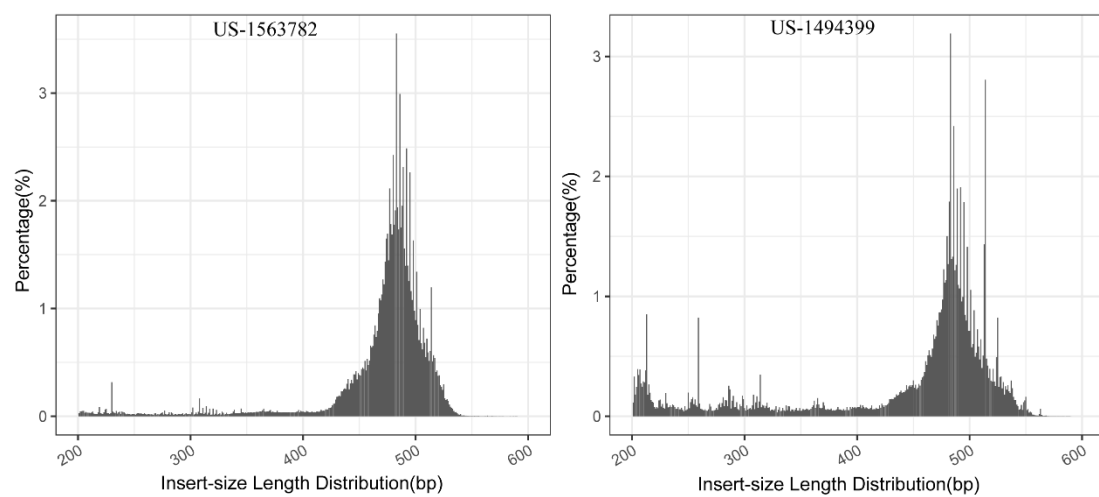
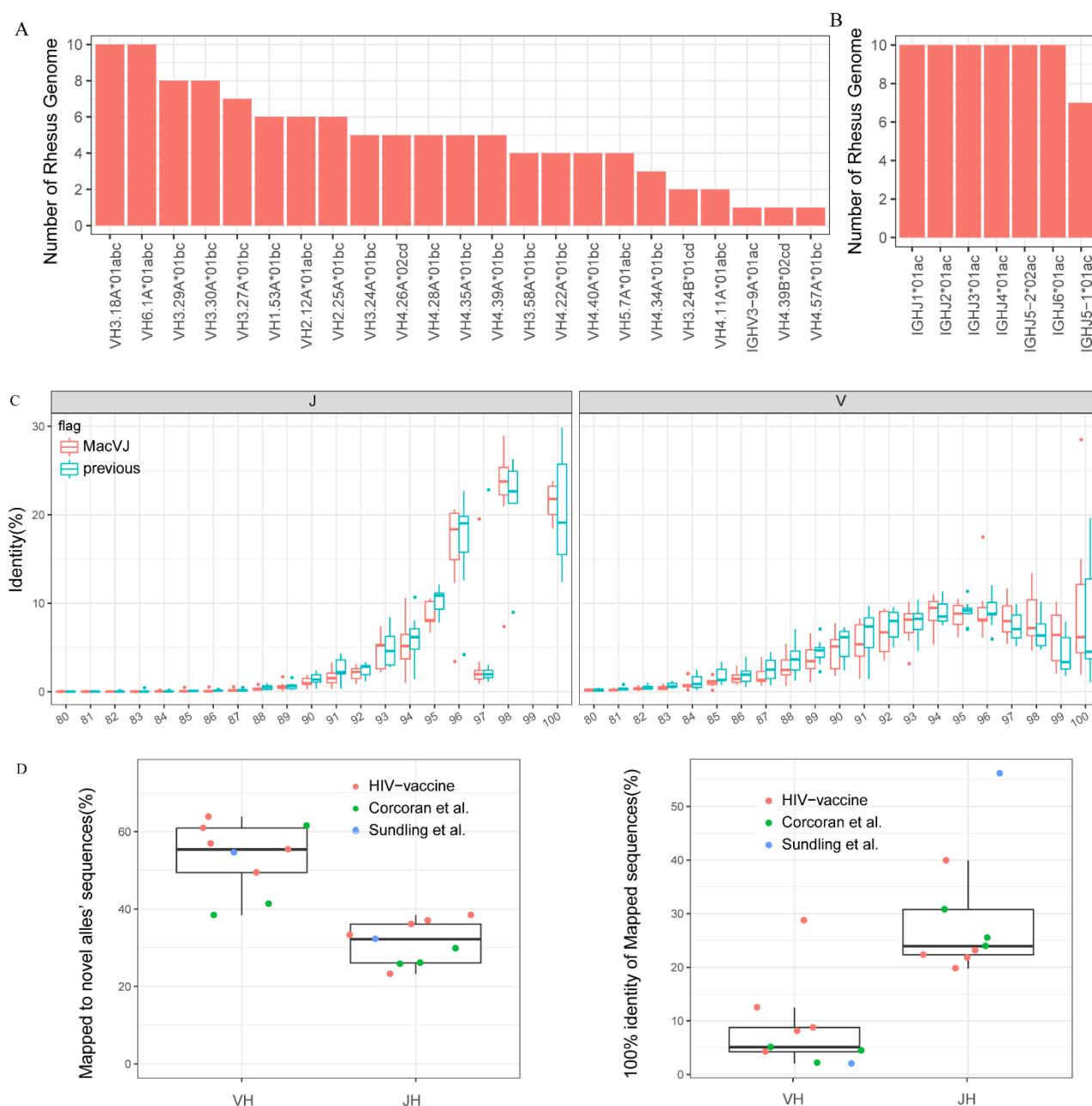


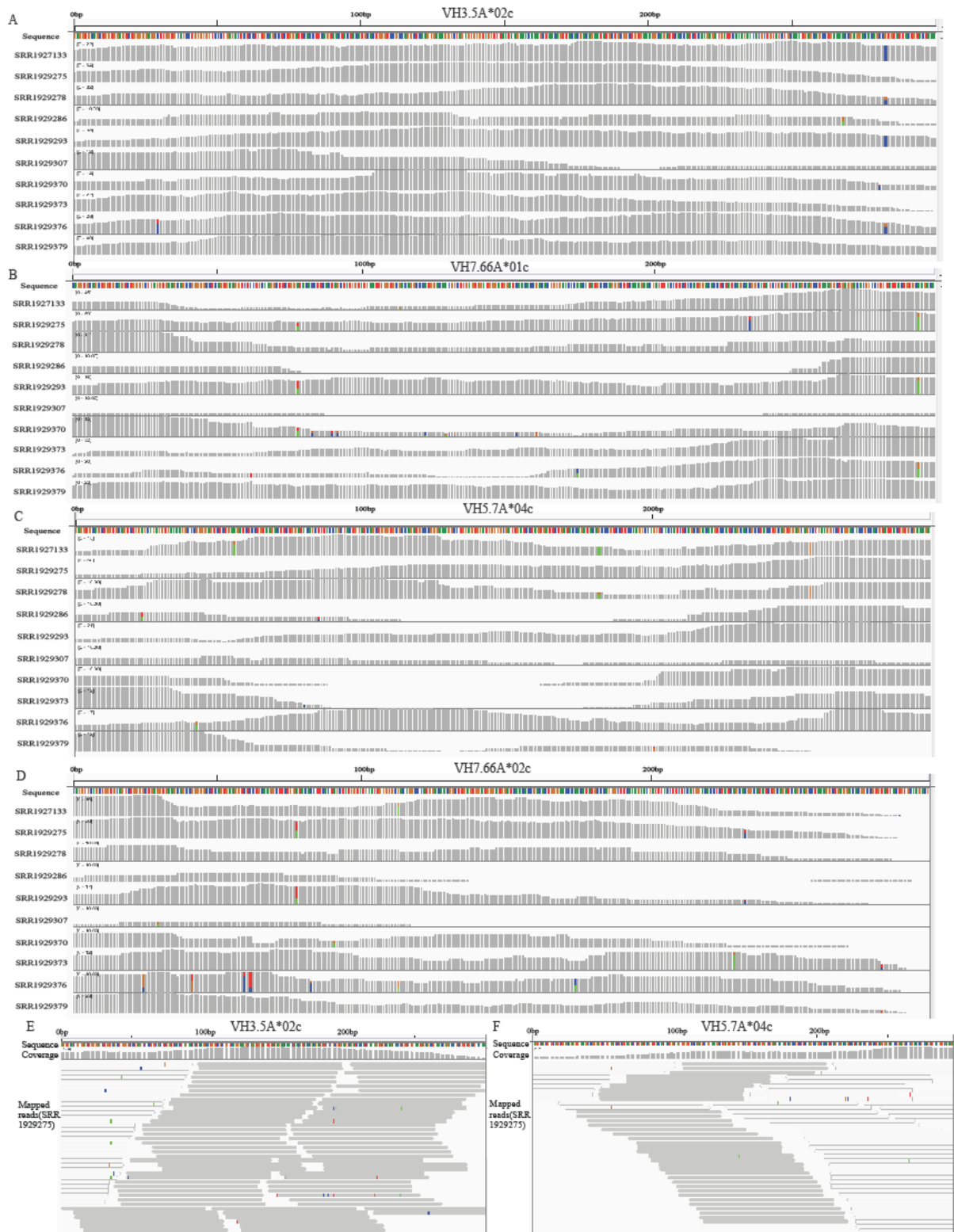
Supplementary Figure 1: Detail evaluation of predicted sequences on Human samples.
(A).H87-LS. (B). H90-LS



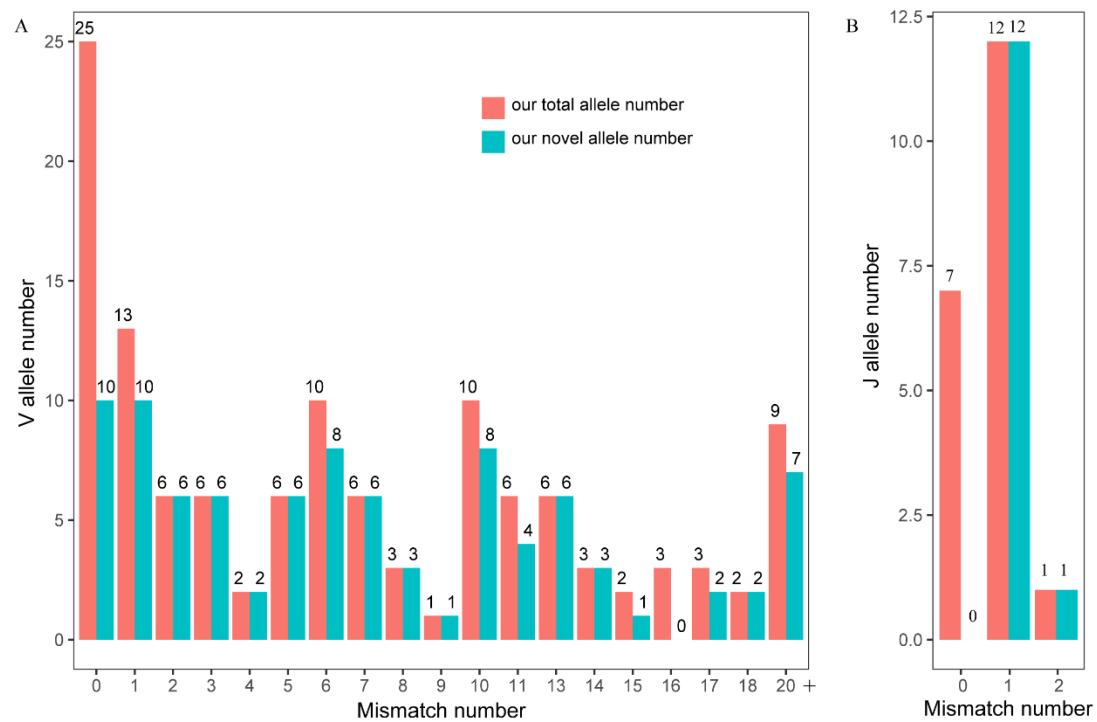
Supplementary Figure 2: The insert-size length distribution for two randomly selected samples.



Supplementary Figure 3: Genome data and other IgH repertoire data analysis. The number of monkeys which supported the VH or JH previously reported alleles: (A). VH alleles. (B) JH alleles. (C, D). Analysis for other IgH repertoire data. The data included three sources: HIV-vaccine, Sundling et al. and Corcoran et al. (C). Identity distribution for the VH and JH between in previous and MacVJ reference. Identity is defined as the percentage of matched bases out of all mapped bases. (D). The proportion of sequences were mapped to the inferred novel alleles.



Supplementary Figure 4: Coverage of multiple alleles in 10 Rhesus genome data. The figures were implemented by IGV (v2.3.97). Colors represent different type of bases (A,C,G,T). (A). VH3.5A*02c. (B). VH7.66A*01c. (C). VH5.7A*04c. (D). VH7.66A*02c. (E, F). Visualization of detailed reads alignment for VH3.5A*02c and VH5.7A*04c. The reads came from one of the Rhesus SRR1929275. Mismatches between the reads and reference are highlighted in different colors. The figure was drawn in the IGV tool.



Supplementary Figure 5: Comparison of novel genes and alleles with Ramesh et al study.

Supplementary Table 1. Primers

Name	Sequence(5'-3')
Reverse transcription(GSP1)	
IGHG	TGCTCTSGGAGGTGCTC
IGHD	GCACGCTGATGTGATGG
IGHA	GACCACGTTATCTGACTG
IGHE	CAGGGGATCAAGGGGAA
IGHM	GGCATTCTCACAGGAGAC
PCR primer synthesis (AAP and GSP2)	
BtgZI-AAP	GATTGACGCGATGGHGGGIIGG
mIGHG	CTSGGAGGTGCTCCTGGA
mIGHD	GCACGCTGATATGATGGGG
mIGHA	AGACCTTGGGKYTGGTCCG
mIGHM	GTTGGGGCGGATGCACTC
mIGHE	ACGAAGGGGCTCTGTATG

The BtgZ I site nucleotides are in orange. The anchor region is in purple. Gene-specific nucleotides are in black.

Supplementary Table 2. Predicted reported and novel V alleles of Rhesus monkey (Mismatch<=7bp)

Sequence ID	Flag	Nearest corresponding alleles	Mismatch/Gap	Supporting Samples	Supporting Individuals
IGHV3-9A*02c	novel_allele	IGHV3-9*01:F	1/0	4	17
IGHV3-9A*01ac	known	IGHV3-9*01:F	0/0	8	35
VH1.16A*02c	novel_allele	IGHV1-1*01 VH1.16	1/0	12	44
VH1.36A*01bc	known	VH1.36	0/0	11	53
VH1.36A*02c	novel_allele	VH1.36	3/0	5	22
VH1.53A*01bc	known	VH1.53	0/0	9	39
VH2.12A*01abc	known	IGHV2-1*01 VH2.12	0/0	9	32
VH2.12A*04c	novel_allele	IGHV2-1*01 VH2.12	5/0	2	6
VH2.12A*02c	novel_allele	IGHV2-1*01 VH2.12	1/0	1	5
VH2.12A*03c	novel_allele	IGHV2-1*01 VH2.12	2/0	5	22
VH2.25A*01bc	known	VH2.25	0/0	10	50
VH2.25A*02c	novel_allele	VH2.25	7/0	5	23
VH3.5A*02c	novel_allele	IGHV3-20*01 VH3.5	1/0	10	37
VH3.8A*02c	novel_allele	IGHV3-14*01 VH3.8	1/0	4	12
VH3.18A*01abc	known	IGHV3-6*01 VH3.18	0/0	1	2
VH3.24A*01bc	known	VH3.24	0/0	8	27
VH3.27A*01bc	known	VH3.27	0/0	2	7
VH3.29A*01bc	known	VH3.29	0/0	10	28
VH3.30A*01bc	known	VH3.30	0/0	10	43
VH3.54A*02c	novel_allele	VH3.54	1/0	2	4
VH3.58A*02c	novel_allele	VH3.58	6/0	4	18
VH3.58A*01bc	known	VH3.58	0/0	9	40
VH4.11A*01abc	known	IGHV4-2*01 VH4.11	0/0	15	75
VH4.11A*04cd	novel_allele	IGHV4-2*01 VH4.11	7/0	4	16
VH4.11A*02c	novel_allele	IGHV4-2*01 VH4.11	3/0	5	25
VH4.11A*05c	novel_allele	IGHV4-2*01 VH4.11	7/0	2	10
VH4.11A*03c	novel_allele	IGHV4-2*01 VH4.11	6/0	2	10
VH4.22A*02c	novel_allele	VH4.22	2/0	2	10
VH4.22A*03c	novel_allele	VH4.22	4/1	6	27
VH4.22A*01bc	known	VH4.22	0/0	9	44
VH4.26A*03c	novel_allele	VH4.26	2/0	2	8
VH4.26A*02cd	novel_allele	VH4.26	1/0	10	50
VH4.28A*02c	novel_allele	VH4.28	6/0	4	15
VH4.28A*01bc	known	VH4.28	0/0	11	54
VH4.34A*02c	novel_allele	VH4.34	1/0	7	35
VH4.34A*03c	novel_allele	VH4.34	2/0	3	12
VH4.34A*01bc	known	VH4.34	0/0	6	28
VH4.34A*04c	novel_allele	VH4.34	5/0	4	20
VH4.34A*05c	novel_allele	VH4.34	6/1	5	25
VH4.35A*02c	novel_allele	VH4.35	2/0	4	16
VH4.35A*01bc	known	VH4.35	0/0	10	48
VH4.37A*02c	novel_allele	VH4.37	1/0	8	34
VH4.37A*04c	novel_allele	VH4.37	4/0	2	9
VH4.37A*03c	novel_allele	VH4.37	3/0	6	27
VH4.38A*02cd	novel_allele	VH4.38	3/0	2	10
VH4.38A*01bc	known	VH4.38	0/0	8	40
VH4.39A*01bc	known	VH4.39	0/0	8	36
VH4.40A*02c	novel_allele	VH4.40	3/0	5	25
VH4.40A*04cd	novel_allele	VH4.40	6/0	5	25
VH4.40A*03c	novel_allele	VH4.40	4/0	2	7
VH4.40A*01bc	known	VH4.40	0/0	10	50
VH4.43A*02c	novel_allele	VH4.43	6/0	4	20
VH4.57A*02c	novel_allele	VH4.57	3/0	4	19
VH4.57A*01bc	known	VH4.57	0/0	7	35
VH5.7A*02c	novel_allele	IGHV5-2*01 VH5.7	2/0	5	24
VH5.7A*03c	novel_allele	IGHV5-2*01 VH5.7	2/0	8	31
VH5.7A*01abc	known	IGHV5-2*01 VH5.7	0/0	4	18
VH5.7A*04c	novel_allele	IGHV5-2*01 VH5.7	2/0	3	15
VH5.46A*03c	novel_allele	VH5.46	2/0	4	18
VH5.46A*02c	novel_allele	VH5.46	1/0	5	19
VH6.1A*01abc	known	IGHV6-1*01 VH6.1	0/0	12	53

Supplementary Table 3. MacVJ: Total Rhesus Monkey IGH germline genes and alleles, including IMGT, CS and our identified.

IGH V Germline sequences:

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[illegible]

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