

Figure 1 – figure supplement 2

A

* - possible false positive

Rank	Motif	P-value	log P-value	% of Targets	% of Background	STD(Bg STD)	Best Match/Details
1	ACCTGTCG	1e-129	-2.984e+02	2.48%	0.12%	48.6bp (143.5bp)	SNAI2/MA0745.1/Jaspar(0.785) More Information Similar Motifs Found
2	TAGACGCG	1e-50	-1.156e+02	2.58%	0.56%	150.2bp (258.0bp)	POL008.1_DCE_S_1/Jaspar(0.624) More Information Similar Motifs Found
3	ATAACACG	1e-47	-1.104e+02	0.71%	0.02%	88.4bp (140.1bp)	PB0119.1_Foxa2_2/Jaspar(0.702) More Information Similar Motifs Found
4	AGTTGTAA	1e-45	-1.039e+02	2.56%	0.61%	207.2bp (403.7bp)	PH0158.1_Rhox11_2/Jaspar(0.710) More Information Similar Motifs Found
5	TCCCCGAT	1e-42	-9.840e+01	1.57%	0.23%	98.2bp (296.8bp)	PB0128.1_Gcm1_2/Jaspar(0.755) More Information Similar Motifs Found
6	TTCGACG	1e-40	-9.420e+01	1.78%	0.32%	182.3bp (156.2bp)	PB0179.1_Sp100_2/Jaspar(0.634) More Information Similar Motifs Found
7	AACTCAGT	1e-40	-9.342e+01	3.57%	1.19%	201.6bp (325.3bp)	POL007.1_BREd/Jaspar(0.642) More Information Similar Motifs Found
8	ACAGCGGT	1e-39	-9.103e+01	1.45%	0.22%	105.5bp (152.4bp)	Myf5(bHLH)/GM-Myf5-ChIP-Seq(GSE24852)/Homer(0.750) More Information Similar Motifs Found
9	CGGTGGCA	1e-38	-8.866e+01	2.35%	0.60%	119.2bp (180.8bp)	Hic1/MA0739.1/Jaspar(0.767) More Information Similar Motifs Found
10	GCCCCACA	1e-37	-8.563e+01	2.34%	0.61%	172.6bp (294.9bp)	PB0110.1_Bcl6b_2/Jaspar(0.728) More Information Similar Motifs Found
11	GCCTAGGT	1e-36	-8.459e+01	1.29%	0.18%	126.0bp (349.6bp)	ZNF711(Zf)/SHS Y5-ZNF711-ChIP-Seq(GSE20673)/Homer(0.705) More Information Similar Motifs Found
12	ATTAGTGC	1e-34	-7.832e+01	0.92%	0.09%	115.0bp (272.0bp)	HOXA5/MA0158.1/Jaspar(0.785) More Information Similar Motifs Found
13	AACCTTAG	1e-32	-7.435e+01	1.10%	0.15%	137.9bp (390.2bp)	HLTF/MA0109.1/Jaspar(0.683) More Information Similar Motifs Found
14	ATGAACGT	1e-31	-7.217e+01	2.27%	0.66%	159.9bp (551.9bp)	PB0178.1_Sox8_2/Jaspar(0.712) More Information Similar Motifs Found
15	GCAATTC	1e-30	-6.991e+01	3.49%	1.37%	162.8bp (344.3bp)	YY2/MA0748.1/Jaspar(0.712) More Information Similar Motifs Found

B

* - possible false positive

Rank	Motif	P-value	log P-value	% of Targets	% of Background	STD(Bg STD)	Best Match/Details
1	GAGTCAAC	1e-22	-5.174e+01	4.19%	0.17%	59.7bp (173.0bp)	FOS::JUN/MA0099.2/Jaspar(0.768) More Information Similar Motifs Found
2	GCTCGTCA	1e-21	-4.890e+01	5.71%	0.50%	122.1bp (237.1bp)	PB0108.1_Atf1_2/Jaspar(0.758) More Information Similar Motifs Found
3	ACAGGGGT	1e-21	-4.856e+01	7.62%	1.05%	95.3bp (288.4bp)	POL009.1_DCE_S_II/Jaspar(0.727) More Information Similar Motifs Found
4	TGGGGCTT	1e-19	-4.436e+01	10.48%	2.33%	169.2bp (240.2bp)	LRF(Zf)/Erythroblasts-ZBTB7A-ChIP-Seq(GSE74977)/Homer(0.724) More Information Similar Motifs Found
5	CGACCGCT	1e-18	-4.334e+01	4.76%	0.38%	460.6bp (190.7bp)	HINFP/MA0131.2/Jaspar(0.692) More Information Similar Motifs Found
6	GAATCAGA	1e-18	-4.152e+01	4.19%	0.28%	95.7bp (251.4bp)	Gfi1/MA0038.1/Jaspar(0.701) More Information Similar Motifs Found
7	TATCAGCG	1e-17	-4.042e+01	2.67%	0.07%	59.6bp (317.5bp)	NRL/MA0842.1/Jaspar(0.689) More Information Similar Motifs Found
8	CGCTTTTCG	1e-17	-3.947e+01	6.10%	0.83%	58.3bp (187.5bp)	IRF7/MA0772.1/Jaspar(0.734) More Information Similar Motifs Found
9	AGTGACAG	1e-17	-3.931e+01	14.67%	4.83%	192.2bp (236.0bp)	PBX1(Homeobox)/MCF7-PBX1-ChIP-Seq(GSE28007)/Homer(0.801) More Information Similar Motifs Found
10	GATCTCAG	1e-16	-3.893e+01	10.86%	2.83%	124.9bp (239.8bp)	PB0126.1_Gata5_2/Jaspar(0.683) More Information Similar Motifs Found
11	GTGCAATC	1e-15	-3.534e+01	6.10%	0.96%	101.4bp (221.4bp)	Ddit3::Cebpa/MA0019.1/Jaspar(0.766) More Information Similar Motifs Found
12	CGTTTTTCG	1e-14	-3.329e+01	6.67%	1.26%	357.8bp (243.3bp)	NFATC2/MA0152.1/Jaspar(0.663) More Information Similar Motifs Found
13	GACCAA	1e-12	-2.932e+01	13.33%	5.01%	399.0bp (268.2bp)	RORA(var.2)/MA0072.1/Jaspar(0.738) More Information Similar Motifs Found