## Homer de novo Motif Results (/rslt/)

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 <u>STAMP</u>

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

Total target sequences = 19632

Total background sequences = 16658

\* - possible false positive

Rank	Motif		log P- pvalue	% of Targets	% of Background	STD(Bg STD)	Best Match/Details	Motif File
1	GASCG	1e- 105	-2.434e+02	31.55%	21.38%		Lm_0254(RRM)/Leishmania_major- RNCMPT00254- PBM/HughesRNA(0.823) More Information   Similar Motifs Found	motif file (matrix)
2	AGGTA	1e- 85	-1.964e+02	30.64%	21.56%	13.6bp (22.5bp)	MOT3/Literature(Harbison)/Yeast(0.955) <u>More Information</u>   <u>Similar Motifs Found</u>	motif file (matrix)
3	CGTCC	1e- 17	-4.120e+01	8.87%	6.42%	14.5bp	FXR2(KH)/Homo_sapiens- RNCMPT00020- PBM/HughesRNA(0.792) <u>More Information</u>   <u>Similar Motifs Found</u>	motif file (matrix)
4 *	<b>TAAGT</b>	1e- 10	-2.384e+01	11.78%	9.66%	16.7bp (17.2bp)	bap/MA0211.1/Jaspar(0.887)  More Information   Similar Motifs Found	motif file (matrix)
5 *	AAAA	1e-7	-1.751e+01	27.96%	25.42%		hb/dmmpmm(SeSiMCMC)/fly(0.978)  More Information   Similar Motifs Found	motif file (matrix)
6 <b>*</b>	CTCTC	1e0	-2.800e-05	12.73%	14.18%	15.5bp (23.2bp)	Trl/dmmpmm(Pollard)/fly(0.895)  More Information   Similar Motifs Found	motif file (matrix)