Fig. S1

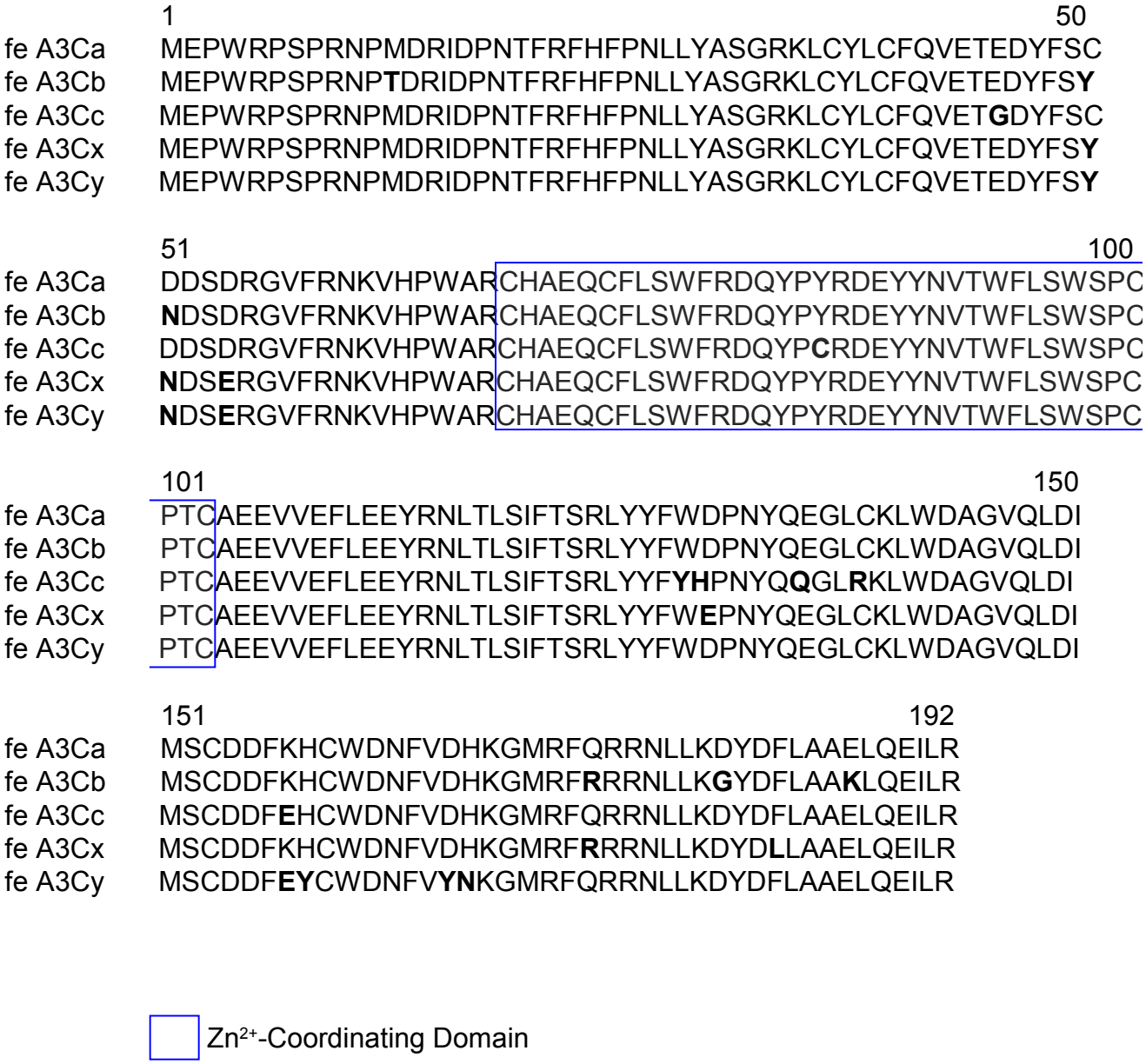

1 50
fe A3Ca MEPWRPSPRNPMDRIDPNTFRFHFPNLLYASGRKLCYLCFQVETEDYFSC
fe A3Cb MEPWRPSPRNPTDRIDPNTFRFHFPNLLYASGRKLCYLCFQVETEDYFSY
fe A3Cc MEPWRPSPRNPMDRIDPNTFRFHFPNLLYASGRKLCYLCFQVETGDYFSC
fe A3Cx MEPWRPSPRNPMDRIDPNTFRFHFPNLLYASGRKLCYLCFQVETEDYFSY
fe A3Cy MEPWRPSPRNPMDRIDPNTFRFHFPNLLYASGRKLCYLCFQVETEDYFSY
51 100
fe A3Ca DDSDRGVFRNKVHPWARCHAEQCFLSWFRDQYPYRDEYYNVTWFLSWSPC
fe A3Cb NDSDRGVFRNKVHPWARCHAEQCFLSWFRDQYPYRDEYYNVTWFLSWSPC
fe A3Cc DDSDRGVFRNKVHPWARCHAEQCFLSWFRDQYPCRDEYYNVTWFLSWSPC
fe A3Cx NDSERGVFRNKVHPWARCHAEQCFLSWFRDQYPYRDEYYNVTWFLSWSPC
fe A3Cy NDSERGVFRNKVHPWARCHAEQCFLSWFRDQYPYRDEYYNVTWFLSWSPC
101 150
fe A3Ca PTCAEEVVEFLEEYRNLTLSIFTSRLYYFWDPNYQEGLCKLWDAGVQLDI
fe A3Cb PTCAEEVVEFLEEYRNLTLSIFTSRLYYFWDPNYQEGLCKLWDAGVQLDI
fe A3Cc PTCAEEVVEFLEEYRNLTLSIFTSRLYYFYHPNYQQGLRKLWDAGVQLDI
fe A3Cx PTCAEEVVEFLEEYRNLTLSIFTSRLYYFWEPNYQEGLCKLWDAGVQLDI
fe A3Cy PTCAEEVVEFLEEYRNLTLSIFTSRLYYFWDPNYQEGLCKLWDAGVQLDI
151 192
fe A3Ca MSCDDFKHCWDNFVDHKGMRFQRRNLLKDYDFLAAELQEILR
fe A3Cb MSCDDFKHCWDNFVDHKGMRFRRRNLLKGYDFLAAKLQEILR
fe A3Cc MSCDDFEHCWDNFVDHKGMRFQRRNLLKDYDFLAAELQEILR
fe A3Cx MSCDDFKHCWDNFVDHKGMRFRRRNLLKDYDLLAAELQEILR
fe A3Cy MSCDDFEYCWDNFVYNKGMRFQRRNLLKDYDFLAAELQEILR
Zn2+-Coordinating Domain

Fig. S2

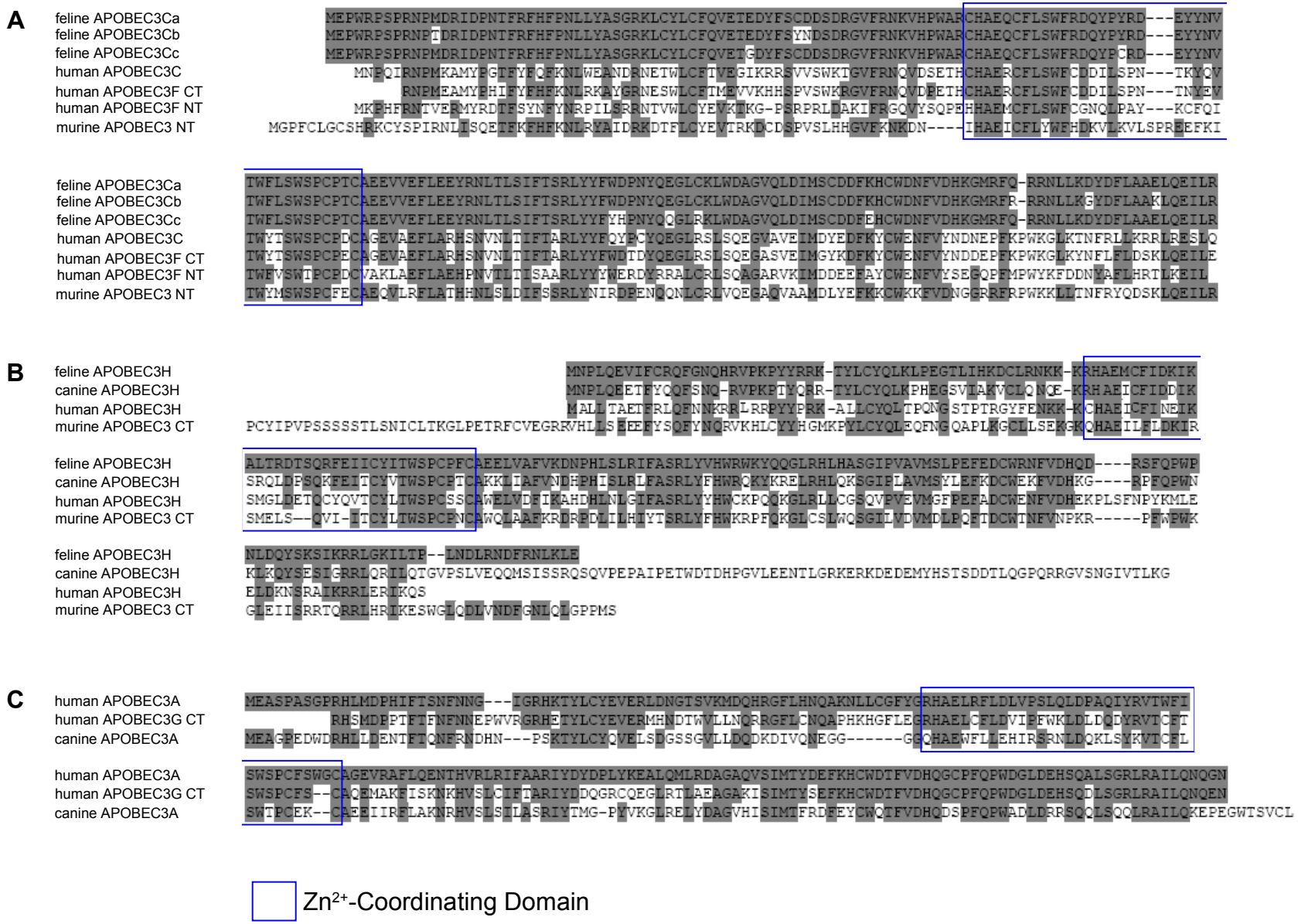

A
feline APOBEC3Ca
feline APOBEC3Cb
feline APOBEC3Cc
human APOBEC3C
human APOBEC3F CT
human APOBEC3F NT
murine APOBEC3 NT
B
feline APOBEC3H
canine APOBEC3H
human APOBEC3H
murine APOBEC3 CT
C
human APOBEC3A
human APOBEC3G CT
canine APOBEC3A
Zn2+-Coordinating Domain

Fig. S3

(first half)

A

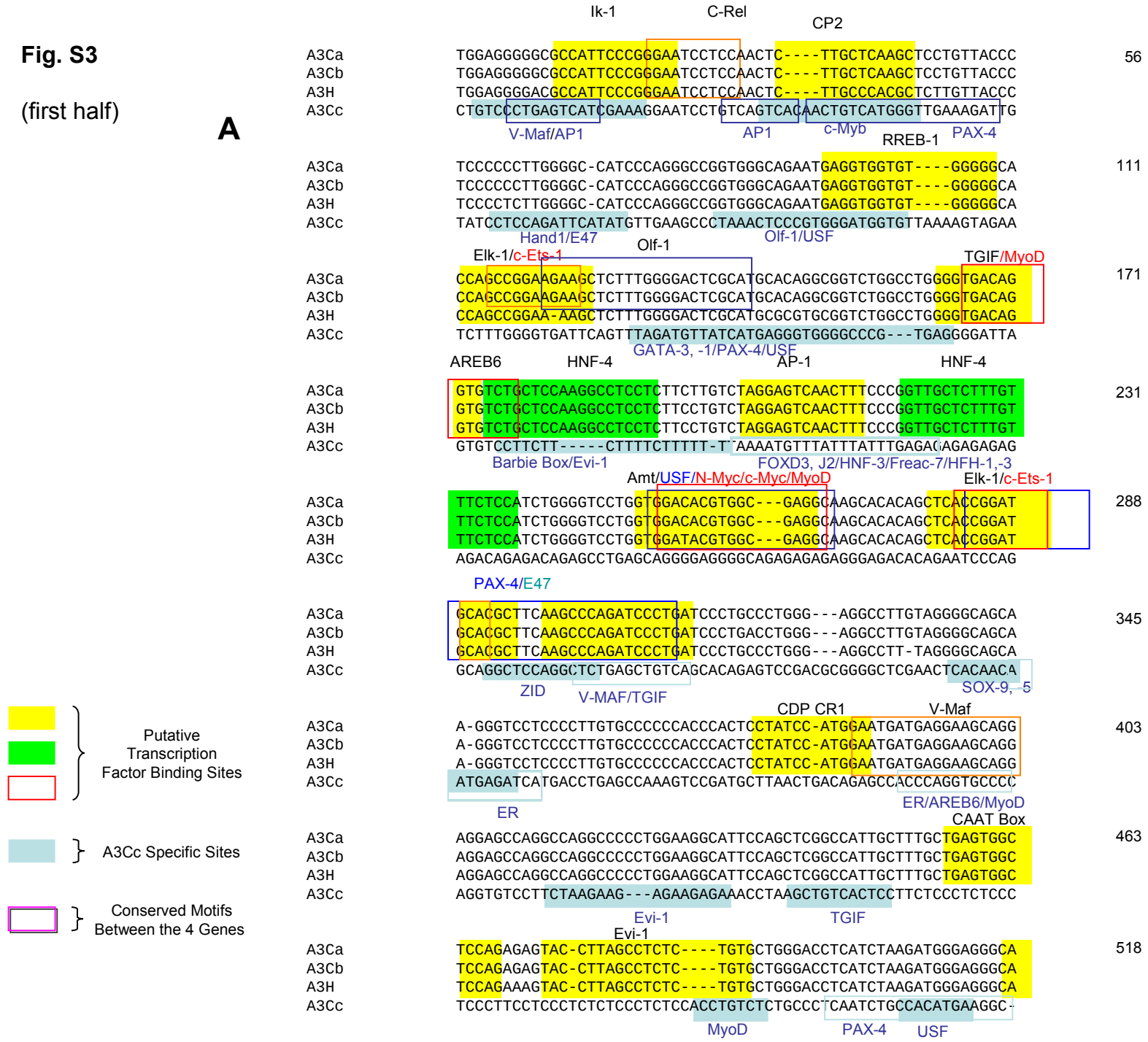


Fig. S3

(second half)

A

Fig. S4

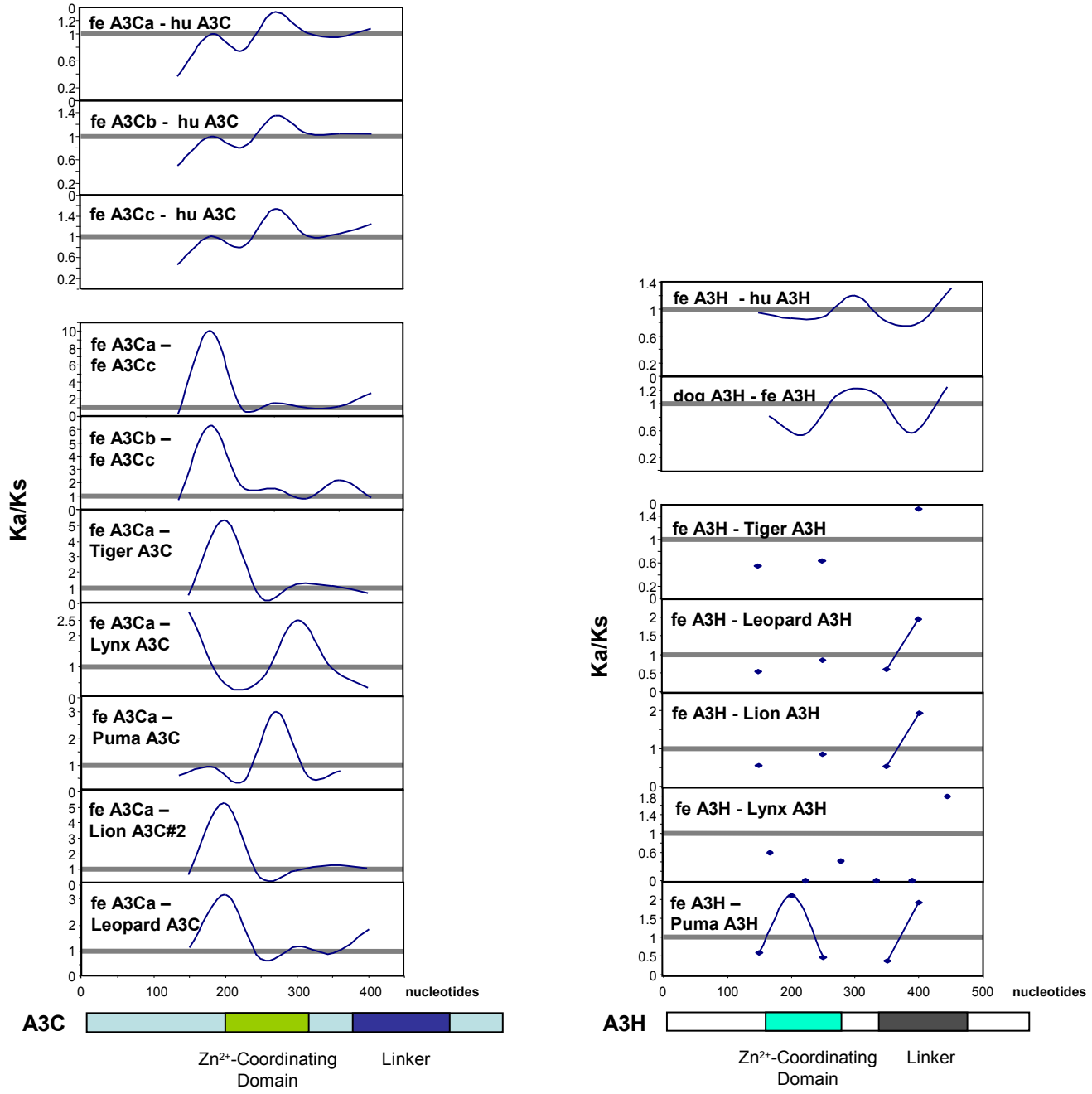

fe A3Ca - hu A3C
fe A3Cb - hu A3C
fe A3Cc - hu A3C
fe A3Ca – fe A3Cc
fe A3Cb – fe A3Cc
fe A3Ca – Tiger A3C
fe A3Ca – Lynx A3C
fe A3Ca – Puma A3C
fe A3Ca – Lion A3C#2
fe A3Ca – Leopard A3C
Ka/Ks
nucleotides
A3C
Zn2+-Coordinating Domain
Linker
fe A3H - hu A3H
dog A3H - fe A3H
fe A3H - Tiger A3H
fe A3H - Leopard A3H
fe A3H - Lion A3H
fe A3H - Lynx A3H
fe A3H – Puma A3H
Ka/Ks
nucleotides
A3H
Zn2+-Coordinating Domain
Linker

Fig. S5

A

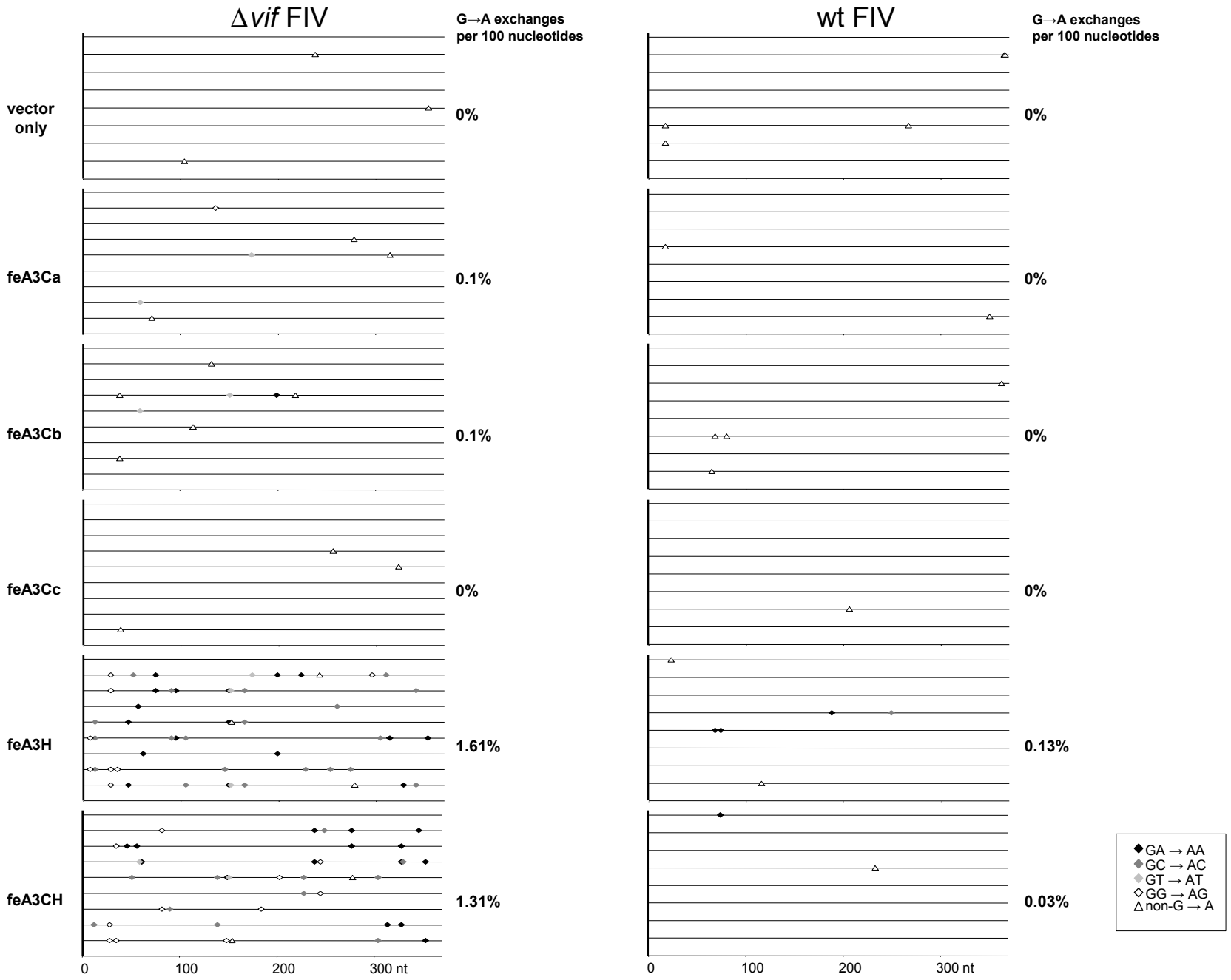
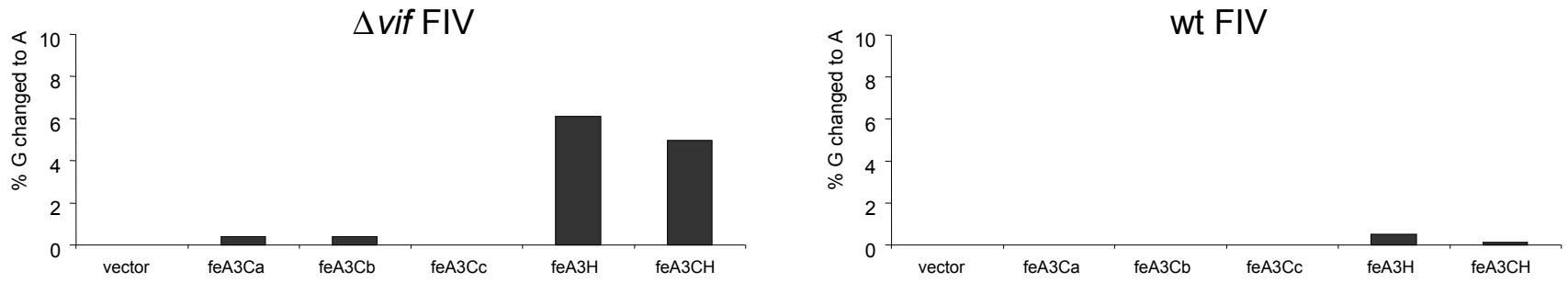
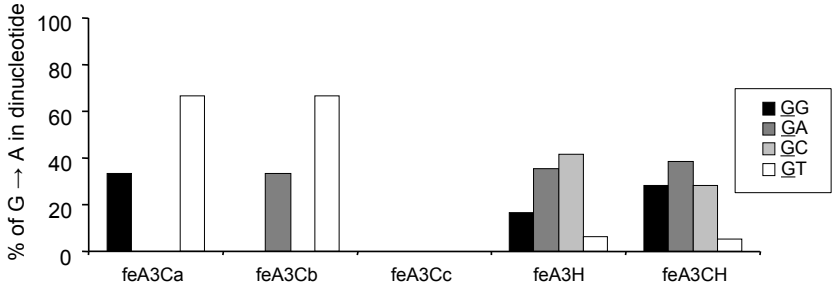

Δvif FIV
G→A exchanges per 100 nucleotides
wt FIV
G→A exchanges per 100 nucleotides
vector only
0%
0%
feA3Ca
0.1%
0%
feA3Cb
0.1%
0%
feA3Cc
0%
0%
feA3H
1.61%
0.13%
feA3CH
1.31%
0.03%
0
100
200
300 nt
0
100
200
300 nt
GA → AA
GC → AC
GT → AT
GG → AG
non-G → A

Fig. S5

B



C



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