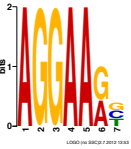
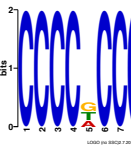
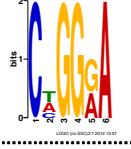
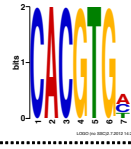
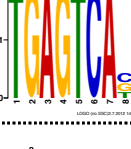
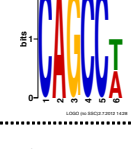
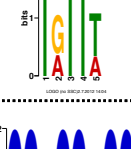
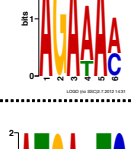
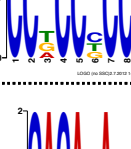
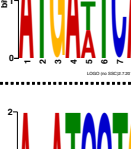
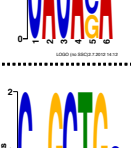
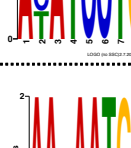
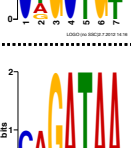
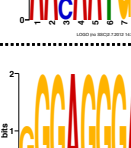
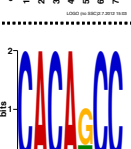
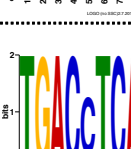
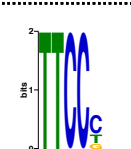
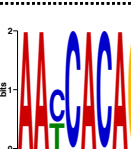
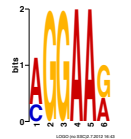
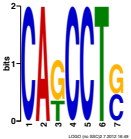
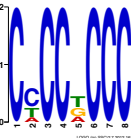
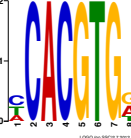
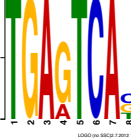
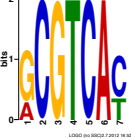
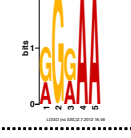
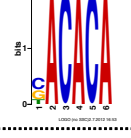
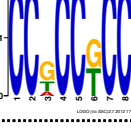
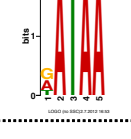
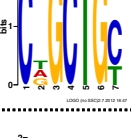
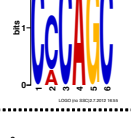
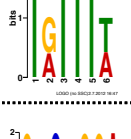
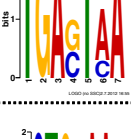
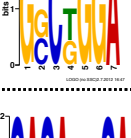
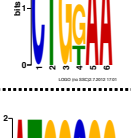
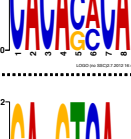
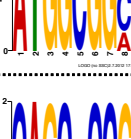
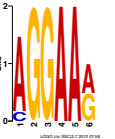
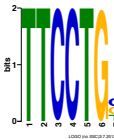
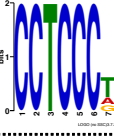
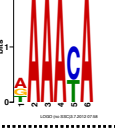
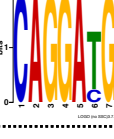
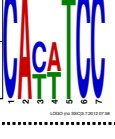
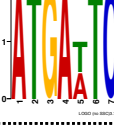
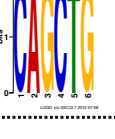
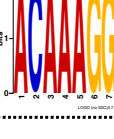
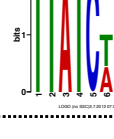
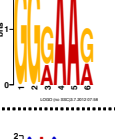
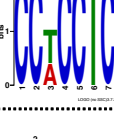
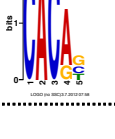
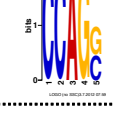
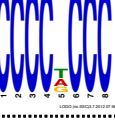
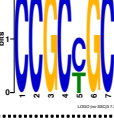
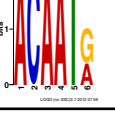
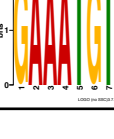


Supplementary Table 3. Motifs enriched under p300 peaks within dynamic, p300-associated H3K27ac clusters. Central 100 bp under p300 peaks was used for de novo motif discovery by DREME. “Motif” indicates the overrepresented motif found by DREME, and its significance score is indicated as the $-\log_{10}$ of the E-value. Top aligned motif indicates the top-scoring JASPAR or Uniprobe position weight matrix. Transcription factors (TFs) with motifs that align with the DREME motif with a p-value of less than 0.001 are listed under candidate TFs. Only vertebrate transcription factor binding motifs were reported. TFs of interest are highlighted in red when common to 3 clusters, green when common to 2 clusters, and blue when unique to 1 cluster.

H0 Cluster							
Motif	E-value (-log ₁₀)	Top aligned motif	Candidate TFs	Motif	E-value (-log ₁₀)	Top aligned motif	Candidate TFs
	234	MA0080.2	ETS, SPI1, ELF3/5, STAT		9	MA0079.2	SP1, KLF4/7, Ascl2, Sox13
	68	MA0144.1	STAT		9	MA0104.1	Mycn, RBP/J, Myc/Max, USF1, Bhlhb2, HIF1a::ARNT
	65	MA0099.2	AP1, Fos		6	No	No
	45	UP00061_2	Fox family, SRY, Sox5		7	No	No
	41	MA0079.2	SP1/4, Egr1, Zfp281		5	MA0099.2	AP1, Fos
	20	UP00042_2	Gm397, Zscan		5	MA0156.1	FEV, ELF5
	19	MA0055.1	Myf, NHLH1, Zic1-3, Ascl2		4	MA0077.1	Sox9
	18	MA0035.2	GATA family		4	MA0079.2	SP1, Obox3
	17	No	No		2	MA0018.2	CREB1, ATF1, Jundm2, NR4A2, RXRa
	13	MA0080.1	SPI1, STAT		2	MA0002.2	RUNX1, GFI

Cluster

Motif	E-value (-log ₁₀)	Top aligned motif	Candidate TFs	Motif	E-value (-log ₁₀)	Top aligned motif	Candidate TFs
	269	MA0156.1	ETS, ELF3/5, SPI1, STAT, FEV		18	No	No
	125	MA0079.2	SP1, KLF4/7, Ascl2, ZFP410, Sox13		17	MA0058.1	Myc::Max, USF1, Mycn, Arnt, Bhlhb2, RBP/J
	116	MA0099.2	AP1, Fos, NFE2L2		10	MA0018.1	CREB1, ATF1
	74	MA0061.1	NF-kB, STAT, ETS, SPI1		8	UP00042_2	Gm397, Sox14, Zscan4
	49	MA0079.2	SP1/4, EGR1, ZFP410		8	No	No
	35	MA0055.1	MYF, NHLH1, Ascl2, Zic1-3		6	UP00057_2	Zic1-3, Swi5,
	34	MA0157.1	FOX family		6	MA0099.1	Fos, AP1, Jundmd2, NFE2L2
	27	No	No		6	MA0144.1	STAT
	23	UP00042_2	Gm397		5	UP00000_2	Smad3
	21	UP00020_1	ATF1, CREB1, Jundm2		5	No	No

H4-12 Cluster							
Motif	E-value (-log ₁₀)	Top aligned motif	Candidate TFs	Motif	E-value (-log ₁₀)	Top aligned motif	Candidate TFs
	422	MA0156.1	ETS, ELF3/5, SPI1, STAT, FEV		9	MA0156.1	FEV, STAT, TEAD
	109	UP00103_2	AP1, Fos, NFE2L2		8	MA0079.2	SP1
	68	MA0157.1	FOX family		11	UP00406_1	Spdef
	36	MA0062.2	GABPA, ELF5, STAT, FEV, ETS		7	MA0099.2	AP1
	34	2MA0048.1	NHLH1, Ascl2, Myf, TGIF		6	UP0030_1	Sox family
	29	MA0090.1	TEAD, NFkB, Rel		6	MA0035.2	GATA family
	21	MA0080.1	SPI1, NFkB		4	MA0079.2	SP1
	18	No	No		4	MA0402.1	SWI5
	13	MA0079.2	SP1, KLF4/7, Ascl2, ZFP281, Sox13		3	MA0079.2	SP1/4, Egr1, Rpn4
	12	MA0078.1	Sox Family, SRY		3	No	No