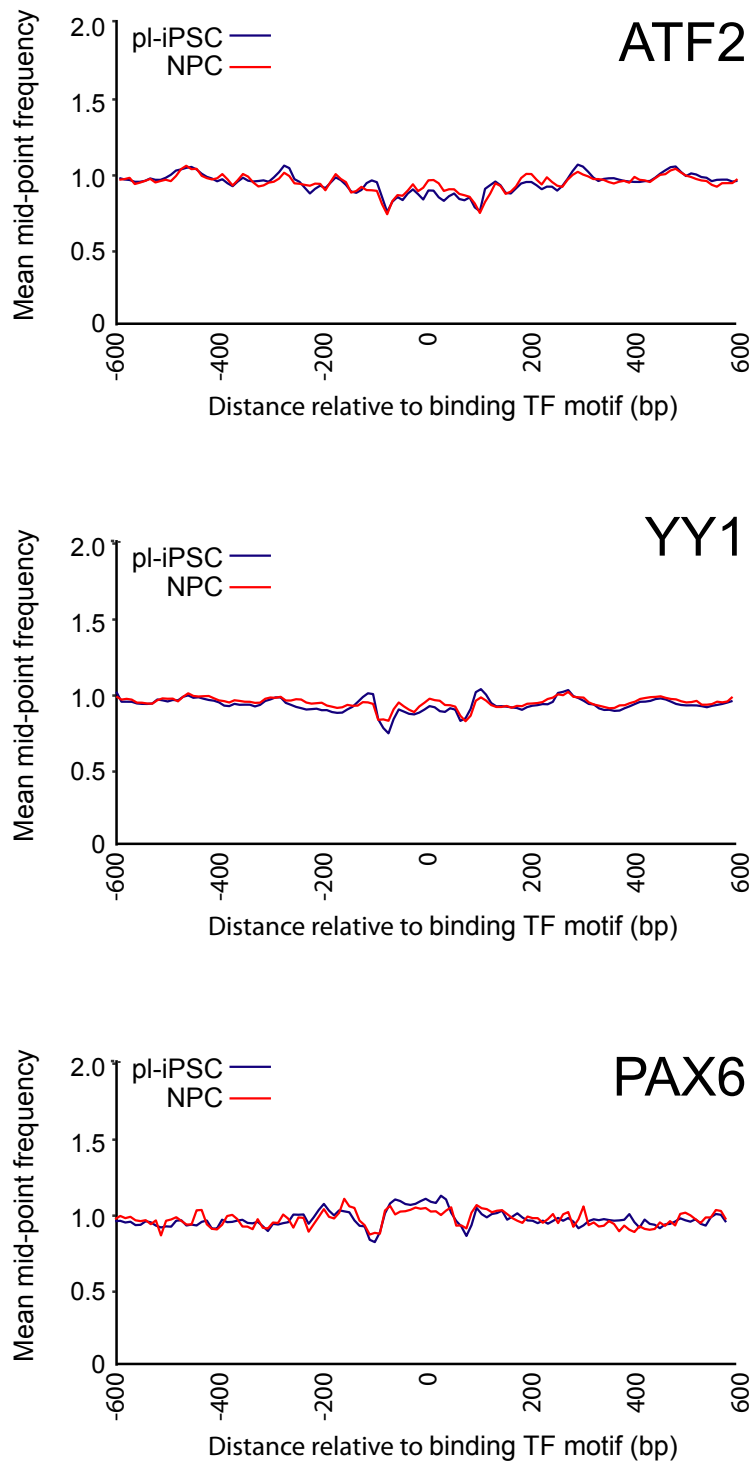


# **Nucleosome dynamics of human iPSC during the early stages of neurodevelopment**

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**SUPPLEMENTAL INFORMATION**



**Fig S1 Nucleosomes are not positioned at several transcription factor binding sites that are involved neurodevelopment.**

Average frequency distribution for sequence read mid-point data at and surrounding transcription factor binding sites ( $\pm 600$  bp) for nucleosomes at A. ATF2 (n=9,881), B. YY1 (n=39,945) and C. PAX6 (n=1,432) binding sites.

**Table S1: Numbers of highly positioned nucleosomes detected.**

<b>Cell type</b>	<b>No. of nucleosomes</b>
pl-iPSC	48,840
NPC	408,152
K562	363,784
GM12878	241,064

**Table S2: Chromatin state calculations for nucleosomes** (see STAR\*METHODS)

	iPS	default	p(default)	expected	O-E	O-E/E	O-E/E*100
1_Active_Promoter	315	9649596	0.00	173.92	141.08	0.81	81.11
2_Weak_Promoter	547	17972821	0.01	323.94	223.06	0.69	68.86
3_Poised_Promoter	188	18382770	0.01	331.33	-143.33	-0.43	-43.26
4_Strong_Enhancer	129	2625615	0.00	47.32	81.68	1.73	172.59
5_Strong_Enhancer	380	7027601	0.00	126.67	253.33	2.00	200.00
6_Weak_Enhancer	1517	34587847	0.01	623.41	893.59	1.43	143.34
7_Weak_Enhancer	1312	65853579	0.02	1186.95	125.05	0.11	10.54
8_Insulator	2725	21846871	0.01	393.77	2331.23	5.92	592.03
9_Txn_Transition	551	25543545	0.01	460.40	90.60	0.20	19.68
10_Txn_Elongation	591	81202908	0.03	1463.61	-872.61	-0.60	-59.62
11_Weak_Txn	7385	496238486	0.19	8944.23	-1559.23	-0.17	-17.43
12_Repressed	530	37571070	0.01	677.18	-147.18	-0.22	-21.73
14_Repetitive/CNV	1201	3946701	0.00	71.14	1129.86	15.88	1588.33
15_Repetitive/CNV	2817	2216760	0.00	39.95	2777.05	69.50	6950.43
13_Heterochrom/lo	28107	1854808938	0.69	33431.17	-5324.17	-0.16	-15.93

**TableS3: Chromatin state calculations for CTCF sites.** (see STAR\*METHODS)

Chromatin state	Observed	p(default)	Expected
1_Active_Promoter	160	0.003601301	34
2_Weak_Promoter	446	0.00670759	64
3_Poised_Promoter	437	0.006860586	65
4_Strong_Enhancer	25	0.000979899	9
5_Strong_Enhancer	66	0.002622753	25
6_Weak_Enhancer	748	0.012908441	123
7_Weak_Enhancer	167	0.024577045	234
8_Insulator	6331	0.008153414	78
9_Txn_Transition	337	0.009533041	91
10_Txn_Elongation	134	0.030305528	288
11_Weak_Txn	149	0.185199887	1762
12_Repressed	39	0.014021802	133
13_Heterochrom/lo	415	0.001472938	14
14_Repetitive/CNV	21	0.000827311	8
15_Repetitive/CNV	3	0.692228464	6587
TOTAL	9478	1	9516
number of CTCF sites = 9516			

**Table S4: Consensus transcription factor binding motif sequences used in this study.**

Transcription factor	Consensus binding motif	Motif length
ATF2	[T][G][A][C][G][T][C][A]	8
YY1	[A][A][G A C][A][T][G][G][C][G C T][G C A][C]	11
PAX6	[A][T][T][C][A][T][G][C][A C G T][T][G][A]	12
CTCF	[C][C][A G][C G][C T][A][G][G A][T G][G][G][C T]	12
RE1	[A C G T][T][T C][A][G][A C][A G][C][C][A C G T] [A C G T][A G][G][A C][G C][A][G]	17