	1 50
fe A3Ca	MEPWRPSPRNPMDRIDPNTFRFHFPNLLYASGRKLCYLCFQVETEDYFSC
fe A3Cb	MEPWRPSPRNP T DRIDPNTFRFHFPNLLYASGRKLCYLCFQVETEDYFS Y
fe A3Cc	MEPWRPSPRNPMDRIDPNTFRFHFPNLLYASGRKLCYLCFQVET G DYFSC
fe A3Cx	MEPWRPSPRNPMDRIDPNTFRFHFPNLLYASGRKLCYLCFQVETEDYFS Y
fe A3Cy	MEPWRPSPRNPMDRIDPNTFRFHFPNLLYASGRKLCYLCFQVETEDYFS Y
	54
fa A 0 0 a	
te A3Ca	
fe A3Cb	NDSDRGVFRNKVHPWARCHAEQCFLSWFRDQYPYRDEYYNVIWFLSWSPC
fe A3Cc	
fe A3Cx	NDSERGVFRNKVHPWARCHAEQCFLSWFRDQYPYRDEYYNVIWFLSWSPC
te A3Cy	NDSERGVFRNKVHPWAR <u>CHAEQCFLSWFRDQYPYRDEYYNVIWFLSWSPC</u>
	101 150
fe A3Ca	PTCAFEV//FELEEYRNI TI SIETSRI YYEW/DPNYOEGI CKI WDAG//OLDI
fe A3Ch	
fe A3Cc	PTCAEEVVELEEPYRNI TI SIETSRI YYE YH PNYO O GI R KI WDAGVOI DI
fe A3Cx	
fe A3Cv	
ic nooy	
	151 192
fe A3Ca	MSCDDFKHCWDNFVDHKGMRFQRRNLLKDYDFLAAELQEILR
fe A3Cb	MSCDDFKHCWDNFVDHKGMRF R RRNLLK G YDFLAA K LQEILR
fe A3Cc	MSCDDF E HCWDNFVDHKGMRFQRRNLLKDYDFLAAELQEILR
fe A3Cx	MSCDDFKHCWDNFVDHKGMRF R RRNLLKDYD L LAAELQEILR
fe A3Cy	MSCDDF EY CWDNFV YN KGMRFQRRNLLKDYDFLAAELQEILR

Fig. S2

Α	feline APOBEC3Ca feline APOBEC3Cb feline APOBEC3Cc human APOBEC3C human APOBEC3F CT human APOBEC3F NT murine APOBEC3 NT	MEFWRPSPRNFMDRIDPNTFRFHFPNLLYASGRKLCYLCFQVETEDYFSCDDSDRGVFRNKVHFWARCHAEQCFLSWFRDQYPRDEYYNV MEFWRPSFRNFTDRIDPNTFRFHFPNLLYASGRKLCYLCFQVETEDYFSYNDSDRGVFRNKVHFWARCHAEQCFLSWFRDQYPYRDEYYNV MEFWRPSFRNFMDRIDPNTFRFHFPNLLYASGRKLCYLCFQVETGDYFSCDDSDRGVFRNKVHFWARCHAEQCFLSWFRDQYPYRDEYYNV MNPQIRNFMKAMYFGTFYFQFKNIWEANDRNETWLCFTVEGIKRRSVVSWKTGVFRNQVDSETHCHAERCFLSWFCDDILSPNTKYCV RNPMEAMYFHIFYFFFKNIRKYGRNESWLCFTMEVVKHHSPVSWKRGVFRNQVDETHCHAERCFLSWFCDDILSPNTNYEW MKFHFRNTVEMYRDFSYNFYNRFIISRRNTVWLCYEVKIKG-PSRPRLBAKIFRGQVFSQPEHHAEMCFLSWFCDDILSPNTKYCV MKFHFRNTVEMYRDFSYNFYNRFIISRRNTVWLCYEVKIKG-PSRPRLBAKIFRGQVFSQPEHHAEMCFLSWFCDDILSPNKCFQI MKFHFRNTVEMYRDFSYNFYNRFIISRRNTVWLCYEVTRKDCDSPVSLHHGVFKNKDNIHAEICFLYWFHDKVTKVLSPREFKI
	feline APOBEC3Ca feline APOBEC3Cb feline APOBEC3Cc human APOBEC3C human APOBEC3F CT human APOBEC3F NT murine APOBEC3 NT	TWFLSWSPCPTCAEEVVEFLEEYRNLTLSIFTSRLYYFWDPNYQEGLCKLWDAGVQLDIMSCDDFKHCWDNFVDHKGMRFQ-RRNLLKDYDFLAAELQEILR TWFLSWSPCPTCAEEVVEFLEEYRNLTLSIFTSRLYYFWDPNYQEGLCKLWDAGVQLDIMSCDDFKHCWDNFVDHKGMRFQ-RRNLLKGYDFLAAELQEILR TWFLSWSPCPTCAEEVVEFLEEYRNLTLSIFTSRLYYFYHPNYQQGLRKLWDAGVQLDIMSCDDFEHCWDNFVDHKGMRFQ-RRNLLKDYDFLAAELQEILR TWYTSWSPCPDCAGEVAEFLARHSNVNLTIFTARLYYFYPTCYQEGLRSLSQEGVAVEINDYEDFKYCWENFVYNDNEFFKPWKGLKTNFRLLKRELRESLQ TWYTSWSPCPECAGEVAEFLARHSNVNLTIFTARLYYFWDTDYQEGLRSLSQEGASVEIMGYKDFKYCWENFVYNDDEFFKPWKGLKYNFLFLDSKLQEILE TWYTSWSPCPECAGEVAEFLARHSNVNLTIFTARLYYFWDTDYQEGLRSLSQEGASVEIMGYKDFKYCWENFVYNDDEFFKPWKGLKYNFLFLDSKLQEILE TWYTSWSPCPECAGEVAEFLARHSNVNLTIFTARLYYFWDTDYQEGLRSLSQEGASVEIMGYKDFKYCWENFVYNDDEFFKPWKGLKYNFLFLDSKLQEILE TWYTSWSPCPECAGEVAEFLARHSNVNLTIFTARLYYFWDTDYQEGLRSLSQEGASVEIMGYKDFKYCWENFVYNDDEFFKPWKKLLTNFYQDSKLQEILE TWYTSWSPCFECAEQVLRFLATHHNLSLDIFSSRLYNIRDFENQONLCRLVQEGAQVAAMDLYEFKKCWKKFVDNGGRRFRPWKKLLTNFRYQDSKLQEILR
В	feline APOBEC3H canine APOBEC3H human APOBEC3H murine APOBEC3 CT	MNPLQEVIFCRQFGNQHRVPKPYYRRK-TYLCYQLKLPEGTLIHKDCLRNKK-KRHAEMCFIDKIK MNPLQEETFYQQFSNQ-RVPKFTYCRR-TYLCYQLKPHEGSVTAKVCLQNQE-KRHAEICFIDDIK MALI TAETFRLQFNNKRRLRRPYYPRK-ALLCYQL TPQNG STFTRGYFENKK-K CHAEICFIDEIK PCYIPVPSSSSSTLSNICLTKGLPETRFCVEGRRVHLLS EEFYSQFYNQRVKHLCYYHGMKPYLCYQLEQFNG QAPLKGCLLSEKGKQHAEILFLDKIR
	feline APOBEC3H canine APOBEC3H human APOBEC3H murine APOBEC3 CT	ALTRDTSQRFEIICYITWSPCPFCAEELVAFVKDNPHLSLRIFASRLYVHWRWKYQQGLRHLHASGIPVAVMSLPEFEDCWRNFVDHQDRSFQPWP SRQLDFSQKFEITCYVTWSPCFTCAKKLIAFVNDHPHISLRLFASRLYFHWRQKYKRELRHLQKSGIFLAVMSYLEFKDCWEKFVDHKGRPFQPWN SMGLDETQCYQVTCYLTWSPCSSCAWELVDFIKAHDHLNLGTFASRLYYHWCKPQQKGLRLLCGSQVPVEVMGFPEFADCWENFVDHEKPLSFNPYKMLE SMELSQVI-TTCYLTWSPCFNC <mark>A</mark> WQLAAFKRDRPDLILHTYTSRLYFHWKRPFQKGLCSLWQSGILMDVMDLPQFTDCWTNFVNPKRPFWPWK
	feline APOBEC3H canine APOBEC3H human APOBEC3H murine APOBEC3 CT	NLDQYSKSIKRRLGKILTFLNDLRNDFRNLKLE KLKQYSESIGRRLQRIQTGVPSLVEQQMSISSRQSQVPEPAIPETWDTDHPGVLEENTLGRKERKDEDEMYHSTSDDTLQGPQRRGVSNGIVTLKG ELLKNSRAIKRRLEETKQS GLEIISRRTQRRLHRTKESWGLCDLVNDFGNLCLGPPMS
С	human APOBEC3A human APOBEC3G CT canine APOBEC3A	MEASPASGPRHIMDPHIFTSNFNNGIGRHKTYLCYEVERIDNGTSVKMDQHRGFIHNQAKNLLCGFYG <mark>RHAEIRFIDIVPSIQIDPAQIYRVTWFI</mark> RHSMDEPTFTFNFNNEPWVRGRHETYLCYEVERMHNDTWVLINQRRGFICNQAPHKHGFIEGRHAEICFIDVIPFWKLDIDQDYRVTCFT MEAGPEDWDRHIIDENTFTQNFRNDHNPSKTYLCYQVEISDGSSGVIIDQDKDIVQNEGGGQQHAEWFIIEHIRSRNIDQKISYKVTCFI
	human APOBEC3A human APOBEC3G CT canine APOBEC3A	SWSPCFSWGCAGEVRAFLQENTHVRLRIFAARIYDYDPLYKEALQMLRDAGAQVSIMTYDEFKHCWDTFVDHQGCPFQPWDGLDEHSQALSGRLRAILQNQGN SWSPCFSCAQEMAKFISKNKHVSLCIFTARIYDDQGRCQEGLRTLAEAGAKISIMTYSEFKHCWDTFVDHQGCPFQPWDGLDEHSQDLSGRLRAILQNQEN SWTPCEKCAEBIIRFLAKNRHVSLSILASRIYTMG-PYVKGLRELYDAGVHISIMTFRDFEYCWQTFVDHQDSPFQPWADLDRRSQQLSQQLRAILQKEPEGWTSVCL

Zn²⁺-Coordinating Domain

			CP2		
TGGAGGGGGGCGC	CATTCCCGGGA	ATCCTCCAACTC-	TTGCTCAAG	CTCCTGTTACCC	
TGGAGGGGGCGC	CATTCCCGGGA	ATCCTCCAACT <mark>C-</mark>	TTGCTCAAG	CTCCTGTTACCC	
TGGAGGGGACGCC	CATTCCCGGGA/	ATCCTCCAACTC-	TTGCCCACG	CTCTTGTTACCC	
CTGTCCCTGAGT	CATCGAAAGGA	ATCCTGTCAGTCA	ACAACTGTCATGG	GTTGAAAGATTG	
V-Maf/AF	21	AP1	c-Myb RR	EB-1 PAX-4	
TCCCCCCTTGGGG	GC-CATCCCAG	GGCCGGTGGGCAG	GAAT <mark>GAGGTGGTG</mark>	<mark>ГGGGGG</mark> CA	
TCCCCCCTTGGGG	GC-CATCCCAG	GGCCGGTGGGCAG	GAAT <mark>GAGGTGGTG</mark>	<mark>FGGGGG</mark> CA	
TCCCCTCTTGGGG	JC-CATCCCAG	GCCCGGTGGGCAG	GAAT <mark>GAGGTGGTG</mark>	<mark>FGGGGG</mark> CA	
TATCCTCCAGATT Hand1/I	rcatatgttga E47 Olf-1	agccctaaactcc Olf-	CCGTGGGATGGTG 1/USF	ITAAAAGTAGAA	
Elk-1/c-Ets-1				TGIF/MyoD	
CCAGCCGGAAGAZ	AGC TCTTTGGGG	GACTCGCATGCAC	CAGGCGGTCTGGC	CTG <mark>GGGIGACAG</mark>	
CCAGCCGGAAGAZ	<mark>agc</mark> tctttgggg	GACTCGCATGCAC	CAGGCGGTCTGGC	CTG <mark>GGG</mark> IGACAG	
CCAGCCGGAA-AA	AGC TCTTTGGGG	GACTCGCATGCGC	CGTGCGGTCTGGC	CTG <mark>GGG<mark>IGACAG</mark></mark>	
TCTTTGGGGTGAT	FTCAGTTTAGA	IGTTATCATGAGO	GTGGGGCCCG	-TGAGGGGATTA	
AREB6 H	HNF-4 GATA	-3, -1/PAX-4/US A	P-1	HNF-4	
GTGTCTCCA/	AGGCCTCCTCTT	ICTTGTC <mark>TAGGAC</mark>	TCAACTTTCCCC	GTTGCTCTTTGT	
GTGTCTCCA2	AGGCCTCCTCTT	fcctgtc <mark>taggag</mark>	TCAACTTTCCCC	GTTGCTCTTTGT	
GTGTCTCCA/	AGGCCTCCTCTT	ICCTGTC <mark>TAGGAG</mark>	TCAACTTTCCCC	GTTGCTCTTTGT	
GTGTCCTTCTT	CTTTTCT	TTTT-T. AAAATO	GTTTATTTATTTG.	AGACAGAGAGAG	
Barbie Box/	Evi-1	FOX	D3, J2/HNF-3/Fr	eac-7/HFH-1,-3	
	Amt/U	SF/N-Myc/c-Myc/	<u>(MyoD</u>	Elk-1/c-Ets-1	
TTCTCCA TCTGGG	3GTCCTG <mark>GTGG</mark> 2	ACACGTGGCC	<mark>BAGG</mark> CAAGCACAC	AG <mark>CTCACCGGAT</mark>	
TTCTCCATCTGGG	3GTCCTG <mark>GT¢G</mark> 2	ACACGTGGCC	<mark>BAGG</mark> CAAGCACAC	AG <mark>CTCACCGGAT</mark>	
TTCTCCATCTGG0	ЗGTCCTG <mark>G‡<mark>¢</mark>G2</mark>	ATACGTGGCC	<mark>BAGG</mark> CAAGCACAC.	AG <mark>CTCA</mark> CCGGAT	
AGACAGAGACAGA	AGCCTGAGCAG	GGGAGGGGCAGAG	BAGAGAGGGAGAC.	ACAGAATCCCAG	
PAX-4/E47					
GCACGCTTCAAGC	CCAGATCCCT	ATCCCTGCCCTG	GGAGGCCTT	GTAGGGGCAGCA	
GCACGCTTCAAGC	CCAGATCCCTC	ATCCCTGCCCTG	GGAGGCCTT	GTAGGGGCAGCA GTAGGGGCAGCA	:
GCACGCTTCAAGC GCACGCTTCAAGC GCACGCTTCAAGC	CCCAGATCCCTC CCCAGATCCCTC CCCAGATCCCTC	ATCCCTGCCCTG ATCCCTGACCTG ATCCCTGCCCTG	GGAGGCCTT GGAGGCCTT GGAGGCCTT	GTAGGGGCAGCA GTAGGGGCAGCA - TAGGGGCAGCA	:
GCACGCTTCAAGC GCACGCTTCAAGC GCACGCTTCAAGC GCAGGCTCCAGGC	CCAGATCCCT CCAGATCCCT CCAGATCCCT CCAGATCCCT TCTGAGCTGT	ATCCCTGCCCTG ATCCCTGACCTG ATCCCTGCCCTG CAGCACAGAGTCC	GG AGGCCTT GG AGGCCTT GG AGGCCTT CACGCGGGGCCTC	STAGGGGCAGCA STAGGGGCAGCA -TAGGGGCAGCA SAACTCACAACA	:
GCACGCTTCAAGC GCACGCTTCAAGC GCACGCTTCAAGC GCAGGCTCCAGGC ZID	CCCAGATCCCTC CCCAGATCCCTC CCCAGATCCCTC TCTGAGCTGTC	ATCCCTGCCCTG ATCCCTGACCTG ATCCCTGCCCTG CAGCACAGAGTCC	GGAGGCCTT GGAGGCCTT GGAGGCCTT CGACGCGGGGGCTC	STAGGGGCAGCA STAGGGGCAGCA -TAGGGGCAGCA SAACTCACAACA SOX-9, -5	:
GCACGCTTCAAGC GCACGCTTCAAGC GCACGCTTCAAGC GCACGCTTCCAGGC GCAGGCTCCAGGC ZID	CCCAGATCCCT CCCAGATCCCTC CCCAGATCCCTC TCTGAGCTGTC V-MAF/TGIF	ATCCCTGCCCTG ATCCCTGACCTG ATCCCTGCCTG CAGCACAGAGTCC CAGCACAGAGTCC	GGAGGCCTT GGAGGCCTT GGAGGCCTT CGACGCGGGGCTC DP CR1	GTAGGGGCAGCA GTAGGGGCAGCA -TAGGGGCAGCA GAACTCACAACA SOX-9, -5 V-Maf	:
GCACGCTTCAAGC GCACGCTTCAAGC GCACGCTTCAAGC GCACGCTTCAGG GCAGGCTCCAGGC ZID A-GGGTCCTCCCC	CCCAGATCCCT CCCAGATCCCTC CCCAGATCCCTC TCTGAGCTGTC V-MAF/TGIF CTTGTGCCCCCC	ATCCCTGCCTG ATCCCTGACCTG ATCCCTGCCTG CAGCACAGAGTCC CACCCACTCCTAT	GGAGGCCTT GGAGGCCTT GGAGGCCTT GACGCGGGGCTC DP CR1 CC-ATGGAATGA	GTAGGGGCAGCA GTAGGGGCAGCA -TAGGGGCAGCA GAACTCACAACA SOX-9, -5 V-Maf TGAGGAAGCAGG	:
GCACGCTTCAAGC GCACGCTTCAAGC GCACGCTTCAAGC GCAGGCTCCAGGC ZID A-GGGTCCTCCCC A-GGGTCCTCCCC	CCCAGATCCCT CCCAGATCCCT CCCAGATCCCT TCTGAGCTGT V-MAF/TGIF CTTGTGCCCCCC CTTGTGCCCCCC	ATCCCTGCCTG ATCCCTGACCTG ATCCCTGCCCTG CAGCACAGAGTCC CACCCACTCCTAT CACCCACTCCTAT	GGAGGCCTT GGAGGCCTT GGAGGCCTT GACGCGGGGCTC DP CR1 CC-ATGGAATGA CC-ATGGAATGA	GTAGGGGCAGCA GTAGGGGCAGCA -TAGGGGCAGCA GAACTCACAACA SOX-9, -5 V-Maf IGAGGAAGCAGG IGAGGAAGCAGG	
GCACGCTTCAAGC GCACGCTTCAAGC GCACGCTTCAAGC GCAGGCTCCAGG ZID A-GGGTCCTCCCC A-GGGTCCTCCCC A-GGGTCCTCCCC	CCCAGATCCCT CCCAGATCCCT CCCAGATCCCT TCTGAGCTGT V-MAF/TGIF CTTGTGCCCCCC CTTGTGCCCCCC	ATCCCTGCCTG ATCCCTGACCTG ATCCCTGCCCTG CAGCACAGAGTCC CACCCACTCCTAT CACCCACTCCTAT CACCCACTCCTAT	GGAGGCCTT GGAGGCCTT GACGCGGGGCTC DP CR1 CC-ATGGAATGA CC-ATGGAATGA CC-ATGGAATGA	GTAGGGGCAGCA GTAGGGGCAGCA -TAGGGGCAGCA GAACTCACAACA SOX-9, -5 V-Maf IGAGGAAGCAGG IGAGGAAGCAGG IGAGGAAGCAGG	
GCACGCTTCAAGC GCACGCTTCAAGC GCACGCTTCAAGC GCAGGCTCCAGG ZID A-GGGTCCTCCCC A-GGGTCCTCCCC A-GGGTCCTCCCC ATGAGATCATGAC	CCCAGATCCCT CCCAGATCCCT CCCAGATCCCT TCTGAGCTGT TCTGAGCTGT V-MAF/TGIF CTTGTGCCCCCC TTGTGCCCCCC CTTGTGCCCCCC CCTGAGCCAAA	ATCCCTGCCTG ATCCCTGACCTG ATCCCTGCCTG CAGCACAGAGTCC CACCCACTCCTAT CACCCACTCCTAT CACCCACTCCTAT CACCCACTCCTAT GTCCGATGCTTA	GGAGGCCTT GGAGGCCTT GACGCGGGGCTC DP CR1 CC-ATGGAATGA CC-ATGGAATGA CC-ATGGAATGA CC-ATGGAATGA	GTAGGGGCAGCA GTAGGGGCAGCA -TAGGGGCAGCA GAACTCACAACA SOX-9, 5 V-Maf IGAGGAAGCAGG IGAGGAAGCAGG IGAGGAAGCAGG CCCAGGTGCCCC	:
GCAGGCTTCAAGG GCAGGCTTCAAGG GCAGGCTTCAAGG GCAGGCTCCCAGG ZID A-GGGTCCTCCCC A-GGGTCCTCCCC A-GGGTCCTCCCC ATGAGATCATGAC	CCCAGATCCCT CCCAGATCCCT CCCAGATCCCT TCTGAGCTGT TCTGAGCTGT V-MAF/TGIF CTTGTGCCCCCC CTTGTGCCCCCC CTGAGCCAAAC	ATCCCTGCCTG ATCCCTGACCTG CACCCTGCCCTG CAGCACAGAGTCC CACCCACTCCTAT CACCCACTCCTAT CACCCACTCCTAT CACCCACTCCTAT GTCCGATGCTTAF	GGAGGCCTT GGAGGCCTT GACGCGGGGCTC DP CR1 CC-ATGGAATGA CC-ATGGAATGA CC-ATGGAATGA CC-ATGGAATGA	GTAGGGGCAGCA GTAGGGGCAGCA -TAGGGGCAGCA GAACTCACAACA SOX-9, -5 V-Maf IGAGGAAGCAGG IGAGGAAGCAGG IGAGGAAGCAGG CCCAGGTGCCCC ER/AREB6/MyoD	
GCACGCTTCAAGC GCACGCTTCAAGC GCACGCTTCAAGC GCAGGCTCCAGG ZID A-GGGTCCTCCCC A-GGGTCCTCCCC A-GGGTCCTCCCC ATGAGATCATGAC ER	CCCAGATCCCT CCCAGATCCCT CCCAGATCCCT TCTGAGCTGT TCTGAGCTGT V-MAF/TGIF CTTGTGCCCCCC CTTGTGCCCCCC CTGAGCCAAAC	ATCCCTGCCTG ATCCCTGACCTG CAGCACAGAGTCC CAGCACAGAGTCC CACCCACTCCTAT CACCCACTCCTAT CACCCACTCCTAT CACCCACTCCTAT GTCCGATGCTTAF	GGAGGCCTT GGAGGCCTT GGAGGCCTT GACGCGGGGGCTC DP CR1 CC-ATGGAATGA CC-ATGGAATGA CC-ATGGAATGA CC-ATGGAATGA	ETAGGGGCAGCA TAGGGGCAGCA TAGGGGCAGCA GAACTCACAACA SOX-9, -5 V-Maf IGAGGAAGCAGG IGAGGAAGCAGG IGAGGAAGCAGG CCCAGGTGCCC¢ ER/AREB6/MyoD CAAT Box	
GCAGGCTTCAAGG GCAGGCTTCAAGG GCAGGCTTCAAGG GCAGGCTCCAGG ZID A-GGGTCCTCCCC A-GGGTCCTCCCC A-GGGTCCTCCCC ATGAGATCATGAC ER AGGAGCCAGGCCZ	CCAGATCCCT CCAGATCCCT CCAGATCCCT CCAGATCCT TCTGAGCTGT V-MAF/TGIF CTTGTGCCCCCC CTTGTGCCCCCC CTTGTGCCCCCCC CCTGAGCCAAAC	ATCCCTGCCTG ATCCCTGCCTG CATCCCTGCCTG CAGCACAGAGTCC CACCCACTCCTAT CACCCACTCCTAT CACCCACTCCTAT CACCCACTCCTAT CACCCACTCCTAT	GGAGGCCTT GGAGGCCTT GGCAGGCCTT GACGCGGGGGCTC DP CR1 CC-ATGGAATGA CC-ATGGAATGA CCC-ATGGAATGA CCC-ATGGAATGA CTGACAGAGCCA	ETAGGGGCAGCA TAGGGGCAGCA TAGGGGCAGCA GACTCACAACA SOX-9, 5 V-Maf IGAGGAAGCAGG IGAGGAAGCAGG IGAGGAAGCAGG CCCAGGTGCCCC ER/AREB6/MyOD CAAT Box ITGCTGAGTGGC	
GCAGGCTTCAAGG GCAGGCTTCAAGG GCAGGCTTCAAGG GCAGGCTCCAGG ZID A-GGGTCCTCCCC A-GGGTCCTCCCC A-GGGTCCTCCCC ATGAGATCATGAC ER AGGAGCCAGGCCZ AGGAGCCAGGCCZ	CCAGATCCCT CCAGATCCCT CCAGATCCCT CCAGATCCT CTGAGCTGT V-MAF/TGIF CTTGTGCCCCC CTTGTGCCCCCC CTGAGCCAAAC	ATCCCTGCCTG ATCCCTGCCTG CATCCCTGCCTG CAGCACAGAGTCC CACCCACTCCTAT CACCCACTCCTAT CACCCACTCCTAT CACCCACTCCTAT GTCCGATGCTTAP AAGGCATTCCAGC	GGAGGCCTT GGAGGCCTT GGAGGCCTT GACGCGGGGGCTC DP CR1 CC-ATGGAATGA CC-ATGGAATGA CC-ATGGAATGA CCGACAGAGCCA CTGGCCATTGCT TCGGCCATTGCT	GTAGGGGCAGCA GTAGGGGCAGCA -TAGGGGCAGCA GACTCACAACA SOX-9, -5 V-Maf IGAGGAAGCAGG IGAGGAAGCAGG IGAGGAAGCAGG CCCAGGTGCCC¢ F/AREB6/MyOD CAAT Box ITGCTGAGTGGC ITGCTGAGTGGC	
GCAGGCTTCAAGG GCAGGCTTCAAGG GCAGGCTTCAAGG GCAGGCTCCAGG ZID A-GGGTCCTCCCC A-GGGTCCTCCCC A-GGGTCCTCCCC ATGAGATCATGAC ER AGGAGCCAGGCCZ AGGAGCCAGGCCZ AGGAGCCAGGCCZ	CCAGATCCCT CCAGATCCCT CCAGATCCCT TCTGAGCTGT V-MAF/TGIF CTTGTGCCCCC CTTGTGCCCCCC CTGAGCCAAAC	ATCCCTGCCTG ATCCCTGACCTG CAGCACAGAGTCC CAGCACAGAGTCC CACCCACTCCTAT CACCCACTCCTAT CACCCACTCCTAT CACCCACTCCTAT GTCCGATGCTTAA AAGGCATTCCAGC AAGGCATTCCAGC	GGAGGCCTT GGAGGCCTT GGAGGCCTT GACGCGGGGGCTC DP CR1 CC-ATGGAATGA CC-ATGGAATGA CC-ATGGAATGA CCC-ATGGAATGA CTGACAGAGCCA TCGGCCATTGCT TCGGCCATTGCT	GTAGGGGCAGCA GTAGGGGCAGCA -TAGGGGCAGCA GACTCACAACA SOX-9, -5 V-Maf IGAGGAAGCAGG IGAGGAAGCAGG IGAGGAAGCAGG CCCAGGTGCCC¢ F/AREB6/MyOD CAAT Box ITGCTGAGTGGC ITGCTGAGTGGC ITGCTGAGTGGC	
GCAGGCTTCAAGG GCAGGCTTCAAGG GCAGGCTTCAAGG GCAGGCTCCAGGG ZID A-GGGTCCTCCCC A-GGGTCCTCCCC A-GGGTCCTCCCC ATGAGATCATGAC ER AGGAGCCAGGCCZ AGGAGCCAGGCCZ AGGAGCCAGGCCZ AGGAGCCAGGCCZ	CCAGATCCCT CCAGATCCCT CCAGATCCCT TCTGAGCTGT V-MAF/TGIF CTTGTGCCCCC CTTGTGCCCCCC CTGAGCCAAAC AGGCCCCCTGG AGGCCCCCTGG AGGCCCCCTGG AGGAGAG	ATCCCTGCCTG ATCCCTGCCTG CCGCACAGAGTCC CAGCACAGAGTCC CCCCCCTCCTAT CACCCACTCCTAT CACCCACTCCTAT CACCCACTCCTAT GTCCGATGCTTAA AAGGCATTCCAGC AAGGCATTCCAGC AAGGCATTCCAGC	GGAGGCCTT GGAGGCCTT GGAGGCCTT GGCCAGGGGGCTC DP CR1 CC-ATGGAATGA CC-ATGGAATGA CCC-ATGGAATGA CTGACAGAGCCA CTGGCCATTGCT TCGGCCATTGCT TCGGCCATTGCT	GTAGGGGCAGCA GTAGGGGCAGCA -TAGGGGCAGCA GAACTCACAACA SOX-9, -5 V-Maf IGAGGAAGCAGG IGAGGAAGCAGG IGAGGAAGCAGG ICCAGGTGCCCC ER/AREB6/MyOD CAAT Box ITGCTGAGTGGC ITGCTGAGTGGC ITGCTGAGTGGC ITGCTGAGTGGC ITGCTGAGTGGC	
GCAGGCTTCAAGG GCAGGCTTCAAGG GCAGGCTTCAAGG GCAGGCTCCAGGG ZID A-GGGTCCTCCCC A-GGGTCCTCCCC A-GGGTCCTCCCC ATGAGATCATGAC ER AGGAGCCAGGCCA AGGAGCCAGGCCA AGGAGCCAGGCCA AGGAGCCAGGCCA	CCAGATCCCT CCAGATCCCT CCAGATCCCT CCAGATCCCT TCTGAGCTGT V-MAF/TGIF CTTGTGCCCCC CTTGTGCCCCCC CTGAGCCAAAC AGGCCCCCTGGZ AGGCCCCCTGGZ AGGAGAGZ	ATCCCTGCCTG ATCCCTGCCTG CCGCACAGAGTCC CAGCACAGAGTCC CCCCCCCTC CACCCACTCCTAT CACCCACTCCTAT CACCCACTCCTAT CACCCACTCCTAT GTCCGATGCTTAA AAGGCATTCCAGC AAGGCATTCCAGC AAGGCATTCCAGC	GGAGGCCTT GGAGGCCTT GGCAGGCCTT CGACGCGGGGCTC DP CR1 CC-ATGGAATGA CC-ATGGAATGA CCC-ATGGAATGA CTGACAGAGCCA TCGGCCATTGCT TCGGCCATTGCT TCGGCCATTGCT TCGGCCATTGCT TGGF	GTAGGGGCAGCA GTAGGGGCAGCA -TAGGGGCAGCA GAACTCACAACA SOX-9, -5 V-Maf IGAGGAAGCAGG IGAGGAAGCAGG IGAGGAAGCAGG ICCAGGTGCCC¢ ER/AREB6/MyOD CAAT Box ITGCTGAGTGGC ITGCTGAGTGGC ITGCTGAGTGGC ITGCTGAGTGGC ITGCTGAGTGGC ITGCTGAGTGGC	
GCACGCTTCAAGC GCACGCTTCAAGC GCACGCTTCAAGC GCACGCTCCAGGC ZID A-GGGTCCTCCCC A-GGGTCCTCCCC ATGAGATCATGAC ER AGGAGCCAGGCCZ AGGAGCCAGGCCZ AGGAGCCAGGCCZ AGGAGCCAGGCCZ	CCAGATCOCT CCAGATCOCT CCAGATCOCT CCAGATCOCT CTCTGAGCTGT V-MAF/TGIF CTTGTGCCCCCC CTTGTGCCCCCCC CTGAGCCCAAAC AGGCCCCCTGGZ AGGCCCCCTGGZ AGGACCCCTGGZ AGGAGAGZ Evi-1 Evi-1	ATCCCTGCCTG ATCCCTGCCTG CCTGCCTGCCTG CAGCACAGAGTCC C CACCCACTCCTAT CACCCACTCCTAT CACCCACTCCTAT GTCCGATGCTTAA AAGGCATTCCAGC AAGGCATTCCAGC AAGGCATTCCAGC AAGGCATTCCAGC	GGAGGCCTT GGAGGCCTT GGCAGGCCTT CGACGCGGGGCTC DP CR1 CC-ATGCAATGA CC-ATGCAATGA CCC-ATGCAATGA CCC-ATGCAATGA CTGACAGAGCCA TCGGCCATTGCT TCGGCCATTGCT TCGGCCATTGCT TGGFCACTCCT TGIF	ETAGGGGCAGCA TAGGGGCAGCA TAGGGGCAGCA GAACTCACAACA SOX-9,-5 V-Maf TGAGGAAGCAGG TGAGGAAGCAGG TGAGGAAGCAGG TGAGGAAGCAGG CCAGGTGCCCC ER/AREB6/MyOD CAAT Box TTGCTGAGTGGC TTGCTGAGTGGC TTGCTGAGTGGC TTGCTGAGTGGC	
GCAGGCTTCAAGG GCAGGCTTCAAGG GCAGGCTTCAAGG GCAGGCTCCAGG ZID A-GGGTCCTCCCC A-GGGTCCTCCCC A-GGGTCCTCCCC ATGAGATCATGAC ER AGGAGCCAGGCCZ AGGAGCCAGGCCZ AGGAGCCAGGCCZ AGGAGCCAGGCCZ AGGAGCCAGGCCZ AGGAGCCAGGCCZ AGGAGCCAGGCCZ AGGAGCCAGGCCZ AGGAGCCAGGCCZ AGGAGCCAGGCCZ AGGAGCCAGGCCZ	CCAGATCOCT CCAGATCOCT CCAGATCOCT CCAGATCOCT CTCTGAGCTGT V-MAF/TGIF CTTGTGCCCCCC CTTGTGCCCCCC CTTGTGCCCCCCC CCTGAGCCCAAAC AGGCCCCCTGGA AGGCCCCCTGGA AGGCCCCCTGGA AGGCCCCCTGGA AGGCCCCCTGGA AGGAG AGA Evi-1 CTTAGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	ATCCCTGCCTG ATCCCTGACCTG ATCCCTGCCTG CAGCACAGAGTCC CAGCACAGAGTCC CCCCCCTCTAT CACCCACTCCTAT CACCCACTCCTAT CACCCACTCCTAT GTCCGATGCTTAA AAGGCATTCCAGC AAGGCATTCCAGC AAGGCATTCCAGC AAGGCATTCCAGC AAGGCATTCCAGC AAGGCATTCCAGC AAGGCATTCCAGC	GGAGGCCTT GGAGGCCTT GGCAGGCCTT CGACGCGGGGCTC DP CR1 CC-ATGCAATGA CC-ATGCAATGA CCC-ATGCAATGA CCC-ATGCAATGA CTGACAGAGCCA TCGGCCATTGCT TCGGCCATTGCT TCGGCCATTGCT TGGFCACTCCT TGIF	GTAGGGGCAGCA GTAGGGGCAGCA -TAGGGGCAGCA GAACTCACAACA SOX-9,-5 V-Maf IGAGGAAGCAGG IGAGGAAGCAGG IGAGGAAGCAGG ICCAGGTGCCCC ER/AREB6/MyOD CAAT Box ITGCTGAGTGGC ITGCTGAGTGGC ITGCTGAGTGGC ITGCTGAGTGGC ITGCTGAGTGGC ITGCTGAGTGGC	:
GCAGGCTTCAAGG GCAGGCTTCAAGG GCAGGCTTCAAGG GCAGGCTCCAGGG ZID A-GGGTCCTCCCCC A-GGGTCCTCCCCC ATGAGATCATGAC ER AGGAGCCAGGCCZ AGGAGCCAGGCCZ AGGAGCCAGGCCZ AGGAGCCAGGCCZ AGGAGCCAGGCCZ AGGAGCCAGGCCZ AGGAGCCAGGCCZ AGGAGCCAGGCCZ AGGAGCCAGGCCZ AGGAGCCAGGCCZ AGGAGCCAGGCCZ AGGAGCCAGGCCZ AGGAGCCAGGCCZ AGGAGCCAGGCCZ AGGAGCCAGGCCZ AGGAGCCAGGCCZ AGGAGCCAGGCCZ AGGAGCCAGGCCZ	CCAGATCOCT CCAGATCOCT CCAGATCOCT CCAGATCOCT CTCTGAGCTGT V-MAF/TGIF CTTGTGCCCCC CTTGTGCCCCCC CTTGTGCCCCCC CTGAGCCCAAAC AGGCCCCCTGG AGGCCCCCTGG AGGCCCCCTGG AGGAGAG Evi-1 -CTTAGCCTCT CTTAGCCTCTC	ATCCCTGCCTG ATCCCTGACCTG ATCCCTGCCTG CAGCACAGAGTCC CACCCACTCTAT CACCCACTCCTAT CACCCACTCCTAT GTCCGATGCTTAT AAGGCATTCCAGC AAGGCATTCCAGC AAGGCATTCCAGC AAGGCATTCCAGC AAGGCATTCCAGC AAGGCATTCCAGC AAGGCATTCCAGC CTGTGCTGC	GGGAGGCCTT GGGAGGCCTT GGGAGGCCTT CGACGCGGGGGCTC DP CR1 CC-ATGCAATGA CC-ATGCAATGA CCC-ATGCAATGA CCC-ATGCAATGA CTGGCCATTGCT TCGGCCATTGCT TCGGCCATTGCT TGGF GGACCTCATCTAA GGACCTCATCTAA	GTAGGGGCAGCA GTAGGGGCAGCA -TAGGGGCAGCA GAACTCACAACA SOX-9,-5 V-Maf IGAGGAAGCAGG IGAGGAAGCAGG IGAGGAAGCAGG ICCAGGTGCCCC ER/AREB6/MyOD CAAT Box ITGCTGAGTGGC ITGCTGAGTGGC ITGCTGAGTGGC ITGCTGAGTGGC ITGCTGAGTGGC ICTCCCTCTCCC	:

lk-1

C-Rel

Fig. S3

A3Ca

A3Cb A3H

A3Cc

A3Ca

A3Cb A3H A3Cc

A3Ca A3Cb A3H A3Cc

A3Ca

A3Cb A3H A3Cc

A3Ca A3Cb A3H A3Cc

A3Ca

A3Cb A3H A3Cc

A3Ca

A3Cb A3H

A3Cc

A3Ca

A3Cb A3H A3Cc

A3Ca A3Cb A3H A3Cc

Putative Transcription

Factor Binding Sites

A3Cc Specific Sites

Conserved Motifs Between the 4 Genes

ł

}

Α

(first half)

MyoD

PAX-4 USF

CDP CR1

A3Ca A3Cb A3H A3Cc	G <mark>TGATCGGCCC</mark> CTCCCAAAGCTCTTGGGGGGCTGTGGTAGAGGATGTGCTCAA <mark>C-GCAC</mark> G <mark>TGATCGGCCC</mark> CTCCCAAAGCTCTTGGGGGGCTGTGGTAGAGGATGTGCTCAA <mark>C-GCAC</mark> GTGATCGGCCCCTCCCAAAGCTCTTGGGGGGCTGTGGTAGAGGATGTGCTCAAC-GCAC -TGAGGGGATTTATGCAGAGGACC-AACCACAGAATTAGGAACCCAAAGCCCATCTGTGC	575
7.	MyoD NKX2-5	
A3Ca A3Cb A3H A3Cc	CTGCCTTCTCCTGGAATGGGGATGAAGATGTGCAGGGCTGAGCCCTGGCC CTGCCTTCTCCTGGAATGGGGATGAAGATCTGCAGGGCTGAGCCCTGGCC CTGCCTTCCTGGAATGGGGATGAAGATCTGCAGGGCTGAGCCCTGGCC CTTTACTACTGTGGAGTCAGGAGAAAACACAGGAGTTCTGACATAAAGTACACACCGCCT	625
	PAX-4 Hand1/E47 CAAT Box	
A3Ca	CTCCCTTTCCAGACACCCAGCGTCCTGCTGGGGGGACTGAATGGCTCCTAAGGGT	679
A3Cb	CTCCCTTTCCAGACACCCAGCGTCCTGCTGGGGGGGCTCGAATGGCTCCTAAGGGT	
АЗН	CTCCCTTTCCAGACACCCAGCGTCCTGCTGGGGGGACTGAATGGCTCCTAAGGGT	
A3Cc	CCTTACCTACATTCTTTCAACAGGCTTGTGGAGAGCAACACCTGGGCCCAGATGTGGGGA	
	ER E47/MyoD/AREB6	
A 3Ca		729
A3Ch		
736		
ASC		
ASCC	TAX/Creh/PAX-4	
	CP2	
A3Ca	TCCCCAGCCACCGGCTTCTGTCCTG	789
A3Ch	TCCCCAGCCACCGCTCTCTCTCCCAGCCACTCTCCAACCCCCACCCCCTCTC	
АЗН	TCCCCAGCCACCGCTCTCTCCCCACCCAGTGTGTTCCCAACCCCCTCTG	
A3Cc	TCCCCAGGAGCCAGCTTCTCTCTCTCTCTCCACCCATCTCTCTC	
11500	Oct.1 CP2	
A3Ca	GCAAAGTACTTTCTCTTTCCCTTTTCCATAACC <mark>TGGGTCCTGCT</mark> GCGCAATGGGGCGCAT	849
A3Cb	SCAAAGTACTTTCTCTTTCCCTTTTCCATAACCTGGGTCCTGCTGCGCGAATGGGGGCGCAT	
АЗН	GCAAAGTACTTTCTCTTTTCCCATAACCT <mark>GGGTCCTGCT</mark> GCCCAATGGGGCCCAT	
A3Cc	GTATCCTCCTTTCTCTTTCCCTTTGCAATAACTCTTCCCAATGGGGCCGGT	
	Evi-1	
A3Ca	CTCCTTCTGAGGGAGGCTGTCCCCCAGGGCAGGGGGGGGG	909
A3Cb	CTCCTTCTGAGGGAGGCTGTCCCCCAGGGCAGGGGGGGGGGGGGAAGGCCTCGGGAGAG	
АЗН	CTCCTTCTGAGGGAGGCTGTGCCCAGGGCGGGGGGGCGTAGCCCTGGGGATG	
A3Cc	CTCCTTCTGAGGGCAGCTGTGTCCAGGGGAGAGGCTTCAGAGAAGGAGAG	
	HNF-4 Barbie Box	
A 3Ca		969
A3Ch	GTGGCTCTGAGCCTGAGGAAGTGCAACCATCTGAGGGCCCACCCTTGGGGGCGAAAG	
АЗН	GTGGCTCTGAGCCTGAGGAAGTGCAACCTTTTGAGGGCCCACCCCCCCC	
A3CC	GCGAGTCTGAACC-AAGGCAGTGCAACCACCTGAGGGGCTCCCCTGAGAACAAAG	
A3Ca	(AGGAAGGAGGTGCGGCTTCTGAGGAGGCAGCCTGGGAGGTGACTGTCACACTG	1029
A3Cb	CAGGAAGGAGGTGCGCCTTCTGAGGAGGCAGCCTGGGAGGTGACTGTCACACTG	
АЗН	CAGGAAGGAGGTGCGGCTTCTGAGGAGGCAGCCTGGGAGGTGACTGTCACACTG	
A3Cc	CAGGAAGGAGGTGCGGCTTCTGAGGAGGCAGCCTGGGAGGTGACTGGCACACTG	
	Flk-1	

_splice acceptor?

Fig. S3

(second half)



Domain





Fig. S5



D

	vector	feA3Ca	feA3Cb	feA3Cc	feA3H	feA3CH
No. of sequences analyzed	8	8	8	8	8	8
Mutations G-A/other	0/3	3/3	3/5	0/3	48/3	39/2
Mutations per 100 nucleotides	0.10	0.20	0.27	0.10	1.71	1.37
Clones without G-A editing	8	5	5	8	0	0
Minimal no. of G-A per clone	0	1	1	0	2	3
Maximal no. of $G \rightarrow A$ per clone	0	1	2	0	8	7
Average no. of $G \rightarrow A$ per clone	0	0.4	0.4	0	6	4.9
G→A exchanges per 100 nucleotides	0	0.10	0.10	0	1.61	1.31