

A comprehensive analysis of the germline and expressed TCR repertoire in White Peking duck

**Zhi Yang^{1,3,+}, Yi Sun^{2,+}, Yonghe Ma^{1,+}, Zhenrong Li¹, Yu Zhao⁴, Liming Ren¹,
Haitang Han¹, Yunliang Jiang^{2,*}, Yaofeng Zhao^{1,*}**

1 State Key Laboratory of Agrobiotechnology, College of Biological Sciences, China Agricultural University, Beijing, 100193, China

2 Shandong Provincial Key Laboratory of Animal Biotechnology and Disease Control and Prevention, College of Animal Science and Veterinary Medicine, Shandong Agricultural University, Taian, 271018, China

3 Beijing Advanced Innovation Center for Food Nutrition and Human Health, College of Food Science and Nutritional Engineering, China Agricultural University, Beijing, 100193, China

4 National Laboratory of Biomacromolecules, Institute of Biophysics, Chinese Academy of Sciences, Beijing, 100101, China

* yaofengzhao@cau.edu.cn; yljiang723@aliyun.com.

⁺ These authors contributed equally to this work.

A

nonamer

heptamer

Jα1: atcttttgttaaagctctttgtcacagtgTAAGTCCATACGTGCCTATGAAACACTCAGTTTGGAGAGGGGACAAGGCTGACTGTTCTTCCAA
N S I R A Y E T L S F G E G T R L T V L P

Jα2: agtttatgttaaagcaccttatcacagtgTACTTGGTACTTATGGAAGTTCACTTTTGGCGGAGGAACTCGCATGTCTGTGCTTCCAA
L G T Y G K F T F G G G T R M S V L P

Jα3: cgtttttgttagtggtgacgtgtcaactgtgTGACTTCAGTATCCAACTGGAAGTCACCTTTGGAAGTGAACACAGCTGGTAGTGAAACCTG
T S V S N W K V T F G S G T Q L V V K P

Jα4: gatttttgtaatgggagggaaatgctgtgTGAATCTGGCTTCAGTGACAAGCTGACCTTTGGCTCAGGAACAGGCTGTCCGTCCAACCAA
E S G F S D K L T F G S G T R L S V Q P

Jα5: gctttttgtaatgggagggaatgctgtgTGACTATGGAACCAACAGGCTGACATTTGGCTCAGGACCAGACTGTCCGTCCAACCAA
D Y G T N R L T F G S G T R L S V Q P

Jα6: catttttgtaatgagatgtgccacagtgCGTACACTGAGGGCAAAGTCACCTTTGGAAGGAAGTGTGCTTTCTGTAGTTCAG
Y T E G K V T F G K G T V L S V V P

Jα7: gctttttgttaggggagggaaatgctgtgTGACTACAGCGGCGACAAGCTGACCTTTGGCTCAGGACCAGGCTGTCTGTCTTACCAA
D Y S G D K L T F G S G T R L S V L P

Jα8: catttgtgtaatggcctttgttgctgtgGGTGTGAATGGAACAGGCTCACCTTTGGAGCTGGATCAAAGCTTTGTGTAAAGCCTC
G A E W N R L T F G A G S K L C V K P

Jα9: gctttttgttagtggtgagggaaatgctgtgTGAATGACTTAAACAAGCTGACTTTTGGCTCAGGACCAGGCTGTCCATCCAACCAA
N D L N K L T F G S G T R L S I Q P

Jα10: catttattttaatggacattgttgctgtgAGTGCTGTCTTGAACAGGCTGAACTTTGGAGCAGGAACAAAGCTTTGTGTAAATACCAG
S A V L N R L N F G A G T K L C V I P

Jα11: ggtttttgttaatggaaggaaatgctgtgTGGCTCTAGCTCTTCATTCGGCAAATTGACCTTTGGCTCGGGGACCAGGCTGTCTGTCCAACCAA
G S S S S F G K L T F G S G T R L S V Q P

Jα12: ggttcttgtgtgtggcaaaaagcaactgtgTGAAGTACGGCAAGATCACCTTTGGGAGCGGAACACGACTTCAGGTTTGCCTA
N Y G K I T L G S G T R L Q V L P

Jα13: gctttttgttaatgggagggaaatgctgtgTGACTATGACTACACCAACAACTGACCTTTGGCTCAGGACCAGGCTGTCCGTCTTACCAA
D Y D Y T N K L T F G S G T R L S V L P

Jα14: catttttgttaatgagacgtgccacagtgAGTTAAATGCGCGCACAGTCACCTTTGGGAAAGGAAGTGTGCTTTTCACTGTGTCCAG
L N A R T V T F G K G T V L S V V P

Jα15: gctttttgttaataggagggaaatgctgtgTGGCACTGGCTCTACATACGGCAAATTGACCTTTGGCTCAGGACCAGGCTGTCTGTCCAACCAA
G T G S T Y G K L T F G S G T R L S V Q P

Jα16: agttcttgttgaggcaaaaagcaactgtgTGAAGTACGACAAGTTACATTTGGAAGGGAACACGACTTCAGGTTTGCCTA
N Y D K F T F G K G T R L Q V L P

Jα17: actttttgttaatgggagtacatgctgtgTGAGTGGCAACTACAAGCTGACCTTTGGCTCAGGAACAGGCTGTCTGTCTTACCAA
S G N Y K L T F G S G T R L S V L P

Jα18: gctttttgttaatgggagggaaatgctgtgTGACACTGGCTACAACAAGCTTACATTTGGCTCAGGACTAGGCTGTCTGTCTTACCAA
D T G Y N K P T F G S G T R L S V L P

Jα19: gctttttgttagtggtgagggaaatgctgtgTGATTTTGGATCCTTCAACAAGCTGATCTTTGGCTCAGGAACAGGCTGTCCGTCTTACCAA
D F G S F N K L I F G S G T R L S V L P

Jα20: gctttttgttaatgggagggaaataactgtgTGGCTATGGCTCTGCATACGGCAGACCAACCTTTGGCACAGGAACAGGCTTTCTGTCCAACCAA
G Y G S A Y G R P T F G T G T R L S V Q P

Jα21: gctttttgttaatgggagggaaatgctgtgTGACTCTGGCTATGGCAACAAGCTGACCTTTGGCTCAGGAACAGGCTGTCCGTCTTACCAA
D S G Y G N K L T F G S G T R L S V L P

Jα22: ggtttttgttagtggtatgtgtcaactgtgTGACTTCAACGTCCACCTGGAAGCCACCTTTGGAAGTGGGACACAGCTGGTGGTGAAACCTG
T S T S T W K A T F G S G T Q L V V K P

Jα23: gctttttgttaatgggagggaaatgctgtgTGAATCTGGCTTCACCAAACTGACCTTTGGCTCAGGACCAGGCTGTCCGTCTTACCAA
E S G F T K L T F G S G T R L S V L P

Jα24: gctttttgtgtgtgggaagaaatgctgtgTCACTACAGCAGTGACAAGCTGACCTTTGGCTCAGGACCAGGCTGTCCGTCTTACCAA

H Y S S D K L T F G S G T R L S V L P

Jα25: gctttttgtagggggaggaaatattgtgTGACTACAGCGGTGACAAGCTGACCTTTGGCTCAGGGACCAGGCTGTCTGTCTTACCAA
D Y S G D K L T F G S G T R L S V L P

Jα26: catttgtgtaatggcctttggtgctgtgGGTGCTGACTGGAACAGGCTCACCTTTGGAGCTGGAACAAAGCTTTGTGTAAAGCCTC
G A D W N R L T F G A G T K L C V K P

Jα27: catttttgtaatgagacgtgccattgtgTGTCCAATGCGTATGCAGTCACCTTTGGAAAAGGAAGTGTGCTTTCAGTTGTACCAG
S N A Y A V T F G K G T V L S V V P

Jα28: gctttttgtaatgggaggaaatgctgtgTGGCTATGGCTCTGGATATGACAGAATGACTTTTGGCTCAGGAACCAGGCTGTCTGTCCAACCAA
G Y G S G Y D R M T F G S G T R L S V Q P

Jα29: agttcttgttgaggcaaaaagcaactgtgTGAACTACGAGAAGCTCACATTTGGGAAGGGAACACGACTTCAGTTTTGCCTA
N Y E K L T F G K G T R L Q V L P

Jα30: aacttttgtaatgggagtaaatgctgtgTGAGTGGCAACTACAAGCTGACCTTTGGCTCAGGAACCAGGCTGTCTGTCTTACCAA
S G N Y K L T F G S G T R L S V L P

Jα31: gctttttgtaatgggaggaaatgctgtgTGACACTGGCTACAACAAGCCTACATTTGGCTCAGGGACTAGGCTGTCTGTCTTACCAA
D T G Y N K P T F G S G T R L S V L P

Jα32: gctttttgtagggggaggaaatgctgtgTGATTCTGGATCCTTAAACAAGCCGACCTTTGGCTCAGGAACCAGGCTGTCCGTCTTACCAA
D S G S L N K P T F G S G T R L S V L P

Jα33: cgtttatttaatggacattgttgctgtgAGTGCTGTCTTGAACAGGCTGAACTTTGGAGCAGGAACAAAGCTTTGTGTAATACCAG
S A V L N R L N F G A G T K L C V I P

Jα34: gctttttgtaatgggaggaaatactgtgTGGCTATGGCTCTGCATACGGCAGACCAACCTTTGGCAGGGACCAGGCTGTCTGTCCAACCAA
G Y G S A Y G R P T F G T G T R L S V Q P

Jα35: gctttttgtaatgggaggaaatgctgtgTGACTTTGGCTCTGGCAACAAGCTGACCTTTGGCTCAGGAACCAGGCTGTCCGTCTTACCAA
D F G S G N K L T F G S G T R L S V L P

Jα36: ggtttttgttagtggatgtgttactgtgTGACTTCAACGTCCACCTGGAAAGCCACCTTTGGAAGTGGGACACAGCTGGTGGTAAACCTG
T S T S T W K A T F G S G T Q L V V K P

Jα37: gctttttgtaatgggaggaaatgctgtgTGAATCTGGCTTCACCAAACTGACCTTTGGCTCAGGGACCAGGCTGTCCGTCTTACCAA
E S G F T K L T F G S G T R L S V L P

Jα38: gctttttgttggtggagaaatgctgtgTCACTACAGCAGTGACAAGCTGACCTTTGGCTCAGGGACCAGGCTGTCCGTCTTACCAA
H Y S S D K L T F G S G T R L S V L P

Jα39: catttgtgtaatggcctttggtgctgtgGGTGCTGAATGGAACAGGCTCACCTTTGGAGCTGGAACAAAGCTTTGTGTAAAGCCTC
G A E W N R L T F G A G T K L C V K P

Jα40: catttttgtaatgagacgtgccattgtgTGTCCAATGCGTATGCAGTCACCTTTGGAAAAGGAAGTGTACTTTCAGTTGTACCAG
S N A Y A V T F G K G T V L S V V P

Jα41: ggtttttgtaatgggaggaaatggtgtgTGGCTCTGGCTCTTCATATGGCAAATTGACCTTTGGCTCAGGGACCAGGCTGTCTGTCCATCCAA
G S G S S Y G K L T F G S G T R L S V H P

Jα42: gctttttgtaatgggaggaaatgctgtgTGACTAACTTATACAAGCTGACTTTTGGCTCAGGGACCAGGCTGTCTGTCTTACCAA
T N L Y K L T F G S G T R L S V L P

Jα43: gctttttgtagtgaggagaaatgctgtgTGATTCTGGATCCTACAACAAGCTGACCTTTGGCTCAGGAACCAGGCTGTCTGTCAAACCAA
D S G S Y N K L T F G S G T R L S V K P

Jα44: agtttttgtaatgaaaggaaatggtgtgTGGCTCTGGCTCTTCATATGGCAAATTGACCTTTGGCTCAGGGACCAGGCTGTCTGTCCATCCAA
G S G S S Y G K L T F G S G T R L S V H P

Jα45: catttttgtaatgagacataccacagtgAGTTAAATGCACGCACAGTCACCTTTGGGAAAAGGAAGTGTGCTTTCAGTTGTCCAG
L N A R T V T F G K G T V L S V V P

Jα46: gctttttgtaatgggaggaaatgctgtgTGGCTATGGCTCTGGATATGACAGACTGACTTTTGGCTCAGGAACCAGGCTGTCTGTCCAACCAA
G Y G S G Y D R L T F G S G T R L S V Q P

Jα47: agttcttgttgaggcaaaaagcaactgtgTGAACTACGACAAGTTCACATTTGGGAAGGGAACACGACTTCAGTTTTGCCTA
N Y D K F T F G K G T R L Q V L P

Jα48: gctttttgtaatgggagtacatgctgtgTGAGTGGCAACTACAAGCTGACCTTTGGCTCAGGAACCAGGCTGTCTGTCTACCAA
S G N Y K L T F G S G T R L S V L P

Jα49: gctttttgtaatgggaagaaatgctgtgTGACACTGGCTACAACAAGCTGACCTTTGGCTCAGGGACTAGGCTGTCTGTCTACCAA
D T G Y N K L T F G S G T R L S V L P

Jα50: gctttttgtagggggaggaaatgctgtgTGACTGGCAACAACAAGCTGACCTTTGGCTCAGGAACCAGGCTGTCCGTCTACCCA
T G N N N K L T F G S G T R L S V L P

Jα51: cattttattaatggacattgttgctgtgAGTGCTGTCTTGAACAGGCTGAACTTTGGAGCAGGAACAAAGCTTTGTGTAAAGCGTG
S A V L N R L N F G A G T K L C V K P

Jα52: gctttttgcaatgggaggaaatactgtgTGGCTATGGCTCTGCATACAACAACCAACTTTGGGTCAGGGACCAGGCTTTCTGTCCAACCAA
G Y G S A Y N K P T F G S G T R L S V Q P

Jα53: gctttttgtaatgggaggaaatgctgtgTGACTTTGGCTCTGGCAACAAGCTGACCTTTGGCTCAGGAACCAGGCTGTCCGTCTACCAA
D F G S G N K L T F G S G T R L S V L P

Jα54: catttgtgtagtggctctttgttgctgtgAGTAATATTTTGAACAGGCTCATCTTTGGAGCTGGAACAAACTTTGTGTAAACCGTG
S N I L N R L I F G A G T K L C V N R

Jα55: catttgtgtagtggctctttgttgctgtgAGTAATATTTTGAACAGGCTCATCTTTGGAGCTGGAACAAACTTTGTGTAAACCGTG
S N I L N R L I F G A G T K L C V N R

Jα56: attttttgtaatgagatgttccacagtgTATACAATGCGGGCAAAGTCACTTTTGGAAAAGGAACTGTGCTTTCAGTTGTACCAG
Y N A G K V T F G K G T V L S V V P

Jα57: gctttttgtaatgggtggaaatgctgtgCGACTATGGGAACAACAACCAACTGACCTTTGGCTCAGGGACCAGGCTGTCTGTCCAACCAA
D Y G N N K L T F G S G T R L S V Q P

Jα58: catttttgtaatgagatatgccacagtgTGTATGATGACCGCACAGTCACTTTTGGAAAAGGAACTGTGCTTTCAGTTGTACCAG
Y D D R T V T F G K G T V L S V V P

Jα59: tctttttgtaatgggaagaaatgctgtgTGGCTCTAGCTCTGGATATGGCAAATAAAGCTTTGGCTCTGGAACCAGGCTGTCTGTCCATCCAA
G S S S G Y G K L N F G S G T R L S V H P

Jα60: gatttttgtaatgtgaggaaatgctgtgTGACTATGGGAACATAAAGCTGACCTTTGGCTCAGGGACCAGGCTGTCCGTCCAACCAA
D Y G N Y K L T F G S G T R L S V Q P

Jα61: gctttttgtaatgggtggaaatgctgtgTGTTTGGCTACAGCCAGCTGACTTTTGGCTCAGGGACCAGGCTGTCCGTCCAACCAA
F G Y S Q L T F G S G T R L S V Q P

Jα62: cttttgcataaatggtatttgttactgtgAGTGCTGACAGTAAGACGCTCACCTTTGGAGCTGGAACAAAGGTTTGTGTAAAGCGTC
S A D S K T L T F G A G T K V C V K P

Jα63: tttttttgttatgggaggaaatgctgtgTGGCTATGGCTCTGGATATGGCAAAGCTGACCTTTGGCTCAGGGACCAGGCTGTCTGTCCAACCAA
G Y G S G Y G K L T F G S G T R L S V Q P

Jα64: ggtttttgttggcttgtttttcatttgtTGAATGTTGGCTATACCATCATCTTTGGAAAAGGGACAAAGCTTCTGTGTAAACCAA
N V G Y T I I F G K G T K L L V K P

Jα65: ccattttgtaaggacctgtcacacagtgCTGATTCTGGAGGATGGGGAAAATATACATGGGGGAGTGAACAAAAGCTTCTGTGTGCCACG
D S G G W G K Y T W G S G T K L L V A P

Jα66: gatttttgtcatggcaacaaacacagtgTGTCTTTGGATACCTACAAGCTAACCTTTGGAGATGGAACAAGGCTCATGGTAAACCAA
S L D T Y K L T F G D G T R L M V K P

Jα67: ggatatgttagaggcctgtgccatttgtTAACACGGTTACAAATTTACATTTGGATCTGGGACAAGACTTCTGGTTCTGCCAG
N Y G Y K F T F G S G T R L L V L P

Jα68: catttttgtagtgattggcatcagtgtgCCAATCAGGGATATGTGAACTGGCATTTGGAGCTGGCACCCAAGCTTCTGTGTATCCCAA
N Q G Y V K L A F G A G T Q L L V I P

B

[illegible]

C

[illegible]

D

nonamer heptamer

J_V1: **gcttattg**caagtcaaaaca**tagtgtg**GACCACATGGATTAATACTTCGGTACAGGAAGCTAATTATCTCCG
T T W I K Y F G T G T K L I I S

J_V2: **agatattg**ctaagtagtatca**gactgtg**GGATGCTGATGTTAAATATTTGGAAGCTGGAAGCTAAGCTTATTGTTTCAG
D A D V K I F G T G T K L I V S

J_V3: **tgttattg**caagactttatg**cactgtg**TCTGGTTATTACTACAAAGTGTTTGGCACCGGTACAAAGCTCATCGTGTCAG
S G Y Y Y K V F G T G T K L I V S

J_V4: **ggtttgtgt**aaaggaaatatag**cagtgtg**GGCAATCTGGTCTTTGGCACAGGCACTAAACTCATCGTTTCCA
G N L V F G T G T K L I V S

J_V5: **aatttgtgt**aaaggcaatatag**cagtgtg**GGCAATCTGGTCTTTGGCACAGGCACTAAACTCATCGTTTCCA
G N L V F G T G T K L I V S

E

nonamer		heptamer		heptamer		nonamer	
D _δ 2:	<u>actttttgt</u>	aactaagtatat	<u>cactgtg</u>	TTGAGAACTTGGAGTAG	<u>cacaata</u>	gcacaaacactctaaggcctcat	<u>acaaaaacc</u>
				L R T W S			
				. E L G V			
				E N L E .			
J _δ 2:	<u>tgttttctg</u>	actatgcagaaa	<u>cactgtg</u>	GAAACAGACAAGCTTGTATTGGAAGTGGGATTGCTTCTCAGTTGAACCAA			
				E T D K L V F G S G I A F S V E P			

Supplementary Figure S1 Nucleotide and deduced amino acid sequences of duck D and J gene segments, J α segments (A), D δ and J δ segments (B), D β and J β segments (C), J γ segments, and D and J segments in the TCR δ 2 locus (E).

A

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<-----FR1-IMGT-----><CDR1-><-----FR2-IMGT-----><CDR2-><-----FR3-IMGT----->

Va1.2 : HAQ-DSVVQFAQETAIQVGHNATLHCNFSSTSSSLPYIFWYQQHLTQSPQFLQVSKFKPHVHSERISSVLSMENSQVLLHVQDAKLQDSAVYLC
Va1.3 : HAQKDSVVQFAQETAIQVGHNATLHCNFSSTSTSPYIFWYQQHLTQSPQFLQVSKFKPHVHSERISSVLSMENSQVLLHVQDAKLQDSAVYLC
Va1.4 : HAQKDSVVQFAQETAIQVGHNATLHCNFSSTSTSPYIFWYQQRLTQSPQFLQVSKFKPHVHSERISSVLSMENSQVLLHVQDAKLQDSAVYLC
Va1.5 : HGQKDSVVQFAQETAIQVGHNATLHCNFSSTSFSAPIYFWYQQRLTQSPQFLQVSKFKPHVHSGRISVLSMENSQVLLHVQDAKLQDSAVYLC

Va2.1 : AAGRAQVQQ-EPWAQTTEGTGINIACSHPNIQSNDIYIYWRQFPFGQPAFLVLAQSGSRDVTDPAGRLSVAGDRRSSTLLLTQPRLRDAAVYYC
Va2.2 : AAGRAQVQQ-EPWSQTREGSGIDIACSHPNIQSNDIYIYWRQFPFGQPAFLVLAQSGSRDVTDPAGRLSVAGDRRSSTLLRTRPLRDAAVYYC
Va2.3 : AAGRAQVQQ-EPWAQTREGSGIDIACSHPNIQSNDIYIYWRQFPFGQPAFLVLAQSGSRDVTDPAGRLSVAGDRRSSTLLRTRPLRDAAVYYC
Va2.4p : AAGRAQVQQ-EPWAHTTEGTGINIACSHPNIQSNDIYIYWRQFPFGQPAFLVLAQSGSRDVTDPAGRLSVAGDRRSSTLLLT*PRLRDAAVYYC
Va2.5 : AVCRAQVQQ-EPWAETREGTGINITCSHPNMQTGYSIYWRHLPGQGPTFLVFGTRGSNALRDLPGWLVAADRSSALWLTDPRLRDAAVYYC
Va2.6 : AVCRAQVQQ-EPRAQTTEGTGINITCSHPNMQTGYSIYWRHLPGQGPTSLVFGTRGSNPLRDLPGWLVAADRSSALWLTDPRLRDAAVYYC
Va2.7 : AVCRAQVQQ-EPWAETRENTGINITCSHPNIQTGEVIYWRHLPGQGPAFLVLAQSGSRDVTDPAGRLSVAGDRRSSTLLRTRPLRDAAVYYC
Va2.8p : AAGRAQVQQ-EPRAQTTEGTGINIACSHPNIQSNDIYIYWR*PFGREPFLVWVAYSQSGKDVNRNPAAGRLSVTGDRSSALWLTDPRLRDAAVYYC
Va2.9 : AVCRAQVQQ-EPWAQTTEGTGINITCSHPNIQIGDSIYWRHVPFGQGPTFLVLGTGKSNPLRDLPGWLVAADRSSALWLTDPRLRDAAVYYC
Va2.10 : AVGRAQVQQ-EPWAETTEGTGINITCSHPNIQTGEVHILPGQGPAFLVFGTRGSRALTDLPGWLVAADRSSALWLTDPRLRDAAVYYC
Va2.11 : AVCRAQVQQ-EPQAQTTEGTGINITCSHPNMQTGYSIYWRHLPGQGPTFLVFGTRGSNALRDLPGWLVAADRSSALWLTDPRLRDAAVYYC
Va2.12 : AVCRAQVQQ-EPWAETREGTGINITCSHPNIQTGEVHILPGQGPAFLVLAQSGSRDVTDPAGRLSVAGDRRSSTLLRTRPLRDAAVYYC
Va2.13 : AVCRAQVQQ-EPRAQTTEGTGINITCSHPNIQTGEVIYWRHLPGQGPAFLVLAQSGSRDVTDPAGRLSVAGDRRSSTLLRTRPLRDAAVYYC
Va2.14 : AAGRAQVQQ-KPWAQTREGTGINIACSHPNIQSFDIYIYWRQFPFGREPFLVLAQSGSRDVTDPAGRLSVAGDRRSSTLLRTRPLRDAAVYYC
Va2.15 : AAGRAQVQQ-EPRAQTTEGTGINIACSHPNIQSYDIYIYWRHLPGRPAFLVLAQSGSRDVTDPAGRLSVAGDRRSSTLLRTRPLRDAAVYYC
Va2.16 : AVCRAQVQQ-EPWAQTDTSTGINITCSHPNIQTGEVIYWRHLPGQGPAFLVLAQSGSRDVTDPAGRLSVAGDRRSSTLLRTRPLRDAAVYYC
Va2.17 : AAGRAQVQQ-EPWAETREGSGIDIACSHPNIQSNDIYIYWRQFPFGQPAFLVLAQSGSRDVTDPAGRLSVAGDRRSSTLLRTRPLRDAAVYYC
Va2.18 : AAGRAQVQQ-EPWAQTTEGTGINIACSHPNIQSNDIYIYWRQFPFGQPAFLVLAQSGSRDVTDPVGRLSVAADRSSSTLLRTRPLRDAAVYYC
Va2.19 : AVCRAQVQQ-EPRAQTREGSGIDITCSHPNIQSYDIYIYWRQFPFGREPFLVLAQSGSRDVTDPAGRLSVAGDRRSSTLLRTRPLRDAAVYYC
Va2.20 : AAGRAQVQQ-EPRAQTREGSGINIACSHPNIQSYDIYIYWRQFPFGREPFLVLAQSGSRDVTDPAGRLSVAGDRRSSTLLRTRPLRDAAVYYC

Va3.1p : AMGQTSVTQEGGQVTVKQKETFTTCTYQIPSLYA-LY*YQKKGQAPQLVIYHTRAG-TKQSGRFTMELNTVKGSSILRLKEVELSDSALYLC
Va3.2 : AMGQTSVTQEGGQVTVKQKETFTTCTYKSSYFYA-LYWYQKKGQAPQLVIYHTSAG-TKQSGRFTMELNTVKGSSILRLKEVELSDSALYLC
Va3.3 : AMGQTSVTQEGGQVTVKQKETFTTCTYQIPSLYG-LYWYQKKGQAPQLLAYITTTG-SMQNIHFTMEMNTVKGSSILQLKEAELSDSALYLC
Va3.4 : AMGQTSVTQEGGQVTVKQKETFTTCTYQIPTFYA-LYWYQKKGQAPQLVYHTEAG-TKQSGRFTTGLNTVKGSSILRLKEVELSDSALYLC
Va3.5 : TTGQVSVTQEGGQVSVQGNFTQTNCTYETSSFNQ-LLWYQKKGQAPQLITHRAIAG-TKQKDRFTTELNTKGSSSVLRLKEVELSDSALYLC
Va3.6 : ATGQVSVTQEGGQVSVQGNFTQTNCTYETSNFNG-LLWYQKKGQAPQRISSYQAGAG-IKQIDRFTTELNTSKSSSVLQLKEVELSDSALYLC
Va3.7 : IMGQVSVTQEGGQVTVQGNFETTTCTYETSYFRG-LLWYQKKGQAPQLLSNQAIAG-TKQKDRFTTELNTTEKSSSVLQLKEVELSDSALYLC
Va3.8 : TMGQVSVTQEGGQVTVQGNFTQTNCTYQSSNFQ-LFWYQKKGQAPQLITRQAGAG-TKQKDRFTTELNTTEKSSSVLQLKEVELSDSALFFC
Va3.9 : TTGQVSVVQEGGQVTVQGNFTQTNCTYETSNFNG-LLWYQKKGQAPQLISYQAGAG-TKQKDRFTTELNTTEKSSSVLQLKEVELSDSALFFC
Va3.10 : TMGQLSVTQEGGQVTVQGNFTQTHCTYQSSSTPDA-WLWYQKKGQAPQRISSYQAGAG-TKQKDRFTTELNTTEKSSSVLCLKEVEPDSALYFC
Va3.11p : TMGQVSVKQEGGQVTVQGNFTQTNCTYQSSNFQ-LFWY*QKKGQVQQLISHQGIQV-TKQKDRFTTELNTTEKSSSVLRLKEVELSDSALYLC
Va3.12 : TMGQVSVTQEGGQVSVQGNFTQTNCTYETSYFQ-LLWYQKKGQAPQLITHQAVAG-TKQKDRFTTELNTKGSSSVLHLKEVELSDSALYLC
Va3.13 : TTGQVSVTQEGGQVSVQGNFTQTNCTYETSNFNG-LLWYQKKGQAPQRISSYQAGAG-TKQIDRFTTELNTTEKSSSVLRLKEVELSDSALYFC
Va3.14 : TTGQVSVTQEGGQVSVQGNFTQTNCTYQSSSTPDA-WLWYQKKGQAPQLISYQAGAG-TKQKDRFTTELNTSEKSSSVLRLKEVELSDSALYFC
Va3.15 : TMGQLSVTQEGGQVTVQGNFTQTHCTYQSSSTPDA-WLWYQKKGQAPQLVYHTSAG-TKQSGRFTMELNTTEKSSSVLRLKEVELSDSALYLC
Va3.16 : -MGQTSVTQEGGQVTVKQKETQATCTYQIPSLYA-LYWYQKKGQAPQLVIYHTSAG-TKQSGRFTMELNTTEKSSSVLRLKEVELSDSALYLC
Va3.17 : TVEQVSVTQEGGQVSVQGNFTQTNCTYETSNFNG-LLWYQKKGQAPQRISSYQAGAG-TKQKDRFTTELNTKGSSSVLHLKEVELSDSALYLC
Va3.18 : IMGQVSVTQEGGQVSVQGNFTQTNCTYETSYFRG-LLWYQKKGQAPQLLSNQAIAG-TKQKDRFTTELNTTEKSSSVLRLKEVELSDSALYLC
Va3.19 : TTGQVSVTQEGGQVTVQGNFTQTNCTYETSRFNG-LLWYQKKGQAPQRISSYQAGAG-TKQKDRFTTELNTTEKSSSVLRLKEVELSDSALYFC
Va3.20 : TTGQVSVTQEGGQVTVQGNFTQTNCTYQSSSTPDA-WFWYQKKGQAPQRISSYQAGAG-TKQKDRFTTELNTTEKSSSVLRLKEVELSDSALYFC
Va3.21 : TTGQVSVTQEGGQVTVQGNFTQTNCTYETSNFNG-LLWYQKKGQAPQLITRQAGAG-TKQKDRFTTELNTTEKSSSVLHLKEVELSDSALYFC
Va3.22 : TMGQVSVTQEGGQVSVQGNFTQTNCTYQSSNFYQ-LFWYQKKGQAPQRISSYQAGAG-TKQKDRFTTELNTSKSSSVLQLKEVELSDSALYLC
Va3.23 : TTGQVSVTQEGGQVTVQGNFTQTNCTYETSRFYQ-LFWYQKKGQAPQLISYQAGAG-TKQKDRFTTELNTTEKSSSVLRLKEVELSDSALYLC
Va3.24 : TTGQVSVTQEGGQVTVQGNFTQTNCTYETSNFDG-LFWYQKKGQAPQLITRQAGAG-TKQKDRFTTELNTTEKSSSVLQLKEVELSDSALYFC

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B

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<-----FR1-IMGT-----><CDR1-><-----FR2-IMGT-----><CDR2-><-----FR3-IMGT----->

Vb1 : VCAELMLVESGGRLR-VPGESVHLSCWGSDFNFAIYSVLWYRQALGGSQWLWLYIN-PDSSYIRYGSVAVKGRATASRDNSKSKTALTILNHLQDSARYFC

Vb2.1 : VWAQWRLVESGGGVK-TPGNSVHLSCWGSDFNFAIRYQAPGGSLWVWSFIN-TYGSTVEYKAVKGRASVSRDNSQSKSSLSLSLVPQDSAHYFC
Vb2.2 : VWAQWRLVESGGGLR-APGDSVHLSCWGSDFNFAIRYQAPGGSLWVWSFIN-TYGSTVEYKAVKGRASVSRDNSQSKSSLSLSLVPQDSAHYFC
Vb2.3 : VWTQSLSVESGGGLR-APGESVHLSCWGSDFNFAIRYQAPGGSLWVWSFIN-TYGSTVEYKAVKGRASVSRDNSQSKSSLSLSLVPQDSAHYFC
Vb2.4 : VWTQSLSVESGGGLR-APGDSVHLSCWGSDFNFAIRYQAPGGSLWVWSFIN-TYGSTVEYKAVKGRASVSRDNSQSKSSLSLSLVPQDSAHYFC
Vb2.5 : VWAELKLVESGGGLR-APGDSVHLSCWGSDFNFAIRYQAPGGSLWVWSFIN-TYGSTVEYKAVKGRASVSRDNSQSKSSLSLSLVPQDSAHYFC
Vb2.6p : VWAQWRLVESGGGLQ-AAGNSVHLSCWGSDFNFAIRYQAPGGSLWVWSFIN-TYGSTVEYKAVKGRASVSRDNSQSKSSLSLSLVPQDSAHYFC
Vb2.7 : VWAELKLVESGGGLR-APGDSVHLSCWGSDFNFAIRYQAPGGSLWVWSFIN-TYGSTVEYKAVKGRASVSRDNSQSKSSLSLSLVPQDSAHYFC
Vb2.8 : VWTQSLSVESGGGLR-APGDSVHLSCWGSDFNFAIRYQAPGGSLWVWSFIN-TYGSTVEYKAVKGRASVSRDNSQSKSSLSLSLVPQDSAHYFC
Vb2.9 : VWAQWRLVESGGGLR-APGDSVHLSCWGSDFNFAIRYQAPGGSLWVWSFIN-TYGSTVEYKAVKGRASVSRDNSQSKSSLSLSLVPQDSAHYFC
Vb2.10 : VWAQWRLVESGGGLR-APGDSVHLSCWGSDFNFAIRYQAPGGSLWVWSFIN-TYGSTVEYKAVKGRASVSRDNSQSKSSLSLSLVPQDSAHYFC
Vb2.11 : -AAQWKLLESGGGLR-APGDSVHLSCWGSDFNFAIRYQAPGGSLWVWSFIN-TYGSTVEYKAVKGRASVSRDNSQSKSSLSLSLVPQDSAHYFC
Vb2.12 : VWAELKLVESGGGLR-APGDSVHLSCWGSDFNFAIRYQAPGGSLWVWSFIN-TYGSTVEYKAVKGRASVSRDNSQSKSSLSLSLVPQDSAHYFC
Vb2.13 : VWTQSLSVESGGGLR-APGDSVHLSCWGSDFNFAIRYQAPGGSLWVWSFIN-TYGSTVEYKAVKGRASVSRDNSQSKSSLSLSLVPQDSAHYFC
Vb2.14 : VWAQWRLVESGGGLR-APGDSVHLSCWGSDFNFAIRYQAPGGSLWVWSFIN-TYGSTVEYKAVKGRASVSRDNSQSKSSLSLSLVPQDSAHYFC
Vb2.15 : VWAQWRLVESGGGLR-APGDSVHLSCWGSDFNFAIRYQAPGGSLWVWSFIN-TYGSTVEYKAVKGRASVSRDNSQSKSSLSLSLVPQDSAHYFC
Vb2.16 : -VWAELKLVESGGGLR-APGDSVHLSCWGSDFNFAIRYQAPGGSLWVWSFIN-TYGSTVEYKAVKGRASVSRDNSQSKSSLSLSLVPQDSAHYFC
Vb2.17 : IWAELKLVESGGGLR-APGDSVHLSCWGSDFNFAIRYQAPGGSLWVWSFIN-TYGSTVEYKAVKGRASVSRDNSQSKSSLSLSLVPQDSAHYFC
Vb2.18 : VWAQWRLVESGGGLQ-AAGNSVHLSCWGSDFNFAIRYQAPGGSLWVWSFIN-TYGSTVEYKAVKGRASVSRDNSQSKSSLSLSLVPQDSAHYFC
Vb2.19 : VWAQWRLVESGGGLR-APGDSVHLSCWGSDFNFAIRYQAPGGSLWVWSFIN-TYGSTVEYKAVKGRASVSRDNSQSKSSLSLSLVPQDSAHYFC
Vb2.20 : VWAQWRLVESGGGLR-APGDSVHLSCWGSDFNFAIRYQAPGGSLWVWSFIN-TYGSTVEYKAVKGRASVSRDNSQSKSSLSLSLVPQDSAHYFC

Vb3.1 : VWTQSLSVESGGGLR-APGDSVHLSCWGSDFNFAIRYQAPGGSLWVWSFIN-TYGSTVEYKAVKGRASVSRDNSQSKSSLSLSLVPQDSAHYFC
Vb3.2 : VWAQWRLVESGGGVQ-APGNTVHLSCWGSDFNFAIRYQAPGGSLWVWSFIN-TYGSTVEYKAVKGRASVSRDNSQSKSSLSLSLVPQDSAHYFC
Vb3.3 : VWAQWRLVESGGGLR-APGDSVHLSCWGSDFNFAIRYQAPGGSLWVWSFIN-TYGSTVEYKAVKGRASVSRDNSQSKSSLSLSLVPQDSAHYFC
Vb3.4 : VWAQWRLVESGGGLR-APGDSVHLSCWGSDFNFAIRYQAPGGSLWVWSFIN-TYGSTVEYKAVKGRASVSRDNSQSKSSLSLSLVPQDSAHYFC
Vb3.5 : VWAQWRLVESGGGVK-TPGNSVHLSCWGSDFNFAIRYQAPGGSLWVWSFIN-TYGSTVEYKAVKGRASVSRDNSQSKSSLSLSLVPQDSAHYFC
Vb3.6 : VWAQWRLVESGGGVR-TRGNSVHLSCWGSDFNFAIRYQAPGGSLWVWSFIN-TYGSTVEYKAVKGRASVSRDNSQSKSSLSLSLVPQDSAHYFC

Vb4.1(4.2) : --QGDEIQPTRTTVMWQAGQETLQCT-YSSNASYIYVAWYRQHPNGSLQYLLQSK-GRGGSYIHTAPFARKRFSGKAD-ESSGTLFHALELKDNALYYC

Vb5 : VWAQPRVSVESGGGLR-APGDSVHLSCWGSDFNFAIRYQAPGGSLWVWSFIN-TYGSTVEYKAVKGRASVSRDNSQSKSSLSLSLVPQDSAHYFC

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C

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<-----FR1-IMGT-----><CDR1-><-----FR2-IMGT-----><CDR2-><-----FR3-IMGT----->
Vβ1.1      : KLITQWPEETLKSRAGETVDISCYQNNSHQLAYMFSWYQQPPG--SSLKLSVASTSLWLQSSYAEGYSEAKFEISRDNSELSVMTIKNVTRKDAATYFC
Vβ1.2p (1.3/1.4) : KLITQWPEETLKSRAGETVDISCYQNNSHQLAYMFR*QQPPG--SSLKLSVASTSLWLQSSYAEGYSEAKFEISRDNSELSVIAIKNVTRKDAATYFC
Vβ2        : WALQQSPDSTVVYE-GDALILNCSEKKESAFSLTMYWYKLPVSGKNATLQLIVNSVEGGRAEIEKEFIN-HFQSSGSTKSSCLSVETSTHVLLNDSGTYYC
Vβ3.1 (3.4) : SALEQSPDSTVIWQ-GEKMSLTCS-KMTPSYIYMYWYKMPSLGNGSGMILMVTAIKSGSKASVEAASFQS-HFTSSGIQSGDGMTLSSTEGAFLNDSGIYYC
Vβ3.2      : LALEQSPDSTVIWQ-GEKMNSVICS-KMKSSSTVMYWYKMPSLGNGSGMILMVTAVKSGAKASVEAASFQS-HFMSSDIQSGDGMTLSSTEGAFLNDSGIYYC
Vβ3.3      : SALEQSPDSTVIWQ-GEKMSLTCS-KMKPSYINMYWYKMPSLGNGSGMILMVTAVKSGAKASVEAASFQS-HFMSSGIQSGDGMTLSSTEGAFLNDSGIYYC
Vβ3.5      : LALEQSPDSTVIWQ-GEKMSLTCS-KMNPSYITMYWYKMPSLGNGSGMILMVTAVKSGAKASVEAASFQS-HFTSSGIQSGDGMTLSSTEGAFLNDSGIYYC
Vβ3.6      : LALEQSPDSTVIWQ-GEKMSLTCS-KMKSSSTVMYWYKMPSLGNGSGMILVVTALVSGKASVEAASFQS-HFTSSDIQSGDGMTLSSTEGAFLNDSGTYYC
Vβ3.7      : LALEQSPDSTVIWQ-GEKMSLTCS-KMKPSSDIMYWYKMPSLGNGSGMILVVTAVKSGKASVEAASFQS-HFTSSGIQSGDGMTLSSTEGAFLNDSGIYYC
Vβ4        : AKITQTSSLVLKEDGE-ATLKCS--QNDNHNYMSWYSLQQPG--KGLQLLYSSIGADQEAVGDTHPG--YKATRLNLSDFHLVIKPVKMNSHADYFC

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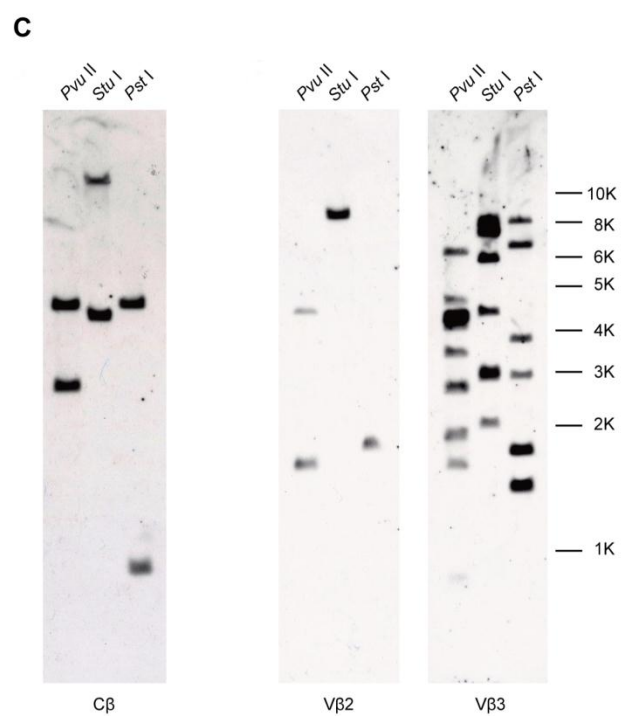
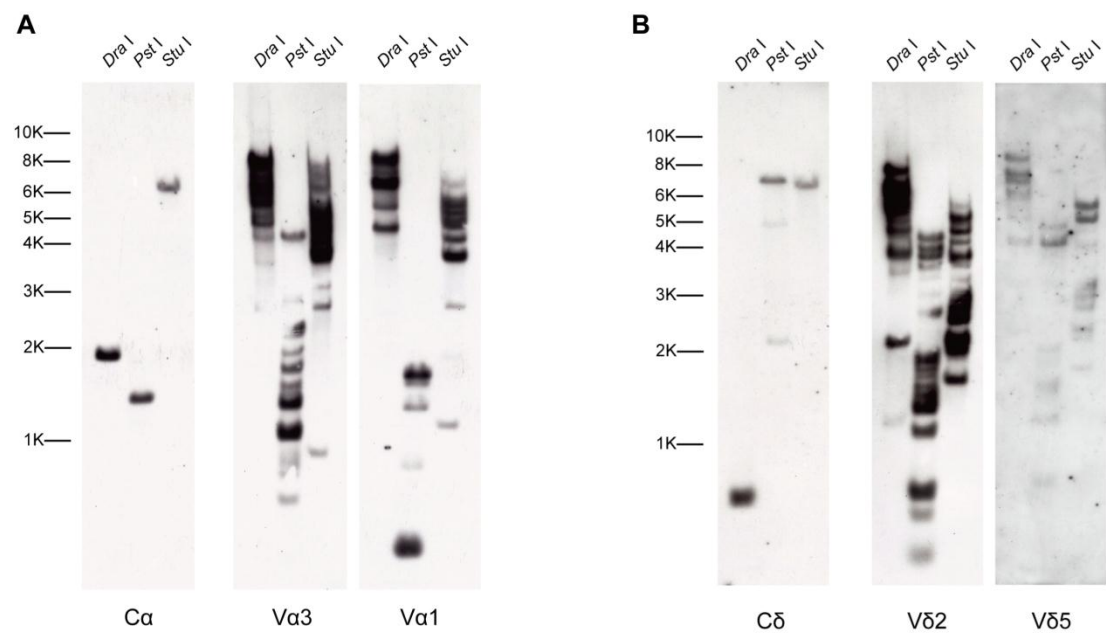
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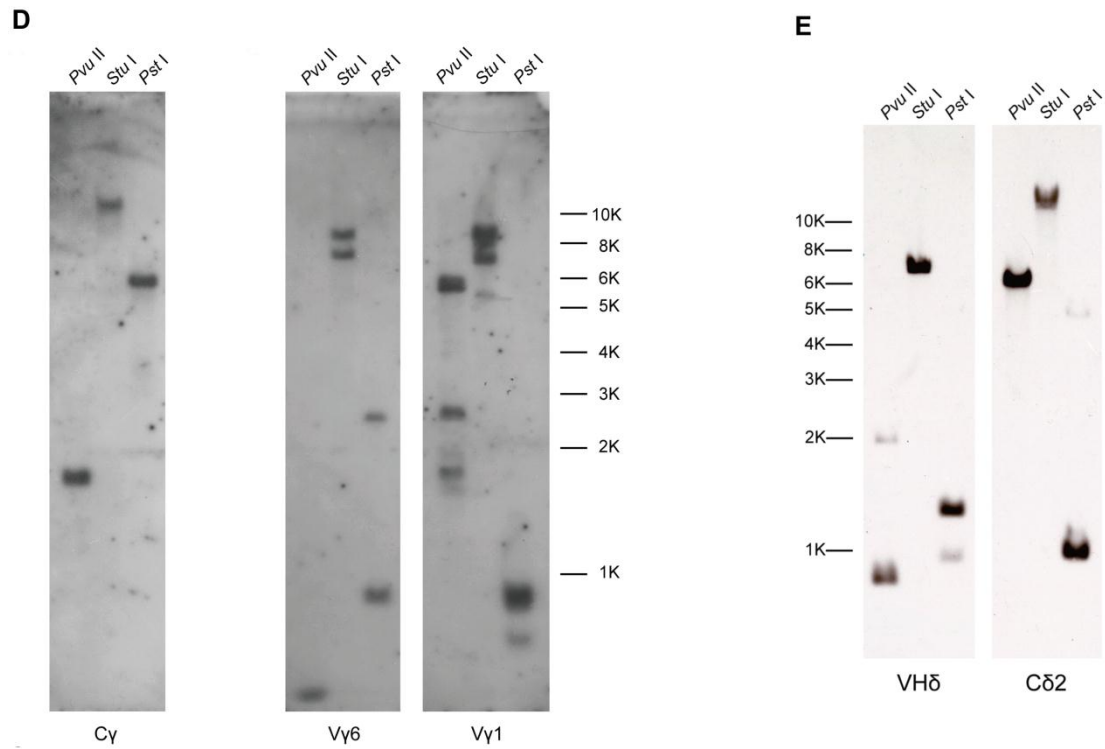
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Vα1.1      : GFAQEIPSIQTSPVSITSMSQG-TARLQSCHFKDVSANFSDNTVSIHWYQSQKENREPVRSMLYISSGTTTSVENNSFQ--RNRYMVQSNLSNQKICILIIKNIGPDDAATYFC
Vα1.2      : GFAQEIPSIQTSPISITSKSQG-STRSLQCHSFKEISANFSDSTTSIHWYQSQKENKAPEWSMFYISTGTTKADKSLQ-GRSTYTIERVSRQKICTLTSIKNIASPDAAATYFC
Vα1.3      : GLAQEIPSIQTSPVSITSKSQG-STRSVLCHSF*RVSANFSDNTTSIHWYQSQKGNKALEWSMFYVTTSTRITSRADKSSFQ-GRSTYTSVESTDQKSMCTLISIKSIVSPDSDATYFC
Vα1.4      : GFAQEIPSIQAPISITSKFQG-STRSLQCHSFKDVSTNSFDSIVSIHWYQSQKENKAPEWSMFYITSTGKTSSVEENSFQ-GRSTYTIERISSRKKICTLTSISNIISPDSDTAIYFC
Vα1.5p     : VFAQEIPSTQTSPISITSKSRG-TTSRLQCHSFKGVSTNSFDDTSIIH*YQSQKENASPERMSFYILTSGTSTASVDESSFQ-SRSTYTIERVSKQKICTLTSIKSIVSPDSDATYFC
Vα1.6      : GFAQEIPSIQAPISITSKFQG-STRSLQCHSFKDVSTNSFDSIVSIHWYQSQKENKAPEWSMFYITSTGKTSAVDESSFQ-GRSTYTIERVSKQKICTLTSIKNIASPDVAATYFC
Vα2.1      : VFAQEIPSIQTSPISITSKFKK-TARSMYCEIKNSLPTSSFDSTSVSIHWYQSQKRENASPERLLFFAEGSTSSVENSGQ-KDRYRAERSVDQSNRSCVLMSIKDVISPDSDAGMYFC
Vα2.2p     : GFSLEIPLQNSISISKSFKK-IS*LSCEIKSLPTIFDSTVLHWHKSWKENEAPERLLFFAEGKTSVESGSFQ-RDSRYRAERSVEQSNRSCVLMSTRDVISPADSSTYH-
Vα3.1      : GDTQAVPVQTLVTRTQAEGRSASMASCQLT-----KEDTVHSWYKQLPGEPPKSRILYVSGQTSPFDDSSD-RQKYQVRKSRASEPLYTLQINNSVNQRDAGTYFC
Vα3.2p     : GDTQAVPVQSPAMRTQAEGRSASMASCRLT-----KEDTVHSWYKQLPGQPIKSRLYVSGQIPAFDDSSD-RQKYQVRKSRASEPLYSLQINNSVNQRDAGT*YFC
Vα3.3p     : GDAQAVPVQSPAMQRQVKSISARMECRLS-----SNAILHSWYKQLPGEPPKSRILYSEMNSPFVDDGSD-RQKYQV*KRASEPLYSLTIDFLSTQRDAGTYFC
Vα3.4      : GDAQVVPVQSPAVRRQVKGSSARMECRLS-----SNTIVHSWYKQLPGEPPKSRILYVSGQSPSTFDDGSD-GRKYQVSWKHASQPLYSLTIDFLNQRDSGTYFC
Vα4        : --QVLLQQRQPSLTKRTSS-TAVIDCKVEGID-DFQDAYIHSWYRHIPSSRAPERLLYVTSTAQISYDKDSYKDKYHSSK-RGKNTCTLSVKDIREDEGTYYC
Vα5        : SPARALQQSPVSVTKPESK-TVLITSCHVS-VP-DFDKAFIHSWYRTRPGAAPERVAYMASTLFLANRED--EGKFSIEKDVGKSLCTLTSVTSTKVTLRSDAGTYFC
Vα6        : GAAQILRQPKPSVRRVAYS-TARIDCHFS-GS-DFPNAYIHSWYQKQPEAPQHLLYVQKEAAAYDQS-YRETFGAEEKKTEPICTLTSIKRVTKQEATYFC

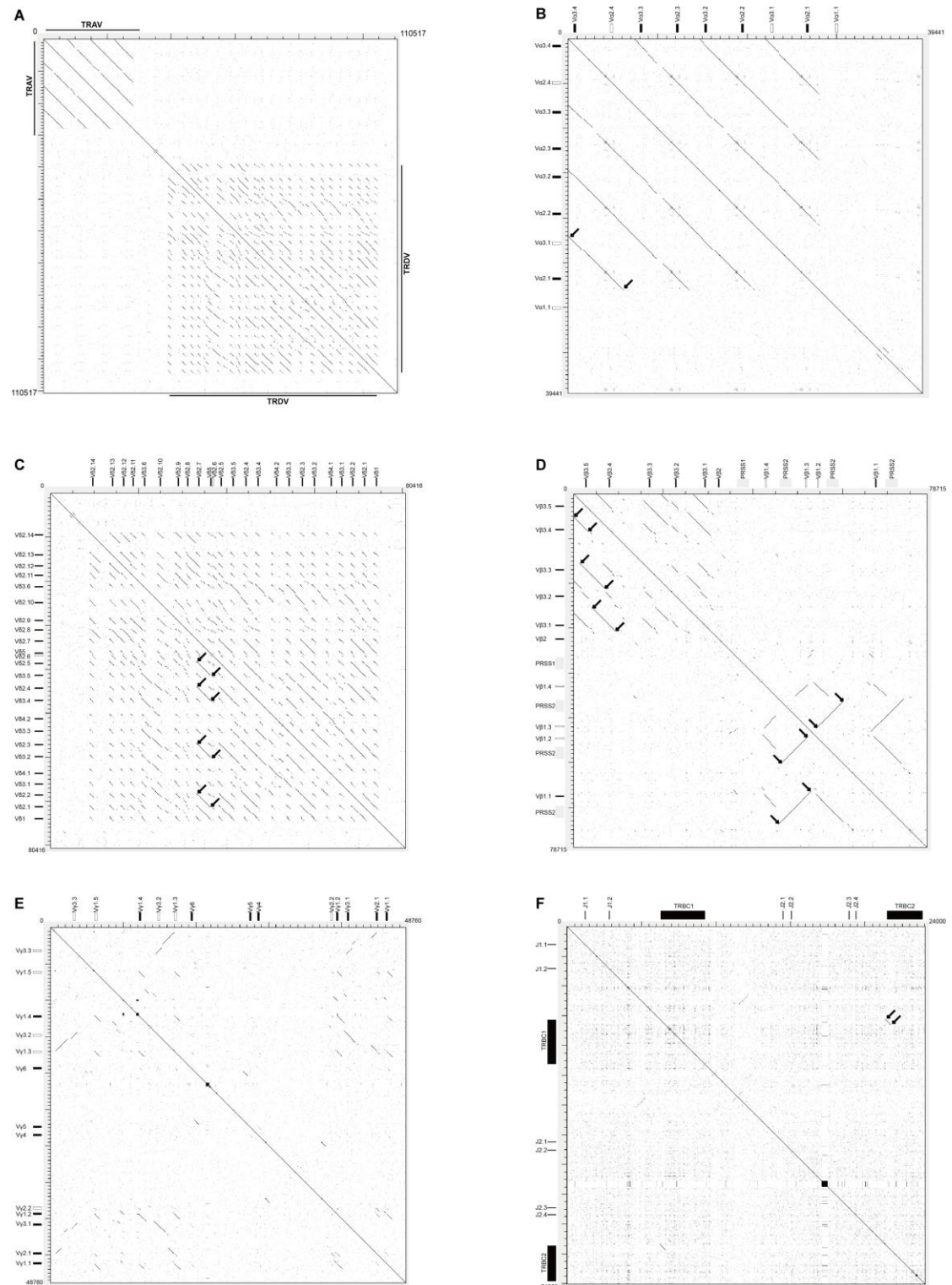
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Supplementary Figure S2 Amino acid sequence alignments of the duck V genes, V α segments (A), V δ segments (B), V β segments (C) and V δ segments (D). Only functional genes and in-frame pseudogenes are shown. The FRs and CDRs were described according to the IMGT unique numbering for the V-REGION. Canonical cysteines and tryptophans are shaded. The pseudogenes are indicated by “p”.





Supplementary Figure S3 Southern blotting detection of duck genomic DNA using the TCR C and V specific probes, C α and V α (A), C δ and V δ (B), C β and V β (C), C γ and V γ (D), and C δ 2 and VH δ (E). The probes used are indicated below each panel. The restriction enzymes used are indicated above each panel. The DNA marker is shown on the left.



Supplementary Figure S4 Dotplot analyses of the V regions of TCR α/δ , TCR β and TCR γ . Approximate V segment locations are shown on each axis. Functional V segments, pseudogenes and non-TCR genes are marked as in Fig. 1. (A) The V α/δ

region of TCR α / δ locus. (B) The incomplete V α region of TCR α / δ locus. Lines parallel to the main diagonal reflect the homology unit containing one V α 2 and one V α 3 segment. (C) The V δ region of TCR α / δ locus. The repeated unit of ~ 4 kb length composed of V segments from V δ 2 and V δ 3 subgroups. (D) The V β region of TCR β locus. The 5' duplicated region corresponds to V β 3 subgroup. One *PRSS2* gene and one V β 1 segment formed a homology unit, which has three copies. Lines perpendicular to the main diagonal reflect the *PRSS2* gene and V β 1 segment with an opposite transcriptional orientation to the relevant C region. (E) The V γ region of TCR γ locus. (F) The J-C region of TCR β locus. Except the well-conserved first exon of two Cb genes, no homologous regions containing coding sequences were found in J-C region of TCR β locus. The solid black region on the diagonal reflects an ~ 400 bp area of short tandem repeats.

A

					CDR3 (nt)
V _h 3.4	Y L C	TACCTCTGTGCTGTGAATGA	F G S G	TGACTGGCAACAACAAGCTGACCTTTGGCTCAGGAACCAAGGCTGTCCGTCTACCCA	J _h 50
V _h 3.4-1		TACCTCTGTGCTGTG-----CGTGATCGATCTGGATCCTTA-----		-----AACAAGCTGACCTTTGGCTCAGGAACCAAGGCTGTCCGTCTACCCA	30
V _h 3.4-2		TACCTCTGTGCTGTGA-----TCG-----	F G K G	CGTACACTGAGGGCAAAGTCACTTTGGAAAAGGAAGTGTGCTTTCTGTAGTTCAG	J _h 6
				-----CGTACACTGAGGGCAAAGTCACTTTGGAAAAGGAAGTGTGCTTTCTGTAGTTCAG	24
V _h 1.2-1	Y L C	TACCTGTGT	F G S G	TGACTTTGGCTCTGGCAACAAGCTGACCTTTGGCTCAGGAACCAAGGCTGTCCGTCTACCAA	J _h 35
		GCACTGGCCGG-----		-----TGGCTCTGGCAACAAGCTGACCTTTGGCTCAGGAACCAAGGCTGTCCGTCTACCAA	24 (*)
V _h 1.2-2	Y L C	TACCTGTGT	F G S G	TGGCTATGGCTCTGGATATGACAGACTGACTTTGGCTCAGGAACCAAGGCTGTCTGTCCAACCAA	J _h 46
		GCACTGAGCCCGCGCCT-----		-----CTATGGCTCTGGATATGACAGACTGACTTTGGCTCAGGAACCAAGGCTGTCTGTCCAACCAA	34
V _h 1.2-4		TACCTGTGT		-----CTATGGCTCTGGATATGACAGACTGACTTTGGCTCAGGAACCAAGGCTGTCTGTCCAACCAA	34
V _h 1.2-5		TACCTGTGT		-----ATGGCTCTGGATATGACAGACTGACTTTGGCTCAGGAACCAAGGCTGTCTGTCCAACCAA	30 (*)
V _h 1.2-3	Y L C	TACCTGTGT	F G S G	TGAACTACGAGAAGCTCACATTTGGGAAGGGAACACGACTTCAGGTTTTCCTTA	J _h 29
		GCACTCCCGGGGAAG-----		-----TGAACACTCGAGAAGCTCACATTTGGGAAGGGAACACGACTTCAGGTTTTCCTTA	24 (*)
V _h 1.2-6	Y L C	TACCTGTGT	F G S G	TAACTACGGTTACAAATTTACATTTGGATCTGGGACAAGACTTCAGGTTCTGCCAG	J _h 67
		GCGAGCCGCTC-----		-----CTACGGTTACAAATTTACATTTGGATCTGGGACAAGACTTCAGGTTCTGCCAG	21
V _h 1.2-7	Y L C	TACCTGTGT	F G S G	TGAATCTGGCTTCACCAAACTGACCTTTGGCTCAGGACCAAGGCTGTCCGTCTACCAA	J _h 37
		GCACTGAGGAC-----		-----CTGGCTTCACCAAACTGACCTTTGGCTCAGGACCAAGGCTGTCCGTCTACCAA	22 (*)
V _h 1.2-8	Y L C	TACCTGTGT	F G S G	TGACTTCAACGCTCCACCTGGAAAGCCACCTTTGGAAAGTGGGACACAGCTGGTGGTGAACCTG	J _h 22
		GCACTGAGCCGTCGT-----		-----ACTTCAACGCTCCACCTGGAAAGCCACCTTTGGAAAGTGGGACACAGCTGGTGGTGAACCTG	33
V _h 1.2-9	Y L C	TACCTGTGT	F G S G	TGGCTATGGCTCTGCATACACAAACCAACTTTGGGTGAGGACCAAGGCTTTCTGTCCAACCAA	J _h 52
		GCACTGGGGGTC-----		-----GGGTATGGCTCTGCATACACAAACCAACTTTGGGTGAGGACCAAGGCTTTCTGTCCAACCAA	33
V _h 1.2-10	Y L C	TACCTGTGT	F G K G	TGTCCAATGCGTATGCAGTCACTTTTGGAAAAGGAAGTGTGCTTTCACTGTGTACCAAG	J _h 27
		GCACTGTACCC-----		-----GTCCAATGCGTATGCAGTCACTTTTGGAAAAGGAAGTGTGCTTTCACTGTGTACCAAG	24 (*)
V _h 1.3-1	Y L C	TACCTGTGT	F G S G	TGAATGACTTAAACAAGCTGACTTTTGGCTCAGGACCAAGGCTGTCCATCCAACCAA	J _h 9
		GCACTGAG-----		-----GAATGACTTAAACAAGCTGACTTTTGGCTCAGGACCAAGGCTGTCCATCCAACCAA	21
V _h 1.3-2	Y L C	TACCTGTGT	F G S G	TGGCTCTAGCTCTTCATTCCGCAAAATGACCTTTGGCTCGGGACCAAGGCTGTCTGTCCAACCAA	J _h 11
		GCACTGAGCC-----		-----GCTCTAGCTCTTCATTCCGCAAAATGACCTTTGGCTCGGGACCAAGGCTGTCTGTCCAACCAA	30
V _h 1.3-3	Y L C	TACCTGTGT	F G S G	TGACTCTGGCTATGGCAACAAGCTGACCTTTGGCTCAGGAACCAAGGCTGTCCGTCTACCAA	J _h 21
		GCACTG-----		-----CTGGCTATGGCAACAAGCTGACCTTTGGCTCAGGAACCAAGGCTGTCCGTCTACCAA	21
V _h 1.3-4	Y L C	TACCTGTGT	F G S G	TGACTATGACTACACCAACAAGTGAACCTTTGGCTCAGGACCAAGGCTGTCCGTCTACCAA	J _h 13
		GCACTGAGACGG-----		-----TATGACTACACCAACAAGTGAACCTTTGGCTCAGGACCAAGGCTGTCCGTCTACCAA	25
V _h 1.3-7		TACCTGTGT		-----ATGACTACACCAACAAGTGAACCTTTGGCTCAGGACCAAGGCTGTCCGTCTACCAA	24
V _h 1.3-5	Y L C	TACCTGTGT	F G S G	TGAGTGGCAACTACAAGCTGACCTTTGGCTCAGGAACCAAGGCTGTCTGTCTACCAA	J _h 17
		GCACTGGA-----		-----GAGTGGCAACTACAAGCTGACCTTTGGCTCAGGAACCAAGGCTGTCTGTCTACCAA	21
V _h 1.3-6	Y L C	TACCTGTGT	F G S G	TGACTTTGGCTCTGGCAACAAGCTGACCTTTGGCTCAGGAACCAAGGCTGTCCGTCTACCAA	J _h 35
		GCACTGAGCCGGGA-----		-----TGACTTTGGCTCTGGCAACAAGCTGACCTTTGGCTCAGGAACCAAGGCTGTCCGTCTACCAA	33
V _h 1.4-1	Y L C	TACCTGTGT	F G S G	TGAGTGGCAACTACAAGCTGACCTTTGGCTCAGGAACCAAGGCTGTCTGTCTACCAA	J _h 17
		GCACTGAGCCGACCC-----		-----TGGCAACTACAAGCTGACCTTTGGCTCAGGAACCAAGGCTGTCTGTCTACCAA	25
V _h 1.4-2	Y L C	TACCTGTGT	F G T G	TGGCTATGGCTCTGCATACGGCAGACCAACCTTTGGCACAGGACCAAGGCTGTCTGTCCAACCAA	J _h 34
		GCACTGAGAAAGTGAC-----		-----GGCTATGGCTCTGCATACGGCAGACCAACCTTTGGCACAGGACCAAGGCTGTCTGTCCAACCAA	36
V _h 1.4-3		TACCTGTGT		-----CTATGGCTCTGCATACGGCAGACCAACCTTTGGCACAGGACCAAGGCTGTCTGTCCAACCAA	30
V _h 1.4-4	Y L C	TACCTGTGT	F G S G	TGACTAACTTATACAAGCTGACTTTTGGCTCAGGACCAAGGCTGTCTGTCTACCAA	J _h 42
		GCACTGATCGCG-----		-----CTAACTTATACAAGCTGACTTTTGGCTCAGGACCAAGGCTGTCTGTCTACCAA	24
V _h 1.4-5	Y L C	TACCTGTGT	F G S G	TGACTATGACTACACCAACAAGTGAACCTTTGGCTCAGGACCAAGGCTGTCCGTCTACCAA	J _h 13
		GCACTGAG-----		-----TGACTATGACTACACCAACAAGTGAACCTTTGGCTCAGGACCAAGGCTGTCCGTCTACCAA	27
V _h 1.4-6	Y L C	TACCTGTGT	F G S G	TGATTCCTGGATCCTTAAACAAGCCGACCTTTGGCTCAGGAACCAAGGCTGTCCGTCTACCCA	J _h 32
		GCACTGGC-----		-----TTCTGGATCCTTAAACAAGCCGACCTTTGGCTCAGGAACCAAGGCTGTCCGTCTACCCA	24
V _h 1.4-7	Y L C	TACCTGTGT	F G K G	TGAATGTTGGCTATACCATCATCTTTGGAAAAGGACAAAGCTTCTTGTGAAACCAA	J _h 64
		GCACTGAGGTG-----		-----GAATGTTGGCTATACCATCATCTTTGGAAAAGGACAAAGCTTCTTGTGAAACCAA	24

V ₀ 1.4-8	Y L C : <u>TACCTGTGT</u>	GCACTGACCCCTCGA-----TCTAGCTCTTCATATGGCAAATTGACCTTTGGCTCAGGGACACAGGCTGTCTGTCCATCCAA	F G S G TGGCTCTGGCTCTTCATATGGCAAATTGACCTTTGGCTCAGGGACACAGGCTGTCTGTCCATCCAA	J ₀ 41	33
V ₀ 1.4-9	Y L C : <u>TACCTGTGT</u>	GCACTGAGAGAGG-----ATGACTTAAACAAGCTGACTTTGGCTCGGGACACAGGCTGTCCATCCAACCAA	F G S G TGAATGACTTAAACAAGCTGACTTTGGCTCAGGGACACAGGCTGTCCATCCAACCAA	J ₀ 9	24
V ₀ 1.4-10	Y L C : <u>TACCTGTGT</u>	GCACTGAGAGGATGG-----CTGGCTACAACAAGCTACATTTGGCTCAGGGACTAGGCTGTCTGTCTACCAA	F G S G TGACACTGGCTACAACAAGCTACATTTGGCTCAGGGACTAGGCTGTCTGTCTACCAA	J ₀ 18	27
V ₀ 1.4-11	Y L C : <u>TACCTGTGT</u>	GCACTGGCCTTATC-----CTATGGAAACACAGGCTGACATTTGGCTCAGGGACACAGCTGTCCGTCCAACCAA	F G S G TGACTATGGAACACACAGGCTGACATTTGGCTCAGGGACACAGCTGTCCGTCCAACCAA	J ₀ 5	27
V ₀ 1.5	Y L C : <u>TACCTGTGT</u>	GCACTGGAGCGC-----AATACGTTTACAAATTACATTTGGATCTGGGACAAGACTTCTGGTTCTGCCAG	F G S G TAACTACGGTTACAAATTACATTTGGATCTGGGACAAGACTTCTGGTTCTGCCAG	J ₀ 67	24
V ₀ 2.5-1	Y Y C : <u>TATTACTGC</u>	GCCCTGAGAACCGGAGG-----GTATGATGACCGACAGTCACTTTGGAAAAGGAAGTGTGCTTTCAGTTGTACCAG	F G K G TGTATGATGACCGACAGTCACTTTGGAAAAGGAAGTGTGCTTTCAGTTGTACCAG	J ₀ 58	30
V ₀ 2.5-2	Y Y C : <u>TATTACTGC</u>	GCCCTGAGAGCTGC-----GGGATATGTGAAACTGGCATTGGAGCTGGCACCCAACTTCTGTATCCCAA	F G A G CCAATCAGGGATATGTGAAACTGGCATTGGAGCTGGCACCCAACTTCTGTATCCCAA	J ₀ 68	24
V ₀ 2.5-3	Y Y C : <u>TATTACTGC</u>	GCCCTGCCGGGGCC-----CTATACCATCATCTTTGGAAAAGGGACAAAGCTTCTGTGAAACCAA	F G K G TGAATGTTGGCTATACCATCATCTTTGGAAAAGGGACAAAGCTTCTGTGAAACCAA	J ₀ 64	18
V ₀ 2.5-4	Y Y C : <u>TATTACTGC</u>	GCCCCCCT-----CTATGGCTCTGGATATGACAGACTGACTTTGGCTCAGGAACACAGGCTGTCTGTCCAACCAA	F G S G TGGCTATGGCTCTGGATATGACAGACTGACTTTGGCTCAGGAACACAGGCTGTCTGTCCAACCAA	J ₀ 46	27
V ₀ 2.5-5	Y Y C : <u>TATTACTGC</u>	GCCCTGTCTCCGA-----TTGGCTCTGGCAACAAGCTGACCTTTGGCTCAGGAACACAGGCTGTCCGTCTACCAA	F G S G TGACTTTGGCTCTGGCAACAAGCTGACCTTTGGCTCAGGAACACAGGCTGTCCGTCTACCAA	J ₀ 35	27
V ₀ 2.5-6	Y Y C : <u>TATTACTGC</u>	GCCCACTACGCGG-----TTGGCTACAGCCAGCTGACTTTGGCTCAGGGACACAGGCTGTCCGTCCAACCAA	F G S G TGTTTGGCTACAGCCAGCTGACTTTGGCTCAGGGACACAGGCTGTCCGTCCAACCAA	J ₀ 61	24
V ₀ 2.5-7	Y Y C : <u>TATTACTGC</u>	GCCCTGAGAGCCCGGGCGGA---TGGCTCTAGCTCTTCATTTCGGCAAATTGACCTTTGGCTCGGGACACAGGCTGTCTGTCCAACCAA	F G S G TGGCTCTAGCTCTTCATTTCGGCAAATTGACCTTTGGCTCGGGACACAGGCTGTCTGTCCAACCAA	J ₀ 11	45
V ₀ 2.5-8	Y Y C : <u>TATTACTGC</u>	GCCCTGAGAGCGCG-----ATGACTACACCAACAACCTGACCTTTGGCTCAGGGACACAGGCTGTCCGTCTACCAA	F G S G TGACTATGACTACACCAACAACCTGACCTTTGGCTCAGGGACACAGGCTGTCCGTCTACCAA	J ₀ 13 (*)	28
V ₀ 2.5-9	Y Y C : <u>TATTACTGC</u>	GCCCTGTGGCTCTGTG-----ATGGGAACACAAACTGACCTTTGGCTCAGGGACACAGGCTGTCCGTCCAACCAA	F G S G TGACTATGGGAACACAAACTGACCTTTGGCTCAGGGACACAGGCTGTCCGTCCAACCAA	J ₀ 60	27
V ₀ 2.6-1	Y Y C : <u>TATTACTGC</u>	GCCCTGAGAGCCGCGG-----CTGGATCCTTAAACAAGCCGACCTTTGGCTCAGGAACACAGGCTGTCCGTCTACCCA	F G S G TGATTCTGGATCCTTAAACAAGCCGACCTTTGGCTCAGGAACACAGGCTGTCCGTCTACCCA	J ₀ 32 (*)	31
V ₀ 2.6-2	Y Y C : <u>TATTACTGC</u>	GCCCTGAACGCGGAGG-----ATGATGACCCGACAGTCACTTTGGAAAAGGAAGTGTGCTTTCAGTTGTACCAG	F G K G TGTATGATGACCCGACAGTCACTTTGGAAAAGGAAGTGTGCTTTCAGTTGTACCAG	J ₀ 58	27
V ₀ 2.6-3	Y Y C : <u>TATTACTGC</u>	GCCCC-----CTATGGCTCTGGATATGACAGACTGACTTTGGCTCAGGAACACAGGCTGTCTGTCCAACCAA	F G S G TGGCTATGGCTCTGGATATGACAGACTGACTTTGGCTCAGGAACACAGGCTGTCTGTCCAACCAA	J ₀ 46	24
V ₀ 2.6-4	Y Y C : <u>TATTACTGC</u>	GCCCTGAGACGACGCC-----CTTTGGCTCTGGCAACAAGCTGACCTTTGGCTCAGGAACACAGGCTGTCCGTCTACCAA	F G S G TGACTTTGGCTCTGGCAACAAGCTGACCTTTGGCTCAGGAACACAGGCTGTCCGTCTACCAA	J ₀ 35	33
V ₀ 2.7	Y Y C : <u>TATTACTGC</u>	GCCCTGAGGGACG-----ATGTTGGCTATACCATCATCTTTGGAAAAGGGACAAAGCTTCTGTGAAACCAA	F G K G TGAATGTTGGCTATACCATCATCTTTGGAAAAGGGACAAAGCTTCTGTGAAACCAA	J ₀ 64	24
V ₀ 2.8	Y Y C : <u>TATTACTGC</u>	GCCCTGATGAGATT-----TACGTGCCTATGAAACACTCAGTTTGGAGAGGGGACAAAGCTGACTGTTCTTCCAA	F G E G TAACTCCATACGTGCCTATGAAACACTCAGTTTGGAGAGGGGACAAAGCTGACTGTTCTTCCAA	J ₀ 1 (*)	28
V ₀ 2.9-1	Y Y C : <u>TATTACTGC</u>	GCCTGGGG-----ATGTTGGCTATACCATCATCTTTGGAAAAGGGACAAAGCTTCTGTGAAACCAA	F G K G TGAATGTTGGCTATACCATCATCTTTGGAAAAGGGACAAAGCTTCTGTGAAACCAA	J ₀ 64 (*)	19
V ₀ 2.9-2	Y Y C : <u>TATTACTGC</u>	GCCCTGAGAGCGCCAGTACGC-----GGGATATGTGAAACTGGCATTGGAGCTGGCACCCAACTTCTGTATCCCAA	F G A G CCAATCAGGGATATGTGAAACTGGCATTGGAGCTGGCACCCAACTTCTGTATCCCAA	J ₀ 68 (*)	31

V ₀ 2.9-3	Y Y C : <u>TATTACTGC</u>	GCCCCCTATC-----	F G T G TGGCTATGGCTCTGCATACGGCAGACCAACCTTTGGCACAGGAACCAAGGCTTTCTGTCCAACCAA	J ₀ 20	30
V ₀ 2.10-1	Y Y C : <u>TATTACTGC</u>	GCCCTGAGAGCCCTCTG-----	F G S G TGTTTGGCTACAGCCAGCTGACCTTTTGGCTCAGGACCAGGCTGTCCGTCCAACCAA	J ₀ 61	30
V ₀ 2.10-2	Y L C : <u>TATTACTGC</u>	GCCCTGAGAGCTAACTACGGAGGT-----	F G S G TAACTACGGTTACAAATTTACATTTGGATCTGGGACAAGACTTCTGGTTCTGCCAG	J ₀ 67	30
V ₀ 2.11	Y Y C : <u>TATTACTGC</u>	GCCCTGAGTGCCCG-----	F G S G CGACTATGGGAACAACAACTGACCTTTGGCTCAGGACCAGGCTGTCTGTCCAACCAA	J ₀ 57	27
V ₀ 2.12-1	Y Y C : <u>TATTACTGC</u>	GCCCTGAGTTGG-----	F G S G TGACACTGGCTACAACAAGCCTACATTTGGCTCAGGACTAGGCTGTCTGTCTACCAA	J ₀ 18	24
V ₀ 2.12-2	Y Y C : <u>TATTACTGC</u>	GCCCTGAG-----	F G S G TGGCTCTGGCTCTCATATGGCAAATTTGACCTTTGGCTCAGGACCAGGCTGTCTGTCCAACCAA	J ₀ 41	24
V ₀ 2.12-3	Y Y C : <u>TATTACTGC</u>	GCTCTCGTACGG-----	F G S G TGAATCTGGCTTCAACAACTGACCTTTGGCTCAGGACCAGGCTGTCTGTCCAACCAA	J ₀ 23	27
V ₀ 2.13-1	Y Y C : <u>TATTACTGC</u>	GCCCTGAGAGCGGCTTCATGGCGGGG-----	F G S G TAACTACGGTTACAAATTTACATTTGGATCTGGGACAAGACTTCTGGTTCTGCCAG	J ₀ 67 (*)	41
V ₀ 2.13-2	Y Y C : <u>TATTACTGC</u>	GCCCTGAGAGCGCTA-----	F G S G TGGCTATGGCTCTGGATATGACAGACTGACCTTTGGCTCAGGAACCAAGGCTGTCTGTCCAACCAA	J ₀ 46	30
V ₀ 2.13-3	Y Y C : <u>TATTACTGC</u>	GCCCTGAGGCGG-----	F G T G TGGCTATGGCTCTGCATACGGCAGACCAACCTTTGGCACAGGAACCAAGGCTTTCTGTCCGACCAA	J ₀ 20	30
V ₀ 2.14	Y Y C : <u>TATTACTGC</u>	GCCCCGCAC-----	F G S G TGACTATGGAACCAACAGGCTGACATTTGGCTCAGGACCAGACTGTCCGTCCAACCAA	J ₀ 5 (*)	22
V ₀ 2.15	Y Y C : <u>TATTACTGC</u>	GCCCTGA-----	F G S G TGGCTATGGCTCTGGATATGGCAAATTTGACCTTTGGCTCAGGACCAGGCTGTCTGTCCAACCAA	J ₀ 63	27
V ₀ 2.16-1	Y Y C : <u>TATTACTGC</u>	GCCCTGATGCTGGCG-----	W G S G CTGATTCTGGAGGATGGGAAAATATACATGGGGGAGTGGACAAAACTTCTGTGTGACCAG	J ₀ 65	30
V ₀ 3.5-1	Y L C : <u>TACCTCTGT</u>	GCTGCCCGGCGCTC-----	F G A G CCAATCAGGGATATGTGAAACTGGCATTGGAGCTGGCACCCAACTTCTGTGTATCCAA	J ₀ 68	27
V ₀ 3.5-4	<u>TACCTCTGT</u>	GCTGTCA-----	F G S G AGGGATATGTGAAACTGGCATTGGAGCTGGCAGCCAACTTCTGTGTATCCAA		18
V ₀ 3.5-2	Y L C : <u>TACCTCTGT</u>	GTGGCGGTCCCGAGCAC-----	F G S G TGGCTATGGCTCTGGATATGGCAAATTTGACCTTTGGCTCAGGACCAGGCTGTCTGTCCAACCAA	J ₀ 63	36
V ₀ 3.5-6	<u>TACCTCTGT</u>	GCTGTGAGGTC-----	F G S G CTATGGCTCTGGATATGGCAAATTTGACCTTTGGCTCAGGACCAGGCTGTCTGTCCAACCAA		30
V ₀ 3.5-3	Y L C : <u>TACCTCTGT</u>	GCTGTGAGACTCCCGGAG-----	F G S G TGACTTTGGCTCTGGCAACAGCTGACCTTTGGCTCAGGAACCAAGGCTGTCCGTCTACCAA	J ₀ 35	33
V ₀ 3.5-5	Y L C : <u>TACCTCTGT</u>	GCTGTGAGAG-----	F G K G TGAATGTTGGCTATACCATCATCTTTGGAAAAGGACAAAGCTTCTGTGAAACCAA	J ₀ 64	21
V ₀ 3.5-7	Y L C : <u>TACCTCTGT</u>	GCTCTCCGAT-----	F G S G TGACTGGCAACAACAACAGCTGACCTTTGGCTCAGGAACCAAGGCTGTCCGTCTACCCA	J ₀ 50	27
V ₀ 3.5-8	Y L C : <u>TACCTCTGT</u>	GCTGTGAGGCCCGCG-----	F G K G TGTCCAATGCGTATGCAGTCACTTTGGAAAAGGAAGTGTACTTTCAAGTTGTACCAG	J ₀ 40	30
V ₀ 3.6	Y L C : <u>TACCTCTGT</u>	GCTGTGAGTGCCCGCTAGGAGACG-----	F G S G TGGCTCTAGCTCTGGATATGGCAAATAAATTTGGCTCTGGAACCAAGGCTGTCTGTCCATCCAA	J ₀ 59	45

V ₀ 3.7-1	Y L C : <u>TACCTCTGT</u>	GCTGTGAGTACAG ~~A~~ -----	F G S G TGGCTATGGCTCTGCATACAACAACCAACTTTGGGTCAGGACCAGGCTTTCTGTCCAACCAA	J ₅₂	36
V ₀ 3.7-2	Y L C : <u>TACCTCTGT</u>	GCTGTGAGTCGACCGGCC--	F G S G TGAATGACTTAAACAAGCTGACCTTTGGGTCAGGACCAGGCTGTCCATCCAACCAA	J ₉ (*)	32
V ₀ 3.7-3	Y L C : <u>TACCTCTGT</u>	GCTGTGAGTGCGCC--	F G S G TGGCTATGGCTCTGGATATGGCAAACTGACCTTTGGGTCAGGACCAGGCTGTCTGTCCAACCAA	J ₆₃	36
V ₀ 3.7-4	Y L C : <u>TACCTCTGT</u>	GCTG-----	F G S G TGACTTTGGCTCTGGCAACAGCTGACCTTTGGGTCAGGAACCAAGGCTGTCCGTCTACCAA	J ₃₅	18
V ₀ 3.7-5	Y L C : <u>TACCTCTGT</u>	GCTGTGAGTGATCCCCGGGCGGGTC-----	F G S G TGAATCTGGATCCTACAACAAGCTGACCTTTGGGTCAGGAACCAAGGCTGTCTGTCAAAACCAA	J ₄₃	42
V ₀ 3.7-6	Y L C : <u>TACCTCTGT</u>	GCTGTGACCCCTC-----	F G K G TGAACCTACGACAACTTACATTGGGAAAGGGAACACGACTTCAGGTTTGCCTA	J ₁₆	24
V ₀ 3.7-7	Y L C : <u>TACCTCTGT</u>	GCTGTGAGTGACGATG-----	F G K G TGAATGTTGGCTATACCATCATCTTTGGAAAAGGGAACAAGCTTCTGTGAAACCAA	J ₆₄	27
V ₀ 3.7-8	Y L C : <u>TACCTCCGT</u>	GCTGTGAGTGATCCCCGGC-----	F G K G TGTCCAATGCGTATGCAGTCACCTTTGGAAAAGGAAGCTGTGCTTTCAGTTGTACCAG	J ₂₇	21
V ₀ 3.8	F F C : <u>TTCTTCTGT</u>	GCTGTGAGTGCGGG-----	F G S G TGAATCTGGCTTCAACAACTGACCTTTGGGTCAGGACCAGGCTGTCCGTCTACCAA	J ₂₃ (*)	29
V ₀ 3.9-1	F F C : <u>TTCTTCTGT</u>	GCTGTGACGATG-----	F G S G TGGCTCTGGCTCTTCATATGGCAAACTGACCTTTGGGTCAGGACCAGGCTGTCTGTCCATCCAA	J ₄₁	30
V ₀ 3.9-7	F F C : <u>TTCTTCTGT</u>	GGTGTGAGTGATCCCGCGC-----	F G S G GGCTCTGGCTCTTCATATGGCAAACTGACCTTTGGGTCAGGACCAGGCTGTCTGTCCATCCAA		42
V ₀ 3.9-2	F F C : <u>TACCTCTGT</u>	GCCCGTATGACG-----	F G S G TGATTTGGATCCTTCAACAAGCTGATCTTTGGGTCAGGAACCAAGGCTGTCCGTCTACCCA	J ₁₉	27
V ₀ 3.9-3	F F C : <u>TTCTTCTGT</u>	GCTGTGG-----	F G S G TGACTATGGAACCAACAGGCTGACATTGGGTCAGGACCAGACTGTCCGTCCAACCAA	J ₅	18
V ₀ 3.9-4	F F C : <u>TTCTTCTGT</u>	GCTGTGAGAG ~~A~~ -----	F G S G TGACTCTGGCTACAACAAGCTGACCTTTGGGTCAGGACTAGGCTGTCTGTCTACCAA	J ₄₉	27
V ₀ 3.9-5	F F C : <u>TTCTTCTGT</u>	GCTGTGACGGGCG-----	F G S G TGAATGACTTAAACAAGCTGACCTTTGGGTCAGGACCAGGCTGTCCATCCAACCAA	J ₉	24
V ₀ 3.9-6	F F C : <u>TACTTCTGT</u>	GCTG-----	F G S G TGAATAACTTAAACAAGCTGACCTTTGGGTCAGGACCAGGCTGTCCGTCTACCAA		18
V ₀ 3.9-8	F F C : <u>TTCTTCTGT</u>	GCTGTGAGTGGAG ~~A~~ -----	F G T G TGGCTATGGCTCTGCATACGGCAGACCAACCTTTGGCACAGGACCAGGCTGTCTGTCCAACCAA	J ₃₄	36
V ₀ 3.9-9	F F C : <u>TTCTTCTGT</u>	GCTGTGGCCCC-----	F G S G TGAGTGGCAACTACAAGCTGACCTTTGGGTCAGGAACCAAGGCTGTCTGTCTACCAA	J ₁₇ (*)	25
V ₀ 3.9-10	F F C : <u>TTCTTCTGT</u>	GCTGTGCGTCGTACAG-----	F G S G TGACTCTGGCTATGGCAACAGCTGACCTTTGGGTCAGGAACCAAGGCTGTCCGTCTACCAA	J ₂₁	33
V ₀ 3.9-11	F F C : <u>TTCTTCTGT</u>	GCTGTGAGTG-----	W G S G CTGATCTGGAGGATGGGGAAATATACATGGGGGAGTGGACAAAACCTTCTGTGTGACCAG	J ₆₅ (*)	29
V ₀ 3.10-1	Y F C : <u>TACTTCTGT</u>	GCTGTGAGTGACGGAACG-----	F G S G TGACTCTGGCTATGGCAACAAGCTGACCTTTGGGTCAGGAACCAAGGCTGTCCGTCTACCAA	J ₂₁	36
V ₀ 3.10-2	Y F C : <u>TACTTCTGT</u>	GCTGTGGGGGG ~~A~~ -----	F G S G TGACTAACTTATACAAGCTGACCTTTGGGTCAGGACCAGGCTGTCTGTCTACCAA	J ₄₂	27
V ₀ 3.10-3	Y F C : <u>TACTTCTGT</u>	GCTGTGGGAGATAACTACGGAGGT-----	F G S G TAACTACGGTTACAAATTTACATTGGATCTGGGACAAGACTTCTGGTTCTGCCAG	J ₆₇ (*)	30
V ₀ 3.10-4	Y F C : <u>TACTTCTGT</u>	GCTGTGAGGATCCCCGTGG-----	F G A G CCAATCAGGGATATGTGAACTGGCATTGGAGCTGGACCCAACTTCTGTGTATCCAA	J ₆₈	36
V ₀ 3.10-5	Y F C : <u>TACTTCTGT</u>	GCTGTGCGAATCCCCAGA-----	F G S G TGAATGACTTAAACAAGCTGACCTTTGGGTCAGGACCAGGCTGTCCATCCAACCAA	J ₉ (*)	33

V ₀ 3.11	Y F C : <u>TACCTCTGT</u>	GCTGTGCGTGAAGAGACGCCCT-----	F G S G TGAATGACTTAACAAGCTGACCTTTGGCTCAGGACCAGGCTGTCCATCCAACCAA -----CTTAACAAGCTGACCTTTGGCTCAGGACCAGGCTGTCCATCCAACCAA	J ₅ 9 (*)	30
V ₀ 3.12-1	Y L C : <u>TACCTCTGT</u>	GCTGTGCGTGGGGA-----	F G S G CGACTATGGGAACAACAAGCTGACCTTTGGCTCAGGACCAGGCTGTCTGTCCAACCAA -----GACTATGGGAACAACAAGCTGACCTTTGGCTCAGGACCAGGCTGTCTGTCCAACCAA	J ₅ 7	30
V ₀ 3.12-8	Y L C : <u>TACCTCTGT</u>	GCTGTGCGCAG-----	F G S G CGACTATGGGAACAACAAGCTGACCTTTGGCTCAGGACCAGGCTGTCTGTCCAACCAA -----CGACTATGGGAACAACAAGCTGACCTTTGGCTCAGGACCAGGCTGTCTGTCCAACCAA	J ₅ 7	27
V ₀ 3.12-2	Y L C : <u>TACCTCTGT</u>	GCTGTGCGTGAGACCCGCGGAGGT-----	F G S G TAATACGGTTACAAATTTACATTTGGATCTGGACAAGACTTCTGGTTCTGCCAG -----GGTTACAAATTTACATTTGGATCTGGACAAGACTTCTGGTTCTGCCAG	J ₆ 7	30
V ₀ 3.12-3	Y L C : <u>TACCTCTGT</u>	GCTGTGCGTGATGACAGG-----	F G S G TGGCACTGGCTCTACATACGCAAAATTGACCTTTGGCTCAGGACCAGGCTGTCTGTCCAACCAA -----GGCTCTGGCTCTACATACGCAAAATTGACCTTTGGCTCAGGACCAGGCTGTCTGTCCAACCAA	J ₁₅	39
V ₀ 3.12-4	Y L C : <u>TACCTCTGT</u>	GCTGTGCGTGCGCCGCC-----	F G S G TGACTTTGGCTCTGGCAACAGCTGACCTTTGGCTCAGGAACAGGCTGTCCGTCTACCAA -----CTTTGGCTCTGGCAACAGCTGACCTTTGGCTCAGGAACAGGCTGTCCGTCTACCAA	J ₃₅	33
V ₀ 3.12-5	Y L C : <u>TACCTCTGT</u>	GCTGTGCGTGGGA-----	F G D G TGCTTTGGATACCTACAAGCTAACCTTTGGAGATGGAACAAGGCTCATGGTAAACCAA -----TGCTCTGGATACCTACAAGCTAACCTTTGGAGATGGAACAAGGCTCATGGTAAACCAA	J ₆₆	30
V ₀ 3.12-6	Y L C : <u>TACCTCTGT</u>	GCTGTGCGTGACCC-----	F G K G TGAATGTTGGCTATACCATCATCTTTGGAAAAGGACAAGCTTCTTGTGAAACCAA -----GAATGCTGGCTATACCATCATCTTTGGAAAAGGACAAGCTTCTTGTGAAACCAA	J ₆₄	27
V ₀ 3.12-7	Y L C : <u>TACCTCTGT</u>	GCCGC-----	L G S G TGAATCAGCGCAAGATCACCTTTGGAGCGGAACACGACTTCAGGTTTGCCTA -----CTACGCAAGATCACCTTTGGAGCGGAACACGACTTCAGGTTTGCCTA	J ₁₂	12
V ₀ 3.12-9	Y L C : <u>TACCTCTGT</u>	GCTGTGCGTGACCGCCCGCGTGGTCA-----	F G S G TGATTCTGGATCCTACAACAGCTGACCTTTGGCTCAGGAACAGGCTGTCTGTCAAACCAA -----TGATTCTGGATCCTACAACAGCTGACCTTTGGCTCAGGAACAGGCTGTCTGTCAAACCAA	J ₄₃	48
V ₀ 3.12-10	Y L C : <u>TACCTCTGT</u>	GCTGTGCGTGCTAACTTAT-----	F G S G TGACTACAGCGGCGACAAGCTGACCTTTGGCTCAGGACCAGGCTGTCTGTCTACCAA -----ACAAGCTGACTTTGGCTCAGGACCAGGCTGTCTGTCTACCAA	J ₇	21
V ₀ 3.12-11	Y L C : <u>TACCTCTGT</u>	GCTGTGCGTGATCCGC-----	F G S G TGACTATGACTACACCAACAAGCTGACCTTTGGCTCAGGACCAGGCTGTCCGTCTACCAA -----CTATGACTACACCAACAAGCTGACCTTTGGCTCAGGACCAGGCTGTCCGTCTACCAA	J ₁₃	33
V ₀ 3.13-1	Y F C : <u>TACTTCTGT</u>	GCTGTGAGAG-----	F G A G CCAATCAGGGATATGTGAAACTGGCATTGGAGCTGGCACCACCAACTTCTTGTATCCAA -----CCAATCAGGGATATGTGAAACTGGCATTGGAGCTGGCACCACCAACTTCTTGTATCCAA	J ₆₈ (*)	28
V ₀ 3.13-2	Y F C : <u>TACTTCTGT</u>	GCTGTGGTTC-----	F G D G TGCTTTGGATACCTACAAGCTAACCTTTGGAGATGGAACAAGGCTCATGGTAAACCAA -----TGGATACCTACAAGCTAACCTTTGGAGATGGAACAAGGCTCATGGTAAACCAA	J ₆₆	21
V ₀ 3.14-1	Y F C : <u>TACTTCTGT</u>	GCTGTGAGTGGACGGGACC-----	F G K G AGTTAAATCGCGCAGCTGACCTTTGGGAAAGGAAGCTGTGCTTTCAGTTGTTCCAG -----ATCGCGCAGCTGACCTTTGGGAAAGGAAGCTGTGCTTTCAGTTGTTCCAG	J ₁₄	27
V ₀ 3.14-2	Y F C : <u>TACTTCTGT</u>	GCTGTGAGCCATCGTCA-----	F G S G TGGCTCTGGCTCTTCATATGGCAAATTGACCTTTGGCTCAGGACCAGGCTGTCTGTCCATCCAA -----TGGCTCTGGCTCTTCATATGGCAAATTGACCTTTGGCTCAGGACCAGGCTGTCTGTCCATCCAA	J ₄₁	39
V ₀ 3.14-3	Y F C : <u>TACTTCTGT</u>	GCTGTGTCCC-----	F G S G TGACTCTGGCTACAACAAGCTGACCTTTGGCTCAGGACTAGGCTGTCTGTCTACCAA -----ACACTGGCTACAACAAGCTGACCTTTGGCTCAGGACTAGGCTGTCTGTCTACCAA	J ₄₉	24
V ₀ 3.14-4	Y F C : <u>TACTTCTGT</u>	GCTGTAGACCT-----	F G S G TGGCTATGGCTCTGGATATGACAGAATGACCTTTGGCTCAGGAACCAAGGCTGTCTGTCCAACCAA -----CTATGGCTCTGGATATGACAGAATGACCTTTGGCTCAGGAACCAAGGCTGTCTGTCCAACCAA	J ₂₈	30
V ₀ 3.14-5	Y L C : <u>TACTTCTGT</u>	GCTGTGATGACCCCACTA-----	F G S G TGACTTTGGCTCTGGCAACAAGCTGACCTTTGGCTCAGGAACCAAGGCTGTCCGTCTACCAA -----TTGGCTCTGGCAACAAGCTGACCTTTGGCTCAGGAACCAAGGCTGTCCGTCTACCAA	J ₃₅	33
V ₀ 3.14-6	Y L C : <u>TACTTCTGT</u>	GCTGTGAGGCGTTGGAGAGGAC-----	F G S G TGACTTTGGCTCTGGCAACAAGCTGACCTTTGGCTCAGGAACCAAGGCTGTCCGTCTACCAA -----GCTCTGGCAACAAGCTGACCTTTGGCTCAGGAACCAAGGCTGTCCGTCTACCAA	J ₃₅	33
V ₀ 3.15	Y L C : <u>TACCTCTGT</u>	GCTGTGAAGGA-----	F G S G TGACTATGACTACACCAACAAGCTGACCTTTGGCTCAGGACCAGGCTGTCCGTCTACCAA -----TGACTATGACTACACCAACAAGCTGACCTTTGGCTCAGGACCAGGCTGTCCGTCTACCAA	J ₁₃	30
V ₀ 3.16-1	Y L C : <u>TACCTCTGT</u>	GCTGTGCC-----	F G S G TGGCTCTAGCTCTTCATTTCGCAAAATTGACCTTTGGCTCGGGACCAGGCTGTCTGTCCAACCAA -----CTCTAGCTCTTCATTTCGCAAAATTGACCTTTGGCTCGGGACCAGGCTGTCTGTCCAACCAA	J ₁₁	27
V ₀ 3.16-2	Y L C : <u>TACCTCTGT</u>	GCTGTGCGTGAAGA-----	F G S G TGACTATGGAACCAACAGGCTGACATTTGGCTCAGGACCAGACTGTCTGTCCAACCAA -----TGACTATGGAACCAACAGGCTGACATTTGGCTCAGGACCAGACTGTCTGTCCAACCAA	J ₅ (*)	27
V ₀ 3.16-3	Y L C : <u>TACCTCTGT</u>	GCTGTGCGTGATACGG-----	F G S G TGACTGGCAACAACAAGCTGACCTTTGGCTCAGGAACCAAGGCTGTCCGTCTACCCA -----ACAAGCTGACCTTTGGCTCAGGAACCAAGGCTGTCCGTCTACCCA	J ₅₀	18
V ₀ 3.17-1	Y L C : <u>TACCTCTGT</u>	GCTGTGCGTGACGG-----	F G S G TGGCTATGGCTCTGGATATGACAGACTGACCTTTGGCTCAGGAACCAAGGCTGTCTGTCCAACCAA -----GGCTATGGCTCTGGATATGACAGACTGACCTTTGGCTCAGGAACCAAGGCTGTCTGTCCAACCAA	J ₄₆	36

	Y L C		F G S G		
V ₀ 3.17-2 :	<u>TAC</u> TCTGT	GCTGTGCGGG-----	TCACTACAGCACTGACAAGCTGACCTTTGGGCTCAGGGACCAAGGCTGTCCGTCTACCAA -----ACAGCACTGACAAGCTGACCTTTGGCTCAGGGACCAAGGCTGTCCGTCTACCAA	J ₀ 24	21
	Y L C		F G K G		
V ₀ 3.18 :	<u>TAC</u> TCTGT	GCTGTAGACACGC-----	TATACAATGCGGGCAAAGTCACCTTTGGGAAAGGAAGCTGTGCTTTCAGTTGTACCAG -----TATACAATGCGGGCAAAGTCACCTTTGGGAAAGGAAGCTGTGCTTTCAGTTGTACCAG	J ₀ 56	27
	Y F C		F G S G		
V ₀ 3.19 :	<u>TACT</u> TCTGT	GCTGTGAGCGAGGGTGG-----	CGACTATGGGAACAACAAGCTGACCTTTGGCTCAGGGACCAAGGCTGTCTGTCCAACCAA -----CGACTATGGGAACAACAAGCTGACCTTTGGCTCAGGGACCAAGGCTGTCTGTCCAACCAA	J ₀ 57	33
	Y F C		F G A G		
V ₀ 3.20-1 :	<u>TACT</u> TCTGT	GCTGTGAGGGG-----	CCAATCAGGGATATGTGAAAGTGGCACTTTGGAGCTGGCACCCTTCTTGTATCCCAA -----TCAGGGATATGTGAAGCTGGCACTTTGGAGCTGGCACCCTTCTTGTATCCCAA	J ₀ 68	24
	Y F C		F G S G		
V ₀ 3.20-2 :	<u>TACT</u> TCTGT	GCTGTGAGTGGCCCGTT-----	TGACTACAGCGGTGACAAGCTGACCTTTGGCTCAGGGACCAAGGCTGTCTGTCTACCAA -----CTACAGCGGTGACAAGCTGACCTTTGGCTCAGGGACCAAGGCTGTCTGTCTACCAA	J ₀ 25	30
V ₀ 3.20-3 :	<u>TACT</u> TCTGT	GCTGTCCAGT-----	CTACAGCGGTGACAAGCTGACCTTTGGCTCAGGGACCAAGGCTGTCTGTCTACCAA -----CTACAGCGGTGACAAGCTGACCTTTGGCTCAGGGACCAAGGCTGTCTGTCTACCAA	(*)	23
	Y F C		F G S G		
V ₀ 3.20-4 :	<u>TACT</u> TCTGT	GCTGTGAAGGGGGTGCAC-----	TGAGTGGCAACTACAAGCTGACCTTTGGCTCAGGAACCAAGGCTGTCTGTCTACCAA -----TGGCACTACAAGCTGACCTTTGGCTCAGGAACCAAGGCTGTCTGTCTACCAA	J ₀ 17	30
	Y F C		F G S G		
V ₀ 3.20-5 :	<u>TACT</u> TCTGT	GCTGTGAGTGATGCG-----	TGACACTGGCTACAACAAGCTGACCTTTGGCTCAGGGACTAGGCTGTCTGTCTACCAA -----ACTGGCTACAACAAGCTGACCTTTGGCTCAGGGACTAGGCTGTCTGTCTACCAA	J ₀ 18	27
	Y F C		F G S G		
V ₀ 3.20-6 :	<u>TACT</u> TCTGT	GCTGTGCGCGA-----	TGATTCTGGATCCTACAACAAGCTGACCTTTGGCTCAGGAACCAAGGCTGTCTGTCAAACCAA -----GGATCCTTCAACAAGCTGACCTTTGGCTCAGGAACCAAGGCTGTCTGTCAAACCAA	J ₀ 43	33
	Y F C		F G S G		
V ₀ 3.21 :	<u>TACT</u> TCTGT	TCTGTGAGTGATGCCCCCGC-----	TGAACACGAGAAGCTCACATTTGGGAAGGGAACACGACTTCAGGTTTGCCTA -----AAGTCCACATTTGGGAAGGGAACACGACTTCAGGTTTGCCTA	J ₀ 29	21
	Y L C		F G S G		
V ₀ 3.22-1 :	<u>TAC</u> TCTGT	GCTGTGAGGGGGCGCC-----	TGATTCTGGATCCTACAACAAGCTGACCTTTGGCTCAGGAACCAAGGCTGTCTGTCAAACCAA -----ATTCTGGATCCTACAACAAGCTGACCTTTGGCTCAGGAACCAAGGCTGTCTGTCAAACCAA	J ₀ 43	33
	Y L C		F G S G		
V ₀ 3.22-2 :	<u>TAC</u> TCTGT	GCTCCGTA-----	TGACACTGGCTACAACAAGCTGACCTTTGGCTCAGGGACTAGGCTGTCTGTCTACCAA -----TGACACTGGCTACAACAAGCTGACCTTTGGCTCAGGGACTAGGCTGTCTGTCTACCAA	J ₀ 49	24
	Y L C		F G S G		
V ₀ 3.22-3 :	<u>TAC</u> TCTGT	GCTGTGCGCCTCG-----	TGATTTTGGATCCTTCAACAAGCTGATCTTTGGCTCAGGAACCAAGGCTGTCCGTCTACCCA -----TTGATCCTTCAACAAGCTGATCTTTGGCTCAGGAACCAAGGCTGTCCGTCTACCCA	J ₀ 19	27
	Y L C		F G K G		
V ₀ 3.23 :	<u>TACT</u> TCTGT	GCTGTGAGTGATCCCCAAG-----	TATACAATGCGGGCAAAGTCACCTTTGGAAAGGAAGCTGTGCTTTTCAGTTGTACCAG -----ACAATGCGGGCAAAGTCACCTTTGGAAAGGAAGCTGTGCTTTTCAGTTGTACCAG	J ₀ 56	30

B

		D _β 1 TTGACTACGTAC	D _β 2 TTTTGGGATTGGAGTAC			CDR3 (nt)
V _β 1	: Y F C TATTCTGTGCTGTTCA TATTCTGTGCTGTTCTCTTTGGGATTGG	-----TAA-----TTGACTACGTAC-----G-----TTGGGATTGG-----	-----TTGGGATTGG-----	F G S G ATAACAGATAAGCTTGCTTTGGGAGTGGAAACCACTCTCACAGTCGAACCAA -----ACAGATAAGCTTGCTTTGGGAGTGGAAACCACTCTCACAGTCGAACCAA	J _β 1	39
V _β 2.1	: Y F C TACTTCTGTGCAGTTTCG TACTTCTGTGCAGTTCTCTTTGGGATTGGAG	-----C-----GAGTAC-----	-----GAGTAC-----	F G S G ATAACAGATAAGCTTGCTTTGGGAGTGGAAACCACTCTCACAGTCGAACCAA -----GATAAGCTTGCTTTGGGAGTGGAAACCACTCTCACAGTCGAACCAA	J _β 1	18
V _β 2.2	: Y F C TACTTCTGTGCAGTTTCG TACTTCTGTGCAGTTCTCTTTGGGATTGGAG	-----GGGGGACGACTTTAC-----	-----GGGGGACGACTTTAC-----	F G S G ATAACAGATAAGCTTGCTTTGGGAGTGGAAACCACTCTCACAGTCGAACCAA -----ACAGATAAGCTTGCTTTGGGAGTGGAAACCACTCTCACAGTCGAACCAA	J _β 1	27
V _β 2.3	: Y F C TACTTCTGTGCAGTTTCG TACTTCTGTGCAGTTCTCTTTGGGATTGGAG	-----AGAGCGCCGAC-----	-----GGGGATTGGAG-----	F G S G ATAACAGATAAGCTTGCTTTGGGAGTGGAAACCACTCTCACAGTCGAACCAA -----CCCTGGATAAGCTTGCTTTGGGAGTGGAAACCACTCTCACAGTCGAACCAA	J _β 1	36
V _β 2.3-1	: TACTTCTGTGCAGTTTCG TACTTCTGTGCAGTTCTCTTTGGGATTGGAG	-----GCCAACGCGGG-----	-----GGAGTA-----	F G S G ATAACAGATAAGCTTGCTTTGGGAGTGGAAACCACTCTCACAGTCGAACCAA -----ATAAGCTTGCTTTGGGAGTGGAAACCACTCTCACAGTCGAACCAA	J _β 1	27
V _β 2.10	: Y F C TACTTTTGTGCAGTTTCG TACTTTTGTGCAGTTCTCTTTGGGATTGGAG	-----CGG-----GACTACG-----TTTGGGATTGGAGTAC-----GTCCTG-----	-----TTTGGGATTGGAGTAC-----GTCCTG-----	F G S G ATAACAGATAAGCTTGCTTTGGGAGTGGAAACCACTCTCACAGTCGAACCAA -----CAGATAAGCTTGCTTTGGGAGTGGAAACCACTCTCACAGTCGAACCAA	J _β 1	45
V _β 2.10-1	: TACTTTTGTGCAGTTTCG TACTTTTGTGCAGTTCTCTTTGGGATTGGAG	-----ACTC-----GACTACGTA-----GCCGA-----TTGGGATTGGAGTAC-----GGGCT-----	-----TTGGGATTGGAGTAC-----GGGCT-----	F G S G ATAACAGATAAGCTTGCTTTGGGAGTGGAAACCACTCTCACAGTCGAACCAA -----ATAAGCTTGCTTTGGGAGTGGAAACCACTCTCACAGTCGAACCAA	J _β 1	45
V _β 2.10-2	: TACTTCTGTGCAGTTTCG TACTTCTGTGCAGTTCTCTTTGGGATTGGAG	-----GAACG-----	-----TTTGGGATTGGAG-----GTGG-----	F G S G ATAACAGATAAGCTTGCTTTGGGAGTGGAAACCACTCTCACAGTCGAACCAA -----GATAAGCTTGCTTTGGGAGTGGAAACCACTCTCACAGTCGAACCAA	J _β 1	33
V _β 2.12	: Y F C TACTTCTGTGCAGTTTCG TACTTCTGTGCAGTTCTCTTTGGGATTGGAG	-----TATGGGGC---TGACTAC-----ACC-----GGATTGGAGTAC-----G-----	-----GGATTGGAGTAC-----G-----	F G S G ATAACAGATAAGCTTGCTTTGGGAGTGGAAACCACTCTCACAGTCGAACCAA -----ACAGATAAGCTTGCTTTGGGAGTGGAAACCACTCTCACAGTCGAACCAA	J _β 1	45
V _β 2.14	: Y F C TACTTCTGTGCAGTTTCG TACTTCTGTGCAGTTCTCTTTGGGATTGGAG	-----TATGGGGC---TGACTAC-----ACC-----GGATTGGAGTAC-----G-----	-----GGATTGGAGTAC-----G-----	F G S G ATAACAGATAAGCTTGCTTTGGGAGTGGAAACCACTCTCACAGTCGAACCAA -----ACAGATAAGCTTGCTTTGGGAGTGGAAACCACTCTCACAGTCGAACCAA	J _β 1	45
V _β 3.1	: Y F C TATTCTGTGCTGTTTCG TATTCTGTGCTGTTCTCTTTGGGATTGGAG	-----ACTACGTA-----TGGGATTGGAGTAC-----GCCG-----	-----TGGGATTGGAGTAC-----GCCG-----	F G K G TGTTACTGCTCCTCTTATCTTCGGGAAGGGGACTCAACTGACCGTGAACCAA -----TACTGCTCCTCTTATCTTCGGGAAGGGGACTCAACTGACCGTGAACCAA	J _β 2	39
V _β 3.1-1	: TATTCTGTGCTGTTTCG TATTCTGTGCTGTTCTCTTTGGGATTGGAG	-----ACGTA-----TACGTAC-----GG-----GGGATTGGAGTAC-----	-----GGGATTGGAGTAC-----	F G S G ATAACAGATAAGCTTGCTTTGGGAGTGGAAACCACTCTCACAGTCGAACCAA -----GATAAGCTTGCTTTGGGAGTGGAAACCACTCTCACAGTCGAACCAA	J _β 1	39
V _β 3.1-2	: TATTCTGTGCTGTTTCG TATTCTGTGCTGTTCTCTTTGGGATTGGAG	-----ACGTA-----TACGTAC-----GG-----GGGATTGGAGTAC-----	-----GGGATTGGAGTAC-----	F G S G ATAACAGATAAGCTTGCTTTGGGAGTGGAAACCACTCTCACAGTCGAACCAA -----GATAAGCTTGCTTTGGGAGTGGAAACCACTCTCACAGTCGAACCAA	J _β 1	27
V _β 3.1-3	: TATTCTGTGCTGTTTCG TATTCTGTGCTGTTCTCTTTGGGATTGGAG	-----CCCC-----CGTAC-----TTTCT-----ATTGG-----	-----ATTGG-----	F G S G ATAACAGATAAGCTTGCTTTGGGAGTGGAAACCACTCTCACAGTCGAACCAA -----GATAAGCTTGCTTTGGGAGTGGAAACCACTCTCACAGTCGAACCAA	J _β 1	27
V _β 3.2	: Y F C TATTCTGTGCTGTTTCG TATTCTGTGCTGTTCTCTTTGGGATTGGAG	-----CCGA-----TTGACTACGTA-----TCCTC-----	-----TCCTC-----	F G S G ATAACAGATAAGCTTGCTTTGGGAGTGGAAACCACTCTCACAGTCGAACCAA -----GATAAGCTTGCTTTGGGAGTGGAAACCACTCTCACAGTCGAACCAA	J _β 1 (*)	25
V _β 3.3	: Y F C TATTCTGTGCTGTTTCG TATTCTGTGCTGTTCTCTTTGGGATTGGAG	-----CGAGAC-----TTGGAG-----CCGTC-----	-----TTGGAG-----CCGTC-----	F G S G ATAACAGATAAGCTTGCTTTGGGAGTGGAAACCACTCTCACAGTCGAACCAA -----ATAAGCTTGCTTTGGGAGTGGAAACCACTCTCACAGTCGAACCAA	J _β 1 (*)	25

	Y F C		F G S G		
V ₅ 5	: <u>TATTCTGCGTGGTTCG</u>		<u>ATAACAGATAAGCTTGTCTTTGGAAGTGGAA</u> CCACTCTCACAGTCGAACCAA	J ₅ 1	
V ₅ 5-1	: TATTCTGCGTGGT-----AACG-----TTTGGGTTTGA-----TAGTG-----		-----TAAGCTTGTCTTTGGAAGTGGAA	(*)	27
V ₅ 5-2	: <u>TATTCTGCGTGGTTCG</u> -----GGTTCCTCC-----		-----CAGATAAGCTTGTCTTTGGAAGTGGAA		24
	Y L C		F G S G		
V ₅ 1.1p	: <u>TACCTGTGTGCACTGAGCC</u>		<u>ATAACAGATAAGCTTGTCTTTGGAAGTGGAA</u> CCACTCTCACAGTCGAACCAA	J ₅ 1	
	<u>TACCTGTGTGCACTGAGC</u> -----GGAA-----TTGACTACG-----CACGAGG-----TTGGA-----AGGTG-----		-----AAGCTTGTCTTTGGAAGTGGAA	(*)	39
	Y Y C		F G S G		
V ₅ 2.1	: <u>TATTACTGCGCCCTGAGAGC</u>		<u>ATAACAGATAAGCTTGTCTTTGGAAGTGGAA</u> CCACTCTCACAGTCGAACCAA	J ₅ 1	
	<u>TATTACTGCGCCCTGAG</u> -----TCA-----TACGTAC-----GGTCTCC-----TGGGATTGGAGTAC-----GGAGG-----		-----AACAGATAAGCTTGTCTTTGGAAGTGGAA		51
	Y Y C		F G S G		
V ₅ 2.2	: <u>TATTACTGCGCCCTGAGAGC</u>		<u>ATAACAGATAAGCTTGTCTTTGGAAGTGGAA</u> CCACTCTCACAGTCGAACCAA	J ₅ 1	
	<u>TATTACTGCGCCCTGAGAGC</u> ---GAGGAGCTG---GACTACGT-----CCG-----TTTGGGA-----CCTT-----		-----ACAGATAAGCTTGTCTTTGGAAGTGGAA		48
	Y Y C		F G S G		
V ₅ 2.3	: <u>TATTACTGCGCCCTGAGAGC</u>		<u>ATAACAGATAAGCTTGTCTTTGGAAGTGGAA</u> CCACTCTCACAGTCGAACCAA	J ₅ 1	
V ₅ 2.3-1	: TATTACTGCGCCCTGAGAGC---GGGACGATCAC-----GGATTGG-----GATTGG-----		-----AGATAAGCTTGTCTTTGGAAGTGGAA		39
V ₅ 2.3-2	: TATTACTGCGCCCTGAGAGC-----ACTACGTAC-----C-----GGATTGGA-----C-----		-----AAGCTTGTCTTTGGAAGTGGAA		30
V ₅ 2.3-3	: <u>TATTACTGCGCCCTGAGAG</u> ---GAAG-----TACGT-----TCC-----TGGGT-----TGGACG-----		-----AGATAAGCTTGTCTTTGGAAGTGGAA	(*)	38
	Y L C		F G K G		
V ₅ 3.2	: <u>TACCTCTGTGCTGTGAATGA</u>		<u>TGTTACTGCTCCTCTTATCTTCGGGAAGGGG</u> ACTCAACTGACCGTGAACCAA	J ₅ 2	
V ₅ 3.2-1	: <u>TACCTCTGTGCTGTGA</u> -----GCTCCTCTTATCTTCGGGAAGGGG		-----GCTCCTCTTATCTTCGGGAAGGGG		18
V ₅ 3.2-2	: <u>TACCTCTGTGCTGTGAATG</u> -----GGCGAGCGGACTCTACGGGGGAATAG		-----TGTACTGCTCCTCTTATCTTCGGGAAGGGG		48
	Y L C		F G S G		
V ₅ 3.3	: <u>TACCTCTGTGCTGTGAATGA</u>		<u>ATAACAGATAAGCTTGTCTTTGGAAGTGGAA</u> CCACTCTCACAGTCGAACCAA	J ₅ 1	
V ₅ 3.3-1	: <u>TACCTCTGTGCTGTGA</u> -----GTG-----TACGTAC-----AAGG-----TGGAGTA-----AGG-----		-----AGCTTGTCTTTGGAAGTGGAA		30
V ₅ 3.3-2	: <u>TACCTCTGTGCTGTGAATGA</u> ---TAT-----GATTGG-----CCG-----		-----GCTTGTCTTTGGAAGTGGAA		21
			F G K G		
V ₅ 3.3-3	: <u>TACCTCTGTGCT</u> -----AGGGG-----TGGGATTGGAGTAC-----GGG-----		<u>TGTTACTGCTCCTCTTATCTTCGGGAAGGGG</u> ACTCAACTGACCGTGAACCAA	J ₅ 2	
			-----ACTGCTCCTCTTATCTTCGGGAAGGGG	(*)	31
	Y L C		F G S G		
V ₅ 3.4	: <u>TACCTCTGTGCTGTGAATGA</u>		<u>ATAACAGATAAGCTTGTCTTTGGAAGTGGAA</u> CCACTCTCACAGTCGAACCAA	J ₅ 1	
V ₅ 3.4-1	: <u>TACCTCTGTGCTGTGA</u> -----GACCGG-----ACGTAC-----GCCGAGGTAC-----		-----GATAAGCTTGTCTTTGGAAGCGGA		33
V ₅ 3.4-2	: <u>TACCTCTGTGCTGTGA</u> ---GCAC---TGACTACGT---CC---TTTGGGATTGGAGT---TCGCCTCTAAT		-----ATAACAGATAAGCTTGTCTTTGGAAGTGGAA	(*)	58

		D ₀ 1	D ₀ 2	F G S G	CDR3 (nt)
		TTGACTACGTAC	TTTTGGGATTGGAGTAC		
V ₀ 2.15-1	Y F C	GCAGTTCGAACCCAGGG-----	-----TTGGAGTA-----GTCGT-----	ATAACAGATAAGCTTGCTTTGGAAAGTGGAAACCACTCTCACAGTCGAACCAA	J ₀ 1
V ₀ 2.15-2	TACTTCTGT	GCACCCCTTCTCCGAGGG-----	-----TTGGAGT-----	-----ATAACAGATAAGCTTGCTTTGGAAAGTGGAAACCACTCTCACAGTCGAACCAA	39
V ₀ 2.15-3	TACTTCTGT	GCAGTCCCCCTC-----GACTAC-----TTCC-----TTTGGGATTGGAGTAC-----CCCAAC-----	-----TTTGGGATTGGAGTAC-----CCCAAC-----	-----ACAGATAAGCTTGCTTTGGAAAGTGGAAACCACTCTCACAGTCGAACCAA	24
				-----TTGGAAAGTGGAAACCACTCTCACAGTCGAACCAA	36 (*)
V ₀ 2.16	Y F C	GCAGTA-----GACTAC-----TCGACC-----TTGGGATTGGAGT-----CGC-----	-----TTGGGATTGGAGT-----CGC-----	TGTTACTGCTCCTCTTATCTTCGGGAAGGGGACTCAACTGACCGTGAACCAA	J ₀ 2
	TACTTCTGT			-----CTCCTCTTATCTTCGGGAAGGGGACTCAACTGACCGTGAACCAA	36
V ₀ 2.17	Y F C	GCAGTTCGCCGA-----GACTACG-----G-----TTGGAG-----AACTC-----	-----TTGGAG-----AACTC-----	ATAACAGATAAGCTTGCTTTGGAAAGTGGAAACCACTCTCACAGTCGAACCAA	J ₀ 1
	TACTTCTGT			-----CAGATAAGCTTGCTTTGGAAAGTGGAAACCACTCTCACAGTCGAACCAA	36
V ₀ 2.18-1	Y F C	GCAGTTAAAC-----GGGGTT-----CGAGT-----	-----GGGGTT-----CGAGT-----	ATAACAGATAAGCTTGCTTTGGAAAGTGGAAACCACTCTCACAGTCGAACCAA	J ₀ 1
	TACTTTTGT			-----ACGTATAAGCTTGCTTTGGAAAGTGGAAACCACTCTCACAGTCGAACCAA	27
V ₀ 2.18-2	TACTTTTGT	GCAGTTCGCGGTG-----TTTGGGATTGGA-----CCGA-----	-----TTTGGGATTGGA-----CCGA-----	TGTTACTGCTCCTCTTATCTTCGGGAAGGGGACTCAACTGACCGTGAACCAA	J ₀ 2
				-----ACTGCTCCTCTTATCTTCGGGAAGGGGACTCAACTGACCGTGAACCAA	36
V ₀ 2.19-1	Y F C	GCAGTTCGCGAGTACGAAGTGC-----TTGGAGTAC-----GTTCTA-----	-----TTGGAGTAC-----GTTCTA-----	TGTTACTGCTCCTCTTATCTTCGGGAAGGGGACTCAACTGACCGTGAACCAA	J ₀ 2
	TACTTCTGT			-----TTACTGCTCCTCTTATCTTCGGGAAGGGGACTCAACTGACCGTGAACCAA	45 (*)
V ₀ 2.19-2	TACTTCTGT	GCAGTCCTACG-----TTGGAG-----AAGT-----	-----TTGGAG-----AAGT-----	ATAACAGATAAGCTTGCTTTGGAAAGTGGAAACCACTCTCACAGTCGAACCAA	J ₀ 1
				-----ATAACAGATAAGCTTGCTTTGGAAAGTGGAAACCACTCTCACAGTCGAACCAA	30
V ₀ 2.20	Y F C	GCAGTTAAAGTCGT-----TTGACTAC-----CCG-----TTTGGGATTGGAGTA-----AGTAGG-----	-----TTTGGGATTGGAGTA-----AGTAGG-----	ATAACAGATAAGCTTGCTTTGGAAAGTGGAAACCACTCTCACAGTCGAACCAA	J ₀ 1
	TACTTCTGT			-----AGCTTGCTTTGGAAAGTGGAAACCACTCTCACAGTCGAACCAA	46 (*)
V ₀ 2.5	Y Y C	GCCCTGAGA-----TTGACTACGTAC-----GATGGC-----	-----TTGACTACGTAC-----GATGGC-----	ATAACAGATAAGCTTGCTTTGGAAAGTGGAAACCACTCTCACAGTCGAACCAA	J ₀ 1
	TATTACTGC			-----GATAAGCTTGCTTTGGAAAGTGGAAACCACTCTCACAGTCGAACCAA	30
V ₀ 2.8	Y Y C	GCCCT-----GAGTAC-----TCCA-----	-----GAGTAC-----TCCA-----	TGTTACTGCTCCTCTTATCTTCGGGAAGGGGACTCAACTGACCGTGAACCAA	J ₀ 2
	TATTACTGC			-----ACTGCTCCTCTTATCTTCGGGAAGGGGACTCAACTGACCGTGAACCAA	21
V ₀ 2.12-1	Y Y C	GCCCTCC-----TTGGGATTG-----CGCA-----	-----TTGGGATTG-----CGCA-----	TGTTACTGCTCCTCTTATCTTCGGGAAGGGGACTCAACTGACCGTGAACCAA	J ₀ 2
	TATTACTGC			-----TGTTACTGCTCCTCTTATCTTCGGGAAGGGGACTCAACTGACCGTGAACCAA	30
V ₀ 2.12-2	Y Y C	GCCCTGAGAGCAATTCTCG-----TGACTACGTA-----G-----GGGATTGG-----C-----	-----TGACTACGTA-----G-----GGGATTGG-----C-----	ATAACAGATAAGCTTGCTTTGGAAAGTGGAAACCACTCTCACAGTCGAACCAA	J ₀ 1
	TATTACTGC			-----TAACAGATAAGCTTGCTTTGGAAAGTGGAAACCACTCTCACAGTCGAACCAA	48

V _a 2.15	: Y Y C : <u>TATTACTGC</u>	GCCCTGAGAGCG-----GACTACGTAC-----CG-----	ATAACAGATAAGCTTGCTTTGGAAGTGGAAACCACTCTCACAGTCGAACCAA	J _o 1	27
			F G S G		
V _a 2.17-1	: Y Y C : <u>TATTACTGC</u>	GCCCTGTATC-----CTACGT-----CGGA-----	ATAACAGATAAGCTTGCTTTGGAAGTGGAAACCACTCTCACAGTCGAACCAA	J _o 1	15
V _a 2.17-2	: <u>TATTACTGC</u>	GCCCTGAGACCC-----TTGACTACGTAC-----GGGTG-----	ATAACAGATAAGCTTGCTTTGGAAGTGGAAACCACTCTCACAGTCGAACCAA		33
V _a 2.17-4	: <u>TATTACTGC</u>	GCCCTAAC-----GACTACGT-----TGGGTTGGAGT-----CG-----	ATAACAGATAAGCTTGCTTTGGAAGTGGAAACCACTCTCACAGTCGAACCAA	(*)	35
			F G K G		
V _a 2.17-3	: <u>TATTACTGC</u>	GCCCTGATCACTCC-----TTTGGGTTGGA-----TCC-----	TGTTACTGCTCCTCTTATCTTCGGGAAGGGGACTCAACTGACCGTGGAAACCAA	J _o 2	36
			F G K G		
V _a 2.18-1	: Y Y C : <u>TATTACTGC</u>	GCCCTGAGAGGAGG-----GGGAT-----GGAG-----	TGTTACTGCTCCTCTTATCTTCGGGAAGGGGACTCAACTGACCGTGGAAACCAA	J _o 2	30
V _a 2.18-3	: <u>TATTACTGC</u>	GCCCTGACTGAG-----CTACGTAC-----ATA-----TTTGGGTTGGAGTAC-----GGGTGTC-----	TGTTACTGCTCCTCTTATCTTCGGGAAGGGGACTCAACTGACCGTGGAAACCAA		57
			F G S G		
V _a 2.18-2	: <u>TATTACTGC</u>	GCCC-----TGACTACGT-----TGCCCC-----	ATAACAGATAAGCTTGCTTTGGAAGTGGAAACCACTCTCACAGTCGAACCAA	J _o 1	21
V _a 2.18-4	: <u>TATTACTGC</u>	GCCCTGAGGGG-----CTACGTAC-----GTTTA-----GGGTTG-----ACC-----	ATAACAGATAAGCTTGCTTTGGAAGTGGAAACCACTCTCACAGTCGAACCAA		39
			F G S G		
V _a 2.19	: Y Y C : <u>TATTACTGC</u>	GCCCTGAGAGGG-----GACTAC-----TTTGGGTTGGAGTAC-----	ATAACAGATAAGCTTGCTTTGGAAGTGGAAACCACTCTCACAGTCGAACCAA	J _o 1	38
			(*)		
			F G S G		
V _a 2.20	: Y Y C : <u>TATTACTGC</u>	GCCC-----TGACTACGTA-----G-----GGGTTGGAGT-----C-----	ATAACAGATAAGCTTGCTTTGGAAGTGGAAACCACTCTCACAGTCGAACCAA	J _o 1	33
			(*)		
			F G S G		
V _a 3.11-1	: Y L C : <u>TACCTCTGT</u>	GCTG-----TACGT-----GTC-----GGGATTGGA-----AGGGTTATAGAG-----	ATAACAGATAAGCTTGCTTTGGAAGTGGAAACCACTCTCACAGTCGAACCAA	J _o 1	39
V _a 3.11-2	: <u>TACTTCTGT</u>	GCTGTGCGTTCGGGGCGAA-----TTGACTACG-----CACCCC-----GGGTTGGAGTAC-----GC-----	ATAACAGATAAGCTTGCTTTGGAAGTGGAAACCACTCTCACAGTCGAACCAA		51
V _a 3.11-3	: <u>TACCTCTGT</u>	GCTGTGCGTA-----CTTCGG-----TTGGGATTGGA-----CTTCGG-----	ATAACAGATAAGCTTGCTTTGGAAGTGGAAACCACTCTCACAGTCGAACCAA		33
			F G S G		
V _a 3.12	: Y L C : <u>TACCTCTGT</u>	GCTGTGCGTGAGCGGGGCCCC-----	ATAACAGATAAGCTTGCTTTGGAAGTGGAAACCACTCTCACAGTCGAACCAA	J _o 1	24
			(*)		
			F G S G		
V _a 3.13-1	: Y F C : <u>TACTTCTGT</u>	GCTGTGAGTGACAC-----TTTTGG-----GTTGG-----	ATAACAGATAAGCTTGCTTTGGAAGTGGAAACCACTCTCACAGTCGAACCAA	J _o 1	32
V _a 3.13-2	: <u>TACTTCTGT</u>	GCTGTGAGGCTCCGTAC-----TGGGTTG-----TTCGTGCT-----	ATAACAGATAAGCTTGCTTTGGAAGTGGAAACCACTCTCACAGTCGAACCAA	(*)	35
			F G K G		
V _a 3.16-1	: Y L C : <u>TACCTCTGT</u>	GCTGTCCAACCA-----TTGACTACG-----GGGA-----	TGTTACTGCTCCTCTTATCTTCGGGAAGGGGACTCAACTGACCGTGGAAACCAA	J _o 2	36
V _a 3.16-2	: <u>TACCTCTGT</u>	GCTGGTACGCTTGTGCTATCG-----	TGTTACTGCTCCTCTTATCTTCGGGAAGGGGACTCAACTGACCGTGGAAACCAA		27
V _a 3.16-5	: <u>TACCTCTGT</u>	GCTGTGCGTGTC-----GACTACG-----GTCTTC-----	TGTTACTGCTCCTCTTATCTTCGGGAAGGGGACTCAACTGACCGTGGAAACCAA	(*)	31
V _a 3.16-9	: <u>TACCTCTGT</u>	GCTGTGCGTGATGGACG-----TTGGAG-----GGTTA-----	TGTTACTGCTCCTCTTATCTTCGGGAAGGGGACTCAACTGACCGTGGAAACCAA		30
V _a 3.16-10	: <u>TACCTCTGT</u>	GCTGTGAA-----TTGGGATTGGA-----TTATGTC-----	TGTTACTGCTCCTCTTATCTTCGGGAAGGGGACTCAACTGACCGTGGAAACCAA		33

				F	G	S	G		J _o
V _o .3.16-3 :	TACCTCTGT	GCTGTGCGTGATCGGGC-----CTACG-----G-----TTGGAGTA-----TCCGC-----ATAACAGATAAGCTTGTC TTTGAAGTGGAA CCACTCTCACAGTCGAACC A	39						
V _o .3.16-4 :	TACCTCTGT	GCTGTGAAGGGC-----GGACTAC-----GTCTC-----CAGATAAGCTTGTC TTTGAAGTGGAA CCACTCTCACAGTCGAACC A	30						
V _o .3.16-6 :	TACCTCTGT	GCTGTGCGTGAG-----TTGAC-----G-----TTGGG TT GAGT-----GGA-----TTGAAGT GGAA CCACTCTCACAGTCGAACC A	(*) 25						
V _o .3.16-7 :	TACCTCTGT	GCTGCCCCCGGT-----TACGTAC-----GGGGCCG-----AATAT-----AGATAAGCTTGTC TTTGAAGTGGAA CCACTCTCACAGTCGAACC A	(*) 45						
V _o .3.16-8 :	TACCTCTGT	GCTGTGCGTGATCGCTC-----TTGGG TT GAGTAC-----G-----ACAGATAAGCTTGTC TTTGAAGTGGAA CCACTCTCACAGTCGAACC A	39						
V _o .3.16-11:	TACCTCTGT	GTCTAG-----TACGTAC-----ACGGTGGGTGG-----AGATAAGCTTGTC TTTGAAGTGGAA CCACTCTCACAGTCGAACC A	30						
V _o .3.16-12:	TACCTCTGT	GCTGTGAATGATC-----GACTACGT-----GGATTGGAG-----TAACAGATAAGCTTGTC TTTGAAGTGGAA CCACTCTCACAGTCGAACC A	39						
V _o .3.16-13:	TACCTCTGT	GCTGTGCGTGACAC-----GGG GT TGGA-----CCGGTATG-----ACAGATAAGCTTGTC TTTGAAGTGGAA CCACTCTCACAGTCGAACC A	39						
V _o .3.16-14:	TACCTCTGT	GCTGTGCGTGACAGG-----TTGGAGTAC-----CTCAGT-----ATAACAGATAAGCTTGTC TTTGAAGTGGAA CCACTCTCACAGTCGAACC A	39						

C

		Dβ GGGACAGGGGATC	F G T G	CDR3 (nt)
V_β2	: TATTTCTGCGCTAAGCAAGATA		AATAATGAAAACTGTTCTTTGGCACTGGGACAAAACCTCACTGTCATAG	J_β1.2
V _β 2-1 (1)	: TATTTCTGCGCTAAGGA-----GATTAAAGGACGATGG-----		-----GAAAAACTGTTCTTTGGCACTGGGACAAAACCTCACTGTCATAG	27
V _β 2-4 (1)	: TATTTCTGCGCTAAG-----TTGCACCGGGACAG-----		-----TAATGAAAACTGTTCTTTGGCACTGGGACAAAACCTCACTGTCATAG	27
V _β 2-6 (1)	: TATTTCTGCGCTAAGCAAGATA-----TGC-----CAGGGGATC-----TCGCGCTGGATGCG-----		-----GAAAAACTGTTCTTTGGCACTGGGACAAAACCTCACTGTCATAG	42
V _β 2-8 (1)	: TATTTCTGCGCTAAGCAAGAT-----GG-----GGGGAT-----GGGTAG-----		-----TAATGAAAACTGTTCTTTGGCACTGGGACAAAACCTCACTGTCATAG	33
V _β 2-9 (1)	: TATTTCTGCGCTAAGCAAGA-----GAAGGAGGGCG-----		-----GAAAAACTGTTCTTTGGCACTGGGACAAAGACTCACTGTCATAG	(*) 25
V _β 2-10 (1)	: TATTTCTGCGCTAAGCAAGATA-----GGAGCTGG-----GGGGATC-----GTCCCG-----		-----TGAAAACTGTTCTTTGGCACTGGGACAAAACCTCACTGTCATAG	39
V _β 2-12 (1)	: TATTTCTGCGC-----CACGGGCCGA-----AGGGGATC-----GGGGTTAGCGAC-----		-----TGAAAACTGTCCTTTGGCACTGGGACAAAACCTCACTGTCATAG	36
V _β 2-13 (1)	: TATTTCTGCGCTAAGCAAGAT-----CTCGCTTCCGTTCCG-----GGGACAGGGGAT-----TACGGG-----		-----AATGAAAACTGTTCTTTGGCACTGGGACAAAACCTCACTGTCATAG	51
V _β 2-14 (1)	: TATTTCTGCGCTAAGCAAGAT-----CCGGCCGACAGTC-----GGGACAGGG-----CTACCA-----		-----TTGGCACTGGGACAAAACCTCACTGTCATAG	(*) 30
V_β2	: TATTTCTGCGCTAAGCAAGATA		ACCAACACTAAGGTGATTTTGGTTTGGGCACAAAAGTTACAGTGATGG	J_β1.1
V _β 2-2 (1)	: TATTTCTGCGC-----CGCGCGGTAC-----		-----CCAACACTAAGGTGATTTTGGTTTGGGCACAAAAGTTACAGTGATGG	21
V _β 2-3 (1)	: TATTTCTGCGCTAAGCA-----GGGT-----AGGGGA-----CACGGACTAT-----		-----ACACTAAGGTGATTTTGGTTTGGGCTCAAAAGTTACAGTGATGG	(*) 33
V _β 2-5 (1)	: TATTTCTGCGCTAAGCAAGA-----CGCCTAC-----GGGACAG-----CCTTACTT-----		-----ACCAACACTAAGGTGATTTTGGTTTGGGCACAAAAGTTACAGTGATGG	42
V_β2	: TATTTCTGCGCTAAGCAAGATA		CAATCTCAACAACTGCATTTTGGAAAGGGCACCCAGCTGACAGTGCTTG	J_β2.2
V _β 2-21 (2)	: TATTTCTGCGCTA-----TCGAC-----GGGAC-----G-----		-----CAATCTCAACAACTGCATTTTGGAAAGGGCACCCAGCTGACAGTGCTTG	24
V_β2	: TATTTCTGCGCTAAGCAAGATA		TTTTATCAATACCCAGTATTTTGGAGAAGGAACAAAAATAACAGTCTCTGG	J_β2.3
V _β 2-15 (2)	: TATTTCTGCGCTAAGCAAGATA-----CCTTACGACGGACCACTGC-----		-----TATCAATACCCAGTATTTTGGAGAAGGAACAAAAATAACAGTCTCTGG	(*) 39
V _β 2-16 (2)	: TATTTCTGCGCTAAGCA-----TC-----GACAGGGGA-----CGGAG-----		-----AATACCCAGTATTTTGGAGAAGGAACAAAAATAACAGTCTCTGG	27
V _β 2-18 (2)	: TATTTCTGCGCTAAGCA-----CCGGCGC-----GGGACA-----CTCT-----		-----TCAATACCCAGTATTTTGGAGAAGGAACAAAAATAACAGTCTCTGG	(*) 30
V _β 2-19 (2)	: TATTTCTGCGCTAAGCAAGAT-----GGGACAGG-----TCCTTCGGGC-----		-----ACCCAGTATTTTGGAGAAGGAACAAAAATAACAGTCTCTGG	30
V _β 2-20 (2)	: TATTTCTGCGCTAAGCAAGAT-----GAGACGAGGC-----CAGGG-----AGTAG-----		-----CAATACCCAGTATTTTGGAGAAGGAACAAAAATAACAGTCTCTGG	36
V_β2	: TATTTCTGCGCTAAGCAAGATA		ATACATATGAGGTTGAGTTTGGTCCTGGGACCCACATAACAGTACTAG	J_β2.1
V _β 2-17 (2)	: TATTTCTGCGCTAAG-----AGGTCCGAAGCT-----		-----ATATGAGGTTGAGTTTGGTCCTGGGACCCACATAACAGTACTAG	(*) 22
V _β 2-22 (2)	: TATTTCTGCGCTAAGCAAGATA-----GGACAGG-----ACGGG-----		-----ATGAGGTTGAGTTTGGTCCTGGGACCCACATAACAGTACTAG	27
V _β 2-23 (2)	: TATTTCTGCGCTAAGC-----GGGGTC-----GACAGG-----CGG-----		-----ATACATATGAGGTTGAGTTTGGTCCTGGGACCCACATAACAGTACTAG	(*) 30
V_β3.1 (3.4)	: TATTACTGTGCTGAAAGTGAAA		TTTTATCAATACCCAGTATTTTGGAGAAGGAACAAAAATAACAGTCTCTGG	J_β2.3
V _β 3.1-7 (2)	: TATTACTGTGCTGAA-----GTAACCGATC-----GGGACAGG-----		-----AATACCCAGTATTTTGGAGAAGGAACAAAAATAACAGTCTCTGG	27
V_β3.1 (3.4)	: TATTACTGTGCTGAAAGTGAAA		AATAATGAAAACTGTTCTTTGGCACTGGGACAAAACCTCACTGTCATAG	J_β1.2
V _β 3.1-2 (1)	: TATTACTGTGCTGAAA-----AGGGAGTACGCG-----GGGGA-----		-----GAAAAACTGTTCTTTGGCACTGGGACAAAACCTCACTGTCATAG	27
V _β 3.1-3 (1)	: TATTACTGTGCTGAAAGTG-----CGGTCGGGGATC-----		-----TAATGAAAACTGTTCTTTGGCACTGGGACAAAACCTCACTGTCATAG	30
V _β 3.1-4 (1)	: TATTACTGTGCTGAAAGTGAA-----GCCGGT-----GACAGGGGATC-----GGG-----		-----TGAAAACTGTTCTTTGGCACTGGGACAAAACCTCACTGTCATAG	36
V _β 3.1-5 (1)	: TATTACTGTGCTGAAAGTGAA-----GCGACCGAGCGAGG-----		-----TGAAAACTGTTCTTTGGCACTGGGACAAAACCTCACTGTCATAG	30
V_β3.1 (3.4)	: TATTACTGTGCTGAAAGTGAAA		ATACATATGAGGTTGAGTTTGGTCCTGGGACCCACATAACAGTACTAG	J_β2.1
V _β 3.1-6 (2)	: TATTACTGTGCTGAA-----GTCTTTGC-----GGGAT-----TC-----		-----GTTGAGTTTGGTCCTGGGACCCACATAACAGTACTAG	18
V _β 3.1-10 (2)	: TATTACTGTGCTGAAAGT-----CCG-----CAGGG-----CCTCT-----		-----GGTTGAGTTTGGTCCTGGGACCCACATAACAGTACTAG	21
V _β 3.1-13 (2)	: TATTACTGTGCTGAAAGTGAA-----GGGATC-----GG-----		-----TGAGGTTGAGTTTGGTCCTGGGACCCACATAACAGTACTAG	(*) 21
V_β3.1 (3.4)	: TATTACTGTGCTGAAAGTGAAA		CAATCTCAACAACTGCATTTTGGAAAGGGCACCCAGCTGACAGTGCTTG	J_β2.2
V _β 3.1-8 (2)	: TATTACTGTGCTGA-----GCTCGATCAGGTGAGGG-----		-----AACAACTGCATTTTGGAAAGGGCACCCAGCTGACAGTGCTTG	24
V _β 3.1-9 (2)	: TATTACTGTGCTGAAAGT-----CCC-----GGGACAGGGGATC-----CTCAGAGAG-----		-----AACAACTGCATTTTGGAAAGGGCACCCAGCTGACAGTGCTTG	36

V _β 3.1-11 (2)	: TATTACTGTGCTGAAAGTGA-----GAGGCGGGAC-----GGGAT-----TAACTATCC-----ATCTCAACAACATGCATTTTGGAAAGGGCACCCAGCTGACAGTGCTTG	42
V _β 3.1-12 (2)	: TATTACTGTGCTGAAAGTGAA-----TGCGATTCCG-----AGGGG-----CAC-----CAACAACATGCATTTTGGAAAGGGCACCCAGCTGACAGTGCTTG	33
V _β 3.2	: Y Y C AATAATGAAAACTGTTCTTTGGCACTGGGACAAAACTCACTGTCATAG J _β 1.2	
V _β 3.2-1 (1)	: -----CGCGGGAC-----GGGAC-----GCGTCCG-----TAATGAAAACTGTTCTTTGGCACTGGGACAAAACTCACTGTCATAG (*)	27
V _β 3.2-2 (1)	: TATTACTGTGCTGAAAGTG-----CCGGGGCC-----GACAG-----ACCGGGGGC-----AATGAAAACTGTTCTTTGGCACTGGGACAAAACTCACTGTCATAG	39
V _β 3.2-3 (1)	: TATTACTGTGCTGAAAGTG-----CCGGGTCTGAAGCGG-----CAGGGGAT-----AGCGAGGG-----TGAAAACTGTTCTTTGGCACTGGGACAAAACTCACTGTCATAG	45
V _β 3.2-5 (1)	: TATTACTGTGCTGAAAGT-----TCGAGTCCC-----GGGAC-----GAAAACTGTTCTTTGGCACTGGGACAAAACTCACTGTCATAG	27
V _β 3.2-6 (1)	: TATTACTGTGCTGAA-----GGTAGCC-----GGGACAG-----CCGCG-----ATGAAAACTGTTCTTTGGCACTGGGACAAAACTCACTGTCATAG	30
V _β 3.2-7 (1)	: TATTACTGTGCTGAAAGTG-----CCTCGGCGGTGACGGCAG-----TAATGAAAACTGTTCTTTGGCACTGGGACAAAACTCACTGTCATAG	30
V _β 3.2-8 (1)	: TATTACTGTGCTGAAAGTGAA-----CA-----GGGATC-----G-----GAAAACTGTTCTTTGGCACTGGGACAAAACTCACTGTCATAG	24
V _β 3.2-9 (1)	: TATTACTGTGCTGAA-----CTACGGGG-----GAAAACTGTTCTTTGGCACTGGGACAAAACTCACTGTCATAG	18
V _β 3.2	: Y Y C TTTTATCAATACCCAGTATTTTGGAGAAGGAACAAAAATAACAGTTCTGG J _β 2.3	
V _β 3.2-12 (2)	: TATTACTGTGCTGAAAGTGA---CGGTCGAGAGGGCCCCGACCAGA-----AATACCCAGTATTTTGGAGAAGGAACAAAAATAACAGTTCTGG	36
V _β 3.2-15 (2)	: TATTACTGTGCTGAAACTGA---TACGCGACCGGGGGTTCCG-----AATACCCAGTATTTTGGAGAAGGAACGAAAAATAACAGTTCTGG	33
V _β 3.2	: Y Y C ATACATATGAGGTTGAGTTTGGTCCTGGGACCCACATAACAGTACTAG J _β 2.1	
V _β 3.2-10 (2)	: TATTACTGTGCTGAAAGTGAA---CGGATGGCGCCCTTCGG-----TGAGGTTGAGTTTGGTCCTGGGACCCACATAACAGTACTAG	30
V _β 3.2-13 (2)	: TATTACTGTGCTGAAAGTGAA-----GGG-----ACAGGG-----TTGAGTTTGGTCCTGGGACCCACATAACAGTACTAG (*)	18
V _β 3.2-14 (2)	: TATTACTGTGCTGAA-----CTCGG-----AGGGGATC-----CGA-----ATATGAGGTTGAGTTTGGTCCTGGGACCCACATAACAGTACTAG	27
V _β 3.2	: Y Y C CAATCTCAACAACATGCATTTTGGAAAGGGCACCCAGCTGACAGTGCTTG J _β 2.2	
V _β 3.2-11 (2)	: TATTACTGTGCTGAAAGTGAA-----GATCGG-----GGGGATC-----AACAACTGCATTTTGGAAAGGGCACCCAGCTGACAGTGCTTG	27
V _β 3.3	: Y Y C AATAATGAAAACTGTTCTTTGGCACTGGGACAAAACTCACTGTCATAG J _β 1.2	
V _β 3.3-1 (1)	: TATTACTGTGCTGAAAGTG-----CTAAGG-----CAGGGGA-----CGTC-----AATGAAAACTGTTCTTTGGCACTGGGACAAAACTCACTGTCATAG	33
V _β 3.3-2 (1)	: TATTACTGTGCTGAAAG-----C-----GGACAGGG-----CGG-----AAAACCTGTTCTTTGGCACTGGGACAAAACTCACTGTCATAG	21
V _β 3.3	: Y Y C ATACATATGAGGTTGAGTTTGGTCCTGGGACCCACATAACAGTACTAG J _β 2.1	
V _β 3.3-6 (2)	: TATTACTGTGCTGAA-----GCGC-----GGGACAGGG-----AAT-----ATACATATGAGGTTGAGTTTGGTCCTGGGACCCACATAACAGTACTAG	30
V _β 3.3-8 (2)	: TATTACTGTGCTGAAAG-----CGAC-----GGGAC-----TACTACGGGC-----GAGGTTGAGTTTGGTCCTGGGACCCACATAACAGTACTAG	27
V _β 3.3-9 (2)	: TATTACTGTGCTGAAAG-----CTACTCC-----GGGAC-----GGGGAACCTC-----GAGGTTGAGTTTGGTCCTGGGACCCACATAACAGTACTAG	30
V _β 3.3	: Y Y C ACCAACACTAAGGTGATTTTGGTTTGGGCACAAAAGTTACAGTGATGG J _β 1.1	
V _β 3.3-5 (1)	: TATTACTGTG-----T-----ACAGGGGA-----ACACTAAGGTGATTTTGGTTTGGGCACAAAAGTTACAGTGATGG	15
V _β 3.3	: Y Y C TTTTATCAATACCCAGTATTTTGGAGAAGGAACAAAAATAACAGTTCTGG J _β 2.3	
V _β 3.3-7 (2)	: TATTACTGTGCTGAAAG-----CGCC-----GGGACAGGG-----CG-----AATACCCAGTATTTTGGAGAAGGAACAAAAATAACAGTTCTGG	27
V _β 3.3	: Y Y C CAATCTCAACAACATGCATTTTGGAAAGGGCACCCAGCTGACAGTGCTTG J _β 2.2	
V _β 3.3-10 (2)	: TATTACTGTGCTGAAAGTGAA-----CGGTT-----GGGGATC-----GCCACAGA-----AATCACAACAACATGCATTTTGGAAAGGGCACCCAGCTGACAGTGCTTG	42
V _β 3.5	: Y Y C AATAATGAAAACTGTTCTTTGGCACTGGGACAAAACTCACTGTCATAG J _β 1.2	
V _β 3.5-1 (1)	: TATTACTGTGCTGAAAGTGAA---TTGGTCGGGG-----AATGAAAACTGTTCTTTGGCACTGGGACAAAACTCACTGTCATAG	30

V _β 3.5-2 (1)	:	TATTACTGTGCTGAAAGTGA-----CCCTCTATTTGG-----	-----AAACTGTTCTTTGGCACTGGGACAAAACCTCACTGTCATAG	24
V _β 3.5-6 (1)	:	TATTACTGTGCTGAAAGTG-----CT-----ACAGGGGATC-----GG-----	-----AATGAAAAACTGTTCTTTGGCGCTGGGACAAAACCTCACTGTCATAG	30
V _β 3.5-8 (1)	:	TATTACTGTGCTGAAAGTGAA-----CCCGAGA-----GACAGGGG-----TCACGCACGG-----	-----ATGAAAAACTGTTCTTTGGCACTGGGACAAAACCTCACTGTTATAG	39
V _β 3.5-10 (1)	:	TATTACTGTGCTGAAAGTG-----CTCC-----GGGACAGGGG-----GATACGG-----	-----TAATGAAAAACTGTTCTTTGGCACTGGGACAAAACCTCACTGTCATAG	39
V _β 3.5	:	Y Y C	F G K G	
V _β 3.5	:	TATTACTGTGCTGAAAGTGAAA	CAATCTCAACAACTGCATTTTGGAAAGGGCACCCAGCTGACAGTGCTTG	J _β 2.2
V _β 3.5-3 (2)	:	TATTACTGTGCTGAAAGTGAAA-----GGTTTTG-----GGGACA-----CCAGCTTGGG-----	-----TCTCAACAACTGCATTTTGGAAAGGGCACCCAGCTGACAGTGCTTG	42
V _β 3.5-7 (2)	:	TATTACTGTGCTGAA-----GAGGCCCTC-----GGGACAGGG-----CGGTTG-----	-----CAACTGCATTTTGGAAAGGGCACCCAGCTGACAGTGCTTG	30
V _β 3.5	:	Y Y C	F G E G	
V _β 3.5	:	TATTACTGTGCTGAAAGTGAAA	TTTTATCAATACCCAGTATTTTGGAGAAGGAACAAAAATAACAGTTCTGG	J _β 2.3
V _β 3.5-4 (2)	:	TATTACTGTGCTGAAAGTGAA--CAGGCGCCGCGTGGTAGTCTGGA-----	-----CAATACCCAGTATTTTGGAGAAGGAACAAAAATAACAGTTCTGG	39
V _β 3.5-11 (2)	:	TATTACTGTGCTGAA-----CTCGTAC-----GGGGATC-----GG-----	-----ATACCCAGTATTTTGGAGAAGGAACAAAAATAACAGTTCTGG	24
V _β 3.5	:	Y Y C	F G P G	
V _β 3.5	:	TATTACTGTGCTGAAAGTGAAA	ATACATATGAGGTTGAGTTTGGTCCTGGGACCCACATAACAGTACTAG	J _β 2.1
V _β 3.5-5 (2)	:	TATTACTGTGCTGAAAGTGAA--GCCGCGATAGGTCG-----	-----TGAGGTTGAGTTTGGTCCTGGGACCCACATAACAGTACTAG	27
V _β 3.5-9 (2)	:	TATTACTGTGCTGAAA-----C-----GACAGG-----CTAC-----	-----GAGGTTGAGTTTGGTCCTGGGACCCACATAACAGTACTAG	18
V _β 3.5	:	Y Y C	F G F G	
V _β 3.5	:	TATTACTGTGCTGAAAGTGAAA	ACCAACACTAAGGTGATTTTGGTTTGGGCACAAAAGTTACAGTGATGG	J _β 1.1
V _β 3.5-12 (2)	:	TATTACTGTGCTGAA-----GCCGT-----CAGGGGA-----GGAACGTCTCGT-----	-----ACCAACACTAAGGTGATTTTGGTTTGGGCACAAAAGTTACAGTGATGG	39
V _β 4	:	Y F C	F G T G	
V _β 4	:	TATTTCTGT	AATAATGAAAAACTGTTCTTTGGCACTGGGACAAAACCTCACTGTCATAG	J _β 1.2
V _β 4-1 (1)	:	TATTTCTGT	GCCAGCACCAAGGGG-----CAGGGGATC---GTCGTGTCACGAGGG-----	42
V _β 4-2 (1)	:	TATTTCTGT	GCCAGCAGTGCGCCCGGACGTCTCGGAG-----ATGAAAAACTGTTCTTTGGCACTGGGACAAAACCTCACTGTCATAG	33
V _β 4-3 (1)	:	TATTTCTGT	GCCAGCAGACCGAAAAAAC-----GGGACAGG-----CTCG-----ATGAAAAACTGTTCTTTGGCACTGGGACAAAACCTCACTGTCATAG	36
V _β 4-4 (1)	:	TATTTCTGT	GCCAGCAGTTTGAAC-----GGGAT-----AGTTTTC-----ATGAAAAACCGTTCTTTGGCACTGGGACAAAACCTCACTGTCATAG	33
V _β 4-5 (1)	:	TATTTCTGT	GCCAGCAGTTTGA-----GGGATC-----G-----ATGAAAAACTGTTCTTTGGCACTGGGACAAAACCTCACTGTCATAG	27
V _β 4-6 (1)	:	TATTTCTGT	GCCAGCAGTT-----CAGGGGATC-----CC-----AACTGTTCTTTGGCACTGGGACAAAACCTCACTGTCATAG	21
V _β 4-7 (2)	:	TATTTCTGT	GCCAGCAGCGGCGC-----GACAGG-----TCCGT-----TGAAAACTGTTCTTTGGCACTGGGACAAAACCTCACTGTCATAG	(*) 30
V _β 4	:	Y F C	F G P G	
V _β 4	:	TATTTCTGT	ATACATATGAGGTTGAGTTTGGTCCTGGGACCCACATAACAGTACTAG	J _β 2.1
V _β 4-8 (2)	:	TATTTCTGT	GCCAGCAGTCA-----GGACAGG-----ATAAGA-----GAGGTTGAGTTTGGTCCTGGGACCCACATAACAGTACTAG	24
V _β 4-9 (2)	:	TATTTCTGT	GCCAGCAGTTTGATAC-----GGGACAGGG-----CGTATAA-----ATATGAGGTTGAGTTTGGTCCTGGGACCCACATAACAGTACTAG	36
V _β 3.6-1 (1)	:	Y Y C	F G T G	
V _β 3.6-1 (1)	:	TATTACTGT	AATAATGAAAAACTGTTCTTTGGCACTGGGACAAAACCTCACTGTCATAG	J _β 1.2
V _β 3.6-2 (1)	:	TATTACTGT	GCTGAAAGTGAGGCC-----GGGATC-----GAACG-----AATGAAAAACTGTTCTTTGGCACTGGGACAAAACCTCACTGTCATAG	33
V _β 3.6-2 (1)	:	TATTACTGT	GCTGA-----ACAGGGGATC-----GCCCCGGG-----AATGAAAAACTGTTCTTTGGCACTGGGACAAAACCTCACTGTCATAG	30
V _β 3.6-3 (1)	:	Y Y C	F G K G	
V _β 3.6-3 (1)	:	TATTACTGT	CAATCTCAACAACTGCATTTTGGAAAGGGCACCCAGCTGACAGTGCTTG	J _β 2.2
V _β 3.6-3 (1)	:	TATTACTGT	GCTGAAAGACGAA-----GGACAGG-----AGG-----CAATCTCAACAACTGCATTTTGGAAAGGGCACCCAGCTGACAGTGCTTG	33
V _β 3.6-4 (2)	:	Y Y C	F G E G	
V _β 3.6-4 (2)	:	TATTACTGT	TTTTATCAATACCCAGTATTTTGGAGAAGGAACAAAAATAACAGTTCTGG	J _β 2.3
V _β 3.6-4 (2)	:	TATTACTGT	GCTGAAAGTGAAATTGAGGG-----GGACA-----CCC-----CAATACCCAGTATTTTGGAGAAGGAACAAAAATAACAGTTCTGG	33
V _β 3.6-5 (2)	:	Y Y C	F G P G	
V _β 3.6-5 (2)	:	TATTACTGT	ATACATATGAGGTTGAGTTTGGTCCTGGGACCCACATAACAGTACTAG	J _β 2.1
V _β 3.6-6 (2)	:	TATTACTGT	GCTGAAACCTTCCCGGTGGGGCCGAAC-----GGGACAGGGGATC-----GGA-----ATGAGGTTGAGTTTGGTCCTGGGACCCACATAACAGTACTAG	45
V _β 3.6-6 (2)	:	TATTACTGT	GCTGAAAGTGAAAGACCCACTTGTCCC-----TTGAGTTTGGTCCTGGGACCCACATAACAGTACTAG	24

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	Y Y C	F G T G	CDR3 (nt)
V _{1.1.1}	: <u>TACTACTGTGCTTACTGGGACTCT</u>	<u>TCTGGTTATTACTACAAAGTGT</u> <u>TTGGCACCGGTACAAAGCTCATCGTGTACG</u>	J ₃
V _{1.1.1-1}	: TACTACTGTGCTTACTGGGACTCT-----GACG-----	CTGGTTATTACTACAAAGTGT <u>TTGGCACCGGTACAAAGCTCATCGTGTACG</u>	30
V _{1.1.1-4}	: TACTACTGTGCTTACTGGGACTCT-----GGG-----	-----GTGTTTGGCACCGGTACAAAGCTCATCGTGTACG	9
V _{1.1.1-7}	: <u>TACTACTGTGCTTACTGGGACTCT</u> -----CGA-----	-----TCTGGTTATTACTACAAAGTGT <u>TTGGCACCGGTACAAAGCTCATCGTGTACG</u>	27
V _{1.1.1}	: <u>TACTACTGTGCTTACTGGGACTCT</u>	<u>GACCACATGGATTAAATACTTCGGTACAGGAAC</u> <u>TAAGCTAATTATCTCCG</u>	J ₁
V _{1.1.1-2}	: TACTACTGTGCTTACTGGGACTCT-----CGAGT-----	-----ATGGATTAAATACTTCGGTACAGGAAC <u>TAAGCTAATTATCTCCG</u>	21
V _{1.1.1-5}	: TACTACTGTGCTTACTGGGACTCT-----ACG-----	-----TGGATTAAATACTTCGGTACAGGAAC <u>TAAGCTAATTATCTCCG</u>	21
V _{1.1.1-8}	: TACTACTGTGCTTACTGGGACTCT-----TGGC-----	-----GGATTAAATACTTCGGTACAGGAAC <u>TAAGCTAATTATCTCCG</u>	21
V _{1.1.1-9}	: <u>TACTACTGTGCTTACTGGGACTCT</u> -----GCCATCTC-----	-----GACCACATGGATTAAATACTTCGGTACAGGAAC <u>TAAGCTAATTATCTCCG</u>	33
V _{1.1.1}	: <u>TACTACTGTGCTTACTGGGACTCT</u>	<u>GGCAATCTGGTCTTTGGCACAGGCAC</u> <u>TAAACTCATCGTTTCCA</u>	J _{4 (J,5)}
V _{1.1.1-3}	: TACTACTGTGCTTACTGGGACTCT-----ATCGTTG-----	-----TGGTCTTTGGCACAGGCAC <u>TAAACTCATCGTTTCCA</u>	18
V _{1.1.1-6}	: <u>TACTACTGTGCTTACTGGGACTCT</u> -----	-----CTGGTCTTTGGCACAGGCAC <u>TAAACTCATCGTTTCCA</u>	12
V _{1.1.2}	: <u>TACTACTGTGCTTACTGGGACTCT</u>	<u>TCTGGTTATTACTACAAAGTGT</u> <u>TTGGCACCGGTACAAAGCTCATCGTGTACG</u>	J ₃
V _{1.1.2-1}	: TACTACTGTGCTTACTGGGACTCT-----A-----	-----TCTGGTTATTACTACAAAGTGT <u>TTGGCACCGGTACAAAGCTCATCGTGTACG</u>	18
V _{1.1.2-3}	: TACTACTGTGCTTACTGGGACTCT-----	-----GGTTATTACTACAAAGTGT <u>TTGGCACCGGTACAAAGCTCATCGTGTACG</u>	24
V _{1.1.2-4}	: <u>TACTACTGTGCTTACTGGGACTCT</u> -----AGAGGTGCCTC-----	-----TTACTACAAAGTGT <u>TTGGCACCGGTACAAAGCTCATCGTGTACG</u>	30
V _{1.1.2}	: <u>TACTACTGTGCTTACTGGGACTCT</u>	<u>GACCACATGGATTAAATACTTCGGTACAGGAAC</u> <u>TAAGCTAATTATCTCCG</u>	J ₁
V _{1.1.2-2}	: TACTACTGTGCTTACTGGGACTCT-----CG-----	-----CATGGATTAAATACTTCGGTACAGGAAC <u>TAAGCTAATTATCTCCG</u>	21
V _{1.1.3p}	: <u>TACTACTGTGCTTACTGGGACTCT</u>	<u>GGCAATCTGGTCTTTGGCACAGGCAC</u> <u>TAAACTCATCGTTTCCA</u>	J _{4 (J,5)}
V _{1.1.3p-1}	: TACTACTGTGCTTACTGGGACTCT-----TTACAC-----	-----GGCAATCTGGTCTTTGGCACAGGCAC <u>TAAACTCATCGTTTCCA</u>	(*) 24
V _{1.1.3-3}	: <u>TACTACTGTGCTTACTGGGACTCT</u> -----GGGG-----	-----AATCTGGTCTTTGGCACAGGCAC <u>TAAACTCATCGTTTCCA</u>	18
V _{1.1.3p}	: <u>TACTACTGTGCTTACTGGGACTCT</u>	<u>TCTGGTTATTACTACAAAGTGT</u> <u>TTGGCACCGGTACAAAGCTCATCGTGTACG</u>	J ₃
V _{1.1.3-2}	: TACTACTGTGCTTACTGGGACTCT-----	-----TGGTTATTACTACAAAGTGT <u>TTGGCACCGGTACAAAGCTCATCGTGTACG</u>	21
V _{1.1.3-4}	: <u>TACTACTGTGCTTACTGGGACTCT</u> -----GGTCG-----	-----AGTGTTTGGCACCGGTACAAAGCTCATCGTGTACG	6
V _{1.1.4}	: <u>TACTACTGTGCTTACTGGGACTCT</u>	<u>GGCAATCTGGTCTTTGGCACAGGCAC</u> <u>TAAACTCATCGTTTCCA</u>	J _{4 (J,5)}
V _{1.1.4-1}	: TACTACTGTGCTTACTGGGACTCT-----TTGAG-----	-----GGCAATCTGGTCTTTGGCACAGGCAC <u>TAAACTCATCGTTTCCA</u>	21
V _{1.1.4-4}	: TACTACTGTGCTTACTGGGACTCT-----CGCGACGGAG-----	-----ATCTGGTCTTTGGCACAGGCAC <u>TAAACTCATCGTTTCCA</u>	21
V _{1.1.4-5}	: <u>TACTACTGTGCTTACTGGGACTCT</u> -----GGAC-----	-----TCTGGTCTTTGGCACAGGCAC <u>TAAACTCATCGTTTCCA</u>	12
V _{1.1.4}	: <u>TACTACTGTGCTTACTGGGACTCT</u>	<u>TCTGGTTATTACTACAAAGTGT</u> <u>TTGGCACCGGTACAAAGCTCATCGTGTACG</u>	J ₃
V _{1.1.4-2}	: TACTACTGTGCTTACTGGGACTCT-----CTCGC-----	-----TTACTACAAAGTGT <u>TTGGCACCGGTACAAAGCTCATCGTGTACG</u>	24
V _{1.1.4-3}	: TACTACTGTGCTTACTGGGACTCT-----CCTC-----	-----ATTACTACAAAGTGT <u>TTGGCACCGGTACAAAGCTCATCGTGTACG</u>	21
V _{1.1.4-8}	: TACTACTGTGCTTACTGGGACTCT-----CGGC-----	-----CTGGTTATTACTACAAAGTGT <u>TTGGCACCGGTACAAAGCTCATCGTGTACG</u>	30
V _{1.1.4}	: <u>TACTACTGTGCTTACTGGGACTCT</u>	<u>GACCACATGGATTAAATACTTCGGTACAGGAAC</u> <u>TAAGCTAATTATCTCCG</u>	J ₁
V _{1.1.4-6}	: TACTACTGTGCTTACTGGGACTCT-----GG-----	-----TGGATTAAATACTTCGGTACAGGAAC <u>TAAGCTAATTATCTCCG</u>	18
V _{1.1.4-7}	: TACTACTGTGCTTACTGGGACTCT-----	-----ATGGATTAAATACTTCGGTACAGGAAC <u>TAAGCTAATTATCTCCG</u>	18
V _{1.1.4-9}	: <u>TACTACTGTGCTTACTGGGACTCT</u> -----AGGA-----	-----GGATTAAATACTTCGGTACAGGAAC <u>TAAGCTAATTATCTCCG</u>	21
V _{1.1.5p}	: <u>TACTACTGTGCTTACTGGGACTCT</u>	<u>GGCAATCTGGTCTTTGGCACAGGCAC</u> <u>TAAACTCATCGTTTCCA</u>	J _{4 (J,5)}
V _{1.1.5p-1}	: TACTACTGTGCTTACTGGGACTCT-----	-----GCAATCTGGTCTTTGGCACAGGCAC <u>TAAACTCATCGTTTCCA</u>	(*) 12
V _{1.1.5p}	: <u>TACTACTGTGCTTACTGGGACTCT</u>	<u>TCTGGTTATTACTACAAAGTGT</u> <u>TTGGCACCGGTACAAAGCTCATCGTGTACG</u>	J ₃
V _{1.1.5p-2}	: TACTACTGTGCTTACTGGGACTCT-----C-----	-----GTTATTACTACAAAGTGT <u>TTGGCACCGGTACAAAGCTCATCGTGTACG</u>	(*) 24
V _{1.1.5p}	: <u>TACTACTGTGCTTACTGGGACTCT</u>	<u>GACCACATGGATTAAATACTTCGGTACAGGAAC</u> <u>TAAGCTAATTATCTCCG</u>	J ₁
V _{1.1.5p-3}	: <u>TACTACTGTGCTTACTGGGACTCT</u> -----CG-----	-----ATGGATTAAATACTTCGGTACAGGAAC <u>TAAGCTAATTATCTCCG</u>	(*) 14
V _{2.1.1}	: <u>TACTACTGCGCTTACTGGGACCT</u>	<u>GACCACATGGATTAAATACTTCGGTACAGGAAC</u> <u>TAAGCTAATTATCTCCG</u>	J ₁
V _{2.1.1-1}	: TACTACTGCGCTTACTGGGACCT-----	-----ACATGGATTAAATACTTCGGTACAGGAAC <u>TAAGCTAATTATCTCCG</u>	18
V _{2.1.1-2}	: <u>TACTACTGCGCTTACTGGGACCT</u> -----ATTACCA-----	-----ATGGATTAAATACTTCGGTACAGGAAC <u>TAAGCTAATTATCTCCG</u>	27
V _{3.1.1}	: <u>TACTACTGTGCGTACTGGTATTATCATCAAGGCAT</u>	<u>GGATGCTGATGTTAAATATT</u> <u>TGGAAC</u> <u>TGGAAC</u> <u>TAAGCTATTGTTTCAG</u>	J ₂
V _{3.1.1-1}	: TACTACTGTGCGTACTGGTATTATCATCAAGGCAT-----C-----	-----GATGTTAAATATTGGAAC <u>TGGAAC</u> <u>TAAGCTATTGTTTCAG</u>	30
V _{3.1.1-10}	: <u>TACTACTGTGCGTACTGGTATTATCATCA</u> -----GCG-----	-----TGTTAAATATTGGAAC <u>TGGAAC</u> <u>TAAGCTATTGTTTCAG</u>	24
V _{3.1.1}	: <u>TACTACTGTGCGTACTGGTATTATCATCAAGGCAT</u>	<u>TCTGGTTATTACTACAAAGTGT</u> <u>TTGGCACCGGTACAAAGCTCATCGTGTACG</u>	J ₃
V _{3.1.1-2}	: TACTACTGTGCGTACTGGTATTATCATCAAGGCAT-----G-----	-----TATTACTACAAAGTGT <u>TTGGCACCGGTACAAAGCTCATCGTGTACG</u>	33
V _{3.1.1-3}	: TACTACTGTGCGTACTGGTATTATCATATC-----GAGAGGG-----	-----TTACTACAAAGTGT <u>TTGGCACCGGTACAAAGCTCATCGTGTACG</u>	30
V _{3.1.1-7}	: TACTACTGTGCGTACTGGTATTATCATATCA-----	-----TTACTACAAAGTGT <u>TTGGCACCGGTACAAAGCTCATCGTGTACG</u>	24
V _{3.1.1-9}	: TACTACTGTGCGTACTGGTATTATCATATC-----CGTTTAAG-----	-----TACTACAAAGTGT <u>TTGGCACCGGTACAAAGCTCATCGTGTACG</u>	30
V _{3.1.1-13}	: TACTACTGTGCGTACTGGTATTATCATATCAAGG-----GGGC-----	-----TCTGGTTATTACTACAAAGTGT <u>TTGGCACCGGTACAAAGCTCATCGTGTACG</u>	39
V _{3.1.1-15}	: <u>TACTACTGTGCGTACTGGTATTATCATATCAAGGCAT</u> ---CGGCTC-----	-----GGTTATTACTACAAAGTGT <u>TTGGCACCGGTACAAAGCTCATCGTGTACG</u>	42

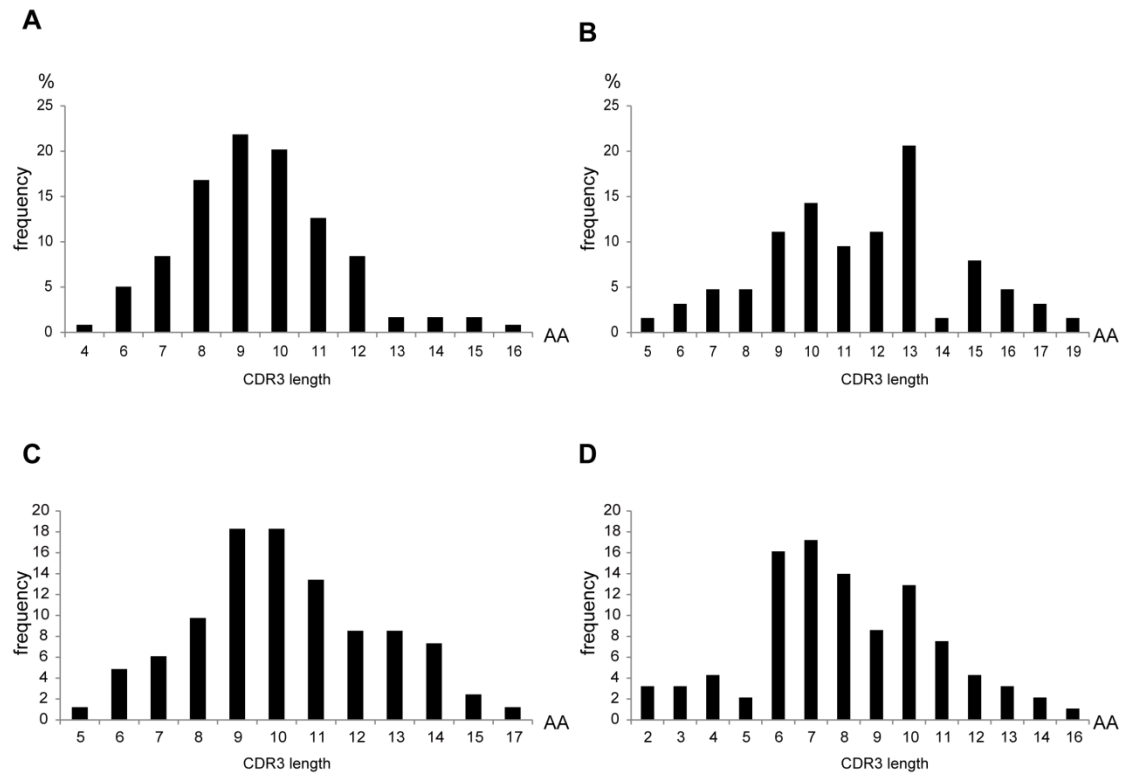
		Y Y C		F G T G		
V ₃ .1	:	<u>TACTACTGTGCGTACTGGTATT</u> CATATCAAGGCAT		<u>GACCACATGGATTAAATACTTCGGTACAGGA</u> ACTAAGCTAATTATCTCCG	J ₁	30
V ₃ .1-4	:	<u>TACTACTGTGCGTACTGGTATT</u> CATATCAAGGCAT	-----	-----ATGGATTAAATACTTCGGTACAGGA	ACTAAGCTAATTATCTCCG	18
V ₃ .1-5	:	<u>TACTACTGTGCGTACTGGT</u> -----	-----CAGG-----	-----ATGGATTAAATACTTCGGTACAGGA	ACTAAGCTAATTATCTCCG	18
V ₃ .1-6	:	<u>TACTACTGTGCGTACTGGTATT</u> CATATCAAGGCAT	-----	-----ACATGGATTAAATACTTCGGTACAGGA	ACTAAGCTAATTATCTCCG	36
V ₃ .1-8	:	<u>TACTACTGTGCGTACTGGTATT</u> CAT-----	-----	-----GGATTAAATACTTCGGTACAGGA	ACTAAGCTAATTATCTCCG	18
V ₃ .1-12	:	<u>TACTACTGTGCGTACTGGTATT</u> CAT-----	-----CGGTTTC-----	-----GACCACATGGATTAAATACTTCGGTACAGGA	ACTAAGCTAATTATCTCCG	33
V ₃ .1-14	:	<u>TACTACTGTGCGTACTGGT</u> -----	-----CCCCGACATCACAAGGC-----	-----GGATTAAATACTTCGGTACAGGA	ACTAAGCTAATTATCTCCG	30
V ₃ .1-16	:	<u>TACTACTGTGCGTACTGGTATT</u> CATATCAAGGC-----	-----G-----	-----CATGGATTAAATACTTCGGTACAGGA	ACTAAGCTAATTATCTCCG	30
V ₃ .1-17	:	<u>TACTACTGTGCGTACTGGT</u> -----	-----GGGAAAGACCG-----	-----CATGGATTAAATACTTCGGTACAGGA	ACTAAGCTAATTATCTCCG	27
		Y Y C		F G T G		
V ₃ .1	:	<u>TACTACTGTGCGTACTGGTATT</u> CATATCAAGGCAT		<u>GGCAATCTGGTCTTTGGCACAGG</u> CACTAAACTCATCGTTTCCA	J ₁ (J ₅)	24
V ₃ .1-11	:	<u>TACTACTGTGCGTACTGGTATT</u> CATCA-----	-----CA-----	-----GCAATCTGGTCTTTGGCACAGG	CACTAAACTCATCGTTTCCA	24
		Y Y C		F G T G		
V ₄	:	<u>TACTACTGTGCGCTACTGGCAGT</u> CT		<u>GGATGCTGATGTTAAATATTTGGA</u> ACTGGAACTAAGCTTATTGTTTCAG	J ₂	21
V ₄ -1	:	<u>TACTACTGTGCGCTACTGGCAGT</u> C-----	-----GCGAC-----	-----ATGTTAAATATTTGGA	ACTGGAACTAAGCTTATTGTTTCAG	27
V ₄ -4	:	<u>TACTACTGTGCGCTACTGGCAGT</u> C-----	-----GAAGAA-----	-----GCTGATGTTAAATATTTGGA	ACTGGAACTAAGCTTATTGTTTCAG	24
V ₄ -7	:	<u>TACTACTGTGCGCTACTGGCAGT</u> C-----	-----CAGACTC-----	-----GATGTTAAATATTTGGA	ACTGGAACTAAGCTTATTGTTTCAG	24
		Y Y C		F G T G		
V ₄	:	<u>TACTACTGTGCGCTACTGGCAGT</u> CT		<u>GACCACATGGATTAAATACTTCGGTACAGGA</u> ACTAAGCTAATTATCTCCG	J ₁	25
V ₄ -2	:	<u>TACTACTGTGCGCTACTGGCAGT</u> C-----	-----	-----GACCACATGGATTAAATACTTCGGTACAGGA	ACTAAGCTAATTATCTCCG (*)	24
V ₄ -3	:	<u>TACTACTGTGCGCTACTGGCAGT</u> C-----	-----AGCGAC-----	-----TGATTAAATACTTCGGTACAGGA	ACTAAGCTAATTATCTCCG	27
V ₄ -5	:	<u>TACTACTGTGCGCTACTGGCAG</u> -----	-----ATCGACG-----	-----CCACATGGATTAAATACTTCGGTACAGGA	ACTAAGCTAATTATCTCCG	27
		Y Y C		F G T G		
V ₄	:	<u>TACTACTGTGCGCTACTGGCAGT</u> CT		<u>GGCAATCTGGTCTTTGGCACAGG</u> CACTAAACTCATCGTTTCCA	J ₁ (J ₅)	28
V ₄ -6	:	<u>TACTACTGTGCGCTACTGGCAG</u> -----	-----CCAATCG-----	-----ATCTGGTCTTTGGCACAGG	CACTAAACTCATCGTTTCCA	28
		Y Y C		F G T G		
V ₆	:	<u>TATTACTGTGCTTACTGGGAG</u> AG		<u>GGATGCTGATGTTAAATATTTGGA</u> ACTGGAACTAAGCTTATTGTTTCAG	J ₂	21
V ₆ -1	:	<u>TATTACTGTGCTTACTGGGAG</u> -----	-----TCCA-----	-----CTGATGTTAAATATTTGGA	ACTGGAACTAAGCTTATTGTTTCAG	21
V ₆ -5	:	<u>TATTACTGTGCTTACTGG</u> -----	-----TCCACCTTA-----	-----ATGTTAAATATTTGGA	ACTGGAACTAAGCTTATTGTTTCAG	21
		Y Y C		F G T G		
V ₆	:	<u>TATTACTGTGCTTACTGGGAG</u> AG		<u>GACCACATGGATTAAATACTTCGGTACAGGA</u> ACTAAGCTAATTATCTCCG	J ₁	24
V ₆ -2	:	<u>TATTACTGTGCTTACTGGGAG</u> -----	-----GTCC-----	-----CCACATGGATTAAATACTTCGGTACAGGA	ACTAAGCTAATTATCTCCG	24
		Y Y C		F G T G		
V ₆	:	<u>TATTACTGTGCTTACTGGGAG</u> AG		<u>TCTGTTTATTACTACAAAGTGT</u> TTGGCACCGGTACAAAGCTCATCGTGTCA	J ₃	24
V ₆ -3	:	<u>TATTACTGTGCTTACTGGGAG</u> -----	-----GCGTATTCTGCTG-----	-----AAAGTGTTTGGCACCGGTACAAAG	CTCATCGTGTCA	24
		Y Y C		F G T G		
V ₆	:	<u>TATTACTGTGCTTACTGGGAG</u> AG		<u>GGCAATCTGGTCTTTGGCACAGG</u> CACTAAACTCATCGTTTCCA	J ₄ (J ₅)	6
V ₆ -4	:	<u>TATTACTGTGCTTACTGGGAG</u> -----	-----GCAT-----	-----TGGTCTTTGGCACAGG	CACTAAACTCATCGTTTCCA	12
V ₆ -6	:	<u>TATTACTGTGCTTACTGGGAG</u> A-----	-----AGG-----	-----TGGTCTTTGGCACAGG	CACTAAACTCATCGTTTCCA	9
V ₆ -7	:	<u>TATTACTGTGCTTACT</u> -----	-----CGCAGCG-----	-----GGTCTTTGGCACAGG	CACTAAACTCATCGTTTCCA	9
		Y Y C		F G T G		
V ₁ .6-1	:	<u>TACTACTGT</u> GCGTCTGA-----	-----	<u>GGCAATCTGGTCTTTGGCACAGG</u> CACTAAACTCATCGTTTCCA	J ₄ (J ₅)	0
V ₁ .6-5	:	<u>TACTACTGT</u> GCGTACTGGGACTTTCTCAG-----	-----	-----TTTGGCACAGG	CACTAAACTCATCGTTTCCA (*)	24
V ₁ .6-8	:	<u>TACTACTGT</u> GCGTACTGGGACTCTATCGT-----	-----	-----GGCAATCTGGTCTTTGGCACAGG	CACTAAACTCATCGTTTCCA	21
V ₁ .6-9	:	<u>TACTACTGT</u> GCGTACTGGGACTCG-----	-----	-----CAATCTGGTCTTTGGCACAGG	CACTAAACTCATCGTTTCCA	18
V ₁ .6-13	:	<u>TACTACTGT</u> GCGTACTGGGACTCCGCGC-----	-----	-----GGCAATCTGGTCTTTGGCACAGG	CACTAAACTCATCGTTTCCA	18
V ₁ .6-15	:	<u>TACTACTGT</u> GCGTACTGGGACTCGAG-----	-----	-----ATCTGGTCTTTGGCACAGG	CACTAAACTCATCGTTTCCA	15
V ₁ .6-16	:	<u>TACTACTGT</u> GCGTACTGGGCGGACTC-----	-----	-----TCTGGTCTTTGGCACAGG	CACTAAACTCATCGTTTCCA	18
V ₁ .6-17	:	<u>TACTACTGT</u> GCGTACTGGGACAC-----	-----	-----CAATCTGGTCTTTGGCACAGG	CACTAAACTCATCGTTTCCA	18
V ₁ .6-19	:	<u>TACTACTGT</u> GCGTACTGGGACTCTCGCA-----	-----	-----GGCAATCTGGTCTTTGGCACAGG	CACTAAACTCATCGTTTCCA	18
		Y Y C		F G T G		
V ₁ .6-2	:	<u>TACTACTGT</u> GCGTACTGGGACCGCGTACATCTA-----	-----	<u>TCTGTTTATTACTACAAAGTGT</u> TTGGCACCGGTACAAAGCTCATCGTGTCA	J ₃	36
V ₁ .6-3	:	<u>TACTACTGT</u> GCGTACTGGGACTCTAGGCCGG-----	-----	-----TCTGTTTATTACTACAAAGTGT	TTGGCACCGGTACAAAGCTCATCGTGTCA	33
V ₁ .6-6	:	<u>TACTACTGT</u> GCGTACTGGGAC-----	-----	-----CTGTTTATTACTACAAAGTGT	TTGGCACCGGTACAAAGCTCATCGTGTCA	24
V ₁ .6-7	:	<u>TACTACTGT</u> GCGTACTGGGACTCGTCG-----	-----	-----TCTGTTTATTACTACAAAGTGT	TTGGCACCGGTACAAAGCTCATCGTGTCA	21
V ₁ .6-11	:	<u>TACTACTGT</u> GCGTACTATCGACA-----	-----	-----TACTACAAAGTGT	TTGGCACCGGTACAAAGCTCATCGTGTCA	21
V ₁ .6-14	:	<u>TACTACTGT</u> GCGTACTGGGACTCTGAGAGTGGA-----	-----	-----TATTACTACAAAGTGT	TTGGCACCGGTACAAAGCTCATCGTGTCA	27
		Y Y C		F G T G		
V ₁ .6-4	:	<u>TACTACTGT</u> GCGTACTGGGACTCTAGTGGGTGG-----	-----	<u>GACCACATGGATTAAATACTTCGGTACAGGA</u> ACTAAGCTAATTATCTCCG	J ₁	33
V ₁ .6-10	:	<u>TACTACTGT</u> GCGTACT-----	-----	-----CCACATGGATTAAATACTTCGGTACAGGA	ACTAAGCTAATTATCTCCG	9
V ₁ .6-18	:	<u>TACTACTGT</u> GCGTACTGGGACTCGTC-----	-----	-----TGATTAAATACTTCGGTACAGGA	ACTAAGCTAATTATCTCCG	27
V ₁ .6-20	:	<u>TACTACTGT</u> GCGTACTGGGACTCGA-----	-----	-----GACCACATGGATTAAATACTTCGGTACAGGA	ACTAAGCTAATTATCTCCG	18
		Y Y C		F G T G		
V ₁ .6-12	:	<u>TACTACTGT</u> GCGTACTGGGACTCCCCCCCCATTCA-----	-----	<u>GGATGCTGATGTTAAATATTTGGA</u> ACTGGAACTAAGCTTATTGTTTCAG	J ₂	36
		Y Y C		F G T G		
V ₃ .4-1	:	<u>TACTACTGT</u> GCACGTTGGTATTATTATCAAGGCCGTGG-----	-----	<u>GACCACATGGATTAAATACTTCGGTACAGGA</u> ACTAAGCTAATTATCTCCG	J ₁	36
		Y Y C		F G T G		
V ₃ .4-2	:	<u>TACTACTGT</u> GCACGTTGGTATTATTATCAAGGCATAGAGGAGGA-----	-----	<u>TCTGTTTATTACTACAAAGTGT</u> TTGGCACCGGTACAAAGCTCATCGTGTCA	J ₃	48
V ₃ .4-6	:	<u>TACTACTGT</u> GCACGTTGGCATTATTATCAAGCGCAG-----	-----	-----TCTGTTTATTACTACAAAGTGT	TTGGCACCGGTACAAAGCTCATCGTGTCA	39
V ₃ .4-9	:	<u>TACTACTGT</u> GCACGTTGGTATTATTATCAAGGACC-----	-----	-----TTGGCACCGGTACAAAGCTCATCGTGTCA		18
V ₃ .4-14	:	<u>TACTACTGT</u> GCCTACTGGGACTTCGGGG-----	-----	-----ATTACTACAAAGTGT	TTGGCACCGGTACAAAGCTCATCGTGTCA	24
V ₃ .4-15	:	<u>TACTACTGT</u> GCACGTTGGTATTATTATCAAGGCACCCGA-----	-----	-----TCTGTTTATTACTACAAAGTGT	TTGGCACCGGTACAAAGCTCATCGTGTCA	42

	Y	Y	C		F	G	T	G		
V _i 3.4-3 :	<u>TACTACTGT</u>			GCACGTTGGCTAT-----	GGCAATCTGGTCTTTGGCACAGGCACTAAACTCATCGTTTCCA				J _i 4 (J _i 5)	12
V _i 3.4-5 :	<u>TACTACTGT</u>			GCACGTTGGTATTATTATCAAGGTCCTCGA-----	-----AATCTGGTCTTTGGCACAGGCACTAAACTCATCGTTTCCA					30
V _i 3.4-7 :	<u>TACTACTGT</u>			GCACGTTGGTATTATTATCAAGGCGAC-----	-----GGCAATCTGGTCTTTGGCACAGGCACTAAACTCATCGTTTCCA					30
V _i 3.4-11 :	<u>TACTACTGT</u>			GCACGTTGGTATTATTATCAAGGCCGT-----	-----GGCAATCTGGTCTTTGGCACAGGCACTAAACTCATCGTTTCCA					30
V _i 3.4-12 :	<u>TACTACTGT</u>			GCACGTTGGTATTATT-----	-----AATCTGGTCTTTGGCACAGGCACTAAACTCATCGTTTCCA					15
V _i 3.4-13 :	<u>TACTACTGT</u>			GCACGTTGGTATTATTATCGGCACA-----	-----GGCAATCTGGTCTTTGGCACAGGCACTAAACTCATCGTTTCCA			(*)		29
V _i 3.4-16 :	<u>TACTACTGT</u>			GCACGTTGGTATTATTATCAA-----	-----GGCAATCTGGTCTTTGGCACAGGCACTAAACTCATCGTTTCCA					24
V _i 3.4-17 :	<u>TACTACTGT</u>			GCACGTTGGTATTATTATCAAGTCCCTCGC-----	-----CAATCTGGTCTTTGGCACAGGCACTAAACTCATCGTTTCCA			(*)		31
V _i 3.4-19 :	<u>TACTACTGT</u>			GCACGTTGGTATTATTATCGGAGGAGCAATCTGGC-----	-----CTTTGGCACAGGCACTAAACTCATCGTTTCCA					27
V _i 3.4-20 :	<u>TACTACTGT</u>			GCACGTTGCTCCTC-----	-----GGCACAGGCACTAAACTCATCGTTTCCA					6
	Y	Y	C		F	G	T	G		
V _i 3.4-4 :	<u>TACTACTGT</u>			GCACGTTGGTATTATTATCAAGGCTCC-----	GGATGCTGATGTTAAAAATATTGGAACTGGAACTAAGCTTATTGTTTCAG			J _i 2		33
V _i 3.4-8 :	<u>TACTACTGT</u>			GCACGTTGGTATTATTATCAAGGCA-----	-----GCTGATGTTAAAAATATTGGAACTGGAACTAAGCTTATTGTTTCAG					33
V _i 3.4-10 :	<u>TACTACTGT</u>			GCACGTTGGTATTATTATCAAGAGCC-----	-----ATGCTGATGTTAAAAATATTGGAACTGGAACTAAGCTTATTGTTTCAG			(*)		29
V _i 3.4-18 :	<u>TACTACTGT</u>			GCACGTTGGTATTATTATCAAGGCATTGACGGGT-----	-----CTGATGTTAAAAATATTGGAACTGGAACTAAGCTTATTGTTTCAG					39

E

	D		J		CDR3 (nt)
	Y F C		F G S G		
	<u>TACTTCTGTGCCAGACAG</u>	<u>TTGAGAACTTGGAGTAG</u>	<u>GAAACAGACAAGCTTGTATTGGAAGTGGGATTGCTTTCTCAGTTGAACCAA</u>		
TRD2-1 :	TACTTCTGTGCCAGACAG-----CT-----	AGAACTTGGAGTAG-----CATCGG-----	CAGACAAGCTTGTATTGGAAGTGGGATTGCTTTCTCAGTTGAACCAA		36
TRD2-2 :	TACTTCTGTGCCAGACAG-----CT-----	CTTGGAGTA--AGCCCGCCTAAGA--	AAACAGACAAGCTTGTATTGGAAGTGGGATTGCTTTCTCAGTTGAACCAA		39
TRD2-3 :	TACTTCTGTGCCAGACAG-----CCGG-----	GGAGTAG-----CCGGGG-----	AGACAAGCTTGTATTGGAAGTGGGATTGCTTCTCAGTTGAACCAA		30
TRD2-4 :	TACTTCTGTGCCAGACAG-----C-----	AGAACTTGGAGTAG-----CTTCG-----	ACAGACAAGCTTGTATTGGAAGTGGGATTGCTTTCTCAGTTGAACCAA	(*)	35
TRD2-5 :	TACTTCTGTGCCAGACAG-----CAA-----	TTGAGAACTTGGAGTAG-----C-----	ACAGACAAGCTTGTATTGGAAGTGGGATTGCTTTCTCAGTTGAACCAA		36
TRD2-7 :	TACTTCTGTGCCAG-----	ACTTGGAGTA-----	ACAGACAAGCTTGTATTGGAAGTGGGATTGCTTTCTCAGTTGAACCAA	(*)	22
TRD2-8 :	TACTTCTGTGCCAGACAG-----CATGGGCTAG-----	GAGAACTTGGAGTAG-----C-----	AACAGACAAGCTTGTATTGGAAGTGGGATTGCTTTCTCAGTTGAACCAA		42
TRD2-9 :	TACTTCTGTGCCAGACAG-----C-----	AACTTGGAGTA-----CCG-----	GAAACAGACAAGCTTGTATTGGAAGTGGGATTGCTTTCTCAGTTGAACCAA		33
TRD2-10 :	TACTTCTGTGCCAGACAG-----CT-----	AGAACTTGGAGTAG-----CATCGG-----	CAGACAAGCTTGTATTGGAAGTGGGATTGCTTTCTCAGTTGAACCAA		36
TRD2-11 :	TACTTCTGTGCCAGACAG-----CATGGGCTAGGT-----	GAACTTGGAGTAG-----T-----	AACAGACAAGCTTGTATTGGAAGTGGGATTGCTTTCTCAGTTGAACCAA		42
TRD2-12 :	TACTTCTGTGCCAGACAG-----CATGGGCTAG-----	GAGAACTTGGAGTAG-----CT-----	ACAGACAAGCTTGTATTGGAAGTGGGATTGCTTTCTCAGTTGAACCAA		42
TRD2-13 :	TACTTCTGTGCCAGACAG-----CATGGGCTAGGT-----	GAACTTGGAGTA-----	GAAACAGACAAGCTTGTATTGGAAGTGGGATTGCTTTCTCAGTTGAACCAA		42
TRD2-14 :	TACTTCTGTGCCAGACAG-----CATGGGCTAGGT-----	GAACTTGGAGTAG-----CT-----	ACAGACAAGCTTGTATTGGAAGTGGGATTGCTTTCTCAGTTGAACCAA		42
TRD2-15 :	TACTTCTGTGCCAGACAG-----CATGGGCTAG-----	GAGAACTTGGAGTAG-----C-----	AACAGACAAGCTTGTATTGGAAGTGGGATTGCTTTCTCAGTTGAACCAA		42
TRD2-16 :	TACTTCTGTGCCAGACAG-----C-----	TGAGAACTTGG-----	ACAGACAAGCTTGTATTGGAAGTGGGATTGCTTTCTCAGTTGAACCAA		27
TRD2-18 :	TACTTCTGTGCCAGACAG-----CA-----	TTGAGAACTTGGAGTAG-----CGCGCGT-----	CAGACAAGCTTGTATTGGAAGTGGGATTGCTTTCTCAGTTGAACCAA	(*)	40

Supplementary Figure S5 Combinatorial and junctional diversity of duck TCR genes expressed in the thymus, TCR α (A), TCR δ (B), TCR β (C), TCR γ (D) and TCR δ 2 (E). The nucleotide sequences of the V(D)J junctions of all unique TCR clones are shown. The germline sequences of the 3'-end of the V, D and J segments are shown above the cDNA clones and in bold. Conserved sequences of the germline V and J segments are underlined. Nucleotides shaded in the junctions are putative P nucleotides. Gaps are indicated by dashes. The CDR3 is defined as the region between the J region-encoded FGXG motif and the nearest preceding V region-encoded cysteine, as described in the IMGT unique numbering for V-DOMAIN. The number on the right-hand side of each cDNA clone indicates the nucleotide length of the CDR3 region. The asterisk indicates nonfunctional transcripts.



Supplementary Figure S6 CDR3 length distributions of duck TCR cDNA clones, TCR α (A), TCR δ (B), TCR β (C) and TCR γ (D). The

x -axis shows the amino-acid length of CDR3, and the y -axis indicates the percentages of CDR3 sequences with the indicated lengths.

Supplementary Table S1 Primer Sequences

Name	Sequence	Purpose
TRBF	5'-CAGATGGGTCTCCCGTAGAA-3'	BAC screening for TCR β locus
TRBR	5'-CCCACCACTGTGAATGTGAG-3'	
TRGF	5'-ATGGTCTGGTGGCAGTAAGG-3'	BAC screening for TCR γ locus
TRGR	5'-TGGCCATGGATTGTTCTGTA-3'	
TRAF	5'-CAAATATGCAGCCTTGCTGA-3'	BAC screening for TCR α/δ locus
TRAR	5'-TTCCTCCTTCCTCTCCCAAT-3'	
TRAF2	5'-GGGATGCACTTCAACCAGAT-3'	BAC screening for the overlap clone
TRAR2	5'-CCCTGTGCAAACCCTAGAAA-3'	
TRD2F	5'-GCAGGCATTTCTTTCTCTCG-3'	BAC screening for TCR δ 2 locus
TRD2R	5'-ACCCAAATTGTCTGCACTCC-3'	
NotI-d(T) ₁₈	5'-AACTGGAAGAATTCGCGGCCGCAGGAATTTTTTTTTTTTTTTTTT-3'	-
RT-P1	5'-AACTGGAAGAATTCGCGGCC-3'	-
RT-P2	5'-AAGAATTCGCGGCCGCAGGAA-3'	-
Cb3F1	5'-CCCCGACACCCTCAATTAG-3'	3'RACE for C β (1 st round RCR)
Cb3F2	5'-AAGGGGTGGGTACAGATGAG-3'	3'RACE for C β (nested RCR)
Cg3F1	5'-TCTGCATTGTCATTTTAAAG-3'	3'RACE for C γ (1 st round RCR)
Cg3F2	5'-GAGCGGATGTTCTACATTTC-3'	3'RACE for C γ (nested RCR)
Ca3F1	5'-CACCACGGAGCTGAACACTG-3'	3'RACE for C α (1 st round RCR)
Ca3F2	5'-CTGACAGCGCCTTGTTCTTC-3'	3'RACE for C α (nested RCR)
Cd3F1	5'-CTTGTTTGGCAAGGAACTTC-3'	3'RACE for C δ (1 st round RCR)
Cd3F2	5'-TTTGCAACACCACAGACATC-3'	3'RACE for C δ (nested RCR)
C2d3F1	5'-TGGAGAAGCCTGCAATGTTC-3'	3'RACE for C δ 2 (1 st round RCR)
C2d3F2	5'-TTTGCTGCAGCCCCCTGAAGG-3'	3'RACE for C δ 2 (nested RCR)

B1gsp1	5'-CTTTCCCACAGAGAATAAG-3'	5'RACE for TCR β 1 (reverse transcription)
B2gsp1	5'-CAAAATGAGCATGATGTACA-3'	5'RACE for TCR β 2 (reverse transcription)
Bgsp2	5'-TCGACTGGTCAGTGAATAAG-3'	5'RACE for both TCR β 1 and β 2 (1 st round RCR)
Bgsp3	5'-TGTGGAAGTCTCATCTGTAC-3'	5'RACE for both TCR β 1 and β 2 (nested RCR)
Ggsp1	5'-TGGGGAGTTTAAAATTCTC-3'	5'RACE for TCR γ (reverse transcription)
Ggsp2	5'-GTGCTGACTGAGTACTTATC-3'	5'RACE for TCR γ (1 st round RCR)
Ggsp3	5'-TGCAGGATTCAGAGTTCTC-3'	5'RACE for TCR γ (nested RCR)
Agsp1	5'-CCCAGCTGTGTGAAAGACAG-3'	5'RACE for TCR α (reverse transcription)
Agsp2	5'-ATCCCTGTTACACAGACAGT-3'	5'RACE for TCR α (1 st round RCR)
Agsp3	5'-TGCTTCCTGTTTATTCTCAG-3'	5'RACE for TCR α (nested RCR)
Dgsp1	5'-TGGCTGGAAAATTTTGTTC-3'	5'RACE for TCR δ (reverse transcription)
Dgsp2	5'-CACATTCACCACTTTAATAG-3'	5'RACE for TCR δ (1 st round RCR)
Dgsp3	5'-GTCCCCTCTGATGTCATAAC-3'	5'RACE for TCR δ (nested RCR)
CbpF	5'-TTTCCCCATCAAAGCAAGA-3'	Southern blotting probe for C β
CbpR	5'-AGCATCACCATAGATGAATC-3'	
Vb3pF	5'-AACAGTCGCCAGACACAGTC-3'	Southern blotting probe for V β III
Vb3pR	5'-GCACTTTCAGCACAGTAATA-3'	
Vb2pF	5'-AATCACCAGGCACAGTTGTC-3'	Southern blotting probe for V β II
Vb2pR	5'-GTGCCTGAGTCATTAAGTAG-3'	
CgpF	5'-GCAGACGAAGCATAAAGATC-3'	Southern blotting probe for C γ
CgpR	5'-ATGGGGAGTTTAAAATTCTC-3'	
Vg1pF	5'-ACACGTCTGCAATGTCATTT-3'	Southern blotting probe for V γ I
Vg1pR	5'-GTAGGCACAGTAGTAGATAG-3'	
Vg6pF	5'-TGCGCGGATCGACTGCCACT-3'	Southern blotting probe for V γ VI
Vg6pR	5'-CCCAGTAAGCACAGTAATAG-3'	

CapF	5'-CAGGCTGACCACTAAAGATG-3'	Southern blotting probe for C α
CapR	5'-CATCCCTGTTACACAGACAG-3'	
Va1pF	5'-TCACCCAGGAAGAAGGACAAG-3'	Southern blotting probe for V α I
Va1pR	5'-GTACAAGGCGCTGTCAGAAAG-3'	
Va3pF	5'-CAGCCTTGTTGGCACTGTCAG-3'	Southern blotting probe for V α III
Va3pR	5'-GAGAAGCACCTGGGAGTTCTC-3'	
CdpF	5'-CTGGCCCAGAAGTTGTTCTG-3'	Southern blotting probe for C δ
CdpR	5'-CCACCACCTTTTCTGATGAC-3'	
Vd2pF	5'-GGCAGGCGTTTGGGCTCAGAG-3'	Southern blotting probe for V δ II
Vd2pR	5'-GAGCTCAGGGACAGAGAAGAC-3'	
Vd5pF	5'-CGCAGCCAAGGATTGTGGAG-3'	Southern blotting probe for V δ V
Vd5pR	5'-GCCATGCAAAAGCAGAAATG-3'	
D2cpF	5'-CCAAGCAGACAAGAATATTC-3'	Southern blotting probe for C δ 2
D2cpR	5'-TTGCAAACCTTTCCTGTCAC-3'	
D2vpF	5'-TTTGCTGCAGCCCCCTGAAGG-3'	Southern blotting probe for V $H\delta$
D2vpR	5'-TCCAAGTTCTCAATCTTTAG-3'	
EF1a1F	5'-GAGCCACCTTACAGCCAGAAGAGATA-3'	Quantitative real-time PCR for <i>EF1a1</i>
EF1a1R	5'-GATTGGCACAAAAGCTACAGTGTCTG-3'	
TRAqF	5'-CCTTCGGTCTACAGGCTGAC-3'	Quantitative real-time PCR for TCR α
TRAqR	5'-TGTTTCCACCTCCACAACAG-3'	
TRBqF	5'-AAGAGCAAAGCCCACTGGT-3'	Quantitative real-time PCR for TCR β
TRBqR	5'-CCCTTCTGTCCTCTCAGCAC-3'	
TRGqF	5'-CTGGAAACAGCACCGTTTTT-3'	Quantitative real-time PCR for TCR γ
TRGqR	5'-GGGAGCTTAGCTGGAGTCCT-3'	
TRDqF	5'-GCAAATGTTTGCAACACCAC-3'	Quantitative real-time PCR for TCR δ

TRDqR	5'-TTTTTGCCAGCAGGACTCTT-3'	
TRD2qF	5'-TTGGCAAGGACATTCTACCC-3'	Quantitative real-time PCR for TCRδ2
TRD2qR	5'-CCCCTTTGCATCTGGTTTTA-3'	
TRD2VH	5'-TGGAGAAGCCTGCAATGTTC-3'	Junctional diversity of TCRδ2 transcripts
TRD2C	5'-TGGGACTCAAAGTTCTACAG-3'	

Supplementary Table S2 Accession numbers for sequences used in phylogenetic analyses

Figure	Accession number
Fig. 3A	Human: A22: DQ097920, A17: DQ097914, A6: X58747, A27: DQ341447, A35: DQ097935, A25: DQ097923, A30: X58768, A34: DQ097934, A10: DQ097904, A21: U50404, A24: M17661, A20: X70305, A41: DQ097943, A36-D7: X61070, A23-D6: D13071, A29-D5: M17664, A1.1: X04939, A14: S51029, A19: Z46641, A38-D8: D13074, D1: AY357942, A9.2: X57531, A40: DQ097942, A16: DQ097913, A3: X57534, A8.4: D13077, A4: M17663, A26.1: L06886, A2: DQ097917, D2: S24406, D3: M23326 Mouse: A4: L47342, A13: M38102, A21-D12: M94080, A11: DQ340292, A10: X57397, A5.4: M38681, A3.1: X02967, A14.3: L77149, A7: X56719, A1: M22604, AVD16D: M16118, D2.2: M37280, A15-D6: M37599, A6: M34200, A12.3: M38680, A9: M33586, A17: X60319, A2: X03760, D4: M23545, D5: X12729 Cow: 013: D90013, 015: D90015, 012: D90012, 011: D90011, D113: D16113, D116: D16116, 014: D90014, 017: D90017, 016: D90016 Sheep: A622: M55622, D3S2: Z12996, D5: Z12995, A35: U78035, D2: AJ005904, D4: AJ005906, D6: AJ005908, D7: AJ809501, D1S1: Z12989 Rabbit: D5: D38121, D1: D26555, A885: M12885, D4: D38120 Chicken: A2: Scaffold AADN03011072.1:23-316, A1: 27:807845-808144, D1: 27:428976-429278 Finch: 066: 27:3077771-3078064, 164: 27:3067882-3068181, 500: 27:3048926-3049222, 516: 27:3033229-3033528, 495: 27:3054225-3054501, 497: 27:3051398-3051700 Parrot: A3: AGAI01023412, A1: AGAI01024880, A2: AGAI01025999, D5: AGAI01011509, D4: AGAI01044297, D6: AGAI01045807 Grouse: GW705681 Turkey: A03: ADDD01149483, A02: ADDD01152688, A01: ADDD01150225, D5: ADDD01052097, D4: ADDD01147795
Fig. 3B	Human: B12.1: X07224, B14: X06154, B11.3: X58797, B2: M64351, B21.1: L27608, B23: L27614, B13: U03115, B5: U03115, B9: M27380, B15: U03115, B3.1: U07977, B7.2: U07975, B19: U48260, B6.9: X61447, B10.3: U17047, B25.1: L27610, B27: U66061, B24.1: L27612, B28: U08314,

	B30: <u>L06893</u>, B20.1: <u>X72719</u>, B29.1: <u>M13847</u>, B4.3: <u>X58812</u> Mouse: B16: <u>L29434</u>, B14: <u>AE000664</u>, B3: <u>AE000663</u>, B21: <u>X16691</u>, B24: <u>M61184</u>, B23: <u>X59150</u>, B26: <u>K02548</u>, B12: <u>M30881</u>, B17: <u>AE000664</u>, B4: <u>X56725</u>, B19: <u>AJ249821</u>, B13.3: <u>M15616</u>, B10: <u>X16694</u>, B29: <u>X00696</u>, B31: <u>X03277</u>, B20: <u>M11859</u>, B30: <u>X16695</u>, B1: <u>X01642</u> Rabbit: B8: <u>BAA04245</u>, B11: <u>BAA04248</u>, B9: <u>BAA04246</u>, B7S1: <u>BAA04241</u>, B1: <u>AAA31472</u>, B5: <u>BAA04239</u>, B10: <u>BAA04247</u>, B2: <u>M13895</u>, B6: <u>BAA04240</u> Cow: B125: <u>PQ0061</u>, B129: <u>PQ0065</u>, B126: <u>PQ0062</u>, B122: <u>JQ0473</u>, B123: <u>PQ0060</u>, B124: <u>PQ0059</u> Sheep: B8S1: <u>AAB88433</u>, B6S1: <u>AAB88431</u>, B10S1: <u>AAB88434</u>, B1S5: <u>AAB88425</u>, B22S1: <u>AAB88440</u>, B7S1: <u>AAB88432</u>, B17S1: <u>AAB88439</u>, B13S1: <u>PQ0068</u>, B12S1: <u>AAB88435</u>, B15S1: <u>AAB88438</u>, B3S1: <u>AAB88427</u>, B2S1: <u>AAB88426</u>, B4S1: <u>AAB88430</u> Chicken: B2: <u>EF554773</u>, B2S2: <u>AAA62753</u>, B1S1: <u>B36198</u>, B1: <u>M37798</u> Axolotl: B3: <u>L29423</u>, B2: <u>L33269</u>, B1.1: <u>L33258</u>, B5: <u>L33337</u>, B6: <u>L33400</u>, B7.1: <u>L33723</u>, B11: <u>AF324475</u>, B4: <u>L29422</u>, B13: <u>AF324477</u>, B10: <u>AF324474</u>, B12: <u>AF324476</u>, B8: <u>L33786</u>, B9: <u>L33787</u> Frog: B1S1: <u>U60425</u>, B9: <u>U60431</u>, B2: <u>U60427</u>, B3: <u>U60432</u>, B4: <u>U60428</u>, B6: <u>U60434</u>, B8: <u>U60435</u>, B5: <u>U60424</u>, B7: <u>U60430</u>, B10: <u>U75994</u>
Fig. 3C	Human: G2: <u>M13429</u>, G9: <u>M27335</u>, G3: <u>S60779</u>, G4: <u>S60780</u> Mouse: G6: <u>M13338</u>, G7: <u>AF037352</u>, G1: <u>Z22847</u>, G3: <u>AF037352</u>, G4: <u>M13336</u> Cow: G5S6: <u>D16129</u>, G5S16: <u>D16133</u>, G5S11: <u>D16126</u>, G5S7: <u>D16130</u>, G1S1: <u>D16119</u>, G1S3: <u>D16131</u>, G6: <u>AY560834</u>, G3S2: <u>U73187</u>, G3S1: <u>U73186</u>, G4S1: <u>U73188</u> Sheep: G5S2: <u>Z13006</u>, G5S1: <u>Z13005</u>, G1S1: <u>Z12998</u>, G2S2: <u>Z13000</u>, G2S1: <u>Z12999</u>, G2S3: <u>Z13001</u>, G2S4: <u>Z13002</u>, G6S1: <u>Z13007</u>, G4S1: <u>Z13004</u>, G3S1: <u>Z13003</u> Opossum: G2: <u>6:283928450-283928153</u>, G1.1: <u>6:283942345-283942040</u>, G1.2: <u>6:283934927-283934623</u>, G1.3: <u>6:283921739-283921428</u>, G1.4: <u>6:283915397-283915042</u>, G1.5: <u>6:283907901-283907590</u>, G4: <u>6:283884333-283884026</u>, G3.1: <u>6:283888100-283887792</u>, G3.2:

6:283879394-283879086

Rabbit: G1S4: D38139, G1S1: D38135, G1S3: D38138, G1S2: D38137, G2S1: D38142

Platypus: G1.1: AAAY82100, G1.2: AAAY82093, G1.3: AAAY82109, G3.1: AAAY82120, G3.2: AAAY82094, G2.3: AAAY82114, G2.1: AAAY82119, G2.2: AAAY82110

Chicken: G1S5: U78213, G1S4: U78212, G1S8: U78216, G1S3: U78210, G2S8: U78226, G2S7: U78225, G2S9: U78227, G3S4: U78231, G3S8: U78235, G3S3: U78230

Frog: G1: AF440824, G13: AF440826, G8: AF440827 , G14: AF440822

Supplementary Table S3 Similarity ranges of new TRV genes identified from cDNA analysis to genomic sequences in each of the subgroups

New genes identified from cDNA analysis		Range
TRAV	V α 1.2	87.4% ~ 96.8%
	V α 1.3	86.8% ~ 96.5%
	V α 1.4	87.5% ~ 96.8%
	V α 1.5	87.5% ~ 96.9%
	V α 2.5	80.6% ~ 96.5%
	V α 2.6	77.8% ~ 96.5%
	V α 2.7	78.9% ~ 95.4%
	V α 2.8p	79.4% ~ 91.8%
	V α 2.9	79.9% ~ 95.7%
	V α 2.10	79.2% ~ 93.3%
	V α 2.11	77.8% ~ 96.5%
	V α 2.12	81.0% ~ 91.8%
	V α 2.13	79.2% ~ 96.1%
	V α 2.14	78.4% ~ 94.7%
	V α 2.15	81.2% ~ 94.7%
	V α 2.16	80.6% ~ 91.8%
	V α 2.17	81.9% ~ 96.4%
	V α 2.18	81.4% ~ 96.4%
	V α 2.19	81.6% ~ 93.3%
	V α 2.20	80.9% ~ 93.6%
	V α 3.5	81.2% ~ 94.6%
	V α 3.6	79.3% ~ 94.3%

	Vα3.7	76.4% ~ 95.3%
	Vα3.8	79.7% ~ 93.2%
	Vα3.9	78.6% ~ 95.7%
	Vα3.10	76.4% ~ 95.7%
	Vα3.11p	80.1% ~ 93.2%
	Vα3.12	79.3% ~ 94.6%
	Vα3.13	79.3% ~ 96.8%
	Vα3.14	77.2% ~ 96.8%
	Vα3.15	80.6% ~ 91.8%
	Vα3.16	79.1% ~ 97.1%
	Vα3.17	80.1% ~ 95.3%
	Vα3.18	77.2% ~ 95.3%
	Vα3.19	79.3% ~ 96.8%
	Vα3.20	78.3% ~ 96.8%
	Vα3.21	80.4% ~ 96.8%
	Vα3.22	81.2% ~ 92.1%
	Vα3.23	80.1% ~ 93.9%
	Vα3.24	80.1% ~ 96.8%
TRDV	Vδ2.15	77.4% ~ 94.1%
	Vδ2.16	76.9% ~ 95.2%
	Vδ2.17	78.5% ~ 96.0%
	Vδ2.18	75.4% ~ 89.6%
	Vδ2.19	76.2% ~ 93.2%
	Vδ2.20	75.1% ~ 91.8%

TRBV	V β 3.6	91.8% ~ 95.0%
	V β 3.7	91.4% ~ 95.3%
TRGV	V γ 1.6	81.0% ~ 93.3%
	V γ 3.4	78.9% ~ 89.6%