



Figure S6 - Theoretical and real mean values of LRR/BAF in different scenarios. 12 manually annotated regions from 4 chromosomes including 6p and 16q are selected for calculating the real LRR/BAF mean values. Based on different combinations of aberration types, the results are classified into four different scenarios: amplification/deletion, amplification/normal, deletion/normal, normal/normal. Real LRR/BAF mean (black) values are illustrated by error bars. Theoretical mean values (yellow) are calculated by equation (1) and equation (3) using parameters estimated by GIANT.