

**Table S2. Putative transcription factor binding sites on the murine *MORG1* promoter sequence.**

Putative transcription factor binding sites on the murine *MORG1* promoter sequence identified by the aid of the ALGGEN-PROMO link ([http://alggen.lsi.upc.es/cgi-bin/promo\\_v3/promo/promoinit.cgi?dirDB=TF\\_8.3](http://alggen.lsi.upc.es/cgi-bin/promo_v3/promo/promoinit.cgi?dirDB=TF_8.3)), which use the TFBS defined in the TRANSFAC database to construct specific binding site weight matrices for TFBS prediction.

Factors predicted within a dissimilarity margin less or equal than 15 % :

Data (txt)
-- Input sequence ----- >Sequence GCAGCTGAGGGAGGGCGGAGGCAGCCAAAGGCTAGGCCAGAGAGAAGGTGGGCCTGAGTCCAGGATCCAA CCCTCCTAGGTGGCATCACCAGGGAGGCGTCATGGGCTGAGGATTCTGCAGATAGGACATCACCACGGCGGA GATAGAGAGCCTGAGATGGAAAAGAGCTGTCAAGTGTGGGGAGCACGCATGGGACCCCATCCCCTTATTAG CATCCTCACATGAAGCTACTCATCTGCTTAGTGTCTCCGAGCTCCGCGAGTTGGCAAAGCTGATAAAGGA GCAGTAGACAGCAACCCAAGCACACCACTTCAGCTGAAGAAAGGTGGGTGAGAAGACCGGGTCAGTGACAA GTATACCAAGGAGCTCCACCACCAAGGTCTCAGATATCAGGTTCTACCTGCAGCTCGGACCTTGTTCCCGGG GAAGCACCTCAACACCAACCCTCAGAGCCTACTCGAAGCAGCAGGCTTCTGATGCCAATGTGTGCTCCTGCACCT CTCACCTACCGCATCCTCTCAGACTGCTTAACATTCCACATGCTAAGGACCCTCCCGGCCTCTTTCCACAA GTCGTCTGTAACCTGCCTAAGTTAGGCTCCACCCTCAGACCCCGCTAGGCAGTGTACAAGTCAAGTGCAAGCCC AACTTCCCCTACGTTTGGGGCGTCACCCTAGCTCCACCCTAGCTGACCTCACCCCTTCCCCACCTCTAGCACA GCCAGAGGACCCGCTCTTTCTGAACCCACCCAGACCTCAGTTTCAGGCGGACCAACAGACACTCAGGGAGG TTCATCCCCACCCACCTTAAGCATGAGGCCACACATGCTGAAGATCATGCCAAGAAGATTATGTAGTCCGGAG TCGGGTCTGTCTAAAGCCGGGTTGCACTCACTCGGGGGAGGCTTATACCTGCGACATGTTCAAGGATCAGGAGC GATCAAGTCCCACCTGGGCCACCTTAGCCATGACCCACGGCCACAACCAAAGACGCCTTGCCATGACTTGCT GGACTGCTCACCTCAGCACTTTGTTGGGCCTTCGTGGGTGCGACATATTGTTAGTGGACATAGCAAAGTGAAG ACCACGCCGTCCTTCTTTACAGCTAGAAGAGCAACTTCCGGGCGTGGAATGAAGGATGGCTTTTAGAGTAA CACCAGTAGCCAGCGCTTCTGTTCCCAATAGCAGTGAGAGGGACGACTCTCAGCCAGAAAAAGGAGAATGAG AAAAGGCCAAAAACAGTTCCTGGAAAGTAGGAAGTCTAGGGAAAAAAACTGAAAGGACTTTTCAGTATCCCC AAAAGTGCATTAACGCGCTGAAATTTTGCACGGAAGTGCAAAGCAGGAAATAAATCCTGGGGGACAATAATA ATGTTACACTCGAGCAAGTCTTTGAAAGCTTGGGAGGACGGTGGTCTCAATACATCAGCAGTAAAGCAGGC AGCGGACTGATGCA
-- Factors predicted by PROMO in this sequence ----- NAME; MATRIX_WIDTH; Myf-3 [T00519]; 8 MyoD [T00525]; 8 MyoD [T01128]; 8 myogenin [T00528]; 7

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Nkx2-1 [T00857]; 7  
COE1 [T01112]; 7  
Elk-1 [T00250]; 5  
WT1 I -KTS [T00900]; 10  
WT1 -KTS [T01839]; 10  
Sp1 [T00759]; 9  
Sp1 [T00755]; 9  
AP-2alphaA [T00035]; 6  
GAL4 [T00302]; 8  
CREMtau [T01309]; 7  
CREMtau1 [T02108]; 7  
CREMtau2 [T02109]; 7  
MF3 [T00507]; 5  
NF-1 [T00535]; 9  
NF-1 [T00536]; 8  
NF-1 [T00538]; 8  
TGGCA-binding protein [T00832]; 7  
LIM1 [T04817]; 4  
C/EBPalpha [T00107]; 3  
TCF-1A [T00999]; 9  
LEF-1 [T02905]; 8  
TCF-4E [T02878]; 7  
HNF-3 [T02277]; 6  
NFI/CTF [T00094]; 8  
NF-AT4 [T01949]; 8  
DEF:GLO:SQUA [T03217]; 7  
SF-1 [T01147]; 9  
NF-1 [T01298]; 6  
GAGA factor [T00301]; 6  
GA-BF [T00297]; 7  
PBF [T02693]; 8  
Zic1 [T04669]; 4  
Zic2 [T04670]; 3  
USF-1 [T00875]; 7  
WT1 I [T01840]; 7  
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Nrf2:MafK [T05666]; 7  
LVb-binding factor [T00477]; 7  
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RC2 [T00724]; 6  
MYB2 [T02536]; 5  
Zic3 [T04671]; 4  
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TF68 [T00809]; 10  
Msx-1 [T02072]; 3

RAR-gamma [T00720]; 8  
ABF1 [T00056]; 6  
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Pax-9b [T03594]; 7  
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Sp3 [T02419]; 11  
USF2 [T02115]; 6  
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MafG [T01437]; 5  
YY1 [T00915]; 7  
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Staf [T02247]; 12  
YY1 [T00865]; 6  
Mitf [T01554]; 13  
NF-1 (-like proteins) [T00601]; 8  
C/EBP [T01386]; 6  
GATA-1 [T05705]; 7  
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GATA-1 [T00306]; 6  
GATA-3 [T00311]; 8  
Pax-6 [T00682]; 5  
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Alfin1 [T04733]; 7  
Vpr [T02399]; 8  
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HES-1 [T01649]; 7  
TCF-1(P) [T01109]; 10  
STAT5A [T04683]; 4  
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IRF-3 [T04673]; 7  
MNB1a [T01059]; 6  
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DI [T00196]; 9  
TGIF [T04076]; 8  
PKNOX1 [T04122]; 11  
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MZF-1 [T00529]; 7  
CP2 [T00152]; 8  
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DBP [T00183]; 7  
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MCB2 [T06036]; 9  
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muEBP-C2 [T00215]; 6  
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LCR-F1 [T01599]; 6  
Stra13 [T02327]; 11  
STE12 [T00772]; 8  
Pax-8 [T01828]; 6  
FOXN2 [T04206]; 11  
E2F-1 [T01542]; 7  
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VDR [T00885]; 4  
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ER-beta [T04651]; 9  
RAR-beta [T00721]; 8  
PPAR-alpha [T00694]; 7  
ER-alpha [T00261]; 8  
USF2b [T02377]; 8  
c-Jun [T00131]; 6

JunB [T00436]; 6  
c-Fos [T00124]; 7  
c-Jun [T00132]; 7  
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JunD [T00437]; 7  
SRY [T00997]; 7  
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Ik-1 [T02702]; 13  
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TFIIB [T00818]; 8  
GATA-2 [T01302]; 8  
Tal-1 [T01799]; 9  
AREB6 [T00625]; 8  
DSXF [T00955]; 7  
DSXM [T00956]; 7  
LVc [T00478]; 5  
NF-1/L [T00599]; 13  
En-1 [T02016]; 6  
PR B [T00696]; 7  
PR A [T01661]; 7  
Sox2 [T01836]; 7  
HMG I(Y) [T02368]; 7  
STAT4 [T01577]; 6  
GR-alpha [T00337]; 8  
PR B [T00697]; 7  
COE2 [T05006]; 9  
GR-beta [T01920]; 8  
c-Ets-1 [T00112]; 7  
E2F [T01547]; 8  
STAT6 [T01581]; 9  
C1 (long form) [T01592]; 8  
C1 (short form) [T01593]; 8  
C1-I [T02946]; 8  
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c-Ets-1 68 [T00115]; 10  
NF-kappaB1 [T00593]; 12  
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RelA [T00595]; 11  
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XBP1 [T03707]; 10  
Myf-5 [T00521]; 13  
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Nkx2-5 [T01675]; 9  
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GBF [T00315]; 11  
USF2 [T00878]; 9  
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DRF1.3 [T05837]; 10  
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TFII-I [T00824]; 11  
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Egr-3 [T05889]; 13  
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ALF1B [T01496]; 8  
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GCMb [T02308]; 9  
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ROM2 [T02810]; 9  
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Fli-1 [T01408]; 13  
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LyF-1 [T00479]; 9  
GT-1 [T00339]; 8  
Su(H) [T01615]; 13  
PEA3 [T00685]; 8  
MIF-1 [T01047]; 13  
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AP-3 [T01150]; 9  
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HOXD10 [T01757]; 10  
HOXD10 [T01758]; 10  
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ANF [T01184]; 12  
CIZ6-1 [T05137]; 10  
FOXM1 [T04208]; 11  
NBF [T00951]; 9  
NBF [T01190]; 9

PPAR-gamma:RXR-alpha [T05236]; 12  
ERR1 [T04849]; 11  
GR [T00333]; 7  
HNF-3alpha [T00371]; 8  
c-Ets-2 [T01397]; 9  
ELF-1 [T01113]; 13  
STAT3 [T01493]; 12  
IRF-2 [T00425]; 13  
PEA3 [T00684]; 8  
c-Ets-2 [T00113]; 8  
Elk-1 [T05013]; 9  
Hb [T00395]; 7  
GATA-2 [T00308]; 9  
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HNF-1B [T01950]; 8  
Ubx [T00863]; 6  
Crx [T03461]; 6  
HNF-1A [T00368]; 8  
HOX11 [T02054]; 7  
SUT1 [T04582]; 10  
POU3F1 [T00969]; 7  
AGL3 [T03025]; 6  
Pax-4a [T02983]; 6  
POU3F2 [T00630]; 7  
RAR-beta2 [T01326]; 12  
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MAC1 [T01265]; 7  
POU2F1 [T01031]; 10  
E74A [T00208]; 10  
GABP [T00268]; 12  
Nkx6-2 [T02050]; 8  
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NERF-1a [T05021]; 12  
Croc [T02291]; 10  
Olf-1 [T01040]; 13  
Sox13 [T02420]; 8  
TII [T00789]; 6  
MBF1 [T00492]; 11  
Antp [T00026]; 6  
Gt [T00328]; 11  
Prd [T00699]; 7  
IPF1 [T02057]; 8  
C/EBPgamma [T00216]; 8  
MRF-2 [T04675]; 10  
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Adf-1 [T00008]; 8  
MATa1 [T00488]; 10  
PUR alpha [T05167]; 10

PUR beta [T05172]; 10  
ATHB-5 [T04066]; 11  
HNF-1C [T01951]; 9  
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ARF1 [T04514]; 13  
POU2F2 (Oct-2.1) [T00646]; 8  
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MED8 [T03491]; 9  
FOXP3 [T04280]; 9  
SBF-1 [T00739]; 9  
HNF-1 [T00369]; 12  
Meis-1a [T03388]; 9  
Meis-1b [T03389]; 9  
Elf-1 [T01019]; 10  
HOXA9 [T01710]; 14  
NF-AT4 [T01946]; 12  
FOXD3 [T02290]; 8  
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Hlf [T01071]; 9  
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NRF-2 [T01199]; 11  
Pax-6 [T01122]; 11  
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AIRE [T05990]; 10  
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Lmo2 [T02251]; 8  
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DTF-1 [T00201]; 11  
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Sry-delta [T00767]; 13  
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SF-1 [T02769]; 11

RXR-beta [T01332]; 10  
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 PHO4 [T00690]; 12  
 Ttk 69K [T00843]; 8  
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 POU2F2B [T01871]; 8  
 POU5F1 (Oct-5) [T00653]; 9  
 POU3F1 [T00656]; 11  
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 POU2F1c [T01863]; 11  
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 AR [T00042]; 7  
 NIT2 [T00627]; 8  
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 RPN4 [T04539]; 9  
 StuAp [T02248]; 8  
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 Egr-1 [T01200]; 13  
 GKLf [T02450]; 13

-- PROMO predictions detail -----

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 Sequence; Myf-3 [T00519]; 960; 967; 0.000000; CCACCTGG; 0.40457; 0.47842;  
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 Sequence; myogenin [T00528]; 0; 6; 0.000000; GCAGCTG; 0.17981; 0.22297;  
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 Sequence; myogenin [T00528]; 21; 27; 11.564188; CAGCCAA; 0.17981; 0.20320;  
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Sequence; myogenin [T00528]; 273; 279; 7.808616; AAAGCTG; 0.44952; 0.42325;  
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Sequence; myogenin [T00528]; 471; 477; 0.482381; CAGCAGG; 0.17981; 0.21833;  
Sequence; myogenin [T00528]; 695; 701; 6.361472; CTAGCTG; 0.53943; 0.64423;  
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Sequence; DEF:GLO:SQUA [T03217]; 273; 279; 9.356185; AAAGCTG; 1.43848; 1.31754;  
Sequence; DEF:GLO:SQUA [T03217]; 282; 288; 1.302806; AAAGGAG; 0.71924; 0.66295;  
Sequence; DEF:GLO:SQUA [T03217]; 327; 333; 1.302806; AAAGGTG; 0.71924; 0.66295;  
Sequence; DEF:GLO:SQUA [T03217]; 568; 574; 10.658991; CCTCTTT; 0.71924; 0.77034;  
Sequence; DEF:GLO:SQUA [T03217]; 744; 750; 10.658991; CCTCTTT; 0.71924; 0.77034;  
Sequence; DEF:GLO:SQUA [T03217]; 889; 895; 10.658991; AAAGCCG; 0.71924; 0.77034;  
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Sequence; Vpr [T02399]; 990; 997; 7.657587; GCCACAAC; 0.40457; 0.56484;  
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Sequence; DEF:GLO [T03216]; 1158; 1165; 9.885571; TTTTAGAG; 0.35962; 0.27695;  
Sequence; DEF:GLO [T03216]; 1222; 1229; 8.211165; CCAGAAAA; 0.26971; 0.22163;  
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Sequence; DI [T00196]; 1240; 1248; 6.438680; GAAAAGGCC; 0.10114; 0.09957;  
Sequence; DI [T00196]; 1280; 1288; 9.739932; GAAAAAAAAA; 0.16857; 0.14545;  
Sequence; DI [T00196]; 1295; 1303; 5.591632; GGACTTTTC; 0.07305; 0.05868;  
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Sequence; AhR [T00018]; 184; 192; 7.262416; GCACGCATG; 0.17981; 0.23424;  
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Sequence; AhR [T00018]; 1135; 1143; 8.794940; CGGGCGTGG; 0.14048; 0.18264;  
Sequence; AhR:Arnt [T05394]; 185; 193; 5.888384; CACGCATGG; 0.28095; 0.34855;  
Sequence; AhR:Arnt [T05394]; 1098; 1106; 4.499480; CACGCCGTC; 0.11238; 0.16806;  
Sequence; AhR:Arnt [T05394]; 1134; 1142; 4.623905; CCGGGCGTG; 0.11238; 0.16806;  
Sequence; PTF1-beta [T00701]; 186; 195; 3.961287; ACGCATGGGA; 0.06743; 0.06108;  
Sequence; PTF1 [T01227]; 186; 196; 6.551229; ACGCATGGGAC; 0.01686; 0.01521;  
Sequence; MYBAS1 [T05553]; 179; 183; 1.530821; GGGGA; 2.87695; 3.94670;  
Sequence; MYBAS1 [T05553]; 195; 199; 0.000000; ACCCC; 1.43848; 1.91318;  
Sequence; MYBAS1 [T05553]; 201; 205; 1.530821; TCCCC; 2.87695; 3.94670;  
Sequence; MYBAS1 [T05553]; 430; 434; 1.530821; GGGGA; 2.87695; 3.94670;  
Sequence; MYBAS1 [T05553]; 620; 624; 0.000000; ACCCC; 1.43848; 1.91318;  
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Sequence; MYBAS1 [T05553]; 672; 676; 1.224657; GGGGC; 1.43848; 2.11265;  
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Sequence; MYBAS1 [T05553]; 707; 711; 0.000000; ACCCC; 1.43848; 1.91318;  
Sequence; MYBAS1 [T05553]; 708; 712; 1.530821; CCCCC; 2.87695; 3.94670;  
Sequence; MYBAS1 [T05553]; 714; 718; 1.530821; TCCCC; 2.87695; 3.94670;  
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Sequence; MYBAS1 [T05553]; 1373; 1377; 1.530821; GGGGA; 2.87695; 3.94670;  
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Sequence; AP-2alpha [T00033]; 671; 679; 4.310562; TGGGGCGTC; 0.13486; 0.18805;  
Sequence; AP-2alpha [T00033]; 711; 719; 3.161178; CCTTCCCA; 0.04495; 0.05164;  
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Sequence; YY1 [T00278]; 98; 104; 8.393145; GTCATGG; 0.89905; 0.92712;  
Sequence; YY1 [T00278]; 154; 160; 2.304535; GAGATGG; 0.26971; 0.23304;  
Sequence; YY1 [T00278]; 187; 193; 7.540151; CGCATGG; 0.98895; 1.08593;

Sequence; YY1 [T00278]; 198; 204; 6.848277; CCATCCC; 0.35962; 0.37333;  
Sequence; YY1 [T00278]; 978; 984; 8.393145; CCATGAC; 0.89905; 0.92712;  
Sequence; YY1 [T00278]; 1011; 1017; 8.393145; CCATGAC; 0.89905; 0.92712;  
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Sequence; MCB1 [T06035]; 198; 206; 5.955048; CCATCCCCT; 0.13486; 0.13165;  
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Sequence; MCB1 [T06035]; 1148; 1156; 2.792877; GAAGGATGG; 0.06743; 0.06427;  
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Sequence; EIIaE-A [T00246]; 372; 378; 13.063953; CTCCCAC; 2.33752; 2.87555;  
Sequence; EIIaE-A [T00246]; 425; 431; 14.472869; TTCCCGG; 2.33752; 2.89592;  
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Sequence; EIIaE-A [T00246]; 561; 567; 10.118218; CTCCCGG; 1.61829; 2.07850;  
Sequence; EIIaE-A [T00246]; 611; 617; 8.709302; CACCCTC; 1.61829; 2.06363;  
Sequence; EIIaE-A [T00246]; 660; 666; 14.472869; TCCCCTA; 2.33752; 2.89592;  
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Sequence; EIIaE-A [T00246]; 708; 714; 8.709302; CCCCCTT; 1.61829; 2.06363;  
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Sequence; EIIaE-A [T00246]; 1276; 1282; 10.118218; TAGGGAA; 1.61829; 2.07850;  
Sequence; EIIaE-A [T00246]; 1417; 1423; 14.472869; TTGGGAG; 2.33752; 2.89592;  
Sequence; FOXO3a [T02938]; 205; 212; 5.687009; CTTATTCA; 0.53943; 0.35590;  
Sequence; FOXO3a [T02938]; 243; 250; 12.629773; CTTAGTGT; 1.61829; 1.37569;  
Sequence; FOXO3a [T02938]; 549; 556; 13.885529; ATGCTAAG; 0.80914; 0.80434;  
Sequence; FOXO3a [T02938]; 595; 602; 8.198520; TGCCTAAG; 0.53943; 0.48667;  
Sequence; FOXO3a [T02938]; 817; 824; 12.629773; ACCTTAAG; 1.61829; 1.37569;  
Sequence; FOXO3a [T02938]; 819; 826; 6.942764; CTTAAGCA; 1.07886; 0.83236;  
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Sequence; FOXO3a [T02938]; 973; 980; 8.198520; CTTAGCCA; 0.53943; 0.48667;  
Sequence; USF [T00873]; 217; 225; 13.317287; CCTCACATG; 0.30343; 0.31650;  
Sequence; USF [T00873]; 676; 684; 14.866241; CGTCACCCT; 0.65743; 0.64129;  
Sequence; muEBP-C2 [T00215]; 220; 225; 0.000000; CACATG; 0.35962; 0.34611;  
Sequence; muEBP-C2 [T00215]; 546; 551; 0.000000; CACATG; 0.35962; 0.34611;  
Sequence; muEBP-C2 [T00215]; 835; 840; 0.000000; CACATG; 0.35962; 0.34611;  
Sequence; USF-1 [T00877]; 216; 226; 8.109390; TCCTCACATGA; 0.02248; 0.02240;

Sequence; USF-1 [T00877]; 542; 552; 1.386985; TTCCCACATGC; 0.01967; 0.01629;  
Sequence; USF-1 [T00877]; 831; 841; 11.576853; GCCACACATGC; 0.00983; 0.01050;  
Sequence; c-Myc [T00143]; 220; 226; 7.324248; CACATGA; 0.53943; 0.50119;  
Sequence; c-Myc [T00143]; 546; 552; 7.324248; CACATGC; 0.53943; 0.50119;  
Sequence; c-Myc [T00143]; 642; 648; 7.324248; TCAAGTG; 0.53943; 0.50119;  
Sequence; c-Myc [T00143]; 835; 841; 7.324248; CACATGC; 0.53943; 0.50119;  
Sequence; c-Myc [T00143]; 961; 967; 3.341592; CACCTGG; 0.08990; 0.10748;  
Sequence; LCR-F1 [T01599]; 97; 102; 0.029165; CGTCAT; 1.43848; 1.27082;  
Sequence; LCR-F1 [T01599]; 223; 228; 5.375891; ATGAAG; 1.79810; 1.43553;  
Sequence; LCR-F1 [T01599]; 231; 236; 5.114259; ACTCAT; 1.07886; 0.91602;  
Sequence; LCR-F1 [T01599]; 234; 239; 3.748626; CATCAT; 1.07886; 0.77796;  
Sequence; LCR-F1 [T01599]; 803; 808; 5.550882; GTTCAT; 1.79810; 1.43553;  
Sequence; LCR-F1 [T01599]; 826; 831; 5.143424; ATGAGG; 1.07886; 0.91602;  
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Sequence; LCR-F1 [T01599]; 861; 866; 5.346725; ATTCAT; 1.79810; 1.43553;  
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Sequence; LCR-F1 [T01599]; 1146; 1151; 5.375891; ATGAAG; 1.79810; 1.43553;  
Sequence; LCR-F1 [T01599]; 1236; 1241; 5.114259; ATGAGA; 1.07886; 0.91602;  
Sequence; LCR-F1 [T01599]; 1318; 1323; 0.000000; TGTCAT; 1.43848; 1.27082;  
Sequence; Stra13 [T02327]; 216; 226; 14.377309; TCCTCACATGA; 0.11800; 0.11394;  
Sequence; Stra13 [T02327]; 219; 229; 14.939254; TCACATGAAGC; 0.09588; 0.08560;  
Sequence; STE12 [T00772]; 223; 230; 14.912281; ATGAAGCT; 0.94400; 0.77963;  
Sequence; STE12 [T00772]; 771; 778; 14.912281; AGTTTCAG; 0.94400; 0.77963;  
Sequence; STE12 [T00772]; 801; 808; 14.912281; AGGTTTCAT; 0.94400; 0.77963;  
Sequence; STE12 [T00772]; 859; 866; 14.912281; AGATTCAT; 0.94400; 0.77963;  
Sequence; Pax-8 [T01828]; 55; 60; 4.910009; GAGTCC; 1.07886; 1.15751;  
Sequence; Pax-8 [T01828]; 229; 234; 5.658723; CTAATC; 0.35962; 0.33755;  
Sequence; Pax-8 [T01828]; 265; 270; 5.938178; GAGTTG; 0.35962; 0.35928;  
Sequence; Pax-8 [T01828]; 461; 466; 5.658723; CTAATC; 0.35962; 0.33755;  
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Sequence; Pax-8 [T01828]; 875; 880; 2.864172; GAGTCG; 1.07886; 0.98072;  
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Sequence; Pax-8 [T01828]; 1391; 1396; 7.145650; ACAAATC; 0.71924; 0.76151;  
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Sequence; FOXN2 [T04206]; 733; 743; 13.336832; CAGAGGACCCG; 0.10957; 0.11488;  
Sequence; FOXN2 [T04206]; 1419; 1429; 12.208624; GGGAGGACGGT; 0.05057; 0.05612;  
Sequence; E2F-1 [T01542]; 13; 19; 5.331496; GGCGGAG; 0.35962; 0.55731;  
Sequence; E2F-1 [T01542]; 136; 142; 5.331496; GGCGGAG; 0.35962; 0.55731;  
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Sequence; E2F-1 [T01542]; 621; 627; 5.126038; CCCCCTC; 0.17981; 0.26581;  
Sequence; E2F-1 [T01542]; 739; 745; 5.944817; ACCCGCC; 0.35962; 0.57368;  
Sequence; E2F-1 [T01542]; 778; 784; 7.879274; GGCGGAC; 0.89905; 1.26476;  
Sequence; E2F-1 [T01542]; 1459; 1465; 9.608274; AGCGGAC; 0.71924; 0.88364;

Sequence; f(alpha)-f(epsilon) [T00287]; 13; 18; 10.521398; GGCGGA; 5.39429; 7.03435;  
Sequence; f(alpha)-f(epsilon) [T00287]; 133; 138; 10.521398; CACGGC; 5.39429; 7.03435;  
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Sequence; f(alpha)-f(epsilon) [T00287]; 260; 265; 10.521398; TCCGCG; 5.39429; 7.03435;  
Sequence; f(alpha)-f(epsilon) [T00287]; 343; 348; 10.521398; ACCGGG; 5.39429; 7.03435;  
Sequence; f(alpha)-f(epsilon) [T00287]; 427; 432; 10.521398; CCCGGG; 5.39429; 7.03435;  
Sequence; f(alpha)-f(epsilon) [T00287]; 515; 520; 14.400746; ACCGCA; 1.43848; 1.62793;  
Sequence; f(alpha)-f(epsilon) [T00287]; 563; 568; 10.521398; CCCGGC; 5.39429; 7.03435;  
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Sequence; f(alpha)-f(epsilon) [T00287]; 892; 897; 0.920900; GCCGGG; 1.07886; 1.60322;  
Sequence; f(alpha)-f(epsilon) [T00287]; 986; 991; 10.521398; CACGGC; 5.39429; 7.03435;  
Sequence; f(alpha)-f(epsilon) [T00287]; 1101; 1106; 10.521398; GCCGTC; 5.39429; 7.03435;  
Sequence; f(alpha)-f(epsilon) [T00287]; 1133; 1138; 5.721149; TCCGGG; 2.15771; 2.97041;  
Sequence; f(alpha)-f(epsilon) [T00287]; 1459; 1464; 10.521398; AGCGGA; 5.39429; 7.03435;  
Sequence; NF-1 [T00539]; 23; 27; 0.000000; GCCAA; 1.43848; 1.59675;  
Sequence; NF-1 [T00539]; 268; 272; 0.000000; TTGGC; 1.43848; 1.59675;  
Sequence; NF-1 [T00539]; 486; 490; 0.000000; GCCAA; 1.43848; 1.59675;  
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Sequence; C/EBPbeta [T00017]; 644; 651; 8.386864; AAGTGCAA; 0.26971; 0.26379;  
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Sequence; C/EBPbeta [T00017]; 1018; 1025; 7.797103; TTGCTGGA; 0.26971; 0.24254;  
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Sequence; C/EBPbeta [T00017]; 1395; 1402; 7.215913; TCGAGCAA; 0.44952; 0.41222;  
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Sequence; HNF-4alpha1 [T02429]; 270; 280; 7.332396; GGCAAAGCTGA; 0.01475; 0.01458;  
Sequence; GATA-1 [T00305]; 276; 283; 1.377780; GCTGATAA; 0.22476; 0.15438;  
Sequence; Ncx [T04368]; 206; 208; 0.000000; TTA; 23.01562; 17.57015;  
Sequence; Ncx [T04368]; 244; 246; 0.000000; TTA; 23.01562; 17.57015;  
Sequence; Ncx [T04368]; 281; 283; 0.000000; TAA; 23.01562; 17.57015;  
Sequence; Ncx [T04368]; 537; 539; 0.000000; TAA; 23.01562; 17.57015;  
Sequence; Ncx [T04368]; 553; 555; 0.000000; TAA; 23.01562; 17.57015;  
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Sequence; GATA-1 [T00267]; 276; 284; 0.371905; GCTGATAAA; 0.02248; 0.01909;  
Sequence; Cdx-1 [T01484]; 205; 208; 2.545394; CTTA; 5.75391; 4.68568;  
Sequence; Cdx-1 [T01484]; 243; 246; 2.545394; CTTA; 5.75391; 4.68568;  
Sequence; Cdx-1 [T01484]; 281; 284; 0.848465; TAAA; 5.75391; 4.15396;  
Sequence; Cdx-1 [T01484]; 537; 540; 1.272697; TAAC; 5.75391; 4.78526;  
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Sequence; STAT6 [T01581]; 542; 550; 11.220546; TTCCACAT; 0.01686; 0.01623;  
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Sequence; STAT6 [T01581]; 1190; 1198; 8.955346; TTCCAATA; 0.07305; 0.06650;  
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Sequence; C1 (short form) [T01593]; 426; 433; 12.500000; TCCCGGGG; 0.53943; 0.77055;  
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Sequence; c-Ets-1 [T00111]; 1342; 1351; 6.833056; CACGGAAGTG; 0.04636; 0.04970;  
Sequence; c-Ets-1 68 [T00115]; 429; 438; 9.959024; CGGGGAAGCA; 0.04636; 0.05288;  
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Sequence; c-Ets-1 68 [T00115]; 1266; 1275; 13.160949; GTAGGAAGTC; 0.06883; 0.06771;  
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Sequence; HNF-3beta [T02344]; 423; 429; 11.542216; TGTTCCC; 0.35962; 0.32089;  
Sequence; HNF-3beta [T02344]; 440; 446; 3.281312; CTCAACA; 0.08990; 0.08738;  
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Sequence; HNF-3beta [T02344]; 933; 939; 10.501356; TGTTCAA; 0.35962; 0.26588;  
Sequence; HNF-3beta [T02344]; 1044; 1050; 2.240452; TGTTGGG; 0.26971; 0.32020;  
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Sequence; HNF-3beta [T02344]; 1164; 1170; 12.911786; AGTAACA; 0.17981; 0.16285;  
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Sequence; LBM1 [T05245]; 445; 456; 6.645768; CACCAACCCTCA; 0.00711; 0.01042;  
Sequence; LBM1 [T05245]; 812; 823; 8.978489; CACCCACCTTAA; 0.01422; 0.02238;  
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Sequence; c-Rel [T01154]; 462; 471; 1.028734; TACTCGAAGC; 0.01686; 0.01798;  
Sequence; XBP1 [T03707]; 463; 472; 1.243456; ACTCGAAGCA; 0.01545; 0.01521;  
Sequence; XBP1 [T03707]; 1393; 1402; 7.348919; ACTCGAGCAA; 0.03652; 0.03963;  
Sequence; Myf-5 [T00521]; 466; 478; 11.871492; CGAAGCAGCAGGC; 0.04748; 0.05693;

Sequence; NF-E4 [T00560]; 474; 483; 12.280901; CAGGCTTCTG; 0.44250; 0.53277;  
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Sequence; NF-E4 [T00560]; 1454; 1463; 12.280901; CAGGCAGCGG; 0.44250; 0.53277;  
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Sequence; POU2F1a [T00644]; 549; 556; 10.378645; ATGCTAAG; 0.04495; 0.03508;  
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Sequence; POU5F1 [T00651]; 484; 491; 4.459547; ATGCCAAT; 0.04495; 0.03545;  
Sequence; LF-A1 [T00467]; 16; 22; 5.631412; GGAGGCA; 0.80914; 0.84678;  
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Sequence; LF-A1 [T00467]; 485; 491; 9.701266; TGCCAAT; 1.61829; 1.82820;  
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Sequence; LF-A1 [T00467]; 626; 632; 4.850633; CTAGGCA; 0.53943; 0.58418;  
Sequence; LF-A1 [T00467]; 851; 857; 8.920488; TGCCAAG; 1.07886; 1.22651;  
Sequence; LF-A1 [T00467]; 1009; 1015; 8.139709; TGCCATG; 0.17981; 0.20741;  
Sequence; LF-A1 [T00467]; 1453; 1459; 5.631412; GCAGGCA; 0.80914; 0.84678;  
Sequence; Cutl1 [T02042]; 486; 491; 0.000000; GCCAAT; 0.71924; 0.66152;  
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Sequence; Cutl1 [T02042]; 1192; 1197; 1.543329; CCAAT; 0.71924; 0.64709;  
Sequence; Cutl1 [T02042]; 1232; 1237; 14.310279; GAGAAT; 2.87695; 2.02230;  
Sequence; Cutl1 [T02042]; 1336; 1341; 11.083515; ATTTTG; 3.59619; 2.81753;  
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Sequence; Cutl1 [T02042]; 1363; 1368; 14.310279; ATAAAT; 2.87695; 2.02230;  
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Sequence; Cutl1 [T02042]; 1382; 1387; 14.310279; AATAAT; 2.87695; 2.02230;  
Sequence; Cutl1 [T02042]; 1433; 1438; 11.083515; CTCAAT; 3.59619; 2.81753;  
Sequence; POU1F1a [T00691]; 112; 116; 4.810880; ATTCT; 2.87695; 2.10214;  
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Sequence; POU1F1a [T00691]; 487; 491; 7.514293; CCAAT; 2.87695; 2.37192;  
Sequence; POU1F1a [T00691]; 541; 545; 5.921083; ATTCC; 4.31543; 3.26086;  
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Sequence; POU1F1a [T00691]; 1333; 1337; 5.921083; GAAAT; 4.31543; 3.26086;  
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Sequence; POU1F1a [T00691]; 1383; 1387; 5.785823; ATAAT; 4.31543; 3.26086;  
Sequence; POU1F1a [T00691]; 1434; 1438; 0.853075; TCAAT; 2.87695; 1.97262;  
Sequence; C/EBPdelta [T00109]; 112; 114; 0.000000; ATT; 23.01562; 17.57015;  
Sequence; C/EBPdelta [T00109]; 208; 210; 0.000000; ATT; 23.01562; 17.57015;

Sequence; C/EBPdelta [T00109]; 489; 491; 0.000000; AAT; 23.01562; 17.57015;  
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Sequence; unc-86 [T01882]; 111; 115; 5.769231; GATTC; 5.75391; 4.66827;  
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Sequence; unc-86 [T01882]; 488; 492; 5.769231; CAATG; 5.75391; 4.66827;  
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Sequence; unc-86 [T01882]; 1435; 1439; 3.846154; CAATA; 8.63086; 6.57590;  
Sequence; POU2F1 [T00641]; 484; 493; 13.626621; ATGCCAATGT; 0.47200; 0.34284;  
Sequence; BR-C Z2 [T01478]; 110; 114; 9.216108; GGATT; 2.87695; 2.37192;  
Sequence; BR-C Z2 [T01478]; 206; 210; 2.971418; TTATT; 1.43848; 1.00552;  
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Sequence; BR-C Z2 [T01478]; 539; 543; 8.363359; ACATT; 2.87695; 2.33413;  
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Sequence; BR-C Z2 [T01478]; 1145; 1149; 6.382414; AATGA; 1.43848; 1.09662;  
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Sequence; BR-C Z2 [T01478]; 1436; 1440; 4.952363; AATAC; 2.87695; 2.05182;  
Sequence; POU2F2B [T00964]; 483; 494; 14.988089; GATGCCAATGTG; 0.09956; 0.07751;  
Sequence; POU2F2 [T00647]; 484; 494; 13.051865; ATGCCAATGTG; 0.29500; 0.22677;  
Sequence; POU2F2 [T00648]; 484; 494; 13.388269; ATGCCAATGTG; 0.35400; 0.26096;  
Sequence; POU2F2 (Oct-2.1) [T01864]; 484; 494; 13.388269; ATGCCAATGTG; 0.35400; 0.26096;  
Sequence; POU2F2 (Oct-2.3) [T01865]; 484; 494; 13.388269; ATGCCAATGTG; 0.35400; 0.26096;  
Sequence; POU2F2 (Oct-2.4) [T01866]; 484; 494; 13.388269; ATGCCAATGTG; 0.35400; 0.26096;  
Sequence; POU2F2 (Oct-2.6) [T01867]; 484; 494; 13.388269; ATGCCAATGTG; 0.35400; 0.26096;  
Sequence; POU2F2 (Oct-2.1) [T01870]; 484; 494; 13.388269; ATGCCAATGTG; 0.35400; 0.26096;  
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Sequence; MATalpha2 [T00487]; 124; 129; 1.844646; GGACAT; 2.15771; 1.88033;  
Sequence; MATalpha2 [T00487]; 219; 224; 2.576772; TCACAT; 0.35962; 0.28781;  
Sequence; MATalpha2 [T00487]; 490; 495; 3.073046; ATGTGT; 1.07886; 1.02079;  
Sequence; MATalpha2 [T00487]; 537; 542; 1.472441; TAACAT; 0.71924; 0.53300;  
Sequence; MATalpha2 [T00487]; 545; 550; 3.073046; CCACAT; 1.07886; 1.02079;  
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Sequence; MATalpha2 [T00487]; 1078; 1083; 1.844646; GGACAT; 2.15771; 1.88033;  
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Sequence; MATalpha2 [T00487]; 1437; 1442; 0.496274; ATACAT; 1.07886; 0.82082;  
Sequence; OSH15 [T05493]; 352; 359; 2.682344; GTGACAAG; 0.04495; 0.04554;  
Sequence; OSH15 [T05493]; 504; 511; 14.878437; CCTCTCAC; 0.40457; 0.45302;  
Sequence; OSH15 [T05493]; 1202; 1209; 14.878437; GTGAGAGG; 0.40457; 0.45302;  
Sequence; PEBP2alphaA1 [T01062]; 512; 521; 7.283639; CCTACCGCAT; 0.03371; 0.04080;  
Sequence; abaA [T01085]; 536; 545; 2.934548; CTAACATTCC; 0.06321; 0.05996;  
Sequence; abaA [T01085]; 1143; 1152; 1.563999; GGAATGAAGG; 0.02107; 0.01849;  
Sequence; RelA [T00594]; 430; 439; 9.226406; GGGGAAGCAC; 0.04636; 0.05075;  
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Sequence; HSF1 (long) [T01042]; 1140; 1147; 14.291973; GTGGGAAT; 0.60686; 0.51527;  
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Sequence; COE3 [T05008]; 539; 551; 12.222268; ACATTCACACATG; 0.02120; 0.02476;  
Sequence; AML1 [T01067]; 540; 552; 14.492509; CATTCCCACATGC; 0.02805; 0.02853;  
Sequence; Nrf2 [T01443]; 208; 218; 9.796651; ATTCAGCATCC; 0.06321; 0.05118;  
Sequence; Nrf2 [T01443]; 547; 557; 12.623767; ACATGCTAAGG; 0.05338; 0.04401;  
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Sequence; c-Ets-1 54 [T00114]; 742; 747; 0.000000; CGCCTC; 0.35962; 0.47174;  
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0.07393;  
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Sequence; TBP [T00794]; 916; 923; 5.472732; GGCTTATA; 0.40457; 0.26887;  
Sequence; FXR [T04494]; 932; 942; 8.275998; ATGTTCAAGGA; 0.01967; 0.01562;  
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Sequence; Clock:Bmal1 [T05866]; 961; 972; 14.945058; CACCTGGGCCAC; 0.10325; 0.12830;  
Sequence; LIP15 [T02803]; 965; 974; 11.934248; TGGGCCACCT; 0.17700; 0.21014;  
Sequence; ROM1 [T02809]; 968; 976; 11.111111; GCCACCTTA; 0.15171; 0.18649;  
Sequence; ROM2 [T02810]; 968; 976; 11.111111; GCCACCTTA; 0.15171; 0.18649;  
Sequence; T3R-alpha [T00838]; 975; 986; 8.047167; TAGCCATGACCC; 0.01475; 0.01493;  
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Sequence; CUTL1 [T00100]; 1192; 1197; 0.880951; CCCAAT; 1.79810; 1.57265;  
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Sequence; CUTL1 [T00100]; 1433; 1438; 1.511826; CTCAAT; 1.07886; 0.81566;  
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Sequence; c-Myb [T00138]; 1311; 1319; 2.302241; CCAAAAGT; 0.04495; 0.04373;  
Sequence; BR-C Z3 [T01479]; 1085; 1094; 14.914334; GCAAAGTAA; 0.06181; 0.05603;  
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Sequence; NF-AT2 [T01947]; 1127; 1139; 11.890307; GCAACTTCCGGGC; 0.02120; 0.02024;  
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Sequence; Arnt [T01346]; 1098; 1106; 9.368188; CACGCCGTC; 0.13486; 0.16677;  
Sequence; Arnt [T01346]; 1134; 1142; 9.895773; CCGGGCGTG; 0.09552; 0.12850;  
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Sequence; MIF-1 [T01047]; 1160; 1172; 14.500958; TTAGAGTAACACC; 0.00878; 0.00730;  
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Sequence; HNF-3alpha [T00371]; 1248; 1255; 3.184334; CAAAACAG; 0.31467; 0.30412;  
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Sequence; c-Ets-2 [T01397]; 1358; 1366; 4.976847; AGGAAATAA; 0.06743; 0.05627;  
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Sequence; Elk-1 [T05013]; 1268; 1276; 1.510524; AGGAAAGTCT; 0.13486; 0.12872;  
Sequence; Hb [T00395]; 1281; 1287; 0.122746; AAAAAAA; 0.26971; 0.22934;  
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Sequence; Ubx [T00863]; 1384; 1389; 1.237209; TAATGT; 1.43848; 0.97968;  
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Sequence; Croc [T02291]; 1360; 1369; 14.947243; GAAATAAATC; 0.23600; 0.14834;  
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Sequence; Gt [T00328]; 1377; 1387; 14.541822; ACAATAATAAT; 0.17454; 0.11594;  
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Sequence; Prd [T00699]; 1319; 1325; 11.870926; GTCATTA; 0.17981; 0.12490;  
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Sequence; IPF1 [T02057]; 1318; 1325; 0.469022; TGTCATTA; 0.08990; 0.06545;  
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Sequence; C/EBPgamma [T00216]; 594; 601; 0.215655; TTGCCTAA; 0.08990; 0.06577;  
Sequence; C/EBPgamma [T00216]; 1018; 1025; 8.367175; TTGCTGGA; 0.17981; 0.17729;  
Sequence; C/EBPgamma [T00216]; 1395; 1402; 7.224460; TCGAGCAA; 0.26971; 0.23019;  
Sequence; MRF-2 [T04675]; 1435; 1444; 10.183125; CAATACATCA; 0.10817; 0.08143;  
Sequence; TSAP [T00855]; 1453; 1462; 12.717730; GCAGGCAGCG; 0.20229; 0.22852;  
Sequence; Adf-1 [T00008]; 0; 7; 3.695360; GCAGCTGA; 0.35962; 0.40372;  
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Sequence; Adf-1 [T00008]; 1457; 1464; 0.989036; GCAGCGGA; 0.24724; 0.33586;  
Sequence; MATA1 [T00488]; 122; 131; 10.503211; TAGGACATCA; 0.04776; 0.04487;  
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Sequence; HNF-1C [T01951]; 1380; 1388; 14.429214; ATAATAATG; 0.13486; 0.08691;  
Sequence; POU4F1(l) [T01877]; 1379; 1388; 6.140450; AATAATAATG; 0.08429; 0.04849;  
Sequence; ARF1 [T04514]; 1370; 1382; 14.033846; CTGGGGGACAATA; 0.01567; 0.01502;  
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Sequence; SBF-1 [T00739]; 1322; 1330; 14.499644; ATTAACGCG; 0.08990; 0.06182;  
Sequence; HNF-1 [T00369]; 1318; 1329; 14.705068; TGTCATTAACGC; 0.01791; 0.01309;  
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Sequence; Meis-1b [T03389]; 165; 173; 0.296000; GAGCTGTCA; 0.05057; 0.04288;  
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Sequence; Elf-1 [T01019]; 1285; 1294; 13.486299; AAAACTGAAA; 0.06743; 0.06031;  
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Sequence; HOXA9 [T01710]; 1309; 1322; 8.828312; CCCCCAACTGTCA; 0.00082; 0.00064;  
Sequence; NF-AT4 [T01946]; 1279; 1290; 5.541758; GGAAAAAAACT; 0.00983; 0.00779;  
Sequence; FOXD3 [T02290]; 1250; 1257; 3.444986; AAACAGTT; 0.08990; 0.07574;  
Sequence; HNF-3beta [T01049]; 1247; 1254; 1.902729; CCAAAACA; 0.22476; 0.19212;  
Sequence; AR [T00040]; 423; 430; 3.768253; TGTTCCTCG; 0.04495; 0.05171;  
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Sequence; R [T00710]; 86; 94; 10.243542; CACCAGGGA; 0.07867; 0.10010;  
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Sequence; Hlf [T01071]; 585; 593; 14.759054; GTCTGTAAC; 0.04495; 0.03510;  
Sequence; Hlf [T01071]; 1161; 1169; 8.501296; TAGAGTAAC; 0.12924; 0.09747;  
Sequence; Elf-1 [T05012]; 1129; 1137; 0.529089; AACTTCCGG; 0.01686; 0.02023;  
Sequence; NRF-2 [T01199]; 1128; 1138; 10.955864; CAACTTCCGGG; 0.00843; 0.00991;  
Sequence; Pax-6 [T01122]; 1112; 1122; 14.220607; TTCACAGCTAG; 0.08042; 0.06939;  
Sequence; POU2F1 [T01466]; 1062; 1069; 13.593447; CGGACATA; 0.47200; 0.45567;  
Sequence; POU2F1 [T01466]; 1077; 1084; 10.506966; TGGACATA; 0.31467; 0.25075;  
Sequence; HNF-3 [T00370]; 1038; 1046; 10.291635; GCACTTTGT; 0.16857; 0.15027;  
Sequence; AIRE [T05990]; 991; 1000; 9.130294; CCACAACCAA; 0.09693; 0.10396;  
Sequence; REB [T02808]; 968; 977; 14.535101; GCCACCTTAG; 0.07586; 0.08713;  
Sequence; PPAR-alpha:RXR-alpha [T05221]; 962; 972; 4.886580; ACCTGGGCCAC; 0.01264; 0.01545;  
Sequence; Lmo2 [T02251]; 960; 967; 0.000000; CCACCTGG; 0.02248; 0.02909;

Sequence; Tal-1 [T00790]; 232; 242; 10.875765; CTCATCATCTG; 0.05057; 0.05418;  
Sequence; Tal-1 [T00790]; 313; 323; 14.153038; CACTTCAGCTG; 0.11379; 0.12009;  
Sequence; Tal-1 [T00790]; 956; 966; 13.546753; AGTCCACCTG; 0.09482; 0.09924;  
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Sequence; DTF-1 [T00201]; 927; 937; 13.860411; GCGACATGTTC; 0.06638; 0.05980;  
Sequence; MEF-2C/delta8 [T01769]; 920; 930; 12.435761; TATACCTGCGA; 0.08218; 0.05845;  
Sequence; B factor [T00061]; 916; 923; 13.449835; GGCTTATA; 0.26971; 0.18075;  
Sequence; TFIID [T00820]; 916; 923; 7.238121; GGCTTATA; 0.08990; 0.06604;  
Sequence; DEAF-1 [T05885]; 878; 886; 3.417227; TCGGGTCGT; 0.07867; 0.09598;  
Sequence; DEAF-1 [T05885]; 908; 916; 7.212653; TCGGGGGAG; 0.15733; 0.20818;  
Sequence; UME6 [T01247]; 904; 914; 12.927645; TCACTCGGGGG; 0.06954; 0.08292;  
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Sequence; ADR1 [T00011]; 195; 202; 3.038707; ACCCCATC; 0.06743; 0.08196;  
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Sequence; ADR1 [T00011]; 691; 698; 6.381348; ACCCCTAG; 0.20229; 0.25206;  
Sequence; ADR1 [T00011]; 707; 714; 7.461305; ACCCCCTT; 0.04495; 0.04915;  
Sequence; ADR1 [T00011]; 759; 766; 8.260309; ACCCCAGA; 0.17981; 0.24509;  
Sequence; Sry-delta [T00767]; 714; 726; 13.356042; TCCCCACCTCTAG; 0.00606; 0.00492;  
Sequence; IA-1 [T05887]; 705; 717; 14.700907; TCACCCCTTCCC; 0.02184; 0.03000;  
Sequence; T3R-alpha1 [T01152]; 700; 710; 13.969556; TGACCTCACCC; 0.24443; 0.22991;  
Sequence; T3R-beta1 [T00853]; 700; 709; 4.183328; TGACCTCACC; 0.01686; 0.01837;  
Sequence; RORalpha1 [T01527]; 700; 709; 6.166756; TGACCTCACC; 0.05479; 0.05980;  
Sequence; SF-1 [T04014]; 700; 709; 9.056375; TGACCTCACC; 0.11379; 0.10641;  
Sequence; COUP-TF1 [T00149]; 700; 708; 1.292649; TGACCTCAC; 0.11238; 0.10486;  
Sequence; T3R-alpha [T01351]; 700; 708; 2.085552; TGACCTCAC; 0.02810; 0.02557;  
Sequence; SF-1 [T02769]; 699; 709; 9.064415; CTGACCTCACC; 0.04214; 0.03890;  
Sequence; RXR-beta [T01332]; 696; 705; 6.413388; TAGCTGACCT; 0.02529; 0.02380;  
Sequence; E4F1 [T00223]; 673; 681; 5.128278; GGGCGTCAC; 0.17981; 0.21682;  
Sequence; Sp3 [T02338]; 672; 680; 11.609185; GGGGCGTCA; 0.09552; 0.12921;  
Sequence; BTEB4 [T05053]; 672; 680; 4.079815; GGGGCGTCA; 0.06743; 0.10474;  
Sequence; Pbx1b [T02088]; 559; 569; 9.987966; CCCTCCCGGCC; 0.05689; 0.07913;  
Sequence; PHO4 [T00690]; 543; 554; 13.124936; TCCCACATGCTA; 0.01291; 0.01629;  
Sequence; Ttk 69K [T00843]; 495; 502; 13.585908; TGTCTCTGC; 0.47200; 0.60786;  
Sequence; CTF [T00174]; 485; 496; 10.779118; TGCCAATGTGTG; 0.02845; 0.03271;  
Sequence; Oct-B1 [T00545]; 484; 491; 12.500000; ATGCCAAT; 0.53943; 0.40002;  
Sequence; POU2F2B [T00662]; 484; 491; 12.500000; ATGCCAAT; 0.53943; 0.40002;  
Sequence; POU2F1 [T00959]; 484; 491; 12.500000; ATGCCAAT; 0.53943; 0.40002;  
Sequence; POU2F2B [T01871]; 484; 491; 12.500000; ATGCCAAT; 0.53943; 0.40002;  
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Sequence; POU3F1 [T00656]; 481; 491; 13.350458; CTGATGCCAAT; 0.25286; 0.20204;  
Sequence; POU2F1b [T01862]; 481; 491; 12.607587; CTGATGCCAAT; 0.53943; 0.40002;  
Sequence; POU2F1c [T01863]; 481; 491; 12.607587; CTGATGCCAAT; 0.53943; 0.40002;  
Sequence; NF-kappaB [T00588]; 431; 440; 4.125075; GGGAAGCACC; 0.01124; 0.01463;  
Sequence; AR [T00042]; 399; 405; 3.321435; AGGTTCT; 0.35962; 0.38993;  
Sequence; NIT2 [T00627]; 116; 123; 5.523088; TGCAGATA; 0.44952; 0.35353;  
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Sequence; mtTFA [T04783]; 278; 287; 3.812478; TGATAAAGGA; 0.08850; 0.06079;  
Sequence; RPN4 [T04539]; 267; 275; 11.111111; GTTGGCAAA; 0.15171; 0.15308;  
Sequence; StuAp [T02248]; 259; 266; 2.687747; CTCCGCGA; 0.35962; 0.44131;  
Sequence; POU2F1 [T00643]; 230; 240; 10.591017; TACTCATCATC; 0.05057; 0.04330;  
Sequence; Sp1 [T00753]; 12; 17; 0.000000; GGGCGG; 0.35962; 0.57664;  
Sequence; Sp1 [T00752]; 11; 20; 2.162070; AGGGCGGAGG; 0.01264; 0.01968;  
Sequence; Sp1 [T00754]; 11; 20; 3.289853; AGGGCGGAGG; 0.04636; 0.07111;  
Sequence; Egr-1 [T01200]; 9; 21; 8.442026; GGAGGGCGGAGGC; 0.00632; 0.01169;  
Sequence; GKLf [T02450]; 7; 19; 13.888051; AGGGAGGGCGGAG; 0.01475; 0.01621;

-- END -----

Distribution of the nucleotides over the given chain:

