

State	H3K36me3	H4K20me1	Control	FAIRE	POL2	H3K27ac	H3K9ac	H3K4me3	H3K4me2	H3K4me1	DNase_UW	DNase_DUKE	CTCF	H3K27me3
1_Tss	1.8	6.4	3.0	33.1	98.5	96.1	99.0	99.9	95.9	43.0	85.9	92.2	36.1	4.9
2_TssF	21.4	23.9	0.7	4.4	55.1	72.4	86.5	97.8	99.4	73.3	24.4	15.4	3.9	1.7
3_PromF	3.3	6.2	0.2	0.6	7.5	2.3	8.2	32.2	89.1	43.8	4.8	4.2	1.7	2.2
4_PromP	0.1	7.1	0.5	7.7	38.4	2.2	37.3	88.0	96.7	61.5	51.3	86.9	31.7	42.1
5_Enh	11.4	7.4	4.0	49.5	68.9	98.4	72.7	33.9	97.1	98.2	89.0	67.3	17.2	0.1
6_EnhF	5.0	2.3	0.6	3.7	10.8	94.3	28.7	1.0	53.9	93.4	20.0	8.1	2.3	0.1
7_EnhWF	0.9	2.2	0.2	0.8	1.4	0.6	1.3	0.0	7.0	88.4	4.4	3.7	1.4	0.4
8_EnhW	0.2	8.3	0.7	16.6	18.9	10.8	6.3	0.6	61.6	93.6	62.6	59.9	17.0	0.7
9_DNaseU	0.4	1.4	0.1	2.8	3.0	1.6	0.5	0.1	2.7	9.1	95.1	13.6	0.3	0.3
10_DNaseD	1.1	3.5	0.2	0.3	1.6	0.5	0.7	0.1	0.3	3.1	2.5	69.5	0.9	0.3
11_FaireW	1.5	1.9	7.9	22.5	0.8	10.1	5.6	1.7	0.2	0.3	0.5	1.5	0.6	2.0
12_CtcfO	5.9	8.8	1.0	34.6	18.6	1.8	1.4	0.3	10.3	16.7	71.4	86.9	99.8	2.0
13_Ctcf	0.3	2.1	0.1	0.5	0.3	0.1	0.2	0.0	0.7	1.4	6.0	16.1	99.1	1.7
14_Gen5'	70.4	35.9	0.7	3.2	52.3	26.2	9.1	1.2	23.4	83.6	9.5	11.6	3.6	0.0
15_Elon	93.2	4.2	0.3	0.7	1.4	0.3	0.2	0.0	0.1	0.3	0.4	1.4	1.0	0.0
16_ElonW	0.0	0.4	0.0	0.3	0.8	0.1	0.0	0.0	0.0	0.1	0.1	0.2	0.0	0.0
17_Gen3'	93.1	17.6	0.4	1.2	83.5	1.2	0.6	0.1	0.1	0.7	2.3	7.5	2.8	0.0
18_Pol2	0.7	5.6	0.1	0.7	82.6	0.9	0.6	0.0	0.1	2.2	2.7	7.1	1.2	0.3
19_H4K20	3.4	85.7	0.3	1.0	2.1	0.2	0.3	0.0	0.2	2.1	0.4	1.4	0.5	0.6
20_ReprD	0.5	15.5	0.5	1.4	2.0	0.5	0.6	1.0	11.4	20.7	4.4	47.9	11.7	90.4
21_Repr	0.0	2.1	0.2	0.1	0.1	0.1	0.0	0.0	0.0	0.0	0.0	1.1	0.1	89.8
22_ReprW	0.0	0.2	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.4	0.0	0.0
23_Low	0.1	0.0	0.0	0.2	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.2	0.0	0.0
24_Quies	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
25_Art	77.0	73.0	40.8	70.2	59.2	34.7	38.3	25.3	31.8	52.4	40.7	63.5	64.5	47.5

state	1_Tss	2_TssF	3_PromF	4_PromP	5_Enh	6_EnhF	7_EnhWF	8_EnhW	9_DNaseU	10_DNaseD	11_FaireW	12_CtcfO	13_Ctcf	14_Gen5'	15_Elon	16_ElonW	17_Gen3'	18_Pol2	19_H4K20	20_ReprD	21_Repr	22_ReprW	23_Low	24_Quies	25_Art	
1_Tss	83	12	1	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2_TssF	15	68	9	0	1	2	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	
3_PromF	1	9	60	5	0	0	4	1	0	0	0	0	0	0	1	0	1	0	1	0	0	2	10	3	0	
4_PromP	5	0	7	75	0	0	0	2	0	1	0	1	0	0	0	0	0	0	0	6	0	0	0	0	0	
5_Enh	2	1	0	0	71	19	0	4	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	
6_EnhF	0	2	0	0	14	62	12	2	0	0	3	0	0	1	0	1	0	0	0	0	0	0	0	0	0	
7_EnhWF	0	0	1	0	0	5	59	8	1	0	1	0	1	0	1	0	0	0	0	0	0	1	19	2	0	
8_EnhW	0	0	1	2	3	2	22	58	1	2	0	1	0	1	0	0	0	1	0	0	0	0	0	0	0	
9_DNaseU	0	0	0	0	0	0	4	2	44	0	1	1	0	0	0	0	0	1	1	0	0	2	32	10	0	
10_DNaseD	0	0	0	0	0	0	1	1	0	75	0	1	0	0	0	0	0	1	1	0	0	4	12	1	0	
11_FaireW	0	0	0	0	0	2	1	0	1	1	65	0	0	0	0	1	0	0	0	1	0	20	4	1	0	
12_CtcfO	0	0	0	1	0	0	2	2	1	4	1	48	23	0	2	1	1	2	1	2	0	1	7	2	0	
13_Ctcf	0	0	0	0	0	0	1	0	0	1	0	10	45	0	0	0	1	0	0	1	0	1	7	19	14	0
14_Gen5'	0	2	0	0	2	1	2	1	0	0	0	0	0	78	4	2	4	1	1	0	0	0	0	0	0	
15_Elon	0	0	0	0	0	0	0	0	0	0	0	0	0	1	75	17	4	0	0	0	0	0	2	0	0	
16_ElonW	0	0	0	0	0	0	0	0	0	0	0	0	0	0	18	77	1	2	1	0	0	0	0	0	0	
17_Gen3'	0	0	0	0	0	0	0	0	0	0	0	0	0	2	10	3	80	4	0	0	0	0	0	0	0	
18_Pol2	0	0	0	0	0	0	0	0	0	0	1	0	1	0	1	0	5	4	69	1	0	0	0	15	2	0
19_H4K20	0	0	0	0	0	0	0	0	0	0	1	0	1	0	1	1	2	0	1	57	0	0	2	30	2	0
20_ReprD	0	0	0	4	0	0	1	0	0	2	0	1	0	0	0	0	0	0	0	0	75	13	4	0	0	0
21_Repr	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	70	24	0	2	0
22_ReprW	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	9	87	1	0	0
23_Low	0	0	0	0	0	0	1	0	0	1	1	0	1	0	0	0	0	0	1	1	0	0	0	94	0	0
24_Quies	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99	0	0
25_Art	0	0	0	0	0	0	0	0	0	0	0	5	1	0	5	1	0	3	0	0	1	0	0	0	80	0

Supplementary Figure 1: Chromatin State Model Parameters (Left) The emission parameters of the chromatin state model. Each row corresponds to a state. Each column of one of the input tracks of the chromatin state model. Each value in the matrix corresponds to the probability the mark is considered present in the state multiplied by 100. **(Right)** The transition parameters of the chromatin state model. An entry in the matrix corresponds to the probability of transitioning to the state of the column when in the state of the row multiplied by 100.

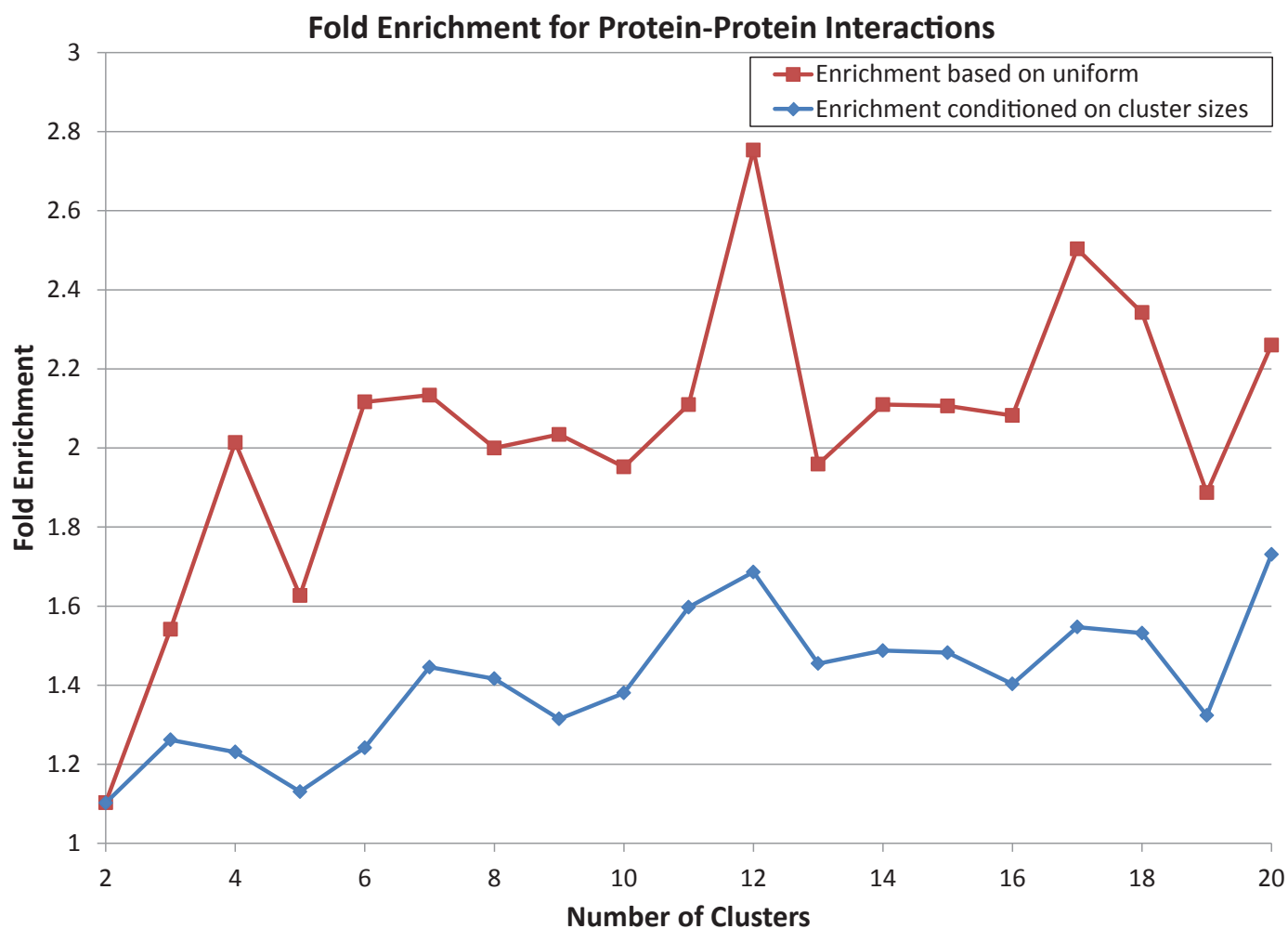
State	GM12878	H1-hESC	HeLa-S3	HepG2	Huvec	K562
1_Tss	0.77	0.46	0.74	0.75	0.62	0.61
2_TssF	0.77	0.22	0.44	0.64	0.35	0.58
3_PromF	0.74	0.46	0.47	0.70	0.29	0.32
4_PromP	0.21	0.72	0.12	0.57	0.28	0.17
5_Enh	0.45	0.14	0.43	0.28	0.85	0.50
6_EnhF	0.70	0.27	0.61	0.52	0.94	0.55
7_EnhWF	1.19	1.62	0.84	1.23	1.27	2.09
8_EnhW	0.38	0.62	0.46	0.36	0.47	0.53
9_DNaseU	0.26	0.64	0.38	0.10	0.20	0.20
10_DNaseD	0.22	1.90	1.21	0.68	0.67	0.46
11_FaireW	0.28	0.42	1.14	0.18	0.46	0.30
12_CtcfO	0.23	0.43	0.30	0.23	0.27	0.24
13_Ctcf	0.63	0.70	0.86	0.65	0.60	0.75
14_Gen5'	0.53	0.28	0.28	0.70	0.61	1.08
15_Elon	3.71	1.36	1.78	4.75	4.15	2.45
16_ElonW	3.49	1.96	1.82	3.40	3.29	2.82
17_Gen3'	1.30	0.77	0.77	1.17	0.83	1.48
18_Pol2	0.57	2.65	0.91	0.51	0.77	0.69
19_H4K20	0.11	0.68	3.01	0.71	0.51	0.28
20_ReprD	0.21	0.46	0.23	1.00	0.45	1.06
21_Repr	2.05	0.44	1.20	3.27	4.33	4.19
22_ReprW	8.34	0.81	4.38	8.98	9.02	9.29
23_Low	13.44	36.19	40.86	13.64	17.39	12.64
24_Quies	59.38	45.75	36.70	54.87	51.35	56.49
25_Art	0.04	0.04	0.07	0.07	0.04	0.23

State	GM12878	H1-hESC	HeLa-S3	HepG2	Huvec	K562
1_Tss	25.0	30.1	26.5	24.8	28.9	27.6
2_TssF	13.1	24.4	21.9	18.0	23.2	20.7
3_PromF	7.9	12.7	11.2	7.8	15.9	9.1
4_PromP	20.4	20.7	16.1	13.6	21.9	19.2
5_Enh	1.2	2.8	1.5	1.1	1.5	2.9
6_EnhF	1.0	1.2	1.7	1.2	1.1	2.4
7_EnhWF	1.3	1.0	1.2	1.4	1.3	2.6
8_EnhW	1.6	3.1	1.2	1.7	1.8	3.1
9_DNaseU	1.0	0.9	0.7	1.9	0.6	1.0
10_DNaseD	3.5	2.5	3.4	2.8	3.3	4.7
11_FaireW	1.5	0.7	0.8	0.7	1.1	1.0
12_CtcfO	1.6	1.6	1.7	1.6	1.6	1.7
13_Ctcf	1.0	0.7	1.2	0.8	1.1	1.0
14_Gen5'	0.9	2.0	2.0	1.1	1.6	2.3
15_Elon	0.3	0.3	0.2	0.3	0.4	0.3
16_ElonW	0.3	0.4	0.3	0.3	0.4	0.3
17_Gen3'	0.8	0.7	0.6	0.7	0.8	0.6
18_Pol2	2.9	1.4	2.4	3.1	1.8	1.7
19_H4K20	0.7	0.4	0.6	0.3	0.2	0.4
20_ReprD	13.4	9.5	1.3	4.3	11.0	4.1
21_Repr	3.4	4.4	1.0	1.8	1.9	1.3
22_ReprW	1.1	2.2	0.9	0.9	1.0	0.9
23_Low	1.0	0.6	0.7	0.8	0.8	0.9
24_Quies	0.3	0.3	0.3	0.3	0.3	0.3
25_Art	1.4	1.8	1.3	2.4	1.9	2.0

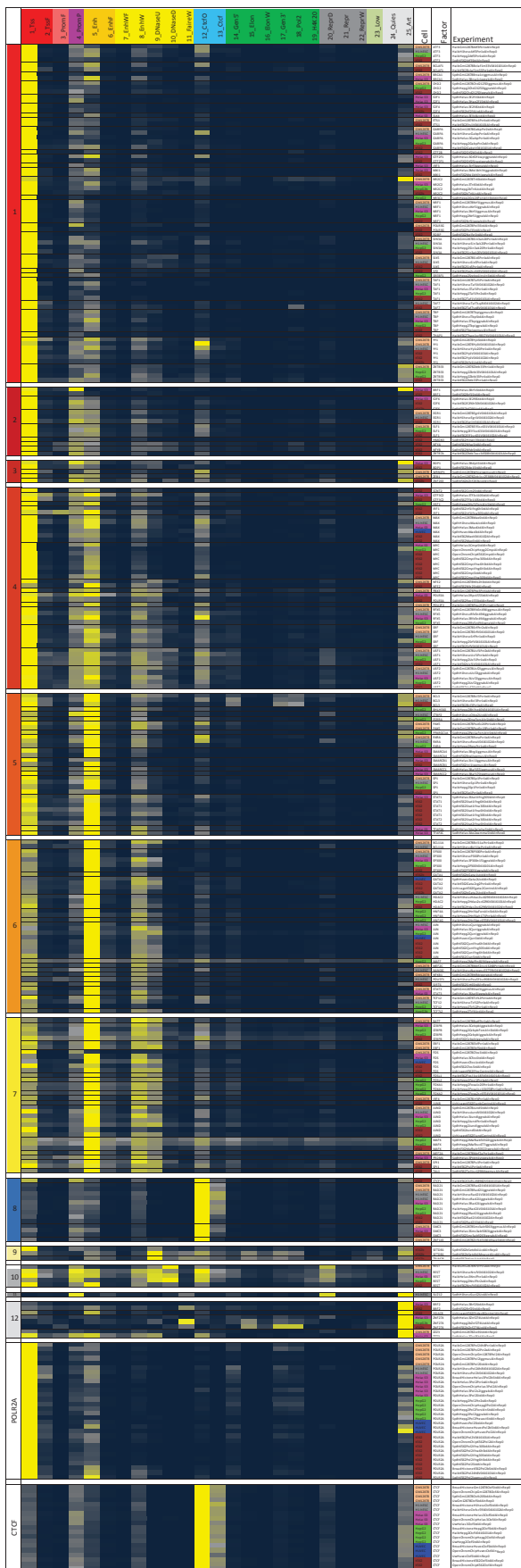
Supplementary Figure 2: Genome Coverage of States and Promoter Region Enrichments (Left) The percentage of the genome assigned to each chromatin state in each cell type. **(Right)** The fold enrichment for each state overlapping regions of the genome within 2000 base pairs of the 5' end of an annotated transcript of GENCODE protein coding gene, where the base percent of the genome is 2.48%. From this figure one can see for instance that State 1 has a much stronger preference to annotated promoter regions than state 5 despite both sharing DNase hypersensitivity, FAIRE, and a number of active histone modifications.

Cluster	1_Tss	2_TssF	3_PromF	4_PromP	5_Enh	6_EnhF	7_EnhWF	8_EnhW	9_DNaseU	10_DNaseD	11_FaireW	12_CtcfO	13_Ctcf	14_Gen5'	15_Elon	16_ElonW	17_Gen3'	18_Pol2	19_H4K20	20_ReprD	21_Repr	22_ReprW	23_Low	24_Quies	25_Art
1	1.0	0.0	0.0	0.1	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1
2	1.0	0.0	0.0	0.4	0.2	0.0	0.0	0.1	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1
3	1.0	0.1	0.0	0.5	0.3	0.0	0.0	0.1	0.0	0.0	0.0	0.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.5
4	1.0	0.0	0.0	0.3	0.6	0.0	0.0	0.2	0.1	0.0	0.0	0.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.2
5	0.9	0.0	0.0	0.2	1.0	0.0	0.0	0.2	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1
6	0.4	0.0	0.0	0.1	1.0	0.1	0.0	0.3	0.1	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1
7	0.5	0.1	0.0	0.2	1.0	0.1	0.0	0.6	0.3	0.0	0.0	0.1	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1
8	0.1	0.0	0.0	0.2	0.1	0.0	0.0	0.1	0.0	0.0	0.0	1.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.2
9	0.5	0.1	0.0	0.1	0.3	0.1	0.0	0.1	1.0	0.2	0.2	0.3	0.1	0.1	0.2	0.1	0.2	0.1	0.0	0.0	0.0	0.0	0.1	0.0	0.5
10	0.9	0.1	0.1	1.0	0.7	0.1	0.1	0.5	0.8	0.7	0.1	1.0	0.2	0.1	0.0	0.0	0.1	0.1	0.2	0.4	0.1	0.1	0.0	0.0	0.3
11	0.0	0.0	0.0	0.9	0.0	0.1	0.0	0.0	0.0	0.0	0.2	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.8	0.0	0.0	0.0	0.0	1.0
12	0.2	0.1	0.0	0.0	0.1	0.1	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.0

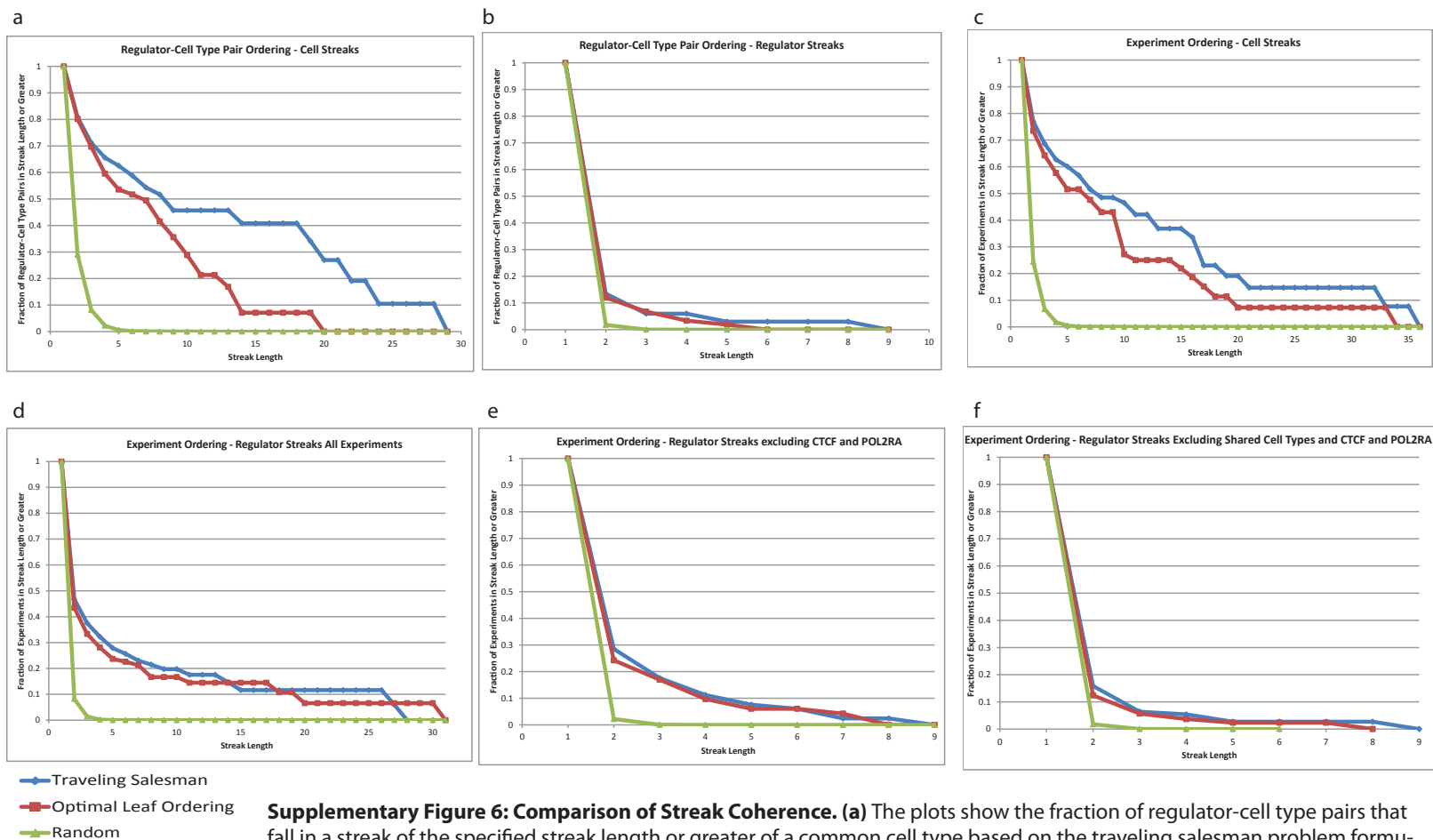
Supplementary Figure 3: K-means cluster averages. The table displays for each cluster from Figure 1, the average row normalized enrichment value for each state.



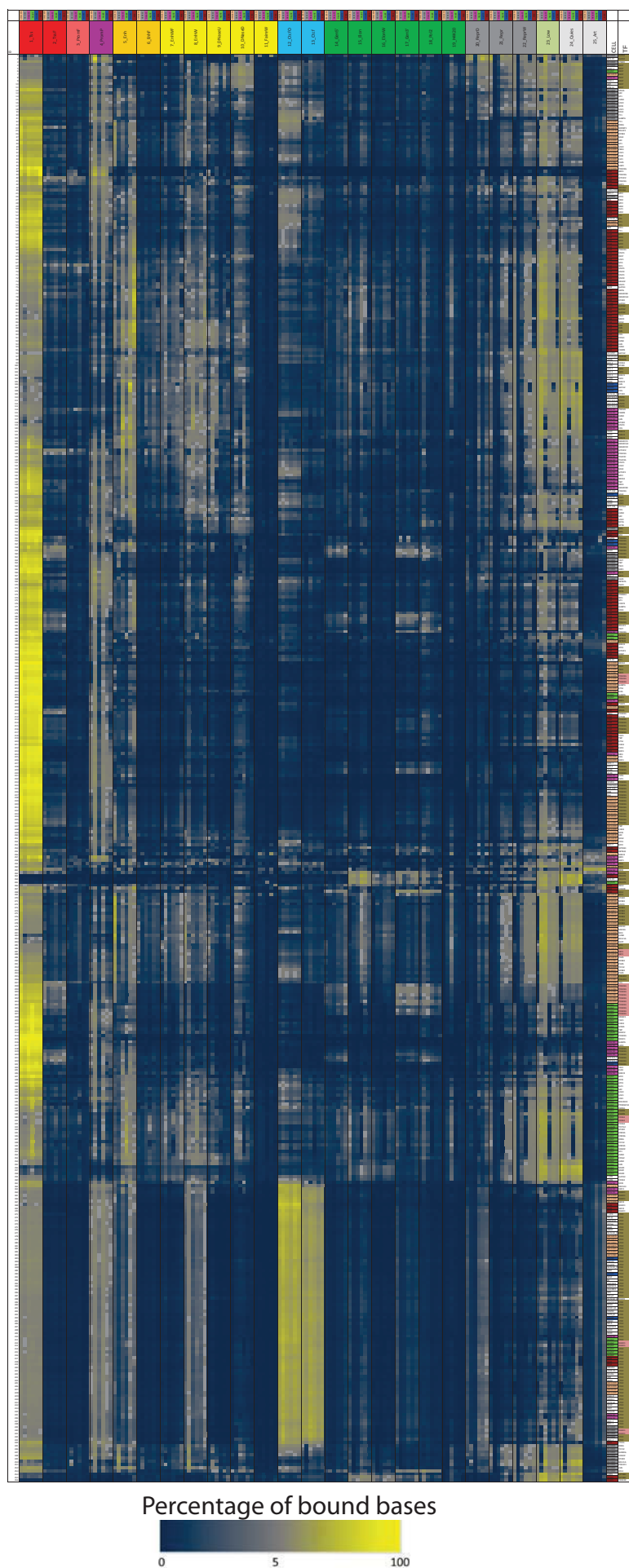
Supplementary Figure 4: Protein-Protein Interaction Enrichments. The figure shows the enrichment for protein-protein interactions falling into the same cluster as a function of the number of clusters. Enrichments are computed two ways. One way assumes a regulator can randomly receive any specific cluster assignment and a second way which first conditions on the size of the clusters (**see Methods**).



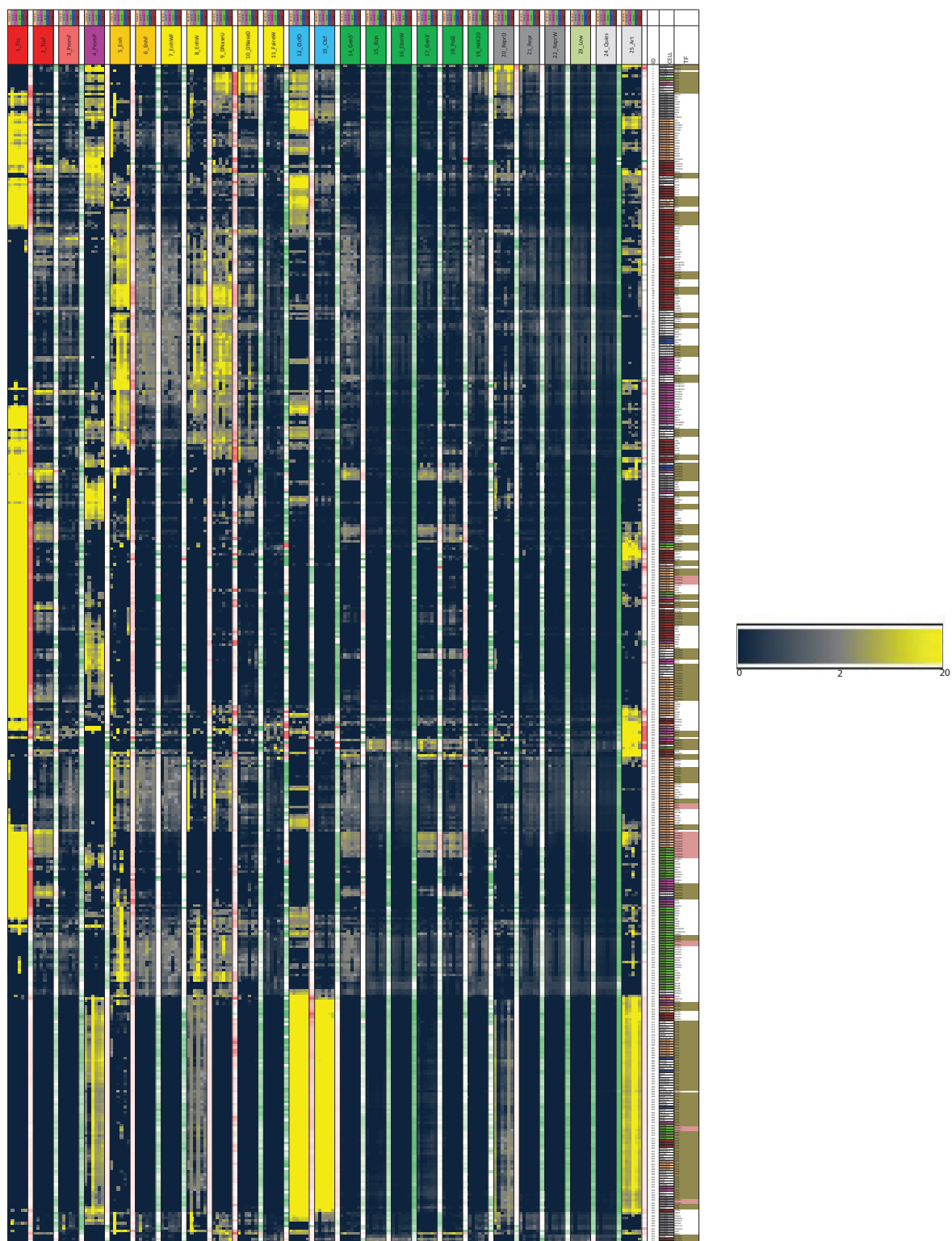
Supplementary Figure 5: Matched Cell Type Chromatin Enrichments. The figure shows the enrichment for each individual experiment with matched chromatin data. The experiments are organized based on the cluster assignment of its corresponding regulator in **Figure 1**. The cell type, regulator, and experiment are displayed in the last three columns. At the bottom are displayed the individual POL2RA and CTCF enrichments not used in the clustering.



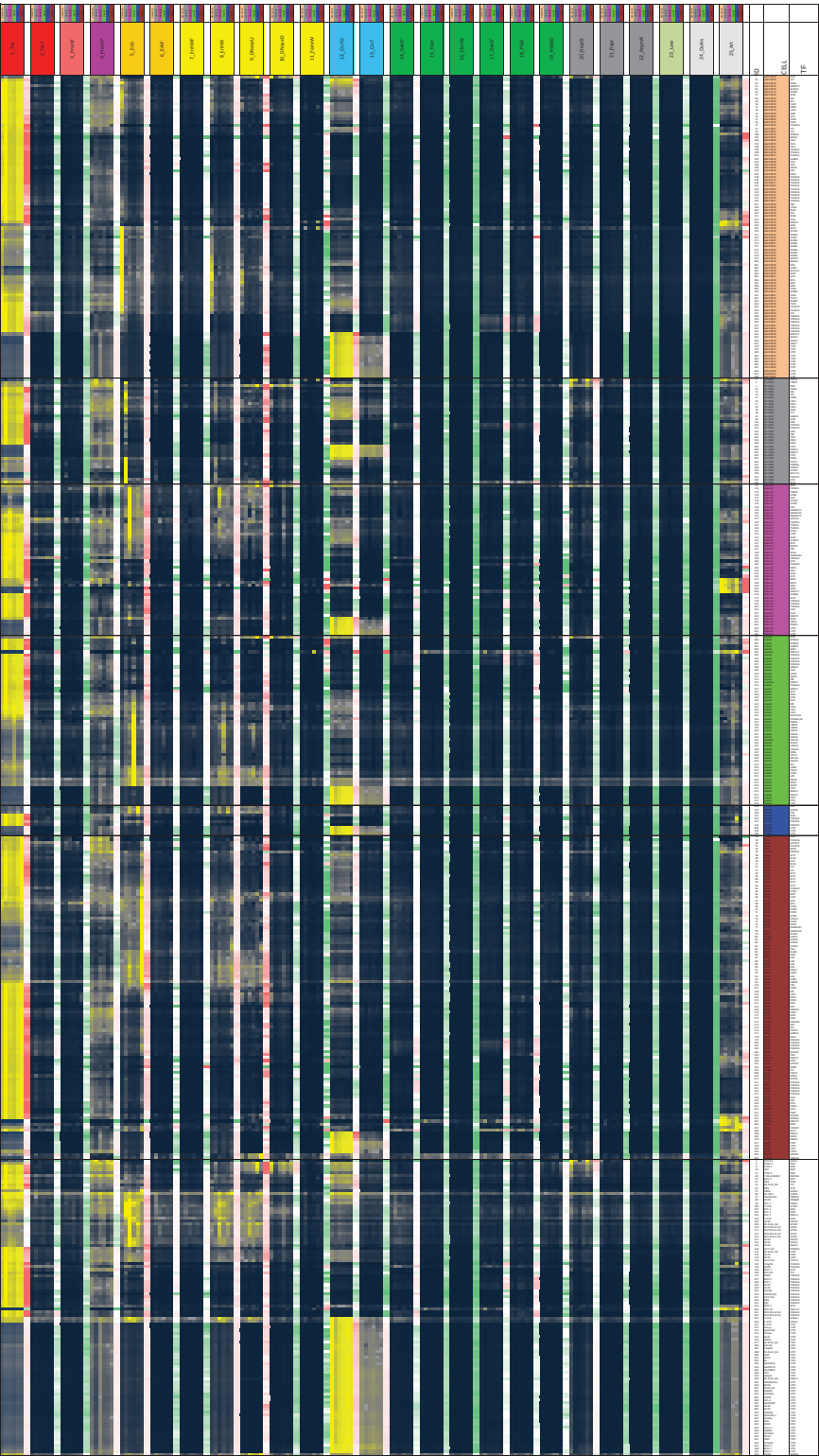
Supplementary Figure 6: Comparison of Streak Coherence. (a) The plots show the fraction of regulator-cell type pairs that fall in a streak of the specified streak length or greater of a common cell type based on the traveling salesman problem formulation in the main text, hierarchical clustering followed by optimal leaf ordering (Bar-Joseph et al, 2001), and a million random orderings. (b) The same as in (a) but for regulators. (c) and (d) The same as (a) and (b) but based on individual experiments. All GM cell lines were considered one cell type in this evaluation. (e) The same as (d) but first excluding CTCF and POL2RA experiments. (f) The same as (e) but only counting once consecutively ordered experiments on the same regulator and cell type.



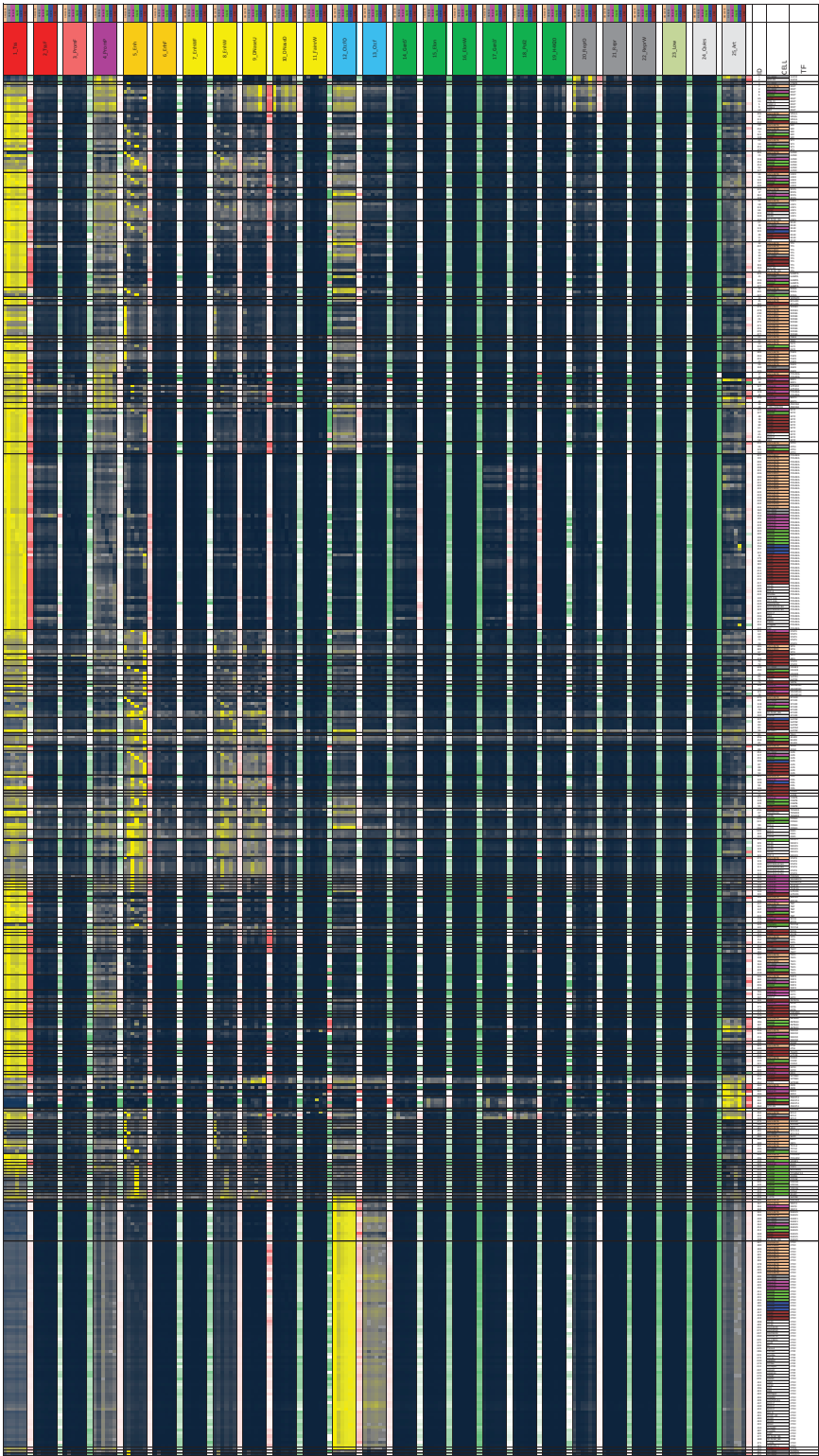
Supplementary Figure 8: Percentage of Bound Locations in Each State. The heatmap indicates for each experiment, chromatin state, and cell type the percentage of bound bases in the experiment that fell in that chromatin state in that cell type. The same ordering as in **Supplementary Figure 7** is shown.



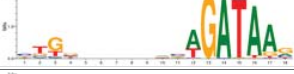
Supplementary Figure 10: Column Subtracted Regulator Binding Enrichment Heat Map. The equivalent figure as **Supplementary Figure 7** except the heat map is colored after subtracting from each fold enrichment value the column median enrichment value using the indicated color scale.



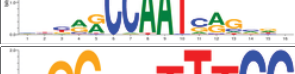
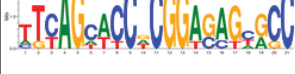
Supplementary Figure 11: Regulator Binding Enrichment Heat Map Ordered Based on Cell Type. The equivalent figure as **Supplementary Figure 7**, except the rows ordered based on cell type. The various GM lines are grouped together. The ordering of cell types is the same ordering used for the columns, with all experiments not corresponding to one of those cell types ordered last. For experiments in the same cell type they were ordered consistent with their order in **Supplementary Figure 7**.



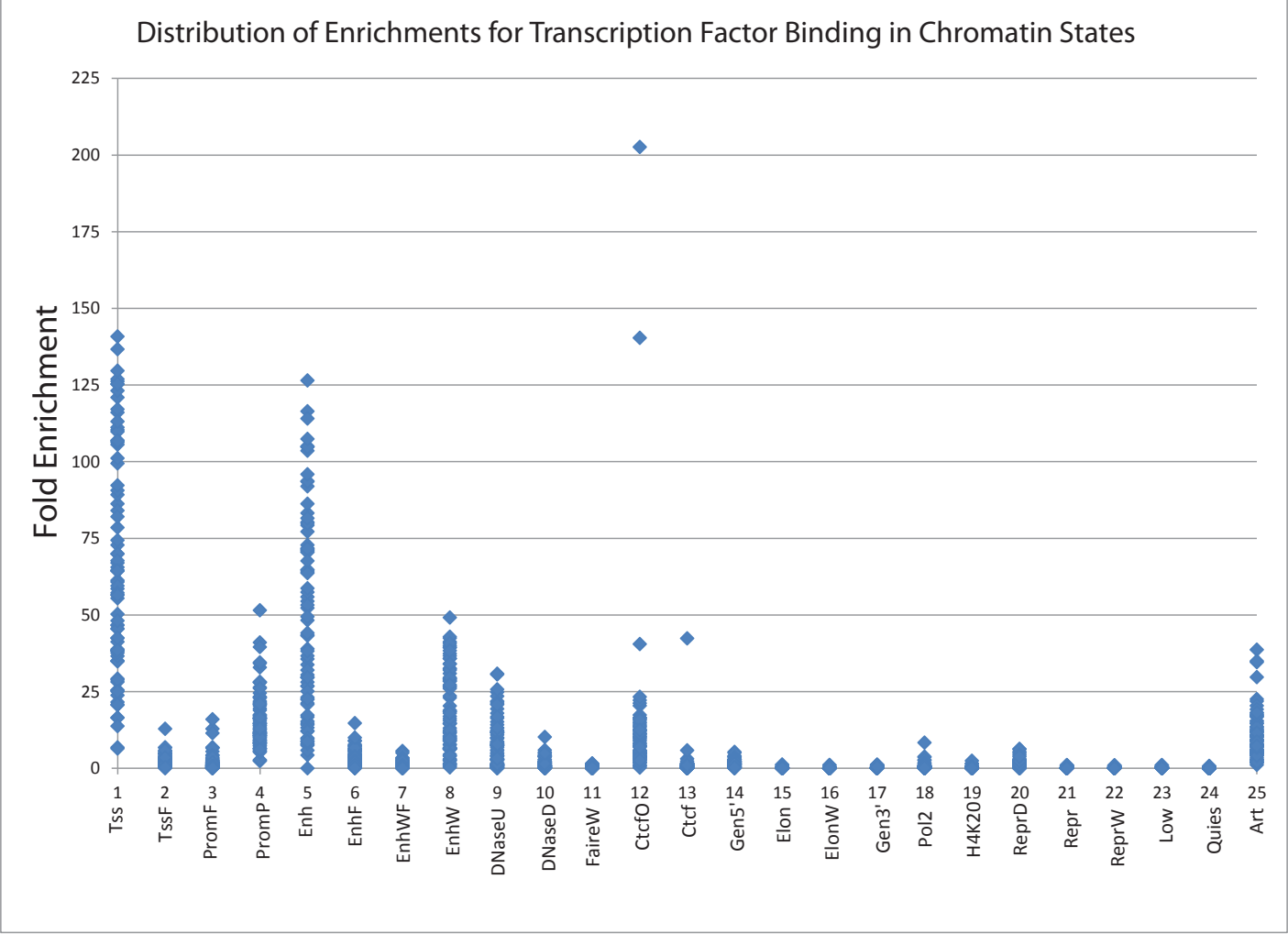
Supplementary Figure 12: Regulator Binding Enrichment Heat Map Ordered Based on Regulator. The equivalent figure as **Supplementary Figure 7** from the main text, except the rows are ordered based on the regulator. The regulators are ordered based on their first appearance in the ordering of **Supplementary Figure 7**. Experiments for the same regulator are ordered based on cell type using the same cell type ordering as the columns treating the various GM lines the same, and then placing experiments on all other cell types last and lexicographically ordered. Experiments on the same regulator and cell type were ordered consistently with **Supplementary Figure 7**.

Motif	TF	Motif Logo	Motif State Enrichment	Relative Motif State Enrichment in Peaks for at least one experiment
AP-1	FOSL2,FOSL1,JUN,JUND,JUNB,FOS		Gm12878 (1,5,7,8,9,10,14) K562 (1,5,6,7,8,9,10,20) Hepg2 (1,4,5,6,8,9,10,20) Huvec (1,5,6,7,8,9,10,14,25) H1hesc (5,7,8,9) Hela3 (1,4,5,6,7,8,9,10,12,14,25)	K562 (4,5,7,8,9,10,14,20,24) Hepg2 (3,4,7,9,10,14,15,20,21,22,23,24) Huvec (1,7,8,9,10,12,14,15,16,23,24) H1hesc (7,8,9,24) Hela3 (1,3,10,12,14,19,20,22,23,24)
AP-2	TFAP2A,TFAP2C		Hela3 (1,4,5,8,9,25)	Hela3 (7,8,9,12,19)
ATF3	ATF3		Gm12878 (1,4,5,8,9,10,20) K562 (1,3,4,5,7,8,9,10,20) Hepg2 (1,4,5,9,10,12) H1hesc (1,4,5,8,9,10,25)	Gm12878 (1) K562 (1) Hepg2 (1) H1hesc (1)
BHLHE40	BHLHE40		Hepg2 (1,17)	Hepg2 (1)
BRCA1	BRCA1			
CEBPB	CEBPB		K562 (8,24) Hepg2 (1,4,5,7,8,10,24) Hela3 (1,4,5,7,8,9,12)	K562 (10,21,22,24) Hepg2 (10,20,21,22,24) Hela3 (10,18,19,21,22,23,24)
CTCF	CTCF		Gm12878 (1,4,5,8,12,13,20,25) K562 (1,4,5,8,12,13,25) Hepg2 (1,4,5,8,12,13,25) Huvec (1,4,5,8,12,13,20,25) H1hesc (1,4,5,8,12,13,25) Hela3 (1,4,5,8,12,13,25)	Gm12878 (8,12,13,15,24,25) K562 (5,12,13,15,24) Hepg2 (8,12,13,15,19,24,25) Huvec (5,8,9,12,13,24,25) H1hesc (12,13,25) Hela3 (8,12,13,15,24,25)
E2F	E2F4,E2F6,E2F1		K562 (1,12,13) Hela3 (1,12,13)	K562 (6,7,12) Hela3 (8)
EBF	EBF1		Gm12878 (5,8,9,24)	Gm12878 (2,3,6,7,9,13,14,15,16,20,21,22,23,24)
ELF1	ELF1		Gm12878 (1,4,5,6,7,8,9,10,12,14) K562 (1,5,6,7,8,9,14) Hepg2 (1,2,3,5,10)	Gm12878 (5,8) K562 (5,6,7,8,9)
ERalpha-a	ESRRA,ESR1		Hepg2 (1,4,5,7,8,9,10,14,17,20)	
Egr-1	EGR1		Gm12878 (1,5,8,9) K562 (1,5,7,8,9)	Gm12878 (2,3,5,6,7,8,9,12,14,23,24) K562 (2,3,5,6,7,8,9,10,12,13,14,15,16,17,18,19,20,21,22,23,24)
Ets	ETS1,ELK4,GABPA		Gm12878 (1,5,6,7,8,9) K562 (1,3,5,9) Hepg2 (1,3) H1hesc (1,5) Hela3 (1,5,6)	Gm12878 (1) K562 (1,3) H1hesc (1)
Foxa	FOXA1,FOXA2		Hepg2 (1,3,4,5,6,7,8,9,10,14,20)	Hepg2 (1,4,8,10,14,18,20,21,24)
GATA	GATA3,GATA2,GATA1		K562 (1,4,5,7,8,9,14,20,25) Huvec (5,7,8,9,10)	K562 (1,4) Huvec (10)
GR	NR3C1			
HNF4	HNF4G,HNF4A		Hepg2 (1,2,3,4,5,6,7,8,9,10,14,17,18,20)	Hepg2 (2,4,12,14)
Hsf	HSF1		Hepg2 (1,4,10,14,15,16,17,20,21,22)	
Irf	IRF4,IRF3,IRF1		Gm12878 (1,3,4,5,7,8,9,14) K562 (1,3,4) Hela3 (1,3)	K562 (4)
Maf	MAFK,MAFF		K562 (1,5,6,7,8,9,10,20) Hepg2 (1,4,5,6,8,9,10,20)	K562 (24) Hepg2 (1,4,9,10,24)

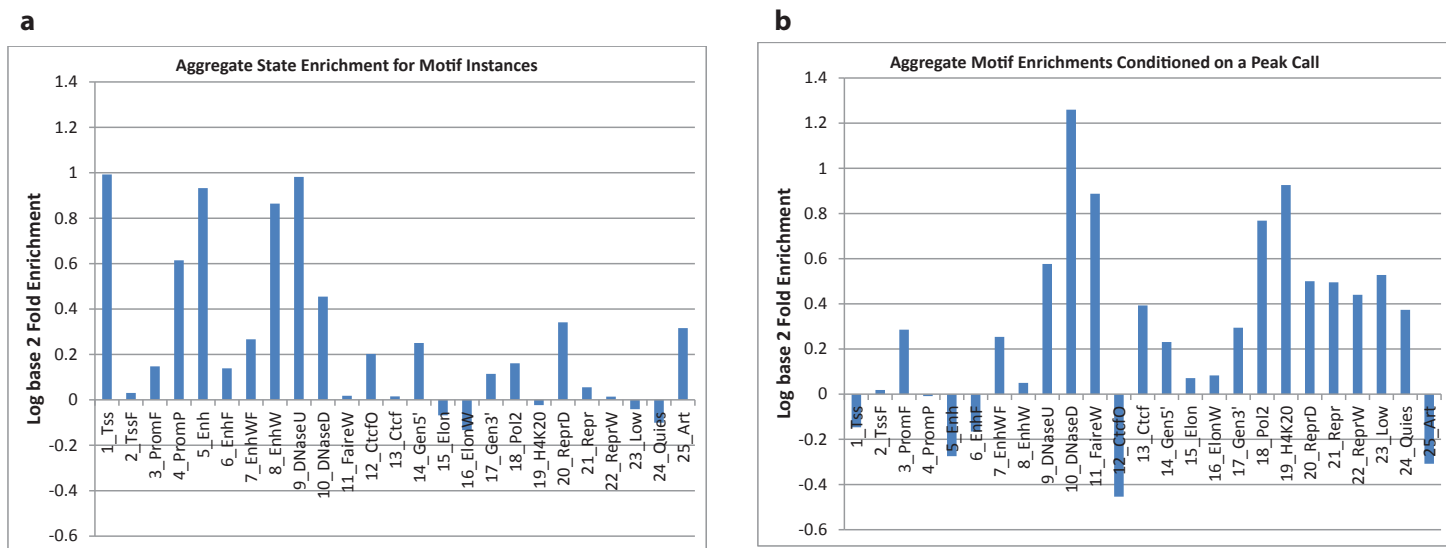
Supplementary Figure 13: Motif Table. The first column gives the motif name. The second column gives the transcription factors associated with the motif. The third column displays the motif logo. The fourth column shows the cell type and state combinations for which there was a significant enrichment of the motif, and at least one of the factors associated with the motif was profiled in that cell type. The last column indicates the cell type and state combinations for which there was at least one factor profiled for which there was a significant relative enrichment for motifs in the peaks in at least one experiment.

Mef2	MEF2A,MEF2C		Gm12878 (1,2,3,4,5,6,7,8,9,10,14,20,22,23)	Gm12878 (1,4,14)
Mxi1	MXI1		K562 (1,14,17) Helas3 (1,18)	
Myc	MAX,MYC,USF2,USF1		Gm12878 (1,4,5,17) K562 (1,4,8,25) Hepg2 (1,4,8,17) Huvec (1,10,11) H1hesc (1,5,10) Helas3 (1,10)	Gm12878 (1,3,6,7,11,20,21,22,23,24) K562 (1,2,6,7,8,9,11,13,14,20,21,22,23,24) Hepg2 (2,3,13,19,21,22,23,24) Huvec (11) H1hesc (1,24) Helas3 (1,19,22,23)
NF-E2	NFE2		Gm12878 (1,5,7,8,9,10,14) K562 (1,5,6,7,8,9,10,14)	K562 (24)
NF-Y	NFYA,NFYB		K562 (1,4,8,9,10)	K562 (1,4)
NF-kappaB	NFKB1		Gm12878 (1,2,4,5,6,7,8,9,10,20)	Gm12878 (6,7,9,14,24)
NRSF	REST		Gm12878 (4,9,10,20) K562 (1,4,9,10,20) Hepg2 (1,4,9,10) H1hesc (1,4,9,12) Helas3 (9,10)	Gm12878 (9,24) K562 (9,10,11,12,17,19,20,22,23,24) Hepg2 (9,19,23,24) H1hesc (9,24) Helas3 (9,10,23,24)
Nanog	NANOG		H1hesc (23,24)	
Nrf1	NRF1		Gm12878 (1,4) K562 (1,4) Hepg2 (1) H1hesc (1,4) Helas3 (1)	Gm12878 (5) K562 (5,8) H1hesc (3,5,8,9,12,20)
PRDM1	PRDM1		Helas3 (1,3,4,5,9,10,12)	Helas3 (3,23)
Pax-5	PAX5		Gm12878 (8,9)	Gm12878 (7,9,22,23,24)
Pbx3	PBX3		Gm12878 (22)	
Pou2f2	POU2F2		Gm12878 (1,4,5,7,8,9,20,24)	Gm12878 (4,7,8,13,22,23)
Pou5f1	POU5F1		H1hesc (1,3,4,5,6,7,8,9,14)	H1hesc (1,4,5,8)
RFX5	RFX5		Gm12878 (1,4,8,9,10,20) Hepg2 (1,4,5,8,9,10,20) H1hesc (1,4,5,6,8,9,10) Helas3 (1,4,9,10)	Gm12878 (4,8) Hepg2 (10) H1hesc (5) Helas3 (1,9,10,19,23)
RXRA	PPARGC1A,RXRA		Gm12878 (1,9,17,18,23) Hepg2 (1,3,4,5,7,8,9,10,14) H1hesc (1,4,10)	H1hesc (1)
SIX5	SIX5		Gm12878 (10,17) K562 (21,22) H1hesc (8,10,13)	
SP1	SP1		Gm12878 (1,4,17) K562 (1,4) Hepg2 (1,4) H1hesc (1,4)	Gm12878 (4) K562 (4) Hepg2 (1,12) H1hesc (4,12)
SREBP	SREBF1		Hepg2 (1,4)	
SRF	SRF		Gm12878 (1,5,16) K562 (1,16) Hepg2 (1,9,16,23) H1hesc (1,5,8,16,23)	Gm12878 (2,6,7,21,22,23,24) K562 (7,8,9,20) Hepg2 (4,7,9,10,20,22,24) H1hesc (8)
STAT	STAT1,STAT2,STAT3		Gm12878 (1,2,4,5,10,12,18,20,21,22) K562 (1,2,3,4,5,7,8,10,20,21)	K562 (1,4,20) Helas3 (1,23)

			Helas3 (1,2,4,5,10,18,20,21)	
TAL1	TAL1		K562 (12,13)	
TATA	TAF1,TAF7,GTF2F1,GTF2B,TBP		Gm12878 (1,4,15,16) K562 (1,11,15,16,20,22) Hepg2 (1,4,10,15,16,23) H1hesc (1,4) Helas3 (1,15,16,17)	K562 (1,4) Hepg2 (4) H1hesc (1,4) Helas3 (1)
TCF12	TCF12		Gm12878 (24) Hepg2 (24) H1hesc (24)	Gm12878 (7,23,24)
TCF4	TCF7L2		Hepg2 (1,4,5,6,7,8,9,10,14,20)	Hepg2 (4,10,14,20,24)
YY1	YY1		Gm12878 (1,12,24) K562 (1,24) H1hesc (1,24)	Gm12878 (1,2,3,7,15,23,24) K562 (1,2,22,23) H1hesc (1,10,23,24)
ZBTB33	ZBTB33		K562 (20,21) Hepg2 (4,10,20,21)	
ZBTB7A	ZBTB7A		K562 (5,7,19,22,23,24)	K562 (2,5,6,8,14)
ZEB1	ZEB1		Gm12878 (1,4,5,6,8,15)	
Znf143	ZNF143		Gm12878 (1)	Gm12878 (1)
p300	EP300		Gm12878 (5) K562 (5) Hepg2 (21) Helas3 (5,9)	Helas3 (5)



Supplementary Figure 14: Distribution of Transcription Factor Binding Enrichments in each Chromatin State. For the 79 transcription factors with a sequence motif considered in **Figure 3**, the chart shows the distribution of their median fold enrichments in each chromatin state.



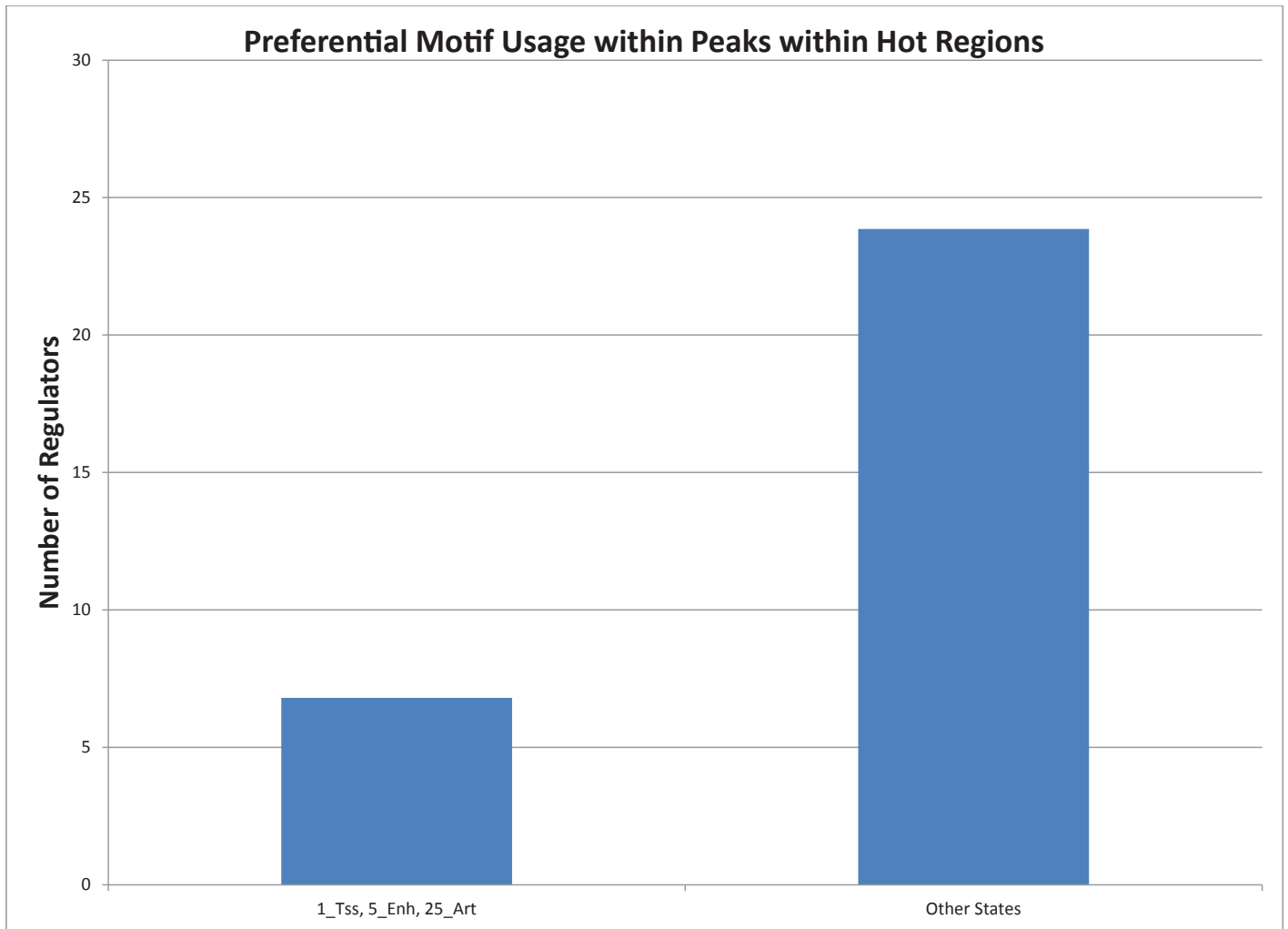
Supplementary Figure 15: Motif enrichments variation across chromatin states. **a.** Aggregate regulatory motif enrichments in each chromatin state mirror overall density of TF binding. **b.** Aggregate motif enrichments in TF binding peak calls lying within each chromatin state relative to the baseline motif enrichment in peak calls. Enriched bars are of states in which peaks are most likely to contain motif bases, while depleted bars are for chromatin states in which peaks are least likely to contain motif bases, suggesting non-specific binding in permissive chromatin states. Motifs for CTCF were excluded from this analysis.

Cluster	1_Tss	2_TssF	3_PromF	4_PromP	5_Enh	6_EnhF	7_EnhWF	8_EnhW	9_DNaseU	10_DNaseD	11_FaireW	12_CtcfO	13_Ctcf	14_Gen5'	15_Elon	16_ElonW	17_Gen3'	18_Pol2	19_H4K20	20_ReprD	21_Repr	22_ReprW	23_Low	24_Quies	25_Art
1	2.1	0.9	1.0	1.3	1.1	1.0	1.0	1.1	1.1	1.0	0.9	1.1	1.0		0.9	0.9	0.9	1.0		0.9			0.9	0.9	1.0
2	1.4	1.0	1.0	1.2	1.3	0.9	1.0	1.4	1.2	1.1		1.2	1.1	0.9	1.0	0.9	1.0	1.0	1.0	1.0	1.0	0.9	0.9	1.0	0.9
4	1.6	0.9	1.0	1.3	1.3	1.0	1.0	1.3	1.4	1.2	1.0	1.0	1.0	1.1	1.0	0.9	1.0	1.0	0.9	1.1	1.0	1.0	1.0	0.9	1.2
5	1.7	1.0	1.1	1.4	1.3	1.0	1.1	1.3	1.3	1.2		1.0	0.9	1.1	1.0	0.9	1.0	1.1	1.0	1.1	1.0	1.0	1.0	0.9	1.1
6	1.4	1.0	1.1	1.3	1.8	1.1	1.2	1.7	1.9	1.2	1.0	1.0	0.9	1.1	0.9	0.9	0.9	1.0		1.1	1.0	1.0	0.9	1.0	1.2
7	1.4	0.9	1.1	1.3	2.1	1.1	1.2	2.1	2.5	1.4	0.9	1.1	1.0	1.1		0.9	0.9	0.9	0.9	1.1	0.9	1.0	0.9	1.0	1.2
10	1.2	1.0	1.0	1.4		1.0	0.9	1.0	2.1	1.5	1.1	1.2	0.9		0.9	0.9	0.9	0.9	0.9	1.0	1.1	1.0	1.0	0.9	1.0

Supplementary Figure 16: Regulatory motif enrichments in each cluster match chromatin state preferences. Each entry indicates the average enrichment in each chromatin state (column) for the known regulatory motifs and cell types of corresponding regulators in a given cluster (row).

state	Gm12878	H1hesc	HeLa3	Hepg2	K562
1_Tss	52.3	59.8	35.8	45.5	45.3
2_TssF	11.3	12.2	16.3	9.6	11.8
3_PromF	0.7	2.0	1.9	1.2	0.7
4_PromP	14.1	27.8	14.3	16.4	9.2
5_Enh	49.0	53.3	47.1	43.8	41.8
6_EnhF	5.6	6.9	6.7	4.9	4.4
7_EnhWF	0.7	0.9	1.8	1.3	0.6
8_EnhW	17.7	19.8	16.9	14.6	10.1
9_DNaseU	2.7	2.1	2.1	1.2	0.7
10_DNaseD	0.6	0.3	0.7	0.7	0.5
11_FaireW	0.8	0.9	2.4	4.5	7.8
12_CtcfO	34.1	35.4	18.5	19.4	14.9
13_Ctcf	0.9	2.5	1.1	0.8	0.4
14_Gen5'	3.2	3.3	10.9	7.4	3.9
15_Elon	0.1	0.0	1.4	0.3	0.3
16_ElonW	0.0	0.0	0.1	0.0	0.0
17_Gen3'	0.3	0.3	3.5	2.7	1.1
18_Pol2	0.2	0.3	0.6	0.9	0.3
19_H4K20	0.2	0.1	0.8	0.4	0.4
20_ReprD	1.5	2.9	3.9	3.4	1.5
21_Repr	0.0	0.1	0.4	0.4	0.1
22_ReprW	0.0	0.0	0.0	0.0	0.0
23_Low	0.0	0.0	0.1	0.1	0.0
24_Quies	0.0	0.0	0.0	0.0	0.0
25_Art	46.6	48.9	53.3	56.4	76.7
Genome %	0.85	0.87	0.84	0.86	0.88

Supplementary Figure 17: HOT Region State Enrichments. The table gives the fold enrichment for HOT regions from (Yip et al, 2012) in each chromatin state.



Supplementary Figure 18: Differential Motif Usage within HOT Regions Based on Chromatin State. The chart shows the number of regulators for which the peaks in HOT regions were significantly more likely if they were in States 1_Tss, 5_Enh, and 25_Art or if they were in one of the other 22 states at a $p < 0.01$. If there were multiple experiments for the same regulator, they were weighted inversely proportional to the number of experiments.

Regulator	Cell Type	Binding Type	1_Tss	2_TssF	3_PromF	4_PromI	5_Enh	6_EnhF	7_EnhWF	8_EnhW	9_DNaseU	10_DNaseD	11_Fairw	12_Ctrf	13_Ctrf	14_Gen5'	15_Elon	16_ElonW	17_Gen3'	18_Po2	19_H4K20	20_ReprD	21_Repr	22_ReprW	23_Low	24_Quies	25_Art	Genome %
ATF3	Gm12878	Shared	105.7	0.1	0.1	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0002	
ATF3	H1hesc	Shared	147.4	0.8	0.0	0.0	0.0	0.0	0.2	0.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0019	
ATF3	Hepg2	Shared	106.0	0.0	0.3	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0007	
ATF3	Hepg2	Excluded	146.6	0.2	0.5	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0004	
ATF3	Gm12878	Unique	67.2	1.0	0.2	0.0	0.0	0.0	0.3	0.7	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0018	
ATF3	H1hesc	Unique	66.0	1.7	0.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0048	
ATF3	Hepg2	Unique	67.2	2.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0007	
ATF3	K562	Unique	91.3	0.4	0.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0026	
ATF3	Gm12878	Excluded	53.0	1.1	0.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0034	
ATF3	H1hesc	Excluded	75.7	2.5	0.6	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0027	
ATF3	Hepg2	Excluded	48.8	0.9	0.5	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0021	
ATF3	K562	Excluded	64.6	1.4	2.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0005	
BC11A	Gm12878	Shared	57.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0002	
BC11A	H1hesc	Shared	84.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0008	
BC11A	Hepg2	Shared	79.4	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0012	
BC11A	H1hesc	Excluded	15.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0009	
BC11A	Gm12878	Unique	2.4	1.5	1.5	0.4	0.7	1.6	1.9	0.0	0.0	0.0	0.0															

[illegible]

[illegible]

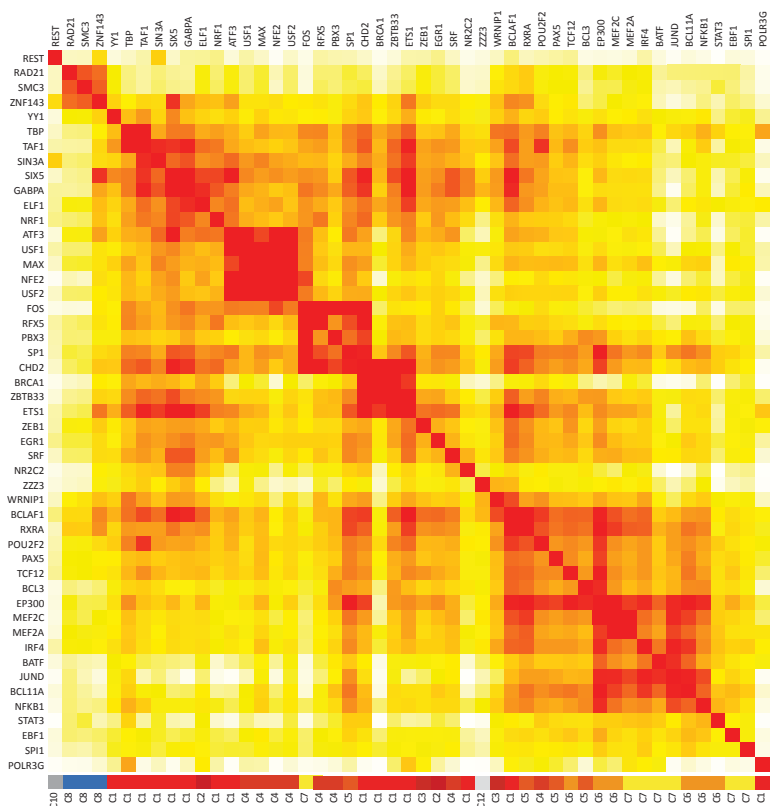
[illegible]

	GM12878 (37)				H1hesc (26)				Hepg2 (27)				Hela3 (33)				K562 (50)		
	Shared	Unique	Excluded		Shared	Unique	Excluded		Shared	Unique	Excluded		Shared	Unique	Excluded		Shared	Unique	Excluded
1 Tss	98.7	64.0	29.5		115.2	39.8	46.4		85.5	52.1	32.1		88.4	40.2	29.6		119.7	64.8	36.2
2 TssF	0.4	1.6	2.3		1.9	4.6	3.6		0.8	2.3	2.6		0.9	2.4	3.2		1.6	3.1	2.8
3 PromF	0.1	0.4	1.6		0.5	2.2	1.6		0.5	1.1	2.4		0.2	0.6	2.1		0.7	1.8	2.5
4 PromP	19.8	14.9	15.8		16.4	19.0	9.4		10.1	11.3	13.5		12.6	12.5	14.4		13.0	12.6	14.0
5 Enh	7.8	42.1	5.6		25.2	57.7	11.5		9.8	57.4	6.5		7.8	60.6	6.0		9.8	36.6	9.1
6 EnhF	0.2	1.4	1.2		1.0	4.0	3.2		0.4	1.9	1.6		0.3	1.7	2.0		0.4	2.0	2.1
7 EnhWF	0.0	0.4	1.4		0.2	0.8	2.2		0.2	0.5	1.5		0.2	0.4	0.9		0.2	0.5	1.9
8 EnhW	5.1	15.3	6.0		6.9	21.5	7.1		4.6	15.2	6.7		3.9	14.0	3.5		5.0	12.0	7.2
9 DNaseU	2.3	3.3	5.6		1.6	5.6	4.4		3.2	5.1	5.3		3.5	2.7	3.1		1.9	2.9	5.1
10 DNaseD	1.1	0.8	4.3		0.4	0.8	1.9		0.5	0.6	5.7		0.3	0.2	2.6		0.5	0.5	2.0
11 FaireW	0.0	0.1	0.8		0.1	0.3	1.5		0.1	0.2	0.5		0.0	0.1	0.4		0.0	0.4	0.6
12 Ctcfo	7.8	4.8	9.2		11.7	14.0	6.5		9.4	3.4	10.4		6.2	8.6	6.8		4.2	4.5	5.9
13 Ctcf	0.1	0.3	2.4		0.2	0.8	1.6		0.2	0.3	2.5		0.2	0.2	2.2		0.2	0.4	1.6
14 Gen5'	0.3	1.2	1.9		0.7	1.9	3.2		0.4	1.4	2.1		0.0	0.6	2.3		0.3	1.1	1.8
15 Elon	0.0	0.0	0.6		0.0	0.0	0.8		0.0	0.0	0.7		0.0	0.0	0.5		0.0	0.1	0.5
16 ElonW	0.0	0.0	0.3		0.0	0.0	0.4		0.0	0.0	0.3		0.0	0.0	0.2		0.0	0.0	0.2
17 Gen3'	0.1	0.2	1.3		0.2	0.2	1.1		0.1	0.2	1.3		0.0	0.1	1.0		0.1	0.2	0.7
18 Pol2	0.2	0.3	2.0		0.2	0.4	1.0		0.2	0.4	1.7		0.1	0.1	1.8		0.2	0.3	0.9
19 H4K20	0.0	0.0	1.1		0.1	0.2	1.4		0.1	0.1	0.8		0.0	0.0	0.9		0.0	0.0	1.0
20 ReprD	1.0	0.8	7.1		0.8	4.0	2.2		0.4	0.7	3.1		0.2	0.1	1.1		0.7	1.0	2.4
21 Repr	0.0	0.0	1.6		0.0	0.1	0.9		0.0	0.0	0.9		0.0	0.0	0.4		0.0	0.1	0.9
22 ReprW	0.0	0.0	0.8		0.0	0.1	0.7		0.0	0.0	0.7		0.0	0.0	0.4		0.0	0.1	0.5
23 Low	0.0	0.0	0.7		0.0	0.0	0.6		0.0	0.0	0.6		0.0	0.0	0.5		0.0	0.1	0.5
24 Quies	0.0	0.0	0.3		0.0	0.0	0.2		0.0	0.0	0.2		0.0	0.0	0.2		0.0	0.0	0.2
25 Art	9.6	11.6	6.9		6.5	7.5	8.0		10.1	15.9	9.3		5.1	9.1	7.0		4.5	10.8	4.5
Median Genome %	0.02	0.01	0.09		0.01	0.02	0.13		0.02	0.04	0.11		0.02	0.02	0.03		0.02	0.02	0.06

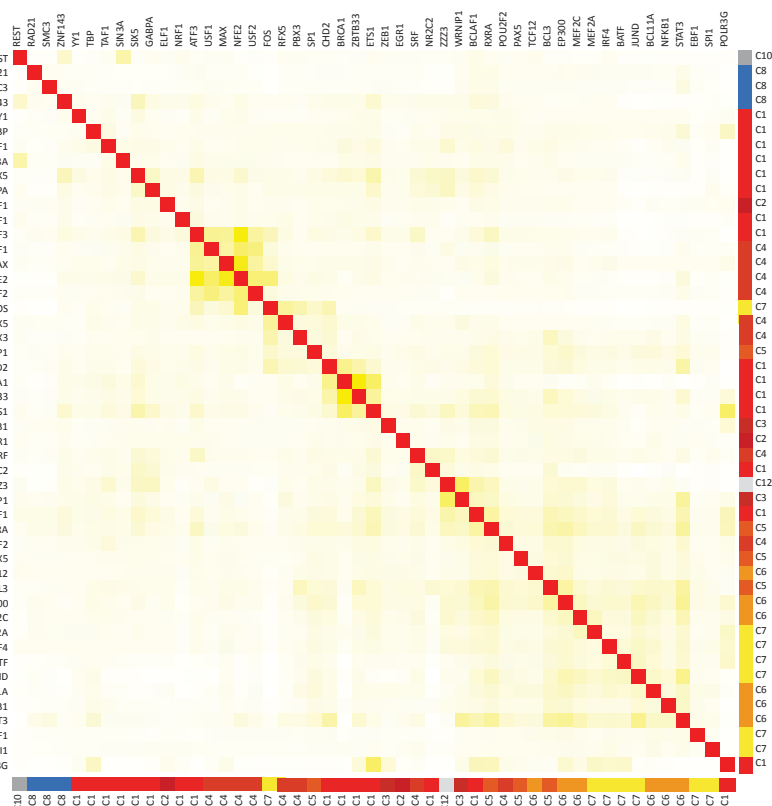
Supplementary Figure 20: Dynamic Binding Enrichments Summary. Each group of three columns corresponds to one cell type and the three columns within each group correspond respectively to bases of shared binding with at least one other cell type, uniquely bound bases, and excluded binding comprising bases only bound in other cell types. The values in each cell correspond to the median fold enrichment. Only regulators mapped in at least one other cell type from the given cell type were considered and the number of such regulators is specified in the parentheses next to the cell type.

a

Co-binding Pairwise Raw Enrichments in Gm12878



Co-binding Pairwise Conditional Enrichments in Gm12878

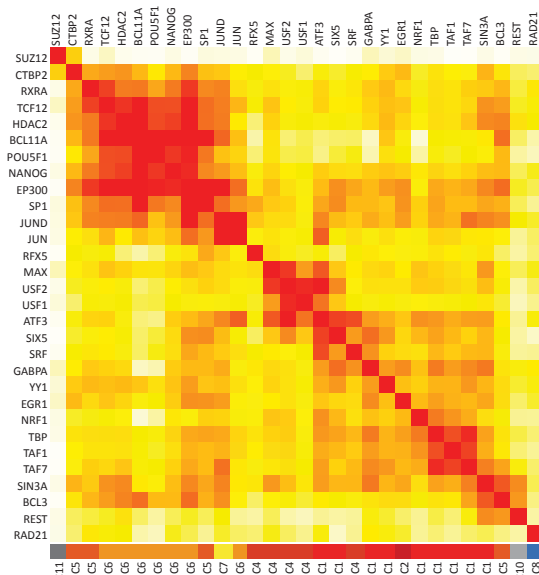


Supplementary Figure 21: Additional Pairwise Regulatory Binding Enrichments. Pairwise enrichments of regulatory binding both (Left) directly and (Right) conditioned on the chromatin state preferences of each factor in the pair as in **Figure 5** of the main text, but shown here for (a) GM12878, (b) H1hesc, (c) HeLa-S3, and (d) Huvec. The cluster assignments correspond to main figure 1.

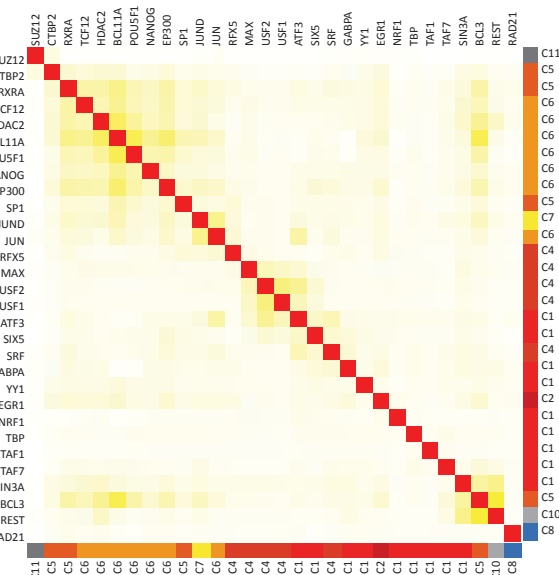


b

Co-binding Pairwise Raw Enrichments in H1hesc

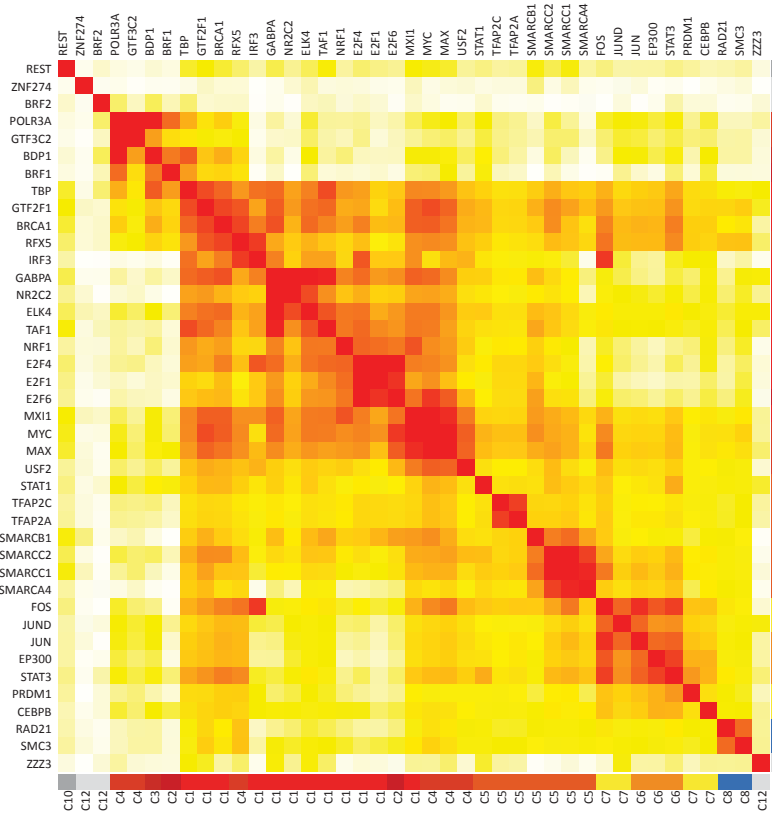


Co-binding Pairwise Conditional Enrichments in H1hesc

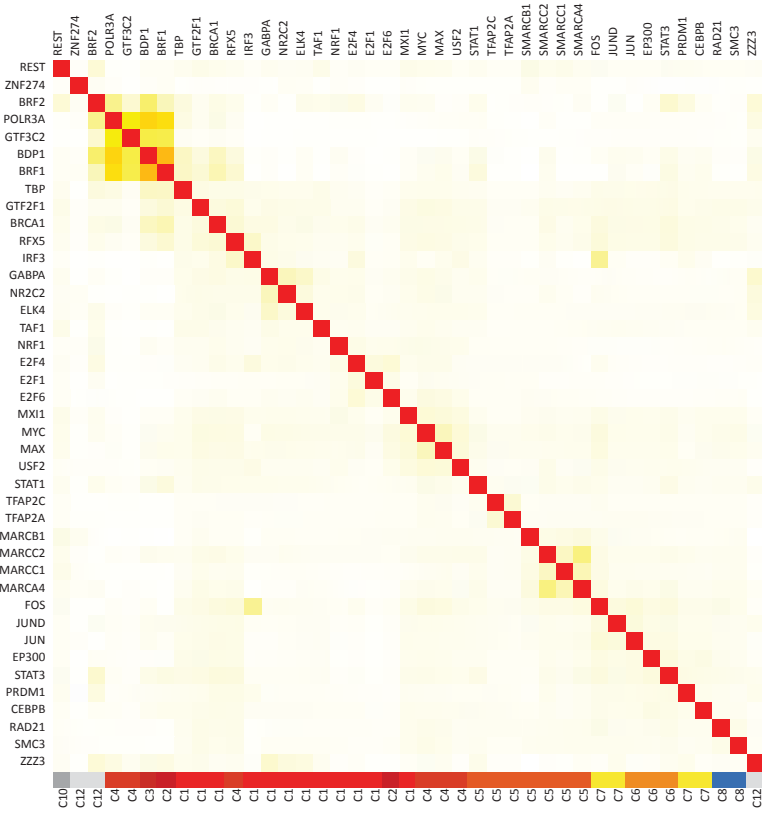


c

Co-binding Pairwise Raw Enrichments in HeLa-S3

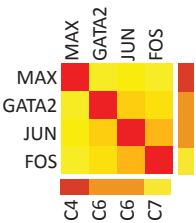


Co-binding Pairwise Conditional Enrichments in HeLa-S3

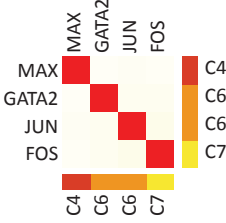


d

Co-binding Pairwise Raw Enrichments in Huvec

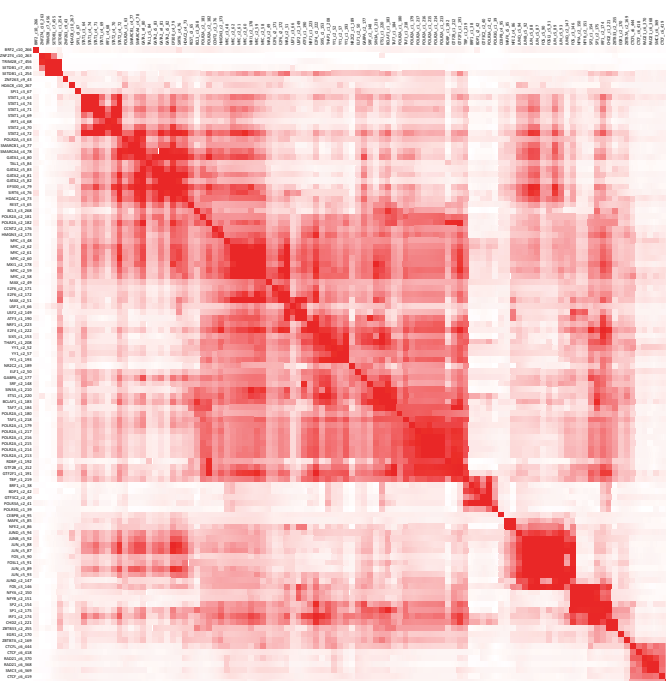


Co-binding Pairwise Conditional Enrichments in Huvec

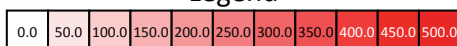


a

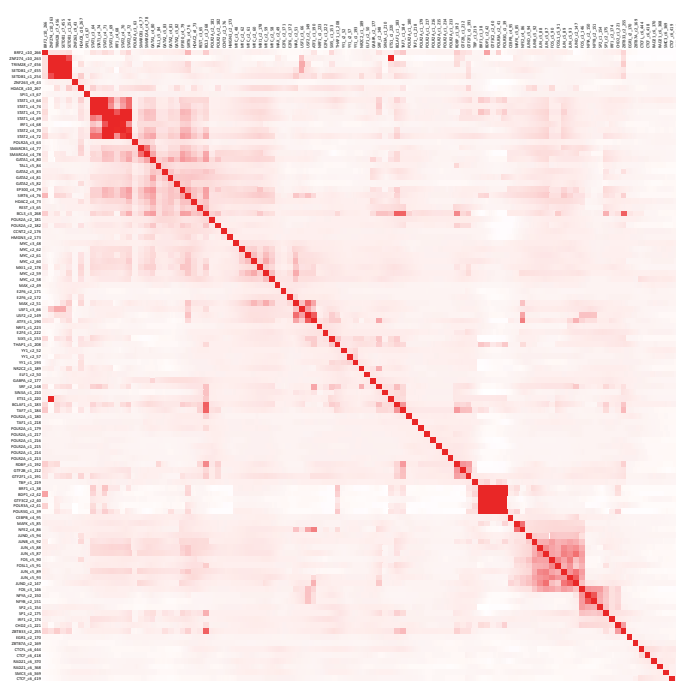
K562 Pairwise Raw Enrichments



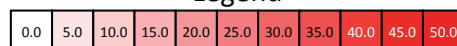
Legend



K562 Pairwise Conditional Enrichments



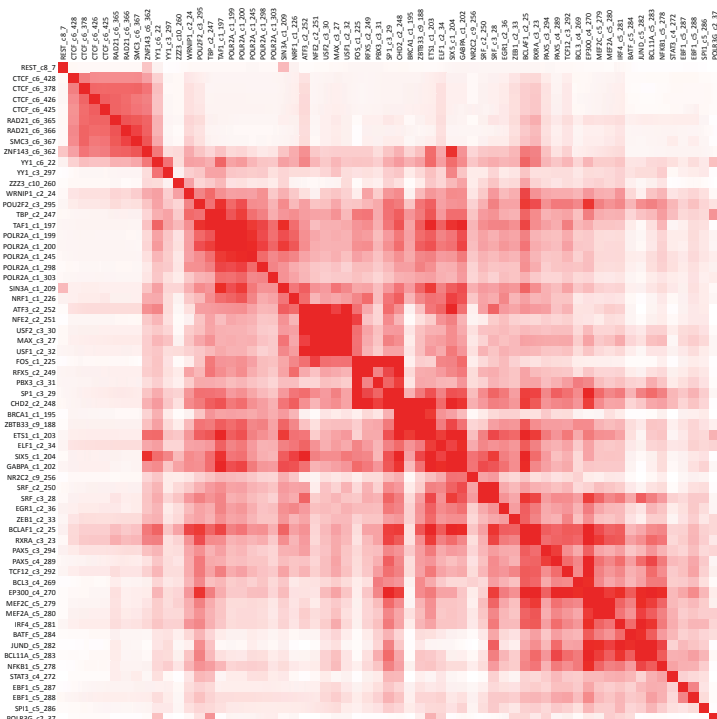
Legend



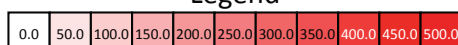
Supplementary Figure 22: Pairwise Regulatory Binding Experiments Enrichments. Pairwise enrichments of regulatory binding at the individual experiment level both (**Left**) directly and (**Right**) conditioned on the chromatin state preferences of each factor in the pair for (**a**) K562, (**b**) GM12878, (**c**) H1hesc, (**d**) HeLa-S3, (**e**) HepG2, and (**f**) Huvec. The color scale for the raw enrichments on left go to 500 while the conditional enrichments on right only go to 50. Next to the regulator name is a cluster assignment based on a 10-state clustering of experiment chromatin state enrichments (not shown) and the experiment ID from **Supplementary Figure 8**.

b

Gm12878 Pairwise Raw Enrichments



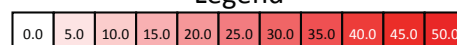
Legend



Gm12878 Pairwise Conditional Enrichments

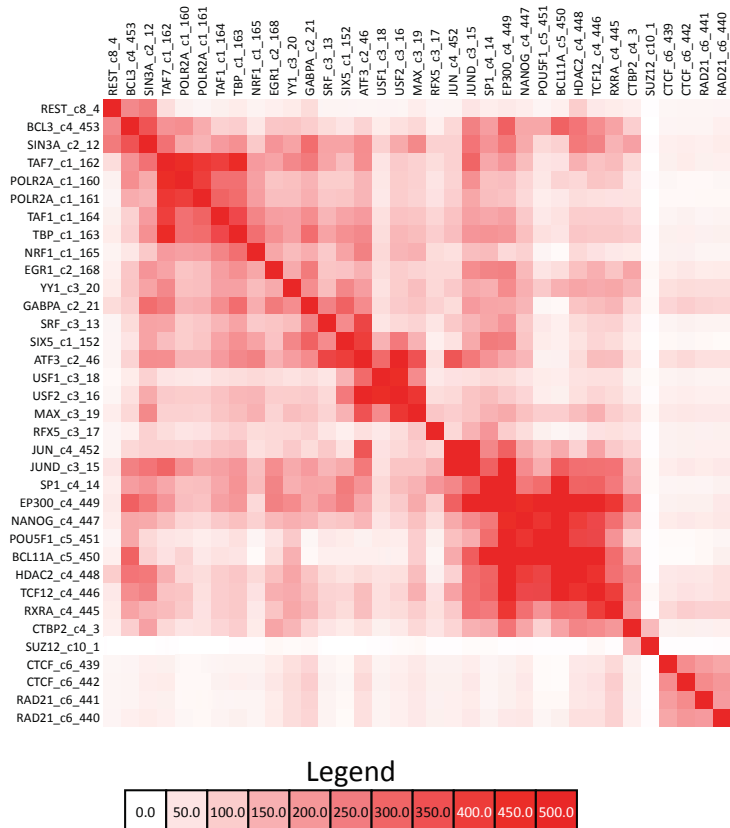


Legend

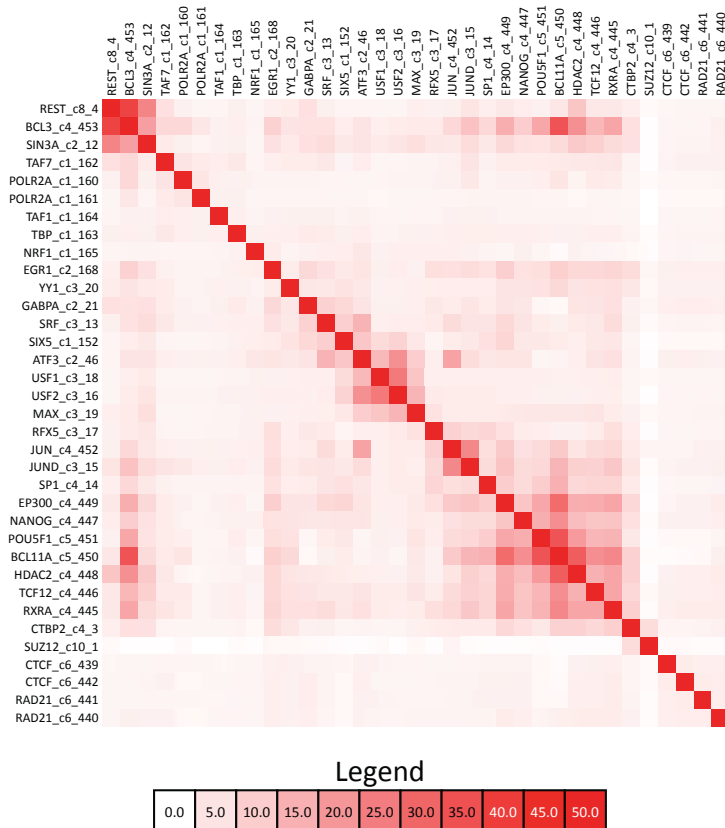


C

H1hesc Pairwise Raw Enrichments

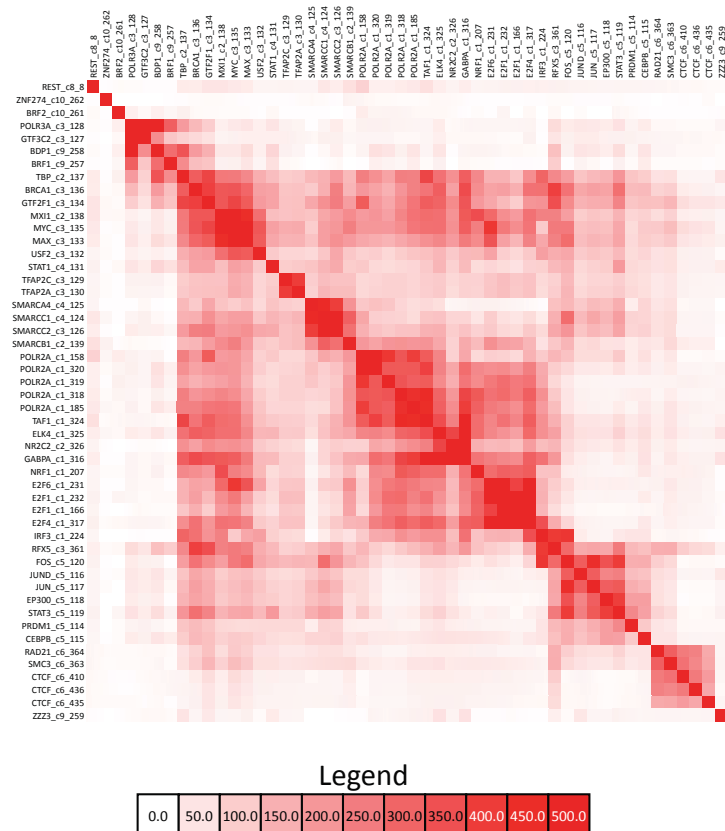


H1hesc Pairwise Conditional Enrichments

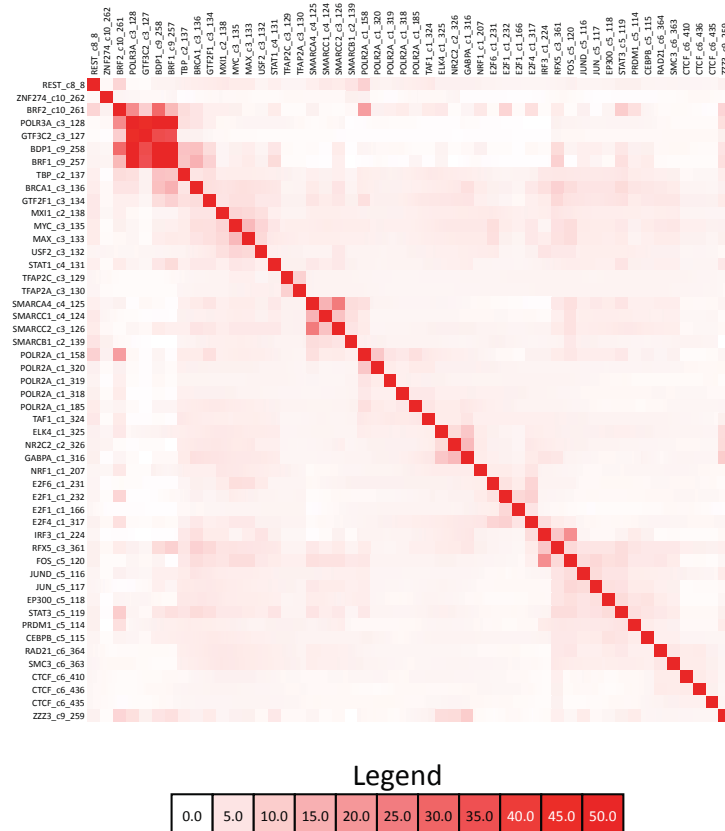


d

HeLa-S3 Pairwise Raw Enrichments

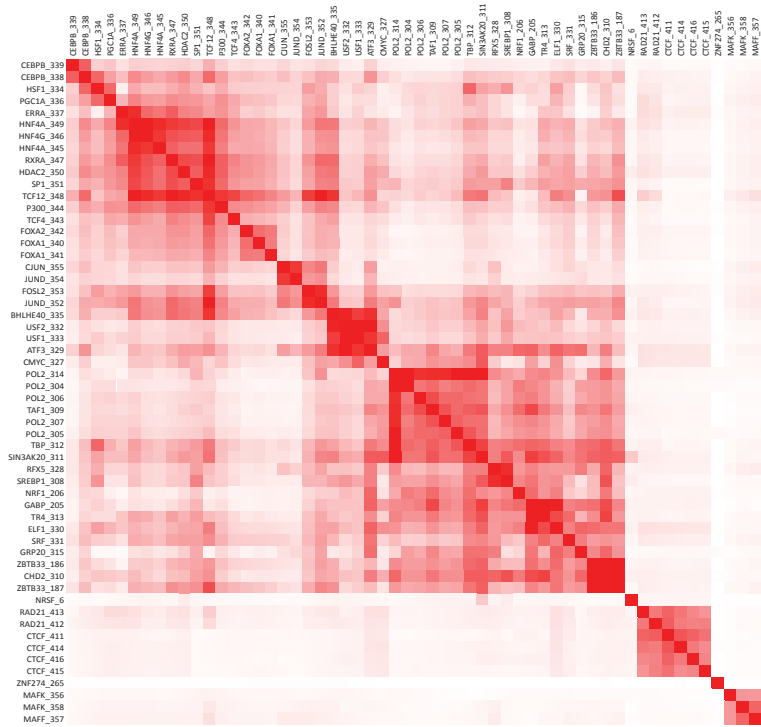


HeLa-S3 Pairwise Conditional Enrichments

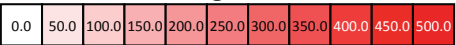


e

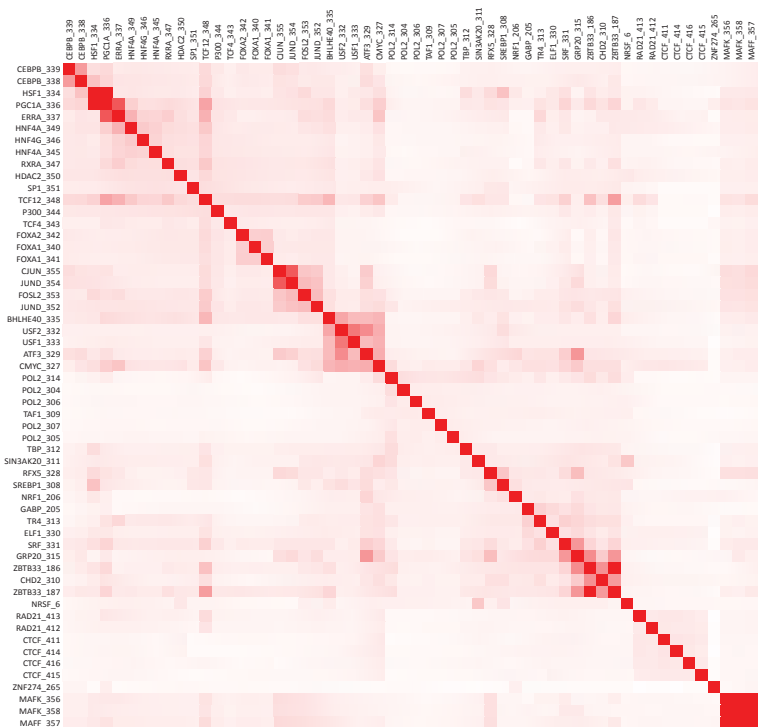
HepG2 Pairwise Raw Enrichments



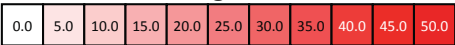
Legend



HepG2 Pairwise Conditional Enrichments

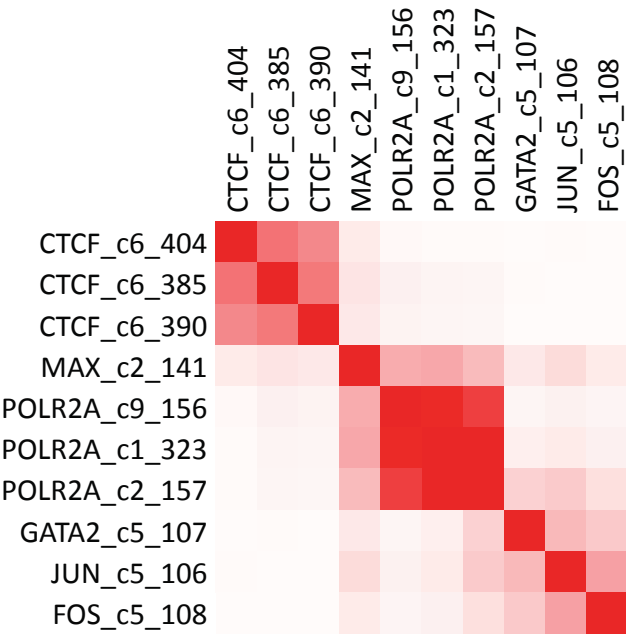


Legend

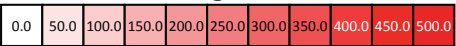


f

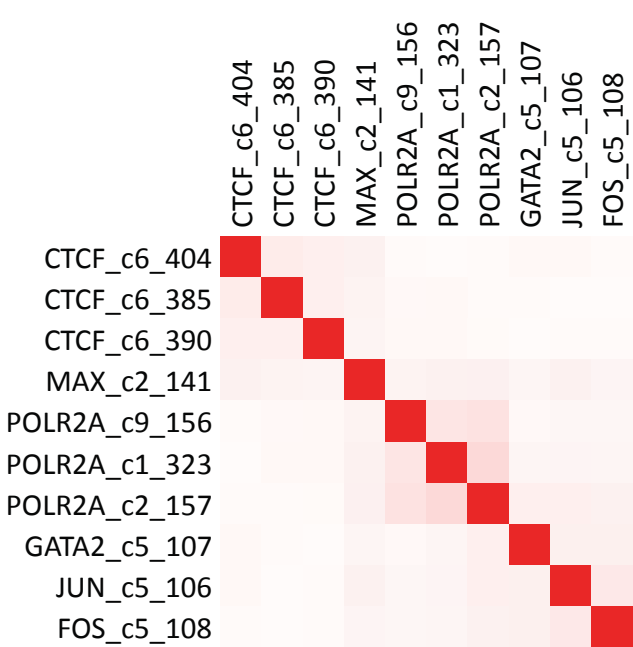
Huvec Pairwise Raw Enrichments



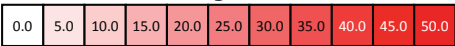
Legend



Huvec Pairwise Conditional Enrichments

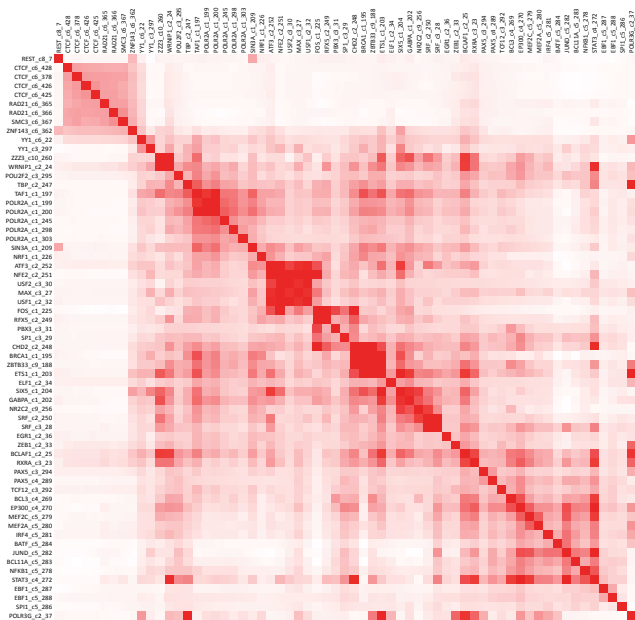


Legend

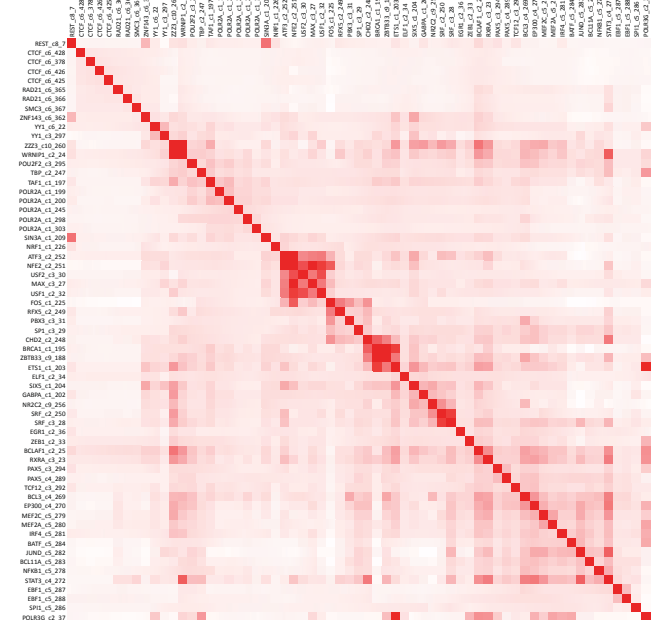


a

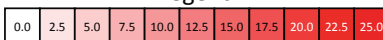
Gm12878 Pairwise Conditional Enrichments DNase



Gm12878 Pairwise Conditional Enrichments DNase+State



Legend



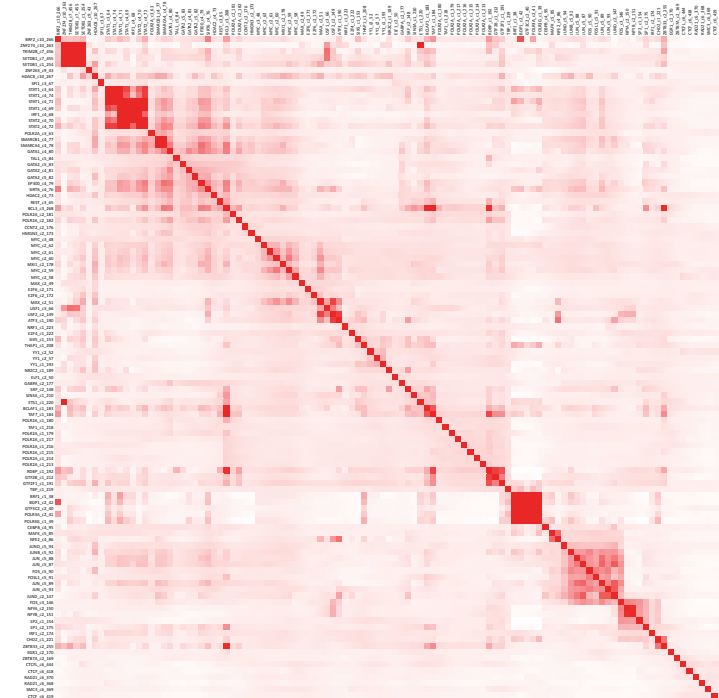
Supplementary Figure 23: Chromatin States Explain Pairwise Regulator Enrichments beyond DNase. The figure illustrates that chromatin states can explain pairwise enrichments of regulators beyond what is captured based on open chromatin as defined by being in a DNase hypersensitive peak from the University of Washington experiments (Thurman et al, 2012). For each cell type the pairwise regulator enrichment conditioning on being in a **(left)** DNase site and **(right)** additionally conditioning on the chromatin state information are shown for **(a)** Gm12878, **(b)** K562, **(c)** H1hesc, **(d)** HeLa-S3, **(e)** HepG2 and **(f)** Huvec.

b

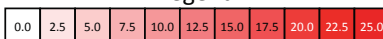
K562 Pairwise Conditional Enrichments DNase



K562 Pairwise Conditional Enrichments DNase+State

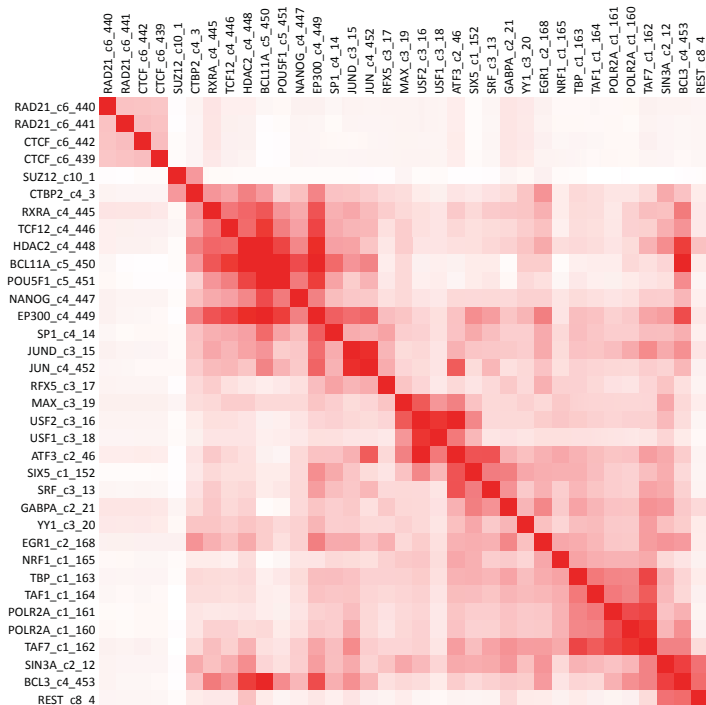


Legend

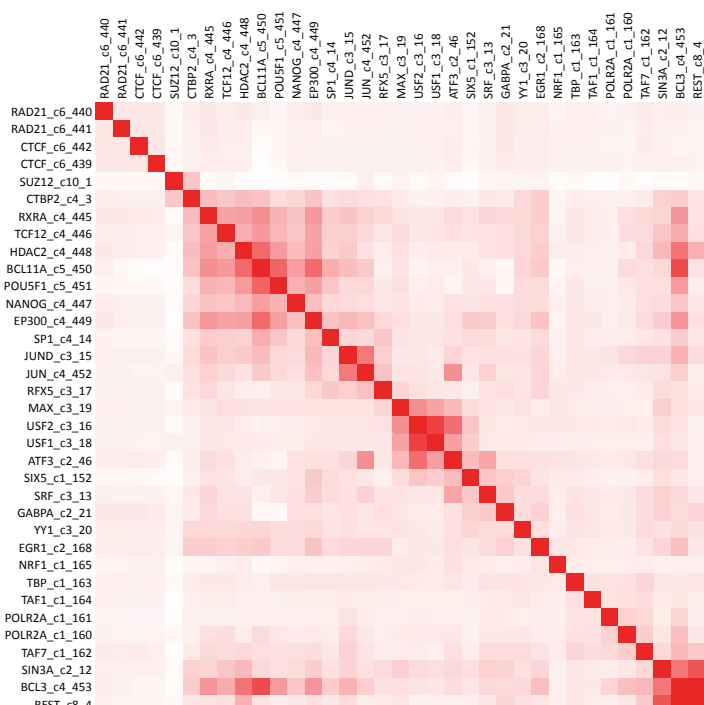


C

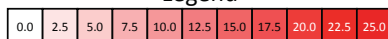
H1hesec Pairwise Conditional Enrichments DNase



H1hesec Pairwise Conditional Enrichments DNase+State

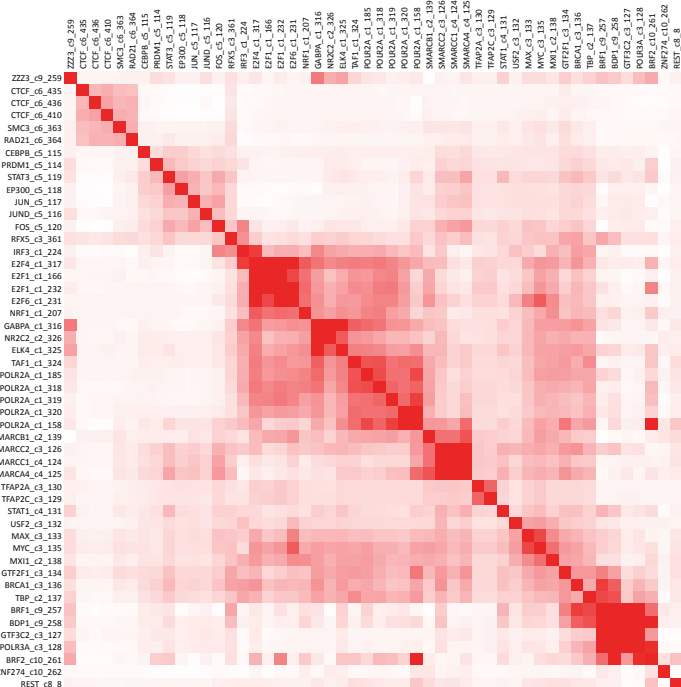


Legend

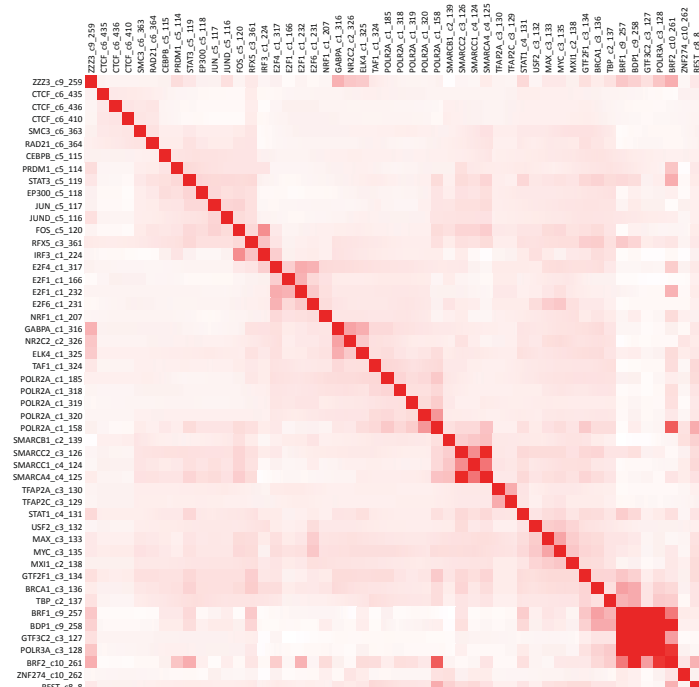


d

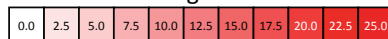
HeLa-S3 Pairwise Conditional Enrichments DNase



HeLa-S3 Pairwise Conditional Enrichments DNase+State

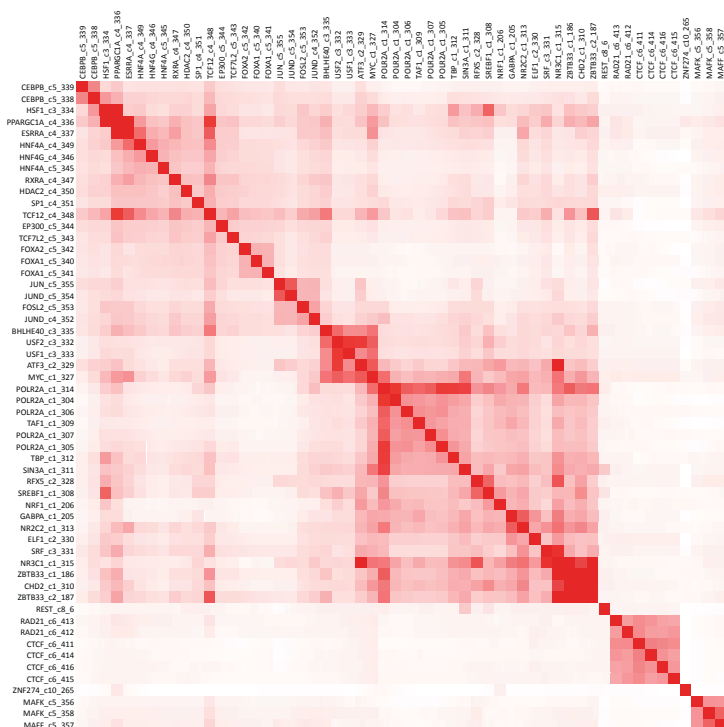


Legend

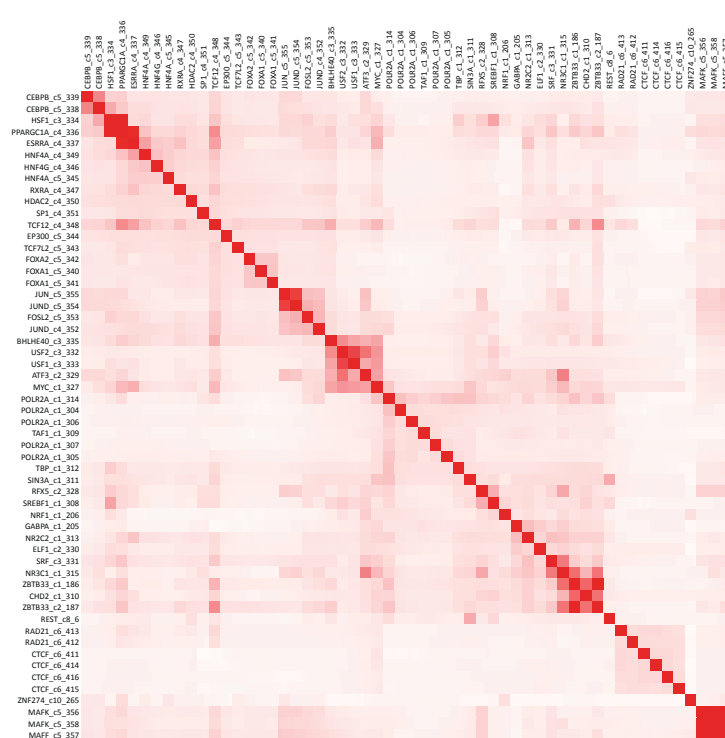


e

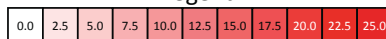
HepG2 Pairwise Conditional Enrichments DNase



HepG2 Pairwise Conditional Enrichments DNase+State

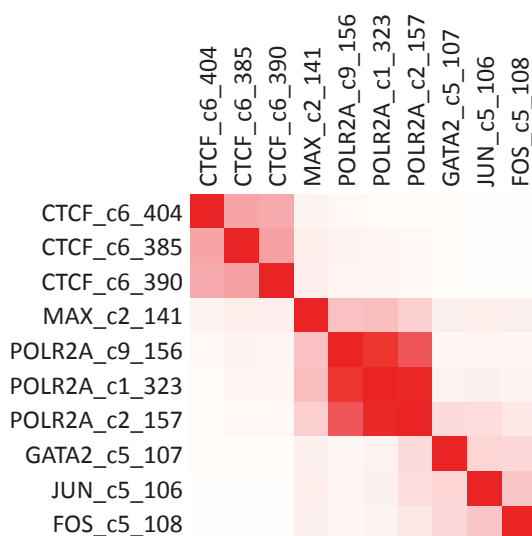


Legend

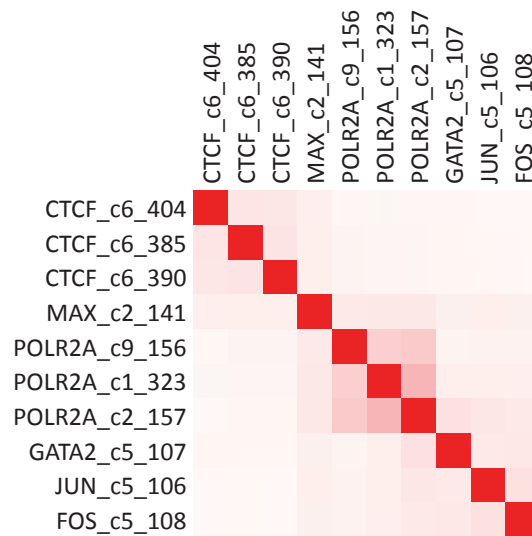


f

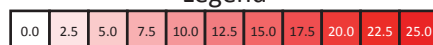
Huvec Pairwise Conditional Enrichments DNase



Huvec Pairwise Conditional Enrichments DNase+State

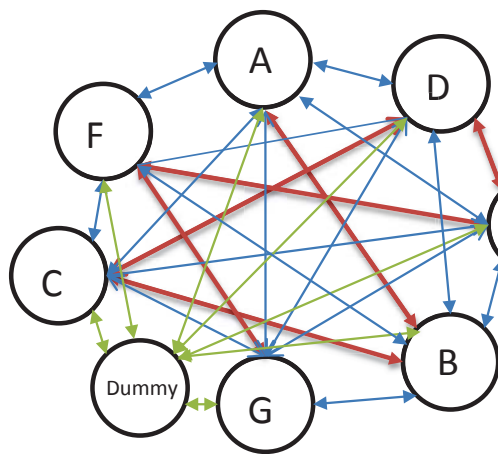


Legend



Unordered Matrix

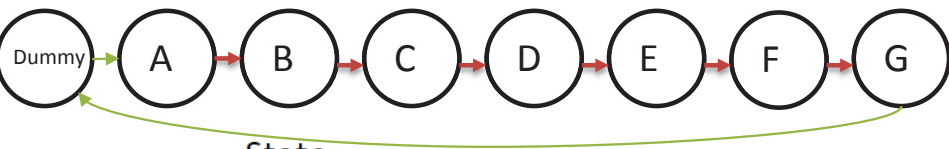
		State							
		1	2	3	4	5	6	7	8
Experiment	A	1	1	0	0	0	0	0	0
	D	0	0	0	1	1	0	0	0
	E	0	0	0	0	1	1	0	0
	B	0	1	1	0	0	0	0	0
	G	0	0	0	0	0	0	1	1
	C	0	0	1	1	0	0	0	0
	F	0	0	0	0	0	1	1	0



Distances



Traveling Salesman Problem



Ordered Matrix

		State							
		1	2	3	4	5	6	7	8
Experiment	A	1	1	0	0	0	0	0	0
	B	0	1	1	0	0	0	0	0
	C	0	0	1	1	0	0	0	0
	D	0	0	0	1	1	0	0	0
	E	0	0	0	0	1	1	0	0
	F	0	0	0	0	0	1	1	0
	G	0	0	0	0	0	0	1	1

Supplementary Figure 24: Illustration of Traveling Salesman Problem formulation to Ordering Rows of Enrichment Matrix. **(Top)** An unordered input matrix. **(Center)** A graph showing distances between each row or equivalently a mapped city. A dummy city has been added with zero distance to all other cities. This graph can be given to a traveling salesman problem solver to provide an optimal ordering of cities or equivalently rows. **(Bottom)** The result matrix now optimally ordered.