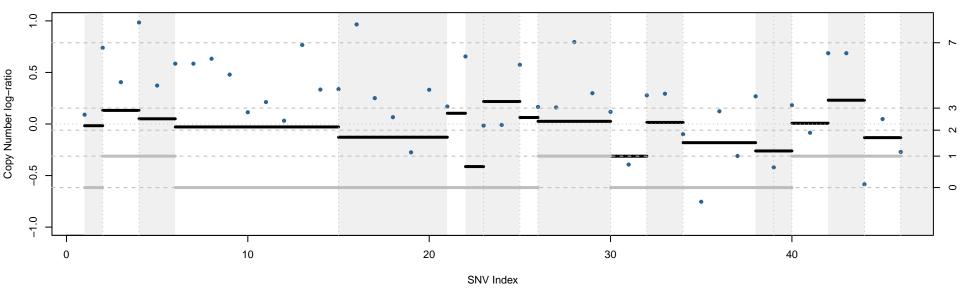


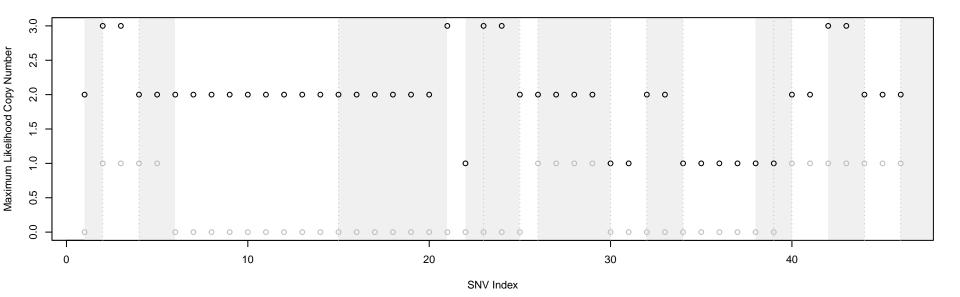
Purity: 0.32 Tumor ploidy: 2.266

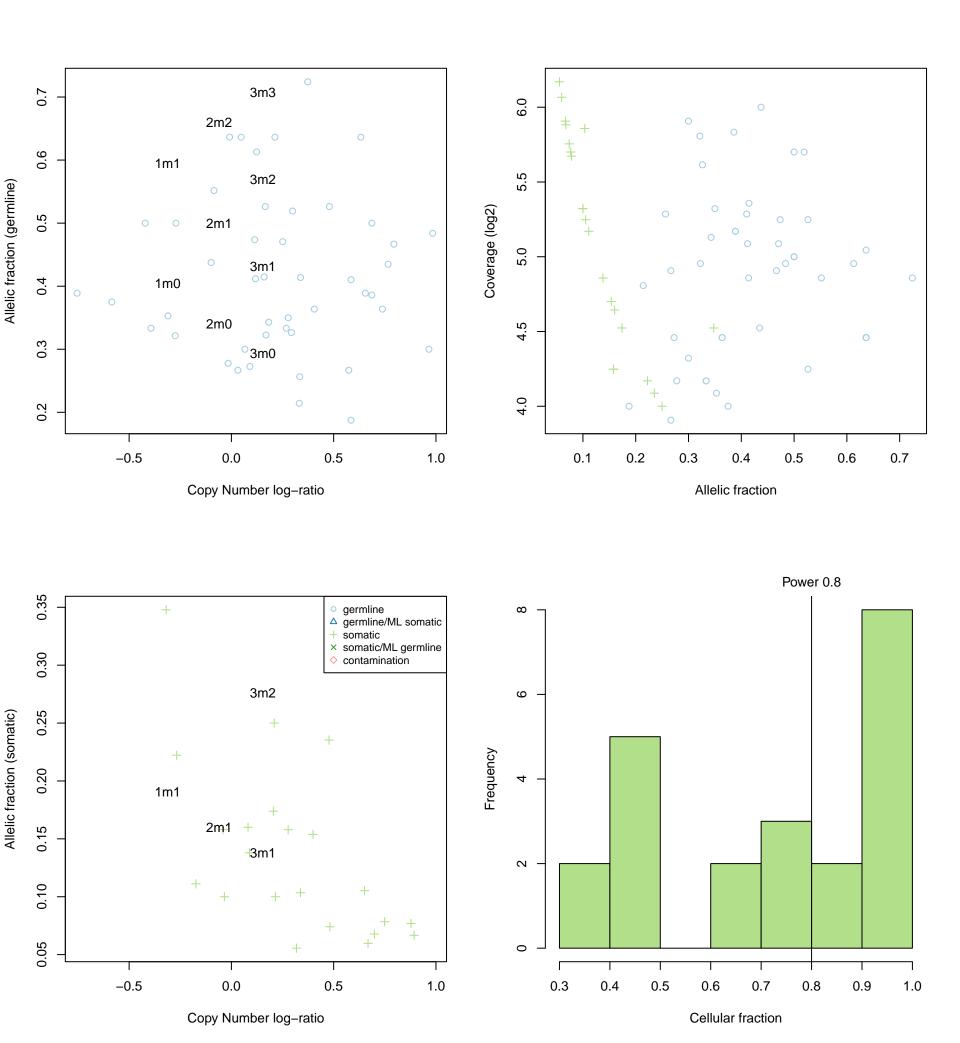




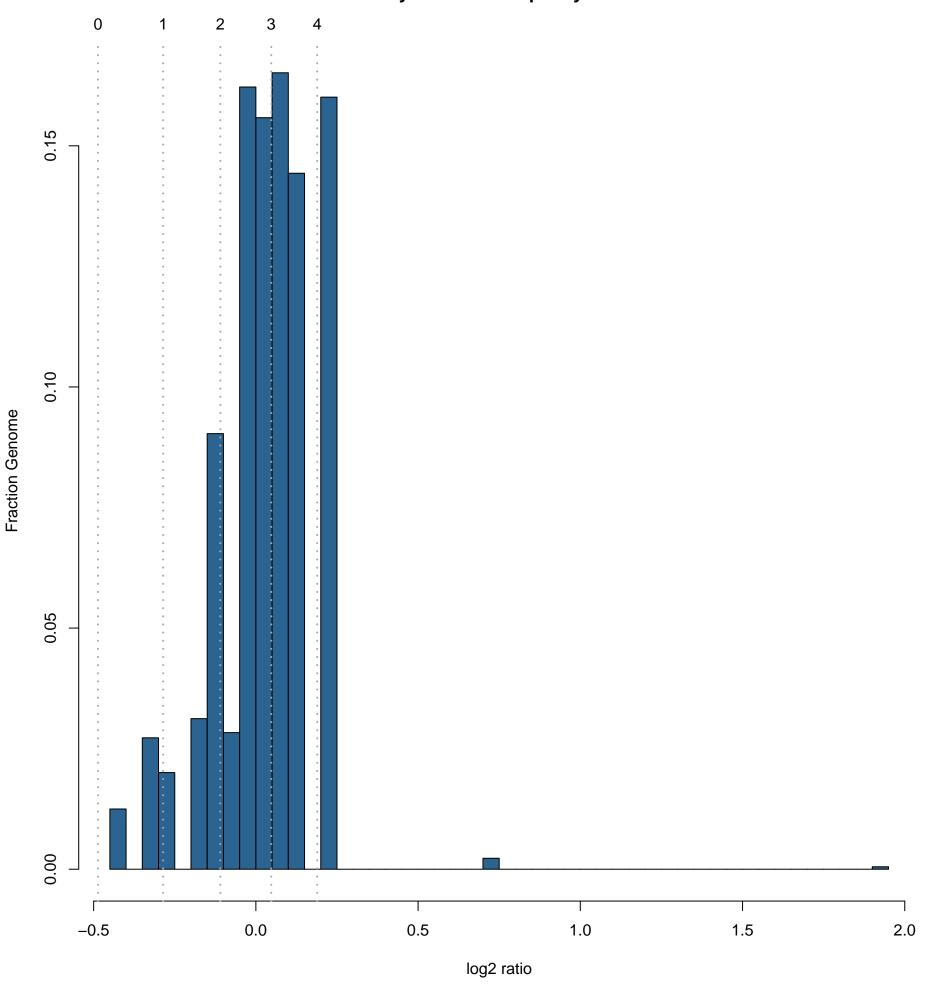
# SCNA-fit log-likelihood: -20176.86

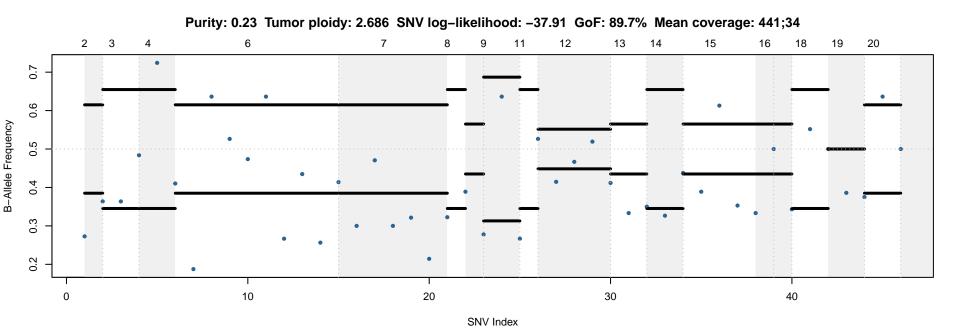




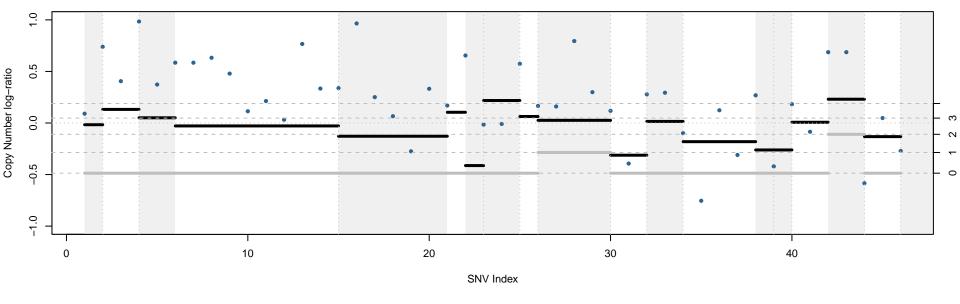


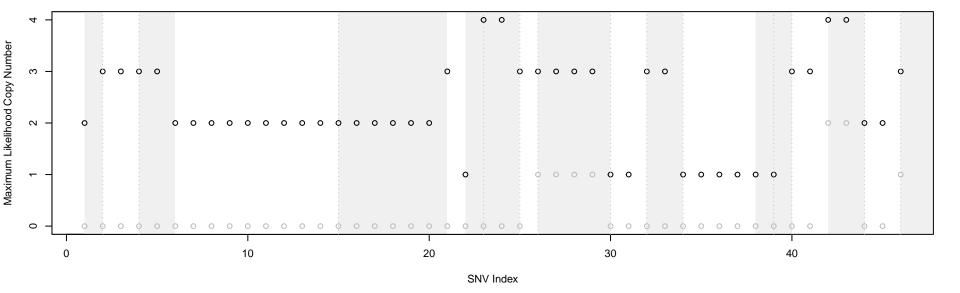
Purity: 0.23 Tumor ploidy: 2.686

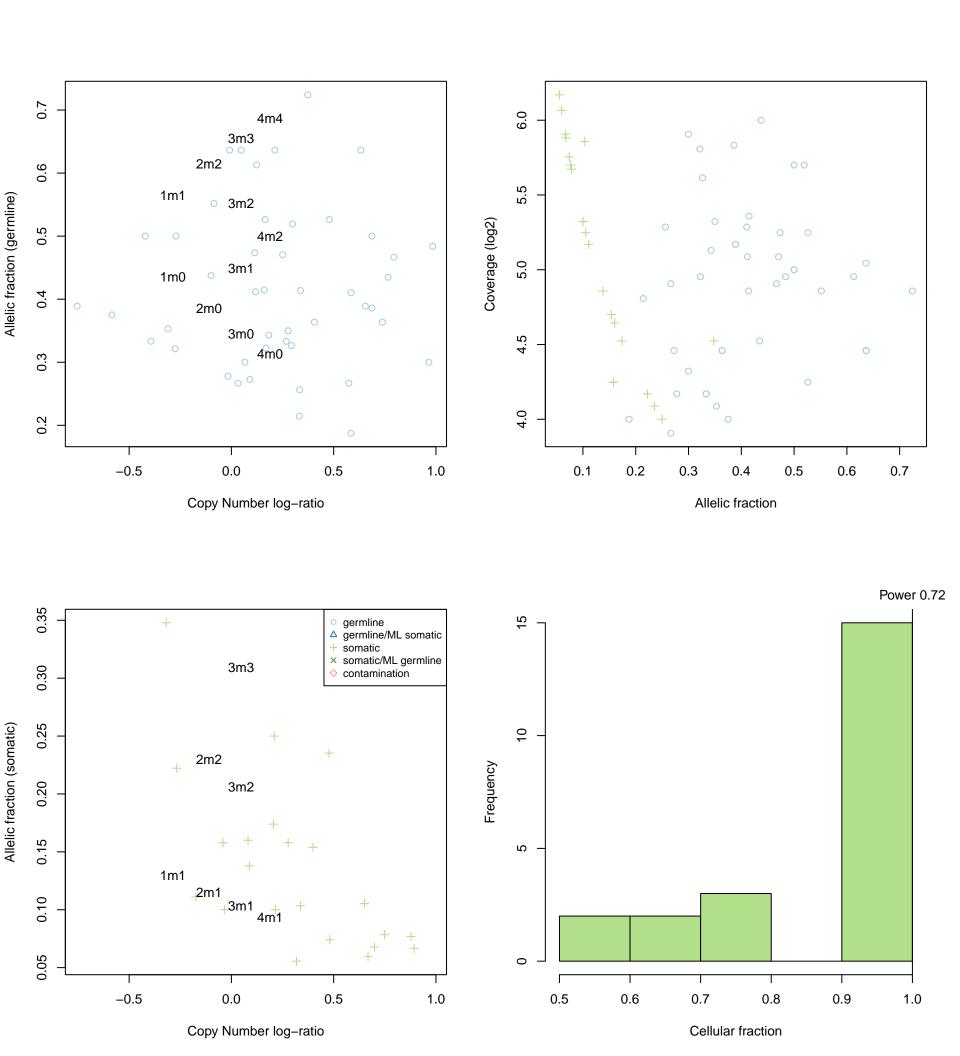




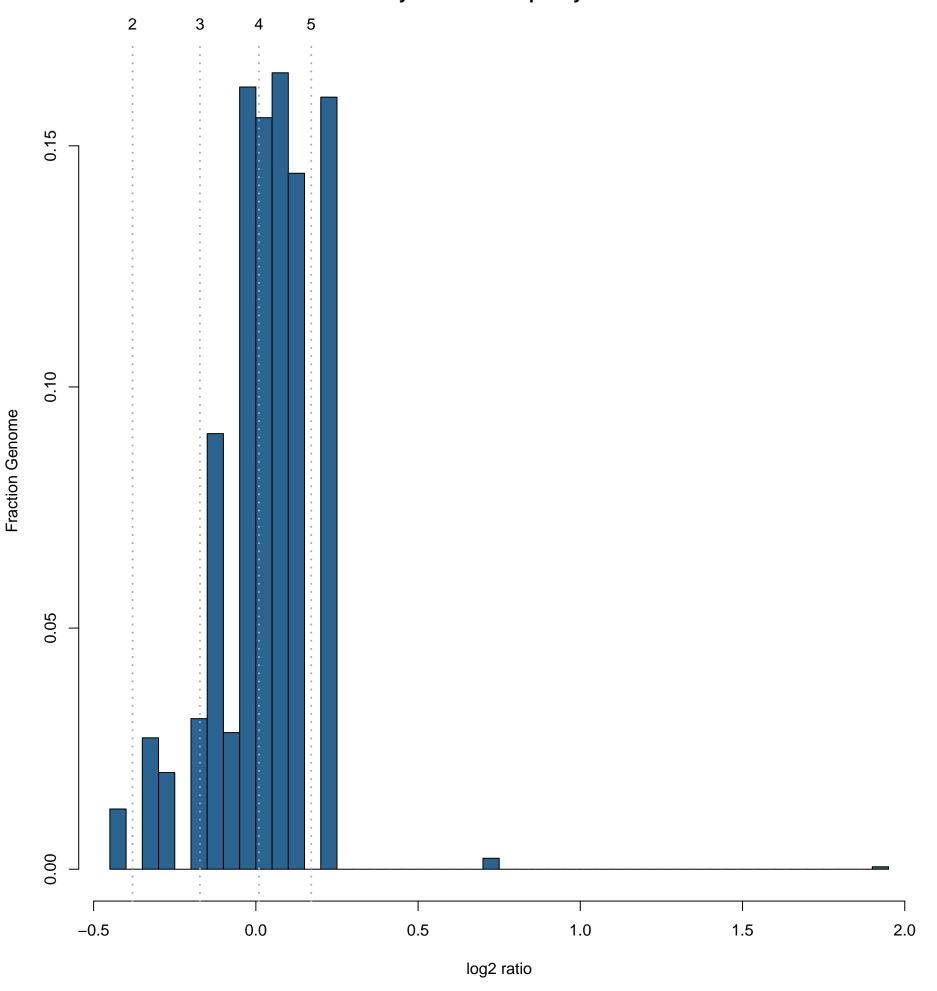
### SCNA-fit log-likelihood: -20156.66







Purity: 0.31 Tumor ploidy: 3.945



B-Allele Frequency

0.3

0.2

0

10

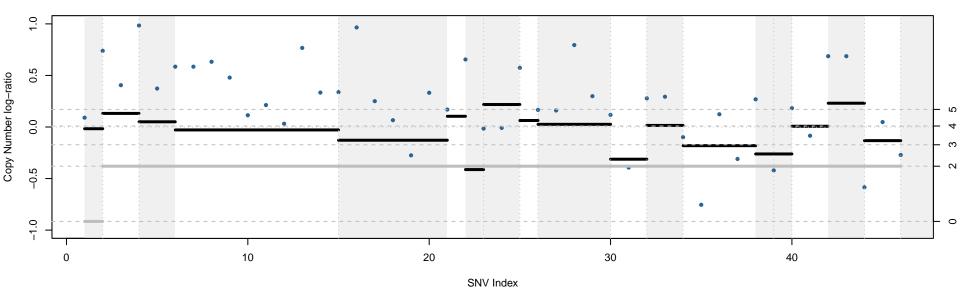
SCNA-fit log-likelihood: -20147.9

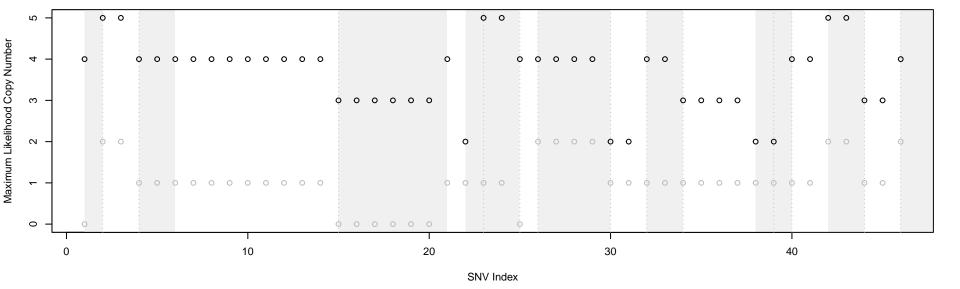
SNV Index

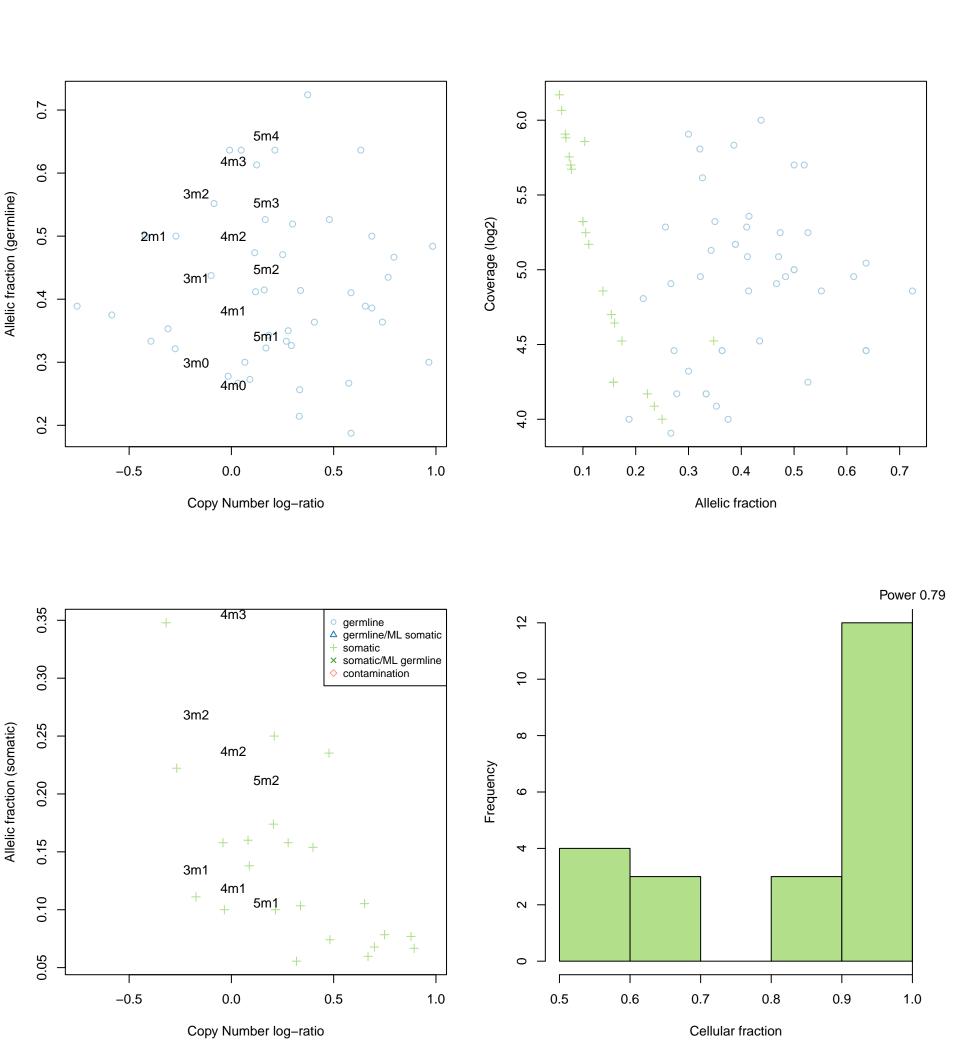
30

40

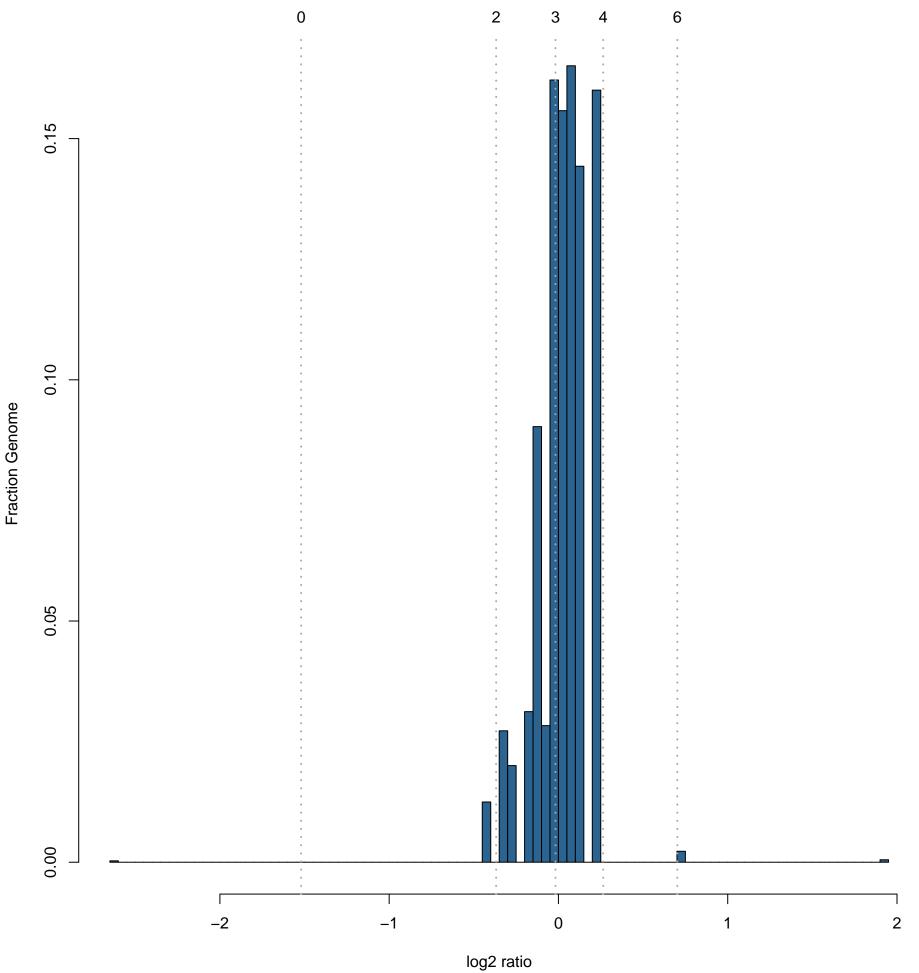
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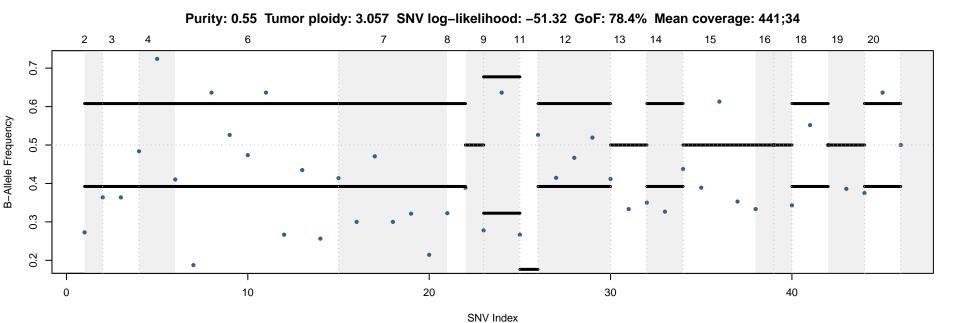




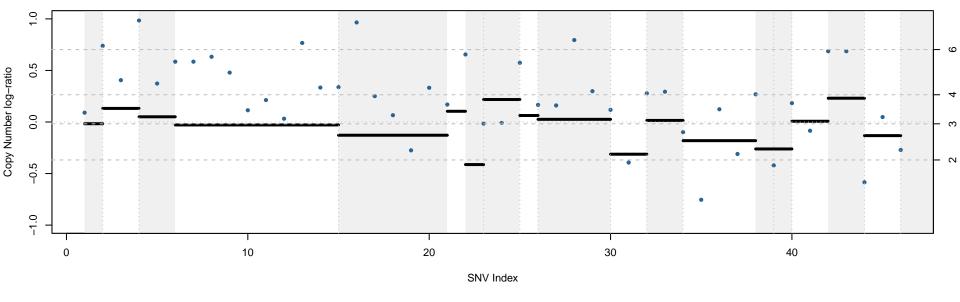


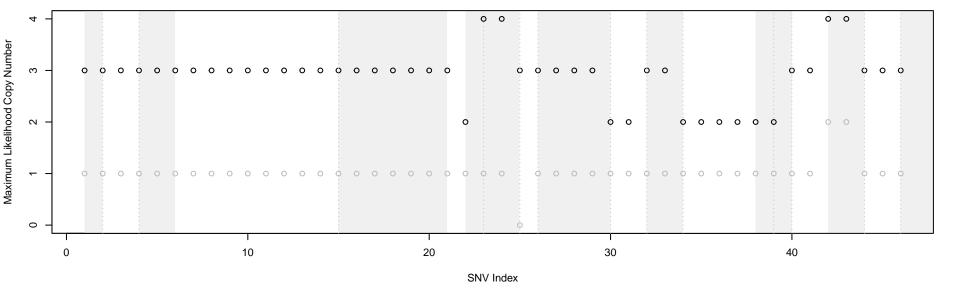
Purity: 0.55 Tumor ploidy: 3.057

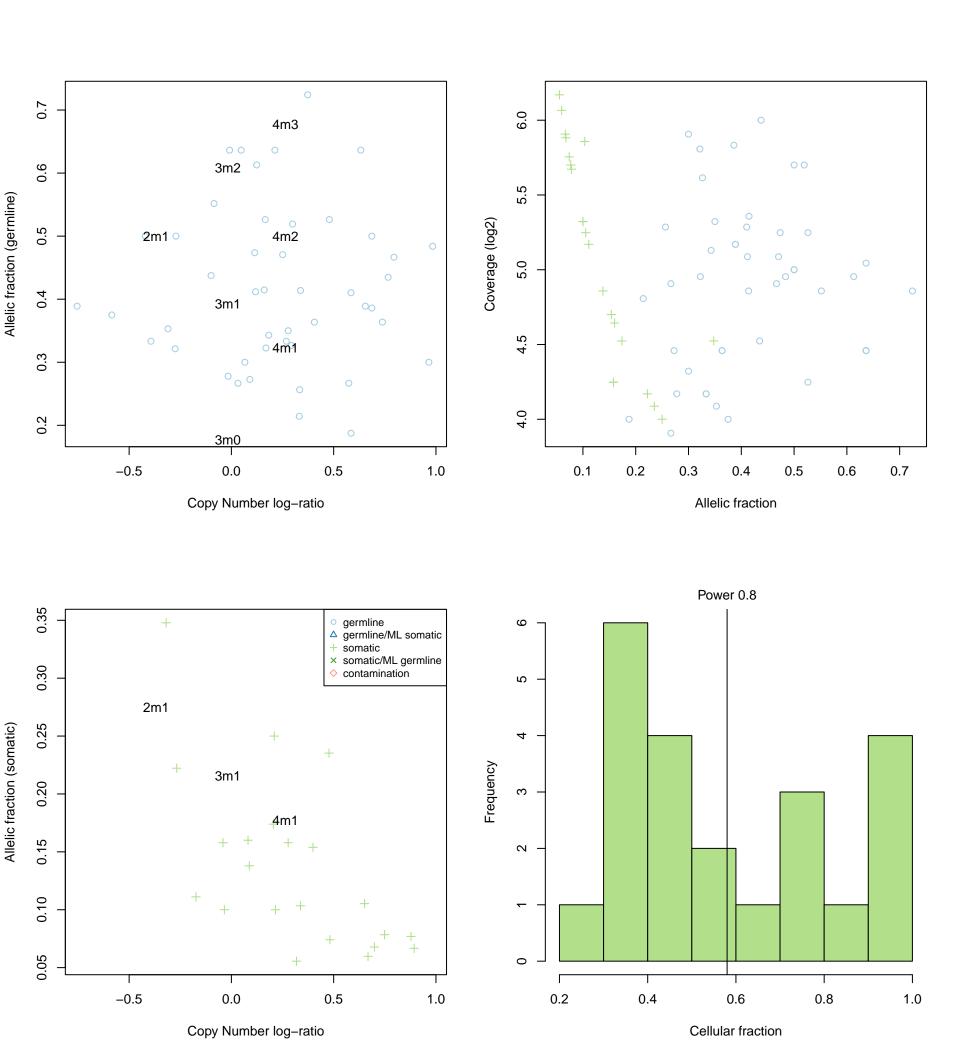




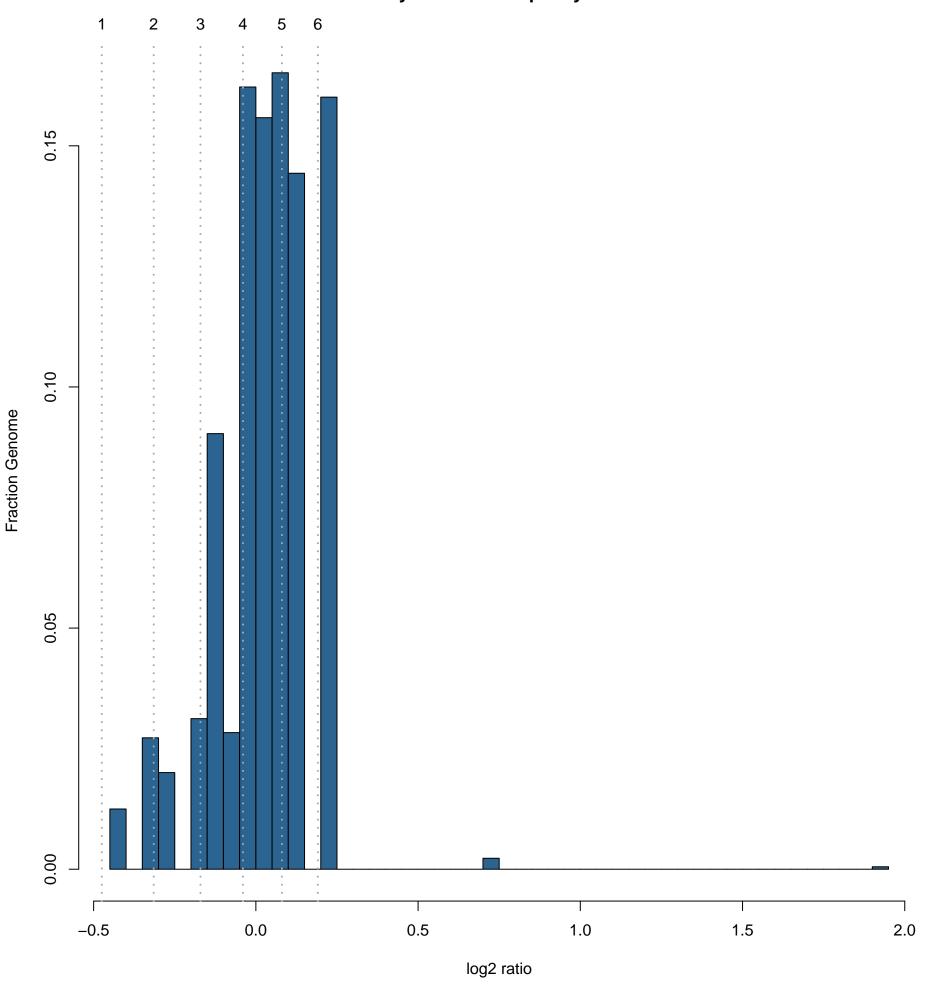
# SCNA-fit log-likelihood: -20207.71

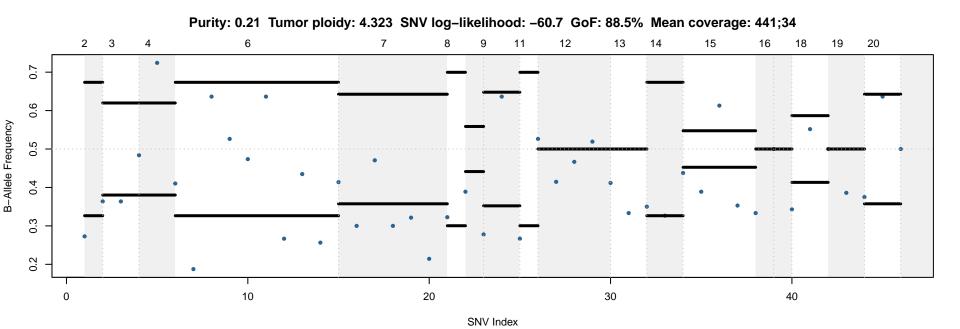




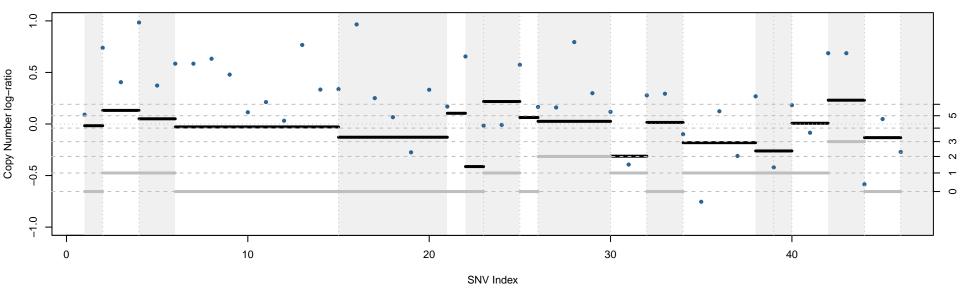


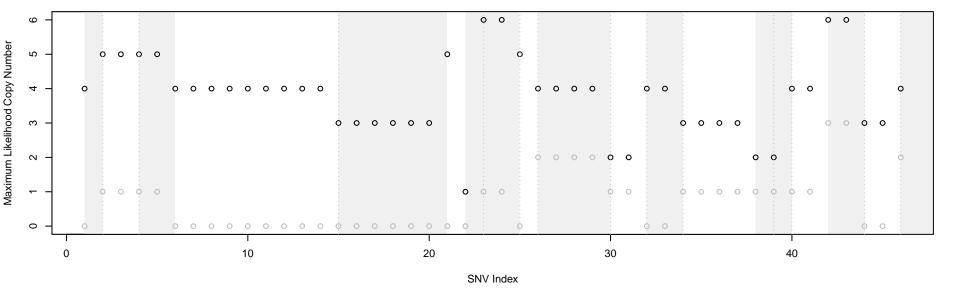
Purity: 0.21 Tumor ploidy: 4.323

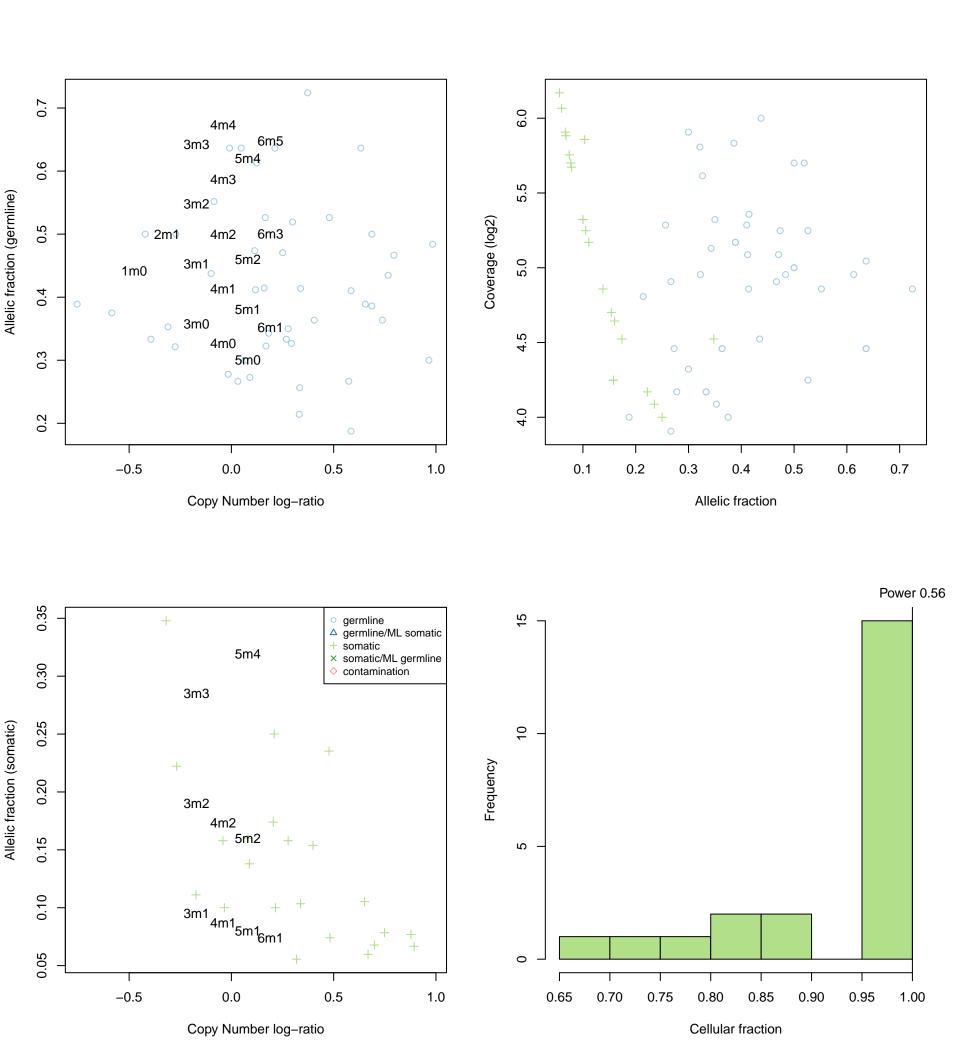




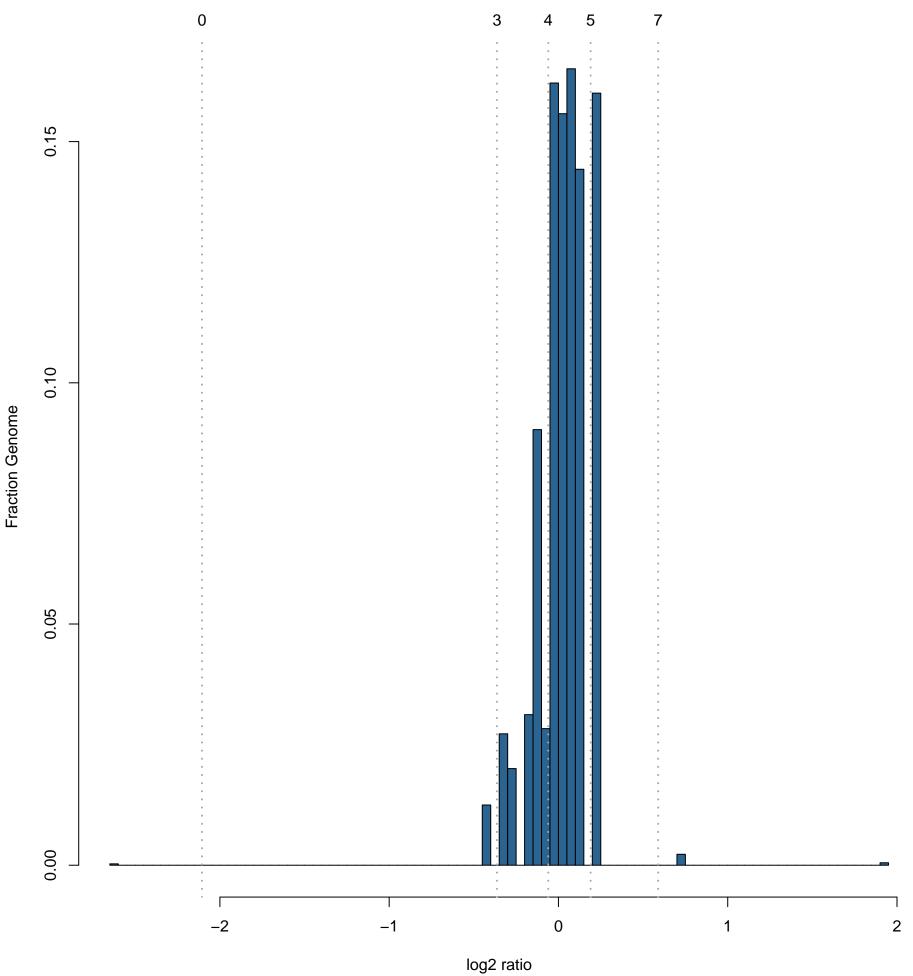
### SCNA-fit log-likelihood: -20130.53

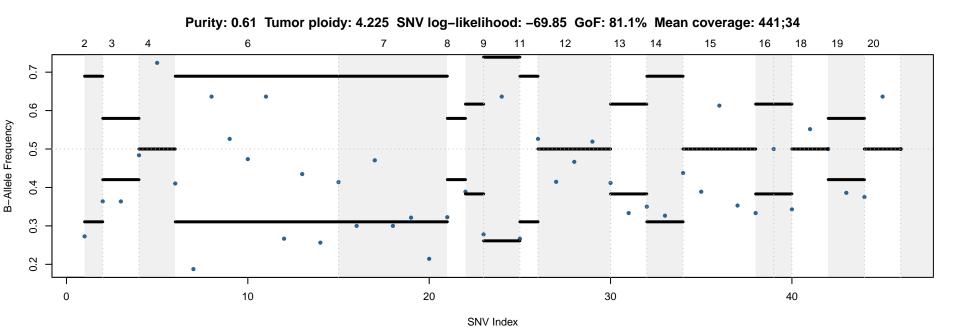




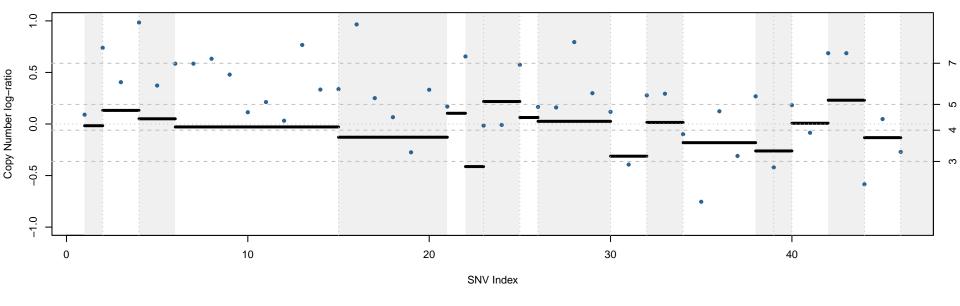


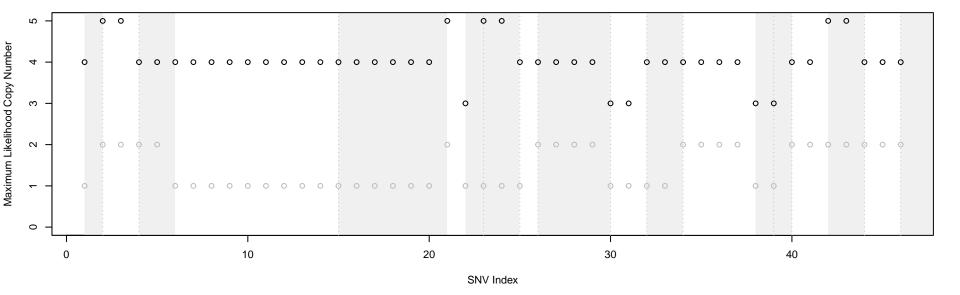
Purity: 0.61 Tumor ploidy: 4.225

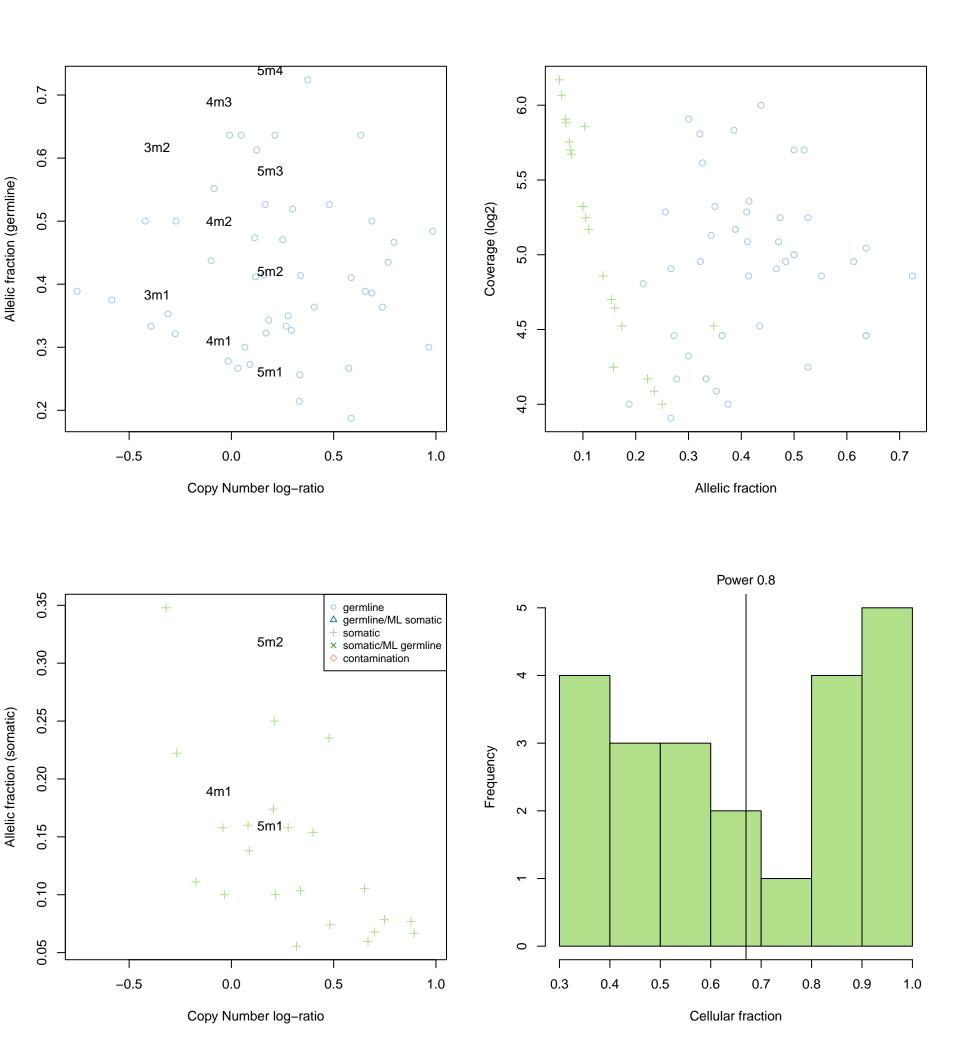




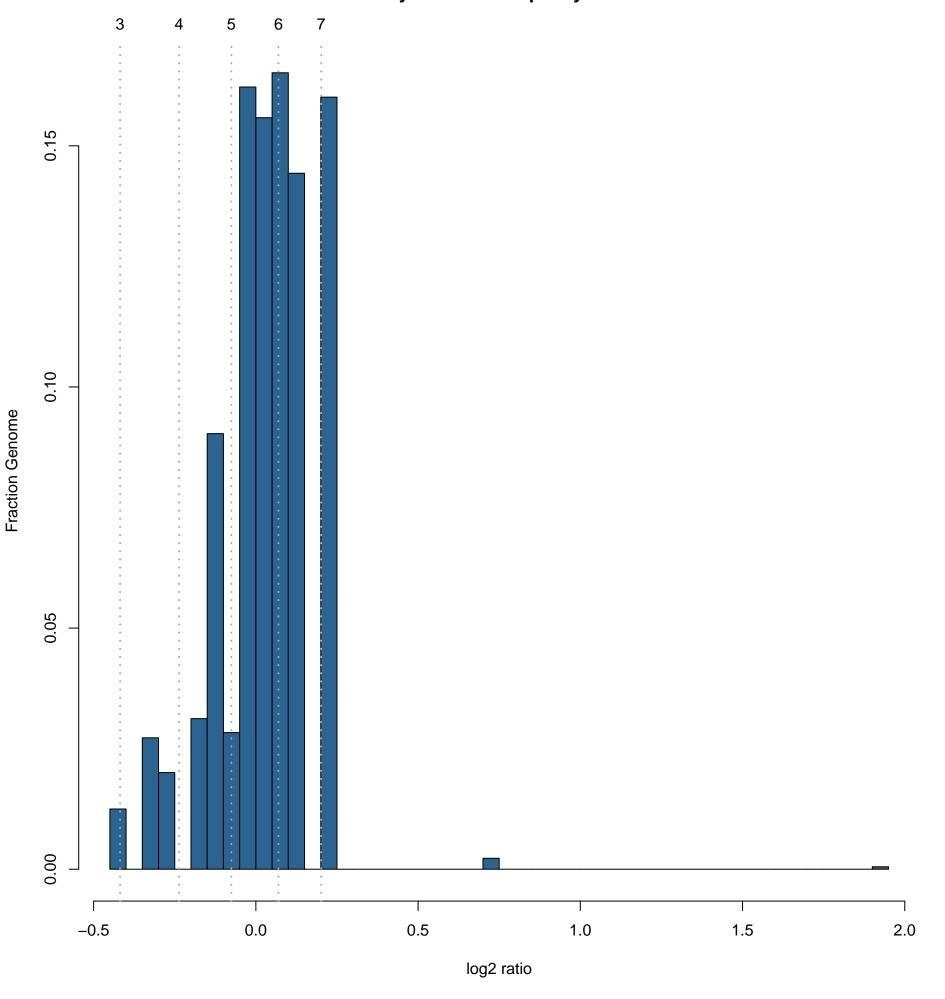
### SCNA-fit log-likelihood: -20192.58

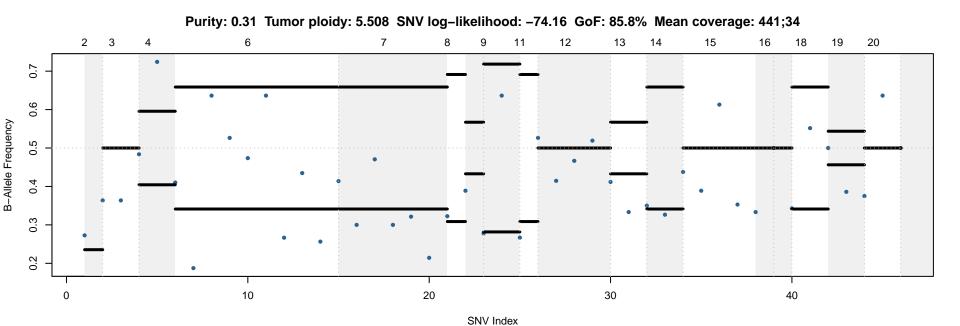




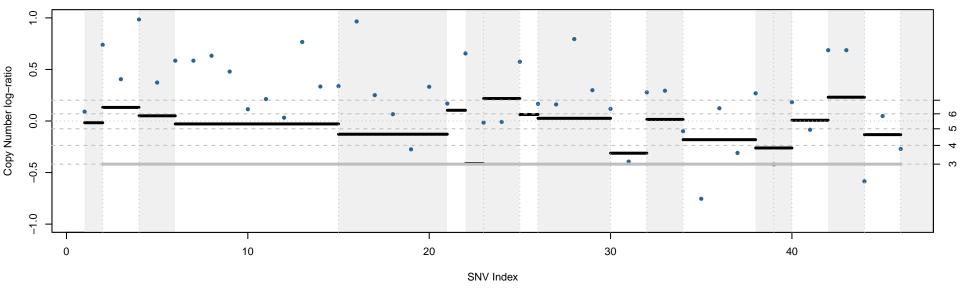


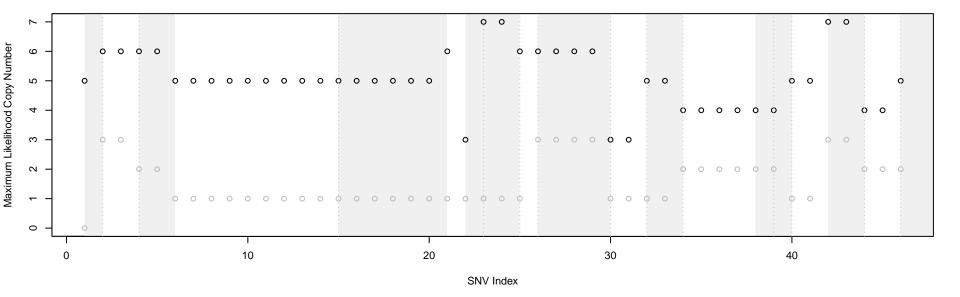
Purity: 0.31 Tumor ploidy: 5.508

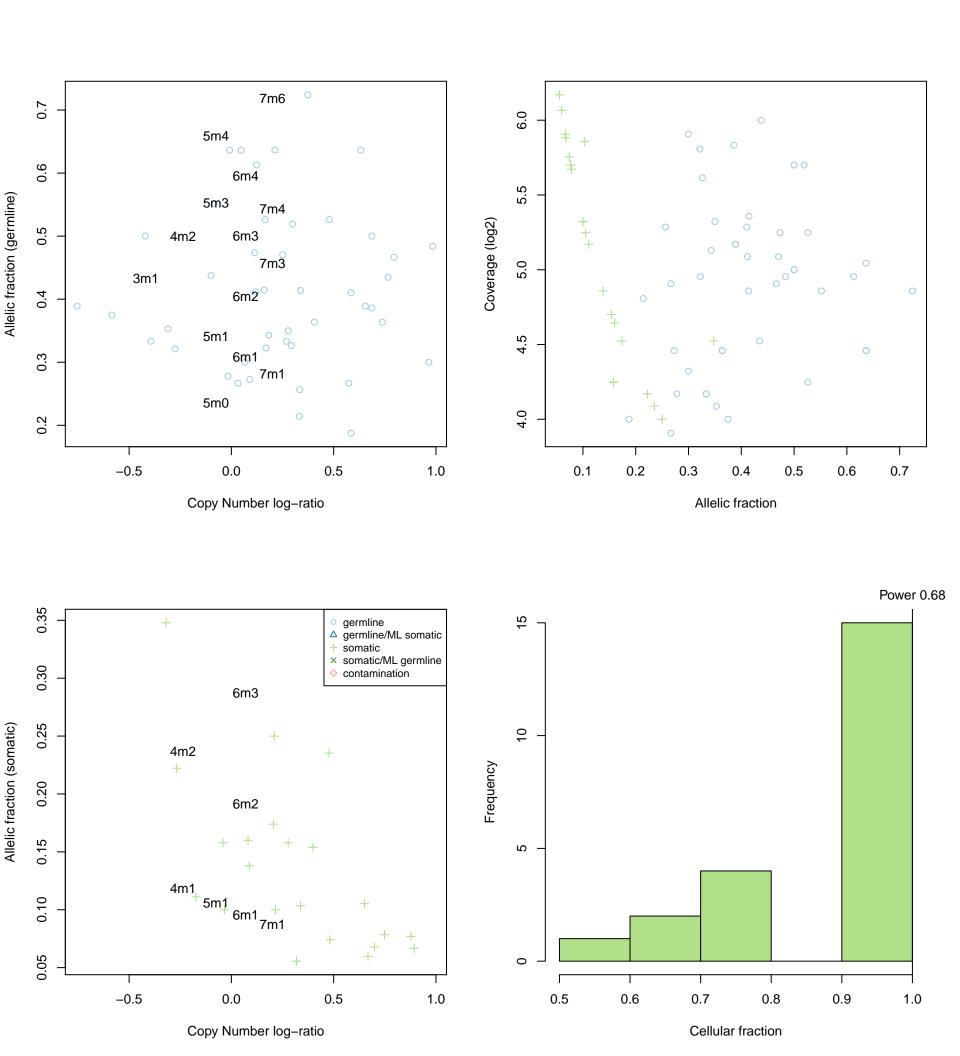




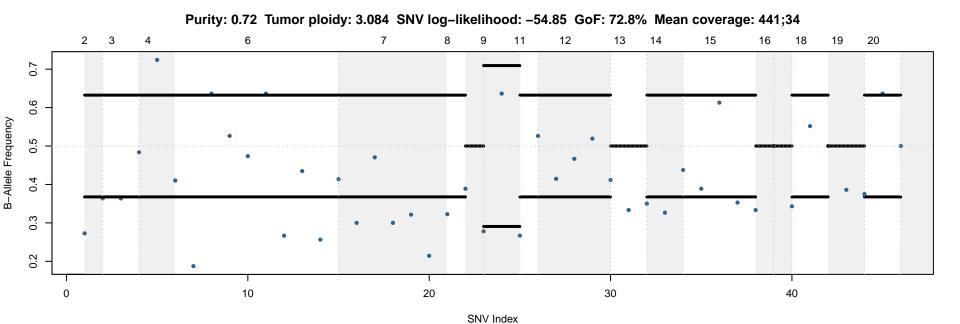
### SCNA-fit log-likelihood: -20148.69



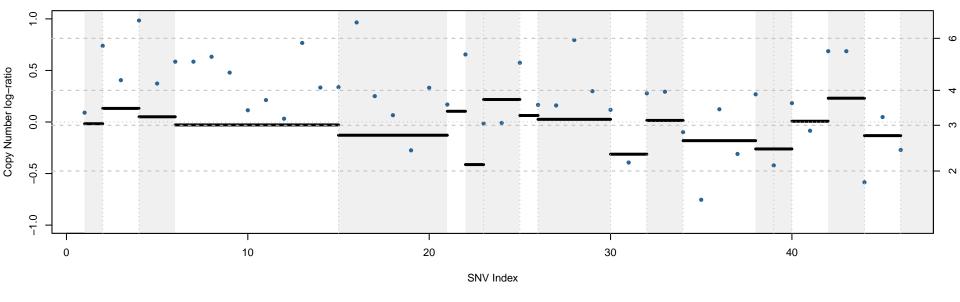


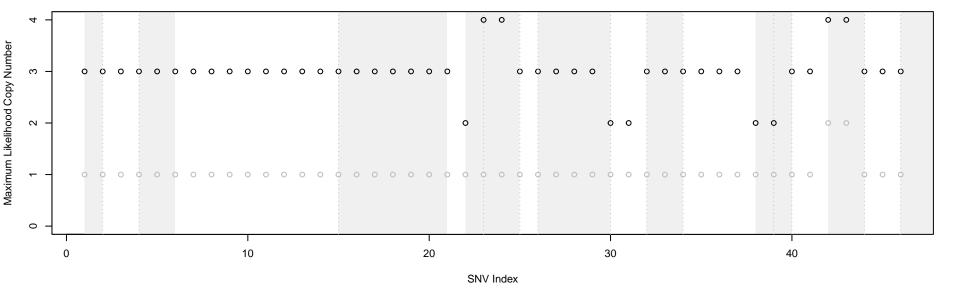


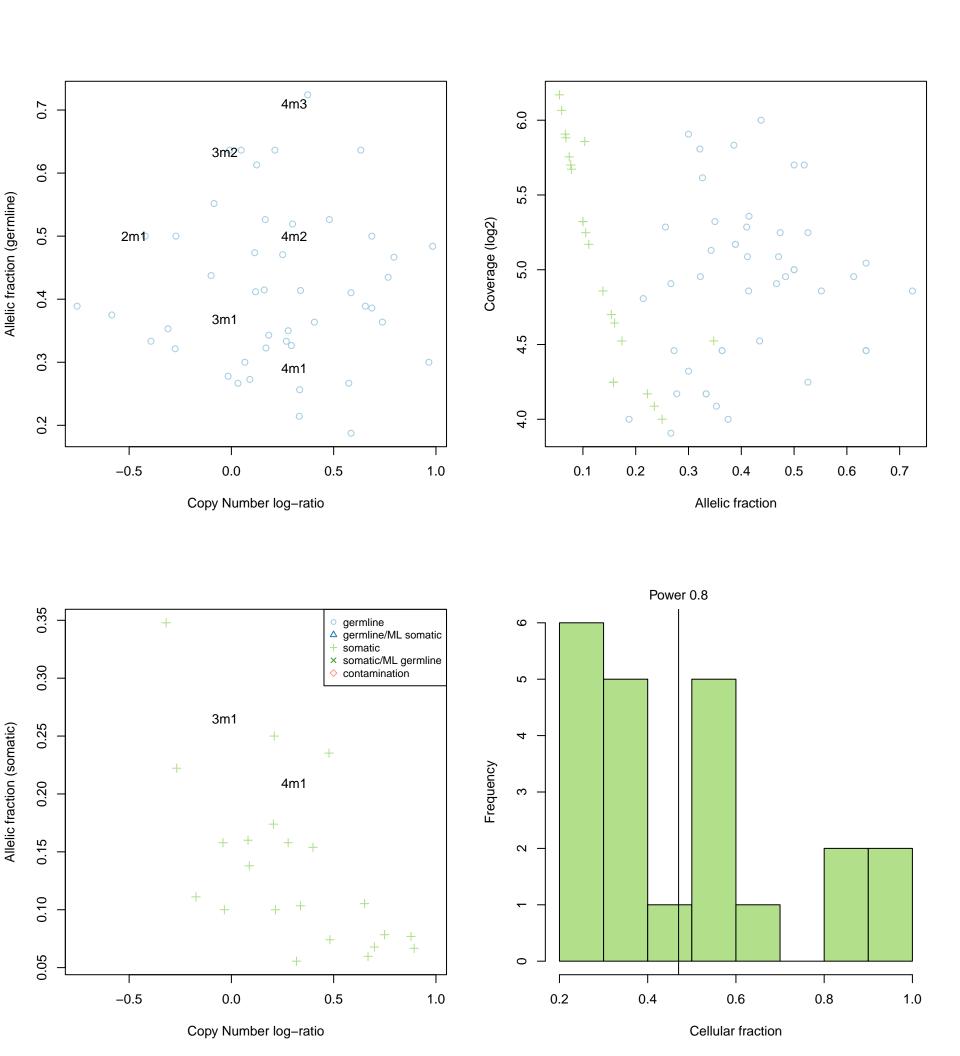
Purity: 0.72 Tumor ploidy: 3.084 6 3 0.30 0.25 0.20 Fraction Genome 0.15 0.05 0.00 -3 -2 -1 0 2 -4 log2 ratio



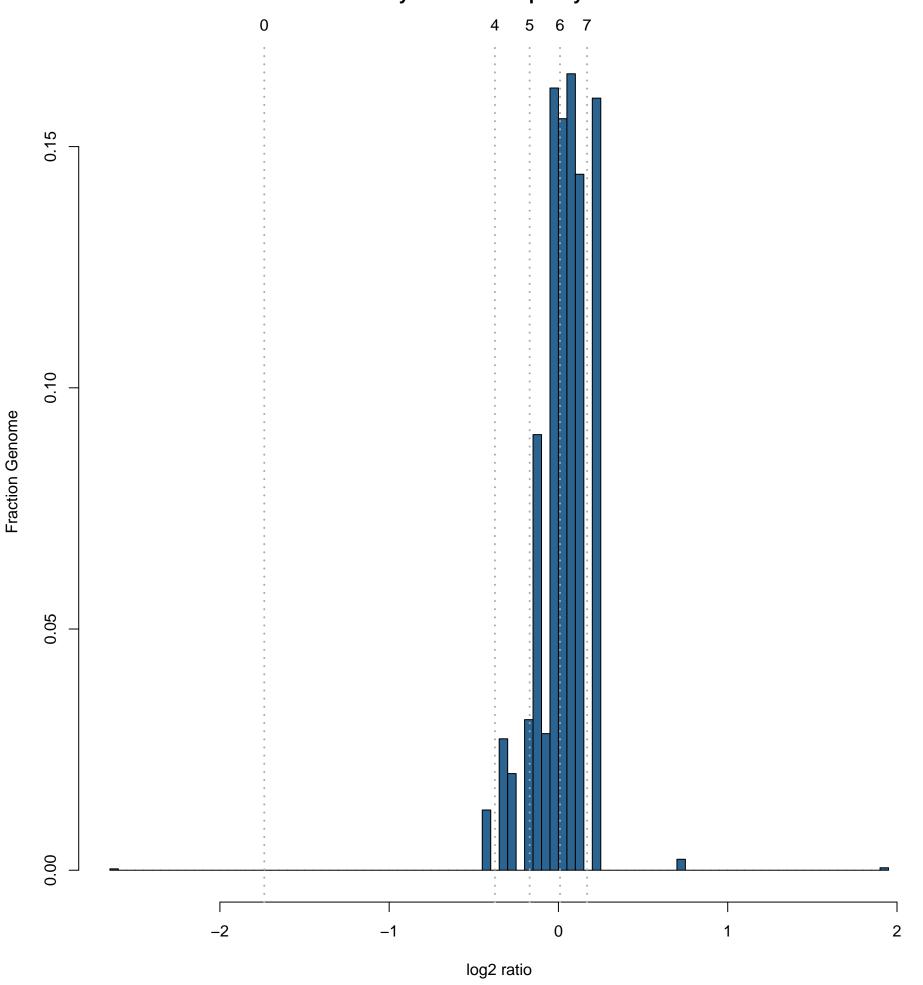
### SCNA-fit log-likelihood: -20249.18

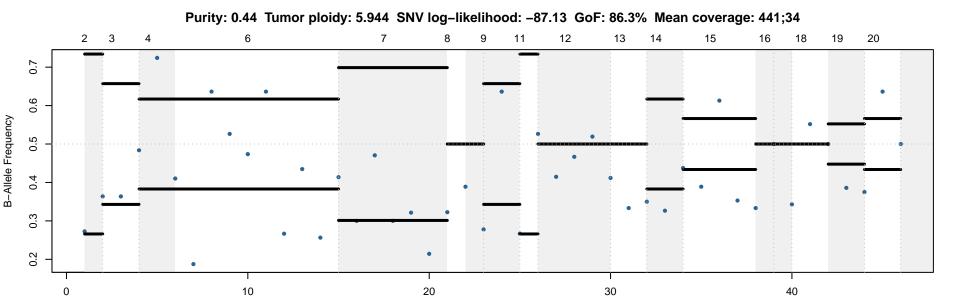






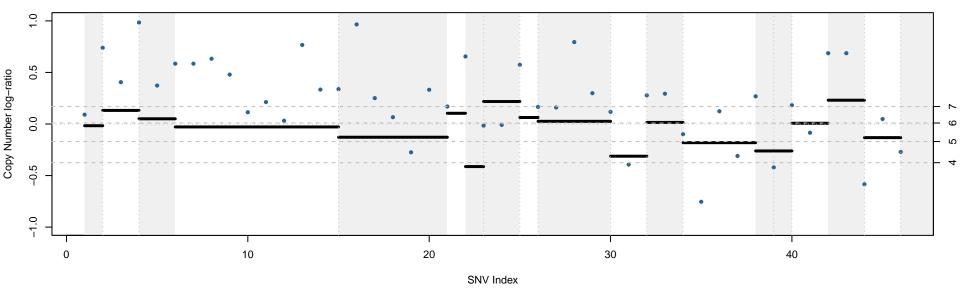
Purity: 0.44 Tumor ploidy: 5.944

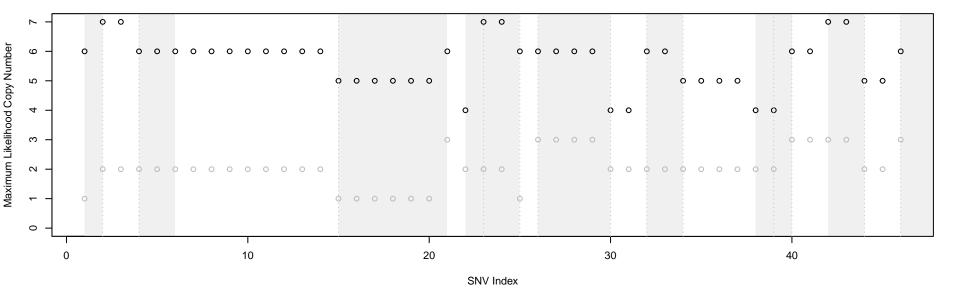


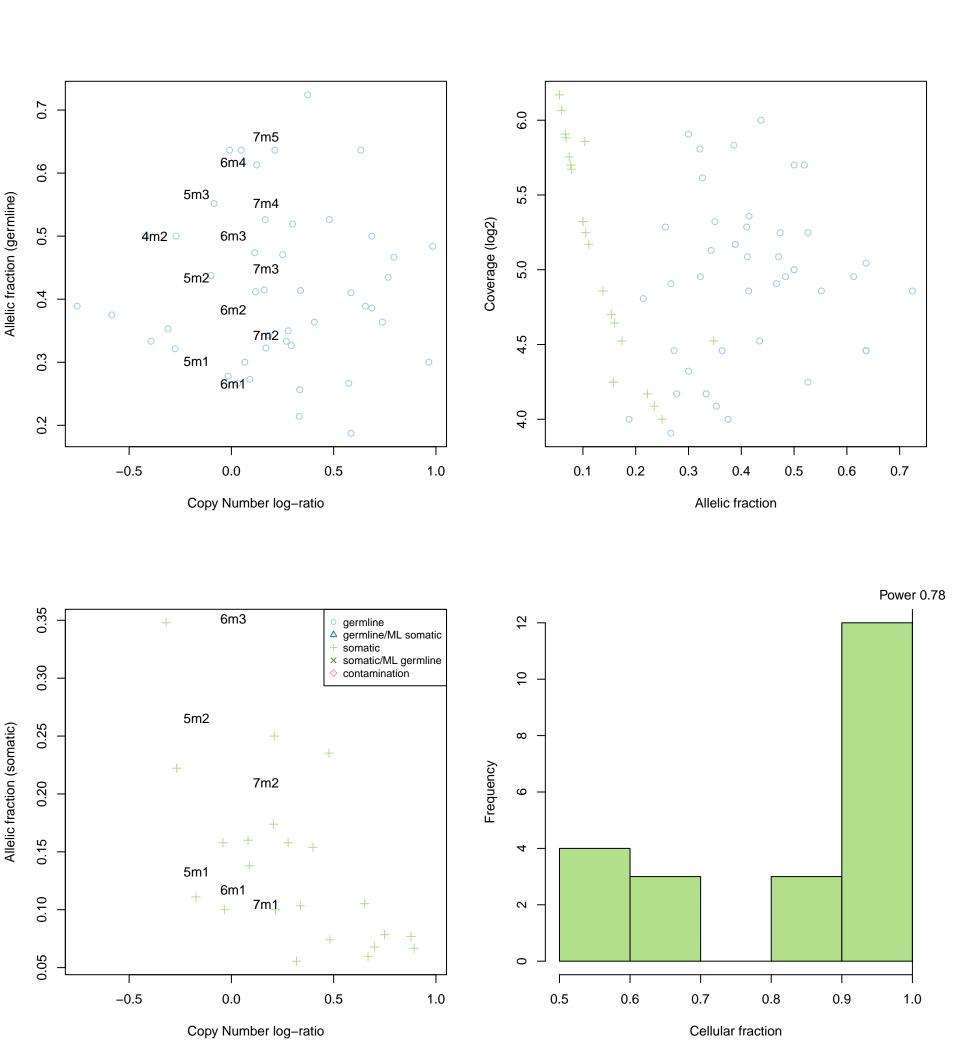


### SCNA-fit log-likelihood: -20147.39

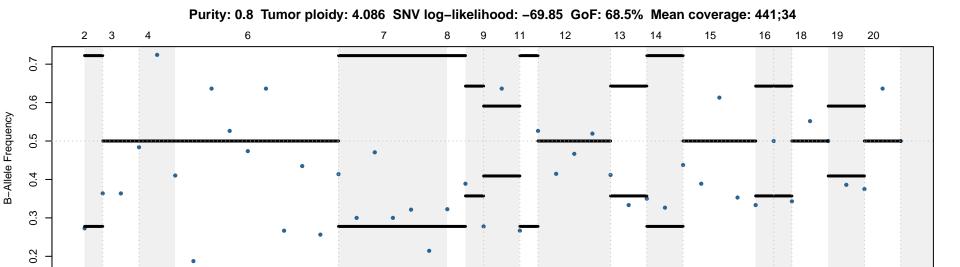
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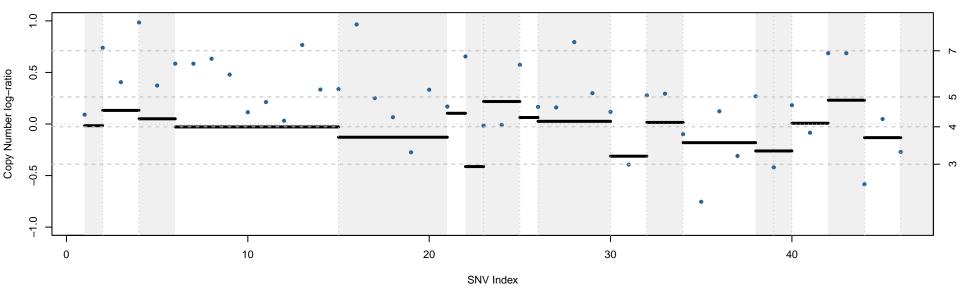


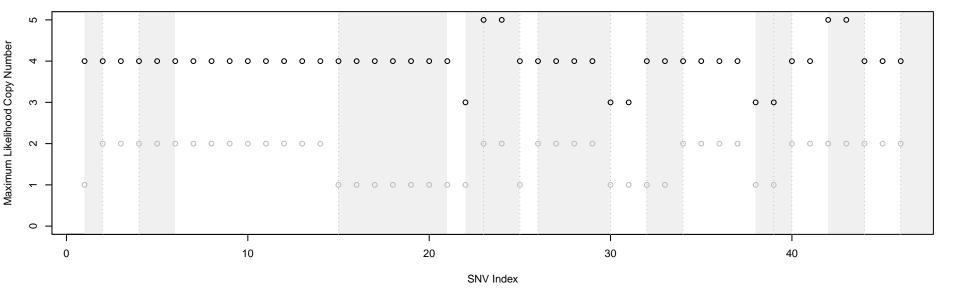
Purity: 0.8 Tumor ploidy: 4.086 0 5 7 0.30 0.25 0.20 Fraction Genome 0.15 0.10 0.05 0.00 0 -3 -2 -1 2 -4 log2 ratio

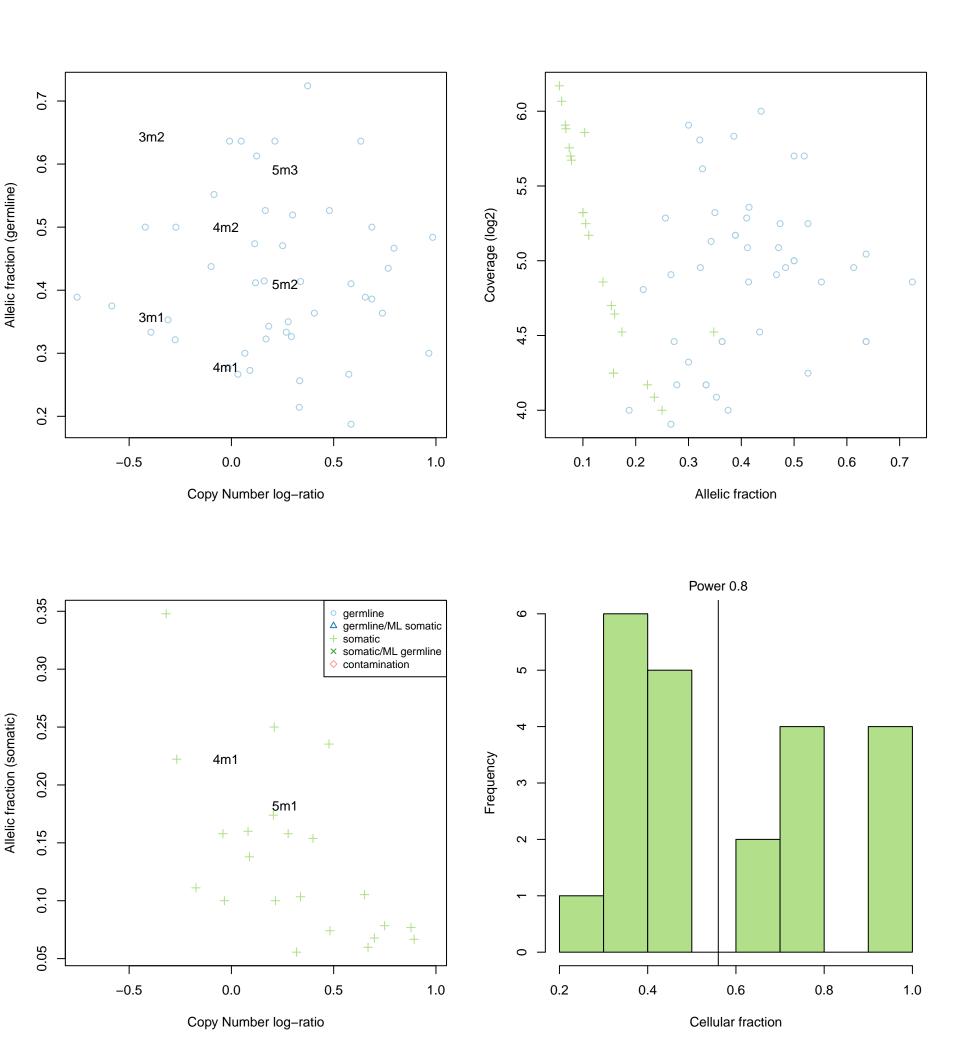


# SCNA-fit log-likelihood: -20214.51

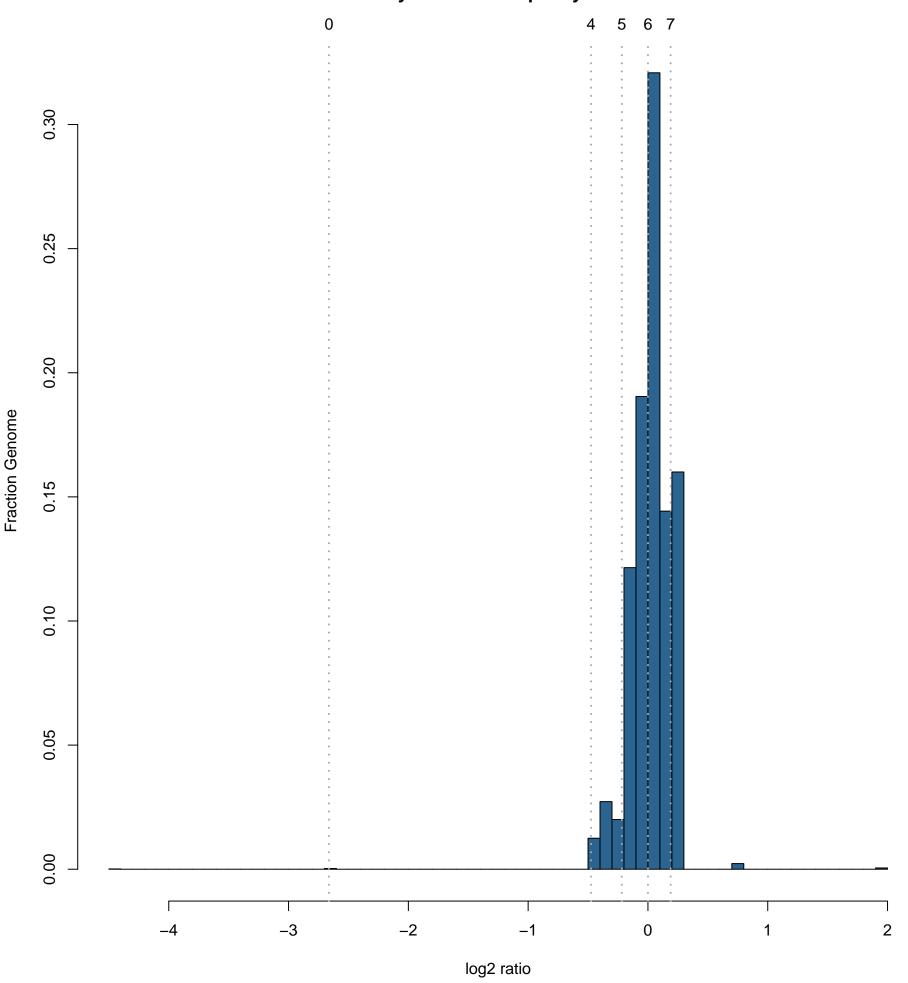
SNV Index

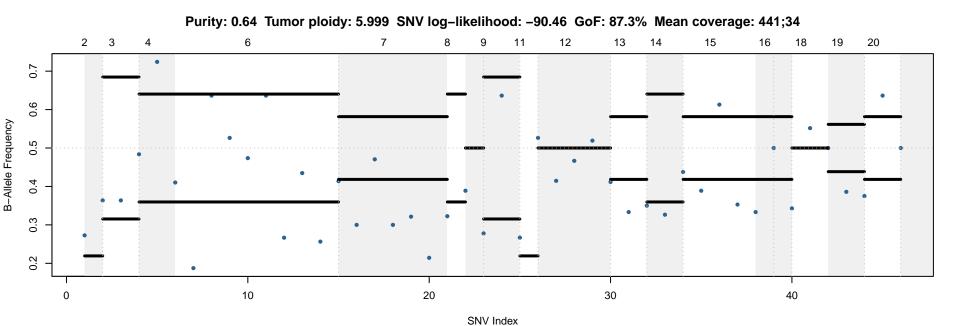




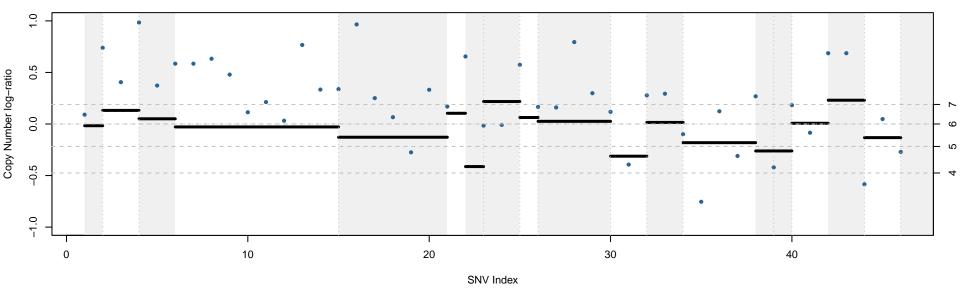


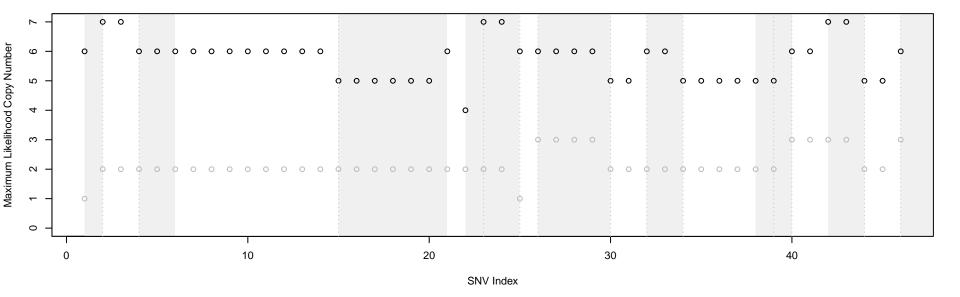
Purity: 0.64 Tumor ploidy: 5.999

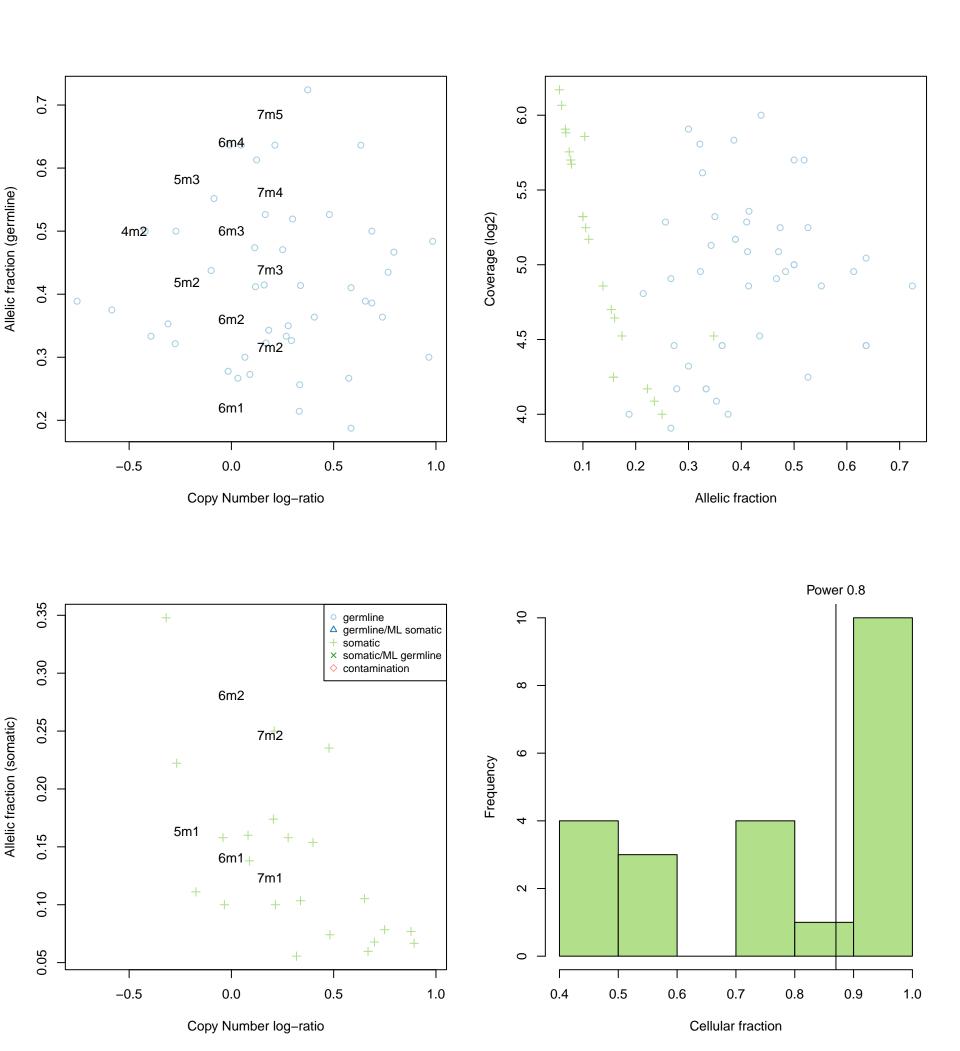




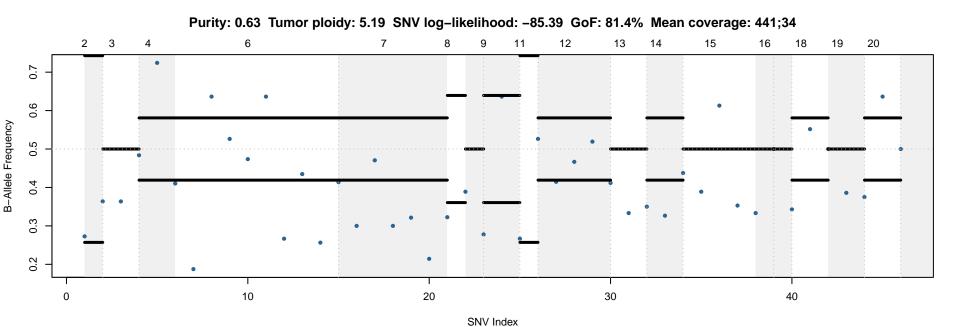
### SCNA-fit log-likelihood: -20161.68



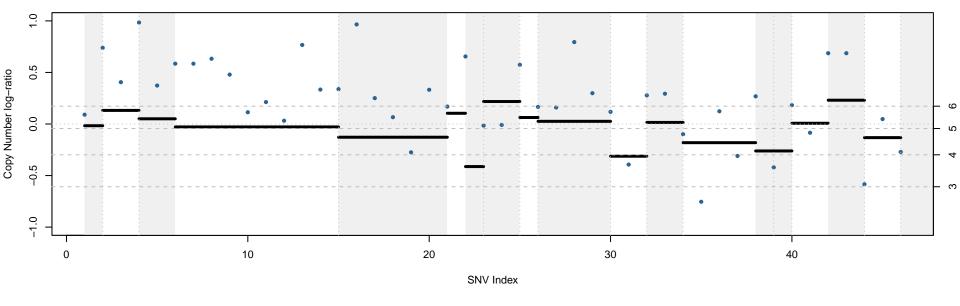


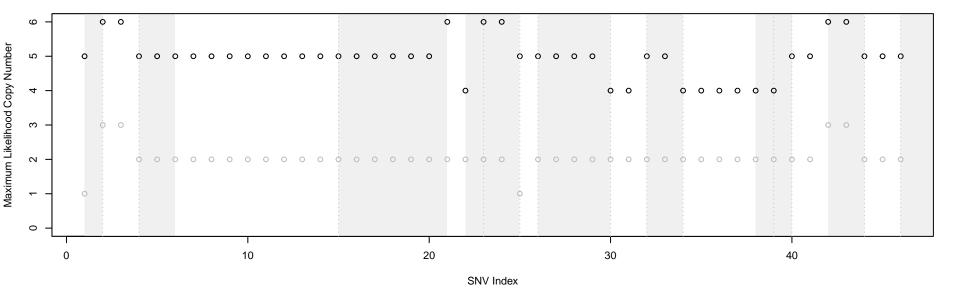


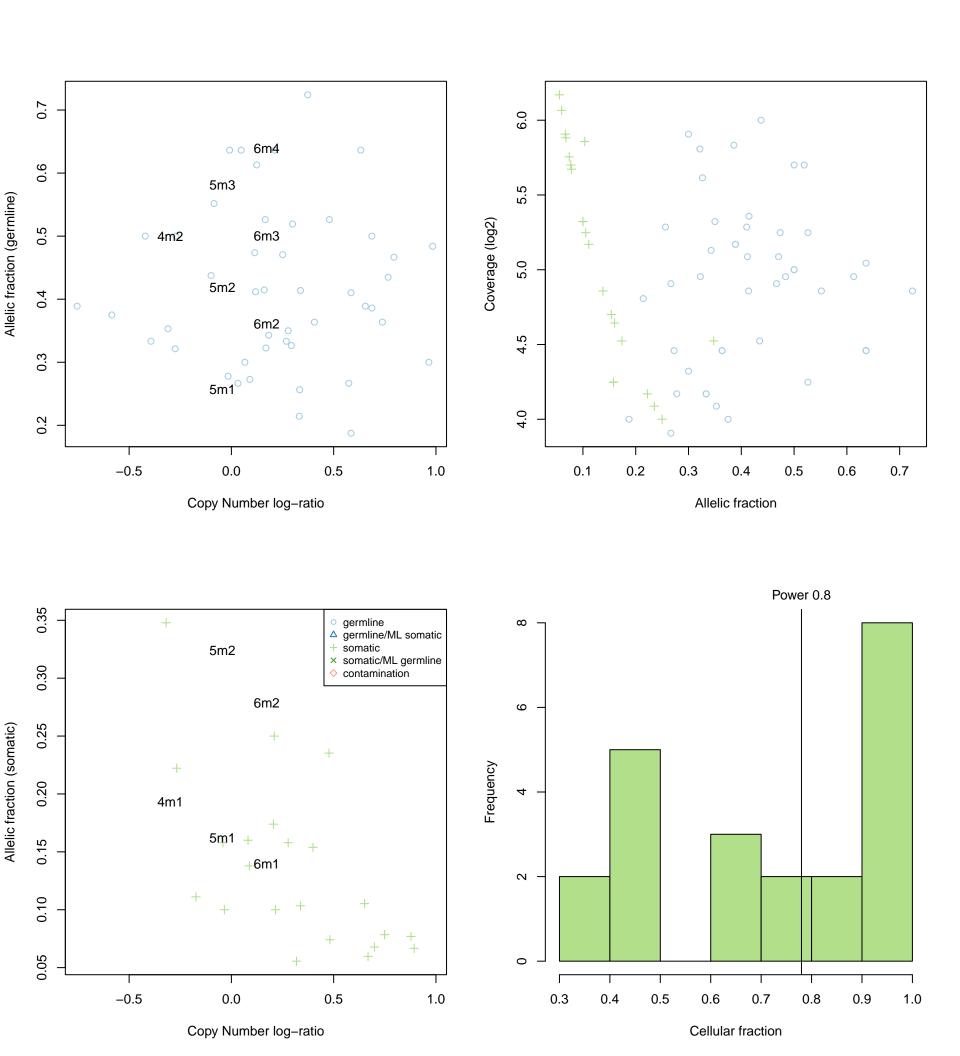
Purity: 0.63 Tumor ploidy: 5.19 5 6 0.30 0.25 0.20 Fraction Genome 0.15 0.10 0.05 0.00 0 -3 -2 -1 2 1 -4 log2 ratio



# SCNA-fit log-likelihood: -20183.94







Purity: 0.75 Tumor ploidy: 1.959 0 Fraction Genome 0.05 0.00 -2 -1 0 1 2 log2 ratio

### SCNA-fit log-likelihood: -20366.6

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