Supplementary Tables

Supplementary Table S1. Primary results of Hi-C libraries sequencing

Sample	Number of reads	Number of mapped contacts (after all filters)*
CEF, replica 1	140 744 763	54 344 109
CEF, replica 2	135 932 850	38 624 661
CME, replica 1	129 824 124	84 643 264
CME, replica 2	131 351 508	85 117 148
CIE, replica 1	139 424 774	93 367 439
CIE, replica 2	139 424 774	92 091 702

*Data provided for standard pipeline executed on contig-level genome assembly. See "*Generation of heatmaps*" for detailed protocol.

Supplementary Table S2. Sizes of TADs identified in CIE and CME

Algorithm	Number	Total Length, Mbp	Genome Coverage, %	Mean Length, Mbp	Median Length, Mbp
CIE Aramtus	3032	781,8	76,54	257.850	200
CIE Dixon	653	927,04	90,76	1419.663	1240
TADtree (Level 0)	1807	623,08	61	344.815	200
TADtree (nested, Level 1)	733	164,28	16,08	224.120	200
TADtree (nested, Level 2)	96	15,48	1,52	161.250	120
TADtree (nested, Level 3)	2	0,28	0,03	140	120
CME Aramtus	3485	806,6	78,96	231.449	200
CME Dixon	805	903	88,4	1121.739	920
CME TADtree (Level 0)	1567	610,28	59,75	389.458	240
CME TADtree (nested, Level 1)	609	129,6	12,69	212.808	160
CME TADtree (nested, Level 2)	73	11,92	1,17	163.288	160
CME TADtree (nested, Level 3)	9	1,4	0,14	155.556	120
CME TADtree (nested, Level 4)	1	0,12	0,01	120	120

Supplementary Table S3. BAC-clones used in this study

BAC CHORI-261	BAC start*	BAC end*	BAC length, bp	Color after detection
177D19	25424085	25632182	208098	red
96F4	26339255	26564682	225428	green
91I5	27261747	27445467	183721	green

*-coordinates in genome assembly Gallus_gallus-5.0

Supplementary Figures

Supplementary Figure 1. Pearson correlation coefficient between biological replicas and different cell types.

Supplementary Figure 2. Analysis of the first Eigenvector values. **A.** Distribution of E1 values in CEF, CIE and CME. **B.** Fraction of positive E1 values (A-compartment) and negative E1 values (B-compartment) on each chromosome. **C.** Scatter plot showing correlation between gene expression levels (measured as FPKM) and E1 values corresponding to promoter region. Each dot represents a single gene. X-axis shows FPKM value, Y-axis shows E1-value of 100KB genomic region containing the gene. If gene spans more than 100 KB, we used E1-value of the 100 KB bin containing transcription start size. Because CME do not exhibit transcriptional activity, we used FPKM values derived from CIE expression data.

Supplementary Figure 3. A/B-compartments in chicken fibroblasts and erythrocytes. **A.** All genomic regions separated into 5 categories according to the E1 values (categories B, b, 0, a, A correspond to ascending E1 values). Heatmaps show average enrichment of interactions between loci belonging to each pair of categories. Compartmentalization strength is calculated as natural logarithm of the AA (bottom right pixel) * BB (upper left pixel) / AB (upper right pixel). **B.** Scatter plots of E1 values. The X- and Y-axes indicate the E1 values derived from two different cell types.

Supplementary Figure 4. The ratio of contact probabilities between pairs of loci of CIE and CEF (green) and of CIE and CEF (blue) at different genomic distances. The X-axis indicates genomic distance, and the Y-axis indicates the ratio of contact probabilities. The black line shows a 1:1 ratio.

Supplementary Figure 5. An example of different compartments pattern in CIE and CME observed on chromosome 9, near LPP gene.

Supplementary Figure 6. Genomic characteristics of TADs identified in chicken fibroblasts. Features shown on Fig. 3 for Dixon TADs presented here for Armatus (left panel, A,C,E,G,I,K) and TADtree (right panel, B,D,F,H,J,L) TADs in a similar manner.

Supplementary Figure 7. CTCF sites contribute to insulation of Dixon TADs. **A.** The drop of contact probability between the genomic loci separated by the CTCF site is shown as on Fig. 3, B. The X-axis shows a distance from the CTCF-site, the Y-axis represents average value of contact frequencies of pairs of loci located 40 KB upstream and 40KB downstream of the point defined by X-axis values. **B.** Orientation of CTCF sites at TAD boundaries. Again, X-axis shows distance

from TAD borders, and Y-axis represents average orientation of CTCF sites in genomic regions defined by X-axis. To obtain Y-values, all CTCF sites in defined genomic regions were summed with a sign according to CTCF site orientation (+1 for forward orientation; -1 for reverse orientation). Obtained results were normalized to the total number of CTCF sites. The graph shows minimum at the -40 KB point, reflecting enrichment of CTCF sites in reverse orientation (-1) near 5'-end of TAD and maximum at the +40 KB point, reflecting enrichment of CTCF sites in forward orientation (+1) near 3'-end of TAD, as shown on schematic illustration below the graph.

Supplementary Figure 8. Comparison of genomic locations of TADs identified by various algorithms in CEF, CIE and CME. **A.** Heatmap showing variation of information coefficient values for pairwise comparisons of TAD sets. Data is presented as ratio of observed information coefficient value (**O**bserbed) to the value obtained for randomly permuted TADs (**E**xpected). For similar TAD sets, variation of information coefficient is equal to 0, thus the resulting O/E ratio is equal to 0. If there is no correlation between positions of TADs of two cell types (or TADs obtained by two different algorithms) observed value would be similar to the expected value, thus resulting O/E ratio will be equal to 1. **B.** Hierarchical clustering of TAD sets based on O/E values.

Supplementary Figure 9. Properties of TADs identified in erythrocytes and fibroblasts. **A, B**. Average number of genes (**A**) and CTCF sites (**B**) near borders of Dixon TADs identified in CIE. Data is presented as on Fig. 3, B. **C, D.** Average Armatus (**C**) and TADtree (**D**) TAD identified in CEF. CIE and CME.

Supplementary Figure 10. Heatmaps showing E1 values of TAD borders and neighboring loci. Each row represents a single TAD, and each pixel reflects E1 value of 40 KB region according to the color scheme shown in the bottom. For each TAD, we show 240 KB (6*40 KB) of genome centered at 3'-border and 240 KB centered at 5'-border.

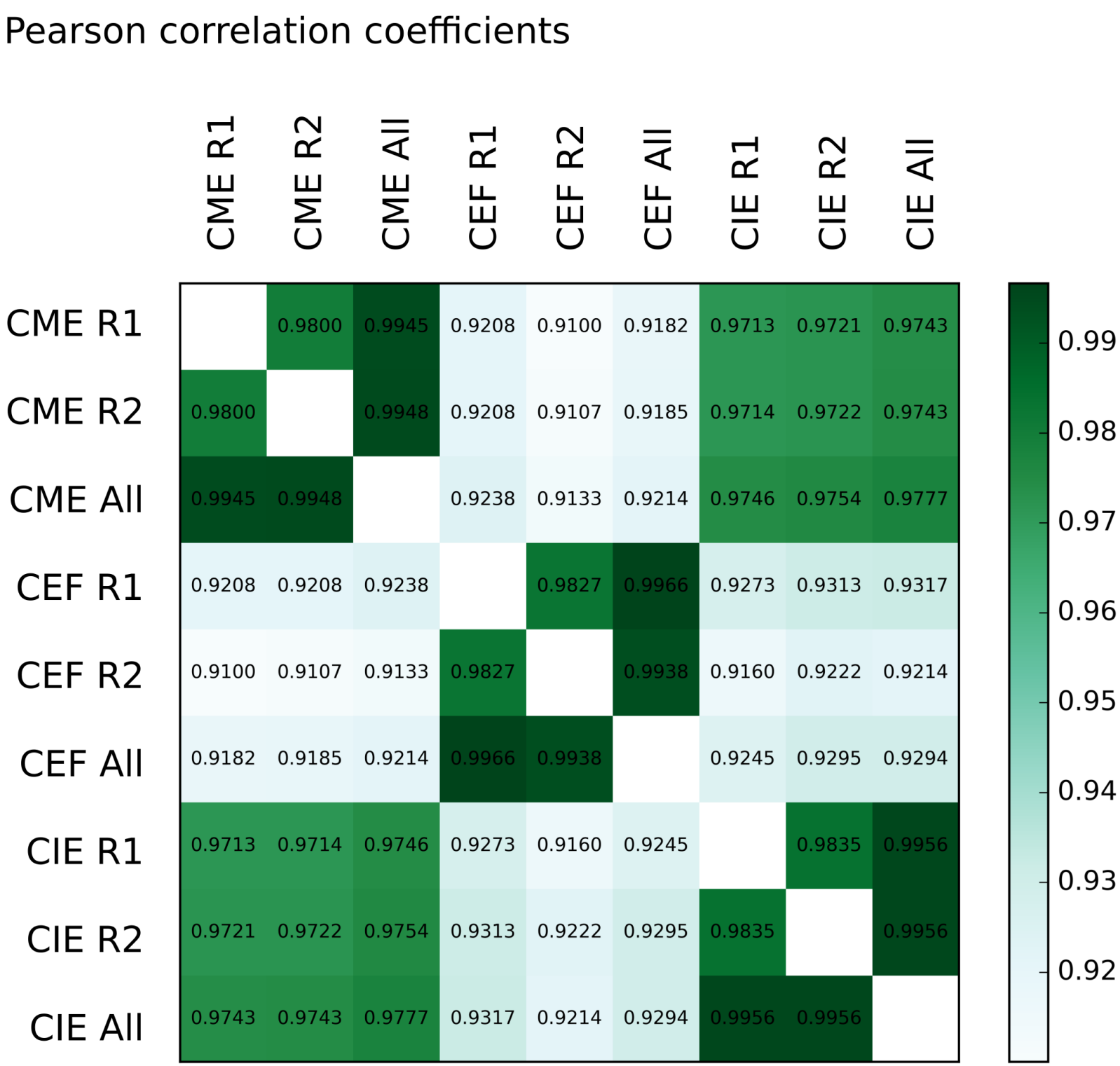
Supplementary Figure 11. The dependence of the contact probability on the genomic distance P(s) calculated separately for micro- and macrochromosomes presented as on Fig. 6.

Supplementary Figure 12. A. Co-occurrence of TAD borders and chicken linage EBRs shown as on Fig. 9, A. **B-D.** Distribution of transposable elements belonging to DNA transposons (B), LINE (C) and LTR (D) families near TAD borders shown as on Fig. 9, C.

Supplementary Figure 13. A-C. The observed/expected ratio for CEF interchromosomal contacts is shown as on Fig. 6, but separately for individual replicas (**A, B**) and merged dataset (**C**).

Supplementary Figure 14. Western blot analysis of CTCF and Rad21, extracted from chicken fibroblasts, erythrocytes, and human HEK293 cells. **A:** Anti-CTCF staining; **B:** anti-Rad21 staining.

Supplementary Figure 15. Distribution of CTCF in CEF and CME (red). DNA is counterstained with DAPI (blue).


Pearson correlation coefficients
CME R1
CME R2
CME All
CEF R1
CEF R2
CEF All
CIE R1
CIE R2
CIE All
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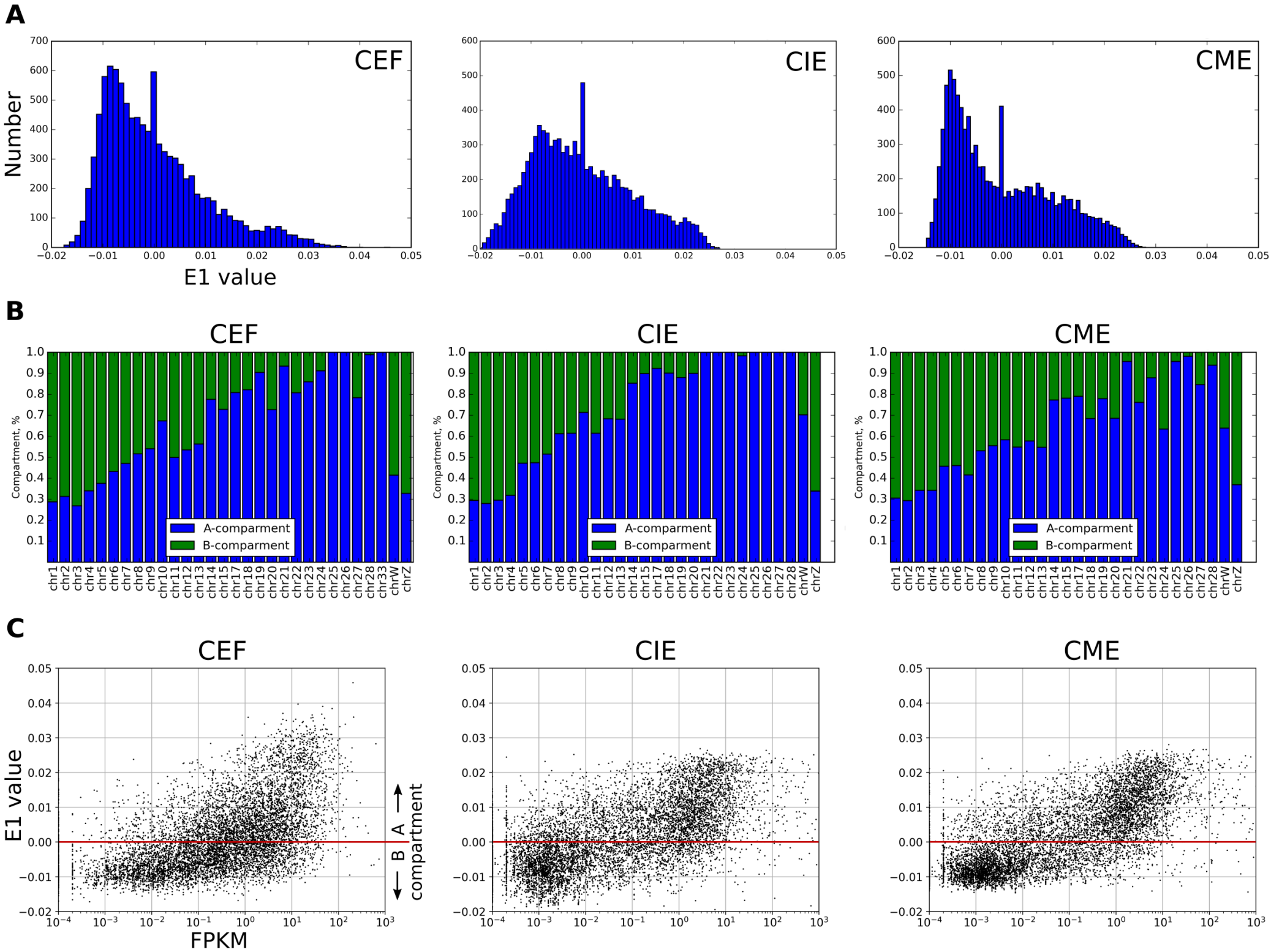
0.9800 0.9948 0.9208 0.9107 0.9185 0.9714 0.9722 0.9743
0.9945 0.9948 0.9238 0.9133 0.9214 0.9746 0.9754 0.9777
0.9208 0.9208 0.9238 0.9827 0.9966 0.9273 0.9313 0.9317
0.9100 0.9107 0.9133 0.9827 0.9938 0.9160 0.9222 0.9214
0.9182 0.9185 0.9214 0.9966 0.9938 0.9245 0.9295 0.9294
0.9713 0.9714 0.9746 0.9273 0.9160 0.9245 0.9835 0.9956
0.9721 0.9722 0.9754 0.9313 0.9222 0.9295 0.9835 0.9956
0.9743 0.9743 0.9777 0.9317 0.9214 0.9294 0.9956 0.9956
0.99
0.98
0.97
0.96
0.95
0.94
0.93
0.92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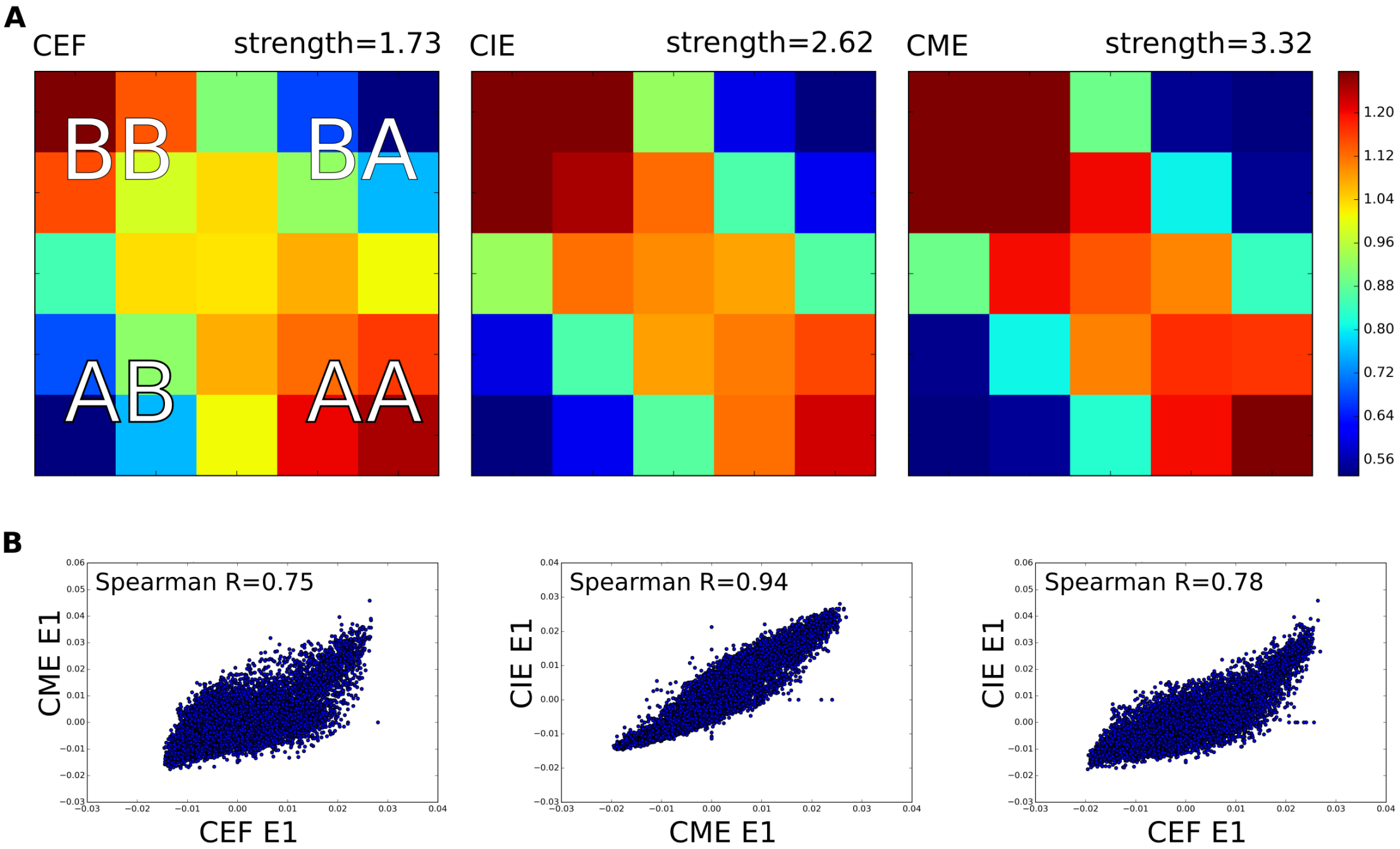
CEF
CIE
CME
Number
E1 value
B
CEF
CIE
CME
Compartment, %
A-comparment
B-comparment
C
CEF
CIE
CME
E1 value
FPKM
A compartment
B compartment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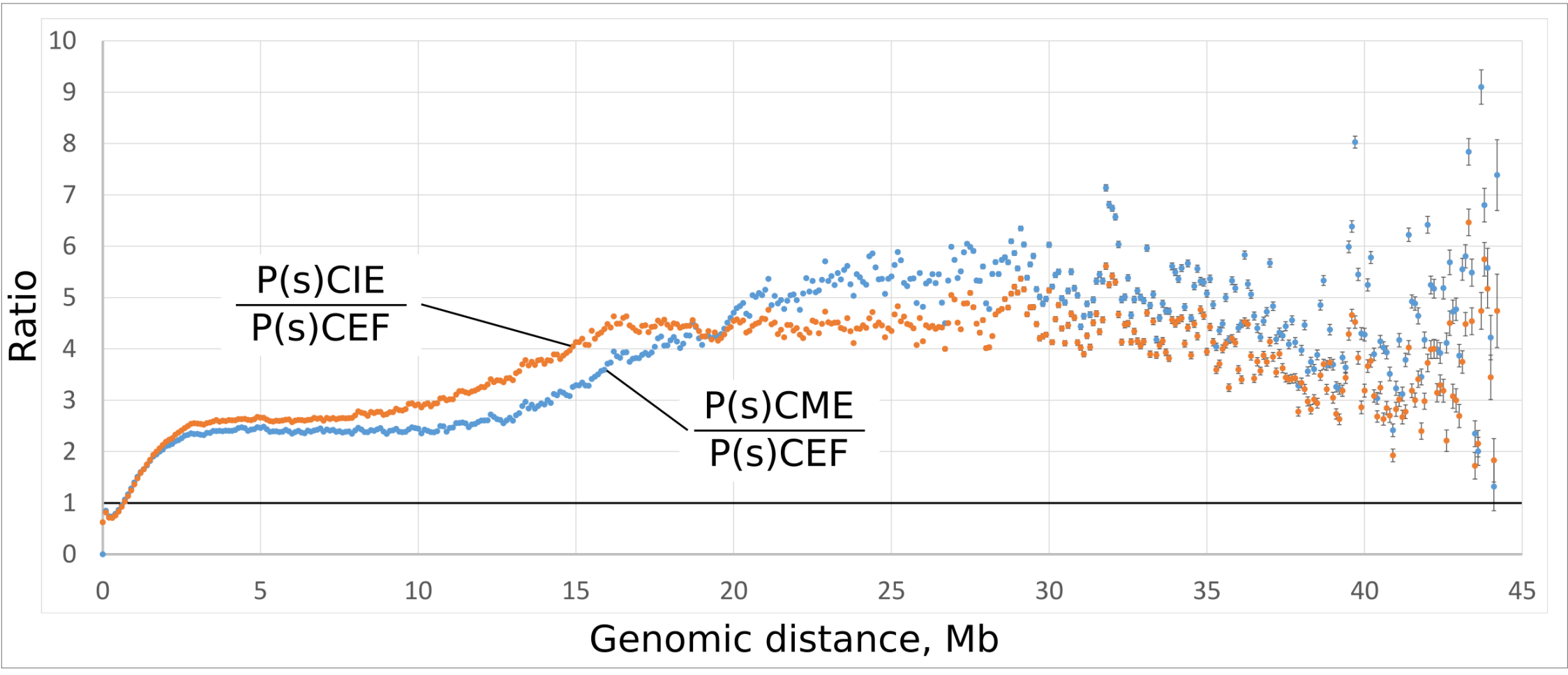
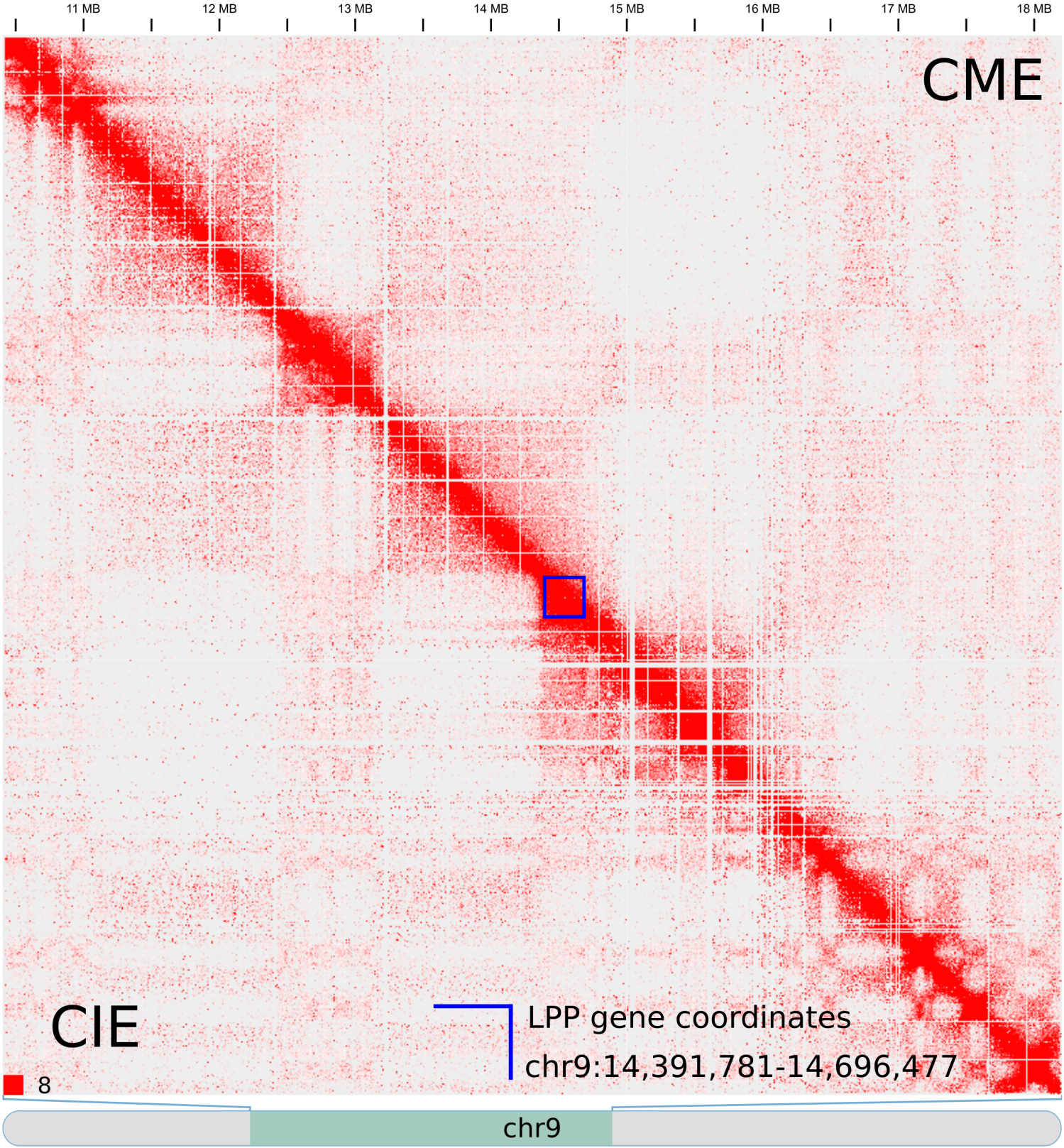
CIE
strength=2.62
CME
strength=3.32
BB
BA
AB
AA
1.20
1.12
1.04
0.96
0.88
0.80
0.72
0.64
0.56
B
Spearman R=0.75
CME E1
CEF E1
Spearman R=0.94
CIE E1
CME E1
Spearman R=0.78
CIE E1
CEF E1


Ratio
10
9
8
7
6
5
4
3
2
1
0
0
5
10
15
20
25
30
35
40
45
Genomic distance, Mb
P(s)CIE
P(s)CEF
P(s)CME
P(s)CEF


11 MB
12 MB
13 MB
14 MB
15 MB
16 MB
17 MB
18 MB
CME
CIE
LPP gene coordinates
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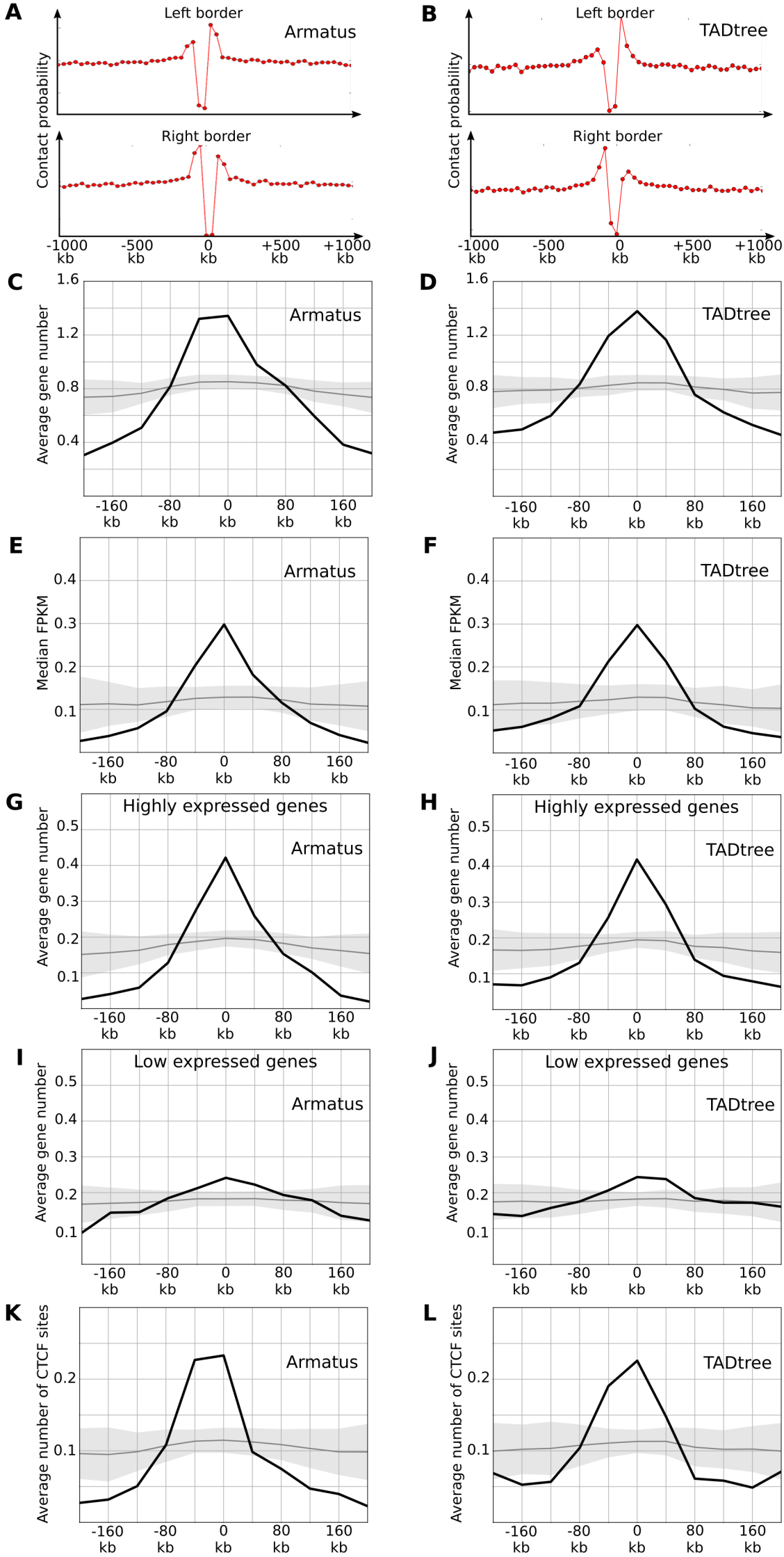
8
chr9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Left border
Armatus
Contact probability
Right border
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-500 kb
0 kb
+500 kb
+1000 kb
B
Left border
TADtree
Contact probability
Right border
-1000 kb
-500 kb
0 kb
+500 kb
+1000 kb
C
Armatus
Average gene number
1.6
1.2
0.8
0.4
-160 kb
-80 kb
0 kb
80 kb
160 kb
D
TADtree
Average gene number
1.6
1.2
0.8
0.4
-160 kb
-80 kb
0 kb
80 kb
160 kb
E
Armatus
Median FPKM
0.4
0.3
0.2
0.1
-160 kb
-80 kb
0 kb
80 kb
160 kb
F
TADtree
Median FPKM
0.4
0.3
0.2
0.1
-160 kb
-80 kb
0 kb
80 kb
160 kb
G
Highly expressed genes
Armatus
Average gene number
0.5
0.4
0.3
0.2
0.1
-160 kb
-80 kb
0 kb
80 kb
160 kb
H
Highly expressed genes
TADtree
Average gene number
0.5
0.4
0.3
0.2
0.1
-160 kb
-80 kb
0 kb
80 kb
160 kb
I
Low expressed genes
Armatus
Average gene number
0.5
0.4
0.3
0.2
0.1
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80 kb
160 kb
J
Low expressed genes
TADtree
Average gene number
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0.4
0.3
0.2
0.1
-160 kb
-80 kb
0 kb
80 kb
160 kb
K
Armatus
Average number of CTCF sites
0.2
0.1
-160 kb
-80 kb
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L
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Average number of CTCF sites
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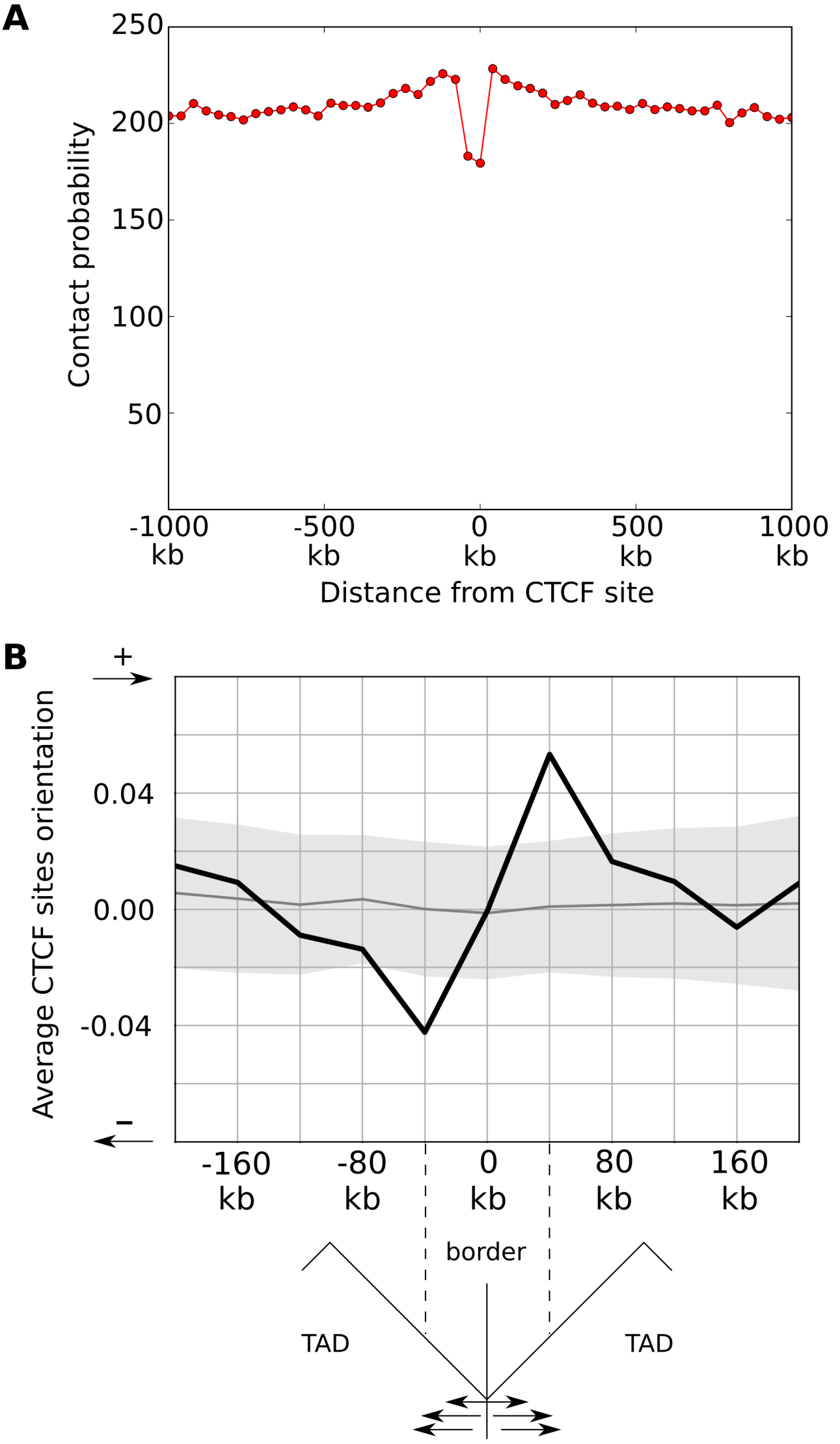
0 kb
80 kb
160 kb


A
250
200
150
100
50
Contact probability
-1000 kb
-500 kb
0 kb
500 kb
1000 kb
Distance from CTCF site
B
+
0.04
0.00
-0.04
–
Average CTCF sites orientation
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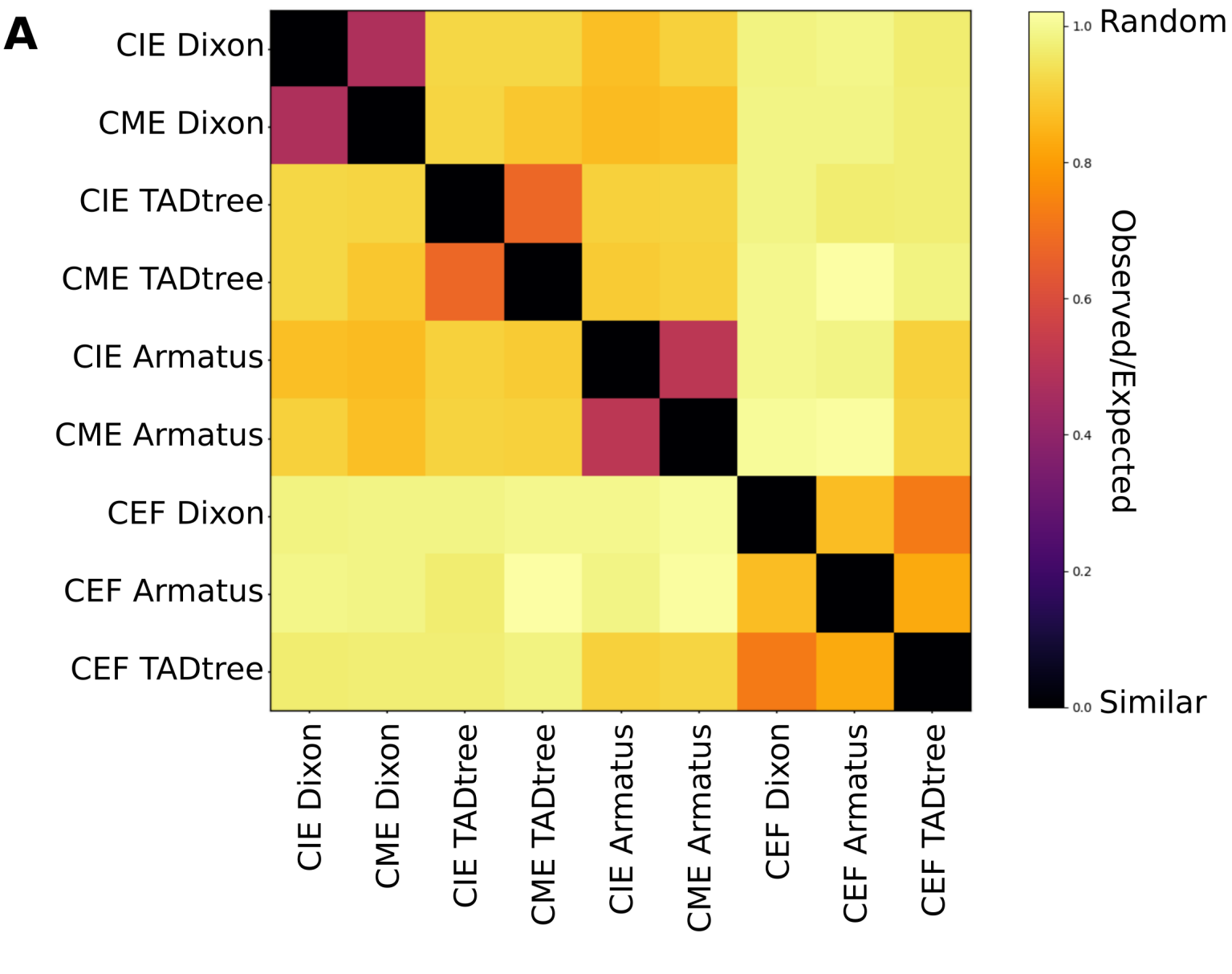
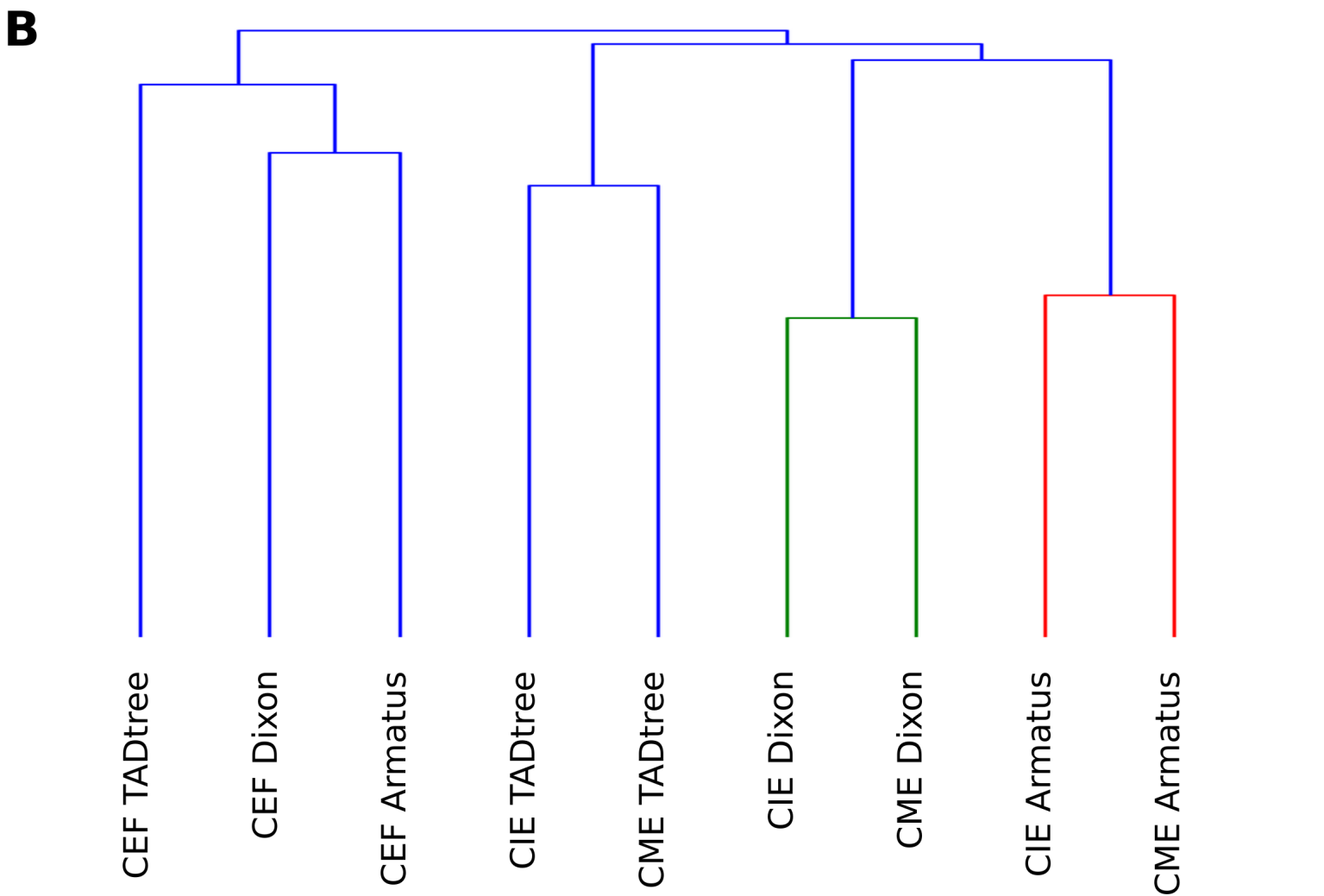
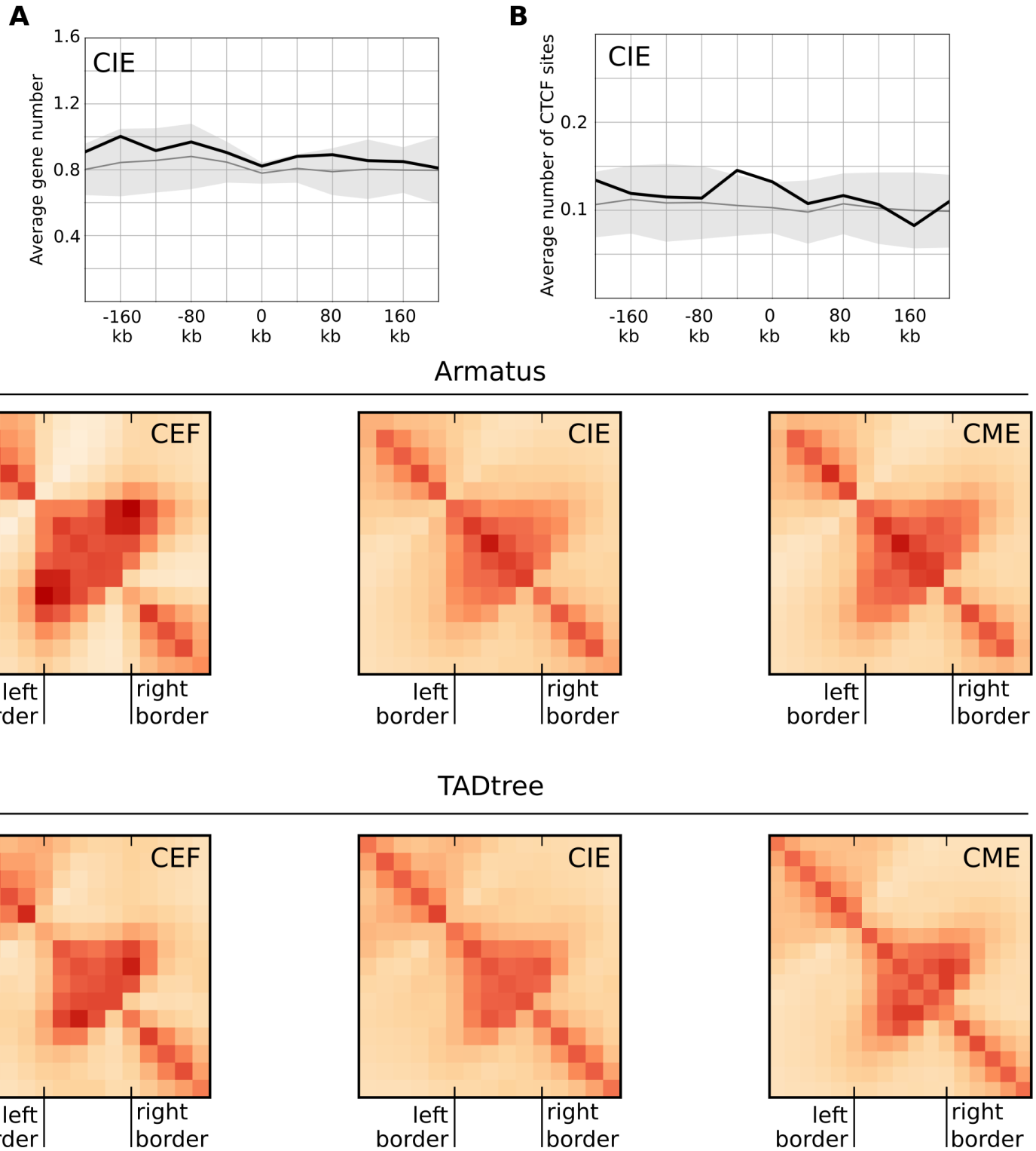
-80 kb
0 kb
80 kb
160 kb
border
TAD
TAD


A
CIE Dixon
CME Dixon
CIE TADtree
CME TADtree
CIE Armatus
CME Armatus
CEF Dixon
CEF Armatus
CEF TADtree
Random
Observed/Expected
Similar
1.0
0.8
0.6
0.4
0.2
0.0


B
CEF TADtree
CEF Dixon
CEF Armatus
CIE TADtree
CME TADtree
CIE Dixon
CME Dixon
CIE Armatus
CME Armatus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1.2
0.8
0.4
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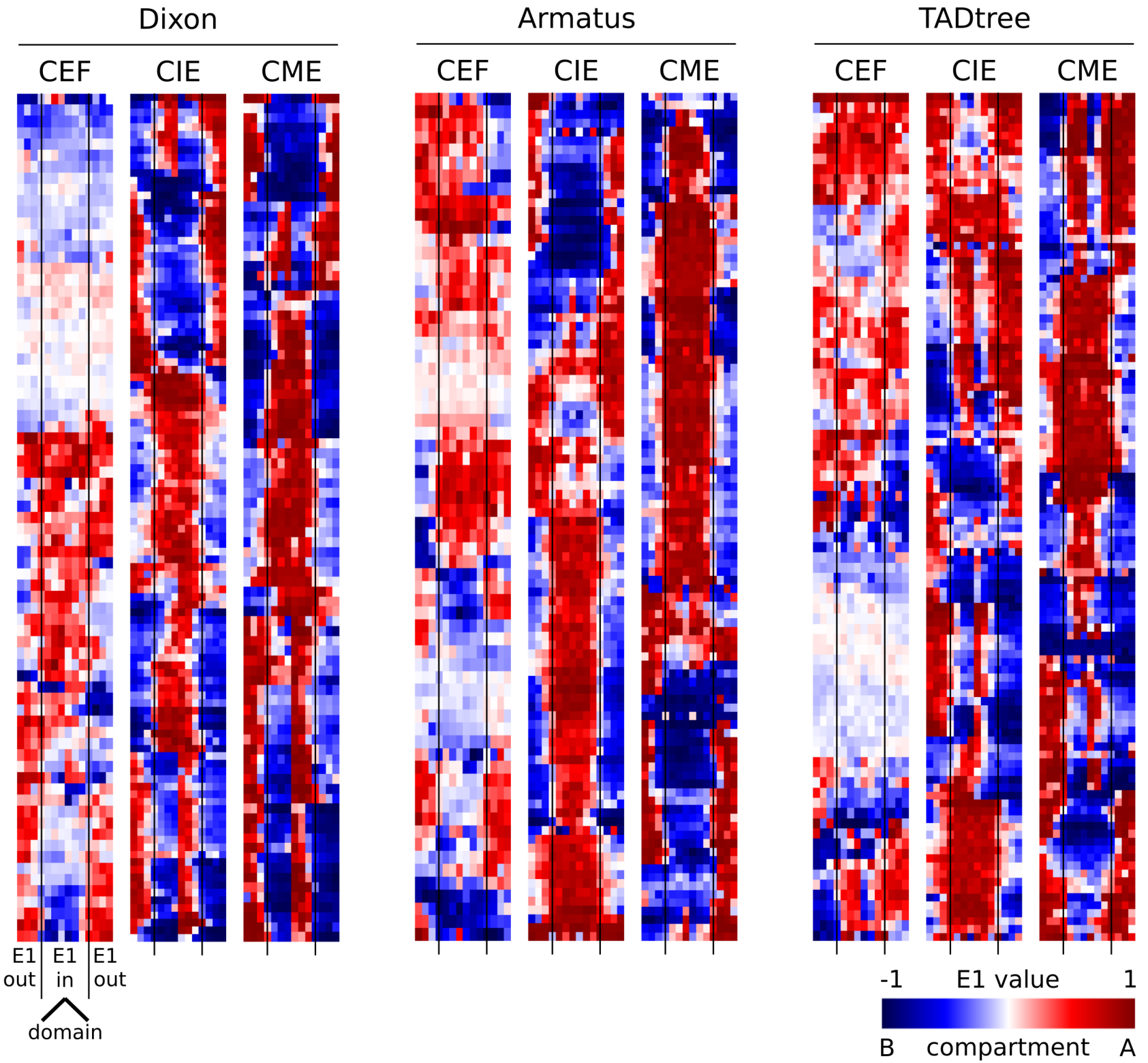
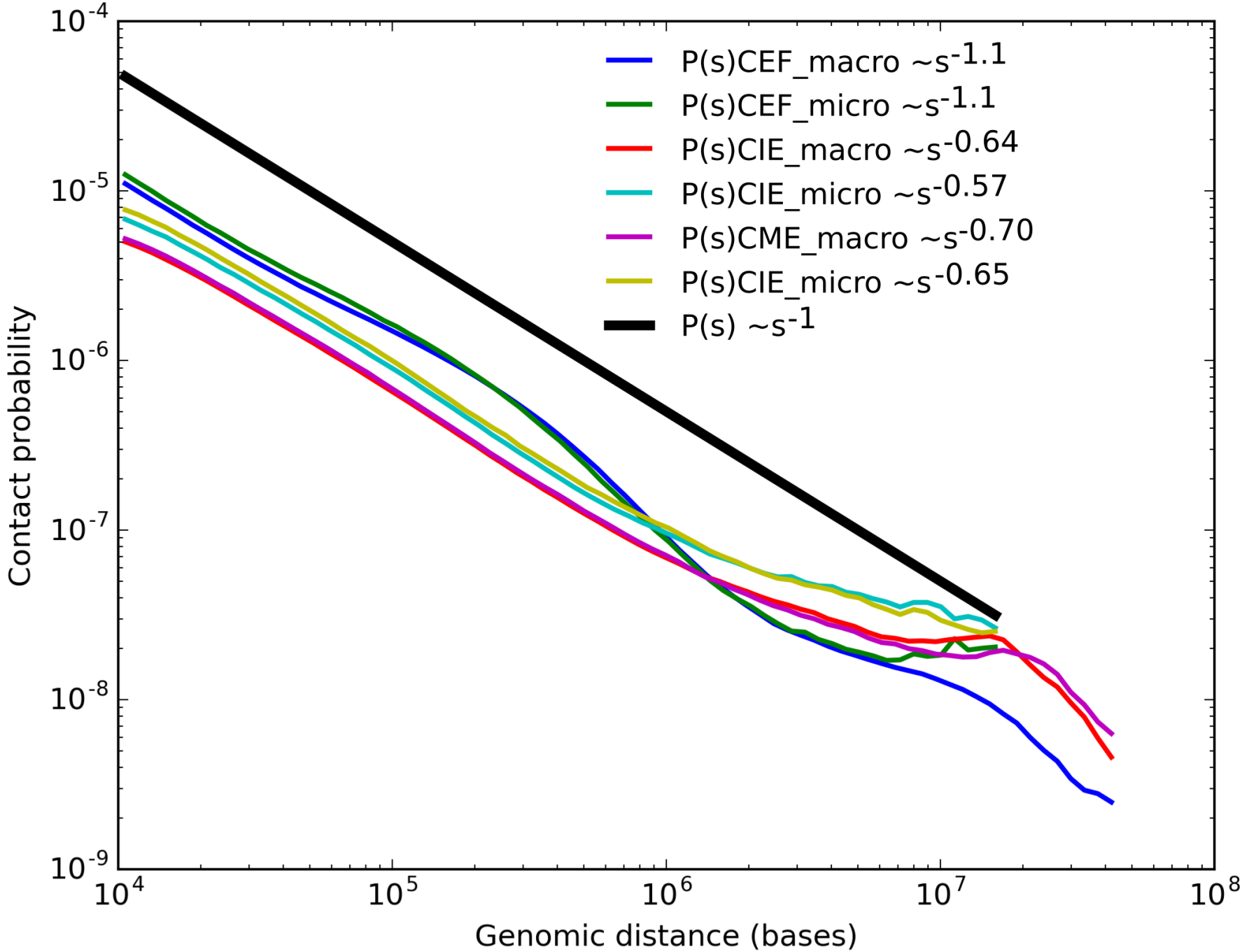
-80 kb
0 kb
80 kb
160 kb
B
CIE
Average number of CTCF sites
0.2
0.1
-160 kb
-80 kb
0 kb
80 kb
160 kb
C
Armatus
CEF
CIE
CME
left border
right border
D
TADtree
CEF
CIE
CME
left border
right border


Dixon
Armatus
TADtree
CEF
CIE
CME
CEF
CIE
CME
CEF
CIE
CME
E1 out
E1 in
E1 out
domain
-1
E1 value
1
B
compartment
A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P(s)CEF_micro ~s-1.1
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P(s)CIE_micro ~s-0.57
P(s)CME_macro ~s-0.70
P(s)CIE_micro ~s-0.65
P(s) ~s-1
Contact probability
Genomic distance (bases)
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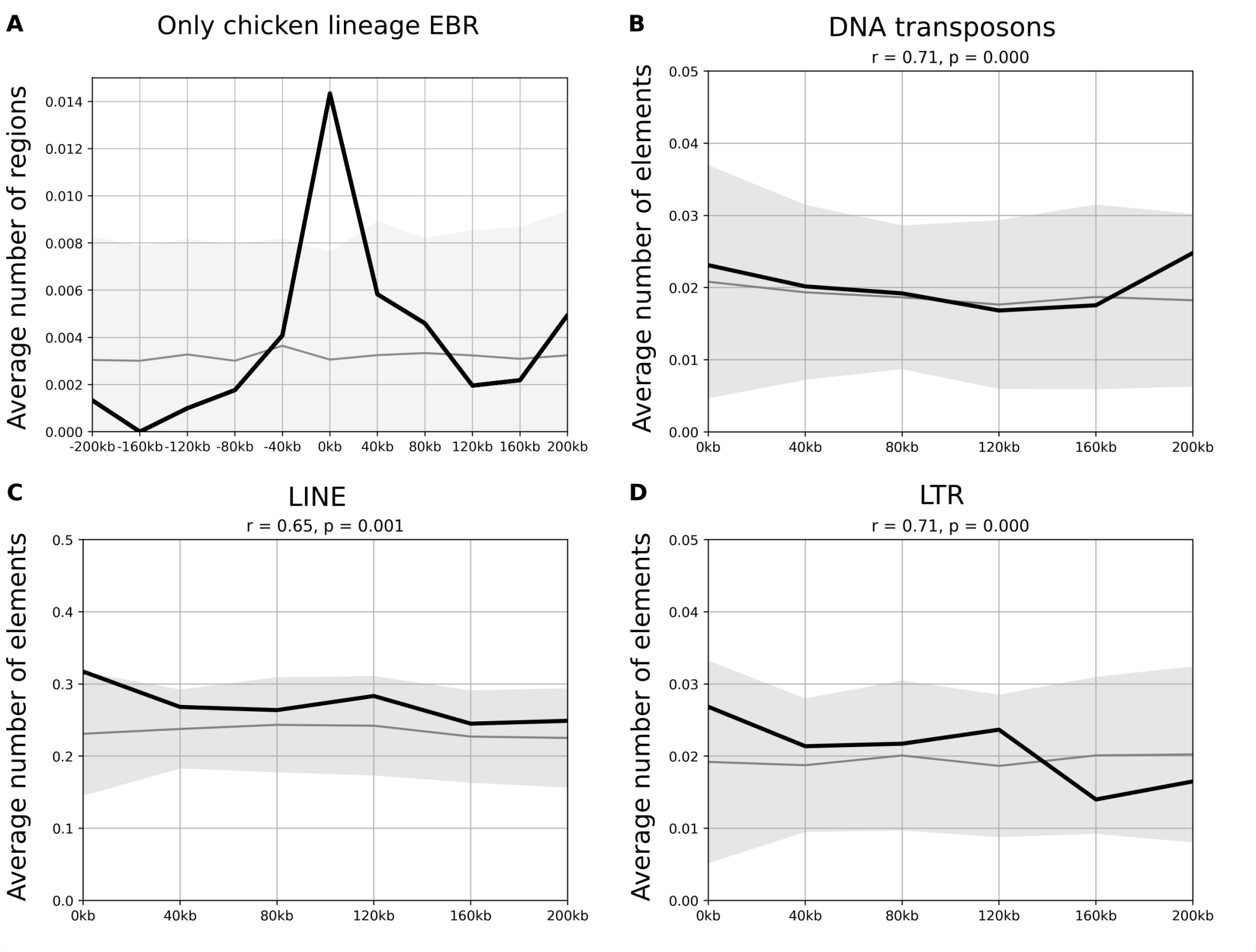
10-5
10-6
10-7
10-8
10-9
10^4
10^5
10^6
10^7
10^8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Average number of regions
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0.012
0.010
0.008
0.006
0.004
0.002
0.000
-200kb -160kb -120kb -80kb -40kb 0kb 40kb 80kb 120kb 160kb 200kb
B
DNA transposons
r = 0.71, p = 0.000
Average number of elements
0.05
0.04
0.03
0.02
0.01
0.00
0kb 40kb 80kb 120kb 160kb 200kb
C
LINE
r = 0.65, p = 0.001
Average number of elements
0.5
0.4
0.3
0.2
0.1
0.0
0kb 40kb 80kb 120kb 160kb 200kb
D
LTR
r = 0.71, p = 0.000
Average number of elements
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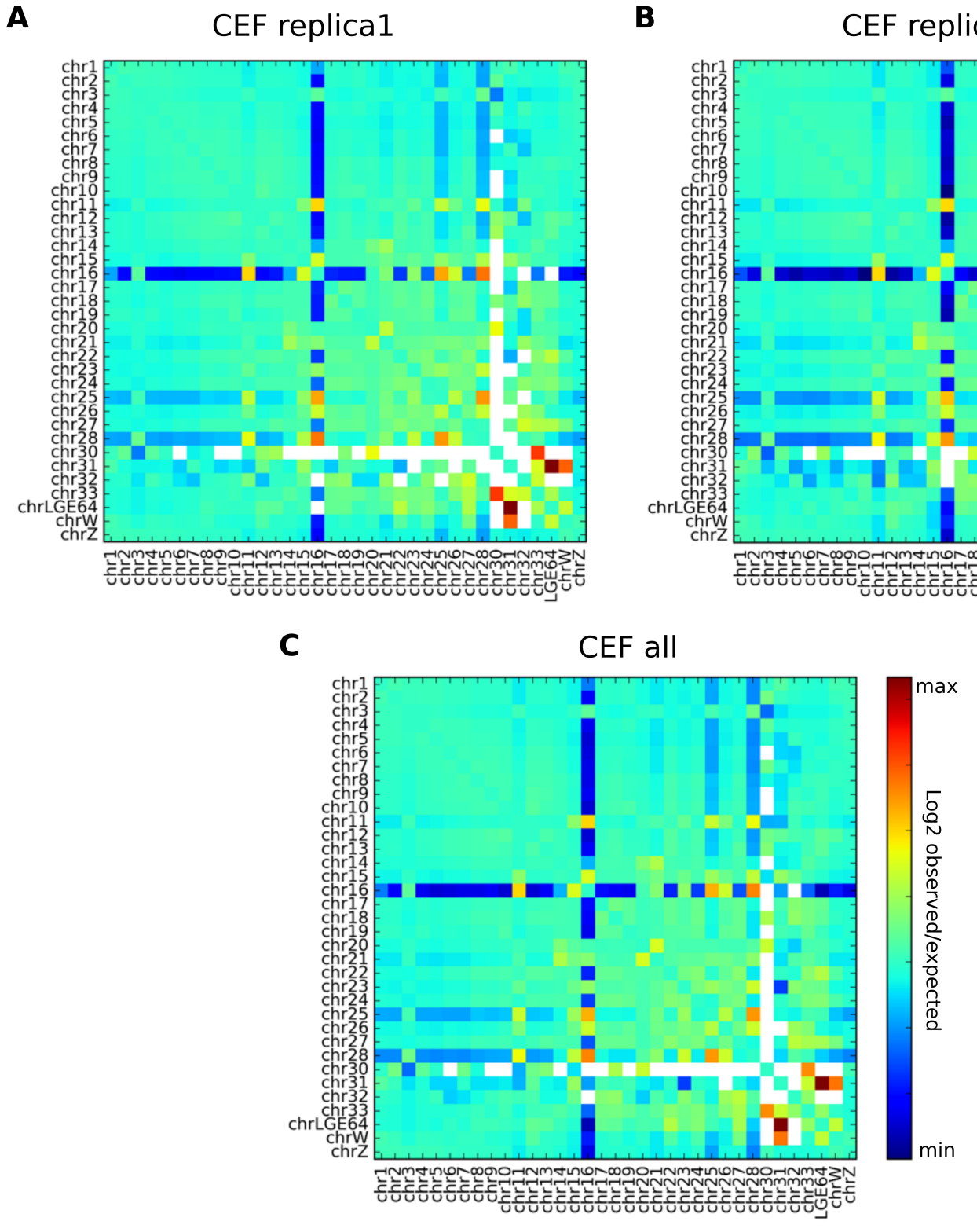
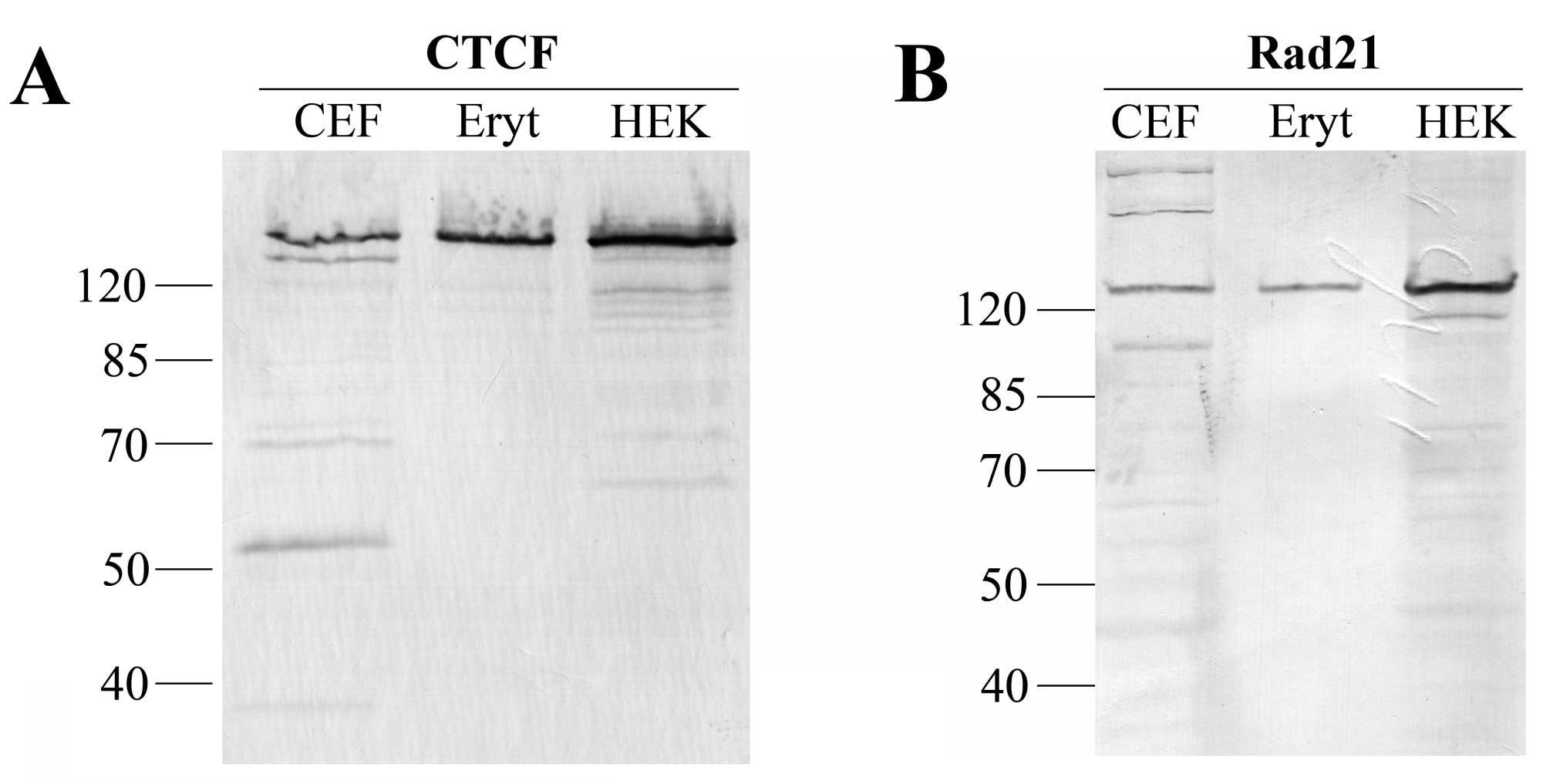
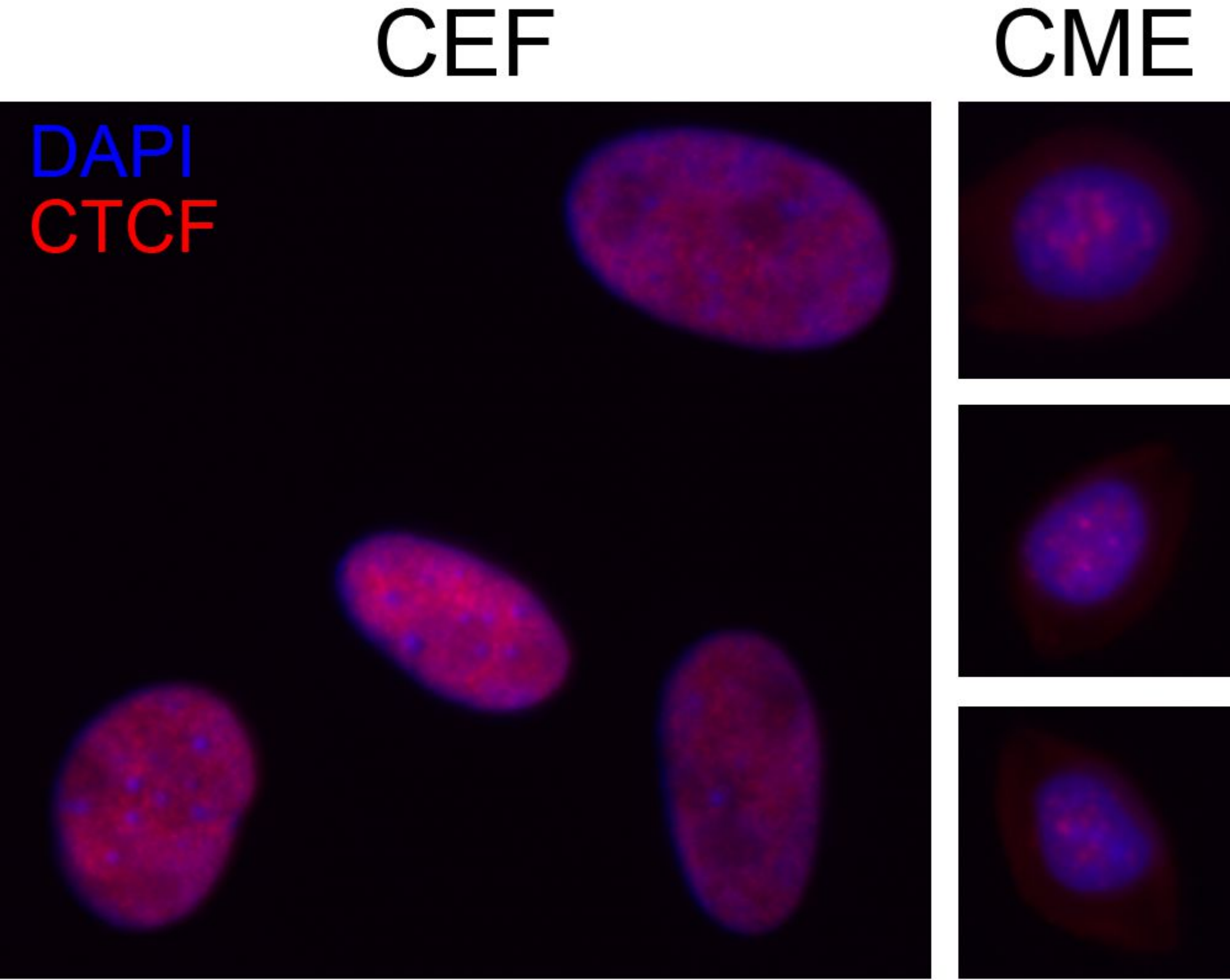
0.04
0.03
0.02
0.01
0.00
0kb 40kb 80kb 120kb 160kb 200kb


A
CEF replica1
B
CEF replica2
C
CEF all
chr1
chr2
chr3
chr4
chr5
chr6
chr7
chr8
chr9
chr10
chr11
chr12
chr13
chr14
chr15
chr16
chr17
chr18
chr19
chr20
chr21
chr22
chr23
chr24
chr25
chr26
chr27
chr28
chr30
chr31
chr32
chr33
chrLGE64
chrW
chrZ
max
Log2 observed/expected
min


A
CTCF
CEF
Eryt
HEK
120
85
70
50
40
B
Rad21
CEF
Eryt
HEK
120
85
70
50
40


CEF
CME
DAPI
CTCF