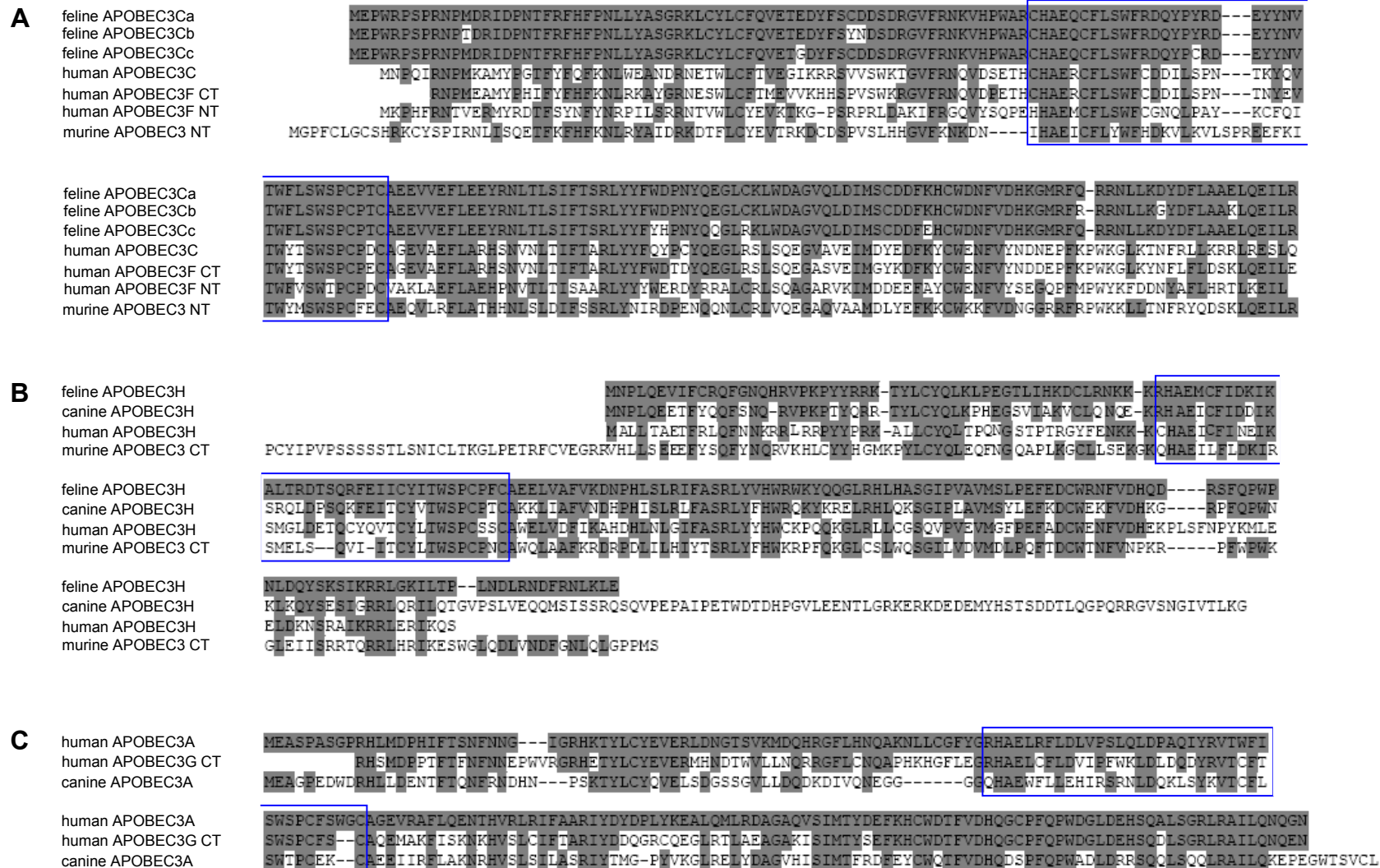


Fig. S1

	1		50
fe A3Ca	M	E	P
fe A3Cb	M	E	P
fe A3Cc	M	E	P
fe A3Cx	M	E	P
fe A3Cy	M	E	P
	51		100
fe A3Ca	D	D	S
fe A3Cb	<b>N</b>	D	S
fe A3Cc	D	D	S
fe A3Cx	<b>N</b>	D	S
fe A3Cy	<b>N</b>	D	S
	101		150
fe A3Ca	P	T	C
fe A3Cb	P	T	C
fe A3Cc	P	T	C
fe A3Cx	P	T	C
fe A3Cy	P	T	C
	151		192
fe A3Ca	M	S	C
fe A3Cb	M	S	C
fe A3Cc	M	S	C
fe A3Cx	M	S	C
fe A3Cy	M	S	C

 Zn<sup>2+</sup>-Coordinating Domain

Fig. S2



 Zn<sup>2+</sup>-Coordinating Domain

**Fig. S3**

(first half)

**A**



Fig. S3

(second half)

A

CDP CR1

A3Ca GTGATCGGCCCTCCCAAAGCTCTTGGGGGCTGTGGTAGAGGAT--GTGCTCAAC-GCAC 575  
 A3Cb GTGATCGGCCCTCCCAAAGCTCTTGGGGGCTGTGGTAGAGGAT--GTGCTCAAC-GCAC  
 A3H GTGATCGGCCCTCCCAAAGCTCTTGGGGGCTGTGGTAGAGGAT--GTGCTCAAC-GCAC  
 A3Cc -TGAGGGGATTTATGCAGAGGACC-AACCACAGAATTAGGAACCCAAAGCCCATCTGTGC

MyoD NKX2-5

A3Ca CTGCCTTCTCCTGGAATGGGGATGAAGATGTGCAGGGCTGA-----GCCCTGGCC 625  
 A3Cb CTGCCTTCTCCTGGAATGGGGATGAAGATGTGCAGGGCTGA-----GCCCTGGCC  
 A3H CTGCCTTCTCCTGGAATGGGGATGAAGATGTGCAGGGCTGA-----GCCCTGGCC  
 A3Cc CTTTACTACTGTGGAGTCAGGAGAAAACACAGGAGTTCTGACATAAAGTACACACCGCCT

Hand1/E47 PAX-4 CAAT Box

A3Ca CTCCTTTCCAGACACCCAGCGTCTGTGGGGACTGAA--TGGCTCCTAA---GGGT 679  
 A3Cb CTCCTTTCCAGACACCCAGCGTCTGTGGGGACTGAA--TGGCTCCTAA---GGGT  
 A3H CTCCTTTCCAGACACCCAGCGTCTGTGGGGACTGAA--TGGCTCCTAA---GGGT  
 A3Cc CCTTACCTACATTCTTTCAACAGGCTTGTGGAGCAACACCTGGGCCCAGATGTGGGGA

ER E47/MyoD/AREB6

A3Ca CA-----CACAGTGGTGGACAGGAGAGGGCTCATGCCA----CTCAGAGAGCCCGCCTC 729  
 A3Cb CA-----CACAGTGGTGGACAGGAGAGGGCTCATGCCA----CTCAGAGAGCCCGCCCC  
 A3H CA-----CACAGTGGTGGACAGGAGAGGGCTCATGCCA----CTCAGAGAGCCCGCCTC  
 A3Cc CATGGGGACGCAGGGTGACCGGGAGAGGGCTCACCCCGAGTCTCAGAGAGCCCGCCCC

TAX/Creb/PAX-4 CP2

A3Ca TCCCCAGCCACCGGCTTCTGTCTGTCTCTCTCCAGCCAGTGTGTGTCCCAACCCCTCTG 789  
 A3Cb TCCCCAGCCACCGGCTTCTGTCTGTCTCTCTCCAGCCAGTGTGTGTCCCAACCCCTCTG  
 A3H TCCCCAGCCACCGGCTTCTGTCTGTCTCTCTCCAGCCAGTGTGTGTCCCAACCCCTCTG  
 A3Cc TCCCCAGGAGCCAGCTTCTGTCTGTCTCTCTCCAGCCCAATCTGT--TCCGACCCCTCTG

Oct-1 CP2

A3Ca GCAAAGTACTTTCTCTTTCCCTTTCCATAACCTGGGTCTCTGCTGCGCAATGGGGCGCAT 849  
 A3Cb GCAAAGTACTTTCTCTTTCCCTTTCCATAACCTGGGTCTCTGCTGCGCAATGGGGCGCAT  
 A3H GCAAAGTACTTTCTCTTTCCCTTTCCATAACCTGGGTCTCTGCTGCGCAATGGGGCCAT  
 A3Cc GTATCCTCCTTTCTCTTTCCCTTTGCAATAACT-----CTTCCAATGGGGCCGGT

Evi-1

A3Ca CTCCTTCTGAGGGAGGCTGTCCCAGGGCAGGGGGTGGGGGGGAAGGCCTCGGGAGAG 909  
 A3Cb CTCCTTCTGAGGGAGGCTGTCCCAGGGCAGGGG--GGGGGGGAAGGCCTCGGGAGAG  
 A3H CTCCTTCTGAGGGAGGCTGTGCCAGGGC-----GGGGGCGTAGCCCTGGGGATG  
 A3Cc CTCCTTCTGAGGGCAGCTGTGTCCAGGG-----AGAGGCTTCAGAGAAGGAGAG

HNF-4 Barbie Box

A3Ca GTGGCTCTGAGCCTGAGGAAGTGAACCATCTGAGGGCCCTCCACCCTTGGGGCCAAAG 969  
 A3Cb GTGGCTCTGAGCCTGAGGAAGTGAACCATCTGAGGGCCCTCCACCCTTGGGGCCAAAG  
 A3H GTGGCTCTGAGCCTGAGGAAGTGAACCTTTTGGGGCCCTCCACCCTTGGGGCCAAAG  
 A3Cc GCGAGTCTGAACC-AAGCAGTGAACACCTGAGGGCTC-----CCCTGAGAACAAG

transcription start?

A3Ca CAGGAAGGAGGTGGGCTTCTGAGGAGGCAGCCTGGGAGGTGACTGTGACTGTACACTG 1029  
 A3Cb CAGGAAGGAGGTGGGCTTCTGAGGAGGCAGCCTGGGAGGTGACTGTGACTGTACACTG  
 A3H CAGGAAGGAGGTGGGCTTCTGAGGAGGCAGCCTGGGAGGTGACTG-----TCACACTG  
 A3Cc CAGGAAGGAGGTGGGCTTCTGAGGAGGCAGCCTGGGAGGTGACTG-----GCACACTG

Elk-1

splice acceptor?

**Fig. S4**

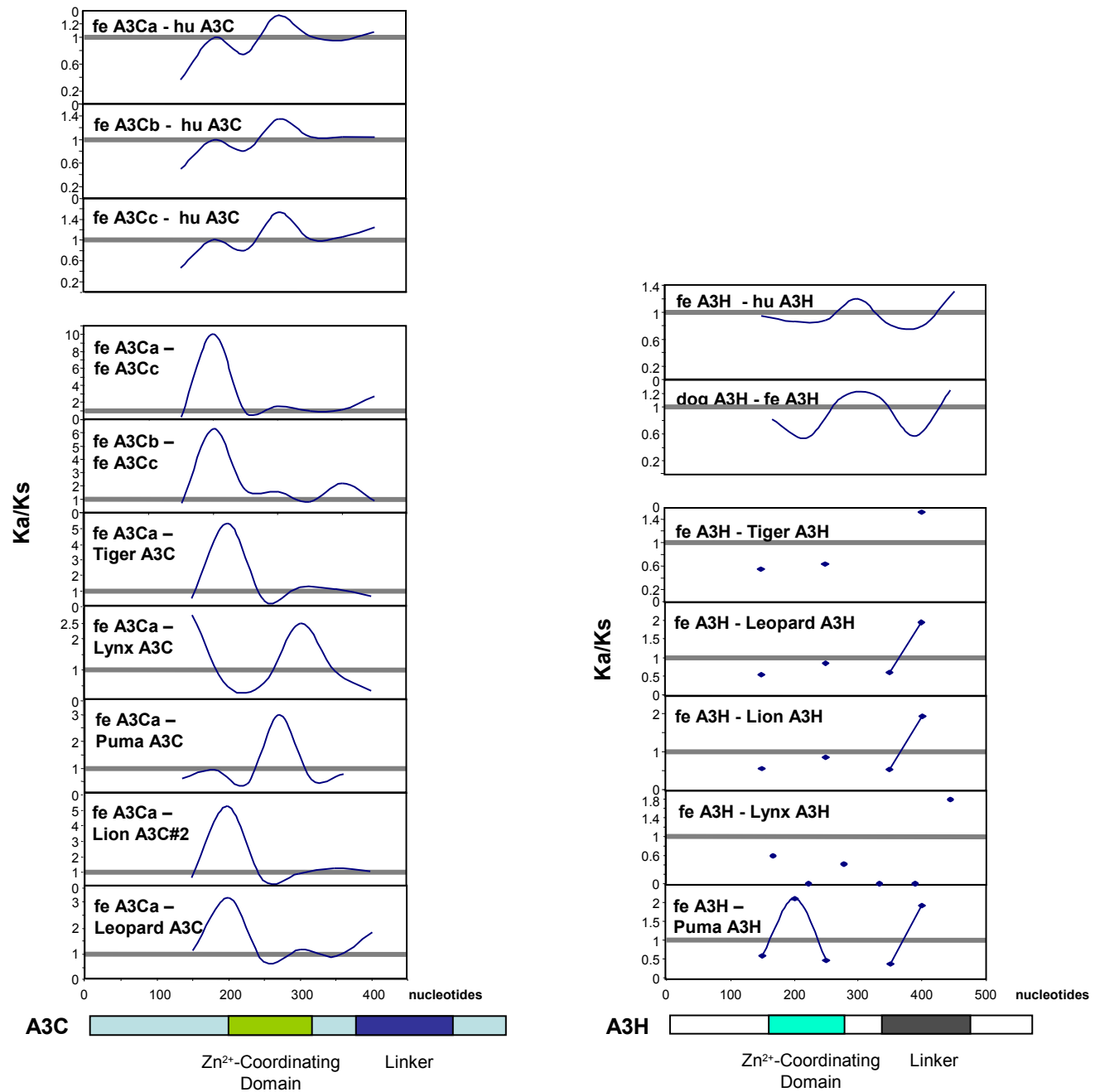
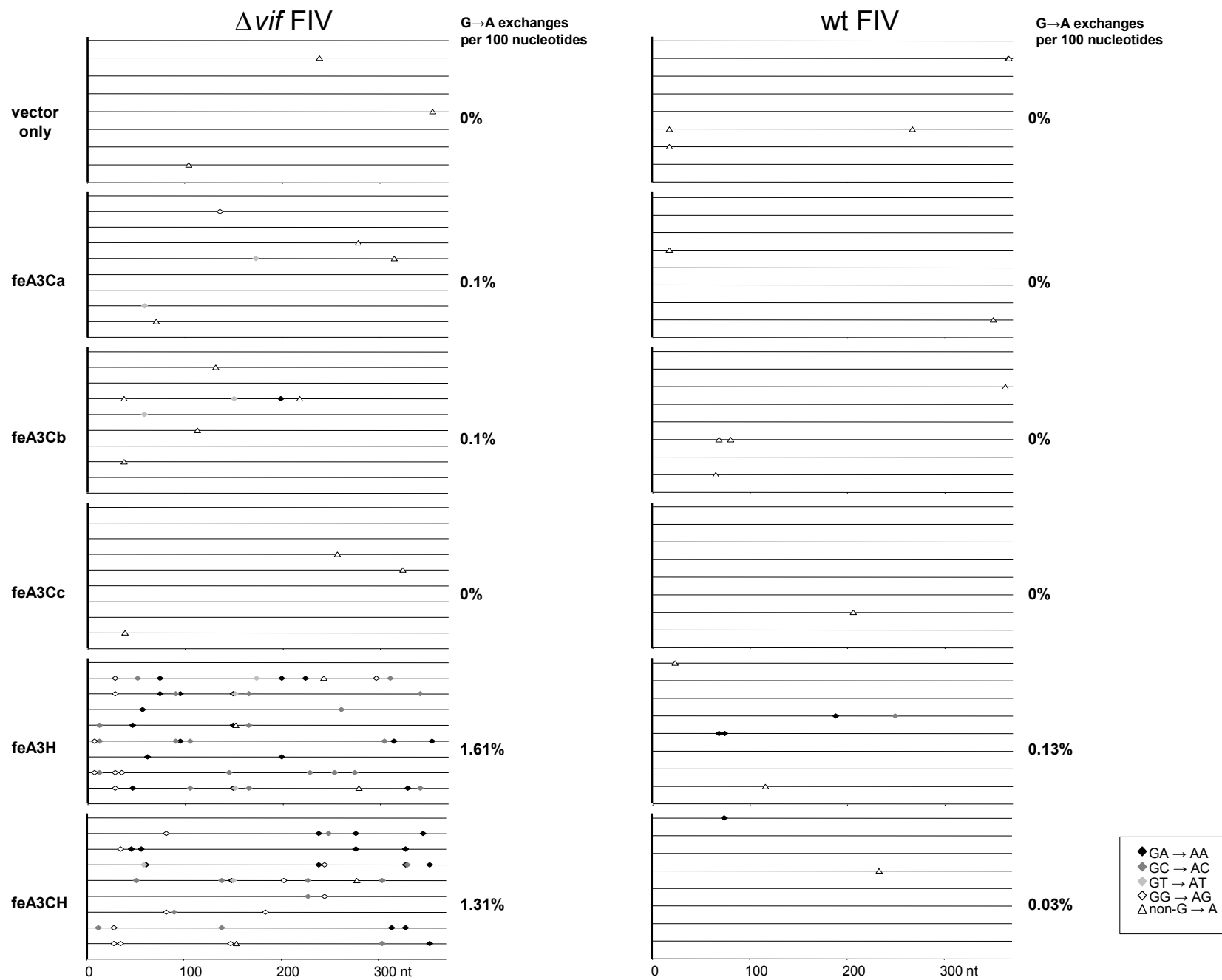
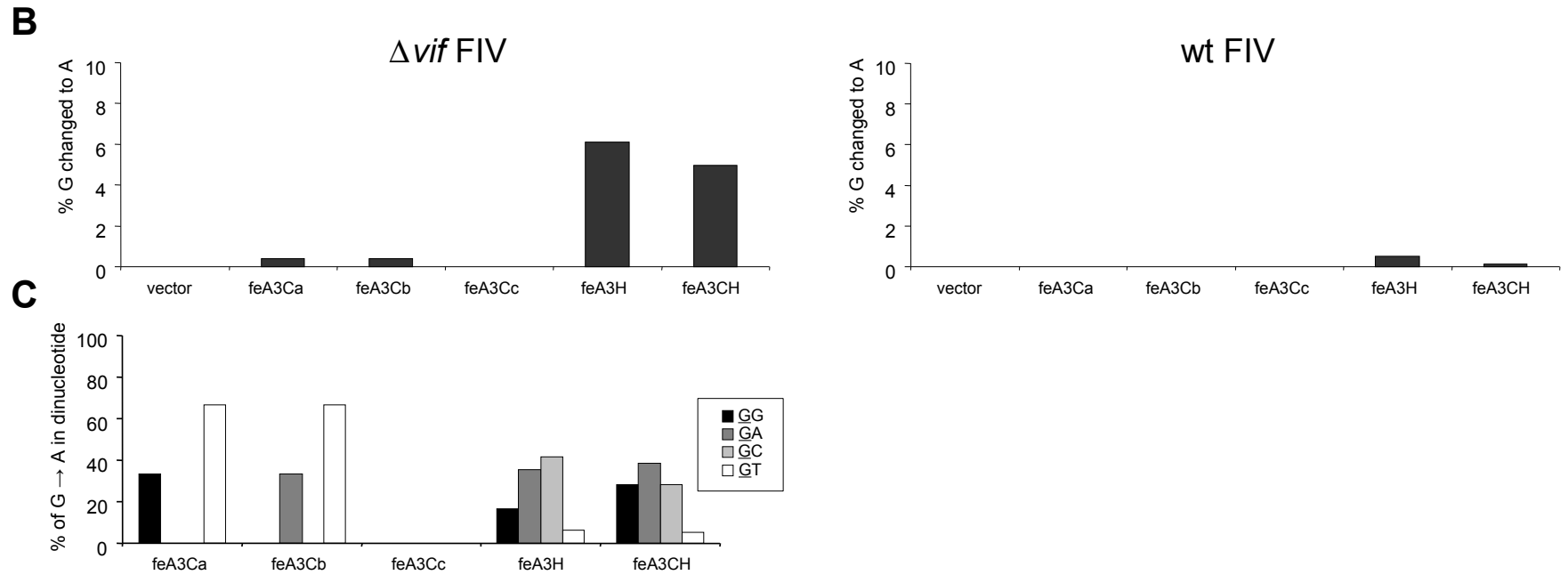


Fig. S5

A



**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→A per clone	0	1	2	0	8	7
Average no. of G→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