

Supplementary Text T7

Publicly available mapped positions of IMR90 [1] and K562 [2] were downloaded from the Gene Expression Omnibus (GEO) [3] and used to build 1Mb contact maps. The contact maps were then corrected as described in the paper. We have then generated 1D contact profiles, where a *cis* contact profile of chromosome *a* is the row sums of the contact map of chromosome *a* with itself, after removing self-interactions (the diagonal), and a *trans* contact profile of chromosome *a* with respect chromosome *b*, is the row sums of the contact map of chromosome *a* and chromosome *b*. Contact profiles were then used for testing the performance of change point analysis for detecting chromosomal aberrations as described in the paper.

References

1. Dixon JR, Selvaraj S, Yue F, Kim A, Li Y, Shen Y, Hu M, Liu JS and Ren B: **Topological domains in mammalian genomes identified by analysis of chromatin interactions.** *Nature* 2012, **485**:376–80.
2. Lieberman-Aiden E, van Berkum NL, Williams L, Imakaev M, Ragooczy T, Telling A, Amit I, Lajoie BR, Sabo PJ, Dorschner MO, Sandstrom R, Bernstein B, Bender MA, Groudine M, Gnirke A, Stamatoyannopoulos J, Mirny LA, Lander ES and Dekker J: **Comprehensive mapping of long-range interactions reveals folding principles of the human genome.** *Science* 2009, **326**:289–93.
3. Edgar R, Domrachev M and Lash AE: **Gene Expression Omnibus: NCBI gene expression and hybridization array data repository.** *Nucl. Acids Res.* 2002, **30**:207-10.