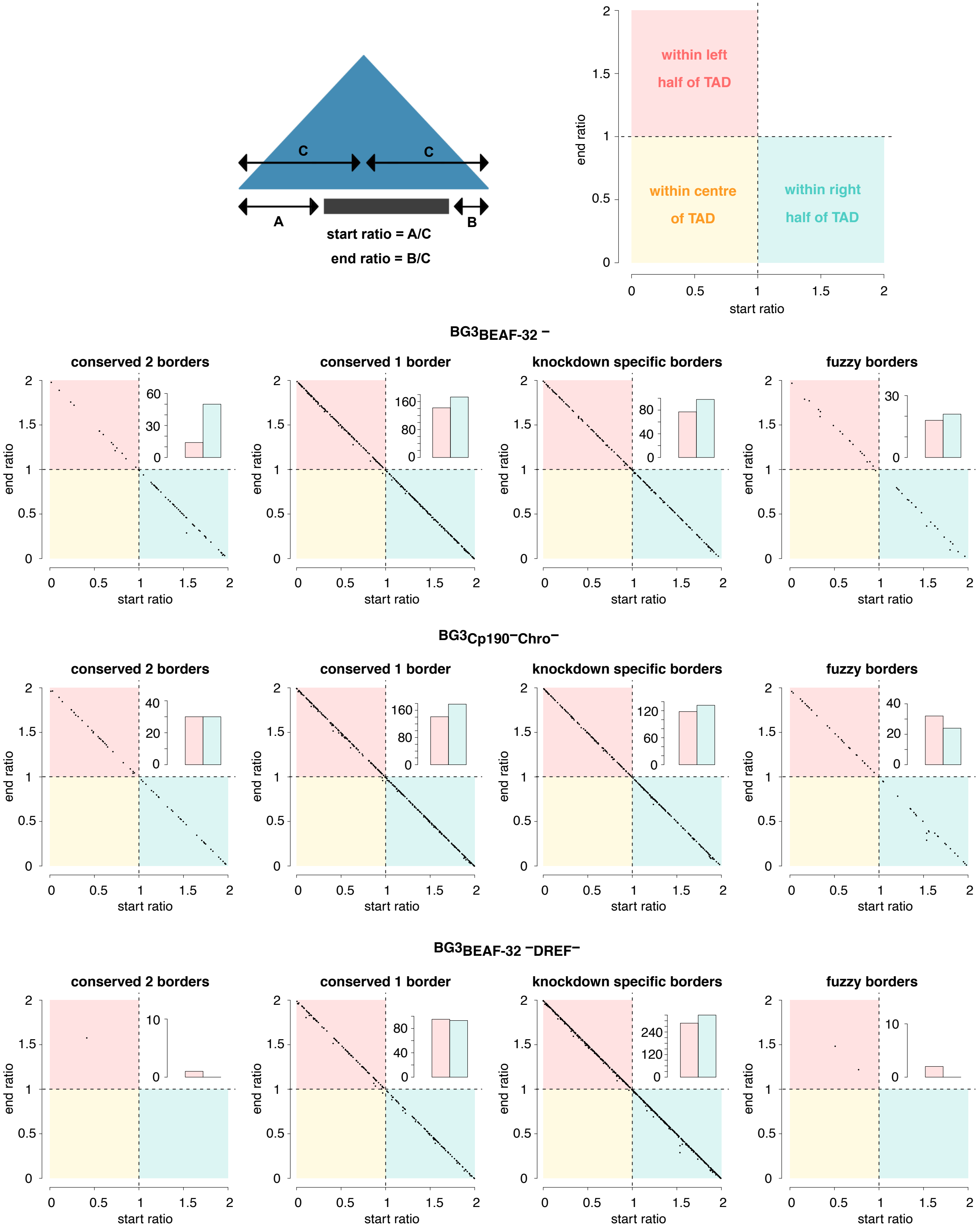
C
C
A
B
start ratio = A/C
end ratio = B/C
within left half of TAD
within centre of TAD
within right half of TAD
end ratio
start ratio
0
0.5
1
1.5
2
BG3BEAF-32 −
BG3Cp190−Chro−
BG3BEAF-32 −DREF−
conserved 2 borders
conserved 1 border
knockdown specific borders
fuzzy borders
60
30
160
80
40
120
240
20
10
0

Figure S7. *The allocation of differentially expressed genes within robust TADs.* Allocation and count of differentially expressed genes within robust TADs in three knockdowns (BEAF-32 knockdown, Cp190 and Chro double knockdown, BEAF-32 Dref double knockdown) based on start and end ratios. The start ratio is defined as a distance from the left border of the TAD to the start position of the gene divided by the half of TAD size, where a start ratio bigger than 1 means that the gene is allocated on the right side of the TAD (green square). The end ratio is defined as a distance from the right border of the TAD to the end position of the gene divided by the half of TAD size, where an end ratio bigger than 1 indicates the gene allocated on the left side of the TAD (red square). Genes having both start and end ratio less than 1 are allocated within TAD centre (yellow square). The majority of differentially expressed genes occupy less than half of the TAD. Only couple of genes are allocated within TAD centre – they are very close to point (1,1) indicating relatively short genes. Majority of genes are allocated either on the left or the right half of the TAD with no strong bias towards TAD borders.