

Table S3. Putative transcription factor binding sites on the human *MORG1* promoter sequence.

Putative transcription factor binding sites on the human *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), 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

```
CAGCTGGGGGCACCGAGACGGCCTCATTCAGGGAAGTCCAGGATGGCAGCTGAAGGCAGCAGGTTTAGCAG
CCAAAGCCCAGGCCTAGTGGATAGACAGGGTCCAAAATGTGACCCTTCTAGGCTGGTATCACCATGGGGGCG
TCATGGGCTGAGGATTCTGCAGATAGGACATCACCACGGCAGAGATGGACAGCCTGAGACAGGAGAGAGGT
GTCAGTCTAGGATGGCCAGGCTGGGGTCCCCCACCCTTACTCAAGAGTCACTTGTTCTGTAGGGCAAGTCTC
ACATGAAGCTACTCATATTTGCTTCGTGTCTCCGAGCTCCGAGAGTTGGCAAAGCTGATGAAGGAGCAGTA
GACAGCGACCCAAGCACACCACTTCAGCTAGGGAAGGTAAGTGGGTGGGCAGGTTAGTGAAAGGCACAAC
AATGAGTCCCCGAAGCCACCTTCCAGACACCAGATCATGCCACTGATTCCATCTGATGCAGCTGGGACCTTG
CCCCACCCGGAATTCCTCAGTCCCACCTGCTCATGGCATACTCTAGATACGTGGTTTCTAGTCTACTGTCTGGC
CTGCGTCTCTCAGGACCAAGAGAGACTCTGACATCCACATGCTTAAGACCCTGCCCTTTTCCACAACCTCTCT
CCAAGTTGCTTCAAAGCCTGGCCCCACTCGCAGACCAATCTGCCACATCCCCAACCTGACTCGAATCCTTGACTT
CACCAAAGACTGGGGCTTTCTCGGCCAGCGTCATCGCAGCCCCACTCCCGGCCGATCTCAGGTCCCGCCCCAT
CAGCAATGACAAGACACCCGCTTATTCCAAACCCGCCCGGGCCTCGTTCTCAGGTCCAACTACACCCATA
GAAGCTCAACCCCGCCACCTTAAGCATGAGGCCGCACATGCTGAAGATCATGCCAGCAGGTTTCATGTAGTC
CGGCGTCGGGTCGTCCAAGGCCGGGTTACATTCGCTCGGCGGGGGCTGTACCTGCGACAGGCTCGAGGGT
CAGGGGCGCTCAGGTCTGCCCCGGGATAGACAGGCGCTTCCAGGGCCCCGATCCACACCCACAACCCGA
ACCCGTGCCCACGACGCTGGGGTCTCACCTCAGCACTTTGTTCCGCTCCGTGGGTCCGACATATTGTTAGTG
GACATAGCGAGTCGAAGGCCAGATCACGCCTCTTCCGCTGCAGGAATCGCAGCTTCCGGCGTGCAAGCTGAG
GGCGGATTTTAGAGTAACACCCGAGGCCCTCGCATTTCCGTTCTCATGACAGAGGCTTGGACTCCCCTTACCC
AGAGAACGGAGATTTAGGAGAAGCCAGAAGTCTTCTTTCAAAGGGGAAAATGGGGAAAAGAACCTGAAAGC
GGGCTTCAATAGTTCCAACCCGATCACCGAAATGCCAAAATGATGAACCCGGAAGTGATAAACAGGAAGTAG
GTCAGGAAGAACAATAAAGGTTACACCCAAGCGTGGGTTTCTAAGGCGCGGAATTTCCGTACAGACCGAT
TTAAGGCTGCAAGGAAGGAGTCCTGGGAGCATGGCTTTCCTGAGC
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-- Factors predicted by PROMO in this sequence -----

NAME; MATRIX_WIDTH;

E47 [T00207]; 7

Tal-1 [T00790]; 11

ETF [T00270]; 9

HSF1 (long) [T01042]; 8

HSF1 (short) [T02104]; 8

STAT5A [T04683]; 4

Elk-1 [T00250]; 5

STAT3 [T01493]; 12

p300 [T01427]; 5

R2 [T00712]; 6

YY1 [T00915]; 7
PEA3 [T00685]; 8
ENKTF-1 [T00255]; 8
Myf-3 [T00519]; 8
MyoD [T00525]; 8
AP-2alphaA [T00035]; 6
TCF-1A [T00999]; 9
LEF-1 [T02905]; 8
TCF-4E [T02878]; 7
NFI/CTF [T00094]; 8
p53 [T00671]; 7
GATA-1 [T00306]; 6
VDR [T00885]; 4
MBF1 [T00492]; 11
POU3F2 [T00630]; 7
FOXP3 [T04280]; 9
USF2b [T02377]; 8
USF2 [T00878]; 9
c-Jun [T00133]; 7
NHP-1 [T00621]; 7
ARP-1 [T00045]; 9
RAR-gamma [T00720]; 8
c-Fos [T00123]; 8
Pax-2 [T01823]; 7
Nkx2-1 [T00857]; 7
NF-X3 [T01514]; 8
GATA-3 [T00311]; 8
TGIF [T04076]; 8
PKNOX1 [T04122]; 11
FOXO3a [T02938]; 8
Hlf [T01071]; 9
AP-1 [T00029]; 8
PR B [T00696]; 7
PR A [T01661]; 7
GR-alpha [T00337]; 8
GR-beta [T01920]; 8
GR [T05076]; 13
LCR-F1 [T01599]; 6
Oct-B1 [T00545]; 8
POU2F2 (Oct-2.1) [T00646]; 8
POU2F2B [T00662]; 8
C/EBPalpha [T00105]; 6
C/EBPbeta [T00581]; 7
FOXN2 [T04206]; 11
NF-1 [T00539]; 5
IRF-1 [T00423]; 9
IRF-3 [T04673]; 7
NF-AT1 [T00550]; 9
WT1 I [T01840]; 7
Pax-6 [T01122]; 11
SRY [T00997]; 7
NF-AT2 [T01945]; 9
NF-AT1 [T01948]; 8

HMG I(Y) [T02368]; 7
STAT4 [T01577]; 6
c-Ets-1 [T00112]; 7
STAT1beta [T01573]; 10
Smad3 [T04096]; 10
ANF [T00025]; 12
Smad4 [T04292]; 11
EllaE-A [T00246]; 7
LF-A1 [T00467]; 7
POU2F2C [T00665]; 8
AP-4 [T00036]; 11
Myf-5 [T00521]; 13
Sp3 [T02338]; 9
TFIIB [T00818]; 8
AREB6 [T00625]; 8
Ik-1 [T02702]; 13
E12 [T00204]; 13
POU6F1 [T04470]; 11
Max [T05056]; 11
AIRE [T05990]; 10
Nrf2 [T01443]; 11
NF-AT4 [T01946]; 12
Pu box binding factor [T00704]; 10
NF-AT3 [T02462]; 10
AML1 [T01067]; 13
c-Myb [T00137]; 8
BTEB3 [T05051]; 9
NF-Y [T00150]; 8
PPAR-alpha:RXR-alpha [T05221]; 11
T3R-alpha1 [T01152]; 11
DP-1 [T01548]; 10
E2F-1 [T01542]; 7
E2F-1:DP-1 [T05204]; 9
GCF [T00320]; 11
MAZ [T00490]; 11
WT1 [T00899]; 11
Egr-3 [T00243]; 13
Pbx1 [T06000]; 12
GCMa [T02306]; 9
PXR-1:RXR-alpha [T05671]; 11
Sp1 [T00759]; 9
WT1 I -KTS [T00900]; 10
WT1 -KTS [T01839]; 10
ER-beta [T04651]; 9
RAR-beta [T00721]; 8
ER-alpha [T00261]; 8
RelA [T00594]; 10
EBF [T05427]; 11
RAR-beta:RXR-alpha [T05420]; 12
USF1 [T00874]; 9
Pax-5 [T00070]; 7
ERRalpha1 [T05682]; 13
HNF-4alpha [T03828]; 13

CUTL1 [T00100]; 6
 AhR:Arnt [T05394]; 9
 c-Ets-2 [T00113]; 8
 Arnt [T01346]; 9
 AhR [T01795]; 8
 MIF-1 [T01047]; 13
 SXR:RXR-alpha [T05670]; 9
 MZF-1 [T00529]; 7
 GABP-alpha [T01390]; 12
 GABP [T00268]; 12
 CDX2 [T03246]; 12
 IRF-2 [T01491]; 11
 FOXJ2 (long isoform) [T04169]; 10
 HNF-3beta [T02513]; 7
 NERF-1a [T05021]; 12
 RORalpha2 [T01528]; 12
 RORalpha1 [T01527]; 10
 COUP-TF1 [T00149]; 9
 SF-1 [T02769]; 11
 AR [T00040]; 8
 HOXD9 [T01424]; 10
 HOXD10 [T01425]; 10
 AP-3 (2) [T00039]; 7
 NF-kappaB [T00590]; 11
 E2F-5 [T01607]; 8
 HNF-1B [T01950]; 8
 RAR-alpha1 [T00719]; 10
 RXR-alpha [T01345]; 9
 ELF-1 [T01113]; 13
 Pbx1b [T02087]; 10
 PU.1 [T02068]; 10
 R1 [T00711]; 12
 TFII-I [T00824]; 11
 T3R-beta1 [T00851]; 11
 CRF [T00170]; 12
 RFX1 [T01673]; 9
 POU2F1 [T00641]; 10
 POU2F2 [T00647]; 11
 octamer-binding factor [T01225]; 11

-- PROMO predictions detail -----

Sequence name; Factor name; Start position; End position; Dissimilarity; String; RE equally; RE query
 Sequence; E47 [T00207]; 1; 7; 4.682492; AGCTGGG; 0.77002; 1.02300;
 Sequence; E47 [T00207]; 36; 42; 5.965250; TCCAGGA; 0.48126; 0.59997;
 Sequence; E47 [T00207]; 77; 83; 5.305872; CCCAGGC; 0.67377; 0.86109;
 Sequence; E47 [T00207]; 121; 127; 4.502284; GGCTGGT; 0.77002; 1.02300;
 Sequence; E47 [T00207]; 228; 234; 4.258142; GCCAGGC; 0.77002; 1.02300;
 Sequence; E47 [T00207]; 232; 238; 4.851527; GGCTGGG; 0.96252; 1.18255;
 Sequence; E47 [T00207]; 454; 460; 0.692900; TCCAGAC; 0.28876; 0.26117;
 Sequence; E47 [T00207]; 461; 467; 0.698487; ACCAGAT; 0.28876; 0.26117;
 Sequence; E47 [T00207]; 493; 499; 4.682492; AGCTGGG; 0.77002; 1.02300;
 Sequence; E47 [T00207]; 574; 580; 0.169035; GTCTGGC; 0.19250; 0.23772;

Sequence; E47 [T00207]; 671; 677; 4.258142; GCCTGGC; 0.77002; 1.02300;
Sequence; E47 [T00207]; 738; 744; 5.533045; GACTGGG; 0.67377; 0.86109;
Sequence; E47 [T00207]; 755; 761; 6.879944; CCCAGCG; 0.48126; 0.64340;
Sequence; E47 [T00207]; 932; 938; 6.034770; CCCAGCA; 0.48126; 0.59997;
Sequence; E47 [T00207]; 1064; 1070; 7.334289; CCCAGGG; 0.19250; 0.30408;
Sequence; E47 [T00207]; 1109; 1115; 6.879944; CGCTGGG; 0.48126; 0.64340;
Sequence; E47 [T00207]; 1186; 1192; 0.000000; GCCAGAT; 0.19250; 0.23772;
Sequence; E47 [T00207]; 1312; 1318; 3.245181; CCCAGAG; 0.19250; 0.24211;
Sequence; E47 [T00207]; 1337; 1343; 1.352278; GCCAGAA; 0.09625; 0.10552;
Sequence; E47 [T00207]; 1551; 1557; 6.489116; TCCTGGG; 0.67377; 0.89212;
Sequence; Tal-1 [T00790]; 0; 10; 12.618019; CAGCTGGGGGC; 0.08121; 0.09181;
Sequence; Tal-1 [T00790]; 478; 488; 12.618019; GATTCCATCTG; 0.08121; 0.09181;
Sequence; Tal-1 [T00790]; 492; 502; 13.546753; CAGCTGGGACC; 0.10152; 0.11094;
Sequence; Tal-1 [T00790]; 524; 534; 13.546753; AGTCCACCTG; 0.10152; 0.11094;
Sequence; ETF [T00270]; 6; 14; 8.217998; GGGGCACCG; 0.21657; 0.41104;
Sequence; ETF [T00270]; 137; 145; 6.076766; GGGGCGTCA; 0.16243; 0.29885;
Sequence; ETF [T00270]; 501; 509; 7.587476; CCTTGCCCC; 0.03609; 0.08254;
Sequence; ETF [T00270]; 672; 680; 7.587476; CCTGGCCCC; 0.03609; 0.08254;
Sequence; ETF [T00270]; 742; 750; 7.000683; GGGGCTTTC; 0.16243; 0.23040;
Sequence; ETF [T00270]; 766; 774; 1.554439; CGCAGCCCC; 0.09024; 0.19704;
Sequence; ETF [T00270]; 794; 802; 0.630521; TCCCGCCCC; 0.03609; 0.09846;
Sequence; ETF [T00270]; 837; 845; 0.630521; ACCCGCCCC; 0.03609; 0.09846;
Sequence; ETF [T00270]; 993; 1001; 6.370162; GGGGCTTGT; 0.10828; 0.18666;
Sequence; ETF [T00270]; 1025; 1033; 6.076766; GGGGCGCTC; 0.16243; 0.29885;
Sequence; ETF [T00270]; 1037; 1045; 3.402275; TCCTGCCCC; 0.07219; 0.16509;
Sequence; ETF [T00270]; 1066; 1074; 8.217998; CAGGGCCCC; 0.21657; 0.41104;
Sequence; HSF1 (long) [T01042]; 25; 32; 7.272359; ATTCAGGG; 0.14438; 0.14291;
Sequence; HSF1 (long) [T01042]; 479; 486; 10.655793; ATTCCATC; 0.79408; 0.50558;
Sequence; HSF1 (long) [T01042]; 511; 518; 7.272359; CCCGGAAT; 0.14438; 0.14291;
Sequence; HSF1 (long) [T01042]; 714; 721; 5.327897; ACTCGAAT; 0.43314; 0.30695;
Sequence; HSF1 (long) [T01042]; 830; 837; 10.655793; ATTCCAAA; 0.79408; 0.50558;
Sequence; HSF1 (long) [T01042]; 981; 988; 14.291973; ATTCGCTC; 0.64970; 0.51288;
Sequence; HSF1 (long) [T01042]; 1208; 1215; 12.600256; GCAGGAAT; 0.86627; 0.71289;
Sequence; HSF1 (long) [T01042]; 1506; 1513; 12.600256; CGCGGAAT; 0.86627; 0.71289;
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Sequence; HSF1 (short) [T02104]; 511; 518; 7.272359; CCCGGAAT; 0.14438; 0.14291;
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Sequence; STAT5A [T04683]; 453; 456; 0.000000; TTCC; 6.16016; 5.86404;
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Sequence; STAT5A [T04683]; 1201; 1204; 0.000000; TTCC; 6.16016; 5.86404;
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Sequence; STAT5A [T04683]; 1368; 1371; 0.000000; GGAA; 6.16016; 5.86404;
Sequence; STAT5A [T04683]; 1398; 1401; 0.000000; TTCC; 6.16016; 5.86404;
Sequence; STAT5A [T04683]; 1436; 1439; 0.000000; GGAA; 6.16016; 5.86404;
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Sequence; STAT5A [T04683]; 1543; 1546; 0.000000; GGAA; 6.16016; 5.86404;
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Sequence; Elk-1 [T00250]; 34; 38; 6.853012; AGTCC; 4.62012; 4.61150;
Sequence; Elk-1 [T00250]; 40; 44; 3.960472; GGATG; 3.08008; 3.84960;
Sequence; Elk-1 [T00250]; 89; 93; 6.081668; GGATA; 3.08008; 2.93146;
Sequence; Elk-1 [T00250]; 99; 103; 6.274504; GGTCC; 3.08008; 3.82271;
Sequence; Elk-1 [T00250]; 154; 158; 6.853012; GGATT; 4.62012; 4.61150;
Sequence; Elk-1 [T00250]; 168; 172; 6.081668; GGACA; 3.08008; 2.93146;
Sequence; Elk-1 [T00250]; 189; 193; 6.081668; GGACA; 3.08008; 2.93146;
Sequence; Elk-1 [T00250]; 204; 208; 7.213232; GGAGA; 4.62012; 4.61150;
Sequence; Elk-1 [T00250]; 223; 227; 3.960472; GGATG; 3.08008; 3.84960;
Sequence; Elk-1 [T00250]; 238; 242; 6.274504; GGTCC; 3.08008; 3.82271;
Sequence; Elk-1 [T00250]; 315; 319; 6.081668; TGTCC; 3.08008; 2.93146;
Sequence; Elk-1 [T00250]; 318; 322; 5.092035; CCTCC; 1.54004; 2.19561;
Sequence; Elk-1 [T00250]; 325; 329; 7.406067; GCTCC; 1.54004; 2.15767;
Sequence; Elk-1 [T00250]; 352; 356; 7.406067; GGAGC; 1.54004; 2.15767;
Sequence; Elk-1 [T00250]; 392; 396; 2.121196; GGAAA; 1.54004; 1.28146;
Sequence; Elk-1 [T00250]; 436; 440; 6.853012; AGTCC; 4.62012; 4.61150;
Sequence; Elk-1 [T00250]; 452; 456; 2.121196; TTTCC; 1.54004; 1.28146;
Sequence; Elk-1 [T00250]; 479; 483; 2.892540; ATTCC; 1.54004; 1.26569;
Sequence; Elk-1 [T00250]; 498; 502; 6.274504; GGACC; 3.08008; 3.82271;
Sequence; Elk-1 [T00250]; 514; 518; 2.892540; GGAAT; 1.54004; 1.26569;
Sequence; Elk-1 [T00250]; 517; 521; 2.892540; ATTCC; 1.54004; 1.26569;
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Sequence; Elk-1 [T00250]; 593; 597; 6.274504; GGACC; 3.08008; 3.82271;
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Sequence; Elk-1 [T00250]; 640; 644; 2.121196; TTTCC; 1.54004; 1.28146;
Sequence; Elk-1 [T00250]; 648; 652; 7.984576; ACTCC; 1.54004; 1.69193;
Sequence; Elk-1 [T00250]; 653; 657; 7.213232; TCTCC; 4.62012; 4.61150;
Sequence; Elk-1 [T00250]; 701; 705; 3.960472; CATCC; 3.08008; 3.84960;
Sequence; Elk-1 [T00250]; 719; 723; 6.853012; AATCC; 4.62012; 4.61150;
Sequence; Elk-1 [T00250]; 775; 779; 7.984576; ACTCC; 1.54004; 1.69193;
Sequence; Elk-1 [T00250]; 792; 796; 6.274504; GGTCC; 3.08008; 3.82271;
Sequence; Elk-1 [T00250]; 830; 834; 2.892540; ATTCC; 1.54004; 1.26569;
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Sequence; Elk-1 [T00250]; 948; 952; 6.853012; AGTCC; 4.62012; 4.61150;
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Sequence; Elk-1 [T00250]; 1035; 1039; 6.274504; GGTCC; 3.08008; 3.82271;
Sequence; Elk-1 [T00250]; 1048; 1052; 6.081668; GGATA; 3.08008; 2.93146;

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Sequence; Elk-1 [T00250]; 1141; 1145; 5.092035; CCTCC; 1.54004; 2.19561;
Sequence; Elk-1 [T00250]; 1149; 1153; 6.274504; GGTCC; 3.08008; 3.82271;
Sequence; Elk-1 [T00250]; 1168; 1172; 6.081668; GGACA; 3.08008; 2.93146;
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Sequence; Elk-1 [T00250]; 1302; 1306; 7.984576; ACTCC; 1.54004; 1.69193;
Sequence; Elk-1 [T00250]; 1322; 1326; 7.213232; GGAGA; 4.62012; 4.61150;
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Sequence; Elk-1 [T00250]; 1450; 1454; 0.000000; GGAAG; 1.54004; 1.65111;
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Sequence; Elk-1 [T00250]; 1509; 1513; 2.892540; GGAAT; 1.54004; 1.26569;
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Sequence; p53 [T00671]; 631; 637; 0.525867; CCTGCCC; 0.19250; 0.30599;
Sequence; p53 [T00671]; 673; 679; 4.325788; CTGGCCC; 0.28876; 0.40491;
Sequence; p53 [T00671]; 743; 749; 8.906038; GGGCTTT; 0.96252; 1.56763;
Sequence; p53 [T00671]; 751; 757; 7.959461; TCGGCCC; 0.57751; 0.84971;
Sequence; p53 [T00671]; 767; 773; 8.739367; GCAGCCC; 0.28876; 0.57878;
Sequence; p53 [T00671]; 795; 801; 3.891597; CCCGCCC; 0.57751; 1.06420;
Sequence; p53 [T00671]; 838; 844; 3.891597; CCCGCCC; 0.57751; 1.06420;
Sequence; p53 [T00671]; 847; 853; 8.472402; GGGCCTC; 0.28876; 0.57878;
Sequence; p53 [T00671]; 889; 895; 3.891597; CCCGCCC; 0.57751; 1.06420;
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Sequence; p53 [T00671]; 1098; 1104; 1.752889; CGTGCCC; 0.09625; 0.17164;
Sequence; p53 [T00671]; 1240; 1246; 7.700559; GGGCGGA; 0.38501; 0.57262;

Sequence; p53 [T00671]; 1263; 1269; 8.472402; GAGGCCCC; 0.28876; 0.57878;
Sequence; p53 [T00671]; 1386; 1392; 8.213500; GGGCTTC; 0.57751; 0.84971;
Sequence; GATA-1 [T00306]; 90; 95; 0.552356; GATAGA; 2.31006; 1.61008;
Sequence; GATA-1 [T00306]; 125; 130; 1.908093; GGTATC; 2.31006; 1.60948;
Sequence; GATA-1 [T00306]; 164; 169; 0.060507; GATAGG; 0.77002; 0.63276;
Sequence; GATA-1 [T00306]; 551; 556; 1.391652; GATACG; 0.77002; 0.63294;
Sequence; GATA-1 [T00306]; 1049; 1054; 0.552356; GATAGA; 2.31006; 1.61008;
Sequence; GATA-1 [T00306]; 1442; 1447; 0.491849; GATAAA; 2.31006; 1.61008;
Sequence; VDR [T00885]; 98; 101; 0.000000; GGGT; 6.16016; 8.05348;
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Sequence; VDR [T00885]; 237; 240; 0.000000; GGGT; 6.16016; 8.05348;
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Sequence; VDR [T00885]; 368; 371; 0.000000; ACCC; 6.16016; 8.05348;
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Sequence; VDR [T00885]; 510; 513; 0.000000; ACCC; 6.16016; 8.05348;
Sequence; VDR [T00885]; 629; 632; 0.000000; ACCC; 6.16016; 8.05348;
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Sequence; VDR [T00885]; 1403; 1406; 0.000000; ACCC; 6.16016; 8.05348;
Sequence; VDR [T00885]; 1432; 1435; 0.000000; ACCC; 6.16016; 8.05348;
Sequence; VDR [T00885]; 1484; 1487; 0.000000; ACCC; 6.16016; 8.05348;
Sequence; VDR [T00885]; 1494; 1497; 0.000000; GGGT; 6.16016; 8.05348;
Sequence; MBF1 [T00492]; 100; 110; 9.143821; GTCCAAAATGT; 0.06091; 0.03491;
Sequence; MBF1 [T00492]; 1244; 1254; 6.505099; GGATTTTAGAG; 0.05076; 0.03144;
Sequence; MBF1 [T00492]; 1418; 1428; 7.302340; TGCCAAAATGA; 0.03722; 0.02489;
Sequence; MBF1 [T00492]; 1467; 1477; 14.636473; AACATAATAA; 0.18273; 0.09655;
Sequence; POU3F2 [T00630]; 105; 111; 7.224857; AAATGTG; 0.57751; 0.39605;
Sequence; POU3F2 [T00630]; 302; 308; 5.457738; ATCATTT; 0.77002; 0.49236;
Sequence; POU3F2 [T00630]; 1243; 1249; 5.710420; CGGATTT; 0.77002; 0.49236;
Sequence; POU3F2 [T00630]; 1271; 1277; 5.457738; CGCATTT; 0.77002; 0.49236;
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Sequence; FOXP3 [T04280]; 1422; 1430; 3.076791; AAAATGATG; 0.10828; 0.04197;
Sequence; FOXP3 [T04280]; 1508; 1516; 7.334112; CGGAATTTT; 0.18047; 0.09883;

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Sequence; USF2b [T02377]; 142; 149; 6.942764; GTCATGGG; 1.15503; 1.08212;
Sequence; USF2b [T02377]; 214; 221; 12.629773; GTCAGTCT; 1.73254; 1.61621;
Sequence; USF2b [T02377]; 262; 269; 1.255756; GTCACCTG; 0.19250; 0.17803;
Sequence; USF2b [T02377]; 605; 612; 12.629773; ACTCTGAC; 1.73254; 1.61621;
Sequence; USF2b [T02377]; 708; 715; 5.687009; AACCTGAC; 0.57751; 0.70456;
Sequence; USF2b [T02377]; 721; 728; 12.629773; TCCTTGAC; 1.73254; 1.61621;
Sequence; USF2b [T02377]; 761; 768; 12.629773; GTCATCGC; 1.73254; 1.61621;
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Sequence; USF2b [T02377]; 1284; 1291; 6.942764; CTCATGAC; 1.15503; 1.08212;
Sequence; USF2b [T02377]; 1458; 1465; 11.374018; GTCAGGAA; 0.86627; 1.05230;
Sequence; USF2 [T00878]; 106; 114; 12.285069; AATGTGACC; 0.14438; 0.15218;
Sequence; USF2 [T00878]; 261; 269; 4.200409; AGTCACTTG; 0.04813; 0.04353;
Sequence; USF2 [T00878]; 708; 716; 14.014611; AACCTGACT; 0.07219; 0.08773;
Sequence; USF2 [T00878]; 1020; 1028; 13.520501; GGTCAGGGG; 0.18047; 0.16808;
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Sequence; c-Jun [T00133]; 139; 145; 4.818265; GGCGTCA; 0.38501; 0.37512;
Sequence; c-Jun [T00133]; 211; 217; 4.951897; GGTGTCA; 0.38501; 0.37512;
Sequence; c-Jun [T00133]; 259; 265; 3.818710; AGAGTCA; 0.38501; 0.29155;
Sequence; c-Jun [T00133]; 609; 615; 6.780539; TGACATC; 0.28876; 0.23770;
Sequence; c-Jun [T00133]; 712; 718; 4.622649; TGAATCG; 0.28876; 0.25611;
Sequence; c-Jun [T00133]; 725; 731; 4.642428; TGAATTC; 0.28876; 0.25611;
Sequence; c-Jun [T00133]; 758; 764; 5.823189; AGCGTCA; 0.57751; 0.51416;
Sequence; c-Jun [T00133]; 811; 817; 9.869451; TGACAAG; 0.19250; 0.15498;
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Sequence; c-Jun [T00133]; 1288; 1294; 5.978259; TGACAGA; 0.57751; 0.51416;
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Sequence; NHP-1 [T00621]; 168; 174; 14.314808; GGACATC; 1.15503; 0.96928;
Sequence; NHP-1 [T00621]; 211; 217; 11.916538; GGTGTCA; 1.73254; 1.69881;
Sequence; NHP-1 [T00621]; 280; 286; 13.454424; CAAGTCT; 0.38501; 0.37974;
Sequence; NHP-1 [T00621]; 498; 504; 9.830000; GGACCTT; 1.44379; 1.33181;
Sequence; NHP-1 [T00621]; 609; 615; 5.345192; TGACATC; 0.57751; 0.45707;
Sequence; NHP-1 [T00621]; 627; 633; 11.916538; AGACCCT; 1.73254; 1.69881;
Sequence; NHP-1 [T00621]; 687; 693; 11.916538; AGACCAA; 1.73254; 1.69881;
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Sequence; NHP-1 [T00621]; 811; 817; 11.056154; TGACAAG; 0.57751; 0.65416;
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Sequence; NHP-1 [T00621]; 1153; 1159; 14.314808; CGACATA; 1.15503; 0.96928;
Sequence; NHP-1 [T00621]; 1168; 1174; 14.314808; GGACATA; 1.15503; 0.96928;
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Sequence; NHP-1 [T00621]; 1341; 1347; 14.314808; GAAGTCT; 1.15503; 0.96928;
Sequence; NHP-1 [T00621]; 1455; 1461; 0.860385; TAGGTCA; 0.28876; 0.25566;
Sequence; NHP-1 [T00621]; 1523; 1529; 11.916538; AGACCGA; 1.73254; 1.69881;
Sequence; ARP-1 [T00045]; 110; 118; 6.071920; TGACCCTTC; 0.04813; 0.06240;
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Sequence; RAR-gamma [T00720]; 126; 133; 3.232527; GTATCACC; 0.19250; 0.18395;
Sequence; RAR-gamma [T00720]; 170; 177; 6.005075; ACATCACC; 0.09625; 0.09416;

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Sequence; RAR-gamma [T00720]; 1406; 1413; 1.839917; CGATCACC; 0.09625; 0.10905;
Sequence; c-Fos [T00123]; 109; 116; 10.552944; GTGACCCT; 0.38501; 0.32576;
Sequence; c-Fos [T00123]; 139; 146; 6.315788; GGCGTCAT; 0.24063; 0.23634;
Sequence; c-Fos [T00123]; 211; 218; 7.473109; GGTGTCAG; 0.09625; 0.10177;
Sequence; c-Fos [T00123]; 259; 266; 5.590539; AGAGTCAC; 0.07219; 0.06130;
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Sequence; c-Fos [T00123]; 711; 718; 5.217470; CTGACTCG; 0.24063; 0.21492;
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Sequence; c-Fos [T00123]; 1287; 1294; 8.912261; ATGACAGA; 0.43314; 0.33991;
Sequence; c-Fos [T00123]; 1455; 1462; 9.187379; TAGGTCAG; 0.43314; 0.33991;
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Sequence; Pax-2 [T01823]; 142; 148; 0.591451; GTCATGG; 0.28876; 0.33662;
Sequence; Pax-2 [T01823]; 214; 220; 3.217275; GTCAGTC; 1.05878; 1.08872;
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Sequence; Nkx2-1 [T00857]; 1283; 1289; 3.178803; CCTCATG; 0.67377; 0.86443;
Sequence; Nkx2-1 [T00857]; 1290; 1296; 5.183213; ACAGAGG; 1.34753; 1.33737;
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Sequence; NF-X3 [T01514]; 162; 169; 12.359921; CAGATAGG; 1.08284; 1.05338;
Sequence; NF-X3 [T01514]; 267; 274; 12.359921; TTGTTCTG; 1.08284; 1.05338;
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Sequence; NF-X3 [T01514]; 690; 697; 12.359921; CCAATCTG; 1.08284; 1.05338;
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Sequence; NF-X3 [T01514]; 1291; 1298; 12.359921; CAGAGGCT; 1.08284; 1.05338;
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Sequence; NF-X3 [T01514]; 1339; 1346; 4.935373; CAGAAGTC; 0.26469; 0.24430;
Sequence; GATA-3 [T00311]; 163; 170; 1.766593; AGATAGGA; 0.33688; 0.20324;
Sequence; GATA-3 [T00311]; 550; 557; 3.975111; AGATACGT; 0.02406; 0.01665;
Sequence; TGIF [T04076]; 210; 217; 1.303150; AGGTGTCA; 0.14438; 0.13398;
Sequence; TGIF [T04076]; 609; 616; 2.318943; TGACATCC; 0.36095; 0.28661;
Sequence; TGIF [T04076]; 811; 818; 2.490395; TGACAAGA; 0.36095; 0.28661;
Sequence; TGIF [T04076]; 1288; 1295; 2.169992; TGACAGAG; 0.31282; 0.27629;
Sequence; PKNOX1 [T04122]; 185; 195; 14.455439; AGATGGACAGC; 0.12182; 0.11413;
Sequence; PKNOX1 [T04122]; 211; 221; 14.455439; GGTGTCTAGTCT; 0.12182; 0.11413;
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Sequence; FOXO3a [T02938]; 251; 258; 6.942764; CTTACTCA; 1.15503; 0.75166;
Sequence; FOXO3a [T02938]; 395; 402; 8.198520; AAGGTAAG; 0.57751; 0.48940;
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Sequence; FOXO3a [T02938]; 1528; 1535; 5.687009; GATTTAAG; 0.57751; 0.28861;
Sequence; Hlf [T01071]; 251; 259; 6.800232; CTTACTCAA; 0.10828; 0.07112;
Sequence; Hlf [T01071]; 1250; 1258; 8.501296; TAGAGTAAC; 0.13836; 0.09026;
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Sequence; AP-1 [T00029]; 712; 719; 7.617752; TGAATCGA; 0.09625; 0.10113;
Sequence; AP-1 [T00029]; 725; 732; 11.843817; TGAATTC; 0.28876; 0.23818;
Sequence; PR B [T00696]; 266; 272; 5.756916; CTTGTTC; 0.57751; 0.45498;
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Sequence; PR B [T00696]; 1132; 1138; 5.756916; TTTGTTC; 0.57751; 0.45498;
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Sequence; LCR-F1 [T01599]; 298; 303; 5.114259; ACTCAT; 1.15503; 0.90891;
Sequence; LCR-F1 [T01599]; 301; 306; 3.748626; CATCAT; 1.15503; 0.69797;
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Sequence; POU2F2 (Oct-2.1) [T00646]; 1274; 1281; 10.519488; ATTTCCGT; 0.19250; 0.10641;
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Sequence; EIIaE-A [T00246]; 509; 515; 14.472869; CACCCGG; 2.50256; 3.60095;
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Sequence; AIRE [T05990]; 556; 565; 10.667168; GTGGTTTCTA; 0.13535; 0.13097;
Sequence; Nrf2 [T01443]; 618; 628; 13.939071; ACATGCTTAAG; 0.10152; 0.06936;
Sequence; Nrf2 [T01443]; 898; 908; 13.939071; CTTAAGCATGA; 0.10152; 0.06936;
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Sequence; PPAR-alpha:RXR-alpha [T05221]; 493; 503; 10.172413; AGCTGGGACCT; 0.06768; 0.12948;
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Sequence; Egr-3 [T00243]; 1079; 1091; 11.366723; CACACCCACAACC; 0.02270; 0.03493;
Sequence; Pbx1 [T06000]; 902; 913; 4.655113; AGCATGAGGCCG; 0.01288; 0.01007;
Sequence; GCMA [T02306]; 916; 924; 12.887507; CATGCTGAA; 0.20454; 0.20859;
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Sequence; Pax-5 [T00070]; 1191; 1197; 2.240452; ATCACGC; 0.28876; 0.39218;
Sequence; Pax-5 [T00070]; 1227; 1233; 7.762216; GCGTGCA; 0.19250; 0.30864;
Sequence; Pax-5 [T00070]; 1490; 1496; 8.803077; GCGTGGG; 0.19250; 0.31999;
Sequence; ERRalpha1 [T05682]; 1118; 1130; 13.621444; CCTCACCTCAGCA; 0.04695; 0.03878;
Sequence; HNF-4alpha [T03828]; 1126; 1138; 13.587440; CAGCACTTTGTTC; 0.02390; 0.01737;
Sequence; CUTL1 [T00100]; 429; 434; 0.925283; AACAAAT; 1.92505; 1.51831;
Sequence; CUTL1 [T00100]; 689; 694; 0.000000; ACCAAAT; 0.38501; 0.29066;
Sequence; CUTL1 [T00100]; 806; 811; 0.967341; AGCAAT; 1.92505; 1.51831;
Sequence; CUTL1 [T00100]; 1159; 1164; 0.925283; ATTGTT; 1.92505; 1.51831;
Sequence; CUTL1 [T00100]; 1390; 1395; 1.732064; TTCAAT; 1.15503; 0.75858;
Sequence; CUTL1 [T00100]; 1467; 1472; 0.925283; AACAAAT; 1.92505; 1.51831;
Sequence; AhR:Arnt [T05394]; 1193; 1201; 9.185597; CACGCCTCT; 0.05414; 0.07277;
Sequence; AhR:Arnt [T05394]; 1223; 1231; 5.810987; TCCGGCGTG; 0.30079; 0.41298;
Sequence; AhR:Arnt [T05394]; 1486; 1494; 5.888384; CCAAGCGTG; 0.30079; 0.41298;
Sequence; c-Ets-2 [T00113]; 515; 522; 2.827022; GAATTCCT; 0.28876; 0.23872;
Sequence; c-Ets-2 [T00113]; 1210; 1217; 2.827022; AGGAATCG; 0.28876; 0.23872;
Sequence; c-Ets-2 [T00113]; 1278; 1285; 2.827022; CCGTTCCT; 0.28876; 0.23872;
Sequence; c-Ets-2 [T00113]; 1344; 1351; 4.629332; GTCTTCCT; 0.43314; 0.36366;
Sequence; c-Ets-2 [T00113]; 1449; 1456; 2.485451; AGGAAGTA; 0.14438; 0.13402;
Sequence; c-Ets-2 [T00113]; 1461; 1468; 4.629332; AGGAAGAA; 0.43314; 0.36366;
Sequence; c-Ets-2 [T00113]; 1542; 1549; 4.629332; AGGAAGGA; 0.43314; 0.36366;
Sequence; Arnt [T01346]; 1193; 1201; 10.241323; CACGCCTCT; 0.10227; 0.16708;
Sequence; Arnt [T01346]; 1223; 1231; 11.217784; TCCGGCGTG; 0.12032; 0.17704;
Sequence; Arnt [T01346]; 1486; 1494; 11.057524; CCAAGCGTG; 0.12032; 0.17704;
Sequence; AhR [T01795]; 1190; 1197; 1.711124; GATCACGC; 0.21657; 0.33487;

Sequence; AhR [T01795]; 1227; 1234; 2.493742; GCGTGCAA; 0.36095; 0.50033;
Sequence; AhR [T01795]; 1490; 1497; 1.766689; GCGTGGGT; 0.21657; 0.27714;
Sequence; MIF-1 [T01047]; 1249; 1261; 14.500958; TTAGAGTAACACC; 0.00940; 0.00714;
Sequence; SXR:RXR-alpha [T05670]; 33; 41; 7.175614; AAGTCCAGG; 0.24063; 0.18748;
Sequence; SXR:RXR-alpha [T05670]; 1297; 1305; 11.263007; CTTGGACTC; 0.09625; 0.08467;
Sequence; MZF-1 [T00529]; 240; 246; 0.056332; TCCCCC; 0.38501; 0.62969;
Sequence; MZF-1 [T00529]; 438; 444; 2.220412; TCCCCGA; 0.38501; 0.48625;
Sequence; MZF-1 [T00529]; 703; 709; 2.107748; TCCCCAA; 0.38501; 0.48625;
Sequence; MZF-1 [T00529]; 1304; 1310; 1.166538; TCCCCTT; 0.38501; 0.46746;
Sequence; MZF-1 [T00529]; 1364; 1370; 1.053874; ATGGGGA; 0.38501; 0.46746;
Sequence; GABP-alpha [T01390]; 1197; 1208; 8.833550; CCTCTTCCGCTG; 0.00865; 0.00930;
Sequence; GABP-alpha [T01390]; 1343; 1354; 14.677905; AGTCTTCCTTTC; 0.02688; 0.02770;
Sequence; GABP-alpha [T01390]; 1432; 1443; 13.457706; ACCCGGAAGTGA; 0.01560; 0.01415;
Sequence; GABP-alpha [T01390]; 1446; 1457; 8.177756; AACAGGAAGTAG; 0.00790; 0.00790;
Sequence; GABP [T00268]; 378; 389; 14.847057; ACCACTTCAGCT; 0.03948; 0.03845;
Sequence; GABP [T00268]; 1196; 1207; 2.995493; GCCTCTCCGCT; 0.00376; 0.00423;
Sequence; GABP [T00268]; 1271; 1282; 13.611252; CGCATTTCCGTT; 0.01579; 0.01518;
Sequence; GABP [T00268]; 1433; 1444; 3.041476; CCCGGAAGTGAT; 0.00376; 0.00423;
Sequence; CDX2 [T03246]; 1436; 1447; 14.892122; GGAAGTGATAAA; 0.05978; 0.03679;
Sequence; IRF-2 [T01491]; 258; 268; 6.873928; AAGAGTCACTT; 0.15227; 0.10956;
Sequence; IRF-2 [T01491]; 1438; 1448; 6.873928; AAGTGATAAAC; 0.15227; 0.10956;
Sequence; FOXJ2 (long isoform) [T04169]; 1440; 1449; 3.916738; GTGATAAACA; 0.03309; 0.01753;
Sequence; HNF-3beta [T02513]; 60; 66; 6.782764; AGGTTTA; 0.19250; 0.10620;
Sequence; HNF-3beta [T02513]; 1245; 1251; 6.557271; GATTTTA; 0.38501; 0.25181;
Sequence; HNF-3beta [T02513]; 1324; 1330; 2.442513; AGATTTA; 0.19250; 0.08011;
Sequence; HNF-3beta [T02513]; 1444; 1450; 4.950880; TAAACAG; 0.38501; 0.25226;
Sequence; HNF-3beta [T02513]; 1527; 1533; 3.053142; CGATTTA; 0.77002; 0.37300;
Sequence; NERF-1a [T05021]; 1448; 1459; 0.000000; CAGGAAGTAGGT; 0.00019; 0.00019;
Sequence; NERF-1a [T05021]; 1460; 1471; 7.088804; CAGGAAGAACAA; 0.00545; 0.00600;
Sequence; RORalpha2 [T01528]; 1450; 1461; 2.181595; GGAAGTAGGTCA; 0.00273; 0.00159;
Sequence; RORalpha1 [T01527]; 1452; 1461; 2.249512; AAGTAGGTCA; 0.04963; 0.04193;
Sequence; COUP-TF1 [T00149]; 1453; 1461; 1.930067; AGTAGGTCA; 0.03008; 0.02415;
Sequence; SF-1 [T02769]; 1452; 1462; 12.020287; AAGTAGGTCA; 0.00602; 0.00615;
Sequence; AR [T00040]; 268; 275; 0.671565; TGTCTGT; 0.19250; 0.14875;
Sequence; AR [T00040]; 1134; 1141; 5.899530; TGTTCCGC; 0.36095; 0.36043;
Sequence; AR [T00040]; 1463; 1470; 0.729340; GAAGAACA; 0.19250; 0.14875;
Sequence; HOXD9 [T01424]; 1470; 1479; 11.174228; AATAATAAGG; 0.14739; 0.08139;
Sequence; HOXD10 [T01425]; 1470; 1479; 11.174228; AATAATAAGG; 0.14739; 0.08139;
Sequence; AP-3 (2) [T00039]; 61; 67; 3.763516; GGTTTAG; 0.57751; 0.46789;
Sequence; AP-3 (2) [T00039]; 412; 418; 11.290546; AGGTTAG; 1.15503; 0.86689;
Sequence; AP-3 (2) [T00039]; 1325; 1331; 0.000000; GATTTAG; 0.28876; 0.19890;
Sequence; AP-3 (2) [T00039]; 1500; 1506; 8.971049; CTAAGGC; 0.48126; 0.40102;
Sequence; NF-kappaB [T00590]; 1508; 1518; 7.571839; CGGAATTTTCC; 0.00602; 0.00476;
Sequence; E2F-5 [T01607]; 1505; 1512; 13.735780; GCGCGGAA; 0.50533; 0.60821;
Sequence; HNF-1B [T01950]; 1472; 1479; 11.219398; TAATAAGG; 0.31282; 0.16536;
Sequence; RAR-alpha1 [T00719]; 1453; 1462; 7.753480; AGTAGGTCA; 0.01203; 0.01443;
Sequence; RXR-alpha [T01345]; 1453; 1461; 2.099821; AGTAGGTCA; 0.15039; 0.14063;
Sequence; ELF-1 [T01113]; 1445; 1457; 5.072491; AAACAGGAAGTAG; 0.00113; 0.00076;
Sequence; Pbx1b [T02087]; 345; 354; 14.774452; TGATGAAGGA; 0.16243; 0.11646;
Sequence; Pbx1b [T02087]; 1285; 1294; 12.747416; TCATGACAGA; 0.11731; 0.10185;
Sequence; PU.1 [T02068]; 514; 523; 3.227625; GGAATTCCTC; 0.02256; 0.01920;
Sequence; PU.1 [T02068]; 1277; 1286; 3.941435; TCCGTTCTC; 0.03158; 0.03628;
Sequence; R1 [T00711]; 1235; 1246; 9.864560; GCTGAGGGCGGA; 0.02331; 0.03759;

Sequence; TFII-I [T00824]; 86; 96; 6.742511; AGTGGATAGAC; 0.02406; 0.02392;
Sequence; TFII-I [T00824]; 220; 230; 9.416256; CTAGGATGGCC; 0.06317; 0.06314;
Sequence; TFII-I [T00824]; 1045; 1055; 6.759160; CCGGGATAGAC; 0.00602; 0.00674;
Sequence; T3R-beta1 [T00851]; 789; 799; 10.019726; TCAGGTCCCGC; 0.01542; 0.01712;
Sequence; T3R-beta1 [T00851]; 858; 868; 10.753334; TCAGGTCCAAC; 0.01955; 0.02161;
Sequence; T3R-beta1 [T00851]; 1032; 1042; 9.756265; TCAGGTCCTGC; 0.01542; 0.01712;
Sequence; CRF [T00170]; 690; 701; 12.356035; CCAATCTGCCAC; 0.05076; 0.06360;
Sequence; RFX1 [T01673]; 660; 668; 9.693213; GTTGCTTCA; 0.04813; 0.04405;
Sequence; POU2F1 [T00641]; 303; 312; 13.518184; TCATTTGCTT; 0.50533; 0.30063;
Sequence; POU2F2 [T00647]; 302; 312; 13.200917; ATCATTTGCTT; 0.31583; 0.20658;
Sequence; octamer-binding factor [T01225]; 302; 312; 14.796379; ATCATTTGCTT; 0.28425; 0.18062;

-- END -----

Distribution of the nucleotides over the given chain:

