## Homer *de novo* Motif Results (homer4.10/Promoter\_500\_200/)

Known Motif Enrichment Results

**Gene Ontology Enrichment Results** 

If Homer is having trouble matching a motif to a known motif, try copy/pasting the matrix file into <a href="STAMP">STAMP</a>

More information on motif finding results: <u>HOMER</u> | <u>Description of Results</u> | <u>Tips</u>

Total target sequences = 237

Total background sequences = 48938

\* - possible false positive

* - possible false positive    David Mark   David   Da							
Rank	Motif	P-value	P-pvalue	ı	Background		Best Match/Detail
1	<b>GCAGÇACATATA</b>	1e-19	-4.395e+01	5.06%	0.06%	178.1bp (204.0bp)	PB0208.1_Zscan4 More Information Found
	CACTAGGTIGCC	1e-18	-4.353e+01	8.44%	0.43%	230.6bp (207.8bp)	GLIS3(Zf)/Thyroi ChIP-Seq(GSE10: /Homer(0.617) More Information Found
3	TACCACCCTEAA	1e-16	-3.778e+01	4.22%	0.05%	173.9bp (169.1bp)	PB0029.1_Hic1_1 More Information Found
4	GGGCCATGCTAA	1e-15	-3.652e+01	4.22%	0.05%	194.3bp (185.0bp)	Brn1(POU,Homeo ChIP-Seq(GSE35-/Homer(0.651) More Information Found
5	TTÇGTÇCAAAAG	1e-15	-3.516e+01	5.06%	0.13%	193.0bp (202.7bp)	CEBP:AP1(bZIP) CEBPb-ChIP-Seq /Homer(0.640) More Information Found
6	ATGCÇGAAÇTIA	1e-14	-3.405e+01	3.80%	0.04%	244.8bp (181.1bp)	Pit1+1bp(Homeok ChIP-Seq(GSE58/ /Homer(0.607) More Information Found
7	<b>CCTGGTTAGTAC</b>	1e-14	-3.341e+01	2.95%	0.01%	216.8bp (168.1bp)	PB0194.1_Zbtb12 More Information Found
8	<b>ITCCAATITTAG</b>	1e-12	-2.989e+01	3.38%	0.04%	ICHEL Inni	<u>r ounu</u>
9	<b><u><u><u>QACTACAGCC</u></u></u></b>	1e-12	-2.874e+01	8.44%	0.96%	184.9bp (197.0bp)	RUNX-AML(Rur ChIP-Seq(Barski_/Homer(0.646) More Information Found
10 *	<b>GGAGAAGGATCA</b>	1e-11	-2.757e+01	13.50%	2.94%	183.3bp (196.6bp)	Znf263(Zf)/K562- Seq(GSE31477)/I More Information

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11 *	<b>TAATTERESTT</b>	1e-11	-2.704e+01	5.49%	0.32%	185.5bp (202.1bp)	RUNX2/MA0511 More Information Found
12 *	<b>ATACAGAGAAGA</b>	1e-11	-2.668e+01	8.44%	1.08%		ZNF768(Zf)/Rajj- Seq(GSE111879), More Information Found
13 *	<b>AAAGTA&amp;TGGCA</b>	1e-11	-2.586e+01	5.06%	0.28%	201.0bp (204.6bp)	NFIA/MA0670.1. More Information Found
14 *	ATEGATECCE	1e-10	-2.384e+01	7.17%	0.86%	177.5bp (204.4bp)	HNF6(Homeobox ChIP-Seq(ERP00 /Homer(0.640) More Information Found
15 *	TGATACT CS	1e-9	-2.284e+01	17.30%	5.57%	197.4bp (200.2bp)	PB0072.1_Sox5_ More Information Found
16 *	CACCACC	1e-9	-2.080e+01	6.75%	0.91%		c-Jun-CRE(bZIP) Seq(GSE31477)/I More Information Found
17 *	<b>GTGCTCGCTI</b>	1e-8	-1.985e+01	6.75%	0.97%	209.4bp (194.4bp)	PB0099.1_Zfp69 More Information Found
18 *	CAACCTGATA	1e-8	-1.953e+01	5.06%	0.49%	204.0bp (205.3bp)	SIX1/MA1118.1/ More Information Found
19 *	CTGCTCCTGG	1e-8	-1.882e+01	16.88%	6.14%	183.0bp (199.7bp)	Znf263(Zf)/K562 Seq(GSE31477)/I More Information Found
20 *	TCTCAAAAGC	1e-5	-1.372e+01	2.95%	0.22%		CHR(?)/Hela-Cel /Homer(0.598) More Information Found
21 *	<b><u>GTACCGCG</u></b>	1e-5	-1.343e+01	9.70%	3.07%	150.1bp (228.9bp)	POL011.1_XCPE More Information Found
22 *	<b>AATTTATTTIAS</b>	1e-5	-1.256e+01	11.39%	4.23%	154.4bp (201.7bp)	Found
23 *	<u>ACACACA JATAT</u>	1e-5	-1.245e+01	4.22%	0.64%	169.3bp (213.2bp)	Found
24 *	AGGCCTAC	1e-5	-1.165e+01	9.28%	3.18%		ZFX(Zf)/mES-Zf Seq(GSE11431)/I More Information Found
25 *	TACCCCTT	1e-3	-9.202e+00	5.06%	1.34%	235.0bp (206.0bp)	MZF1(var.2)/MA /Jaspar(0.721) More Information Found

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26 *	TCCAATCAGA	1e-3	-9.200e+00	2.53%	0.30%	141.3bp (190.1bp)	NFYA/MA0060.3 More Information Found
27 *	TTTIGCC	1e-3	-9.004e+00	20.68%	12.10%	221.00p (202.4bp)	PB0145.1_Mafb_ More Information Found
28 *	CATAGATAACAT	1e-3	-8.598e+00	0.84%	0.01%	(232.2bp)	TRPS1(Zf)/MCF7 Seq(GSE107013)/ More Information Found
29 *	<b>GATCGCGGATT</b> I	1e-3	-8.598e+00	0.84%	0.01%	158.9bp (143.0bp)	Gfi1/MA0038.1/J More Information Found
30 *	TATTTAAAATAT	1e-3	-8.476e+00	4.64%	1.23%	171.4bp (212.8bp)	Phox2b(Homeobc PHOX2B-ChIP-S /Homer(0.683) More Information Found
31 *	<b>GTCTTCCGGCCG</b>	1e-3	-8.155e+00	0.84%	0.01%	92.3bp (171.2bp)	MF0001.1_ETS_c More Information Found
32 *	<b>STATASTTGT</b>	1e-3	-6.942e+00	2.95%	0.65%	192.5bp	PB0172.1_Sox1_2 More Information Found
33 *	<b>ATGIATGCATAC</b>	1e-2	-6.784e+00	0.84%	0.02%	7717hn	PH0148.1_Pou3f3 More Information Found
34 *	<u>ATCCGIATAC</u>	1e-1	-3.605e+00	1.69%	0.47%	75.2bp (206.8bp)	PB0198.1_Zfp128 More Information Found
35 *	<b>ATATAATATTAT</b>	1e-1	-3.300e+00	0.84%	0.13%	11637hn	Arid5a/MA0602.1 More Information Found

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