



Figure S3 - Comparison of estimated normal cell contamination levels and tumor average copy number for simulated tumor SNP arrays. Simulated tumor dilution SNP arrays are analyzed by three methods for evaluating the performance in aberration identification, and both estimated normal cell level and average copy number are illustrated for comparison. (a) Estimated normal cell levels by GIANT (blue), ASCAT (red) and OncoSNP (yellow). (b) Tumor average copy number calculated based on the results for different tumor SNP arrays with normal contamination level ranging from 0% to 95%.