

# Information from STAMP

The following results were obtained using default options from STAMP

Phylogenetic tree from the obtained motifs



YY1\_100\_c1\_2W1



Motif Name	E-Value	Alignment	Weblogo
T	6.2805e-03	--CACACA--- TTCACACCTAG	
BRACH_01	8.2514e-03	----CACACA----- AATTCACACCTAGGTGTSANNNN	
AR_02	9.9081e-03	-----CACACA----- NNNNNNAGAACACNNTGTNCYNNNNNN	

SMAD3_Q6	1.4280e-02	---CACACA AGNCAGACA	
AHR_Q5	1.7541e-02	--TGTGTG--- NTNGCGTGNNN	

YY1_100_c1_2W2	
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Motif Name	E-Value	Alignment	Weblogo
HFH4_01	4.4017e-03	---ACACACAC-- TAAACAAACAMWN	
HMX1_01	9.9625e-03	ACACACAC--- -CACGCACTTG	
SMAD3_Q6	1.0812e-02	--ACACACAC AGNCAGACA-	
TAXCREB_02	1.4057e-02	---GTGTGTGT--- GGGRTATGCGTCAY	
CF2II_01	1.4826e-02	GTGTGTGT- RTATATRTA	

YY1\_100\_c1\_2W3

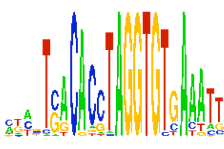
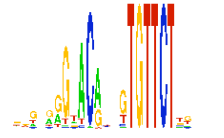




Motif Name	E-Value	Alignment	Weblogo
SMAD3_Q6	3.4640e-03	CACACACACA -AGNCAGACA	
HFH4_01	5.1153e-03	--CACACACACA- TAAACAAACAMWN	
GCM_Q2	7.7969e-03	--TGTGTGTGTG NATGCGGGYNNK	
GBF_Q6	2.2250e-02	-TGTGTGTGTG TTNGGGGTN--	
CACCCBINDINGFACTOR_Q6	2.6641e-02	-CACACACACA----- CCNCACCCWNNKGTG	


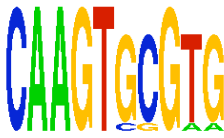

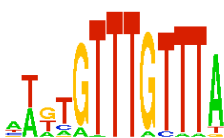
YY1\_100\_c1\_2W4

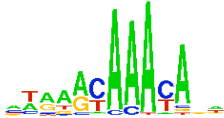


Motif Name	E-Value	Alignment	Weblogo
T	6.2563e-03	-ACACAC---- TTCACACCTAG	

BRACH_01	8.2113e-03	----ACACAC----- AATTCACACCTAGGTGTSANNNN	
AR_02	1.0043e-02	-----GTGTGT----- NNNNNNNRGNACANNGTGTTCTNNNNNN	
SMAD3_Q6	1.4316e-02	-GTGTGT-- TGTCTGNCT	
Fos	1.5272e-02	--ACACAC TGANTCAC	




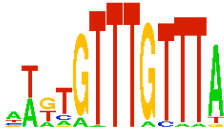
Motif Name	E-Value	Alignment	Weblogo
SMAD3_Q6	8.0682e-03	-YRCACACA AGNCAGACA	
HMX1_01	1.3660e-02	--TGTGTGYR CAAGTGC GTG	
GBF_Q6	1.4767e-02	YRCACACA- NACCCCNAA	
HFH4_01	1.5818e-02	-TGTGTGYR---- NWKTGTTTGT TTA	

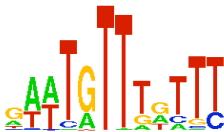
HNF3\_Q6 2.0826e-02 ---YRCACACA--  
NNRNRYYAAAYANN 

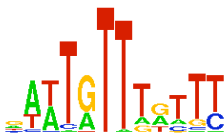
YY1\_100\_c1\_2W6 

Motif Name	E-Value	Alignment	Weblogo
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SMAD3_Q6	3.4142e-03	GTGTGTGTGT -TGTCTGNCT	
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HFH4_01	5.2908e-03	-ACACACACAC-- TAAACAAACAMWN	
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Foxd3	2.6210e-02	ACACACACAC-- AAANAAACAWTN	
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FOXD3_01	2.7585e-02	ACACACACAC-- AAANAAACAWTN	
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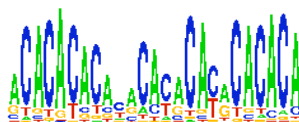
GBF_Q6	2.9191e-02	GTGTGTGTGT TTNGGGGTN-	
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YY1\_100\_c1\_2M1 

Motif Name	E-Value	Alignment	Weblogo
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NRF1_Q6	2.5324e-02	ACACACAYRCACACAC ---CGCRTGCGCR---	
HMG-IY	2.7719e-02	GTGTGTGYRTGTGTGT RTTTYKNYNTTTNTNN	
GCM_Q2	3.6770e-02	-GTGTGTGYRTGTGTGT NATGCGGGYNNK----	
SMAD3_Q6	3.6827e-02	ACACACAYRCACACAC -----AGNCAGACA-	
TAXCREB_02	4.0343e-02	GTGTGTGYRTGTGTGT- --GGGRTATGCGTCAY	

YY1\_100\_c1\_2M11



Motif Name	E-Value	Alignment	Weblogo
GCM_Q2	3.4610e-02	TGTGTGYRTGTGTGNNTGTGTGTGT -----NATGCGGGYNNK-----	
SMAD3_Q6	3.9057e-02	ACACACACANNCACACAYRCACACA --AGNCAGACA-----	
CF2II_01	6.2164e-02	ACACACACANNCACACAYRCACACA -----TAYATATAY-----	


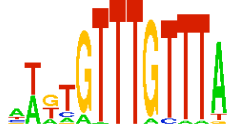
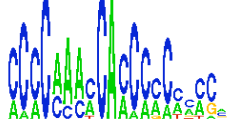
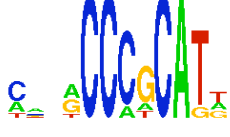
HFH4_01	6.7524e-02	ACACACACANNCACACAYRCACACA -----TAAACAAACAMWN---	
HMX1_01	8.8041e-02	TGTGTGYRTGTGTGNNTGTGTGTGT CAAGTGCCTG-----	

YY1_100_c1_2M12		
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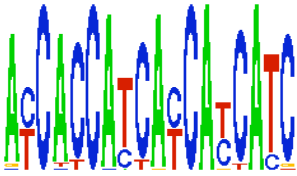
Motif Name	E-Value	Alignment	Weblogo
RREB1	1.3722e-02	TGTGTGTGNNKGTGTNTGTG NGKKKGKGGGTGKTTTGGGG	
TAXCREB_02	4.2602e-02	TGTGTGTGNNKGTGTNTGTG -GGGRTATGCGTCAY----	
GBF_Q6	5.1749e-02	CACANACACMNNCACACACA- -----NACCCCNAA	
SMAD3_Q6	7.1080e-02	CACANACACMNNCACACACA ---AGNCAGACA-----	
HFH4_01	7.1939e-02	CACANACACMNNCACACACA --TAAACAAACAMWN-----	



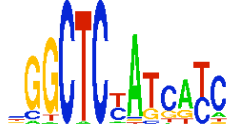

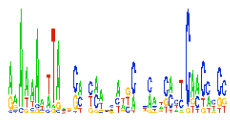
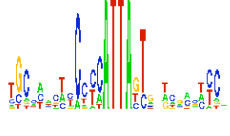


SMAD3_Q6	4.9961e-02	TGTGTGYRTGNRTGTGTG TGTCTGNCT-----	
HFH4_01	5.8172e-02	CACACAYNCAYRCACACA- -----TAAACAAACAMWN	
RREB1	6.5049e-02	--CACACAYNCAYRCACACA CCCCAAAMCACCCMCMMMCNC	
GCM_Q2	6.6679e-02	TGTGTGYRTGNRTGTGTG -----NATGCGGGYNNK	

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YY1_100_c1_2M3		
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Motif Name	E-Value	Alignment	Weblogo
ZID_01	1.7454e-02	GATGRTGRTGATGGTGR- -----GRTGATRGAGCCN	
CACBINDINGPROTEIN_Q6	4.1883e-02	AYCACCATCAYCAYCATC CCCASCCYC-----	
PAX4_04	4.7036e-02	-----AYCACCATCAYCAYCATC RNAAAWTANNNNNNNNNNNNNNNNNNNNCACNCN-	
HOX13_01	4.8970e-02	-----GATGRTGRTGATGGTGR- NGRNNNNNNNNNANTAATGRNGNNNNNNNGCN--	

HAHB4\_01

5.2765e-02

AYCACCATCA YCAYCATC  
----NAATYATTA-----

