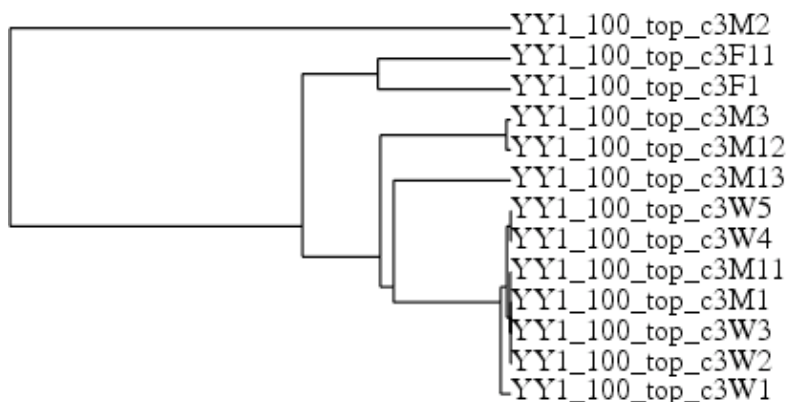


Information from STAMP

The following results were obtained using default options from STAMP



Phylogenetic tree from the obtained motifs





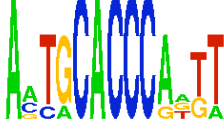
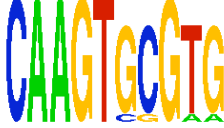
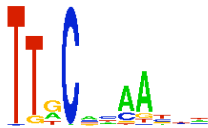
YY1_100_top_c3W1



Motif Name	E-Value	Alignment	Weblogo
RCS1_Q2	1.3519e-02	----YNTGCA-- AANTGGGTGCAKT	
MTF1_Q4	1.5009e-02	-----YNTGCA-- GGGCCGNGTGCANA	
HIF1_Q3	1.6387e-02	----YNTGCA--- GNNKACGTGCNNNN	

AR_Q6	1.8503e-02	-YNTGCA-- NNNTGCTCN	
MYC_Q2	2.3323e-02	TGCANR-- -NCACGTG	

YY1_100_top_c3W2	
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Motif Name	E-Value	Alignment	Weblogo
NRF1_Q6	1.6618e-03	TGTGCAYG-- YGC GCAYGCG	
SGF3_Q6	7.6906e-03	CRTGCACA- --TGMAYAA	
RCS1_Q2	1.1676e-02	----TGTGCAYG AANTGGGTGCAKT	
HMX1_01	1.3798e-02	--TGTGCAYG CAAGTGC GTG	
CEBP_Q2_01	1.8142e-02	----TGTGCAYG NNNTTNGNAAN	

YY1_100_top_c3W3



Motif Name	E-Value	Alignment	Weblogo
RCS1_Q2	1.3515e-02	---GTGTGCATGT AANTGGGTGCAKT-	
NRF1_Q6	1.6721e-02	GTGTGCATGT- -YGCGCAYGCG	
MTF1_Q4	1.6942e-02	----GTGTGCATGT GGGCCGNGTGCANA-	
HMX1_01	2.7825e-02	ACATGCACAC- -CACGCACTTG	
SGF3_Q6	2.9423e-02	ACATGCACAC ---TGMAYAA	

YY1_100_top_c3W4



Motif Name	E-Value	Alignment	Weblogo
AHR_Q5	2.0589e-03	--TGYGTG--- NTNGCGTGNNN	






HMX1_01	2.8228e-03	CACRCA--- CACGCACTTG	
T	1.3027e-02	--CACRCA--- TTCACACCTAG	
PAX3_01	1.3323e-02	---TGYGTG--- KNAAGYGTGACGA	
Pax6	1.4568e-02	-----TGYGTG-- MANTSAWGCCTGAA	



Motif Name	E-Value	Alignment	Weblogo
RCS1_Q2	1.3293e-03	--TGCACACA--- AMTGCACCCANTT	
MTF1_Q4	3.4169e-03	--TGCACACA--- TNTGCACNCGGCC	
SGF3_Q6	6.5074e-03	TGCACACA TGMAYAA-	
SN_02	9.2128e-03	-----TGTGTGCA NNNANNTGNTNNA	






T 1.4106e-02 TGCACACA---
TTCACACCTAG 

YY1_100_top_c3F1 




Motif Name	E-Value	Alignment	Weblogo
Snail	1.3231e-01	NNNNCCTGGNNN --CACCTG----	
TTK69_01	2.5154e-01	NNNCCAGGNNNN --GCAGGACC-	
E2A_Q6	2.5372e-01	NNNCCAGGNNNN --RNCAGNTG--	
PAX6_Q2	2.9323e-01	--NNNCCAGGNNNN KAGTTCAGGTCAG	
GRH_01	3.0462e-01	NNNNCCTGGNNN ----ACYGGTTT	

YY1_100_top_c3F1 

Motif Name	E-Value	Alignment	Weblogo
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CACBINDINGPROTEIN_Q6	1.7774e-01	NNNNNCNCAGNNNN ----CCASCCYC	
SREBP1_Q6	3.2505e-01	NNNNCTGNGNNNNN ----TGGSGTG--	
CP2_01	3.5878e-01	NNNNCTGNGNNNNN- ---CTGGKTNGNGC	
LYF1_01	3.5976e-01	NNNNNCNCAGNNNN --YCTCCCAA---	
GRH_01	3.6524e-01	NNNNNCNCAGNNNN ---AAACCRGT---	



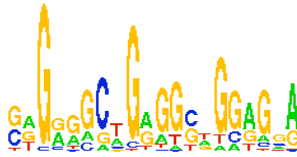
Motif Name	E-Value	Alignment	Weblogo
NRF1_Q6	2.6638e-03	ACACACACAYGCAYACA ----CGCRTGCGCR--	
HMX1_01	3.8553e-03	ACACACACAYGCAYACA -CACGCACTTG-----	
HMG-IY	1.5594e-02	ACACACACAYGCAYACA- --NNANAAANRNMRAAY	

SMAD3_Q6	2.1546e-02	ACACACACAYGCAYACA AGNCAGACA-----	
GCM_Q2	2.7866e-02	TGTRTGCRTGTGTGTGT --NATGCGGGYNNK--	



Motif Name	E-Value	Alignment	Weblogo
HMG-IY	3.0976e-03	-TGTNTGNNTGYNTKTRTGTR RTTTYKNYNTTNTNN----	
HFH4_01	2.2476e-02	YACAYAMANRCANNCANACA TAAACAAACAMWN-----	
DBP_Q6	3.4526e-02	YACAYAMANRCANNCANACA -----AGCANWN-	
HNF3ALPHA_Q6	3.4540e-02	YACAYAMANRCANNCANACA -----NWRARCAAAYA	
GCM_Q2	3.6773e-02	TGTNTGNNTGYNTKTRTGTR -----NATGCGGGYNNK--	

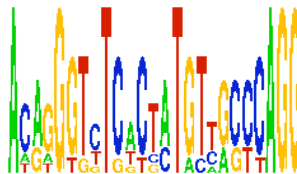
YY1_100_top_c3M12



Motif Name	E-Value	Alignment	Weblogo
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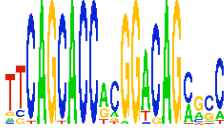
TANTIGEN_B	1.3023e-04	SNGRRGCWGRGGSNGGRGNA RGGAGGCAGAGGCAGGYGG-	
CACBINDINGPROTEIN_Q6	5.9844e-04	TNCYCCNSCCYCWGCYYCNS -----CCCASCCYC--	
BARBIE_01	2.1313e-03	TNCYCCNSCCYCWGCYYCNS -CMNNCNSCTTTNNNT----	
KROX_Q6	8.4973e-03	SNGRRGCWGRGGSNGGRGNA --GNNGNGGGGGCGGN----	
VDR_Q3	1.3035e-02	SNGRRGCWGRGGSNGGRGNA--- -----GGGKNARNRRGGWSA	

YY1_100_top_c3M13

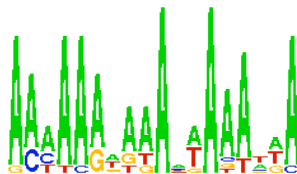


Motif Name	E-Value	Alignment	Weblogo
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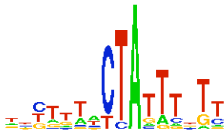
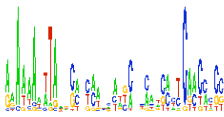
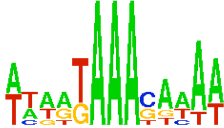

IRF1	7.1374e-03	CCTGGGCRACATAGWGARACCCTGT -----NAAANYGAAACC----	
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SF1_Q6	3.7769e-02	ACAGGGTYTCWCTATGTYGCCCAGG -CAAGGTCA-----	
Spz1	4.5909e-02	CCTGGGCRACATAGWGARACCCTGT --AGGGTAWCAGC-----	
Broad-complex_2	4.7074e-02	CCTGGGCRACATAGWGARACCCTGT -----AAATAGNW-----	
NRSF_01	4.7354e-02	ACAGGGTYTCWCTATGTYGCCCAGG --GSYGCTGTCCGTGGTGCTGAA-	

YY1_100_top_c3M2



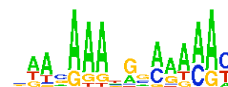
Motif Name	E-Value	Alignment	Weblogo
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BRCZ2_01	2.0783e-03	TNNTTTWNTTTNTTTKTT --NNNNWNCTATTTNTY	
PAX4_04	4.8213e-03	-----TNNTTTWNTTTNTTTKTT NGNGTGNNNNNNNNNNNNNNNTAWTTTNY	
BRCZ4_01	7.3178e-03	TNNTTTWNTTTNTTTKTT ---TTWTSTTTAYWWW--	
EVI1_04	8.7746e-03	TNNTTTWNTTTNTTTKTT TATCTTNTCNTATCN---	

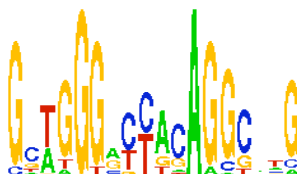
HMG-IY

8.8691e-03

-AAMAAANAAANWAAANNA
 NNANAAANRNMRAAY---



YY1_100_top_c3M3

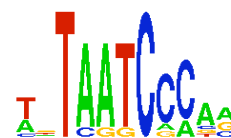


Motif Name	E-Value	Alignment	Weblogo
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PITX2_Q2

4.5305e-03

CNNGCCTGTRGNCCCANC
 -----WNTAATCCCAN-



AML1_Q1

1.4789e-02

GNTGGGNCYACAGGCNNG
 -----ACCACA-----



AML1_Q6

1.7440e-02

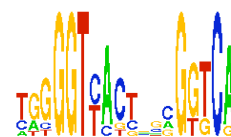
GNTGGGNCYACAGGCNNG
 -----ACCACA-----



LXR_Q3

2.7733e-02

--CNNGCCTGTRGNCCCANC
 TGACCNNNAGTRACCCCA--



CF1_Q2

2.8680e-02

CNNGCCTGTRGNCCCANC
 -----NGTGACCCC---

