

Supplementary Text T8

For comparison of Hi-C data sets, we have downloaded publicly available mapped positions of IMR90 [1] and embryonic human stem cells (ESC) [1] from the Gene Expression Omnibus (GEO) [2] and transformed them into 1Mb contact maps (a contact map for each replicate, with 2 replicates for IMR90 and 2 replicates of ESC). Following appropriate correction (as described in the paper) we have next performed a comparison, within and between cell lines (comparison procedure as described in the paper). For within-comparison we have compared replicates' contact maps (2 comparisons in total: one for comparing the 2 replicates of IMR90 and another for comparing the 2 replicates of ESC). For between-comparison we have compared replicates' contact maps from different cell lines (4 comparisons in total, see Table 2). Pairs achieving a BF value larger than the permissive threshold (6.10) were reported as differentially interacting regions (Supplementary Table ST2).

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. 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.