SUPPLEMENTARY FIGURE LEGENDS

Figure S1. Chromatin loops cluster transcriptionally silent 5'end *HoxA* genes in a cell type independent manner. Chromatin contacts between regions surrounding the *HoxA9, A10, A11, and A13* genes were measured using libraries from untreated (undifferentiated) NT2/D1 and PMA treated (differentiated) THP-1 cells. The *y*-axis indicates normalized interaction frequency. The *x*-axis shows the genomic position relative to beginning of the cluster. The genomic domain is drawn to scale above the graphs. Solid orange vertical lines identify the position of "fixed" 3C region in each graph. Shaded yellow vertical lines illustrate DNA looping contacts with the fixed region. Each data point is an average of at least 3 PCR reactions and error bars represent standard error of the mean (s.e.m.).

Figure S2. Chromatin looping is a conserved feature of the transcriptionally silent *HoxB* cluster. (**A**) Linear schematic representation of the *HoxB* cluster on human chromosome 17. Cluster features are as described in Figure 1A.

(**B**) 3C interaction frequency heat map of the silent *HoxB* cluster. Pair-wise interaction frequencies were measured by 3C in undifferentiated NT2/D1 cells. Heat map features are as described in Figure 1B.

(**C**) Two-dimensional schematic representation of the silent human *HoxB* cluster *in vivo*. The model is based on heat map results presented in (**B**) and is as described in Figure 1C. Note that the yellow circles simply highlight an area encompassing looping contacts and not the number of interactions.

Figure S3. Chromatin looping is a conserved feature of the transcriptionally silent *HoxC* cluster. (**A**) Linear schematic representation of the *HoxC* cluster on human chromosome 12. Cluster features are as described in Figure 1A.

(**B**) 3C interaction frequency heat map of the silent *HoxC* cluster. Pair-wise interaction frequencies were measured by 3C in undifferentiated NT2/D1 cells. Heatmap features are as described in Figure 1B.

(**C**) Two-dimensional schematic representation of the silent human *HoxC* cluster *in vivo*. The model is based on heat map results presented in (**B**) and is as described in Figure 1C. Yellow circles highlight an area containing looping interactions.

Figure S4. Chromatin looping is a conserved feature of the transcriptionally silent *HoxD* cluster. (**A**) Linear schematic representation of the *HoxD* cluster on human chromosome 2. Cluster features are as described in Figure 1A.

(**B**) 3C interaction frequency heat map of the silent *HoxD* cluster. Pair-wise interaction frequencies were measured by 3C in undifferentiated NT2/D1 cells. Heatmap features are as described in Figure 1B.

(**C**) Two-dimensional schematic representation of the silent human *HoxD* cluster *in vivo*. The model is based on heat map results presented in (**B**) and is as described in Figure 1C. Yellow circles highlight an area containing looping interactions.

Figure S5. *HoxD* chromatin loops are conserved in different 3C libraries. (**A**) Linear schematic representation of the *HoxD* cluster on human chromosome 2. Cluster features are as described in Figure 1A, except that the predicted HindIII restriction pattern in the *HoxD* region is illustrated below linear diagram.

(**B**) 3C interaction frequency heat map of the silent *HoxD* cluster. Pair-wise interaction frequencies were measured by 3C in undifferentiated NT2/D1 cells. Heat map features are as described in Figure 1B.

(**C**) Two-dimensional schematic representation of the silent human *HoxD* cluster *in vivo*. The model is based on heat map results presented in (**B**) and is as described in Figure 1C. Yellow circles highlight an area containing looping interactions.

Figure S6. Three-dimensional modeling of the silent *HoxB* cluster identifies CTCF as a likely candidate mediating chromatin loops.

(**A**) Example of a 5C3D output model of the transcriptionally silent *HoxB* cluster. Green lines represent genomic DNA, and vertices define boundaries between consecutive restriction fragments. Colored spheres as indicated in the legend below identify the transcription start site of corresponding paralogue group.

(**B**) Three-dimensional local base density scan of the transcriptionally silent *HoxB* cluster. Local base densities at consecutive ten base pairs was estimated in one hundred possible 5C3D outputs models with Microcosm 1.0 (*y-axis*) and represented graphically along the corresponding genomic region (ENCODE hg18 Chr17:43960763 to 44065377) (*x-axis*). The weight of the trace is proportional to the standard deviation with sharper areas indicating smaller deviations. A linear schematic representation of the *HoxB* cluster is shown to scale at the top of the graph and is as described in Figure

1. Shaded yellow vertical lines identify the position of CTCF binding sites mapped in various cell lines as illustrated in (**C**).

(**C**) CTCF binds to multiple discrete sites conserved in various cell lines at the 5’end of the *HoxB* cluster. CTCF binding was identified by ChIP-seq and ChIP-chip in different cell lines as described in MATERIALS AND METHODS. Binding sites conserved in most cell lines are numbered and highlighted by yellow vertical lines, which are contiguous with lines in panel (**B**).

(**D**) Conserved CTCF binding sites in *HoxB* are clustered three-dimensionally. The position CTCF binding sites numbered in (**C**) are illustrated in the example 5C3D output model presented in (**A**). CTCF binding sites are represented by colored spheres as indicated in the legend below.

(**E**) CTCF binding sites are significantly close to each other in three-dimensional models. Distances between pairs of CTCF binding sites were measured in one hundred possible 5C3D outputs models with Microcosm 2.0. The significance of spatial proximity between pair-wise CTCF binding sites is expressed as p-values summarized in a heatmap. Numbers at the top and on the left of heatmap identify CTCF binding sites. Intersecting column and row number identifies the CTCF pair corresponding to p-value. p-values are color-coded based on the scale presented on the *right*, with white indicating low significance and red highly significant proximity. p-values represent the fraction of fragment pairs separated by the same linear genomic distance, which are closer or at the same distance to CTCF pairs in 5C3D output models (see MATERIALS AND METHODS for details).

Figure S7. Three-dimensional modeling of the silent *HoxC* cluster identifies CTCF as a likely candidate mediating chromatin loops.

(**A**) Example of a 5C3D output model of the transcriptionally silent *HoxC* cluster. Green lines represent genomic DNA, and vertices define boundaries between consecutive restriction fragments. Colored spheres as indicated in the legend below identify the transcription start site of corresponding paralogue group.

(**B**) Three-dimensional local base density scan of the transcriptionally silent *HoxC* cluster. Local base densities at consecutive ten base pairs was estimated in one hundred possible 5C3D outputs models with Microcosm 1.0 (*y-axis*) and represented graphically along the corresponding genomic region (ENCODE hg18 Chr12:52593459 to 52739739) (*x-axis*). The weight of the trace is proportional to the standard deviation with sharper areas indicating smaller deviations. A linear schematic representation of the *HoxC* cluster is shown to scale at the top of the graph and is as described in Figure 1. Shaded yellow vertical lines identify the position of CTCF binding sites mapped in various cell lines as illustrated in (**C**).

(**C**) CTCF binds to multiple discrete sites conserved in various cell lines at the 5'end of the *HoxC* cluster. CTCF binding was identified by ChIP-seq and ChIP-chip in different cell lines as described in MATERIALS AND METHODS. Binding sites conserved in most cell lines are numbered and highlighted by yellow vertical lines, which are contiguous with lines in panel (**B**).

(**D**) Conserved CTCF binding sites in *HoxC* are clustered three-dimensionally. The position CTCF binding sites numbered in (**C**) are illustrated in the example 5C3D output model presented in (**A**). CTCF binding sites are represented by colored spheres as indicated in the legend below.

(**E**) CTCF binding sites are significantly close to each other in three-dimensional models. Distances between pairs of CTCF binding sites were measured in one hundred possible 5C3D outputs models with Microcosm 2.0. The significance of spatial proximity between pair-wise CTCF binding sites is expressed as p-values summarized in a heatmap. Numbers at the top and on the left of heatmap identify CTCF binding sites. Intersecting column and row number identifies the CTCF pair corresponding to p-value. p-values are color-coded based on the scale presented on the *right*, with white indicating low significance and red highly significant proximity. p-values represent the fraction of fragment pairs separated by the same linear genomic distance, which are closer or at the same distance to CTCF pairs in 5C3D output models (see MATERIALS AND METHODS for details).

Figure S8. Three-dimensional modeling of the silent *HoxD* cluster identifies CTCF as a likely candidate mediating chromatin loops.

(**A**) Example of a 5C3D output model of the transcriptionally silent *HoxD* cluster. Green lines represent genomic DNA, and vertices define boundaries between consecutive restriction fragments. Colored spheres as indicated in the legend below identify the transcription start site of corresponding paralogue group.

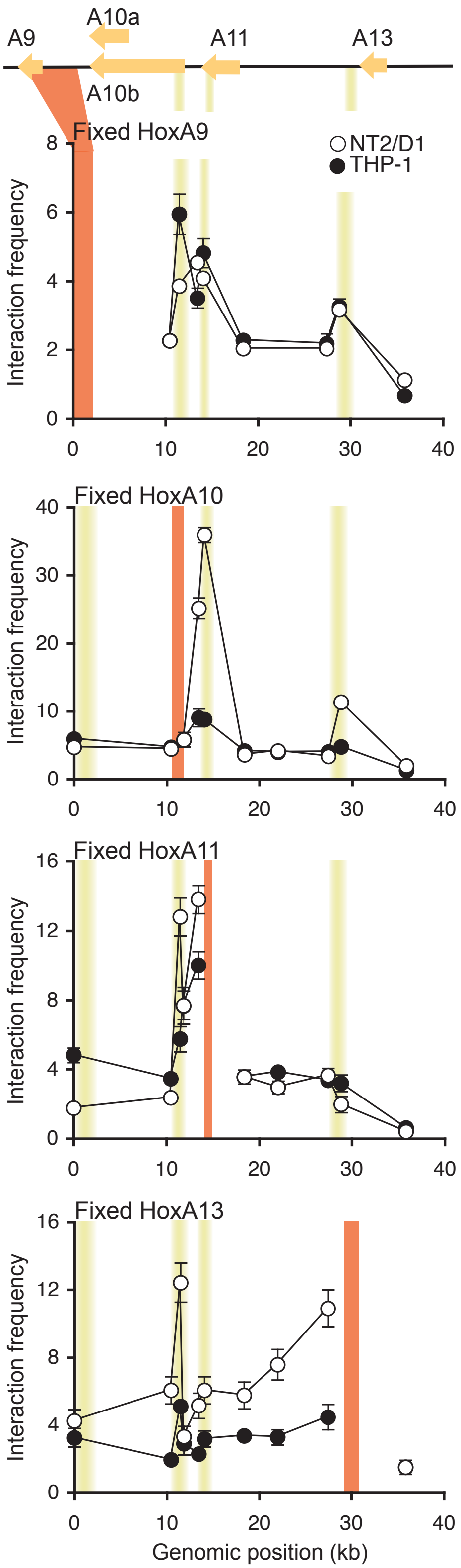
(**B**) Three-dimensional local base density scan of the transcriptionally silent *HoxD* cluster. Local base densities at consecutive ten base pairs was estimated in one hundred possible 5C3D outputs models with Microcosm 1.0 (*y-axis*) and represented graphically along the corresponding genomic region (ENCODE hg18 Chr2:176658690 to 176766146) (*x-axis*). The weight of the trace is proportional to the standard deviation with sharper areas indicating smaller deviations. A linear schematic representation of the *HoxD* cluster is shown to scale at the top of the graph and is as described in Figure 1. Shaded yellow vertical lines identify the position of CTCF binding sites mapped in various cell lines as illustrated in (**C**).

(**C**) CTCF binds to multiple discrete sites conserved in various cell lines at the 5'end of the *HoxD* cluster. CTCF binding was identified by ChIP-seq and ChIP-chip in different cell lines as described in MATERIALS AND METHODS. Binding sites conserved in most cell lines are numbered and highlighted by yellow vertical lines, which are contiguous with lines in panel (**B**).

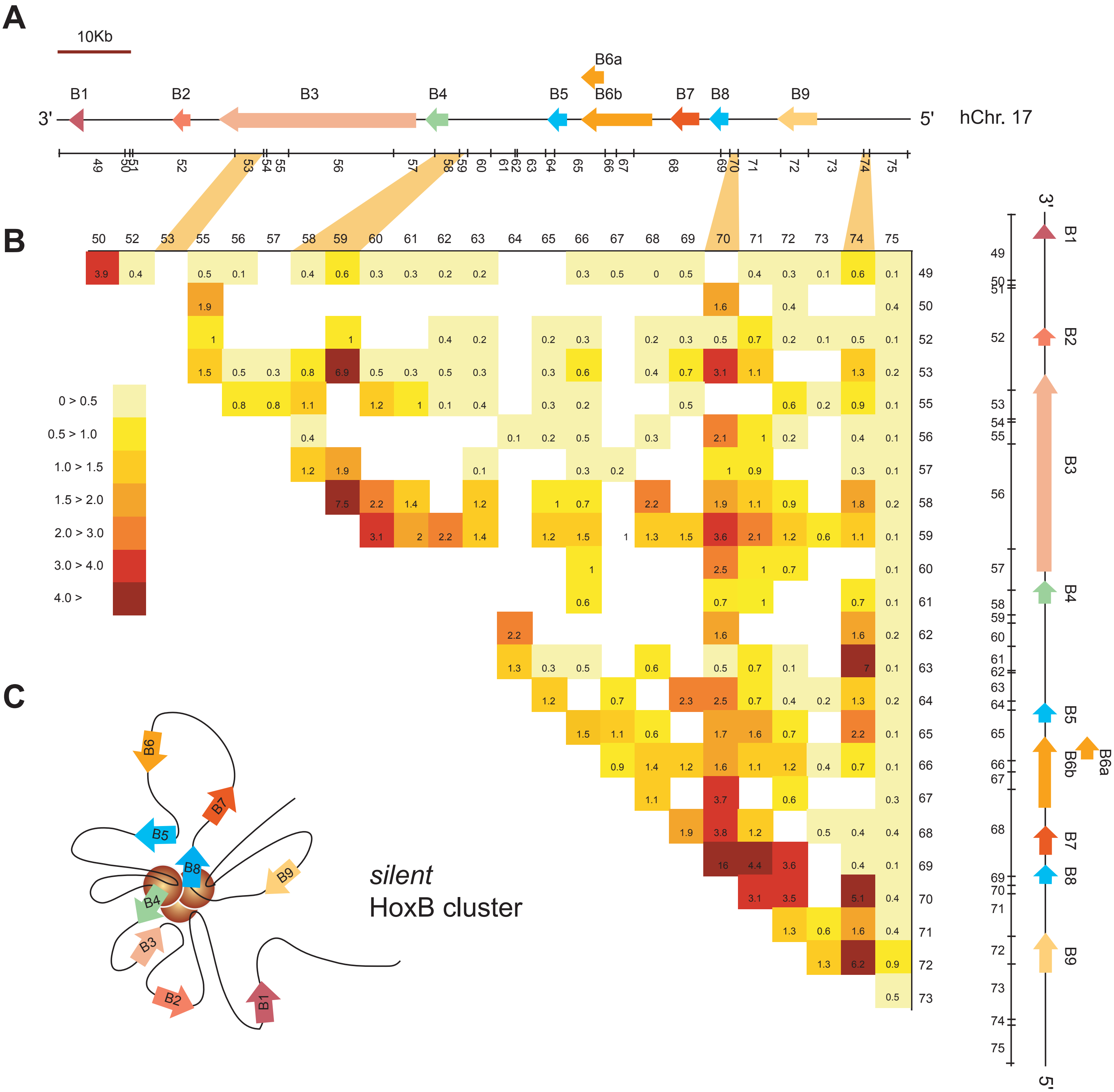
(**D**) Conserved CTCF binding sites in *HoxD* are clustered three-dimensionally. The position CTCF binding sites numbered in (**C**) are illustrated in the example 5C3D output model presented in (**A**). CTCF binding sites are represented by colored spheres as indicated in the legend below.

(**E**) CTCF binding sites are significantly close to each other in three-dimensional models. Distances between pairs of CTCF binding sites were measured in one hundred possible 5C3D outputs models with Microcosm 2.0. The significance of spatial proximity between pair-wise CTCF binding sites is expressed as p-values summarized in a heatmap. Numbers at the top and on the left of heatmap identify CTCF binding sites. Intersecting column and row number identifies the CTCF pair corresponding to p-value. p-values are color-coded based on the scale presented on the *right*, with white indicating low significance and red highly significant proximity. p-values represent the fraction of fragment pairs separated by the same linear genomic distance, which are closer or at the same distance to CTCF pairs in 5C3D output models (see MATERIALS AND METHODS for details).

Ferraiuolo et al. Supplementary Figure 1



Ferraiuolo et al. Supplementary Figure 2



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50				1.9															1.6		0.4			0.4
52				1				1			0.4	0.2		0.2	0.3		0.2	0.3	0.5	0.7	0.2	0.1	0.5	0.1
53				1.5	0.5	0.3	0.8	6.9	0.5	0.3	0.5	0.3		0.3	0.6		0.4	0.7	3.1	1.1			1.3	0.2
55					0.8	0.8	1.1		1.2	1	0.1	0.4		0.3	0.2			0.5			0.6	0.2	0.9	0.1
56							0.4						0.1	0.2	0.5		0.3		2.1	1	0.2		0.4	0.1
57							1.2	1.9				0.1			0.3	0.2			1	0.9			0.3	0.1
58								7.5	2.2	1.4		1.2		1	0.7		2.2		1.9	1.1	0.9		1.8	0.2
59									3.1	2	2.2	1.4		1.2	1.5	1	1.3	1.5	3.6	2.1	1.2	0.6	1.1	0.1
60															1				2.5	1	0.7			0.1
61															0.6				0.7	1			0.7	0.1
62													2.2						1.6				1.6	0.2
63													1.3	0.3	0.5		0.6		0.5	0.7	0.1		7	0.1
64														1.2		0.7		2.3	2.5	0.7	0.4	0.2	1.3	0.2
65															1.5	1.1	0.6		1.7	1.6	0.7		2.2	0.1
66																0.9	1.4	1.2	1.6	1.1	1.2	0.4	0.7	0.1
67																	1.1		3.7		0.6			0.3
68																		1.9	3.8	1.2		0.5	0.4	0.4
69																			16	4.4	3.6		0.4	0.1
70																				3.1	3.5		5.1	0.4
71																					1.3	0.6	1.6	0.4
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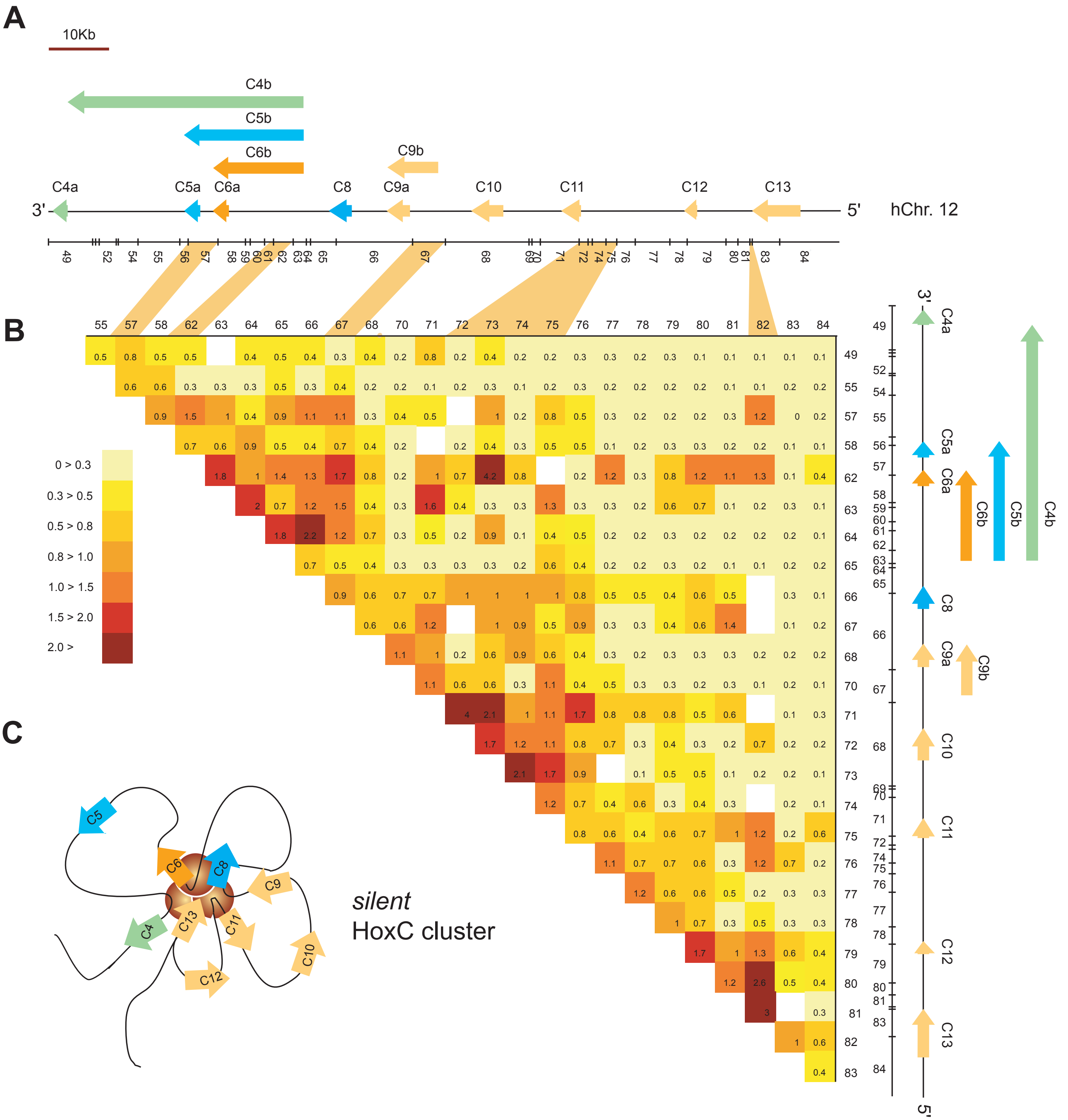
73																								0.5

Ferraiuolo et al. Supplementary Figure 3



	55	57	58	62	63	64	65	66	67	68	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84
49	0.5	0.8	0.5	0.5		0.4	0.5	0.4	0.3	0.4	0.2	0.8	0.2	0.4	0.2	0.2	0.3	0.3	0.2	0.3	0.1	0.1	0.1	0.1	0.1
55		0.6	0.6	0.3	0.3	0.3	0.5	0.3	0.4	0.2	0.2	0.1	0.2	0.3	0.1	0.2	0.3	0.2	0.2	0.2	0.2	0.1	0.1	0.2	0.2
57			0.9	1.5	1	0.4	0.9	1.1	1.1	0.3	0.4	0.5		1	0.2	0.8	0.5	0.3	0.2	0.2	0.2	0.3	1.2	0	0.2
58				0.7	0.6	0.9	0.5	0.4	0.7	0.4	0.2		0.2	0.4	0.3	0.5	0.5	0.1	0.2	0.3	0.3	0.2	0.2	0.1	0.1
62					1.8	1	1.4	1.3	1.7	0.8	0.2	1	0.7	4.2	0.8		0.2	1.2	0.3	0.8	1.2	1.1	1.3	0.1	0.4
63						2	0.7	1.2	1.5	0.4	0.3	1.6	0.4	0.3	0.3	1.3	0.3	0.3	0.2	0.6	0.7	0.1	0.2	0.3	0.1
64							1.8	2.2	1.2	0.7	0.3	0.5	0.2	0.9	0.1	0.4	0.5	0.2	0.2	0.3	0.2	0.2	0.2	0.2	0.1
65								0.7	0.5	0.4	0.3	0.3	0.3	0.3	0.2	0.6	0.4	0.2	0.2	0.3	0.2	0.1	0.1	0.2	0.2
66									0.9	0.6	0.7	0.7	1	1	1	1	0.8	0.5	0.5	0.4	0.6	0.5		0.3	0.1
67										0.6	0.6	1.2		1	0.9	0.5	0.9	0.3	0.3	0.4	0.6	1.4		0.1	0.2
68											1.1	1	0.2	0.6	0.9	0.6	0.4	0.3	0.2	0.3	0.3	0.3	0.2	0.2	0.2
70												1.1	0.6	0.6	0.3	1.1	0.4	0.5	0.3	0.3	0.2	0.3	0.1	0.2	0.1
71													4	2.1	1	1.1	1.7	0.8	0.8	0.8	0.5	0.6		0.1	0.3
72														1.7	1.2	1.1	0.8	0.7	0.3	0.4	0.3	0.2	0.7	0.2	0.2
73															2.1	1.7	0.9		0.1	0.5	0.5	0.1	0.2	0.2	0.1
74																1.2	0.7	0.4	0.6	0.3	0.4	0.3		0.2	0.1
75																	0.8	0.6	0.4	0.6	0.7	1	1.2	0.2	0.6
76																		1.1	0.7	0.7	0.6	0.3	1.2	0.7	0.2
77																			1.2	0.6	0.6	0.5	0.2	0.3	0.3
78																				1	0.7	0.3	0.5	0.3	0.3
79																					1.7	1	1.3	0.6	0.4
80																						1.2	2.6	0.5	0.4
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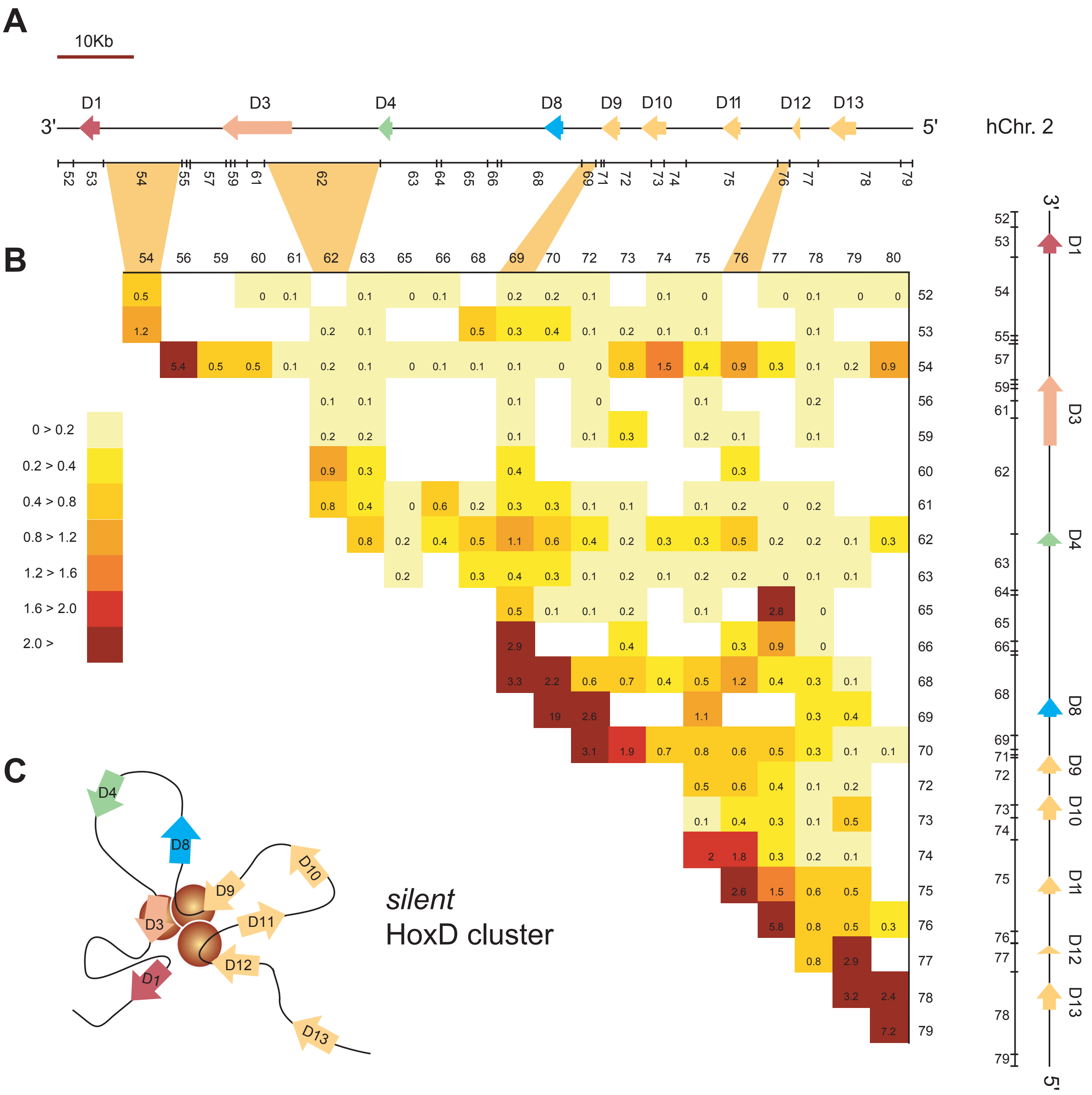
82																								1	0.6
83																									0.4

Ferraiuolo et al. Supplementary Figure 4



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2.0 >

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53	1.2					0.2	0.1			0.5	0.3	0.4	0.1	0.2	0.1	0.1			0.1		
54		5.4	0.5	0.5	0.1	0.2	0.1	0	0.1	0.1	0.1	0	0	0.8	1.5	0.4	0.9	0.3	0.1	0.2	0.9
56						0.1	0.1				0.1		0			0.1			0.2		
59						0.2	0.2				0.1		0.1	0.3		0.2	0.1		0.1		
60						0.9	0.3				0.4						0.3				
61						0.8	0.4	0	0.6	0.2	0.3	0.3	0.1	0.1		0.1	0.2	0	0.2		
62							0.8	0.2	0.4	0.5	1.1	0.6	0.4	0.2	0.3	0.3	0.5	0.2	0.2	0.1	0.3
63								0.2		0.3	0.4	0.3	0.1	0.2	0.1	0.2	0.2	0	0.1	0.1	
65											0.5	0.1	0.1	0.2		0.1		2.8	0		
66											2.9			0.4			0.3	0.9	0		
68											3.3	2.2	0.6	0.7	0.4	0.5	1.2	0.4	0.3	0.1	
69												19	2.6			1.1			0.3	0.4	
70													3.1	1.9	0.7	0.8	0.6	0.5	0.3	0.1	0.1
72																0.5	0.6	0.4	0.1	0.2	
73																0.1	0.4	0.3	0.1	0.5	
74																2	1.8	0.3	0.2	0.1	
75																	2.6	1.5	0.6	0.5	
76																		5.8	0.8	0.5	0.3
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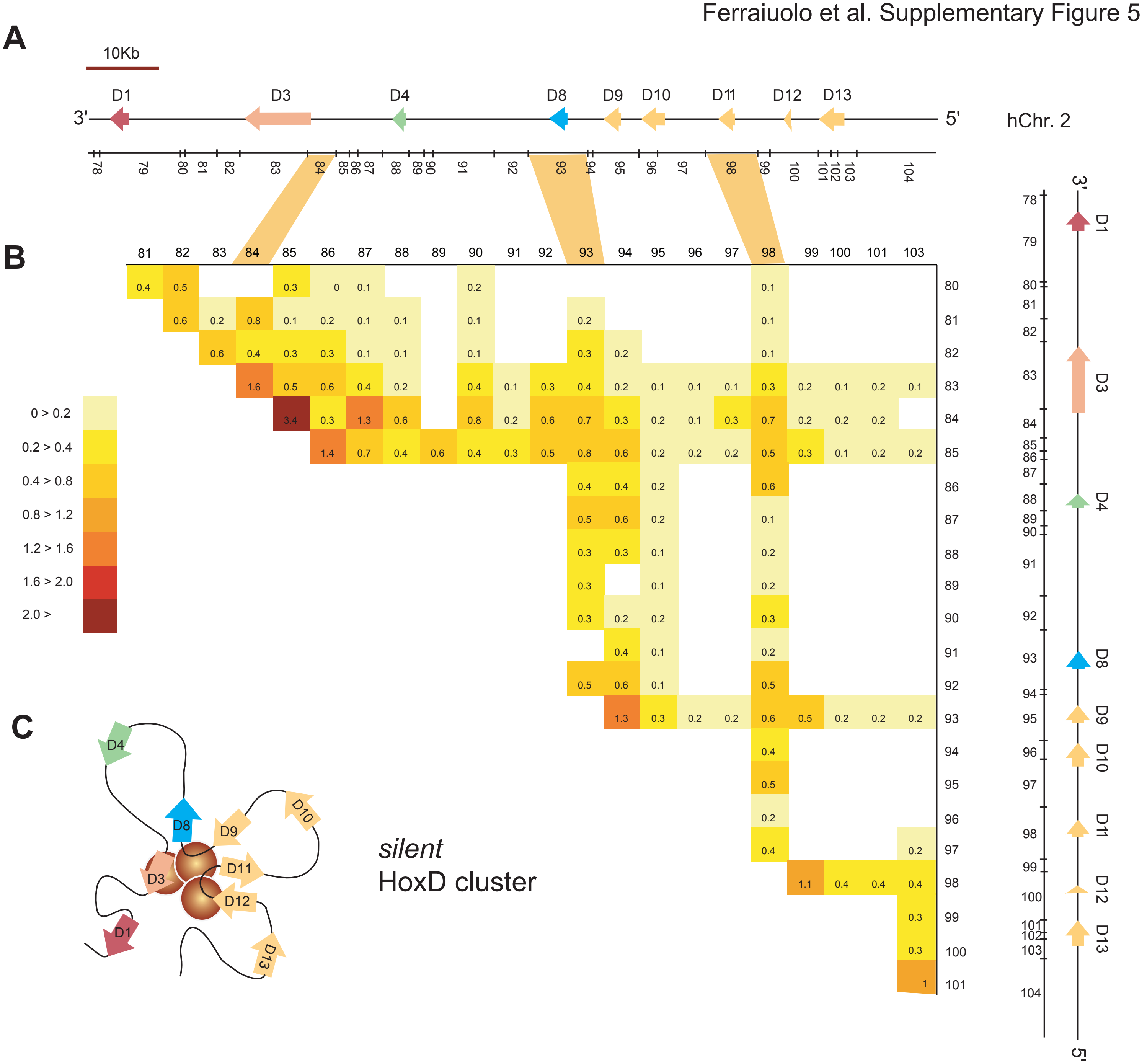
Ferraiuolo et al. Supplementary Figure 5



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2.0 >	🟫

	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	103
80	0.4	0.5			0.3	0	0.1			0.2								0.1				
81		0.6	0.2	0.8	0.1	0.2	0.1	0.1		0.1			0.2					0.1				
82			0.6	0.4	0.3	0.3	0.1	0.1		0.1			0.3	0.2				0.1				
83				1.6	0.5	0.6	0.4	0.2		0.4	0.1	0.3	0.4	0.2	0.1	0.1	0.1	0.3	0.2	0.1	0.2	0.1
84					3.4	0.3	1.3	0.6		0.8	0.2	0.6	0.7	0.3	0.2	0.1	0.3	0.7	0.2	0.2	0.2	
85						1.4	0.7	0.4	0.6	0.4	0.3	0.5	0.8	0.6	0.2	0.2	0.2	0.5	0.3	0.1	0.2	0.2
86													0.4	0.4	0.2			0.6				
87													0.5	0.6	0.2			0.1				
88													0.3	0.3	0.1			0.2				
89													0.3		0.1			0.2				
90													0.3	0.2	0.2			0.3				
91														0.4	0.1			0.2				
92													0.5	0.6	0.1			0.5				
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94																		0.4				
95																		0.5				
96																		0.2				
97																		0.4				0.2
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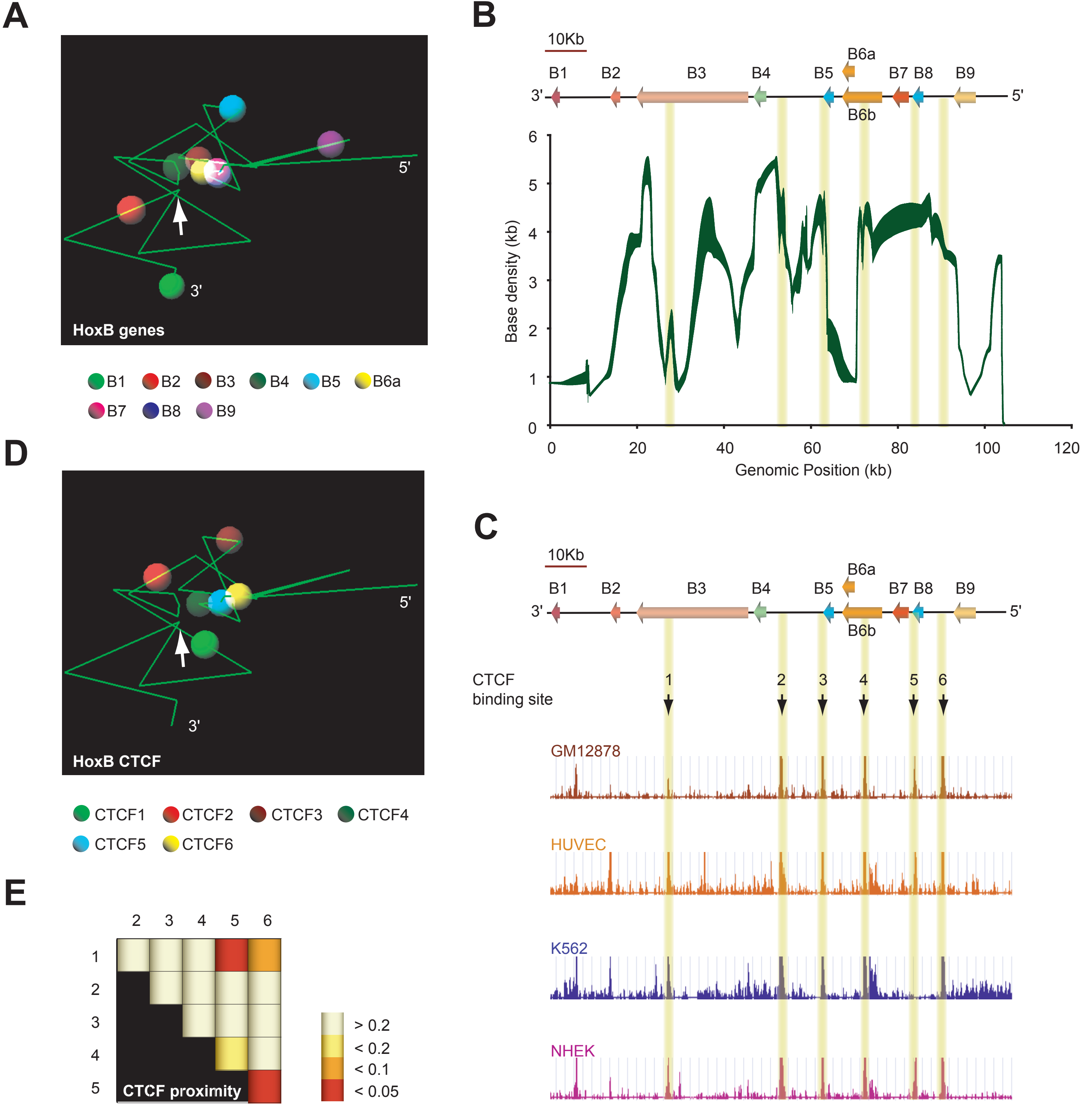
Ferraiuolo et al. Supplementary Figure 6



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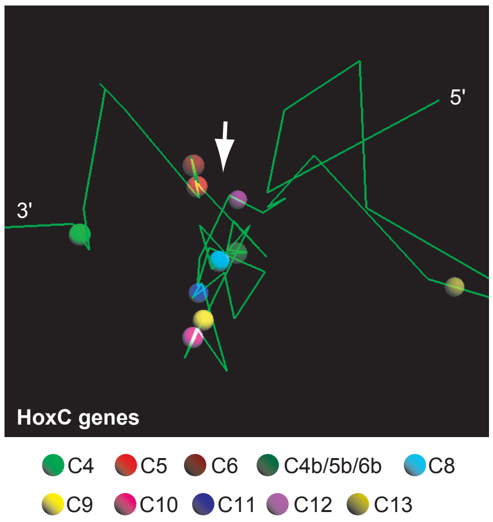
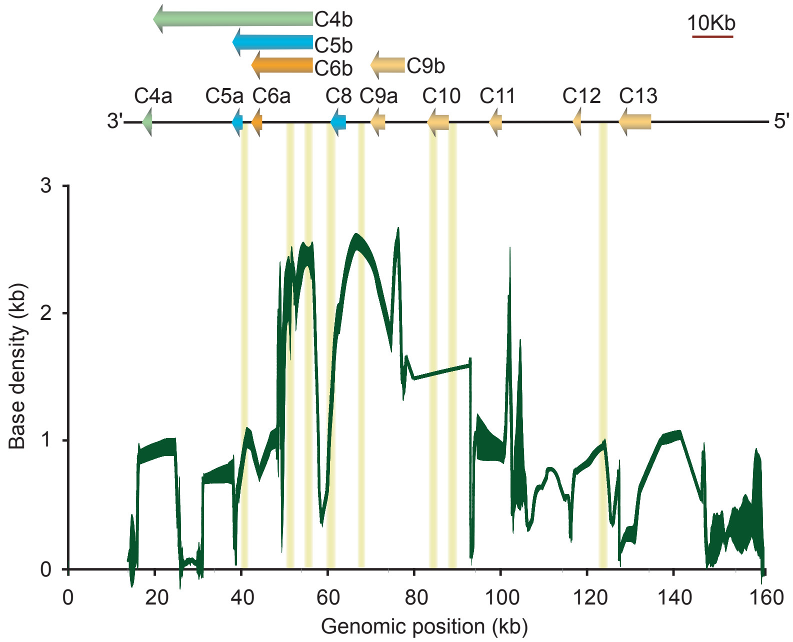

5'
3'
HoxC genes
C4
C5
C6
C4b/5b/6b
C8
C9
C10
C11
C12
C13

B


C4b
C5b
C6b
C9b
10Kb
C4a
C5a
C6a
C8
C9a
C10
C11
C12
C13
3'
5'
Base density (kb)
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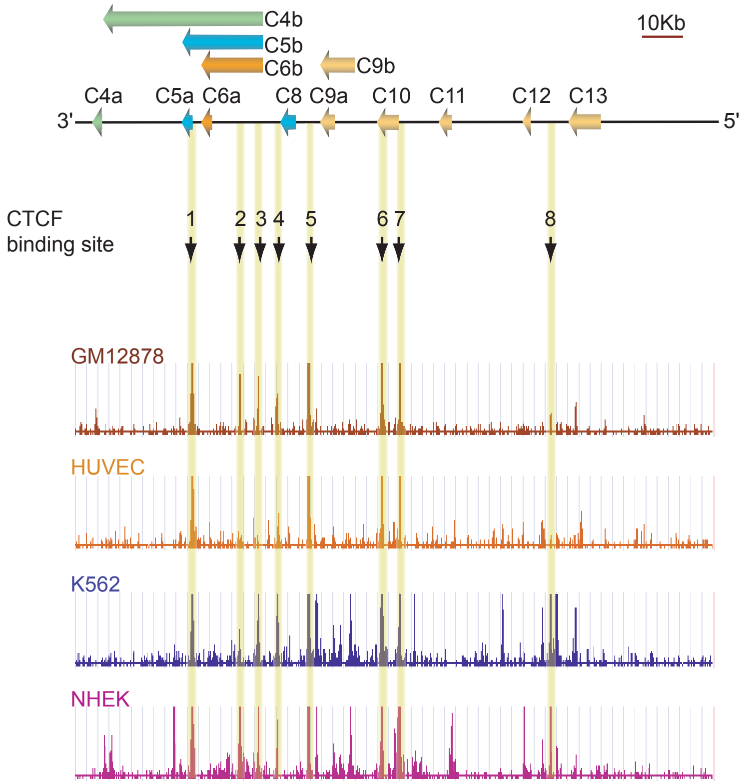
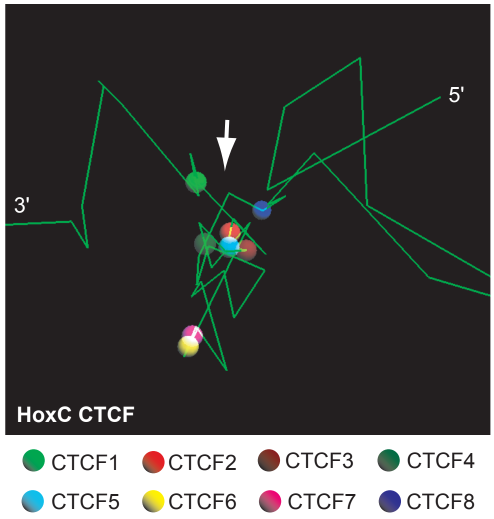
2
1
0
0
20
40
60
80
100
120
140
160
Genomic position (kb)

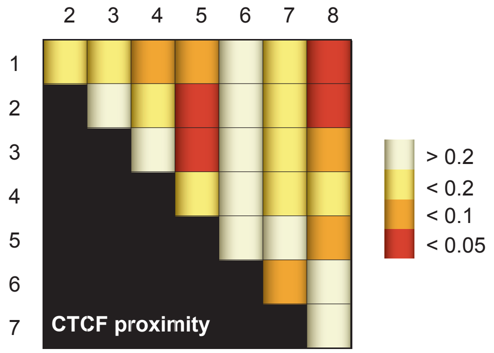
C


C4b
C5b
C6b
C9b
10Kb
C4a
C5a
C6a
C8
C9a
C10
C11
C12
C13
3'
5'
CTCF
binding site
1
2
3
4
5
6
7
8
GM12878
HUVEC
K562
NHEK

D


5'
3'
HoxC CTCF
CTCF1
CTCF2
CTCF3
CTCF4
CTCF5
CTCF6
CTCF7
CTCF8

E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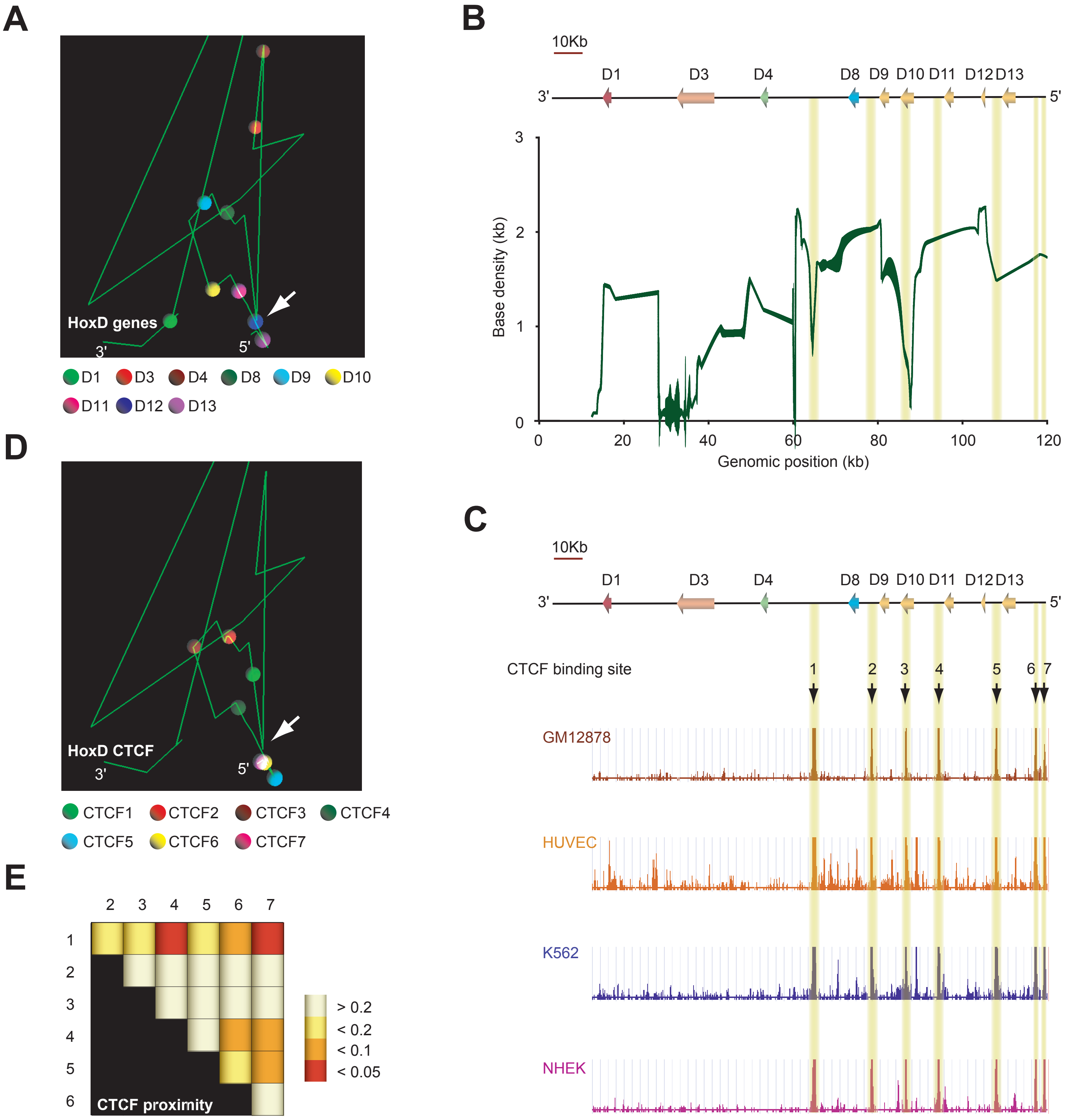

	2	3	4	5	6	7
1	🟨	🟨	🟥	🟨	🟧	🟥
2		⬜	⬜	⬜	⬜	⬜
3			⬜	⬜	⬜	⬜
4				⬜	🟧	🟧
5					🟨	🟧
6						⬜

Supplementary Table 1 Human 3C primer sequences for HoxA, HoxB, and HoxC analysis in BglII 3C libraries

Primer Name	Primer Sequence (5'-3')	BglII fragment position[a]	
		start	end
1. HoxA cluster (Chr. 7)			
HoxA BglF47	CAAAGTACCCAAACTGCTCTACCACTGG	27079118	27085686
HoxA BglF48	GAGTCATGAACCACATTAGAATAGCTGAGAGG	27085687	27086789
HoxA BglF49	CAACAGCAACTGACTATGGGTGTTTTAATTGG	27086790	27090631
HoxA BglF50	GCTTGGGCAGGGCAATTATAAAGCTTGC	27090632	27092571
HoxA BglF51	CGAAGAGCTGGACTTCTCTGAGGATTCC	27092572	27100768
HoxA BglF52	GACAGTGCTAGAGGGTTCAAAAGATAACACC	27100769	27110440
HoxA BglF53	CGAATGCATAGAGTTCAGATAGCCACCG	27110441	27114681
HoxA BglF55	CAACCCAGCCCCCAAAGTTTGCAACCTAG	27115729	27119306
HoxA BglF58	CATTAATGACTTGGGGTGGGATGGGTGA	27121876	27126958
HoxA BglF59	CAGAACATTACCAACTGTCTGCGCATCCG	27126959	27130638
HoxA BglF60	GGTTTTTGTGGTCTTATTGTAGGGAACTCCC	27130639	27133878
HoxA BglF61	CCAGCACAGACTCTTAACCGGATAATGTC	27133879	27135357
HoxA BglF62	GTGTGGGCTCTGAGTTTGTGCTTTCCCTG	27135358	27135550
HoxA BglF63	CATGGCACCAGTAAGCATTTTGTCACTGG	27135551	27141654
HoxA BglF64	CTAAACGAGATTGAAGGGGGACTTTTTGTGTG	27141655	27147801
HoxABglF64b	GAGTGCAACACACAACATTGGCACTAAACG		
HoxA BglF64REV	CCTTTATTTGAAAAGAGGGATTCTGATTGGC		
HoxA BglF65	GCGTGGATTTAGAAAAAGGCTGGCTTTACC	27147802	27149225
HoxA BglF66	CGCTGGGCTGCGTGGAATTGATGAGCTTG	27149226	27151902
HoxA BglF67	GTTTGTTGGGCTTGTAAAACCCCTTGAATTAGC	27151903	27155489
HoxA BglF68	GGAAACATCAGGGCGTACATATTTAACACAGC	27155490	27160284
HoxA BglF69	GCAGTCGGACCTTCGTCCTTATGCTCTTTC	27160285	27161219
HoxA BglF70	CCCAAATGGCATCACTCGTCTTTTGCTCGG	27161220	27169811
HoxA BglF71	CAGTCAAGCTTTGCCCTAGCCAGTCTCC	27169812	27174699
HoxA BglF72	GATGACAACCCCAATGGAGTGATTGCTCCG	27174700	27185151
HoxA BglF73	GCTTTGACATTGATCGGAAGTGCGCCATC	27185152	27186177
HoxA BglF74	GACTCTCTCTAGCAACTTGAGAGACTTTGG	27186178	27186535
HoxA BglF75	CAGAAGCTTCCAAGCTCAGTTCAAGAGCC	27186536	27188136
HoxA BglF76	CACCAGGGGTCCCAAACCTGTCATTCTAG	27188137	27188771
HoxA BglF77	CTTGGAAGGATCTGGGATGTTGCTGAAGG	27188772	27193079
HoxA BglF78	CAGAGCTCTTCTCCATTACAGGAATATCTCC	27193080	27196708
HoxA BglF79	CAATAGCTCTAATTACAGTGTGAGACCACCC	27196709	27202119
HoxA BglF80	GTGCACAAATACATTTTCACAGTGTGCTGAATGTC	27202120	27203509
HoxA BglF80-2	CCAGCAAATGTTTAGCAAATATTGGGAAATGCC		
HoxA BglF81	GTTGACGTTTGACATTTAACGGGCTGGGC	27203510	27204194
HoxA BglF82	GAGCAGATCATTTGGGAAAGGAGCAAGTGG	27204195	27210535
HoxA BglF87	CTTGTGTGGGATCCAGGGTGCATTTTCTG	27216438	27220562
HoxA BglF88	CAAGTTAATGCCCCATATGCCCCCATAATCC	27220563	27230964
HoxA BglF93	GCAGTTCCAGAGCAGTTTCTAACCTGCTG	27236536	27240602
HoxA BglF94	CTAAGACTGGCCAGTCAGCTTTGAAAGAGC	27240603	27246456
HoxA BglF95	GGAAACAGGAATCATCGCTTGGGTCTTGG	27246457	27267169
2. HoxB cluster (Chr. 17)			
HoxB BglF49	CTTGGAAACTGTCCATCCTAGAGGTGACC	43960763	43969183
HoxB BglF50	GGAGAGAGAGAAAGTTTTAAGAGGGCTCC	43969184	43969745
HoxB BglF52	GGTCATGGAGTGTAAGGCGTTCATGAAGC	43969947	43983290
HoxB BglF53	CAGCAAGTTTTGGGAGCTGGAGGTAACC	43983291	43987251
HoxB BglF55	GGGTGGGAGCTATTTTTCTGTGTTTATTAGC	43987305	43990264
HoxB BglF56	GAGGGAAAGAAGTCAAAAGGTTGGGAGG	43990265	44003885
HoxB BglF57	GGATCTTGGTGTTGGGCAACTTGTGGTC	44003886	44009216
HoxB BglF58	GCGGAGTGTTTATGTCAACTACATATTCCCC	44009217	44012306
HoxB BglF59	CTCAACTCCCTAGGTCTGAGAAATACTTGC	44012307	44013496
HoxB BglF60	GAGTCTCTCTAGGCATTTGCTCATGAGC	44013497	44016543
HoxB BglF61	CCTCAGAGTCCCTTAGGGAGAAATATCC	44016544	44019680
HoxB BglF62	GAGCTCATTCTTGCTAGCCCTGTCTTCC	44019681	44019964
HoxB BglF63	CTAGTGGAAGACCAGGATGAAGTCTAGC	44019965	44023541
HoxB BglF64	GCCAGGCTCATACTTTTCAATTTGTTGTCC	44023542	44024661
HoxB BglF65	GGTGAGAAGAGTTCTCCGCTAAGATAAGC	44024662	44031190
HoxB BglF66	CTAGAGAGGACTAGGGGCCATTTGAACAGG	44031191	44032711
HoxB BglF67	CCTTTTTATATATGCCCTAGAGGAAGCCGC	44032712	44034978
HoxB BglF68	GACACAAGTGAATCTAAGGGAGCCAGAAAGG	44034979	44046148
HoxB BglF69	GAGAGAGAGAAAAAAACGCGGATTCGCCG	44046149	44047255
HoxB BglF70	GGTGACGAAGCCGAAATGAGAATGATTATGG	44047256	44048594
HoxB BglF71	GAGTAAGCTTCCATCTGATGCTTAGGTGC	44048595	44053925
HoxB BglF72	CAGAAAAGGAAGCGGTAGCCCCTGCGAGG	44053926	44057561
HoxB BglF73	CTCTGGAAAGTTCTGGATGTAGTTGAGAGC	44057562	44064710
HoxB BglF74	GCCTCTTTGATATACCTGCTCAGTCTCTGC	44064711	44065376
HoxB BglF75	GCATTTGGGTCTTGGAATTAGCCAGTTAATTGCC*	44065377	44070696
HoxB BglF77	GGGTTTGGAGTGTAAGTATGTATGGAGGG	44070752	44072427
HoxB BglF78	CTCTGGACTGCTGGGACTCTAAGCTAGG	44072428	44075054
HoxB BglF80	GGTCTTTCAGTTTTCTGGCTAAATCTGGC	44075093	44076323
HoxB BglF81	GGGTTTGTGGTAATCTTGCAATGAGGTTTTTTGC	44076324	44082501
HoxB BglF83	GGTCAGGATTTCTTTCATTTCAACTAACTGTTGG	44085694	44087225
HoxB BglF84	GGAGGGAGGCAGTAATTTTAGTAGTATAGAAGC	44087226	44091634
HoxB BglF85	CAGGGTTAGGGGCCACTTTCATGACAGC	44091635	44094179
HoxB BglF86	CTTGAGGGAATCTCTAATGGTCTATGAGGC	44094180	44099475
HoxB BglF87	CTGGCACGATGACCACAGACCATTAAGG	44099476	44104697
HoxB BglF88	GAGTGTCAAGGCCCTATCAAAGTTAAAAG	44104698	44106165
HoxB BglF94	GATTAGGTAGGCCTGTGAGGCAAAATGAAGG	44114099	44117257
HoxB BglF96	CTCTTGAGACTTCCCTTTTTCGTCCATGG	44119800	44129710
3. HoxC cluster (Chr. 12)			
HoxC BglF48	CAAGTAACAACCAGCAAGTGGTTCAAAAGG	52737153	52739739
HoxC BglF49	GTTAGACAGAGTGACCTGCATTTCACCTCG	52729290	52737152
HoxC BglF50	GATGTGTGGATGCAGGAACCTTGCTGTGC	52728908	52729289
HoxC BglF52	GAGACAGAATTACTTGCTTTAATAAGCC	52725707	52728280
HoxC BglF54	GAGAACGACAGTCAAAAAGAGAAAGTTTACC	52722453	52725608
HoxC BglF55	CTCTAGAGGCCCTTATGAGACCAAATGG	52715790	52722452
HoxC BglF56	GAGGAAAGGCGAAAAGGAAAGGCGCAGG	52714476	52715789
HoxC BglF57	CGCGTTAGGTAGCGATTGAAGTGAAATTCC	52709745	52714475
HoxC BglF58	GTTAAGTGTTTTATGACGTCCCTAAACAGAGGG	52705529	52709744
HoxC BglF59	GACTGGACCCAGCCTGAAGAAGTTCGTGG	52704593	52705528
HoxC BglF60	GTTATACATGGCAGGAGTTTTGTGTGTGGG	52702611	52704592
HoxC BglF61	GAAAGGAGGCCCATCAATTCTCAGCCTTGG	52701334	52702610
HoxC BglF62	CAATGGGCACAGCCTCTAAGTTCTCTCTC	52697799	52701333
HoxC BglF63	GAGGTGAGAATTGGGGTCAACTTCTAGGACC	52696062	52697798
HoxC BglF64	CTTTCCCAGCCAGCAGGCAGTCATTAGG	52695263	52696061
HoxC BglF65	GCTACCATAAAACGAAACTTCAAGGGAGTTGC	52691287	52695262
HoxC BglF66	GGGGTAGAACCTCAGGATCTCATACACC	52679298	52691286
HoxC BglF67	CTGCCGCCGTCTTCTTCACCTGTTCTC	52674120	52679297
HoxC BglF68	CTTGCACACAGATGCTACGGAGTTCAGC	52661098	52674119
HoxC BglF69	GCTTCTAAGTTGCCCCCAGTAAGTCAGG	52660795	52661097
HoxC BglF70	GGGAAGGTCTTGTCATGCTGATATTGTCC	52659517	52660794
HoxC BglF71	CATAGCAGGAGGAGTAGCTGTTCCGATGG	52653468	52659516
HoxC BglF72	GAAGAGACTAACCAGACAGTGGAAAGGAGC	52651995	52653467
HoxC BglF73	GCTCAGCATTTAAGTGACACCTGAGTGG	52651310	52651994
HoxC BglF74	GATGCTAGCAACCCGACCCTATTTCTTCC	52649156	52651309
HoxC BglF75	CACCGAACTCTAGATACTGCCAAAGAGAGC	52647540	52649155
HoxC BglF76	GAAGTGCAGGGGACAGAATTCCAAATGG	52644510	52647539
HoxC BglF77	CTGGTTTCAACCTCCTTTAGGCTGTCCAC	52639188	52644509
HoxC BglF78	CAAAACAGACAAGAGGATATCCAGGGAGG	52636547	52639187
HoxC BglF79	CAGTGAATCGTCTCCACCGACCTCTAAGC	52630388	52636546
HoxC BglF80	CCTTTTTAGGCTTACCAGTGTCCCAATGC	52628427	52630387
HoxC BglF81	CCAGTCCTGAACTGGCTGAAGGTATTCG	52626916	52628426
HoxC BglF82	GAACACTGTTTTGTAATGCACCAGTGGG	52626325	52626915
HoxC BglF83	CAGACTACCACAGATGAGGATTCTCAGAGC	52621925	52626324
HoxC BglF84	GGAGAGTACTCTTTCTCCATGTCGAAAGG	52608656	52621924
HoxC BglF85	CCAAAAGCCATTTTTCAAGAGGCGCAGG	52607711	52608655
HoxC BglF86	GAATTGTAGAGATAAGCCAACTAGATCAGGGC	52605458	52607710
HoxC BglF87	GATGCAGTTATCTGTCATCAGCTGTACAGC	52603135	52605457
HoxC BglF88	CTAAAGTTTCTTCTAGCTATAGTCTTAGG	52602340	52603134
HoxC BglF89	CACTGTACTACAAACTGGGTAACAGAGC	52597569	52602339
HoxC BglF90	CCTCTTTATCAAGCCACCCAGGAATTGC	52594432	52597568
HoxC BglF91	GCAATAAACCCTTAACCAGTCTTCTTGC	52593460	52594431
HoxC BglF92	GTTGAAGATGTGCATACCCCATCATCTGCC	52585275	52593459
4. Gene desert (Encode region ENr313 Chr. 16)			
GD BglF34	GTGATGTTAAATGAAGGATTGGCAAACAGGAG	60835052	60838561
GD BglF35	GGGGTACGCCTGATAGGAATATTACAAGG	60838562	60841364
GD BglF36	CAGGCTTTATTTCCATTCCTCTAATTGAGTTCCC	60841365	60843243
GD BglF37	GTATGACACAGAGAAAATGTGGTGCATTCACC	60843244	60846741
GD BglF39	GCTGTGCATACCCTAAAGATTTGGTAAAGCC	60847305	60847852
GD BglF40	GCACATCACCTACAACCAACAAACAGGAAAC	60847853	60849318
GD BglF41	CTCTCTCTCTCACATACAAGATGGGCAGC	60849319	60851533
GD BglF42	CAACCTGCTCCTCAGTAGTGACTTTTGGG	60851534	60857366
GD BglF43	CATCCAAATGAAGCACCAATTCAGGAATGCAATC	60857367	60858960
GD BglF45	CCAATTCCATTTAACAATGAGCATGCACTGAGC	60859657	60861091
GD BglF46	GTCTACAAATATGTATCTCCCTTTCAAGTCCAC	60861092	60861612
GD BglF47	CAGTGTCTTTCAGATTCTATCCTAGTCTTACTGG	60861613	60863515
GD BglF48	CATGAGTACACAAAAATGGCTGCTTGATGCC	60863516	60866664
GD BglF49	CTTCTTGTTGAACTGTAATTATAACAGAGCCACC	60866665	60868158
GD BglF50	CAGGAGGCCGAGTTATGCTACCCATTTGG	60868159	60869137
GD BglF51	CACCATATCTGGCCACTATAATAGATTTCTGACTC	60869138	60874749
GD BglF52	GATGAGAGAAAGGTGGTTCTATGAGAACATATGC	60874750	60878548
GD BglF53	CTTTGTGGAACAGCCATTGGCAAAAGTCC	60878549	60883452
GD BglF54	CATCGGGTAGGAATACCTCCCATACTACC	60883453	60887859
GD BglF55	CAGTCAAACTTAGATACGCAGAGGCAAGG	60887860	60899665
GD BglF57	GCACACCTGTTTCAGACTAGGCTCCTCC	60901176	60903390
GD BglF58	CATCTCACTGCCATAAAGCACTTCAGAATGG	60903391	60908428

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[a] corresponds to position in human genome sequence version 18.

Supplementary Table 2 Human 3C primer sequences for HoxD analysis in BglII and HindIII 3C libraries

1. HoxD cluster (Chr. 2)

Primer Name	Primer Sequence (5'-3')	BglII fragment position[a]	
		start	end
HoxD BglF47	CACATAGGTCATACATGAGGTATGCTTGG	176786769	176794243
HoxD BglF48	CAATGTAACTAATAATCCCTGCCTCACCAGG	176784080	176786768
HoxD BglF49	CTTTAAAGTCTCCCTCCATACCTCAGTCC	176777979	176784079
HoxD BglF50	GACAGAACGGAGCATTCACTTCAGAATCC	176768993	176777978
HoxD BglF51	GTATTCATCCTTGTAACAGATCACTGGAGGG	176766147	176768992
HoxD BglF52	CTTTTTGATGTGCAGCTGCCTTTCTCAGG	176764529	176766146
HoxD BglF53	GTGGAACACTCCTTATGCTCCTTTCTGG	176760706	176764528
HoxD BglF54	CAGGTAAAAACACTGCCTGTACCAGAGC	176750510	176760705
HoxD BglF56	GCAGAAAGTGCAGAGGACTTATGTACCC	176749897	176750467
HoxD BglF57	TGATTTATGGCGAGTCACCCAAAGGACG	176745185	176749896
HoxD BglF59	CTGGTAAGGCCTCCCTCTGTCAAAGAAGG	176743976	176744667
HoxD BglF60	CATATGACCTCCAAGGTTGCATTTCCAGC	176742567	176743975
HoxD BglF61	GACTTGCAGACTTCCAGACTCATTTTGAGG	176740374	176742566
HoxD BglF62	CTTCTATAAGGTCGTCAGGTCCGTGTGG	176725747	176740373
HoxD BglF63	GAGGAAGGTCAAAAGCCACTTCTTATTTGC	176718675	176725746
HoxD BglF64	GTTGCCACCAAACAGTGTAAAAACGTGTGG	176717939	176718674
HoxD BglF65	GGTGAAATACTGTCTTTGTTCGATTTCCCTTGC	176712037	176717938
HoxD BglF66	GTTTCAGTTCAGCAGTTTTGAAGTTGAGG	176710807	176712036
HoxD BglF68	GGCATCTTGTAGAACTGTGTGATTCCTCG	176700459	176710731
HoxD BglF69	CCTCGGCTCTTCCTGTTTTCAAAGAGCC	176698663	176700458
HoxD BglF70	CAGAGTTCGTGGAGGACCTTGAACCAGG	176698025	176698662
HoxD BglF71	CATTTACAACTGGTCCTCGGGCAGGAACC	176697695	176698024
HoxD BglF72	GATGCCACATTACTTAAATGACATGATGGCAGG	176691586	176697694
HoxD BglF73	GAGTTTGTTGCGCTTATCAGAATACATGCAGC	176690066	176691585
HoxD BglF74	GGGTTTAAACATTACCTTTCCACAGGGGTGG	176687205	176690065
HoxD BglF75	CTCAAATCTTTACAGACCCCGAATACCAGC	176675684	176687204
HoxD BglF76	CCAGCTGGAAATAGGCCAGCCTATTTCG	176674316	176675683
HoxD BglF77	GGATTTGGCTGAGGAGCGAATAGAGAGC	176670609	176674315
HoxD BglF78	GTTTGGGTATTTCATCAAAAAGCATCAACAGGGAG	176660295	176670608
HoxD BglF79	GCCGAGGGGAACAGAAGATAAACTTTTGGC	176658691	176660294
HoxD BglF80	CTGCTATCAAATCGTCCAGCCTAGTTCG	176657859	176658690

Primer Name	Primer Sequence (5'-3')	HindIII fragment position[a]	
		start	end
HoxD Hind76	CACTAACTTGAACCATTCCACATCCTGGG	176767257	176769904
HoxD Hind77	CAGAGGTCACCTAGTTCATCCCGATCTCC	176765801	176767256
HoxD Hind79	GTATACACCTGCCACAATTCATTTAGCC	176754265	176765654
HoxD Hind80	CTCTATACTACACCATTCCACACAGGGC	176753783	176754264
HoxD Hind81	CAAGAACTCCCAGATGAAGAGGACCTTCC	176749498	176753782
HoxD Hind82	GCCCATTTTGTATAAGAAACAGGAGTAAACAAGG	176746547	176749497
HoxD Hind83	GAGCAACGATTCTCCCTTTCCTGTTGGC	176737444	176746546
HoxD Hind84	GTGGTCGTTTCTGGATTTGGAGAGAGCC	176733563	176737443
HoxD Hind85	GTCTCGCACCCTTTCAGGAATTACTTACG	176731864	176733562
HoxD Hind86	CGGTTTTTTACAACTCCTGTTGTCTTGGAGC	176730585	176731863
HoxD Hind87	GAACAAGCCTACAGAGAAACTCTTTTTTCCC	176727467	176730584
HoxD Hind88	GAGTAACCGCCATGCTTTCTACCAGTGC	176723799	176727466
HoxD Hind89	CGACTTGTTCAGACAGGTCAAAGCCAACG	176721871	176723798
HoxD Hind90	GCTAATTAGCAAGCTCTTAACAGAAGTGAGCG	176720831	176721870
HoxD Hind91	GAGCTTGGGAACCTCATCTCAAGAAGCAGG	176712617	176720830
HoxD Hind92	CTAACTTTGCTGGAGGGAACCGCAGCAGC	176707878	176712616
HoxD Hind93	CTGTGACTGTCAACAAGTCAAGAGCAGC	176699966	176707877
HoxD Hind94	CCAGAGGAACCAGACACTTTGGCAACC	176699633	176699965
HoxD Hind95	GCCAGAAATCACCAAGATGCCACTGAAAGC	176693282	176699632
HoxD Hind96	CATGATCATTGGGCTCAAGGCAAAACTGG	176690783	176693281
HoxD Hind97	CCTATTAGAATCCAGTGTTGGACAGACAAGG	176684300	176690782
HoxD Hind98	GACACTGTCTGGCAGCTCTCGTAAAAGC	176677295	176684299
HoxD Hind99	GTAAACCTGCTGGTATCAAGGATTTAGCAGG	176675771	176677294
HoxD Hind100	GCAAAAAGGCCTCAAACAGAAAATTCTAGTGCC	176669406	176675770
HoxD Hind101	CTGGGATATTCGGAGCACCTAGCTGAGG	176667195	176669405
HoxD Hind103	CTGCCTTAGGAACAATATTAGATCCAATGAGC	176664233	176667023
HoxD Hind104	GAGTAATGCAGGGTGACAGCTGCTGCAGG	176648489	176664232

2. Gene desert (Encode region ENr313 Chr. 16)

GD Hind F28	GATACTTATACCCTGAGGCTAGAGACAGGC	60825408	60839352
GD Hind F29	GGTCTGAGGATTACTACCTGTGGAAAGC	60839353	60841760
GD Hind F30	CAATAGGACTCAATTGCTTTAAGTTCCTGG	60841761	60847237
GD Hind F31	GTATAACAAACCTCCATGGAACATGTTACC	60847238	60854675
GD Hind F33	GAAATGACCAAGAAGACATTACTATTGACCC	60854745	60857748
GD Hind F34	CTAGGGTATACAAAATGAGATGAGAGAGGG	60857749	60863902
GD Hind F35	CAGGATGTTTGGCAACACTGTTGTGTGAGG	60863903	60864738
GD Hind F36	CAAAATGCCATGTATTGAGAAGCAGCTAAGG	60864739	60869243
GD Hind F37	GGAAGTGAGTCTAAATCTGTCCTGTGGAC	60869244	60871568
GD Hind F38	CAGAGTAAGAAGACAACTCCATCTGCCACG	60871569	60876856
GD Hind F39	CATGGATTTACTTTGAGTATGCACCAGCC	60876857	60879766
GD Hind F40	GCTGCAATTTCTCTAATTTCCATACCACC	60879767	60880485
GD Hind F41	GGCTCTAGGAAAACACACATGCAGAAGC	60880486	60881926
GD Hind F42	GCTATTCATGGGGAAAGGGTAACTGAGG	60881927	60884454
GD Hind F43	GTACAGGCTTTTAATTCAGACAGACCCG	60884455	60889381
GD Hind F44	GCTTTCATATTTATCTTCTTCCAACCTACCACC	60889382	60892213
GD Hind F45	GCCAATCACCATTCTATATATTGCATTGGTGG	60892214	60892916
GD Hind F46	CAAAAGCCTGTGGGAGCTGACTATTTACTGG	60892917	60894162
GD Hind F47	CTTTCCAGGACATCAATTCCTTGATGCTACC	60894163	60895710
GD Hind F48	CTTTTAGTGAGTGCTACTGCAGAACACTTCCC	60895711	60904905
GD Hind F49	CTGCAACTGTCTGTGTCACATTGTGGCC	60904906	60905984
GD Hind F50	CAGAAGCAGTGTTGAGTAATTCAGAGGTTCC	60905985	60907740
GD Hind F51	CCTTCCTCTATGCCCACGGTAGAATTCC	60907741	60908483

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[a] corresponds to position in human genome sequence version 18.

Supplementary Table 3 3C datasets of transcriptionally silent human Hox clusters

Fragment 1	Fragment 2	Average IF	s.e.m.	no contacts
1. HoxA cluster (hChr. 7) BglII 3C library				
47	51	0.414194445	0	1
47	73	0.322412505	0.046490454	4
48	51	0.482283377	0.065933482	4
48	52	0.402829519	0	2
48	53	0.270229157	0.012441755	3
49	51	0.435287278	0.019700641	9
49	53	0.345776014	0.018578581	6
50	51	1.033674	0.045216309	6
50	52	0.408951441	0.032247265	9
50	61	0.563337406	0.009093233	4
50	73	0.242977425	0	2
51	52	0.508432889	0.014494916	15
51	53	0.350714829	0.026353801	4
51	55	0.499060169	0.03200887	9
51	58	0.547624209	0.025439577	4
51	61	0.348828064	0.022713966	8
51	63	0.487562296	0.009754516	6
51	65	0.499858403	0.018636574	9
51	66	0.256831633	0	2
51	68	0.289501383	0.025371782	6
51	71	0.41029731	0.033620065	6
51	73	0.542177454	0.027344585	12
51	76	0.420373683	0.013567676	6
52	53	1.038519978	0.053390628	13
52	55	0.69389344	0.020397082	9
52	58	0.775872533	0.029673209	6
52	59	0.52346826	0.019732379	6
52	61	0.724593987	0.074806142	13
52	62	0.314587093	0.027666771	4
52	63	0.64342892	0	2
52	64	0.697230857	0.036087796	6
52	65	0.640347287	0.038656013	9
52	66	0.338518941	0.024424181	6
52	67	0.337769366	0.021397269	6
52	68	0.494818316	0.043878939	4
52	69	0.763626681	0.076160005	9
52	70	0.66029296	0.004580538	3
52	71	0.720223959	0.036186498	6
52	72	0.829160023	0.012924961	4
52	73	1.084580535	0.042895478	15
52	74	0.235675703	0	2
52	75	0.529297544	0.049946141	9
52	76	0.825180961	0.033929037	4
52	78	0.463784789	0.019153342	9
52	79	0.58038402	0.072952465	6
52	80	0.531771375	0.020988545	9
52	81	0.663207012	0.005313093	4
52	82	0.445118597	0	1
52	87	0.310519631	0.004342971	6
52	88	0.435821776	0.028146321	6

52	93	0.225671988	0.025592371	3
53	55	0.770370148	0.004649755	4
53	58	0.449916677	0.037488151	9
53	60	0.690134132	0.028443537	6
53	61	0.607170389	0.072937046	4
53	63	0.525576101	0.076914249	4
53	64	0.700140564	0.038099486	6
53	65	0.506411622	0.064739597	6
53	67	0.282775704	0.006209215	3
53	68	0.320903328	0.023538446	6
53	69	0.16303447	0.02728403	9
53	71	0.529743303	0.015657752	9
53	73	1.134705687	0.142641223	12
53	74	0.288815145	0.01094816	6
53	76	0.868908089	0.036999764	9
53	77	0.562211603	0.035766446	9
53	78	0.58062122	0.043479465	6
53	79	0.413020902	0	2
53	80	0.602665666	0.043227608	6
53	82	0.590987046	0.028887168	6
53	87	0.290412537	0.020952852	6
53	88	0.421198425	0.007395883	6
55	60	0.622649093	0.044308693	9
55	61	0.983719794	0.062129744	6
55	62	0.068322544	0.003728017	6
55	63	0.967874346	0.082655612	9
55	73	1.246116158	0.140115267	4
58	60	1.456676874	0.030385639	6
58	62	0.291341819	0.019253966	6
58	63	1.16276911	0.169746954	9
58	64	0.927935783	0.055141313	9
59	60	1.692871419	0.051181111	4
59	62	0.53860932	0.052747068	6
59	63	0.935437616	0	1
59	64	1.130799851	0.033570548	9
59	65	1.168336633	0.140758484	9
60	61	4.45667491	0.208148665	24
60	62	1.368815028	0.039005937	18
60	63	1.367139369	0.073510047	13
60	64	1.005669365	0.056404864	42
60	65	1.672915141	0.200179713	18
60	66	1.071661134	0.162069557	30
60	67	0.414862448	0.067250317	27
60	68	0.52303337	0.023134308	15
60	69	0.506726511	0.02054491	6
60	70	0.422921906	0.05688156	12
60	71	0.732098883	0.055638696	9
60	72	0.728582568	0.069139937	3
60	73	0.299345285	0.022614939	15
60	74	0.103836314	0.02569295	9
60	75	0.277610277	0.025736797	9
60	76	0.570550628	0.112497304	9
60	77	0.299179524	0.030591859	9
60	78	0.370263656	0.015409257	9

60	79	0.326590433	0.012975354	9
60	81	0.211006825	0.022538128	9
60	82	0.398271981	0.026126504	15
61	62	3.230853012	0.191737719	15
61	63	3.183482973	0.241574826	36
61	64	2.687491108	0.314049749	13
61	65	1.200765467	0.105491277	9
61	66	0.886294211	0.125499109	9
61	67	0.789002954	0.084160314	12
61	68	0.533791866	0.023340051	4
61	69	0.503471963	0.054569281	6
61	70	0.467885947	0.036743662	15
61	71	0.879885635	0.110225362	9
61	72	0.470061836	0.072749348	13
61	73	0.616486508	0.060238001	6
61	77	0.372281225	0.06040483	9
61	79	0.220167828	0.059385156	6
61	82	0.215139953	0.016028258	18
62	63	1.08940284	0.032665377	21
62	64	0.184160439	0.015798601	15
62	65	0.302487273	0.019116152	9
62	70	0.100848226	0.008066981	9
62	71	0.11492603	0.005821974	9
62	73	0.082240041	0.007323438	6
62	82	0.067278458	0.001441366	6
63	64	1.930621761	0.072209916	6
63	65	2.511194401	0.201670468	18
63	66	1.054221571	0.065247303	15
63	67	0.325495806	0.024857864	24
63	68	0.865693839	0.186880563	3
63	69	0.617794743	0.106477359	15
63	70	0.670303359	0.09381115	10
63	71	0.757113662	0.060305679	9
63	72	0.73979845	0.028229854	6
63	73	1.674403868	0.277674135	4
63	74	0.183609089	0.02638284	9
63	75	0.256024594	0.017806475	9
63	76	0.352035877	0.027150116	6
63	77	0.344171632	0.029362949	9
63	78	0.29312008	0.0180315	9
63	79	0.300389456	0.014933219	9
63	80	0.254222611	0.061161813	6
63	81	0.391994854	0.066182174	9
63	82	0.336018381	0.024998831	9
64	65	5.971019576	0.407797376	18
64	68	1.648341853	0.219451797	9
64	69	0.748140488	0.079585265	9
64	70	0.409112252	0.020766929	15
64	71	1.604835564	0.210186709	6
64	72	1.053528306	0.082217397	15
64	73	0.599436342	0.046887967	18
64	74	0.296619394	0.04295461	6
64	75	0.236824787	0.029968383	6
64	76	0.087222541	0.003105728	6

64	77	0.26775705	0.047999112	9
64	78	0.321615502	0.01760215	6
64	79	0.324599374	0.009163773	9
64	81	0.228437908	0.039984669	3
64	82	0.322196409	0.026829913	9
65	66	7.480581844	0.532226335	9
65	67	2.795064778	0.365882002	9
65	68	1.866088391	0.168406628	15
65	69	1.762617924	0.12850221	9
65	71	2.089831491	0.09611347	15
65	72	1.254867771	0.033678652	9
65	73	2.261379291	0.198170461	6
65	74	0.55581326	0.024768115	9
65	75	1.157782133	0.09731478	6
65	76	1.971223856	0.462596255	3
65	77	1.958696475	0.08316037	4
65	78	1.134593558	0.063956422	9
65	79	1.827079432	0.099120302	9
65	80	1.641681501	0.11192296	6
65	81	0.533428651	0.068829935	9
65	82	0.480007533	0.011588694	18
66	67	7.206744355	1.269303785	24
66	70	0.432299423	0.032484353	15
66	71	0.821088254	0.078663242	3
66	72	0.580983289	0.070467453	15
66	74	0.138078163	0.006198256	9
66	75	0.283655285	0	2
66	76	0.387196458	0.076478243	9
66	77	0.684481874	0.053764719	9
66	78	0.159869261	0.016529572	18
66	79	0.138316891	0.011844948	18
66	80	0.164659111	0.030390068	6
66	81	0.230857858	0.021770415	9
66	82	0.283435357	0.007397951	6
67	68	1.429402595	0.08279281	10
67	69	2.361025279	0.166434607	9
67	70	0.88775219	0.146208192	18
67	71	0.736290753	0.041384892	15
67	72	0.643034125	0.038193565	12
67	73	0.950210667	0.023217123	9
67	74	0.319429798	0.021889108	9
67	75	0.173827584	0.021225456	18
67	76	0.136129262	0.010435198	12
67	77	0.581822712	0.053302425	9
67	78	0.146336324	0.024184736	15
67	79	0.156894297	0.024069607	18
67	80	0.147253409	0.034145097	3
67	81	0.333922477	0.054824419	6
67	82	0.131464063	0.005973513	9
68	69	3.450940547	0.130373587	6
68	70	1.91760252	0.140647337	9
68	71	1.019901647	0.024468455	15
68	72	0.841778918	0.048621719	3
68	73	1.033270386	0.032348139	6

68	74	0.14031112	0.01464122	13
68	75	0.216998439	0.040690884	13
68	76	0.411455575	0.048278402	21
68	77	0.710372791	0.04339726	9
68	78	0.269618482	0.053687249	15
68	79	0.732857372	0.110833226	12
68	80	0.231938533	0.033960079	10
68	81	0.621344576	0.129810479	6
68	82	0.243802449	0.014432211	9
69	70	3.561994897	0.211859573	18
69	71	1.81224299	0.130431661	24
69	73	1.792351047	0.085953533	9
69	74	0.6595067	0.158880954	6
69	76	0.934912757	0.15135422	4
69	78	1.089852043	0.186131027	18
69	79	1.157283237	0.180672783	6
69	80	4.86069545	0.47231656	9
69	82	0.102658966	0.012970953	9
70	71	1.233151835	0.027585977	14
70	72	1.057379828	0.072199794	3
70	74	0.801662966	0.068816672	6
70	75	1.307659574	0	1
70	76	0.456471409	0.050013966	9
70	77	0.920192132	0.025405181	15
70	78	0.947409889	0.025218559	12
70	79	0.947574416	0.144685738	3
70	80	3.487517886	0.749609751	9
70	81	0.236372816	0.017624332	6
70	82	0.509038819	0.020125444	18
71	72	0.998139494	0.015867797	16
71	73	1.665696566	0.15093774	15
71	75	1.954598509	0.116285792	18
71	76	1.75501778	0.110756314	21
71	77	0.936461153	0.015330918	11
71	79	0.7828894	0.027802879	12
71	80	1.436208625	0.023229439	9
71	82	0.502032036	0.0256664	18
71	88	0.657877814	0.010750486	9
72	73	1.572196044	0.069432023	9
72	74	1.406649628	0.062996236	6
72	75	1.652735993	0.119747873	10
72	76	2.351327314	0.13213865	18
72	77	0.892791311	0.028726189	10
72	78	1.106041921	0.067598917	7
72	79	0.743536609	0.021767146	4
72	80	1.97788457	0.063140852	6
72	82	0.878453766	0.013115261	4
73	74	2.072473765	0.06317638	4
73	75	9.081264902	1.500179359	10
73	76	12.65854275	1.095366515	15
73	77	1.316081613	0.070457465	7
73	78	1.512895205	0.099635607	15
73	79	1.211374583	0	2
73	80	4.065999732	0.361642193	12

73	82	0.717293482	0.11892534	11
73	87	0.757509635	0.105465617	6
73	88	0.614910304	0.033016059	6
73	93	0.322353632	0.03368495	4
74	75	9.39432081	0.614630577	9
74	76	7.790409344	0.824259626	9
74	77	1.454569604	0.173243811	11
74	78	0.644867527	0.072574369	12
74	80	1.116073046	0.253430195	6
74	82	0.266843777	0.0139702	18
75	76	13.6915759	0.803865396	18
75	77	2.226200261	0.242996854	15
75	78	1.782634725	0.147039533	9
75	79	1.98837385	0.23314637	4
75	80	1.667258038	0.308971045	4
75	82	0.444322131	0.008264697	6
76	77	3.646078421	0.399125286	6
76	78	2.975304492	0.358469664	15
76	79	3.71189538	0.404132861	9
76	80	2.026248283	0.459702363	6
76	82	0.438980792	0.021309842	9
77	78	1.246767732	0.098301826	11
77	80	1.901806781	0.216985268	24
77	82	0.668277664	0.043411832	21
77	87	0.5928332	0.012691578	4
77	88	0.753749006	0.02137388	6
78	79	1.220649309	0.08393796	9
78	80	2.4891864	0.13611383	12
78	81	4.586875726	0.287105289	3
78	82	0.813537664	0.014812253	18
79	80	3.629343792	0.226700493	9
79	82	1.079302684	0.018528068	9
80	82	0.462242373	0.095234501	9
80	87	3.11261305	0.801832267	9
81	82	1.295838184	0.090118851	9

2. HoxB cluster (hChr. 17) BglII 3C library

49	50	3.94464834	0.493744051	9
49	52	0.380715059	0.029796363	9
49	55	0.471149847	0.071599459	10
49	56	0.088108728	0.004319589	9
49	58	0.386284542	0.028042481	9
49	59	0.628978555	0.105687995	6
49	60	0.25145725	0.037469743	9
49	61	0.288632272	0.026763982	9
49	62	0.243953822	0.012139122	6
49	63	0.212289274	0.021231924	9
49	66	0.297382357	0.057476754	9
49	67	0.483835694	0.04953558	9
49	68	0.038192384	0.002523056	9
49	69	0.46263655	0.021828268	6
49	71	0.445612374	0.059526829	4
49	72	0.316057114	0.04030683	9
49	73	0.100291557	0.00394179	6

49	74	0.627421996	0.207106048	9
49	75	0.078964538	0.010695379	6
50	55	1.904574252	0.550069323	6
50	70	1.61092051	0.24921696	3
50	72	0.406145579	0.067781893	4
50	75	0.405733037	0.037060875	3
52	55	0.959682875	0.057691094	4
52	59	0.952593313	0.052766309	9
52	62	0.386281175	0.056065939	9
52	63	0.185717848	0.028227212	9
52	65	0.173858113	0.020512526	9
52	66	0.286258508	0.02100948	9
52	68	0.188083081	0.022174053	9
52	69	0.254831256	0.045275474	9
52	70	0.542846157	0.049891183	6
52	71	0.701313857	0.046622643	6
52	72	0.199482742	0.020400603	6
52	73	0.074169409	0.002461158	9
52	74	0.510566048	0.098741056	6
52	75	0.060323992	0.003787749	9
53	55	1.475213482	0.184987557	15
53	56	0.462450237	0.018589183	9
53	57	0.324516596	0.016789629	9
53	58	0.801974758	0.077002329	9
53	59	6.867219917	0	2
53	60	0.48948569	0.032489996	9
53	61	0.275104022	0.013742084	9
53	62	0.530559654	0.061777454	9
53	63	0.314460395	0.044970921	9
53	65	0.293899784	0.03733071	9
53	66	0.576162638	0.071223018	9
53	68	0.381521723	0.019776246	9
53	69	0.687046498	0.071507051	9
53	70	3.148404635	0.445046411	4
53	71	1.059490579	0.00514746	4
53	74	1.286434855	0.362807334	4
53	75	0.185486772	0.036464238	9
55	56	0.835618545	0.029746196	6
55	57	0.758977336	0.031253123	9
55	58	1.123382221	0.023321781	9
55	60	1.188566608	0.068796143	9
55	61	0.974069677	0.152800573	6
55	62	0.094915967	0.006353615	4
55	63	0.434245785	0.080687084	9
55	65	0.260724666	0.022366712	9
55	66	0.191310018	0.011295335	18
55	69	0.516429161	0.069456704	4
55	72	0.579630016	0.066908236	9
55	73	0.167080758	0.007722549	9
55	74	0.911963646	0.12091639	12
55	75	0.102678776	0.016379822	9
56	58	0.421901272	0.015529482	6
56	64	0.127106295	0.017473475	9
56	65	0.180510122	0.006150878	9

56	66	0.469892692	0	2
56	68	0.328206086	0.025370037	6
56	70	2.054238785	0.111944294	6
56	71	1.036084326	0.010474908	3
56	72	0.230163434	0.012212589	9
56	74	0.350877078	0.013404548	6
56	75	0.115109	0.011625048	9
57	58	1.240436168	0.114078843	9
57	59	1.912773452	0.165833755	9
57	63	0.123069266	0.00197624	9
57	66	0.331914697	0.056400334	4
57	67	0.238334062	0.020911442	9
57	70	0.966622744	0.101470814	9
57	71	0.884073061	0.028035176	6
57	74	0.29575195	0.036967955	9
57	75	0.147330715	0.008832945	9
58	59	7.470070486	0.388966052	6
58	60	2.239951039	0.29983072	6
58	61	1.422630323	0.157419547	9
58	63	1.194252017	0.061259644	9
58	65	0.965311166	0.094803244	9
58	66	0.68339902	0.071197457	7
58	68	2.23666321	0.211098824	6
58	70	1.888123119	0.187322144	12
58	71	1.062625061	0.129982958	15
58	72	0.902987282	0.129108592	6
58	74	1.846667026	0.064143512	6
58	75	0.156223911	0.014240473	6
59	60	3.09583237	0.225878784	3
59	61	2.000950874	0.181147238	9
59	62	2.218612556	0.49593837	6
59	63	1.367234629	0.279898324	6
59	65	1.214196099	0.106191066	9
59	66	1.52976173	0.296672824	6
59	67	1.045356925	0.029197356	3
59	68	1.347087495	0.107429372	6
59	69	1.519671773	0.194499789	9
59	70	3.640702125	0.620242616	15
59	71	2.086773037	0.338537485	25
59	72	1.165046812	0.059463823	15
59	73	0.577132574	0.085758769	6
59	74	1.086394712	0.1360811	6
59	75	0.135618877	0.009530517	9
60	66	0.952014009	0.22973856	4
60	70	2.480315046	0.208854125	9
60	71	1.022865662	0.080093272	9
60	72	0.72232455	0.01715041	4
60	75	0.146827988	0.015146688	9
61	66	0.579804438	0.012056311	9
61	70	0.704604834	0.05521611	9
61	71	1.045634076	0.089705527	6
61	74	0.665366563	0.041924281	9
61	75	0.141592031	0.01690941	9
62	64	2.19560908	0.292930963	9

62	70	1.601745691	0.373953316	15
62	74	1.569631145	0.035175264	4
62	75	0.169029109	0.009278236	6
63	64	1.288796314	0.028469302	9
63	65	0.315811274	0.024752779	9
63	66	0.534908219	0.019297918	3
63	68	0.588908936	0.043553329	9
63	70	0.517991853	0.02085252	6
63	71	0.67740104	0.07455875	9
63	72	0.085915129	0.004604819	9
63	74	6.990279655	0.473922797	3
63	75	0.070138247	0.005648225	9
64	65	1.193576171	0.111345188	6
64	67	0.719153983	0.044353967	6
64	69	2.308342069	0.246240573	9
64	70	2.522424142	0.291879552	12
64	71	0.744532846	0.080503997	6
64	72	0.439446672	0.059406541	6
64	73	0.17857748	0.042752877	6
64	74	1.270458789	0.176517982	9
64	75	0.154119561	0.011697246	9
65	66	1.541149859	0.063856912	6
65	67	1.102939568	0.079882185	9
65	68	0.619394316	0.032918068	9
65	70	1.706422269	0.127631611	9
65	71	1.586629944	0.135669219	4
65	72	0.684455975	0.088900608	9
65	74	2.203364067	0.659174542	6
65	75	0.110308373	0.009029518	9
66	67	0.920302304	0.052238651	4
66	68	1.372962863	0.167562412	4
66	69	1.164849639	0.05599233	6
66	70	1.600309738	0.296281076	12
66	71	1.113192975	0.158836011	3
66	72	1.181767406	0.28357446	4
66	73	0.385077032	0.071775013	4
66	74	0.729716506	0	2
66	75	0.096366065	0.009171836	6
67	68	1.08391302	0.156111305	6
67	70	3.660969574	0.564057933	6
67	72	0.598017569	0.061009522	6
67	75	0.312657573	0	2
68	69	1.880723925	0.243326191	3
68	70	3.770305648	0.052517774	6
68	71	1.192866823	0.173236044	9
68	73	0.48384426	0.034440483	9
68	74	0.404988739	0.03618024	9
68	75	0.376238293	0.017311961	9
69	70	15.9642219	0.440985702	6
69	71	4.3682899	0.715141929	9
69	72	3.617031549	0.564039191	4
69	74	0.418240899	0.070586747	4
69	75	0.118300876	0.01253451	4
70	71	3.106239585	0.254476284	10

70	72	3.531625189	0.232789071	12
70	74	5.058870968	0.141893273	4
70	75	0.351818062	0.060137387	6
70	77	0.628249026	0.089632458	6
70	78	0.442087511	0.018664457	6
70	80	1.222205562	0.027062245	4
70	81	0.391067133	0.011822535	9
70	85	0.221159591	0.048806578	4
70	86	0.204743692	0.007870742	6
70	87	0.438326336	0.044300378	6
70	94	0.232655308	0.030502144	3
70	96	0.14097326	0.020478443	9
71	72	1.258844762	0.068650731	9
71	73	0.621827872	0.08219513	4
71	74	1.62132894	0.294082432	5
71	75	0.384247789	0.064587627	9
71	77	0.596519467	0.147660798	6
71	78	0.604571909	0.084870718	9
71	80	0.826866092	0	2
71	81	0.498398992	0.069430069	9
71	83	0.520725985	0.081353255	9
71	84	0.334881248	0.033975899	9
72	73	1.295031084	0.103251838	4
72	74	6.194947137	1.659041652	9
72	75	0.928503399	0	2
72	77	1.31470881	0.135124791	4
72	80	1.276715504	0	2
72	81	0.910922656	0.072353929	6
72	83	1.053094543	0.130426232	4
73	75	0.544874309	0.052651172	6

3. HoxC cluster (hChr. 12) BglII 3C library

48	49	0.388667105	0.013619573	9
49	50	1.888432056	0.078807519	18
49	52	1.004400198	0.074311175	9
49	54	0.232012027	0.011668751	6
49	55	0.496446532	0.022643749	9
49	57	0.829543051	0.072400891	19
49	58	0.523949902	0.026590899	9
49	62	0.495275389	0.013783722	9
49	64	0.406755652	0.032142501	12
49	65	0.516639066	0.030890298	9
49	66	0.427399662	0.027371599	9
49	67	0.270652833	0.02105288	21
49	68	0.442630643	0.007240932	9
49	70	0.244059329	0.014045823	9
49	71	0.787696921	0.041999648	9
49	72	0.166245452	0.018282054	9
49	73	0.357896776	0.037227155	6
49	74	0.205313386	0.004269685	9
49	75	0.209199369	0.028195736	9
49	76	0.293611441	0.027382137	9
49	77	0.303694709	0.020410898	6
49	78	0.229586219	0.027365067	9

49	79	0.296509314	0.015473162	24
49	80	0.13810626	0.034210313	6
49	81	0.144833203	0.022020443	9
49	82	0.096282502	0.011584219	6
49	83	0.1080673	0.004326067	9
49	84	0.130854458	0.007623735	9
55	56	2.419725737	0.072335843	3
55	57	0.617504178	0.039379306	18
55	58	0.565667894	0.013980478	9
55	59	0.433246746	0.012818986	6
55	62	0.311660394	0.042379939	9
55	63	0.288844147	0.020928558	9
55	64	0.254569374	0.054851075	6
55	65	0.516502153	0.026529922	9
55	66	0.269332636	0.022415176	9
55	67	0.372193885	0.046611	18
55	68	0.180570864	0.020518776	9
55	70	0.175221875	0.002631237	6
55	71	0.120997564	0.010431374	6
55	72	0.206667982	0.012321795	6
55	73	0.29034873	0.030330004	3
55	74	0.12593622	0.018160733	9
55	75	0.191668005	0.014775253	9
55	76	0.311665256	0.024703054	15
55	77	0.179249993	0.004467855	6
55	78	0.227774112	0.040306081	6
55	79	0.18224212	0.011673007	9
55	80	0.231795176	0.021164556	9
55	81	0.06843926	0.005317264	4
55	82	0.120361758	0	2
55	83	0.176000195	0.030315289	4
55	84	0.185695935	0.010210208	4
56	79	0.726365944	0.0755813	9
57	58	0.936429644	0.022660143	9
57	59	2.797492073	0.364326466	6
57	62	1.451356386	0.327177554	6
57	63	0.99249847	0.197231637	9
57	64	0.391098194	0.019613121	4
57	65	0.857999764	0.127874126	9
57	66	1.091222519	0.231266106	6
57	67	1.065802302	0.128192863	37
57	68	0.319528044	0.07384598	9
57	70	0.373561386	0.072741297	9
57	71	0.516198912	0.051897544	6
57	73	1.007562134	0.099603313	6
57	74	0.223228145	0.037333111	6
57	75	0.770999096	0.195822474	6
57	76	0.482420042	0.032142877	9
57	77	0.275379577	0.066711582	9
57	78	0.247802346	0.056750831	9
57	79	0.230962451	0.03334609	6
57	80	0.205285411	0.079084876	6
57	81	0.257975288	0.068459327	6
57	82	1.212765368	0	1

57	83	0.030866124	0.006355574	6
57	84	0.198992944	0.023072005	6
58	59	1.707984174	0.026930657	6
58	61	0.938913273	0.033332687	9
58	62	0.737150334	0.046671808	9
58	63	0.612577481	0.014497158	9
58	64	0.900594371	0.112347713	9
58	65	0.499854515	0.01625087	9
58	66	0.435363391	0.037434324	9
58	67	0.733688731	0.094595844	9
58	68	0.381369285	0.050166499	6
58	70	0.225430735	0.025118771	3
58	72	0.235326653	0.029310176	9
58	73	0.382152554	0.022148317	9
58	74	0.262267569	0.019826273	9
58	75	0.508979562	0.061093697	4
58	76	0.511852634	0.010732393	6
58	77	0.141754069	0.006462196	4
58	78	0.1576619	0.005363052	6
58	79	0.265084073	0.006565558	4
58	80	0.264357261	0.05016243	4
58	81	0.20105928	0.065891672	4
58	82	0.245947157	0.038463068	9
58	83	0.124502418	0.004252762	6
58	84	0.142826916	0.007546671	9
60	75	2.078374353	0	1
61	66	1.636225063	0.213301752	6
61	75	0.94608474	0	2
61	90	0.835439854	0.064148268	9
62	63	1.763984363	0.104221277	18
62	64	1.025762439	0.044070957	9
62	65	1.405873442	0.077668645	9
62	66	1.257840126	0.167680141	24
62	67	1.725824863	0.227278296	12
62	68	0.809226023	0.081970539	15
62	70	0.180733276	0.032002901	9
62	71	0.967653834	0	2
62	72	0.712618646	0.110702199	9
62	73	4.170538846	1.692906	4
62	74	0.804989642	0.084938814	9
62	76	0.216256167	0.030250245	9
62	77	1.152663761	0.040512993	3
62	78	0.260629116	0.008229392	9
62	79	0.7528756	0.046375039	6
62	80	1.203640624	0.158286757	4
62	81	1.06991716	0.08043382	9
62	82	1.286495777	0	2
62	83	0.091967185	0.005733246	6
62	84	0.410412848	0.025614247	6
62	90	0.364055581	0.024546035	15
63	64	1.997016301	0.100033074	6
63	65	0.699816674	0.009273898	9
63	66	1.187457416	0.095092628	18
63	67	1.523454745	0.140043969	30

63	68	0.432779492	0.035491766	21
63	70	0.341132877	0.040926614	9
63	71	1.56360756	0	2
63	72	0.445201925	0.039694543	9
63	73	0.280168382	0.036948379	9
63	74	0.265037215	0.043287806	6
63	75	1.257933706	0.096093808	6
63	76	0.301829603	0.030061409	9
63	77	0.335046326	0.045139492	9
63	78	0.183674238	0.01661576	6
63	79	0.559782654	0.040996467	9
63	80	0.733298191	0.049052492	9
63	81	0.108815006	0.010864081	9
63	82	0.204906275	0.03305415	9
63	83	0.254315165	0.012703525	3
63	84	0.149016749	0.008279022	9
63	87	0.789461219	0	2
63	90	0.405733594	0.021313125	6
64	65	1.79668251	0.130177714	18
64	66	2.183977067	0.027145035	3
64	67	1.20375552	0.053469433	3
64	68	0.739737461	0.11103071	6
64	70	0.331758712	0.052573421	9
64	71	0.547709999	0.161393448	4
64	72	0.231203018	0.04102432	9
64	73	0.887879344	0.064557398	4
64	74	0.112032678	0.021054397	6
64	75	0.364354411	0.04530044	9
64	76	0.543372467	0.052172525	6
64	77	0.235679097	0.041243997	15
64	78	0.175500504	0.014525968	9
64	79	0.291731951	0.028621055	4
64	80	0.164287335	0.032510381	6
64	81	0.179620647	0.012538933	6
64	82	0.245251231	0.072669195	3
64	83	0.205723497	0.037490041	6
64	84	0.140560082	0.028022898	4
65	66	0.69337832	0.049552054	36
65	67	0.524636336	0.058349002	6
65	68	0.418331586	0.038861411	9
65	70	0.287937472	0.041208174	6
65	71	0.316849814	0.053330746	6
65	72	0.29874047	0.015706221	6
65	73	0.307499207	0.057999322	9
65	74	0.160068931	0.011870576	9
65	75	0.590501211	0	2
65	76	0.350120908	0.016265861	9
65	77	0.2272442	0.017176143	9
65	78	0.225555903	0.022314102	9
65	79	0.284764596	0.030230191	9
65	80	0.20133729	0.013105938	9
65	81	0.091926993	0.004483017	6
65	82	0.107124761	0.018803784	6
65	83	0.159654242	0.011380204	9

65	84	0.172445152	0.010015587	9
66	67	0.925546197	0.092144792	21
66	68	0.551143165	0.058485491	24
66	69	1.335902174	0.046973702	6
66	70	0.744234045	0.074605344	9
66	71	0.708571196	0.123625031	6
66	72	0.994188681	0.072198108	9
66	73	1.001753376	0.099693916	9
66	74	0.983744749	0.154686636	9
66	75	1.000042729	0.084605274	13
66	76	0.847867617	0.054811009	13
66	77	0.513871132	0.022061518	9
66	78	0.478655148	0.06588806	4
66	79	0.448521864	0.043408123	18
66	80	0.56762239	0.058215115	9
66	81	0.501036179	0.069251498	9
66	83	0.344478369	0.039161329	9
66	84	0.14178051	0.005240807	9
66	89	0.191829793	0.009728297	9
66	90	0.259080216	0.028539724	9
66	91	0.921969986	0.173523289	9
66	92	0.181884107	0.018840405	9
67	68	0.585493639	0.031376178	19
67	70	0.591328227	0.039827077	6
67	71	1.249741542	0.143495597	4
67	73	0.983705884	0.148240598	4
67	74	0.870002861	0.050352762	4
67	75	0.477187748	0.063007764	6
67	76	0.887994228	0.111893981	27
67	77	0.251226037	0.061523761	6
67	78	0.28444967	0.042396489	9
67	79	0.448655584	0.06938404	6
67	80	0.612382432	0.110550817	9
67	81	1.402282954	0	2
67	83	0.122527296	0.011017503	6
67	84	0.248385235	0.021725014	9
68	69	2.368098162	0.131502894	9
68	70	1.123067622	0.006705267	3
68	71	1.038487104	0	2
68	72	0.217338134	0.006231674	18
68	73	0.612826818	0.081947997	6
68	74	0.920195811	0.080962727	6
68	75	0.643078384	0.017835259	6
68	76	0.389025585	0.022716496	15
68	77	0.278491224	0.019353001	9
68	78	0.212805985	0.011562837	6
68	79	0.319967542	0.021661691	6
68	80	0.271122165	0.012529952	9
68	81	0.294577659	0.0321107	3
68	82	0.151609743	0.023407433	9
68	83	0.166171846	0.006416444	6
68	84	0.185838106	0.01460667	9
68	86	0.159688807	0.002346058	6
68	87	0.205773337	0.021548647	6

68	89	0.109844352	0.006361887	9
68	90	0.119649697	0.008981673	9
68	91	0.297127396	0.007940254	6
68	92	0.130152049	0.014723878	9
70	71	1.131664137	0.127428393	9
70	72	0.612073504	0.076079041	6
70	73	0.564374787	0.066934735	9
70	74	0.282778473	0.033562803	9
70	75	1.086236214	0.138226778	4
70	76	0.431940528	0.068486466	11
70	77	0.4969336	0.029893427	9
70	78	0.293241738	0.033690087	9
70	79	0.299825173	0.029009315	9
70	80	0.232902776	0.055860725	9
70	81	0.281137273	0.049396355	9
70	82	0.134536457	0	2
70	83	0.204561448	0.005842197	4
70	84	0.108672124	0.014479559	9
70	86	0.19563312	0.016829207	6
70	87	0.007768552	8.35619E-05	3
70	89	0.101487757	0.0118314	6
70	90	0.137445465	0.003283993	4
70	91	0.210184543	0.035433184	4
71	72	3.965240879	0.492288706	15
71	73	2.143861343	0.067893446	6
71	74	1.00965613	0.093850856	3
71	75	1.128521773	0.045108846	9
71	76	1.665046293	0.113186599	4
71	77	0.769857344	0.057350004	3
71	78	0.760944623	0.069418532	4
71	79	0.81222131	0.089047423	24
71	80	0.525429047	0.071919601	6
71	81	0.601811988	0.078794022	4
71	83	0.126335866	0.013061096	6
71	84	0.272469643	0.035282517	9
71	87	0.118877546	0.0262969	6
71	89	0.155016354	0	2
72	73	1.670605018	0.121402018	9
72	74	1.190170524	0.049751404	9
72	75	1.056641488	0.052421437	6
72	76	0.832208061	0.057280163	6
72	77	0.74688533	0.06581514	9
72	78	0.33622032	0.020774589	6
72	79	0.398928225	0.041493864	6
72	80	0.283674974	0.030260126	6
72	81	0.242215395	0.015169981	6
72	82	0.739668671	0.118649385	18
72	83	0.204349011	0.021316249	9
72	84	0.235343601	0.012846922	9
72	86	0.054141827	0.018485338	6
72	87	0.137472102	0.018939176	9
72	89	0.191604287	0.010467974	6
72	90	0.102483461	0.018409276	9
73	74	2.101760998	0.278376543	9

73	75	1.710752783	0.132973588	4
73	76	0.866249049	0.116986499	9
73	78	0.124829992	0.018539809	6
73	79	0.470798828	0.058103399	9
73	80	0.487211459	0.057779695	9
73	81	0.099335974	0	2
73	82	0.214921728	0.031348322	3
73	83	0.241554082	0.046324093	9
73	84	0.115742977	0.026658665	9
73	86	0.108493349	0.014202169	9
73	87	0.08286908	0.010693956	15
73	89	0.125674589	0.013011874	6
73	91	0.052413044	0.013576963	6
74	75	1.171505596	0.026289456	9
74	76	0.717233666	0.014535659	15
74	77	0.443796471	0.032204348	9
74	78	0.560781272	0.0344206	9
74	79	0.328122046	0.015823049	15
74	80	0.37937868	0.030552147	6
74	81	0.292584961	0.059675017	4
74	83	0.242971604	0.019061682	6
74	84	0.128107376	0.007592584	9
74	86	0.075454436	0.012619237	9
74	87	0.099909941	0.013280324	9
74	89	0.082048655	0.002120137	6
74	90	0.289880522	0.015458489	6
75	76	0.769679867	0.01455191	18
75	77	0.64164004	0.022951278	18
75	78	0.409620169	0	1
75	79	0.570552438	0.032885556	6
75	80	0.710079524	0.037679661	3
75	81	1.00611093	0.068637607	9
75	82	1.180704534	0	2
75	83	0.205311929	0.008475231	6
75	84	0.602398085	0.1689048	6
75	87	0.68251501	0.122155927	9
75	89	0.414247447	0.029174311	6
75	90	0.576535122	0.041424351	9
75	92	0.339964195	0.02189774	9
76	77	1.125673097	0.033678655	4
76	78	0.729203782	0.022427494	9
76	79	0.71129059	0.016140349	18
76	80	0.589842566	0.076650891	9
76	81	0.317545546	0.027198037	15
76	82	1.154036945	0.070587303	6
76	83	0.679275573	0.014413245	9
76	84	0.221874922	0.009235736	9
77	78	1.234188689	0.076012169	15
77	79	0.587311119	0.021916842	9
77	80	0.632157569	0.029293726	9
77	81	0.520600086	0.019898371	6
77	82	0.237929775	0.012785089	4
77	83	0.325197191	0.024482329	11
77	84	0.299957539	0.009977604	9

77	86	0.131973052	0.01395041	10
77	87	0.154153826	0.037051049	6
77	89	0.129890318	0.010392682	9
77	90	0.137763023	0.018893159	9
77	91	0.251557473	0.029851517	9
77	92	0.125266401	0.00655573	4
78	79	0.967115415	0.031679242	18
78	80	0.686042333	0.041959981	9
78	81	0.322349979	0.045067697	9
78	82	0.519722154	0.079216064	10
78	83	0.261408675	0.026279971	9
78	84	0.31441517	0.01808045	9
78	86	0.128110499	0.002545731	6
78	87	0.250169233	0.029701611	9
78	89	0.147676347	0.017872408	9
78	90	0.25040069	0.024052124	8
78	91	0.151909079	0.016157225	6
78	92	0.088338254	0.009072846	6
79	80	1.669484124	0.09084514	9
79	81	0.972259461	0.100584846	9
79	82	1.29842738	0.107301859	15
79	83	0.589442418	0.012557876	9
79	84	0.390526781	0.030858915	9
79	87	0.329584374	0.043774289	6
79	91	0.384376037	0.043649576	6
80	81	1.247024372	0.038545845	9
80	82	2.607089654	0.319596584	9
80	83	0.548280583	0.0281921	9
80	84	0.40296962	0.022982289	18
80	86	0.139876355	0.008099089	6
80	87	0.264390573	0.017944395	9
80	89	0.313281962	0.055713667	9
80	90	0.1740151	0.023270953	9
80	91	0.197052729	0.023350184	9
81	82	2.956722224	0.513201965	4
81	84	0.346403819	0.021531503	9
81	90	0.693144378	0.014702882	6
82	83	1.019438958	0.031367892	6
82	84	0.575061177	0.01129176	6
82	87	0.691378974	0.052936023	6
82	89	0.528755283	0.050870638	9
82	90	0.516466995	0.016122077	9
82	91	0.687192795	0.10687253	8
82	92	0.458807956	0	1
83	84	0.373175996	0.035228458	9
83	90	0.420026074	0.008853916	6
84	86	0.718856611	0.01917806	9
84	87	0.560083359	0.019539507	9
84	89	0.224861254	0.038801079	9
84	90	0.184813063	0.005473869	9
84	91	0.293998297	0.018407982	9
84	92	0.263569474	0.018383042	9

4. HoxD cluster (hChr. 2) BglII 3C library

47	63	0.01157912	0.000625791	6
48	63	0.036420086	0.007589193	9
49	62	0.02470507	0.003889242	9
49	63	0.022360558	0.005694188	9
49	69	0.002443007	7.66836E-05	6
50	63	0.024759587	0.002044597	9
50	69	0.11959954	0.00500194	3
50	75	0.032958102	0.005802507	6
51	54	0.223622117	0.025152983	9
51	62	0.051938182	0.012810664	9
51	63	0.05649947	0.014307655	9
51	69	0.053330597	0.012933753	9
51	75	0.019595687	0.001483559	3
52	54	0.530468194	0.015252301	9
52	60	0.004903139	0.000330631	6
52	61	0.135774151	0.013995596	9
52	63	0.143996001	0.011467827	15
52	65	0.047191517	0.002094412	6
52	66	0.105846283	0.002623477	4
52	69	0.207251461	0.052934188	15
52	70	0.153424989	0.036611197	9
52	72	0.112384012	0.032427483	6
52	74	0.139912823	0.020875929	9
52	75	0.035247606	0.007975779	9
52	77	0.022987089	0.005805597	6
52	78	0.114092967	0.026216519	9
52	79	0.034627678	0.001190239	4
52	80	0.033592397	0.003527728	6
53	54	1.170315292	0.073758679	9
53	62	0.199408377	0.025029868	9
53	63	0.093963486	0.013243443	9
53	68	0.475666988	0.038057096	9
53	69	0.262575292	0.039099967	18
53	70	0.400568778	0.061494953	9
53	72	0.104405302	0.007043762	9
53	73	0.206954189	0.034054805	9
53	74	0.077890583	0.011693533	6
53	75	0.142869809	0.027806127	9
53	78	0.06615926	0.0176479	9
54	56	5.389183236	0.675675969	9
54	59	0.522715167	0.164864037	6
54	60	0.488025747	0.061645126	9
54	61	0.13790567	0.015506727	6
54	62	0.207455878	0.009286868	12
54	63	0.100357992	0.010609776	18
54	65	0.033816141	0.00684642	9
54	66	0.084140865	0.019587115	6
54	68	0.097553439	0.013833663	9
54	69	0.108819236	0.023091486	15
54	70	0.028905269	0.002098777	6
54	72	0.04765301	0.004706307	9
54	73	0.811719002	0.031463538	9
54	74	1.465004622	0.066790857	6
54	75	0.367592222	0.078303312	18

54	76	0.913886641	0.10110693	9
54	77	0.317321345	0.045326841	6
54	78	0.10859094	0.025782235	12
54	79	0.162692935	0.057039394	6
54	80	0.887696884	0.282631386	9
56	62	0.130578703	0.023455847	9
56	63	0.087730284	0.013453417	6
56	69	0.10865671	0.013662135	6
56	72	0.038115242	0.014724587	4
56	75	0.123688426	0.006953948	9
56	78	0.195439324	0.017826918	6
57	63	0.337297118	0.135384589	6
57	75	0.100572369	0.007980904	6
59	62	0.237550257	0.055410448	9
59	63	0.164238729	0.013053584	9
59	69	0.067592684	0.025326201	6
59	72	0.068917076	0.011148167	6
59	73	0.317906371	0.101047436	9
59	75	0.231650556	0.014140864	9
59	76	0.086121122	0	2
59	78	0.090008951	0.024099921	9
60	62	0.915412751	0.053869801	9
60	63	0.269409626	0.048794231	9
60	69	0.379532245	0.124161666	9
60	76	0.289214099	0.048372218	9
61	62	0.775672653	0.046683513	9
61	63	0.396321795	0.03595493	9
61	65	0.034610468	0.001704929	6
61	66	0.601101588	0.157467741	9
61	68	0.159297162	0.012947724	9
61	69	0.264490385	0.066013491	9
61	70	0.282682574	0.062053884	9
61	72	0.140400435	0.015714979	9
61	73	0.127889243	0.016800283	6
61	75	0.108083937	0.016005051	18
61	76	0.161612731	0.012698438	9
61	77	0.020977737	0.005249364	3
61	78	0.188337324	0.029886651	9
62	63	0.763364833	0.032677569	27
62	65	0.158522254	0.030539806	9
62	66	0.410043686	0.018011885	6
62	68	0.461325071	0.012288181	18
62	69	1.138675419	0.07493686	27
62	70	0.557056622	0.077353303	15
62	72	0.35746854	0.025209582	9
62	73	0.163328326	0.021887652	9
62	74	0.299782797	0.016717918	9
62	75	0.319448289	0.011024206	24
62	76	0.522886361	0.048362055	18
62	77	0.167795789	0.012375174	6
62	78	0.159361281	0.022725774	9
62	79	0.146018436	0.006368698	6
62	80	0.306677635	0.064142326	6
63	64	4.61867188	0.301166852	9

63	65	0.223296719	0.050143293	18
63	68	0.270851848	0.012168193	9
63	69	0.393584053	0.037062605	9
63	70	0.332559782	0.038782036	15
63	71	0.039735869	0.009733017	9
63	72	0.083114165	0.022719667	9
63	73	0.177239408	0.011308681	9
63	74	0.092666658	0.025671591	9
63	75	0.171294173	0.009551223	24
63	76	0.16226801	0.022279826	18
63	77	0.043563069	0.006508188	6
63	78	0.104455745	0.005161622	9
63	79	0.130874082	0.014914311	9
64	70	0.160666969	0.052105431	9
65	69	0.468161833	0.03983373	9
65	70	0.136118799	0.024951876	6
65	72	0.124402625	0.0096685	9
65	73	0.246590413	0.045089128	6
65	75	0.075407636	0.006705602	18
65	77	2.830573248	0.840409434	3
65	78	0.043712632	0.011874276	6
66	69	2.913046705	0.514950985	9
66	73	0.394186427	0.127578804	9
66	76	0.257041697	0.081791508	9
66	77	0.928039324	0.255323159	6
66	78	0.02953769	0.003566499	9
68	69	3.349712634	0.353678055	9
68	70	2.21636748	0.172064591	9
68	72	0.599990462	0.013133965	9
68	73	0.664673876	0.054101214	9
68	74	0.419027406	0.065547279	9
68	75	0.502235807	0.037567769	15
68	76	1.212059803	0.138667747	9
68	77	0.403815363	0.050093153	9
68	78	0.257968011	0.019811918	18
68	79	0.137881911	0.016202529	9
69	70	18.97160533	0.411405698	9
69	72	2.596834627	0.058684512	6
69	75	1.093906978	0.014616301	6
69	78	0.337769285	0.023617012	9
69	79	0.412101152	0.044213859	9
70	71	8.120111488	0.209020837	6
70	72	3.066151806	0.080575907	9
70	73	1.942633407	0.205123116	9
70	74	0.730546923	0.096282863	9
70	75	0.766711155	0.072584043	15
70	76	0.592584819	0.064562624	9
70	77	0.52839102	0.047018707	18
70	78	0.319221812	0.047697385	15
70	79	0.135643654	0.005783741	6
70	80	0.067154844	0.013456031	6
72	75	0.454405202	0.027470812	9
72	76	0.625014475	0.053757367	9
72	77	0.36599296	0.030091523	9

72	78	0.132849165	0.010800555	9
72	79	0.201179705	0.003907295	4
73	75	0.064644621	0.013913054	6
73	76	0.406643422	0.017568999	9
73	77	0.310072833	0.016634351	9
73	78	0.129511771	0.020159794	6
73	79	0.45960647	0.085384935	9
74	75	2.015540169	0.139598041	9
74	76	1.828820812	0.253671272	9
74	77	0.34089806	0.057902551	9
74	78	0.180053165	0.011781978	9
74	79	0.100449378	0.009451037	9
75	76	2.584536658	0.06369268	9
75	77	1.473864701	0.071991158	18
75	78	0.567402686	0.034264357	9
75	79	0.524504465	0.130069063	9
76	77	5.848185921	0.389671752	9
76	78	0.815686393	0.074079406	9
76	79	0.518598307	0.021929117	9
76	80	0.281424387	0.032093122	6
77	78	0.846185808	0.108442432	9
77	79	2.93053088	0.252116579	6
78	79	3.235804	0.322903924	18
78	80	2.375043951	0.199113399	9
79	80	7.183029633	1.072657337	9

5. HoxD cluster (hChr.2) HindIII 3C library

76	85	0.105334983	0.008584528	3
76	93	0.024097511	0.003365362	9
77	85	0.072835398	0.00349924	6
77	93	0.05770575	0.005762809	9
79	81	0.276306869	0.01631304	9
79	82	0.152039955	0.037501696	6
79	83	0.132427837	0.006551934	9
79	84	0.109351306	0.008227966	6
79	85	0.096185962	0.004209614	6
79	86	0.125831396	0.005743939	9
79	87	0.046538586	0.00411821	9
79	88	0.044296484	0.001713328	9
79	93	0.133518961	0.007904945	18
79	98	0.053003201	0.01217096	9
80	81	0.400251383	0.019872293	9
80	82	0.517995243	0.016997625	9
80	85	0.325022133	0.057497073	6
80	86	0.046993293	0.001172316	4
80	87	0.108480599	0.007884975	9
80	90	0.194913579	0.02266323	3
80	98	0.062444518	0.006825416	6
81	82	0.56524625	0.034305697	9
81	83	0.241887222	0.017989556	9
81	84	0.768128635	0.059136234	6
81	85	0.138311024	0.010548364	9
81	86	0.168473834	0.018510257	6
81	87	0.077624054	0.003411896	6

81	88	0.122132514	0.007923806	9
81	90	0.128796541	0.024175612	9
81	93	0.173021977	0.013419977	15
81	98	0.063080142	0.003207557	6
82	83	0.59514323	0.011478081	6
82	84	0.396183593	0.04207913	9
82	85	0.273269133	0.042836593	6
82	86	0.274427155	0.026143462	6
82	87	0.131863578	0.011536482	6
82	88	0.136618426	0.013764537	9
82	90	0.059209253	0.000968246	6
82	93	0.313001755	0.026334663	18
82	94	0.168185542	0.006560169	9
82	98	0.135223457	0.020666663	6
83	84	1.611524056	0.076777458	6
83	85	0.470788226	0.0297113	9
83	86	0.56787186	0.047819238	6
83	87	0.408503799	0.048959181	9
83	88	0.188983498	0.008997461	9
83	90	0.372077125	0.035047766	9
83	91	0.133082761	0.002966725	9
83	92	0.261341285	0.003813395	9
83	93	0.403562428	0.025685121	9
83	94	0.215551547	0.008673574	9
83	95	0.113621674	0.008567332	9
83	96	0.059402626	0.003419267	9
83	97	0.147187991	0.00953425	6
83	98	0.301059899	0.030154787	9
83	99	0.209591211	0.005082283	6
83	100	0.113168984	0.004165872	6
83	101	0.153941063	0.005473137	6
83	103	0.103614797	0.006949853	9
84	85	3.356238212	0.1617265	9
84	86	0.259603499	0.046456087	6
84	87	1.28717193	0.191192111	6
84	88	0.605971277	0.093581684	9
84	90	0.783987391	0.171737882	6
84	91	0.200719958	0.010191694	6
84	92	0.57276385	0.073479364	4
84	93	0.722056185	0.037917843	9
84	94	0.284169748	0.072922016	6
84	95	0.248041086	0.031771886	6
84	96	0.141985577	0.022317253	9
84	97	0.257962232	0.018361582	3
84	98	0.718473857	0.053929206	9
84	99	0.249596024	0.027891935	9
84	100	0.199451524	0.000308947	4
84	101	0.185196548	0	2
85	86	1.354907989	0	2
85	87	0.733341394	0.130535462	9
85	88	0.371032483	0.042670186	9
85	89	0.561881136	0.069862568	6
85	90	0.442207126	0.049921567	6
85	91	0.271228735	0.019918783	6

85	92	0.468232699	0.013463933	6
85	93	0.777078431	0.028492089	18
85	94	0.584528739	0.053195795	15
85	95	0.204276919	0.012526574	9
85	96	0.150784432	0.010899307	9
85	97	0.17044664	0.005558876	9
85	98	0.450902457	0.026876218	18
85	99	0.344945903	0.038801097	9
85	100	0.128133505	0.005268756	9
85	101	0.183701314	0.026121622	9
85	103	0.173575355	0.022993291	6
85	104	0.092458438	0.015215878	9
86	93	0.400291911	0.043890627	10
86	94	0.389451645	0.017481851	4
86	95	0.229045578	0.023313409	6
86	98	0.560698207	0.044260572	9
87	93	0.46680754	0.036118148	18
87	94	0.603934226	0.107919698	9
87	95	0.219149726	0.025886833	9
87	98	0.128563694	0.009961838	6
88	93	0.288988378	0.024006636	18
88	94	0.29356331	0.045825838	9
88	95	0.101732999	0.005220265	6
88	98	0.220297846	0.027511547	9
89	93	0.267033549	0.014825826	6
89	95	0.107348735	0.010812869	9
89	98	0.177684968	0.000502591	6
90	93	0.291274108	0.023958377	18
90	94	0.167671136	0.015868251	4
90	95	0.16577654	0.022700181	9
90	98	0.269002884	0.040985101	6
91	94	0.38836699	0.049016827	6
91	95	0.105793178	0.004179667	9
91	98	0.173240703	0.01757952	9
92	93	0.522550065	0.037946512	15
92	94	0.554093917	0.042146337	9
92	95	0.112806785	0.005525207	6
92	98	0.504146791	0.036339851	6
93	94	1.264904749	0.062106945	9
93	95	0.334837362	0.010808618	9
93	96	0.20343215	0.01332561	15
93	97	0.155308364	0.012031706	13
93	98	0.603735363	0.028669137	9
93	99	0.548977248	0.045838964	15
93	100	0.218071032	0.011373878	15
93	101	0.210236854	0.021439339	15
93	103	0.182269541	0.0059596	9
94	98	0.445567963	0.04935346	9
95	98	0.507750942	0.02657871	6
96	98	0.214433739	0.028157352	9
97	98	0.367981157	0.016854571	9
97	103	0.161854519	0.023030797	9
98	99	1.128734183	0.065987206	9
98	100	0.419369424	0.024472178	9

98	101	0.365926341	0.018271555	9
98	103	0.445790234	0.036662766	9
98	104	0.158467448	0.018144003	9
99	103	0.337341534	0.060250364	6
100	103	0.333712008	0.031226585	9
101	103	0.960069795	0.061624324	9

Supplementary Table 4 CTCF binding sites spatial proximity pvalues

CTCF binding site no.	CTCF binding site no.	spatial proximity pvalue
1. HoxA cluster (hChr.7)		
1	2	0.02678203
1	3	0.31070582
1	4	0.13829335
1	5	0.15077596
1	6	0.0389216
1	7	0.07878337
2	3	0.36581353
2	4	0.24963315
2	5	0.20176091
2	6	0.08902356
2	7	0.04752285
3	4	0.23697267
3	5	0.33403211
3	6	0.00442767
3	7	0.00465001
4	5	0.19716172
4	6	0.0173232
4	7	0.028764
5	6	0.1122355
5	7	0.19742217
6	7	0.03869927
2. HoxB cluster (hChr.17)		
1	2	0.41633609
1	3	0.53089901
1	4	0.23939206
1	5	0.04427663
1	6	0.05616785
2	3	0.6740716
2	4	0.46478994
2	5	0.3613153
2	6	0.27453042
3	4	0.6005353
3	5	0.25438991
3	6	0.23983176
4	5	0.17808154

4	6	0.26319362
5	6	0.03994647

3. HoxC cluster (hChr.12)

1	2	0.18062496
1	3	0.18832248
1	4	0.08762587
1	5	0.07488327
1	6	0.26323993
1	7	0.17818445
1	8	0.0446196
2	3	0.24570518
2	4	0.19256089
2	5	0.01144373
2	6	0.2037175
2	7	0.11639926
2	8	0.04037435
3	4	0.46231568
3	5	0.01901819
3	6	0.21360259
3	7	0.13021513
3	8	0.05475762
4	5	0.18242971
4	6	0.24095405
4	7	0.16004813
4	8	0.17501248
5	6	0.31995269
5	7	0.22065067
5	8	0.07451412
6	7	0.07382367
6	8	0.4363793
7	8	0.44610715

4. HoxD cluster (hChr.2)

1	2	0.16015709
1	3	0.14159152
1	4	0.02713644
1	5	0.10446039
1	6	0.05235583
1	7	0.04996417
2	3	0.36911509

2	4	0.26814447
2	5	0.38422811
2	6	0.26165815
2	7	0.32729371
3	4	0.68014182
3	5	0.47995943
3	6	0.30230697
3	7	0.2585034
4	5	0.38293457
4	6	0.06399769
4	7	0.05015029
5	6	0.15009725
5	7	0.09429818
6	7	0.41942358