

Fig S1

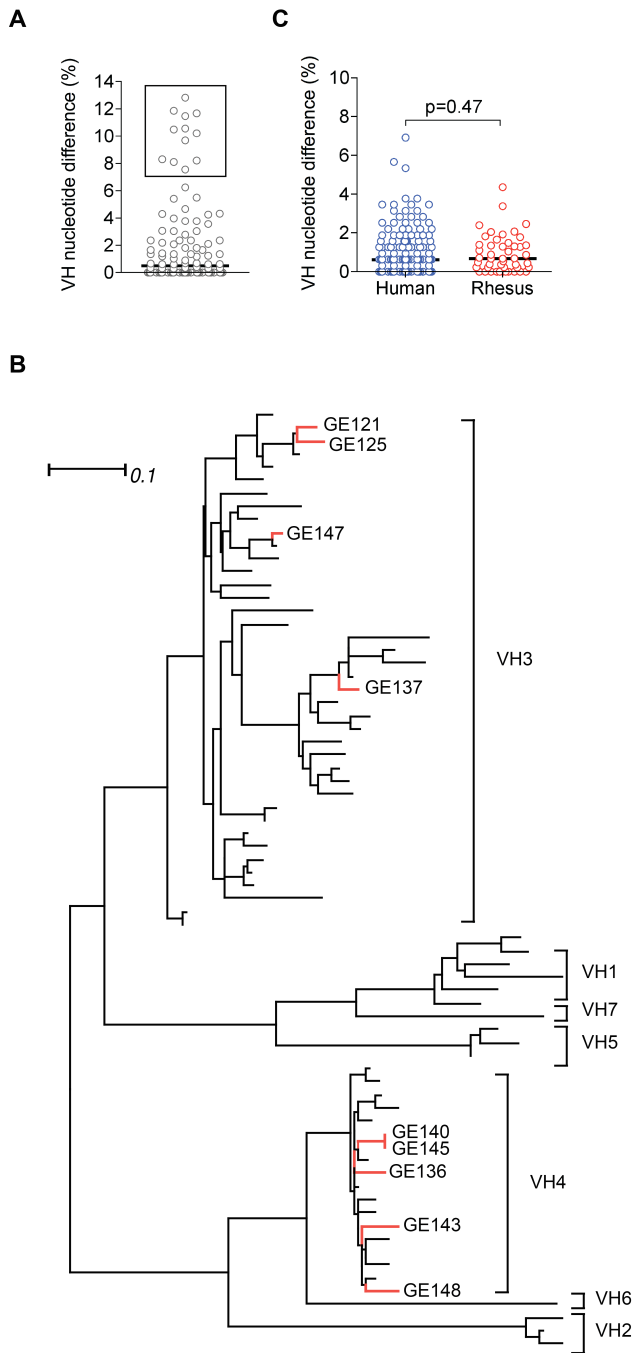


Figure S1. Examination of VH sequences.

(A) Sequences of published rhesus macaque heavy chain germline VH genes were aligned to VH genes identified in the rhesus macaque reference genome (19). Deviations from germline were determined and presented as percent VH nucleotide difference. The box indicates deviations larger than those observed between allelic variants of human VH genes, indicating that these sequences may represent unique VH genes that are not available in the current reference genome. (B) The phylogenetic relationship of the VH regions of the isolated GE121, GE125, GE136, GE137, GE140, GE143, GE145, GE147, and GE148 MAbs compared to VH genes identified from the rhesus macaque reference genome. (C) Nucleotide variation among allelic variants of human VH genes compared to allele *01 (blue) and between a collection of Chinese and Indian rhesus macaque VH genes (red). There was no significant difference between the groups as determined with a Mann-Whitney test, indicating that the variation observed between Chinese and Indian rhesus VH genes fall within normal allelic variation.

Fig S2

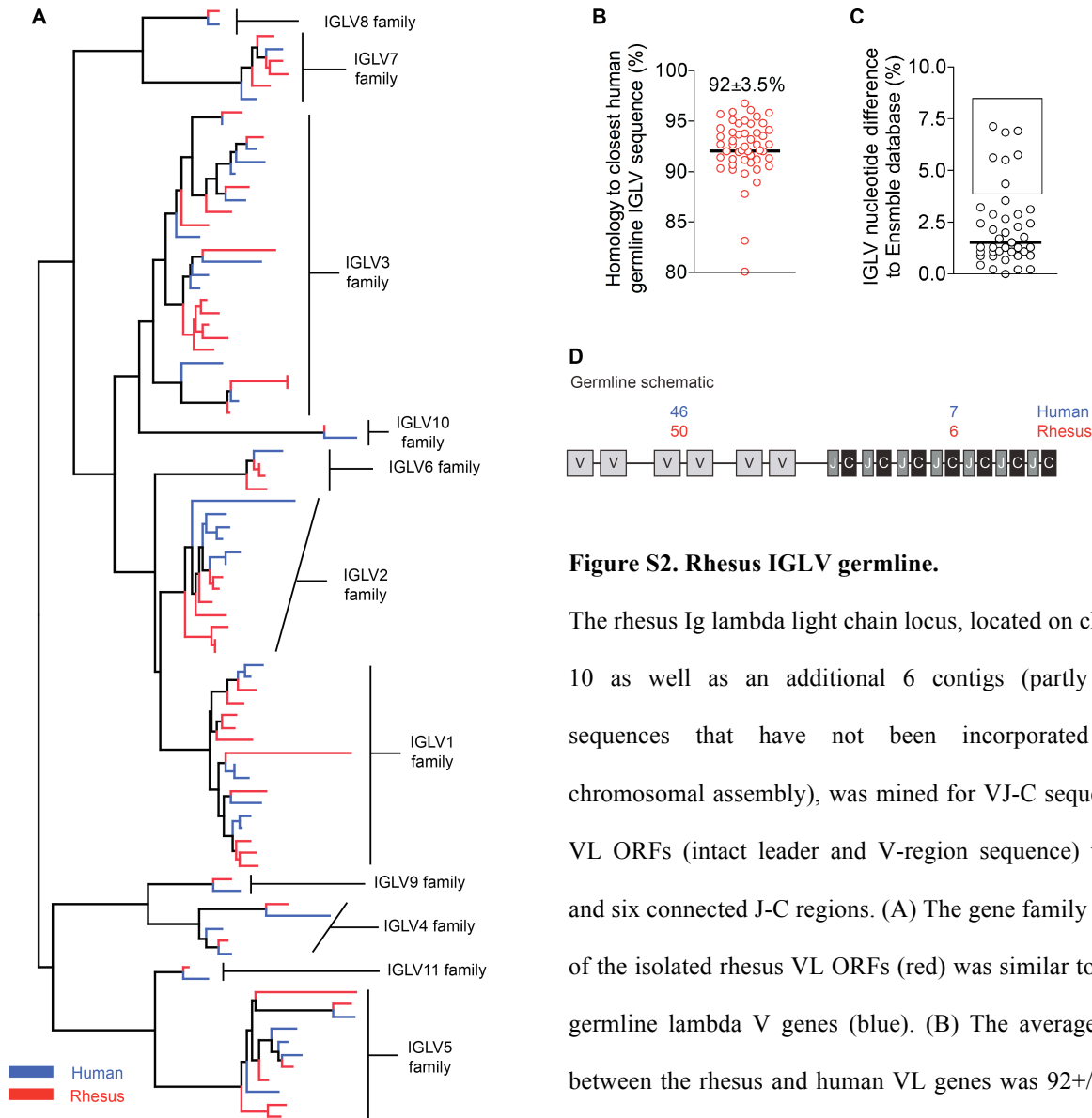


Figure S2. Rhesus IGLV germline.

The rhesus Ig lambda light chain locus, located on chromosome 10 as well as an additional 6 contigs (partly assembled sequences that have not been incorporated into the chromosomal assembly), was mined for VJ-C sequences. Fifty VL ORFs (intact leader and V-region sequence) were found and six connected J-C regions. (A) The gene family distribution of the isolated rhesus VL ORFs (red) was similar to the human germline lambda V genes (blue). (B) The average homology between the rhesus and human VL genes was $92 \pm 3.5\%$ (SD; $n=50$). (C) When comparing allelic variation to previously isolated VL germline genes (23) there were some sequences displaying a higher level of diversity ($>4\%$ difference) indicating that perhaps not all VL germline genes are identified in the current rhesus genome assembly (19). (D) Schematic representation of the rhesus lambda locus indicating general VJ-C gene organization and number of genes found.

Fig S3

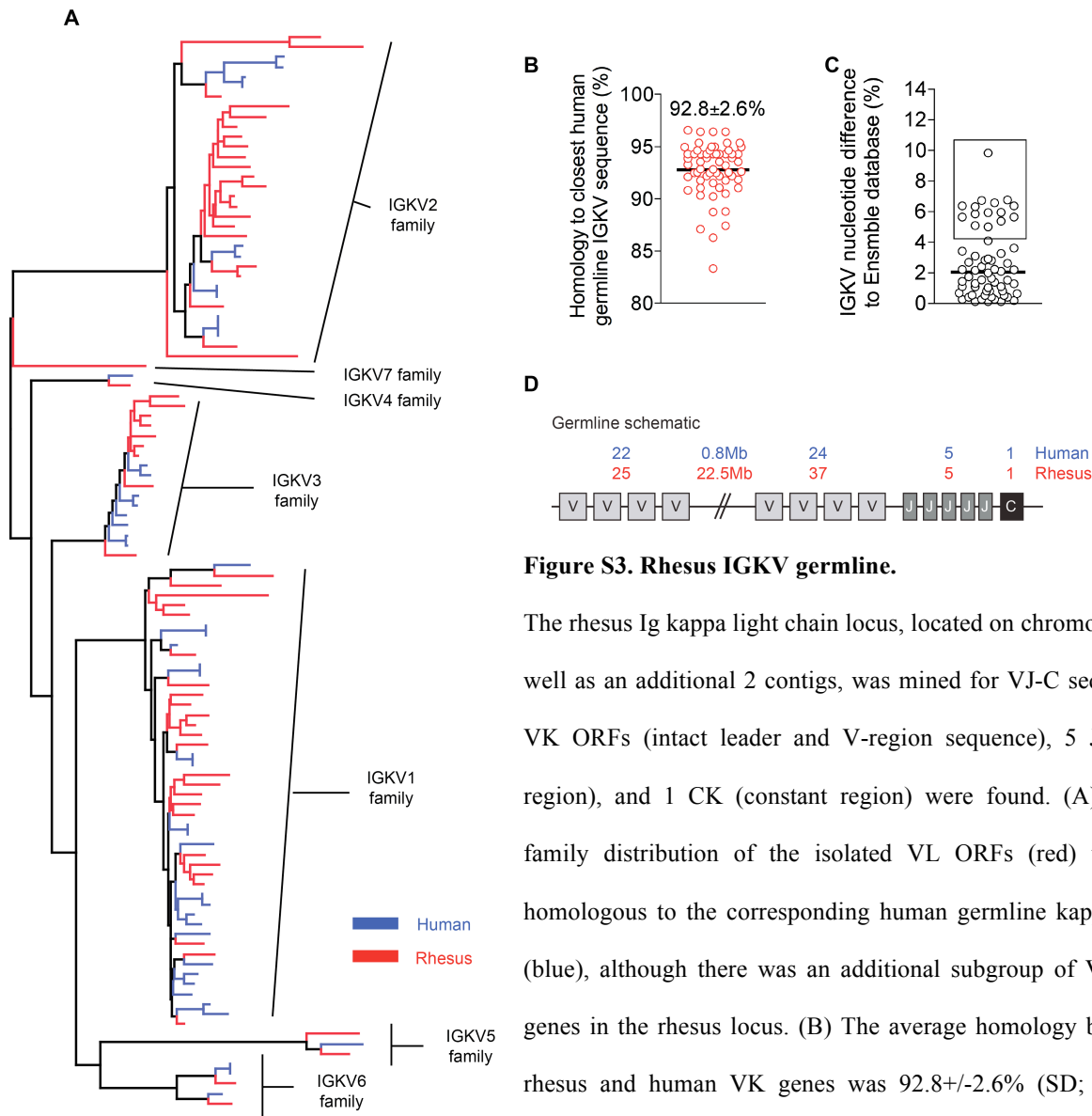


Figure S3. Rhesus IGKV germline.

The rhesus Ig kappa light chain locus, located on chromosome 13 as well as an additional 2 contigs, was mined for VJ-C sequences. 62 VK ORFs (intact leader and V-region sequence), 5 JK (joining region), and 1 CK (constant region) were found. (A) The gene family distribution of the isolated VL ORFs (red) was highly homologous to the corresponding human germline kappa V-genes (blue), although there was an additional subgroup of VK2 family genes in the rhesus locus. (B) The average homology between the rhesus and human VK genes was 92.8+/-2.6% (SD; n=62). (C) When comparing allelic variation to previously isolated VK germline genes (24) there were some sequences displaying a higher level of divergence (>4% difference) indicating that possibly not all VK germline genes are represented in the current rhesus genome assembly (19). (D) Schematic representation of the rhesus lambda locus indicating general VJ-C gene distribution and the number of genes found. Two distant clusters of VK genes were found in the assembled rhesus macaque genome.

Fig S4

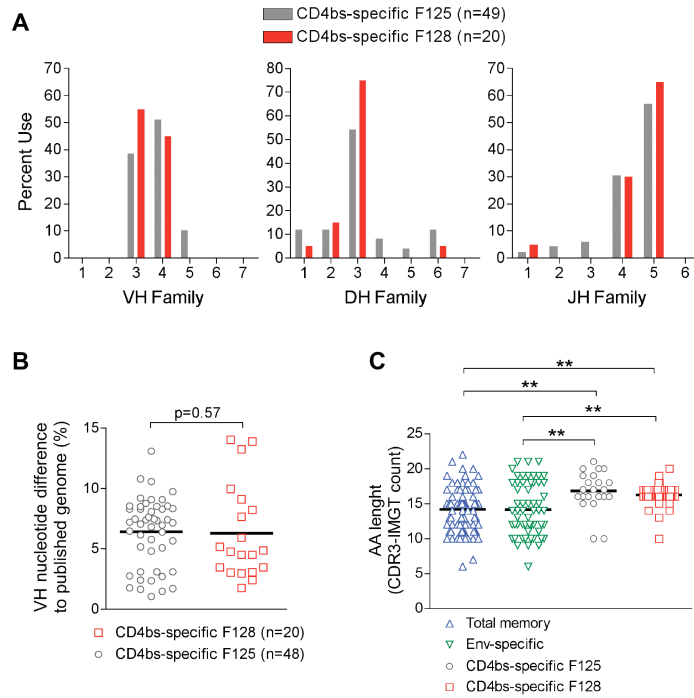


Figure S4. CD4bs-specific VDJ sequence evaluation in monkeys F125 and F128.

CD4bs-specific memory B cells were sorted and antibody genes amplified and sequenced from one additional monkey (F125; n=49, gray circles) two weeks following the fifth immunization with gp140-F in adjuvant (as described for F128 and in reference (26)) and compared to sequences from monkey F128 (red boxes). (A) Heavy chain VDJ gene family usage was evaluated, using IMGT/V-Quest, and was highly homologous between the two monkeys. (B) SHM levels were determined via aligning the V-regions to the germline counterpart. There was no statistically significant difference in the SHM level of the CD4bs-specific sequences in the two monkeys as determined by the Mann-Whitney test. (C) The CDR3 lengths were significantly longer for the CD4bs-specific sequences in both monkeys in comparison to total memory (CD20+CD27+IgG+) and total Env-specific (CD20+CD27+IgG+gp140-FT+) memory B cells. Statistics was determined by the Kruskal-Wallis test followed by Dunn's multiple comparison test, where $**p<0.01$. In conclusion the CD4bs-specific sequences were highly homologous between the different monkeys.

Fig S5

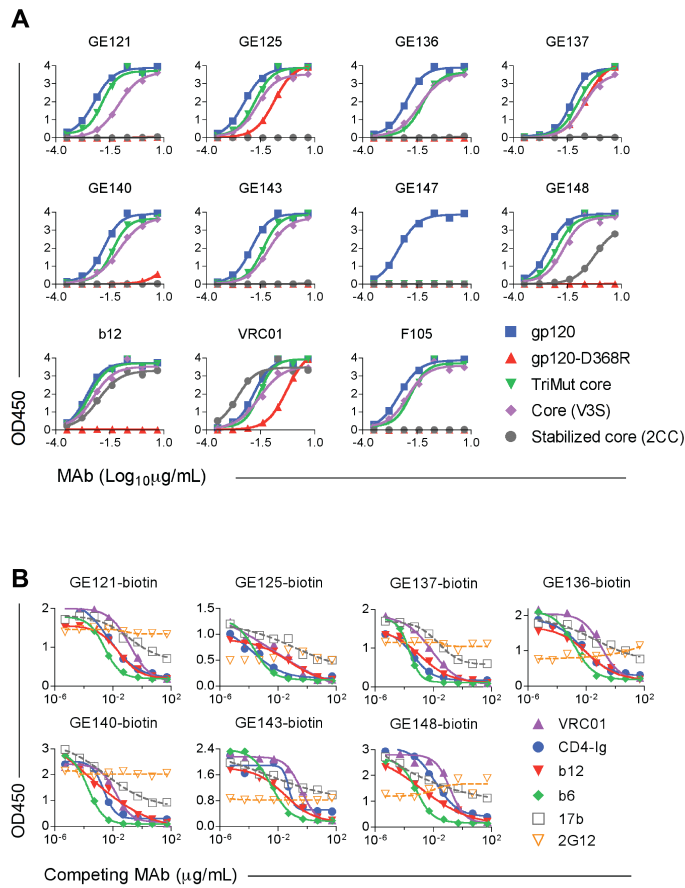


Figure S5. Binding specificities of isolated MAbs. (A) The NHP MAbs and known human CD4bs-directed MAbs, b12, VRC01 and F105, were characterized for their capacity to bind gp120, gp120-D368R, core (V3S), stabilized core (2CC) and TriMut core by ELISA. Titration curves are shown as Log_{10} dilutions ($\mu\text{g/mL}$). (B) Binding by the biotinylated NHP MAbs to gp120 in the presence of increasing concentrations of competing ligands (CD4bs-directed human MAbs, b6, b12, VRC01 and CD4-Ig, CoRbs-directed MAb, 17b, and a control MAb, 2G12) is shown as titration curves of the competing ligand in $\mu\text{g/mL}$.

Fig S6

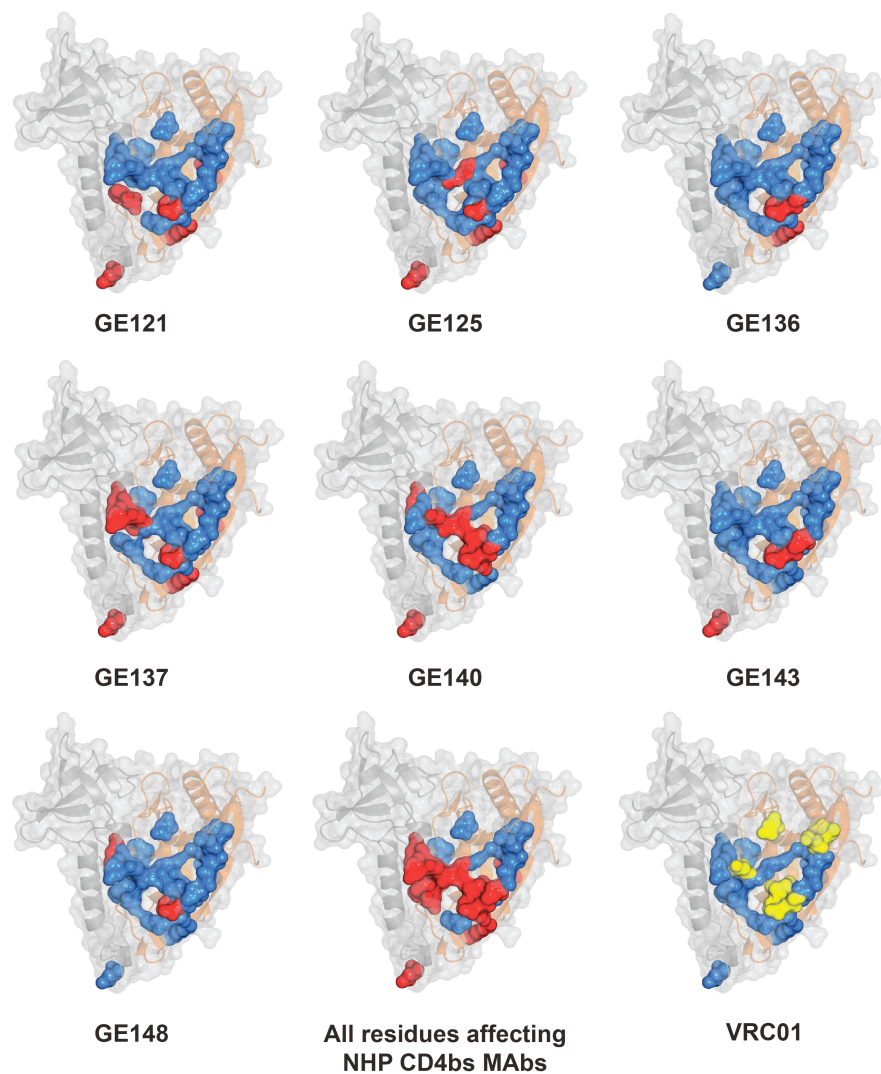


Figure S6. Amino acid residues affecting individual MAb binding to gp120 modeled on the core structure. Residues identified in the Ala scan that result in a 3-fold reduction in gp120 binding by the individual vaccine-elicited NHP MAbs are marked in red and those affecting VRC01 binding are marked in yellow. Shown in blue are the combined residues targeted in the Ala scan analysis. Behind the transparent surface of the core, the alpha carbon backbone of the inner domain and bridging sheet are shown in gray and the outer domain in salmon. Lower-mid panel shows the combined residues affecting recognition of the NHP MAbs to gp120.

Table S1. Heavy chain germline V-gene analysis and annotation

Sequence ID ^a	Closest corresponding human IGHV gene ^b	Homology (%) ^c	Sequence	Genomic location ^d
VH6.1	IGHV6-1*01 F	95.3	cagggtcagctgcaggagtcagggtccaggactgggtaagccctcacagaccctgtc actcaccctgtccatctccggggacagtgctctagcaacagtgctacttggaaactgg atcaggcagtcgcatctcgagagcccttgagtgctgggaaggacatactacaggtc caagtggtataatgatgatgcaaatctgtgcaaaatcgaataagatcaaccaggca cacatccaagaaccagttctccctgcagctgaactctgtgacccccgagggacatgg ccgtgtattactgtcaagaga	Ch7
VH3.2	IGHV3-66*02 F	91.6	gaggtgcagttggtgagctcggggaggcttggtacagcctggggctccctgag actctctgtacaggtctggattcaccttcagtagctactacatgactgggtccgcca ggctccagggaaagggctggaggggtctcagcttaataactgtgggggtgagca catggtacacagactccgtgaagggccgattccatctccaagaagaaacgcca gaacacactgtattccaatggagacccctgagagctgaggacacggctgtattata ctgtgcgaagaga	Ch7
VH2.3	IGHV2-70*10 F	94.5	caggctacctgaaggagctgatctgcgctagtgaaaccacacagaccctcac gctgacctgcacctctcgggttctcactcagcactctggaatgggtgtggacggga tcgctgacccccagggaagggcctggagtgctgcacgactgattgggtgagtg ataaatactacagccatctgctgaagagcaggctcaccatctccaaggacacctcc aagaaccaggtgtcctcaatgacccaactggaccctgtggacacagccaacata ttactgtgcagggagac	Ch7
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VH4.35	IGHV4-39*07 F	90.4	caggtgcagctcaggagctggggccaggactggtgaagcctcggagaccctgt ccctcactcgtctgtctcgttggctccatcagcagtagtaactggtgagctggatc cgccagctccagggaaagggctggaaatgattgggggtatctatgtagtggtgg gagcaccgaatacaacccccctcaagagctcagctcaccattcaatagacagct ccaagaaccagttctcctgaagctgagctctgtgaccgccggacacggcctgt tattactgtgcgagaga	C1
VH1.36	IGHV1-69*10 F	94.8	caggtccagctgggtcagctcggggctgaggtgaagagcctggggcctcagtg aggittcctgcaagctcctggattcaactcggcagctatctatcagctgggtgca caggccccggacaagggctgagtgattggagtgatccctctgtgtgataaa caaacctacgagaaagttccagggcagagctcagctaccggcagacagctccac aagcacagcctaactggagctgagcagcctgagatctgaggacacggcctgtatt actgtgcgagagg	C1
VH4.37	IGHV4-4*07 F	90.0	cagctgcagctcaggagctggggccaggactggtgaagcctcggagaccctgtc tgtcactcgtctgtctcgttggctctatcagcagtagctactggagctggatccgc aggccccagggaaagggactggagtggttgggtatctatgtagtgtagtagca ccaactcaacccccctcaagagctcagctcaccctcagtagacacgctcaag aacagctctcctgaagctgagctctgtgaccgccggacacggcctgtattac tgtgcgagcga	C1
VH4.38	IGHV4-39*07 F	90.1	caggtgcagctcaggagctggggccaggactggtgaagcctcggagaccctgt ccctcactcgtctgtctcgttggctccatcagcagtagtaactggtgagctggatc cgcaacccccagggaaagggctggagtggttgggaatctatgtagtagtagc gagcactctacaacccccctcaagagctcagctcaccattcaaaagacagct ccaagaaccagttctcctgaagctgagctctgtgaccgccggacacggcctgt attactgtgcgagaga	C1
VH4.39	IGHV4-4*07 F	91.6	caggtgcagctcaggagctggggccaggactggtgaagcctcggagaccctgt ccctcactcgtctgtctcgttggctccatcagcagtagtaactggtgagctggatc cgccagccccagggaaagggactggagtggttgggtatctatgtagtagtagc gagcaccactcaacccccctcaagagctcagctcaccattcaaaagacagct ccaagaaccagttctcctgaagctgagctctgtgaccgccggacacggcctgt attactgtgcgagaga	C1
VH4.40	IGHV4-39*07 F	91.1	caggtgcagctcaggagctggggccaggactggtgaagcctcggagaccctgt ccctcactcgtctgtctcgttggctctatcagcagtagtaactggtgagctggatc cgccagccccagggaaagggctggagtggttgggaatctcgttggtagtagt gtagcactctacaacccccctcaagagctcagctcaccattcaaaagacagct ccaagaaccagttctcctgaagctgagctctgtgaccgccggacacggcctgt tattactgtgcgagaga	C1
VH3.41	IGHV3-h*01 P	91.6	gaggtgcagctggtggagctggtggggcggtggtaaagcctggggggccctga gactctcctgcgcagcctcgtgattcaactcagtagctactacactgactggctcgc caggctccagggaaagggctggagtggttctcagttattgtaatgggtggtagc acatgtgacgagactcctgtgaagggcagattccacctccagagagaaccca agaacacactgtatttcaaatgacagcctgagagctgaggacacggcctgtclatta ctgtgcgagaga	C1
VH3.42	IGHV3-22*02 P	88.1	gaggtgcagctggtgaaactggcggaggctggtgaagcctggggggccctgag gactctcctgtgcagactcgtgattcaactcagtagcactacatgagtggtccgc caggctccagggaaagggctggagtggttggatgaatgaaacaaagctgatg gtgagacaacagactatctgcatctgtgaaagggcagattccacctccagagatg attcgaaagcactacactctcgaatgaacaaactgaaacccagggacacggcgc cgtgtattactgtgcgaggaa	C1
VH4.43	IGHV4-39*07 F	90.4	cagctgcagctcaggagctggggccaggactggtgaagcctcggagaccctgtc cctcactcgtctgtctcgttggctccatcagcagtagtaactggtgagctggatcc gccagccccagggaaagggactggagtggttgggtatctctgttagtggtggg agcaccagcgacaacccccctcaagagctcagctcaccattcaaaagacagct ccaagaaccagttctcctgaagctgagctctgtgaccgccggacacggcctgt attactgtgcgagaaa	C1
VH3.44	IGHV3-33*01 F	93.1	gaggtgcagctggtggagctggtggggaggctggtcagcctggggggccctgag actctcctgtgcagcctcggattcaactcagtagctatgcatgcaactgggtccgc aggctccagggaaagggctggagtggttgggtatattgtagtagtgaagtaag aaatactcagcagactctgtgaagggcagattccacctccagagacaactccaa gaaactgctatctcaaatgaacaaactgaaatggaggacacggcctgtattac tgtgcgagaga	C1
VH3.45	IGHV3-52*01 P	92.0	gaggtgcagctggtggagctggtggggaggctggtgacagcctggggggccctgag actctcctgtacagcctcgtgattcaactcagtagcaccagataaactggtaccga cagctccagggaaagggctggagtggttggcagataaagtaacagatggaagtg agaaatactatgtagactctgtgaagggccgattcaactctccagagacaactgcca agaaactcctctatcgaatgaacagcctgagagctgaggacacagcctgtatt actgtgcgagaga	C1
VH5.46	IGHV5-51*01 F	95.1	gaggtgcagctggtgagctggagcagaggtgaaagggccggggagctctgga	C1

			agatctcctgtaagactctggatacagcttaccagcagctggatcagctgggtgcg ccagatgccgggaaaggcctggagtgaggggagcatctatcctgggtctgta taccaaatacaaccgctcctcaaggccacgtcaatctcagccgcaagtcacat cagccaccactcctcagctggagcagcctgaaggcctggaccaccgccaagctat tactgtgcgaaagt	
VH3.47	IGHV3-72*01 F	95.9	gaggtgcaagctggtagctggtggggcgctggcacagcctgggggtccctgag actctcctgtgacgctctggattcacctcagtgaccactacatggaactgggtccgc aggctccagggaaggcctggagtggtgacccgtatgaaacaaagtcaacag ttacaacaagaalacgcgcgtctggaaggcagattccatctcaagggatg attcaaaagaacactgtatctgcaaatgagcagcctgaaaacccgaggaacagcgc tgtattactgtctagaga	C1
VH3.48	IGHV3-48*04 F	91.0	gaggtgcaagctggtagctggtggggaggctggccagcctggcggtccctgag gctctcctgtgcaacctctggattcacctcagtaactactggatgtctgggtcccca ggctccagggaaggcctggagtggtctcaagtattagtgtagcagtagtagca catactaccagactctgcaaggccgattaccatctccagagacaacccaag aacacgctgtatctgcaaatgaacagcccggagcggaggaacagcgtcttatta ctgtgcgagaga	C1
VH3.49	IGHV3-22*01 P	88.4	gaggtgcaagctggtagctggtggggaggctggcaacagcctgggggtccctga gactctcctgtgattcacctcagtgaccactacatgagctgggtccgcaaggctcc agggaaggccggcagtggtgagtttcatgagaacaaagttaagtgggaac aacagaatacagcagctgtgaaaggcagattcactctcaagagctgattccaa aagcattggccagctgcaaatgagcagcctgaaaacccgaggaacagcgcgtg tactgtccagaag	C1
VH3.50	IGHV3-48*04 F	91.3	gaggtgcaagctggtagctggtggggaggctggccagcctggcggtccctgag actctcctgtgacgctctggattcacctcagtaactactggatgtctgggtcccca ggctccagggaaggcctggagtggtctcaagtattagtgtagcagtagtagca catactaccagactctgcaaggccgattaccatctccagagacaacccaag aacacgctgtatctgcaaatgaacagcccggagcggaggaacagcgtcttatta ctgtgcgagaga	C1
VH3.51	IGHV3-48*04 F	91.9	gaggtgcaagctggtagctggtggggaggctggcaacagcctgggggtccctgag actctcctgtgacgctccgattcacctcgggtaactctgactgtatctggatccgc aggctccagggaaggcctggagtggtctcacaattagtggtgtagcatata ctactcagactctgaaaggccgattaccatctccagagacaacccaagaa cgctgtatctgcaaatgagcagcctgagagtgagggaacagcgcgtgattactgtg caaaaga	C1
VH3.52	IGHV3-h*01 P	91.6	gaagtgcaagctggtagctggtggggaggctggtaacagcctgggggtccctgag actctcctgtgacgctctggattcacctcagtgaccactacatgactgggtccgc aggctccagggaaggcctggagtggtctcaagtattagcagtggtgtagta ccattgtaccagactctgcaaggccgattaccatctccagagacaaccca agaacacagctgtatctgcaaatgaacagcctgagagccgaggaacagcgtctat tactgtgcgagaga	C2
VH1.53	IGHV1-f*01 F	95.1	gaggtcagctggtagctggtggggaggctggtaacagcctgggggtccctgaa aatctcctgcaagcctctggatacactcaccgactactcctgactgggtcga caggctcctggaaaggcctggagtggtggagcgtgtgactgcaagatgggtgaa gcaatacagcagagaagttccaggaagagtcaccatccagcagcagcagctca cagacacagcctacatggagctgagcagcctgagatctgagggaacagcgcgtgta ttactgtgcaacaga	C2
VH3.54	IGHV3-15*08 F	91.2	gaggtgcaagctggtagctggtggggaggctggccagcctggggatccctgag actctcctgtgacgctctggattcacctcagtaactactggatgaactgggtccgc aggctccagggaaggcctggagtggtggttattaaacaaagcagatgt ggaaacagcagcatacggccaatctgaaaggcagattcactctcaagagatga ttcaaaagaacacactgtactgcaaatgaacagcctgaaaacccgaggaacagcgc cgtgtattactgtactagaga	C3
VH3.55	IGHV3-66*02 F	87.4	gaggtgcaagcgggtggagctggtggggaggctggcaacctgggggtccctga gactctcctgtgacgctctgattcacctcagtagctcctggatgaactgggactc caggctccaggaaggcctggagtggtctcacaattagtggtgtagcaca gaclaccagattctcaaggcccaattcaccatctccagagacaatccagagac catgctgtatgcaaatgaacagcctgagagctgaggacatggctgtgaattactgt gcaagaga	C4
VH3.56	IGHV3-48*04 F	91.7	gaggtgcaagctggtagctggtggggaggctggccagcctggcggtccctgag actctcctgtgcaacctctggattcacctcagtaactactggatgactggtcccca ggctccagggaaggcctggagtggtctcaagtattagtgtagcagtaglaaca catactaccagactctgcaaggccgattaccatctccagagacaacccaag aacacgctgtatctgcaaatgaacagcctgagagccgaggaacagcgtcttatta ctgtgcgagaga	C7
VH4.57	IGHV4-39*02 F	92.1	caggtgcaagctgaggagctggggaggctggtaacagcctgggagaccctgt ccctcactgctgtctggtgctccatcagcagtggttactactgagctg atccgcccagcccccagggaaggcctggagtggtgggtggtatctatglaaag tgagagtaaccaactacaacccctccctcaagagctcaggtcaccattcaaaagaca cgtccaagaacagctctcctgaaagctgagctctgtgaccgcccgggacagcggc gtgtattactgtgagaga	C8
VH3.58	IGHV3-66*02 F	92.3	gaggtgcaagctggtagctggtggggaggctggcaaacgctgggggtccctga gactctcctgtgacgctctgattcacctcagtagctcctggatgaactgggtccgc agactccagggaaggcctggagtggtctcagctattaatagtggtgggtgagc acatactcagcagactcctgaaaggccgattaccatctccagagacaactcaaa gaacacgctctcctgcaaatgaacagcctgagagctgaggacaacagcgtgtatt actgtgtaaaaga	C9
VH1.59	IGHV1-24*01 F	95.14	gaggtcagctggtagctggtggggaggctggtaacagcctgggggtccctgag aggctcctgcaaggttccgatacactcaccgaattaccatgactgggtgca caggccctgaaaggcctggagtggtggaggtgtgactctgatatgggtgaa ataatacacgagagaagttccaggcagagtcaccatgaccagaggaacagctca cagacacagcctacatggagctgagcagcctgagatctgaggacaacagcgcgtgta ttactgtgcgaga	C10
VH3.60	IGHV3-48*04 F	90.88	gaggtgcaagctggtagctggtggggaggctggccagcctgggggtccctgag actctcctgtgacgctccggattcacctcgggtaactctgactgtgactggtccgc aggctccagggaaggcctggagtggtctcacaattagtggtgtagcatata ctactcagactctgcaaggccgattaccatctccagagacaacccaagaa cagctgtatctgcaaatgagcagcctgagagtgagggaacagcgtgtattactgtg aaaaga	C11
VH1.A	IGHV1-8*02 F	85.07	caggtcagctggtagctggtggggaggctggcaacagcctgggggtccctgaa gctctcacaagcctctggttacccttccagcactatataaactgggtgagac aggccctgaaacagctgctgactggatggatgattaaccttagcaatgtaata	C1

			caggctacgcacagaagtccagggcagagtcacatgaccagggacacgtcca caagcacagcctacatggagctgaacagcctgagatctgaggacacggcgtgtatt actgtcggagaga	
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^aVH Open reading frames (ORFs) were annotated based on gene family usage and position relative to the junction between the V and D regions, with the most proximal gene segment receiving number 1 (e.g. VH6.1 correspond to family 6, VH ORF number 1 from the V-D junction). Since the locations of the contigs in the chromosome were unknown they were annotated as if following after the assembled genomic chromosomal sequence. F indicates functional. P indicates pseudogene. Annotations were given a dot (.) between the V family name and the family member gene number instead of a dash (-), as in the annotations for human Ab genes, to minimize confusion with the final annotations of the rhesus Ig loci that will be possible to do when a complete genome assembly is available.

^bClosest matching human germline VH gene was determined via IMGT/V-Quest

^cHomology (%) between the rhesus and closest matching human germline as determined by IMGT/V-Quest or AlignX

^dRaw sequences are available via www.ensembl.org

Sequences were extracted from genome assembly: MMUL 1.0, Feb 2006, database v. 66.10
Ch7 corresponds to chromosome 7 region: 169,100,000-169,801,366.

C1 corresponds to contig MMUL: 1099548049584

C2 corresponds to contig MMUL: 1099214726682

C3 corresponds to contig MMUL: 1099214740059

C4 corresponds to contig MMUL: 1099214735892

C6 corresponds to contig MMUL: 1099214757507 (region spanning VH3.5 in Ch7)

C7 corresponds to contig MMUL: 1099214739418

C8 corresponds to contig MMUL: 1099214811615

C9 corresponds to contig MMUL: 1099214148171

C10 corresponds to contig MMUL: 1099214764051

C11 corresponds to contig MMUL: 1099214792373

Table S2. Lambda germline gene analysis and annotation

Sequence ID ^a	Closest corresponding human IGLV gene ^b	Homology (%) ^c	Sequence	Genomic location ^d
VL3.1	IGLV3-1*01 F	87.8	tcctatgagctgactcagcccccctcagtgctcagtgccccaggacagccagccagcatcacctgc ctggagataaattgggaatgcalatgcttactggtaccagcagaagccagggcctccctgta ctggatcatalaataaaatgcaaccggccctcaggatccctgagcgattctcggctccaactcg gggaacacggccaccctgacatcagcggggctgaggctggggatgaggccgactattactgt gctacaagctatggcag	Ch10
VL4.2	IGLV4-3*01 F	91.2	ctgcctgtgctgactcagccccctgctcctgctgggacctctgcaagctcacctgcac cctgagcagtgagcagcagaactcttattttctggtatcaacagagaccggggaggctccccg gtalataatgaaggttaacagtgatggcaccagagcaaggggagggatccccgatcctct tgggtccagctcggggctgacgctaccctaccatccaacctccagctgacgacagggctg agttactgtggagagtgccacagattgatggccagctacgtt	Ch10
VL2.3	IGLV2-14*01 F	95.0	caggctgcccctgactcagctccctctgctgctgggtctcctggacagctggctaccatctcgtcact ggaaccagcagtgacattgggtgataaccgtgctcctggtaccacagcaccagggcaaaag ccccaaactcagttatgaggtcagtaagcggccctcagggtctctgatcgtctctggtcc aagtctggcaacacggcctcctgaccatctctgggtccaggctgaggacagggctgatttac tgacgtcatalcga	Ch10
VL3.4	IGLV3-10*01 F	96.8	tcctatgagctgacacagcccccctcgggtcagtgctcccaggacagacggccaggatcacct gctctggagatgattgcaaaaaaatgcttattgttccagcagaagccagggcctccctg tctgatcattgagcagcaaacggccctcgggtcctggagagattctcgtccagctc agggacagtgccaccctgactatcagtgggggccagggtggagatgaagctgactactactgt actcaacagatgacagtgtaacatag	Ch10
VL2.5	IGLV2-23*02 F	93.1	caggctgccccgactcagctccctctgctgctgggtctgctggacagctggctaccatctcctgac tggaaaccagcagtgatattgggtattataatgctgctggttaccacagatccagggcaaaagcc cccaaaactcagttatgaggtcagtaagcggccctcagggtctctgatcgtctctggtccaa gtctggcaacacggcctcctgaccatctctgggtccaggctgaggacagggctgattactg cagctcatgacaggtatggtacttct	Ch10
VL3.6	IGLV3-9*01 F	83.1	ttctgtaactgacacagtcaccctcagtgctcagtgggccccaggacagatgaccaggatcacctgt gaagaagaatcattggaagtaaaagtctcaatggtaccggcagaagccagggccagggccg gtttggctcattctgggatalagcaggcggcctcaggaatctgagagattctcggctccaact ggagaacacagccaaacctgaccatcaacagggccaggctggggatgaggctattactgtaag atgtgggacatt	Ch10
VL2.7	IGLV2-8*01 F	96.1	caggctgcccctgactcagctccctcaatgctcgggtctcctggacagctggctaccatctcctgca ctggaaaccagcagtgacattgggtgataaccgtctcctggtaccacagcaccagggcaaa gccccaaactcagttatgaggtcagtaagcggccctcagggtctctgatcgtctctggtcc caagtctggcaacacggcctcctgaccatctctgggtccaggctgaggatgaggctgattata ctgcagctcatatgca	Ch10
VL3.8	IGLV3-21*02 F	93.8	tcctatgagctgactcagcccccctcgggtcagtcggcctcaggacagacggccaggatcacct gtggggagacaaactggaagtaaaatgctcactggtaccagcagaagccagggcagggcc cctgtgctgctatctatgctatagcaaacggccctcagggtaccctgagcgattctcgtgctca ctcagggaaacacggccaccctgaccatcagcaggggtgagggccgggagaggctgactatt actgacaggtggtggacagt	Ch10
VL2.9	IGLV2-18*02 F	88.9	caggctgcccctgactcagctccctcagtgctcaagctcctggtcagctggctaccatctcctgctg ctggaaaccagcagtgacattgggtgataaccgtctcctggtaccacagcaccagggcaaa gccccagactcctgattaccgtgctcagtaacgaccctcagggtctctgatcgtctctggtcc aagtctggcagcagcctccctgaccatctctgggtccaggctgaggacagggctattactg ctgctcatata	Ch10
VL3.10	IGLV3-19*01 F	95.7	ttctgagctgactcaggaacctcagtgctgctggcctgggacagacagctcaggatcactgtcc aaggagacagcctcagaagctattatgcaagctggtaccagcagaagccagggccagggccct gtcgtgctgctatgataaacaacacggccctcagggtaccctgagcgattctcgtgctcaagc tcagaaacacagctcctcagaccatcagtggggtcagggtggaagatgaggctgactattactg gactcctgggacagcagcggtaccatc	Ch10
VL3.11	IGLV3-12*02 F	92.1	tcctatgatgactcagccacgctcagtgctgctgctcccaggacagacggccaggatcacctgt gggggagacaacttggaaatgaaatgctcactggtaccagcagaagccagggcagggccct gtcgtgctcattatagatagcaaacggccctcagggtaccctgagcgattctcgtgctcaact cagggaacacggccaccctgaccatcagcggggctgagggccgggagtgaggctgactattact gtcaggtggtggacagtagtagtcatcc	Ch10
VL3.12	IGLV3-22*01 F	90.3	tcctatgagctgacacagcccccctgggtcagtgctcccaggacagacggccaggatcacctg ctctggagatgactgaagaaaatattgctgactggtaccagcagaagccggccagggccct gtgctgctgatacgaagatagtaagcagccctctggaatccctgagcgattctcgtgctcaact caggggacacgcaaccctgaccatcagcagcaccctgagtgaagatgaggctgactattactg ttttctgggaatgagaacaatcc	Ch10
VL2.13	IGLV2-11*01 F	95.8	caggctgcccctgactcagctcctcagtgctcgtgggtctcctggacagctggctaccatctcctgca ctgaaaccagcagtgacatcgtggtgataactgtctcctggtaccacagcaccagggcaca gccccaaactcagttatgaggtcagtaagcggccctcagggtctctgatcgtctctggtcc caagtctggcaacacggcctcctgaccatctctgggtccaggctgaggacagggctgattata ctgctgctcatatgacggcagctacacttcc	Ch10
VL3.14	IGLV3-19*01 F	91.4	tcctgagctgactcaggaacctcagtgctgctggcctgggacatacagtcaggatgactgctcc aaggagacagcctcaaacctattatgcaagctggtaccagcagaagccagggcagggccctg tctgtgctcattatgtaaacactcggccctcagggtaccagcgattctctgctggctca ggaaacacaggttctgaccatcactgctcaggtggaagatgaggctgactattactgtaac tctgggacagcagcggtaccatct	Ch10
VL3.15	IGLV3-21*01 F	93.6	tcctatgagctgactcagcccccctcgggtcagtgctcccaggacagacggccaggatcacctg tggggagacaaccttggaaatgaaatgctcactggtaccagcagaagccagggcagggcccc tggctgctcattatgatagtgaccggccctcagggtaccctgagcgattctcgtcctcaact agggaacaccggccaccctgaccatcagcggggctgagggccgggagtgaggctgactattactg tcaggtggtggacagtagtagtcatcc	Ch10
VL1.16	IGLV1-36*01 F	90.9	cagctgtgctgactcagctccctcagcgtcagggccggcaggaagagtgctaccatctcctgtt ctgaaagcagctccaacatggaaatgaaatgctgctggtaccagcagctccaggaacagc tccaacactcctcattatgatacgaagcctcaggtgctcctgacagattctcgtcctcaac gtctggcaagcagctcctggccatcagtggtgctccagcagggatgaggctgattactg cgacatgggagtagacgtgagcgtcc	Ch10
VL5.17	IGLV5-45*01 F	90.2	aagcctatgctgactcagccggcctcctcagcactcctggagatcagccagctcactatgc accctcagcgggtgacatcaattgtgctgctaccatattctggtaccagcagaagccagggag ctccccggtatctctgaggtcaaacactcagactcagataaaggccagggctctggagctccag ccgtctctggtccaagaatgctcagcgaacacagggattttacgactctctgggtccagctg aggatgaggtgactattactgtccattgggacagcagcgggtcct	Ch10

VL1.18	IGLV1-40*01 F	91.2	cagctctgtgctgacagccgcccctcagctgtctggggccccagggcagagggtaaccatctctg cactggagcagctccaacattggagttatgtatctctggtaccagcagctccaggaaca cccccaaacctctcatatcaagataaagcgaccctcaggggttctgaccgattctctggctcc aagctctggtacctcagctccctgaccatcagggctccagactgaggatgaggctgattact gctctctatgacagcagcctgagtg	Ch10
VL1.19	IGLV1-50*01 ORF	89.8	cagctctgtgctgacagccgcccctcagctgtctggggccccagggcagagggtaaccatctctg cactggagcagctccaacattggagttatgtatctctggtaccagcagctccaggaaca cccccaaacctctcatatgacaataaagcgaccctcaggggttctgaccgattctctgctcc aagctctggtacctcagctccctgaccatcagggctccagcctgggatgaggctgattact gaggagcatgggatagcagcctgagtgctca	Ch10
VL1.20	IGLV1-51*02 F	93.5	Cagctctgtgctgacagccgcccctcagctgtctggggccccagggcagagggtaaccatctctg cctggaaagcagctccaacatcgggagaaattgtatctctggtaccagcagctccaggaaca gcccccaaacctctcatatcaagataaagcgaccctcaggggttctgaccgattctctgct cgaagctctggtacctcagctccctggccatcac (partial sequence)	Ch10
VL7.21	IGLV7-43*01 F	92.7	caggctgtgtagtactcaggagccctcactgactgtctccaggaggagcagctactctcacctg ctctcagcagctggagcagctcaccagtggtactctccacactggtccagcagaagcctggcc aagccccagggactgattataatacaagctcaaacactctgactctgcccgttctcag gctccctctggggcaaaagctcgcctgatactgacaggtgcacagcctgaggcagaggtgag tattactgtgctgactatagtggtctcag	Ch10
VL1.22	IGLV1-47*02 F	95.1	cagctctgtgctgactcaaccacctcagctctggggccccagggcagagtgctaccatctctgt ctggaagcagctccaacatcgggagaaattgtatctctggtaccagcagctcaggaaagggc cccaaacctctataataatacaagcagccctcaggggtccctgactctctggctcca agctctgcaagctcagctccctggccatcagtggtccagctccagggatgaggctgattactg cagcagctgggatagcagcctgagcgttc	Ch10
VL5.23	IGLV5-48*01 ORF	91.2	cagcctgtgctgactcagccaaacctcctctcagcactctctggagcatcagctcagctcactgc acctcagcagctggcagctcagtggtggctcaatatacactggtaccagcagaagcaggag tctccccgtactctgtaactactcagactcaaaagggcagggctctggagctccag ccctctctggatccaaagatgctccgccaatgagggtttactctctggttccagctgga ggtagggctgactattactgtaactggtgcaacaactgctct	Ch10
VL7.24	IGLV7-43*01 F	92.7	caggctgtgtagtactcaggagccctcaatgactgtctccagggaggagcagctactctcacctg ctctccagcagctggagcagctcaccagtggtcactctccactggttccagcagaacctggaca agcccccaagcactgattataatacaaacactcctgactctctgcccgggtctcag ctccctctgggggaaagctgcccctgacactgctgagctgagcagcctgaggataaggtgag tattactgctgctgactatagtggtctcag	Ch10
VL1.25	IGLV1-44*01 F	93.7	cagctctgtgctgactcagccacctcagctctggggccccagggcagagtgctaccatctctgt ctggaagcagctccaacatcagaggtatgggtgtaactggtaccagcagctcaggaaagggc cccccaaacctctcatataataatacagcagccctcaggggtccctgaccgattctctgctcc aagctctggcactcagctccctggccatcactggtctccagctgaggatgaggcagattact cgaagcagtggaataacagcctgagcgttc	Ch10
VL7.26	IGLV7-43*01 F	91.3	caggctgtgtagtactcaggagccctcactgactgtctccaggaggagcagctactctcacctg ctctccagcagctggagcagctcaccagtggtcacttccactggttccagcagaacctggaca agcccccaagcactgattatgatacaagcaaacctctctggaccctgcccgttctcag gctccctgtctgggtaagctcctcagcacttctgggtgagcagccccagggagcagctgag tattactgctggctgactcagtggtgctcag	Ch10
VL1.27	IGLV1-47*02 F	94.7	cagctctgtgctgactcagccacctcagctctggggctccgggagagtgctaccatctctgt ctggaagcagctccaacatggaagtaattgtatctggtaccagcagctccaggaagcggcc ccccaaactctcatatagtaatacagcagccctcaggggtccctgaccgattctctgctctaa ctgtggcaactcagctccctggccatcactggtctccgactgaggatgagggtgattactgtg cagcagtggaataacagcctgagcagcttc	Ch10
VL5.28	IGLV5-48*01 ORF	93.8	cagcctgtgctgactcagccaaacctcctctcagcactctctggagcatcagcagactcactgc acctcgcagctggcactcagtggtgtagttacaggatattctggtaccagcagaagcaggag ctcccccgtatcttgaactcaccacagactcagataagcaccagggatctggagctccag ccgctctctggatccaaagatgctccggccaatgagggtttactcactctgggctcagctga ggtagggctgactattactgattggtggcaacaactgctct	Ch10
VL9.29	IGLV9-49*01 F	94.3	cagcctgtgctgactcagccaaacctcctctcagcactctctggagcatcagcagactcactgc acctcagtagcggctcagtaattatgctggactggtcaccagcagaagcagggaagggc cctcagttgtgctgagtgggcagcaggtgggattggggtccaaggggagtggaactcctgat cctctcagctcgggctccggcctgaaatcgttaccctgacctcaagaacattcaggaagagga tgagagtgactcactctggggcagaccagcctggggagcagctctg	Ch10
VL1.30	IGLV1-40*01 F	91.9	cagctctgtgctgacagccgcccctcagctgtctggggccccagggcagagggtaaccatctctg cactggagcagctccaacattggagttatgtgctggtaccagcagctccaggaacgg cccccaaacctctcatataaataaagcgaccctcaggggttctgactgattctctgctcc cagctctgtaacctcagctccctgaccatcactgactcagctgaggatgaggctgattactg ccagctctatgacagcagctgagtg	Ch10
VL1.31	IGLV1-41*01 ORF	90.5	cagctctgtgctgacagccgcccctcagctgtctggggccccagggcagagggtaaccatctctg ctctggaagcagctccaactcaggagttatgtgctggtaccagcagctccagggagcagc cccccaaacctctcatatgattataaagcgaccctcaggggttctgaccgattctctgctcc agctctggcactcagccctgggatcagtgactcggcctgaggatgaggcagattact gctcagcagtggtatagcagcctgag	Ch10
VL5.32	IGLV5-39*01 F	90.2	cagcctgtgctgactcagccagcctcctctcagcactctctggagcatcagcagctcactgc acctcagtggtggcaccatgttgggtgactcactatacactggtaccagcagaagcaggggag tctccccgtatctctgaaagtaacaactcagactcagataagcaccagggctctggagctccag tgctctctggatccaaagatgctcagcagaacagggatttaccgactctgggctccagctg aggatgagctgactattactgctcattggcagcagcagctct	Ch10
VL7.33	IGLV7-46*01 F	92.0	caggctgtgtagtactcaggagccctcactgactgtctccaggaggagcagctactctcactgt ggctccagctctggagcagctcaggggacttattctccactggttccagcagaagcctggccaa gccccagaacaactgattatgatacaagcaaacagctctctggaacccctgcccgttctcagc tccctctggggtaaaagctcctcagcactgctgagctgagcagctgaggatgaggctgagat tactgtgctgactatagtggtgctc	Ch10
VL6.34	IGLV6-57*01 F	92.7	ccccattgtctggggctcggggcagacggctccatctctgaccaccagcagtgggcag cattgacaacagctatgltactggtaccagcagcggccggcagcggccccaccactgtagct acaatgatgccaagacccctgggtccctgactcggctctctggctccatgacagcctccca actctgctccctcaactctctgactgaaagctgaggagcagggctgactattactgctgattatg acagcagc	Ch10
VL5.35	IGLV5-52*01 F	94.1	cagcctgtgctgactcagccatctccatctcctgctgagcggcagcagactcactgc acgtgagcagtggtcactcagtggtgactctgatacgtggtaccacaacaagcaggag ccctccccgtatctctgtaactcactcagactcagataagcacaaggctctggagctccag ccctctctggatccaatgatgcatcagccaatgagggttctgcatatctctggctccagcctg aggatgagctgactattactgtgactcagctggcactgcaactcaagactca	Ch10
VL4.36	IGLV4-69*01 F	95.9	cagcctgtgctgactcagccctcctcctgctcctccctgggagcctcggtaagctcactgca ctgagcagtgggcagcagcagctcagcactcagctggtcagcagcagcagcaagggagggc cctgactctaatgagcctaacagctatgacagccacagcaagggggagggatcctctgac	Ch10

				gcttcaggctccagctccgggctgagcgtacctccacctccaacctccagctgaggatgaggctgattactgctcagaccctggatactggcattca	
VL1.37	IGLV1-40*01 F	78.8		cagctgtgctgactcagccaccctcagtgctgggcccacagggccaggctcactatctctgca ttggaagcagctcactggtcagctggtataatgtaaaactgttgccagtggtcccaagaactga tcccaaaactctcagtgtaataagaaactgggctcctgggcatcagcaaatctctgctcc aagtctggcaactggctccctggccaccactggctctggactgaggacagactgagatca ctccagctccacggcagcagcagtgct	Ch10
VL5.38	IGLV5-45*01 F	80.1		cagcctgtgctgactcagccctcctctctgctatcaggagcatcagccagactcctgc accctgagcagtggtcagtgctgactctctggtataactggataaccagataagccagggagc cctccccgtatctcctgagcctcaccaaaattcattcatgacctggctccgggtccccagggc gcatctctggtatggaagactggtccaaataaaggctctgctcactatctgctccagcctgag gatggcctgactattactglatgattgagcagggcagagctct	Ch10
VL6.39	IGLV6-57*01 F	91.6		ccccattctgtgctggggtctccggggcagacgggtaccatctctgaccocgcagctggcag cactgacagtaataatgtcagtggtaccagcagcccccggcaatgcccccaccagtgattt acaaaataacaaagaccctcgggtccctgactggttctctggtccattgacagctcctcca actctgctccctgctcactctgggctaaagtctgaggacgaggctgactactctgctgctgct gatggcagc	Ch10
VL6.40	IGLV6-57*01 F	92.7		ccccattctgtgctggggtctccggggcagacgggtaccatctctgaccocgcagctggcag cactgacagtaataatgtcagtggtaccagcagcccccggcagtgccccaccagtgattt acaaaataacaaagaccctcgggtccctgactggttctctggtccattgacagctcctcca actctgctccctgctcactctgggctaaagtctgaggacgaggctgactactctgctgctgct gatggcagc	Ch10
VL10.41	IGLV10-54*01 F	95.4		caggcagggtgactcagccaccctcagtgccaagggttgagacagacggccacgctcacc tgcactgagaagtagtgctcagtggtaccagcagcccccggcagtgccccaccagtgattt acaaaataacaaagaccctcgggtccctgactggttctctggtccattgacagctcctcca actctgctccctgctcactctgggctaaagtctgaggacgaggctgactactctgctgctgct gatggcagc	Ch10
VL11.42	IGLV11-55*01 ORF	94.8		cagcctgtgctgactcagccaccctcctctgctgctcctccgggagcagctggccagactcccctgc accctgagaagtagtgctcagtggtgtaaaaaactgtaactgctgacagcagaagccaggga ggcctccaggttattctgctactactcctcagcagcaagcagctgggacctgggtccccca atcagctctggtcccaaggagcctcaagtaacacagcgttttctgctcactctgggtccagcct gaggacgaggccgattattactgctcaggtgtagcagctgctgctaat	Ch10
VL8.43	IGLV8-61*01 F	94.8		gagactgtgggtagccaggagccatggtgctgactgactcctggaggaaacagtcacactcactg tggctgagctggtcagctcctcaccagtaactccccagctggtaccagcagacccccaggcc aggtcccaagcagcctcactcagcacaacacctcctctggggtccctgctgctctctggt cctcacttgggaaacaaagctcctcaccatcagggggctcaggcagcagtgatgattctgattt actctgactcctcactggtgtagtggcatttc	Ch10
VL2.44	IGLV2-11*01 F	92.0		cagctgcccctgactcagccctcctcagtgccaagtctctggacagctgggtccacctctgctc ac tggaaaccagcagtgactggtgtataatgactctcctggtaccagcagccccaggccacag cccccagactcctgattatgactgaagacggccctcagggtctctgctgctctctgctcc aagtctggcaacacggcctcctgaccatctgggtccaggctgaggacgaggctgattattac tgcctcactatagggtaggaagcatttc	CAL:175-471
VL3.45	IGLV3-27*01 F	92.5		tcctatgactgactcagccaccctcctgctcagtgctccctggacagcagcccaagattcctgc tctggagatgactgcaaaaatattatgctcattggtaccagcagaagccaggccagcctctg ctgtgattataaagcagtgagagccctcaggatcctgagcagctctggtccacgtca gggaccagtcaccctgaccatcagcggggccagggtgaggatgaggctgactactgctt actctgggtagcaacaact	CCL:5110-5393
VL3.46	IGLV3-21*01 F	93.2		tcctatgactgactcagccaccctcctgctcagtgctccctggacagcagcccaagattcctgc tctggagatgactgcaaaaatattatgctcattggtaccagcagaagccaggccagcctctg ctgtggtcactctgctgtagcgaacggcctcaggatcctgagcagctctgctgctcaca ctacgggaacacggcctcctgaccatcagcggggctgaggccgggtagggtgactatta ctgctcaggtgggacagtagtagtacc	CDL:227-516
VL3.47	IGLV3-21*02 F	92.1		tcctatgactgactcagccaccctcctgctcagtgctccctggacagcagcccaagattcctgc tggggagacaacattggaagtgaagtgtaactggtaccagcagaagccacggcagggccct gtgctgctcactctgctgtagcgaacggcctcaggatcctgagcagctctgctgctcaca ctacgggaacacggcctcctgaccatcagcggggctgaggccgggtagggtgactattact gtacaggtgggacagtagtagtacc	CEL:20227-20516
VL3.48	IGLV3-19*01 F	90.7		tcctcgggctgactcagggcctgctgctgctggcctgggacacagtcaggatgactgccc aaggagacagcctcaaaaactattatgcaagctggtaccagcagaagccaggccaggtccctg tctgctcactctggtataaagcagtgagagggcctcaggatcctgagcagctctgctgctcaga ggaacaacaggtcctgaccatcactgctcaggtggaagtagggtgactattactgtaac tctgggacagcagcagtagcctcc	CEL:27670-27959
VL3.49	IGLV3-25*02 F	93.9		tcctatgactgactcagccaccctcctgctcagtgctccctggacagcagcccaagattcctgc tctggagaataactcggcaaaaaatgctcagtggttcacagcagaagccaggccagggccc ctgctggtgtagatataaagcagtgagagggcctcaggatcctgagcagctctgctgctcaga gttcagggaacacagttactgaccatcagtgggggccaggcagaagtagggtgactattac tgcactcagcagcagcagtggtatcctc	CFL:1449-1738
VL2.50	IGLV2-18*02 F	92.0		cagctgcccctgactcagccctcctcagtgccaagtctctggacagctgggtccacctctgctc ac tggaaaccagcagtgactggtgtataatgactctcctggtaccagcagccccaggccacag cccccagactcctgattatgaggtcagtaagcggccctcagggtctctgactcctctggtccc aagtctggcaacacggcctcctgaccatctctgggtccaggctgaggacgaggctgattattac tgcctcactatagggtaggaagcatttc	CGL:8640-8936
JL1	IGLJ1*01	81.6		ttacatctcgggtctgggaccggctcaccgtcctag	Ch10
CL1	IGLC1*01	92.6		cccaaggctccccacggctcactctgctccgccctcctctgaggagctccaagcaaaacagggc cacactagtgctgactcagtgactctccccgggagctggaagtgccctggaggcagctgagg cagcgtctcaatggggtagtgagaccaccgcccctcaaacagagcaacaacaagattg cagccagcagctactgagcctgactcctgaccagtggaagtcacaagagctcagctgccc aggtcaccgacgaaggagcagctgggagaagcagtgggccctcgagaattgta	Ch10
JL2	IGLJ2*01	84.2		tggtattcggaggagggaccggctgaccgtcctag	Ch10
CL2	IGLC2*01	92.7		cagcccaaggctccccctgctcactctctcccgcctcctctgaggagcttaagccaacaag gccacaactagtgctgactcagtgactctccccgggagcgtggaaagtgccctggaggcagga tggcagcagtcacacggggagtgagaccaccaaacctcaaacagagcaacaaca (partial sequence)	Ch10
JL3	IGLJ3*01	89.5		tgtgtattcggaggagggaccggctgaccgtcctag	Ch10
CL3	IGLC3*01	92.1		cagcccaaggctccccctgctcactctctcccgcctcctctgaggagcttaagccaacaag gccacaactagtgctgactcagtgactctccccgggagcgtggaaagtgccctggaggcaga tggcagcgtctcaacggggagtgagaccaccaaacctcaaacagagcaacaacaagt acggccagcagctactgactgactgctgaccagctggaagctcccaagagctacagct	Ch10

			gccagggtcacgcacgaaggagcaccgtggagaagacagtgcccccgcagaatgtca	
JL4	IGLJ4*01	84.2	tttggattctgtggaggaccagctgaccattgtag	Ch10
CL4P	IGLC4*01 P	88.5	ctggctactgagacacctcctcctgacccagaggcaggagttccaagacaagaccac actggtatgtctcatgagtgacttctacctgagagccatgacagtgccctggaagctagatgacatc tccatcacctagtgtagagaccaccacccctccaacagagcaacaaggctacctgagcct gggcccagacagtggaagtcccacaacctctcatctgccaggtcacgcaggaagggaacacc gtggaaaagacagtgcccccgcagcatgttct	Ch10
JL5	IGLJ5*01	86.8	ttgggtgttcggcgaggggaccaagctgaccatcctag	Ch10
CL5P	IGLC5*01 P	86.4	cagccacaaggccacccttggctactctgttcccacctcctctgaggagctccaagccaaca ggccacactagtgctcataaalgccctctacccaggagccatgacagtgccctggaaggcag atggcaccacagtcaccaagggcatggagacaagcaccctccaacagagcaacaagtat gcggccagcagttacctaagcctgatgctgagcagtgaaagtcccccaagactaccgctcc aggtcacacacgaagggaaccacctggagaagacagtgcccatgcagaatgttc	Ch10
JL6	IGLJ6*01	92.1	tgatgttgcggaagtgccaccaagttgaccgtcctcg	Ch10
CL6	IGLC6*01	94.3	cagcccaaggctcccccttggctactctgttcccacctcctctgaggagctccaagccaaca ggccacactagtgctcctgactgacttctacccgggagctgaaagtgccctggaaggcagat ggcaactctgtcaacacgggagtgagaccaccacccctccaacagagcaacaacaagta cggccagcagctactgagcctgacgtccgaccagtggaagtcccaagagctacagttg ccaggtcacgcacgaaggagcaccctggagaagacagtgcccccctgcagaatgtca	Ch10
JL7	IGLJ7*01	-	No NHP sequence was found	-
CL7	IGLC7*01	91.4	caccccaaggctcccccttggctactctgttcccacctcctctgaggagctccaagccaaca ggccacactagtgctcctgactgacttctacccgggagccgtggaagtgccctggaaggcagat ggagcccccgtcaacatgggagtgagaccaccacccctccaacagagcaacaacaagt acggccagcagctaccctgagcctgacgtccgaccagtgagggtcccaacagctacagct gccagggtcacgcacgaaggagcaccctggagaagacaatggcctgtgcagaatgtctct	Ch10

^aOpen reading frames (ORFs) were annotated based on gene family usage and position relative to the junction between the V and J regions, with the most proximal gene segment receiving number 1 (e.g VL1.30 correspond to family 1, VL ORF number 30 from the V-J junction, JL2 is the second J gene segment from the V-J junction). Since the locations of the contigs in the chromosome were unknown they were annotated as if following after the assembled chromosomal sequence. F indicates functional. P indicates pseudogene. Annotations were given a dot (.) between the V family name and the family member gene number instead of a dash (-), as in the annotations for human Ab genes, to minimize confusion with the final annotations of the rhesus Ig loci that will be possible to do when a complete genome assembly is available.

^bClosest matching human germline VH gene was determined via IMGT/V-Quest. JL and CL gene segments were compared to allele *01.

^cHomology (%) between the rhesus and closest matching human germline as determined by IMGT/V-Quest or AlignX

^dRaw sequences are available via www.ensembl.org

Sequences were extracted from genome assembly: MMUL 1.0, Feb 2006, database v. 66.10

Ch10 corresponds to chromosome 10 region: 65,700,000-67,300,000.

CAL corresponds to contig MMUL:1099214728802

CCL corresponds to contig MMUL:1099214729065

CDL corresponds to contig MMUL:1099214790287

CEL corresponds to contig MMUL:1099548049764

CFL corresponds to contig MMUL:1099214733386

CGL corresponds to contig MMUL:1099214725231

Table S3. Kappa germline gene analysis and annotation

Sequence ID ^a	Closest corresponding human IGKV gene ^b	Homology (%) ^c	Sequence	Genomic location ^d
VK4.1	IGKV4-1*01 F	94.9	Gacattgtagtaccagctccagactccctggctgtctctgggagagaggtccaccatcaac tgcaagtcagccagagctctttatcacgctccaacaataagaactctagcctggtagccagcag aaaccaggacaggtcctaaagctctcattatctgggcatctaccgggaatccgggctcctaa ccgattcagtgccagtgatctgggtcagattcactctcaccatcagtgccctcaggctgaagat gtggcagtgattactctcagcagattatagcactctc	Ch13:1
VK5.2	IGKV5-2*01 F	87.1	gaaatgatactcacacagctccggcattgtgtcagcagactccaggagacaaagtcaccatctcc tcagagctggccaagacattgatgatgatgaactggatcaacaggaaaccaggagaagctc tcaaacctatttaaagatgtaactctctctgtttggcaatcccaactcaattcagtgagtgga tgggatagatttaccctgacaattaatagcatgaaatctgaggatactcatattactctgccaac agagggataatcacctct	Ch13:1
VK3.3	IGKV3D-7*01 F	91.0	caagtataattgacacagctccagccaacctgtcttctccagggaagagccactctctctg cagggccagtcagagctttagcagctactagcctggatccagcagaaaccctggcaggtccc aggctctcattcaacagtgctccagcaggccactggcctccagacagagctcagtgccagc ggctgggacagattcaccctcaccatcagcagcctggagcctgaagatgtggagttatcact cctatcagattacagcgggtacc	Ch13:1
VK5.4	IGKV5-2*01 F	92.5	gaaacgatactcacacagctccggcattgtgtcagcagactccaggagacaaagtcaccatctc ctcagagctggccaagacattgatgatgatgaactggatcaacaggaaaccaggagaagc tccaactcatttaaagatgtaactctctctgtttggcaatcccaactcagttcagtgccagc gtaggaaacagatttaccctcacaattaatagtaactcagagctgctcatattactctgtcta caacatgataattccctct	Ch13:1
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VK1.49	IGKV1-27*01 F	91.8	Gacatccagatgaccagctccactccctgcccgtcaccctggagagccggcctccatcct gcccgggacagtcaggcctcctgtagatgtaggatacactattgtagtactgcagaagc ctacactcctctcattctgtagcaggttgcatacaggggtcccactcagttcagtgccagtgat ctgggacagatttcaactcaccatcagcagcctgagcctgaagatttgcactattactgtcga caggattataatcccc	Ch13:2
VK2.50	IGKV2-40*01 F	92.5	Gatattgtagtaccagactccactccctgcccgtcaccctggagagccggcctccatcct tgaggcttagtcagagcctcctggatagtaggatacactattgtagtactgcagaagc caggccagctccacagcctctgatttggctcacaacgggcccctggagtcacagacaggtt cagtgccagtggtcagcagcactgatttcaactgaaatcagcaggggtggagggctgaggatgtg gggttattactgcatgcaaaactcacaactcct	Ch13:2
VK2.51	IGKV2-28*01 F	93.5	Gatattgtagtaccagactccactccctgcccgtcaccctggagagccggcctccatcct gcaggtctagtcagagcctctgcatagtaagtgatacactattgtagtactgcagaagcca ggccagctccacagcctctgatttggctcacaacgggcccctggagtcacagcaggttca gtggcagtggtcagcagcactgatttcaactgaaatcagccgggtggagggctgaggatgtgg gtttattactgctgcaagatatacagcttctc	Ch13:2
VK1.52	IGKV1-12*01 F	90.2	gatatccagatgaccagctccactccctgcccgtcaccctggagagccggcctccatcct gcccggcgagtcagaacattatagtggttagcgtgtagcagcagaaccaggaaagccctta agctcctgactatgctgcaaccagattgaaagtggttccctcggctcagcggcagtggtat gggacagatttcaactcaccatcagcagcctgagcctgaagatttgcactattactgtcaac aggtttagtaacccctc	Ch13:2
VK2.53	IGKV2-40*01 F	92.2	Gatattgtagtaccagactccactccctgcccgtcaccctggagagccggcctccatcct caggtctagtcagagcctctgcatagtgatgatacactattgtagtactgcagaagcc agccagctccacagcctctgatttggctcacaacgggcccctggagtcacagaggttca gtggcagtggtcagcagcactgatttcaactgaaatcagcaggggtggagggctgaggatgtgg gtttattactgctgcaagatatacagcttctc	Ch13:2
VK1.54	IGKV1-27*01 F	91.8	Gacatccagatgaccagctccactccctgcccgtcaccctggagagccggcctccatcact gcccagggagtcaggccttaactatgatttagcctgtagcagcagaaccagggaaacactcct aagcctgactatgagcctcaggttgcagaagtggttccctcctgctcagcggcagtgat ctggacagatttcaactcaccatcagcagcctgagcctgaagatttgcactattactgtcaac	Ch13:2

			attattacagtagccccctcc	
VK1.55	IGKV1-16*01 F	93.2	Gacatccagatgaccagctccatctccctgctgcatctgtaggagacagagtcaccatcactgcccagggagtcagggcattagcaataaattagcctggatcagcagaaaacggggaagcccctaagctcctgatctataagccatccactctgcaaaagtggggtccatcaagggtcagcggcaggtgacitgggacagattcactctcaccatcagcagcctgagcctgaagatttgcaacttattactgtagcaatggtatggtatcc	Ch13:2
VK2.56	IGKV2-40*01 F	92.6	Gatattgtagtagccagactccactctccctgcccacccccggagagccggcctccatctctcaggtctagtcagagctctctggatagtagtgatgatacacatttgattggtactcgcagaagccagggccagcctccacagcccataatctatttttcaagccggcctctggagtcocagacaggttcagtgggcagtgatcaggcaggtattcacactgaaaatcagcgggtggaggtgagtagtggtgggttattactgcatgcaatgtagatgatttcc	Ch13:2
VK1.57	IGKV1-39*01 F	93.9	Gacatccagatgaccagctccatctccctgctgcatctgtaggagacagagtcaccatcactgcccagggcaagtgagaacttaacaacttattacatggatcagcagaaaacagggaaagccccaaagcctctgatctatgctcctcctcctgcaaaagtggggtccatcaagggtcagcggcagtgtagctggagcagatttcaactcaccatcagcagcctgagaggtgcaacttattactgtagcacaatgtagtaccctcc	Ch13:2
VK2.58	IGKV2-29*02 F	91.8	Gatattgtagtagccagactccactctccctgcccagtcaccctggagagccggcctccatctctcaggtctagtcagagcctcctgatagtaggaaatactatttgattggtactacagaagcccagggcagctccacggctcctcaattatagagtttccaacgggttctctggagtcacagacaggttagtgccagtgatcagcagcagatttcaactgaaaatcagcgggtggaaggtgaggtgtaggggttattactgcatgcaagcttcaaaactcctcc	Ch13:2
VK2.59	IGKV2-40*01 F	92.2	Gatattgtagtagccagactccactctccctgcccacccccggagagccggcctccatctctcaggtctagtcagagcctcctcctgatagtaaggaacaactatttgactgtagcctgcagaagccaaagcctctgatctatagggcctcctcaattgggggttccaacagagcctctggagtcocagacaggttcagtgccagtggtcaggcagctgattcacactgaaaatcagcagggtgagggcggaggtgtaggggttattactgcatgcaagcttcaaaactcctcc	Ch13:2
VK2.60	IGKV2-29*02 F	92.9	Gatattgtagtagccagactccactctccctgcccagtcaccctggagagccggcctccatctctcaggtctagtcagagcctcctcctgatagtaaggaatactatttgattggtactcgcagaagcccagggcagctccacggctcctcaatctatagagtttccaacgggttctctggagtcacagacaggttagtgccagtgatcagcagcagatttcaactgaaaatcagcgggtgagggctgaggtgtaggggttattactgcatgcaagcttcaaaactcctcc	Ch13:2
VK1.61	IGKV1-33*01 F	92.5	Gacatccagatgaccagctccatctccctgctgcatctgtaggagacagagtcaccatcactgcccagggcagtgaggtattagcaactggtggcctggatcacaagaaaacagggaaagcccctaagctcctgatctatagggcctcaattggaaacaggggtccatcaagggtcagtggaaggtgacitgggacagatttcaactcaccatcagcagcctgagcctgaagatagcacaatattactgtagcacaagcagataatccctcc	Ch13:2
VK2.62	IGKV2-40*01 F	91.5	Gatattgtagtagccagactccactctccctgcccagtcaccctggagagccggcctccatctctcaggtctagtcagagcctcctcctgatagtaaggaacaactatttgattggtactcgcagaagccagggcagctccacggctcctgatctataaagttaccaatcgggaatcggggtccagacaggttcagtgccagtggtcaggcagagattcacactgaaaatcagcagggtgagcctgaggtgtaggggttattactgcatgcaagctcaaaaagatcc	Ch13:2
JK1	IGKJ1*01	100	gtggacgttcggccaagggaccaaggtggaatcaaac	Ch13:1
JK2	IGKJ2*01	92.3	tgtagcagtttggccaggggaccaaaagtgtagatcaaac	Ch13:1
JK3	IGKJ3*01	94.7	attcactttcggccccgggacaaactggatcaaac	Ch13:1
JK4	IGKJ4*01	100	gctcactttcggcggaggaccaaggtgtagatcaaac	Ch13:1
JK5	IGKJ5*01	100	gatcacttcggccaagggacacagcagctggagattaaac	Ch13:1
CK1	IGKC1*01	91.9	gagcgtggctgcccactctgcttctcctcctccatctgaggtcaggtgaaatcggaaactgctctctgtgctgctgtaataactctatcccagagagggcagcgtaaagtggaaggtgaggtgctcctcaaaaacggglaactcccagagaggtgtagcagagcagggcagcagaagcaaacactacagcctgagcagcaccctgacgctgagcagcagactaccagaggtcacaatgctatgctcggaaagtcacccatcagggcctgagcctgcccctcaccagagcttcaacagagggaggtg	Ch13:1

^aOpen reading frames (ORFs) were annotated based on gene family usage and position relative to the junction between the V and J regions, with the most proximal gene segment receiving number 1 (e.g VK5.2 correspond to family 5, VK ORF number 2 from the V-J junction, JK2 is the second J gene segment from the V-J junction). Since the locations of the contigs in the chromosome were unknown they were annotated as if following after the first assembled chromosomal sequence. F indicates functional. P indicates pseudogene. Annotations were given a dot (.) between the V family name and the family member gene number instead of a dash (-), as in the annotations for human Ab genes, to minimize confusion with the final annotations of the rhesus Ig loci that will be possible to do when a complete genome assembly is available.

^bClosest matching human germline VH gene was determined via IMGT/V-Quest. JK and CK gene segments were compared to allele *01.

^cHomology (%) between the rhesus and closest matching human germline as determined by IMGT/V-Quest or AlignX

^dRaw sequences are available via www.ensembl.org

Sequences were extracted from genome assembly: MMUL 1.0, Feb 2006, database v. 66.10

Ch13:1 corresponds to chromosome 13 region: 89,000,000-90,500,000

Ch13:2 corresponds to chromosome 13 region: 112,900,000-113,700,000

CAK corresponds to contig MMUL:1099548049606

Table S4. Properties of the CD4bs-specific flow cytometric sorts.

Animal	F125	F128
Immunization	2 weeks post imm 5	1 week post imm 5
Probe	gp140-F/ gp140-F-D368R	gp140-F/ gp140-F-D368R
Total PBMC	2552940	521082
Total Memory B cell CD20+IgG+CD27+	102789	6990
Total Memory B cell %	4.0	1.3
Total Memory B cell Env+ CD20+IgG+CD27+gp140-F+	4737	270
Memory B cell Env+ %	4.6	3.9
^a CD4bs Memory B cell CD20+IgG+CD27+ gp140-F+ gp140-F-D368R-	287	34
CD4bs % (of total Env+)	6.1	12.6
Sorted cells	264	29
Productive Ab sequences with matching HC+LC ^b	25 (from 88 wells)	17
Expressed MAbs	Not done	11
Env-specific	Not done	9 (8 unique clones) ^c

^aCD4-binding site directed memory B cell

^bAll RT-PCR sequences were antibody specific

^cGE140 and GE145 were identical clones

Table S5. Binding affinities of vaccine- and infection-elicited MAbs to a panel of Env ligands

CD4bs ligands	gp120			gp120-D368R			Core (V3S)			Stabilized core (2CC)			TriMut core			
	K_D (nM)	on-rate ($M^{-1}s^{-1}$)	off-rate (s^{-1})	K_D (nM)	on-rate ($M^{-1}s^{-1}$)	off-rate (s^{-1})	K_D (nM)	on-rate ($M^{-1}s^{-1}$)	off-rate (s^{-1})	K_D (nM)	on-rate ($M^{-1}s^{-1}$)	off-rate (s^{-1})	K_D (nM)	on-rate ($M^{-1}s^{-1}$)	off-rate (s^{-1})	
NHP MAbs	GE121	9.7	2.8×10^4	2.7×10^{-4}	>5000	NB	NB	0.9	3.2×10^5	2.9×10^{-4}	>8000	NB	NB	4.4	1.7×10^5	7.5×10^{-4}
	GE125	4.2	3.9×10^4	1.7×10^{-4}	247.3	6.7×10^3	1.7×10^{-3}	0.4	3.5×10^5	1.5×10^{-4}	>8000	NB	NB	2.3	1.8×10^5	4.0×10^{-4}
	GE136	13.7	3.9×10^4	5.3×10^{-4}	>5000	NB	NB	1.4	3.2×10^5	4.5×10^{-4}	>8000	NB	NB	4.3	1.7×10^5	7.2×10^{-4}
	GE137	14.8	3.8×10^4	5.6×10^{-4}	66.7	1.7×10^4	1.1×10^{-3}	7.5	2.3×10^5	1.7×10^{-3}	>8000	NB	NB	15.9	1.4×10^5	2.2×10^{-3}
	GE140	7.1	4.6×10^4	3.3×10^{-4}	>5000	NB	NB	1.8	4.0×10^5	7.0×10^{-4}	>8000	NB	NB	3.2	2.0×10^5	6.4×10^{-4}
	GE143	2	2.6×10^4	5.0×10^{-5}	>5000	NB	NB	2	1.6×10^5	3.2×10^{-4}	>8000	NB	NB	5.6	8.0×10^4	4.4×10^{-4}
	GE147	103.4	6.0×10^3	6.5×10^{-4}	>5000	NB	NB	2840	1.3×10^3	3.6×10^{-3}	>8000	NB	NB	>5000	NB	NB
GE148	4.2	5.6×10^4	2.3×10^{-4}	>5000	NB	NB	0.6	5.0×10^5	2.9×10^{-4}	2042	5.6×10^3	1.0×10^{-2}	2	2.3×10^5	4.5×10^{-4}	
Receptor	CD4-Ig	14	3.6×10^4	5.0×10^{-4}	>5000	NB	NB	4.4	1.1×10^5	4.7×10^{-4}	5.7	1.5×10^5	7.5×10^{-4}	812.7	9.5×10^4	7.7×10^{-2}
bNAbs (CD4 bs)	VRC01	9.5	1.8×10^4	1.7×10^{-4}	348.8	1.5×10^4	5.4×10^{-3}	2.7	4.5×10^4	1.2×10^{-4}	0.7	8.3×10^4	0.6×10^{-4}	36.6	1.7×10^4	6.3×10^{-4}
	b12	27.4	9.8×10^4	2.7×10^{-3}	>5000	NB	NB	5.9	4.6×10^5	2.7×10^{-3}	54.7	1.6×10^5	8.8×10^{-3}	18	3.0×10^5	5.4×10^{-3}
	HJ16	643.8	7.7×10^4	5.0×10^{-2}	203.6	5.8×10^4	1.2×10^{-2}	22.4	3.6×10^4	8.1×10^{-4}	182.7	9.4×10^3	1.7×10^{-3}	62.6	2.0×10^4	1.2×10^{-3}
non- bNAbs (CD4bs)	b6	1.2	8.3×10^4	1.0×10^{-4}	3.8	7.0×10^4	2.7×10^{-4}	0.5	5.4×10^5	2.5×10^{-4}	>8000	NB	NB	0.5	3.5×10^5	1.7×10^{-4}
	b13	17.4	2.7×10^4	4.8×10^{-4}	>5000	NB	NB	7.4	7.6×10^4	5.6×10^{-4}	2151	3.5×10^3	7.4×10^{-3}	13.5	6.8×10^4	9.1×10^{-4}
	F105	19.1	7.0×10^4	1.3×10^{-3}	>5000	NB	NB	7.8	5.0×10^5	3.9×10^{-3}	>8000	NB	NB	17.6	2.7×10^5	4.7×10^{-3}

NB, No binding observed

Affinity (KD) was calculated by dividing the on-rate with the off-rate, as determined by Bio-Layer interferometry

Table S6. Antibody conjugates used for flow cytometric sorting of memory B cells.

Antibody Conjugate	Manufacturer	Clone name
CD3 APC-Cy7	BD Pharmingen	SP34-2
CD8 Pacific Blue	BD Pharmingen	RPA-T8
CD14 Qdot 605	Vaccine Research Center, NIH	M5E2
CD20 PE-Alexa Fluor 700	Vaccine Research Center, NIH	2H7
CD27 PE-Cy7	BD Pharmingen	M-T271
IgG FITC	BD Pharmingen	G18-14
IgM PE-Cy5	BD Pharmingen	G20-12