Additional file 3: Transcription factor prediction in LEAP-2 gene promoter

Table S2A. Prediction of putative transcription factor binding sites in mud loach LEAP-2A 5'-flanking region based on TRANSFAC search

Matrix	Factor name	Position (strand)	Core score	Matrix score	Sequence
V$AHR_Q6	AhR	1899 (+)	1	1	CACGCa
V$AHR_Q6	AhR	517 (-)	1	0.998	gGCGTG
V$AP1_Q6_02	AP-1	1214 (+)	1	1	TGACTcaa
V$AP1_Q6_02	AP-1	1761 (-)	1	1	atgAGTCA
V$AP1_Q6_02	AP-1	2121 (-)	1	1	atgAGTCA
V$AP1_Q6_02	AP-1	1914 (-)	1	0.964	atcAGTCA
V$ARID5A_03	Arid5a	1034 (-)	1	0.992	cattacaATATTaa
V$ARID5A_03	Arid5a	1417 (+)	1	0.979	gtAATATtattacg
V$ARID5A_03	Arid5a	1413 (-)	1	0.966	aaaagtaATATTat
V$ARID5A_03	Arid5a	1354 (-)	1	0.963	atctaaaATATTaa
V$ARID5A_03	Arid5a	1038 (+)	1	0.958	acAATATtaagtta
V$ARID5A_03	Arid5a	1358 (+)	1	0.952	aaAATATtaatgtg
V$CREBP1_01	ATF-2 group	1426 (+)	1	1	TTACGtaa
V$CREBP1_01	ATF-2 group	1426 (-)	1	1	ttaCGTAA
V$BEN_01	BEN	1821 (-)	1	0.96	actCGCTG
V$BRCA_01	BRCA1	2202 (-)	1	0.999	CAACAcaa
V$BRCA_01	BRCA1	499 (+)	1	0.997	tttTGTTG
V$BRCA_01	BRCA1	2765 (+)	1	0.997	tttTGTTG
V$BRCA_01	BRCA1	336 (+)	1	0.987	gttTGTTG
V$BRCA_01	BRCA1	701 (-)	1	0.979	CAACAcag
V$BRCA_01	BRCA1	2094 (-)	1	0.963	CAACActa
V$BRCA_01	BRCA1	218 (-)	0.997	0.958	CAACCata
V$BRCA_01	BRCA1	821 (+)	0.994	0.958	ggtCGTTG
V$BRCA_01	BRCA1	2144 (-)	1	0.955	CAACAtct
V$CEBPA_Q6	C/EBP group	1596 (-)	0.997	0.99	agTTGCTtaatct
V$CEBPA_Q6	C/EBP group	1788 (+)	0.997	0.973	agctggAGCAAac
V$CEBPA_Q6	C/EBP group	1579 (-)	0.998	0.972	ttTTGCCacatga
V$CEBPA_Q6	C/EBP group	2191 (-)	1	0.964	caTTGCAttagca
V$CEBPA_Q6	C/EBP group	1128 (-)	1	0.963	ttTTGCAttactt
V$CEBPA_Q6	C/EBP group	1331 (-)	1	0.962	acTTGCAttactt
V$CEBPA_Q6	C/EBP group	1070 (-)	0.996	0.961	aaTTGCGttactt
V$CEBPA_Q6	C/EBP group	1447 (-)	0.996	0.96	taTTGCGttaccc
V$CEBPA_Q6	C/EBP group	2543 (+)	0.996	0.957	ttctctCGCAAag
V$CEBPA_Q6	C/EBP group	2194 (+)	0.997	0.956	tgcattAGCAAca
V$CEBPA_Q6	C/EBP group	461 (-)	0.997	0.953	agTTGCTtattaa
V$CDX2_01	CDX group	2289 (+)	1	0.96	aaatgtaATAAAataa
V$CDX2_01	CDX group	2307 (+)	1	0.959	atgtgtaATAAAatac
V$CDX2_Q5_02	CDX group (half-site)	810 (+)	1	1	TTTATa
V$CDX2_Q5_02	CDX group (half-site)	1298 (+)	1	1	TTTATa
V$CDX2_Q5_02	CDX group (half-site)	1376 (+)	1	1	TTTATa
V$CDX2_Q5_02	CDX group (half-site)	1378 (-)	1	1	tATAAA
V$CDX2_Q5_02	CDX group (half-site)	681 (+)	1	0.999	TTTATg
V$CDX2_Q5_02	CDX group (half-site)	1707 (+)	1	0.999	TTTATg
V$CDX2_Q5_02	CDX group (half-site)	1950 (+)	1	0.999	TTTATg
V$CDX2_Q5_02	CDX group (half-site)	2061 (+)	1	0.999	TTTATg
V$CDX2_Q5_02	CDX group (half-site)	67 (-)	1	0.998	aATAAA
V$CDX2_Q5_02	CDX group (half-site)	207 (+)	1	0.998	TTTATt
V$CDX2_Q5_02	CDX group (half-site)	1292 (+)	1	0.998	TTTATt
V$CDX2_Q5_02	CDX group (half-site)	1879 (+)	1	0.998	TTTATt
V$CDX2_Q5_02	CDX group (half-site)	2016 (+)	1	0.998	TTTATt
V$CDX2_Q5_02	CDX group (half-site)	2286 (-)	1	0.998	aATAAA
V$CDX2_Q5_02	CDX group (half-site)	2295 (-)	1	0.998	aATAAA
V$CDX2_Q5_02	CDX group (half-site)	2313 (-)	1	0.998	aATAAA
V$CDX2_Q5_02	CDX group (half-site)	567 (-)	1	0.994	gATAAA
V$CDX2_Q5_02	CDX group (half-site)	854 (+)	1	0.994	TTTATc
V$CDX2_Q5_02	CDX group (half-site)	862 (-)	1	0.994	gATAAA
V$CDX2_Q5_02	CDX group (half-site)	1911 (+)	1	0.994	TTTATc
V$CDX2_Q5_02	CDX group (half-site)	1955 (-)	1	0.994	gATAAA
V$CDX2_Q5_02	CDX group (half-site)	2427 (-)	1	0.994	gATAAA
V$CDX2_Q5_02	CDX group (half-site)	2496 (+)	1	0.994	TTTATc

V$CHCH_01	Churchill	1226 (-)	0.998	0.995 tTCCCG
V$CHCH_01	Churchill	2531 (-)	1	0.993 gCCCCG
V$CHCH_01	Churchill	1722 (-)	0.998	0.987 aTCCCG
V$CIZ_01	CIZ	374 (-)	1	0.998 tacTTTTTc
V$CIZ_01	CIZ	1136 (-)	1	0.998 tacTTTTTc
V$CIZ_01	CIZ	318 (-)	1	0.997 gttTTTTTc
V$CIZ_01	CIZ	587 (+)	1	0.997 gAAAAAgtt
V$CIZ_01	CIZ	193 (-)	1	0.995 attTTTTTc
V$CIZ_01	CIZ	553 (+)	1	0.995 gAAAAAaat
V$CIZ_01	CIZ	1925 (-)	1	0.994 ttcTTTTTc
V$CIZ_01	CIZ	1058 (+)	1	0.985 cAAAAAgta
V$CIZ_01	CIZ	2162 (+)	1	0.985 cAAAAAagc
V$CIZ_01	CIZ	506 (-)	1	0.984 gttTTTTTg
V$CIZ_01	CIZ	1868 (-)	1	0.984 actTTTTTg
V$CIZ_01	CIZ	443 (-)	1	0.983 tagTTTTTg
V$CP2_Q6	CP2-related factors	2022 (-)	1	0.997 tgCCAGTcag
V$CP2_Q6	CP2-related factors	2487 (+)	1	0.994 atgACTGGtt
V$CP2_Q6	CP2-related factors	51 (-)	1	0.979 aaCCAGAgag
V$CP2_Q6	CP2-related factors	1747 (-)	1	0.979 atCCAGTaaa
V$DLX3_02	Dlx group	1312 (-)	1	0.993 ctAATTAa
V$DLX3_02	Dlx group	2301 (+)	1	0.992 aTAATTat
V$DLX3_02	Dlx group	2301 (-)	1	0.992 atAATTAt
V$DLX3_02	Dlx group	1312 (+)	1	0.989 cTAATTaa
V$DLX3_02	Dlx group	1068 (+)	1	0.974 cTAATTgc
V$DLX3_02	Dlx group	309 (+)	1	0.972 tTAATTgc
V$DLX3_02	Dlx group	2369 (+)	1	0.966 aTAATTgt
V$DRI1_01	DRI1	309 (-)	1	1 TTAATt
V$DRI1_01	DRI1	1275 (-)	1	1 TTAATt
V$DRI1_01	DRI1	1314 (+)	1	1 aATTAA
V$E2A_Q6_01	E2A group	1176 (-)	1	0.971 cttacAGGTGttt
V$E2A_Q6_01	E2A group	713 (-)	1	0.964 tacacAGGTGctt
V$E2A_Q6_01	E2A group	724 (-)	1	0.963 ttcacAGGTGcta
V$E2A_Q6_01	E2A group	658 (+)	1	0.962 tagCACCTgtgta
V$E2A_Q6_01	E2A group	702 (-)	1	0.962 aacacAGGTGcta
V$EBOX_Q6_01	Ebox	992 (-)	1	0.986 tgacACGTGc
V$EBOX_Q6_01	Ebox	660 (+)	0.998	0.956 gCACCTgtgt
V$EBOX_Q6_01	Ebox	703 (-)	0.998	0.956 acacAGGTGc
V$EBOX_Q6_01	Ebox	714 (-)	0.998	0.956 acacAGGTGc
V$EBOX_Q6_01	Ebox	725 (-)	0.998	0.954 tcacAGGTGc
V$ETS_Q6	Ets-related factors	1591 (-)	1	0.99 aaGGAAGt
V$ETS_Q6	Ets-related factors	491 (+)	1	0.975 cCTTCCta
V$HNF3B_Q6	FOX factors	1751 (-)	1	0.987 agtAAACAc
V$HNF3B_Q6	FOX factors	2591 (-)	1	0.987 agtAAACAt
V$HNF3B_Q6	FOX factors	801 (+)	1	0.979 cTGTTTgtt
V$HNF3B_Q6	FOX factors	2580 (-)	1	0.973 cgcAAACAt
V$HNF3B_Q6	FOX factors	2427 (-)	1	0.97 gatAAACAa
V$HNF3B_Q6	FOX factors	2058 (+)	1	0.963 tTGTTTatg
V$HNF3B_Q6	FOX factors	851 (+)	1	0.962 aTGTTTatc
V$HNF3B_Q6	FOX factors	504 (+)	1	0.955 tTGTTTttt
V$HNF3B_Q6	FOX factors	2393 (+)	1	0.955 tTGTTTttt
V$HNF3B_Q6	FOX factors (HNF-3 isoforms)	1836 (+)	1	1 tTGTTTgct
V$GATA_Q6	GATA	566 (+)	1	0.995 aGATAAa
V$GATA_Q6	GATA	854 (-)	1	0.995 tTTATCt
V$GATA_Q6	GATA	2496 (-)	1	0.995 tTTATCt
V$GATA_Q6	GATA	1609 (+)	1	0.994 tGATAAg
V$GATA_Q6	GATA	2150 (-)	1	0.994 cTTATCa
V$GATA_Q6	GATA	2466 (+)	1	0.994 tGATAAg
V$GATA_Q6	GATA	861 (+)	1	0.989 tGATAAa
V$GATA_Q6	GATA	1911 (-)	1	0.989 tTTATCa
V$GATA_Q6	GATA	1954 (+)	1	0.989 tGATAAa
V$GATA_Q6	GATA	2426 (+)	1	0.989 tGATAAa
V$GATA_Q6	GATA	486 (-)	1	0.978 cTTATCc
V$GATA_Q6	GATA	1731 (+)	1	0.978 gGATAAg
V$GATA_Q6	GATA	2501 (-)	1	0.978 cTTATCc
V$GEN_INI_B	general initiator	244 (+)	0.995	0.995 cctCAGTT
V$GEN_INI_B	general initiator	2119 (-)	1	0.969 GAATGagt

V$GEN_INI_B	general initiator	839 (+)	0.996	0.969	ccaCATTT
V$GEN_INI_B	general initiator	360 (+)	0.996	0.966	actCATTT
V$GEN_INI_B	general initiator	271 (-)	1	0.962	GAATGaca
V$GEN_INI_B	general initiator	201 (+)	0.996	0.961	cggCATTT
V$GEN_INI_B	general initiator	2408 (+)	0.996	0.958	agtCATTT
V$GEN_INI_B	general initiator	882 (+)	1	0.957	ctgCATTC
V$GEN_INI_B	general initiator	2538 (+)	1	0.957	ctgCATTC
V$GEN_INI_B	general initiator	1764 (+)	0.995	0.957	agtCAGTT
V$GEN_INI_B	general initiator	383 (-)	0.996	0.954	AAATGaac
V$GEN_INI_B	general initiator	2112 (-)	0.996	0.954	AAATGcag
V$GEN_INI_B	general initiator	1268 (+)	0.995	0.953	gttCAGTT
V$GEN_INI_B	general initiator	2434 (-)	0.995	0.953	AACTGaac
V$GEN_INI_B	general initiator	2381 (-)	0.991	0.953	AATTGaca
V$GEN_INI_B	general initiator	2281 (-)	0.996	0.951	AAATGaat
V$GEN_INI_B	general initiator	2640 (-)	0.996	0.951	AAATGaaa
V$GFI1_Q6_01	GFI1 factors	167 (-)	1	0.993	cagTGATTtt
V$GFI1_Q6_01	GFI1 factors	759 (-)	1	0.977	ctaTGATTac
V$GFI1_Q6_01	GFI1 factors	1525 (+)	0.992	0.976	taAATCTttg
V$GFI1_Q6_01	GFI1 factors	2386 (-)	1	0.966	acaTGATTtg
V$GMEB2_04	GMEB	1426 (-)	1	1	tTACGTaa
V$GMEB2_04	GMEB	1426 (+)	1	1	ttACGTAa
V$HIF1A_Q5	HIF1	993 (-)	1	0.992	gaCACGTgc
V$HIF1A_Q5	HIF1	994 (+)	1	0.992	acACGTGca
V$HIF1A_Q5	HIF1	1434 (-)	1	0.992	tgCACGTta
V$HIF1A_Q5	HIF1	1469 (-)	1	0.992	gaCACGTcg
V$HIF1A_Q5	HIF1	1975 (-)	1	0.986	acCACGTaa
V$RUSH1A_02	hltf	1481 (+)	1	0.997	gtcCTTATta
V$RUSH1A_02	hltf	1906 (+)	0.997	0.995	gtcCTTTTat
V$RUSH1A_02	hltf	1956 (-)	0.997	0.993	atAAAAGgga
V$RUSH1A_02	hltf	1668 (-)	0.993	0.987	acACAAGgcc
V$RUSH1A_02	hltf	1731 (-)	1	0.978	ggATAAGtaa
V$RUSH1A_02	hltf	587 (-)	0.997	0.976	gaAAAAGttt
V$RUSH1A_02	hltf	1113 (+)	0.997	0.976	taaCTTTTaa
V$RUSH1A_02	hltf	1220 (+)	0.997	0.976	aaaCTTTTcc
V$RUSH1A_02	hltf	1016 (+)	0.997	0.975	ttaCTTTTaa
V$RUSH1A_02	hltf	1022 (-)	0.997	0.975	ttAAAAGtaa
V$RUSH1A_02	hltf	1085 (+)	0.997	0.975	ttaCTTTTca
V$RUSH1A_02	hltf	1124 (+)	0.997	0.975	ttaCTTTTgc
V$RUSH1A_02	hltf	1322 (-)	0.997	0.975	tgAAAAGtaa
V$RUSH1A_02	hltf	1346 (-)	0.997	0.975	ttAAAAGtat
V$RUSH1A_02	hltf	1411 (-)	0.997	0.975	agAAAAGtaa
V$RUSH1A_02	hltf	373 (+)	0.997	0.974	ttaCTTTTtc
V$RUSH1A_02	hltf	1058 (-)	0.997	0.974	caAAAAGtaa
V$RUSH1A_02	hltf	1135 (+)	0.997	0.974	ttaCTTTTtc
V$RUSH1A_02	hltf	1338 (+)	0.997	0.974	ttaCTTTTtt
V$RUSH1A_02	hltf	1866 (+)	0.997	0.974	ttaCTTTTtt
V$RUSH1A_02	hltf	1440 (+)	0.993	0.972	ttaCTTGTat
V$RUSH1A_02	hltf	2403 (-)	0.993	0.966	aaACAAGtca
V$IK_Q5_01	Ikaros	2691 (+)	1	0.991	TGGGAgt
V$IK_Q5_01	Ikaros	8 (-)	1	0.986	ctTCCCA
V$IK_Q5_01	Ikaros	1491 (+)	1	0.982	TGGGAtg
V$IK_Q5_01	Ikaros	2503 (-)	1	0.977	taTCCCA
V$IK_Q5_01	Ikaros	529 (+)	1	0.973	TGGGAtt
V$IK_Q5_01	Ikaros	284 (+)	1	0.963	TGGGAcc
V$ING4_01	ING4	238 (+)	1	1	cCACCA
V$ING4_01	ING4	1054 (+)	1	1	cCACCA
V$IRF1_Q5	IRF factors	2636 (+)	1	0.988	gagaaaaTGAAAga
V$IRF1_Q5	IRF factors	1315 (+)	1	0.959	attaaacTGAAAag
V$ISL1_Q3	ISL-1	2196 (-)	1	0.994	CATTAgca
V$ISL1_Q3	ISL-1	277 (-)	1	0.989	CATTAagt
V$ISL1_Q3	ISL-1	2586 (-)	1	0.989	CATTAagt
V$ISL1_Q3	ISL-1	2669 (-)	1	0.989	CATTAggt
V$ISL1_Q3	ISL-1	843 (+)	1	0.986	attTAATG
V$ISL1_Q3	ISL-1	1428 (+)	1	0.986	acgTAATG
V$ISL1_Q3	ISL-1	1514 (+)	1	0.986	gtgTAATG
V$ISL1_Q3	ISL-1	255 (+)	1	0.984	aacTAATG

V$ISL1_Q3	ISL-1	947 (-)	1	0.984	CATTAaaa
V$ISL1_Q3	ISL-1	1362 (+)	1	0.982	tatTAATG
V$ISL1_Q3	ISL-1	121 (+)	1	0.981	ttgTAATG
V$ISL1_Q3	ISL-1	1026 (+)	1	0.981	aagTAATG
V$ISL1_Q3	ISL-1	1034 (-)	1	0.981	CATTAcaa
V$ISL1_Q3	ISL-1	1099 (+)	1	0.981	aagTAATG
V$ISL1_Q3	ISL-1	1133 (-)	1	0.981	CATTActt
V$ISL1_Q3	ISL-1	1286 (-)	1	0.981	CATTAttt
V$ISL1_Q3	ISL-1	1336 (-)	1	0.981	CATTActt
V$ISL1_Q3	ISL-1	1382 (+)	1	0.981	aagTAATG
V$ISL1_Q3	ISL-1	1864 (-)	1	0.981	CATTActt
V$ISL1_Q3	ISL-1	23 (+)	1	0.979	taaTAATG
V$ISL1_Q3	ISL-1	1633 (-)	1	0.979	CATTActa
V$CPBP_Q6	KLF6	2531 (+)	1	1	GCCCCgg
V$CPBP_Q6	KLF6	58 (-)	0.997	0.997	gaGGGTC
V$CPBP_Q6	KLF6	2215 (-)	0.997	0.997	atGGGTC
V$CPBP_Q6	KLF6	512 (-)	1	0.996	ttGGGGG
V$CPBP_Q6	KLF6	687 (+)	1	0.996	GCCCCta
V$CPBP_Q6	KLF6	1457 (+)	1	0.996	CCCCCaa
V$CPBP_Q6	KLF6	283 (-)	0.995	0.995	gtGGGAC
V$CPBP_Q6	KLF6	1960 (-)	0.995	0.995	aaGGGAG
V$CPBP_Q6	KLF6	2560 (-)	0.995	0.995	aaGGGAC
V$CPBP_Q6	KLF6	2659 (-)	0.995	0.995	gaGGGAG
V$CPBP_Q6	KLF6	2690 (-)	0.995	0.995	ctGGGAG
V$CPBP_Q6	KLF6	2158 (+)	0.997	0.994	GACCCaa
V$CPBP_Q6	KLF6	513 (-)	1	0.993	tgGGGGC
V$CPBP_Q6	KLF6	514 (-)	0.992	0.988	ggGGGCG
V$CPBP_Q6	KLF6	686 (+)	0.992	0.988	GGCCCct
V$LRH1_Q5_01	LRH-1 group	1930 (+)	1	0.983	tttCAAGGact
V$LRH1_Q5_01	LRH-1 group	575 (-)	1	0.979	ggtCCTTGggc
V$LRH1_Q5_01	LRH-1 group	1618 (-)	1	0.978	tagCCTTGagc
V$LRH1_Q5_01	LRH-1 group	1668 (+)	1	0.977	acaCAAGGcca
V$MAFA_Q4	MafA group	2462 (-)	1	0.998	atGCTGA
V$MAFA_Q4	MafA group	582 (-)	1	0.96	ggGCTGA
V$MAFA_Q4	MafA group	2028 (+)	1	0.96	TCAGCtt
V$MEF2A_Q6	Mef-2	1294 (-)	1	0.993	TATTTttata
V$MEF2A_Q6	Mef-2	2073 (+)	1	0.982	ctttaAAATA
V$MEF2A_Q6	Mef-2	61 (+)	1	0.976	ggtcaAAATA
V$MEF2A_Q6	Mef-2	1374 (-)	1	0.976	TATTTataaa
V$MEF2A_Q6	Mef-2	1888 (-)	1	0.951	TATTTtttaa
V$MEIS1_01	MEIS, PKNOX, TGIF	1539 (+)	1	0.996	actTGACAgaga
V$MTF1_Q5	MTF-1	2135 (-)	1	0.955	aTGCACactc
V$MYB_Q4	Myb-like factors	456 (+)	1	0.992	gaaaCAGTTgct
V$MYB_Q4	Myb-like factors	82 (-)	1	0.991	gtcAACTGaaag
V$MYB_Q4	Myb-like factors	958 (+)	1	0.99	tttaCAGTTgtg
V$MYB_Q4	Myb-like factors	2175 (+)	1	0.99	ggtaCAGTTgtt
V$MYB_Q4	Myb-like factors	2431 (-)	1	0.99	aacAACTGaact
V$MYB_Q4	Myb-like factors	1763 (+)	1	0.982	gagtCAGTTtga
V$MYB_Q4	Myb-like factors	1712 (-)	1	0.98	gtgAACTGaaat
V$MYB_Q4	Myb-like factors	1849 (-)	1	0.975	ctaAACTGttgc
V$MYB_Q4	Myb-like factors	330 (+)	1	0.974	tgtgCAGTTtgt
V$MYB_Q4	Myb-like factors	312 (+)	1	0.973	attgCAGTTttt
V$MYB_Q4	Myb-like factors	1267 (+)	1	0.973	tgttCAGTTtaa
V$MYB_Q4	Myb-like factors	1316 (-)	1	0.973	ttaAACTGaaaa
V$MYB_Q4	Myb-like factors	243 (+)	1	0.972	acctCAGTTtta
V$MZF1_Q5	MZF1	1007 (+)	1	0.993	tGGGGAa
V$MZF1_Q5	MZF1	185 (+)	1	0.967	aGGGGAa
V$NF1_Q6	NF-1 factors	2267 (-)	1	0.966	taaaaatgtctGCCAAat
V$NF1_Q6	NF-1 factors	1147 (+)	1	0.961	acTTGGCagaggcttgat
V$NFAT1_Q4	NFAT-related factors	1224 (-)	1	1	tTTTCC
V$NFAT1_Q4	NFAT-related factors	1010 (+)	1	0.992	GGAAAg
V$NFAT1_Q4	NFAT-related factors	1096 (+)	1	0.992	GGAAAg
V$NFAT1_Q4	NFAT-related factors	407 (-)	1	0.991	aTTTCC
V$NFAT1_Q4	NFAT-related factors	1185 (-)	1	0.991	gTTTCC
V$NKX25_Q6	Nkx group	1536 (+)	1	0.979	tcCACTTgaca
V$NKX25_Q6	Nkx group	277 (-)	1	0.963	cattAAGTGgg

V$P53_Q3	p53 related factors	1647 (-)	1	0.978	tggGCATGcta
V$P53_Q3	p53 related factors	1155 (-)	0.993	0.97	gagGCTTGatc
V$CRX_Q4_01	paired related HD factors	1602 (+)	1	1	tTAATC
V$CRX_Q4_01	paired related HD factors	763 (-)	1	0.992	GATTAc
V$CRX_Q4_01	paired related HD factors	922 (-)	1	0.991	GATTAt
V$IPF1_Q5	PDX group	257 (+)	1	1	cTAATGg
V$IPF1_Q5	PDX group	276 (-)	1	0.994	aCATTAa
V$IPF1_Q5	PDX group	845 (+)	1	0.994	tTAATGa
V$IPF1_Q5	PDX group	946 (-)	1	0.994	tCATTAa
V$IPF1_Q5	PDX group	1364 (+)	1	0.994	tTAATGt
V$IPF1_Q5	PDX group	2585 (-)	1	0.994	aCATTAa
V$IPF1_Q5	PDX group	2195 (-)	1	0.991	gCATTAg
V$IPF1_Q5	PDX group	2668 (-)	1	0.991	gCATTAg
V$IPF1_Q5	PDX group	1384 (+)	1	0.979	gTAATGa
V$IPF1_Q5	PDX group	1516 (+)	1	0.979	gTAATGa
V$IPF1_Q5	PDX group	1632 (-)	1	0.979	tCATTAc
V$IPF1_Q5	PDX group	1863 (-)	1	0.979	tCATTAc
V$IPF1_Q5	PDX group	123 (+)	1	0.978	gTAATGt
V$IPF1_Q5	PDX group	25 (+)	1	0.972	aTAATGt
V$IPF1_Q5	PDX group	1285 (-)	1	0.972	aCATTAt
V$IPF1_Q5	PDX group	1028 (+)	1	0.97	gTAATGc
V$IPF1_Q5	PDX group	1033 (-)	1	0.97	gCATTAc
V$IPF1_Q5	PDX group	1101 (+)	1	0.97	gTAATGc
V$IPF1_Q5	PDX group	1132 (-)	1	0.97	gCATTAc
V$IPF1_Q5	PDX group	1335 (-)	1	0.97	gCATTAc
V$IPF1_Q5	PDX group	1430 (+)	1	0.97	gTAATGc
V$POU2F1_Q6	POU domain group	1493 (-)	1	0.989	ggATGCAaatat
V$POU2F1_Q6	POU domain group	1126 (+)	1	0.962	actttTGCATta
V$PIT1_Q6_01	POU1F1	2283 (-)	1	0.995	aTGAATaaat
V$PIT1_Q6_01	POU1F1	1561 (+)	1	0.982	atagATTCAt
V$RFX1_01	RFX-related factors	1074 (-)	0.992	0.964	gcGTTACttagttactt
V$RFX_Q6	RFX-related factors (half-site)	1854 (+)	1	0.962	ctGTTGCtt
V$RFX_Q6	RFX-related factors (half-site)	460 (+)	1	0.956	caGTTGCtt
V$RFX_Q6	RFX-related factors (half-site)	2199 (-)	1	0.952	taGCAACac
V$RORALPHA_Q4	RORalpha	2201 (+)	1	0.952	gcaacacaaaGGTCAt
V$SF1_Q5_01	SF-1 group	1670 (-)	1	0.985	aCAAGGcca
V$SF1_Q5_01	SF-1 group	1618 (+)	1	0.961	tagCCTTGa
V$SMAD4_Q6_01	SMAD factors	2273 (+)	1	1	tGTCTGc
V$SMAD4_Q6_01	SMAD factors	2218 (+)	1	0.979	gGTCTGa
V$SOX10_Q3	Sox10	424 (-)	1	0.991	tgcATTGT
V$SOX10_Q3	Sox10	1528 (-)	0.992	0.981	atcTTTGT
V$SOX10_Q3	Sox10	2567 (-)	0.992	0.98	agcTTTGT
V$SOX10_Q3	Sox10	1776 (-)	0.992	0.979	accTTTGT
V$SOX10_Q3	Sox10	2206 (+)	0.992	0.979	ACAAAggt
V$SOX10_Q3	Sox10	2054 (-)	1	0.976	gatATTGT
V$SOX10_Q3	Sox10	2083 (-)	1	0.969	tgtATTGT
V$SOX10_Q3	Sox10	134 (-)	0.992	0.969	gctTTTGT
V$SOX10_Q3	Sox10	2763 (-)	0.992	0.969	ggtTTTGT
V$SOX10_Q3	Sox10	2369 (-)	1	0.966	ataATTGT
V$SOX10_Q3	Sox10	1038 (+)	1	0.964	ACAATatt
V$SOX10_Q3	Sox10	2000 (+)	1	0.964	ACAATttt
V$SOX10_Q3	Sox10	1870 (-)	0.992	0.962	tttTTTGT
V$SOX10_Q3	Sox10	497 (-)	0.992	0.961	tatTTTGT
V$SOX10_Q3	Sox10	1832 (-)	0.992	0.961	tgtTTTGT
V$SOX10_Q3	Sox10	2389 (-)	0.992	0.961	tgaTTTGT
V$SOX10_Q3	Sox10	893 (-)	0.992	0.959	catTTTGT
V$SOX10_Q3	Sox10	117 (-)	0.992	0.958	agtTTTGT
V$SOX10_Q3	Sox10	926 (-)	0.992	0.958	ataTTTGT
V$SOX10_Q3	Sox10	2108 (+)	0.992	0.958	ACAAAaat
V$SOX10_Q3	Sox10	801 (-)	0.992	0.955	ctgTTTGT
V$SOX10_Q3	Sox10	334 (-)	0.992	0.954	cagTTTGT
V$SRY_Q6	Sox-related factors	138 (+)	1	1	TTGTTt
V$SRY_Q6	Sox-related factors	504 (+)	1	1	TTGTTt
V$SRY_Q6	Sox-related factors	805 (+)	1	1	TTGTTt
V$SRY_Q6	Sox-related factors	1836 (+)	1	1	TTGTTt
V$SRY_Q6	Sox-related factors	1998 (-)	1	1	aAACAA

V$SRY_Q6	Sox-related factors	2058 (+)	1	1	TTGTTt
V$SRY_Q6	Sox-related factors	2393 (+)	1	1	TTGTTt
V$SRY_Q6	Sox-related factors	2403 (-)	1	1	aAACAA
V$SRY_Q6	Sox-related factors	2430 (-)	1	1	aAACAA
V$SOX2_Q3_01	Sox-related factors	1527 (-)	1	0.98	aatcTTTGTtccact
V$SOX2_Q3_01	Sox-related factors	1775 (-)	1	0.969	aaccTTTGTgatgag
V$SOX2_Q3_01	Sox-related factors	2200 (+)	1	0.969	agcaacACAAAggtc
V$SRY_Q6	Sox-related factors	2182 (+)	1	0.967	TTGTTa
V$TATA_01	TBP-related factors	802 (-)	1	0.991	tgtttgttTTTATag
V$TATA_01	TBP-related factors	1290 (-)	1	0.979	attttattTTTATat
V$TATA_01	TBP-related factors	1368 (-)	1	0.959	tgtgtataTTTATaa
V$TBX5_01	TBX5	2671 (+)	1	0.962	ttaGGTGTctat
V$TBX5_01	TBX5	1179 (+)	1	0.957	acaGGTGTttcc
V$LEF1_Q5_01	TCF-7-related factors	982 (+)	1	0.996	tCAAAGc
V$LEF1_Q5_01	TCF-7-related factors	1777 (-)	1	0.985	cCTTTGt
V$LEF1_Q5_01	TCF-7-related factors	2206 (+)	1	0.985	aCAAAGg
V$LEF1_Q5_01	TCF-7-related factors	2568 (-)	1	0.982	gCTTTGt
V$LEF1_Q5_01	TCF-7-related factors	1529 (-)	1	0.981	tCTTTGt
V$LEF1_Q5_01	TCF-7-related factors	2550 (+)	1	0.963	gCAAAGt
V$LEF1_Q5_01	TCF-7-related factors	771 (+)	1	0.962	gCAAAGa
V$LEF1_Q5_01	TCF-7-related factors	265 (-)	1	0.959	tCTTTGg
V$LEF1_Q5_01	TCF-7-related factors	1943 (-)	1	0.959	gCTTTGg
V$LEF1_Q5_01	TCF-7-related factors	2031 (-)	1	0.959	gCTTTGg
V$LEF1_Q5_01	TCF-7-related factors	2259 (-)	1	0.959	gCTTTGg
V$TEF1_Q6_04	Tef-1-related factors	266 (-)	1	0.958	ctttGGAATga
V$TTF1_Q5_01	TTF-1 (Nkx2.1)	2556 (-)	1	1	tcTCAAG
V$TTF1_Q5_01	TTF-1 (Nkx2.1)	1622 (+)	1	0.999	CTTGAgc
V$TTF1_Q5_01	TTF-1 (Nkx2.1)	1540 (+)	1	0.989	CTTGAca
V$TTF1_Q5_01	TTF-1 (Nkx2.1)	453 (+)	1	0.978	CTTGAaa
V$TTF1_Q5_01	TTF-1 (Nkx2.1)	859 (+)	1	0.978	CTTGAta
V$TTF1_Q5_01	TTF-1 (Nkx2.1)	1607 (+)	1	0.978	CTTGAta
V$TTF1_Q5_01	TTF-1 (Nkx2.1)	1930 (-)	1	0.978	ttTCAAG
V$TTF1_Q5_01	TTF-1 (Nkx2.1)	74 (-)	1	0.976	gaTCAAG
V$TTF1_Q5_01	TTF-1 (Nkx2.1)	1159 (+)	1	0.976	CTTGAtc
V$YY1_Q6_03	YY1-like factors	33 (-)	1	1	aaAATGG
V$YY1_Q6_03	YY1-like factors	619 (+)	1	1	CCATTtt
V$YY1_Q6_03	YY1-like factors	892 (+)	1	1	CCATTtt
V$YY1_Q6_03	YY1-like factors	1829 (+)	0.996	0.996	CCATGtt
V$YY1_Q6_03	YY1-like factors	1201 (+)	0.999	0.982	CCATCtc
V$YY1_Q6_03	YY1-like factors	631 (+)	0.996	0.98	CCATAta
V$YY1_Q6_03	YY1-like factors	692 (-)	0.996	0.98	taTATGG
V$YY1_Q6_03	YY1-like factors	735 (-)	0.996	0.98	taTATGG
V$YY1_Q6_03	YY1-like factors	156 (+)	0.996	0.979	CCATGta
V$YY1_Q6_03	YY1-like factors	12 (+)	1	0.965	CCATTct
V$YY1_Q6_03	YY1-like factors	1487 (-)	0.996	0.963	atTATGG
V$DELTAEF1_01	ZEB1 group	538 (-)	1	0.983	gttAGGTGgtc
V$DELTAEF1_01	ZEB1 group	239 (+)	1	0.98	cacCACCTcag
V$DELTAEF1_01	ZEB1 group	2670 (-)	1	0.979	attAGGTGtct
V$DELTAEF1_01	ZEB1 group	1178 (-)	1	0.975	tacAGGTGttt
V$DELTAEF1_01	ZEB1 group	658 (+)	1	0.974	tagCACCTgtg
V$DELTAEF1_01	ZEB1 group	704 (-)	1	0.974	cacAGGTGcta
V$DELTAEF1_01	ZEB1 group	715 (-)	1	0.974	cacAGGTGctt
V$DELTAEF1_01	ZEB1 group	726 (-)	1	0.974	cacAGGTGcta
V$DELTAEF1_01	ZEB1 group	871 (+)	1	0.97	agcCACCTaca
V$ZNF333_01	ZNF333	25 (+)	1	1	ATAAT
V$ZNF333_01	ZNF333	401 (+)	1	1	ATAAT
V$ZNF333_01	ZNF333	404 (+)	1	1	ATAAT
V$ZNF333_01	ZNF333	923 (-)	1	1	ATTAT
V$ZNF333_01	ZNF333	1250 (+)	1	1	ATAAT
V$ZNF333_01	ZNF333	1287 (-)	1	1	ATTAT
V$ZNF333_01	ZNF333	1422 (-)	1	1	ATTAT
V$ZNF333_01	ZNF333	1487 (-)	1	1	ATTAT
V$ZNF333_01	ZNF333	2301 (+)	1	1	ATAAT
V$ZNF333_01	ZNF333	2304 (-)	1	1	ATTAT
V$ZNF333_01	ZNF333	2348 (-)	1	1	ATTAT
V$ZNF333_01	ZNF333	2369 (+)	1	1	ATAAT

V$ZNF333_01	ZNF333	2681 (-)	1	1 ATTAT

TRANSFAC software (http://genexplain.com/transfac): GeneXplain GmbH, Wolfenbüttel, Germany
Only factor binding sites predicted with core and matrix scores respectively higher than 0.99 and 0.95 are listed.
For nucleotide sequence of LEAP-2B gene, refer to GenBank accession no. KX372541.1

Table S2B. Prediction of putative transcription factor binding sites in mud loach LEAP-2B 5'-flanking region based on TRANSFAC search

Matrix	Factor name	Position (strand)	Core score	Matrix score	Sequence
V$AHR_Q6	AhR	2468 (-)	1	1	tGCGTG
V$AP1_Q6_02	AP-1	1676 (+)	1	0.971	TGACTaat
V$AP1_Q6_02	AP-1	2745 (-)	1	0.971	attAGTCA
V$ARID5A_03	Arid5a	1395 (+)	1	0.98	taAATATtgccatc
V$ARID5A_03	Arid5a	3172 (-)	1	0.98	cctggaaATATTaa
V$ARID5A_03	Arid5a	2265 (+)	1	0.976	tcAATATtaataaa
V$ARID5A_03	Arid5a	2261 (-)	1	0.975	atgatcaATATTaa
V$ARID5A_03	Arid5a	1391 (-)	1	0.954	cagataaATATTgc
V$ARID5A_03	Arid5a	1693 (+)	1	0.953	caAATATttttgga
V$ARID5A_03	Arid5a	3410 (+)	1	0.953	caAATATttactaa
V$ARID5A_03	Arid5a	3176 (+)	1	0.952	gaAATATtaaatga
V$BBX_04	Bbx	823 (+)	1	0.98	taaaaGTTAAcaacaca
V$BBX_04	Bbx	1129 (-)	1	0.977	agacttgTTAACcttct
V$BEN_01	BEN	156 (-)	1	0.989	tctCGCTG
V$BEN_01	BEN	123 (-)	1	0.986	catCGCTG
V$BLIMP1_Q4	Blimp-1	3526 (+)	1	0.975	agagagaGAAAG
V$BLIMP1_Q4	Blimp-1	3546 (+)	1	0.975	agagagaGAAAG
V$BRCA_01	BRCA1	833 (-)	1	0.999	CAACAcaa
V$BRCA_01	BRCA1	1283 (+)	1	0.999	ttgTGTTG
V$BRCA_01	BRCA1	2654 (-)	1	0.997	CAACAaaa
V$BRCA_01	BRCA1	1337 (+)	1	0.99	gtcTGTTG
V$BRCA_01	BRCA1	2971 (-)	1	0.987	CAACAaac
V$BRCA_01	BRCA1	502 (+)	0.997	0.975	ataGGTTG
V$BRCA_01	BRCA1	2 (+)	1	0.974	tgtTGTTG
V$BRCA_01	BRCA1	1286 (+)	1	0.974	tgtTGTTG
V$BRCA_01	BRCA1	144 (+)	1	0.967	ggcTGTTG
V$BRCA_01	BRCA1	838 (-)	1	0.956	CAACAggt
V$CEBPA_Q6	C/EBP group	2610 (+)	1	0.996	tttttgTGCAAgc
V$CEBPA_Q6	C/EBP group	2646 (+)	1	0.996	tttttgTGCAAca
V$CEBPA_Q6	C/EBP group	1096 (-)	0.998	0.995	atTTGCCaaactc
V$CEBPA_Q6	C/EBP group	638 (+)	1	0.993	cacttaTGCAAaa
V$CEBPA_Q6	C/EBP group	1214 (-)	0.997	0.991	caTTGCTtaaaaa
V$CEBPA_Q6	C/EBP group	1544 (+)	0.997	0.984	cccttcAGCAAat
V$CEBPA_Q6	C/EBP group	2674 (+)	1	0.966	tgttatTGCAAtg
V$CEBPA_Q6	C/EBP group	2785 (-)	0.998	0.958	acTTGCCcattat
V$CEBPA_Q6	C/EBP group	2930 (+)	0.997	0.958	gagatgAGCAAgc
V$CEBPA_Q6	C/EBP group	2543 (-)	1	0.957	aaTTGCAtattgg
V$CEBPA_Q6	C/EBP group	1828 (+)	0.997	0.957	tgtattAGCAAtt
V$CDX2_Q5_02	CDX group (half-site)	1065 (+)	1	1	TTTATa
V$CDX2_Q5_02	CDX group (half-site)	1109 (-)	1	1	tATAAA
V$CDX2_Q5_02	CDX group (half-site)	1231 (-)	1	1	tATAAA
V$CDX2_Q5_02	CDX group (half-site)	1443 (-)	1	1	tATAAA
V$CDX2_Q5_02	CDX group (half-site)	1482 (+)	1	1	TTTATa
V$CDX2_Q5_02	CDX group (half-site)	1683 (-)	1	1	tATAAA
V$CDX2_Q5_02	CDX group (half-site)	2214 (-)	1	1	tATAAA
V$CDX2_Q5_02	CDX group (half-site)	2458 (+)	1	1	TTTATa
V$CDX2_Q5_02	CDX group (half-site)	3119 (-)	1	1	tATAAA
V$CDX2_Q5_02	CDX group (half-site)	3591 (-)	1	1	tATAAA
V$CDX2_Q5_02	CDX group (half-site)	1557 (+)	1	0.999	TTTATg
V$CDX2_Q5_02	CDX group (half-site)	2360 (+)	1	0.999	TTTATg
V$CDX2_Q5_02	CDX group (half-site)	436 (-)	1	0.998	aATAAA
V$CDX2_Q5_02	CDX group (half-site)	766 (-)	1	0.998	aATAAA
V$CDX2_Q5_02	CDX group (half-site)	1057 (-)	1	0.998	aATAAA
V$CDX2_Q5_02	CDX group (half-site)	1487 (-)	1	0.998	aATAAA
V$CDX2_Q5_02	CDX group (half-site)	1505 (-)	1	0.998	aATAAA
V$CDX2_Q5_02	CDX group (half-site)	1509 (-)	1	0.998	aATAAA
V$CDX2_Q5_02	CDX group (half-site)	1886 (+)	1	0.998	TTTATt
V$CDX2_Q5_02	CDX group (half-site)	2273 (-)	1	0.998	aATAAA
V$CDX2_Q5_02	CDX group (half-site)	2642 (+)	1	0.998	TTTATt
V$CDX2_Q5_02	CDX group (half-site)	2660 (-)	1	0.998	aATAAA
V$CDX2_Q5_02	CDX group (half-site)	2765 (-)	1	0.998	aATAAA

V$CDX2_Q5_02	CDX group (half-site)	2903 (-)	1	0.998	aATAAA
V$CDX2_Q5_02	CDX group (half-site)	3082 (-)	1	0.998	aATAAA
V$CDX2_Q5_02	CDX group (half-site)	3140 (+)	1	0.998	TTTATt
V$CDX2_Q5_02	CDX group (half-site)	3249 (+)	1	0.998	TTTATt
V$CDX2_Q5_02	CDX group (half-site)	1393 (-)	1	0.994	gATAAA
V$CDX2_Q5_02	CDX group (half-site)	3072 (-)	1	0.994	gATAAA
V$CDX2_Q5_02	CDX group (half-site)	3433 (+)	1	0.994	TTTATc
V$CDX2_Q5_02	CDX group (half-site)	3623 (+)	1	0.994	TTTATc
V$CHCH_01	Churchill	36 (-)	0.997	0.994	tACCCG
V$CHCH_01	Churchill	49 (-)	0.998	0.991	gTCCCG
V$CHCH_01	Churchill	724 (+)	0.998	0.987	CGGGAt
V$CIZ_01	CIZ	1819 (-)	1	0.999	gacTTTTTc
V$CIZ_01	CIZ	3251 (-)	1	0.999	tatTTTTTc
V$CIZ_01	CIZ	3281 (+)	1	0.997	gAAAAAaac
V$CIZ_01	CIZ	3667 (+)	1	0.997	gAAAAAaac
V$CIZ_01	CIZ	448 (+)	1	0.987	cAAAAAata
V$CIZ_01	CIZ	1902 (+)	1	0.986	cAAAAAact
V$CIZ_01	CIZ	2436 (-)	1	0.986	acaTTTTTc
V$CIZ_01	CIZ	1086 (+)	1	0.985	gAAAAAtaa
V$CIZ_01	CIZ	2607 (-)	1	0.985	cacTTTTTg
V$CIZ_01	CIZ	2940 (-)	1	0.985	agcTTTTTg
V$CP2_Q6	CP2-related factors	997 (+)	1	0.997	ctgACTGGaa
V$CP2_Q6	CP2-related factors	1183 (-)	1	0.982	ttCCAGTgag
V$CP2_Q6	CP2-related factors	14 (-)	1	0.981	tcCCAGAaag
V$CP2_Q6	CP2-related factors	1156 (-)	1	0.979	ccCCAGTgaa
V$CP2_Q6	CP2-related factors	649 (-)	1	0.977	aaCCAGAtag
V$CP2_Q6	CP2-related factors	124 (+)	1	0.976	atcGCTGGtc
V$CP2_Q6	CP2-related factors	1565 (-)	1	0.976	caCCAGTgat
V$CP2_Q6	CP2-related factors	629 (-)	1	0.975	caCCAGTaac
V$CREB1_Q6	CREB group	923 (-)	1	0.986	taTGACGtaggg
V$CREB1_Q6	CREB group	64 (+)	1	0.982	aggcaCGTCAtc
V$DLX3_02	Dlx group	2742 (+)	1	0.996	cTAATTag
V$DLX3_02	Dlx group	2742 (-)	1	0.996	ctAATTAg
V$DLX3_02	Dlx group	1068 (+)	1	0.966	aTAATTgt
V$DLX3_02	Dlx group	1862 (+)	1	0.963	gTAATTga
V$DRI1_01	DRI1	687 (-)	1	1	TTAATt
V$DRI1_01	DRI1	1637 (+)	1	1	aATTAA
V$E2A_Q6_01	E2A group	1668 (-)	1	0.972	tgcccAGGTGact
V$E2A_Q6_01	E2A group	1789 (-)	1	0.959	ctgtcAGGTGaga
V$EBOX_Q6_01	Ebox	1790 (-)	0.998	0.987	tgtcAGGTGa
V$EBOX_Q6_01	Ebox	1669 (-)	0.998	0.957	gcccAGGTGa
V$ETS_Q6	Ets-related factors	3653 (+)	1	0.981	gCTTCCtt
V$HNF3B_Q6	FOX factors	887 (+)	1	1	tTGTTTgct
V$HNF3B_Q6	FOX factors	873 (-)	1	0.987	agtAAACAt
V$HNF3B_Q6	FOX factors	1687 (-)	1	0.987	aacAAACAa
V$HNF3B_Q6	FOX factors	1927 (-)	1	0.979	aacAAACAg
V$HNF3B_Q6	FOX factors	283 (+)	1	0.975	aTGTTTacc
V$HNF3B_Q6	FOX factors	1372 (-)	1	0.973	tgtAAACAg
V$HNF3B_Q6	FOX factors	1683 (-)	1	0.969	tatAAACAa
V$HNF3B_Q6	FOX factors	2214 (-)	1	0.961	tatAAACAt
V$HNF3B_Q6	FOX factors	1659 (-)	1	0.96	cacAAACAg
V$HNF3B_Q6	FOX factors	1715 (+)	1	0.96	cTGTTTgtg
V$HNF3B_Q6	FOX factors	2575 (-)	1	0.957	gccAAACAa
V$HNF3B_Q6	FOX factors	3261 (-)	1	0.956	actAAACAg
V$HNF3B_Q6	FOX factors	2221 (-)	1	0.955	attAAACAt
V$GATA_Q6	GATA	2822 (+)	1	1	aGATAAg
V$GATA_Q6	GATA	1392 (+)	1	0.995	aGATAAa
V$GATA_Q6	GATA	3623 (-)	1	0.995	tTTATCt
V$GATA_Q6	GATA	2868 (-)	1	0.992	gTTATCt
V$GATA_Q6	GATA	1053 (+)	1	0.99	aGATAAt
V$GATA_Q6	GATA	2793 (-)	1	0.99	aTTATCt
V$GATA_Q6	GATA	3071 (+)	1	0.989	tGATAAa
V$GATA_Q6	GATA	3433 (-)	1	0.989	tTTATCa
V$GATA_Q6	GATA	963 (+)	1	0.971	cGATAAc
V$GEN_INI_B	general initiator	1802 (-)	0.995	0.995	AACTGagg
V$GEN_INI_B	general initiator	1521 (+)	0.995	0.976	catCAGTT
V$GEN_INI_B	general initiator	2242 (-)	0.995	0.965	AACTGagt

V$GEN_INI_B	general initiator	1176 (+)	0.991	0.964 ccaCAATT
V$GEN_INI_B	general initiator	2951 (+)	1	0.963 ctcCATTC
V$GEN_INI_B	general initiator	2748 (+)	0.999	0.961 agtCAGTC
V$GEN_INI_B	general initiator	2875 (-)	1	0.958 GAATGaac
V$GEN_INI_B	general initiator	2893 (+)	1	0.958 gttCATTC
V$GEN_INI_B	general initiator	354 (+)	0.996	0.958 agtCATTT
V$GEN_INI_B	general initiator	562 (+)	0.996	0.958 agtCATTT
V$GEN_INI_B	general initiator	2525 (+)	0.996	0.958 tgtCATTT
V$GEN_INI_B	general initiator	1753 (+)	1	0.953 gatCATTC
V$GEN_INI_B	general initiator	303 (-)	0.995	0.953 GATTGaac
V$GEN_INI_B	general initiator	1344 (-)	1	0.951 GAATGggc
V$GEN_INI_B	general initiator	3184 (-)	0.996	0.951 AAATGaaa
V$GFI1_Q6_01	GFI1 factors	3426 (-)	1	0.999 ctgTGATTtt
V$GFI1_Q6_01	GFI1 factors	1111 (+)	1	0.989 taAATCAgtg
V$GFI1_Q6_01	GFI1 factors	1735 (-)	0.992	0.982 cacAGATTtt
V$GFI1_Q6_01	GFI1 factors	1568 (-)	1	0.981 cagTGATTac
V$GFI1_Q6_01	GFI1 factors	2483 (+)	1	0.981 tcAATCAcag
V$GFI1_Q6_01	GFI1 factors	1386 (+)	1	0.978 gaAATCAgat
V$GFI1_Q6_01	GFI1 factors	2146 (-)	1	0.977 ctaTGATTac
V$GFI1_Q6_01	GFI1 factors	2682 (-)	1	0.971 caaTGATTat
V$GFI1_Q6_01	GFI1 factors	3156 (+)	1	0.971 acAATCAgtg
V$GFI1_Q6_01	GFI1 factors	3003 (-)	0.992	0.965 ataAGATTtc
V$GFI1_Q6_01	GFI1 factors	1864 (-)	1	0.964 aatTGATTtt
V$GFI1_Q6_01	GFI1 factors	968 (+)	1	0.959 acAATCAgat
V$GFI1_Q6_01	GFI1 factors	681 (-)	0.992	0.958 cgaAGATTaa
V$GFI1_Q6_01	GFI1 factors	438 (+)	0.992	0.957 taAATCTatt
V$GFI1_Q6_01	GFI1 factors	453 (-)	0.992	0.957 aatAGATTta
V$GFI1_Q6_01	GFI1 factors	1627 (+)	1	0.956 aaAATCAtca
V$GFI1_Q6_01	GFI1 factors	461 (+)	1	0.955 taAATCAaca
V$HIC1_08	HIC1	2338 (+)	1	0.997 aTGCCAact
V$HIC1_08	HIC1	494 (+)	1	0.98 aTGCCAgca
V$HIF1A_Q5	HIF1	65 (-)	1	0.993 ggCACGTca
V$HIF1A_Q5	HIF1	1574 (+)	1	0.987 ttACGTGtt
V$RUSH1A_02	hltf	1221 (-)	0.997	0.996 taAAAAGgtg
V$RUSH1A_02	hltf	2599 (+)	0.997	0.995 gtcCTTTTca
V$RUSH1A_02	hltf	3655 (+)	0.997	0.994 ttcCTTTTtt
V$RUSH1A_02	hltf	883 (+)	0.993	0.993 tacCTTGTtt
V$RUSH1A_02	hltf	1489 (-)	0.997	0.99 taAAAAGgct
V$RUSH1A_02	hltf	3447 (+)	0.993	0.987 tgcCTTGTgg
V$RUSH1A_02	hltf	361 (-)	1	0.978 tcATAAGtaa
V$RUSH1A_02	hltf	637 (+)	1	0.976 acaCTTATgc
V$RUSH1A_02	hltf	822 (-)	0.997	0.976 ttAAAAGtta
V$RUSH1A_02	hltf	2342 (+)	0.997	0.976 caaCTTTTca
V$RUSH1A_02	hltf	3122 (+)	0.997	0.976 aaaCTTTTga
V$RUSH1A_02	hltf	1879 (+)	1	0.975 gcaCTTATtt
V$RUSH1A_02	hltf	1948 (-)	0.997	0.973 ctAAAAGtgg
V$RUSH1A_02	hltf	2166 (+)	0.997	0.973 ccaCTTTTag
V$RUSH1A_02	hltf	2606 (+)	0.997	0.972 tcaCTTTTtg
V$RUSH1A_02	hltf	43 (-)	0.997	0.97 gcAAAAGtcc
V$RUSH1A_02	hltf	1818 (+)	0.997	0.969 ggaCTTTTtc
V$RUSH1A_02	hltf	557 (-)	0.993	0.967 atACAAGtca
V$RUSH1A_02	hltf	1129 (+)	0.993	0.967 agaCTTGTta
V$HNF4A_Q3	HNF-4 group	213 (-)	1	0.982 atgtcCTTTGacct
V$HSF1_01	HSF dimer	1752 (-)	1	0.956 agatcATTCT
V$IK_Q5_01	Ikaros	12 (-)	1	0.977 atTCCCA
V$IK_Q5_01	Ikaros	2966 (-)	1	0.977 atTCCCA
V$IK_Q5_01	Ikaros	3078 (+)	1	0.977 TGGGAat
V$IK_Q5_01	Ikaros	130 (-)	1	0.963 ggTCCCA
V$ING4_01	ING4	111 (+)	1	1 cCACCA
V$IRF1_Q5	IRF factors	2602 (-)	1	0.974 ctTTTCActtttg
V$IRF1_Q5	IRF factors	859 (+)	1	0.972 actaaagTGAAAct
V$IRF1_Q5	IRF factors	3011 (+)	0.992	0.969 tcaaaatAGAAAtt
V$IRF1_Q5	IRF factors	1031 (+)	0.992	0.958 cttaaaaAGAAAga
V$IRF1_Q5	IRF factors	1710 (-)	0.992	0.954 taTTTCTgtttgtg
V$ISL1_Q3	ISL-1	3378 (+)	1	0.994 cgtTAATG
V$ISL1_Q3	ISL-1	2792 (-)	1	0.993 CATTAtct
V$ISL1_Q3	ISL-1	1274 (+)	1	0.992 gctTAATG

V$ISL1_Q3	ISL-1	2220 (-)	1	0.989 CATTAaac
V$ISL1_Q3	ISL-1	2753 (+)	1	0.989 gtcTAATG
V$ISL1_Q3	ISL-1	242 (-)	1	0.984 CATTAaag
V$ISL1_Q3	ISL-1	3333 (+)	1	0.984 cttTAATG
V$ISL1_Q3	ISL-1	278 (+)	1	0.982 tatTAATG
V$ISL1_Q3	ISL-1	2807 (-)	1	0.982 CATTAatg
V$ISL1_Q3	ISL-1	2807 (+)	1	0.982 catTAATG
V$ISL1_Q3	ISL-1	2999 (-)	1	0.981 CATTAtaa
V$GKLF_Q4	KLF4 group	3556 (-)	1	1 agGGAGG
V$GKLF_Q4	KLF4 group	60 (-)	1	0.999 gaGGAGG
V$GKLF_Q4	KLF4 group	3092 (-)	1	0.998 taGGAGG
V$GKLF_Q4	KLF4 group	1167 (+)	1	0.954 CCTCCat
V$GKLF_Q4	KLF4 group	188 (+)	1	0.953 CCTCCac
V$GKLF_Q4	KLF4 group	139 (-)	1	0.952 ctGGAGG
V$GKLF_Q4	KLF4 group	1702 (-)	1	0.952 ttGGAGG
V$CPBP_Q6	KLF6	2034 (-)	1	1 atGGGGG
V$CPBP_Q6	KLF6	265 (+)	0.997	0.997 GACCCac
V$CPBP_Q6	KLF6	905 (+)	0.997	0.997 CACCCag
V$CPBP_Q6	KLF6	2446 (-)	0.997	0.997 gtGGGTG
V$CPBP_Q6	KLF6	3559 (-)	0.997	0.997 gaGGGTG
V$CPBP_Q6	KLF6	930 (-)	1	0.996 taGGGGC
V$CPBP_Q6	KLF6	1350 (+)	1	0.996 GCCCCta
V$CPBP_Q6	KLF6	1358 (+)	1	0.996 CCCCCta
V$CPBP_Q6	KLF6	49 (+)	0.995	0.995 GTCCCgg
V$CPBP_Q6	KLF6	131 (+)	0.995	0.995 GTCCCac
V$CPBP_Q6	KLF6	1617 (+)	0.995	0.995 CTCCCtt
V$CPBP_Q6	KLF6	3555 (-)	0.995	0.995 aaGGGAG
V$CPBP_Q6	KLF6	269 (+)	0.997	0.994 CACCCct
V$CPBP_Q6	KLF6	2036 (-)	0.997	0.994 ggGGGTC
V$CPBP_Q6	KLF6	2398 (+)	0.997	0.994 CACCCta
V$CPBP_Q6	KLF6	1346 (-)	0.992	0.992 atGGGCC
V$CPBP_Q6	KLF6	1327 (+)	0.995	0.991 GTCCCct
V$CPBP_Q6	KLF6	931 (-)	0.992	0.988 agGGGCG
V$CPBP_Q6	KLF6	1349 (+)	0.992	0.988 GGCCCct
V$CPBP_Q6	KLF6	1154 (+)	0.995	0.987 GTCCCca
V$MAFA_Q4	MafA group	507 (-)	1	0.998 ttGCTGA
V$MAFA_Q4	MafA group	538 (+)	1	0.998 TCAGCaa
V$MAFA_Q4	MafA group	1548 (+)	1	0.998 TCAGCaa
V$MAFA_Q4	MafA group	1721 (-)	1	0.998 gtGCTGA
V$MAFA_Q4	MafA group	2228 (-)	1	0.998 atGCTGA
V$MAFA_Q4	MafA group	2326 (+)	1	0.998 TCAGCac
V$MAFA_Q4	MafA group	1494 (-)	1	0.96 agGCTGA
V$MAFA_Q4	MafA group	1381 (-)	1	0.952 gcGCTGA
V$MEF2A_Q6	Mef-2	697 (+)	1	0.99 cttaaAAATA
V$MEF2A_Q6	Mef-2	1509 (+)	1	0.989 aataaAAATA
V$MEF2A_Q6	Mef-2	1888 (-)	1	0.989 TATTTtaaac
V$MEF2A_Q6	Mef-2	2419 (+)	1	0.978 gttcaAAATA
V$MEF2A_Q6	Mef-2	3589 (+)	1	0.978 gttatAAATA
V$MEF2A_Q6	Mef-2	3009 (+)	1	0.976 tttcaAAATA
V$MEF2A_Q6	Mef-2	760 (+)	1	0.969 tctttAAATA
V$MEF2A_Q6	Mef-2	1253 (-)	1	0.968 TATTTtgatg
V$MEF2A_Q6	Mef-2	3234 (-)	1	0.965 TATTTaaaca
V$MEF2A_Q6	Mef-2	819 (-)	1	0.962 TATTTaaaag
V$MEF2A_Q6	Mef-2	447 (+)	1	0.953 tcaaaAAATA
V$MEIS1_01	MEIS, PKNOX, TGIF	483 (-)	1	0.997 ctacTGTCAtga
V$MEIS1_01	MEIS, PKNOX, TGIF	1786 (-)	1	0.997 catcTGTCAggt
V$MEIS1_01	MEIS, PKNOX, TGIF	658 (-)	1	0.996 gagcTGTCAaca
V$MYB_Q4	Myb-like factors	3575 (+)	1	0.989 ttcaCAGTTgaa
V$MYB_Q4	Myb-like factors	366 (-)	1	0.985 agtAACTgttat
V$MYB_Q4	Myb-like factors	465 (+)	1	0.975 tcaaCAGTTtct
V$MYB_Q4	Myb-like factors	1520 (+)	1	0.975 acatCAGTTtcc
V$MYB_Q4	Myb-like factors	3065 (-)	1	0.974 ttaAACTgataa
V$MYB_Q4	Myb-like factors	1799 (-)	1	0.973 agaAACTgaggc
V$MYB_Q4	Myb-like factors	2239 (-)	1	0.973 caaAACTgagtt
V$MZF1_Q5	MZF1	1154 (-)	1	0.989 gTCCCCa
V$NF1_Q6	NF-1 factors	1089 (-)	1	0.961 aaataacatttGCCAAac
V$NF1_Q6	NF-1 factors	1208 (+)	1	0.96 tcTTGGCattgcttaaaa

V$NF1_Q6	NF-1 factors	2329 (-)	1	0.96	gcacaggacatGCCAAct
V$NF1_Q6	NF-1 factors	2564 (-)	1	0.96	aagacctgaaaGCCAAac
V$NF1_Q6	NF-1 factors	578 (-)	1	0.957	ccaactagctaGCCAAat
V$NF1_Q6	NF-1 factors	566 (-)	1	0.955	attttagcttaGCCAAct
V$NFAT1_Q4	NFAT-related factors	176 (-)	1	1	tTTTCC
V$NFAT1_Q4	NFAT-related factors	3666 (+)	1	1	GGAAAa
V$NFAT1_Q4	NFAT-related factors	184 (-)	1	0.992	cTTTCC
V$NFAT1_Q4	NFAT-related factors	1181 (-)	1	0.991	aTTTCC
V$NFAT1_Q4	NFAT-related factors	1526 (-)	1	0.991	gTTTCC
V$NFAT1_Q4	NFAT-related factors	3175 (+)	1	0.991	GGAAAt
V$NKX25_Q6	Nkx group	2494 (-)	1	0.978	taccAAGTGag
V$NKX25_Q6	Nkx group	2127 (+)	1	0.97	ggCACTTaaaa
V$NKX25_Q6	Nkx group	1948 (-)	1	0.961	ctaaAAGTGgt
V$NKX25_Q6	Nkx group	2165 (+)	1	0.961	acCACTTttag
V$NKX25_Q6	Nkx group	30 (+)	1	0.953	gaCACTTaccc
V$NKX25_Q6	Nkx group	859 (-)	1	0.953	actaAAGTGaa
V$NKX25_Q6	Nkx group	2665 (+)	1	0.953	aaCACTTactg
V$HNF6_Q4	ONECUT factors	2626 (-)	1	1	tATTGAtt
V$HNF6_Q4	ONECUT factors	1864 (-)	1	0.962	aATTGAtt
V$P53_Q3	p53 related factors	1811 (-)	1	0.983	tggGCATGgac
V$P53_Q3	p53 related factors	2334 (+)	1	0.978	ggaCATGCcaa
V$P53_Q3	p53 related factors	2256 (-)	1	0.974	aagGCATGatc
V$P53_Q3	p53 related factors	1963 (-)	0.993	0.956	atgGCTTGtaa
V$CRX_Q4_01	paired related HD factors	685 (-)	1	1	GATTAa
V$CRX_Q4_01	paired related HD factors	692 (+)	1	1	tTAATC
V$CRX_Q4_01	paired related HD factors	718 (-)	1	1	GATTAg
V$CRX_Q4_01	paired related HD factors	1726 (-)	1	1	GATTAa
V$CRX_Q4_01	paired related HD factors	2279 (-)	1	1	GATTAa
V$CRX_Q4_01	paired related HD factors	2630 (-)	1	1	GATTAg
V$CRX_Q4_01	paired related HD factors	2981 (+)	1	1	cTAATC
V$CRX_Q4_01	paired related HD factors	3371 (-)	1	1	GATTAa
V$CRX_Q4_01	paired related HD factors	1572 (-)	1	0.992	GATTAc
V$CRX_Q4_01	paired related HD factors	2150 (-)	1	0.992	GATTAc
V$CRX_Q4_01	paired related HD factors	951 (+)	1	0.991	aTAATC
V$CRX_Q4_01	paired related HD factors	2686 (-)	1	0.991	GATTAt
V$IPF1_Q5	PDX group	241 (-)	1	0.995	cCATTAa
V$IPF1_Q5	PDX group	2809 (+)	1	0.995	tTAATGg
V$IPF1_Q5	PDX group	280 (+)	1	0.994	tTAATGt
V$IPF1_Q5	PDX group	1276 (+)	1	0.994	tTAATGa
V$IPF1_Q5	PDX group	2219 (-)	1	0.994	aCATTAa
V$IPF1_Q5	PDX group	3335 (+)	1	0.994	tTAATGa
V$IPF1_Q5	PDX group	2755 (+)	1	0.991	cTAATGc
V$IPF1_Q5	PDX group	2806 (-)	1	0.986	gCATTAa
V$IPF1_Q5	PDX group	3380 (+)	1	0.986	tTAATGc
V$IPF1_Q5	PDX group	2791 (-)	1	0.973	cCATTAt
V$IPF1_Q5	PDX group	2998 (-)	1	0.972	aCATTAt
V$POU2F1_Q6	POU domain group	641 (-)	1	0.964	ttATGCAaaacc
V$POU2F1_Q6	POU domain group	2234 (-)	1	0.962	acATGCAaaact
V$PIT1_Q6_01	POU1F1	1847 (-)	1	1	aTGAATatat
V$PIT1_Q6_01	POU1F1	2459 (+)	1	1	ttatATTCAt
V$PIT1_Q6_01	POU1F1	2762 (-)	1	0.994	aTGAATaaag
V$RORALPHA_Q4	RORalpha	3352 (-)	1	0.971	tTGACCtatctcagaa
V$RORALPHA_Q4	RORalpha	2886 (-)	1	0.96	aTGACCtgttcattca
V$AML3_Q6	Runt-related factors	521 (+)	1	1	aACCACaa
V$AML3_Q6	Runt-related factors	2060 (+)	1	0.984	cACCACat
V$SMAD4_Q6_01	SMAD factors	201 (-)	1	1	tCAGACa
V$SMAD4_Q6_01	SMAD factors	941 (-)	1	1	aCAGACa
V$SMAD4_Q6_01	SMAD factors	994 (+)	1	1	tGTCTGa
V$SMAD4_Q6_01	SMAD factors	3644 (-)	1	1	aCAGACa
V$SMAD4_Q6_01	SMAD factors	3040 (+)	1	0.981	aGTCTGc
V$SMAD4_Q6_01	SMAD factors	1336 (+)	1	0.98	aGTCTGt
V$SMAD4_Q6_01	SMAD factors	3268 (+)	1	0.98	aGTCTGa
V$SOX10_Q3	Sox10	612 (+)	1	0.999	ACAATgcc
V$SOX10_Q3	Sox10	410 (-)	1	0.991	tacATTGT
V$SOX10_Q3	Sox10	2918 (-)	1	0.991	tgcATTGT
V$SOX10_Q3	Sox10	1586 (-)	0.992	0.991	gacTTTGT
V$SOX10_Q3	Sox10	2580 (+)	0.992	0.991	ACAAAgtc

V$SOX10_Q3	Sox10	2316 (+)	1	0.989	ACAATgtg
V$SOX10_Q3	Sox10	2508 (-)	0.992	0.981	cacTTTGT
V$SOX10_Q3	Sox10	3648 (+)	0.992	0.98	ACAAAgct
V$SOX10_Q3	Sox10	1178 (+)	1	0.976	ACAATttc
V$SOX10_Q3	Sox10	554 (+)	1	0.969	ACAATaca
V$SOX10_Q3	Sox10	1868 (-)	0.992	0.969	gatTTTGT
V$SOX10_Q3	Sox10	3227 (-)	1	0.968	taaATTGT
V$SOX10_Q3	Sox10	1068 (-)	1	0.966	ataATTGT
V$SOX10_Q3	Sox10	968 (+)	1	0.963	ACAATcag
V$SOX10_Q3	Sox10	1007 (-)	1	0.963	tagATTGT
V$SOX10_Q3	Sox10	3156 (+)	1	0.963	ACAATcag
V$SOX10_Q3	Sox10	1279 (-)	1	0.961	atgATTGT
V$SOX10_Q3	Sox10	1015 (+)	0.992	0.961	ACAAAata
V$SOX10_Q3	Sox10	2656 (+)	0.992	0.961	ACAAAata
V$SOX10_Q3	Sox10	2375 (-)	0.992	0.96	ctaTTTGT
V$SOX10_Q3	Sox10	2609 (-)	0.992	0.96	cttTTTGT
V$SOX10_Q3	Sox10	2592 (+)	0.992	0.959	ACAAAatg
V$SOX10_Q3	Sox10	1692 (+)	0.992	0.958	ACAAAtat
V$SOX10_Q3	Sox10	2645 (-)	0.992	0.958	attTTTGT
V$SOX10_Q3	Sox10	1688 (+)	0.992	0.957	ACAAAcaa
V$SOX10_Q3	Sox10	1660 (+)	0.992	0.955	ACAAAcag
V$SOX10_Q3	Sox10	1715 (-)	0.992	0.955	ctgTTTGT
V$SOX10_Q3	Sox10	1928 (+)	0.992	0.955	ACAAAcag
V$SOX10_Q3	Sox10	752 (+)	0.992	0.954	ACAAAcgg
V$SOX10_Q3	Sox10	2188 (-)	0.992	0.954	ccgTTTGT
V$SOX10_Q3	Sox10	2973 (+)	0.992	0.952	ACAAAcct
V$SRY_Q6	Sox-related factors	887 (+)	1	1	TTGTTt
V$SRY_Q6	Sox-related factors	1686 (-)	1	1	aAACAA
V$SRY_Q6	Sox-related factors	1690 (-)	1	1	aAACAA
V$SRY_Q6	Sox-related factors	1926 (-)	1	1	aAACAA
V$SRY_Q6	Sox-related factors	2192 (+)	1	1	TTGTTt
V$SRY_Q6	Sox-related factors	2578 (-)	1	1	aAACAA
V$SOX2_Q3_01	Sox-related factors	2574 (+)	1	0.978	agccaaACAAAgtct
V$SRY_Q6	Sox-related factors	7 (+)	1	0.967	TTGTTa
V$SRY_Q6	Sox-related factors	414 (+)	1	0.967	TTGTTa
V$SRY_Q6	Sox-related factors	750 (-)	1	0.967	tAACAA
V$SRY_Q6	Sox-related factors	830 (-)	1	0.967	tAACAA
V$SRY_Q6	Sox-related factors	966 (-)	1	0.967	tAACAA
V$SRY_Q6	Sox-related factors	1072 (+)	1	0.967	TTGTTa
V$SRY_Q6	Sox-related factors	1133 (+)	1	0.967	TTGTTa
V$SOX2_Q3_01	Sox-related factors	1585 (-)	1	0.952	ggacTTTGTattgcc
V$STAT1_Q6	STAT factors	12 (-)	1	0.992	aTTCCCagaa
V$STAT1_Q6	STAT factors	3661 (+)	0.991	0.97	tttttAGGAAa
V$TATA_01	TBP-related factors	1230 (+)	1	0.972	gtATAAAacatttaa
V$TATA_01	TBP-related factors	1442 (+)	1	0.967	atATAAAatatagta
V$TATA_01	TBP-related factors	2450 (-)	1	0.966	gtgaaagtTTTATat
V$TATA_01	TBP-related factors	3590 (+)	1	0.965	ttATAAAtacagtgg
V$TATA_01	TBP-related factors	1108 (+)	1	0.96	ctATAAAtcagtgga
V$TATA_01	TBP-related factors	1474 (-)	1	0.96	aaacagcaTTTATaa
V$TBX5_01	TBX5	1224 (+)	1	0.958	aaaGGTGTataa
V$LEF1_Q5_01	TCF-7-related factors	217 (-)	1	1	cCTTTGa
V$LEF1_Q5_01	TCF-7-related factors	1143 (-)	1	0.996	tCTTTGa
V$LEF1_Q5_01	TCF-7-related factors	1601 (+)	1	0.996	tCAAAGa
V$LEF1_Q5_01	TCF-7-related factors	2561 (+)	1	0.996	tCAAAGa
V$LEF1_Q5_01	TCF-7-related factors	2736 (+)	1	0.996	tCAAAGc
V$LEF1_Q5_01	TCF-7-related factors	2818 (+)	1	0.996	tCAAAGa
V$LEF1_Q5_01	TCF-7-related factors	1587 (-)	1	0.982	aCTTTGt
V$LEF1_Q5_01	TCF-7-related factors	2509 (-)	1	0.982	aCTTTGt
V$LEF1_Q5_01	TCF-7-related factors	2580 (+)	1	0.982	aCAAAGt
V$LEF1_Q5_01	TCF-7-related factors	3648 (+)	1	0.982	aCAAAGc
V$LEF1_Q5_01	TCF-7-related factors	2797 (-)	1	0.959	tCTTTGg
V$LEF1_Q5_01	TCF-7-related factors	3213 (-)	1	0.959	tCTTTGg
V$TTF1_Q5_01	TTF-1 (Nkx2.1)	2157 (-)	1	0.99	agTCAAG
V$TTF1_Q5_01	TTF-1 (Nkx2.1)	256 (+)	1	0.989	CTTGAca
V$TTF1_Q5_01	TTF-1 (Nkx2.1)	349 (+)	1	0.978	CTTGAag
V$TTF1_Q5_01	TTF-1 (Nkx2.1)	2882 (+)	1	0.977	CTTGAtg
V$TTF1_Q5_01	TTF-1 (Nkx2.1)	3302 (+)	1	0.977	CTTGAac

V$XVENT1_01	Xvent-1	2372 (+)	1	0.974	accctATTTGtcc
V$YY1_Q6_03	YY1-like factors	1985 (+)	1	1	CCATTtt
V$YY1_Q6_03	YY1-like factors	2134 (-)	1	1	aaAATGG
V$YY1_Q6_03	YY1-like factors	3134 (+)	1	1	CCATTtt
V$YY1_Q6_03	YY1-like factors	180 (+)	0.999	0.999	CCATCtt
V$YY1_Q6_03	YY1-like factors	2307 (-)	0.996	0.997	aaTATGG
V$YY1_Q6_03	YY1-like factors	3074 (-)	1	0.983	taAATGG
V$YY1_Q6_03	YY1-like factors	2090 (-)	0.996	0.98	taTATGG
V$YY1_Q6_03	YY1-like factors	2122 (-)	0.996	0.98	taTATGG
V$YY1_Q6_03	YY1-like factors	1404 (+)	0.999	0.979	CCATCtg
V$YY1_Q6_03	YY1-like factors	114 (+)	0.996	0.979	CCATAtc
V$YY1_Q6_03	YY1-like factors	259 (-)	0.996	0.979	gaCATGG
V$YY1_Q6_03	YY1-like factors	1170 (+)	0.996	0.979	CCATAtc
V$YY1_Q6_03	YY1-like factors	2030 (+)	0.996	0.976	CCATAtg
V$YY1_Q6_03	YY1-like factors	2031 (-)	0.996	0.976	caTATGG
V$YY1_Q6_03	YY1-like factors	3442 (+)	0.996	0.976	CCATGtg
V$YY1_Q6_03	YY1-like factors	2791 (+)	1	0.966	CCATTat
V$YY1_Q6_03	YY1-like factors	2953 (+)	1	0.965	CCATTct
V$DELTAEF1_01	ZEB1 group	1791 (-)	1	0.997	gtcAGGTGaga
V$DELTAEF1_01	ZEB1 group	1670 (-)	1	0.98	cccAGGTGact
V$DELTAEF1_01	ZEB1 group	1223 (-)	1	0.973	aaaAGGTGtat
V$DELTAEF1_01	ZEB1 group	2003 (+)	1	0.97	tagCACCTatg
V$ZNF333_01	ZNF333	951 (+)	1	1	ATAAT
V$ZNF333_01	ZNF333	1055 (+)	1	1	ATAAT
V$ZNF333_01	ZNF333	1068 (+)	1	1	ATAAT
V$ZNF333_01	ZNF333	1485 (+)	1	1	ATAAT
V$ZNF333_01	ZNF333	1533 (+)	1	1	ATAAT
V$ZNF333_01	ZNF333	1857 (-)	1	1	ATTAT
V$ZNF333_01	ZNF333	1973 (+)	1	1	ATAAT
V$ZNF333_01	ZNF333	2296 (+)	1	1	ATAAT
V$ZNF333_01	ZNF333	2386 (+)	1	1	ATAAT
V$ZNF333_01	ZNF333	2687 (-)	1	1	ATTAT
V$ZNF333_01	ZNF333	2793 (-)	1	1	ATTAT
V$ZNF333_01	ZNF333	2963 (+)	1	1	ATAAT
V$ZNF333_01	ZNF333	3000 (-)	1	1	ATTAT

TRANSFAC software (http://genexplain.com/transfac): GeneXplain GmbH, Wolfenbüttel, Germany
Only factor binding sites predicted with core and matrix scores respectively higher than 0.99 and 0.95 are listed.
For nucleotide sequence of LEAP-2B gene, refer to GenBank accession no. KX372542.1