

Figure S1 – Average detection offset for simulated chromosomal aberrations

The average offset for detecting simulated chromosomal aberrations (deletions, duplication sand translocations) of sizes of 0.01-3Mb. Corrected 1D contact profiles of IMR90 were used for simulation. Deletions and duplications were simulated using the *cis* 1D contact profile of chromosome 3. The *trans* 1D contact profile of chromosomes 9, with respect to chromosome 12, was used for simulating translocations. At each iteration (in a given simulation), a single region was chosen and change points were detected given a simulated aberration (for each of the given sizes). The average detection offset (up to 5Mb) was reported for different aberrations sizes (Y axis).

