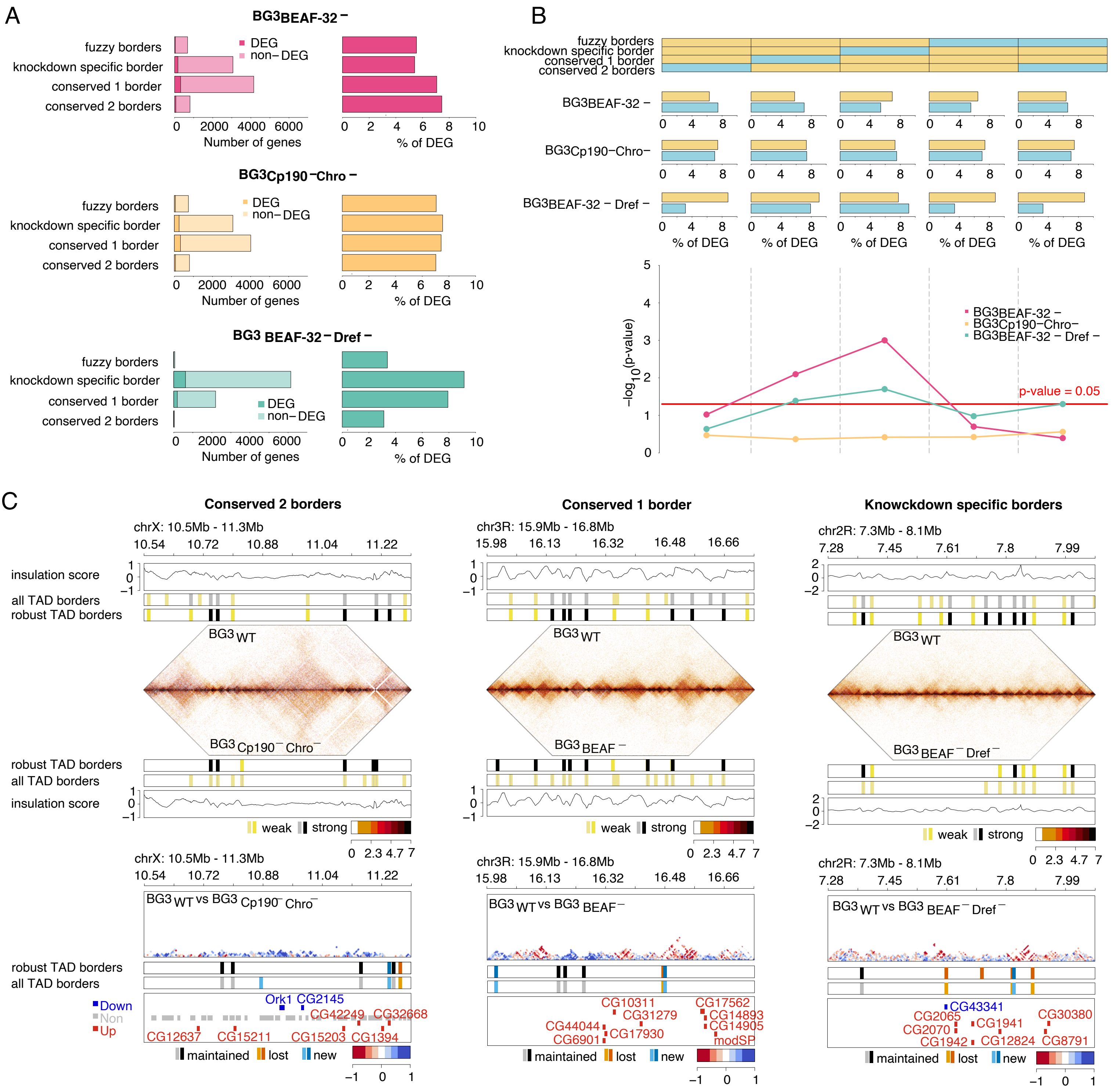
A
BG3BEAF-32 −
fuzzy borders
knockdown specific border
conserved 1 border
conserved 2 borders
DEG
non− DEG
0 2000 4000 6000
Number of genes
0 2 4 6 8 10
% of DEG
BG3Cp190 −Chro −
BG3 BEAF-32 − Dref −
B
BG3BEAF-32 −
BG3Cp190−Chro−
BG3BEAF-32 − Dref −
0 4 8
% of DEG
−log10(p-value)
0 1 2 3 4 5
p-value = 0.05
C
Conserved 2 borders
Conserved 1 border
Knowckdown specific borders
chrX: 10.5Mb - 11.3Mb
10.54 10.72 10.88 11.04 11.22
chr3R: 15.9Mb - 16.8Mb
15.98 16.13 16.32 16.48 16.66
chr2R: 7.3Mb - 8.1Mb
7.28 7.45 7.61 7.8 7.99
insulation score
all TAD borders
robust TAD borders
BG3 WT
BG3 Cp190− Chro−
BG3 BEAF −
BG3 BEAF− Dref−
weak
strong
0 2.3 4.7 7
BG3 WT vs BG3 Cp190− Chro−
BG3 WT vs BG3 BEAF−
BG3 WT vs BG3 BEAF− Dref−
Down
Non
Up
Ork1 CG2145
CG42249 CG32668
CG12637 CG15211 CG15203 CG1394
CG10311 CG17562
CG31279 CG14893
CG44044 CG14905
CG6901 CG17930 modSP
CG43341
CG2065 CG1941 CG30380
CG2070
CG1942 CG12824 CG8791
maintained
lost
new
−1 0 1

Figure S6. *Comparison of differentially and non-differentially expressed genes within different TAD classes in the knockdowns.* (A) Count and proportion of DEG and non-DEG in the three knockdowns (BEAF-32 knockdown, Cp190 Chro double knockdown and BEAF-32 Dref double knockdown) within TADs that: are fully conserved; lose one or both borders; have slightly shifted borders in the knockdowns. (B) We group different TAD classes in two subgroups (blue and yellow) and performed a permutation test to investigate if DEG overlap with any of the class more than expected by chance and plot the corresponding proportion of DEG over non-DEG for each group together with the corresponding -$\log_{10}$ p-values. (C) Examples of DEGs inside TADs that have: *(i)* both borders conserved, *(ii)* one border conserved or *(iii)* both borders are knockdown specific. From top to bottom we plot the insulation score, TAD borders in full dataset (grey are strong and yellow are weak), TAD borders recovered both in full and downsampled dataset (black are strong and yellow are weak) and contact map in WT cells. We also plot a mirror plot in the knockdowns and $\log_2$ fold change between WT and knockdown. To compute the $\log_2$FC, we followed the steps and parameters recommended in diffHiC package (Lun and Smyth 2015). Briefly, we consider individual replicates and use edgeR package (Robinson et al. 2010) to compute the $\log_2$FC in 5 kb bins. On the last row, we plot the position of the non-differentially expressed (grey), upregulated (blue) and downregulated (red) genes.