

Supplemental Table S3: Alignment of pII_E and pII_S across all variable regions

nt position	160	162	163	167-168	173	176	180-181	187-188	195-199	205-210	223-234	239	253	255-258	262-264	267-273	282	289-290	295-298	301-302	304-305	315	322	326	332	347	350	355	358-359	364	394-395	400-441	445	447	452	474	477-492
1c1	G	T	G	GG	G	C	TC	AC	GAAAG	GGTAT	TCCCCCGCGACAAA	A	C	GAAA	GAA	CGAAAA	T	GA	AAAC	AG	GG	A	A	G	A	C	A	G	GA	T	AA	GACGCCGGCCAAAGCCGACGACGTCAAAGCCGACGCCCAACGCC	G	A	A	C	TGAATCATCTGCCACC
1c2	G	T	A	GG	G	C	TC	AA	GAAAG	ACTTCT	TCCCCCGCGGAA	A	A	AAGC	ACG	CGAAAA	T	CA	AATC	AG	GG	T	A	A	A	C	A	G	AA	T	AC	AACGACGCCAAAGCCGACGCCAAAGACGACACCGTCAACGCC	G	A	A	C	TGAATCATCTGCC
1c3	G	T	G	GG	G	C	TC	AA	GGAAA	ACTTCT	TCCCCCCTCCGAC	A	A	AGAG	GAA	TAAAAAC	T	AC	CTTT	AG	GG	T	A	G	A	C	G	G	AA	T	AC	GCCAAAGCCGACGCGACCGGACGCCGCGGCAAGACACCAAC	G	C	A	C	TGAATCATCTGCCGTT
1c4	G	T	G	GG	G	T	TC	GA	GGAAG	ACTTCT	TCCCCCCCACCGAC	A	A	AAGC	ACG	CGAAAA	C	GA	GCTT	AC	GG	T	A	G	A	C	A	C	GA	-	AA	GACGCCGGCCAAACCCGGCCGACGACGTCAAAGCCGACGCCAAAGACACCGACAAA	A	C	A	C	TAAATCATCTGCCGTT
1c5	G	T	A	AG	A	T	TC	GA	CAAAG	GGTCT	TCCGCTTCAAAA	T	A	GGAA	AAA	CGAAAA	C	CA	GCTT	AG	AA	A	A	A	A	C	A	G	AA	T	AA	ACCGAAGCCAAACGCCAAAGCCGGCCGACGACGTGCGCCAAAGACGACACCGCCGGCACAAA	G	C	G	C	TGAATCATCTG
2c1	G	C	A	AA	A	C	TA	GA	CGCCG	GGCGT	TCCGTTCAACA	A	C	GAAA	GAA	CGAAAA	T	CA	GCTT	AC	GG	A	C	A	A	C	A	C	GA	T	AC	ACCGGACAAACGACGACACCGTTGCCGACGCCAACACGCC	G	C	A	C	TAAACATGATGCCAAA
2c2	G	T	A	AG	G	C	TC	GA	GAAAG	GACAAG	TCCCCCCTCCAAC	A	G	AAGC	ACG	CACAAAC	T	AC	CTTT	AG	GG	T	A	G	A	C	A	C	GC	T	CA	GCCAAAGCCGACGACGCGCTCACCGCCGACGCCAACACGCC	G	C	A	T	TACGTATCTGCCAAA
2c3	G	T	A	AG	A	T	TC	AT	GGAAA	GACAAG	TCTTCTTCATCA	A	A	GGAA	AAA	CGAAAA	C	AC	AATT	AG	AA	A	A	A	G	C	A	G	AA	T	AA	GCCAAAGTTCGCGCCGCAAGACGACGACGTACCGACGCAAAAAACAACACGGC	G	C	A	C	TAAATCATCTGCC
2c4	G	T	G	GG	G	T	TC	GA	GGAAG	ACTTCT	TCCCCCCCACCGA	A	A	AAGC	ACG	CGAAAA	C	GA	GCTT	AC	GG	T	A	G	A	C	A	C	GA	T	AA	GCCGACAAACACGGCAACATTACCGCCGACAAACGGCAACGCC	G	A	A	C	TGAATCATCTGCC
2c5	G	T	G	GG	A	T	TC	GA	GGAAA	GACAAG	TCCGCTCCGAC	A	A	AAGC	ACG	CGAAAA	T	GA	GCTT	AC	GG	A	C	G	A	C	A	G	AA	T	AA	ACCGAAGCCAAACGCCAAAGCCGGCCGACGACGTGCGCCAAAGACGACACCGCCGGCACAAA	G	C	A	C	TGAATCATCTG
2c6	G	T	A	GG	G	C	TC	AT	GAAAG	ACTTCT	TCCCTCCGCGCCGAC	A	C	GAAA	GAA	CAACAAC	T	AC	GCTT	AG	AA	A	C	G	G	C	A	G	AA	-	AC	GACGACAAAGCCAAAGACGACGTCAAAGCCGACGCCACCGCCGGCACAAA	G	C	A	C	TGAATCATCTG
3c1	G	T	G	GG	A	T	TC	GA	GGAAA	ACTTCT	TCCCTCCGACAAA	A	C	GAAA	GAA	CGAAAA	T	CA	GCTT	AC	GG	A	C	G	A	C	A	C	GA	T	AC	AACGACGCCAAAGCCGACGACGTCAAAGCCGACGCCCAACGCC	G	A	A	C	TGAATCATCTGCCACC
3c2	C	C	A	AA	A	T	-A	GA	CAAAG	GGTCT	TCCGTTCAACA	A	C	GAAA	GAA	CACAAAC	T	CA	GCTT	AC	GG	A	A	G	A	C	G	C	GA	T	AA	GACGACGCCGCGCCAAAGACGACACCGTACCGCCGACGCCACCGGCAACGACGCAAA	G	C	A	C	TAAATCAACTGCCGTT
3c3	G	C	A	AG	A	T	TC	AT	GAAAG	ACTTCT	AACCCACCGAC	A	G	AAGC	ACG	CACAAAC	T	AA	CTTT	AG	GG	A	C	G	G	C	A	G	GC	T	AA	ACCGAAGCCAAACGCCGACGCCCGCCGCAAGACACCAACACGGC	A	C	A	C	CCCCTTCTCTGCTAGC
6c1	G	T	A	GG	A	T	TA	AA	CGCCG	GGCGT	TCCCCCGCCACCGA	A	A	GGAA	AAA	CGAAAA	C	CA	GCTT	AC	GG	T	A	G	A	C	A	C	GA	T	AA	GACGCCGGCCAAACCCGGCCGACGACGTCAAAGCCGACGCCAACACGGC	A	C	A	C	TAAACATGATGCCAAA
6c2	G	T	G	GG	A	C	TC	AA	GGAAG	ACTTCT	TCCCCCCTCCGAC	A	C	AAGC	ACG	CGAAAC	T	GA	AAAT	GA	GG	A	A	G	A	G	G	AA	T	AA	GACGCCAAACACGCCAACACGACGCGCTACCGACGACACCAACCGGCAACGGCAACGAAAA	G	A	A	C	TGAATCATCTGCCGTT	
6c3	-	-	-	--	A	C	TA	AA	CGCAA	GGCGT	TCCGCTCCGAC	A	G	AAGC	ACG	CGAAAA	T	AA	CTTT	AG	GG	A	C	G	A	C	A	G	GC	T	AA	AACGACGCCCAACGACGACGTACCGACGACGCCGACGCCAACGGGCAAGGCAAA	G	C	A	C	TAAATCAACTGCCGTT
7c1	G	C	A	AG	A	T	TC	AC	GGAAA	ACTTCT	TCCCTCCGACCGAC	A	C	AAGC	ACG	CGAAAC	T	GA	AAAT	GA	GG	A	C	G	G	C	G	G	GC	T	AC	GCCAAAGCCAAAGACGCGGACGACGTACCGACGACGCCGACGCCAACGCCGCAAGGCAAA	G	C	A	C	TAAATCAACTGCCAAA
us	-	-	-	--	-	-	--	-	GGTAT	TCCCTCCGCGAA	A	A	AAGC	ACG	CGAAAC	T	GA	GCTT	AG	GG	A	A	G	G	C	G	C	GA	T	AC	AACGACGCCGCGCAACGACGACGTGCGCCAAAGACGACGCCGCGGCAACGCC	G	A	A	C	TGAACCAACTGCCACC	
1-81-S2	G	C	A	AG	A	T	TC	AT	GAAAG	ACTTCT	TCCGTTCAACA	A	C	GAAA	GAA	CGAAAA	T	CA	GCTT	AC	GG	A	C	A	A	C	A	C	GA	T	AC	ACCGGACAAACGACGACACCGTTGCCGACGCCAACACGCC	G	C	A	C	TGAATCATCTGCCACC