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
