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Supplemental Material to:

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The clustering of CpG islands may constitute an important determinant of the 3D organization of interphase chromosomes

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SUPPLEMENTARY TABLES

Table S1. The reference bait-originated subsequences for the 4C anchors. These sequences appeared at the beginning of the 4C reads before the *Hind*III restriction sites and originated from the anchor DNA fragments. The sequences were trimmed (see Material and Methods).

Anchor	Reference sequence
TSR3	CACTCATCTCCCCGTACTTTGCCCTAATTCCTCAAGCTT
GENE-Des	AATTTGTGAAGCAGTTGTATGTAGTCAGCAACAGAAGTACAAGCTT
NPRL3	GCCAGGATATAGATTCTGCTTTTAAGCTT
TRAP1	CCAGAGATTCTCAAATCACAGCACAGAAGCTT
PPL	AAAGCATCTCCTCTCCCTGAAGAGCAGAGAGCGGCTCCAAAGCTT

SUPPLEMENTARY FIGURE LEGENDS

Figure S1. Scatterplots and box-plots showing the relationships between the TSR3 4C signal (y-axis) in HD3 cells and the densities of various genomic features (x-axis). (A-G) The correlation of the TSR3 4C signal with the CGI density (A), Sp1 motifs (B), CTCF motifs (C), CTCF deposition sites, as determined by ChIP-Seq (D), NF-E2 binding motifs (E), GATA1 binding motifs (F), and G-quadruplex motifs (G) is shown. Other designations are as in Figure 3.

Figure S2. Scatterplots and box-plots showing the relationships between the GENE-Des 4C signal (y-axis) in HD3 cells and the densities of various genomic features (x-axis). (A-G) The correlation of the GENE-Des 4C signal with the CGI density (A), Sp1 motifs (B), CTCF motifs (C), CTCF deposition sites, as determined by ChIP-Seq (D), NF-E2 binding motifs (E), GATA1 binding motifs (F), and G-quadruplex motifs (G) is shown. Other designations are as in Figure 3.

Figure S3. Scatterplots and box-plots showing the relationships between the TRAP1 4C signal (y-axis) in HD3 cells and the densities of various genomic features (x-axis). (A-G) The correlation of the TRAP1 4C signal with the CGI density (A), Sp1 motifs (B), CTCF motifs (C),

CTCF deposition sites, as determined by ChIP-Seq (D), NF-E2 binding motifs (E), GATA1 binding motifs (F), and G-quadruplex motifs (G) is shown. Other designations are as in Figure 3.

Figure S4. Scatterplots and box-plots showing the relationships between the PPL 4C signal (y-axis) in HD3 cells and the densities of various genomic features (x-axis). (A-G) The correlation of the PPL 4C signal with the CGI density (A), Sp1 motifs (B), CTCF motifs (C), CTCF deposition sites, as determined by ChIP-Seq (D), NF-E2 binding motifs (E), GATA1 binding motifs (F), and G-quadruplex motifs (G) is shown. Other designations are as in Figure 3.

Figure S5. Distribution of the CTCF deposition sites in the upstream area of the chicken c-myc gene. The figure demonstrates the position of the CTCF binding site reported by Lobanenkov et al (site V)[78] and CTCF binding sites found in our ChIP-Seq experiments (shown are the raw data of the ChIP-Seq analysis and CTCF deposition peaks identified as described in Material and Methods); visualization in the UCSC browser. Genomic coordinates are according to the galGal4 assembly.

SUPPLEMENTARY FIGURES

Figure S1

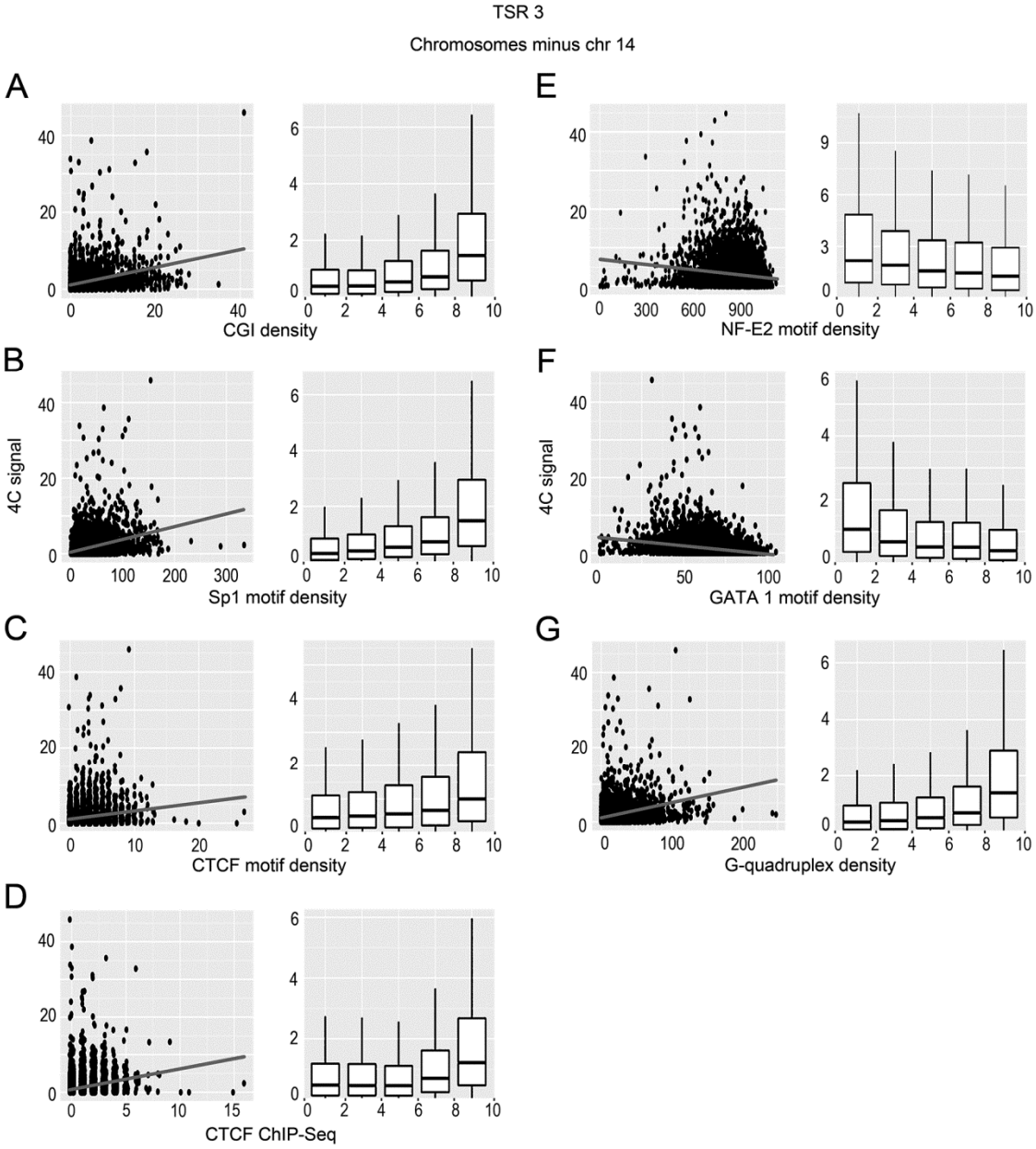


Figure S2

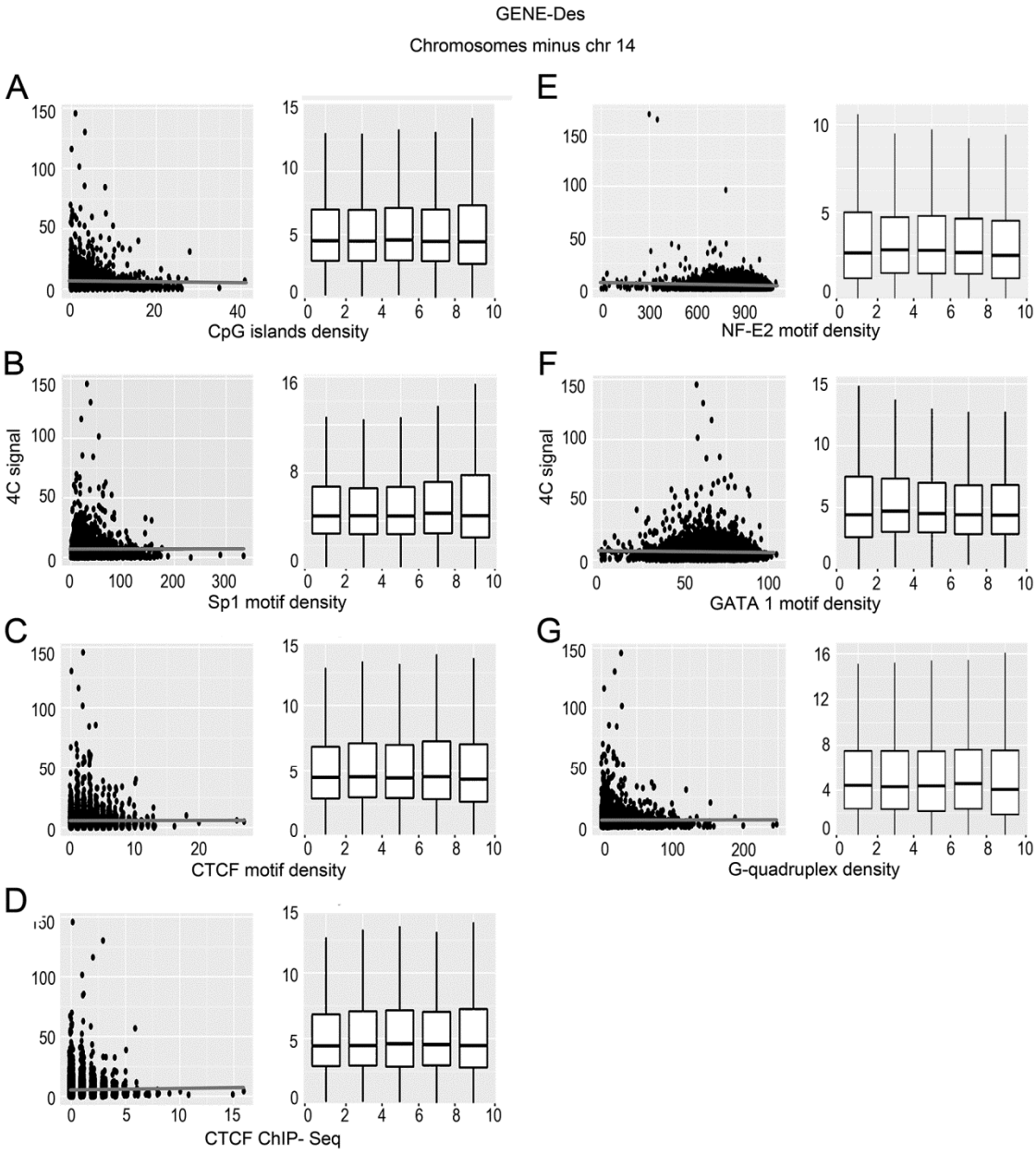

GENE-Des
Chromosomes minus chr 14
A
CpG islands density
B
4C signal
Sp1 motif density
C
CTCF motif density
D
CTCF ChIP- Seq
E
NF-E2 motif density
F
4C signal
GATA 1 motif density
G
G-quadruplex density

Figure S3

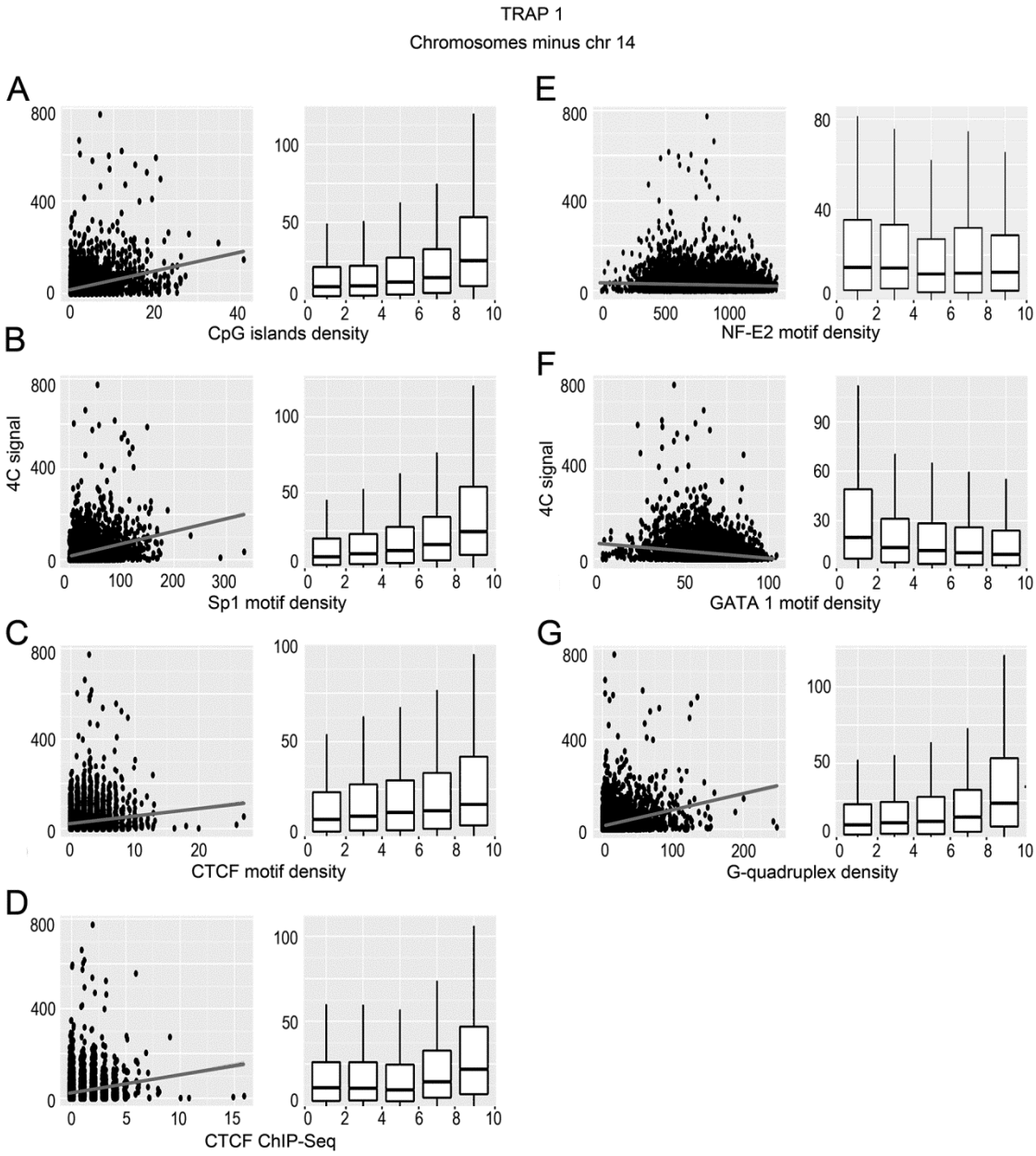

TRAP 1
Chromosomes minus chr 14
A
B
C
D
E
F
G
4C signal
CpG islands density
Sp1 motif density
CTCF motif density
CTCF ChIP-Seq
NF-E2 motif density
GATA 1 motif density
G-quadruplex density

Figure S4

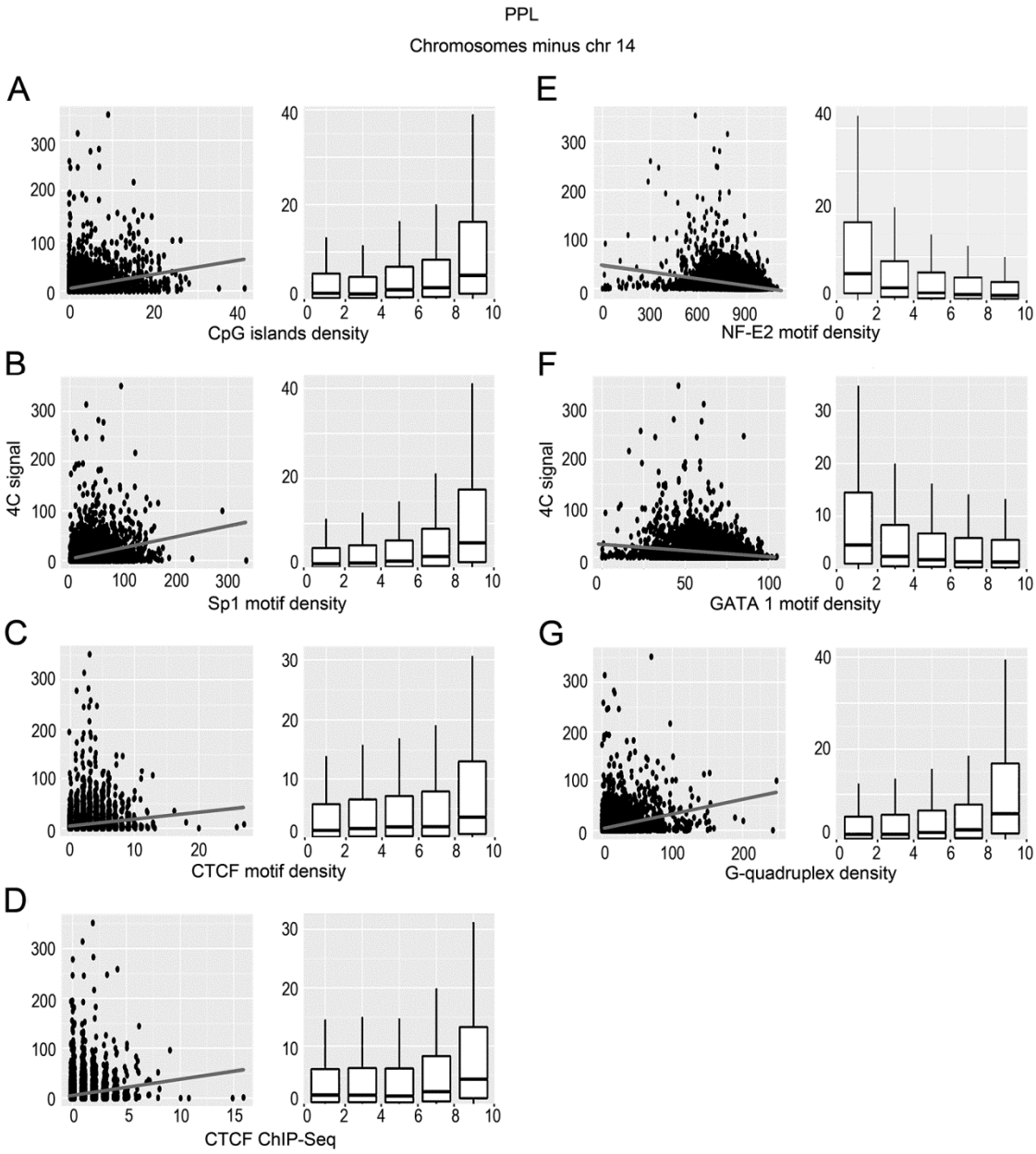
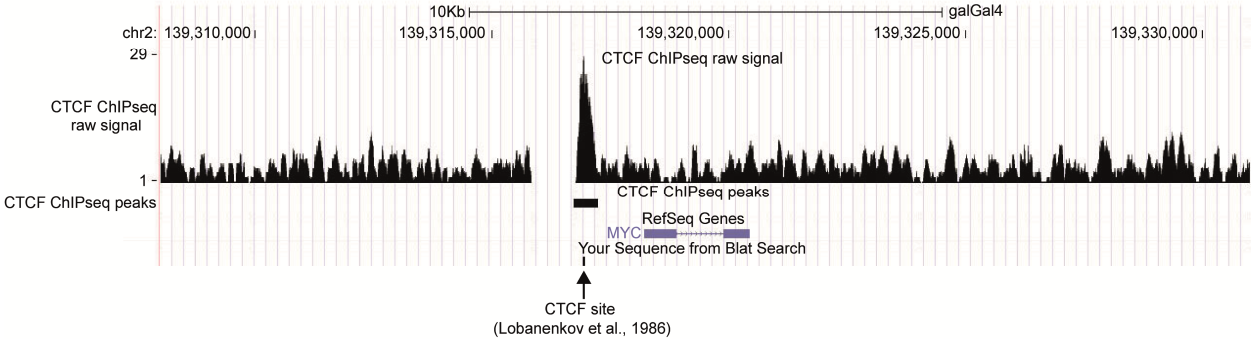

PPL
Chromosomes minus chr 14
A
CpG islands density
E
NF-E2 motif density
B
4C signal
Sp1 motif density
F
4C signal
GATA 1 motif density
C
CTCF motif density
G
G-quadruplex density
D
CTCF ChIP-Seq

Figure S5


10Kb
galGal4
chr2: 139,310,000
139,315,000
139,320,000
139,325,000
139,330,000
29
CTCF ChIPseq raw signal
CTCF ChIPseq raw signal
1
CTCF ChIPseq peaks
CTCF ChIPseq peaks
RefSeq Genes
MYC
Your Sequence from Blat Search
CTCF site
(Lobanenkov et al., 1986)