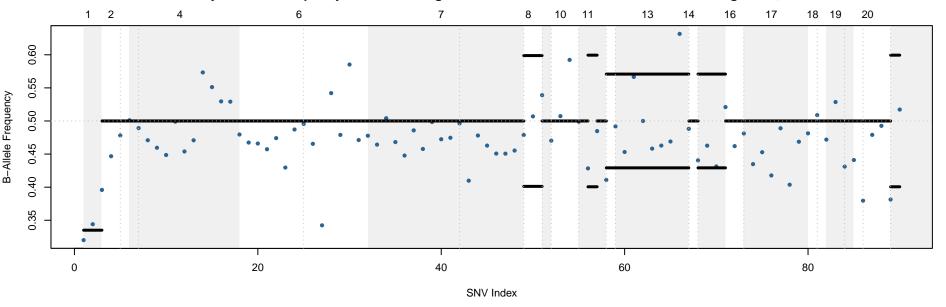
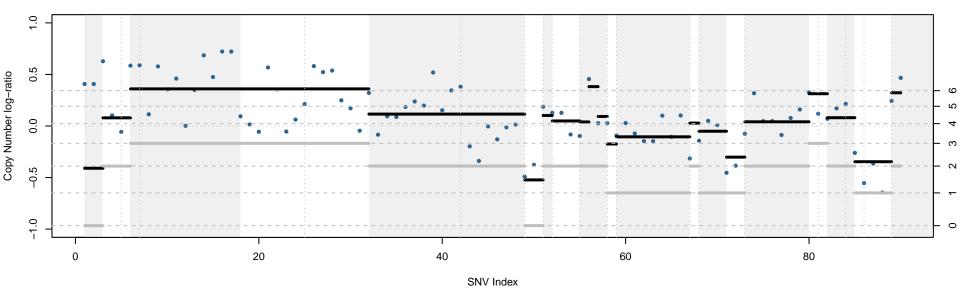
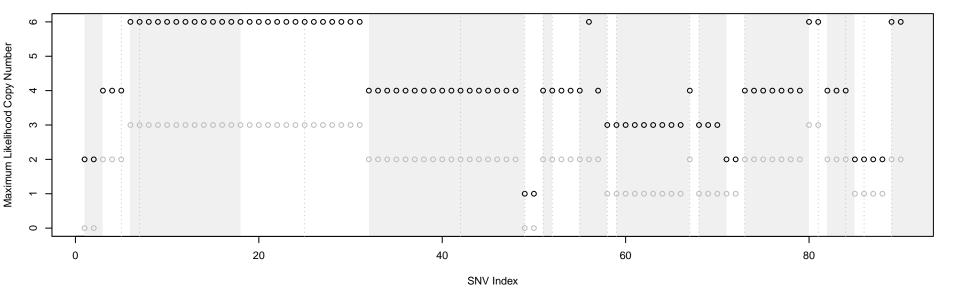
Purity: 0.33 Tumor ploidy: 3.874 0 3 2 5 0.10 0.08 Fraction Genome 90.0 0.04 0.02 0.00 -1.0 -0.5 0.0 0.5 1.0 log2 ratio

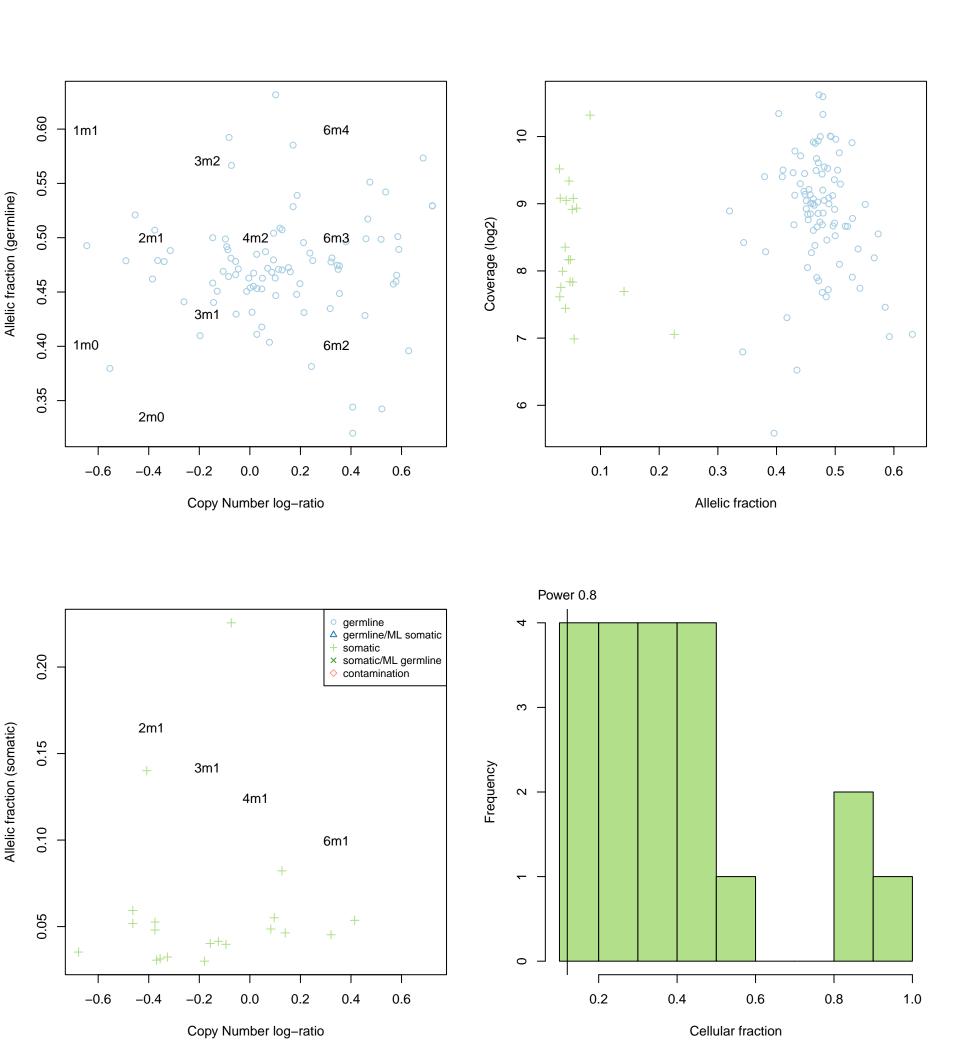
Purity: 0.33 Tumor ploidy: 3.874 SNV log-likelihood: -29.33 GoF: 91.1% Mean coverage: 454;525

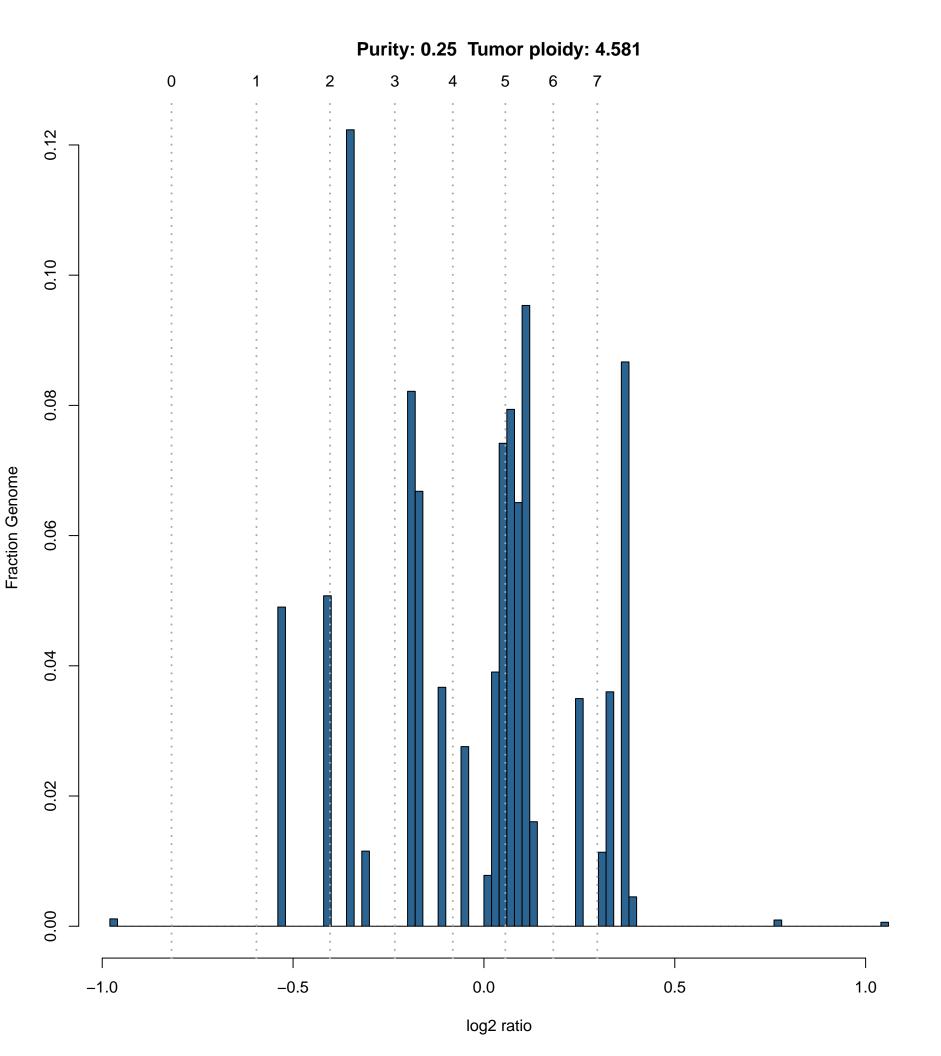


SCNA-fit log-likelihood: -5215.59

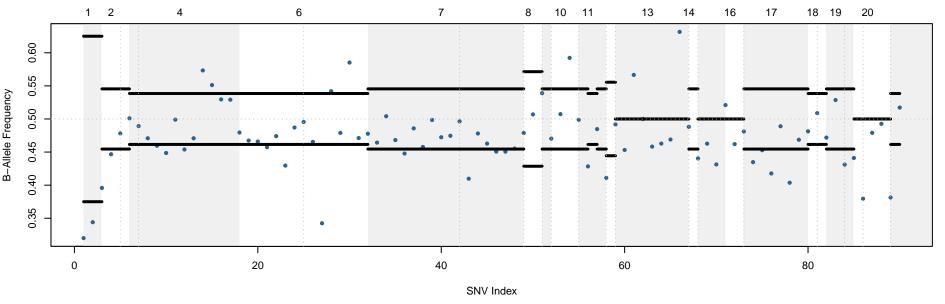




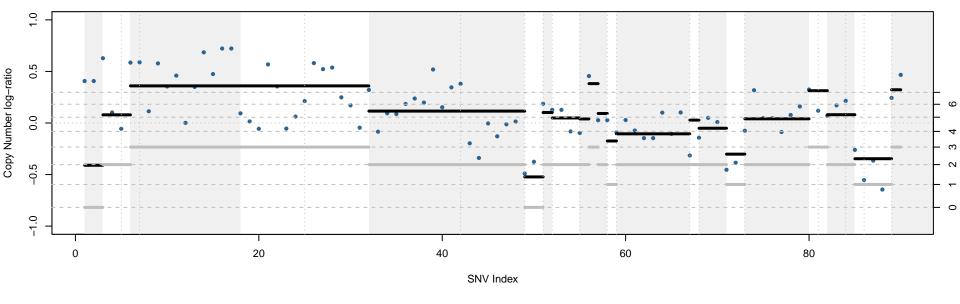


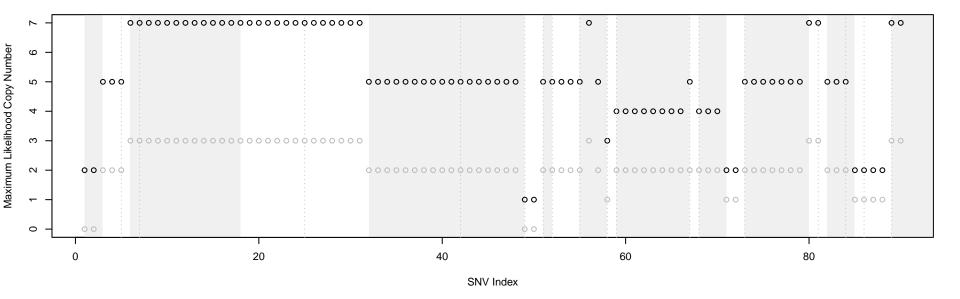


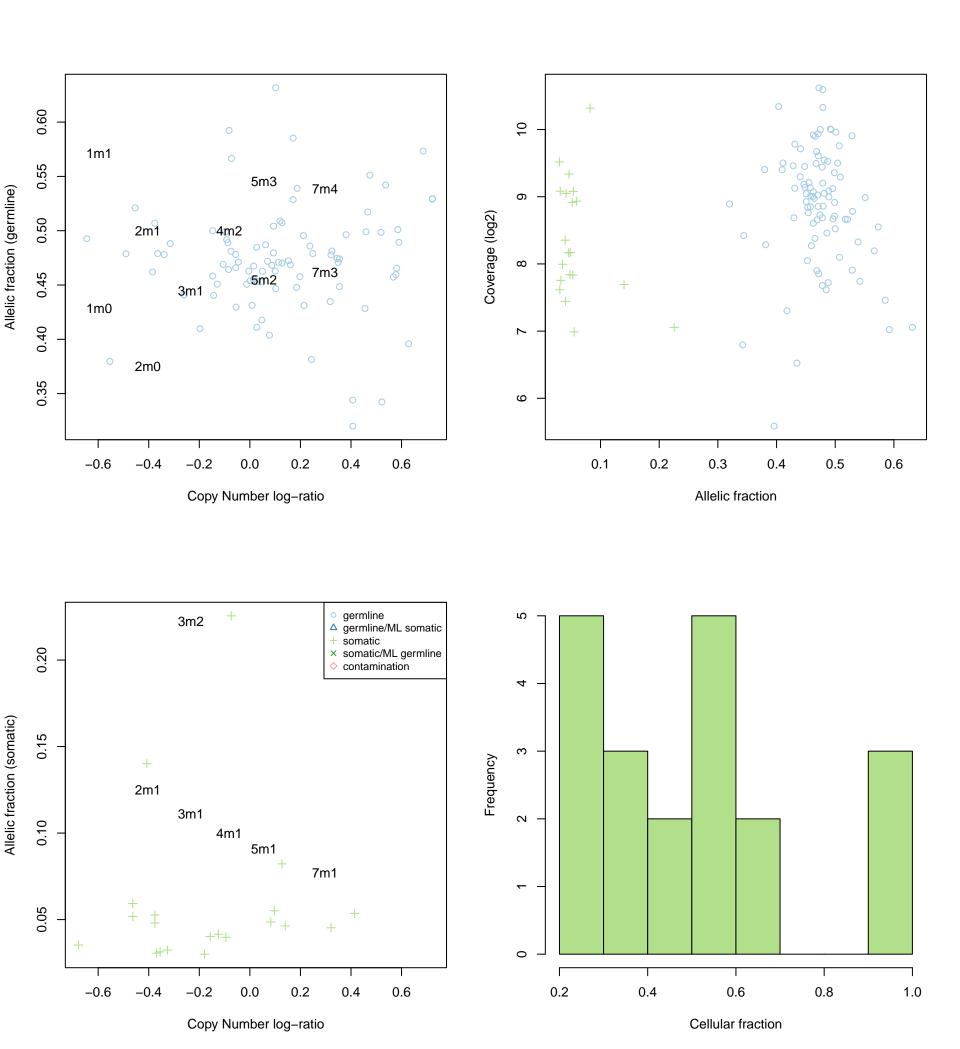




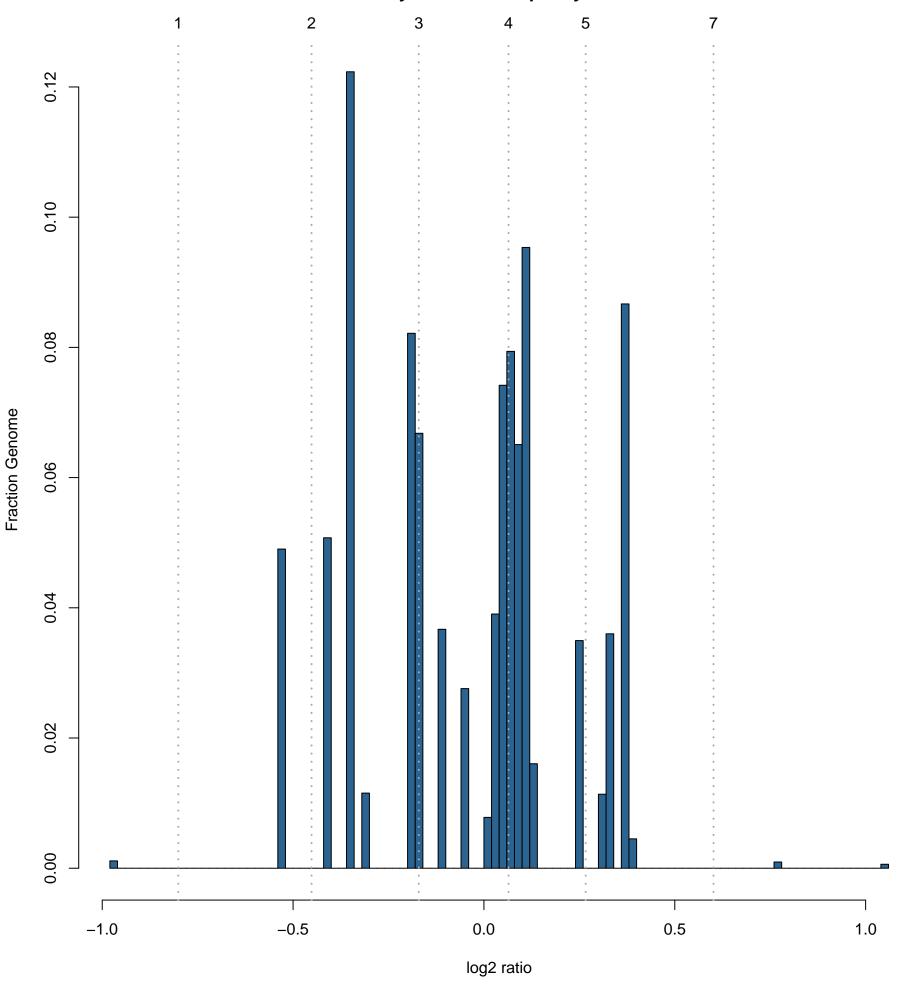
SCNA-fit log-likelihood: -5191.05



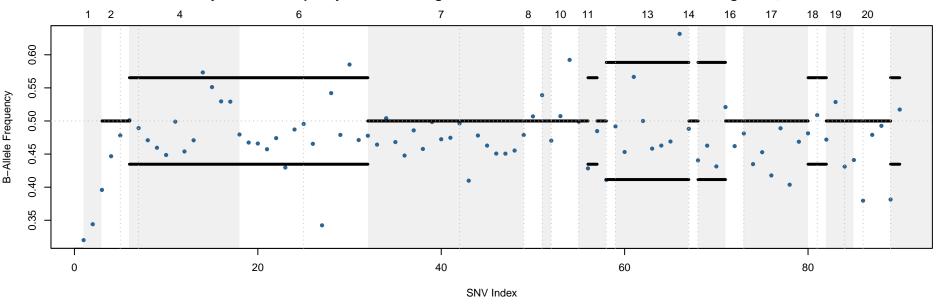




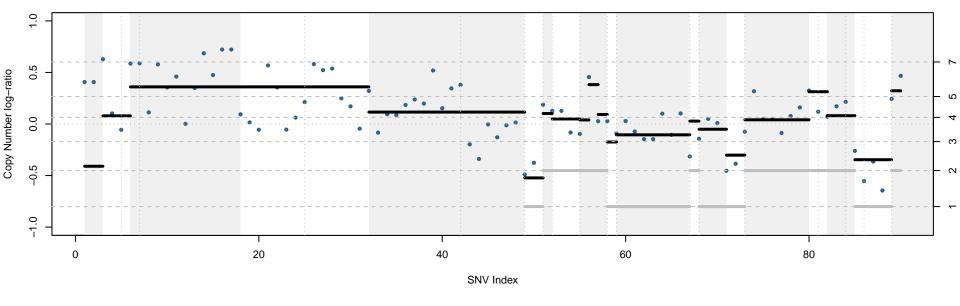
Purity: 0.43 Tumor ploidy: 3.709

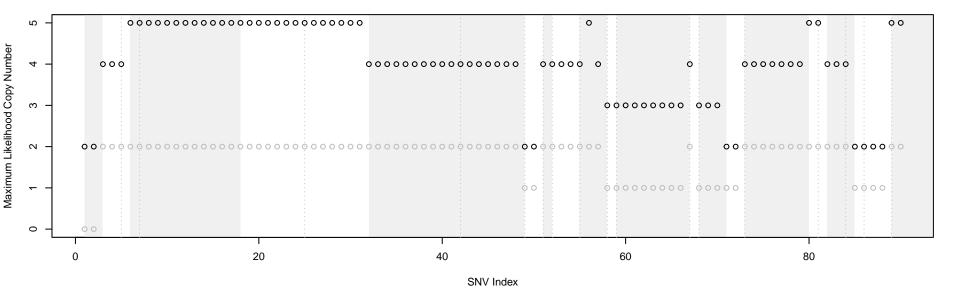


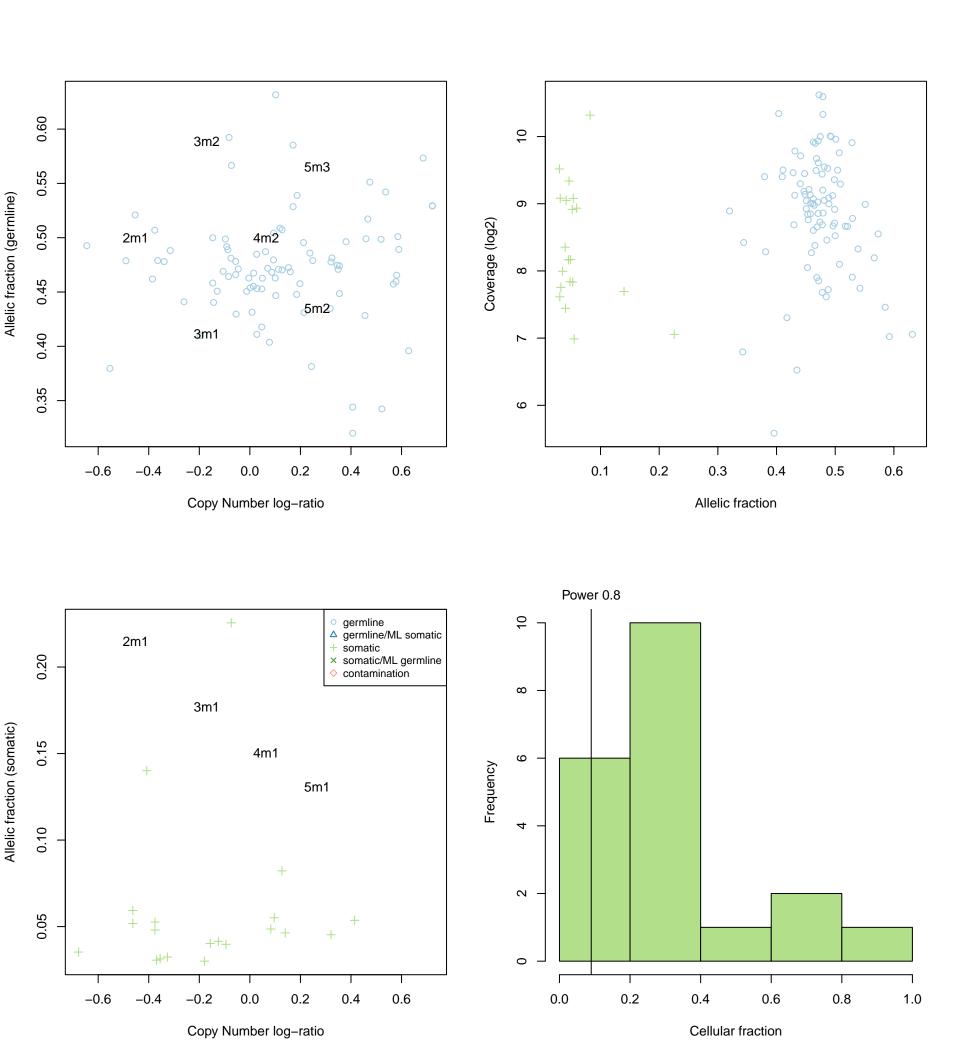
Purity: 0.43 Tumor ploidy: 3.709 SNV log-likelihood: -55.86 GoF: 87.4% Mean coverage: 454;525



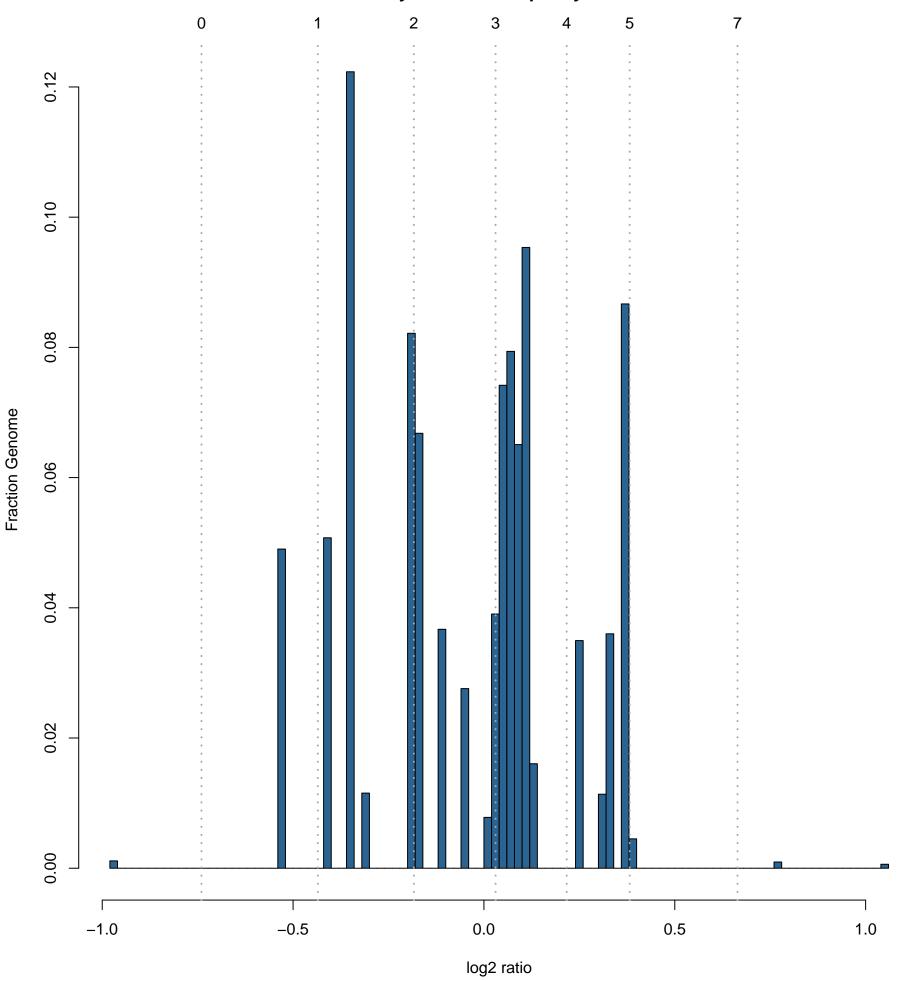
SCNA-fit log-likelihood: -5244.45



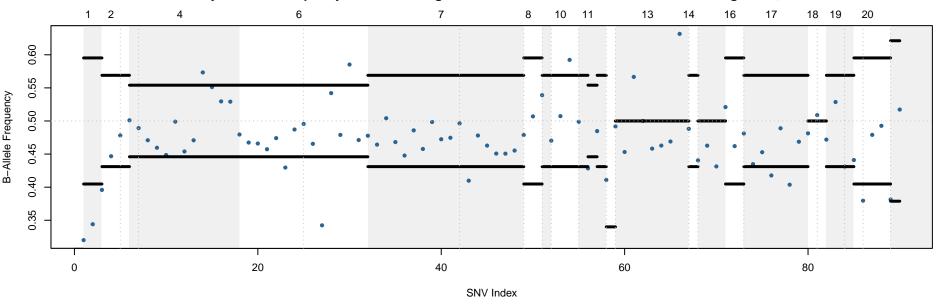




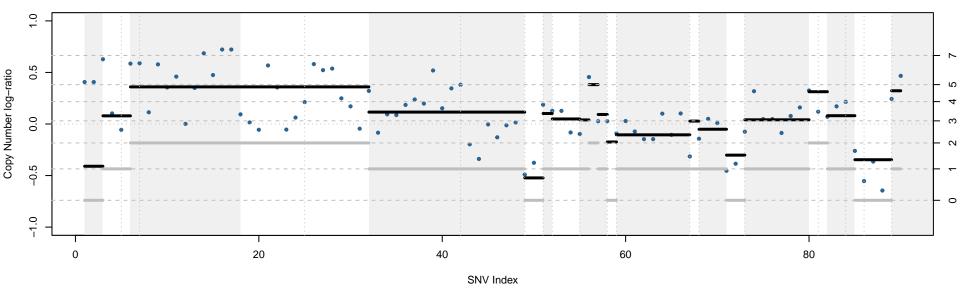
Purity: 0.32 Tumor ploidy: 2.848

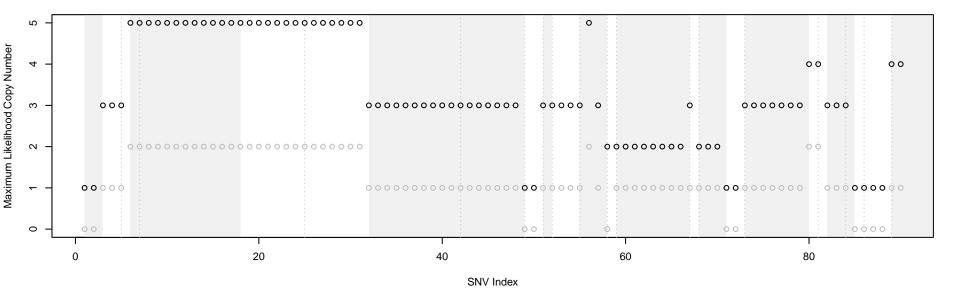


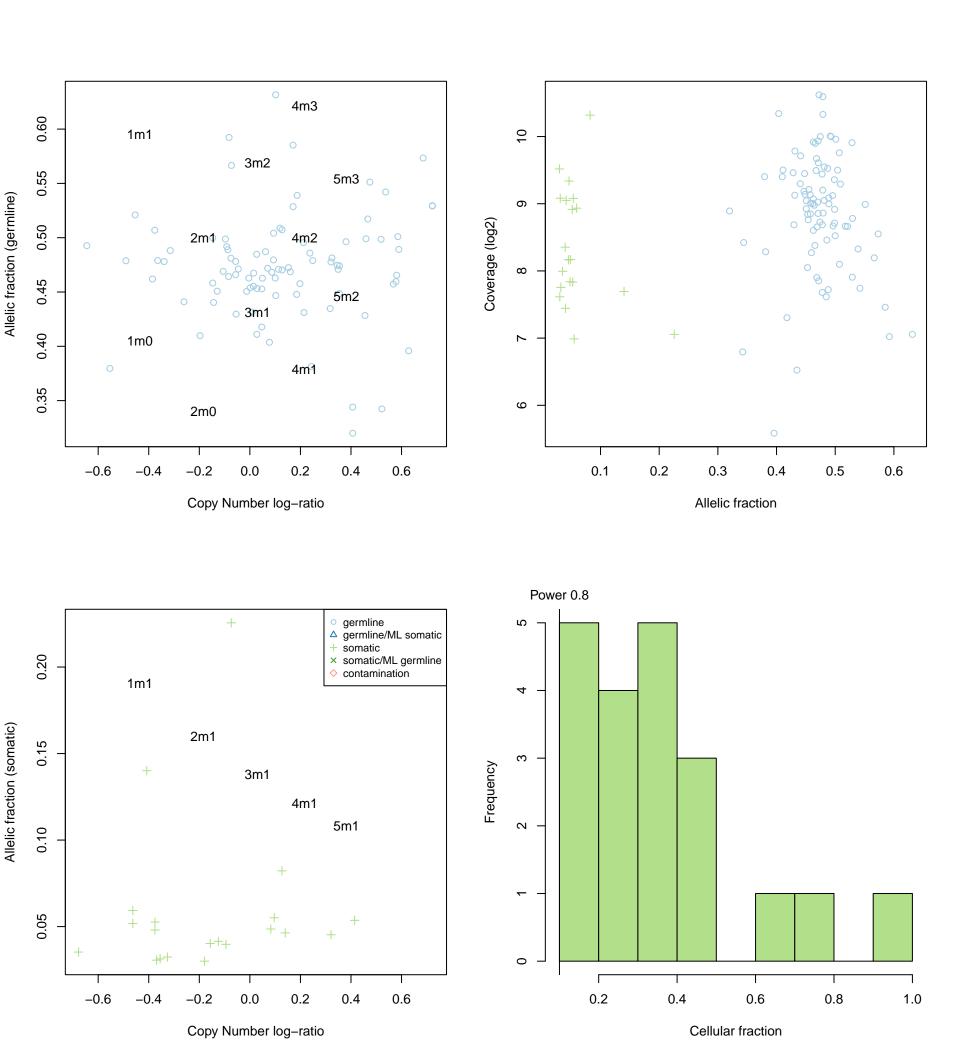
Purity: 0.32 Tumor ploidy: 2.848 SNV log-likelihood: -51.37 GoF: 89.5% Mean coverage: 454;525



SCNA-fit log-likelihood: -5237.95



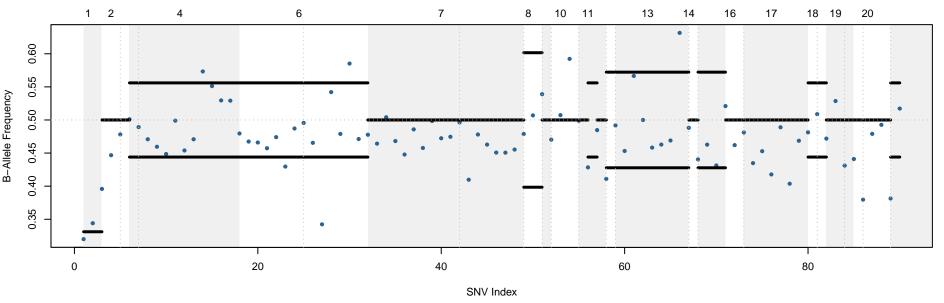




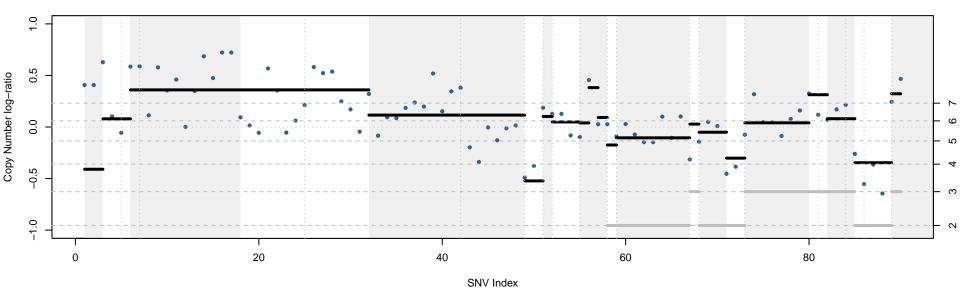
Purity: 0.51 Tumor ploidy: 5.679 5 2 3 6 7 0.10 0.08 Fraction Genome 90.0 0.04 0.02 0.00 -1.0 -0.5 0.0 0.5 1.0

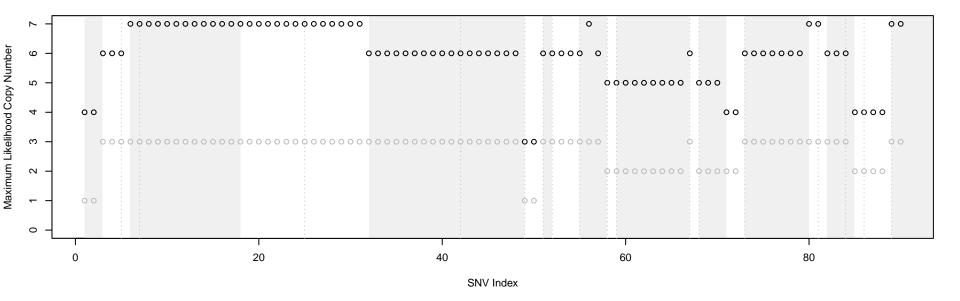
log2 ratio

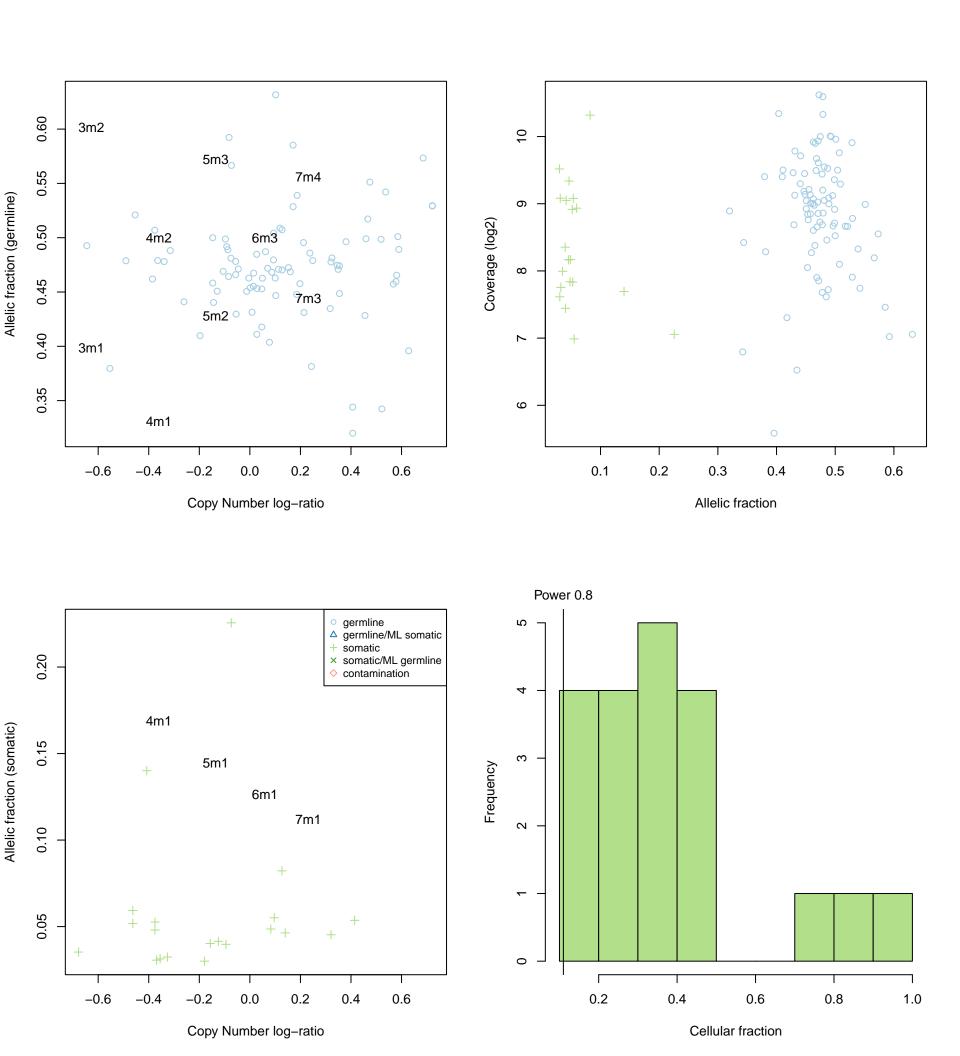
Purity: 0.51 Tumor ploidy: 5.679 SNV log-likelihood: -76.18 GoF: 91.4% Mean coverage: 454;525



SCNA-fit log-likelihood: -5261.41

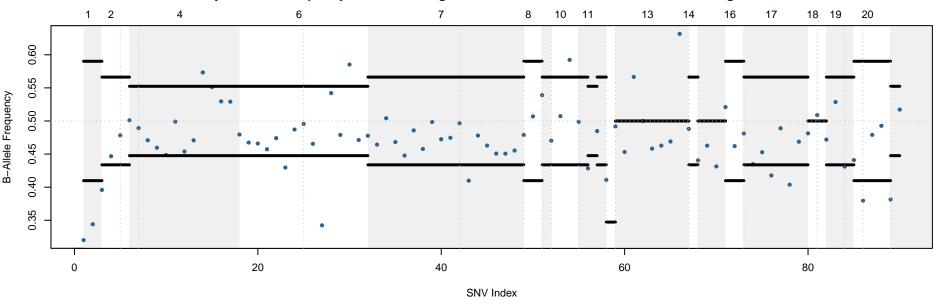




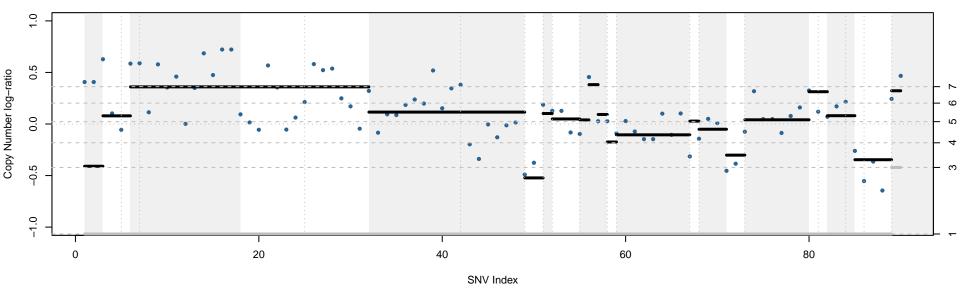


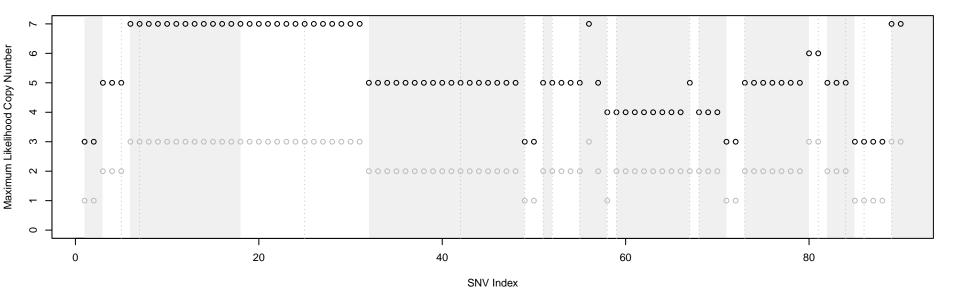
Purity: 0.44 Tumor ploidy: 4.881 3 5 6 0.10 0.08 Fraction Genome 90.0 0.04 0.02 0.00 -1.0 -0.5 0.0 0.5 1.0 log2 ratio

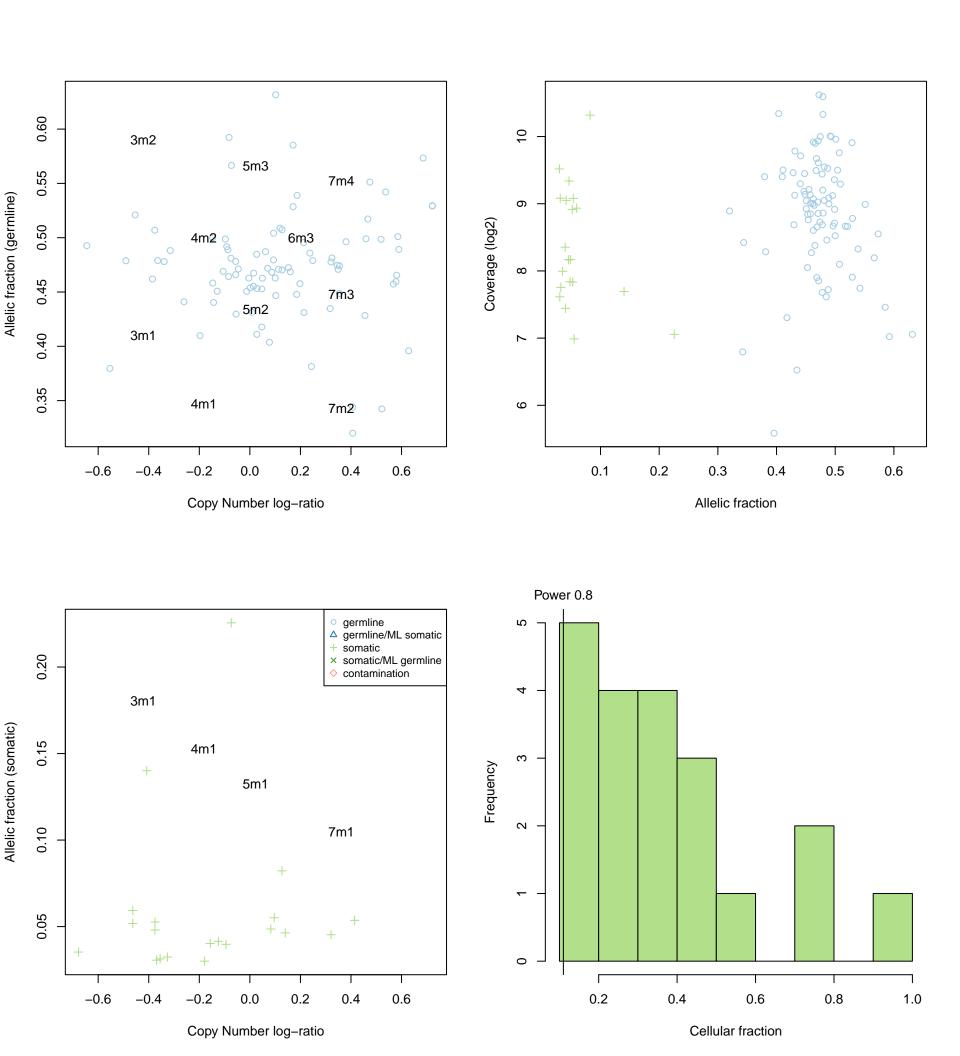
Purity: 0.44 Tumor ploidy: 4.881 SNV log-likelihood: -90.6 GoF: 90.7% Mean coverage: 454;525



SCNA-fit log-likelihood: -5243.86

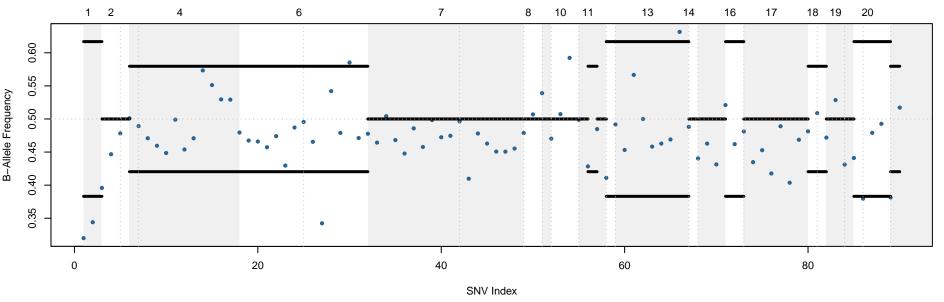




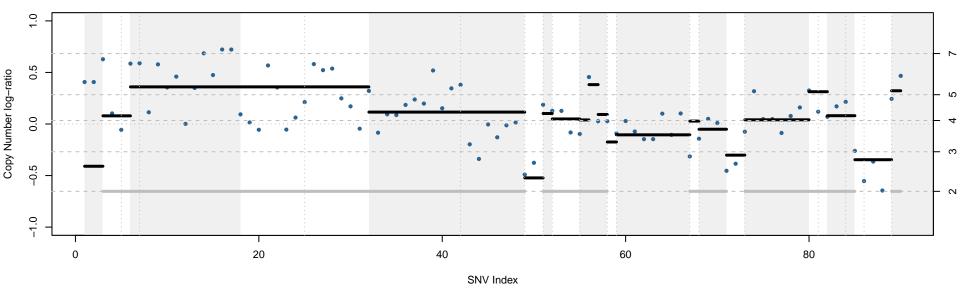


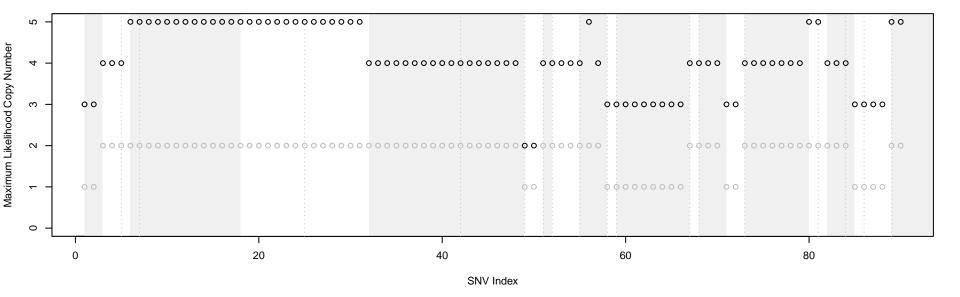
Purity: 0.61 Tumor ploidy: 3.877 2 3 7 5 0.10 0.08 Fraction Genome 90.0 0.04 0.02 0.00 -1.0 -0.5 0.0 0.5 1.0 log2 ratio

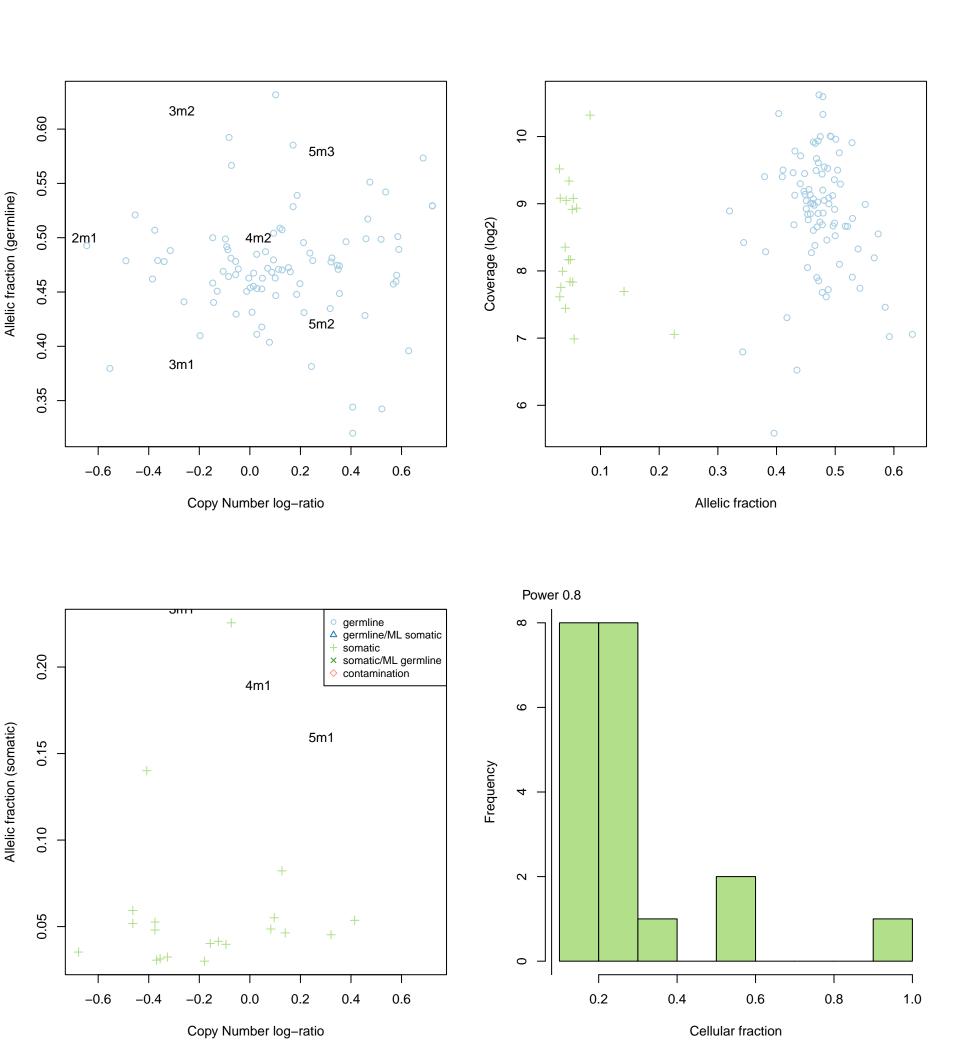




SCNA-fit log-likelihood: -5353.03

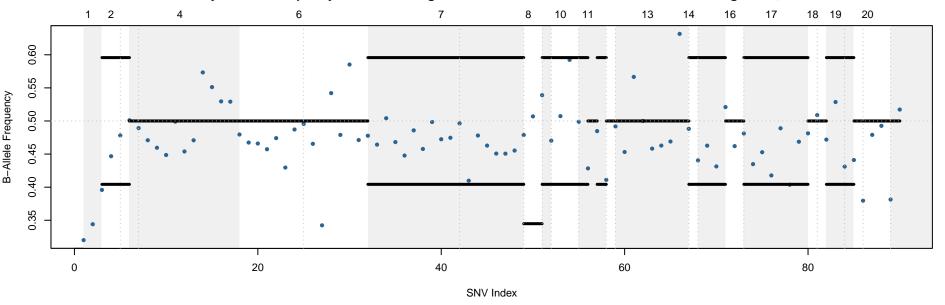




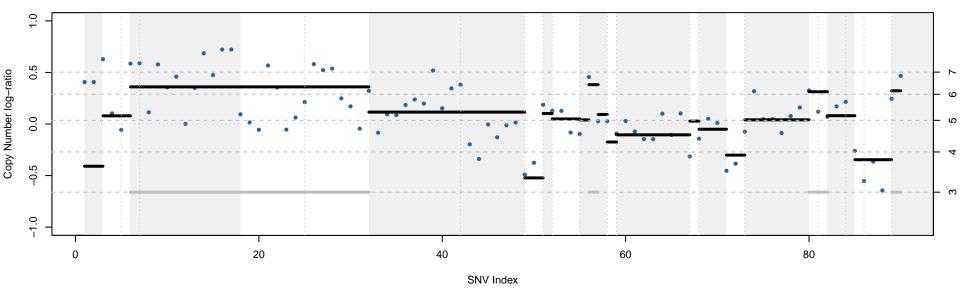


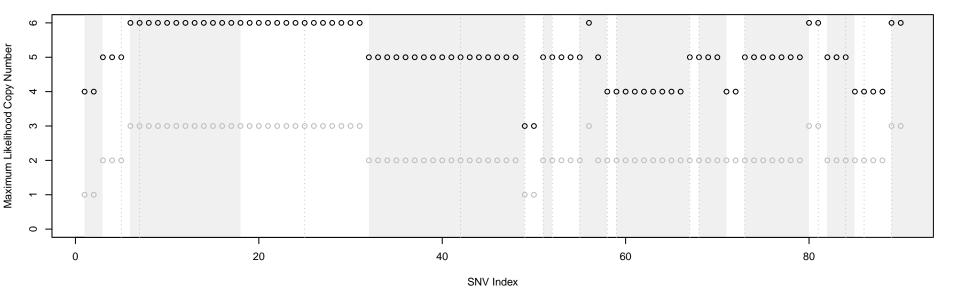
Purity: 0.9 Tumor ploidy: 4.874 7 3 5 6 0.10 0.08 Fraction Genome 90.0 0.04 0.02 0.00 -1.0 -0.5 0.0 0.5 1.0 log2 ratio

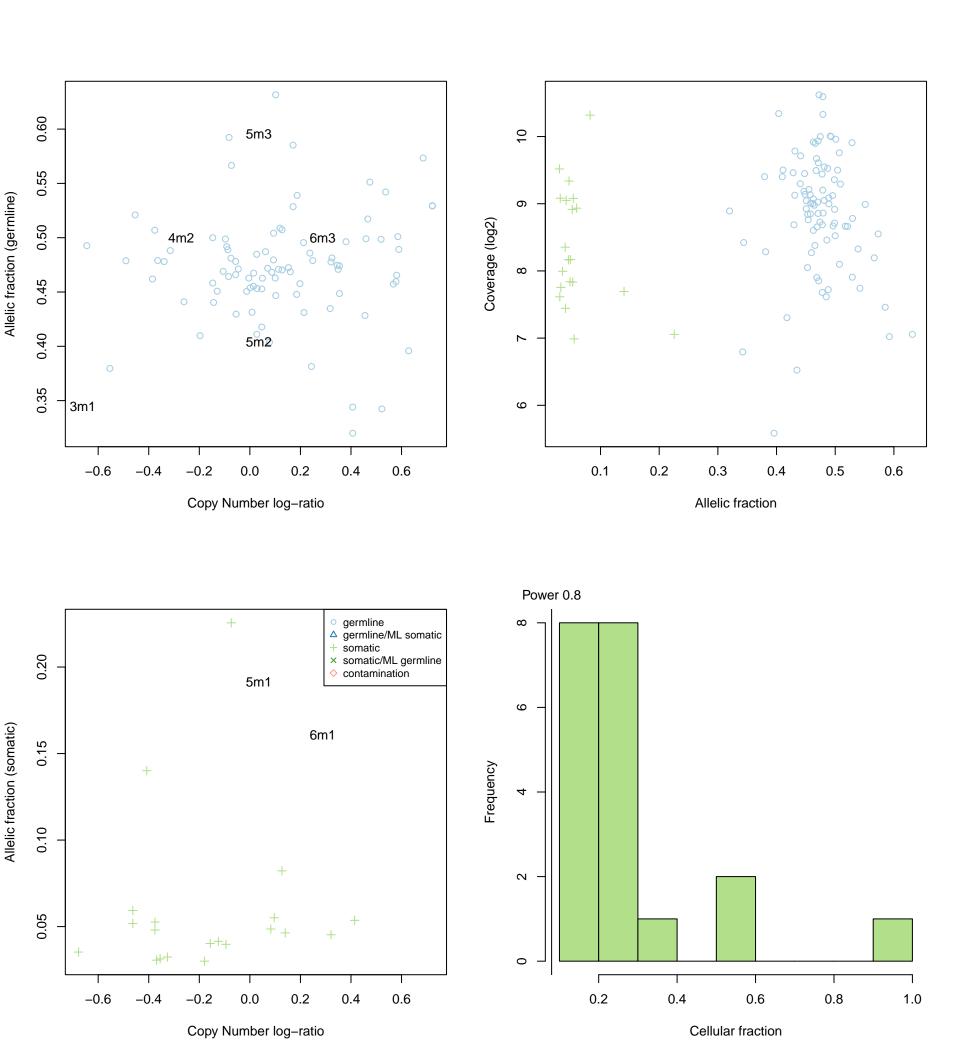
Purity: 0.9 Tumor ploidy: 4.874 SNV log-likelihood: -182.43 GoF: 80.2% Mean coverage: 454;525



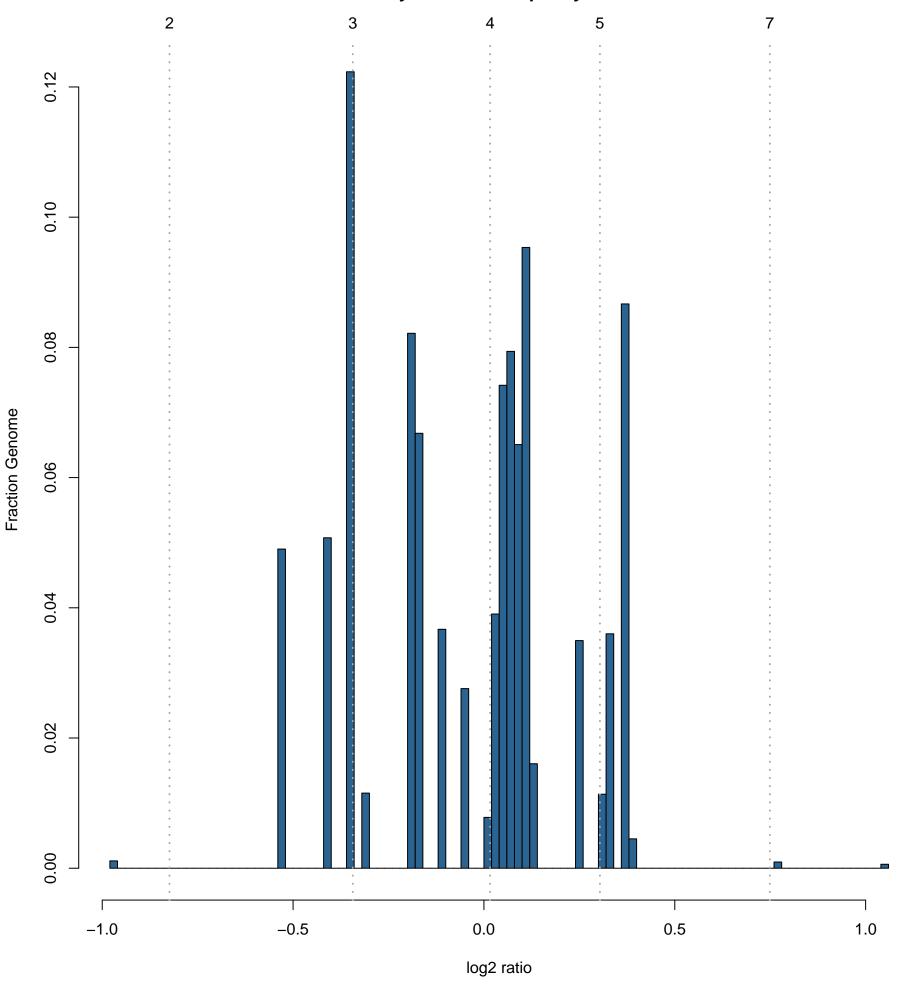
SCNA-fit log-likelihood: -5355.93



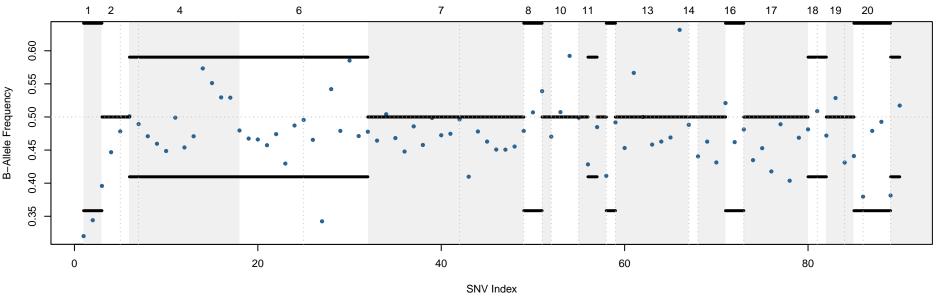




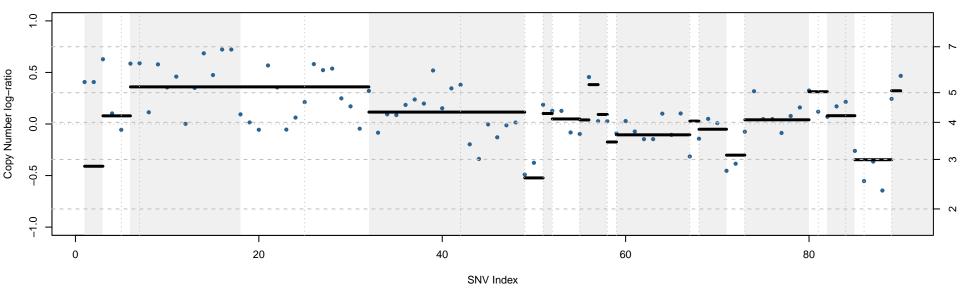
Purity: 0.79 Tumor ploidy: 3.949

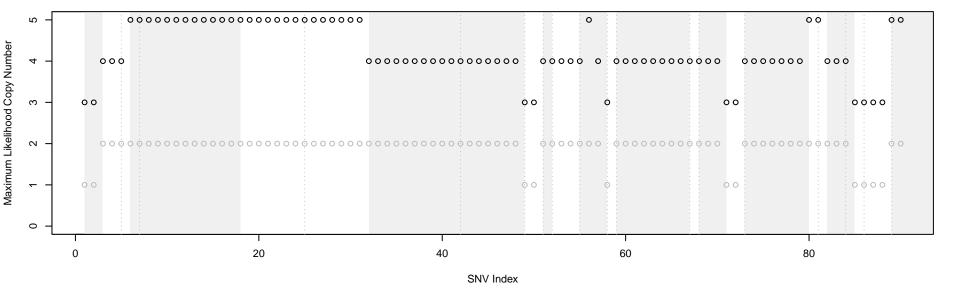


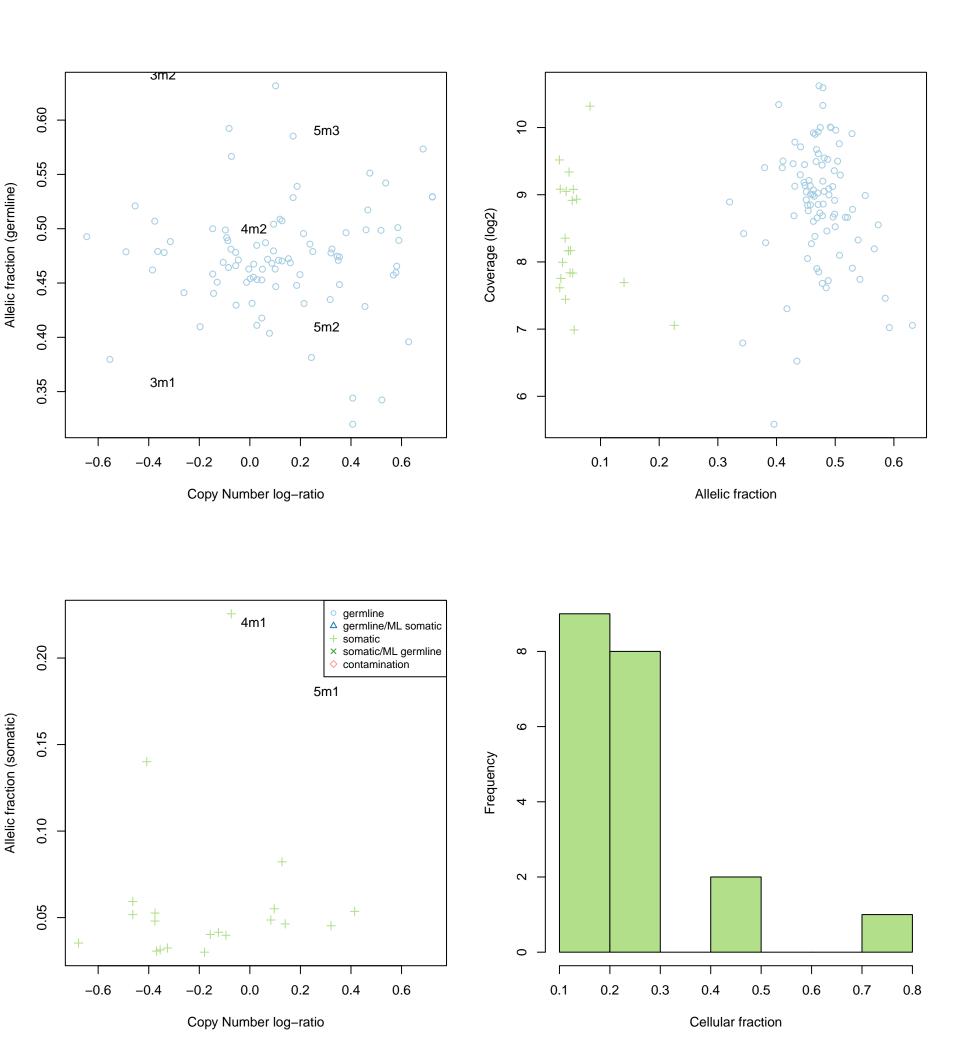




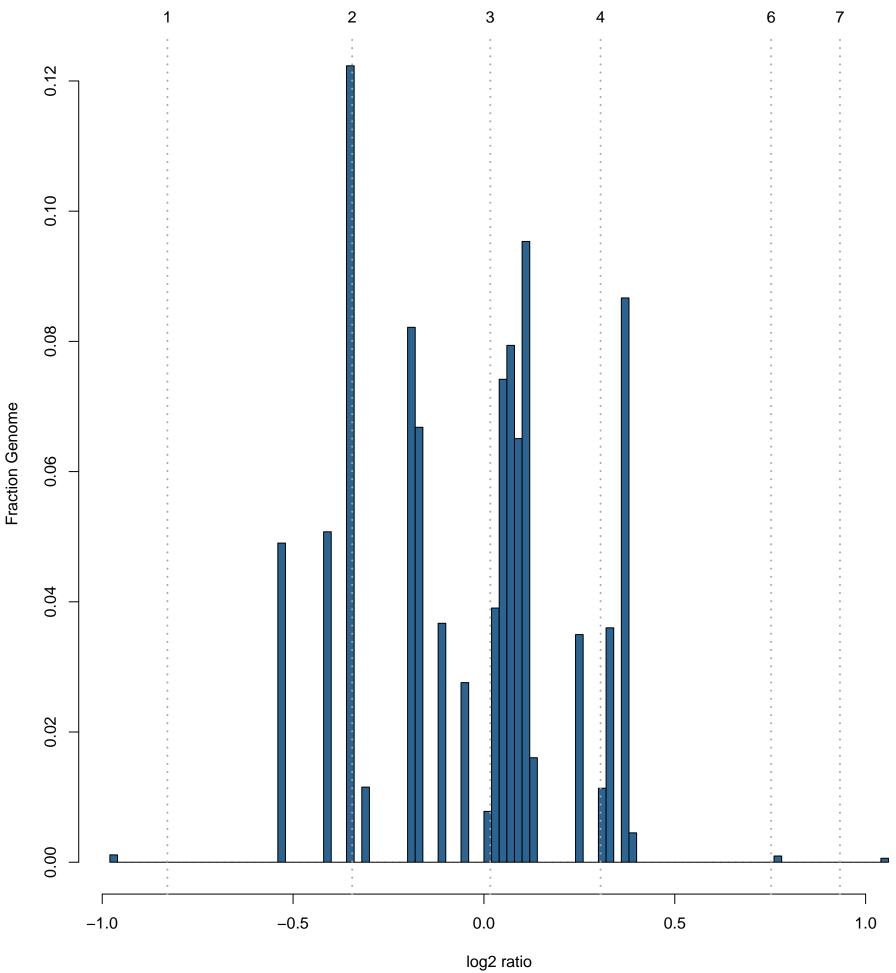
SCNA-fit log-likelihood: -5425.36



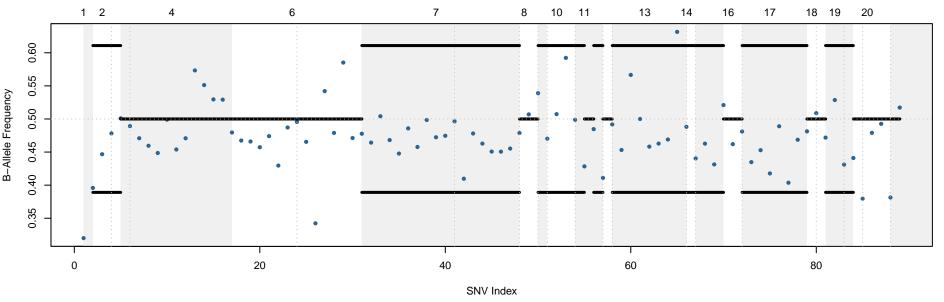




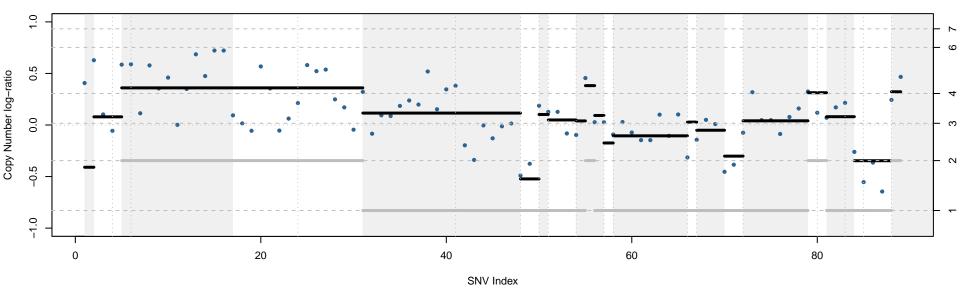
Purity: 0.57 Tumor ploidy: 2.949

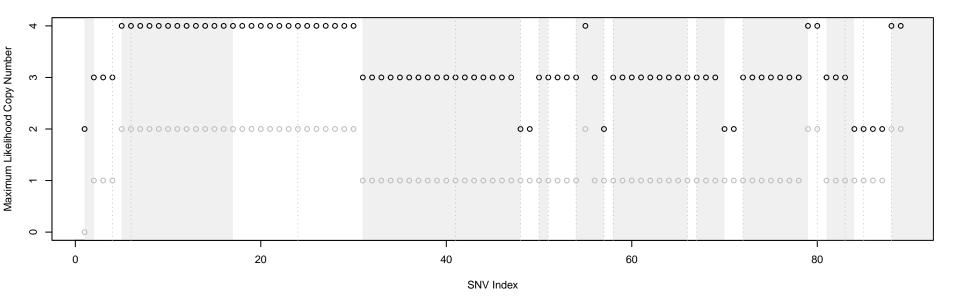


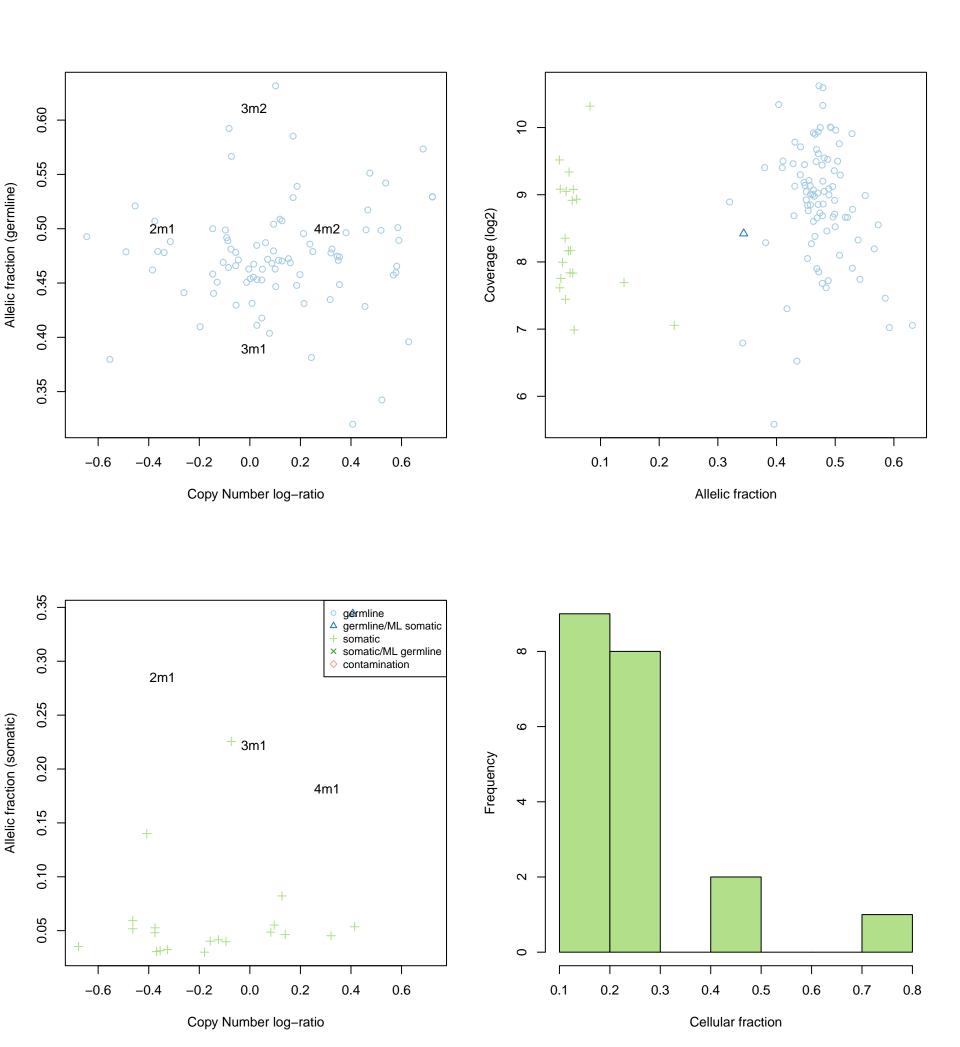




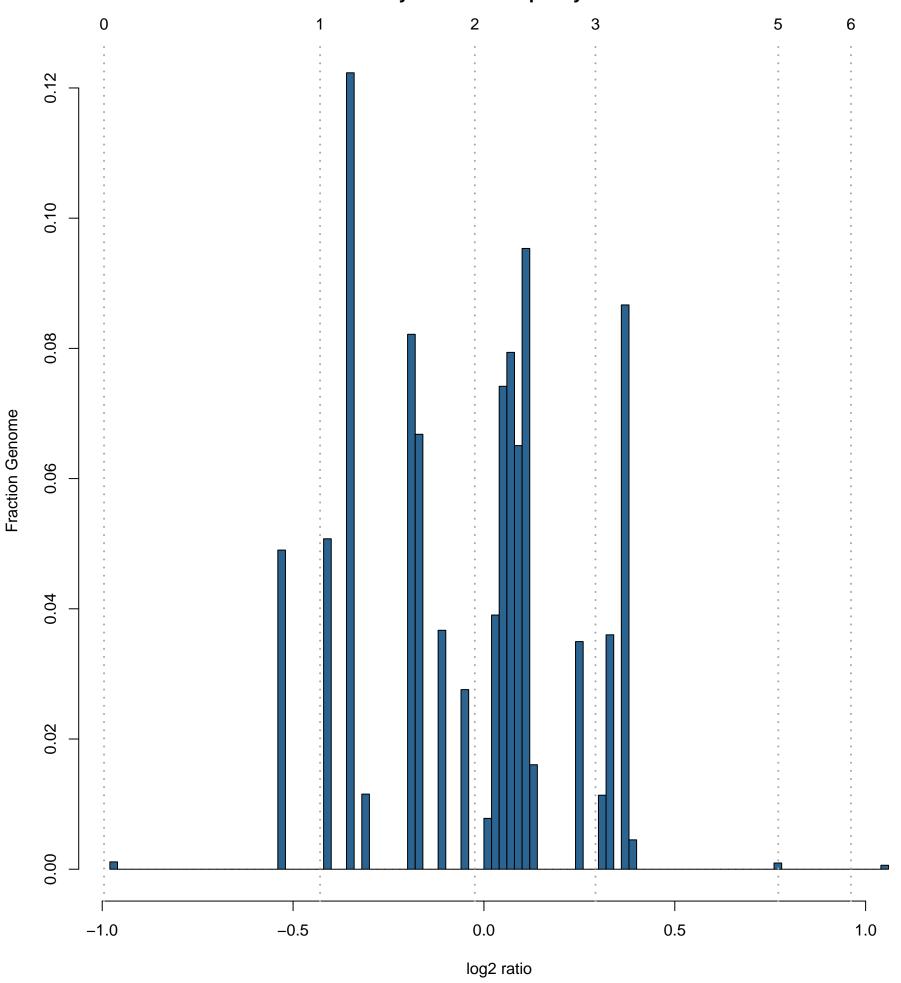
SCNA-fit log-likelihood: -5417.11



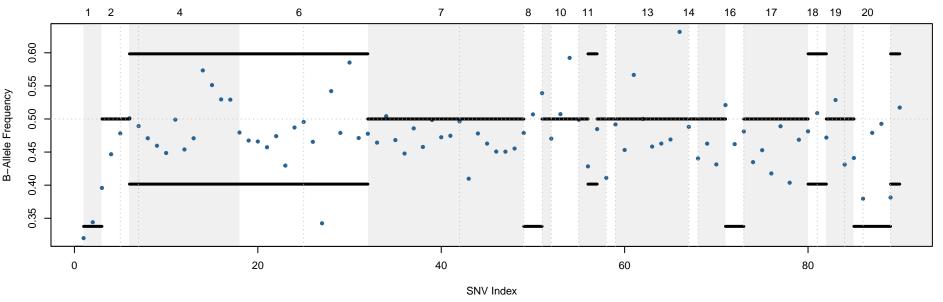




Purity: 0.49 Tumor ploidy: 2.068







SCNA-fit log-likelihood: -5486.99

