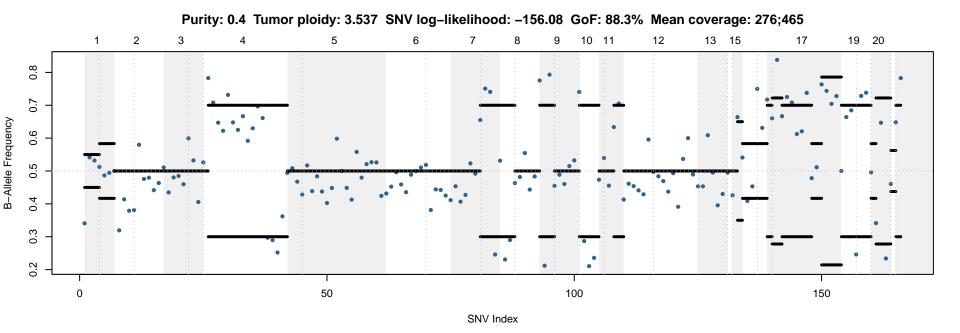
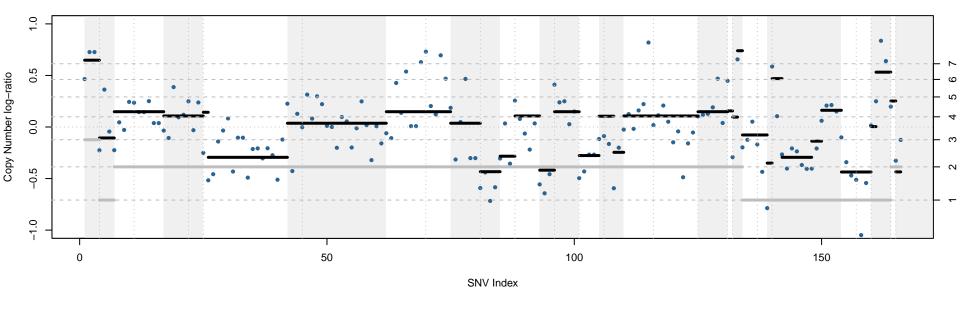
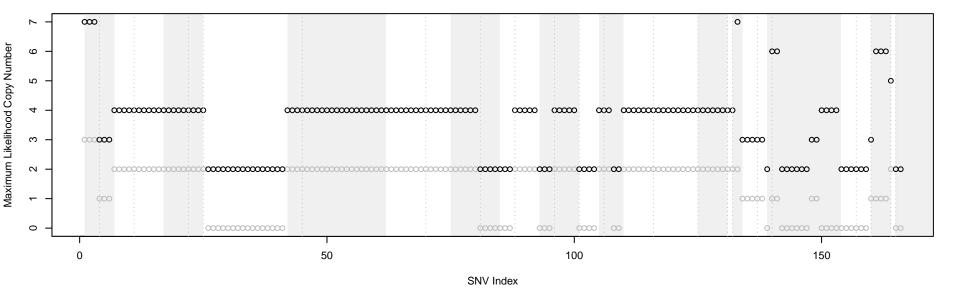
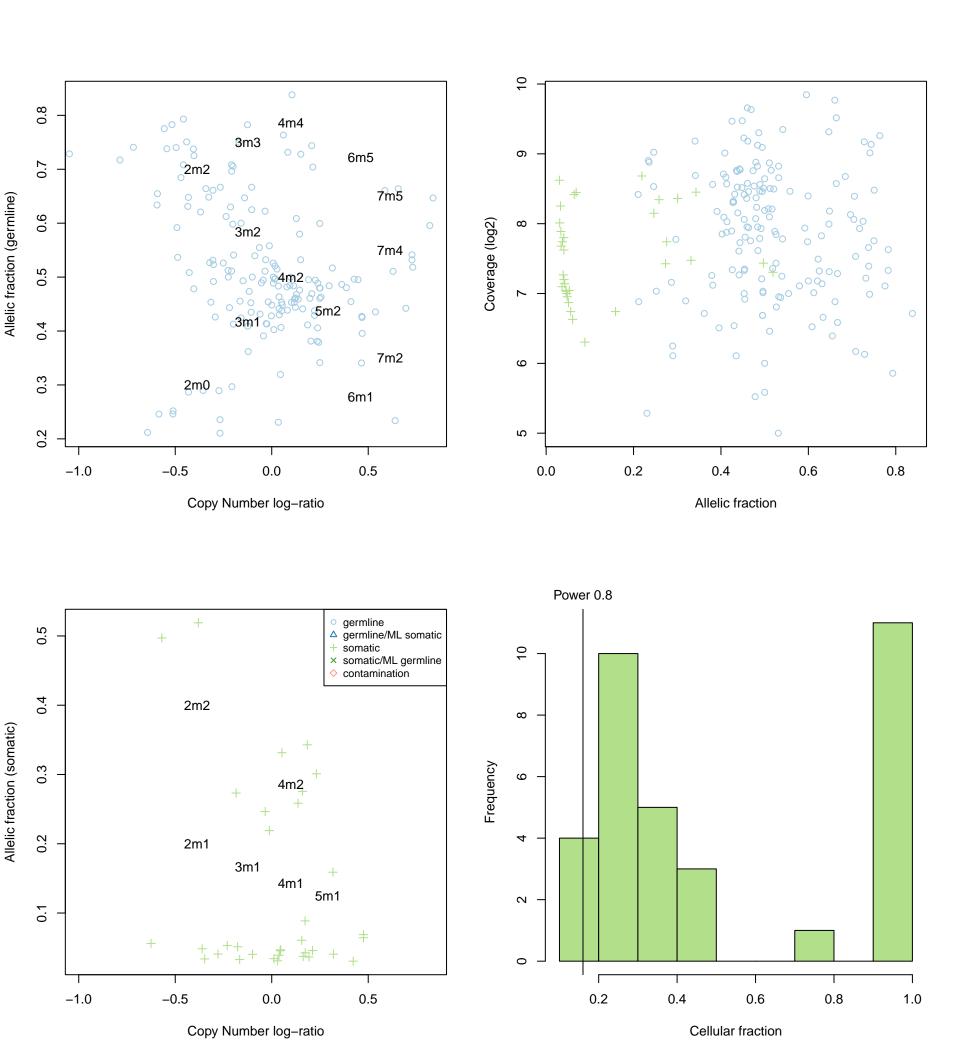
Purity: 0.4 Tumor ploidy: 3.537 2 3 6 5 0.20 Fraction Genome 0.10 0.05 0.00 -0.5 0.0 0.5 1.0 log2 ratio



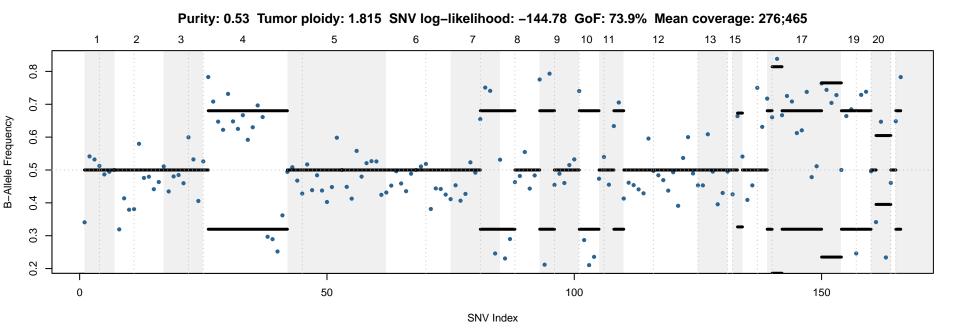
SCNA-fit log-likelihood: -9821.99



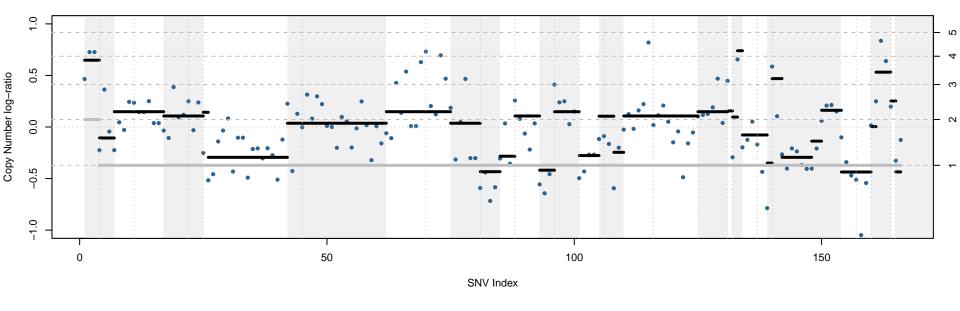


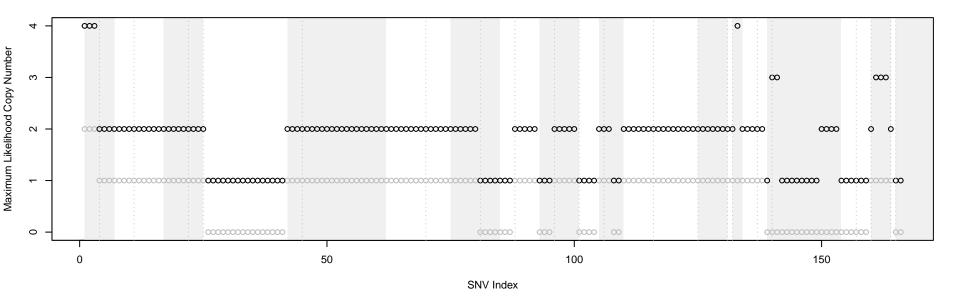


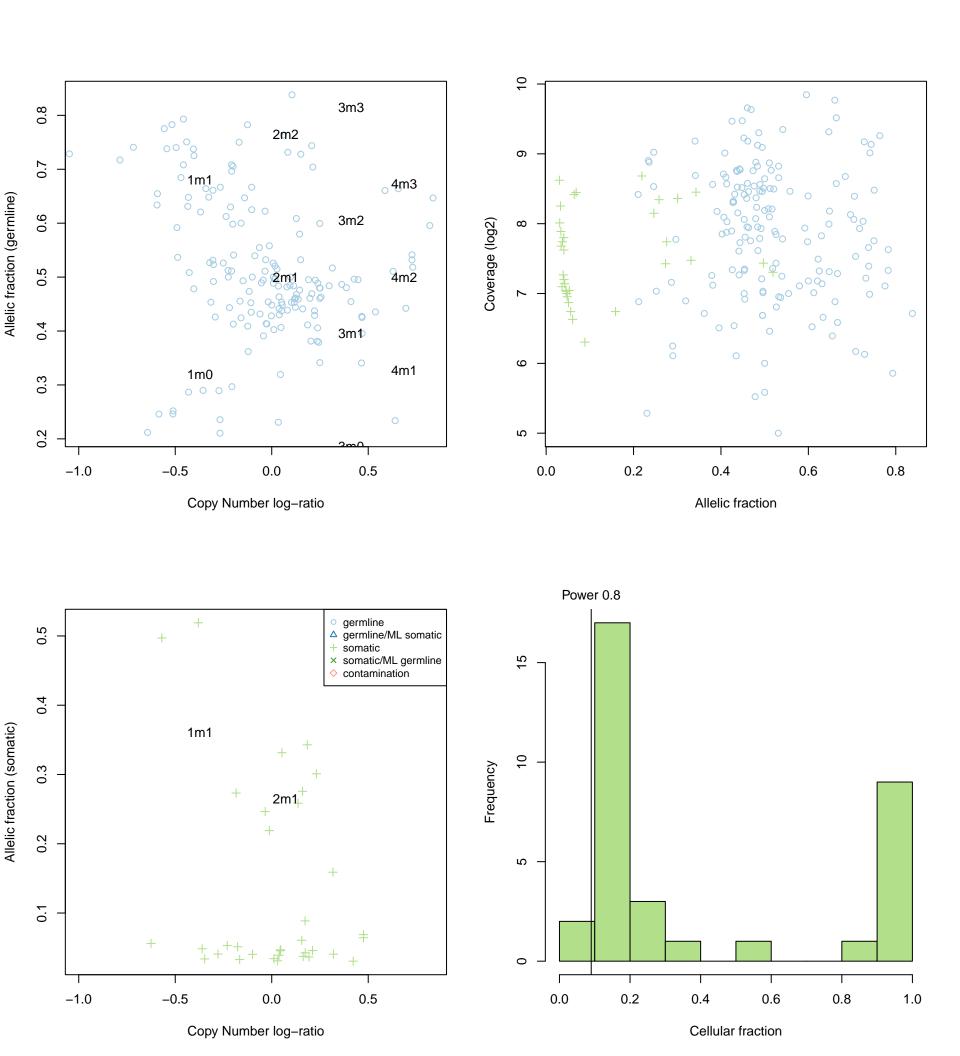
Purity: 0.53 Tumor ploidy: 1.815 2 6 3 5 0.20 Fraction Genome 0.05 0.00 -0.5 0.0 0.5 1.0 log2 ratio



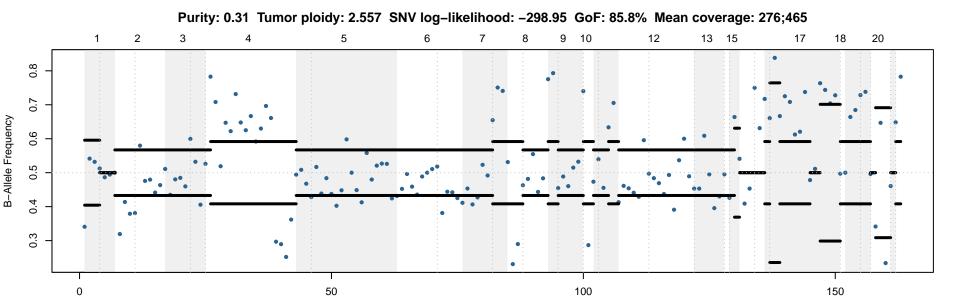
SCNA-fit log-likelihood: -9997.48





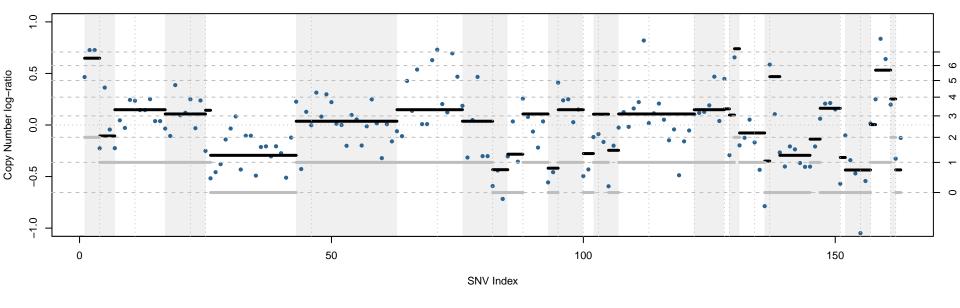


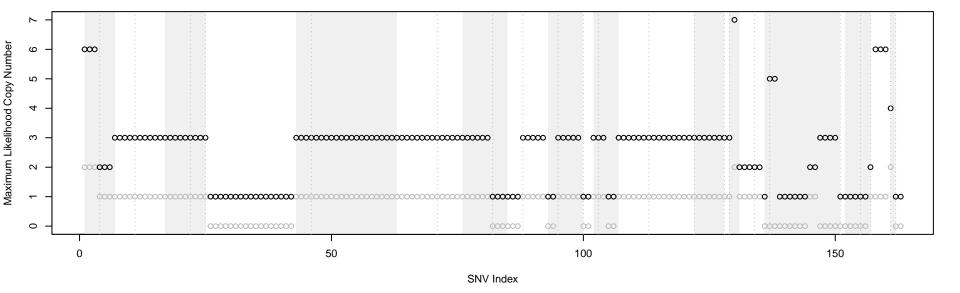
Purity: 0.31 Tumor ploidy: 2.557 5 0 2 6 0.25 0.20 Fraction Genome 0.10 0.05 0.00 -0.5 0.0 0.5 1.0 log2 ratio

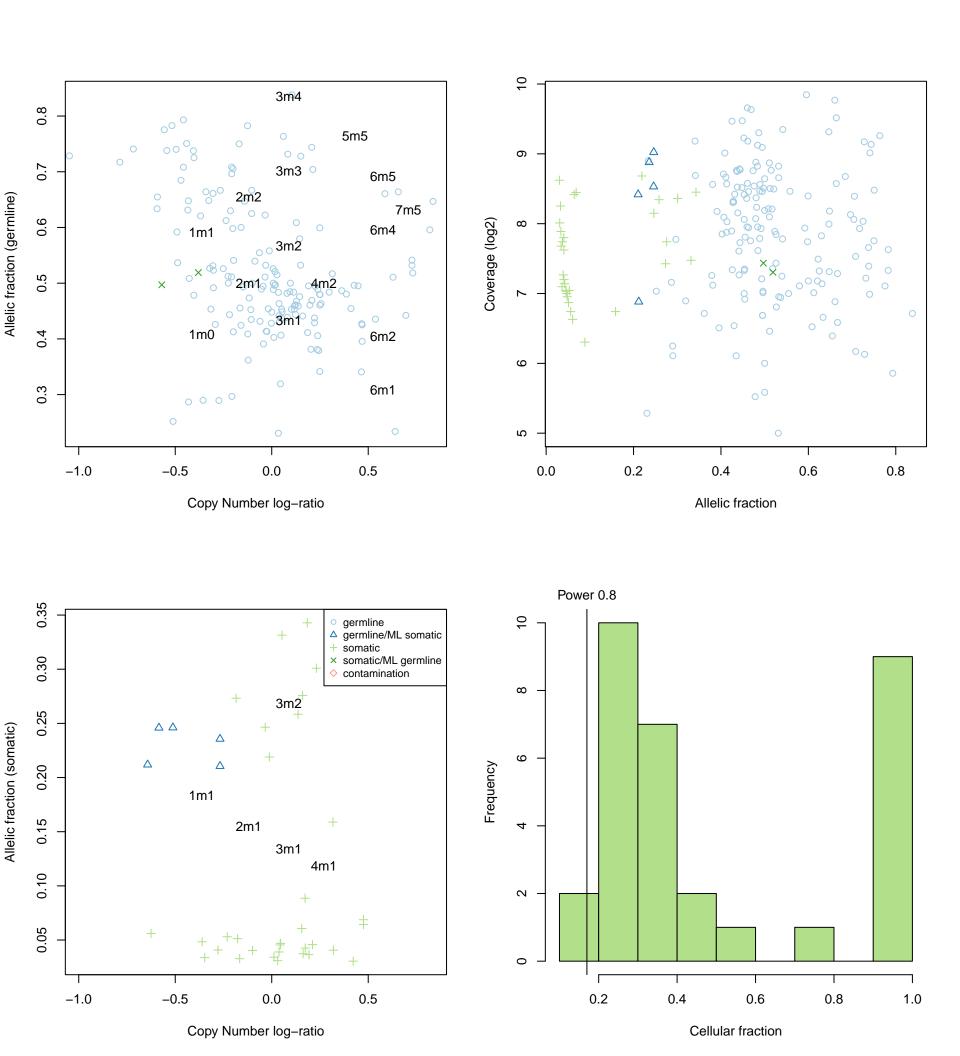


SCNA-fit log-likelihood: -9798.34

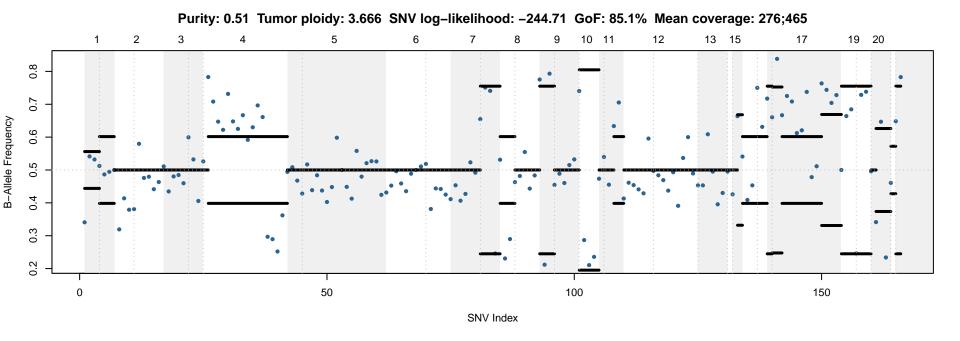
SNV Index



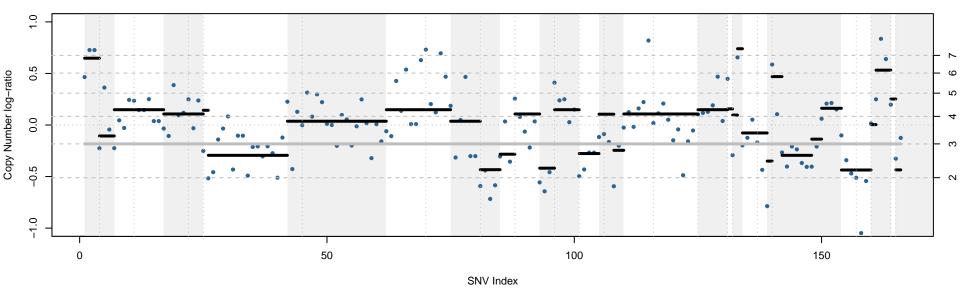


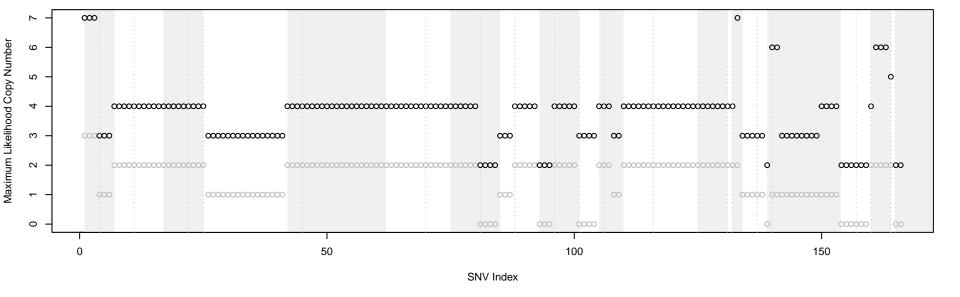


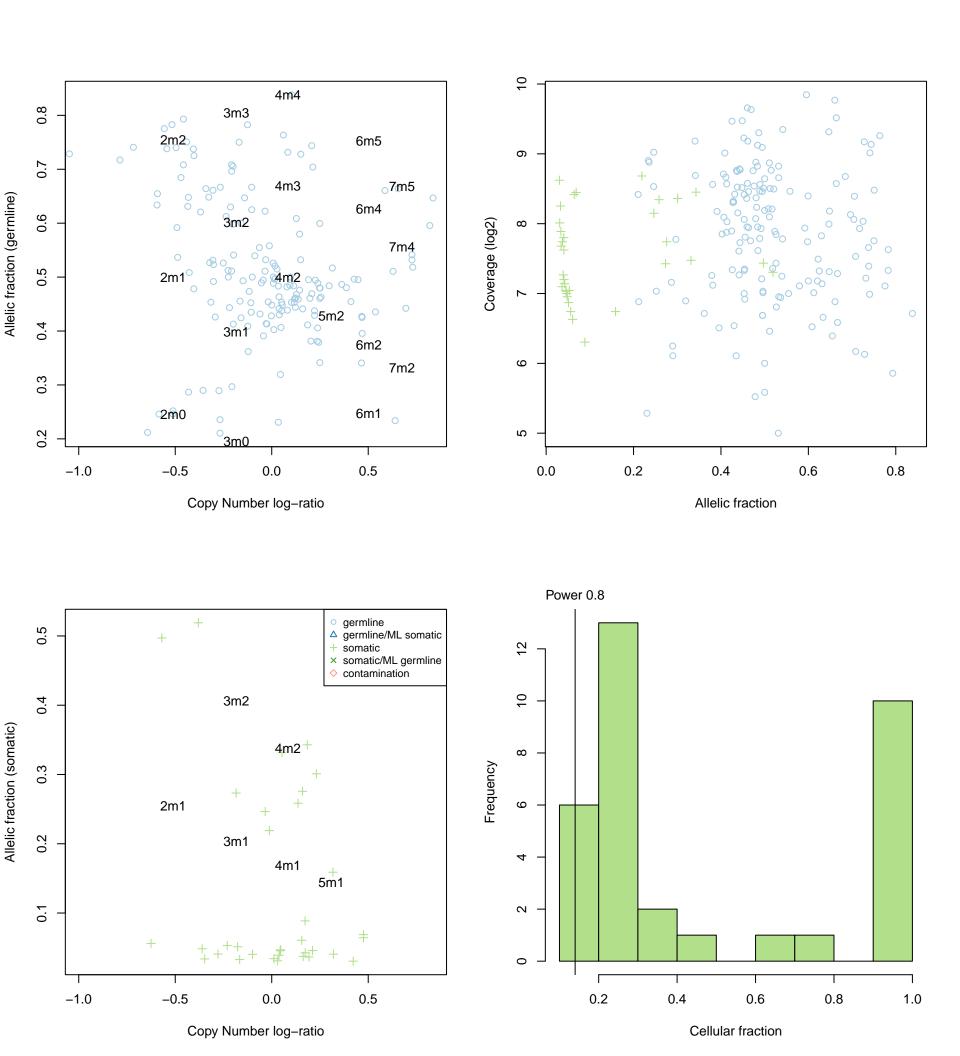
Purity: 0.51 Tumor ploidy: 3.666 2 6 3 5 7 0.20 Fraction Genome 0.10 0.05 0.00 -0.5 0.0 0.5 1.0 log2 ratio



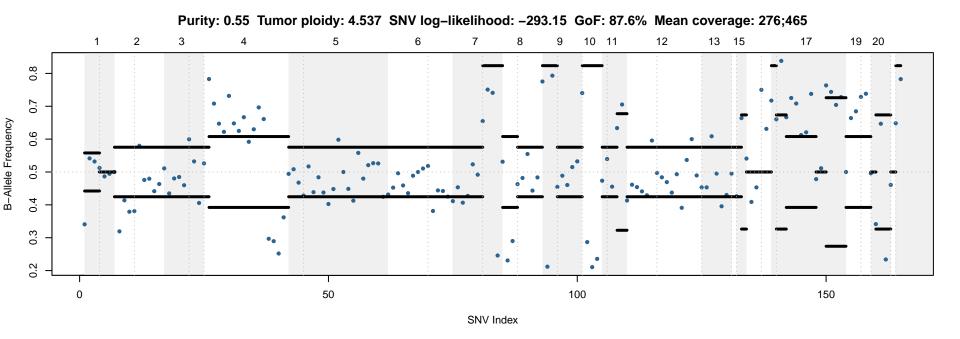
SCNA-fit log-likelihood: -9947.23



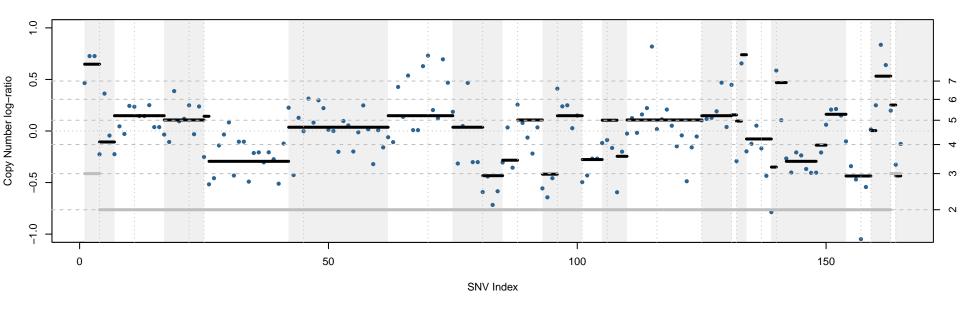


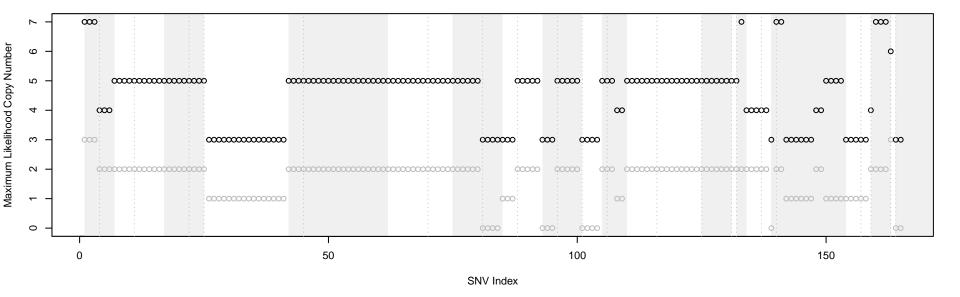


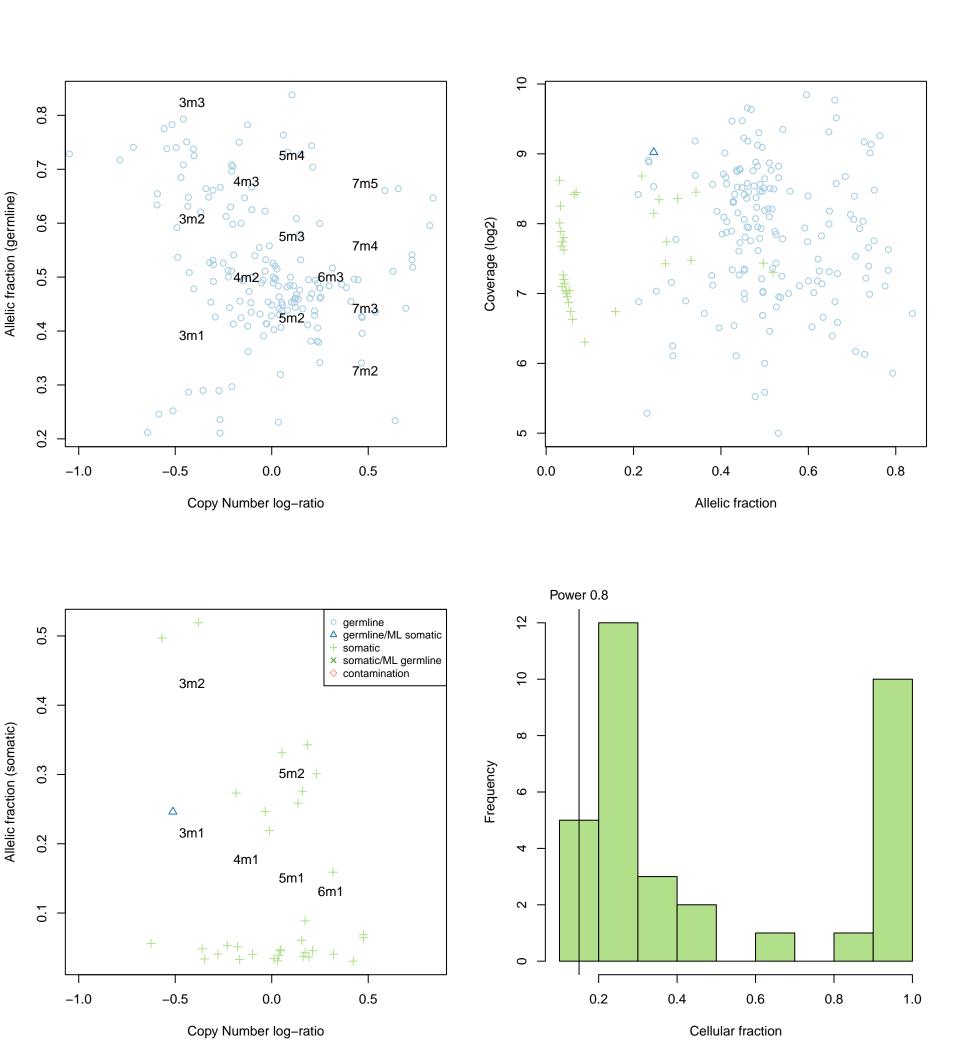
Purity: 0.55 Tumor ploidy: 4.537 3 5 6 4 0.20 Fraction Genome 0.10 0.05 0.00 -0.5 0.0 0.5 1.0 log2 ratio



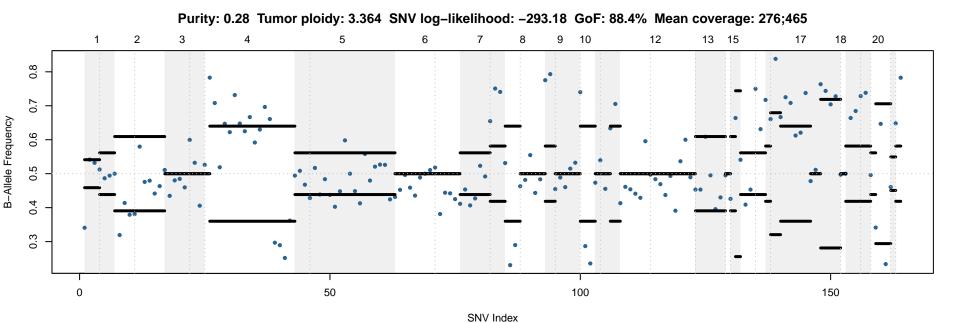
SCNA-fit log-likelihood: -9992.61



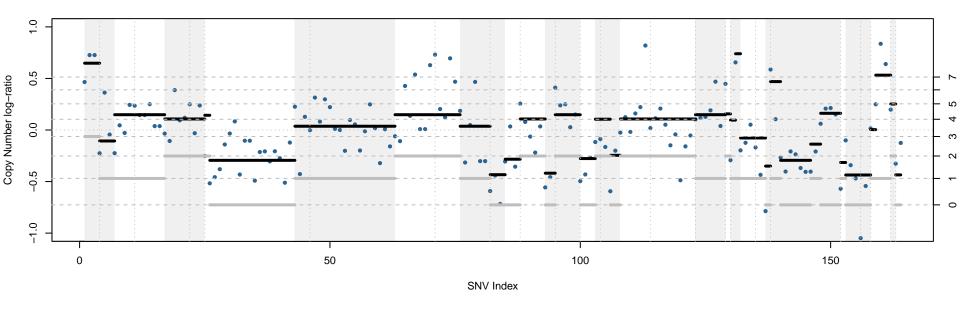


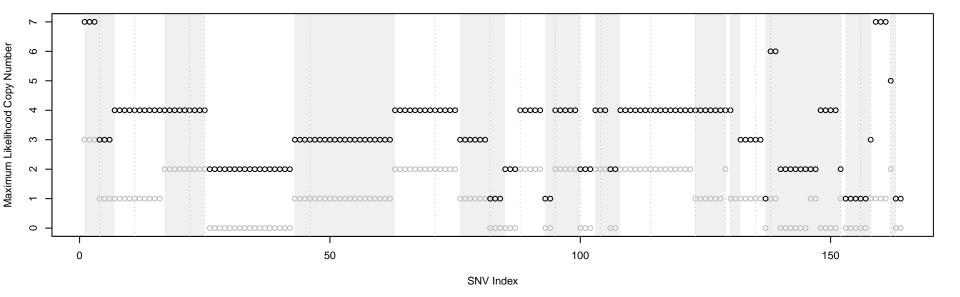


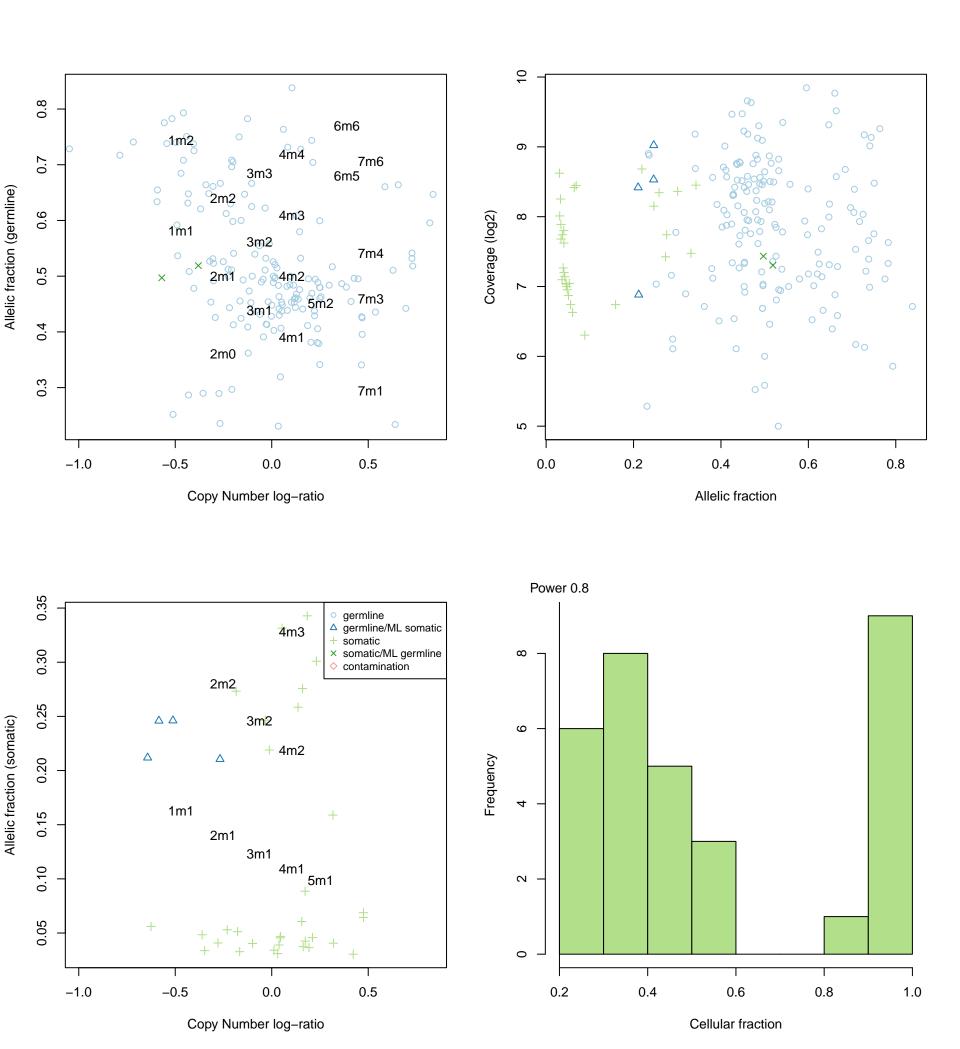
Purity: 0.28 Tumor ploidy: 3.364 2 3 5 6 0.20 Fraction Genome 0.10 0.05 0.00 -0.5 0.0 0.5 1.0 log2 ratio



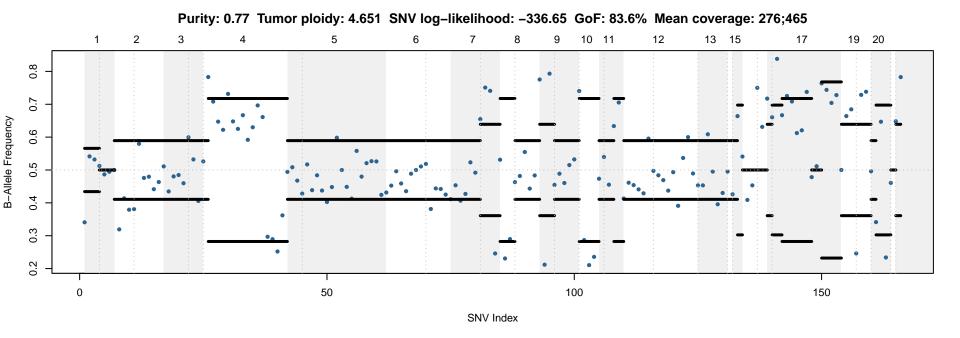
SCNA-fit log-likelihood: -10036



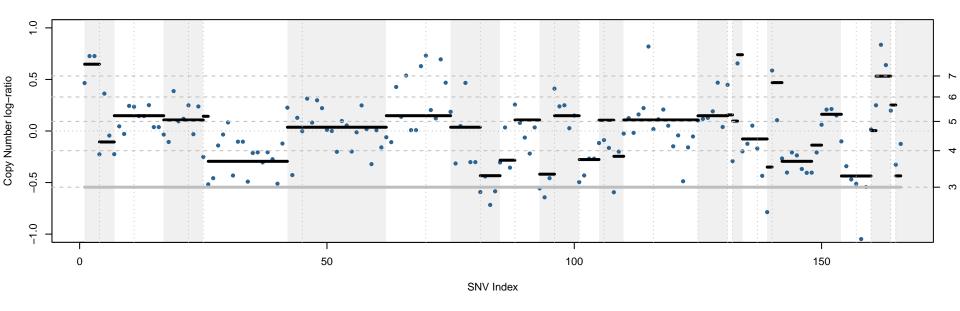


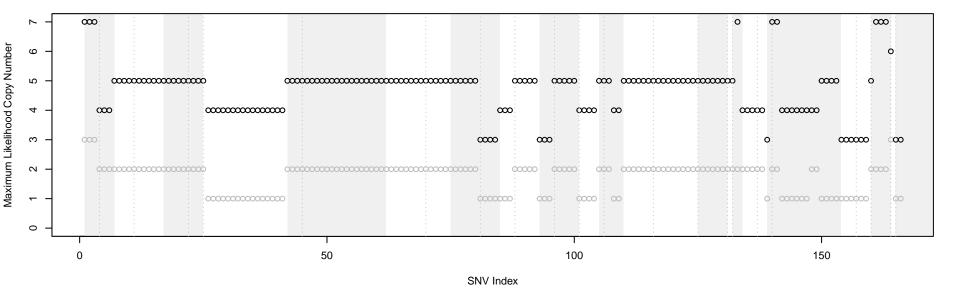


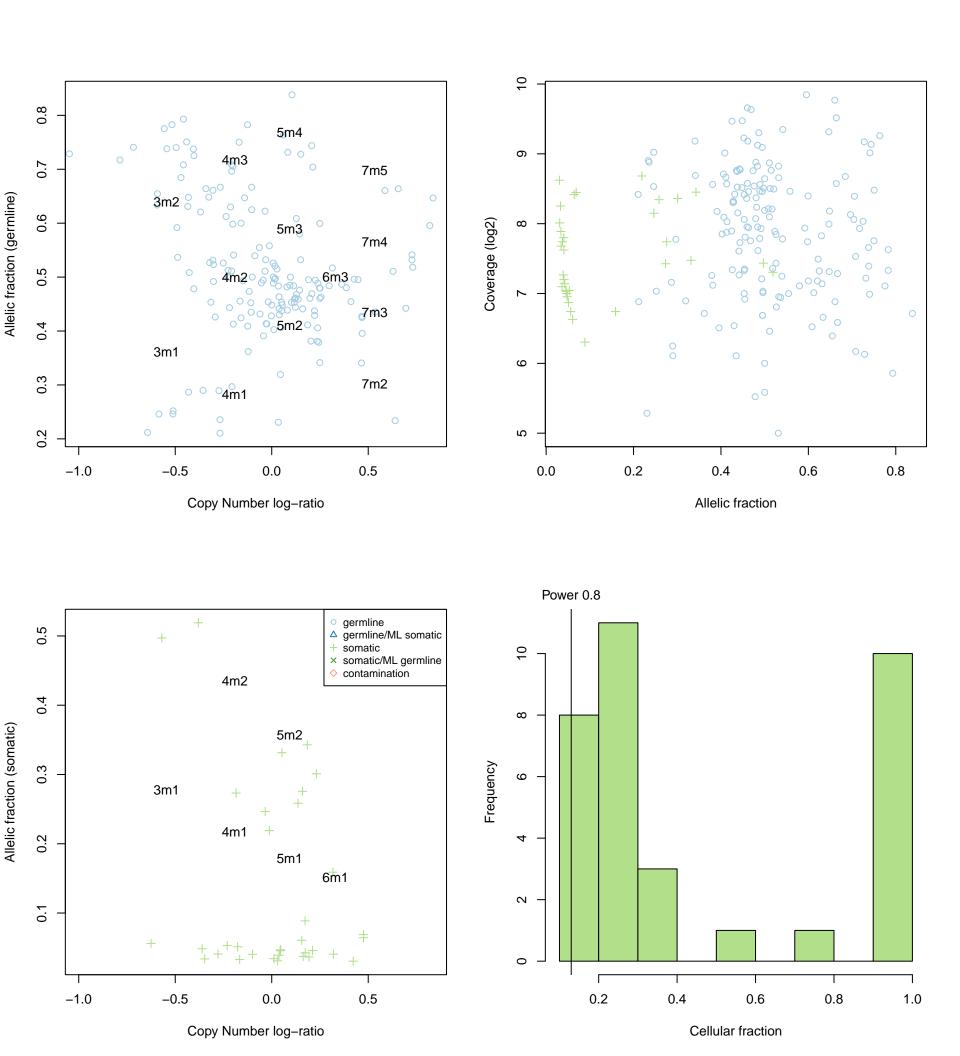
Purity: 0.77 Tumor ploidy: 4.651 3 4 0.20 Fraction Genome 0.10 0.05 0.00 -0.5 0.0 0.5 1.0 log2 ratio



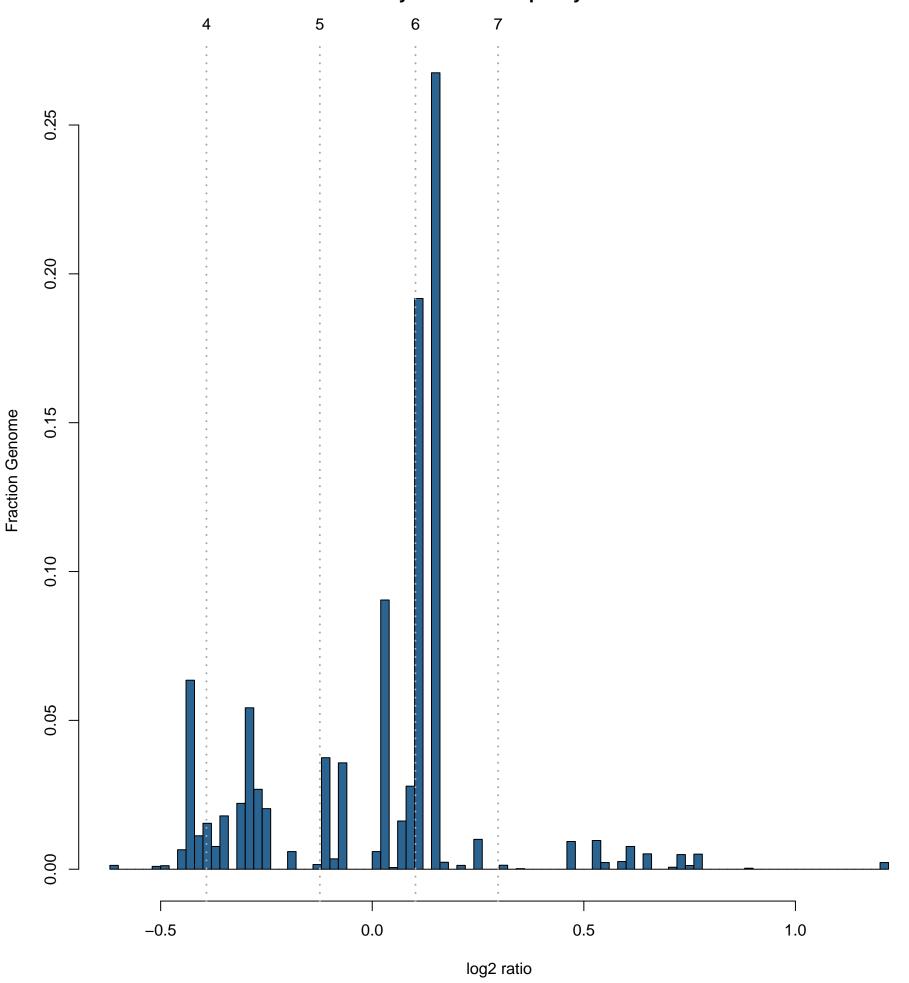
SCNA-fit log-likelihood: -10028.71

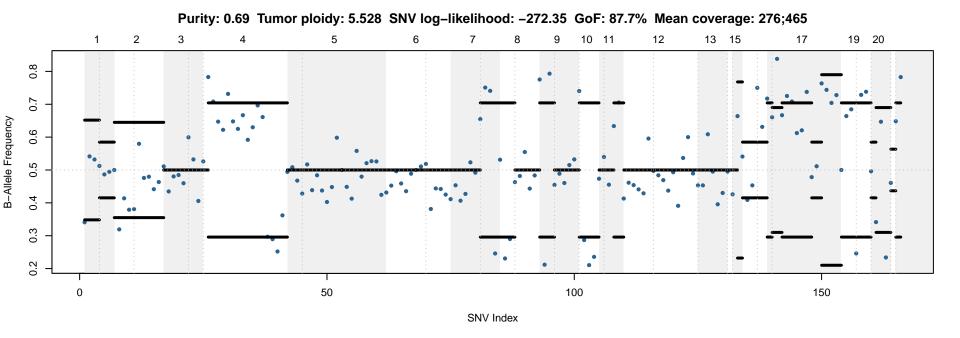




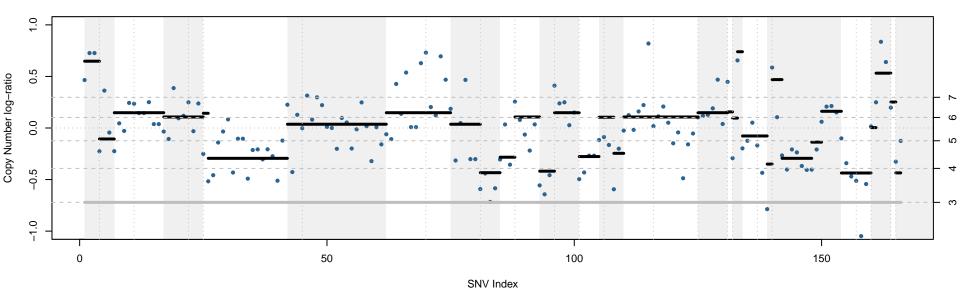


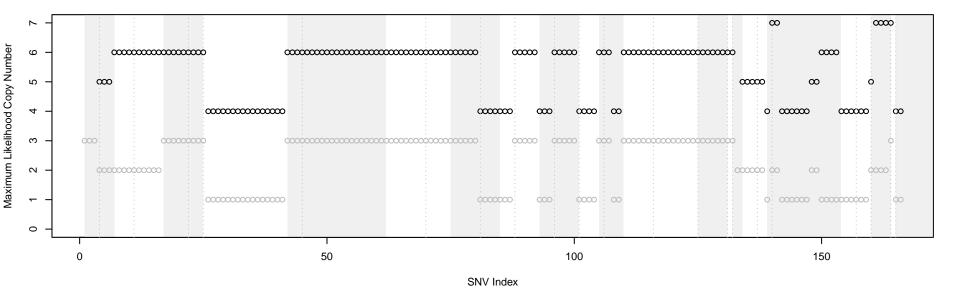
Purity: 0.69 Tumor ploidy: 5.528

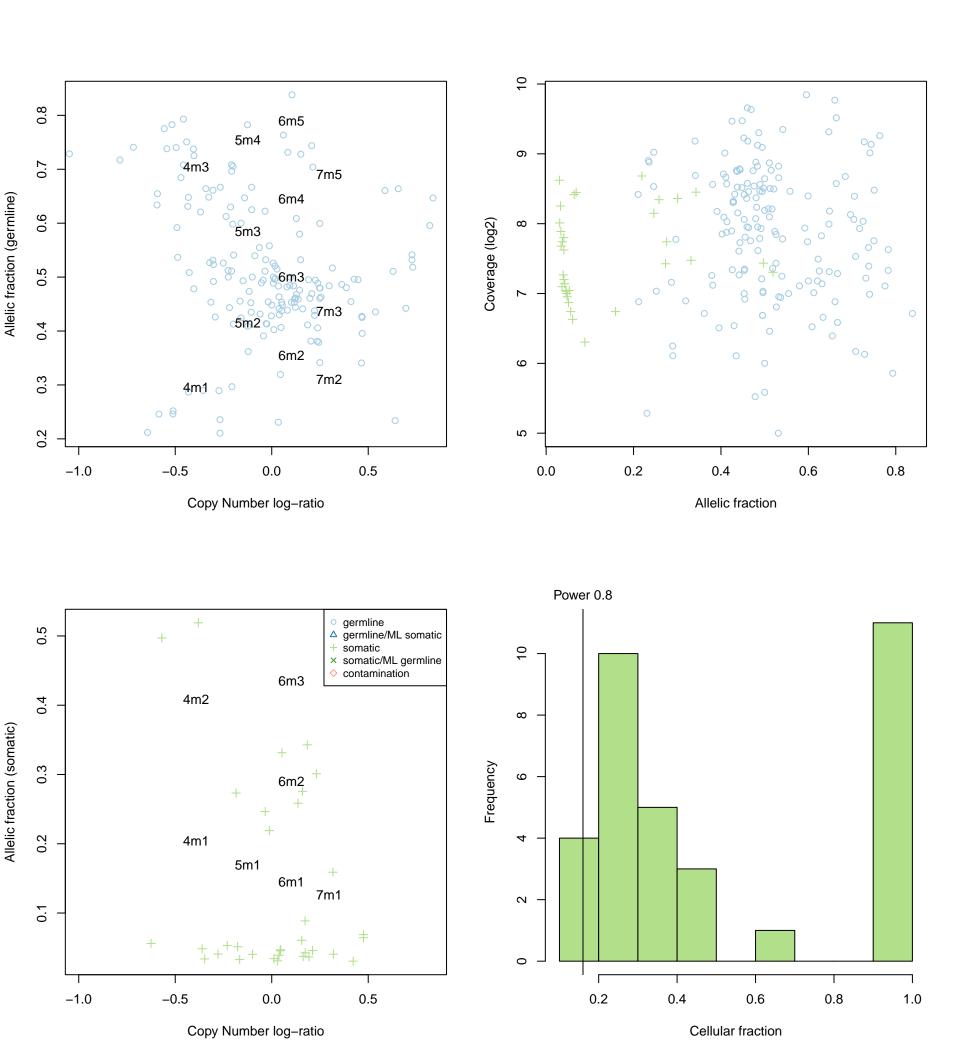




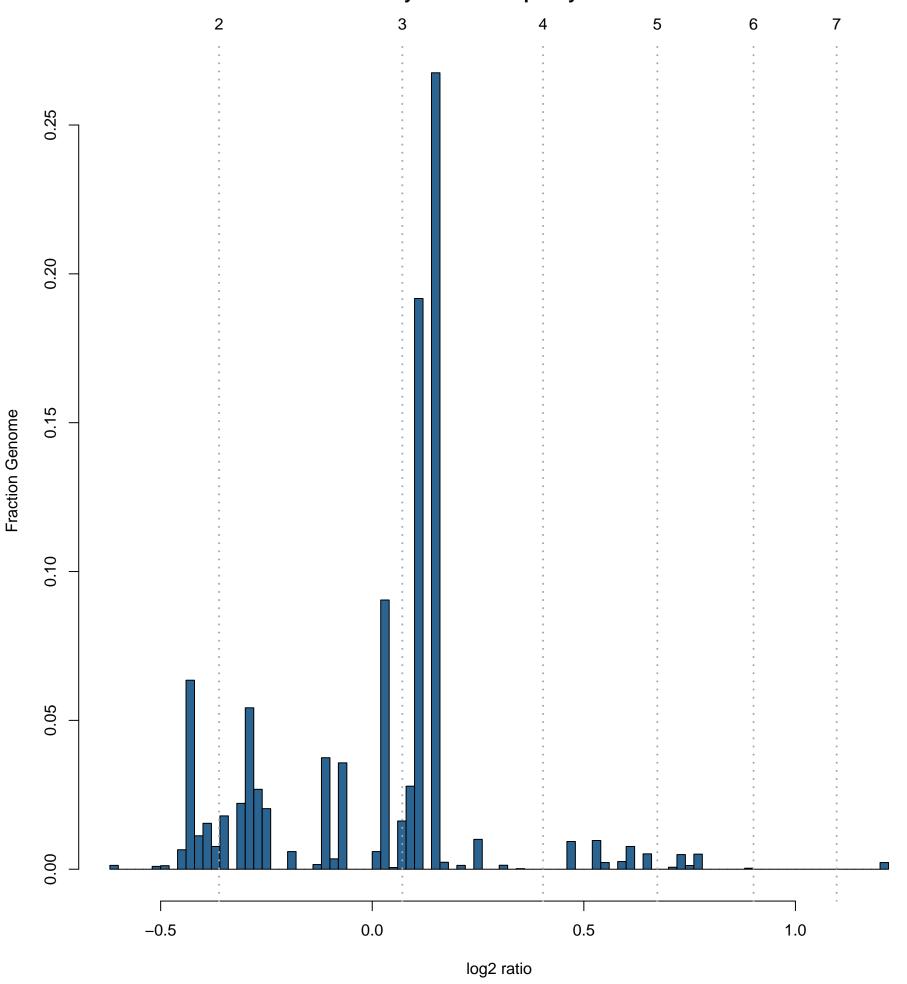
SCNA-fit log-likelihood: -10461.81

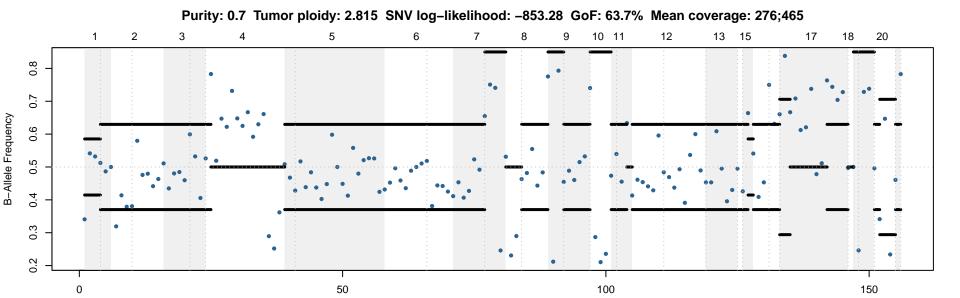






Purity: 0.7 Tumor ploidy: 2.815





SCNA-fit log-likelihood: -9998.45

SNV Index

