



Figure S5: Sensitivities for distinguishing aberrations from normal regions by five different methods.

Sensitivity is calculated by using the simulated tumor SNP arrays, which contains ten known altered regions with various aberration types, and results are illustrated for comparing the performance in identifying genomic aberration regions with respect to increasing normal cell contamination levels. Different lines correspond to the sensitivities for GIANT (blue), ASCAT (red), OncoSNP (yellow), PSCN (green) and PSCBS (black).