Homer Known Motif Enrichment Results
/:/zfs/venom/Crotalus_genomes/Ctigris_CLP2741/ATAC_Seq/HOMER/Genrich_Run1/Genrich_Filtered_Hard50Overlap_ATAC_All_VG_Combined/

Homer de novo Motif Results
Gene Ontology Enrichment Results
Known Motif Enrichment Results (vs file)
Total Target Sequences = 2446, Total Background Sequences = 44046

Rank	Motif	Name	P-value	log P-value	q-value (Benjamini)	# Target Sequences with Motif	% of Target Sequences with Motif	# of Background Sequences with Motif	% of Background Sequences with Motif	Details / Matrix File	AVG
1	AAACRTTTTAAACGCGTTT	GRHL2/CP2/HBE-GRHL2 ChIP-Seq(GSE48194)/Homer	1e-183	-421.6e+02	0.000	454.0	18.56%	1546.0	3.51%	logo	bed
3	AAAGTAAACA	FOXA1(Forkhead)/LNCAP FOXA1 ChIP-Seq(GSE27824)/Homer	1e-111	-255.6e+02	0.000	679.0	27.76%	4925.2	11.19%	logo	bed
4	CCTGTTTACATA	Foxa2(Forkhead)/Liver-Foxa2 ChIP-Seq(GSE25094)/Homer	1e-106	-246.6e+02	0.000	496.0	20.28%	2948.2	6.70%	logo	bed
5	AAACTAAACA	FOXA1(Forkhead)/MCF7-FOXA1 ChIP-Seq(GSE26231)/Homer	1e-94	-216.6e+02	0.000	588.0	24.04%	4075.0	9.26%	logo	bed
6	TATCTTTTACATTTGCCA	NF1-FOXA1(CTF)(Forkhead)/LNCAP-FOXA1 ChIP-Seq(GSE28275)/Homer	1e-92	-213.6e+02	0.000	339.0	5.68%	227.7	0.52%	logo	bed
7	CCCATCTTTACATAGA	Foxa3(Forkhead)/Liver-Foxa3 ChIP-Seq(GSE37765)/Homer	1e-92	-212.6e+02	0.000	276.0	11.28%	110.5	2.52%	logo	bed
8	CTGCCAGCCTGGGA	Fox:Elox21(Forkhead:bHLH)/Panc1-Foxa2-ChIP-Seq(GSE41290)/Homer	1e-86	-198.6e+02	0.000	488.0	19.95%	3296.5	7.49%	logo	bed
9	CTGCCAAG	NF1-half(inv(CTF))/LNCAP NF1-ChIP-Seq(Unpublished)/Homer	1e-79	-181.6e+02	0.000	873.0	35.69%	8519.2	19.35%	logo	bed
10	TATTTACTTTA	FOXM1(Forkhead)/MCF7-FOXM1-ChIP-Seq(GSE72377)/Homer	1e-75	-172.6e+02	0.000	576.0	23.55%	4617.7	10.53%	logo	bed
11	TCTTTACTTTACC	Foxf2(Forkhead)/Zebrafish(embryo-Foxf2-Isoxin ChIP-Seq(GSE41066)/Homer	1e-74	-169.6e+02	0.000	490.0	20.03%	3915.5	8.89%	logo	bed
12	AATCATAAACAG	Foxl2.2(Forkhead)/Ovary-Foxl2.2 ChIP-Seq(GSE60858)/Homer	1e-73	-167.6e+02	0.000	430.0	17.58%	3353.9	7.62%	logo	bed
13	CTTGGCAGCCTCCAG	NF1(CTF)/LNCAP-NF1 ChIP-Seq(Unpublished)/Homer	1e-56	-130.6e+02	0.000	231.0	9.53%	1232.2	2.80%	logo	bed
14	AGTAAACA	Foxo3(Forkhead)/U2OS-Foxo3 ChIP-Seq(E-MTAB-2701)/Homer	1e-49	-120.6e+02	0.000	363.0	14.84%	2707.5	6.15%	logo	bed
15	AAAGCTAAACAA	Foxf1(Forkhead)/Lung-Foxf1 ChIP-Seq(GSE37995)/Homer	1e-45	-111.6e+02	0.000	432.0	17.66%	3647.8	8.29%	logo	bed
16	TTTTTACAAACA	FOXK1(Forkhead)/HEK293-FOXK1 ChIP-Seq(GSE31475)/Homer	1e-45	-111.6e+02	0.000	470.0	19.22%	4134.5	9.39%	logo	bed
17	ACCAGGAAGT	ELF5(ETS)/PDAC ELF5 ChIP-Seq(GSE64537)/Homer	1e-45	-104.6e+02	0.000	551.0	14.35%	2768.2	6.29%	logo	bed
18	CTTGTTTACA	FOXP1(Forkhead)/H9-FOXP1 ChIP-Seq(GSE31006)/Homer	1e-42	-97.26e+01	0.000	237.0	9.69%	1549.9	3.52%	logo	bed
19	CTGCCAGCCTCCCA	Tfs1Nf1(NF)/IUR(Ame)-Tfs1 ChIP-Seq(GSE31829)/Homer	1e-38	-88.6e+01	0.000	227.0	9.28%	1528.7	3.47%	logo	bed
20	CCATGTTTACAT	FOXK2(Forkhead)/U2OS FOXK2-ChIP-Seq(E-MTAB-2264)/Homer	1e-33	-85.87e+01	0.000	303.0	12.39%	2437.0	5.54%	logo	bed
21	ACCAGGAAGT	EHF(ETS)/LoVo-EHF ChIP-Seq(GSE49402)/Homer	1e-33	-77.70e+01	0.000	550.0	22.49%	5914.9	13.44%	logo	bed
22	CTGTTTAC	Foxo3(Forkhead)/EOM-Foxo1 ChIP-Seq(Tan_et_al)/Homer	1e-31	-72.1e+01	0.000	655.0	26.86%	7597.6	17.26%	logo	bed
23	ACTTCCTGCA	EHF(ETS)/BMDM-EHF ChIP-Seq(GSE68009)/Homer	1e-29	-70.63e+01	0.000	428.0	17.50%	4331.1	9.84%	logo	bed
24	ACAGCGAAGT	ELF5(ETS)/T47D-ELF5 ChIP-Seq(GSE30407)/Homer	1e-29	-70.03e+01	0.000	317.0	12.96%	2846.8	6.47%	logo	bed
25	CCTGCCTCGT	SPDEF(ETS)/VCaP-SPDEF ChIP-Seq(GSE41421)/Homer	1e-29	-67.6e+01	0.000	402.0	16.43%	4047.4	9.19%	logo	bed
26	CCTGGCCGGAGC	Sp2(Zf)/mES-Sp2.Flag ChIP-Seq(GSE72989)/Homer	1e-28	-66.01e+01	0.000	419.0	17.13%	4299.7	9.77%	logo	bed
27	AACCGGAAGT	ETV1(ETS)/GIST48-ETV1 ChIP-Seq(GSE22441)/Homer	1e-26	-61.47e+01	0.000	547.0	22.36%	6178.8	14.04%	logo	bed
28	GTGACCTGA	AP1(bZIP)/K562-AP1 ChIP-Seq(GSE31477)/Homer	1e-26	-61.13e+01	0.000	234.0	9.57%	1945.2	4.42%	logo	bed
29	ACAGGAAGTG	ERG(ETS)/VCaP-ERG ChIP-Seq(GSE14097)/Homer	1e-23	-54.89e+01	0.000	567.0	23.18%	6766.7	15.37%	logo	bed
30	GCCAATTCC	NF(CCAAT)/Promoter/Homer	1e-22	-52.82e+01	0.000	592.0	16.03%	8217.8	9.58%	logo	bed
31	CCAGTTTCCTGCC	Ets2(ETS)/E8T1-Ets2 ChIP-Seq(GSE59402)/Homer	1e-22	-51.92e+01	0.000	361.0	14.76%	3800.2	8.63%	logo	bed
32	ACAGGAAGTG	ETS1(ETS)/Jurkat-ETS1 ChIP-Seq(GSE17954)/Homer	1e-22	-51.08e+01	0.000	410.0	16.76%	4524.2	10.28%	logo	bed
33	AGAGGAAGTG	PU.1(ETS)/Thp1Mac-PU.1 ChIP-Seq(GSE21512)/Homer	1e-21	-49.3e+01	0.000	184.0	7.52%	1515.5	3.44%	logo	bed
34	ACACGGAAGT	Ehf-Ehsf(ETS)/CD4+-Ehf8 ChIP-Seq(Bonelli_et_al.)/Homer	1e-20	-48.70e+01	0.000	129.0	5.27%	904.9	2.06%	logo	bed
35	GCCCCCCCCCCC	Sp1(Zf)/Promoter/Homer	1e-19	-44.07e+01	0.000	152.0	6.21%	1202.5	2.73%	logo	bed
36	GCTGCCCGTA	Elk1(ETS)/Hela-Elk1 ChIP-Seq(GSE31477)/Homer	1e-18	-41.6e+01	0.000	280.0	11.45%	2910.2	6.61%	logo	bed
37	CCGCCCCCCCCC	Sp2(Zf)/HEK293-Sp2.mGFP ChIP-Seq(Encode)/Homer	1e-17	-41.19e+01	0.000	485.0	19.83%	5910.1	13.42%	logo	bed
38	CCCTTCCCCC	Elk1(ETS)/CD8-FLI1 ChIP-Seq(GSE20898)/Homer	1e-17	-40.67e+01	0.000	467.0	19.09%	5653.3	12.84%	logo	bed
39	CTTGACCTCA	Atf3(bZIP)/TU9.1-Atf3 ChIP-Seq(GSE50872)/Homer	1e-17	-40.02e+01	0.000	142.0	5.81%	417.7	2.58%	logo	bed
40	TGTTTACCATGCGAA	X-box(HTH)/NPC-H3K4me1 ChIP-Seq(GSE16256)/Homer	1e-17	-39.86e+01	0.000	71.0	2.90%	177.9	0.86%	logo	bed
41	CCTTCCAGCAGGAA	Stat1+(2)/Stat2/CD4-Stat1 ChIP-Seq(GSE19198)/Homer	1e-16	-38.90e+01	0.000	260.0	10.63%	2688.2	6.11%	logo	bed
42	CTGCTCAGTCAG	Pknox1(Homeobox)/ES-Pknox1 ChIP-Seq(GSE62820)/Homer	1e-16	-38.87e+01	0.000	91.0	3.72%	584.7	1.33%	logo	bed
43	CCGGGAAGTG	ETV4(ETS)/HepG2-ETV4 ChIP-Seq(ENCODE)/Homer	1e-16	-38.76e+01	0.000	442.0	18.07%	5356.8	12.21%	logo	bed
44	ACCCGGAAGT	ELF1(ETS)/Jurkat-ELF1 ChIP-Seq(GSE40251)/Homer	1e-16	-37.31e+01	0.000	246.0	10.06%	2535.0	5.76%	logo	bed
45	ACCAGGAAGT	GABPA(ETS)/Jurkat-GABPA ChIP-Seq(GSE17954)/Homer	1e-15	-33.53e+01	0.000	354.0	14.47%	4130.9	9.38%	logo	bed
46	CCTGACCTCA	Atf2(bZIP)/T47d-Atf2 ChIP-Seq(GSE50872)/Homer	1e-15	-33.48e+01	0.000	97.0	3.97%	691.0	1.57%	logo	bed
47	ACCCGGAAGT	ETS(ETS)/Promoter/Homer	1e-15	-33.46e+01	0.000	166.0	6.79%	1524.0	3.46%	logo	bed
48	CCTCTCAGTCAG	Pbx3(Homeobox)/GM12878-PBX3 ChIP-Seq(GSE32465)/Homer	1e-14	-32.69e+01	0.000	84.0	3.43%	555.8	1.26%	logo	bed
49	CTGCTCAGTCAG	ERG:ERG fusion(ETS)/CADO_ES1-ERG ChIP-Seq(GSE61021)/Homer	1e-14	-32.62e+01	0.000	277.0	11.32%	3043.0	6.91%	logo	bed
50	AAAGCAGGAAGTG	Spib(ETS)/OCI-LY3-SPIB ChIP-Seq(GSE56457)/Homer	1e-14	-31.92e+01	0.000	111.0	4.54%	865.9	1.97%	logo	bed
51	GTTACCTAATCCCAA	NFIL3(bZIP)/HepG2-NFIL3 ChIP-Seq(Encode)/Homer	1e-14	-31.34e+01	0.000	237.0	9.69%	2499.8	5.68%	logo	bed
52	TCTCACTT	Tgif2(Homeobox)/mES-Tgif2 ChIP-Seq(GSE35404)/Homer	1e-13	-31.62e+01	0.000	862.0	35.24%	12417.5	28.21%	logo	bed
53	ACCGCCACCCGCCC	KLF3(Zf)/MEF-KD3 ChIP-Seq(GSE44748)/Homer	1e-12	-27.99e+01	0.000	167.0	6.83%	1668.2	3.79%	logo	bed
54	ATGACCTCATCC	c-Jun-CRE(bZIP)/K562-Jun ChIP-Seq(GSE31477)/Homer	1e-11	-27.04e+01	0.000	84.0	3.43%	633.5	1.44%	logo	bed
55	ACTGGCGTGGCT	KLF1(EZ)/MEP-KD1 ChIP-Seq(GSE31477)/Homer	1e-11	-27.02e+01	0.000	534.0	21.83%	7212.8	16.38%	logo	bed
56	ACCAGCAGCAGGCT	ZNF768(Zf)/iPSC-ZNF768 ChIP-Seq(GSE111875)/Homer	1e-11	-26.66e+01	0.000	21.0	0.86%	50.8	0.12%	logo	bed
57	ATGACCTCATCG	Jun(bZIP)/K562-Jun8 ChIP-Seq/Homer	1e-11	-26.62e+01	0.000	43.0	1.76%	219.0	0.50%	logo	bed
58	TTCCCGCAA	Stat3(Stat)/mES-Stat3 ChIP-Seq(GSE11431)/Homer	1e-11	-25.97e+01	0.000	187.0	7.65%	1985.7	4.51%	logo	bed
59	CCTGTCAGTCAA	PBX1(Homeobox)/MCF7-PBX1 ChIP-Seq(GSE28007)/Homer	1e-10	-25.56e+01	0.000	37.0	1.51%	170.1	0.39%	logo	bed
60	TCCCACG	HIC1(Zf)/Trog-ZBTB29 ChIP-Seq(GSE99089)/Homer	1e-10	-25.52e+01	0.000	647.0	26.45%	9149.8	20.78%	logo	bed
61	CCTAATCCGT	Dux20(Homeobox)/EpiLC-Dux2 ChIP-Seq(GSE36090)/Homer	1e-10	-24.48e+01	0.000	250.0	10.22%	3916.0	8.62%	logo	bed
62	AGGATTAA	GSC(Homeobox)/FrogEmbryos-GSC ChIP-Seq(GSE40057)/Homer	1e-10	-24.40e+01	0.000	347.0	14.19%	4381.6	9.95%	logo	bed
63	ACAAGGAAAT	ERS:FLI1 fusion(ETS)/SK_N_MC-ERS ChIP-Seq(GSE41021)/Homer	1e-9	-22.42e+01	0.000	239.0	9.77%	2714.0	6.30%	logo	bed
64	GTTCCAGGAAA	STAT4(Stat)/CD4-Stat4 ChIP-Seq(GSE22104)/Homer	1e-9	-21.95e+01	0.000	322.0	13.16%	4023.5	9.14%	logo	bed
65	CTAATCC	CRX(Homeobox)/Retina-Crx ChIP-Seq(GSE20299)/Homer	1e-9	-21.22e+01	0.000	652.0	26.66%	9336.9	21.21%	logo	bed
66	GCTTCCCATGCGGAC	IOA:1(HTH)/NPC-H3K4me1 ChIP-Seq(GSE16256)/Homer	1e-9	-21.06e+01	0.000	90.0	3.68%	765.4	1.74%	logo	bed
67	CTTCCTCCGGC	Elk4(ETS)/Hela-Elk4 ChIP-Seq(GSE31477)/Homer	1e-9	-21.26e+01	0.000	262.0	10.71%	3163.3	7.19%	logo	bed
68	TGGCCGTGGC	KLF5(Zf)/LoVo-KLF5 ChIP-Seq(GSE49402)/Homer	1e-9	-21.09e+01	0.000	343.0	14.02%	4457.7	10.13%	logo	bed
69	AACAATGCT	Isx(Homeobox)/CPA-Isx13 ChIP-Seq(GSE62969)/Homer	1e-9	-21.08e+01	0.000	139.0	13.86%	1403.6	10.00%	logo	bed
70	CTGCACC	Tgif1(Homeobox)/mES-Tgif1 ChIP-Seq(GSE35404)/Homer	1e-8	-19.94e+01	0.000	763.0	31.19%	11421.7	25.94%	logo	bed
71	CCTCGTCACGTCAC	CREB2(bZIP)/Promoter/Homer	1e-7	-18.8e+01	0.000	92.0	3.76%	884.5	2.01%	logo	bed
72	CCTGCACAC	Max(bHLH)/mESC-Mxd1 ChIP-Seq(GSE48087)/Homer	1e-7	-17.51e+01	0.000	388.0	15.86%	5329.6	12.11%	logo	bed
73	CCTGACTCATCC	Jun-AP1(bZIP)/K562-c-Jun ChIP-Seq(GSE31477)/Homer	1e-7	-17.74e+01	0.000	75.0	3.07%	670.3	1.52%	logo	bed
74	GTTCCCATGCGGACG	CTCF(Zf)/Colo-CTCF ChIP-Seq(Encode)/Homer	1e-7	-17.16e+01	0.000	55.0	2.25%	432.7	0.98%	logo	bed
75	CCTGACTCATCC	Bz3(bZIP)/Lung-Bz3 ChIP-Seq(GSE49402)/Homer	1e-7	-17.30e+01	0.000	42.0	1.72%	287.1	0.65%	logo	bed
76	ATTATCAAAG	Jun(bZIP)/Daudi-Jun8 ChIP-Seq(GSE36009)/Homer	1e-7	-16.64e+01	0.000	149.0	6.09%	1689.3	3.84%	logo	bed
77	ATGACTCAT	HLF(bZIP)/HEK293-HLF.Flag ChIP-Seq(GSE69817)/Homer	1e-6	-15.962e+01	0.000	271.0	11.08%	3568.6	8.11%	logo	bed
78	ATGACTCAT	BATF(bZIP)/Th17-BATF ChIP-Seq(GSE39756)/Homer	1e-6	-15.53e+01	0.000	169.0	6.91%	2027.9	4.61%	logo	bed
79	CGTTCCCATGCGAAC	RFX(HTH)/K562-RFX5 ChIP-Seq(GSE41270)/Homer	1e-6	-14.46e+01	0.000	35.0	1.43%	238.1	0.54%	logo	bed
80	CCCATTGTC	Nr2e3(HMG)/mES-Nr2e3 ChIP-Seq(GSE11431)/Homer	1e-6	-14.41e+01	0.000	278.0	11.37%	3745.7	8.51%	logo	bed
81	ATTTCGATA	Oct1(POU,Homeobox)/NCBI1048-POU2F1A ChIP-Seq(GSE21512)/Homer	1e-5	-13.30e+01	0.000	120.0	4.91%	1384.6	3.15%	logo	bed
82	CTCTCCCGAGAC	ZBTB33(Zf)/GM12878-ZBTB33 ChIP-Seq(GSE32465)/Homer	1e-5	-12.67e+01	0.000	26.0	1.06%	35.2	0.38%	logo	bed
83	ACGCACATCTGTCG	PKNX1(TF/Zf)/PR-CEBP ChIP-Seq(GSE31383)/Homer	1e-5	-12.22e+01	0.000	551.0	22.53%	8332.9	18.93%	logo	bed
84	CTCTTCCCACGGAA	Bz8b(Zf)/Lung-Bz8 ChIP-Seq(GSE49402)/Homer	1e-5	-12.01e+01	0.000	560.0	14.72%	8176.9	11.78%	logo	bed
85	ATCTGGGATTC	Foxh1(Forkhead)/hESC-FOXH1 ChIP-Seq(GSE29422)/Homer	1e-5	-11.12e+01	0.000	176.0	7.20%	2274.1	5.17%	logo	bed
86	CCCTTGTGCC	Sox10(HMG)/pmel8-Sox8 ChIP-Seq(GSE50066)/Homer	1e-4	-11.22e+01	0.000	261.0	10.67%	3620.1	8.22%	logo	bed
87	GCAACCACTTCGAACCAGCT	Tcfcp2l1(CP2)/mES-Tcfcp2l1 ChIP-Seq(GSE11431)/Homer	1e-4	-11.09e+01	0.000	53.0	2.17%	505.0	1.15%	logo	bed
88	CTCTCCCATGCCTC	Foxj2(bZIP)/Neuron-Foxj2 ChIP-Seq(GSE61429)/Homer	1e-4	-10.09e+01	0.000	129.0	5.27%	583.4	3.60%	logo	bed
89	CCATTGTC	Sox3(HMG)/NPC-Sox3 ChIP-Seq(GSE30389)/Homer	1e-4	-10.67e+01	0.000	512.0	20.93%	7795.5	17.70%	logo	bed
90	CCATTGTCA	Sox10(HMG)/Sciatic/Nerve-Sox3 ChIP-Seq(GSE35132)/Homer	1e-4	-10.06e+01	0.000	470.0	19.22%	7088.5	16.10%	logo	bed
91	CCTGACTCATCC	Fos2(bZIP)/T47d_E-fos2 ChIP-Seq(GSE50872)/Homer	1e-4	-10.07e+01	0.000	89.0	3.64%	1014.9	2.31%	logo	bed
92	CCATTGTTGC	Tcf15(HMG)/Endoderm-Sox17 ChIP-Seq(GSE61473)/Homer	1e-4	-10.61e+01	0.000	232.0	9.48%	3202.0	7.27%	logo	bed
93	CTCTCCCAGA	GFX(?)/Promoter/Homer	1e-4	-9.91e+01	0.000	22.0	0.49%	32.1	0.12%	logo	bed
94	TACGTCCG	HIF-1a(bHLH:MCF)? HIF1a ChIP-Seq(GSE28352)/Homer	1e-4	-9.902e+01	0.000	87.0	3.56%	1002.0	2.28%	logo	bed
95	CCCTGACTCATCC	Fos1(bZIP)/BT549 Fos1 ChIP-Seq(GSE41404)/Homer	1e-4	-9.824e+01	0.000	141.0	5.76%	1808.5	4.11%	logo	bed
96	ATATGCAAAT	Ox21(POU,Homeobox)/Brain-Ox21 ChIP-Seq(GSE21512)/Homer	1e-4	-9.275e+01	0.000	105.0	4.29%	1286.2	2.92%	logo	bed
97	GCACGTGC	HIF-1(bHLH)/T47D-HIF1b ChIP-Seq(GSE35957)/Homer	1e-3	-8.99e+01	0.000	296.0	12.10%	4319.8	9.81%	logo	bed
98	CTTTCCCACG	Rbp1(?)/Panc1-Rbp1 ChIP-Seq(GSE47459)/Homer	1e-3	-8.741e+01	0.000	342.0	13.98%	5095.4	11.57%	logo	bed
99	CTGCCCATGCCTC	NR1(NR)/hESC7-NR1 ChIP-Seq(Unpublished)/Homer	1e-3	-8.586e+01	0.000	105.0	4.29%	1311.9	2.98%	logo	bed
100	ATGACTCATC	AP-1(bZIP)/ThinMac-PU.1 ChIP-Seq(GSE21512)/Homer	1e-3	-8.431e+01	0.000	178.0	7.28%	2448.8	5.56%	logo	bed
101	GGGGGGGG	Mzf2(Zf)/Hep(G2-Mzf ChIP-Seq(GSE81475)/Homer	1e-3	-8.138e+01	0.000	435.0	17.78%	6699.8	15.22%	logo	bed
102	TCGTGACTCA	Bach2(bZIP)/OCI-Ly7-Bach2 ChIP-Seq(GSE116422)/Homer	1e-3	-8.035e+01	0.000	46.0	2.45%	670.5	1.52%	logo	bed
103	ACATCGTGCGCACATCTGCG	c/Ap3(?)/Saos-p53 ChIP-Seq(GSE135780)/Homer	1e-3	-8.014e+01	0.000	28.0	1.14%	242.2	0.55%	logo	bed
104	ACATCGTGCGCACATCTGCG	c/Ap3(?)/Saos-p53 ChIP-Seq/Homer	1e-3	-8.014e+01	0.000	28.0	1.14%	242.2	0.55%	logo	bed
105	CTCCCGCACAC	NT1(?)/Kidney-WT1 ChIP-Seq(GSE90816)/Homer	1e-3	-8.003e+01	0.000	154.0	6.30%	2091.6	4.75%	logo	bed
106	CATTACACCTCTTCAAA	Brachyury(T-box)/Mesoendoderm-Brachyury ChIP-Seq(GSE54696)/Homer	1e-3	-7.973e+01	0.000	68.0	2.78%	786.1	1.79%	logo	bed
107	ACTTTCCATTTC	HF1(HD)/iMEM-hf1 ChIP-Seq(GSE56743)/Homer	1e-3	-7.856e+01	0.000	92.0	3.76%	1143.3	2.60%	logo	bed
108	TCGCTGGCGG	Egr1(ZF)/K562-Egr1 ChIP-Seq(GSE32465)/Homer	1e-3	-7.847e+01	0.000	164.0	6.87%	2320.0	5.27%	logo	bed
109	CCAGCCAACTCCCCACATCCT	E7/p53(?)/Tonsilx-p53 ChIP-Seq(PRJNA331011)/Homer	1e-3	-7.799e+01	0.000	16.0	0.65%	106.6	0.24%	logo	bed
110	ATGACTCATCC	Atf3(bZIP)/GBM-ATF3 ChIP-Seq(GSE39213)/Homer	1e-3	-7.395e+01	0.000	160.0	6.54%	2127.6	5.04%	logo	bed
111	CCAGCCATGCCTCCACATCCT	p63(p53)/Keratinocyte-p63 ChIP-Seq(GSE81761)/Homer	1e-3	-7.291e+01	0.000	89.0	3.64%	1119.5	2.54%	logo	bed
112	CCGTGGCGGG	Ep2(Zf)/Thymocytes-Ep2 ChIP-Seq(GSE34224)/Homer	1e-3	-7.140e+01	0.000	48.0	1.96%	525.2	1.19%	logo	bed
113	TTGTCTAG	Smad3/MA0(MA)/NPC-Smad3 ChIP-Seq(GSE36671)/Homer	1e-3	-7.089e+01	0.000	697.0	28.50%	1130.1	25.67%	logo	bed
114	AGGAAACAGCTG	ETS:E-twx(ETS:bHLH)/HCT-Sc1 ChIP-Seq(GSE22178)/Homer	1e-3	-6.954e+01	0.000	27.0	1.10%	248.0	0.56%	logo	bed
115	CCTGACTCATCAAAAATACG	Mafk(bZIP)/MA0(MA)0139.1.Mafk ChIP-Seq(GSE24865)/Homer	1e-3	-6.948e+01	0.000	125.0	5.11%	1688.6	3.84%	logo	bed
116	GGAAGTGAAACT	Zic(Zf)/ZiCKO-Zic2(ko) ChIP-Seq(GSE61147)/Homer	1e-3	-6.939e+01	0.000	456.0	18.64%	7180.4	16.31%	logo	bed
117	CGCGGGAAGT	PU.1(ETS)/BF/cDC-Idb ChIP-Seq(GSE60589)/Homer	1e-3	-6.627e+01	0.000	53.0	2.17%	610.0	1.39%	logo	bed
118	CCCTACGAACAG	E2F6(E2F)/Hela-E2F6 ChIP-Seq(GSE31477)/Homer	1e-2	-6.554e+01	0.000	204.0	8.34%	2936.8	6.70%	logo	bed
119	ACTATTTAGCG	Rfx5(RFX)/GM12878-Rfx5 ChIP-Seq(GSE31477)/Homer	1e-2	-6.348e+01	0.000	127.0	5.19%	1749.7	3.97%	logo	bed
120	CTATTTAGCG	Mef2b(MADS)/HEK293-Mef2b.V5 ChIP-Seq(GSE67037)/Homer	1e-2	-6.210e+01	0.000	230.0	9.40%	3419.1	7.77%	logo	bed
121	CGGGGATTTCCC	NFkB:p65(RHD)/GM12787-p65 ChIP-Seq(GSE19403)/Homer	1e-2	-6.199e+01	0.000	134.0	5.48%	1868.2	4.24%	logo	bed
122	CACGTGCCCC	Hif2a(bHLH:PAS)/786-O-HIF2a ChIP-Seq(GSE34871)/Homer	1e-2	-6.009e+01	0.000	93.0	3.80%	1233.1	2.80%	logo	bed
123	CCGCGGGAAG	E2F4(E2F)/K562-E2F4 ChIP-Seq(GSE31477)/Homer	1e-2	-5.952e+01	0.000	206.0	8.42%	3050.8	6.93%	logo	bed
124	GAAAGCGAAAGG	HF2(HD)/EryhoSolas-HF2 ChIP-Seq(GSE30987)/Homer	1e-2	-5.884e+01	0.000	33.0	1.35%	348.9	0.79%	logo	bed
125	AGAAACATTGTTC	PQR(NR)/EndoStromal-PGR ChIP-Seq(GSE69135)/Homer	1e-2	-5.835e+01	0.000	70.0	2.86%	887.2	2.02%	logo	bed
126	CGGGGCTGTCG	KLF10(Zf)/HEK293-KLF10 GFP-ChIP-Seq(GSE58341)/Homer	1e-2	-5.563e+01	0.000	146.0	5.97%	2085.2	4.74%	logo	bed
127	CCCACACCCAC	Klf9(Zf)/GBM-KLF9 ChIP-Seq(GSE62221)/Homer	1e-2	-5.391e+01	0.000	103.0	4.21%	1409.7	3.20%	logo	bed
128	ATGAATATCC	Pit1(Homeobox)/GCut-Pit1 ChIP-Seq(GSE58009)/Homer	1e-2	-5.570e+01	0.000	2.5.0	10.51%	9525.8	8.92%	logo	bed
129	ACACCTG	Mycn(bHLH:bCZ)/2-Mycn4 ChIP-Seq(GSE36024)/Homer	1e-2	-5.558e+01	0.000	32.0	13.16%	919.1	11.40%	logo	bed
130	ATTTCCATAA	Gata6(POU,Homeobox)/mES-Gata6 ChIP-Seq(GSE31411)/Homer	1e-2	-5.164e+01	0.000	128.0	5.23%	1831.7	4.16%	logo	bed
131	ATGAATATCC	Brn2(POU,Homeobox)/NPC-Brn2 ChIP-Seq(GSE35496)/Homer	1e-2	-5.126e+01	0.000	28.0	1.14%	297.6	0.68%	logo	bed
132	CCTATTTTAAGCG	Mef2d(MADS)/Retina-Mef2d ChIP-Seq(GSE18841)/Homer	1e-2	-5.109e+01	0.000	53.0	2.17%	659.1	1.50%	logo	bed
133	GAAACGCGAAAGT	STAT1(Stat)/HuSA5-STAT1 ChIP-Seq(GSE21792)/Homer	1e-2	-5.088e+01	0.000	80.0	3.27%	1073.6	2.44%	logo	bed
134	AATCGAAATGCC	Bf(HOX)/BMDM-BF8 ChIP-Seq(GSE77788)/Homer	1e-2	-5.044e+01	0.000	128.0	5.14%	1716.3	3.90%	logo	bed
135	GGAAATTCCC	Oct6(POU,Homeobox)/NPC-Pou3f1 ChIP-Seq(GSE35496)/Homer	1e-2	-4.830e+01	0.000	112.0	4.58%	1593.4	3.62%	logo	bed
136	GCTAATTA	SFKB:p65-RelA(RHD)/TissueMac-LPS-Expression(GSE23622)/Homer	1e-2	-4.809e+01	0.000	21.0	0.86%	209.5	0.48%	logo	bed
137	CCCGCCATTGT	LXR9(Homeobox)/Hu116-LXR9 ChIP-Seq(GSE110822)/Homer	1e-2	-4.752e+01	0.000	345.0	14.10%	5490.5	12.47%	logo	bed
138	CTCCCCATTGT	Sox9(HMG)/Lung8-SOX9 ChIP-Seq(GSE73227)/Homer	1e-2	-4.743e+01	0.000	202.0	8.30%	3092.4	7.02%	logo	bed
139	CTCACCTGTCTGCT	ZNF317(ZF)/HEK293-ZNF317.GFP ChIP-Seq(GSE58341)/Homer	1e-2	-4.739e+01	0.000	24.0	0.98%	251.8	0.57%	logo	bed
140	ATTCCCCAAC	CEBPD(bZIP)/ThinMac-CEBPD ChIP-Seq(GSE21512)/Homer	1e-2	-4.617e+01	0.000	238.0	9.73%	3689.8	8.38%	logo	bed