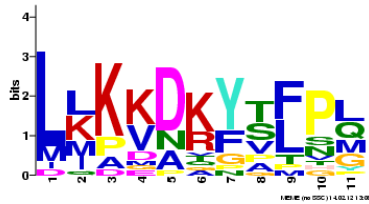


Group SoxB

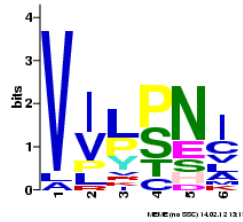
Group B motif

Name	Start	p-value	Sites		
HsaSox14	85	3.61E-13	KYRPRRKPKN	LLKKDRYVFPL	PYLGDTDPLK
MmSox14	243	3.61E-13	KYRPRRKPKN	LLKKDRYVFPL	PYLGDTDPLK
MmSox2	120	1.22E-11	KYRPRRKTKT	LMKKDKYTLPG	GLLAPGGNSM
XlaSox3	117	8.07E-11	KYRPRRKTKT	LLKKDKYSLPG	NLLAPGVSPV
AmiSoxB1	108	8.39E-10	YRPRRKSRTL	LKKDNKYTLSM	LGAQGGPPVQ
CinSoxB2	90	1.12E-09	YRPRRKPKSL	IKPKDRFAFPL	FPSSGMSSPT
AmiSoxBb	87	2.33E-09	YKPRRRKQKQ	LIKKATYSFPY	TGTENAAHAA
NvSoxB1	111	4.36E-09	YRPRRKSRTL	LKKDNKYALSM	LSAGQAGGQV
NvSoxB2	104	8.89E-08	SPVFSPPYAAS	MMAVDKFSTNQ	LPQTIAHSVA
AmiSoxBa	104	1.29E-07	GPMFSPYSSP	MMAVDKFPTNQ	LPQTIAHSTA
CinSoxB1	174	4.38E-07	YRPRRKTKAI	LKKENKFGMGP	GGIMGGGAGP
SciSoxB	199	9.30E-07	NAATIVPAGS	LQVPVNVFPQ	ANPPAPGRQV
AmqSoxB2	249	1.21E-06	DGAKQGGQTI	LIKMDAGTPHQ	VISPSYITAA
AmqSoxB1	422	1.30E-06	SSNXTNSAES	LLDGAGGTLPL	QHLM
LcoSoxB	254	7.08E-06	FAYMSTAAKP	DIPVAQPTFVM	AANPALPAPG



Conserved region I

Name	Start	p-value	Sites		
HsaSox14	198	7.28E-09	THPSPTNPGY	VVPCNC	TAWSASTLQP
MmSox14	356	7.28E-09	THPSPTNPGY	VVPCNC	TAWSASTLQP
AmqSoxB1	336	2.05E-08	PVESLDSYSE	VILSNC	KVSDDCSTSIH
AmiSoxBa	151	2.79E-07	FHHSVSPGYP	VIYPNV	TAVNSHHSVT
LcoSoxB	297	1.47E-06	GHIEQPQVTY	VILPNK	A
AmqSoxB2	317	1.72E-06	QSTPTSSTTP	VIVSEI	KSHSTPQVNS
CinSoxB1	21	1.91E-06	QIPYPTSGVP	VIPSNA	HLPPPAPIAG
AmiSoxB1	233	6.23E-06	PLSYSQPSNQ	VLIPNI	KQEMPSPGSQ
NvSoxB2	150	6.67E-06	FHHSVSPGYP	VIYPSV	SNGGNVHSGS
NvSoxB1	241	9.08E-06	ITPPYTQHSP	LILPNI	KQEMPSPTGN
CinSoxB2	222	1.68E-05	ATTGANKIKS	VLYPNL	LYTFNETEEK
MmSox2	244	2.69E-05	PGMALGSMGS	VVKSEA	SSSPPVVTSS
XlaSox3	236	8.36E-05	TVMSLASMGS	VVKSEP	SSPPPAITSH
SciSoxB	249	1.16E-04	LYTAAPQYQT	FILPSA	APGQPQAVMA
AmiSoxBb	173	2.40E-04	ANSVHELPYP	VRPSEM	MIPTPTGPHG



Conserved region II

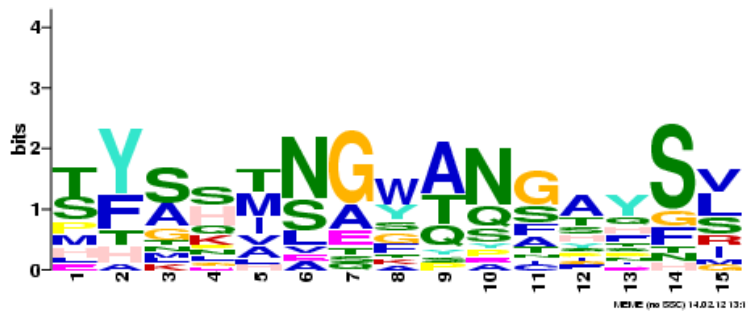
Name	Start	p-value	Sites		
MmSox3	396	1.91E-18	PAIASHSQRA	CLGDLRDMISMYLP	PGGDAADAAS
XlaSox3	256	1.91E-18	PAITSHQRA	CLGDLRDMISMYLP	PGGDASDPSL
MmSox2	267	2.11E-14	TSSSHSRAPC	QAGDLRDMISMYLP	GAEVPEPAAP
NvSoxB1	266	6.54E-14	NMNVGGVTRN	CADQLGDMINTYLP	PADTANPVST
AmiSoxB1	255	1.13E-13	PGSQSSRGRS	CTDQLGDMINTYLP	GESAAASANA
AmqSoxB1	357	4.64E-10	CTSIHSNDSG	AESDLRNMISTYLE	ESNSXPGPTE
CinSoxB2	274	1.88E-09	HGSRCEYQRL	CDEHTRCWLVAFP	AKPNPINAES
HsaSox14	97	2.11E-08	KKDRYVFPLP	YLGDTDPLKAAGLP	VGASDGLLSA
MmSox14	255	2.11E-08	KKDRYVFPLP	YLGDTDPLKAAGLP	VGASDGLLSA
AmiSoxpB	98	3.58E-08	KVDRYPFITLP	CLPTTDELLKCAPT	GIPITTSFVTD
AmqSoxB2	395	1.77E-07	ALRSAEIPYR	VYPDLSSMPLCLVP	VVDQASPGSN
LcoSoxB	180	9.92E-07	VDVRLQRASA	SMPNLHSAQTVYQP	AAPIQHHVVP
NvSoxB2	213	1.15E-06	LHSQVQQRLS	QVEDSRGMKSMNAT	PSPPVSSPDP
CinSoxB1	243	4.88E-06	PSPHAYPAMA	NSGTAANRYDMYYP	SYSTPTTLPS
AmiSoxBb	137	5.23E-06	QQYYQMSQHA	PYPPTYDMAAVHAQ	RQTHSFSTPP
SciSoxB	235	1.99E-05	TTQALNGGSS	SATNLYTAAPQYQT	FILPSAAPGQ
AmiSoxBa	201	2.26E-05	HNRALYTSQA	FQPTLPSQIQQRIS	SVDEPRGGSL



Conserved region

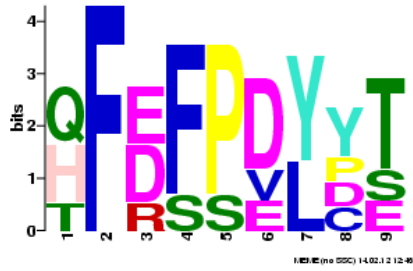
III

Name	Start	p-value	Sites		
XlaSox3	149	3.74E-17	SSVGVGQRID	TYAHMNGWTNGAYSL	MQDQLGYSQH
MmSox3	263	5.57E-16	SPVGVGQRLD	TYTHVNGWANGAYSL	VQEQLGYAQP
MmSox2	160	2.59E-12	LGGGLNQRM	SYAHMNGWSNGSYSM	MQEQLGYPOH
HsaSox14	164	2.17E-09	VPHTLATGAL	PYASTLGYQNGAFGS	LSCPSQHTHT
MmSox14	322	2.17E-09	VPHTLATSAL	PYASTLGYQNGAFGS	LSCPSQHTHT
NvSoxB2	130	5.22E-09	AHSVVALSQDP	MYSKINGGPPFHHSV	SPGYPVIYPS
CinSoxB1	270	5.26E-08	TP TTLPSMSS	LTSQHNSYAQSAYSV	GGSPAYSVAQ
AmiSoxB1	138	1.49E-07	QRSMVQNPAD	HFGQMNGFAYSPITG	YNQMNNDPY
AmqSoxB1	394	1.70E-07	PSGSSRPPTA	EFKLLNASAQCTDFI	ASNSSNXTNS
AmiSoxBa	130	2.38E-07	AHSTALSADP	MYSKINGAAAFAHHS	VSPGYPVIYP
NvSoxB1	192	7.13E-07	PPMNGLPFHG	SYSNMSASAQIYPSV	SVMTSQPVGA
LcoSoxB	148	7.60E-07	TLARAGSATF	SFGSTSEWQSNSSSR	TGSTGSQVDV
AmiSoxBb	203	9.75E-07	IYGSTMESGP	TTSGVSAFTNATQNI	HAQQIAEASP
AmqSoxB2	157	1.17E-06	PQQVVTSHGL	HHSPIATTTNFIQSL	QPAASIAGGG
CinSoxB2	230	1.59E-06	KSVLYPNLLY	TFNETEEKYETHNFR	RRLPMWITTS
SciSoxB	151	2.89E-06	TRASSAFNFP	TAMSASGWTSSGTSL	FSSTTPIGQY



Group SoxC

Name	Start	P-value	Sites		
HsaSox12	283	1.50E-12	PDLQPPSGTS	HFEFPDYCT	PEVTEMIAGD
AmiSoxC	263	3.56E-12	LLDLHGTSAG	QDFPDLYT	PPEVSELIQG
CiSoxC	494	3.26E-10	AYADPCRRKS	HFEFSDYDT	DEVKRMIESS
AmqSoxC	368	1.55E-07	FSPFNIDSCS	TFDFPELPS	DFADIFAQNA
SciSoxC	554	2.26E-07	EYSCDSNRPL	QFRSPVYYE	SRHTSSMWAP



Group SoxE

Conserved motif I

Name	Start	P-value	Sites
HsaSox9	75	2.56E-27	EDKFPVCIRE AVSQVLKGYDWTLPMPVVRVN GSSKNKPHVK
CinSoxE	177	3.52E-26	KDDMSKDIKD AVSQVLKGYDWTLPMPVRMN GSQKTKPHVK
MmSox10	74	7.28E-26	DDKFPVCIRE AVSQVLSGYDWTLPMPVVRVN GASKSKPHVK
NvSoxE1	34	3.21E-25	NHQLSNAIAS AVNHVLDGYDWSLIPLPVRVN GIKTQKPHVK
AmiSoxE1	29	3.21E-25	NMDLSSAIAT AVNHVLDGYDWSLIPLPVRVN GGHKHKPHVK
HsaSox8	70	1.81E-22	DERFPACIRD AVSQVLKGYDWSLVPMPVRGG GGGALKAKPH
LcoSoxE	345	1.04E-10	DPLTKSFKAG EWEHVLAAYVSEKCFSPDIFN TTGFSFSSSA
SciSoxE	67	9.03E-10	LTTSPRASPA PINNEEEQVDAVQKPKNVRKR KRGGDDRVR



Conserved motif II

Name	Start	P-value	Sites
HsaSox9	266	9.10E-21	RPLPEGGRQP PIDFRDVDIGELSSDVISNI ETFDVNEFDQ
HsaSox8	257	4.08E-20	GRRPVDSGRQ NIDFSNVDISELSSEVMGTM DAFDVHEFDQ
MmSox10	269	1.69E-19	GRSLGEGGKP HIDFGNVDIGEISHEVMSNM ETFDVTELDQ
SciSoxE	233	4.83E-13	TPSLSACGSV TGGSSDVDVDWLLKDTIQTC KVSPMSLNS
NvSoxE1	235	2.72E-12	FPSCSKKDDS NSHAIDFDVGDLTDDLAMG DVDSTEFDQY
CinSoxE	155	8.99E-11	SSARSASPGT NDDLSDRDSNPEKDDMSKDI KDAVSQVLKG
LcoSoxE	176	2.14E-09	EDTERLEEPT AKRFNNTISPALSVDALLQV QGQYPVDLSR
AmiSoxE1	1	6.13E-09	M TEEATNGEITNTDQRQPKNM DLSSAIATAV



Group SoxF

Name	Start	P-value	Sites
HsaSox17	354	1.19E-19	GTDPSQPAEL LGEVDRTEFEQYLHFVCK PEMGLPYQGH
MmSox17	359	3.06E-18	GTESNQPTTEL LGEVDRTEFEQYLPFVYK PEMGLPYQGH
XSiSox17	324	3.53E-16	RADHIQQVDM LAEVDRTTEFEQYLSYVAK SDLGMHYHGQ
SciSoxF1	146	1.40E-14	RIKQEEISRV FKLLSQQEITQYVGLAEK KRKTKTPKRS
AmiSoxF	346	2.29E-14	SSFHITELIP EEDFNREEFDQYLDGTET ANISWM
LcoSoxF1	142	2.35E-13	RIKQEEISRV FKLSQDEITQYVGLASK KRERPPRRKI
NvSoxF1	324	1.60E-12	SIPLSDLLLD DLNLNTNELDQYLDGTEL DAFDYVI
LcoSoxF2	90	2.65E-11	IDSADQNQRL FGNNITNEDTQGLPLVRS KKLVDQASRI
SciSoxF2	248	1.10E-10	RLDSDALNRV TKALTQQEINECVSGCIS PLMKRAPRPS
AmqSoxF	26	1.03E-09	RDREGSEVGE EENETRNGFQEEEEVVDK QEEKESKGKK
CinSoxF	732	1.12E-09	RKMSVYYDPA TTAENDAEFAKYEGKATA AQESVDIKTA

