A

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1    GCA CGA GGG AAC ACA TCA GCG GGT GTT TTG GCC GTC GGA TAT TTT TTG CCG AAG
57   AAA TTT CAT TTC GAG ACA AGT TGG TTG TCG ACT CGA AGT CTG CCA GTC ATG CAT
                                                                     M   H   2

111  GAG GTT GAC CGT ATG CTC CTA TCC GAT CGC AGG ACA GAG CGA AAC AAG AGA GTC
      E   V   D   R   M   L   L   S   D   R   R   T   E   R   N   K   R   V  20

165  CCA GCA CCT CTG TCT TCG ATG CGA GTT TTA AGC CCC TCG GGG TTT AAC AAT TCC
      P   A   P   L   S   S   M   R   V   L   S   P   S   G   F   N   N   S  38

219  ATC GGT TGT CAC TCA GTT CAG CCT GAA CAG AAC CAA AGC TAC GTC AAG CTA CTT
      I   G   C   H   S   V   Q   P   E   Q   N   Q   S   Y   V   K   L   L  56

273  CGC GGG TCG CAA GAG CAA GAC AGC AAC CCG AAG AAA GAG CTT AGC ATG GAC AGC
      R   G   S   Q   E   Q   D   S   N   P   K   K   E   L   S   M   D   S  74

327  GAC ACT GAT AGA ATT AAA AGA CCC ATG AAC GCT TTT ATG GTG TGG GCC CAA GTT
      D   T   D   R   I   K   R   P   M   N   A   F   M   V   W   A   Q   V  92

381  GAG CGA AGA CGA CTG GCT GAC GCG AAC CCA GAA CTT CAC AAC GCA GAA CTT AGT
      E   R   R   R   L   A   D   A   N   P   E   L   H   N   A   E   L   S 110

435  AAA ATC CTT GGG CAA GCT TGG AGA GCC TTG AAC GGT TTG CAG AAA AGA CCA TTC
      K   I   L   G   Q   A   W   R   A   L   N   G   L   Q   K   R   P   F 128

489  GTT GAA GAG GCC GAA CGC TTG CGA CAA CAA CAC ATC AAA GAT CAC CCT GAC TAT
      V   E   E   A   E   R   L   R   Q   Q   H   I   K   D   H   P   D   Y 146

543  AAA TAT CGG CCG CGG CGA AGA AAA CAT CCT AAA AGG GTG ATA AAA AAG ATG TCA
      K   Y   R   P   R   R   R   K   H   P   K   R   V   I   K   K   M   S 164

597  TCT ACC AAT CCA GCG GTC TGT GCC TTG GTC CAA GAG CGC AAA GAC GCA TCC CCT
      S   T   N   P   A   V   C   A   L   V   Q   E   R   K   D   A   S   P 182

651  CGC GTC TCT CGA TTG AAT CCA ACA ACT GAC TGT GGA CGC CTC CCG TTC AAC CCT
      R   V   S   R   L   N   P   T   T   D   C   G   R   L   P   F   N   P 200

705  TCA GAT GGA AAT CCG ATA GGT TTT GCG CCT CTC CCG AAG CAG ACG GGA TTT CCT
      S   D   G   N   P   I   G   F   A   P   L   P   K   Q   T   G   F   P 218

759  AGT GGA GAA ATG AAA CTT TCG CAT CTT GGA AGT CCG CCT GTT TTG CCC AAG TTG
      S   G   E   M   K   L   S   H   L   G   S   P   P   V   L   P   K   L 236

813  CCC GAG ATA AGT CTC CTC ACA CCC GAG CCA AGT CCT GGT TCA AGC GAG TTT GGC
      P   E   I   S   L   L   T   P   E   P   S   P   G   S   S   E   F   G 254

867  AGC GAG TTC AAT TTT CCA AGC GGC TGG CAA GAC CTG CCT AAC GCG CCG GTA AAT
      S   E   F   N   F   P   S   G   W   Q   D   L   P   N   A   P   V   N 272

921  CTA CAA CCC AAA ACG TTG CAA TCA ACC TCG CCA GCG TCG TAC GTC GGT GTA TCC
      L   Q   P   K   T   L   Q   S   T   S   P   A   S   Y   V   G   V   S 290

975  ACC GCA AAT TCG ACG CTT GCC AGC CAG CTC TAT TTC TCG AAC GGA AGT GTA AAT
      T   A   N   S   T   L   A   S   Q   L   Y   F   S   N   G   S   V   N 308

1029 GCA ATG ACA TTG AAC CCA TCG ATC GCT GGC AGC GTG AAT GCA GCT CAC CTG CAG
      A   M   T   L   N   P   S   I   A   G   S   V   N   A   A   H   L   Q 326

1083 AAC AGC GTT GCA AGT TCA AGC CAA CTT TTC TCG TCT TTT CAC ATC ACA GAA TTA
      N   S   V   A   S   S   S   Q   L   F   S   S   F   H   I   T   E   L 344

1137 ATA CCC GAG GAG GAT TTC AAC CGA GAG GAG TTT GAT CAA TAC CTT GAT GGG ACA
      I   P   E   E   D   F   N   R   E   E   F   D   Q   Y   L   D   G   T 362

1191 GAA ACG GCG AAC ATT TCT TGG ATG TAA GCT GCT GGA ATG ACA GCT TGG AAA CGA
      E   T   A   N   I   S   W   M   *                                     370

1245 GAA TGA ACT CGG TCG TAA TCG CAG AAG CAA ATC TTT TAG GTG CGA TCA AGA CAT
1299 TTA GTC AAT ATT ATC ATG CGA CGG ATT TAG TAC ATC GTC AAG ATC GTT GCA AGC
1353 GAA CAT TTC TCT TGT CAT CAT AGT ATT AGT TTG TCC AAA TAT TTT CAT GCG CGA
1407 TGC GTA CGC TTT CTA TTT TTT TCT CGC TGT ACA GTT TAC ATA TCG CAG AGG TCA
1461 AAC GCT TGG GCT GTA GAC AGT TGA AAG CTT AAA GTC TCG AAG GAG CCC CGC AGA
1515 GTT TCA AAT TCC GTT TCT TAA ACT TAT ACG TGG GTA TAC ATT GTC ATA GTT TAT
1569 ATT TTG ATG TAA ATT TAT TGT GGG TTG CTA TCG AAA TAA AGA TTT TGT AAT GAA
1623 AAA AAA AAA AAA AAA A
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B

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AmSoxF      1 ----------------------------------------------------------------------------MHEVDRMLLSDRRTER
NvSoxF1     1 ----------------------------------------------------------------------------MRAPEELKLEPDEKRI
DmSoxF      1 MEPSYDHEHPHRLLTNYNSKKYPHVSRTPEYSHSTGSDYPEHGGYLTDGRLMHESNSDAGIYHVRQGSEHSSPSLHSPAIQSSGYENEHL
CiSoxF      1 ----MTGLLHVVPPNNAGSGTLPYTIPSDEYSRSLTSFVDPYSSPSGYSPQRDYLESMGLLTRAVSGSSPESSKSVSTPSIFTAGLNSGL
XlSox17a    1 ----------------------------------------------------------------------------MSSPDGGYASDDQNQG
HsSox17     1 ----------------------------------------------------------------------------MSSPDAGYASDDQSQT
HsSox7      1 ----------------------------------------------------------------------------------------------
MmSox7      1 ----------------------------------------------------------------------------------------------
FrSox18     1 ----------------------------------------------------------------------------MNLAESRLS

AmSoxF     17 NKEWPAPLSSWRVLSPSGFNNSFCCHSVQPEQNQSYVKLLRGSQEQDSNP-----------------------------------------
NvSoxF1    17 AEGKRPVPLPFTIPNATFTQAAQMRDRDLPYTNWLGSLSGSSGRARTEK-----------------------------------------
DmSoxF     91 NEAWLAAHSHSHSPMPMVSSAYWGGGTASGSLINSNIPLLGGGGNSVLNKFLSHPHAGMVGGGTGQMEDCTSHSPIEAASMWSYDYKGDL
CiSoxF     87 FYSQYSTVTSSTTSPYTSSSQWLSPQVTNAGHYQQYACPYNLTNASQPSLAVNDQTSYLSSYPELYADTITN-------------------
XlSox17a   17 KCSWPIMMTGLGQCQWAEPMTSLGEGKLKSDAGS-------ANSRS-------------------------------------------
HsSox17    17 QSALPAVMAGLGPCPWAESLSPLGDMKVKGEAPANSGAPAGAAGRA-----------------------------------------
HsSox7      1 ------MASLLGAYPWTEGLECPALEARLSDGLSPPAVPRPSGDK-----------------------------------------------
MmSox7      1 ------MASLLGAYPWTEGLECPALEARLSDGLSPPAVPRPSGDK-----------------------------------------------
FrSox18    10 RETLLHGARLSLRGPWASRTPSPASDSDMGFEQNLSGDSSSPDVRRTEPRISLTSGG-------------------------------

                                                                   *                   *
AmSoxF     67 ----------------------KKELSMDSDTDRIKRPMNAFMVWAQVERRRLADANPELHNAELSKLLGQAWRALNGLQKRPFVEEAER
NvSoxF1    67 ---------------------------DDETERIKRPMNAFMVWAQVERRRLADANPELHNAELSKLLGLTWRALNSTQKRPFVEEAER
DmSoxF    181 CAPNCGYLERHKPLPADLKYRPPGGTQSKSAKESRIRRPMNAFMVWAKIERKKLADENPELHNAELSKLLGKKWRSLTPQDRRPVVEEAER
CiSoxF    159 -------------NTSVRSRKSTETAKAAKDEPRIRRPMNAFMCWAKTERRRQAAAFPDHNAELSKLLGKKWKESNEDKRPYLTSAEK-
XlSox17a   56 ------------------------------KAEARIRRPMNAFMVWAKDERRRLAQQNPDLHNAELSKLLGKKWSMTLAERPEVEEAER
HsSox17    63 ------------------------------KGESRIRRPMNAFMVWAKDERRRLAQQNPDLHNAELSKLLGKKWMATLAERPFVEEAER
HsSox7     40 ------------------------------GSESRIRRPMNAFMVWAKDERRRLAVQNPDLHNAELSKLLGKKWMATLSQKRPVVEEAER
MmSox7     40 ------------------------------SSESRIRRPMNAFMVWAKDERRRLAVQNPDLHNAELSKLLGKKWMATLSQKRPVVEEAER
FrSox18    67 ----------QSPAMSSTGGVPSGDGKAAGGSQRIRRPMNAFMVWAKDERRRLALQNPDLHNAWLSKLLGQSWMALSATDKRPFVEEAER
                                                                                   HMG domain

AmSoxF    135 LRQQHIKDHPDYKYRPRRRKHPKKVLKKMSSTNPAVCALVQERKDASPRVSRLNPTTDCGRLPFNPSDG---------------------
NvSoxF1   129 LRLQHMQDYPNYKYRPRRRKHSKNAAKRSTGAAAGSKVNGTACEKSSGQETVSRFNCLVESSFFQVPG-----------------------
DmSoxF    271 LRVIHMTHPDWKYRPRRRKQSSLRANQPGGKKQSESSPNPSTGGSKSNPKLATPPLATASSSYTTPTDESTCNSYNQHGQSTPGGLYE
CiSoxF    236 LRMKHMQEHPDYKYRPRKFKPKSRRGKTTAADDKGVTGDHFGGSTNCGKTLNTKLGTTGKLVNGKS-----------------------
XlSox17a  117 LRVQHMQDHPNYKYRPRRRKQVKRMKRAENGFMHMAEAQESAVLGADG-RMCLENFSLGYHEQTYSHG----QVPQSSHYREPQ-AVAP-
HsSox17   124 LRVQHMQDHPNYKYRPRRRKQVKRLKRVEGGFLHGLAEPQAAALGPEGGRVAMDGLGLQFPEQGFPAGPPLLPPHMGGHYRDCQSLGAP-
HsSox7    101 LRLQHMQDYPNYKYRPRRRKQAKRLGCRVDPGFLLSSLSRDQNALPEKRSGSRGALGEKEDRGEYSPGTALPSLRGCYHEGPAGGGGG--
MmSox7    101 LRLQHMQDYPNYKYRPRRRKQAKRLGCRVDPGFLLSSLSRDQNTLPEKNGIGR---GEKEDRGEYSPGATLPGLHSCYREGAAAAPG---
FrSox18   147 LRVQHLQDHPNYKYRPRRRKQTKKLKRVEPGLLLHSLAQASSSGLGMGPGMSPVAAEAIAGGPVYGHHGSLPPYHPSHHLSTSHGHFRDL

AmSoxF    204 ------------------------------------------------------NPIGFAPLPKQTGFPSGEMKLSHLGSPPVLPKLPPITS
NvSoxF1   197 ------------------------------------------------------TPNSPIPSPEPKPGKSQFSALTDPEVSMLPAPFPNLE
DmSoxF    361 QPLKPTYSPSSVDCYSNADSTEQIESLAANCPPALLNESSPTGGGYDNSLLLKKLTKPSPSSKAAKSRQEKLAKSEEKNKGSQSQGQSQQG
CiSoxF    304 ------------------------------------------------------IYSANSLFSSDQAHVRRNHSNNNSRHGNKYGPGF
XlSox17a  200 ------------------------------------------------HYDGYSLPTP-ESSPLDLAEA---DPVFFTSPAQDPCQ
HsSox17   213 ------------------------------------------------PLDGYPLPTP-DTSPLDGVDP---DPAFFAAPMPGDCP
HsSox7    189 ------------------------------------------GTPSSVDTPYPGLPTPEMSPLDVLEP---EQTFFSSPCQEPHG
MmSox7    185 ------------------------------------------------SVDTPYPGLPTPEMSPLDALEP---EQTFFSSSCQEPHG
FrSox18   237 Q-----------------------------------------------AVPGHLELESYGLPTP-EMSPLDILEEGAGESVFFPQHMQEPAG

AmSoxF    241 LLTPEPSPGSSEPGSSFNFPSGWQDLPNNPWNLQPKTLQSTSPASYWGVSTANSTLASQLYFSNGSVN-------AMTLNPSIAGSVNAA
NvSoxF1   234 DIDLPTPESSPGRAETSKVFTFPTAAVAAAWEFRSTLLGMLASQSASVHSTHNTSLFGTGNVSYSSQS-----------SIVNAQASTGP
DmSoxF    451 IYAATYPLAPTSVAVVAARGMVTCNNKGLLDHGHSVKGTFVPVPVSPSEDNSTSMRNSISALQQHCN-------VVTSTPSSSPGTMPT
CiSoxF    338 SNSFSPYDSTASPPYASLESLFSNTPNSSSYQIKHKSPGERMESLPDSCSSTSKCDINFDGQAYTNRAN-------QSSLFNYNTTVSS
XlSox17a  234 MMPYSYNGSYPHQQNSMLVRQMPQTEQMG---QVSPVQGMMACQSSPHMYYGQMYLPGSAR----------------HHQLHQAPQPSPP
HsSox17   247 AAGTYSYAQVSDYAGPPEPPAGPMHPRLGPEPAGPSIPGLLAPPSALHVYYGAMGSPGAGGRGFQMQPQHQHQHPHPGPPQPSPP
HsSox7    230 HPRRIPHLPGHPYSPEYAPSPLHCSHPLGSLALGQS------PGVSMMSPVPGCPPSPAYYSPATYHP-------LHSNLQAHLPQLSPP
MmSox7    222 HPHHLPHLPGPPYSPEFTPSPLHCSHPLGSLALGQS------PGVSMMSPVSGCPPSPAYYSHATYHP-------LHPNLQAHLPQLSPP
FrSox18   281 MVGWSSYHQHHQLHHNQQYSQAPLSESTSSYSFSHLPASLPQPAKSQQTSHHSAAPAGYFSYASSTPN-------STYHMSCHLPQLSPP

AmSoxF    324 HLQNSVASSS-------------------QLFSSFHIPEEHPMPEEPDYYDGTETANISWM-----------------------
NvSoxF1   313 QQSIP-----------------------------LSDLLLDDLNLNTNPEDQYLDGTELDAFDYVI-------------------
DmSoxF    534 SEMSSYTVSMADNCGNLRLSMNELSGNEYLPSANAYGMQYEDFLRYQSNDMDYSTSAVEHKETTSDSASGQKCLKYPDTNQNYDDYEAEA
CiSoxF    420 PQIRN-----------------------------PIDPSCFTKYTAPSTNRYTDFTAVTTCQSTGLEP-------------------
XlSox17a  305 PEAQQMGR-----------------------ADHIQPADMLAEVDPTEPEQYISYVAKSDLGMHY-------------HAQESVVPT
HsSox17   337 PEALPCRDG-----------------------TDPSQPAELLGEVDPTEPEQYISFVCKPEMGLPY-------------QGHDSGVNL
HsSox7    307 PEHPG---------------------------FDALDQLSQVELLGPMDPNEPDQYINTPGHPDSATGAMALSGHVP-------VSQVTPT
MmSox7    299 PEHPG---------------------------FDTLDQLSQVELLGPMDPNEPDQYINTPGHPDSAAGVGTLTGHVP--------LSQGTPT
FrSox18   364 PETPPSSCSSSSIIQSTFPNSIPLEHLNPETTSHLNSSSGEFWSPVDPNEPDQYVNAGRIREEALGRGVGVLKGPSGRGSSSVMSAAPSC

AmSoxF        ------------------------------------------------------------------------------------------
NvSoxF1       ------------------------------------------------------------------------------------------
DmSoxF    624 YSNAMLPATAASYYTQLPYPPTSLAAFPLQLAVPPQQTTSGAYGAQPIQSGYLHYGNYGGYEGMARVSHRTKRPSTISRHPTRLRPPCQC
CiSoxF        ------------------------------------------------------------------------------------------
XlSox17a  356 AD-NGPISSVLSDASTAVYYCNYPSA-------------------------------------------------------------
HsSox17   389 PDSHGAISSVVSDASSAVYYCNYPDV-------------------------------------------------------------
HsSox7    364 GPTETSLISVLADATATYYNSYSVS-----------------------------------------------------------------
MmSox7    356 GPTETSLISVLADATATYYNSYSVS-----------------------------------------------------------------
FrSox18   454 DEGGSSLISALSDASSAVYYNTCITG-----------------------------------------------------------------

AmSoxF        -----
NvSoxF1       -----
DmSoxF    714 HPTRR
CiSoxF        -----
XlSox17a      -----
HsSox17       -----
HsSox7        -----
MmSox7        -----
FrSox18       -----
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