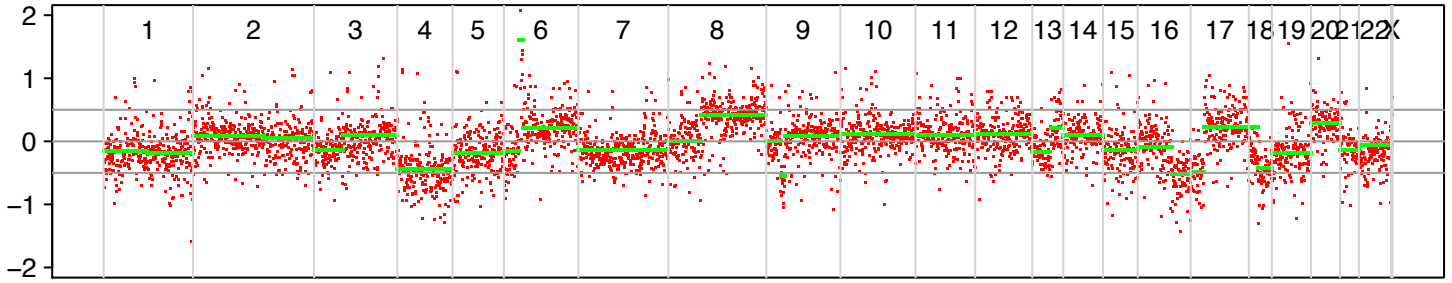
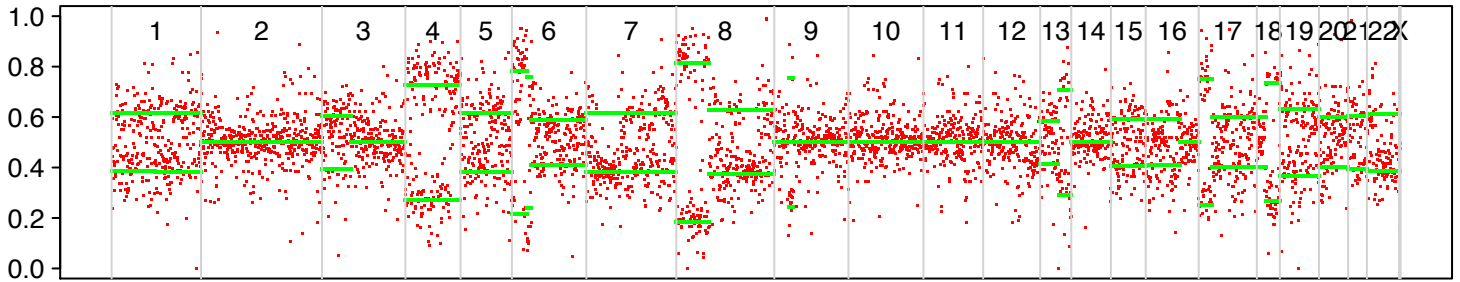


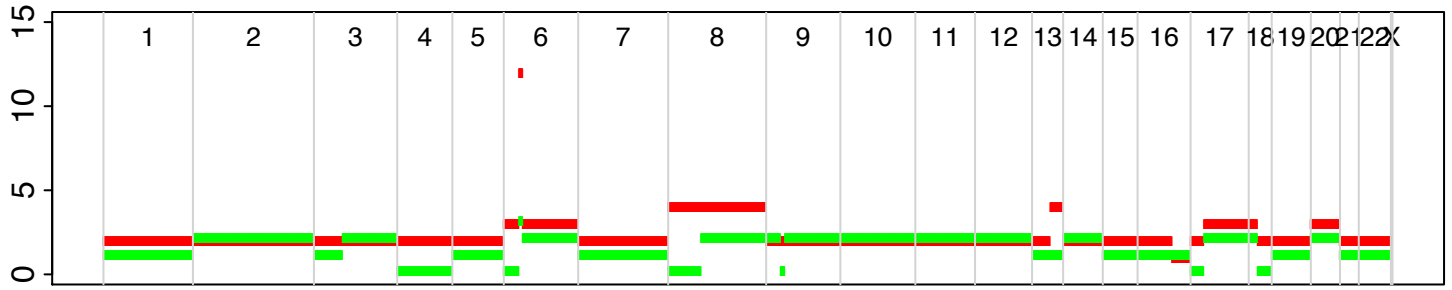
T_T019A, LogR



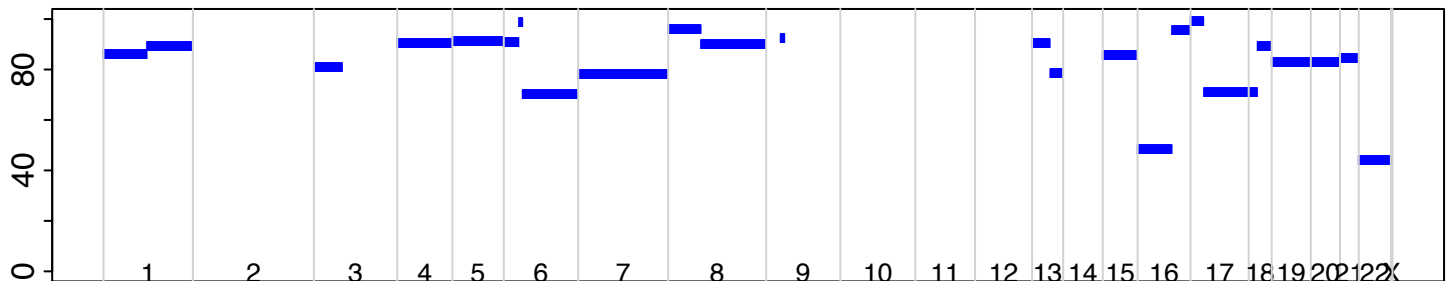
T_T019A, BAF



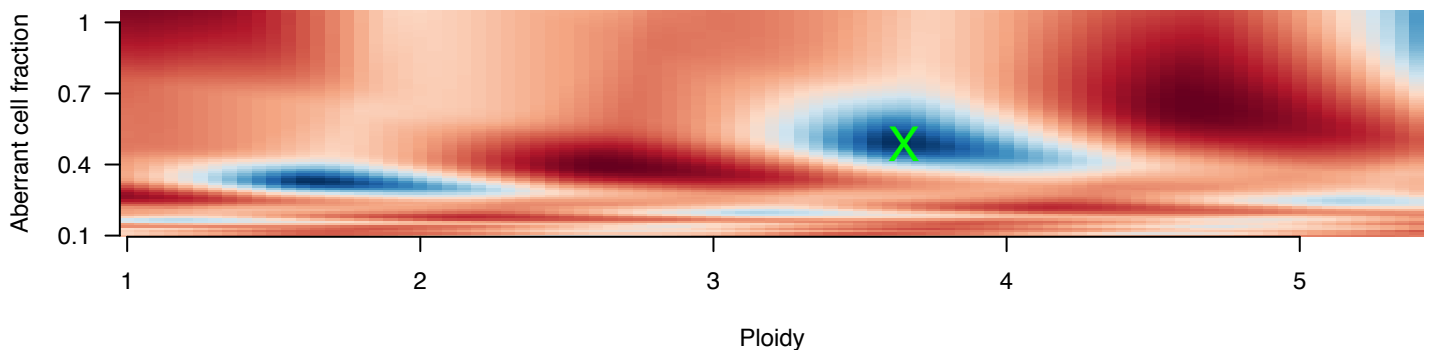
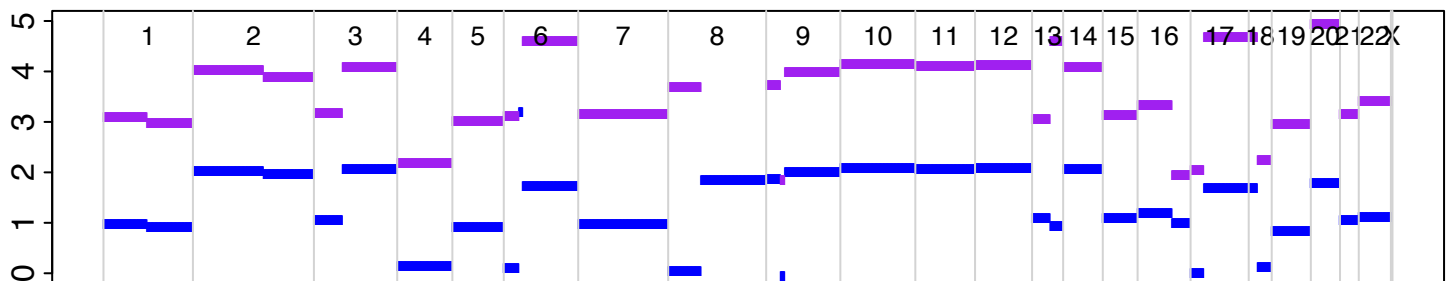
Ploidy: 3.72, aberrant cell fraction: 49%, goodness of fit: 99.6%



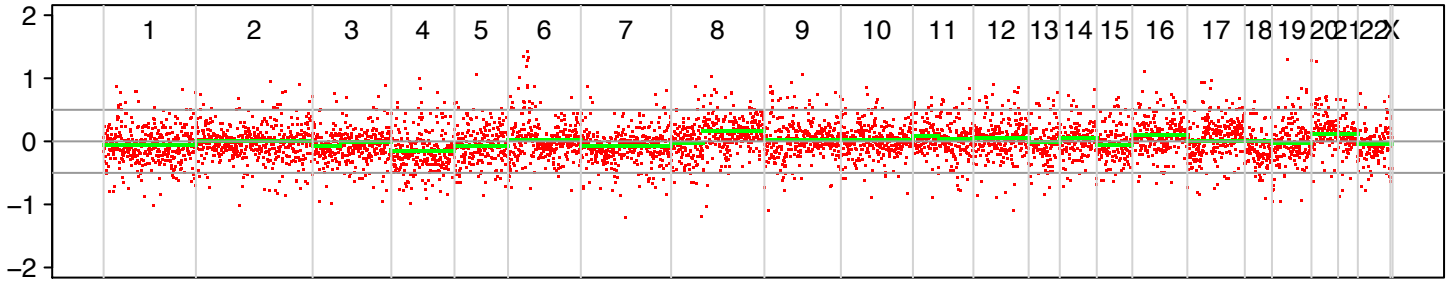
Aberration reliability score (%), average: 81%



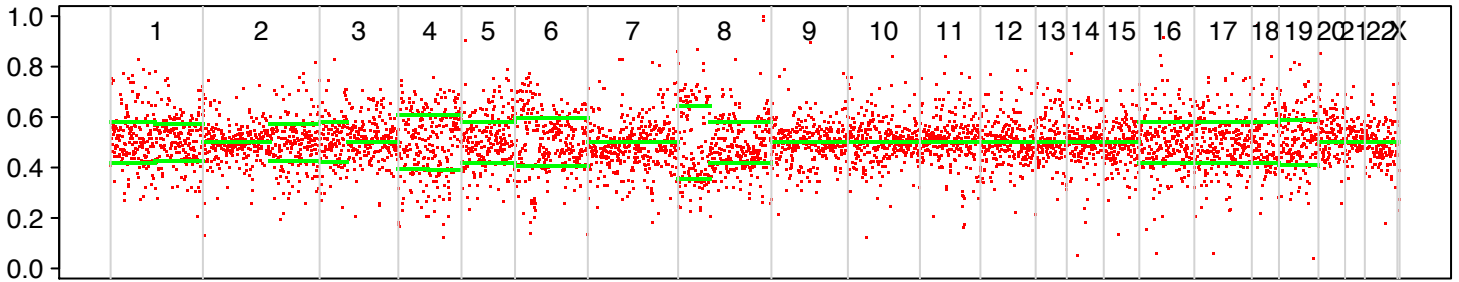
Ploidy: 3.72, aberrant cell fraction: 49%, goodness of fit: 99.6%



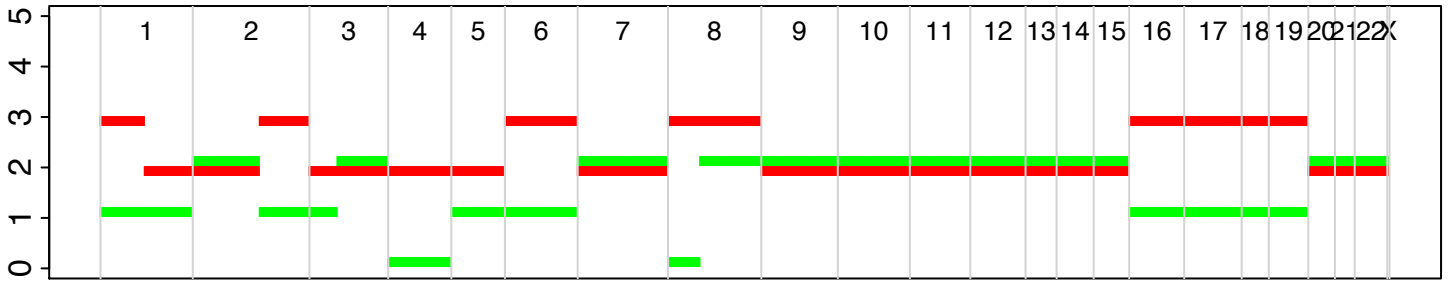
T_T019B, LogR



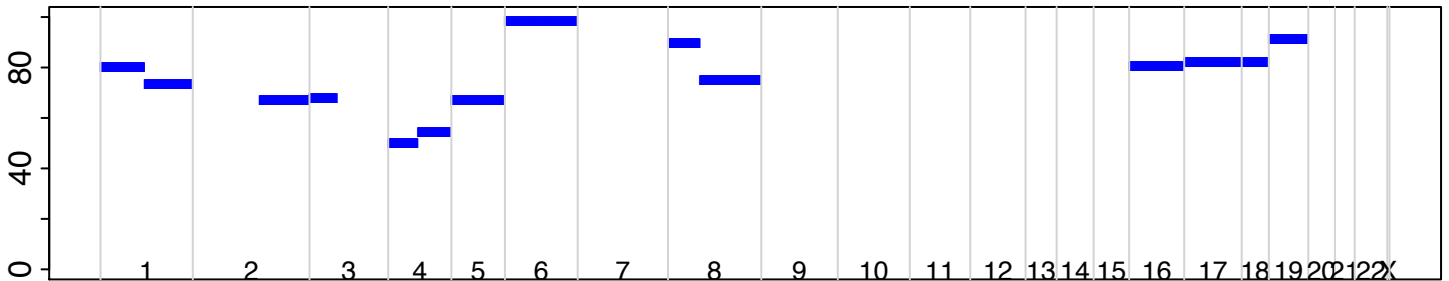
T_T019B, BAF



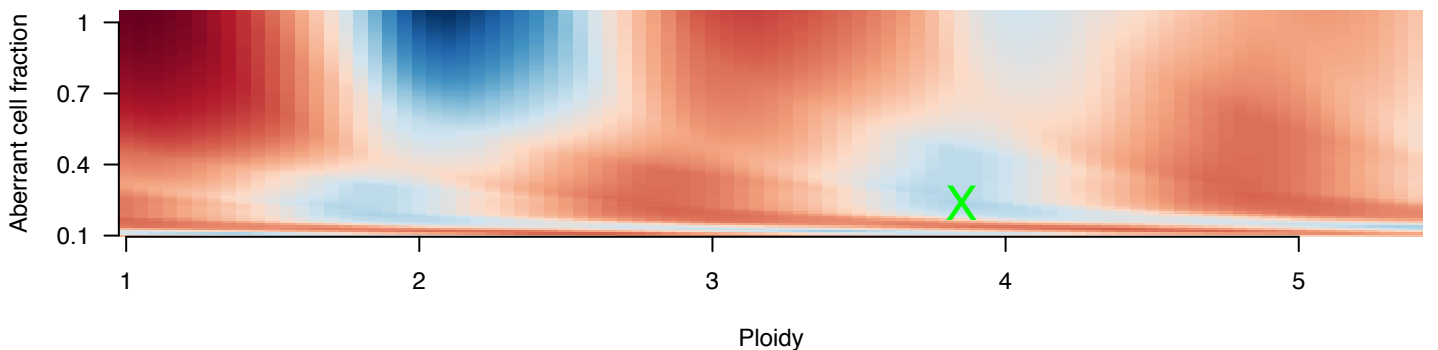
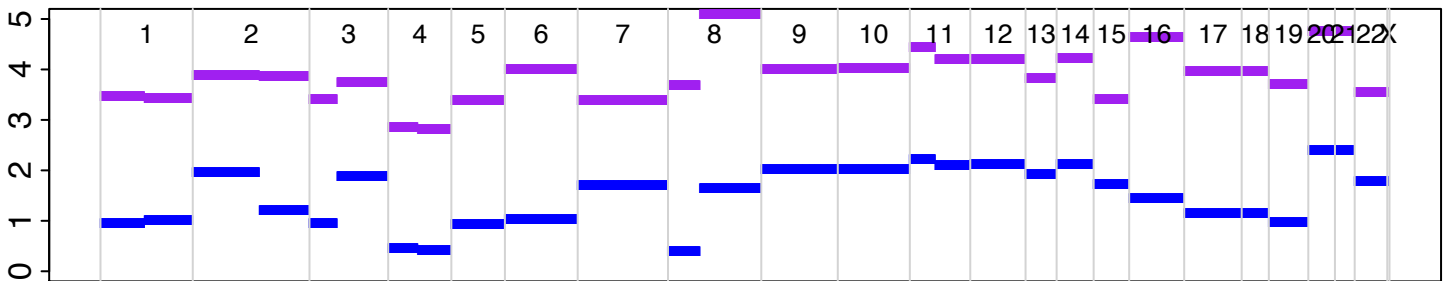
Ploidy: 3.87, aberrant cell fraction: 24%, goodness of fit: 99.3%



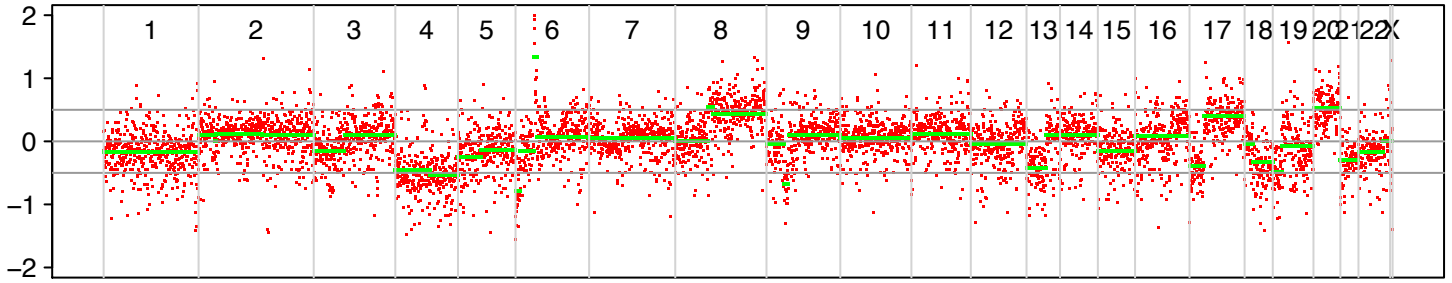
Aberration reliability score (%), average: 77%



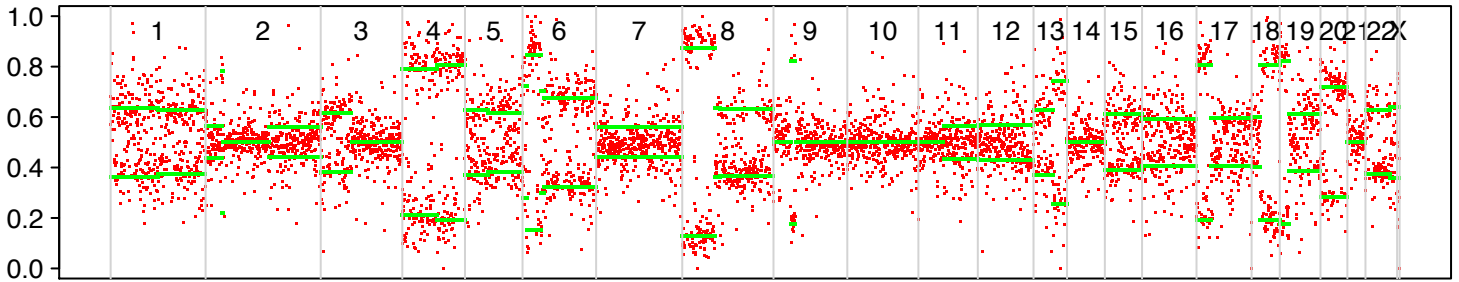
Ploidy: 3.87, aberrant cell fraction: 24%, goodness of fit: 99.3%



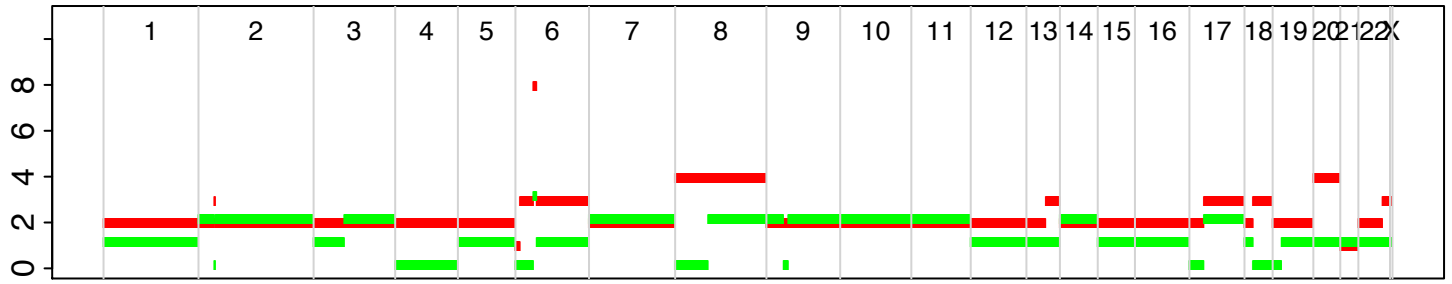
T_T019C, LogR



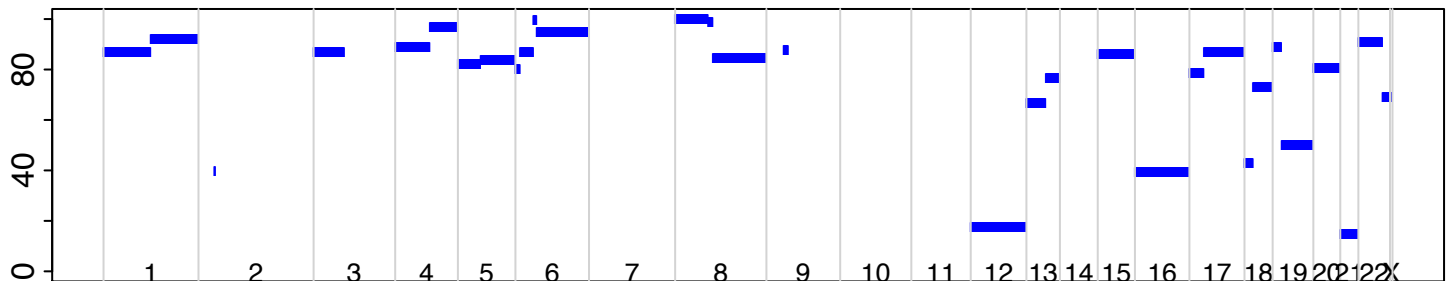
T_T019C, BAF



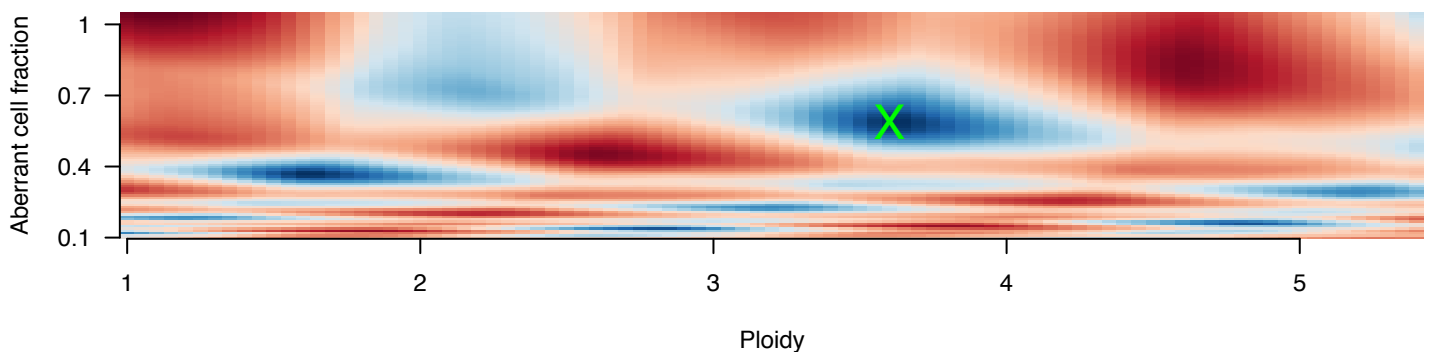
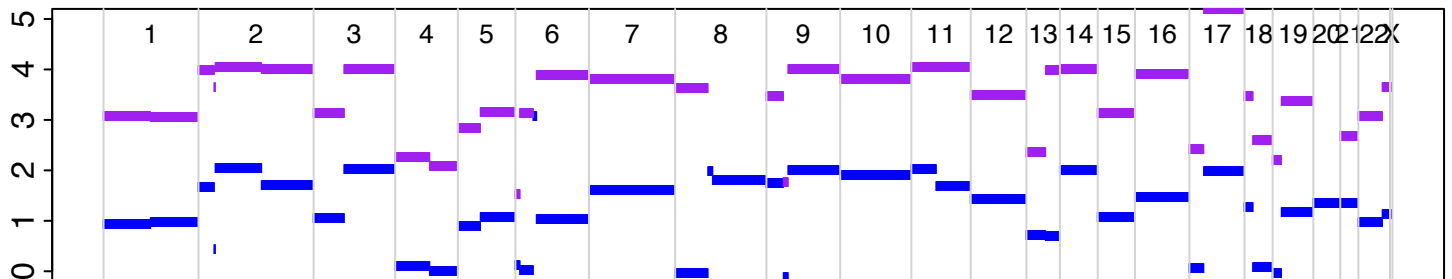
Ploidy: 3.66, aberrant cell fraction: 59%, goodness of fit: 99.5%



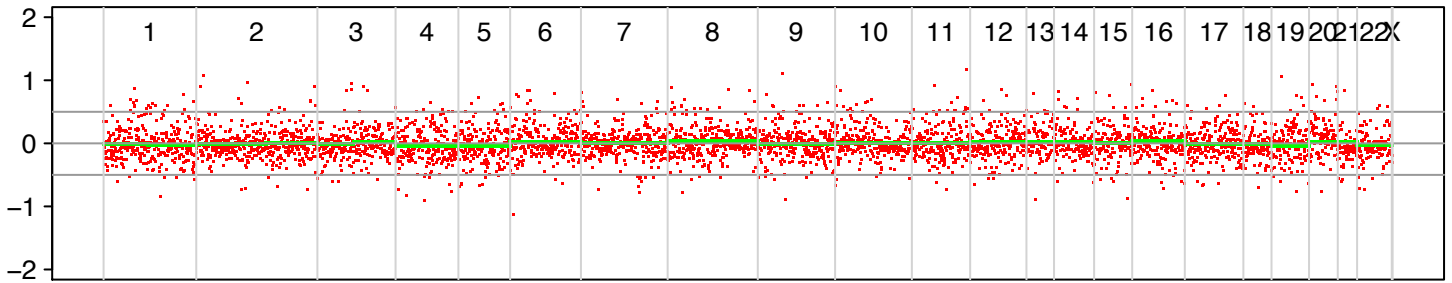
Aberration reliability score (%), average: 75%



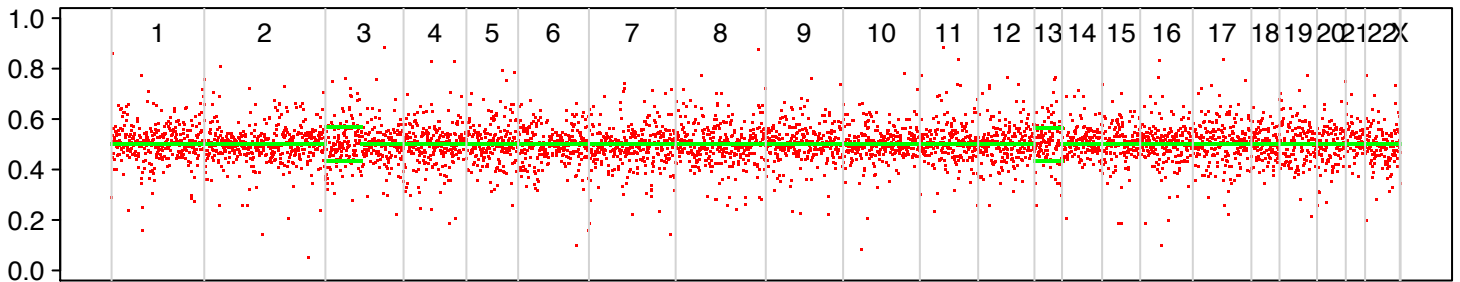
Ploidy: 3.66, aberrant cell fraction: 59%, goodness of fit: 99.5%



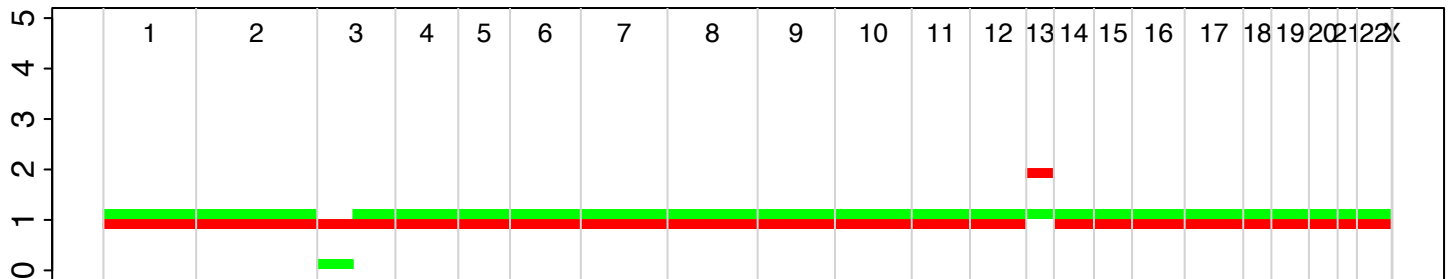
T_T019D, LogR



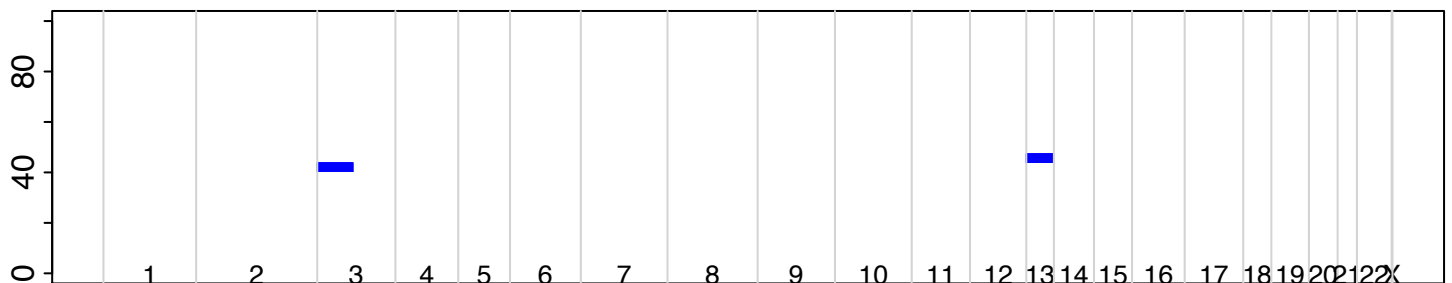
T_T019D, BAF



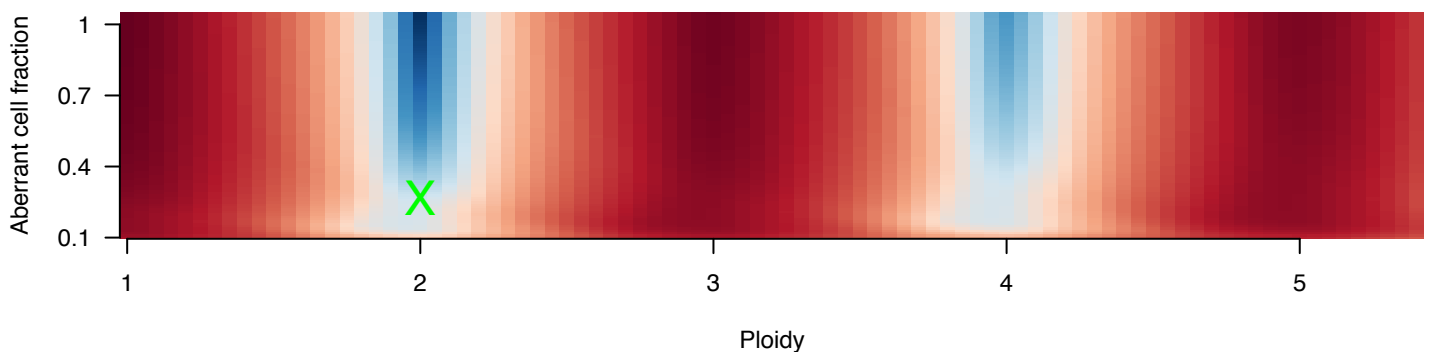
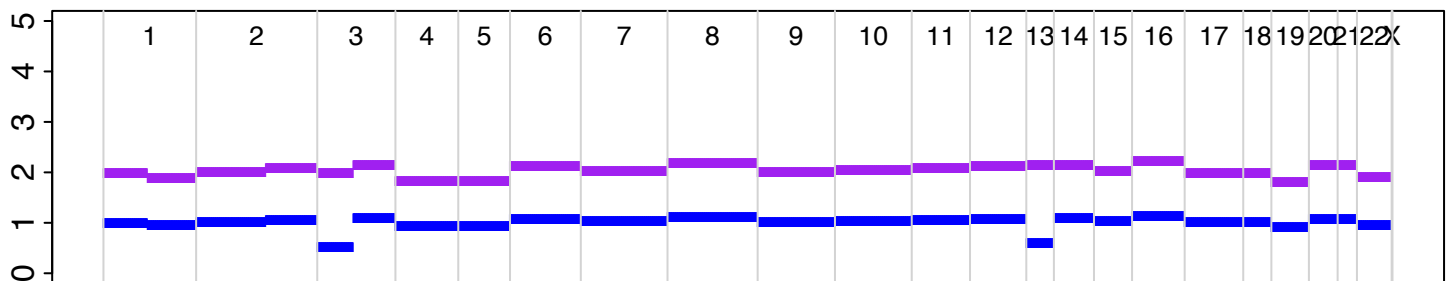
Ploidy: 2.01, aberrant cell fraction: 27%, goodness of fit: 98.2%



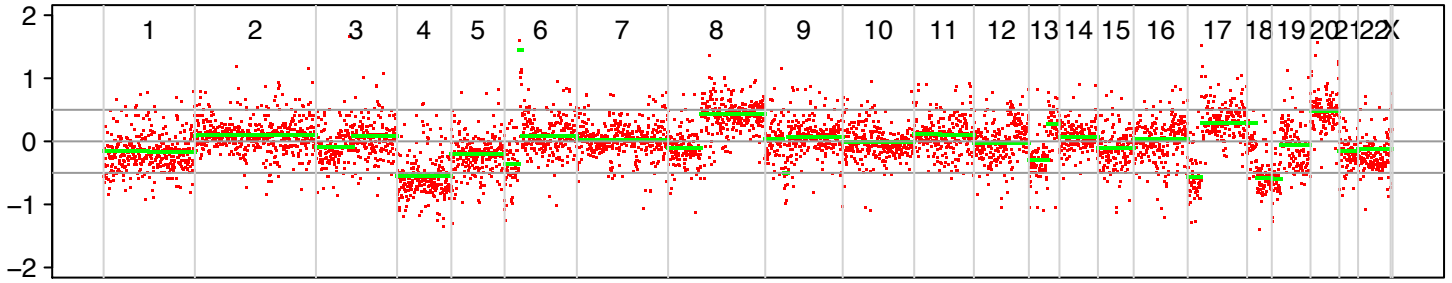
Aberration reliability score (%), average: 43%



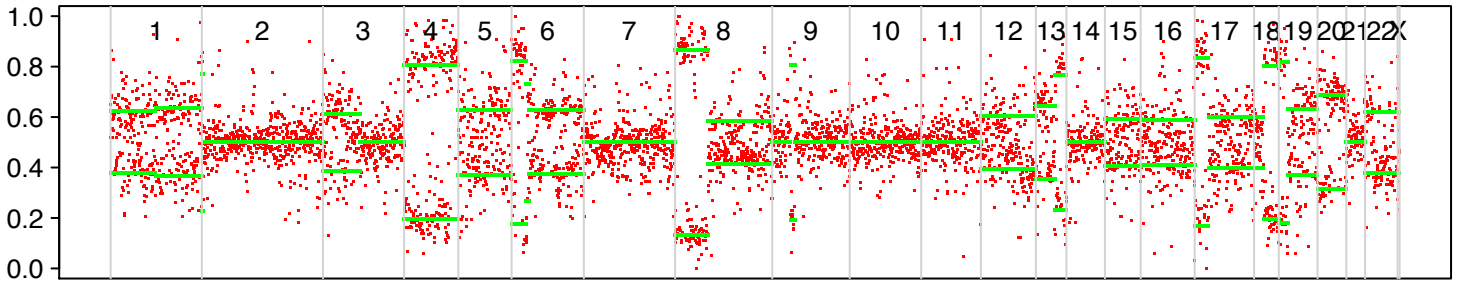
Ploidy: 2.01, aberrant cell fraction: 27%, goodness of fit: 98.2%



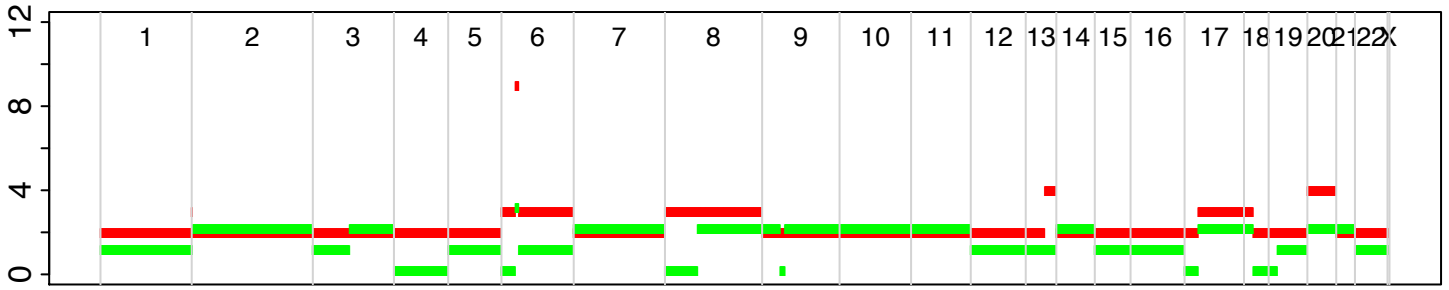
T_T019E, LogR



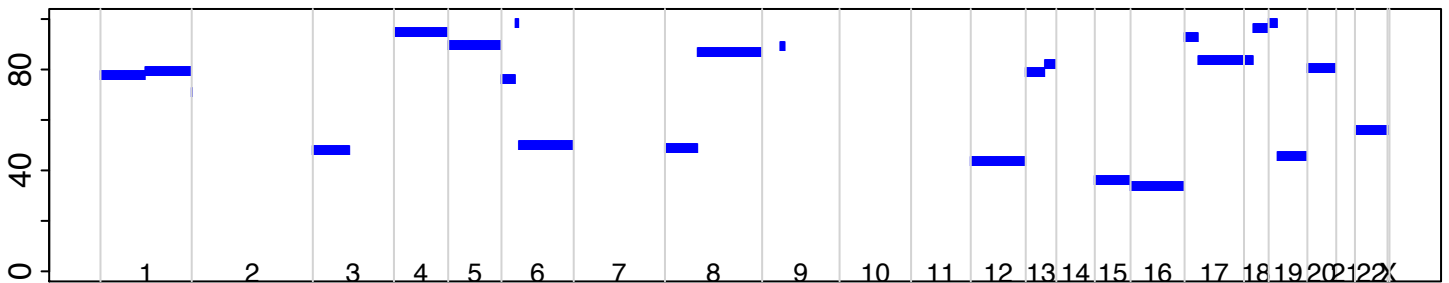
T_T019E, BAF



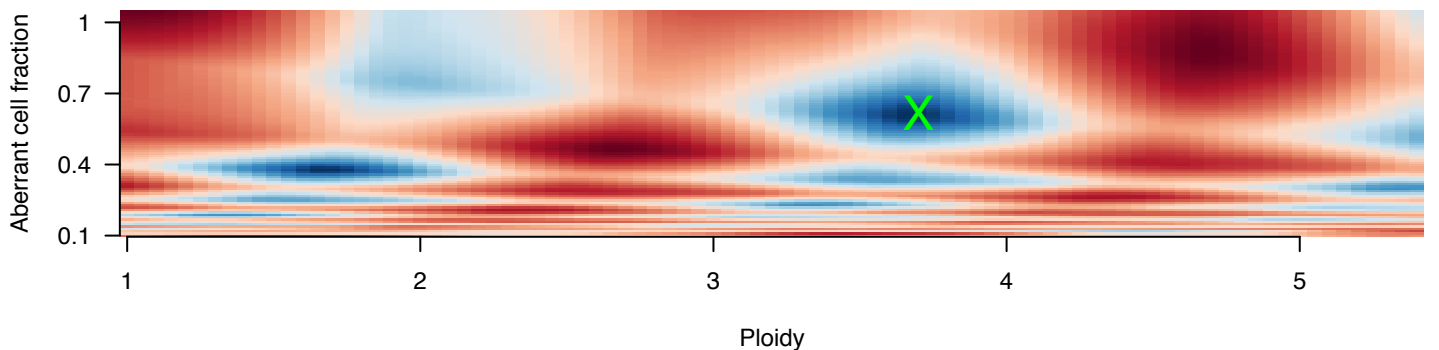
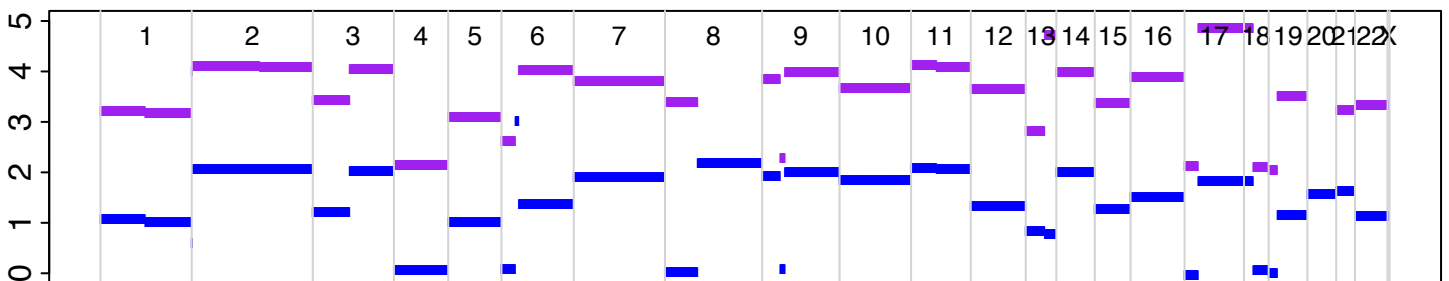
Ploidy: 3.76, aberrant cell fraction: 62%, goodness of fit: 99.4%



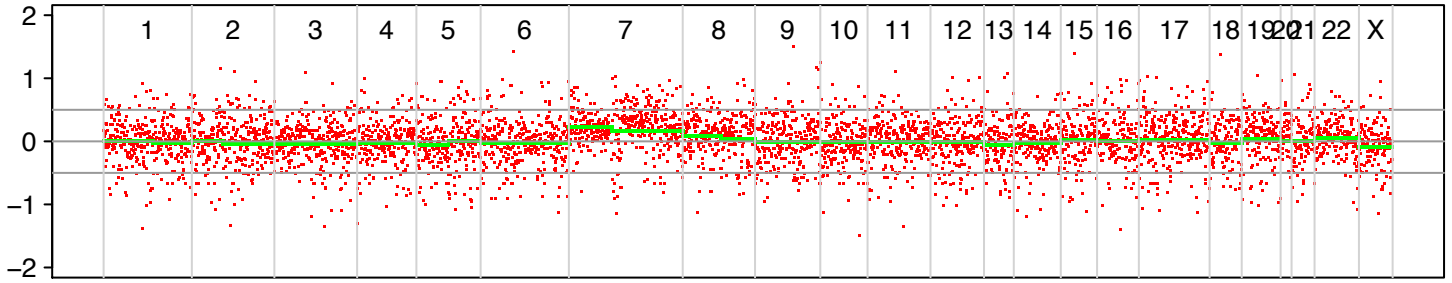
Aberration reliability score (%), average: 68%



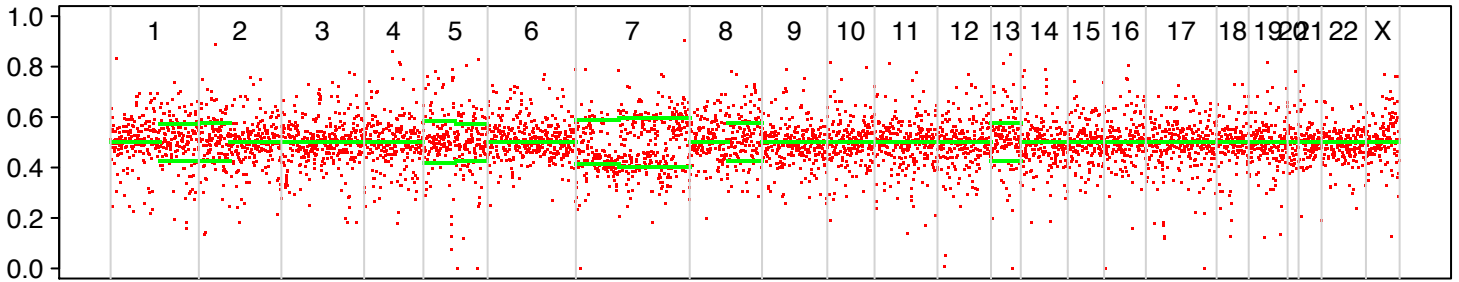
Ploidy: 3.76, aberrant cell fraction: 62%, goodness of fit: 99.4%



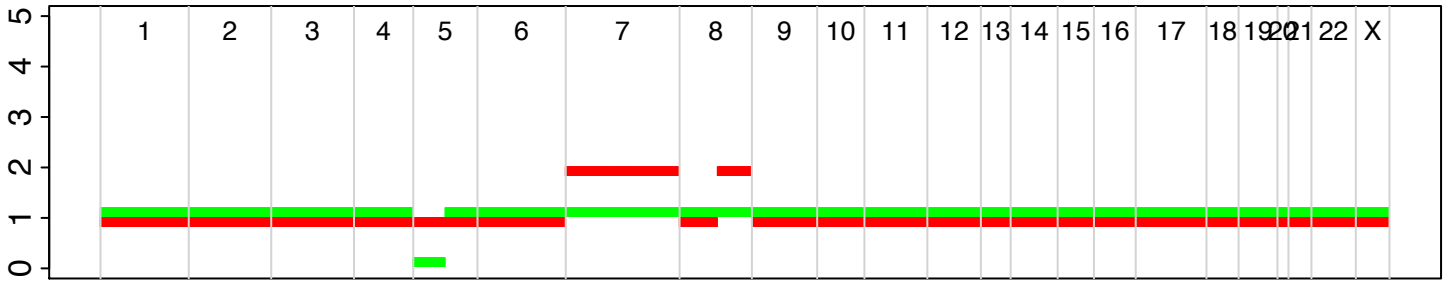
T_520A, LogR



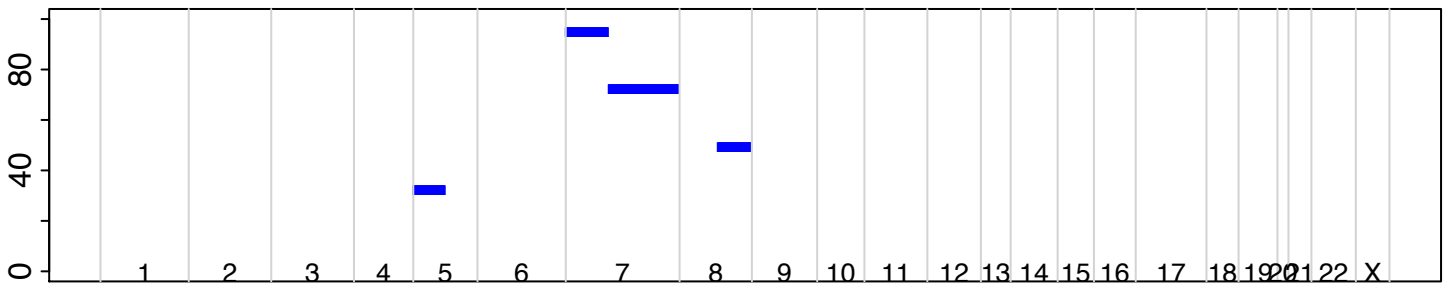
T_520A, BAF



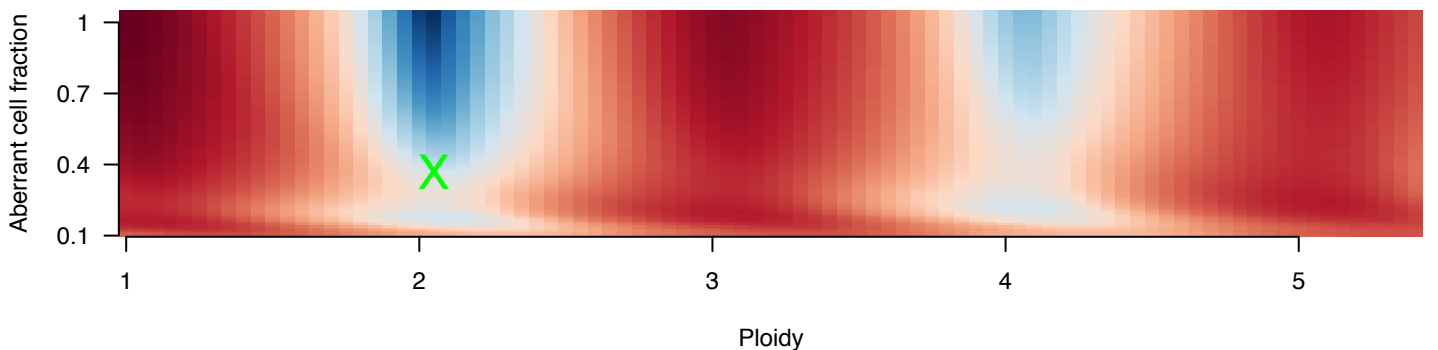
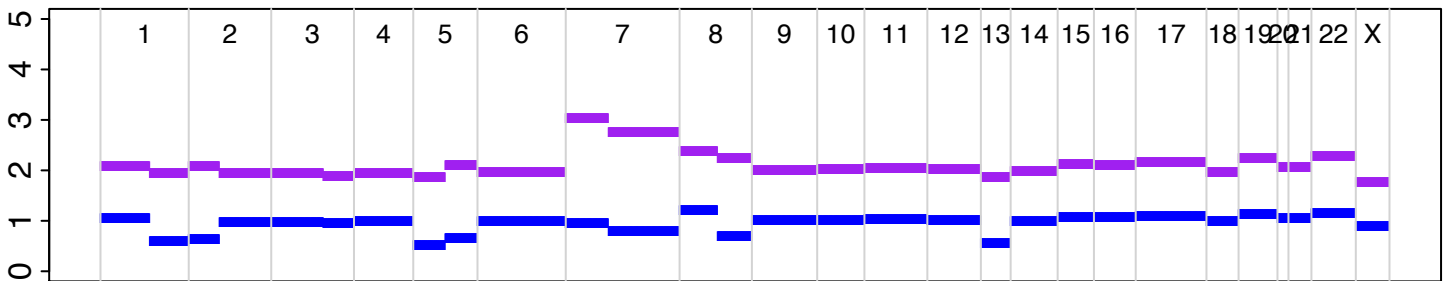
Ploidy: 2.09, aberrant cell fraction: 37%, goodness of fit: 98.9%



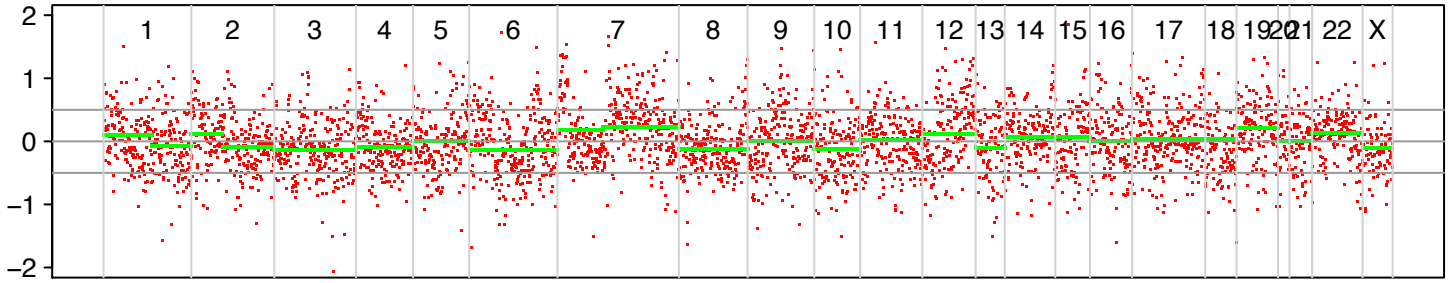
Aberration reliability score (%), average: 66%



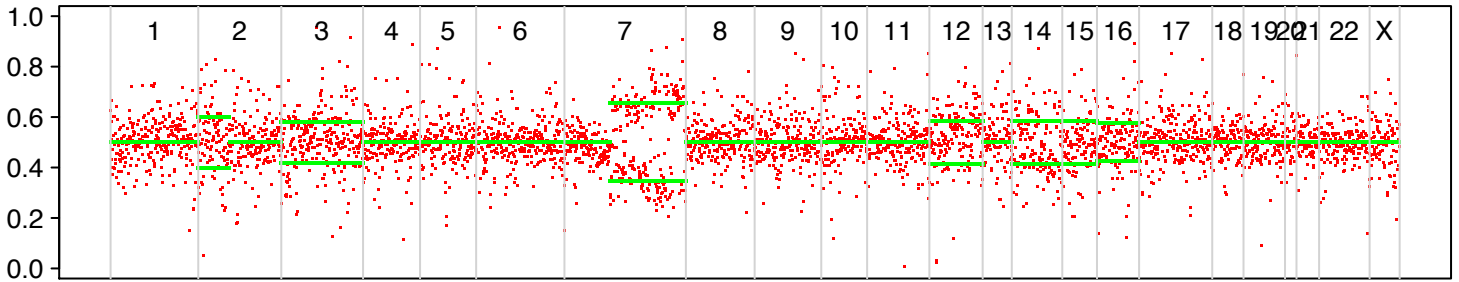
Ploidy: 2.09, aberrant cell fraction: 37%, goodness of fit: 98.9%



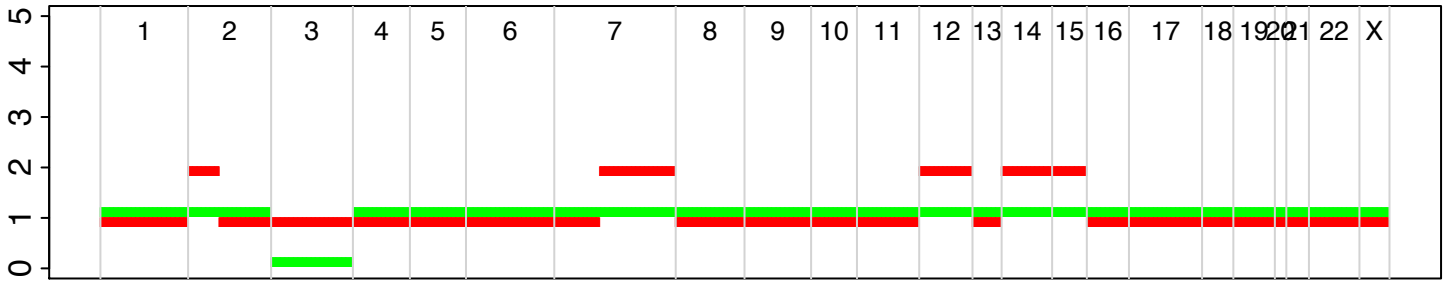
T_520B, LogR



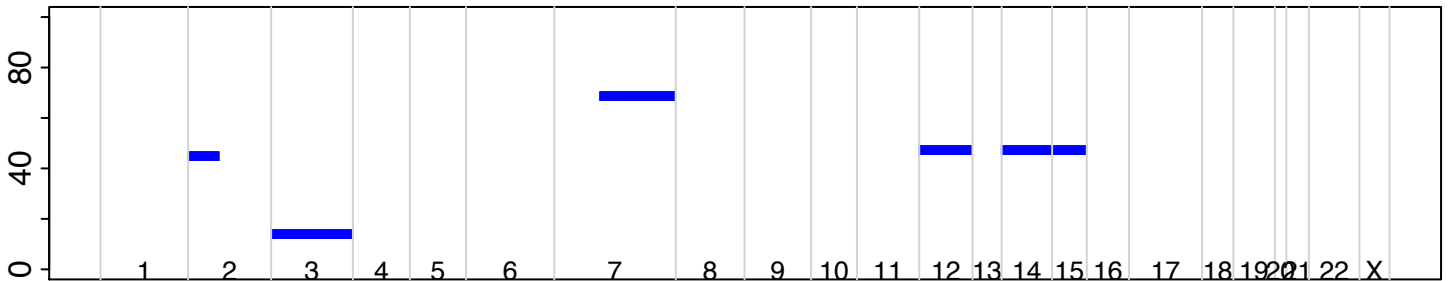
T_520B, BAF



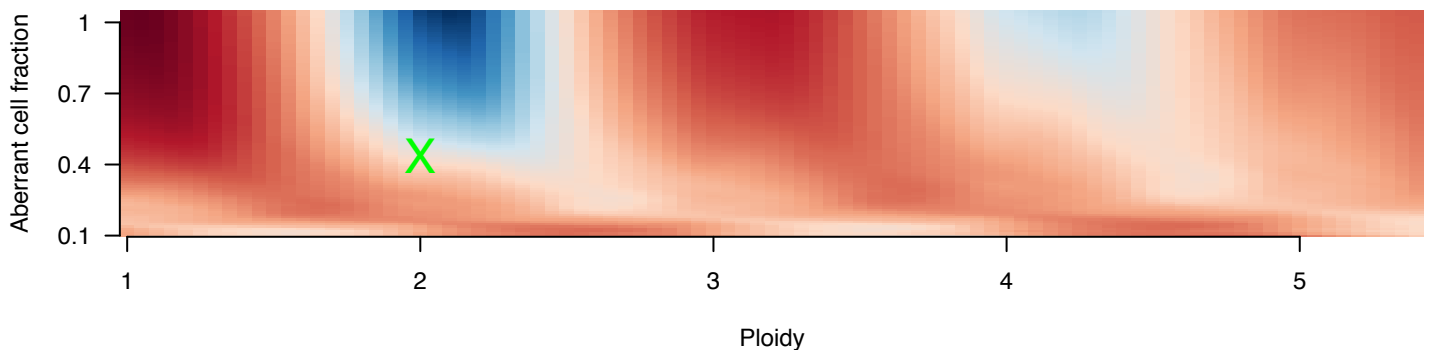
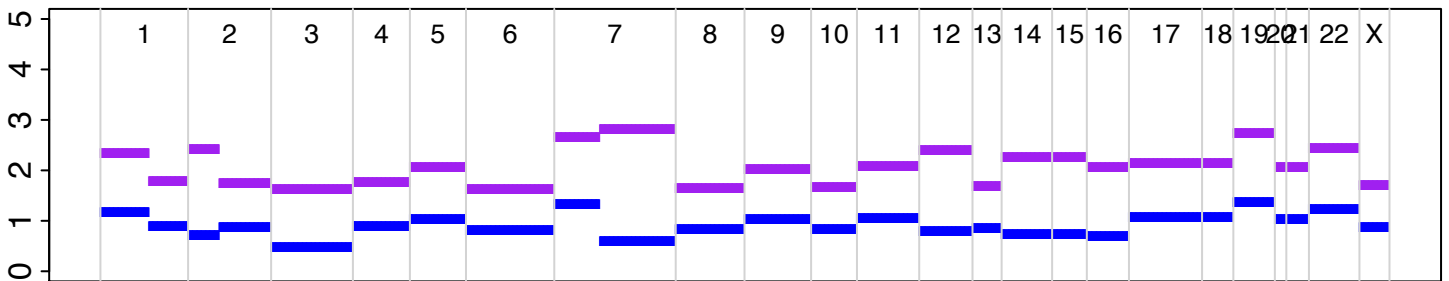
Ploidy: 2.05, aberrant cell fraction: 44%, goodness of fit: 98.7%



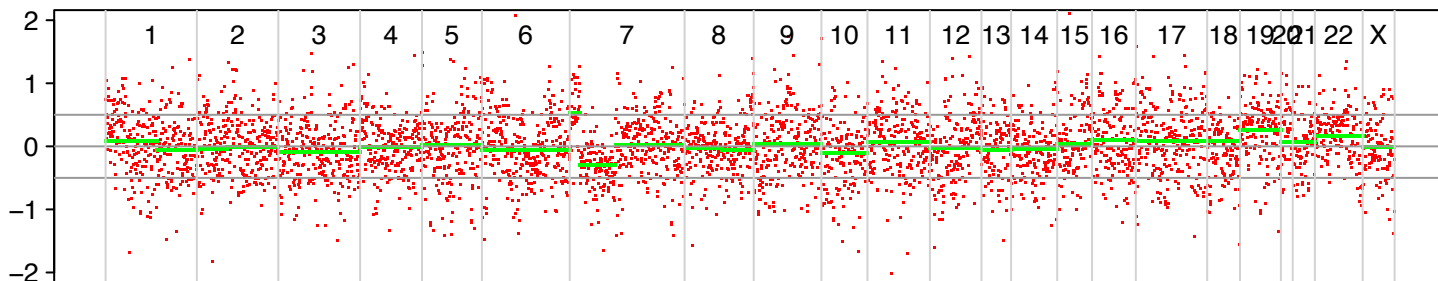
Aberration reliability score (%), average: 43%



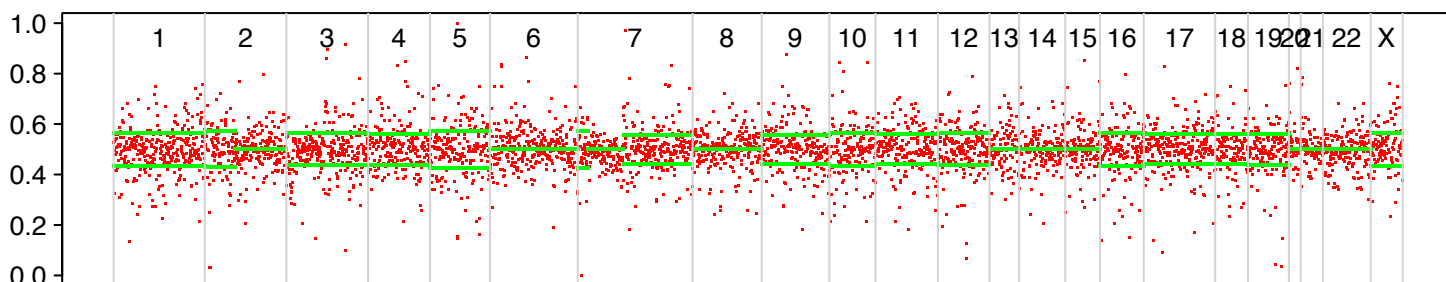
Ploidy: 2.05, aberrant cell fraction: 44%, goodness of fit: 98.7%



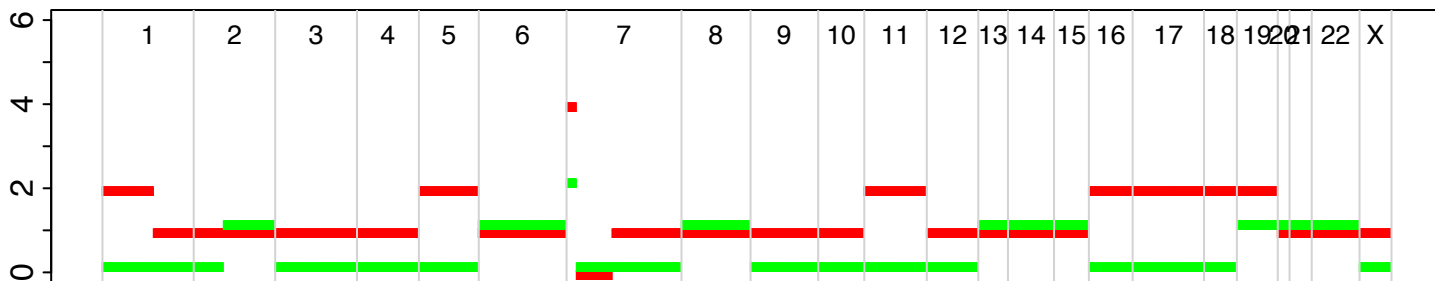
T_520C, LogR



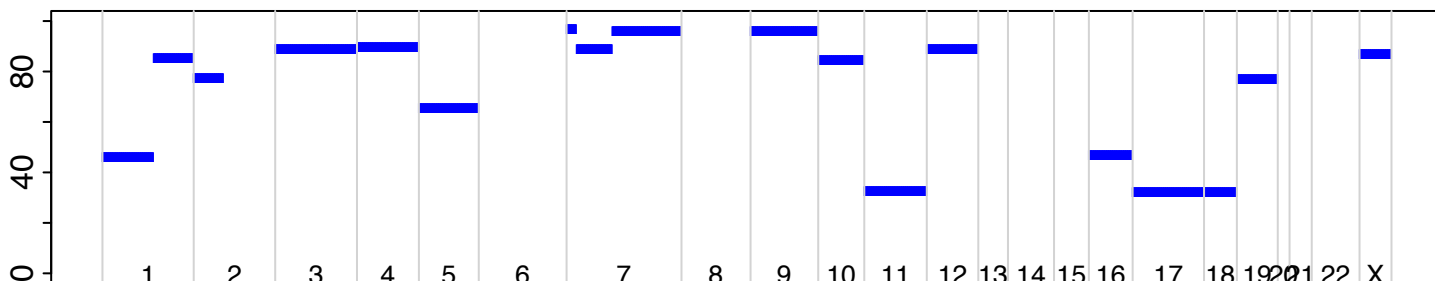
T_520C, BAF



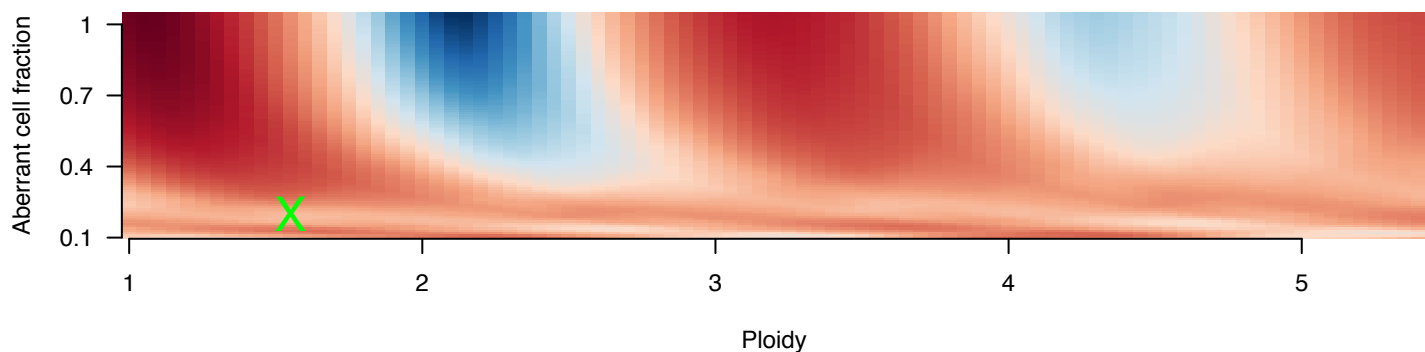
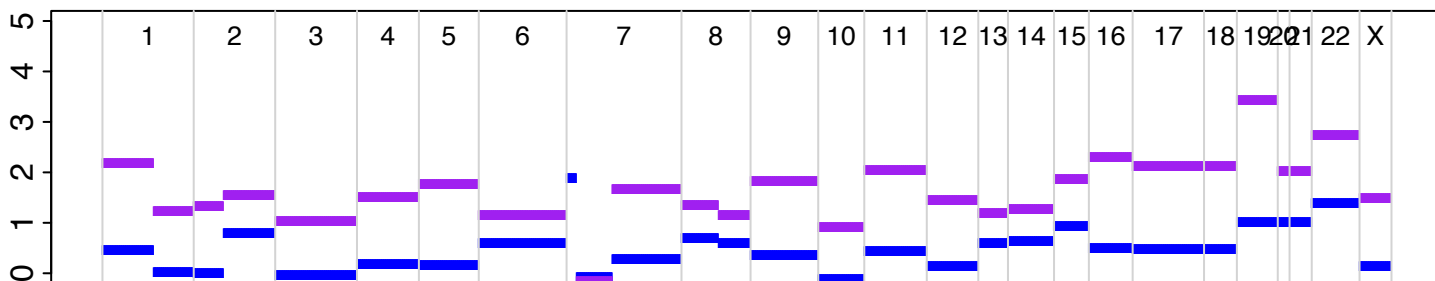
Ploidy: 1.65, aberrant cell fraction: 20%, goodness of fit: 99.2%



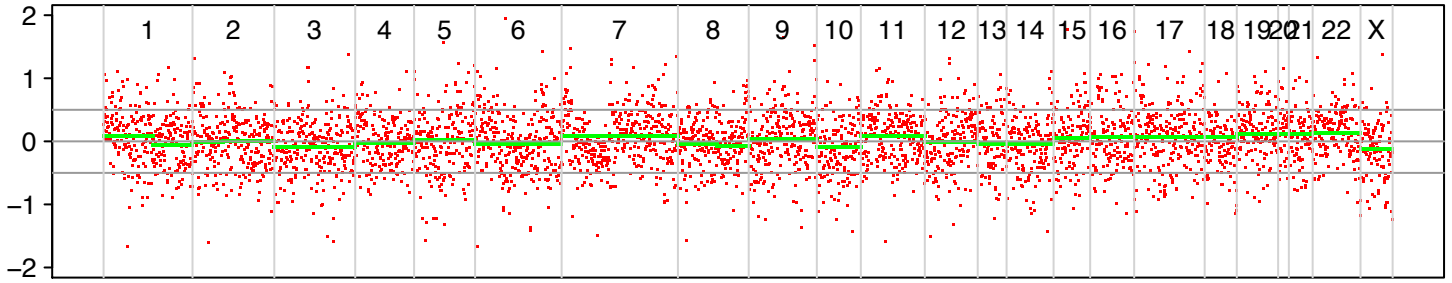
Aberration reliability score (%), average: 72%



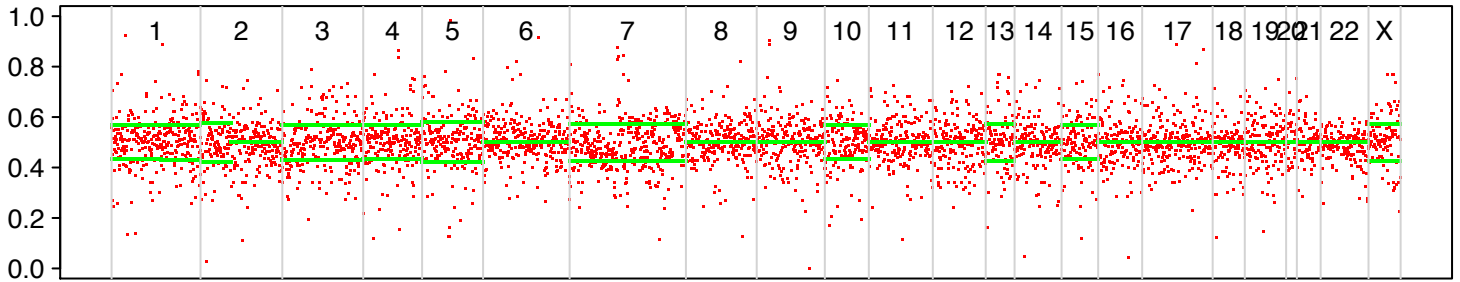
Ploidy: 1.65, aberrant cell fraction: 20%, goodness of fit: 99.2%



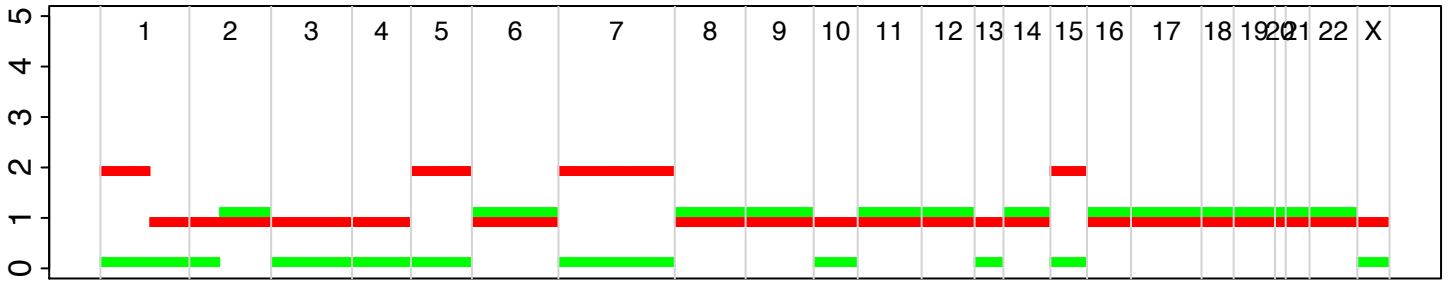
T_520D, LogR



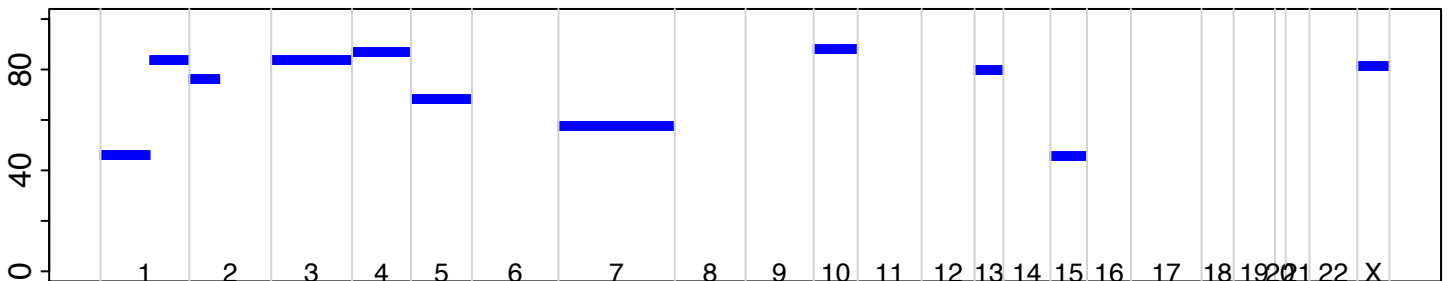
T_520D, BAF



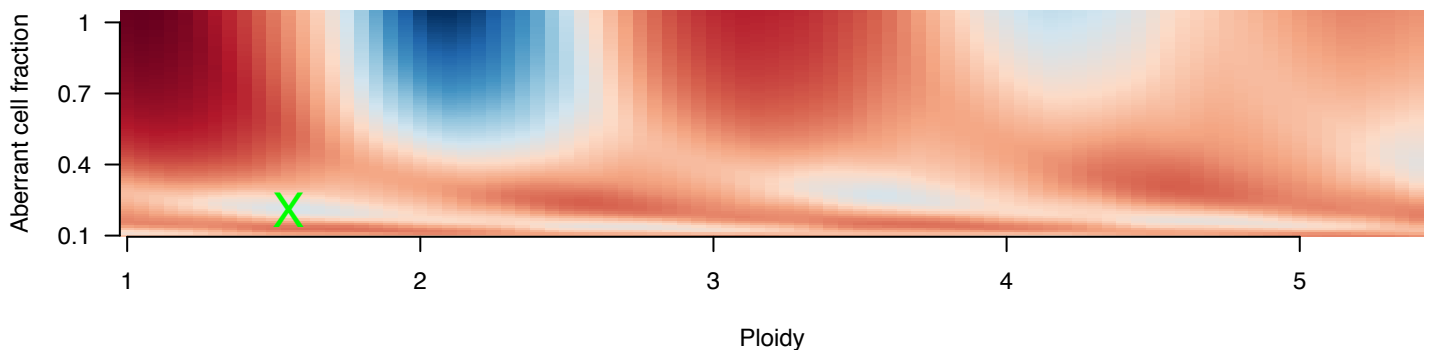
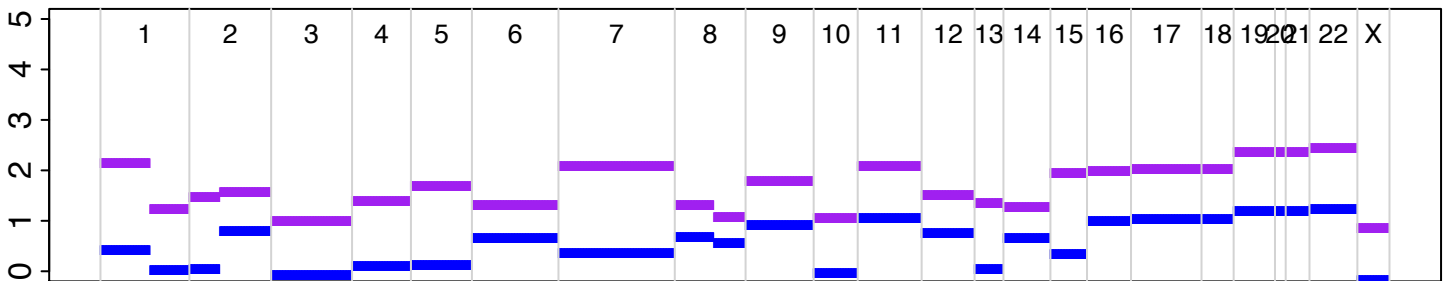
Ploidy: 1.65, aberrant cell fraction: 21%, goodness of fit: 99.2%



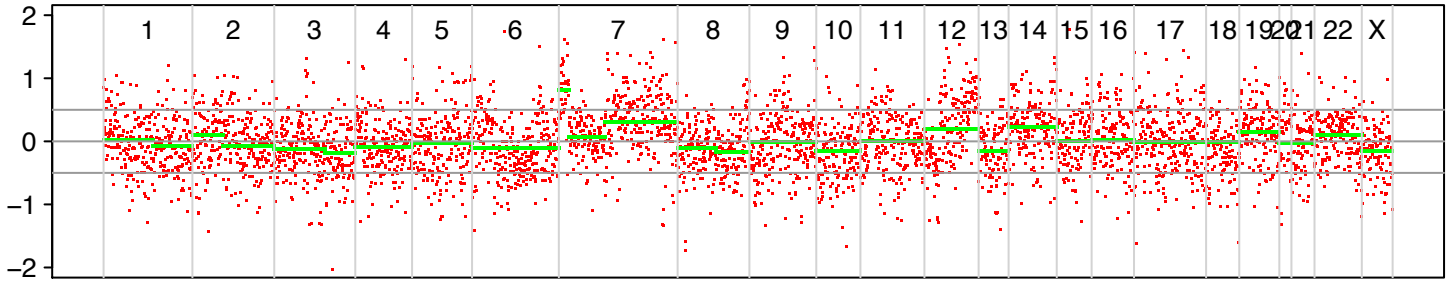
Aberration reliability score (%), average: 71%



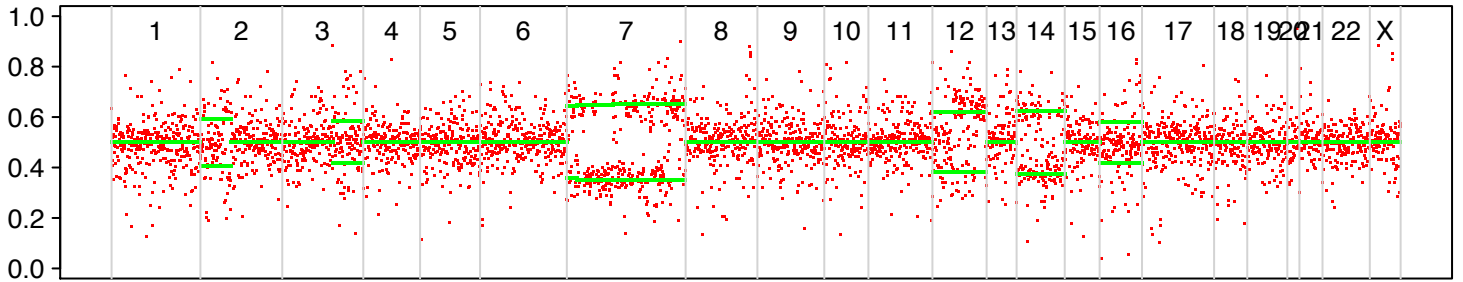
Ploidy: 1.65, aberrant cell fraction: 21%, goodness of fit: 99.2%



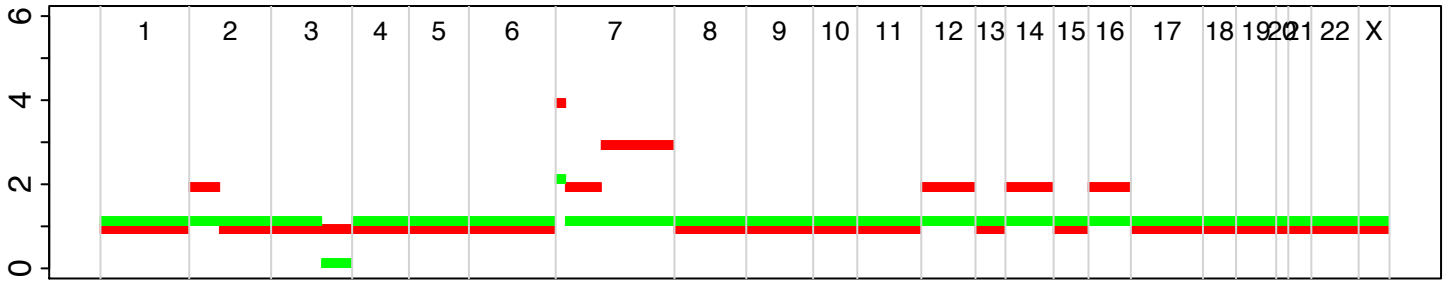
T_520E, LogR



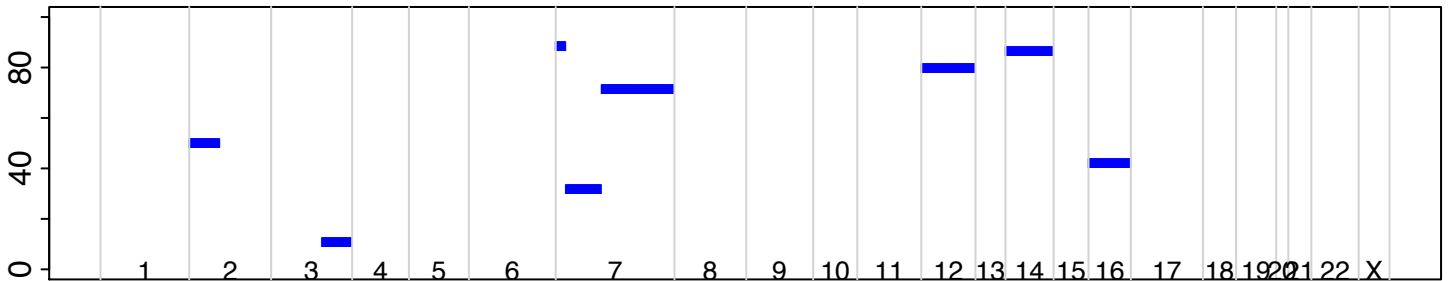
T_520E, BAF



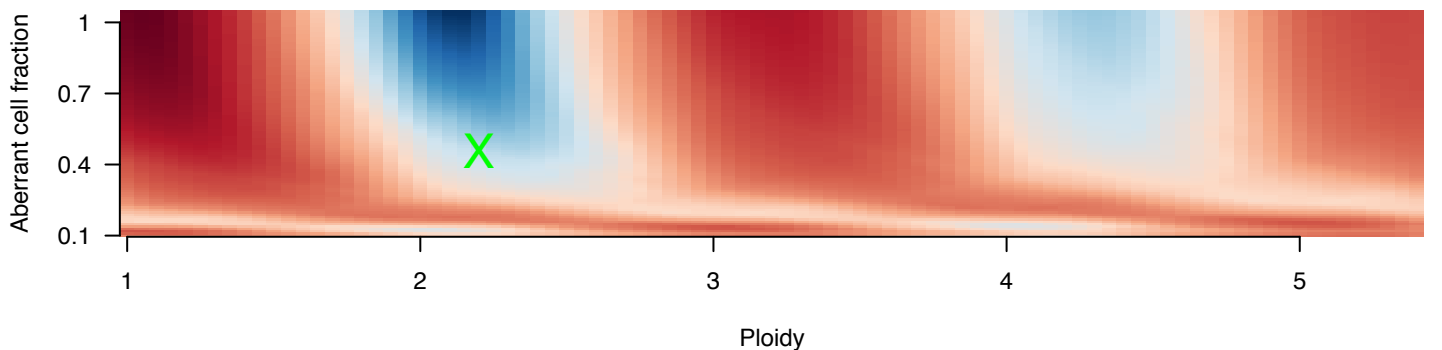
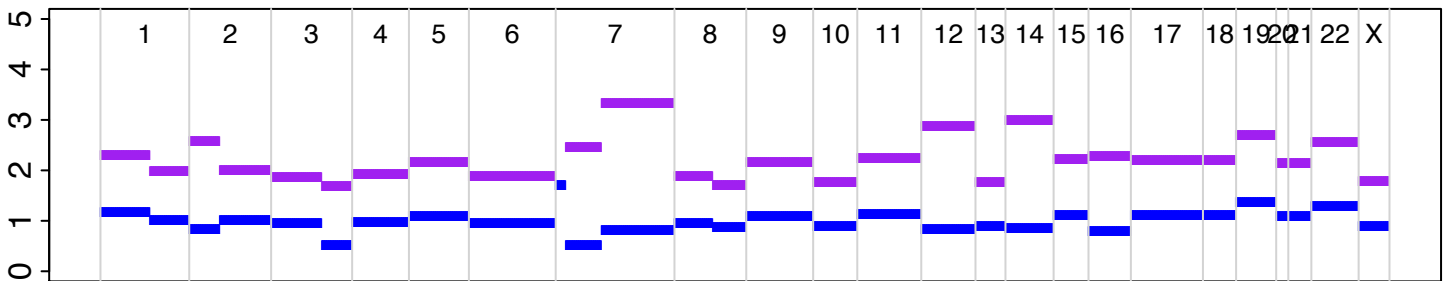
Ploidy: 2.25, aberrant cell fraction: 46%, goodness of fit: 98.6%



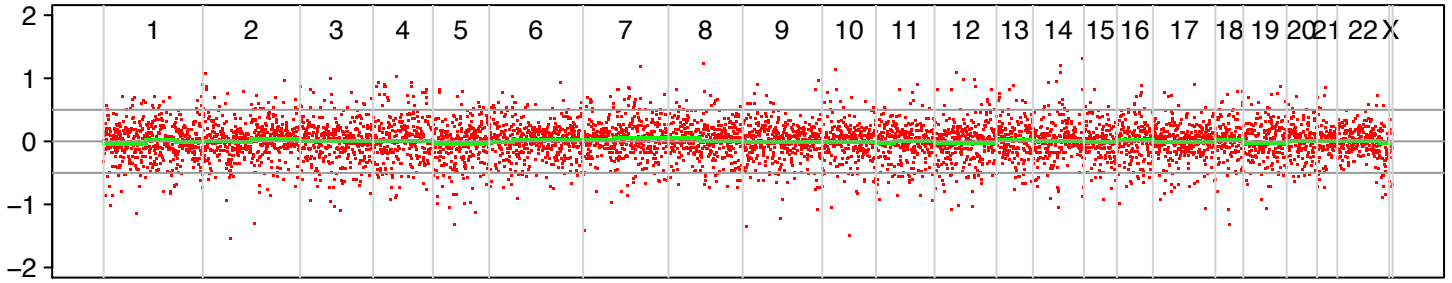
Aberration reliability score (%), average: 59%



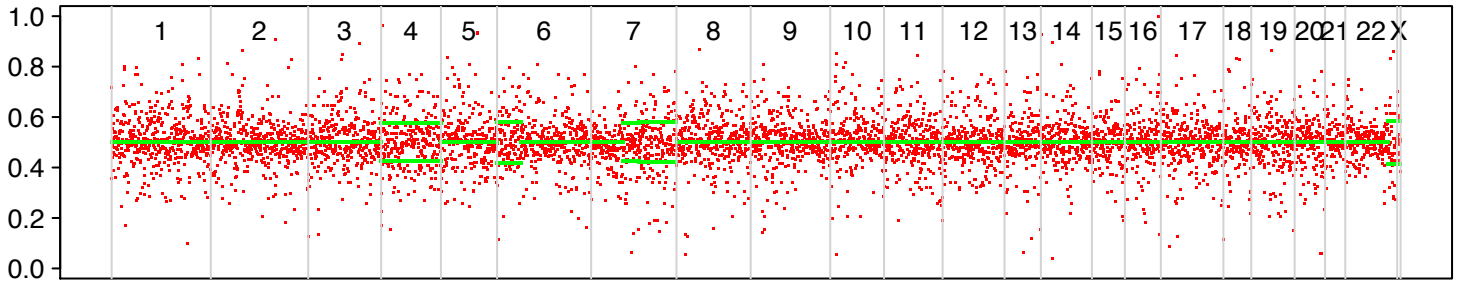
Ploidy: 2.25, aberrant cell fraction: 46%, goodness of fit: 98.6%



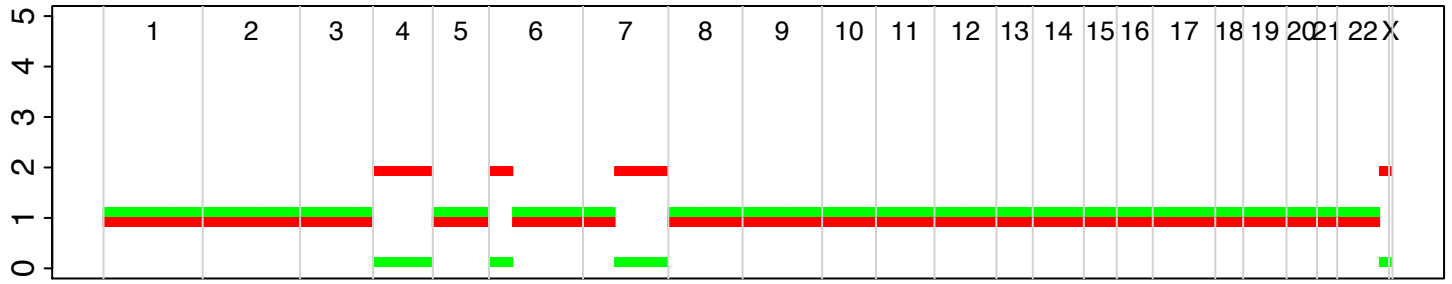
T_699A, LogR



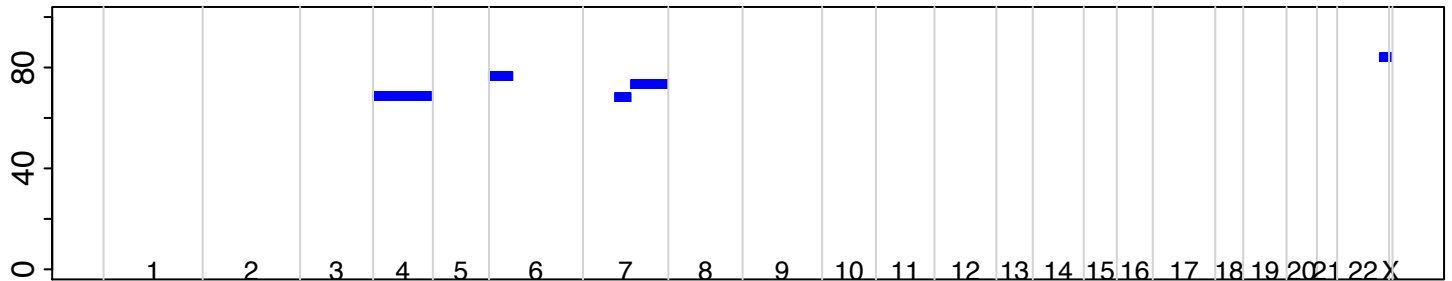
T_699A, BAF



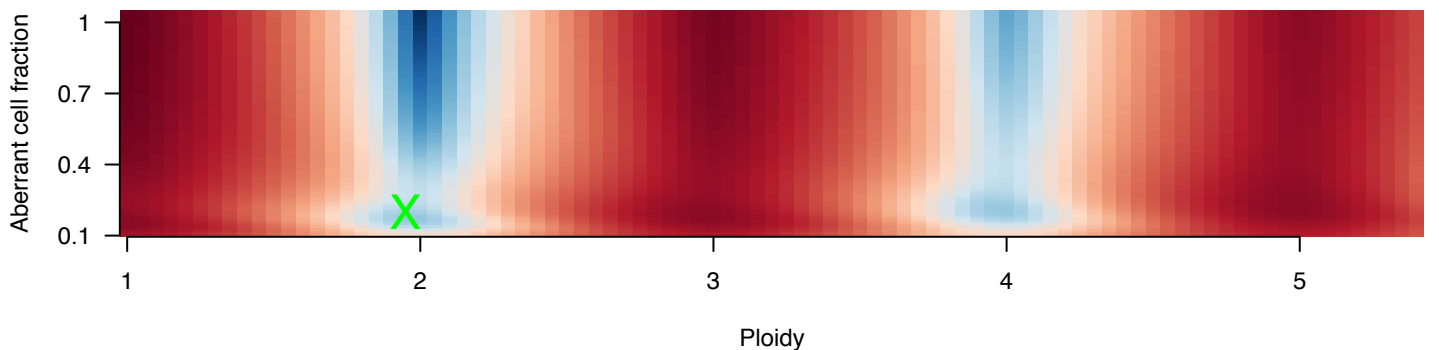
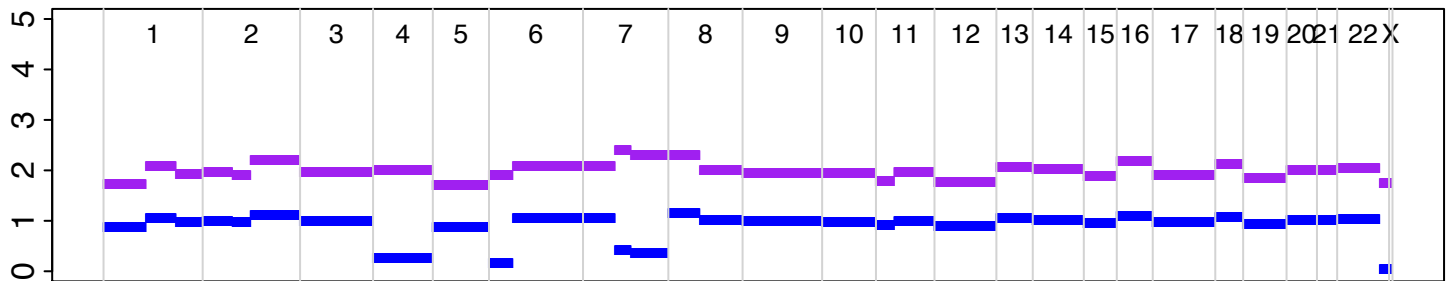
Ploidy: 1.96, aberrant cell fraction: 20%, goodness of fit: 98.9%



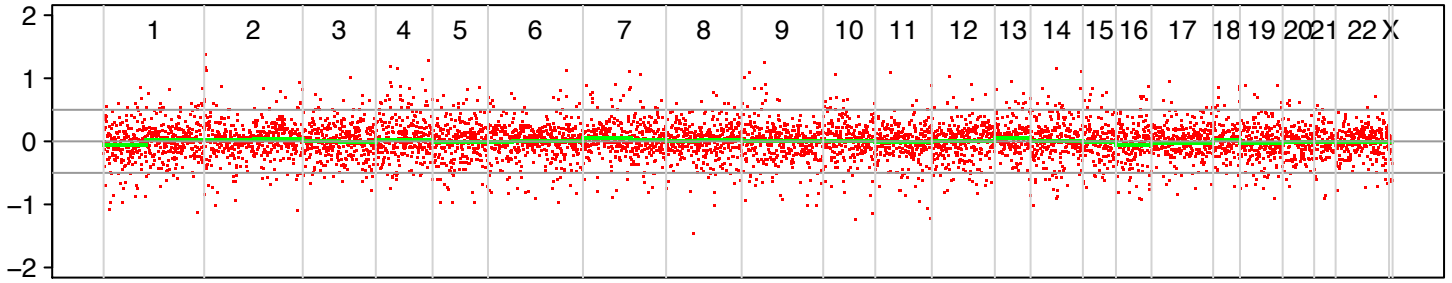
Aberration reliability score (%), average: 72%



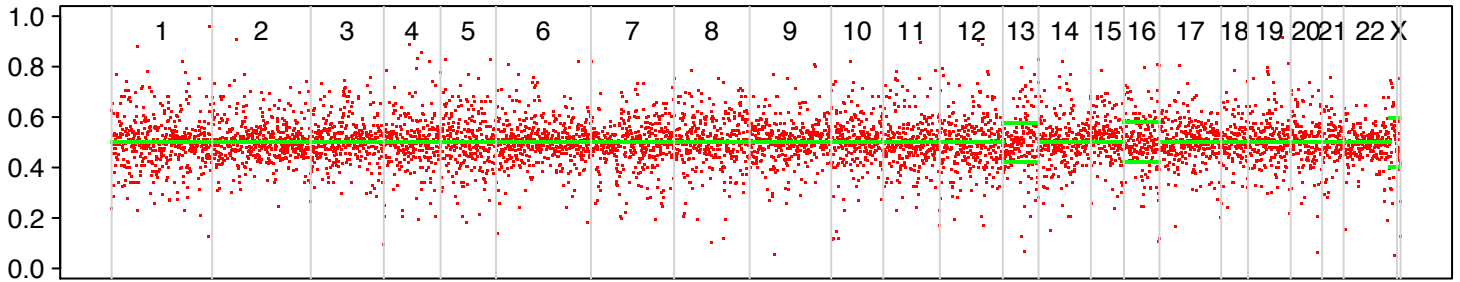
Ploidy: 1.96, aberrant cell fraction: 20%, goodness of fit: 98.9%



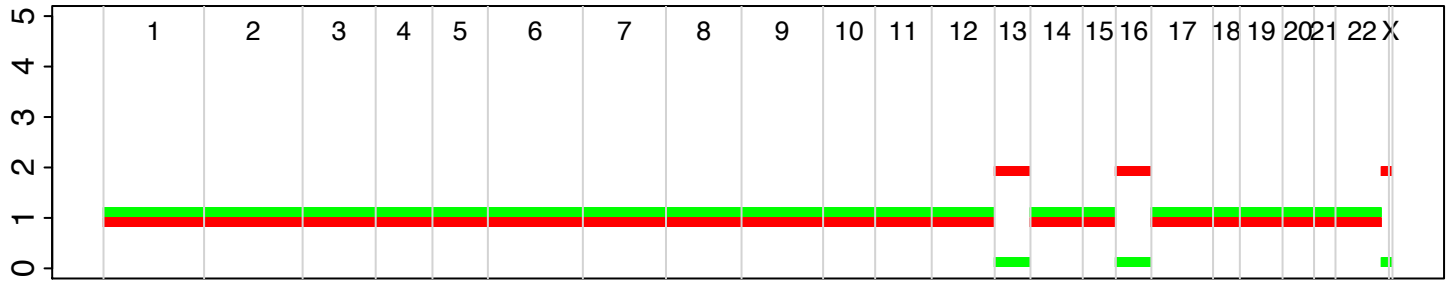
T_699B, LogR



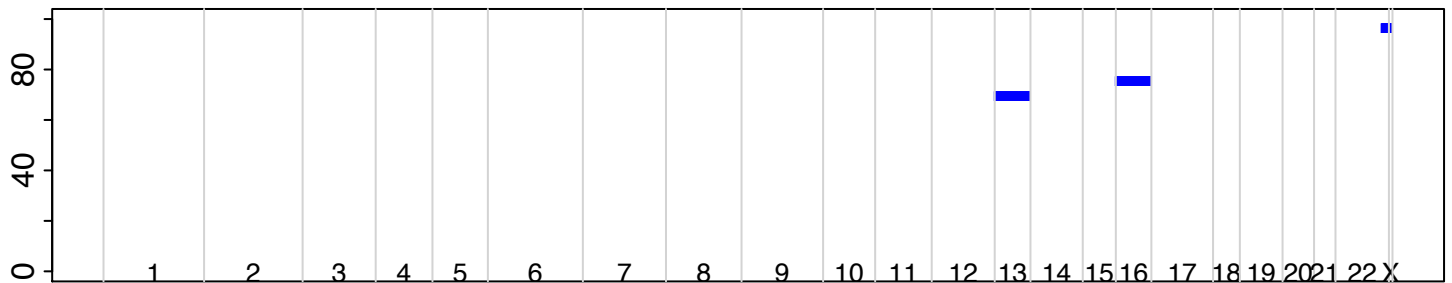
T_699B, BAF



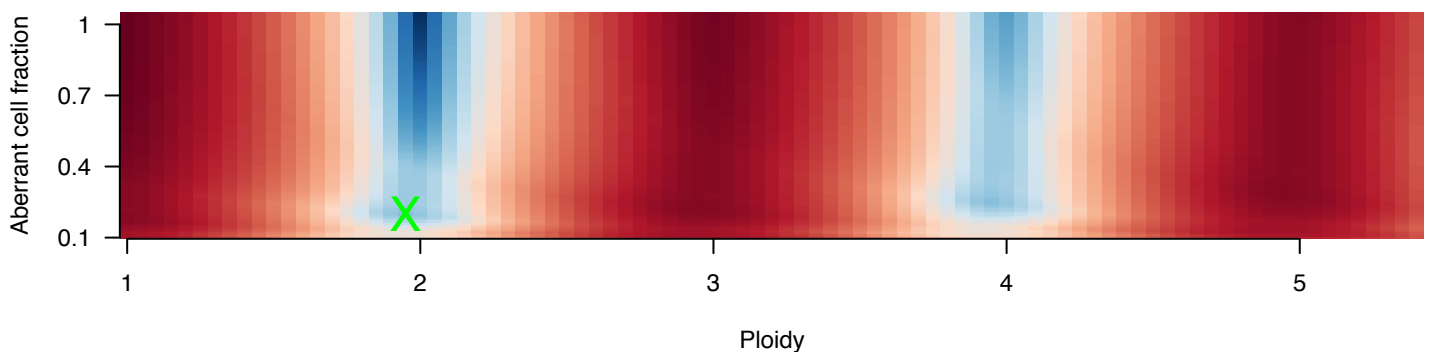
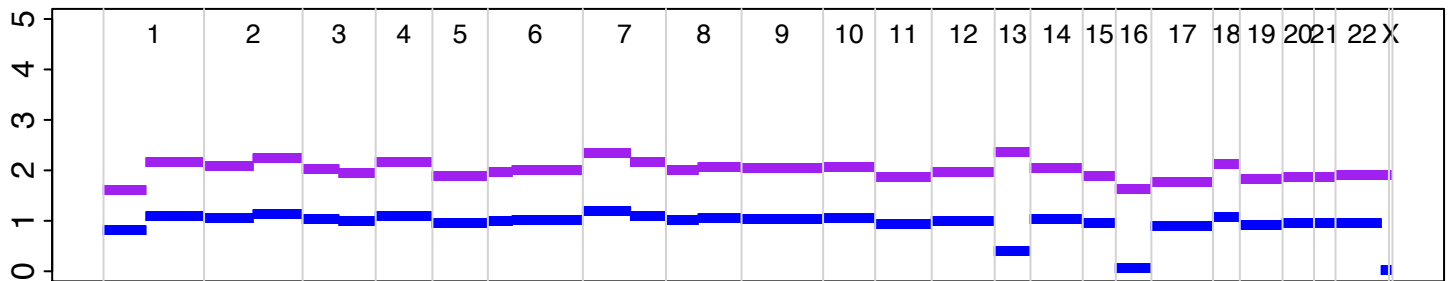
Ploidy: 1.98, aberrant cell fraction: 20%, goodness of fit: 98.8%



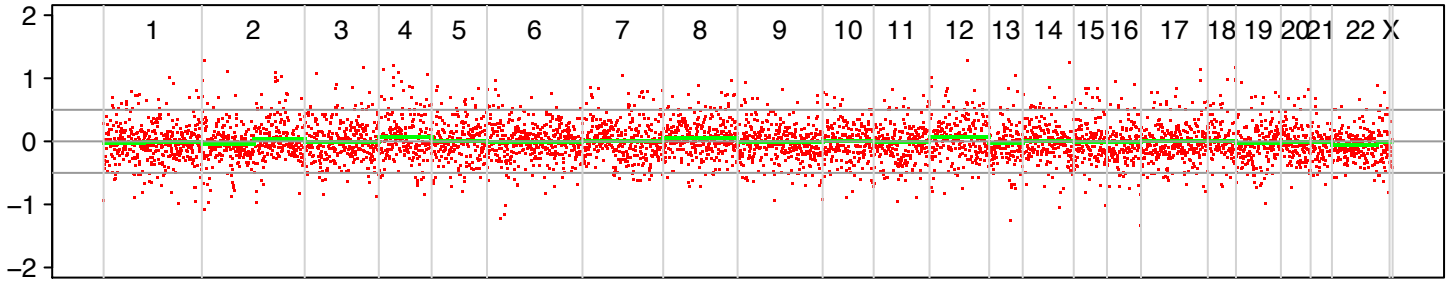
Aberration reliability score (%), average: 75%



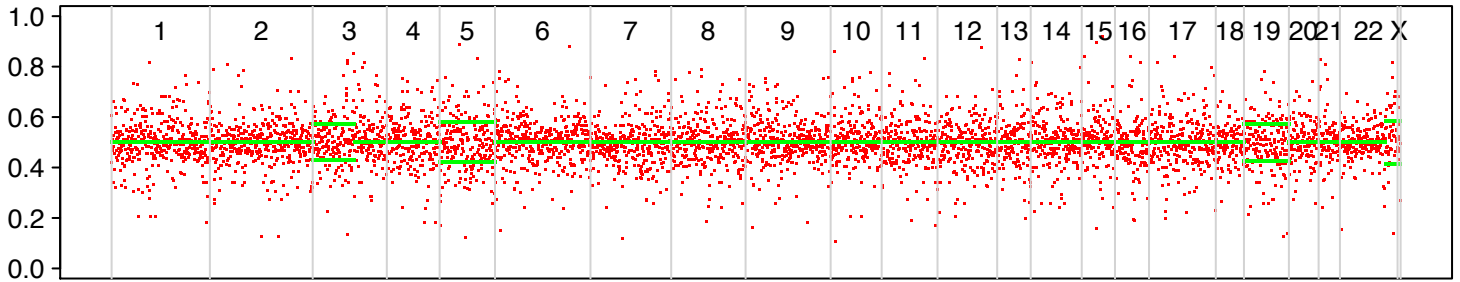
Ploidy: 1.98, aberrant cell fraction: 20%, goodness of fit: 98.8%



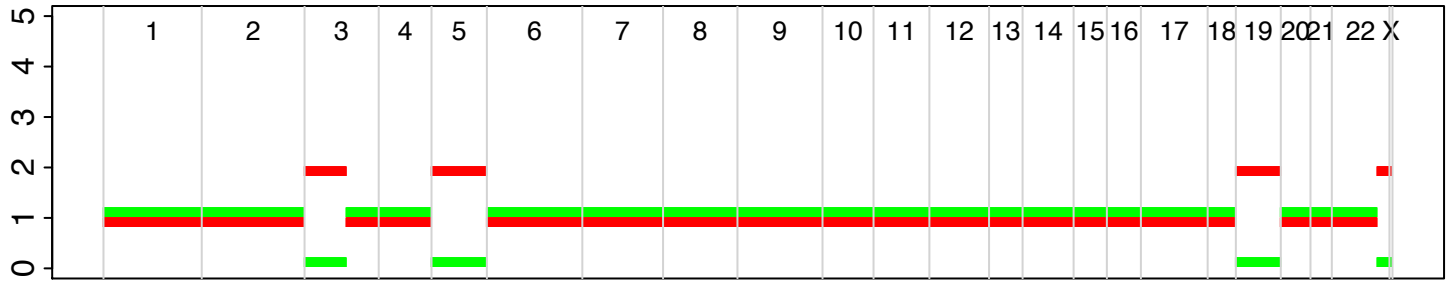
T_699C, LogR



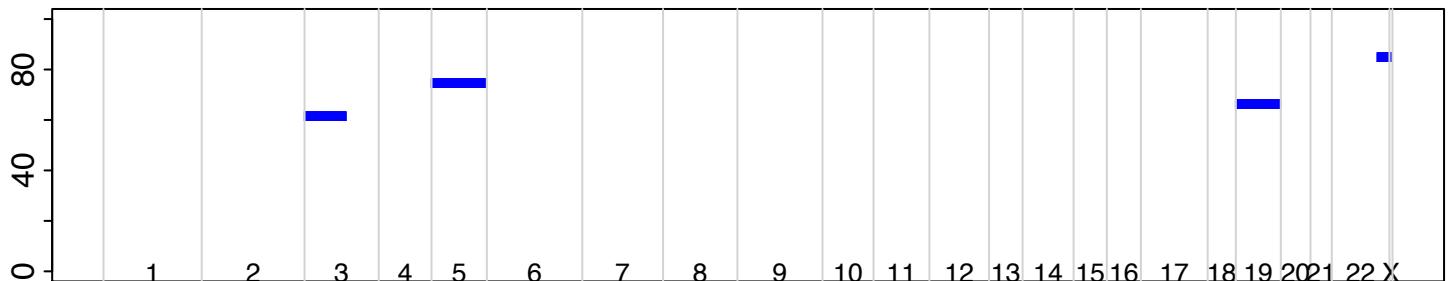
T_699C, BAF



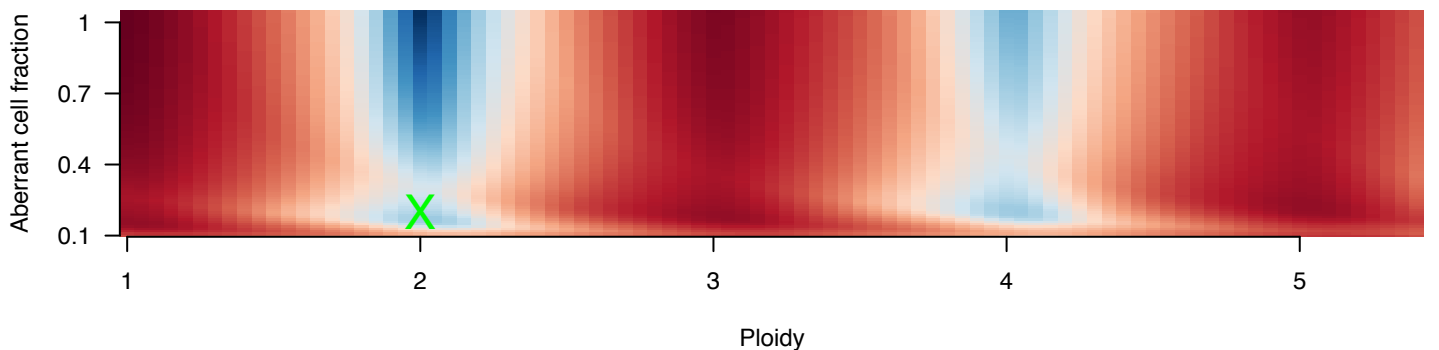
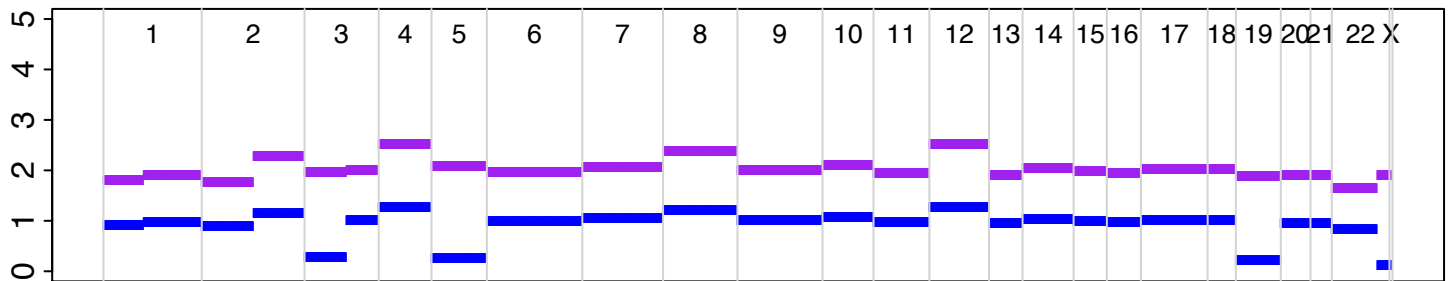
Ploidy: 2.02, aberrant cell fraction: 20%, goodness of fit: 98.8%



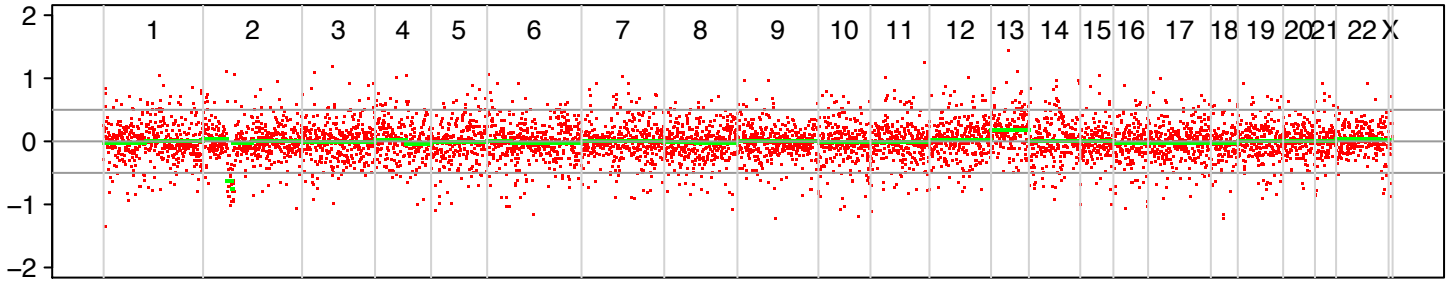
Aberration reliability score (%), average: 69%



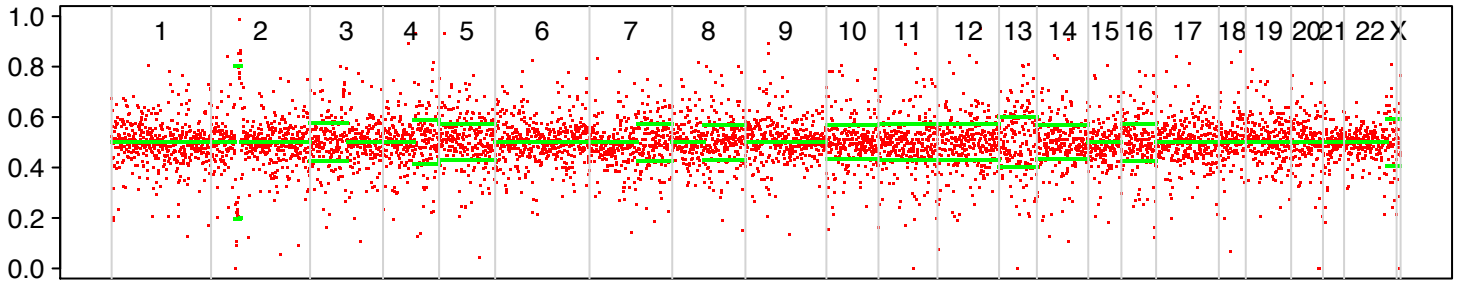
Ploidy: 2.02, aberrant cell fraction: 20%, goodness of fit: 98.8%



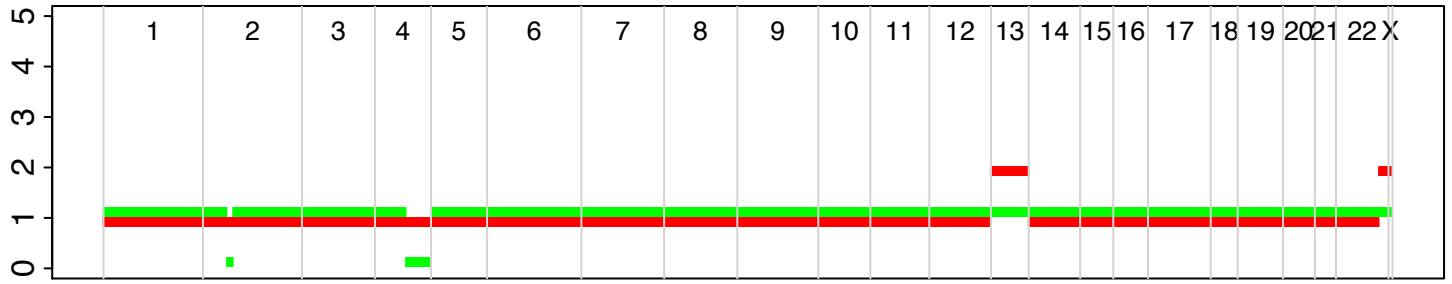
T_699D, LogR



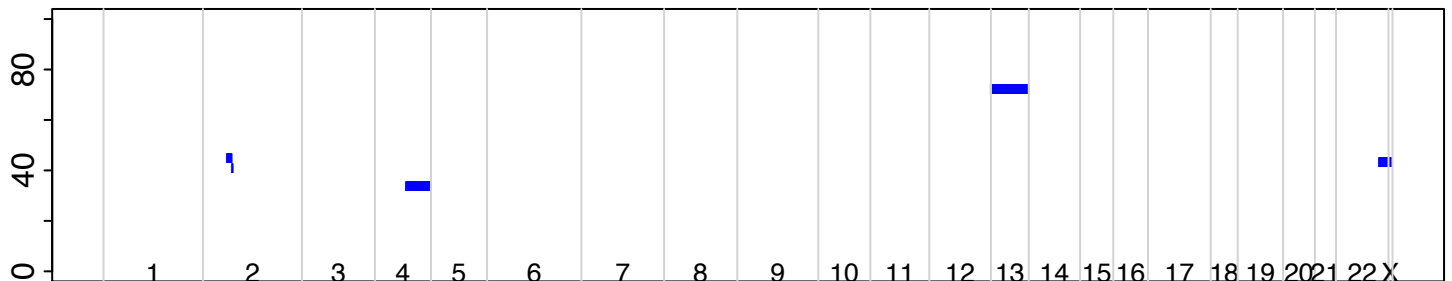
T_699D, BAF



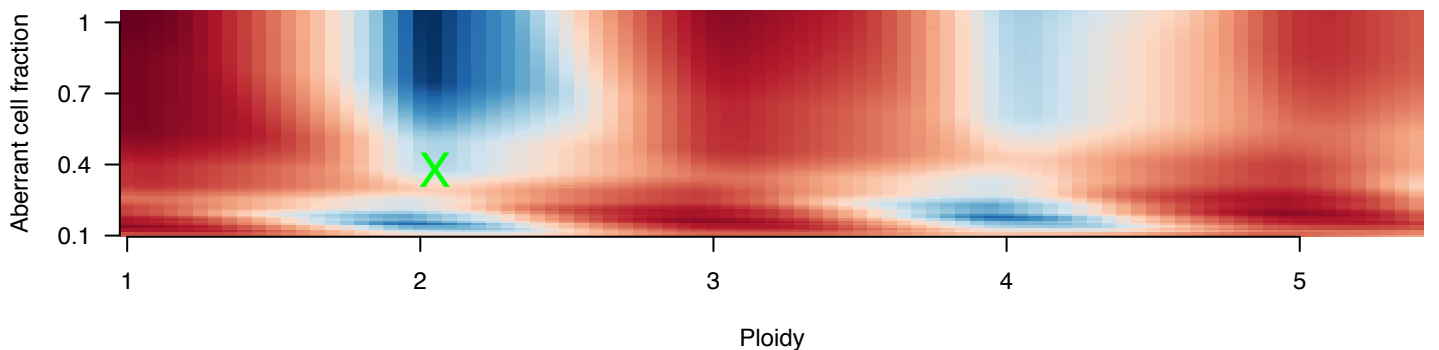
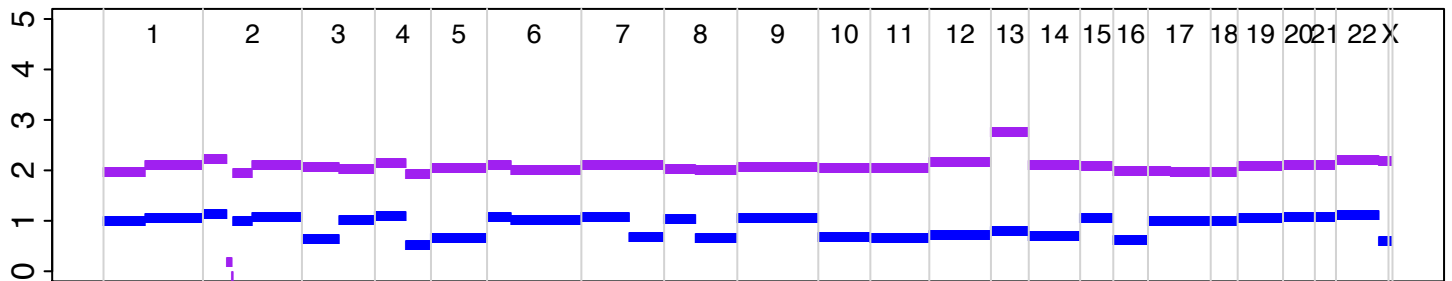
Ploidy: 2.05, aberrant cell fraction: 38%, goodness of fit: 99.2%



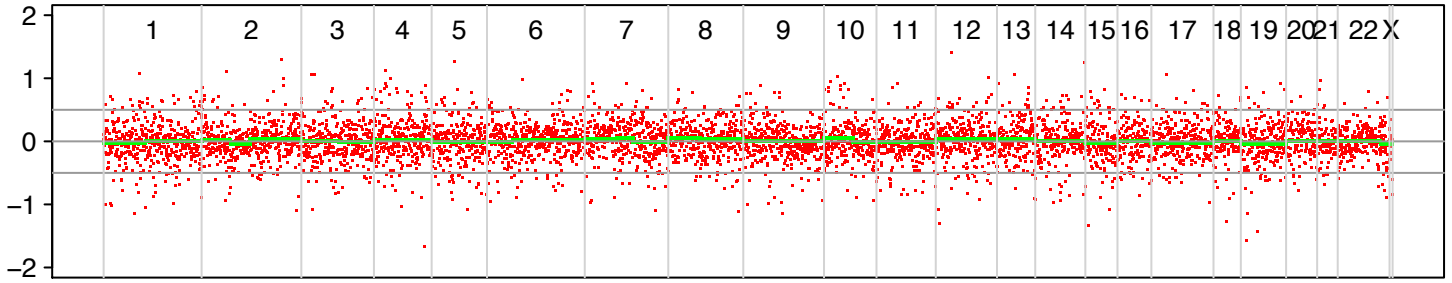
Aberration reliability score (%), average: 53%



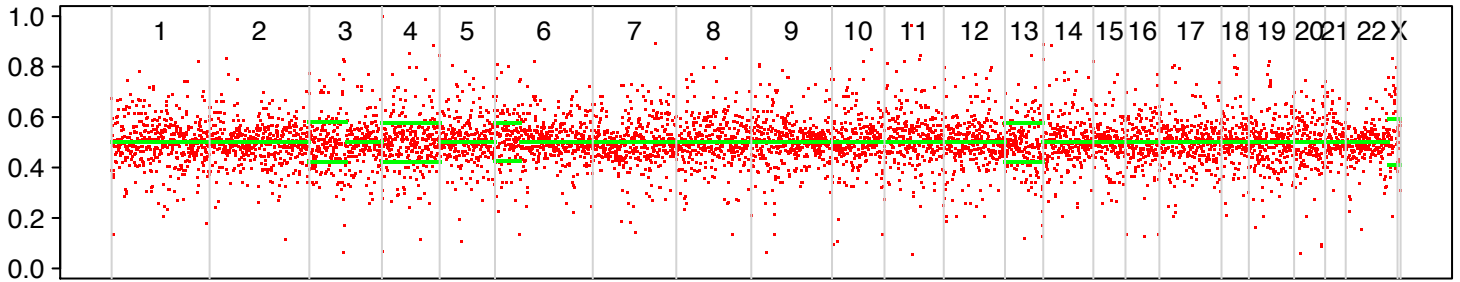
Ploidy: 2.05, aberrant cell fraction: 38%, goodness of fit: 99.2%



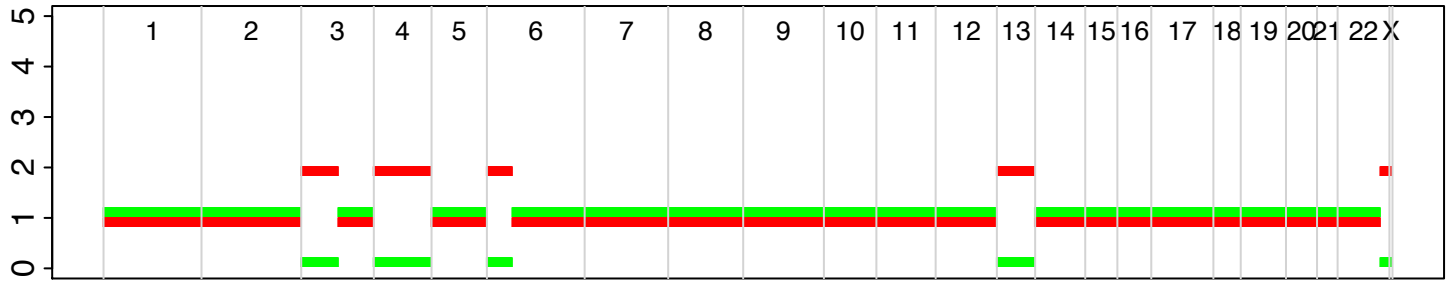
T_699E, LogR



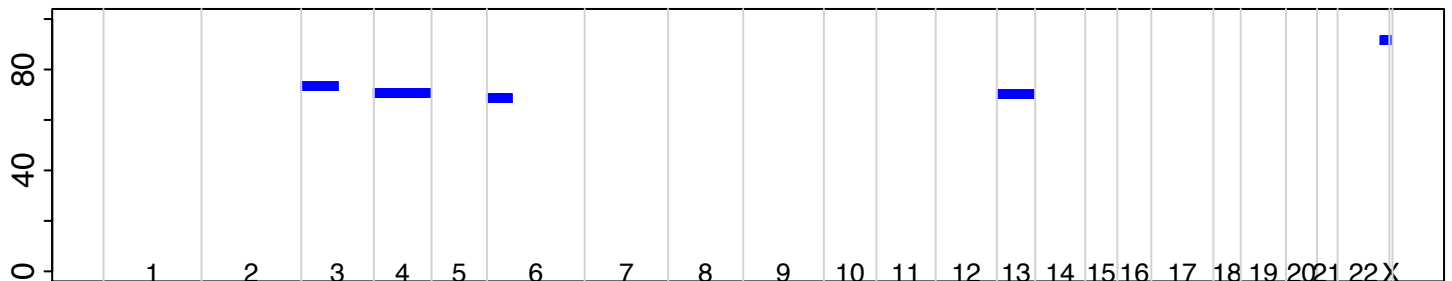
T_699E, BAF



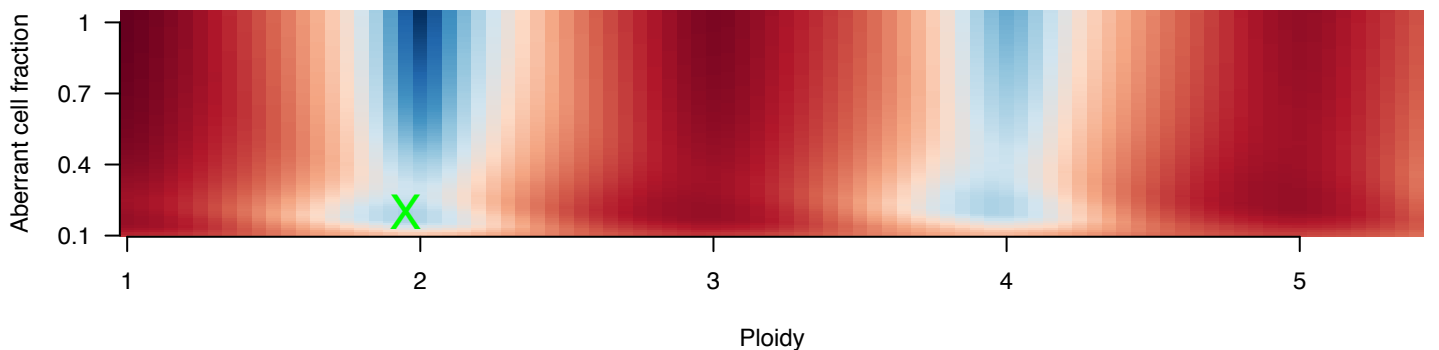
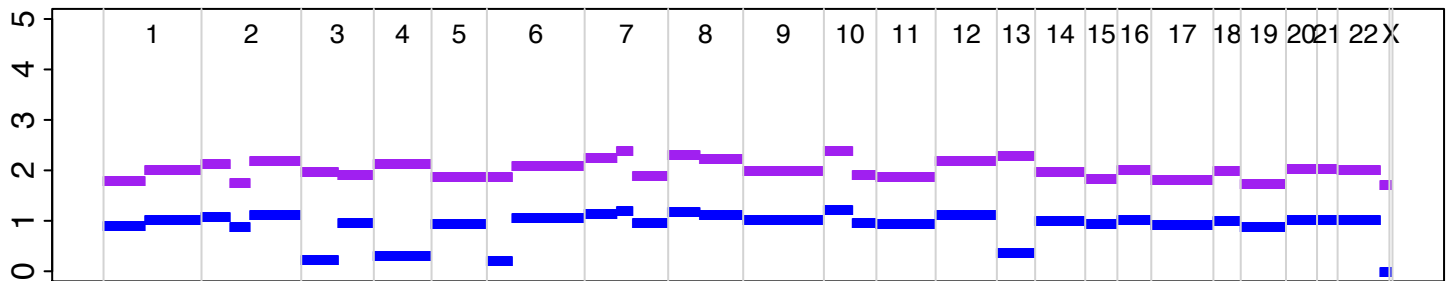
Ploidy: 1.99, aberrant cell fraction: 20%, goodness of fit: 98.8%



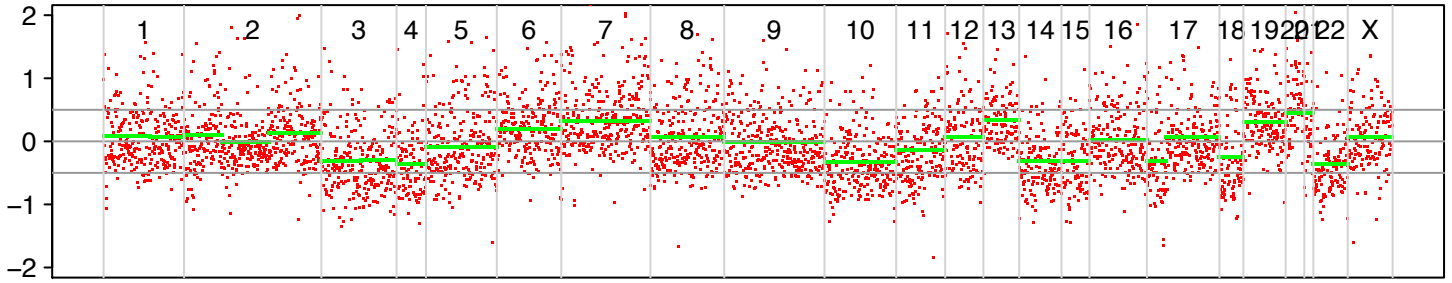
Aberration reliability score (%), average: 72%



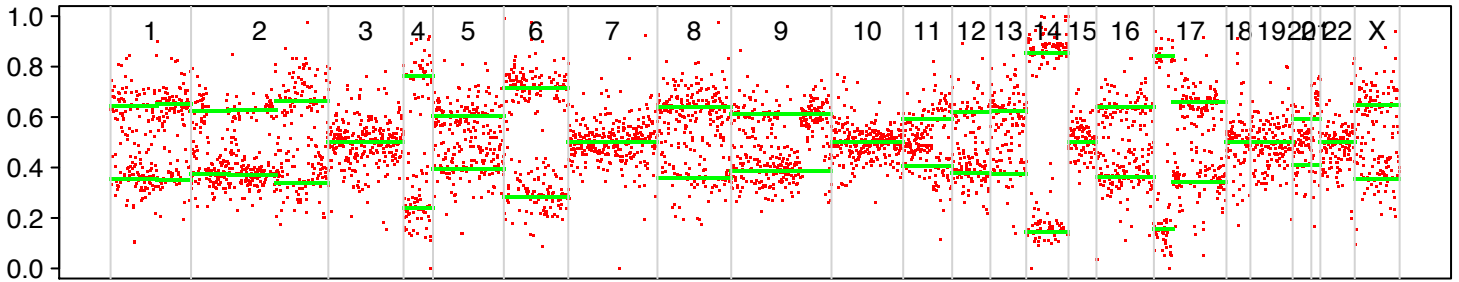
Ploidy: 1.99, aberrant cell fraction: 20%, goodness of fit: 98.8%



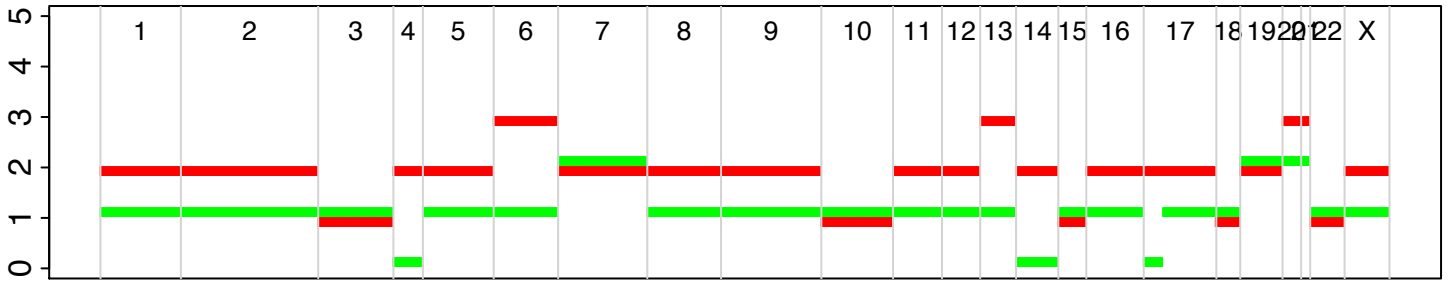
T_T720A, LogR



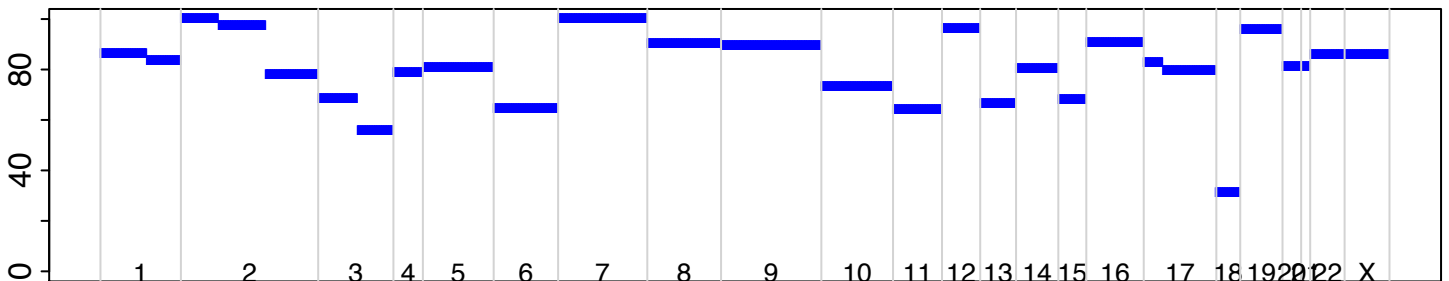
T_T720A, BAF



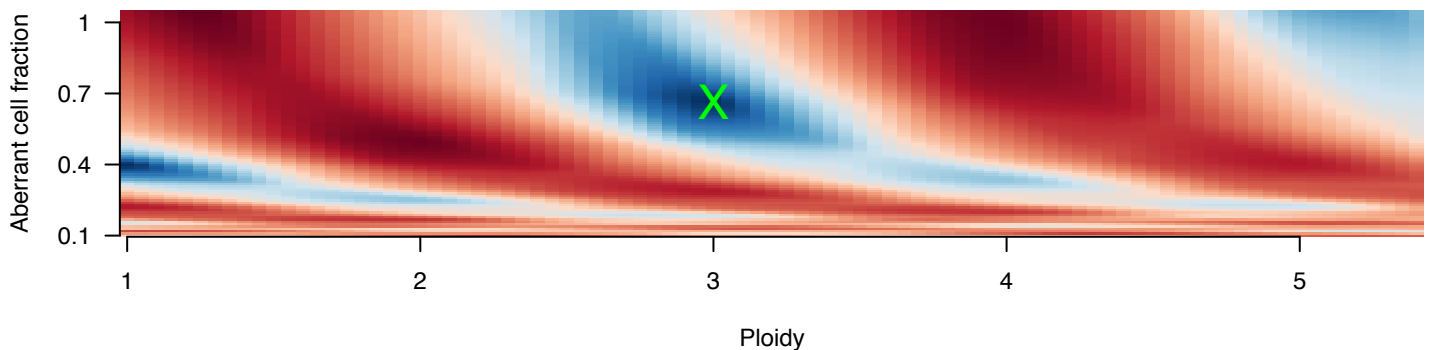
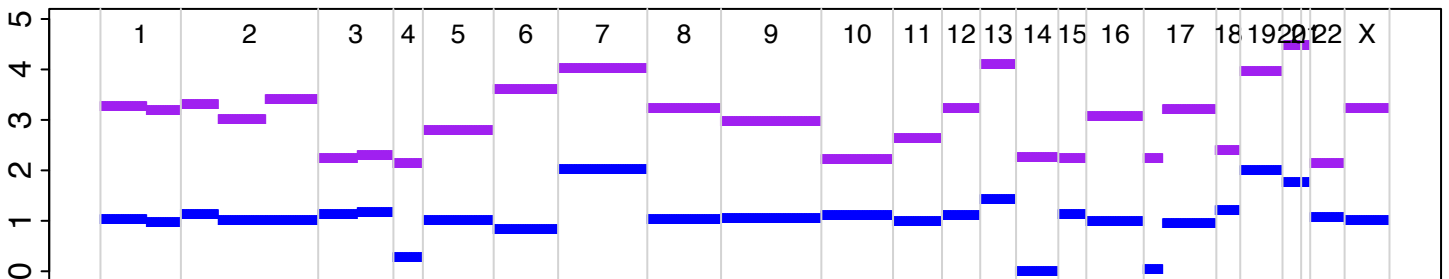
Ploidy: 3.03, aberrant cell fraction: 67%, goodness of fit: 99.7%



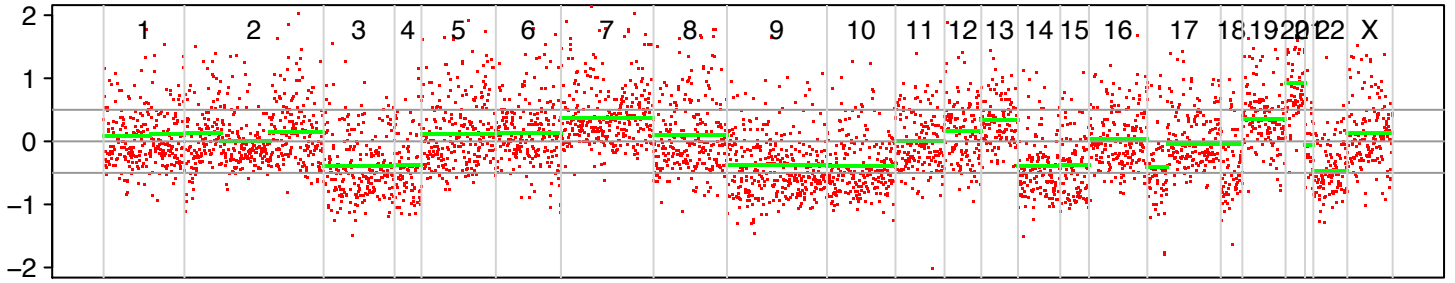
Aberration reliability score (%), average: 81%



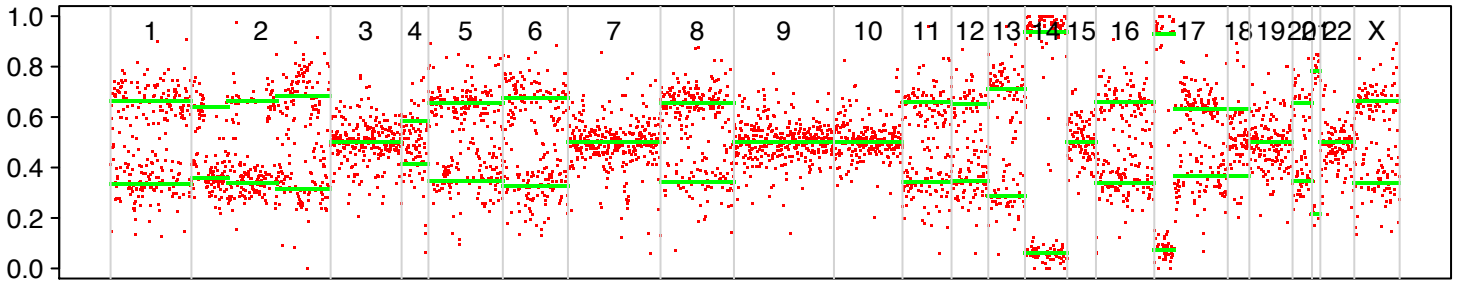
Ploidy: 3.03, aberrant cell fraction: 67%, goodness of fit: 99.7%



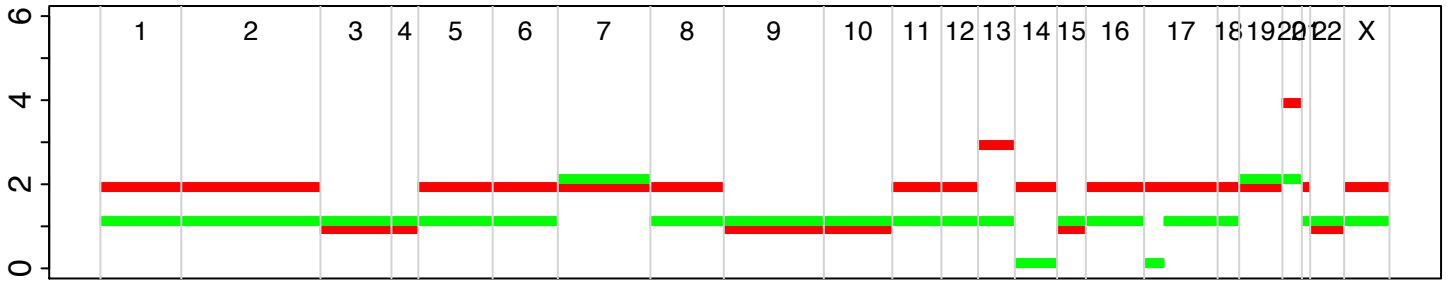
T_T720B, LogR



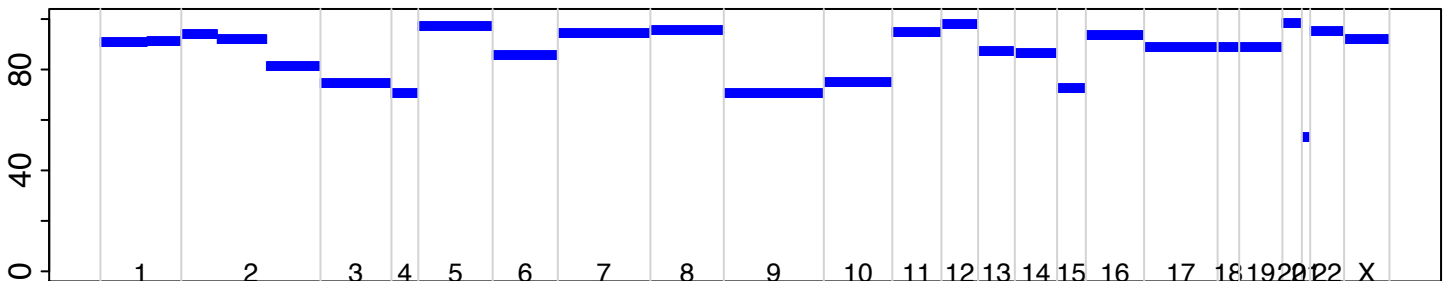
T_T720B, BAF



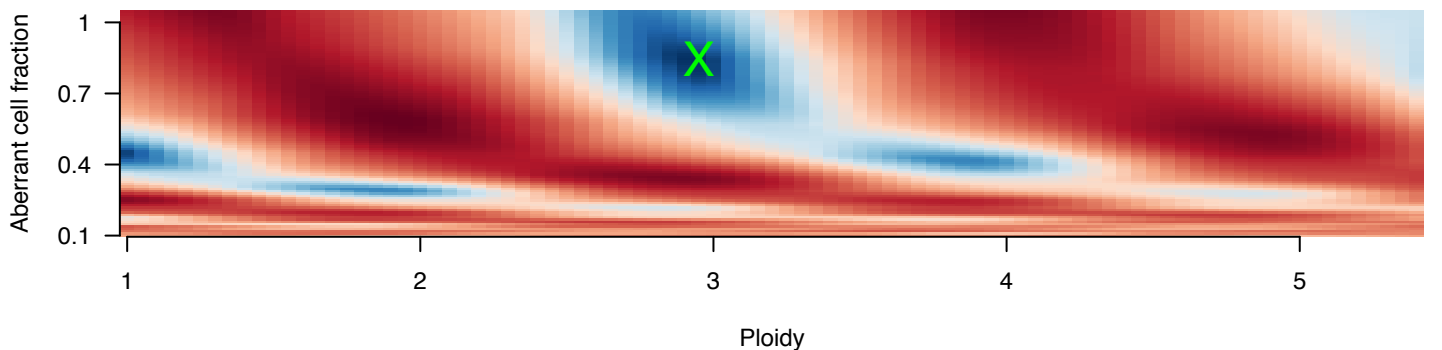
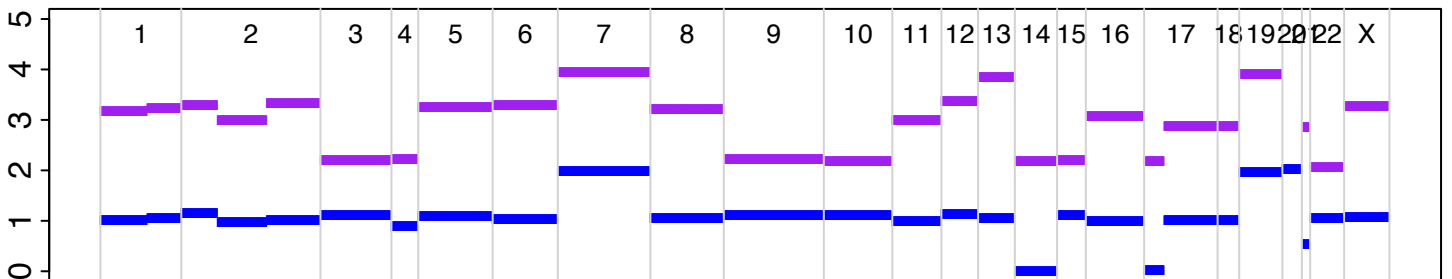
Ploidy: 2.99, aberrant cell fraction: 85%, goodness of fit: 99.8%



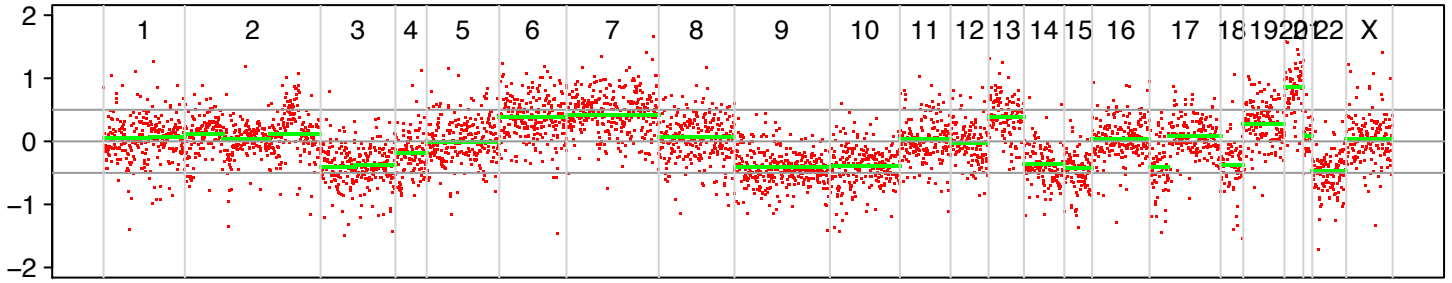
Aberration reliability score (%), average: 87%



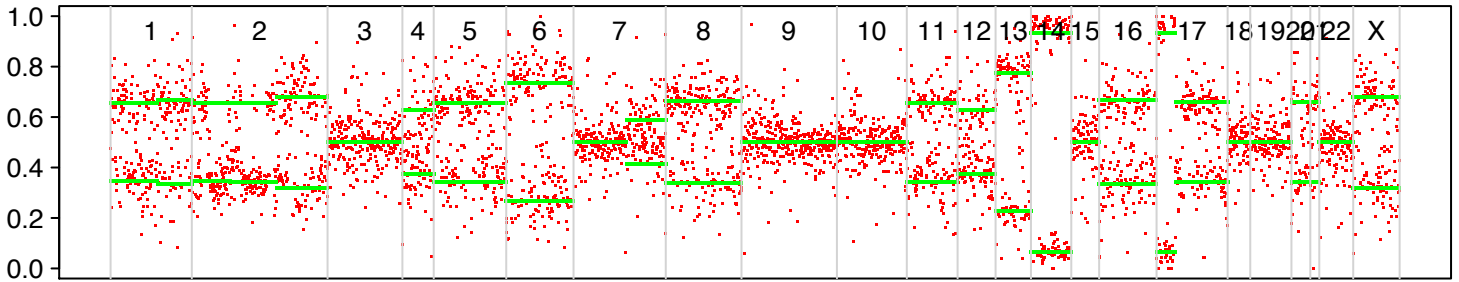
Ploidy: 2.99, aberrant cell fraction: 85%, goodness of fit: 99.8%



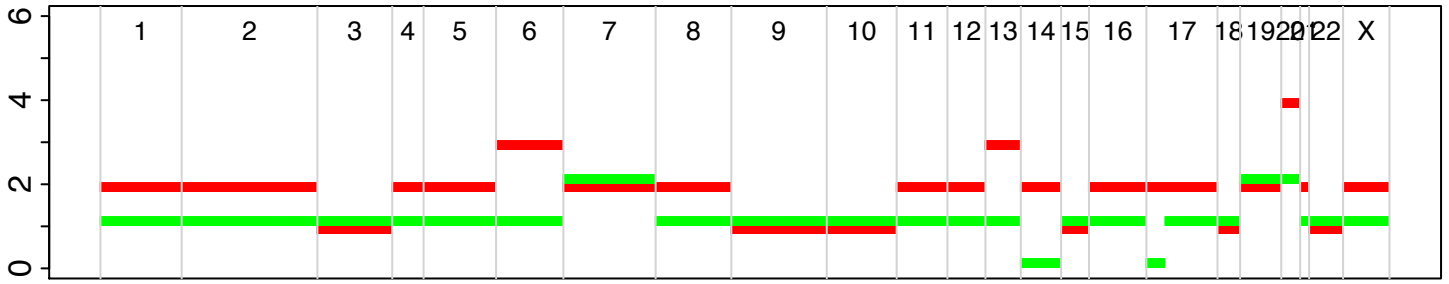
T_T720C, LogR



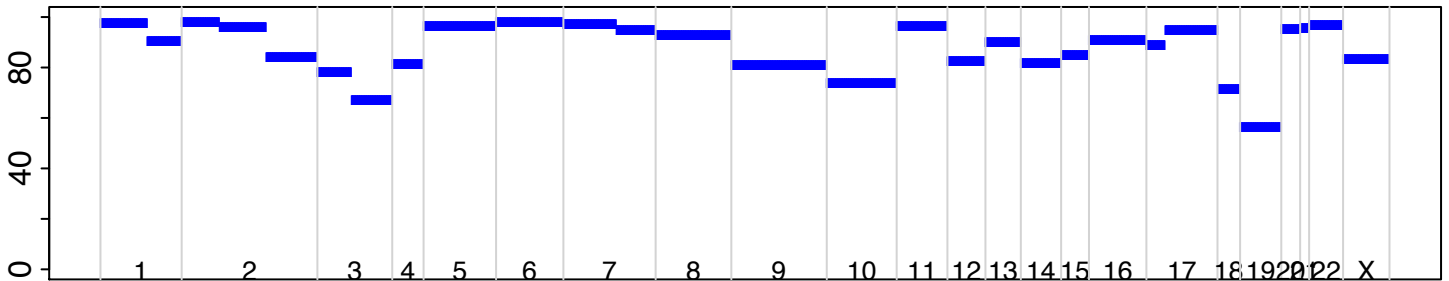
T_T720C, BAF



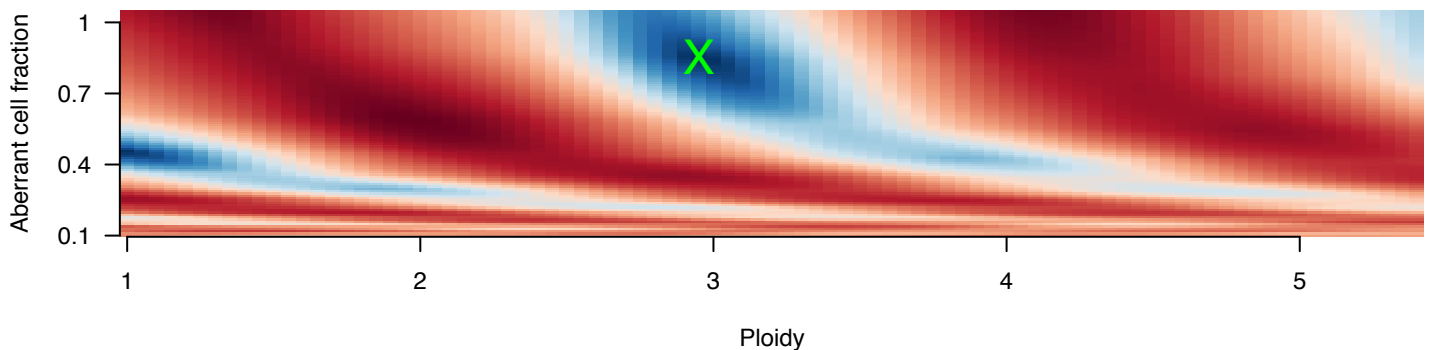
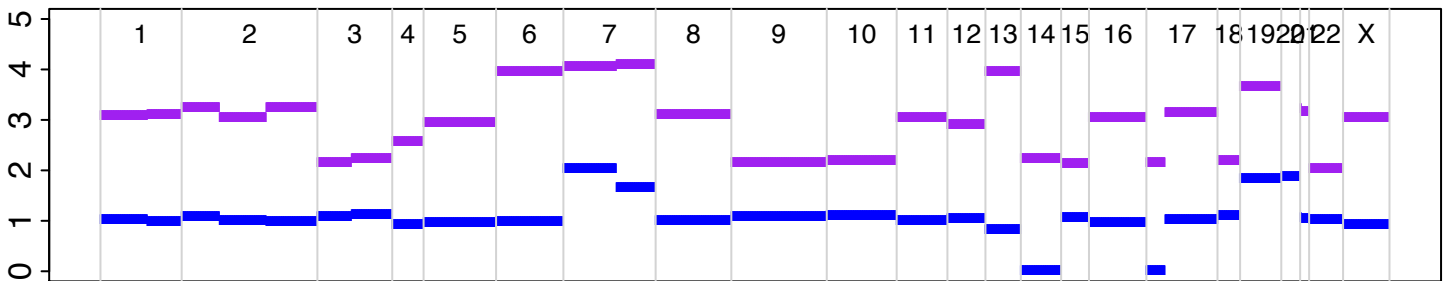
Ploidy: 2.98, aberrant cell fraction: 86%, goodness of fit: 99.7%



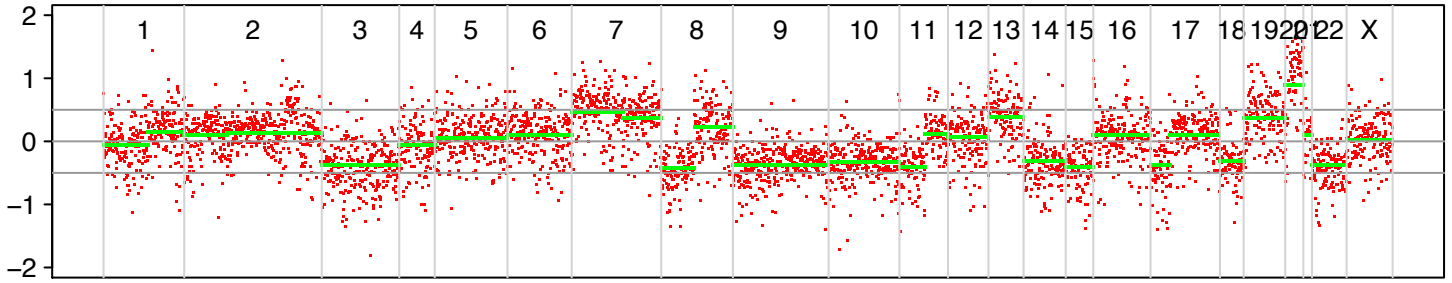
Aberration reliability score (%), average: 87%



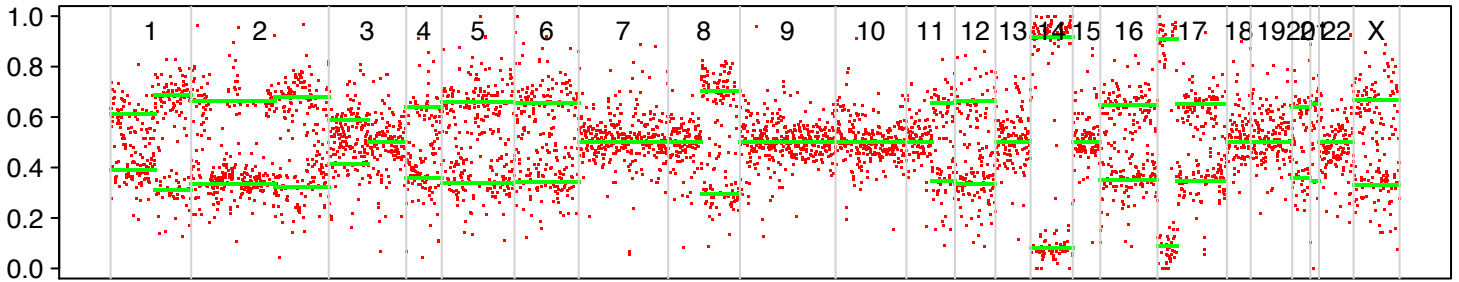
Ploidy: 2.98, aberrant cell fraction: 86%, goodness of fit: 99.7%



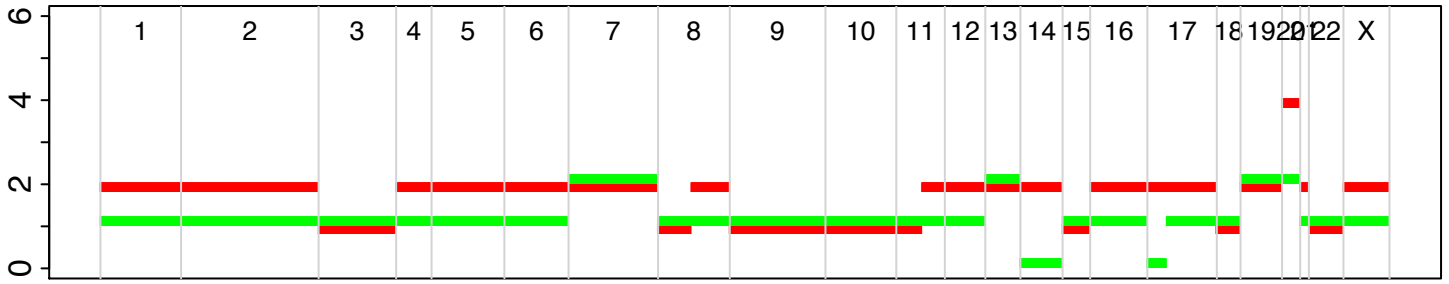
T_T720D, LogR



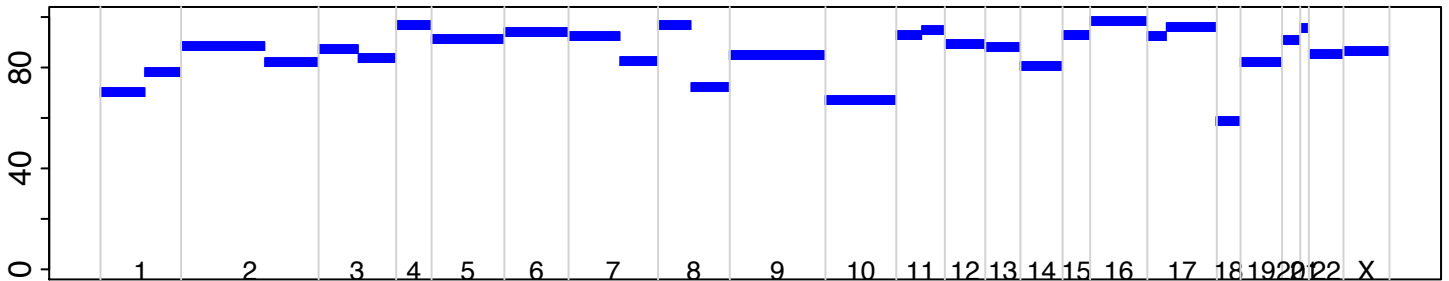
T_T720D, BAF



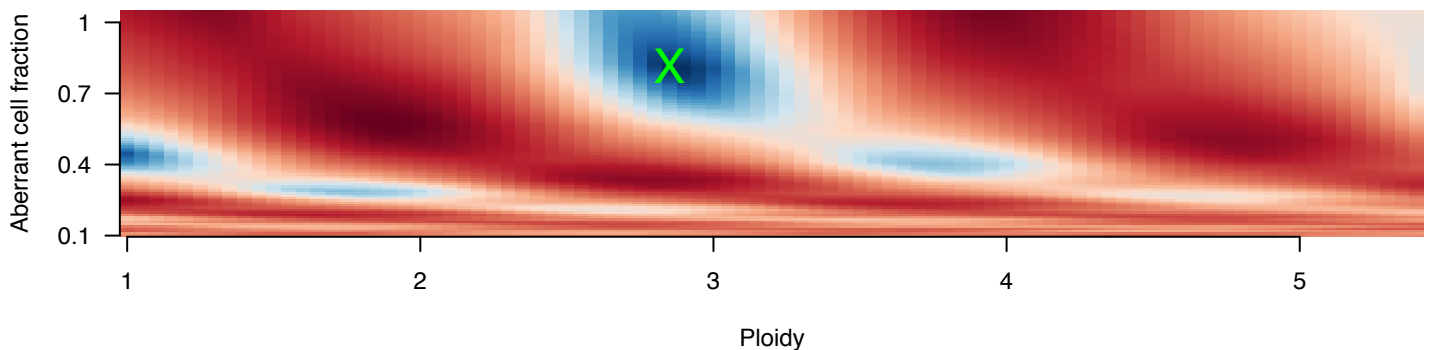
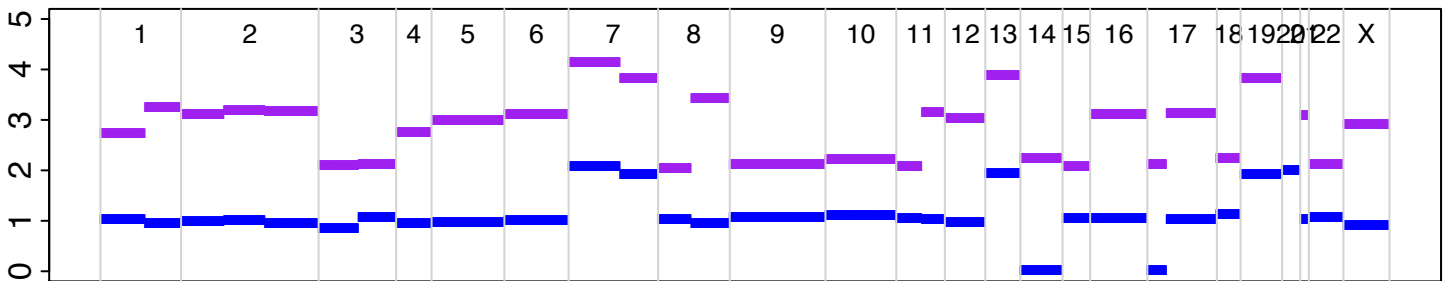
Ploidy: 2.87, aberrant cell fraction: 82%, goodness of fit: 99.8%



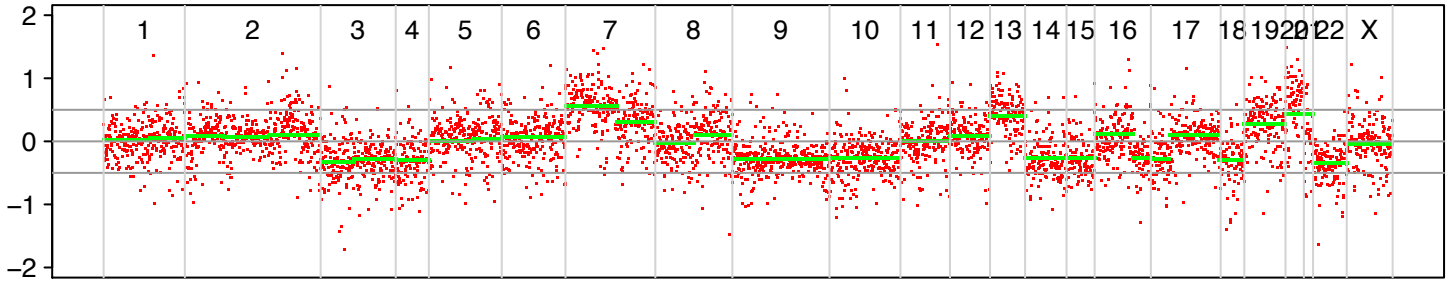
Aberration reliability score (%), average: 86%



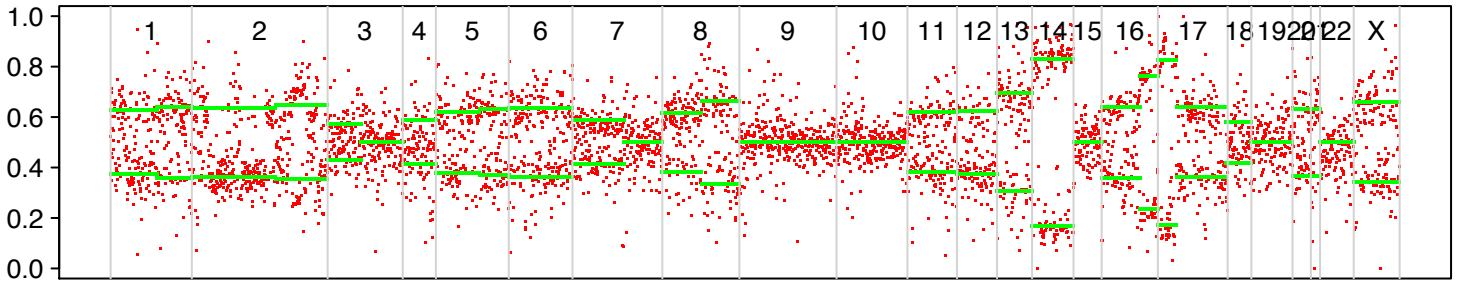
Ploidy: 2.87, aberrant cell fraction: 82%, goodness of fit: 99.8%



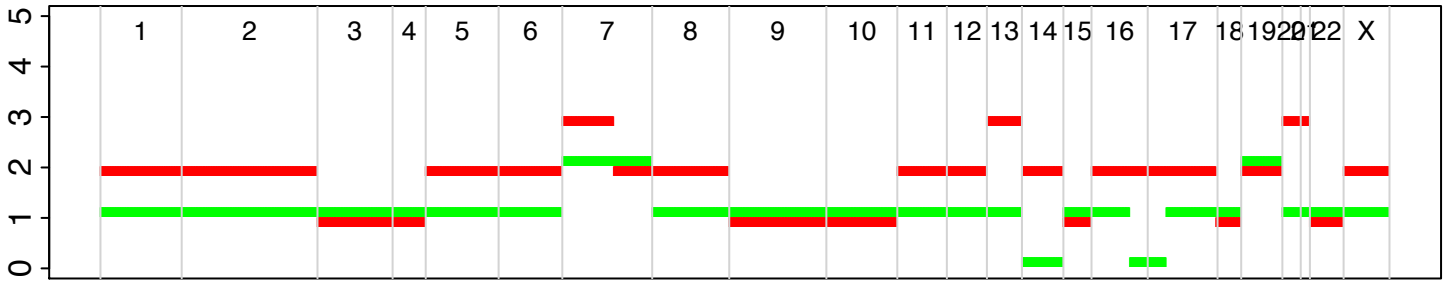
T_T720E, LogR



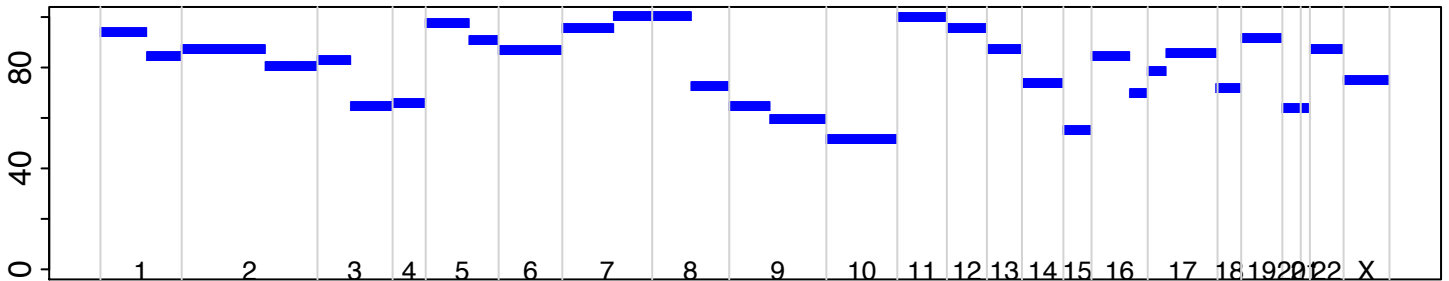
T_T720E, BAF



Ploidy: 3.03, aberrant cell fraction: 62%, goodness of fit: 99.7%



Aberration reliability score (%), average: 80%



Ploidy: 3.03, aberrant cell fraction: 62%, goodness of fit: 99.7%

