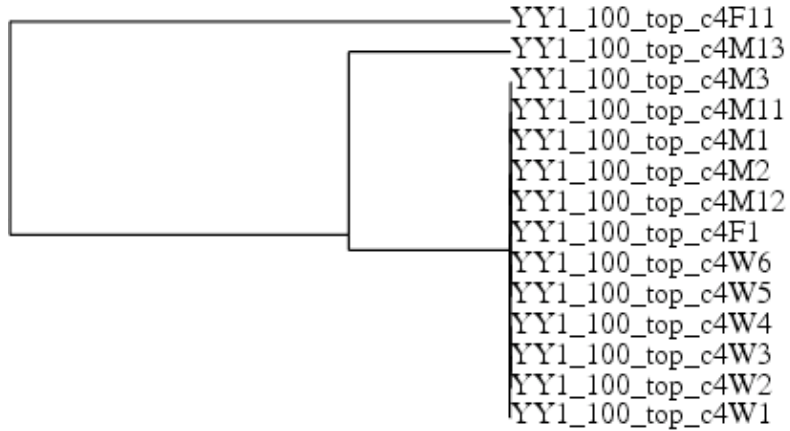


Information from STAMP

The following results were obtained using default options from STAMP

Phylogenetic tree from the obtained motifs



YY1_100_top_c4W1


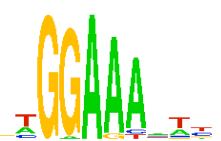


Motif Name	E-Value	Alignment	Weblogo
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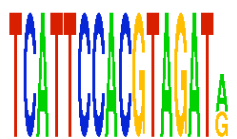
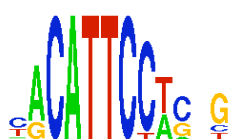
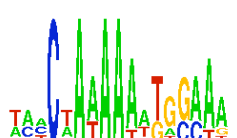
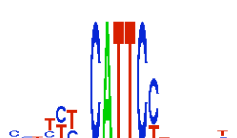
O2_01	4.1849e-04	-----TSGAAT-- YATCTACGTGGAATGA	
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TEAD	9.2747e-03	---TSGAAT--- CNSWGGAAATGTR	
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PAX_Q6	1.1704e-02	---ATTCSA- GTKAGTTCCAG	
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IK1_01	1.6130e-02	---ATTCSA--- NNNATTCCCANN	
NFAT_Q4_01	1.6979e-02	---ATTCSA- NWNTTCCWN	

YY1_100_top_c4W2	
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Motif Name	E-Value	Alignment	Weblogo
TEF1_Q6	4.1004e-04	ATGGAATG --GRRATG	
O2_01	8.5142e-04	-----ATGGAATG- YATCTACGTGGAATGA	
TEAD	2.6430e-03	--ATGGAATG-- CNSWGAATGTR	
MADSB_Q2	1.4302e-02	CATTCCAT----- -TTTSCATTTTTRGNW	
ABAA_01	1.5916e-02	---ATGGAATG----- NNNNNNGGAATGNRRNNNN	

YY1_100_top_c4W3



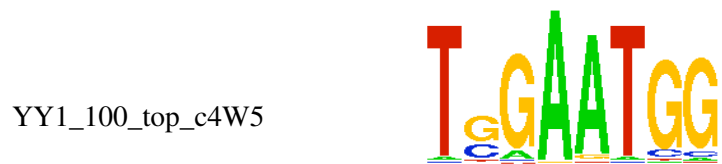
Motif Name	E-Value	Alignment	Weblogo
TEF1_Q6	1.3260e-03	TCCATTCSAT --CATYYC--	
O2_01	9.1075e-03	-----ATSGAATGGA YATCTACGTGGAATGA-	
TEAD	1.1252e-02	--ATSGAATGGA CNSWGAATGTR	
HMG-IY	1.5516e-02	----TCCATTCSAT- RTTTYKNYNTTNTNN	
CAT8_Q6	2.2166e-02	TCCATTCSAT- -CCATTNNCC	

YY1_100_top_c4W4

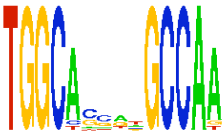


Motif Name	E-Value	Alignment	Weblogo
MADSB_Q2	6.2071e-04	-TTCCAT----- TTTSCATTTTTRGNW	


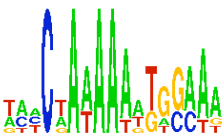
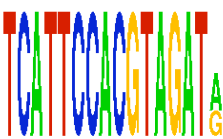
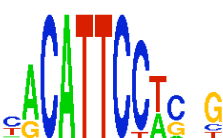
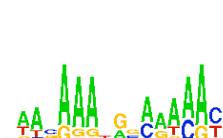
HMG-IY	4.2636e-03	----TTCCAT----- RTTTYKKNYNTTNTNN	
PAX_Q6	8.1370e-03	----TTCCAT GTKAGTTCCAG	
SQUA	8.8104e-03	--TTCCAT----- NTTNCYATWWTGK	
AGL3_01	8.9079e-03	-----ATGGAA-- NNWNCTATAWWTGGNANN	



Motif Name	E-Value	Alignment	Weblogo
TEF1_Q6	4.0887e-04	CCATTCSA -CATYYC-	
O2_01	9.3282e-04	-----TSGAATGG YATCTACGTGGAATGA	
CAT8_Q6	1.4163e-03	--TSGAATGG GGNNAATGG	
TEAD	2.8498e-03	--TSGAATGG- CNSWGAATGTR	

Hox11-CTF1 5.6165e-03 -TSGAATGG-----
TTGGCNNNSTGCCA 

YY1_100_top_c4W6 

Motif Name	E-Value	Alignment	Weblogo
TEF1_Q6	1.2919e-03	TTCCATTCSA ---CATYYC-	
MADSB_Q2	5.9286e-03	----TSGAATGGAA- WNCYAAAAAATGSAAA	
O2_01	8.9285e-03	-----TSGAATGGAA YATCTACGTGGAATGA--	
TEAD	1.0927e-02	TTCCATTCSA--- -YACATTCCWSNG	
HMG-IY	1.1203e-02	----TTCCATTCSA-- RTTTYKKNYNTTNTNN	



YY1_100_top_c4F1 

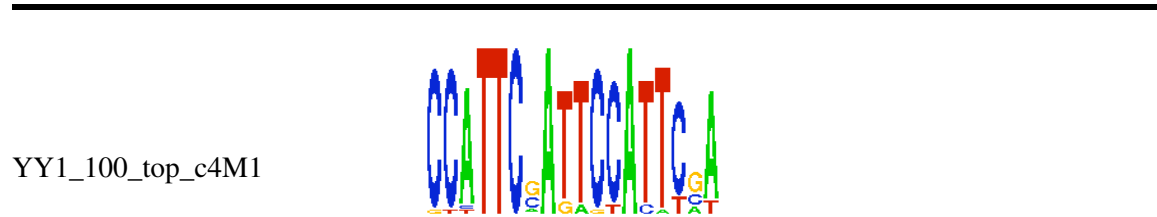
Motif Name	E-Value	Alignment	Weblogo
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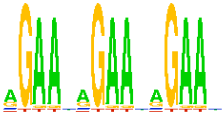
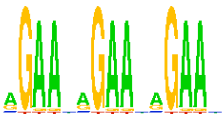

CAT8_Q6	8.5272e-03	--TNGAATGGAATS GGNNAATGG----	
HMG-IY	1.5847e-02	--TNGAATGGAATS-- NNANAAANRRNMRAAY	
TEF1_Q6	1.8311e-02	SATTCCATTCNA ----CATYYC-	
MADSB_Q2	2.1575e-02	SATTCCATTCNA---- -TTTSCATTTTTRGNW	
UNC86_Q2	3.8897e-02	SATTCCATTCNA--- ----CATWMRAAAT	

YY1_100_top_c4F11

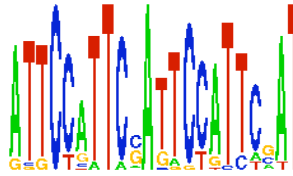
Motif Name	E-Value	Alignment	Weblogo
TEF1_Q6	2.3544e-02	NNNNYNNYCCNNNN ----CATYYC----	
MAZ_Q6	7.7755e-02	NNNNYNNYCCNNNN ---CCCTCCCC---	
SPI1	1.1927e-01	NNNNYNNYCCNNNN ----STTCN---	

ZIC2_01	1.6547e-01	NNNNYNNYCCNNNN --NACCACCCN---	
ZIC3_01	1.9008e-01	NNNNYNNYCCNNNN --GANCMCCCN---	



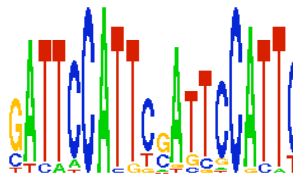
Motif Name	E-Value	Alignment	Weblogo
CAT8_Q6	2.4550e-02	--TNGAATGGAATSGAATGG GGNNNAATGG-----	
TEF1_Q6	2.4808e-02	CCATTCSATTCCATTCNA -CATYYC-----	
HSF_02	2.8796e-02	CCATTCSATTCCATTCNA --NTTCTNTTCTNTTCT-	
HSF_02	3.5271e-02	CCATTCSATTCCATTCNA --NTTCNNTTCNNTTCN-	
UNC86_Q2	5.5979e-02	---TNGAATGGAATSGAATGG ATTTYKWATG-----	

YY1_100_top_c4M11

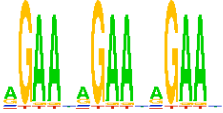





Motif Name	E-Value	Alignment	Weblogo
CAT8_Q6	6.6035e-03	-ATNGAATGGAATSGAATGGAAT GGNNNAATGG-----	
TGA1A_Q2_01	8.2001e-03	ATNGAATGGAATSGAATGGAAT--- ---RANWNNNTNNNNNANGTCATCNA	
TEF1_Q6	1.4645e-02	ATNGAATGGAATSGAATGGAAT -----GRRATG----	
UNC86_Q2	2.6710e-02	--ATNGAATGGAATSGAATGGAAT ATTTYKWATG-----	
HMG-IY	3.1864e-02	ATCCATTCSATTCCATTTCNAT- -----RTTTYKNYNTTTNTNN	

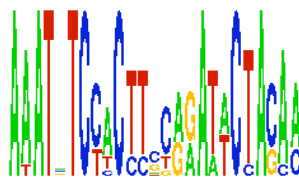
YY1_100_top_c4M12







Motif Name	E-Value	Alignment	Weblogo
HSF_02	6.3785e-03	GAATGGAATSGAATGGAATC ---AGAANAGAANAGAAN-	


HSF_02	8.8997e-03	GATTCCATTCSATTCCATTC- -----NTTCNNTTCNNTTCN	
HMG-IY	1.2033e-02	--GATTCCATTCSATTCCATTC RTTYKKNYNTTNTNN-----	
TEF1_Q6	3.7612e-02	GATTCCATTCSATTCCATTC ----CATYYC-----	
CAT8_Q6	4.1736e-02	GAATGGAATSGAATGGAATC ----GGNNAATGG----	

YY1_100_top_c4M13

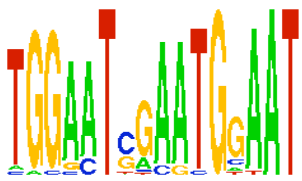


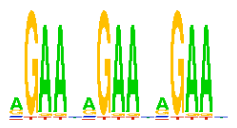
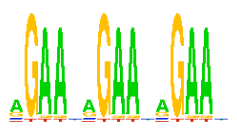


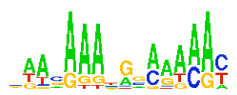
Motif Name	E-Value	Alignment	Weblogo
ELK4	7.2446e-03	TTGTAGWATYYGNAAGTGGANATTT -----ACCGGAAGT-----	
E74A	7.4745e-03	TTGTAGWATYYGNAAGTGGANATTT -----CCGGAAR-----	
IRF1_Q6	1.0237e-02	TTGTAGWATYYGNAAGTGGANATTT -----AANTGAA-----	
TEL2_Q6	1.2002e-02	TTGTAGWATYYGNAAGTGGANATTT -----CAGGAAGTAN-----	

AP3_Q6 2.1066e-02 AAATNTCCACTTNCRRATWCTACAA
 -----TCYMAATT-----



YY1_100_top_c4M2



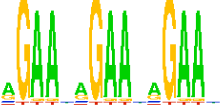



Motif Name	E-Value	Alignment	Weblogo
HSF_02	6.2123e-03	TGGAATSGAATGGAAT -AGAANAGAANAGAAN	
HSF_02	9.0021e-03	ATTCCATTCSATTCCA NTTCNNTTCNNTTCN-	
TEF1_Q6	1.4537e-02	ATTCCATTCSATTCCA ---CATYYC-----	
CAT8_Q6	1.8480e-02	TGGAATSGAATGGAAT --GNNAATGG--	
HMG-IY	3.4876e-02	---ATTCCATTCSATTCCA RTTTYKNYNTTNTNN---	

YY1_100_top_c4M3



Motif Name	E-Value	Alignment	Weblogo
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HMG-IY	6.9031e-03	GANGWTTCCMTTCNAKTN -RTTTYKKNYNTTNTNN-	
TEF1_Q6	8.1047e-03	GANGWTTCCMTTCNAKTN -----CATYYC----	
HSF_02	5.2437e-02	GANGWTTCCMTTCNAKTN- ----NTTCTNTTCTNTTCT	
CAT8_Q6	6.0870e-02	NAMTNGAAKGGAAWCNTC -GGNNNAATGG-----	
HSF_02	6.5988e-02	GANGWTTCCMTTCNAKTN- ----NTTCNNTTCNNTTCN	