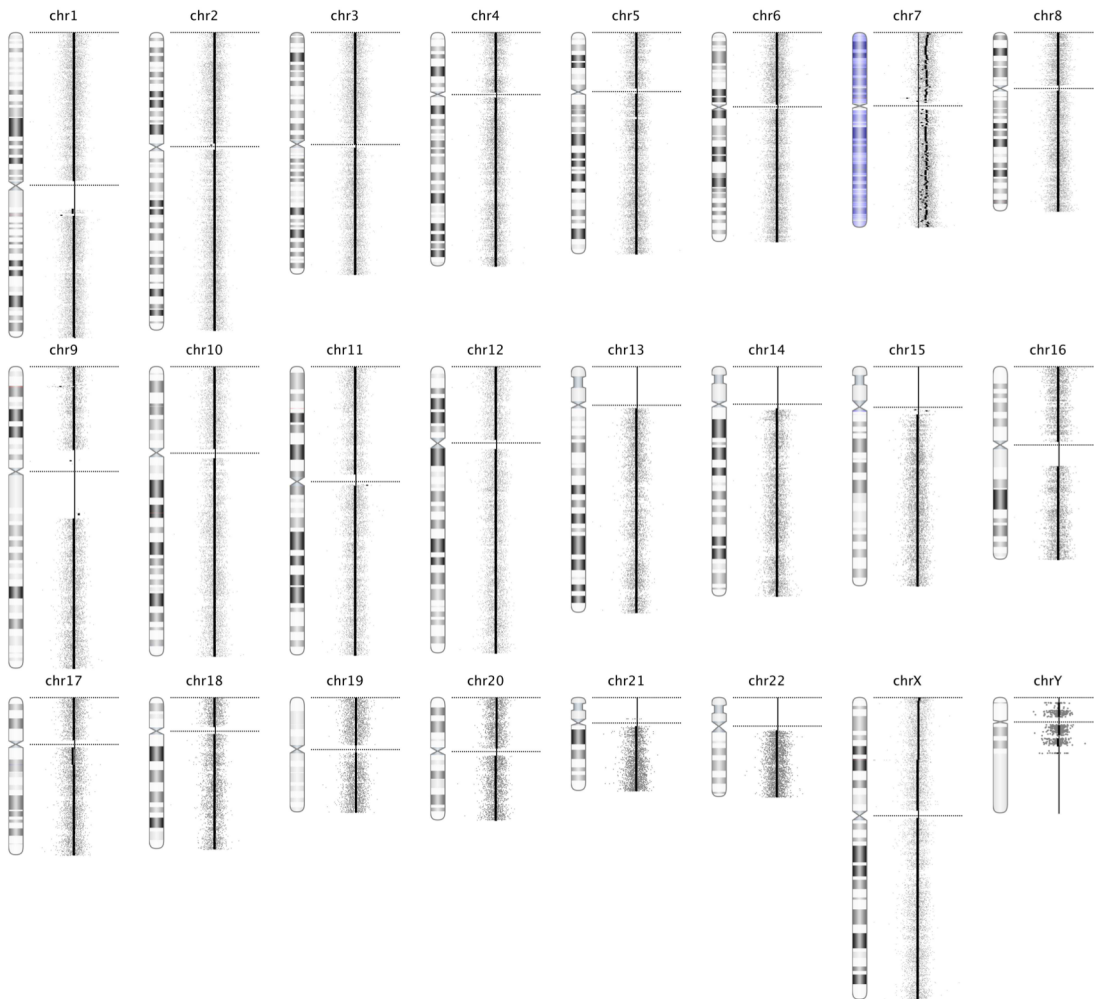
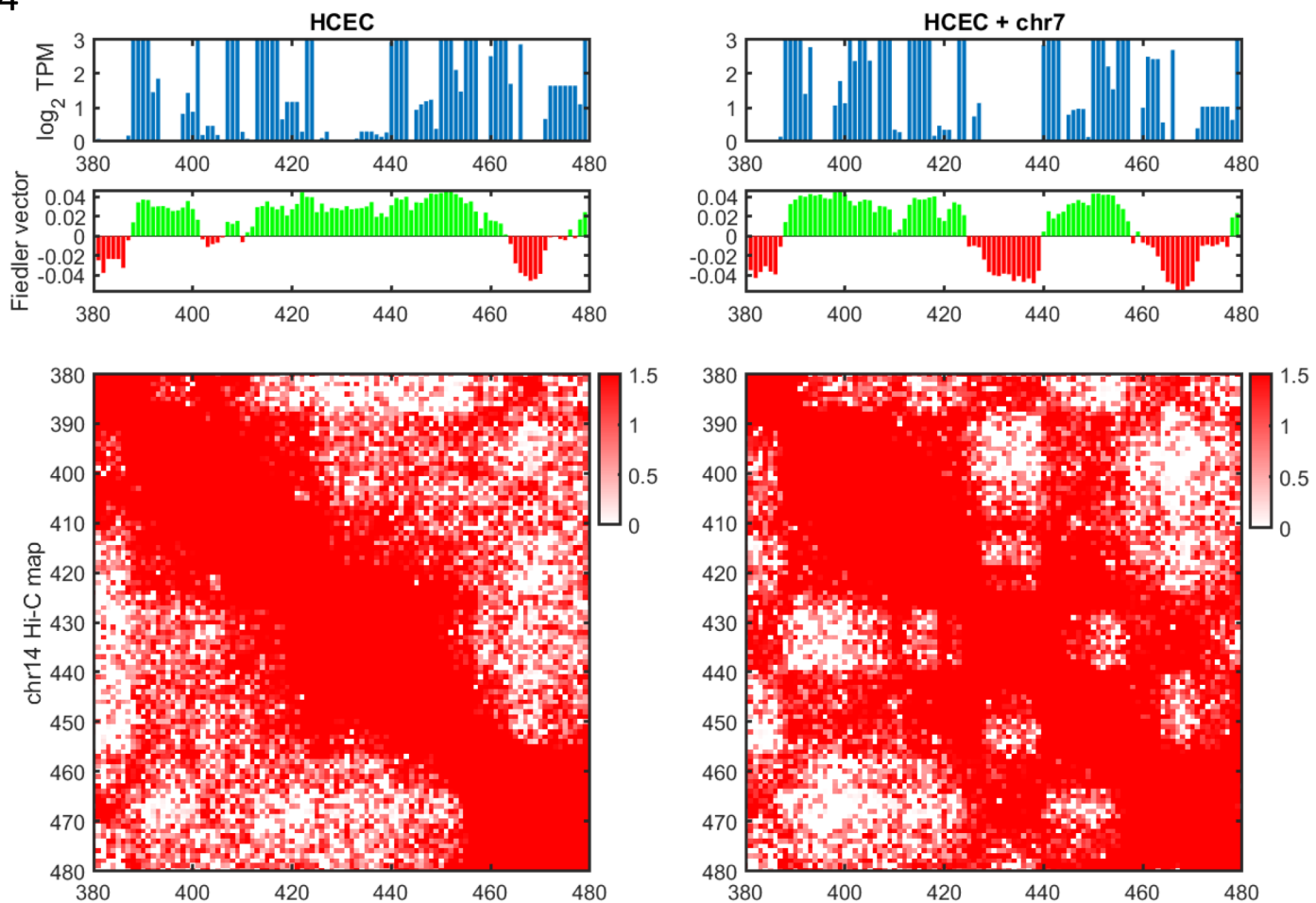


Supplementary Figure 1

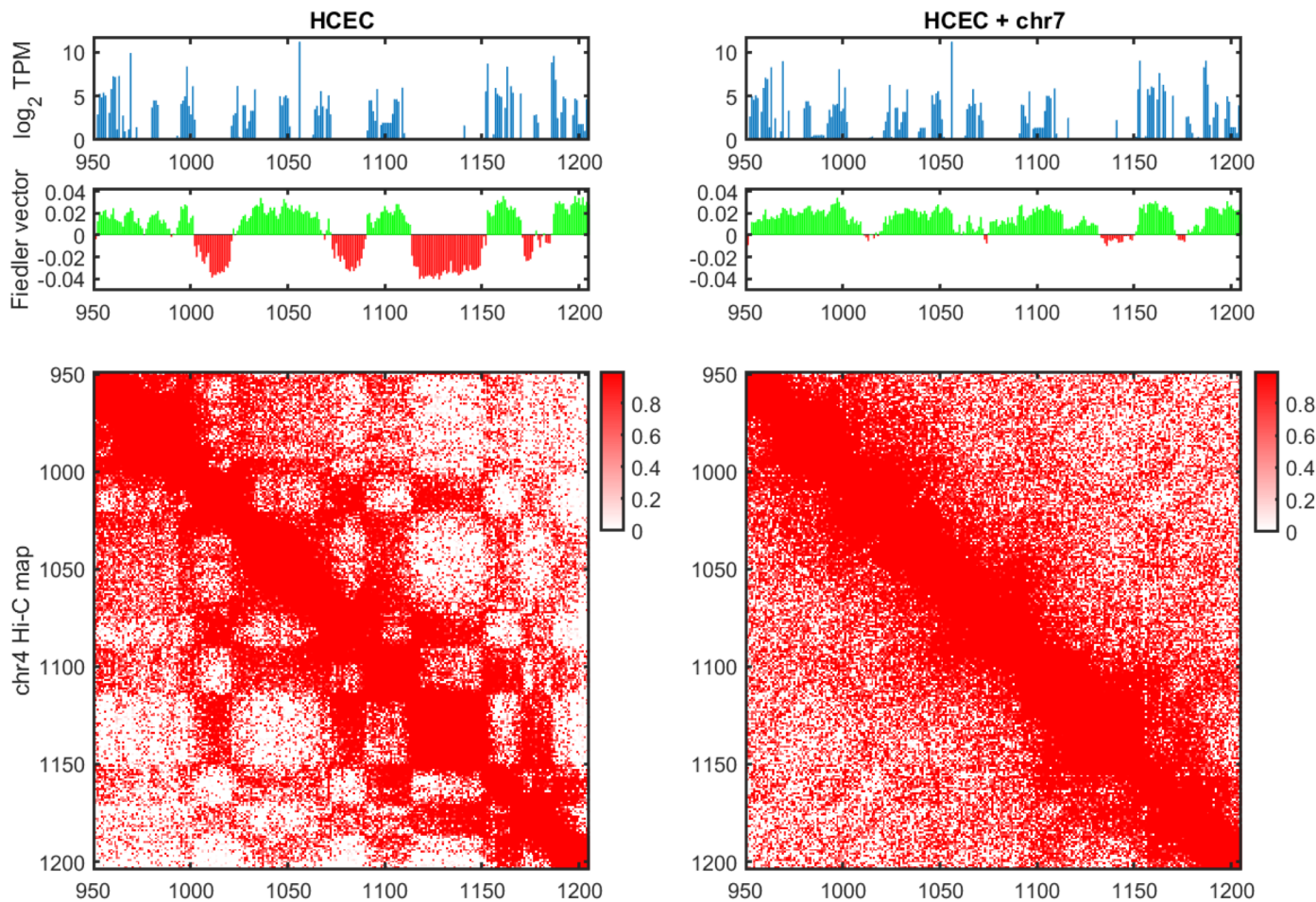


Supplementary Figure 2

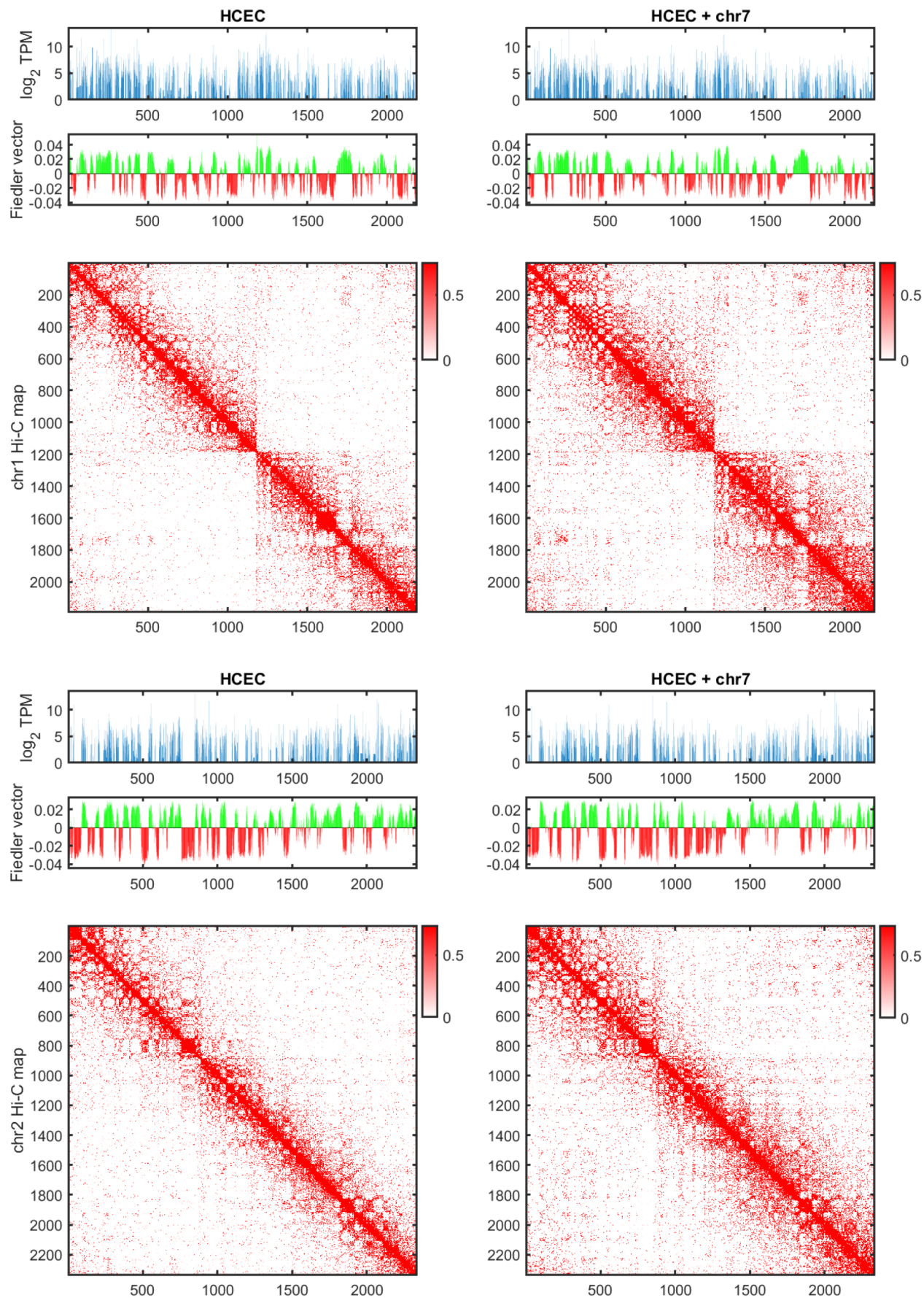
chr14



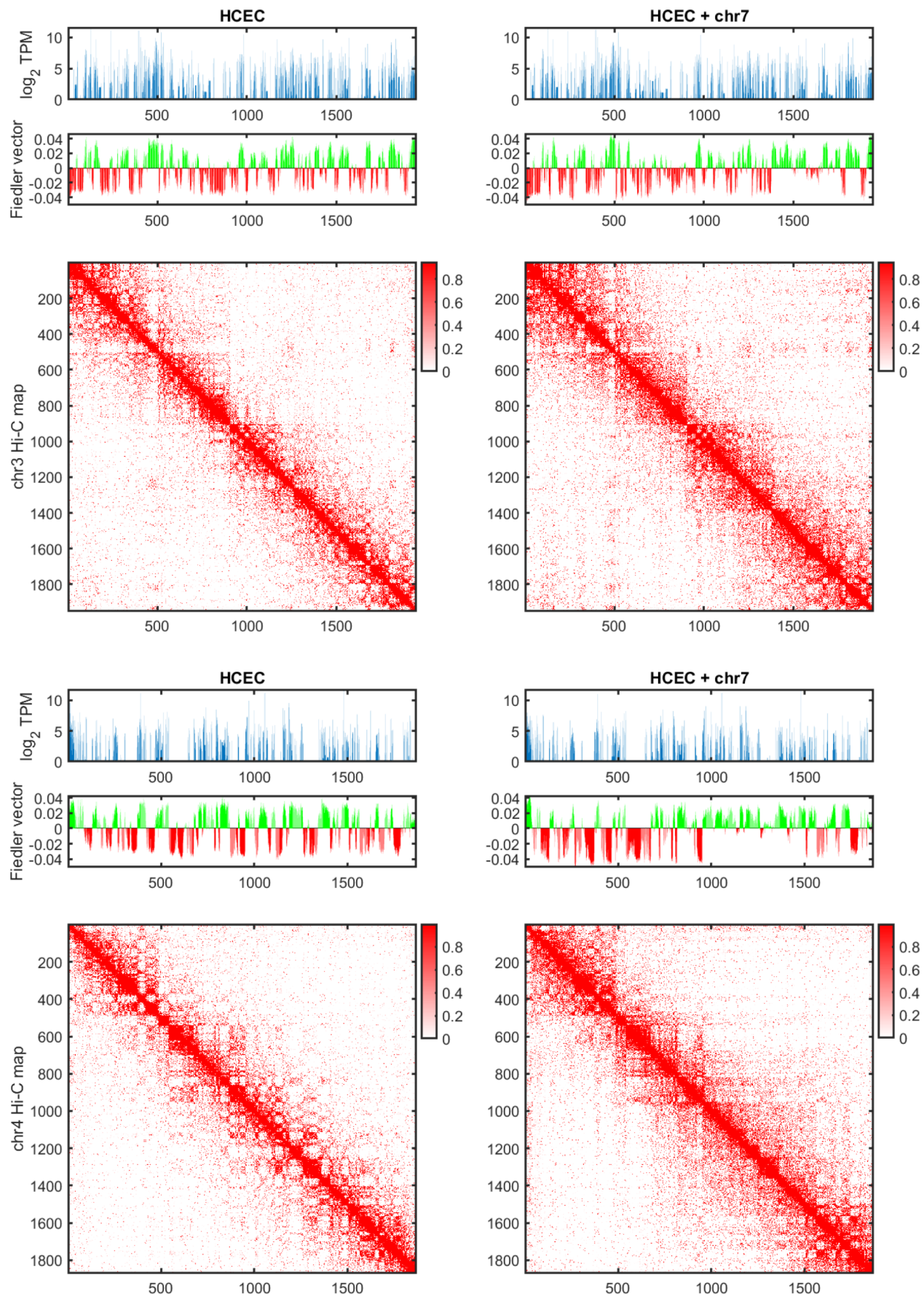
chr4



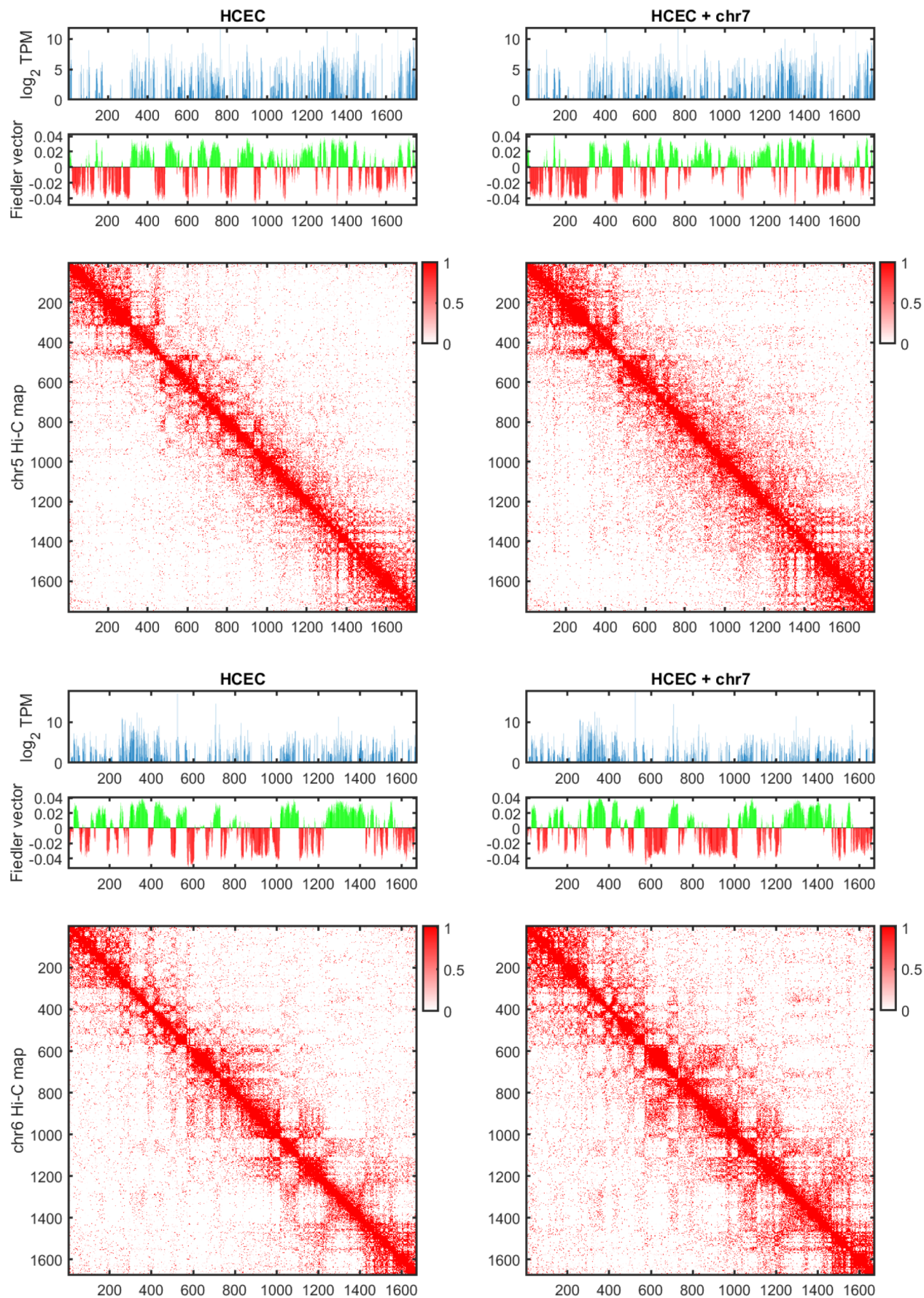
Supplementary Figure 3A



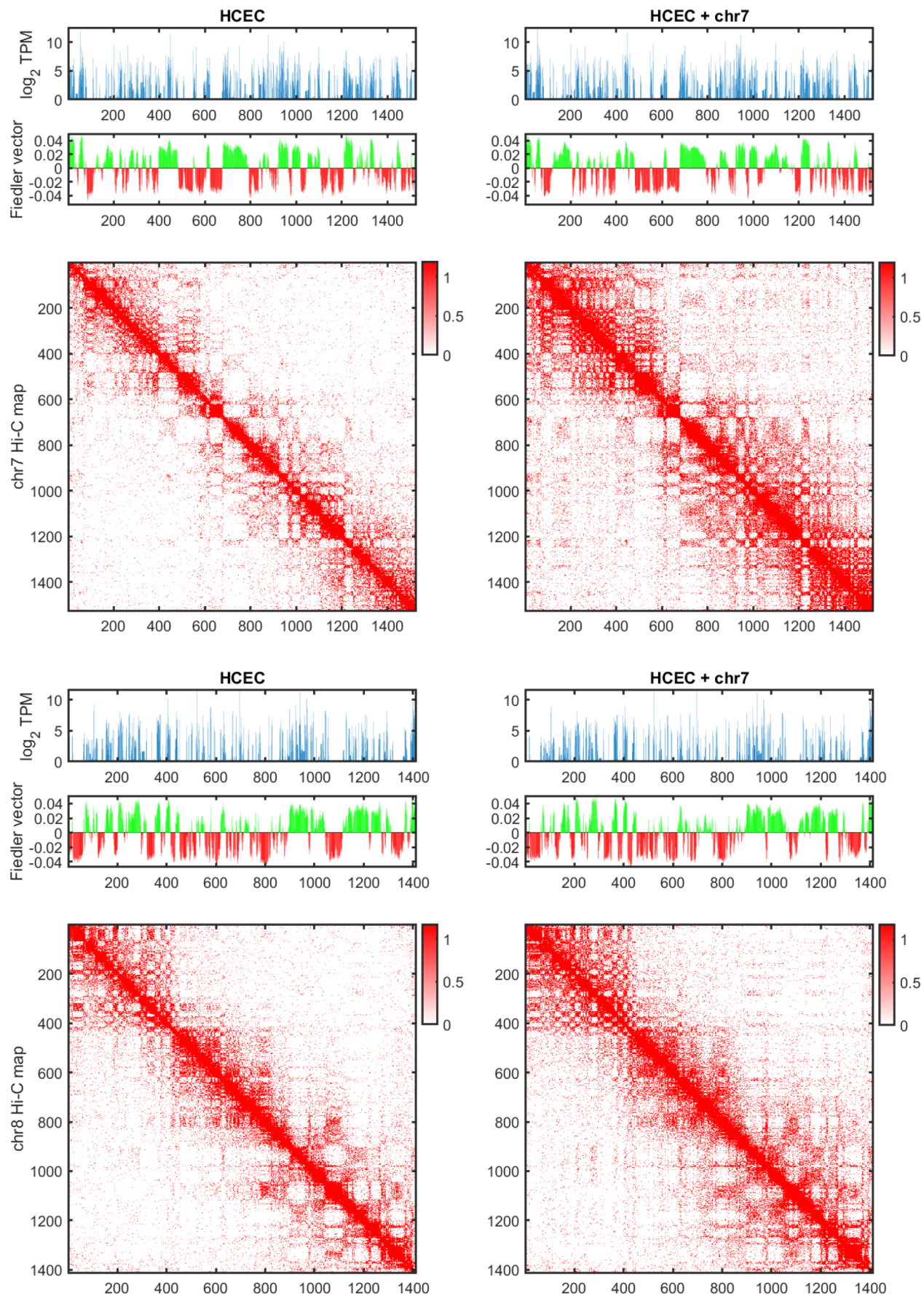
Supplementary Figure 3B



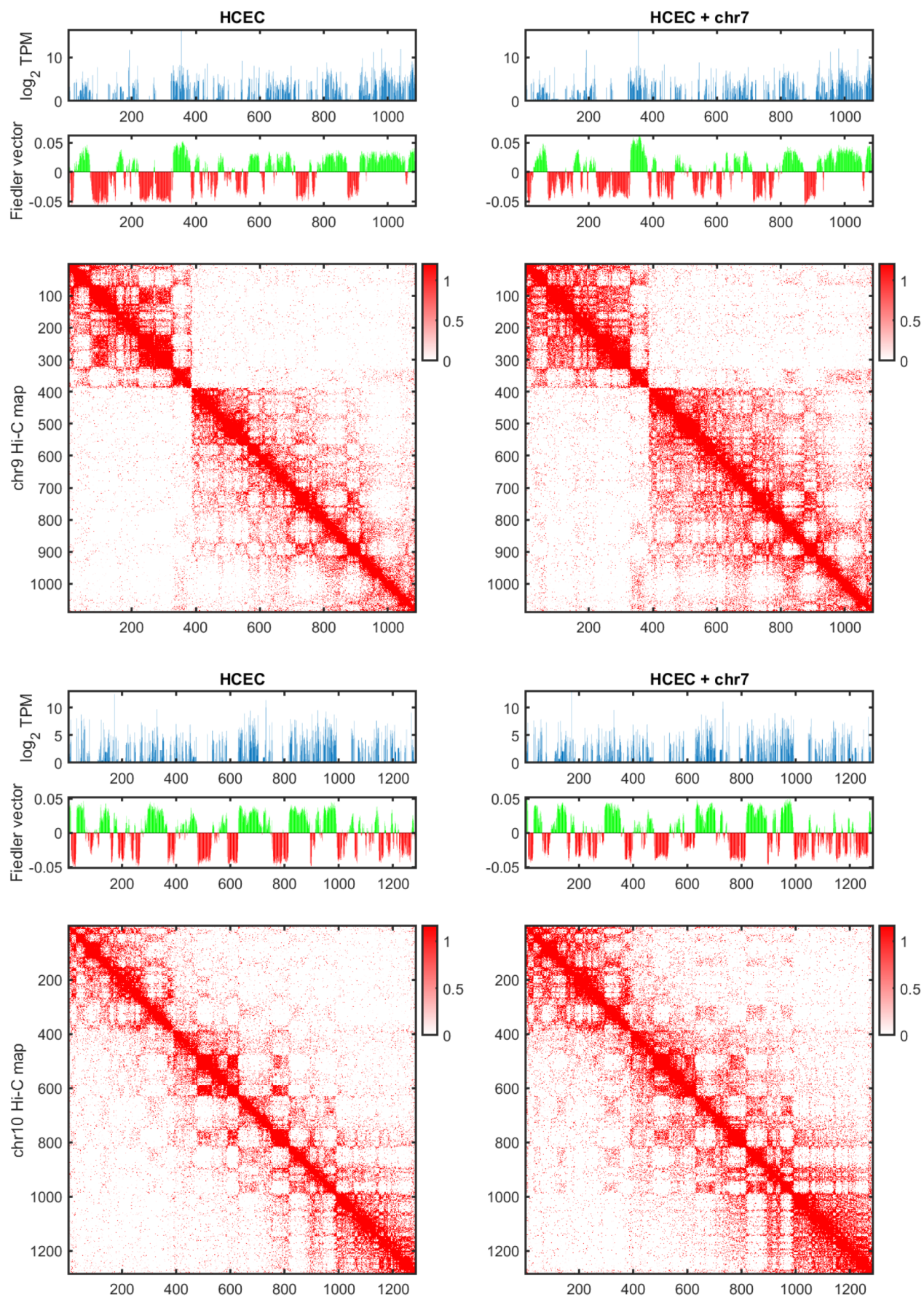
Supplementary Figure 3C



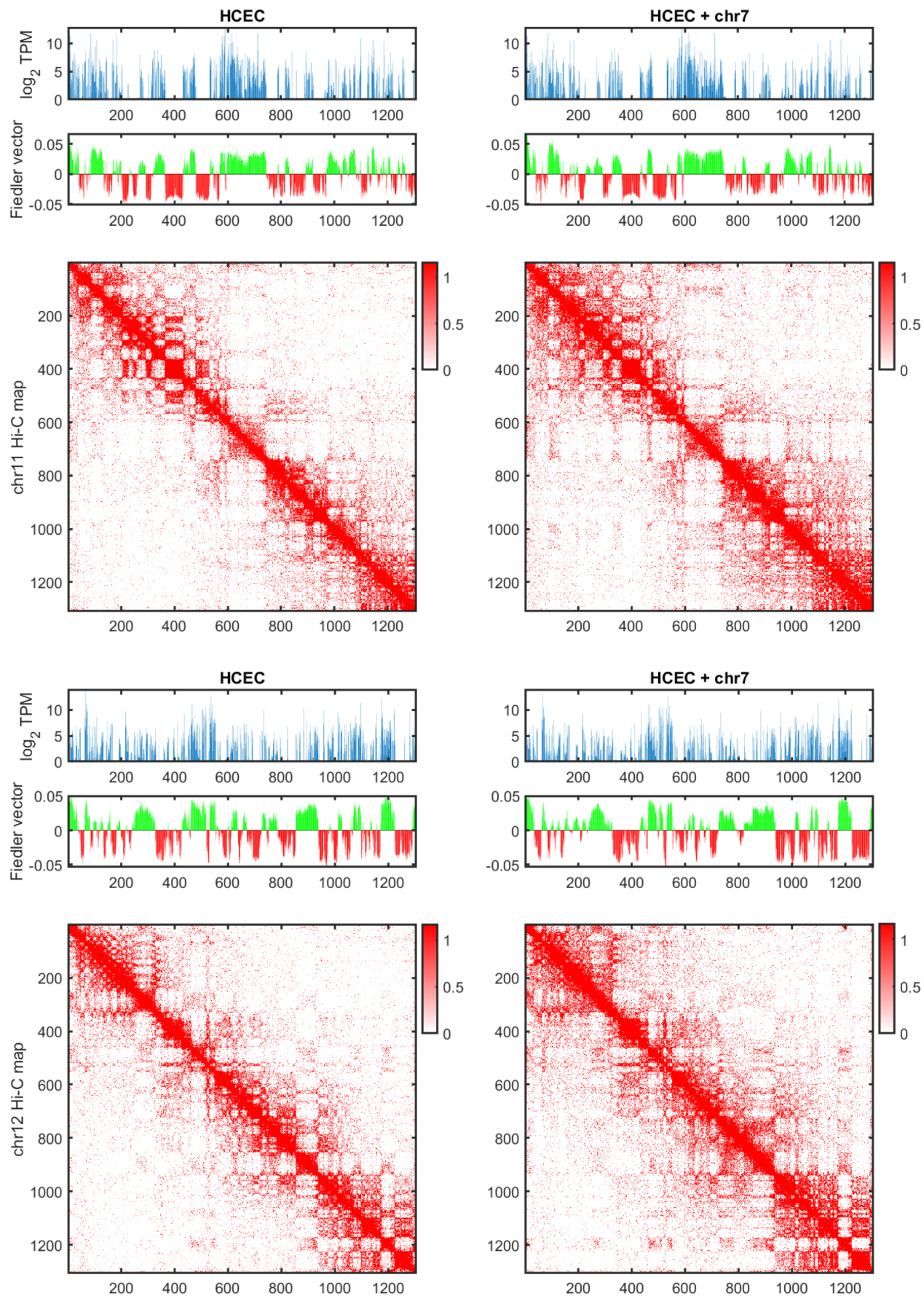
Supplementary Figure 3D



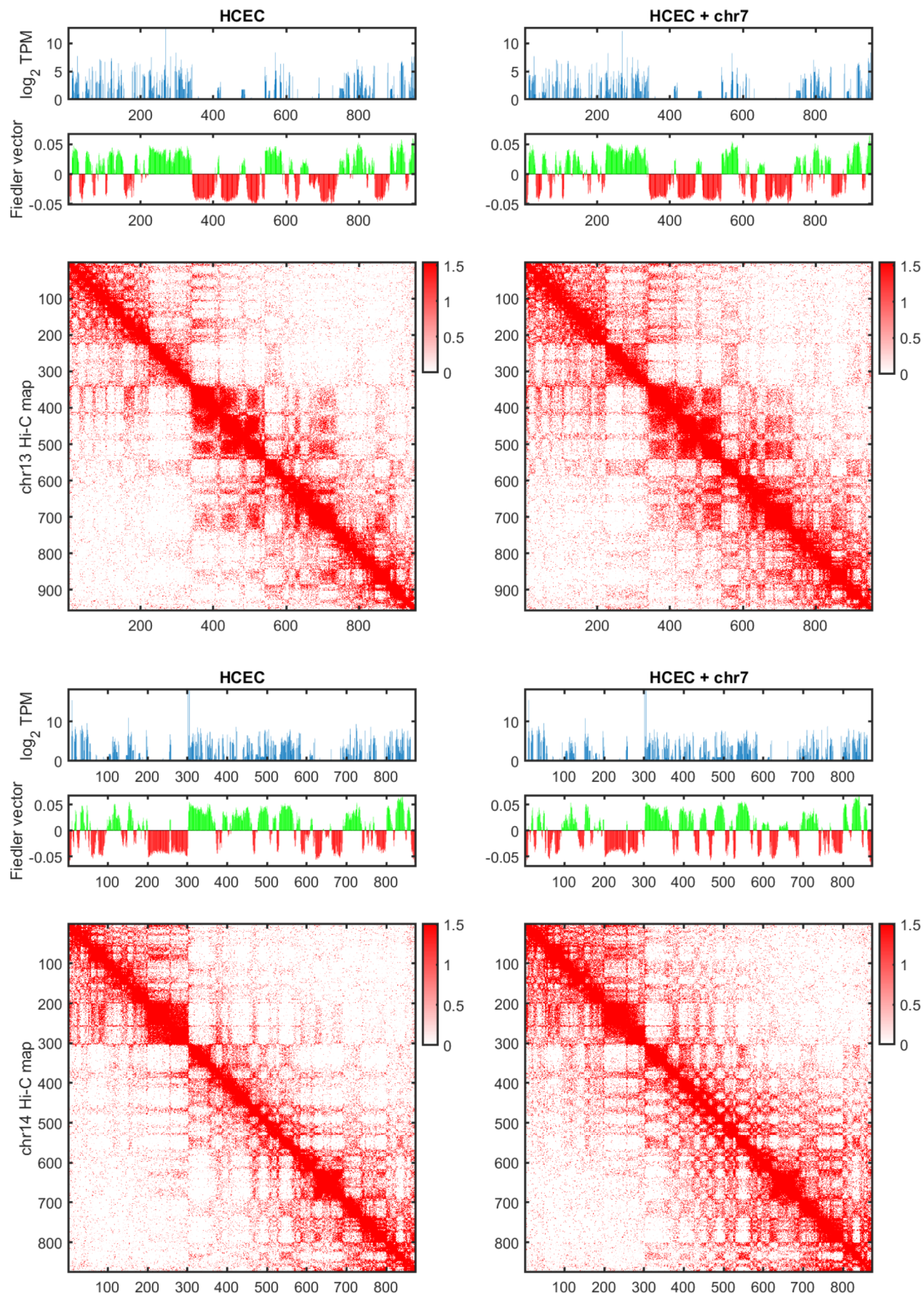
Supplementary Figure 3E



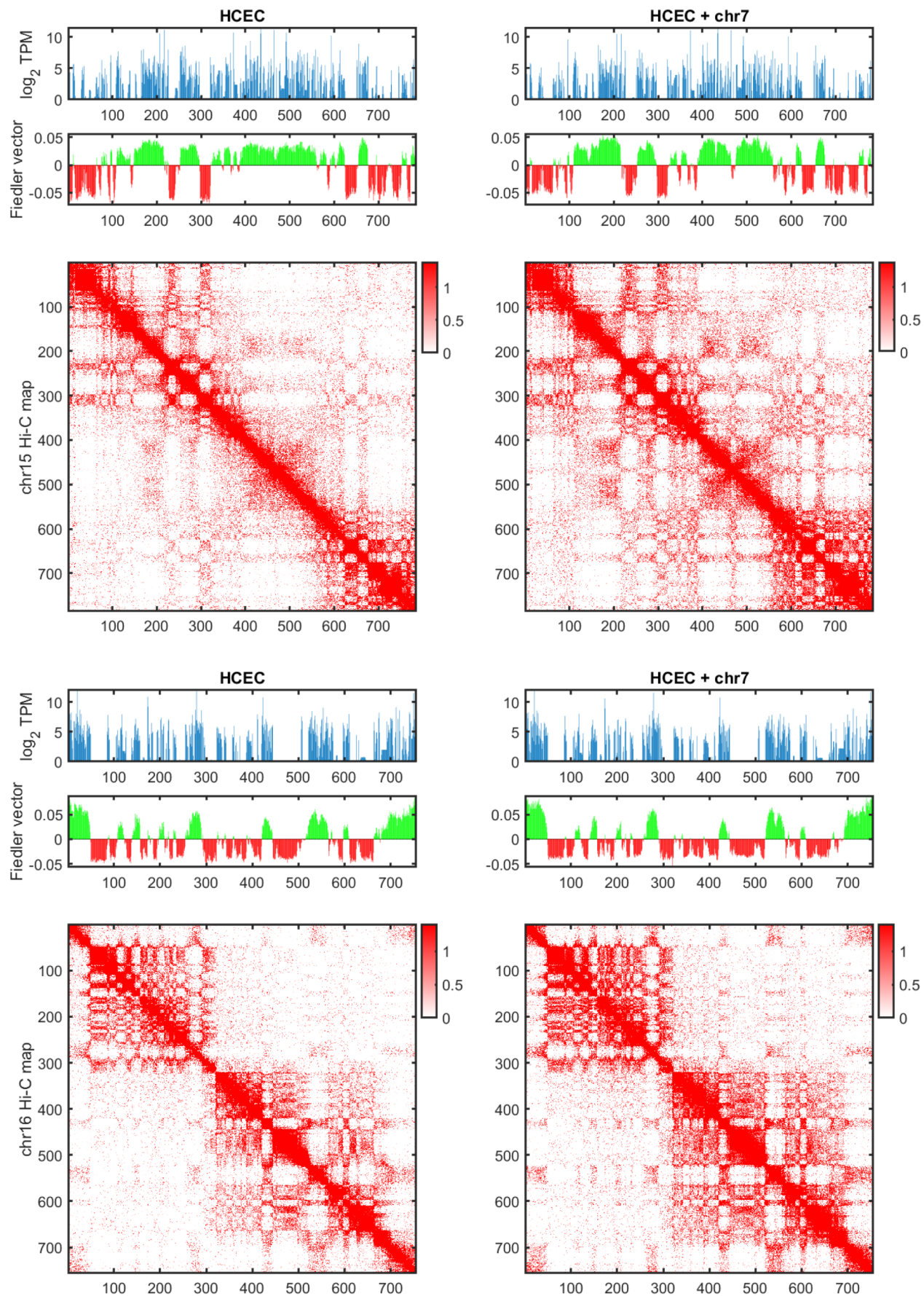
Supplementary Figure 3F



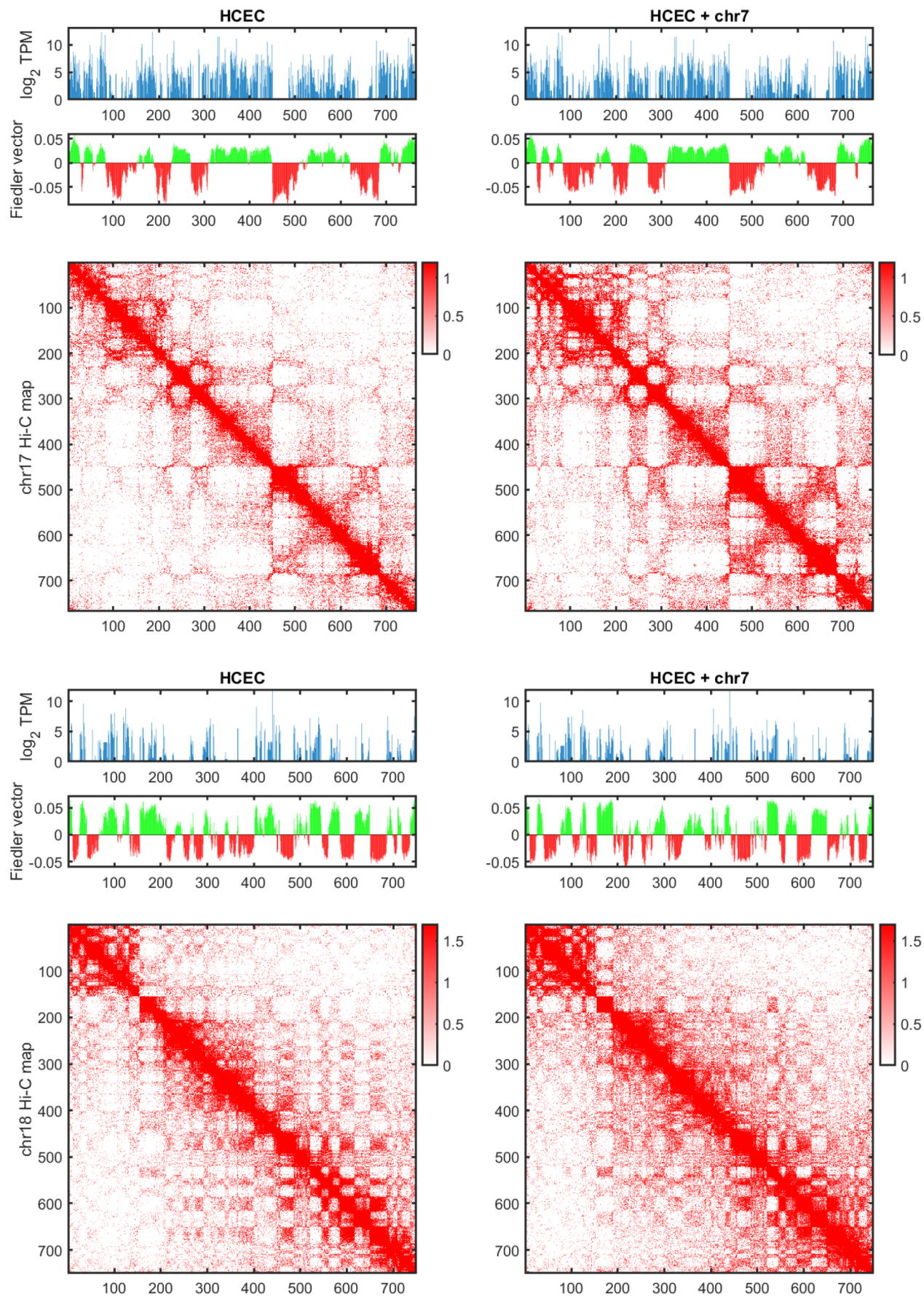
Supplementary Figure 3G



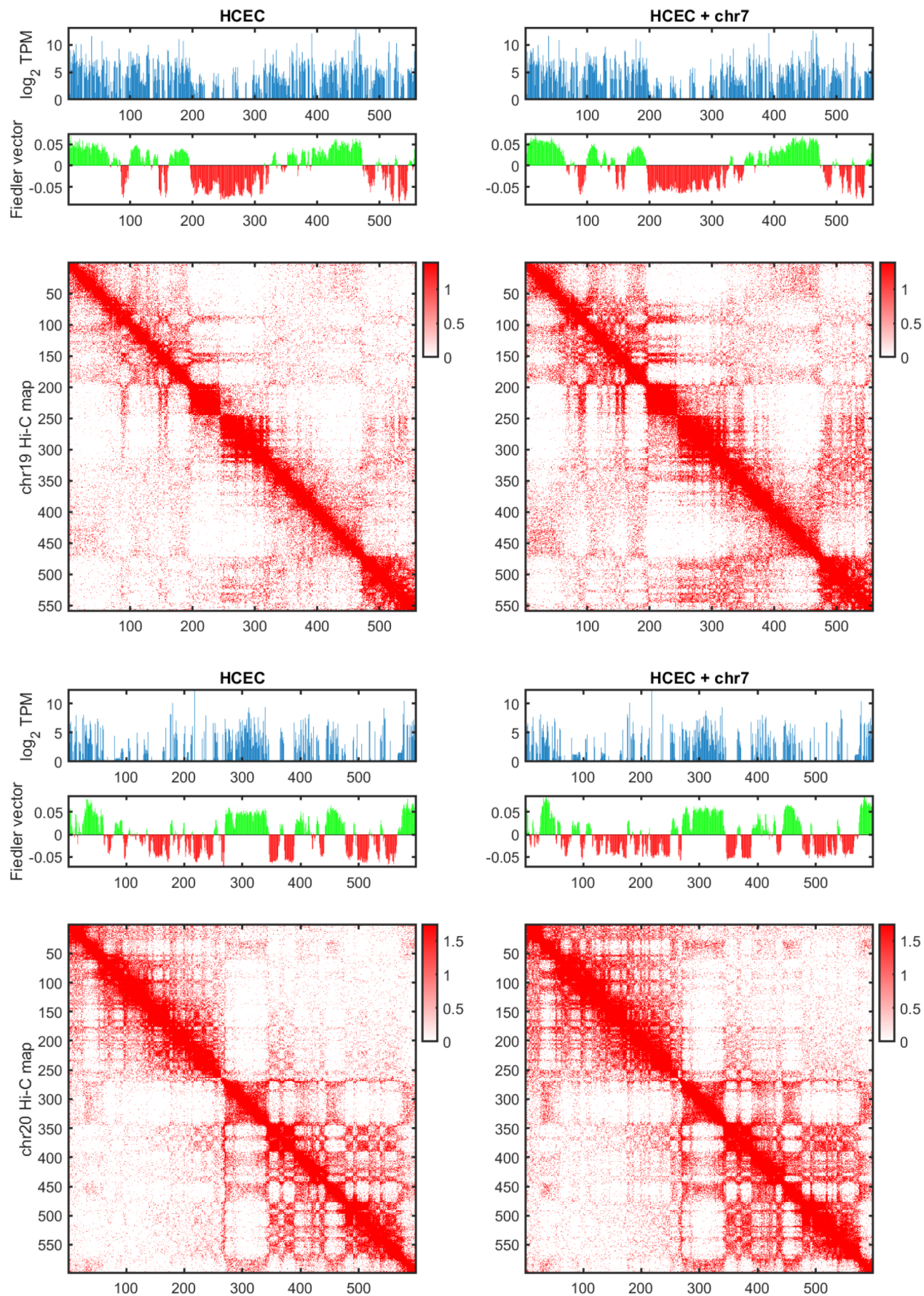
Supplementary Figure 3H



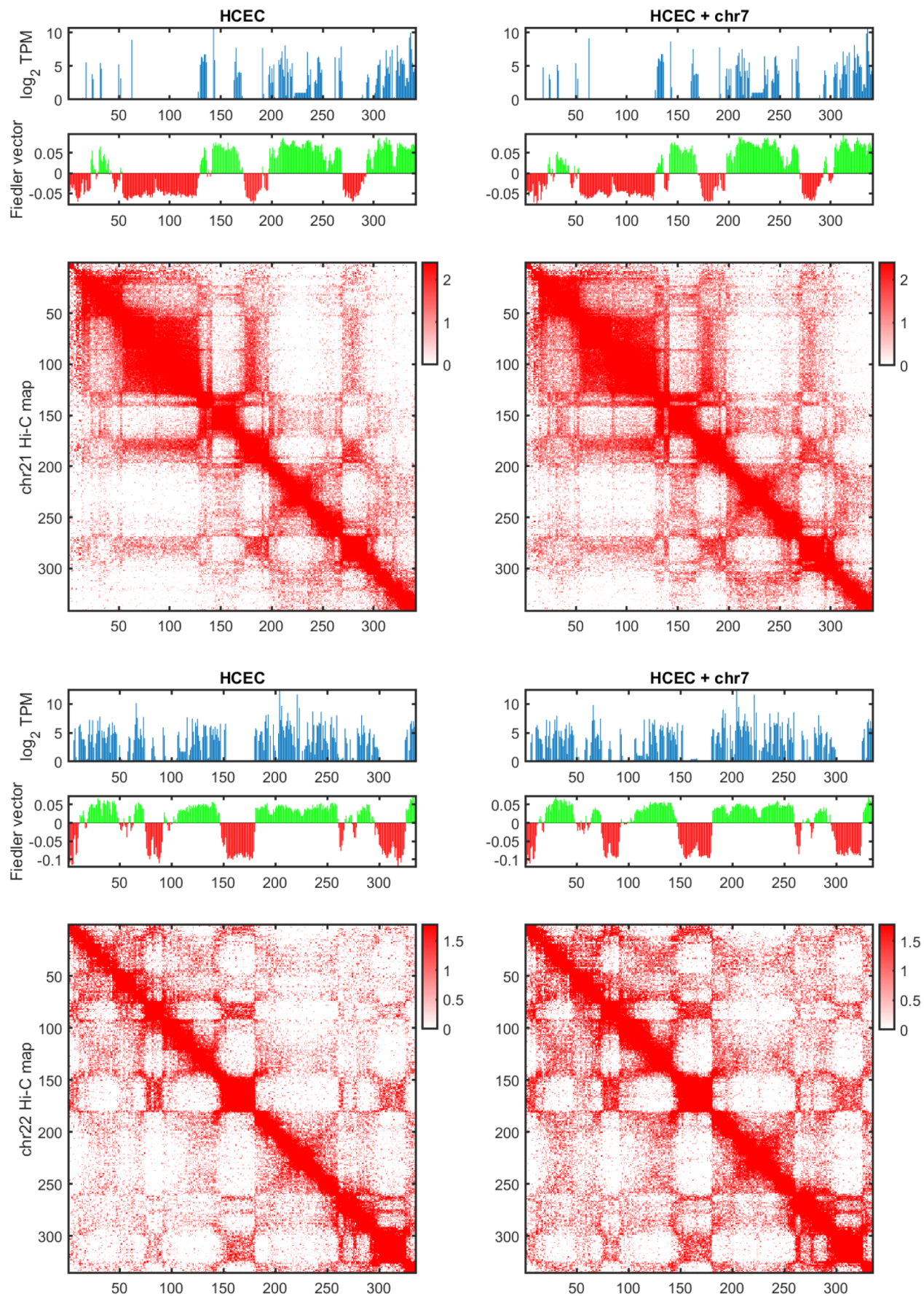
Supplementary Figure 3I



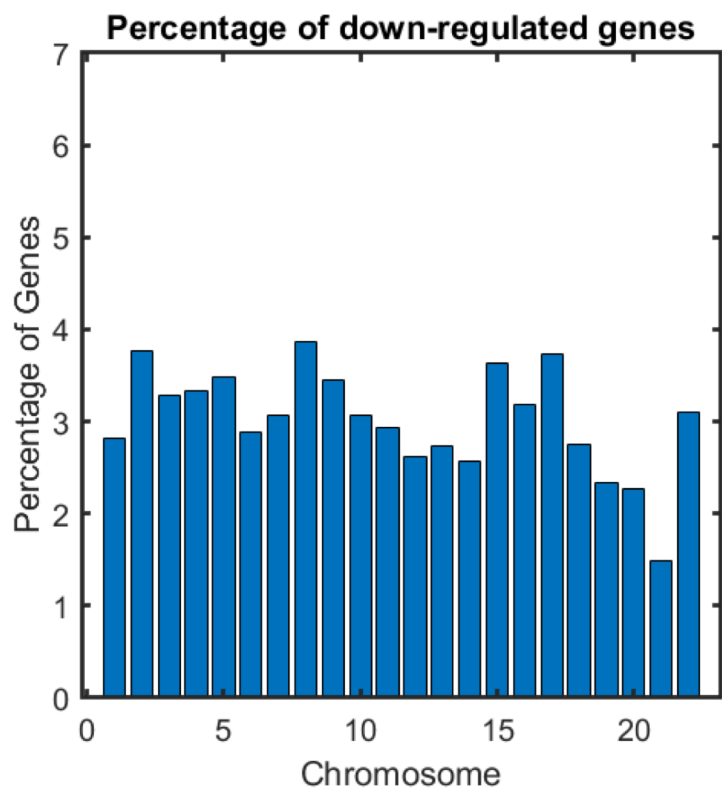
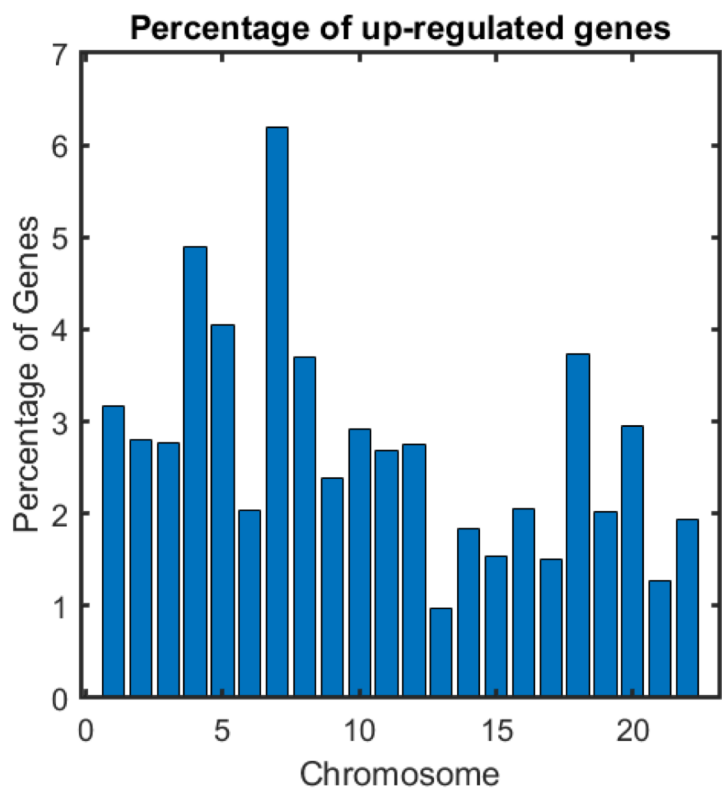
Supplementary Figure 3J



Supplementary Figure 3K

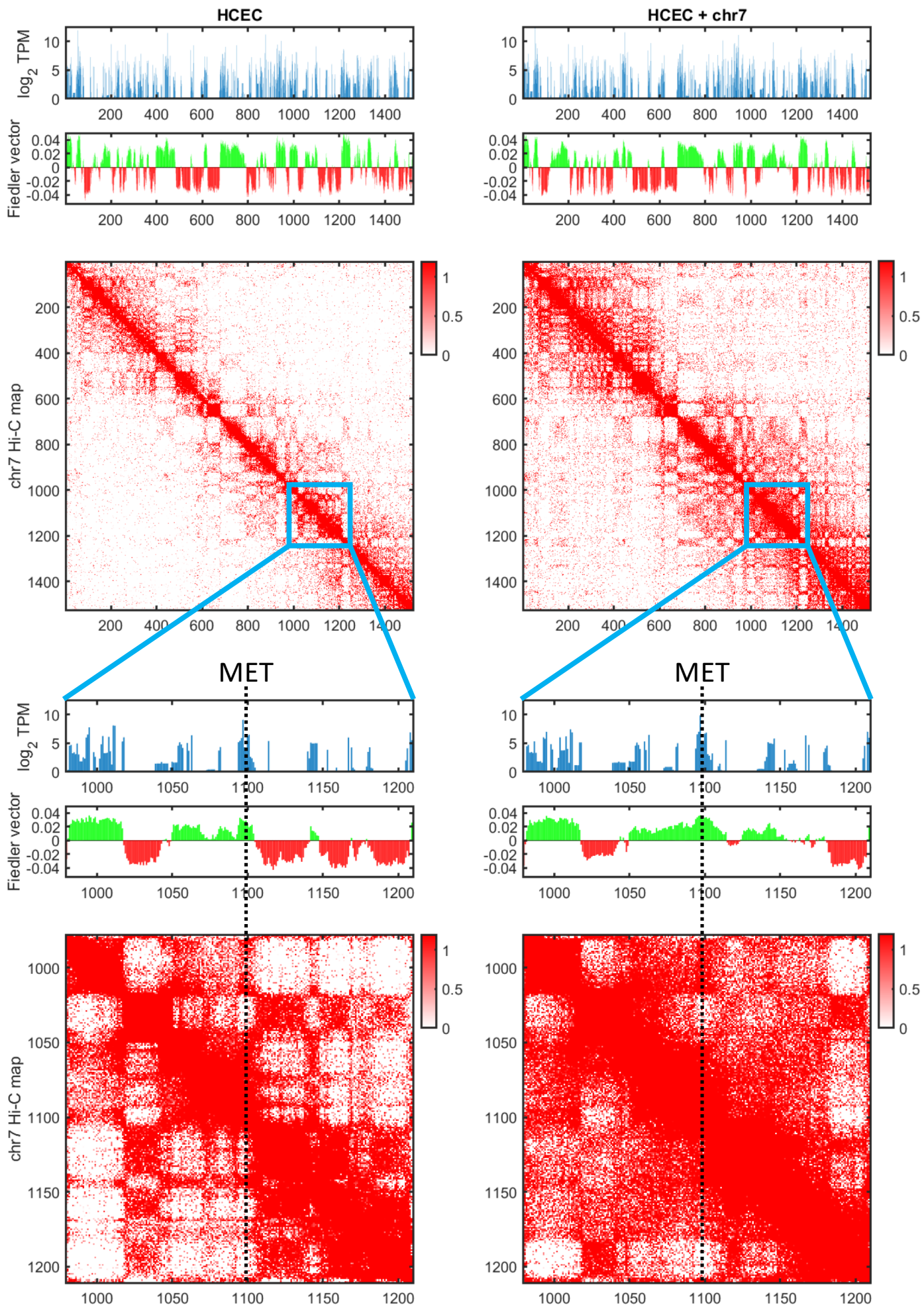


Supplementary Figure 4

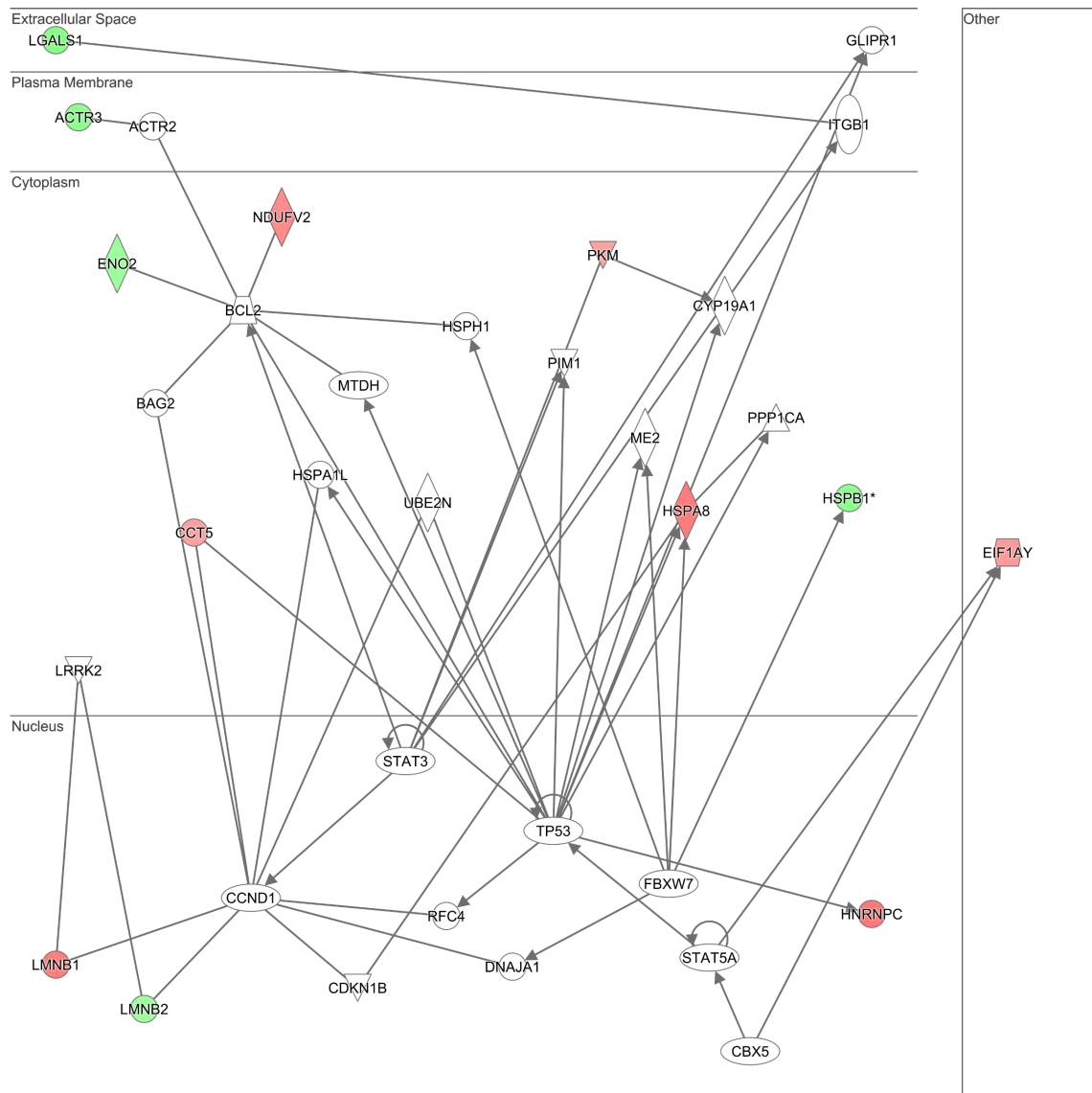


chr7

Supplementary Figure 5



Supplementary Figure 6



Supplementary Figure 1: Array Comparative Genome Hybridization (aCGH) of the HCEC 1CT+7 cell line. A gain of a chromosomal region is depicted in blue, while neutral copy number is depicted in grey. The location of the corresponding probe is graphed immediately to the left of the chromosomal region, with gains depicted as a shift to the right of the center line while probes displaying neutral copy number overlap the center line. These results demonstrate that trisomy 7 is the sole cytogenetic aberration in the HCEC 1CT +7 cell line.

Supplementary Figure 2: Comparison of gene expression and chromatin structure on chromosomes 14 and 4 in the HCEC 1CT (left) and HCEC 1CT+7 lines (right). The average gene expression within each 100kb bin across the region of the respective chromosomes (chr14:57,900,000-67,900,000 and chr4: 99,000,000-124,000,000) is shown as \log_2 TPM. Chromatin compartments, as determined by the Fiedler vector, are plotted directly underneath the gene expression data. The Hi-C contact map is plotted shown below the Fiedler at 100kb resolution, log-scale.

Supplementary Figure 3: (A-K) Comparison of gene expression and chromatin structure, genome-wide in the HCEC 1CT (left) and HCEC 1CT+7 lines (right). Average gene expression (\log_2 TPM), Fiedler vector, and log-scale Hi-C contact map at 100kb resolution are shown for all chromosomes.

Supplementary Figure 4: Percentage of up-regulated (left) and down-regulated (right) genes as a result of trisomy 7. As expected, the highest percentage of up-regulated genes localize to chromosome 7.

Supplementary Figure 5: Comparison of gene expression and chromatin structure in chromosome 7 in the HCEC 1CT (left) and HCEC 1CT+7 lines (right). Average gene expression (\log_2 TPM), Fiedler vector, and log-scale Hi-C contact map at 100kb resolution are shown for chromosome 7 (top). The blue box denotes a region around the gene MET. This region has been shown in greater detail in the bottom half of the figure.

Supplementary Figure 6: Colon specific IPA network analysis of differentially expressed proteins identified by 2-DIGE and MS. The network Cell Death and Survival and 27 Cancer with TP53 as a central node was identified to be significant with a score of 20. Red indicates overexpression, green indicates underexpression.