

Supplemental Tables

Table S1, Spearman's Rank Order Correlation Coefficients between the Relative Interaction Frequencies of each 5C Replicate

ES 2i 1						
ES 2i 2	0.96697874					
ES Serum 1	0.90833291	0.93463038				
ES Serum 2	0.90105915	0.92885156	0.96734117			
pNPC 1	0.88150638	0.89151858	0.87489302	0.86904787		
pNPC 2	0.88047355	0.89716557	0.88978209	0.88753915	0.93984855	
	ES 2i 1	ES 2i 2	ES Serum 1	ES Serum 2	pNPC 1	pNPC 2

Table S2: Summary of new CHIP-seq datasets provided in this study

Target Protein	Cell Type	Total Mapped Test ChIP-Seq reads	Number non-redundant tags utilized (after down-sampling)	Control Samples	Total Mapped Control ChIP-Seq reads	Number non-redundant tags utilized (after down-sampling)
CTCF	mES (V6.5) in 2i/LIF media	37958347	11000000	mES (V6.5) in 2i/LIF whole cell extract	41629078	15000000
CTCF	mES (V6.5) in serum/LIF media	48653104	11000000	mES (V6.5) in serum/LIF whole cell extract	29243502	15000000
CTCF	Primary NPCs	67490709	11000000	Primary NPCs whole cell extract	41249127	15000000

Table S3: Summary of new 5C datasets provided in this study

Condition	Cell Type	5C/ Sequencing Run*	Total Mapped Reads (Paired end 1)	Total Mapped Reads (Paired end 2)	5C/ Sequencing Run*	Total Mapped Reads (Paired end 1)	Total Mapped Reads (Paired end 2)
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Scramble siRNA Rep 1	Primary NPCs	1	15564299	15493210	2	17519692	17451775
Scramble siRNA Rep 2	Primary NPCs	1	9893122	9840016	2	22108742	21989501
YY1 siRNA Rep 1	Primary NPCs	1	12062591	12019219	2	19736186	19631975
YY1 siRNA Rep 2	Primary NPCs	1	12191408	12143821	2	49818851	49599774

* Footnote: Runs were subsequently merged for analysis.

Table S4: Summary of publically available ChIP-seq datasets analyzed

Target Protein	Cell Type	Mapped Test ChIP-Seq reads (after down-sampling)	Test ChIP Reference	Test Sample GEO ID	Control Samples	Mapped Control ChIP-Seq reads (after down-sampling)	Control Sample GEO ID
YY1	mES Cells	7200000	(Sigova et al. 2015)	GSM1665555	Whole Cell Extract	7700000	GSM1665554
YY1	ES-derived NPC	7200000	(Mendenhall et al. 2010)	GSM628032	NPC Whole Cell Extract	7700000	GSM883648
YY1	ProB Cells (Rag2 ^{-/-})	7200000	(Medvedovic et al. 2013)	GSM1145864	ProB Input	7700000	GSM1145867
H3K27ac	mES (V6.5)	7000000	(Creyghton et al. 2010)	GSM594579 Rep2	V6.5 Whole Cell Extract	7000000	GSM594599
H3K27ac	ES-derived NPC	7000000	(Creyghton et al. 2010)	GSM594585	NPC Whole Cell Extract	7000000	GSM883648

Table S5: Significant CTCF Peaks in ES cells in 2i Conditions

Provided in separate spreadsheet.

Table S6: Significant CTCF Peaks in ES cells in Serum Conditions

Provided in separate spreadsheet.

Table S7: Significant CTCF Peaks in NPCs

Provided in separate spreadsheet.

Table S8: Significant CTCF Peaks present only in the 2i condition (classified as '2i only')

Provided in separate spreadsheet.

Table S9: Significant CTCF Peaks present only in the NPC condition (classified as 'NPC only')

Provided in separate spreadsheet.

Table S10: Significant CTCF Peaks present in the ES 2i and ES serum cellular states (classified as '2i + serum')

Provided in separate spreadsheet.

Table S11: Significant CTCF Peaks present in the ES 2i, ES serum, and NPC cellular states (classified as 'constitutive')

Provided in separate spreadsheet.

Table S12: Significant YY1 Peaks in NPCs

Provided in separate spreadsheet.

Table S13: Significant YY1 Peaks in ES cells in Serum

Provided in separate spreadsheet.

Table S14: ES Enhancer Annotations

Provided in separate spreadsheet.

Table S15: NPC Enhancer Annotations

Provided in separate spreadsheet.

Table S16: ES Gene Annotations

Provided in separate spreadsheet.

Table S17: NPC Gene Annotations

Provided in separate spreadsheet.

Table S18: Constitutive Gene Annotations

Provided in separate spreadsheet.