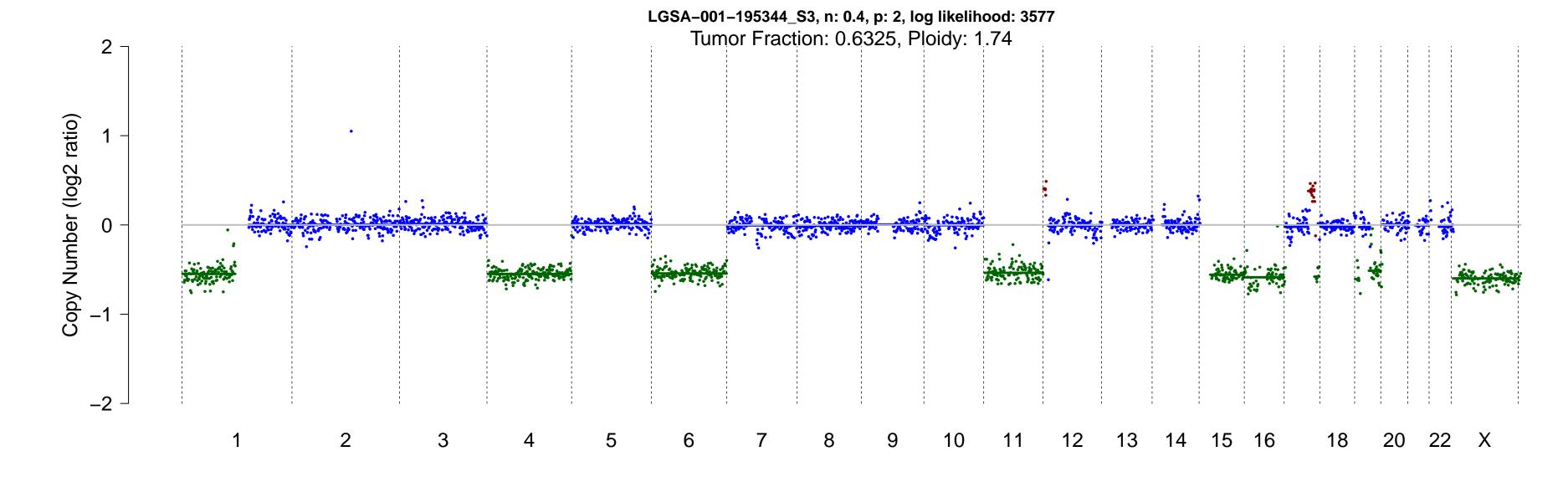
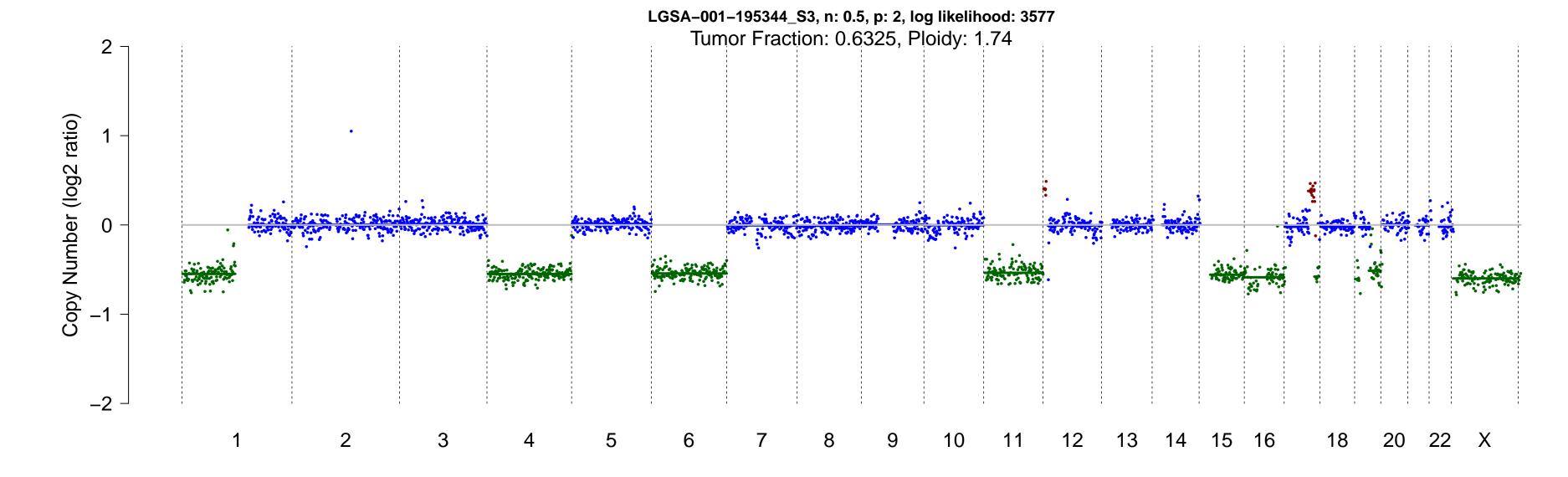
LGSA-001-195344_S3, n: 0.6, p: 2, log likelihood: 3601 Tumor Fraction: 0.6334, Ploidy: 1.74 Subclone Fraction: 0.151, Frac. Genome Subclonal: 0.01, Frac. CNA Subclonal: 0.03 Copy Number (log2 ratio)





LGSA-001-195344_S3, n: 0.3, p: 2, log likelihood: 3576 Tumor Fraction: 0.6326, Ploidy: 1.74 Subclone Fraction: 0.872, Frac. Genome Subclonal: 0.01, Frac. CNA Subclonal: 0.04 Copy Number (log2 ratio)

LGSA-001-195344_S3, n: 0.5, p: 3, log likelihood: 3375 Tumor Fraction: 0.9199, Ploidy: 2.74
Subclone Fraction: 0.07, Frac. Genome Subclonal: 0.08, Frac. CNA Subclonal: 0.11 Copy Number (log2 ratio)

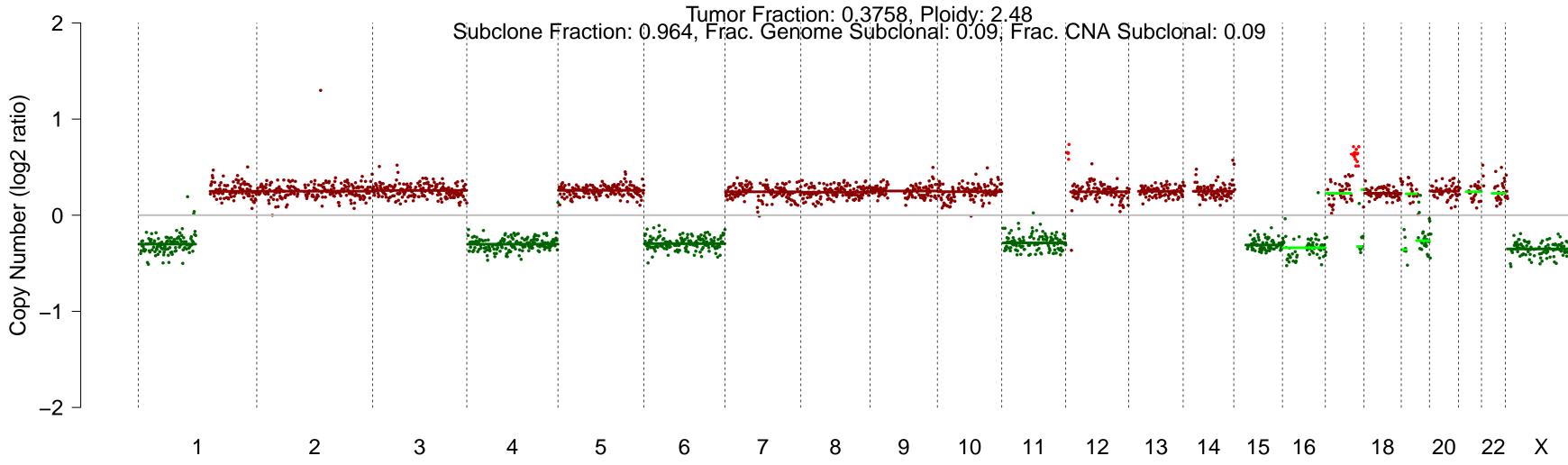
LGSA-001-195344_S3, n: 0.2, p: 3, log likelihood: 3352 Tumor Fraction: 0.9222, Ploidy: 2.74 Subclone Fraction: 0.172, Frac. Genome Subclonal: 0.02, Frac. CNA Subclonal: 0.03 Copy Number (log2 ratio)

LGSA-001-195344_S3, n: 0.3, p: 3, log likelihood: 3352 Tumor Fraction: 0.9222, Ploidy: 2.74 Subclone Fraction: 0.172, Frac. Genome Subclonal: 0.02, Frac. CNA Subclonal: 0.03 Copy Number (log2 ratio)

LGSA-001-195344_S3, n: 0.4, p: 3, log likelihood: 3352 Tumor Fraction: 0.9222, Ploidy: 2.74 Subclone Fraction: 0.171, Frac. Genome Subclonal: 0.02, Frac. CNA Subclonal: 0.03 Copy Number (log2 ratio)

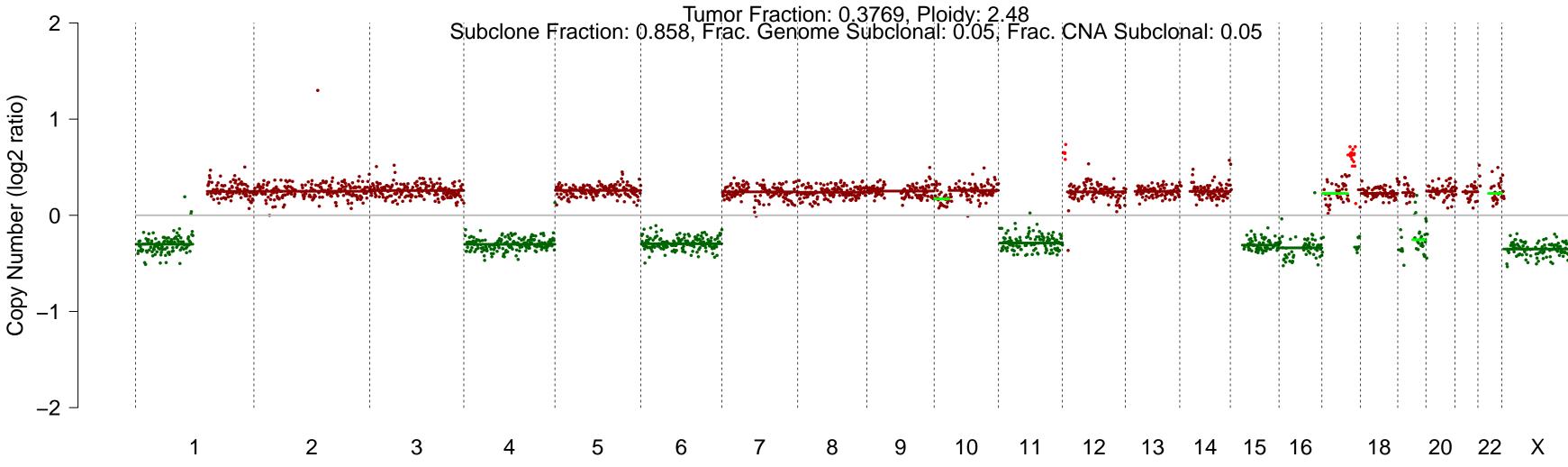
LGSA-001-195344_S3, n: 0.9, p: 2, log likelihood: 3315 Tumor Fraction: 0.3766, Ploidy: 2.48
Subclone Fraction: 0.985, Frac. Genome Subclonal: 0.17, Frac. CNA Subclonal: 0.17 Copy Number (log2 ratio)

LGSA-001-195344_S3, n: 0.8, p: 2, log likelihood: 3256

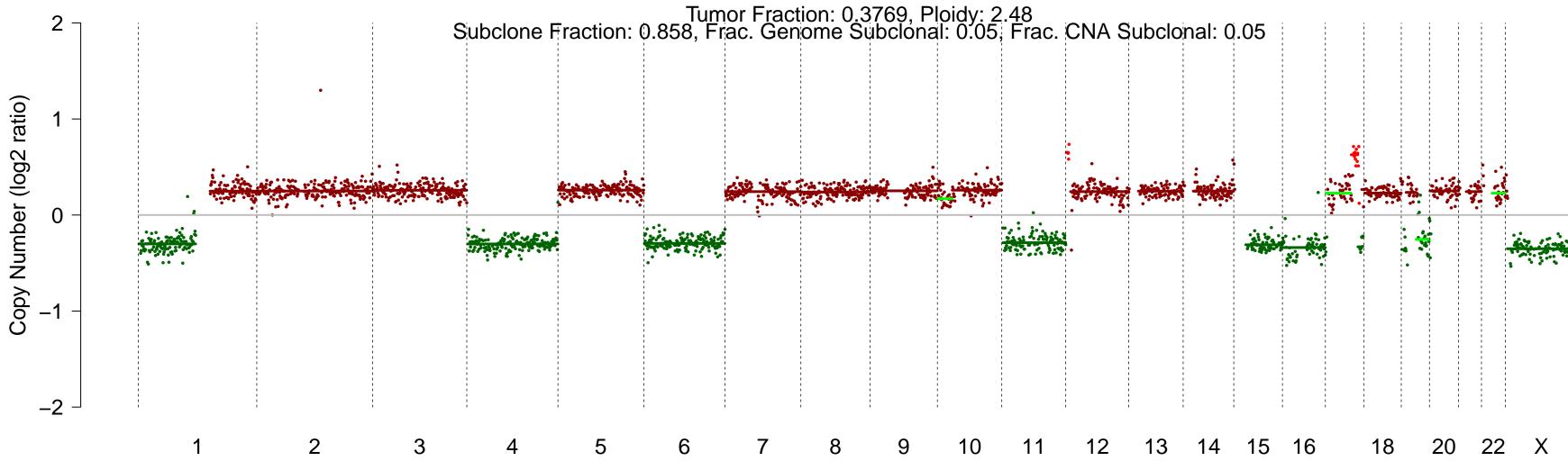


LGSA-001-195344_S3, n: 0.9, p: 3, log likelihood: 3241 Tumor Fraction: 0.3769, Ploidy: 2.48
Subclone Fraction: 0.89, Frac. Genome Subclonal: 0.07, Frac. CNA Subclonal: 0.07 Copy Number (log2 ratio)

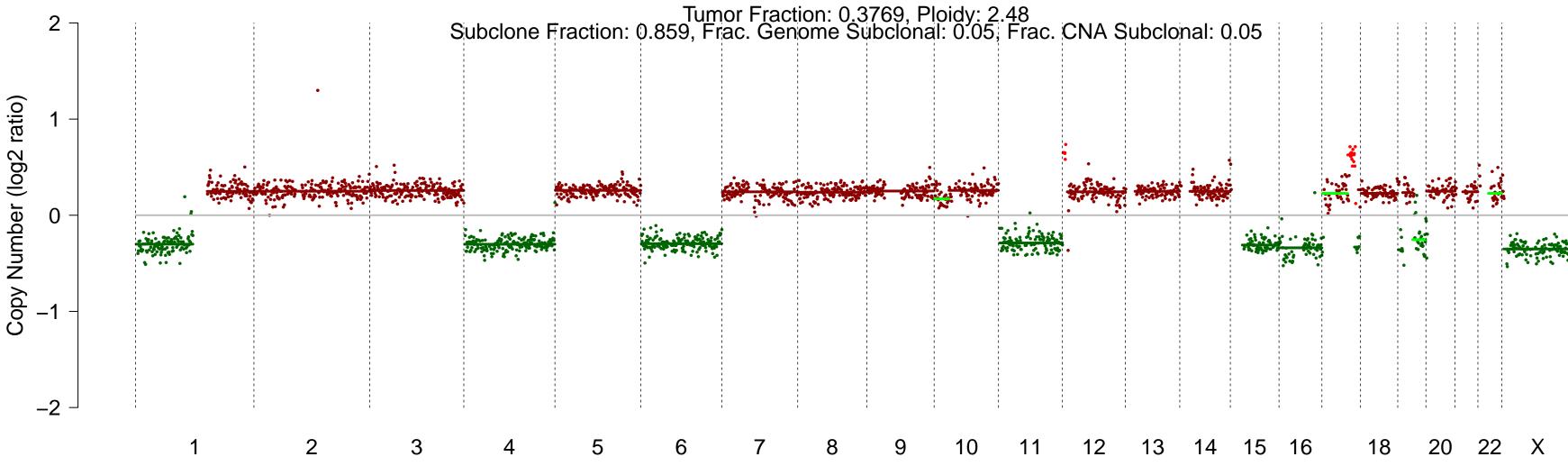
LGSA-001-195344_S3, n: 0.7, p: 2, log likelihood: 3223



LGSA-001-195344_S3, n: 0.8, p: 3, log likelihood: 3223



LGSA-001-195344_S3, n: 0.6, p: 3, log likelihood: 3222



LGSA-001-195344_S3, n: 0.7, p: 3, log likelihood: 3222 Tumor Fraction: 0.3769, Ploidy: 2.48
Subclone Fraction: 0.857, Frac. Genome Subclonal: 0.05, Frac. CNA Subclonal: 0.05 Copy Number (log2 ratio)