Jump to: <u>Multiple Alignment Motif Tree Motif Matching</u> <u>Input file: 593 motifs loaded</u>

Settings: Metric=PCC, Alignment=SWU, Gap-open=1000, Gap-extend=1000, -nooverlapalign
Multiple Alignment=IR, Tree=UPGMA, Matching against: JASPAR
e: All results files are removed nightly at midnight EST. Please save your results by saving "Webs

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Multiple Alignment

(Consensus sequence representations shown, but multiple alignment was carried out on the matrices)

54_CAA_LMYQR:	NCTTGTTARN
otp:	NYAATTAN
NEMVEDRAFT_v1g113057:	NNGGATTARN
53_CAC_ERVSR:	NCGTGTTAA
LHX1:	NYNATTAN
LHX2:	NNNNTTNNNN
LHX3:	NNAWTTAATTANN
LHX4:	NTAATTAN
LHX6:	NNTAATTA
CBG04010:	NNNMATTAANN
LHX9:	NNTNATTAN
PK24181.1:	NNNNNNNNNNNN
21_TAC_ERVSV:	NCGYATTANN
ceh-74:	NNNCCTCACNN
IRX5:	NNNTGTNNNACAYNN
IRX1:	NNCANNNNNNNNNTGNN
IRX3:	WACAYGNWWWWNCRTGTW
IRX2:	NWACAYGACANN
10_TGG_KSVMQ:	NNCATTARNN
pal-1:	TTWATTAC
GSC2:	NNNATTAN
Isl1:	NCCATTAGN
Isl2:	NNNTNNN
18_TAG_RLTQA:	NNCAATTARN
271_AAC_KLQRF:	NCGTYTTANN
HGTX:	NTMATTAN
WOX11:	NNTAATTAANT
WOX13:	NNTGATTGAN
Q0N4F9_NEMVE:	MTAATTAN
hox12:	GTMATWAA

OdsH:	eve:	NSTAATTAGN
FGRRES_07914: NNGTYTTARN	OdsH:	NYAATTAN
225_AAC_SLQRF: NNGTYTTARN	unc-62:	NNNTNTNNN
HMLALPHA2:	FGRRES_07914:	NNACATGTANN
59_ATC_TRMAF: GATTTANNNN	225_AAC_SLQRF:	NNGTYTTARN
Q7M3U4_ACRFO: NNWTGATTANN	HMLALPHA2:	NNNGTNNN
SNOG_11642: NNWTGATTANN	59_ATC_TRMAF:	GATTTANNNN
Hoxb8: NNNNATWNN	Q7M3U4_ACRFO:	NNNAATTANNN
Hoxb9: NNNNRTWAAN	SNOG_11642:	NNWTGATTANN
Six4: NNNKNTNNN	Hoxb8:	NNNNATWNN
Hoxb3: NNNNATTAN	Hoxb9:	NNNNRTWAAN
GSX1: NTNATKAN	Six4:	NNNKNTNNN
Hoxb6: NNNNNNN	Hoxb3:	NNNNATTAN
Six1:	GSX1:	NTNATKAN
Six2: NNNTATNN	Hoxb6:	NNNNNNN
HOS66:NNNNNNNN	Six1:	NNNRTATNNN
Hoxc10: NTTTTAYGAC	Six2:	NNNTATNN
Hoxc10: NTTTTAYGAC Hoxc12: NNTWAYNNNN 264_ACT_KVYHV: NNGTTTANNN HOXB8: GYMATTAN HOXB9: NTTTTACGAC SNAPOd2T00006145001: NNTATTRNN Q6Y859_MARMO: NNNATTNNNNN	HOS66:	NNNNNNNN
Hoxc12: NNTWAYNNNN	Hoxc11:	NNNNRTWAAN
264_ACT_KVYHV: NNGTTTANNN	Hoxc10:	NTTTTAYGAC
HOXB8: GYMATTAN	Hoxc12:	NNTWAYNNNN
HOXB9: NTTTTACGAC SNAPOd2T00006145001: NNTRATTRNN Q6Y859_MARMO: NNATNNNNN HOXB2: NYAATTAN zfhx4: NYAATTAN	264_ACT_KVYHV:	NNGTTTANNN
SNAPOd2T00006145001: NNTRATTRNN	HOXB8:	GYMATTAN
Q6Y859_MARMO: NNNATNNNNN HOXB2: NYAATTAN zfhx4: NYAATTANN HOXB1: NTAATTAC HOXB6:	HOXB9:	NTTTTACGAC
HOXB2: NYAATTAN	SNAPOd2T00006145001:	NNTRATTRNN
zfhx4: NYAATTANN	Q6Y859_MARMO:	NNNATNNNNN
HOXB1: NTAATTAC HOXB6: GYMATTAN HOXB5: NYMATTAN HOXC11: NTTTACGAYN HOXC10: NTTTTATKRCN HOXC12: NTTTTATTACN Hoxd12_CONSTRUCT: NNTNAYNNNN 272_AAC_VAQRC: NCGTTTTANN	HOXB2:	NYAATTAN
HOXB6: GYMATTAN HOXC11: NYMATTAN HOXC10: NTTTATKRCN HOXC12: NTTTTATTACN Hoxd12_CONSTRUCT: NNTNAYNNNN 272_AAC_VAQRC: NCGTTTTANN hbn: NTAATTAAATTAN HOX6: NTGATTGNNN	zfhx4:	NYAATTANN
HOXB5: NYMATTAN HOXC11: NNTTTACGAYN HOXC10: NTTTTATKRCN HOXC12: NTTTTATTACN Hoxd12_CONSTRUCT: NNTNAYNNNN 272_AAC_VAQRC: NCGTTTTANN hbn: NTGATTGNNN HOX6: NNNNATTAN HOxa6: NNNNATTAN	HOXB1:	NTAATTAC
HOXC11: NNTTTACGAYN HOXC10: NNTTTATKRCN HOXC12: NTTTTATTACN Hoxd12_CONSTRUCT: NNTNAYNNNN 272_AAC_VAQRC: NCGTTTTANN hbn: NTAATTAAATTAN HOX6: NTGATTGNNN Hoxa6: NNNNATTAN	HOXB6:	GYMATTAN
HOXC10: NTTTATKRCN HOXC12: NTTTTATTACN Hoxd12_CONSTRUCT: NTGTTTTANN 272_AAC_VAQRC: NTGATTANATTAN hbn: NTGATTGNNN HOX6: NNNNATTAN HDG11: NCATTWAWKN	HOXB5:	NYMATTAN
HOXC12: NTTTTATTACN Hoxd12_CONSTRUCT: NNTNAYNNNN 272_AAC_VAQRC: NCGTTTTANN hbn: NTAATTAAATTAN HOX6: NTGATTGNNN Hoxa6: NNNNATTAN HDG11: NNNTTGAGAKN CAD25866: NNNNATTAN barx1: NNNNATTAN	HOXC11:	NNTTTACGAYN
Hoxd12_CONSTRUCT: NNTNAYNNNN 272_AAC_VAQRC: NCGTTTTANN hbn: NTAATTAAATTAN HOX6: NTGATTGNNN Hoxa6: NNNNATTAN HDG11: NCATTWAWKN CAD25866: NNNTTGAGAKN barx1: NNNNATTAN	HOXC10:	NNTTTATKRCN
272_AAC_VAQRC: NCGTTTTANN hbn: NTAATTAAATTAN HOX6: NTGATTGNNN Hoxa6: NNNNATTAN HDG11: NCATTWAWKN CAD25866: NNNTTGAGAKN barx1: NNNNATTAN	HOXC12:	NTTTTATTACN
hbn: NTAATTAAATTAN HOX6: NTGATTGNNN Hoxa6: NNNNATTAN HDG11: NCATTWAWKN CAD25866: NNNTTGAGAKN barx1: NNNNATTAN	Hoxd12_CONSTRUCT:	NNTNAYNNNN
HOX6: NTGATTGNNN Hoxa6: NNNNATTAN HDG11: NCATTWAWKN CAD25866: NNNTTGAGAKN barx1: NNNNATTAN	272_AAC_VAQRC:	NCGTTTTANN
Hoxa6: NNNNATTAN HDG11: NCATTWAWKN CAD25866: NNNTTGAGAKN barx1: NNNNATTAN	hbn:	NTAATTAAATTAN
HDG11: NCATTWAWKN CAD25866: NNNTTGAGAKN barx1: NNNNATTAN	HOX6:	NTGATTGNNN
CAD25866:NNNTTGAGAKN barx1:NNNATTAN	Hoxa6:	NNNNATTAN
barx1:NNNNATTAN	HDG11:	NCATTWAWKN
	CAD25866:	NNNTTGAGAKN
Duxbl1:NTGATTRNN	barx1:	
	Duxbl1:	NTGATTRNN

Hmx2:	NNNCRNTTNN
243_GGT_ATKSM:	NTMCTTARNN
ceh-24:	NNYNCTYNN
ceh-23:	NNNTAATTAN
ceh-22:	NNNCACTTNA
vis:	NTGTCA
Dfd:	NNYCATTANN
MTAL2_KLUDE:	WTTACAYG
BSX:	NNCGTTAN
B-H2:	NNCGTTTANN
B-H1:	NNCGTTTANN
HNF1B:	GTTAATNATTAAY
20_TAC_QRVSA:	CGYATTARNN
CG5369:	TAATNNAATTA
24_GTG_HLIQY:	NCACTTANNN
ceh-90:	NGTTTTANN
BARX1:	NNATTAAAWANCNATTA
CNK00090:	ATAATTAA
mirr:	TGTTWNNN
Dbx2:	NNNANNN
Gbx2:	NNYAATTANN
Gbx1:	NNYAATTANN
Dbx1:	TAATTAAT
Hlx:	NNNAWNN
SNOG_08903:	TTGATTTR
EMX2:	NTAATTAG
EMX1:	NTAATTAN
HAT1:	NNATGATTRN
Q1WMN9_COPDI:	NNGATTNNNN
GRMZM2G087741:	NGMYGTCANN
Pdx1:	NNNATTAN
15_TCC_RMIKS:	NGGATTARNN
cad:	NTTTTATKGCNN
Q0N4H2_NEMVE:	ANYAATTA
Q9GP48_9TURB:	NTAATTAN
Q24782_9CNID:	TTAATTAA
FGRRES_01100:	YAATTAAW
229_TTC_GRISA:	NNYATTANNN
<pre>estExt_gwp_gw1.C_702:</pre>	NNNNTNATTN
218_CTG_KQNQK:	NNTRGTTAAN
Bsx:	NNNNATTAN
ceh-5:	NNNATTANN
39_CTA_IFNAK:	NCTMGTTANN

MTR_2g038000:	NNNNNAGNNN
POU5F1B:	NNNTTNN
AAZ08039:	NNYAATTANN
YHP1:	NWWATTRNN
255_CCT_RADGK:	NNNGGTTANN
ATEG_00670:	NNNNACNNN
TVAG_451170:	NNCRCATCAN
lab:	STAATTAN
Nkx2-9:	NNRAGTRNNN
HB−5:	-NWNNNNNCAATTATTGNTNN
Nkx2-1:	NNRAGNRN
Nkx2-6:	NNNCACTTNN
Nkx2-4:	NNRAGNRNNN
43_CCT_MTNGK:	NTGGTTAANN
34_GAT_RTMRY:	NGTCTTARNN
HMBOX1:	NCTAGTTAN
caup:	NWNTAACA
so:	NGTATCAN
48_CCA_EHNAK:	NNTRGTTANN
NEMVEDRAFT_v1g101664:	GATYGATT
unc-4:	TAATTNAATTA
Ubx:	NYAATTAN
Rx:	NYAATTAN
SNAPOd2T00005194001:	NNTACATGTNN
CBG24578:	NNNTGACAGSTN
HAT3.1:	NNNGGTKYAN
Nkx6-3:	NNNATNANN
Nkx6-1:	NYNATTANN
Q6WL90_TRICY:	NNNATTAN
Q9C1N5_COPSC:	NNGATTGNN
SIX4:	NNGTATCRNN
SIX5:	ACTACAAYTC
SIX1:	NCGTATCRNN
SIX2:	NNGTATCRNN
Barx2:	NNNNATTAN
HNF1A:	NRTTAATNATTAACN
Vsx1:	NCAATTAN
Vsx2:	NYAATTAN
RAX:	YTAATTAN
WUS:	TCAWTCAWTCA
GRMZM2G135447:	SMYGTCAN
HDG7:	NCATTAAWTRN
HDG1:	NCATTAATTRN

DPRX:	NGGATTATCN
ESX1:	NYAATTAN
SHOX2:	NYAATTAN
270_AAG_RAQWF:	CCTYTTNNNN
NEMVEDRAFT_v1g129868:	NNNNTNRN
CADAORAG00002315:	NNNNACANNN
203_GTC_VQKRF:	NCGTCTTAR
ATHB-53:	NCAATTATTGN
Tlx2:	ATTAAWTA
ATHB-51:	ATWATTNN
ceh-62:	NNTAATTANN
CaO19.4000:	NNNNATTRN
Rax:	NNAATTANN
49_CAT_LSQSR:	NNTGTTARN
en:	NYAATTAN
Nobox:	NNYNATNNN
221_CTG_RLYQK:	NNTRGTTAAN
abd-A:	NGTAATTANN
Dll:	NYAATTAN
Lhx6_CONSTRUCT:	NYAATYANN
pha-2:	NNNATNNNNN
MNX1:	NTAATTAN
Cphx1:	WGATNNNNN
CG11085:	NCRATTAN
ftz:	GTAATTAA
uncx:	NYAATTANN
EN1:	NNTAATTA
EN2:	NTAATTAN
42_CGA_TFYAA:	NCTCGTTAN
E5:	NNNATTAN
HAT22:	AATGATTRNN
ro:	TAATTARN
2_TTT_RTVSA:	NNNATTARNN
lms:	NYAATTAN
ENSCING00000016045:	NCYAATTARNN
En1:	NNNANNN
Hoxa5:	NNNNATTAN
egl-5:	CCCATTAAAT
Hoxa3:	NNNYNATTAN
Hoxa2:	NNTAATTANN
Hoxa1:	NNYNATTNN
PK19166.1:	RTTAGGGG
26_GGT_ALKNM:	NCGCCTTAAN

Hoxa9:	NNNNNNN
CIMG_06089:	NNNNNNNNNNNN
Nanog:	NNNNATNNN
Gsx2:	NNNNATTAN
HAT3:	NTGATTRN
HAT2:	NNAATGATTRN
HAT5:	WNAATTATTNN
Dbx:	ATTAATTA
223_CTC_RTFGK:	NTTAGTTANN
NCU03266:	NYNATTWNNN
Q0N4H9_NEMVE:	NNNNTYRNN
PDX1:	NTMATTAR
NK7.1:	NACCGTTTAAN
ISX:	CTAATTAN
Q70LF3_ARTSF:	NTAATTAN
Hoxa11:	NNNTTTACGANN
Hoxa10:	NNNNTNNN
Nkx2-2:	NNNRAGNRN
303_CTC_VMNRK:	NTGAGTTANN
CAD26261:	TWWATTANN
KNAT4:	NNNNGTCNN
KNAT7:	AGAYGTCA
KNAT6:	NNNNGTCNNN
Hmx:	NCAMTTAN
KNAT3:	NNNNGTCNNN
Lim3:	NTAATTAN
Lim1:	NYAATTAN
lin-39:	GATTGATG
PRH_PETCR:	ATATATWA
Abd-B:	NWTTTACGACN
Q9BJW6_9CNID:	NCTAATTANN
Nkx3-1:	NNAAGTGNNN
Otp:	NNATTANN
Nkx3-2:	NNAAGTRNN
ceh-19:	NNCNATTAN
247_GCG_RTDRS:	NKKCTTARNN
Meis3:	NTGTCAN
55_CAA_LHYVR:	NNTTGTTANN
Q24780_9CNID:	NNTAATTAANN
Hdx:	NNATNNN
ATHB-12:	NNNNNNN
ATHB-13:	NNAATTATTRN
ATHB-16:	AATKATTA

ATHB-15:	AATAATTACT
Q00354_COPCI:	NGATTGGT
AGAP009986:	NNNNTGTNNN
Mnx1:	NNNNNATTAN
Q86SD7_PODCA:	NNTAATTANN
HOXA6:	NGYMATTANN
HOXA5:	STAATTAS
HOXA2:	NTAATTAN
HOXA1:	NNTAATTANN
Q8VHG7_MOUSE:	NGGATTAW
4_TTC_VRVSA:	NNNATTARNN
HOXA9:	NNNTTTAYGAYN
Obox6:	NNRGATTAN
Obox5:	NNNATNAN
Obox3:	NNATNWN
Obox1:	NNNGGATTAN
lbe:	NNTCGTTA
38_CTA_LHYAK:	NCTAGTTARN
256_CCA_RLYQK:	NNTRGTTANN
lbl:	CTMATTAN
HXD12_HETFR:	TTAATTAC
DMBX1:	NGGATTAN
ALX3:	NYAATTAN
73_AAT_KLTAF:	NTACTTARNN
Emx2:	NNNNATTAN
ALX4:	NYAATTAN
75_AAC_SISRF:	NNTCTTAANN
NEMVEDRAFT_v1g114268:	AYCNATTAN
vnd:	TYTCAAGTR
Smp_158000:	CYAATTAA
CG32105:	YTAATTAA
DRGX:	NYAATTAN
46_CCC_RLDSK:	NCGGGTTAR
Dlx4:	NNNATTAN
bsh:	TAATYTAATTA
ATEG_04171:	NNNYAATTWN
exex:	NNNNYAATTNNCNN
SNAPOd2T00003340001:	NWWATTANNN
CBG10835:	NNNTCANN
schlank:	AWNTTGGTRG
TLX2:	NYAATTAN
TLX3:	NAATTGNNNNNNNNNNNNCAATTN
GSX2:	SYMATTAN

37_GAA_RFQKF:	NSTTCTTAAN
TGIF2:	TGACANNTGTCA
TGIF1:	TGACAGCTGTCA
Dmbx1:	NNRGATTAN
Rhox6:	NNNATTAN
CG18599:	TAATTAN
Rhox8:	NTTACACCN
Uncx:	NTAATTNRATTAN
40_CGG_STRER:	YCCGTTAANN
13_TCT_ATVKA:	NGGATTARNN
Hoxb5:	NNNNATNAN
Tgif2:	NNNTGTCANN
Tgif1:	NNNTGTCANN
PK20392.1:	NNATKATTNN
C4B866_NEMVE:	NNNTAATTAANN
Hoxd8:	NNNNNNNN
Hoxd9:	NCCATWAAA
yox1:	NNNNATNNNN
Hoxd1:	NNNNATYN
Hoxd3:	NNYAATTANN
14_TCG_KGTQM:	CCCATTARNN
POU6F1:	NNTAATTANN
Y749_MIMIV:	TATATTAA
Q0N4H7_NEMVE:	NNNNNATNNN
Meox1:	NNYMATTAN
HOXD8:	GYMATTAN
HOXD9:	NTTTTATTGC
EVX1:	NTAATTAN
HOXD1:	NTAATTAN
EVX2:	NTAATTAN
repo:	NYTAATTAAN
PDF2:	NANRGAATATTCNNN
hbx4:	NNNYGTCANN
hbx2:	NNATATATWN
bap:	NNCACTTANN
PK25034.1:	NNMNGTCANN
SNAPOd2T00006620001:	NYAATTAN
ems:	NTAATTAN
PRRX1:	NYAATTAN
CG15696:	NNNATTRNN
PRRX2:	NNCRTNAN
NCU03070:	WWTATTGRNN
FGRRES_17238:	NNNNACNNNN

hbx5-2:	WTGATTRN
Meis2:	NTGTCAN
Meis1:	NNNTGTCAN
hbx5-1:	TTGATTGR
ara:	NNAWAACA
CG2808:	TAATSNAATTA
btn:	NNTMATTANN
CAGL0H02959g:	NNNYGTCANN
CAD25284:	TTAATTAN
HMRA2:	WTTACAYG
ATHB-22:	NNNWAWATTATNN
ATHB-21:	NNAATWATTGNTNN
ATHB-20:	NNAATTATTRN
MEIS3:	TGACANNTGTCA
MEIS2:	TGACAGCTGTCA
MEIS1:	NTGTCAN
tup:	CMATTAWS
ceh-58:	NNYAATTANN
Awh:	NTAATTAN
ceh-54:	NNYAATTAN
Dobox5_CONSTRUCT:	NNRGATTAN
ceh-57:	NNNNNTWAN
ceh-51:	NNNATNRNN
ceh-53:	NRGATTAN
PHO2:	NNNNNATNNN
LBX2:	CTCRTTAA
LBX1:	CTAATTAN
226_TTT_KMISA:	NNNATTANNN
Q5EVH4_OIKDI:	NCTGTCAN
Q1WMN0_COPDI:	NNGATTGNN
PKNOX1:	TGACASSTGTCA
PKNOX2:	TGACANNTGTCA
Hnf1b:	NNNGTNNN
ANHX:	TTGACAWG
253_CGT_VANSR:	NNTGTTANN
NEMVEDRAFT_v1g81436:	NNNNTNNNNN
Hnf1a:	NNNGTTAN
220_CTG_LTYQK:	NCTRGTTANN
ENSTNIG00000017092:	NTGATTAN
H2.0:	TNATWAA
NEMVEDRAFT_v1g80394:	NNNATNNNN
unpg:	NNCAATTANN
NEMVEDRAFT_v1g164989:	CTAATTAR

308_GCG_RLDRF:	NNTCTTAANN
216_TGC_NRVMM:	NGCATTARNN
250_GAT_AGKTF:	NNTCTTARNN
310_GTC_YRRGA:	NTACTTARNN
ANIA_01217:	NNTATTNNNN
Noto:	NNNNATNNNN
MEOX1:	NSTAATTANN
MEOX2:	NNTAATTANN
Nkx1-1:	NNNNATTANN
pdm3:	CTAATTAN
UM04928:	NNNATNNNNN
Hmbox1:	NNNGTNNN
Alx3:	NNNATTA
CG11617:	WTTTWACA
ZHX1:	
HOXA11:	NTTTTACGACN
HOXA10:	NTTTTACGACN
pb:	GTMATTAN
Alx4:	NTAATYNAATTAN
Barx1:	NNNNATTANN
ATHB-4:	NNMTGCATRNN
ATHB-5:	NNAATTATTGN
ATHB-6:	NATNATTNN
ATHB-7:	NNATGATTGN
ATHB-9:	NTAATCATTAYNWTN
Rhox11:	NNNTGTWNNN
ventx3.2:	TAATTAAT
208_CTC_HFNRK:	NCKASTTAAN
phx1:	NNTAATTAANN
CBG23031:	NNNNATWAAN
CBG08197:	NNNGTNNN
Cdx4:	TGATTTATNGNN
ATHB-X:	NCAATYATTNN
51_CAG_MSHWR:	NCTGTTAN
Prrx2:	NYAATTAN
si_dkey-43p13.5:	NNNNWWNNNN
Lbx2:	NNNNTTNN
CG9876:	NNYRATTANS
NEMVEDRAFT_v1g8907:	NNNYMATTAN
ind:	TAATTARNR
7_TTA_RVLRA:	TAATTARNN
237_TAG_YAVNA:	NMATTARNNN
C15:	YMWTTAAN

hbx7:	NNNNGCATNTNNN
UNCX:	NNAATTNN
TGIF2LY:	TGACANNTGTCA
TGIF2LX:	TGACAGNTGTCA
CBG00023:	NNNNNATWAN
Prrx1:	NNNAATTA
236_TAG_KSTQM:	NCCATTANNN
CG34031:	NNNNNNRN
mixl1.S:	NNTAATTAANN
NEMVEDRAFT_v1g205636:	NTAATTAN
CBG07641:	NNTAATTANN
NEMVEDRAFT_v1g197288:	NNAAGTRNNN
dharma:	GGATNNN
gsc:	NGGATTAN
Q68SS9_PLEDJ:	NGATTGNN
Dlx5:	NNNATTW
Dlx1:	NYAATTAN
Dlx2:	NYAATTAN
Dlx3:	NNNNATTAN
Hmx1:	NNNCRNTTNN
260_ATA_KAYNA:	NTNGTTARNN
CDX1:	NTTTTATGGCN
ISL1:	SCACTTAN
ISL2:	NCACTTAN
CDX2:	NNTTAYRAYN
SPU_026099:	NTAATTAA
GSC:	NGGATTAN
ARGFX:	NCTAATTARN
ENSTNIG0000004116:	CTAATTAA
NKX2-1:	NTKGAGTGNN
Phyra73700:	NNNNNTCAN
prd-b:	NTRATTRNN
268_AAT_KLQAF:	NTWCTTAANN
227_TTT_YRIAA:	NAATTANNNN
ANIA_00885:	NNTKACANNN
ventx1.1.L:	NNNNNNNNNN
En2:	NSTAATTANN
CBG00029:	TAATTAAT
FGRRES_17152:	ATGACATG
FGRRES_17150:	NWTGACAWNN
210_CCG_RSNQK:	NTGGTTAANN
YOX1:	YNATWWN
Hoxd10:	NNNNNNN

Hoxd11:	NNNNNNNN
MTAL2_PICAN:	NNNTGTNNN
NKX6-2:	NYAATTAN
NKX6-3:	NTCATTAWN
NKX6-1:	NATYAWWWNNNMATTWNTN
Hoxc9:	NTTAATTACN
Hoxc8:	NNNNNNNNN
BARHL2:	ANCGTTTAN
BARHL1:	NCGTTTAN
Hoxc6:	RTAATTAA
Shox2:	NYAATTAN
vab-7:	MTAATTAA
ENSTNIG00000006040:	NNNYNATTANNNN
HOXC9:	NTTTATKGCN
lim-4:	NNTAATTAR
Evx1:	NNNNATTAN
Evx2:	NNATTANN
Isx:	NNATTNNN
NEMVEDRAFT_v1g136480:	NNNNNNNNNN
258_ATT_RTVQQ:	NTMATTANNN
Lhx1:	NNNNNATTA
Lhx2:	NYMATTAN
Lhx3:	NNNTAATNN
Lhx4:	NTAATTAN
Lhx5:	NNNYAATTA
Lhx6:	NTRATTRN
Lhx8:	NTRATTANNNNTRATTAN
Lhx9:	NYNATTAN
GRMZM2G038252:	NCAATCAN
Pknox1:	NGACANNN
Pknox2:	TGACACCTGTCA
DLX4:	NCAATTAN
DLX5:	NCAATTAN
DLX6:	NCAATTAN
DLX1:	NYAATTAN
DLX2:	NYAATTAN
DLX3:	NYAATTAN
44_CCT_RGDSK:	CGGGTTAN
241_GTT_GLRAF:	NTACTTANNN
ATML1:	NNNANTNANN
ceh-34:	NNNRKATNNN
LMX1A:	TTAATTAN
LMX1B:	NNNTAATTAN

MATALPHA2:	NNNGNNNN
Gsc:	TWANNGGATTA
achi:	NTGTCA
252_CTC_LRYSK:	NTAGTTANNN
HOXB3:	NNYMATTANN
RLT1:	NANGAANN
HOXD12:	NTTTACGAYN
HOXD10:	NTTTTATKRC
HOXD11:	NTWANNNTTTACGAYN
CUP9:	NWTGTGTCAN
UM00578:	NNGATNNNN
FGRRES_16926_M:	NNNACANN
Scr:	NYMATTAN
TVAG_493070:	NNCACATCANN
Q4RRY4_TETNG:	NTRATTRNN
Q0ZPQ4_NEMVE:	CTTCTTAA
267_ACA_RVSHT:	NTGTTTAANN
Q00352_COPCI:	TGATTGGTT
TOS8:	NNNTGACGTMW
56_ATT_HRVQA:	NYAATTARNN
NOBOX:	NNNNATNRNN
GBX2:	NYAATTAN
GBX1:	NSYAATTANN
076842_CUPSA:	NTAATTAA
NANOG:	NCNRTYAN
kal-1:	NNNTNNNN
AAEL012091:	NNGATNNNN
36_GAC_ATRRF:	NCGTCTTAN
scro:	NCACTYNNN
HHEX:	WTNAATTA
PK25011.1:	NNNNNNAWNN
Q0ZPQ8_NEMVE:	NNNYGTCAN
NCU09556:	TATATTAA
MIXL1:	NNYAATTANN
HDX:	NNNNNN
60_ATA_KTVQV:	NTMATTARNN
CG4328:	NWTWATTR
CNG03450:	NNWATTAAN
232_TCG_IKNQM:	NYCATTARNN
dve:	NNTAATTAGN
Q0N4M8_NEMVE:	GTAATTAN
NKX3-2:	NCCACTTANN
NKX3-1:	NCCACTTANN

Irx5:	NNTGTNNNN
Irx4:	NTNTNNNN
CBG20882:	NYNATNNNN
Irx6:	NTNTNNN
Irx3:	YWACATGAMAAA
Irx2:	NNNTGTNNN
HMX1:	NCAMTTANN
HMX3:	NNCAMTTANNN
HMX2:	NCACTTRNC
NEMVEDRAFT_v1g81309:	NNNNATTAN
Cdx1:	NNYNATWNN
inv:	TAATTARW
Cdx2:	NNYNATWWN
hbx10:	NWWATTRN
ENSCING00000007395:	NWNNNNNN
RHOXF1:	GGATNATCN
ap:	TAATTARN
Q70HR3_PLEPI:	NNNTACTTAN
Sebox:	NNTTAATTAN
263_AGA_VRFAA:	NNTACTTANN
235_TAT_RAVSV:	NNCATTARNN
17_TAT_TRVSA:	NNYATTARNN
249_GCA_QLKQS:	NNNNAAGTAN
XP_003689450.1:	NNNANMCNNN
Lmx1a:	NNNATNRN
Lmx1b:	NNATNAN
217_GGG_KSKEG:	NCCCTTARNN
ANL2:	NCATTAATTNN
304_CTG_TTNQK:	CCRGTTANNN
AGAP006642:	GGATTANN
slou:	NNYAATTANN
Meox2:	NTAATTAN
RAX2:	NYAATTAN
SHOX:	NYAATTAN
76_AAA_RAQWF:	CCTYTTAANN
NEMVEDRAFT_v1g105595:	NNAATTAN
CG11294:	TAATTNNATTA
Nkx1-2:	NNNATTANN
Barh12:	NNYNNTTAN
Barhl1:	NNCRTTTANN
bcd:	GGATTAN
64_AGA_AFRAH:	NNTMCTTAAN
242_GTC_LQRGA:	NTACTTANNN

205_GAA_TQRQW:	NTACTTANNN
Q8I9J5_9BILA:	NRTWATTANN
NOTO:	NYAATTAN
KIJAO D10043a:	NNNNNNNNNN

Familial Profile:
 (click for matrix)

Motif Tree

Tree (drawn by Phylip) Click here for Newick-format tree (viewable with MI)	EGA) Input Motif	Best match in JASPAR
	54 CAA LMYQR	MA0217.1_caup (E val: 8.9496e-06)
	42 CGA TFYAA	MA0186.1_Dfd (E val: 2.4354e-03)
		M. 0.106.1 P.01
	<u>lbe</u>	MA0186.1_Dfd (E val: 4.2043e-04)
	LBX2	MA0186.1_Dfd (E val: 5.8346e-08)
	39 CTA IFNAK	MA0231.1_lbe

	(E val: 8.3745e-06)
HMBOX1	MA0231.1_lbe (E val: 4.3822e-07)
38 CTA LHYAK	MA0231.1_lbe (E val: 7.0847e-07)
220 CTG LTYQK	MA0231.1_lbe (E val: 4.1962e-05)
260 ATA KAYNA	MA0231.1_lbe (E val: 5.8661e-04)
223 CTC RTFGK	MA0231.1_lbe (E val: 1.4477e-06)
252 CTC LRYSK	MA0231.1_lbe (E val: 1.8927e-06)
303 CTC VMNRK	MA0099.2_AP1 (E val: 6.0862e-05)
53 CAC ERVSR	MA0173.1_CG11617 (E val: 2.3925e-06)

46 CCC RLDSK	MA0421.1_YDR026C (E val: 5.5305e-06)
44 CCT RGDSK	MA0452.1_Kr (E val: 4.6188e-05)
218 CTG KQNQK	MA0231.1_lbe (E val: 1.0395e-05)
43 CCT MTNGK	MA0231.1_lbe (E val: 9.6156e-04)
221 CTG RLYQK	MA0231.1_lbe (E val: 4.9698e-05)
210 CCG RSNQK	MA0231.1_lbe (E val: 2.4988e-04)
48 CCA EHNAK	MA0231.1_lbe (E val: 1.4619e-05)
256 CCA RLYQK	MA0231.1_lbe (E val: 8.6188e-06)

<u>BSX</u>	MA0217.1_caup (E val: 4.8362e-03)
PRRX2	MA0186.1_Dfd (E val: 2.6340e-03)
40 CGG STRER	MA0248.1_tup (E val: 8.8280e-04)
255 CCT RADGK	MA0217.1_caup (E val: 5.1581e-03)
<u>ceh-57</u>	MA0217.1_caup (E val: 6.2734e-03)
<u>Hnf1b</u>	MA0217.1_caup (E val: 4.2044e-03)
<u>Hnfla</u>	MA0217.1_caup (E val: 2.6865e-03)
<u>Hmbox1</u>	MA0231.1_lbe (E val: 9.7179e-02)

271 AAC KLQRF	MA0127.1_PEND (E val: 4.1253e-03)
203 GTC VQKRF	MA0127.1_PEND (E val: 3.2871e-04)
36 GAC ATRRF	MA0127.1_PEND (E val: 5.6761e-04)
225 AAC SLQRF	MA0393.1_STE12 (E val: 2.3663e-03)
34 GAT RTMRY	MA0211.1_bap (E val: 1.1833e-03)
272 AAC VAQRC	MA0393.1_STE12 (E val: 3.5152e-04)
<u>ceh-90</u>	MA0393.1_STE12 (E val: 1.3427e-03)
250 GAT AGKTF	MA0127.1_PEND (E val: 1.6496e-02)

26 GGT ALKNM	MA0211.1_bap (E val: 8.8493e-04)
217 GGG KSKEG	MA0211.1_bap (E val: 4.4540e-05)
247 GCG RTDRS	MA0211.1_bap (E val: 1.2248e-03)
37 GAA RFQKF	MA0127.1_PEND (E val: 4.5636e-06)
Q0ZPQ4 NEMVE	MA0127.1_PEND (E val: 1.6660e-08)
268 AAT KLQAF	MA0211.1_bap (E val: 1.1050e-05)
75 AAC SISRF	MA0211.1_bap (E val: 8.0890e-04)
308 GCG RLDRF	MA0211.1_bap (E val: 8.1581e-04)

270 AAG RAQWF	MA0053.1_MNB1A (E val: 2.4849e-02)
76 AAA RAQWF	MA0211.1_bap (E val: 8.9918e-04)
243 GGT ATKSM	MA0124.1_NKX3-1 (E val: 6.9614e-06)
64 AGA AFRAH	MA0211.1_bap (E val: 5.1182e-06)
73 AAT KLTAF	MA0211.1_bap (E val: 8.0708e-07)
208 CTC HFNRK	MA0211.1_bap (E val: 1.6084e-05)
310 GTC YRRGA	MA0124.1_NKX3-1 (E val: 1.3755e-06)
242 GTC LQRGA	MA0124.1_NKX3-1 (E val: 1.3807e-06)

241 GTT GLRAF	MA0124.1_NKX3-1 (E val: 1.5270e-06)
205 GAA TOROW	MA0124.1_NKX3-1 (E val: 1.8120e-06)
	MA0124.1_NKX3-1
263 AGA VRFAA	(E val: 2.0316e-06)
Q70HR3 PLEPI	MA0124.1_NKX3-1 (E val: 1.7532e-06)
249 GCA QLKQS	MA0124.1_NKX3-1 (E val: 7.5248e-04)
<u>ceh-22</u>	MA0211.1_bap (E val: 4.4240e-08)
<u>vnd</u>	MA0253.1_vnd (E val: 1.1102e-16)
24 GTG HLIQY	MA0211.1_bap (E val: 1.9677e-06)

<u>bap</u>	MA0211.1_bap (E val: 2.1113e-06)
ISL1	MA0211.1_bap (E val: 7.7296e-07)
ISL2	MA0211.1_bap (E val: 6.2608e-07)
HMX1	MA0063.1_Nkx2-5 (E val: 2.2710e-06)
HMX2	MA0211.1_bap (E val: 1.1516e-08)
<u>NKX3-2</u>	MA0211.1_bap (E val: 2.0976e-06)
<u>NKX3-1</u>	MA0211.1_bap (E val: 2.0256e-06)
<u>Nkx2-6</u>	MA0211.1_bap (E val: 7.4956e-04)

Nkx3-1	MA0211.1_bap (E val: 8.3180e-04)
<u>Nkx2-9</u>	MA0211.1_bap (E val: 1.9645e-03)
<u>Nkx2-1</u>	MA0211.1_bap (E val: 9.7504e-04)
<u>Nkx2-2</u>	MA0211.1_bap (E val: 2.2528e-03)
<u>Nkx3-2</u>	MA0211.1_bap (E val: 6.6546e-04)
<u>scro</u>	MA0211.1_bap (E val: 1.4217e-03)
<u>Nkx2-4</u>	MA0211.1_bap (E val: 2.2018e-03)
NEMVEDRAFT v1g197288	MA0211.1_bap (E val: 2.4841e-03)

<u>ceh-24</u>	MA0211.1_bap (E val: 5.8321e-02)
ENSCING00000007395	MA0211.1_bap (E val: 3.0174e-02)
<u>Hoxb9</u>	MA0165.1_Abd-B (E val: 1.0286e-03)
<u>CBG23031</u>	MA0174.1_CG42234 (E val: 8.4823e-04)
Hoxc11	MA0165.1_Abd-B (E val: 2.3036e-03)
<u>Hoxa9</u>	MA0307.1_GLN3 (E val: 6.1601e-03)
Hoxd10	MA0307.1_GLN3 (E val: 4.1907e-03)
<u>Hoxd11</u>	MA0307.1_GLN3 (E val: 1.4126e-02)

Hoxa10	MA0307.1_GLN3 (E val: 8.7847e-03)
Cdx2	MA0307.1_GLN3 (E val: 8.2090e-03)
Cdx1	MA0307.1_GLN3 (E val: 7.8786e-03)
<u>Hoxc10</u>	MA0165.1_Abd-B (E val: 2.4823e-08)
HOXB9	MA0165.1_Abd-B (E val: 2.2251e-06)
Abd-B	MA0165.1_Abd-B (E val: 1.4554e-06)
HOXA10	MA0165.1_Abd-B (E val: 7.2371e-06)
HOXA11	MA0165.1_Abd-B (E val: 2.0449e-05)

Hoxa11	MA0165.1_Abd-B (E val: 6.8791e-06)
HOXD11	MA0153.1_HNF1B (E val: 2.3770e-05)
HOXC11	MA0165.1_Abd-B (E val: 6.4582e-06)
HOXD12	MA0165.1_Abd-B (E val: 1.5126e-05)
HOXA9	MA0165.1_Abd-B (E val: 4.9453e-07)
CDX2	MA0165.1_Abd-B (E val: 1.8242e-04)
HOXC10	MA0216.1_cad (E val: 2.9939e-09)
HOXC9	MA0216.1_cad (E val: 1.5245e-08)

HOXC12	MA0216.1_cad (E val: 4.7854e-09)
<u>cad</u>	MA0216.1_cad (E val: 2.2162e-08)
HOXD9	MA0216.1_cad (E val: 6.3975e-10)
HOXD10	MA0216.1_cad (E val: 5.7397e-10)
CDX1	MA0216.1_cad (E val: 1.0263e-07)
Hoxd9	MA0165.1_Abd-B (E val: 4.1215e-07)
Cdx4	MA0216.1_cad (E val: 4.8203e-07)
Hoxc12	MA0151.1_ARID3A (E val: 3.9486e-02)
	20

Hoxd12 CONSTRUCT	MA0151.1_ARID3A (E val: 4.2453e-02)
264 ACT KVYHV	MA0297.1_FKH2 (E val: 6.6792e-04)
267 ACA RVSHT	MA0297.1_FKH2 (E val: 1.1765e-06)
<u>B-H2</u>	MA0168.1_B-H1 (E val: 3.6424e-04)
<u>B-H1</u>	MA0168.1_B-H1 (E val: 3.8028e-04)
BARHL1	MA0168.1_B-H1 (E val: 5.0670e-05)
Barhl1	MA0168.1_B-H1 (E val: 2.9661e-04)
<u>HAT3.1</u>	MA0218.1_ct (E val: 8.9984e-04)

MTR 2g038000	MA0132.1_Pdx1 (E val: 2.8654e-02)
59 ATC TRMAF	MA0434.1_YPR013C (E val: 4.2834e-03)
Q9C1N5 COPSC	MA0037.1_GATA3 (E val: 5.0444e-03)
Q1WMN0 COPDI	MA0037.1_GATA3 (E val: 6.7599e-03)
<u>UM00578</u>	MA0190.1_Gsc (E val: 1.1501e-02)
AAEL012091	MA0212.1_bcd (E val: 1.3723e-02)
<u>Hdx</u>	MA0212.1_bcd (E val: 2.0846e-02)
<u>dharma</u>	MA0234.1_oc (E val: 4.8065e-04)

NEMVEDRAFT v1g113057	MA0212.1_bcd (E val: 2.6743e-08)
15 TCC RMIKS	MA0212.1_bcd (E val: 2.6557e-08)
<u>DPRX</u>	MA0190.1_Gsc (E val: 2.8082e-08)
RHOXF1	MA0234.1_oc (E val: 4.4835e-08)
<u>Q8VHG7 MOUSE</u>	MA0201.1_Ptx1 (E val: 2.4983e-10)
<u>GSC</u>	MA0234.1_oc (E val: 3.9560e-09)
<u>ceh-53</u>	MA0190.1_Gsc (E val: 4.6874e-09)
gsc	MA0190.1_Gsc (E val: 5.2033e-09)

AGAP006642	MA0190.1_Gsc
AGAF000042	(E val: 4.0356e-09)
<u>bcd</u>	MA0190.1_Gsc (E val: 9.0637e-10)
DMBX1	MA0234.1_oc (E val: 8.8704e-09)
<u>Obox6</u>	MA0190.1_Gsc (E val: 2.0177e-08)
Dobox5 CONSTRUCT	MA0190.1_Gsc (E val: 2.6002e-08)
Obox1	MA0190.1_Gsc (E val: 3.5326e-08)
13 TCT ATVKA	MA0234.1_oc (E val: 3.1024e-08)
<u>Gsc</u>	MA0234.1_oc (E val: 6.2323e-08)

Dmbx1	MA0234.1_oc (E val: 4.4797e-05)
Q1WMN9 COPDI	MA0212.1_bcd (E val: 1.7040e-02)
<u>SNOG 11642</u>	MA0235.1_onecut (E val: 5.9581e-06)
ENSTNIG00000017092	MA0235.1_onecut (E val: 1.9058e-05)
<u>HNF1B</u>	MA0153.1_HNF1B (E val: 5.5378e-13)
<u>HNF1A</u>	MA0153.1_HNF1B (E val: 6.3727e-14)
<u>ATHB-15</u>	MA0223.1_exex (E val: 5.4407e-09)
<u>ATHB-9</u>	MA0186.1_Dfd (E val: 1.5656e-05)

Duxbl1	MA0235.1_onecut (E val: 4.4831e-04)
<u>HDX</u>	MA0235.1_onecut (E val: 1.7708e-04)
Cphx1	MA0235.1_onecut (E val: 1.1410e-03)
Lhx6 CONSTRUCT	MA0075.1_Prrx2 (E val: 2.2088e-04)
<u>WOX13</u>	MA0070.1_PBX1 (E val: 5.5638e-06)
Q00354 COPCI	MA0316.1_HAP5 (E val: 3.4094e-09)
Q00352 COPCI	MA0060.1_NFYA (E val: 4.3583e-09)
Q68SS9 PLEDJ	MA0315.1_HAP4 (E val: 9.4207e-07)

HOX6	MA0235.1_onecut (E val: 1.7458e-04)
HAT1	MA0235.1_onecut (E val: 1.4678e-04)
hbx5-2	MA0235.1_onecut (E val: 9.7419e-08)
hbx5-1	MA0070.1_PBX1 (E val: 4.1702e-10)
<u>ATHB-7</u>	MA0070.1_PBX1 (E val: 1.0559e-04)
HAT3	MA0235.1_onecut (E val: 2.3651e-05)
GRMZM2G038252	MA0426.1_YHP1 (E val: 9.8215e-06)
<u>WUS</u>	MA0070.1_PBX1 (E val: 1.4198e-05)

<u>HAT22</u>	MA0008.1_HAT5 (E val: 2.6746e-05)
HAT2	MA0008.1_HAT5 (E val: 1.8572e-05)
<u>АТНВ-Х</u>	MA0110.1_ATHB-5 (E val: 1.8404e-07)
SNOG 08903	MA0235.1_onecut (E val: 1.5205e-10)
NEMVEDRAFT v1g101664	MA0070.1_PBX1 (E val: 5.5008e-06)
<u>lin-39</u>	MA0070.1_PBX1 (E val: 6.2232e-08)
estExt gwp gw1.C 702	MA0235.1_onecut (E val: 4.9964e-03)
BARX1	MA0151.1_ARID3A (E val: 1.2246e-06)

NKX6-1	MA0214.1_bsh (E val: 8.3352e-07)
Q0N4H2 NEMVE	MA0188.1_Dr (E val: 5.7239e-10)
NEMVEDRAFT v1g114268	MA0188.1_Dr (E val: 6.9261e-05)
<u>NK7.1</u>	MA0054.1_myb.Ph3 (E val: 5.3691e-06)
BARHL2	MA0054.1_myb.Ph3 (E val: 6.5933e-07)
304 CTG TTNQK	MA0188.1_Dr (E val: 1.8802e-04)
PK19166.1	MA0372.1_RPH1 (E val: 9.3146e-09)
Lhx8	MA0198.1_OdsH (E val: 9.5457e-08)

TLX3	MA0188.1_Dr (E val: 1.1926e-03)
Q0N4H7 NEMVE	MA0094.1_Ubx (E val: 2.9184e-02)
ventx1.1.L	MA0075.1_Prrx2 (E val: 1.2557e-02)
LHX2	MA0075.1_Prrx2 (E val: 8.0794e-03)
NEMVEDRAFT v1g129868	MA0075.1_Prrx2 (E val: 5.9220e-03)
<u>Q0N4H9 NEMVE</u>	MA0075.1_Prrx2 (E val: 2.6414e-02)
Hoxa3	MA0075.1_Prrx2 (E val: 4.2577e-03)
Barx1	MA0094.1_Ubx (E val: 4.4172e-03)

Mnx1	MA0075.1_Prrx2 (E val: 4.4611e-03)
Nkx1-1	MA0075.1_Prrx2 (E val: 4.6337e-03)
<u>Hlx</u>	MA0075.1_Prrx2 (E val: 9.7967e-03)
Lmx1b	MA0075.1_Prrx2 (E val: 2.9556e-03)
Lmx1a	MA0075.1_Prrx2 (E val: 5.3755e-03)
<u>CaO19.4000</u>	MA0075.1_Prrx2 (E val: 8.5189e-03)
<u>kal-1</u>	MA0075.1_Prrx2 (E val: 6.1057e-03)
<u>PHO2</u>	MA0075.1_Prrx2 (E val: 1.2104e-02)

<u>ceh-51</u>	MA0075.1_Prrx2 (E val: 4.0765e-02)
VII 40 40 50	MA0075.1_Prrx2
<u>UM04928</u>	(E val: 1.3088e-02)
<u>otp</u>	MA0426.1_YHP1 (E val: 2.8789e-08)
<u>OdsH</u>	MA0426.1_YHP1 (E val: 2.3854e-08)
<u>DII</u>	MA0426.1_YHP1 (E val: 2.2713e-08)
Vsx2	MA0426.1_YHP1 (E val: 2.3819e-08)
DLX5	MA0426.1_YHP1 (E val: 2.1206e-08)
DLX4	MA0426.1_YHP1 (E val: 2.6660e-08)

DLX6	MA0426.1_YHP1 (E val: 2.4257e-08)
DLX1	MA0426.1_YHP1 (E val: 3.6604e-08)
GBX2	MA0426.1_YHP1 (E val: 4.0831e-08)
<u>lms</u>	MA0426.1_YHP1 (E val: 3.2934e-08)
<u>Rx</u>	MA0426.1_YHP1 (E val: 2.5179e-08)
<u>Vsx1</u>	MA0426.1_YHP1 (E val: 1.3173e-08)
LHX1	MA0426.1_YHP1 (E val: 3.7149e-08)
<u>Lim1</u>	MA0426.1_YHP1 (E val: 4.6222e-08)
	41

ESX1	MA0426.1_YHP1 (E val: 9.7762e-08)
SHOX2	MA0232.1_lbl (E val: 1.2365e-07)
Shox2	MA0232.1_lbl (E val: 9.8309e-08)
TLX2	MA0232.1_lbl (E val: 8.2750e-08)
DLX2	MA0232.1_lbl (E val: 1.1128e-07)
RAX2	MA0232.1_lbl (E val: 1.1674e-07)
PRRX1	MA0232.1_lbl (E val: 6.1316e-08)
DLX3	MA0232.1_lbl (E val: 1.1929e-07)

<u>en</u>	MA0426.1_YHP1 (E val: 6.3159e-08)
<u>Dlx1</u>	MA0426.1_YHP1 (E val: 7.3537e-08)
<u>Dlx2</u>	MA0426.1_YHP1 (E val: 8.3123e-08)
SNAPOd2T00006620001	MA0426.1_YHP1 (E val: 5.3836e-08)
<u>ceh-54</u>	MA0426.1_YHP1 (E val: 3.0546e-07)
Gbx2	MA0426.1_YHP1 (E val: 2.9462e-07)
Gbx1	MA0426.1_YHP1 (E val: 3.9716e-07)
<u>AAZ08039</u>	MA0426.1_YHP1 (E val: 2.2824e-07)

<u>CG11085</u>	MA0426.1_YHP1 (E val: 2.0173e-08)
<u>Hmx</u>	MA0426.1_YHP1 (E val: 4.3245e-08)
GBX1	MA0232.1_lbl (E val: 4.9552e-07)
<u>CG9876</u>	MA0426.1_YHP1 (E val: 4.0548e-07)
unpg	MA0426.1_YHP1 (E val: 2.0776e-07)
18 TAG RLTQA	MA0426.1_YHP1 (E val: 1.1960e-07)
<u>ceh-58</u>	MA0232.1_lbl (E val: 4.0935e-07)
Barhl2	MA0426.1_YHP1 (E val: 5.7920e-07)

<u>ceh-19</u>	MA0426.1_YHP1 (E val: 4.4632e-07)
<u>YHP1</u>	MA0232.1_lbl (E val: 5.2801e-06)
ATEG 04171	MA0232.1_lbl (E val: 4.6903e-06)
NCU03266	MA0196.1_NK7.1 (E val: 1.9654e-08)
HMX3	MA0426.1_YHP1 (E val: 2.8398e-07)
ENSTNIG00000006040	MA0426.1_YHP1 (E val: 8.7845e-07)
<u>Rax</u>	MA0075.1_Prrx2 (E val: 3.8995e-06)
ALX4	MA0075.1_Prrx2 (E val: 1.8830e-06)

Alx3	MA0075.1_Prrx2 (E val: 8.5973e-07)
<u>Dlx5</u>	MA0075.1_Prrx2 (E val: 1.2097e-06)
Prrx1	MA0075.1_Prrx2 (E val: 1.7693e-06)
NEMVEDRAFT v1g105595	MA0075.1_Prrx2 (E val: 2.2012e-06)
<u>Lhx 1</u>	MA0075.1_Prrx2 (E val: 5.0294e-06)
LHX3	MA0194.1_Lim1 (E val: 1.8346e-09)
<u>Dbx1</u>	MA0194.1_Lim1 (E val: 4.3593e-11)
<u>Dbx</u>	MA0194.1_Lim1 (E val: 2.3550e-11)

ventx3.2	MA0194.1_Lim1 (E val: 1.7841e-11)
<u>CBG00029</u>	MA0194.1_Lim1 (E val: 1.6173e-11)
FGRRES 01100	MA0226.1_hbn (E val: 2.2507e-11)
Tlx2	MA0194.1_Lim1 (E val: 2.7621e-10)
<u>WOX11</u>	MA0240.1_repo (E val: 7.1158e-10)
<u>Q24782 9CNID</u>	MA0194.1_Lim1 (E val: 1.4038e-11)
<u>CG32105</u>	MA0236.1_otp (E val: 3.4164e-11)
<u>pal-1</u>	MA0448.1_H2.0 (E val: 2.2106e-10)

<u>hox12</u>	MA0174.1_CG42234 (E val: 1.3600e-10)
HXD12 HETFR	MA0206.1_abd-A (E val: 9.0750e-11)
<u>ftz</u>	MA0226.1_hbn (E val: 2.0192e-11)
<u>Hoxc6</u>	MA0194.1_Lim1 (E val: 1.9802e-11)
Hoxc9	MA0240.1_repo (E val: 7.4846e-10)
<u>H2.0</u>	MA0448.1_H2.0 (E val: 2.5989e-11)
Q0N4F9 NEMVE	MA0180.1_Vsx2 (E val: 1.1622e-12)
SPU 026099	MA0180.1_Vsx2 (E val: 8.9306e-13)

vab-7	MA0180.1_Vsx2 (E val: 1.7780e-12)
ENSTNIG00000004116	MA0180.1_Vsx2 (E val: 5.9242e-13)
Smp 158000	MA0180.1_Vsx2 (E val: 4.7229e-13)
NEMVEDRAFT v1g164989	MA0180.1_Vsx2 (E val: 7.4326e-12)
<u>ARGFX</u>	MA0180.1_Vsx2 (E val: 1.2971e-10)
<u>repo</u>	MA0240.1_repo (E val: 2.8598e-10)
ENSCING00000016045	MA0180.1_Vsx2 (E val: 5.3273e-10)
<u>CNK00090</u>	MA0240.1_repo (E val: 2.3502e-11)

CAD25284	MA0194.1_Lim1 (E val: 1.5897e-11)
<u>076842 CUPSA</u>	MA0194.1_Lim1 (E val: 1.6400e-11)
LMX1A	MA0172.1_CG11294 (E val: 1.7100e-11)
<u>HHEX</u>	MA0172.1_CG11294 (E val: 2.1773e-10)
<u>lim-4</u>	MA0181.1_Vsx1 (E val: 9.2564e-11)
<u>Sebox</u>	MA0194.1_Lim1 (E val: 2.5830e-10)
<u>Q24780 9CNID</u>	MA0194.1_Lim1 (E val: 7.3681e-10)
mix11.S	MA0194.1_Lim1 (E val: 6.0393e-10)

phx1	MA0194.1_Lim1 (E val: 1.0717e-09)
C4B866 NEMVE	MA0194.1_Lim1 (E val: 1.2649e-09)
<u>CNG03450</u>	MA0444.1_CG34031 (E val: 7.7102e-07)
<u>hbn</u>	MA0229.1_inv (E val: 1.1169e-09)
<u>CG5369</u>	MA0194.1_Lim1 (E val: 1.2872e-09)
unc-4	MA0178.1_CG32105 (E val: 1.8305e-08)
<u>bsh</u>	MA0229.1_inv (E val: 3.9607e-11)
<u>Uncx</u>	MA0172.1_CG11294 (E val: 3.7957e-09)

Alx4	MA0194.1_Lim1 (E val: 6.3149e-08)
<u>CG2808</u>	MA0188.1_Dr (E val: 1.4849e-08)
<u>CG11294</u>	MA0229.1_inv (E val: 6.6941e-10)
LHX4	MA0232.1_lbl (E val: 1.2360e-07)
<u>HGTX</u>	MA0232.1_lbl (E val: 6.2738e-09)
HOXB2	MA0232.1_lbl (E val: 1.5599e-08)
<u>NOTO</u>	MA0232.1_lbl (E val: 1.6063e-08)
<u>NKX6-2</u>	MA0232.1_lbl (E val: 1.8473e-08)

HOXA2	MA0232.1_lbl (E val: 8.6640e-09)
PDX1	MA0232.1_lbl (E val: 1.1612e-08)
<u>Ubx</u>	MA0232.1_lbl (E val: 1.5127e-08)
Lhx2	MA0232.1_lbl (E val: 9.1589e-09)
Lhx9	MA0232.1_lbl (E val: 1.1389e-08)
EMX1	MA0232.1_lbl (E val: 1.3018e-08)
<u>lab</u>	MA0232.1_lbl (E val: 1.0849e-08)
<u>CG18599</u>	MA0232.1_lbl (E val: 1.9400e-09)

Meox2	MA0232.1_lbl (E val: 7.1346e-09)
<u>ems</u>	MA0232.1_lbl (E val: 9.6821e-09)
EVX1	MA0232.1_lbl (E val: 1.2369e-08)
EVX2	MA0232.1_lbl (E val: 1.2336e-08)
<u>Lim3</u>	MA0232.1_lbl (E val: 2.1239e-08)
Lhx4	MA0232.1_lbl (E val: 2.0476e-08)
HOXD1	MA0232.1_lbl (E val: 2.0307e-08)
Q9GP48_9TURB	MA0232.1_lbl (E val: 3.8246e-08)

Q70LF3 ARTSF	MA0232.1_lbl (E val: 2.7533e-08)
NEMVEDRAFT v1g205636	MA0232.1_lbl (E val: 3.7288e-08)
MNX1	MA0232.1_lbl (E val: 2.6559e-08)
	MA0232.1_lbl
<u>DRGX</u>	(E val: 3.1653e-08)
EN2	MA0232.1_lbl (E val: 3.0403e-08)
Prrx2	MA0232.1_lbl (E val: 2.7448e-08)
EN1	MA0232.1_lbl (E val: 2.6907e-08)
ALX3	MA0232.1_lbl (E val: 2.1881e-08)
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SHOX	MA0232.1_lbl (E val: 2.2701e-08)
<u>Awh</u>	MA0232.1_lbl (E val: 1.6501e-08)
zfhx4	MA0232.1_lbl (E val: 5.4071e-08)
<u>Lhx5</u>	MA0232.1_lbl (E val: 7.9458e-08)
<u>uncx</u>	MA0232.1_lbl (E val: 9.0879e-08)
Lhx3	MA0232.1_lbl (E val: 6.3907e-08)
Hoxa1	MA0232.1_lbl (E val: 3.8787e-08)
LHX6	MA0232.1_lbl (E val: 1.0164e-07)

Lhx6	MA0232.1_lbl (E val: 1.2291e-06)
<u>prd-b</u>	MA0232.1_lbl (E val: 7.3149e-07)
<u>Q4RRY4 TETNG</u>	MA0232.1_lbl (E val: 2.1430e-07)
7 TTA RVLRA	MA0232.1_lbl (E val: 5.5511e-08)
HOXA1	MA0232.1_lbl (E val: 1.4927e-07)
<u>ceh-23</u>	MA0232.1_lbl (E val: 1.3081e-07)
56 ATT HRVQA	MA0232.1_lbl (E val: 1.9416e-07)
MIXL1	MA0232.1_lbl (E val: 2.4876e-07)
	57

slou	MA0232.1_lbl (E val: 1.4101e-07)
<u>En2</u>	MA0232.1_lbl (E val: 6.0426e-08)
Hoxd3	MA0232.1_lbl (E val: 1.0207e-07)
GSX1	MA0232.1_lbl (E val: 6.6879e-08)
HOXB5	MA0232.1_lbl (E val: 5.6550e-08)
<u>Scr</u>	MA0232.1_lbl (E val: 4.3130e-08)
HOXB8	MA0232.1_lbl (E val: 1.3096e-07)
HOXD8	MA0232.1_lbl (E val: 2.2035e-07)

HOXB6	MA0232.1_lbl (E val: 3.1744e-08)
HOXA6	MA0223.1_exex (E val: 8.5000e-08)
HOXB1	MA0223.1_exex (E val: 2.3787e-10)
HOXA5	MA0223.1_exex (E val: 3.9288e-10)
Q0N4M8 NEMVE	MA0223.1_exex (E val: 2.3856e-09)
GSX2	MA0232.1_lbl (E val: 8.5976e-09)
abd-A	MA0223.1_exex (E val: 1.9332e-08)
<u>pb</u>	MA0232.1_lbl (E val: 6.8619e-08)

HOXB3	MA0232.1_lbl (E val: 5.6179e-08)
NEMVEDRAFT v1g8907	MA0232.1_lbl (E val: 1.4668e-07)
Hoxa2	MA0232.1_lbl (E val: 3.9527e-08)
MEOX2	MA0232.1_lbl (E val: 7.0922e-08)
<u>eve</u>	MA0241.1_ro (E val: 7.8255e-10)
EMX2	MA0241.1_ro (E val: 2.5200e-11)
<u>ro</u>	MA0241.1_ro (E val: 1.2763e-11)
<u>ap</u>	MA0209.1_ap (E val: 1.2763e-11)

RAX	MA0202.1_Rx (E val: 5.1507e-11)
inv	MA0229.1_inv (E val: 6.5503e-15)
<u>ind</u>	MA0228.1_ind (E val: 7.6496e-11)
<u>ISX</u>	MA0241.1_ro (E val: 8.0527e-11)
LBX1	MA0241.1_ro (E val: 4.2517e-10)
pdm3	MA0241.1_ro (E val: 1.8173e-10)
<u>lbl</u>	MA0241.1_ro (E val: 1.9839e-09)
<u>dve</u>	MA0241.1_ro (E val: 9.7944e-10)
	· '

Q9BJW6_9CNID	MA0241.1_ro (E val: 8.0265e-10)
MEOX1	MA0223.1_exex (E val: 5.9674e-09)
<u>exex</u>	MA0198.1_OdsH (E val: 1.1913e-08)
60 ATA KTVQV	MA0221.1_eve (E val: 4.0308e-10)
LHX9	MA0232.1_lbl (E val: 2.4650e-07)
POU6F1	MA0232.1_lbl (E val: 1.9095e-07)
Q86SD7_PODCA	MA0232.1_lbl (E val: 2.5359e-07)
<u>CBG07641</u>	MA0232.1_lbl (E val: 1.8462e-07)

<u>ceh-62</u>	MA0232.1_lbl (E val: 2.4811e-07)
<u>btn</u>	MA0232.1_lbl (E val: 7.5444e-08)
258 ATT RTVQQ	MA0232.1_lb1 (E val: 8.0329e-08)
LMX1B	MA0232.1_lbl (E val: 2.8185e-07)
SNAPOd2T00006145001	MA0232.1_lbl (E val: 2.6419e-06)
227 TTT YRIAA	MA0075.1_Prrx2 (E val: 6.0657e-06)
<u>CAD26261</u>	MA0178.1_CG32105 (E val: 2.6988e-08)
Y749 MIMIV	MA0346.1_NHP6B (E val: 3.8384e-06)

NCU09556	MA0379.1_SIG1 (E val: 2.9552e-06)
<u>ATHB-22</u>	MA0356.1_PHO2 (E val: 3.7090e-05)
SNAPOd2T00003340001	MA0232.1_lbl (E val: 6.4014e-06)
<u>CG4328</u>	MA0182.1_CG4328 (E val: 1.4526e-07)
hbx10	MA0182.1_CG4328 (E val: 1.1851e-05)
Q8I9J5 9BILA	MA0448.1_H2.0 (E val: 3.6600e-05)
Q7M3U4 ACRFO	MA0075.1_Prrx2 (E val: 1.9488e-05)
<u>CBG04010</u>	MA0206.1_abd-A (E val: 7.7487e-06)

10 TGG KSVMQ	MA0203.1_Scr (E val: 4.2788e-06)
237 TAG YAVNA	MA0238.1_pb (E val: 2.3898e-06)
2 TTT RTVSA	MA0203.1_Scr (E val: 1.5232e-05)
4 TTC VRVSA	MA0203.1_Scr (E val: 1.0721e-04)
17 TAT TRVSA	MA0203.1_Scr (E val: 3.5384e-05)
<u>HDG11</u>	MA0151.1_ARID3A (E val: 3.6185e-06)
HDG7	MA0170.1_C15 (E val: 6.0448e-09)
HDG1	MA0226.1_hbn (E val: 3.0337e-09)

ANL2	MA0206.1_abd-A (E val: 4.3694e-06)
<u>egl-5</u>	MA0248.1_tup (E val: 3.1483e-08)
14 TCG KGTQM	MA0248.1_tup (E val: 4.2624e-08)
<u>NKX6-3</u>	MA0215.1_btn (E val: 3.0070e-09)
<u>tup</u>	MA0248.1_tup (E val: 2.1446e-11)
<u>C15</u>	MA0170.1_C15 (E val: 1.2763e-11)
232 TCG IKNQM	MA0248.1_tup (E val: 3.8435e-09)
ATML1	MA0186.1_Dfd (E val: 8.4622e-05)
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226 TTT KMISA	MA0075.1_Prrx2 (E val: 2.0502e-04)
<u>Isl1</u>	MA0132.1_Pdx1 (E val: 2.3124e-06)
236 TAG KSTQM	MA0248.1_tup (E val: 4.8824e-06)
<u>NANOG</u>	MA0214.1_bsh (E val: 1.0306e-04)
<u>Dfd</u>	MA0232.1_lbl (E val: 1.7692e-06)
<u>HB-5</u>	MA0110.1_ATHB-5 (E val: 2.0816e-07)
<u>ATHB-21</u>	MA0110.1_ATHB-5 (E val: 6.3559e-07)
<u>ATHB-53</u>	MA0110.1_ATHB-5 (E val: 4.4373e-10)

HAT5	MA0008.1_HAT5 (E val: 2.8499e-08)
<u>ATHB-13</u>	MA0008.1_HAT5 (E val: 4.2208e-08)
<u>ATHB-16</u>	MA0008.1_HAT5 (E val: 1.8398e-09)
<u>ATHB-20</u>	MA0008.1_HAT5 (E val: 2.7583e-08)
ATHB-5	MA0008.1_HAT5 (E val: 1.9168e-07)
<u>NCU03070</u>	MA0216.1_cad (E val: 6.3417e-05)
<u>ATHB-51</u>	MA0008.1_HAT5 (E val: 1.7745e-05)
PK20392.1	MA0008.1_HAT5 (E val: 9.0427e-05)

ATHB-6	MA0110.1_ATHB-5 (E val: 6.6140e-05)
GSC2	MA0094.1_Ubx (E val: 2.0696e-03)
<u>Isl2</u>	MA0094.1_Ubx (E val: 3.3589e-03)
Obox3	MA0094.1_Ubx (E val: 1.7438e-03)
POU5F1B	MA0075.1_Prrx2 (E val: 3.0457e-03)
<u>En1</u>	MA0075.1_Prrx2 (E val: 2.1945e-03)
<u>Dlx4</u>	MA0075.1_Prrx2 (E val: 2.1990e-03)
Pdx1	MA0094.1_Ubx (E val: 2.5080e-03)

<u>E5</u>	MA0075.1_Prrx2 (E val: 1.9975e-03)
<u>Isx</u>	MA0094.1_Ubx (E val: 2.0861e-03)
<u>Hoxd1</u>	MA0075.1_Prrx2 (E val: 2.9738e-03)
Q6WL90 TRICY	MA0075.1_Prrx2 (E val: 1.9260e-03)
<u>Otp</u>	MA0075.1_Prrx2 (E val: 2.0878e-03)
Rhox6	MA0094.1_Ubx (E val: 2.0443e-03)
Evx2	MA0075.1_Prrx2 (E val: 2.3487e-03)
<u>Hoxb6</u>	MA0094.1_Ubx (E val: 2.5913e-03)

Dbx2	MA0094.1_Ubx (E val: 4.4778e-03)
<u>Hoxd8</u>	MA0094.1_Ubx (E val: 4.7931e-03)
Obox5	MA0094.1_Ubx (E val: 2.4391e-03)
Barx2	MA0094.1_Ubx (E val: 3.1310e-03)
<u>Hoxa5</u>	MA0094.1_Ubx (E val: 3.3308e-03)
<u>barx1</u>	MA0075.1_Prrx2 (E val: 3.1848e-03)
<u>Nkx6-1</u>	MA0075.1_Prrx2 (E val: 3.4714e-03)
Hoxb3	MA0075.1_Prrx2 (E val: 3.1781e-03)

Dlx3	MA0075.1_Prrx2 (E val: 3.2354e-03)
Gsx2	MA0075.1_Prrx2 (E val: 3.0869e-03)
Evx1	MA0075.1_Prrx2 (E val: 3.1475e-03)
<u>Hoxb5</u>	MA0094.1_Ubx (E val: 3.7479e-03)
<u>Nkx6-3</u>	MA0075.1_Prrx2 (E val: 3.8618e-03)
Emx2	MA0075.1_Prrx2 (E val: 3.2531e-03)
<u>Nkx1-2</u>	MA0075.1_Prrx2 (E val: 3.3875e-03)
<u>Bsx</u>	MA0075.1_Prrx2 (E val: 3.4670e-03)
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Lbx2	MA0094.1_Ubx (E val: 5.3979e-03)
NEMVEDRAFT v1g81309	MA0075.1_Prrx2 (E val: 3.3645e-03)
<u>CBG20882</u>	MA0094.1_Ubx (E val: 4.1346e-03)
<u>Hoxa6</u>	MA0094.1_Ubx (E val: 3.7532e-03)
<u>ceh-5</u>	MA0075.1_Prrx2 (E val: 3.4502e-03)
<u>Nobox</u>	MA0094.1_Ubx (E val: 4.8980e-03)
<u>Nanog</u>	MA0075.1_Prrx2 (E val: 4.5812e-03)
Meox1	MA0075.1_Prrx2 (E val: 4.5297e-03)

YOX1	MA0094.1_Ubx (E val: 1.1609e-02)
NEMVEDRAFT v1g136480	MA0094.1_Ubx (E val: 7.7218e-03)
21 TAC ERVSV	MA0212.1_bcd (E val: 2.7894e-03)
20 TAC QRVSA	MA0203.1_Scr (E val: 1.4870e-04)
216 TGC NRVMM	MA0212.1_bcd (E val: 6.8226e-04)
235 TAT RAVSV	MA0186.1_Dfd (E val: 9.5367e-04)
229 TTC GRISA	MA0356.1_PHO2 (E val: 1.8486e-03)
Hoxb8	MA0094.1_Ubx (E val: 6.4583e-03)

Hoxc8	MA0094.1_Ubx (E val: 8.9132e-03)
CBG00023	MA0094.1_Ubx (E val: 5.4028e-03)
Hmx2	MA0426.1_YHP1 (E val: 3.6198e-04)
<u>Hmx1</u>	MA0426.1_YHP1 (E val: 3.2593e-04)
SIX5	MA0335.1_MET4 (E val: 2.1780e-03)
<u>schlank</u>	MA0193.1_Lag1 (E val: 2.2828e-10)
yox1	MA0075.1_Prrx2 (E val: 7.7965e-03)
<u>Noto</u>	MA0075.1_Prrx2 (E val: 6.3461e-03)

<u>UNCX</u>	MA0075.1_Prrx2 (E val: 1.8805e-03)
<u>pha-2</u>	MA0426.1_YHP1 (E val: 4.0154e-02)
<u>CG15696</u>	MA0426.1_YHP1 (E val: 2.0724e-02)
<u>CG34031</u>	MA0426.1_YHP1 (E val: 2.0324e-02)
NEMVEDRAFT v1g80394	MA0426.1_YHP1 (E val: 1.3574e-02)
<u>NOBOX</u>	MA0426.1_YHP1 (E val: 3.2827e-02)
IRX5	MA0328.1_MATALPHA2 (E val: 3.9553e-05)
MTAL2 KLUDE	MA0328.1_MATALPHA2 (E val: 6.6896e-12)

HMRA2	MA0328.1_MATALPHA2 (E val: 1.7878e-12)
Rhox8	MA0392.1_STB5 (E val: 2.3740e-05)
<u>mirr</u>	MA0233.1_mirr (E val: 1.6159e-06)
<u>ara</u>	MA0210.1_ara (E val: 1.6159e-06)
<u>caup</u>	MA0217.1_caup (E val: 1.6159e-06)
<u>CG11617</u>	MA0173.1_CG11617 (E val: 1.4526e-07)
51 CAG MSHWR	MA0217.1_caup (E val: 1.9443e-06)
49 CAT LSQSR	MA0173.1_CG11617 (E val: 1.9340e-06)

253 CGT VANSR	MA0217.1_caup (E val: 4.9392e-06)
55 CAA LHYVR	MA0217.1_caup (E val: 8.1367e-06)
HMLALPHA2	MA0210.1_ara (E val: 1.2090e-02)
MATALPHA2	MA0210.1_ara (E val: 2.0207e-02)
<u>CBG08197</u>	MA0210.1_ara (E val: 1.5637e-02)
<u>Irx4</u>	MA0210.1_ara (E val: 8.5641e-03)
<u>Irx6</u>	MA0210.1_ara (E val: 5.7942e-03)
<u>Irx2</u>	MA0210.1_ara (E val: 1.6628e-02)

<u>Irx5</u>	MA0210.1_ara (E val: 1.3053e-02)
<u>AGAP009986</u>	MA0210.1_ara (E val: 2.8411e-02)
Rhox11	MA0210.1_ara (E val: 2.0801e-02)
MTAL2 PICAN	MA0318.1_HMRA2 (E val: 1.0682e-01)
IRX1	MA0328.1_MATALPHA2 (E val: 9.6004e-06)
IRX3	MA0328.1_MATALPHA2 (E val: 8.9355e-05)
<u>FGRRES 07914</u>	MA0328.1_MATALPHA2 (E val: 2.1882e-04)
SNAPOd2T00005194001	MA0328.1_MATALPHA2 (E val: 1.7656e-04)

ATHB-4	MA0254.1_vvl (E val: 8.1236e-04)
<u>hbx7</u>	MA0322.1_INO4 (E val: 2.4836e-03)
IRX2	MA0207.1_achi (E val: 6.9992e-04)
<u>Irx3</u>	MA0143.1_Sox2 (E val: 2.4858e-09)
<u>vis</u>	MA0252.1_vis (E val: 8.8622e-07)
<u>achi</u>	MA0252.1_vis (E val: 8.7480e-07)
Meis2	MA0252.1_vis (E val: 6.4391e-06)
MEIS1	MA0252.1_vis (E val: 6.6419e-06)

Meis3	MA0227.1_hth (E val: 6.6077e-06)
	(E val. 0.00776-00)
Meis1	MA0252.1_vis (E val: 4.1357e-05)
ANHX	MA0408.1_TOS8 (E val: 5.5807e-06)
FGRRES 17152	MA0328.1_MATALPHA2 (E val: 7.6247e-08)
FGRRES 17150	MA0252.1_vis (E val: 1.0847e-04)
Tgif1	MA0227.1_hth (E val: 6.8698e-05)
Tgif2	MA0227.1_hth (E val: 6.9961e-05)
CUP9	MA0288.1_CUP9 (E val: 3.7091e-11)

hbx4	MA0227.1_hth (E val: 1.0419e-04)
CAGL0H02959g	MA0227.1_hth (E val: 1.1990e-04)
ANIA 00885	MA0207.1_achi (E val: 1.9445e-04)
GRMZM2G087741	MA0227.1_hth (E val: 1.3141e-06)
GRMZM2G135447	MA0227.1_hth (E val: 5.9773e-09)
KNAT7	MA0018.2_CREB1 (E val: 2.6336e-07)
CBG24578	MA0207.1_achi (E val: 1.4139e-07)
TGIF2	MA0227.1_hth (E val: 3.1704e-07)

TGIF1	MA0207.1_achi (E val: 1.8587e-07)
MEIS3	MA0227.1_hth (E val: 1.3353e-06)
MEIS2	MA0207.1_achi (E val: 3.0941e-07)
PKNOX1	MA0227.1_hth (E val: 5.8002e-07)
PKNOX2	MA0227.1_hth (E val: 5.7190e-07)
TGIF2LY	MA0227.1_hth (E val: 3.0965e-07)
TGIF2LX	MA0227.1_hth (E val: 2.5463e-07)
Pknox2	MA0207.1_achi (E val: 1.0777e-07)

Q5EVH4 OIKDI	MA0227.1_hth (E val: 5.3087e-09)
<u>HOS66</u>	MA0089.1_NFE2L1_MafG (E val: 2.0629e-02)
KNAT4	MA0089.1_NFE2L1_MafG (E val: 1.2367e-02)
Q0ZPQ8 NEMVE	MA0207.1_achi (E val: 1.1053e-02)
KNAT3	MA0207.1_achi (E val: 1.4978e-02)
PK25034.1	MA0207.1_achi (E val: 1.4895e-02)
KNAT6	MA0207.1_achi (E val: 1.6623e-02)
<u>unc-62</u>	MA0207.1_achi (E val: 1.5344e-02)

MA0227.1_hth (E val: 7.0473e-03)
MA0207.1_achi (E val: 1.4605e-02)
MA0207.1_achi (E val: 2.7682e-02)
MA0227.1_hth (E val: 2.1428e-02)
MA0227.1_hth (E val: 3.4042e-02)
MA0246.1_so (E val: 1.2975e-03)
MA0129.1_TGA1A (E val: 2.3900e-03)
MA0018.2_CREB1 (E val: 8.6372e-07)

CBG10835	MA0199.1_Optix (E val: 1.5682e-02)
<u>Phyra73700</u>	MA0199.1_Optix (E val: 1.5829e-02)
si dkey-43p13.5	MA0210.1_ara (E val: 7.5942e-02)
PK24181.1	MA0227.1_hth (E val: 4.3791e-02)
Six4	MA0204.1_Six4 (E val: 3.2262e-02)
Six2	MA0246.1_so (E val: 1.2907e-02)
Six1	MA0246.1_so (E val: 2.2537e-02)
<u>so</u>	MA0246.1_so (E val: 7.0329e-09)

SIX2	MA0246.1_so (E val: 2.7271e-07)
SIX4	MA0246.1_so (E val: 1.5465e-07)
SIX1	MA0246.1_so (E val: 9.5689e-05)
<u>ceh-34</u>	MA0246.1_so (E val: 3.0430e-02)
XP 003689450.1	MA0036.1_GATA2 (E val: 5.8039e-02)
Q6Y859 MARMO	MA0199.1_Optix (E val: 5.3920e-03)
PRH PETCR	MA0345.1_NHP6A (E val: 4.6352e-09)
hbx2	MA0379.1_SIG1 (E val: 6.3617e-06)

PDF2	MA0277.1_AZF1 (E val: 1.1933e-03)
KLLA0 D10043g	MA0379.1_SIG1 (E val: 8.4022e-03)
NEMVEDRAFT v1g81436	MA0216.1_cad (E val: 9.7454e-02)
<u>ANIA 01217</u>	MA0216.1_cad (E val: 6.6209e-02)
ZHX1	MA0129.1_TGA1A (E val: 1.0082e-01)
<u>ceh-74</u>	MA0436.1_YPR022C (E val: 6.6468e-03)
<u>CAD25866</u>	MA0227.1_hth (E val: 2.3133e-03)
<u>NKX2-1</u>	MA0211.1_bap (E val: 7.5503e-05)

<u>ATHB-12</u>	MA0089.1_NFE2L1_MafG (E val: 2.0267e-01)
RLT1	MA0127.1_PEND (E val: 3.5933e-02)
PK25011.1	MA0089.1_NFE2L1_MafG (E val: 1.5545e-01)
<u>CIMG 06089</u>	MA0318.1_HMRA2 (E val: 3.1007e-01)

Motif Similarity Matches

54_CAA_LMYQR

forward reverse compliment

Name E value Alignment Motif

MA0217.1_caup 8.9496e-06 NCTTGTTARN ---TGTTA--

42_CGA_TFYAA

forward reverse compliment

Name	E value	Alignment	Motif
MA0186.1_Dfd	2.4354e-03	NCTCGTTAN TCATTAA	

lbe

	forward	reverse compliment	
Name	E value	Alignment	Motif
MA0186.1_Dfd	4.2043e-04	NNTCGTTA- TCATTAA	

LBX2

	forward	reverse compliment	
Name	E value	Alignment	Motif
MA0186.1_Dfd	5.8346e-08	CTCRTTAA -TCATTAA	

39_CTA_IFNAK

forward reverse compliment

Name E value Alignment Motif

MA0231.1_lbe 8.3745e-06 NCTMGTTANN --TNRTTA--

HMBOX1

forward reverse compliment

Name E value Alignment Motif

38_CTA_LHYAK

forward reverse compliment

Name E value Alignment Motif

 $\begin{array}{ccc} \text{MA0231.1_lbe} & 7.0847\text{e-}07 & & \text{NCTAGTTARN} \\ & & -\text{TNRTTA}- & & \end{array}$

220_CTG_LTYQK

forward reverse compliment

MA0231.1_lbe 4.1962e-05

NNTAACYAGN --TAAYNA--

260_ATA_KAYNA

forward

reverse compliment

Name E value Alignment

Motif

MA0231.1_lbe 5.8661e-04

NTNGTTARNN -TNRTTA---

223_CTC_RTFGK

forward

reverse compliment

Name E value

Alignment

Motif

MA0231.1_lbe 1.4477e-06

NNTAACTAAN --TAAYNA--

252_CTC_LRYSK

forward

reverse compliment

Alignment

Name E value

MA0231.1_lbe 1.8927e-06

NTAGTTANNN -TNRTTA---

303_CTC_VMNRK

forward

reverse compliment

Name E value

Alignment

MA0099.2_AP1 6.0862e-05

NTGAGTTANN -TGAGTCA--

53_CAC_ERVSR

forward

reverse compliment

Name

E value

Alignment

Motif

Motif

MA0173.1_CG11617 2.3925e-06

NCGTGTTAA --ATGTWAA

46_CCC_RLDSK

forward

reverse compliment

Name

E value

Alignment

MA0421.1_YDR026C 5.5305e-06

-NCGGGTTAR NCCGGGTAAA

44_CCT_RGDSK

forward reverse compliment

Name E value Alignment Motif

MA0452.1_Kr 4.6188e-05 NTAACCCG----TAACCCYTTNN

218_CTG_KQNQK

forward reverse compliment

Name E value Alignment Motif

43_CCT_MTNGK

forward reverse compliment

MA0231.1_lbe 9.6156e-04

NTGGTTAANN -TNRTTA---

221_CTG_RLYQK

forward

reverse compliment

Name E value

Alignment

Motif

MA0231.1_lbe 4.9698e-05

NNTRGTTAAN
--TNRTTA--

210_CCG_RSNQK

forward

reverse compliment

Name

E value

Alignment

Motif

MA0231.1_lbe 2.4988e-04

NTGGTTAANN -TNRTTA---

48_CCA_EHNAK

forward

reverse compliment

Name

E value

Alignment

MA0231.1_lbe 1.4619e-05

NNTRGTTANN --TNRTTA--

256_CCA_RLYQK

forward

reverse compliment

Name E value

Alignment

MA0231.1_lbe 8.6188e-06

NNTRGTTANN
--TNRTTA--

BSX

forward

reverse compliment

Name

E value

Alignment

Motif

Motif

MA0217.1_caup 4.8362e-03

NNCGTTAN
--TGTTA-

PRRX2

forward

reverse compliment

Name E value

Alignment

MA0186.1_Dfd 2.6340e-03

NNCRTNAN -TCATTAA

40_CGG_STRER

forward

reverse compliment

Name E value

Alignment Motif

MA0248.1_tup 8.8280e-04

YCCGTTAANN -CMATTAW--

255_CCT_RADGK

forward

reverse compliment

Name

E value

Alignment

Motif

MA0217.1_caup 5.1581e-03

NNNGGTTANN
---TGTTA--

ceh-57

forward

reverse compliment

Name E value

Alignment

MA0217.1_caup 6.2734e-03

NNNNNTWAN
---TGTTA-

Hnf1b

forward

reverse compliment

Name E value

Alignment

MA0217.1_caup 4.2044e-03

NNNGTNNN --TGTTA-

Hnf1a

forward

reverse compliment

Name

E value

Alignment

Motif

Motif

MA0217.1_caup 2.6865e-03

NNNGTTAN --TGTTA-

Hmbox1

forward

reverse compliment

Name

E value

Alignment

9.7179e-02 MA0231.1_lbe

NNNACNNN -TAAYNA-

271_AAC_KLQRF

forward reverse compliment

Name E value Alignment Motif

NCGTYTTANN MA0127.1_PEND 4.1253e-03 ANTTCTTATK

203_GTC_VQKRF

forward reverse compliment

E value Name Alignment Motif

-YTAAGACGN MA0127.1_PEND 3.2871e-04 MATAAGAANT

36_GAC_ATRRF

forward reverse compliment

Name E value Motif Alignment

MA0127.1_PEND 5.6761e-04 -NTAAGACGN

MATAAGAANT

225_AAC_SLQRF

forward

reverse compliment

Name E value

Alignment

MA0393.1_STE12 2.3663e-03

NNGTYTTARN
-YGTTTCA--

34_GAT_RTMRY

forward

reverse compliment

Name

E value

Alignment

Motif

Motif

MA0211.1_bap 1.1833e-03

NNYTAAGACN --TTAAGTG-

272_AAC_VAQRC

forward

reverse compliment

Name

E value

Alignment

NCGTTTTANN -YGTTTCA--

ceh-90

forward reverse compliment

Name E value Alignment Motif

NGTTTTANN YGTTTCA--

250_GAT_AGKTF

forward reverse compliment

Name E value Alignment Motif

NNYTAAGANN-MA0127.1_PEND 1.6496e-02

-MATAAGAANT

26_GGT_ALKNM

forward reverse compliment

E value Motif Name Alignment

MA0211.1_bap 8.8493e-04

NTTAAGGCGN -TTAAGTG--

217_GGG_KSKEG

forward reverse compliment

Name E value Alignment Motif

MA0211.1_bap 4.4540e-05 NNYTAAGGGN --TTAAGTG-

247_GCG_RTDRS

forward reverse compliment

Name E value Alignment Motif

MA0211.1_bap 1.2248e-03 NKKCTTARNN -CACTTAA--

37_GAA_RFQKF

forward reverse compliment

Name E value Alignment Motif

MA0127.1_PEND 4.5636e-06 NTTAAGAASN MATAAGAANT

Q0ZPQ4_NEMVE

forward

reverse compliment

Name E value

Alignment

Motif

MA0127.1_PEND 1.6660e-08

-TTAAGAAG-MATAAGAANT

268_AAT_KLQAF

forward

reverse compliment

Name

E value

Alignment

Motif

MA0211.1_bap 1.1050e-05

NTWCTTAANN -CACTTAA--

75_AAC_SISRF

forward

reverse compliment

Name

E value

Alignment

MA0211.1_bap 8.0890e-04

NNTCTTAANN -CACTTAA--

308_GCG_RLDRF

forward reverse compliment

Name E value Alignment Motif

MA0211.1_bap 8.1581e-04 NNTCTTAANN -CACTTAA--

270_AAG_RAQWF

forward reverse compliment

Name E value Alignment Motif

MA0053.1_MNB1A 2.4849e-02 CCTYTTNNNN NCTTT----

76_AAA_RAQWF

forward reverse compliment

MA0211.1_bap 8.9918e-04

CCTYTTAANN -CACTTAA--

243_GGT_ATKSM

forward reverse compliment

Name E value Alignment Motif

MA0124.1_NKX3-1 6.9614e-06 NTMCTTARNN ATACTTA---

64_AGA_AFRAH

forward reverse compliment

Name E value Alignment Motif

MA0211.1_bap 5.1182e-06 NNTMCTTAAN --CACTTAA-

73_AAT_KLTAF

forward reverse compliment

MA0211.1_bap 8.0708e-07

NTACTTARNN -CACTTAA--

208_CTC_HFNRK

forward reverse compliment

Name E value Alignment Motif

MA0211.1_bap 1.6084e-05 NCKASTTAAN --CACTTAA-

310_GTC_YRRGA

forward reverse compliment

Name E value Alignment Motif

MA0124.1_NKX3-1 1.3755e-06 NNYTAAGTAN ---TAAGTAT

242_GTC_LQRGA

forward reverse compliment

MA0124.1_NKX3-1 1.3807e-06

NNNTAAGTAN
---TAAGTAT

241_GTT_GLRAF

forward reverse compliment

Name E value Alignment Motif

MA0124.1_NKX3-1 1.5270e-06 NNNTAAGTAN ---TAAGTAT

205_GAA_TQRQW

forward reverse compliment

Name E value Alignment Motif

MA0124.1_NKX3-1 1.8120e-06 NNNTAAGTAN ---TAAGTAT

263_AGA_VRFAA

forward reverse compliment

MA0124.1_NKX3-1 2.0316e-06

NNTACTTANN -ATACTTA--

Q70HR3_PLEPI

forward reverse compliment

Name E value Alignment Motif

MA0124.1_NKX3-1 1.7532e-06 NTAAGTANNN
-TAAGTAT--

249_GCA_QLKQS

forward reverse compliment

Name E value Alignment Motif

MA0124.1_NKX3-1 7.5248e-04 NNNNAAGTAN ---TAAGTAT

ceh-22

forward reverse compliment

4.4240e-08 MA0211.1_bap

NNNCACTTNA ---CACTTAA

vnd

forward reverse compliment

Name E value Alignment Motif

YACTTGARA $MA0253.1_vnd$ 1.1102e-16 YACTTGARA

24_GTG_HLIQY

forward reverse compliment

Motif E value Name Alignment

NNNTAAGTGN MA0211.1_bap 1.9677e-06

--TTAAGTG-

bap

forward reverse compliment

E value Motif Name Alignment

2.1113e-06 MA0211.1_bap NNCACTTANN

--CACTTAA-

ISL1

	forward	reverse compliment	
Name	E value	Alignment	Motif
MA0211.1_bap	7.7296e-07	SCACTTAN -CACTTAA	

ISL2

	forward	reverse compliment	
Name	E value	Alignment	Motif
MA0211.1_bap	6.2608e-07	NCACTTAN -CACTTAA	

HMX1

	forward	reverse compliment	
Name	E value	Alignment	Motif
MA0063.1_Nkx2-5	2.2710e-06	NCAMTTANN -CAMTTAW-	

HMX2

forward reverse compliment

Name E value Alignment Motif

MA0211.1_bap 1.1516e-08 NCACTTRNC -CACTTAA-

NKX3-2

forward reverse compliment

Name E value Alignment Motif

 $\begin{array}{ccc} \text{MA0211.1_bap} & 2.0976\text{e-}06 & & \text{NCCACTTANN} \\ & --\text{CACTTAA-} & & \end{array}$

NKX3-1

forward reverse compliment

10/21/20

MA0211.1_bap 2.0256e-06

NNTAAGTGGN -TTAAGTG--

Nkx2-6

forward reverse compliment

Name E value Alignment Motif

MA0211.1_bap 7.4956e-04 NNNCACTTNN ---CACTTAA

Nkx3-1

forward reverse compliment

Name E value Alignment Motif

MA0211.1_bap 8.3180e-04 NNNCACTTNN ---CACTTAA

Nkx2-9

forward reverse compliment

MA0211.1_bap 1.9645e-03

NNRAGTRNNN TTAAGTG---

Nkx2-1

forward reverse compliment

Name E value Alignment Motif

MA0211.1_bap 9.7504e-04 NYNCTYNN -CACTTAA

Nkx2-2

forward reverse compliment

Name E value Alignment Motif

Nkx3-2

forward reverse compliment

MA0211.1_bap 6.6546e-04

NNYACTTNN --CACTTAA

scro

forward reverse compliment

Name E value Alignment Motif

Nkx2-4

forward reverse compliment

Name E value Alignment Motif

MA0211.1_bap 2.2018e-03 NNRAGNRNNN TTAAGTG---

NEMVEDRAFT_v1g197288

forward reverse compliment

MA0211.1_bap 2.4841e-03

NNNYACTTNN ---CACTTAA

ceh-24

forward reverse compliment

Name E value Alignment Motif

MA0211.1_bap 5.8321e-02 NNYNCTYNN --CACTTAA

ENSCING00000007395

forward reverse compliment

Name E value Alignment Motif

MA0211.1_bap 3.0174e-02 NWNNNNNN CACTTAA-

Hoxb9

forward reverse compliment

MA0165.1_Abd-B 1.0286e-03

NNNNRTWAAN --TMATAAA-

CBG23031

forward reverse compliment

Name E value Alignment Motif

NNNNATWAAN MA0174.1_CG42234 8.4823e-04 --TMATWAA-

Hoxc11

forward reverse compliment

Name E value Alignment Motif

NNNNRTWAAN MA0165.1_Abd-B 2.3036e-03

--TMATAAA-

Hoxa9

forward reverse compliment

MA0307.1_GLN3 6.1601e-03

NNNNNNN -TTATC--

Hoxd10

forward reverse compliment

Name E value Alignment Motif

MA0307.1_GLN3 4.1907e-03 NNNNNNNN -TTATC--

Hoxd11

forward reverse compliment

Name E value Alignment Motif

Hoxa10

forward reverse compliment

MA0307.1_GLN3 8.7847e-03

NNNNNTNNN ---GATAA-

Cdx2

forward reverse compliment

Name E value Alignment Motif

NWWATNRNN MA0307.1_GLN3 8.2090e-03 -TTATC---

Cdx1

forward reverse compliment

E value Motif Name Alignment

NNWATNRNN MA0307.1_GLN3 7.8786e-03

-TTATC---

Hoxc10

forward reverse compliment

Name E value Motif Alignment

MA0165.1_Abd-B 2.4823e-08 NTTTTAYGAC --TTTATKA- HOXB9

forward reverse compliment

Name E value Alignment Motif

MA0165.1_Abd-B 2.2251e-06 GTCGTAAAAN -TMATAAA--

Abd-B

forward reverse compliment

Name E value Alignment Motif

HOXA₁₀

forward reverse compliment

MA0165.1_Abd-B 7.2371e-06

NTTTTACGACN
--TTTATKA--

HOXA11

forward reverse compliment

Name E value Alignment Motif

MA0165.1_Abd-B 2.0449e-05 NGTCGTAAAAN --TMATAAA--

Hoxa11

forward reverse compliment

Name E value Alignment Motif

MA0165.1_Abd-B 6.8791e-06 NNTCGTAAANNN --TMATAAA---

HOXD11

forward reverse compliment

MA0153.1_HNF1B 2.3770e-05

NRTCGTAAANNNTWAN ----GTTAAWYATTAA

HOXC11

forward reverse compliment

Name E value Alignment Motif

NNTTTACGAYN MA0165.1_Abd-B 6.4582e-06 --TTTATKA--

HOXD12

forward reverse compliment

E value Name Alignment Motif

NRTCGTAAAN MA0165.1_Abd-B 1.5126e-05

--TMATAAA-

HOXA9

forward reverse compliment

Name E value Motif Alignment

MA0165.1_Abd-B 4.9453e-07 NNNTTTAYGAYN ---TTTATKA--

CDX2

forward reverse compliment

Name E value Alignment Motif

MA0165.1_Abd-B 1.8242e-04 NRTYRTAANN --TMATAAA-

HOXC10

forward reverse compliment

Name E value Alignment Motif

MA0216.1_cad 2.9939e-09 NNTTTATKRCN --TTTATTR--

HOXC9

forward reverse compliment

Name E value Alignment Motif

HOXC12

forward reverse compliment

Name E value Alignment Motif

 $\begin{array}{ccc} \text{MA0216.1_cad} & \text{4.7854e-09} & & \text{NGTAATAAAAN} \\ & & -\text{YAATAAA--} \end{array}$

cad

forward reverse compliment

Name E value Alignment Motif

 $\begin{array}{ccc} \text{MA0216.1_cad} & \text{2.2162e-08} & & \text{NNGCMATAAAAN} \\ & & --\text{YAATAAA--} \end{array}$

HOXD9

forward reverse compliment

MA0216.1_cad 6.3975e-10

GCAATAAAN -YAATAAA--

HOXD10

forward reverse compliment

Name E value Alignment Motif

MA0216.1_cad 5.7397e-10 GYMATAAAAN -YAATAAA--

CDX1

forward reverse compliment

Name E value Alignment Motif

MA0216.1_cad 1.0263e-07 NTTTTATGGCN --TTTATTR--

Hoxd9

forward reverse compliment

Name E value Alignment Motif

MA0165.1_Abd-B 4.1215e-07 NCCATWAAA -TMATAAA-

Cdx4

forward reverse compliment

Name E value Alignment Motif

 $\begin{array}{ccc} \text{MA0216.1_cad} & \text{4.8203e-07} & & \text{NNCNATAAATCA} \\ & & -\text{YAATAAA---} \end{array}$

Hoxc12

forward reverse compliment

Name E value Alignment Motif

MA0151.1_ARID3A 3.9486e-02 NNTWAYNNNN
-TTTAAT---

Hoxd12_CONSTRUCT

forward reverse compliment

MA0151.1_ARID3A 4.2453e-02

NNTNAYNNNN -TTTAAT---

264_ACT_KVYHV

forward reverse compliment

Name E value Alignment Motif

267_ACA_RVSHT

forward reverse compliment

Name E value Alignment Motif

B-H2

forward reverse compliment

MA0168.1_B-H1 3.6424e-04

NNCGTTTANN --CAATTAA-

B-H1

forward reverse compliment

E value Name Alignment Motif

NNCGTTTANN MA0168.1_B-H1 3.8028e-04 --CAATTAA-

BARHL1

forward reverse compliment

E value Motif Name Alignment

NCGTTTAN MA0168.1_B-H1 5.0670e-05 -CAATTAA

Barhl1

forward reverse compliment

Name E value Motif Alignment

MA0168.1_B-H1 2.9661e-04 NNCRTTTANN --CAATTAA-

HAT3.1

forward reverse compliment

Name E value Alignment Motif

MA0218.1_ct 8.9984e-04 NTRMACCNNN TTRAAC----

MTR_2g038000

forward reverse compliment

Name E value Alignment Motif

MA0132.1_Pdx1 2.8654e-02 NNNNNAGNNN -AATTAG---

59_ATC_TRMAF

forward reverse compliment

MA0434.1_YPR013C 4.2834e-03

-GATTTANNNN NGATYTACN--

Q9C1N5_COPSC

forward reverse compliment

Name E value Alignment Motif

MA0037.1_GATA3 5.0444e-03 NNCAATCNN --YTATCN-

Q1WMN0_COPDI

forward reverse compliment

Name E value Alignment Motif

MA0037.1_GATA3 6.7599e-03 NNCAATCNN --YTATCN-

UM00578

forward reverse compliment

MA0190.1_Gsc 1.1501e-02

NNGATNNNN -GGATTA--

AAEL012091

forward reverse compliment

Name E value Alignment Motif

MA0212.1_bcd 1.3723e-02 NNGATNNNN
-GGATTA--

Hdx

forward reverse compliment

Name E value Alignment Motif

MA0212.1_bcd 2.0846e-02 NNATNNN GGATTA-

dharma

forward reverse compliment

MA0234.1_oc 4.8065e-04

NNNATCC -TAATCC

NEMVEDRAFT_v1g113057

forward reverse compliment

Name E value Alignment Motif

MA0212.1_bcd 2.6743e-08 NNGGATTARN --GGATTA--

15_TCC_RMIKS

forward reverse compliment

Name E value Alignment Motif

MA0212.1_bcd 2.6557e-08 NGGATTARNN
-GGATTA---

DPRX

forward reverse compliment

MA0190.1_Gsc 2.8082e-08

NGGATTATCN -GGATTA---

RHOXF1

forward reverse compliment

Name E value Alignment Motif

MA0234.1_oc 4.4835e-08 GGATNATCN GGATTA---

Q8VHG7_MOUSE

forward reverse compliment

Name E value Alignment Motif

MA0201.1_Ptx1 2.4983e-10 NGGATTAW -GGATTAA

GSC

forward reverse compliment

MA0234.1_oc 3.9560e-09

NTAATCCN -TAATCC-

ceh-53

forward

reverse compliment

Name E value

Alignment

MA0190.1_Gsc 4.6874e-09

NRGATTAN -GGATTA-

gsc

forward

reverse compliment

Name E value

Alignment

Motif

Motif

MA0190.1_Gsc 5.2033e-09

NGGATTAN -GGATTA-

AGAP006642

forward

reverse compliment

Name E value

Alignment

Motif

MA0190.1_Gsc 4.0356e-09

GGATTANN GGATTA--

bcd

forward reverse compliment

Name E value Alignment Motif

MA0190.1_Gsc 9.0637e-10 GGATTAN GGATTA-

DMBX1

forward reverse compliment

Name E value Alignment Motif

MA0234.1_oc 8.8704e-09 NGGATTAN -GGATTA-

Obox6

forward reverse compliment

MA0190.1_Gsc 2.0177e-08

NNRGATTAN
--GGATTA-

Dobox5_CONSTRUCT

forward reverse compliment

Name E value Alignment Motif

MA0190.1_Gsc 2.6002e-08 NTAATCYNN -TAATCC--

Obox1

forward reverse compliment

Name E value Alignment Motif

 $\begin{array}{ccc} \text{MA0190.1_Gsc} & 3.5326\text{e-}08 & & \text{NNNGGATTAN} \\ & ---\text{GGATTA-} & & \end{array}$

13_TCT_ATVKA

forward reverse compliment

MA0234.1_oc 3.1024e-08

NGGATTARNN -GGATTA---

Gsc

forward reverse compliment

Name E value Alignment Motif

MA0234.1_oc 6.2323e-08 TAATCCNNTWA TAATCC----

Dmbx1

forward reverse compliment

Name E value Alignment Motif

MA0234.1_oc 4.4797e-05 NNRGATTAN --GGATTA-

Q1WMN9_COPDI

forward reverse compliment

MA0212.1_bcd 1.7040e-02

NNGATTNNNN -GGATTA---

SNOG_11642

forward reverse compliment

Name E value Alignment Motif

ENSTNIG00000017092

forward reverse compliment

Name E value Alignment Motif

MA0235.1_onecut 1.9058e-05

NTAATCAN
-NAATCAA

HNF1B

forward reverse compliment

MA0153.1_HNF1B 5.5378e-13

RTTAATNATTAAC GTTAAWYATTAA-

HNF1A

forward reverse compliment

E value Name Alignment Motif

NRTTAATNATTAACN MA0153.1_HNF1B 6.3727e-14 --TTAATRWTTAAC-

ATHB-15

forward reverse compliment

Alignment E value Motif Name

AATAATTACT MA0223.1_exex 5.4407e-09

--TAATTAN-

ATHB-9

forward reverse compliment

MA0186.1_Dfd 1.5656e-05

NTAATCATTAYNWTN
----TCATTAA----

Duxbl1

forward reverse compliment

Name E value Alignment Motif

MA0235.1_onecut 4.4831e-04 NNYAATCAN
--NAATCAA

HDX

forward reverse compliment

Name E value Alignment Motif

Cphx1

forward reverse compliment

MA0235.1_onecut 1.1410e-03

NNNNNATCW-----NAATCAA

Lhx6_CONSTRUCT

forward reverse compliment

Name E value Alignment Motif

MA0075.1_Prrx2 2.2088e-04 NNTRATTRN --TAATT--

WOX13

forward reverse compliment

Name E value Alignment Motif

MA0070.1_PBX1 5.5638e-06 NNTGATTGAN-NTTGATTGATNN

Q00354_COPCI

forward reverse compliment

MA0316.1_HAP5 3.4094e-09

ACCAATCN----ACCAATNAGMNNSSN

Q00352_COPCI

forward

reverse compliment

Name E value

Alignment

Motif

MA0060.1_NFYA 4.3583e-09

---TGATTGGTT---NNNCYSATTGGYYNNN

Q68SS9_PLEDJ

forward

reverse compliment

Name

E value

Alignment

Motif

MA0315.1_HAP4 9.4207e-07

NNCAATCN-----

NCCAATCARNNNNN

HOX6

forward

reverse compliment

Name E value

Alignment

Motif

MA0235.1_onecut 1.7458e-04

NNNCAATCAN
---NAATCAA

HAT1

forward reverse compliment

Name E value Alignment Motif

hbx5-2

forward reverse compliment

Name E value Alignment Motif

MA0235.1_onecut 9.7419e-08 NYAATCAW -NAATCAA

hbx5-1

forward reverse compliment

MA0070.1_PBX1 4.1702e-10

-TTGATTGR---NTTGATTGATNN

ATHB-7

forward reverse compliment

Name E value Alignment Motif

MA0070.1_PBX1 1.0559e-04 NNATGATTGN---NTTGATTGATNN

HAT3

forward reverse compliment

Name E value Alignment Motif

MA0235.1_onecut 2.3651e-05

NYAATCAN
-NAATCAA

GRMZM2G038252

forward reverse compliment

MA0426.1_YHP1 9.8215e-06

NCAATCAN -CAATTA-

WUS

forward reverse compliment

E value Motif Name Alignment

TGAWTGAWTGA---MA0070.1_PBX1 1.4198e-05 --NTTGATTGATNN

HAT22

forward reverse compliment

E value Alignment Motif Name

AATGATTRNN MA0008.1_HAT5 2.6746e-05 AATAATTN--

HAT2

forward reverse compliment

E value Name Alignment Motif MA0008.1_HAT5 1.8572e-05

NNAATGATTRN
--AATAATTN-

ATHB-X

forward reverse compliment

Name E value Alignment Motif

MA0110.1_ATHB-5 1.8404e-07 NNAATRATTGN --AATMATTGN

SNOG_08903

forward reverse compliment

Name E value Alignment Motif

 $\begin{array}{cccc} \text{MA0235.1_onecut} & 1.5205\text{e-}10 & & \text{YAAATCAA} \\ & -\text{NAATCAA} & & \end{array}$

NEMVEDRAFT_v1g101664

forward reverse compliment

MA0070.1_PBX1 5.5008e-06

---GATYGATT-NTTGATTGATNN

lin-39

forward reverse compliment

Name E value Alignment Motif

MA0070.1_PBX1 6.2232e-08 -CATCAATC--NNATCAATCAAN

estExt_gwp_gw1.C_702

forward reverse compliment

Name E value Alignment Motif

BARX1

forward reverse compliment

MA0151.1_ARID3A 1.2246e-06

NNATTAAAWANCNATTA
--ATTAAA-----

NKX6-1

forward reverse compliment

Name E value Alignment Motif

MA0214.1_bsh 8.3352e-07 NATYAWWWNNNMATTWNTN -----YMATTAA--

Q0N4H2_NEMVE

forward reverse compliment

Name E value Alignment Motif

MA0188.1_Dr 5.7239e-10 TAATTRNT TAATTGG-

NEMVEDRAFT_v1g114268

forward reverse compliment

NTAATNGRT MA0188.1_Dr 6.9261e-05 -TAATTGG-

NK7.1

forward reverse compliment

E value Name Alignment Motif

-NACCGTTTAAN MA0054.1_myb.Ph3 5.3691e-06 TAACNGTTW---

BARHL2

forward reverse compliment

E value Name Alignment Motif

NTAAACGNT--MA0054.1_myb.Ph3 6.5933e-07

--WAACNGTTA

 304_CTG_TTNQK

forward reverse compliment

Name E value Motif Alignment

MA0188.1_Dr 1.8802e-04 CCRGTTANNN

CCAATTA---

PK19166.1

forward reverse compliment

Name E value Alignment Motif

MA0372.1_RPH1 9.3146e-09 RTTAGGGG-TTAGGGGN

Lhx8

forward reverse compliment

Name E value Alignment Motif

MA0198.1_OdsH 9.5457e-08 NTRATTANNNNTRATTAN -----YTAATTR-

TLX3

forward reverse compliment

Name E value Alignment Motif

MA0188.1_Dr 1.1926e-03 NAATTGNNNNNNNNNNNNNNNNNCAATTN

TAATTGG-----

Q0N4H7_NEMVE

forward

reverse compliment

Name E value

Alignment

MA0094.1_Ubx 2.9184e-02

NNNNNATNNN ----ATTA-

ventx1.1.L

forward

reverse compliment

Name

E value

Alignment

Motif

Motif

MA0075.1_Prrx2 1.2557e-02

NNNNNNNNN --TAATT---

LHX2

forward

E value

reverse compliment

Name

Alignment

Motif

MA0075.1_Prrx2 8.0794e-03

NNNNAANNNN ---TAATT--

NEMVEDRAFT_v1g129868

forward reverse compliment

Name E value Alignment Motif

Q0N4H9_NEMVE

forward reverse compliment

Name E value Alignment Motif

MA0075.1_Prrx2 2.6414e-02 NNYRANNNN --TAATT--

Hoxa3

forward reverse compliment

MA0075.1_Prrx2 4.2577e-03

NTAATNRNNN -TAATT----

Barx1

forward reverse compliment

Name E value Alignment Motif

Mnx1

forward reverse compliment

Name E value Alignment Motif

Nkx1-1

forward reverse compliment

MA0075.1_Prrx2 4.6337e-03

NNNNATTANN ---AATTA--

Hlx

forward reverse compliment

Name E value Alignment Motif

MA0075.1_Prrx2 9.7967e-03 NNWTNNN TAATT--

Lmx1b

forward reverse compliment

Name E value Alignment Motif

Lmx1a

forward reverse compliment

MA0075.1_Prrx2 5.3755e-03

NYNATNNN -TAATT--

CaO19.4000

forward

reverse compliment

Name E value

Alignment Motif

MA0075.1_Prrx2 8.5189e-03

NYAATNNNN -TAATT---

kal-1

forward

reverse compliment

Name

E value

Alignment

Motif

MA0075.1_Prrx2 6.1057e-03

NNNNANNN --TAATT-

PHO₂

forward

reverse compliment

Name

E value

Alignment

Motif

MA0075.1_Prrx2 1.2104e-02

NNNATNNNNN -TAATT----

ceh-51

forward reverse compliment

Name E value Alignment Motif

UM04928

forward reverse compliment

Name E value Alignment Motif

otp

forward reverse compliment

MA0426.1_YHP1 2.8789e-08

NYAATTAN -CAATTA-

OdsH

forward reverse compliment

E value Motif Name Alignment

NYAATTAN MA0426.1_YHP1 2.3854e-08 -CAATTA-

Dll

forward reverse compliment

Alignment E value Motif Name

NYAATTAN MA0426.1_YHP1 2.2713e-08

-CAATTA-

Vsx2

forward reverse compliment

MA0426.1_YHP1 2.3819e-08

NYAATTAN -CAATTA-

DLX5

forward reverse compliment

Name E value Alignment Motif

NTAATTGN MA0426.1_YHP1 2.1206e-08 -TAATTG-

DLX4

forward reverse compliment

E value Motif Name Alignment

NCAATTAN MA0426.1_YHP1 2.6660e-08 -CAATTA-

DLX6

forward reverse compliment

Name E value Motif Alignment

MA0426.1_YHP1 2.4257e-08 NCAATTAN

-CAATTA-

DLX1

forward reverse compliment

Name E value Alignment Motif

GBX2

forward reverse compliment

Name E value Alignment Motif

lms

forward reverse compliment

MA0426.1_YHP1 3.2934e-08

NTAATTRN -TAATTG-

Rx

forward reverse compliment

Name E value Alignment Motif

MA0426.1_YHP1 2.5179e-08 NYAATTAN -CAATTA-

Vsx1

forward reverse compliment

Name E value Alignment Motif

LHX1

forward reverse compliment

MA0426.1_YHP1 3.7149e-08

NYNATTAN -CAATTA-

Lim1

forward reverse compliment

Name E value Alignment Motif

 $\begin{array}{ccc} \text{MA0426.1_YHP1} & \text{4.6222e-08} & & \text{NYAATTAN} \\ & -\text{CAATTA-} \end{array}$

ESX1

forward reverse compliment

Name E value Alignment Motif

MA0426.1_YHP1 9.7762e-08 NYAATTAN -CAATTA-

SHOX2

forward reverse compliment

NYAATTAN MA0232.1_lbl 1.2365e-07 -TMATTA-

Shox2

forward reverse compliment

E value Name Alignment Motif

NYAATTAN MA0232.1_lbl 9.8309e-08 -TMATTA-

TLX2

forward reverse compliment

E value Motif Name Alignment

NYAATTAN 8.2750e-08 MA0232.1_lbl -TMATTA-

DLX2

forward reverse compliment

Name E value Motif Alignment

MA0232.1_lbl 1.1128e-07 NYAATTAN -TMATTA-

RAX2

forward reverse compliment

Name E value Alignment Motif

MA0232.1_lbl 1.1674e-07 NTAATTRN -TAATKA-

PRRX1

forward reverse compliment

Name E value Alignment Motif

MA0232.1_lbl 6.1316e-08 NTAATTRN -TAATKA-

DLX3

forward reverse compliment

MA0232.1_lbl 1.1929e-07

NYAATTAN -TMATTA-

en

forward reverse compliment

Name E value Alignment Motif

Dlx1

forward reverse compliment

Name E value Alignment Motif

MA0426.1_YHP1 7.3537e-08 NYAATTAN -CAATTA-

Dlx2

forward reverse compliment

MA0426.1_YHP1 8.3123e-08

NYAATTAN -CAATTA-

SNAPOd2T00006620001

forward reverse compliment

Name E value Alignment Motif

ceh-54

forward reverse compliment

Name E value Alignment Motif

Gbx2

forward reverse compliment

MA0426.1_YHP1 2.9462e-07

NNYAATTANN --CAATTA--

Gbx1

forward reverse compliment

Name E value Alignment Motif

AAZ08039

forward reverse compliment

Name E value Alignment Motif

MA0426.1_YHP1 2.2824e-07 NNTAATTRNN --TAATTG--

CG11085

forward reverse compliment

MA0426.1_YHP1 2.0173e-08

NCRATTAN -CAATTA-

Hmx

forward reverse compliment

Name E value Alignment Motif

GBX1

forward reverse compliment

Name E value Alignment Motif

CG9876

forward reverse compliment

MA0426.1_YHP1 4.0548e-07

NNYRATTANS --CAATTA--

unpg

forward reverse compliment

Name E value Alignment Motif

NNCAATTANN MA0426.1_YHP1 2.0776e-07 --CAATTA--

18_TAG_RLTQA

forward reverse compliment

Name E value Alignment Motif

NNCAATTARN MA0426.1_YHP1 1.1960e-07

--CAATTA--

ceh-58

forward reverse compliment

MA0232.1_lbl 4.0935e-07

NNYAATTANN --TMATTA--

Barhl2

forward reverse compliment

Name E value Alignment Motif

MA0426.1_YHP1 5.7920e-07 NNYNNTTAN --CAATTA-

ceh-19

forward reverse compliment

Name E value Alignment Motif

YHP1

forward reverse compliment

MA0232.1_lbl 5.2801e-06

NNYAATWWN --TMATTA-

ATEG_04171

forward reverse compliment

Name E value Alignment Motif

NCU03266

forward reverse compliment

Name E value Alignment Motif

MA0196.1_NK7.1 1.9654e-08 NYNATTWNNN -CAATTAA--

HMX3

forward reverse compliment

MA0426.1_YHP1 2.8398e-07

NNCAMTTANNN --CAATTA---

ENSTNIG00000006040

forward reverse compliment

Name E value Alignment Motif

MA0426.1_YHP1 8.7845e-07 NNNYNATTANNNN ---CAATTA----

Rax

forward reverse compliment

Name E value Alignment Motif

ALX4

forward reverse compliment

MA0075.1_Prrx2 1.8830e-06

NTAATTRN -TAATT--

Alx3

forward reverse compliment

Name E value Alignment Motif

MA0075.1_Prrx2 8.5973e-07 TAATNNN TAATT--

Dlx5

forward reverse compliment

Name E value Alignment Motif

MA0075.1_Prrx2 1.2097e-06 WAATNNN TAATT--

Prrx1

forward reverse compliment

MA0075.1_Prrx2 1.7693e-06

TAATTNNN TAATT---

NEMVEDRAFT_v1g105595

forward reverse compliment

Name E value Alignment Motif

MA0075.1_Prrx2 2.2012e-06 NTAATTNN -TAATT--

Lhx1

forward reverse compliment

Name E value Alignment Motif

MA0075.1_Prrx2 5.0294e-06 TAATNNNNN TAATT----

LHX3

forward reverse compliment

MA0194.1_Lim1 1.8346e-09

NNTAATTAAWTNN --TAATTAA----

Dbx1

forward reverse compliment

Name E value Alignment Motif

ATTAATTA MA0194.1_Lim1 4.3593e-11 -TTAATTA

Dbx

forward reverse compliment

E value Motif Name Alignment

ATTAATTA MA0194.1_Lim1 2.3550e-11

-TTAATTA

ventx3.2

forward reverse compliment

Name E value Motif Alignment

MA0194.1_Lim1 1.7841e-11 ATTAATTA

-TTAATTA

CBG00029

forward reverse compliment

Name E value Alignment Motif

MA0194.1_Lim1 1.6173e-11 TAATTAAT TAATTAA-

FGRRES_01100

forward reverse compliment

Name E value Alignment Motif

 $\begin{array}{ccc} MA0226.1_hbn & 2.2507e\text{-}11 & & & \\ YAATTAAW \\ YAATTAA- & & \end{array}$

Tlx2

forward reverse compliment

MA0194.1_Lim1 2.7621e-10

TAWTTAAT TAATTAA-

WOX11

forward reverse compliment

Name E value Alignment Motif

 $\begin{array}{ccc} \text{MA0240.1_repo} & 7.1158\text{e-}10 & & \text{NNTAATTAANT} \\ & & -\text{TAATTAA}-- \end{array}$

Q24782_9CNID

forward reverse compliment

Name E value Alignment Motif

MA0194.1_Lim1 1.4038e-11 TTAATTAA -TAATTAA

CG32105

forward reverse compliment

10/21/20

TTAATTAR 3.4164e-11 MA0236.1_otp -TAATTAR

pal-1

forward reverse compliment

E value Name Alignment Motif

TTWATTAC MA0448.1_H2.0 2.2106e-10 NTWATNA-

hox12

forward reverse compliment

E value Motif Name Alignment

GTMATWAA MA0174.1_CG42234 1.3600e-10

-TMATWAA

HXD12_HETFR

forward reverse compliment

Name E value Motif Alignment

MA0206.1_abd-A 9.0750e-11 GTAATTAA -TAATTAA

ftz

forward reverse compliment

Name E value Alignment Motif

 $\begin{array}{ccc} MA0226.1_hbn & 2.0192e\text{-}11 & & \text{GTAATTAA} \\ & & -\text{YAATTAA} \end{array}$

Hoxc6

forward reverse compliment

Name E value Alignment Motif

Hoxc9

forward reverse compliment

MA0240.1_repo 7.4846e-10

NGTAATTAAN --TAATTAA-

H2.0

forward reverse compliment

Name E value Alignment Motif

MA0448.1_H2.0 2.5989e-11 TNATWAA TNATWAN

Q0N4F9_NEMVE

forward reverse compliment

Name E value Alignment Motif

 $\begin{array}{cccc} MA0180.1_Vsx2 & 1.1622e\text{-}12 & & \text{MTAATTAN-} \\ & & \text{CTAATTAAM} \end{array}$

SPU_026099

forward reverse compliment

MA0180.1_Vsx2 8.9306e-13

NTAATTAA-CTAATTAAM

vab-7

forward reverse compliment

Name E value Alignment Motif

ENSTNIG00000004116

forward reverse compliment

Name E value Alignment Motif

Smp_158000

forward reverse compliment

MA0180.1_Vsx2 4.7229e-13

CYAATTAA-CTAATTAAM

NEMVEDRAFT_v1g164989

forward reverse compliment

Name E value Alignment Motif

CTAATTAR-MA0180.1_Vsx2 7.4326e-12 CTAATTAAM

ARGFX

forward reverse compliment

Motif E value Name Alignment

NCTAATTARN MA0180.1_Vsx2 1.2971e-10

-CTAATTAAM

repo

forward reverse compliment

MA0240.1_repo 2.8598e-10

NYTAATTAAN --TAATTAA-

ENSCING00000016045

forward

reverse compliment

Name E value

Alignment

MA0180.1_Vsx2 5.3273e-10

NCYAATTARNN -CTAATTAAM-

CNK00090

forward

reverse compliment

Name E value

Alignment

Motif

Motif

MA0240.1_repo 2.3502e-11

ATAATTAA -TAATTAA

CAD25284

forward

reverse compliment

Name E value

Alignment

Motif

MA0194.1_Lim1 1.5897e-11

TTAATTAN TTAATTA-

O76842_CUPSA

forward reverse compliment

Name E value Alignment Motif

MA0194.1_Lim1 1.6400e-11 NTAATTAA -TAATTAA

LMX1A

forward reverse compliment

Name E value Alignment Motif

MA0172.1_CG11294 1.7100e-11 TTAATTAN

TTAATTA-

HHEX

forward reverse compliment

Name E value Alignment Motif

MA0172.1_CG11294 2.1773e-10 TAATTNAW

TAATTAA-

lim-4

forward reverse compliment

Name E value Alignment Motif

MA0181.1_Vsx1 9.2564e-11 NNTAATTAR --TAATTAR

Sebox

forward reverse compliment

Name E value Alignment Motif

MA0194.1_Lim1 2.5830e-10 NTAATTAANN -TAATTAA--

Q24780_9CNID

forward reverse compliment

MA0194.1_Lim1 7.3681e-10

NNTAATTAANN --TAATTAA--

mixl1.S

forward reverse compliment

Name E value Alignment Motif

MA0194.1_Lim1 6.0393e-10 NNTAATTAANN
--TAATTAA--

phx1

forward reverse compliment

Name E value Alignment Motif

MA0194.1_Lim1 1.0717e-09 NNTAATTAANN --TAATTAA--

C4B866_NEMVE

forward reverse compliment

MA0194.1_Lim1 1.2649e-09

NNNTAATTAANN ---TAATTAA--

CNG03450

forward reverse compliment

Name E value Alignment Motif

MA0444.1_CG34031 7.7102e-07 NNWATTAAN -CAATTAA-

hbn

forward reverse compliment

Name E value Alignment Motif

CG5369

forward reverse compliment

MA0194.1_Lim1 1.2872e-09

TAATTNNATTA
TAATTAA----

unc-4

forward reverse compliment

Name E value Alignment Motif

MA0178.1_CG32105 1.8305e-08 TAATTNAATTA TAATTAA----

bsh

forward reverse compliment

Name E value Alignment Motif

MA0229.1_inv 3.9607e-11 TAATTARATTA TAATTARW---

Uncx

forward reverse compliment

MA0172.1_CG11294 3.7957e-09

NTAATTNRATTAN -TAATTAA----

Alx4

forward reverse compliment

Name E value Alignment Motif

NTAATYNAATTAN MA0194.1_Lim1 6.3149e-08 -TAATTAA----

CG2808

forward reverse compliment

Name E value Motif Alignment

TAATTNSATTA MA0188.1_Dr 1.4849e-08

TAATTGG----

CG11294

forward reverse compliment

Alignment E value Motif Name

MA0229.1_inv 6.6941e-10

TAATNNAATTA
---WYTAATTA

LHX4

forward reverse compliment

Name E value Alignment Motif

MA0232.1_lbl 1.2360e-07 NTAATTAN -TMATTA-

HGTX

forward reverse compliment

Name E value Alignment Motif

MA0232.1_lbl 6.2738e-09 NTMATTAN -TMATTA-

HOXB2

forward reverse compliment

MA0232.1_lbl 1.5599e-08

NYAATTAN -TMATTA-

NOTO

forward reverse compliment

Name E value Alignment Motif

 $\begin{array}{ccc} \text{MA0232.1_lbl} & 1.6063\text{e-}08 & & \text{NYAATTAN} \\ & & -\text{TMATTA-} \end{array}$

NKX6-2

forward reverse compliment

Name E value Alignment Motif

 $\begin{array}{ccc} \textbf{MA0232.1_lbl} & 1.8473\text{e-}08 & & \textbf{NTAATTRN} \\ & & -\texttt{TAATKA-} \end{array}$

HOXA2

forward reverse compliment

NTAATTAN MA0232.1_lbl 8.6640e-09 -TMATTA-

PDX1

forward reverse compliment

E value Motif Name Alignment

YTAATKAN MA0232.1_lbl 1.1612e-08 -TAATKA-

Ubx

forward reverse compliment

E value Motif Name Alignment

NYAATTAN MA0232.1_lbl 1.5127e-08 -TMATTA-

Lhx2

forward reverse compliment

Name E value Motif Alignment

MA0232.1_lbl 9.1589e-09 NYMATTAN

-TMATTA-

Lhx9

Name

E value	Alignment	Motif

reverse compliment

MA0232.1_lbl 1.1389e-08 NYNATTAN -TMATTA-

forward

EMX1

forward reverse compliment

Name E value Alignment Motif

 $\begin{array}{ccc} \text{MA0232.1_lbl} & \text{1.3018e-08} & & \text{NTAATTAN} \\ & & -\text{TMATTA-} \end{array}$

lab

forward reverse compliment

MA0232.1_lbl 1.0849e-08

STAATTAN -TMATTA-

CG18599

forward reverse compliment

Name E value Alignment Motif

MA0232.1_lbl 1.9400e-09 TAATTAN TMATTA-

Meox2

forward reverse compliment

Name E value Alignment Motif

 $\begin{array}{ccc} \text{MA0232.1_lbl} & 7.1346\text{e-09} & & \text{NTAATTAN} \\ & & -\text{TMATTA-} \end{array}$

ems

forward reverse compliment

NTAATTAN MA0232.1_lbl 9.6821e-09 -TMATTA-

EVX1

forward reverse compliment

E value Name Alignment Motif

NTAATTAN MA0232.1_lbl 1.2369e-08 -TMATTA-

EVX2

forward reverse compliment

E value Motif Name Alignment

NTAATTAN 1.2336e-08 MA0232.1_lbl -TAATKA-

Lim3

forward reverse compliment

Name E value Motif Alignment

MA0232.1_lbl 2.1239e-08 NTAATTAN

-TAATKA-

Lhx4

	forward	reverse compliment	
Name	E value	Alignment	Motif
MA0232.1_lbl	2.0476e-08	NTAATTAN -TMATTA-	

HOXD1

	forward	reverse compliment	
Name	E value	Alignment	Motif
MA0232.1_lbl	2.0307e-08	NTAATTAN -TAATKA-	

Q9GP48_9TURB

	Jorwara	reverse compument	
Name	E value	Alignment	Motif
MA0232.1_lbl	3.8246e-08	NTAATTAN -TMATTA-	

Q70LF3_ARTSF

forward reverse compliment

Name E value Alignment Motif

MA0232.1_lbl 2.7533e-08 NTAATTAN -TMATTA-

NEMVEDRAFT_v1g205636

forward reverse compliment

Name E value Alignment Motif

MA0232.1_lbl 3.7288e-08 NTAATTAN -TMATTA-

MNX1

forward reverse compliment

MA0232.1_lbl 2.6559e-08

NTAATTAN -TMATTA-

DRGX

forward reverse compliment

Name E value Alignment Motif

 $\begin{array}{ccc} \text{MA0232.1_lbl} & 3.1653\text{e-}08 & & \text{NYAATTAN} \\ & & -\text{TMATTA-} \end{array}$

EN₂

forward reverse compliment

Name E value Alignment Motif

MA0232.1_lbl 3.0403e-08 NTAATTAN -TMATTA-

Prrx2

forward reverse compliment

MA0232.1_lbl 2.7448e-08

NTAATTRN -TAATKA-

EN1

forward reverse compliment

Name E value Alignment Motif

MA0232.1_lbl 2.6907e-08 TAATTANN TAATKA--

ALX3

forward reverse compliment

Name E value Alignment Motif

 $\begin{array}{ccc} \text{MA0232.1_lbl} & 2.1881\text{e-}08 & & \text{NTAATTRN} \\ & & -\text{TAATKA-} \end{array}$

SHOX

forward reverse compliment

MA0232.1_lbl 2.2701e-08

NYAATTAN -TMATTA-

Awh

forward reverse compliment

Name E value Alignment Motif

 $\begin{array}{ccc} \text{MA0232.1_lbl} & \text{1.6501e-08} & & \text{NTAATTAN} \\ & & -\text{TMATTA-} \end{array}$

zfhx4

forward reverse compliment

Name E value Alignment Motif

MA0232.1_lbl 5.4071e-08 NYAATTANN -TMATTA--

Lhx5

forward reverse compliment

MA0232.1_lbl 7.9458e-08

NNNYAATTA ---TMATTA

uncx

forward reverse compliment

Name E value Alignment Motif

MA0232.1_lbl 9.0879e-08 NNTAATTRN --TAATKA-

Lhx3

forward reverse compliment

Name E value Alignment Motif

MA0232.1_lbl 6.3907e-08 NNATTANNN TAATKA---

Hoxa1

forward reverse compliment

MA0232.1_lbl 3.8787e-08 NNYNATTNN --TMATTA-

LHX6

forward reverse compliment

Name E value Alignment Motif

TAATTANN MA0232.1_lbl 1.0164e-07 TMATTA--

Lhx6

forward reverse compliment

Name E value Alignment Motif

NYAATYAN MA0232.1_lbl 1.2291e-06 -TMATTA-

prd-b

forward reverse compliment

E value Alignment Name Motif MA0232.1_lbl 7.3149e-07

NTRATTRNN -TAATKA--

Q4RRY4_TETNG

forward

reverse compliment

Name E value

Alignment

Motif

MA0232.1_lbl 2.1430e-07

NNYAATYAN --TMATTA-

7_TTA_RVLRA

forward

reverse compliment

Name

E value

Alignment

Motif

MA0232.1_lbl

5.5511e-08

TAATTARNN TMATTA---

HOXA1

forward

reverse compliment

Name

E value

Alignment

Motif

MA0232.1_lbl 1.4927e-07

NNTAATTANN --TAATKA--

ceh-23

forward reverse compliment

Name E value Alignment Motif

MA0232.1_lbl 1.3081e-07 NTAATTANNN -TAATKA---

56_ATT_HRVQA

forward reverse compliment

Name E value Alignment Motif

MA0232.1_lbl 1.9416e-07 NYAATTARNN
-TMATTA---

MIXL1

forward reverse compliment

MA0232.1_lbl 2.4876e-07

NNYAATTANN --TMATTA--

slou

forward reverse compliment

Name E value Alignment Motif

En2

forward reverse compliment

Name E value Alignment Motif

MA0232.1_lbl 6.0426e-08 NSTAATTANN --TMATTA--

Hoxd3

forward reverse compliment

MA0232.1_lbl 1.0207e-07 NNYAATTANN --TMATTA--

GSX1

forward reverse compliment

E value Motif Name Alignment

NTMATNAN 6.6879e-08 MA0232.1_lbl -TAATKA-

HOXB5

forward reverse compliment

Name E value Alignment Motif

NYMATTAN MA0232.1_lbl 5.6550e-08

-TMATTA-

Scr

forward reverse compliment

MA0232.1_lbl 4.3130e-08

NYMATTAN -TMATTA-

HOXB8

forward reverse compliment

Name E value Alignment Motif

MA0232.1_lbl 1.3096e-07 NTAATKRC -TAATKA-

HOXD8

forward reverse compliment

Name E value Alignment Motif

 $\begin{array}{ccc} \text{MA0232.1_lbl} & 2.2035\text{e-07} & & \text{NTAATKRC} \\ & -\text{TAATKA-} & & \end{array}$

HOXB6

forward reverse compliment

MA0232.1_lbl 3.1744e-08

GYMATTAN
-TMATTA-

HOXA6

forward reverse compliment

Name E value Alignment Motif

MA0223.1_exex 8.5000e-08 NNTAATKRCN --TAATTAN-

HOXB1

forward reverse compliment

Name E value Alignment Motif

 $\begin{array}{ccc} \text{MA0223.1_exex} & 2.3787\text{e-}10 & & \text{NTAATTAC} \\ & & -\text{TAATTAN} \end{array}$

HOXA5

forward reverse compliment

MA0223.1_exex 3.9288e-10

STAATTAS -TAATTAN

Q0N4M8_NEMVE

forward reverse compliment

Name E value Alignment Motif

GTAATTAN MA0223.1_exex 2.3856e-09 NTAATTA-

GSX2

forward reverse compliment

Motif E value Name Alignment

NTAATKRS 8.5976e-09 MA0232.1_lbl

-TAATKA-

abd-A

forward reverse compliment

E value Motif Name Alignment

MA0223.1_exex 1.9332e-08 NGTAATTANN -NTAATTA--

pb

forward reverse compliment

Name E value Alignment Motif

MA0232.1_lbl 6.8619e-08 GTMATTAN -TMATTA-

HOXB3

forward reverse compliment

Name E value Alignment Motif

MA0232.1_lbl 5.6179e-08 NNYMATTANN --TMATTA--

NEMVEDRAFT_v1g8907

forward reverse compliment

10/21/20

MA0232.1_lbl 1.4668e-07

NTAATKRNNN -TAATKA---

Hoxa2

forward reverse compliment

Name E value Alignment Motif

MA0232.1_lbl 3.9527e-08 NNTAATTANN --TMATTA--

MEOX2

forward reverse compliment

Name E value Alignment Motif

 $\begin{array}{ccc} \text{MA0232.1_lbl} & 7.0922\text{e-}08 & & \text{NNTAATTANN} \\ & & -\text{TMATTA--} \end{array}$

eve

forward reverse compliment

MA0241.1_ro 7.8255e-10

NSTAATTAGN --TAATTAR-

EMX2

forward reverse compliment

Name E value Alignment Motif

MA0241.1_ro 2.5200e-11 NTAATTAG -TAATTAR

ro

forward reverse compliment

Name E value Alignment Motif

MA0241.1_ro 1.2763e-11 TAATTARN TAATTAR-

ap

forward reverse compliment

MA0209.1_ap 1.2763e-11

TAATTARN TAATTAR-

RAX

forward reverse compliment

Name E value Alignment Motif

 $\begin{array}{ccc} \text{MA0202.1_Rx} & 5.1507\text{e-}11 & & \text{NTAATTAR} \\ & -\text{TAATTAR} \end{array}$

inv

forward reverse compliment

Name E value Alignment Motif

MA0229.1_inv 6.5503e-15 TAATTARW TAATTARW

ind

forward reverse compliment

MA0228.1_ind 7.6496e-11

TAATTARNR TAATTAR--

ISX

forward	reverse compliment
jorwara	reverse compliment

Name E value Alignment Motif

MA0241.1_ro 8.0527e-11 CTAATTAN YTAATTA-

LBX1

forward reverse compliment

Name E value Alignment Motif

 $\begin{array}{ccc} \text{MA0241.1_ro} & \text{4.2517e-10} & & \text{NTAATTAG} \\ & -\text{TAATTAR} \end{array}$

pdm3

forward reverse compliment

MA0241.1_ro 1.8173e-10

CTAATTAN YTAATTA-

lbl

forward reverse compliment

Name E value Alignment Motif

MA0241.1_ro 1.9839e-09 NTAATKAG -TAATTAR

dve

forward reverse compliment

Name E value Alignment Motif

MA0241.1_ro 9.7944e-10 NCTAATTANN
-YTAATTA--

Q9BJW6_9CNID

forward reverse compliment

MA0241.1_ro 8.0265e-10

NNTAATTAGN
--TAATTAR-

MEOX1

forward reverse compliment

Name E value Alignment Motif

MA0223.1_exex 5.9674e-09 NNTAATTASN --TAATTAN-

exex

forward reverse compliment

Name E value Alignment Motif

MA0198.1_OdsH 1.1913e-08 NNNNYAATTNNCNN ----YAATTAR---

60_ATA_KTVQV

forward reverse compliment

Name E value Alignment Motif

MA0221.1_eve 4.0308e-10 NTMATTARNN -TMATTAR--

LHX9

forward reverse compliment

Name E value Alignment Motif

MA0232.1_lbl 2.4650e-07 NNTNATTAN --TMATTA-

POU6F1

forward reverse compliment

Name E value Alignment Motif

MA0232.1_lbl 1.9095e-07 NNTAATTANN --TAATKA--

Q86SD7_PODCA

forward reverse compliment

MA0232.1_lbl 2.5359e-07

NNTAATTANN --TMATTA--

CBG07641

forward

reverse compliment

Name E value

Alignment Motif

MA0232.1_lbl 1.8462e-07

NNTAATTANN --TMATTA--

ceh-62

forward

reverse compliment

Name E value

Alignment

Motif

MA0232.1_lbl 2.4811e-07

NNTAATTANN --TMATTA--

btn

forward

reverse compliment

Name E value

Alignment

Motif

MA0232.1_lbl 7.5444e-08

NNTMATTANN
--TMATTA--

258_ATT_RTVQQ

forward reverse compliment

Name E value Alignment Motif

MA0232.1_lbl 8.0329e-08 NTMATTANNN -TMATTA---

LMX1B

forward reverse compliment

Name E value Alignment Motif

MA0232.1_lbl 2.8185e-07 NNNNTAATTAN ----TMATTA-

SNAPOd2T00006145001

forward reverse compliment

MA0232.1_lbl 2.6419e-06

NNYAATYANN --TMATTA--

227_TTT_YRIAA

forward

reverse compliment

Name E value

Alignment Motif

MA0075.1_Prrx2 6.0657e-06

NAATTANNNN -AATTA----

CAD26261

forward

reverse compliment

Name

E value

Alignment

Motif

MA0178.1_CG32105 2.6988e-08

TWWATTANN TTAATTA--

Y749_MIMIV

forward

reverse compliment

Name

E value

Alignment

MA0346.1_NHP6B 3.8384e-06

----TATATTAA----

NCU09556

forward reverse compliment

Name E value Alignment Motif

MA0379.1_SIG1 2.9552e-06 TTAATATA ---ATATA

ATHB-22

forward reverse compliment

Name E value Alignment Motif

MA0356.1_PHO2 3.7090e-05 NNNWAWATTATNN ----TAWTAW--

SNAPOd2T00003340001

forward reverse compliment

MA0232.1_lbl 6.4014e-06

NWWATTANNN -TAATKA---

CG4328

forward reverse compliment

Name E value Alignment Motif

MA0182.1_CG4328 1.4526e-07 YAATWAWN YAATWAW-

hbx10

forward reverse compliment

Name E value Alignment Motif

MA0182.1_CG4328 1.1851e-05 NWWATTRN WTWATTR-

Q8I9J5_9BILA

forward reverse compliment

MA0448.1_H2.0 3.6600e-05

NRTWATTANN
-NTWATNA--

Q7M3U4_ACRFO

forward

reverse compliment

Name E value

Alignment Motif

MA0075.1_Prrx2 1.9488e-05

NNNTAATTNNN ---TAATT---

CBG04010

forward

reverse compliment

Name E value

Alignment

Motif

MA0206.1_abd-A 7.7487e-06

NNTTAATKNNN --TTAATTA--

10_TGG_KSVMQ

forward

reverse compliment

Name E value

Alignment

MA0203.1_Scr 4.2788e-06

NNYTAATGNN --YTAATGA-

237_TAG_YAVNA

forward

reverse compliment

Name E value

Alignment

Motif

MA0238.1_pb 2.3898e-06

NMATTARNNN TMATTAR---

2_TTT_RTVSA

forward

reverse compliment

Name

E value

Alignment

Motif

MA0203.1_Scr 1.5232e-05

NNYTAATNNN --YTAATGA-

4_TTC_VRVSA

forward

reverse compliment

Name

E value

Alignment

MA0203.1_Scr 1.0721e-04 NNNATTARNN -TCATTAR--

17_TAT_TRVSA

forward reverse compliment

E value Name Alignment Motif

NNYATTARNN MA0203.1_Scr 3.5384e-05 -TCATTAR--

HDG11

forward reverse compliment

Name E value Alignment Motif

NCATTWAWKN MA0151.1_ARID3A 3.6185e-06

--ATTAAA--

HDG7

forward reverse compliment

Alignment Name E value Motif MA0170.1_C15 6.0448e-09

NCATTAAWTRN
---TTAAWKR-

HDG1

forward reverse compliment

Name E value Alignment Motif

 $\begin{array}{ccc} \text{MA0226.1_hbn} & 3.0337\text{e-09} & & \text{NYAATTAATGN} \\ & & -\text{YAATTAA}--- \end{array}$

ANL2

forward reverse compliment

Name E value Alignment Motif

 $\begin{array}{ccc} \text{MA0206.1_abd-A} & \text{4.3694e-06} & & \text{NNAATTAATGN} \\ & & -\text{TAATTAA---} \end{array}$

egl-5

forward reverse compliment

MA0248.1_tup 3.1483e-08

CCCATTAAAT -CMATTAW--

14_TCG_KGTQM

forward

reverse compliment

Name E value

Alignment

MA0248.1_tup 4.2624e-08

NNYTAATGGG --WTAATKG-

NKX6-3

forward

reverse compliment

Name

E value

Alignment

Motif

Motif

MA0215.1_btn 3.0070e-09

NTCATTAWN
-TCATTAN-

tup

forward

reverse compliment

Name E value

Alignment

SWTAATKG 2.1446e-11 MA0248.1_tup -WTAATKG

C15

forward reverse compliment

E value Name Alignment Motif

NTTAAWKR MA0170.1_C15 1.2763e-11 -TTAAWKR

232_TCG_IKNQM

reverse compliment forward

E value Motif Name Alignment

NYCATTARNN MA0248.1_tup 3.8435e-09

-CMATTAW--

ATML1

forward reverse compliment

Name E value Motif Alignment

MA0186.1_Dfd 8.4622e-05 NNNANTNANN

-TCATTAA--

226_TTT_KMISA

forward reverse compliment

Name E value Alignment Motif

MA0075.1_Prrx2 2.0502e-04 NNNATTANNN --AATTA---

Isl1

forward reverse compliment

Name E value Alignment Motif

MA0132.1_Pdx1 2.3124e-06 NCCATTAGN --AATTAG-

236_TAG_KSTQM

forward reverse compliment

10/21/20

MA0248.1_tup 4.8824e-06

NCCATTANNN -CMATTAW--

NANOG

forward

reverse compliment

Name E value

Alignment

MA0214.1_bsh 1.0306e-04

NCNRTYAN -YMATTAA

Dfd

forward

reverse compliment

Name

E value

Alignment

Motif

Motif

MA0232.1_lbl 1.7692e-06

NNYCATTANN
--TMATTA--

HB-5

forward

reverse compliment

Name

E value

Alignment

MA0110.1_ATHB-5 2.0816e-07

NNANCAATAATTGNNNNNWN ----AATMATTGN-----

ATHB-21

forward reverse compliment

E value Name Alignment Motif

NNAATWATTGNTNN MA0110.1_ATHB-5 6.3559e-07 NCAATKATT----

ATHB-53

forward reverse compliment

E value Motif Name Alignment

NCAATTATTGN MA0110.1_ATHB-5 4.4373e-10

NCAATKATT--

HAT5

forward reverse compliment

MA0008.1_HAT5 2.8499e-08

NNAATAATTNW --AATAATTN-

ATHB-13

forward reverse compliment

Name E value Alignment Motif

NNAATTATTRN MA0008.1_HAT5 4.2208e-08 -NAATTATT--

ATHB-16

forward reverse compliment

E value Motif Name Alignment

TAATMATT-MA0008.1_HAT5 1.8398e-09

-AATAATTN

ATHB-20

forward reverse compliment

Name E value Motif Alignment

MA0008.1_HAT5 2.7583e-08 NYAATAATTNN --AATAATTN-

ATHB-5

forward reverse compliment

Name E value Alignment Motif

NCU03070

forward reverse compliment

Name E value Alignment Motif

 $\begin{array}{ccc} \text{MA0216.1_cad} & 6.3417\text{e-}05 & & \text{NNYCAATAWW} \\ & ---\text{YAATAAA} & & \end{array}$

ATHB-51

forward reverse compliment

MA0008.1_HAT5 1.7745e-05

NNAATWAT----AATAATTN

PK20392.1

forward reverse compliment

Name E value Alignment Motif

MA0008.1_HAT5 9.0427e-05 NNAATMATNN --AATAATTN

ATHB-6

forward reverse compliment

Name E value Alignment Motif

MA0110.1_ATHB-5 6.6140e-05 NNAATNATN---AATMATTGN

GSC₂

forward reverse compliment

MA0094.1_Ubx 2.0696e-03

NTAATNNN -TAAT---

Isl2

forward reverse compliment

Name E value Alignment Motif

MA0094.1_Ubx 3.3589e-03 NNNTNNN --ATTA-

Obox3

forward reverse compliment

Name E value Alignment Motif

MA0094.1_Ubx 1.7438e-03 NNATNWN --ATTA-

POU5F1B

forward reverse compliment

MA0075.1_Prrx2 3.0457e-03

NNAANNN -TAATT-

En1

forward reverse compliment

Name E value Alignment Motif

MA0075.1_Prrx2 2.1945e-03 NNNANNN -TAATT-

Dlx4

forward reverse compliment

Name E value Alignment Motif

MA0075.1_Prrx2 2.1990e-03 NTAATNNN -TAATT--

Pdx1

forward reverse compliment

MA0094.1_Ubx 2.5080e-03

NNNATTAN ---ATTA-

E5

forward reverse compliment

Name E value Alignment Motif

Isx

forward reverse compliment

Name E value Alignment Motif

MA0094.1_Ubx 2.0861e-03 NNATTNNN --ATTA--

Hoxd1

forward reverse compliment

Name E value Alignment Motif

MA0075.1_Prrx2 2.9738e-03 NNNNATYN

Q6WL90_TRICY

forward reverse compliment

Name E value Alignment Motif

Otp

forward reverse compliment

Name E value Alignment Motif

MA0075.1_Prrx2 2.0878e-03 NNTAATNN --TAATT-

Rhox6

forward reverse compliment

10/21/20

NTAATNNN MA0094.1_Ubx 2.0443e-03 -TAAT---

Evx2

forward reverse compliment

Name E value Alignment Motif

NNATTANN MA0075.1_Prrx2 2.3487e-03 -AATTA--

Hoxb6

forward reverse compliment

Alignment E value Motif Name

NNNNNN MA0094.1_Ubx 2.5913e-03 TAAT---

Dbx2

forward reverse compliment

Name E value Alignment Motif

MA0094.1_Ubx 4.4778e-03 NNNTNNN TAAT---

Hoxd8

forward reverse compliment

Name E value Alignment Motif

MA0094.1_Ubx 4.7931e-03 NNNNNNNN ---ATTA-

Obox5

forward reverse compliment

Name E value Alignment Motif

MA0094.1_Ubx 2.4391e-03 NNNATNAN ---ATTA-

Barx2

forward reverse compliment

MA0094.1_Ubx 3.1310e-03

NNNNATTAN
----ATTA-

Hoxa5

forward reverse compliment

Name E value Alignment Motif

MA0094.1_Ubx 3.3308e-03 NTAATNNNN -TAAT----

barx1

forward reverse compliment

Name E value Alignment Motif

MA0075.1_Prrx2 3.1848e-03 NNNNATTAN ---AATTA-

Nkx6-1

forward reverse compliment

MA0075.1_Prrx2 3.4714e-03

NNTAATNRN --TAATT--

Hoxb3

forward reverse compliment

Name E value Alignment Motif

Dlx3

forward reverse compliment

Name E value Alignment Motif

Gsx2

forward reverse compliment

MA0075.1_Prrx2 3.0869e-03

NTAATNNNN -TAATT---

Evx1

forward reverse compliment

Name E value Alignment Motif

MA0075.1_Prrx2 3.1475e-03 NTAATNNNN -TAATT---

Hoxb5

forward reverse compliment

Name E value Alignment Motif

MA0094.1_Ubx 3.7479e-03 NTNATNNNN -TAAT----

-TAAT-

Nkx6-3

forward reverse compliment

MA0075.1_Prrx2 3.8618e-03

NNNATNANN
--AATTA--

Emx2

forward reverse compliment

Name E value Alignment Motif

Nkx1-2

forward reverse compliment

Name E value Alignment Motif

Bsx

forward reverse compliment

MA0075.1_Prrx2 3.4670e-03

NTAATNNNN -TAATT---

Lbx2

forward reverse compliment

Name E value Alignment Motif

MA0094.1_Ubx 5.3979e-03 NNAANNNN -TAAT---

NEMVEDRAFT_v1g81309

forward reverse compliment

Name E value Alignment Motif

CBG20882

forward reverse compliment

MA0094.1_Ubx 4.1346e-03

NYNATNNNN ---ATTA--

Hoxa6

forward

reverse compliment

Name E value

Alignment

MA0094.1_Ubx 3.7532e-03

NNNNATTAN
----ATTA-

ceh-5

forward

reverse compliment

Name

E value

Alignment

Motif

Motif

MA0075.1_Prrx2 3.4502e-03

NNTAATNNN --TAATT--

Nobox

forward

reverse compliment

Name E value

Alignment

MA0094.1_Ubx 4.8980e-03

NNYNATNNN ----ATTA-

Nanog

forward

reverse compliment

Name E value

Alignment

MA0075.1_Prrx2 4.5812e-03

NNNATNNNN -TAATT---

Meox1

forward

reverse compliment

Name

E value

Alignment

Motif

Motif

MA0075.1_Prrx2 4.5297e-03

NTAATKRNN -TAATT---

YOX1

forward

reverse compliment

Name

E value

Alignment

MA0094.1_Ubx 1.1609e-02

YNATWWN
--ATTA-

NEMVEDRAFT_v1g136480

forward reverse compliment

Name E value Alignment Motif

MA0094.1_Ubx 7.7218e-03 NNNNNNNNN ----ATTA--

21_TAC_ERVSV

forward reverse compliment

Name E value Alignment Motif

MA0212.1_bcd 2.7894e-03 NCGYATTANN
--GGATTA--

20_TAC_QRVSA

forward reverse compliment

MA0203.1_Scr 1.4870e-04

CGYATTARNN -TCATTAR--

216_TGC_NRVMM

forward

reverse compliment

Name E value

Alignment

MA0212.1_bcd 6.8226e-04

NGCATTARNN -GGATTA---

235_TAT_RAVSV

forward

reverse compliment

Name

E value

Alignment

Motif

Motif

MA0186.1_Dfd 9.5367e-04

NNYTAATGNN --TTAATGA-

229_TTC_GRISA

forward

reverse compliment

Name

E value

Alignment

MA0356.1_PHO2 1.8486e-03

NNYATTANNN --TAWTAW--

Hoxb8

forward reverse compliment

Name E value Alignment Motif

MA0094.1_Ubx 6.4583e-03 NNNNATWNN ----ATTA-

Hoxc8

forward reverse compliment

Name E value Alignment Motif

MA0094.1_Ubx 8.9132e-03 NNNNNNNN ----ATTA-

CBG00023

forward reverse compliment

MA0094.1_Ubx 5.4028e-03

NNNNNATWAN
----ATTA-

Hmx2

forward

reverse compliment

Name E value

Alignment

MA0426.1_YHP1 3.6198e-04

NNNCRNTTNN ---CAATTA-

Hmx1

forward

reverse compliment

Name

E value

Alignment

Motif

Motif

MA0426.1_YHP1 3.2593e-04

NNNCRNTTNN
---CAATTA-

SIX5

forward

reverse compliment

Name

E value

Alignment

MA0335.1_MET4 2.1780e-03

GARTTGTAGT -ANCTGTGG-

schlank

forward reverse compliment

E value Name Alignment Motif

AWNTTGGTRG MA0193.1_Lag1 2.2828e-10 ---TTGGTRG

yox1

forward reverse compliment

Name E value Alignment Motif

NNNNATNNNN MA0075.1_Prrx2 7.7965e-03

--TAATT---

Noto

forward reverse compliment

MA0075.1_Prrx2 6.3461e-03

NNNNATNNNN ---AATTA--

UNCX

forward reverse compliment

Name E value Alignment Motif

MA0075.1_Prrx2 1.8805e-03 NNAATTNN
-TAATT--

pha-2

forward reverse compliment

Name E value Alignment Motif

CG15696

forward reverse compliment

MA0426.1_YHP1 2.0724e-02

NNYAATNNN --CAATTA-

CG34031

forward reverse compliment

Name E value Alignment Motif

MA0426.1_YHP1 2.0324e-02 NYNNNNNN -CAATTA-

NEMVEDRAFT_v1g80394

forward reverse compliment

Name E value Alignment Motif

NOBOX

forward reverse compliment

MA0426.1_YHP1 3.2827e-02

NNYNATNNNN --CAATTA--

IRX5

forward reverse compliment

Name E value Alignment Motif

MA0328.1_MATALPHA2 3.9553e-05

NNNTGTNNNACAYNN
----AATTACATG-

MTAL2_KLUDE

forward reverse compliment

Name E value Alignment Motif

MA0328.1_MATALPHA2 6.6896e-12 CRTGTAAW-CATGTAATT

HMRA2

forward reverse compliment

MA0328.1_MATALPHA2 1.7878e-12

-WTTACAYG AATTACATG

Rhox8

forward reverse compliment

Name E value Alignment Motif

MA0392.1_STB5 2.3740e-05 NTTACACCN
-TANNNCCG

mirr

forward reverse compliment

Name E value Alignment Motif

ara

forward reverse compliment

1.6159e-06 MA0210.1_ara

TGTTWTNN TGTTW---

caup

forward reverse compliment

E value Name Alignment Motif

TGTTANWN MA0217.1_caup 1.6159e-06 TGTTA---

CG11617

forward reverse compliment

Motif E value Name Alignment

-TGTWAAAW MA0173.1_CG11617 1.4526e-07

ATGTWAA--

51_CAG_MSHWR

forward reverse compliment

Name E value Motif Alignment

MA0217.1_caup 1.9443e-06 NCTGTTAN --TGTTA-

49_CAT_LSQSR

forward

reverse compliment

Name E value

Alignment

Motif

MA0173.1_CG11617 1.9340e-06

NNTGTTARN
-ATGTWAA-

253_CGT_VANSR

forward

reverse compliment

Name

E value

Alignment

Motif

MA0217.1_caup 4.9392e-06

NNTGTTANN --TGTTA--

55_CAA_LHYVR

forward

reverse compliment

Name E value

Alignment

Motif

MA0217.1_caup 8.1367e-06

NNTTGTTANN
---TGTTA--

HMLALPHA2

forward reverse compliment

Name E value Alignment Motif

MATALPHA2

forward reverse compliment

Name E value Alignment Motif

MA0210.1_ara 2.0207e-02 NNNGNNNN --TGTTW-

CBG08197

forward reverse compliment

10/21/20

MA0210.1_ara 1.5637e-02

NNNGTNNN --TGTTW-

Irx4

forward

reverse compliment

Name E value

Alignment

MA0210.1_ara 8.56

8.5641e-03

NTNTNNNN -TGTTW--

Irx6

forward

reverse compliment

Name

E value

Alignment

Motif

Motif

MA0210.1_ara 5.7942e-03

NTNTNNN -TGTTW-

Irx2

forward

reverse compliment

Name

E value

Alignment

Motif

MA0210.1_ara 1.6628e-02

NNNTGTNNN ---TGTTW-

Irx5

forward reverse compliment

Name E value Alignment Motif

MA0210.1_ara 1.3053e-02 NNTGTNNNN --TGTTW--

AGAP009986

forward reverse compliment

Name E value Alignment Motif

MA0210.1_ara 2.8411e-02 NNNNTGTNNN ----TGTTW-

Rhox11

forward reverse compliment

MA0210.1_ara 2.0801e-02

NNNTGTWNNN ---TGTTW--

MTAL2_PICAN

forward reverse compliment

Name E value Alignment Motif

MA0318.1_HMRA2 1.0682e-01 NNNACANNN WTTACAYG-

IRX1

forward reverse compliment

Name E value Alignment Motif

MA0328.1_MATALPHA2 9.6004e-06

NNCANNNNNNNNNNNNTGNN
-----AATTACATG--

IRX3

forward reverse compliment

MA0328.1_MATALPHA2 8.9355e-05

WACAYGNWWWWNCRTGTW
----AATTACATG--

FGRRES_07914

forward reverse compliment

Name E value Alignment Motif

MA0328.1_MATALPHA2 2.1882e-04 NNACATGTANN---CATGTAATT

SNAPOd2T00005194001

forward reverse compliment

Name E value Alignment Motif

MA0328.1_MATALPHA2 1.7656e-04 -NNTACATGTNN AATTACATG---

ATHB-4

forward reverse compliment

8.1236e-04 MA0254.1_vvl

NNYATGCAKNN --TATKCA---

hbx7

forward reverse compliment

Name E value Alignment Motif

NNNANATGCNNNN MA0322.1_INO4 2.4836e-03 TTCACATGC----

IRX2

forward reverse compliment

Name E value Alignment Motif

NNTGTCRTGTWN MA0207.1_achi 6.9992e-04

-CTGTCA----

Irx3

forward reverse compliment

Alignment E value Motif Name

MA0143.1_Sox2 2.4858e-09

--TTTKTCATGTWR-CCWTTGTNATGCANA

vis

forward reverse compliment

Name E value Alignment Motif

MA0252.1_vis 8.8622e-07 NTGTCA NTGTCA

achi

forward reverse compliment

Name E value Alignment Motif

MA0252.1_vis 8.7480e-07 NTGTCA NTGTCA

Meis2

forward reverse compliment

MA0252.1_vis 6.4391e-06

NTGTCAN NTGTCA-

MEIS1

forward reverse compliment

Name E value Alignment Motif

MA0252.1_vis 6.6419e-06 NTGACAN
-TGACAN

Meis3

forward reverse compliment

Name E value Alignment Motif

 $\begin{array}{ccc} \text{MA0227.1_hth} & 6.6077\text{e-}06 & & \text{NTGTCAN} \\ & & \text{CTGTCA-} \end{array}$

Meis1

forward reverse compliment

Name E value Alignment Motif

ANHX

forward reverse compliment

Name E value Alignment Motif

MA0408.1_TOS8 5.5807e-06 CWTGTCAA--NTGTCAAN

FGRRES_17152

forward reverse compliment

Name E value Alignment Motif

MA0328.1_MATALPHA2 7.6247e-08 -ATGACATG AATTACATG

FGRRES_17150

forward reverse compliment

NNWTGTCAWN 1.0847e-04 MA0252.1_vis --NTGTCA--

Tgif1

forward reverse compliment

Alignment Name E value Motif

NNNTGTCANN MA0227.1_hth 6.8698e-05 --CTGTCA--

Tgif2

forward reverse compliment

E value Name Alignment Motif

NNNTGTCANN 6.9961e-05 MA0227.1_hth

--CTGTCA--

CUP9

forward reverse compliment

Name E value Motif Alignment

MA0288.1_CUP9 3.7091e-11 NWTGTGTCAN WWTGTGTCA-

hbx4

forward reverse compliment

Name E value Alignment Motif

 $\begin{array}{ccc} MA0227.1_hth & 1.0419e\text{-}04 & & NNNYGTCANN \\ & & --\text{CTGTCA}\text{-}- \end{array}$

CAGL0H02959g

forward reverse compliment

Name E value Alignment Motif

ANIA_00885

forward reverse compliment

Name E value Alignment Motif

MA0207.1_achi 1.9445e-04 NNNTGTMANN

--CTGTCA--

GRMZM2G087741

forward

reverse compliment

Name E value

Alignment

Motif

MA0227.1_hth 1.3141e-06

NGMYGTCANN --CTGTCA--

GRMZM2G135447

forward

reverse compliment

Name

E value

Alignment

Motif

MA0227.1_hth 5.9773e-09

SMYGTCAN -CTGTCA-

KNAT7

forward

reverse compliment

Name

E value

Alignment

Motif

MA0018.2_CREB1 2.6336e-07

TGACRTCT TGACGTCA

CBG24578

forward reverse compliment

Name E value Alignment Motif

MA0207.1_achi 1.4139e-07 NNNTGACAGSTN ---TGACAG---

TGIF2

forward reverse compliment

Name E value Alignment Motif

 $\begin{array}{ccc} MA0227.1_hth & 3.1704e\text{-}07 & & \texttt{TGACANNTGTCA} \\ & & -----\texttt{CTGTCA} \end{array}$

TGIF1

forward reverse compliment

MA0207.1_achi 1.8587e-07

TGACAGCTGTCA
----CTGTCA

MEIS3

forward reverse compliment

Name E value Alignment Motif

 $\begin{array}{ccc} MA0227.1_hth & 1.3353e\text{-}06 & & \texttt{TGACANNTGTCA} \\ & -----\texttt{CTGTCA} & & \end{array}$

MEIS2

forward reverse compliment

Name E value Alignment Motif

MA0207.1_achi 3.0941e-07 TGACAGCTGTCA TGACAG-----

PKNOX1

forward reverse compliment

MA0227.1_hth 5.8002e-07

TGACASSTGTCA
----CTGTCA

PKNOX2

forward reverse compliment

Name E value Alignment Motif

MA0227.1_hth 5.7190e-07 TGACANNTGTCA ----CTGTCA

TGIF2LY

forward reverse compliment

Name E value Alignment Motif

 $\begin{array}{lll} MA0227.1_hth & 3.0965e\text{-}07 & & \texttt{TGACANNTGTCA} \\ & -----\texttt{CTGTCA} & & \end{array}$

TGIF2LX

forward reverse compliment

MA0227.1_hth 2.5463e-07

TGACANCTGTCA
----CTGTCA

Pknox2

forward reverse compliment

Name E value Alignment Motif

 $\begin{array}{ccc} MA0207.1_achi & 1.0777e\text{-}07 & & \text{TGACAGGTGTCA} \\ & & \text{TGACAG-----} \end{array}$

Q5EVH4_OIKDI

forward reverse compliment

Name E value Alignment Motif

 $\begin{array}{ccc} MA0227.1_hth & 5.3087e\text{-}09 & & \text{NCTGTCAN} \\ & -\text{CTGTCA-} \end{array}$

HOS66

forward reverse compliment

MA0089.1_NFE2L1_MafG 2.0629e-02

NNNNNNN --GTCATN

KNAT4

forward reverse compliment

Name E value Alignment Motif

MA0089.1_NFE2L1_MafG 1.2367e-02 NNNNGTCNN---GTCATN

Q0ZPQ8_NEMVE

forward reverse compliment

Name E value Alignment Motif

 $\begin{array}{ccc} \text{MA0207.1_achi} & 1.1053\text{e-}02 & & \text{NTGACRNNN} \\ & -\text{TGACAG--} & & & \end{array}$

KNAT3

forward reverse compliment

MA0207.1_achi 1.4978e-02 NNNNGTCNNN --CTGTCA--

PK25034.1

forward reverse compliment

Name E value Alignment Motif

NNMNGTCANN MA0207.1_achi 1.4895e-02 --CTGTCA--

KNAT6

reverse compliment forward

Motif E value Name Alignment

NNNNGTCNNN MA0207.1_achi 1.6623e-02

--CTGTCA--

unc-62

forward reverse compliment

Name E value Motif Alignment

MA0207.1_achi 1.5344e-02 NNNTNTNNN

--CTGTCA-

Pknox1

forward reverse compliment

Name E value Alignment Motif

 $\begin{array}{ccc} \text{MA0227.1_hth} & 7.0473\text{e-}03 & & \text{NNNTGTCN} \\ & & --\text{CTGTCA} & & \end{array}$

$FGRRES_16926_M$

forward reverse compliment

Name E value Alignment Motif

FGRRES_17238

forward reverse compliment

MA0207.1_achi 2.7682e-02

NNNNACNNNN --TGACAG--

CADAORAG00002315

forward reverse compliment

Name E value Alignment Motif

MA0227.1_hth 2.1428e-02 NNNTGTNNNN --CTGTCA--

ATEG_00670

forward reverse compliment

Name E value Alignment Motif

 $\begin{array}{ccc} \text{MA0227.1_hth} & 3.4042\text{e-}02 & & \text{NNNGTNNNN} \\ & & -\text{CTGTCA--} \end{array}$

TVAG_451170

forward reverse compliment

1.2975e-03 MA0246.1_so

NNCRCATCAN ---GTATCA-

TVAG_493070

forward reverse compliment

E value Name Alignment Motif

NNTGATGTGNN MA0129.1_TGA1A 2.3900e-03 --TGACGTN--

TOS8

forward reverse compliment

E value Motif Name Alignment

WKACGTCANNN MA0018.2_CREB1 8.6372e-07

TGACGTCA---

CBG10835

forward reverse compliment

MA0199.1_Optix 1.5682e-02

NNNNTCANN --TATCA--

Phyra73700

forward

reverse compliment

Name E value

Alignment

MA0199.1_Optix 1.5829e-02

NNNNNTCAN
---TATCA-

si_dkey-43p13.5

forward

reverse compliment

Name

E value

Alignment

Motif

Motif

MA0210.1_ara 7.5942e-02

NNNNWWNNNN --TGTTW---

PK24181.1

forward

reverse compliment

Name

E value

Alignment

Motif

10/21/20

MA0227.1_hth 4.3791e-02

NNNNNNNNN-----CTGTCA

Six4

Name E value Alignment Motif

Six2

forward reverse compliment

Name E value Alignment Motif

MA0246.1_so 1.2907e-02 NNNTATNN --GTATCA

Six1

forward reverse compliment

Name E value Alignment Motif

MA0246.1_so 2.2537e-02 NNNRTATNNN ---GTATCA-

SO

Name	E value	Alignment	Motif

reverse compliment

MA0246.1_so 7.0329e-09 NGTATCAN -GTATCA-

forward

SIX2

forward reverse compliment

Name E value Alignment Motif

MA0246.1_so 2.7271e-07 NNYGATACNN --TGATAC--

SIX4

forward reverse compliment

MA0246.1_so 1.5465e-07

NNYGATACNN --TGATAC--

SIX1

forward reverse compliment

Name E value Alignment Motif

MA0246.1_so 9.5689e-05 NCGTATCRNN --GTATCA--

ceh-34

forward reverse compliment

Name E value Alignment Motif

MA0246.1_so 3.0430e-02 NNNRKATNNN ---GTATCA-

XP_003689450.1

forward reverse compliment

MA0036.1_GATA2 5.8039e-02

NNNGKNTNNN ---NGATN--

Q6Y859_MARMO

forward reverse compliment

Name E value Alignment Motif

NNNATNNNNN MA0199.1_Optix 5.3920e-03 --TATCA---

PRH_PETCR

forward reverse compliment

E value Name Motif Alignment

----TWATATAT----MA0345.1_NHP6A 4.6352e-09 NNNNNTTATATANNRNNNNN

hbx2

forward reverse compliment

E value Motif Name Alignment

MA0379.1_SIG1 6.3617e-06 NNATATATWN

---TATAT--

PDF2

forward reverse compliment

Name E value Alignment Motif

MA0277.1_AZF1 1.1933e-03 NNNGAATATTCYNTN----TTTCTTTTT

KLLA0_D10043g

forward reverse compliment

Name E value Alignment Motif

MA0379.1_SIG1 8.4022e-03 NNNNNNNNN --TATAT---

NEMVEDRAFT_v1g81436

forward reverse compliment

10/21/20

MA0216.1_cad 9.7454e-02

NNNNNANNNN ---YAATAAA

ANIA_01217

forward reverse compliment

Name E value Alignment Motif

 $\begin{array}{ccc} \text{MA0216.1_cad} & 6.6209\text{e-}02 & & \text{NNNNAATANN} \\ & --\text{YAATAAA} & & \end{array}$

ZHX1

forward reverse compliment

Name E value Alignment Motif

MA0129.1_TGA1A 1.0082e-01 NNNNRNNN TGACGTN-

ceh-74

forward reverse compliment

MA0436.1_YPR022C 6.6468e-03

NNGTGAGGNNN -NGTGGGG---

CAD25866

forward reverse compliment

Name E value Alignment Motif

 $\begin{array}{ccc} \text{MA0227.1_hth} & 2.3133\text{e-}03 & & \text{NMTCTCAANNN} \\ & -\text{CTGTCA----} \end{array}$

NKX2-1

forward reverse compliment

Name E value Alignment Motif

MA0211.1_bap 7.5503e-05 NNCACTCMAN --CACTTAA-

ATHB-12

forward reverse compliment

MA0089.1_NFE2L1_MafG 2.0267e-01

NNNNNNN -NATGAC-

RLT1

forward reverse compliment

Name E value Alignment Motif

MA0127.1_PEND 3.5933e-02 --NANGAANN
MATAAGAANT

PK25011.1

forward reverse compliment

Name E value Alignment Motif

MA0089.1_NFE2L1_MafG 1.5545e-01 NNNNNNAWNN ---GTCATN-

CIMG_06089

forward reverse compliment

MA0318.1_HMRA2 3.1007e-01

NNNNNNNNN----CRTGTAAW

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