

Figure S1

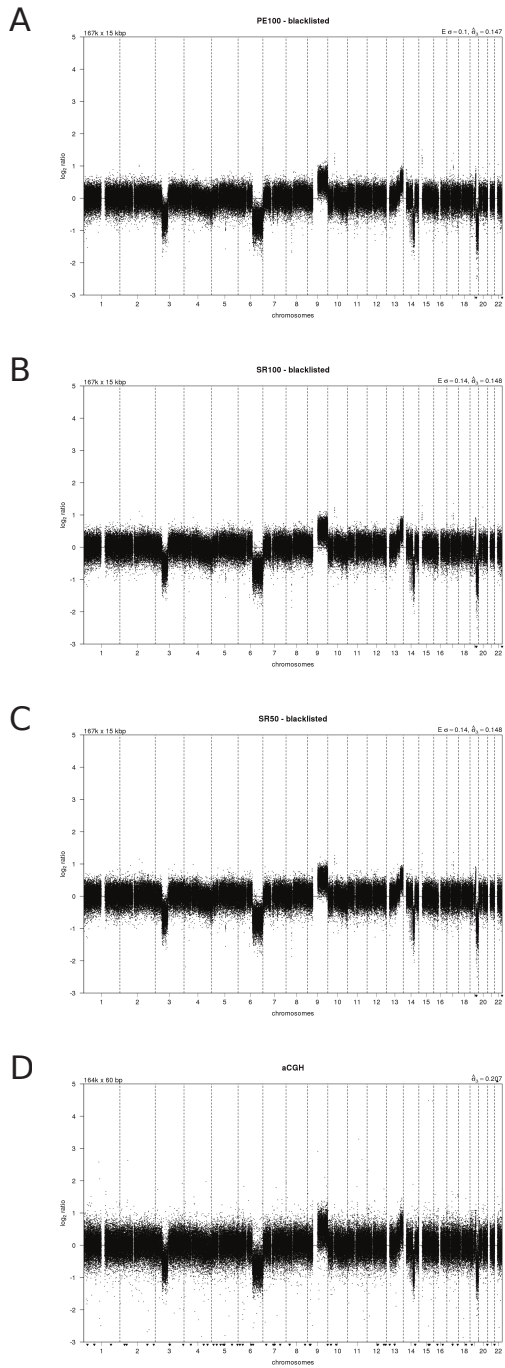
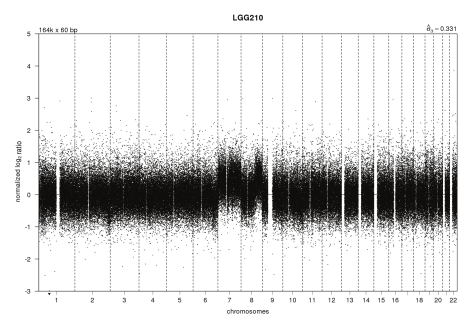
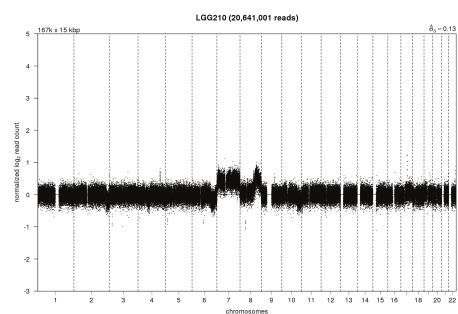
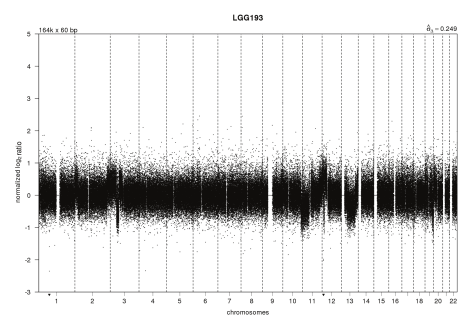
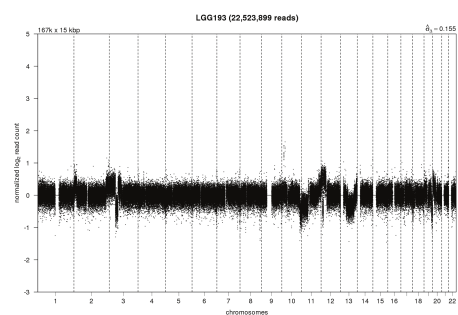
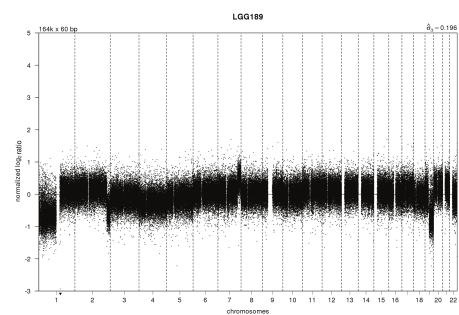
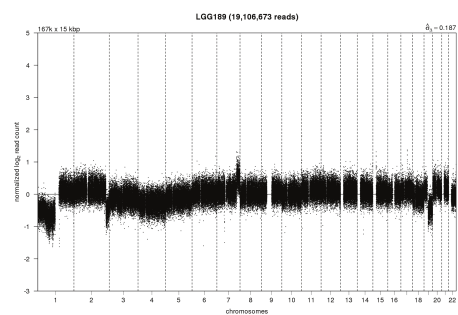
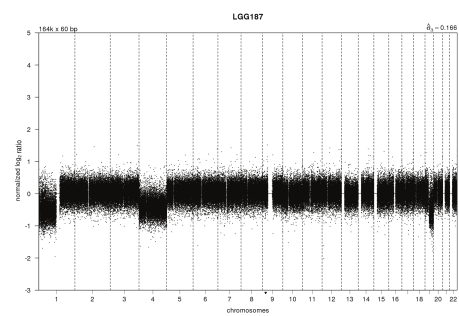
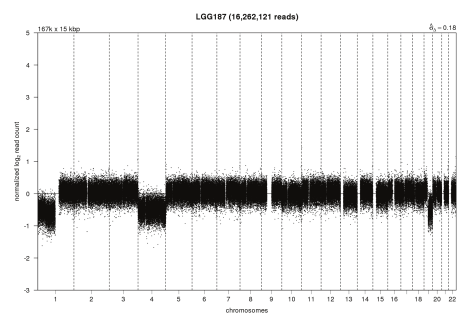
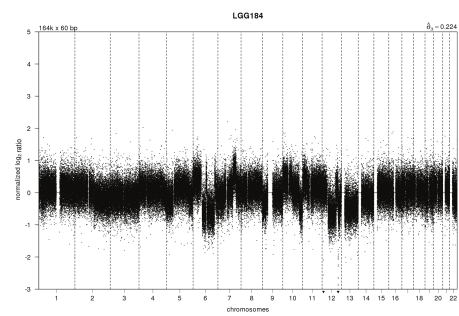
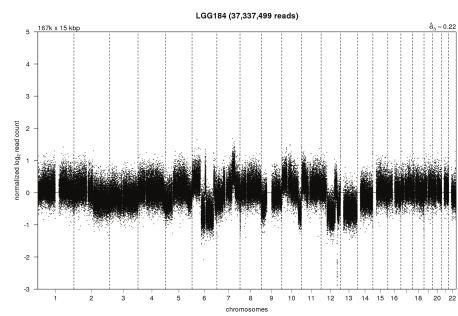
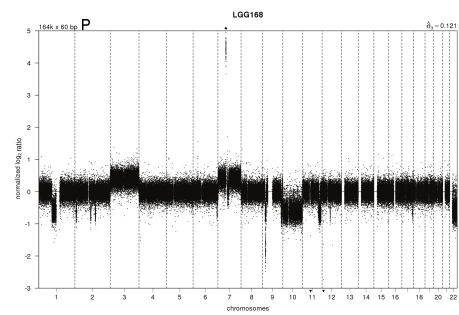
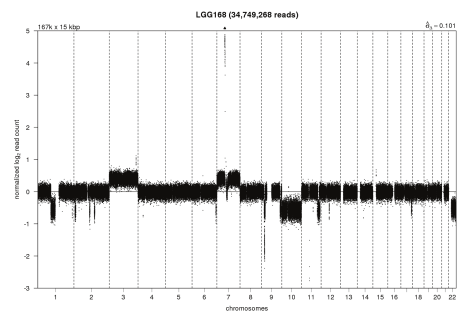


Figure S1. The standard deviation of a profile, denoted by $\hat{\sigma}_\Delta$, and the theoretically expected standard deviation based on read counting, denoted by $E \sigma$, are given in the top right corner of each profile. In the top left corner the number and size of bins used for counting of reads are indicated.

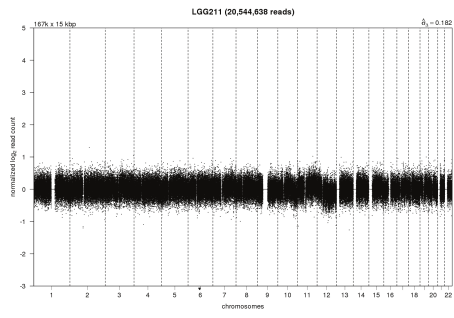
Figure S2

WGS

arrayCGH



WGS



arrayCGH

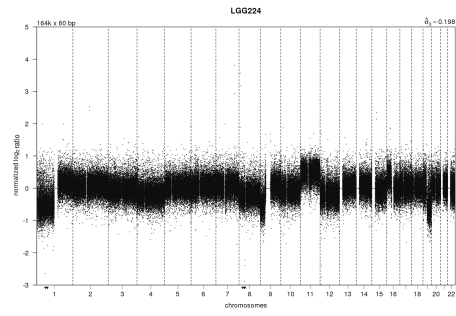
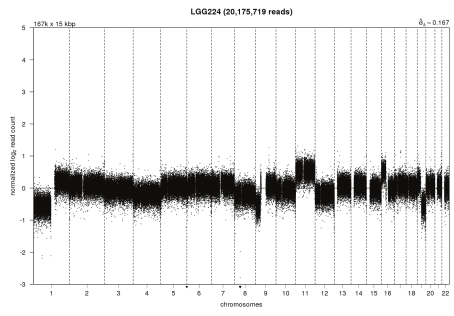
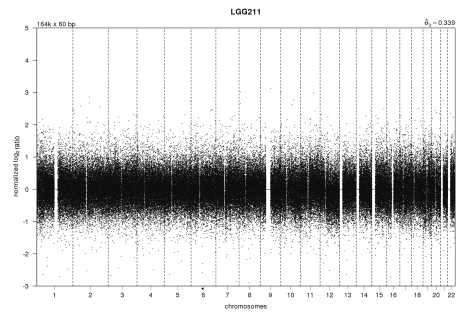


Figure S3

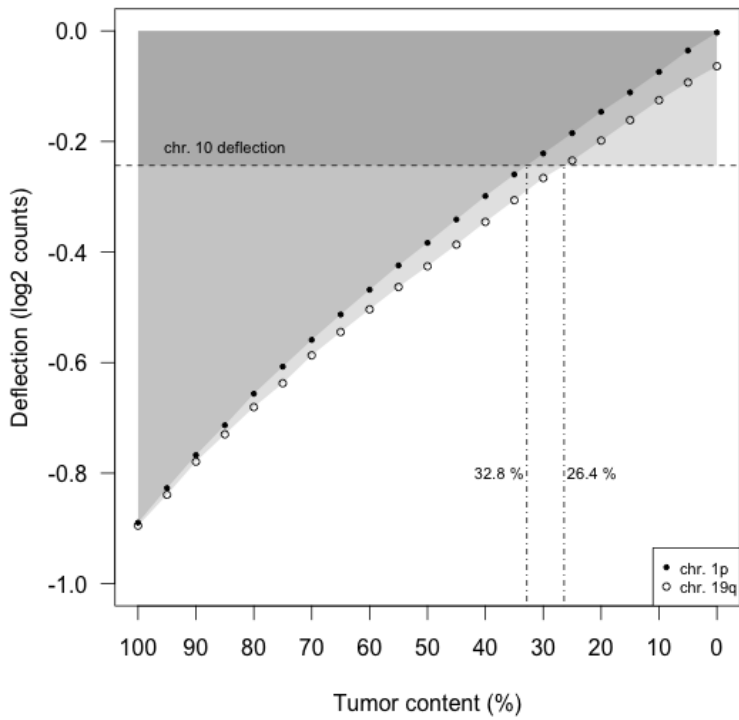


Figure S3. A mixture series, ranging from 100% to 0% with steps of 5% (x-axis), is performed while maintaining a total of 10 million reads for each mixture. The deflection of chromosome 1p and 19q deletion (y-axis) decreases with lower tumor content and intersects with the level of chromosome 10 at respectively 32.8% and 26.4% tumor content. Given the high repeat and GC content of chromosome 19, the intersection with chromosome 1p (32.8%) is considered a more realistic estimate for the percentage of tumor cells containing the chromosome 10 deletion.

Figure S4

WGS

arrayCGH

