

Supplemental data, Table I. Identification of BAC clones carrying nurse shark IgM heavy chain genes by subfamily (Group).

| Group 1 | plate address |
|----------------|----------------------|
| B4 | 078G19 |
| G5 | 367D16 |
| B6 | 080D10 |
| F6 | 354D16 |
| A7 | 031M3 |
| A8 | 031M4 |
| D8 | 269O10 |

| Group 3 | plate address |
|----------------|----------------------|
| D1 | 214G21 |
| F4 | 350G3 |
| D5 | 265A13 |
| F7 | 354F3 |
| A11 | 055A21 |
| A12 | 055A22 |

| Group 5 | plate address |
|----------------|----------------------|
| C2 | 113G13 |
| B7 | 080I3 |

| Group 7+8 | plate address |
|------------------|----------------------|
| F5 | 352J19 |
| D7 | 269E20 |

| Group 2 | plate address |
|----------------|----------------------|
| G2A, V1 | |
| F1 | 323F7 |
| G6 | 368M21 |
| C9 | 157A9 |
| G9 | 370J21 |
| E10 | 312E1 |
| G2A, V2 | |
| F2 | 338E17 |
| G2 | 364B20 |
| G4 | 365B19 |
| A9 | 049M15 |
| B9 | 099B16 |
| H9 | 408F7 |
| E11 | 314P9 |
| G2B, V3 | |
| E1 | 295L7 |
| E2 | 295L8 |
| G3 | 364N19 |
| C4 | 129F19 |
| A6 | 031H4 |
| C7 | 148I2 |
| H10 | 411H9 |
| F11 | 359D24 |
| F12 | 362N22 |

| Group 4 | plate address |
|----------------|----------------------|
| A1 | 009F6 |
| B1 | 060K19 |
| D2 | 219M8 |
| C3 | 124H21 |
| D3 | 241N2 |
| F3 | 344N19 |
| H3 | 406E11 |
| H4 | 406E12 |
| B5 | 079P8 |
| C5 | 129I8 |
| E5 | 299E14 |
| C6 | 130L3 |
| D6 | 266E5 |
| E6 | 299F14 |
| H6 | 406H11 |
| E7 | 301K11 |
| H7 | 408A17 |
| E8 | 301K12 |
| G8 | 370F16 |
| H8 | 408B17 |
| C10 | 176D23 |
| F10 | 359B6 |
| B11 | 100O14 |
| C11 | 194M2 |
| G11 | 392F4 |
| C12 | 196O2 |
| D12 | 293A21 |
| E12 | 319N8 |
| H12 | 413F5 |

| 2 Loci | plate address |
|---------------|----------------------|
| B3 | 075N10 |

| C-Only | plate address | Group |
|---------------|----------------------|--------------|
| A10 | 053N16 | G1 |
| D10 | 273J10 | G1 |
| C1 | 111K3 | G2C |
| A4 | 019J22 | G4 |
| H11 | 411K9 | G4 |
| B10 | 099K21 | G5 |
| H2 | 399C2 | G2B |

Supplemental data Figure 1. Alignment of nurse shark H chain sequences. The VH gene segment, exons CH1, CH2, CH3, CH4 (including tailpiece) are aligned. The positions causing gaps (one codon in FR1, positions in the 5' region of CH2 in lower case and shaded) are not included in the phylogenetic analyses.

| | | |
|------|---|-----|
| | VH gene segment | |
| G4B3 | GTGTCCAGTCGGAG---GTTACTTTGACTCAACCAGAGGCAGAGAACAGCCAACCTGGAGGCTCGCTGACACTTACCTGTA AAACTAGCGGGTTCGATCTTAGCAGCTACTATATGGGTT | 117 |
| G4B2 | GTGTCCAGTCGGAG---GTTACTTTGACTCAACCAGAGGCAGAGAACAGCCAACCTGGAGGCTCGCTGACACTTACCTGTA AAACTAGCGGGTTCGATCTTAGCAGCTACTATATGGGTT | 117 |
| G4E2 | GTGTCCAGTCGGAG---GTTACTTTGACTCAACCAGAGGCAGAGAACAGCCAACCTGGAGGCTCGCTGACACTTACCTGTA AAACTAGCGGGTTCGATCTTAGCAGCTACTATATGGGTT | 117 |
| G4S5 | GTGTCCAGTCGGAG---GTTACTTTGACTCAACCAGAGGCAGAGAACAGCCAACCTGGAGGCTCGCTGACACTTACCTGTA AAACTAGCGGGTTCGATCTTAGCAGCTACTATATGGGTT | 117 |
| G3 | GTGTCCAGTCGGAG---GTTACTTTGACTCAACCAGAGGCAGAGAACAGCCAACCTGGAGGCTCGCTGACACTTACCTGTA AAACTAGCGGGTTCGATCTTAGCAGCTACTATATGGGTT | 117 |
| G2A | GTGTCCAGTCGGAGgagGTTACTTTGATTCAACCAGAGGCAGAGAACAGCCATCCTGGAGGTTCCATGAGACTGACCTGTA AAAACAGCGGGTTCGATCTTAGCAGCTATGCCATGAGTT | 120 |
| G2B | GTGTCCAGTCGGAGgagGTTACTTTGATTCAACCAGAGGCAGAGAACAGCCATCCTGGAGGTTCCATGAGACTGACCTGTA AAAACAGCGGGTTCGATCTTAGCAGCTATGCCATGAGTT | 120 |
| G5 | GTGTCCAGTCGGAA---GTTACTTTGATTCAACCAGAGGCAGAGACCGCCATCCTGGAGGCTCGCTGAGTCTGACCTGTA AAAACAGTGGGTTCAATCTTAGCAGCTCCTCCATGTATT | 117 |
| G1 | GTGTCCAATCGCAA---ATTATTTTGACTCAAAAAGTGGCAGAACTGGCCGGCTGGAGGCACCTAACACTGACCTGTA AAAACAGCGGGTTCGATCTTAGCAGCTACTATATGGGTT | 117 |
| | | |
| G4B3 | GGTCCGCGCAGGTTCCCGGACAGGGTCTGGAGTGGTTGGTTAGCTACTATAGTTTACATCGAGCAATTACTATGCGCCAGCGATTAAAGGTCGATTTACTGCGTCCAAAGACACTTCAAACA | 237 |
| G4B2 | GGTCCGCGCAGGTTCCCGGACAGGGTCTGGAGTGGTTGGTTAGCTACTATAGTTTACATCGAGCAATTACTATGCGCCAGCGATTAAAGGTCGATTTACTGCGTCCAAAGACACTTCAAACA | 237 |
| G4E2 | GGTCCGCGCAGGTTCCCGGACAGGGTCTGGAGTGGTTGGTTAGCTACTATAGTTTACATCGAACAATTACTATGCGCCAGCGATTAAAGATCGATTTACTGCGTCCAAAGACACTTCAAACA | 237 |
| G4S5 | GGTCCGCGCAGGTTCCCGGACAGGGTCTGGAGTGGTTGGTTAGCTACTATAGTTTACATCGAACAATTACTATGCGCCAGCGATTAAAGATCGATTTACTGCGTCCAAAGACACTTCAAACA | 237 |
| G3 | GGTCCGCGCAGGTTCCCGGACAGGGTCTGGAGTGGTTGGTTAGCTACTATAGTTTACATCGAACAATTACTATGCGCCAGCGATTAAAGATCGATTTACTGCGTCCAAAGACACTTCAAACA | 237 |
| G2A | GGTCCGACAGGTTCCCGGACAGGGGCTGGAGTGGATAGTTTACTCTTATGGTTTACATAGCAATGACTATGCGCCAGCGATTAAAGATCGATTTACTGCGTCCATAGACACTTCAAACA | 240 |
| G2B | GGTCCGACAGGTTCCCGGACAGGGGCTGGAGTGGATAGTTTACTCTTATGGTTTACATAGCAATGACTATGCGCCAGCGATTAAAGATCGATTTACTGCGTCCATAGACACTTCAAACA | 240 |
| G5 | GGATCCGACAGGTTCCCGGACAGGGGCTGGAGTGGATAGTTTACTCTTATGGTTTACATAGCAATGACTATGCGCCAGCGATTAAAGATCGATTTACTGCGTCCAAAGACACTTCAAACA | 237 |
| G1 | GGATCCGACAAGTTCCAGGACAGGGCTGGAGTGGCTGCTTGAATACAAAAGTTCGTCGAGCAATAACTATGCCCCAGGGGTTAAGGCCGATTTACTGCGTCCAAAGACACTTCAAACA | 237 |
| | | |
| | CH1 | |
| G4B3 | ACATCTTCGCGTTGGAATGAAGAGACTGAAGATCGAAGACACCGCCATCTATTACTGTGCAAGAGAC/GTGACACCGTCTTCCCGGACACTTTATGGTCTCGTCTCCTCCTGCGTGCAAC | 357 |
| G4B2 | ACATCTTCGCGTTGGAATGAAGAGACTGAAGATCGAAGACACCGCCATCTATTACTGTGCAAGAGAC/GTGACACCGTCTTCCCGGACACTTTATGGTCTCGTCTCCTCCTGCGTGCAAC | 357 |
| G4E2 | ACATCTTCGCGTTGGAATGAAGAGCCTGAAGATCGAAGACACCGCCATCTATTACTGTGCAAGAGAC/GTGACACCGTCTTCCCGGACACTTTATGGTCTCGTCTCCTCCTGCGGAGCAAC | 357 |
| G4S5 | ACATCTTCGCGTTGGAATGAAGAGCCTGAAGATCGAAGACACCGCCATCTATTACTGTGCAAGAGAC/GTGACACCGTCTTCCCGGACACTTTATGGTCTCGTCTCCTCCTGCGGAGCAAC | 357 |
| G3 | ACATCTTCGCGTTGGAATGAAGAGCCTGAAGATCGAAGACACCGCCATCTATTACTGTGCAAGAGAC/GTGACACCGTCTTCCCGGACACTTTATGGTCTCGTCTCCTCCTGCGGAGCAAC | 357 |
| G2A | ATATCTTCGCGTTGGAATGAAGAGCCTGAAGATCGAAGACACCGCCATCTATTACTGTGCAAGAGAC/GTGACACCGTCTTCCCGGACGCTTTATGGTCTCGTCTCCTCCTGTCAGCAAC | 360 |
| G2B | ATATCTTCGCGTTGGAATGAAGAGCCTGAAGATCGAAGACACCGCCATCTATTACTGTGCAAGAGAC/GTGACACCGTCTTCCCGGACGCTTTATGGTCTAGTCTCCCTCCTGTCAGCAAC | 360 |
| G5 | ACATCTTCGATTTGGAATGAGGAGCGTGAAGATCGAGACACCGCCATCTATTACTGTGCAACAGAT/GCAACACCGTCTTCTCCGACACTTTATGGCTTAGTCTCCTCCTGTCAGCAAG | 357 |
| G1 | ACATCTTCGCGTTGGAATGAAGAACCTGAAGATCGAAGACACCGCCATCTATTACTGTGCAAAAAGC/GTGACAACATCTTCTCCCTACTTTATGGCTTAGTCTCCTCCTGTCAGCAAC | 357 |
| | | |
| G4B3 | ACAGCACTGACGGTTCGTGATTTTTGGTTGTTGGCGATGGACTACTCCCCGACGCCACCAGTGTGACCTGGAAGAAAGGTGGGAAGCCCTTACAGACTGGATTTATGACATACCCAT | 477 |
| G4B2 | ACAGCACTGACGGTTCGTGATTTTTGGTTGTTGGCGATGGACTACTCCCCGACGCCACCAGTGTGACCTGGAAGAAAGGTGGGAAGCCCTTACAGACTGGATTTATGACATACCCAT | 477 |
| G4E2 | ACAGCACTGACGGTTCGTGATTTTTGGTTGTTGGCGATGGACTACTCCCCGACGCCACCAGTGTGACCTGGAAGAAAGGTGGGAAGCCCTTACAGCTGGATTTATGACATACCCAT | 477 |
| G4S5 | ACAGCACTGACGGTTCGTGATTTTTGGTTGTTGGCGATGGACTACTCCCCGACGCCACCAGTGTGACCTGGAAGAAAGGTGGGAAGCCCTTACAGACTGGATTTATGACATACCCAT | 477 |
| G3 | ACAGCACTGACGGTTCGTGATTTTTGGTTGTTGGCGATGGACTACTCCCCGATGACCCAGTGTGACCTGGAAGAAACATGGGGAGCCGATCAGCACTGGATTTATGACATACCCAT | 477 |
| G2A | AGACCAATGACGGTTCGTGATTTTTGGTTGTTGGCGATGGACTACTCCCCGACACCAGTGTGACCTGGAAGAAACATGGGGAGCCGATCAGCACTGGATTTAAGACATACCCAT | 480 |
| G2B | AGAACAATGACGGTTCGTGATTTTTGGTTGTTGGCGATGGACTACTCCCCGACACCAGTGTGACCTGGAAGAAACATGGGGAGCTGATCAGCACTGGATTTAAGACATACCCAT | 480 |
| G5 | GCAACATGACGGTTCGTGATCTATGGTTGTTGGCGATGGACTACTCCCCGACGTCGCGAGTGTGACCTGGAAGAAACATGGGGAGCTGATCAGCACTGGAGTTCAGAGCTACCCAT | 477 |
| G1 | ACAACACCGATGGTTCGTGATCTTTGGTTGCTTGGCAATGGGCTATTCCCTGACGTCCTAAGGTGACCTGGAAGAAAGGTGGGAAGCCGATCTCGACTGGATTGAAGACTTACCCAT | 477 |
| | | |
| G4B3 | CGGTGAGAAGCAAGAAGGGAACCTACACCTGAGCAGTCAGTTAGCGGTTCATCGAGTCAGAGGCAGAAATGCCAGAAAATACCTGTGAGGTTTCGACACAGCGGTTCCGACAAGAGCACTG | 597 |
| G4B2 | CGGTGAGAAGCAAGAAGGGAACCTACACCTGAGCAGTCAGTTAGCGGTTCATCGAGTCAGAGGCAGAAATGCCAGAAAATACCTGTGAGGTTTCGACACAGCGGTTCCGACAAGAGCACTG | 597 |
| G4E2 | CGGTGAGAAGCAAGAAGGGAACCTACACCTGAGCAGTCAGTTAGCGGTTCACCGAGTCAGAGGCAGAAATGCAGAGAAAATATCTGCGAGGTTTCGACACAGCGGTTCCGACAAGAGCACTG | 597 |
| G4S5 | CGGTGAGAAGCAAGAAGGGAACCTACACCTGAGCAGTCAGTTAGCGGTTCACCGAGTCAGAGGCAGAAATGCCAGAAAATACCTGTGAGGTTTCGACACAGCGGTTCCGACAAGAGCACTG | 597 |
| G3 | CGGTGAGAAGCAAGAAGGGAACCTACACCTGAGCAGTCAGTTAGCGGTTCACCGAGTCAGAGGCAGAAATGCCAGAAAATCTCCTGTGAGGTTTCGACACAGTGGGTTCCGACAAGAGCACTG | 597 |
| G2A | CGGTGAGAAGCAAGAAGGGAACCTACACCTGAGCAGTCAGTTAGCGGTTCACCGAGTCAGAGGCAGAAATGCCAGAAAATCTCCTGTGAGGTTTCGACACAGCGGTTCCGACAAGAGCACTG | 600 |
| G2B | CGGTGAGAAGCAAGAAGGGAACCTTACAGCTGAGCAGTCAGTTAGCGGTTCACCGAGTCAGAGGCAGAAATGCCAGAAAATCTCCTGTGAGGTTTCGACATAGCGGTTCCGACAAGAGCACTG | 600 |
| G5 | CGGTGAGAAGCAAGAAGGGAACCTACAGCTGAGCAGTCAGTTAGCGGTTCACCGAGTCAGAGGCAGAAATGCCAGAAAATCTCCTGTGAGGTTTCGACACAGCGGTTCCGACAAGAGCACTG | 597 |
| G1 | CAGTGAGAAGCAAGAAGGGAACCTACACCTGAGCAGTCAGTTAACCCTGACTGAGTCAGAAAGTGAATGCAGGAAAATCTACTGTGAAGTTCAACACGAAGGTTTCAGAGAAGAGCGGTTG | 597 |

CH2

G4B3 GAATGCCAT/gtcaaatcggt---GTCAGTCCAACCTCTTCTCCTAACTGTGAGTTCAGTGAAGAAATCGAGAGCAAAAAAGTTGCGACGATCGTCTGTCAATCTTTGGACTTCAATCCAA 714
G4B2 GAATGCCAT/gtccaccagataagGTCACCTCCAACCTCTTCTCCTAACTGTGAGTTCAGTGAAGAAATCGAGAGCAAAAAAGTTGCGACGATCGTCTGTCAATCTTTGGACTTCAATCCAA 717
G4E2 GAATGCCAT/gtcaattaaatggtGTCACCTCCAACCTCTTCTCCTAACTGTGAGTTCAGTGAAGAAATCGAGAGCAAAAAAGTTGCGACGATCGTCTGTCAATCTTTGGACTTCAATCCAA 717
G4S5 GAATGCCAT/gtccaccagataagGTCACCTCCAACCTCTTCTCCTAACTGTGAGTTCAGTGAAGAAATCGAGAGCAAAAAAGTTGCGACGATCGTCTGTCAATCTTTGGACTTCAATCCAA 717
G3 GAATGCCAT/gcaaacagattacGTCCCTCCAAGTTTCTCCTAACTGTGAGTTCAGTGAAGAAATCGAGAGCAAAAAAGTTGCGACGATCGTCTGTCAATCTTTGGACTTCAATCCAA 717
G2A GAATGCCAT/gtggaaacggt---GACCCCTCCGACTGTTCTCCTAACTGTGAGTTCAGTGAAGAAATCGAGAGCATAAAAAATTTGCAACCATCGTCTGTCAATCATTTGACTTCCATTCAA 717
G2B GAATGCCAT/gtcgaatcgat---GGCCCTCCAACCTGTTCTCCTAACTGTGAGTTCAGTGAAGAAATCGAGATCATAAAAAATTTGCAACCATCGTCTGTCAATCATTTGACTTCCATTCAA 717
G5 GAATGCCAT/gtc---ctgat---GGCTTCCGACTGCTCTCCTAACTGTGAGTTCAGTGAAGAAATCGAGAGCAAAAAATTTGCAATCATCGTCTGTCAATCATTTGACTTCCATTCAA 711
G1 GAATGCCAT/gtccaattatt---GTCCATCCAACCTCTTCTCCTAACTGTGAGTTCAGTGAAGAAATTTGCAACCATCGTCTGTCAATCATTTGACTTCCATTCAA 714

G4B3 GAAAAATCTCCGTGATTTGGTTGAAGAATGGAAAACAGGTGAATTCGGTACCTTCACTTTTCCCGTGTGTGAAGCGAATGGAACTTCTCAACGACCAGTCAGCTGAGAGTCCCTTATC 834
G4B2 GAAAAATCTCCGTGATTTGGTTGAAGAATGGAAAACAGGTGAATTCGGTACCTTCACTTTTCCCGTGTGTGAAGCGAATGGAACTTCTCAACGACCAGTCAGCTGAGAGTCCCTTATC 837
G4E2 GAAAAATCTCCGTGATTTGGTTGAAGAATGGAAAACAGGTGAATTCGGTACCTTCACTTTTCCCGTGTGTGAAGCGAATGGAACTTCTCAACGACCAGTCAGCTGAGAGTCCCTTATC 837
G4S5 GAAAAATCTCCGTGATTTGGTTGAAGAATGGAAAACAGGTGAATTCGGTACCTTCACTTTTCCCGTGTGTGAAGCGAATGGAACTTCTCAACGACCAGTCAGCTGAGAGTCCCTTATC 837
G3 GAAAAATCTCCGTGATTTGGTTGAAGAATGGAAAACAGATGAATTCGGTACCTTCACTTTTCCCGTGTGTGAAGCGAATGGAACTTCTCAACGACCAGTCAGCTGAGAGTCCCTTATC 837
G2A GTCAATCTCCGTCAATTTGGTTGAAGAACGGAGGACGTGTCATTCTGCATCCTAACTTCTCCCGTGTGTGAAGCGAATGGAACTTCTCAACGACCAGTCAGCTGAGAGTCCCTTATG 837
G2B GTCAATCTCCGTCAATTTGGTTGAAGAACGGAGGACGTGTCATTCTGCATCCTAACTTCTCCCGTGTGTGAAGCGAATGGAACTTCTCAACGACCAGTCAGCTGAGAGTCCCTTATG 837
G5 GTCAATCTCCGTGACTTTGGTTGAAGAACGGAGGACGTGTCATTCTGCATCCTAACTTCTCCCGTGTGTGAAGCGAATGGAACTTCTCAAGTACCAGTCAGCTGAGAGTCCCTTATG 831
G1 GTCAATCTCAGTGACTTTGGTTGAAGAATGGACAATCCGTGGATTCTGGCTTCTTCACTTCTCCTGCGTATGAACGAAACAAGAACTTCTCAGTGACCAGTTGGCTGAGAGTCCCTTATA 834

CH3

G4B3 GTGAATGGTTCGACAGAGCAGTCTATACATGCCAGGTCGATCATGAAGGGGTCATTCAAAGTCAGAACATCACCGGACCTCAGG/TTTCGGAGTGCCCGTGATTACACAGCTAAAATACTAC 954
G4B2 GTGAATGGTTCGACAGAGCAGTCTATACATGCCAGGTCGATCATGAAGGGGTCATTCAAAGTCAGAACATCACCGGACCTCAGG/TTTCGGAGTGCCCGTGATTACACAGCTAAAATACTAC 957
G4E2 GTGAATGGTTCGACAGAGCAGTCTATACATGCCAGGTCGATCATGAAGGGGTCATTCAAAGTCAGAACATCACCGGACCTCAGG/TTTCGGAGTGCCCGTGATTACACAGCTAAAATACTAC 957
G4S5 GTGAATGGTTCGACAGAGCAGTCTATACATGCCAGGTCGATCATGAAGGGGTCATTCAAAGTCAGAACATCACCGGACCTCAGG/TTTCGGAGTGCCCGTGATTACACAGCTAAAATACTAC 957
G3 GTGAATGGTTCGACAGAGCAGTCTATACATGCCAGGTCGATCATGAAGGGGTCATTCAAAGTCAGAACATCACCGGACCTCAGG/TTTCGGAGTGCCCGTGATTACACAGCTAAAATACTAC 957
G2A CTGAATGGTTCGACAAAAGCAGTCTATACATGCCAGGTCATTATGATGGGGTCACTCAAAGTTGGAACATCACTGGACCTCAGG/TTTCGGAGTGCCATGGTTACACAGCCAAAATACTAC 957
G2B CTGAATGGTTCGACAAAAGCAGTCTATACATGCCAGGTCATTATGATGGGGTCACTCAAAGTTGGAACATCACTGGACCTCAGG/TTTCGGAGTGCCATGGTTACACAGCCAAAATACTAC 957
G5 CTGAATGGTTCGACAGAGCAGTCTATACATGCCAGGTCAGTATAAAGAGGTCATTCAAAGTTGGAACATCACCGGACCTCAGG/TTTCGGAGTGCCATGGTTACACAGCTAAAATACTAC 951
G1 GTGAATGGTTCACAGTGCAGTCTATACTTGCCAGGTCACCCATGAAGGGTCACTCAAAGTCAGAACATCACCGGATTCAGG/TTACCGAGTGCCCGTGATTACACAGTAAAATACTAC 954

G4B3 CGCCACCAGTTGAACAGGTCTTACTGGAGGCGACGGTGACGTTAACCTGCGTTGTGTACAATCTTCAATTTTGAAGCCAACCTTCACTGGATACACGACAAGAAGACTCTGAAATCAGAGA 1074
G4B2 CGCCACCAGTTGAACAGGTCTTACTGGAGGCGACGGTGACGTTAACCTGCGTTGTGTACAATCTTCAATTTTGAAGCCAACCTTCACTGGATACACGACAAGAAGACTCTGAAATCAGAGA 1077
G4E2 CGCCACCAGTTGAACAGGTCTTACTGGAGGCGACGGTGACGTTAACCTGCGTTGTGTACAATCTTCAATTTTGAAGCCAACCTTCACTGGATACACGACAAGAAGACTCTGAAATCAGAGA 1077
G4S5 CGCCACCAGTTGAACAGGTCTTACTGGAGGCGACGGTGACGTTAACCTGCGTTGTGTACAATCTTCAATTTTGAAGCCAACCTTCACTGGATACACGACAAGAAGACTCTGAAATCAGAGA 1077
G3 CGCCACCAGTTGAACAGGTCTTACTGGAGGCGACGGTGACGTTAACCTGCGTTGTGTACAATCTTCAATTTTGAAGCCAACCTTCACTGGATACACGACAAGAAGACTCTGAAATCAGAGA 1077
G2A CACCACCAGTTCGAACAGGTCTTACTGGAGGCGACGGTGACATTAACCTTGTGTGTCGATCCTTCACTTGGAGTCAACTTCACTGGATGCAAGGCAAGAAGACTCTGAAATCAGAGA 1077
G2B CACCACCAGTTCGAACAGGTCTTACTGGAGGCGACGGTGACGTTAACCTGCGTTGTGTGTCGATCCTTCACTTGGAGTCAACTTCACTGGATGCAAGGCAAGAAGACTCTGAAATCAGAGA 1077
G5 CACCACCAGTTCGAACAGGTCTTACTGGAGGCGACGGTGACATTAACCTGCGTTGTGTGTCGATCCTTCACTTGGAGTCAACTTCACTGGATGCAAGGCAAGAAGACTCTGAAATCAGAGA 1071
G1 CGCCGCAATTTGAACAGGTCTTACTGGAGGCGACGGTGACGTTGACCTGCGTTGTATTCAGTCTTCTTTTGGAGTCAACGTCACCTGGACACAGGAAAATAAGCCTCTGAAATCAGAGA 1074

G4B3 TTGTTGACCAGTCCGGAGAGCATTCCGAAGGTGTGATCAGCAAGTTAGATATTTTACTGAAGCCTGGCTGAGTGGGGATAAAATTTGAATGCGTGGTGAACAATCAGTATTTACCGACTC 1194
G4B2 TTGTTGACCAGTCCGGAGAGCATTCCGAAGGTGTGATCAGCAAGTTAGATATTTTACTGAAGCCTGGCTGAGTGGGGATAAAATTTGAATGCGTGGTGAACAATCAGTATTTACCGACTC 1197
G4E2 TTGTTGACCAGTCCGGAGAGCATTCCGAAGGTGTGATCAGCAAGTTAGATATTTTACTGAAGCCTGGCTGAGTGGGGATAAAATTTGAATGCGTGGTGAACAATCAGTATTTACCGACTC 1197
G4S5 TTGTTGACCAGTCCGGAGAGCATTCCGAAGGTGTGATCAGCAAGTTAGATATTTTACTGAAGCCTGGCTGAGTGGGGATAAAATTTGAATGCGTGGTGAACAATCAGTATTTACCGACTC 1197
G3 TTGTTGACCAGTCCGGAGAGCATTCCGAAGGTGTGATCAGCAAGTTAGATATTTTACTGAAGCCTGGCTGAGTGGGGATAAAATTTGAATGCGTGGTGAACAATCAGTATTTACCGACTC 1197
G2A TTGCTCAGACTCCGGAGAGCATTCCGATGGTACGATCAGCAAGTTAGATATTTTCCGACTGAATCCTGGCTGAGTGGGGATAAAATTTGACTGCGTGGTGAATCATCAGTATCTACCGACTC 1197
G2B TTGCTCAGGATTTCCGGAGAGCATTCCGATGGTGCATCAGCAAAATAGATATTTTCCGACTGAAGCCTGGCTGAGTGGGGATAAAATTTGCAATGCGTGGTGAATCATCAGTATCTACCGACTC 1197
G5 TTGCTCAGACTCTGGAGAGCATTCCGATGGTGCATCAGCAAAATGGATATTTTACTGAAGCCTGGCTGAGTGGGGATAAAATTTGCAATGCGTGGTGAATCATCAGTATCTACCGACTC 1191
G1 TTGCTGACCAAGCCGGAGGATCCCGACAGCGTGATCAGCAAAATGGATATTTTACTGAAGCCTGGCTGAGTGGGGATAAAATTTTACTGCGTGGTGAACGATCAGACTC 1194

CH4

G4B3 CACTGAGAAACTCCATCCACAAGAGAAAT / TGGTAAATCCGCTGGAACCATCGGTGTCCGTCCCTCCTGCCAGCGACAGAAGAAGTCTCCGCACAGAGGTTTGTTCGCTCACCTGTTT 1314
 G4B2 CACTGAGAAACTCCATCCACAAGAGAAAT / TGGTAAATCCGCTGGAACCATCGGTGTCCGTCCCTCCTGCCAGCGACAGAAGAAGTCTCCGCACAGAGGTTTGTTCGCTCACCTGTTT 1317
 G4E2 CACTGAGAAACTCCATCCACAAGAGAAAT / TGGTAAATCCGCTGGAACCATCGGTGTCCGTCCCTCCTGCCAGCGACAGAAGAAGTCTCCGCACAGAGGTTTGTTCGCTCACCTGTTT 1317
 G4S5 CACTGAGAAACTCCATCCACAAGAGAAAT / TGGTAAATCCGCTGGAACCATCGGTGTCCGTCCCTCCTGCCAGCGACAGAAGAAGTCTCCGCACAGAGGTTTGTTCGCTCACCTGTTT 1317
 G3 CACTGAGAGACTCCATCCACAAGGAGAAAT / TGGTAAATCCGCTGGAGCCATCGGTGTCCATCCCTGCCAACGACAGAAGAAGTCTCCGCACAGAGGTTTGTTCGCTCACCTGTTT 1317
 G2A CTCTGAGAGACTCCATACACAAGGAGACAA / TTAAAAATCCACTGGAGCCATCAGTGTCTGTCTCTACTGCCAACACAGAAGAAGTCTCCGCAGAGGTTTGTTCCTTACCTGTTTGG 1317
 G2B CTCTGAGAGACTCCATCCACAAGGAGACAA / TTGAAAAATCCACTGGAGCCATCGGTGTCTGTCTCTCCTGCCAACGACAGAAGAAGTCTCCGCAGAGGTTTGTTCCTTACCTGTTT 1317
 G5 CTCTGAGAGACTCCATCCACAAGGAGAGAA / TTGAAAAATCCACTGGAGCCATCGGTGTCTGTCTCTCCTGCCAACGACAGAAGAAGTCTCCGCAGAGGTTTGTTCCTTACCTGTTT 1311
 G1 CTCTCAGAGACTCCATCCACAAGGAGAAAC / CAATAAAATCCATTGGAGCCATCAGTGTCTGTCTCTTGGCACCGGAGGAAGAAGTCTCCACTCAGAGGTTTGTCTCCCTCACTTGTTCG 1314

G4B3 TGAGAGGTTTTCAGGCCCCGAGAGATCTTTGTCAAGTGGACAACCAACGACAAGCCGGTTAATCCCCTAATACTATAAGAACACCGAGGTGACGGCAGAGAGCGATAACACCTCCTTCTTCT 1434
 G4B2 TGAGAGGTTTTCAGGCCCCGAGAGATCTTTGTCAAGTGGACAACCAACGACAAGCCGGTTAATCCCCTAATACTATAAGAACACCGAGGTGACGGCAGAGAGCGATAACACCTCCTTCTTCT 1437
 G4E2 TGAGAGGTTTTCAGGCCCCGAGAGATCTTTGTCAAGTGGACAACCAACGACAAGCCGGTTAATCCCCTAATACTATAAGAACACCGAGGTGACGGCAGAGAGCGATAACACCTCCTTCTTCT 1437
 G4S5 TGAGAGGTTTTCAGGCCCCGAGAGATCTTTGTCAAGTGGACAACCAACGACAAGCCGGTTAATCCCCTAATACTATAAGAACACCGAGGTGACGGCAGAGAGCGATAACACCTCCTTCTTCT 1437
 G3 TGAGAGGTTTTCAGGCCCCGAGAGATCTTTGTCAAGTGGACAACCAACGACAAGCCGGTTAATCCCCTAATACTATAAGAACACCGAGGTGACGGCAGAGAGCGGTAACACCTCCTTCTTCT 1437
 G2A TGAGAGGTTTTCAGGCCCCGAGAGATCTTTGTCAAGTGGACAACCAACGACAAGCCGGTTAATCCCAGTAACACAGAACACCGAAGTACGGCAGAGAGCGACAACACCTCCTTCTTCT 1437
 G2B TGAGAGGTTTTCAGGCCCCGAGAGATCTTTGTCAAGTGGACAACCAACGACAAGCCGGTTAATCCCAGTAACACAGAACACCGAAGTACGGCAGAGAGCGACAACACCTCCTTCTTCT 1437
 G5 TGAGAGGTTTTCAGGCCCCGAGAGATCTTTGTCAAGTGGACAACCAACGACAAGCCGGTTAATCCCAGTAACACAGAACACCGAAGTACGGCAGAGAGCGACAACACCTCCTTCTTCT 1431
 G1 TGAGAGGTTTTCAGGCCCCGAGAGATCTTTGTCAAGTGGACAACCAATGATAAGCCGGTGAATCCCAGTAATACAGAACACCGAGGTGACGGCAGAGAGCGACAACGCTCCTTTTCA 1434

G4B3 TGTACAGCCTATTGTCCATTGCTGCGGAGGAGTGGGCCAGCGGTGCTTCTTACTCCTGTGTGGTGGGACATGAAGCGATTTCCTTTGAAGATCATCAACAGAACCATGGATAAATCCAGCG 1554
 G4B2 TGTACAGCCTATTGTCCATTGCTGCGGAGGAGTGGGCCAGCGGTGCTTCTTACTCCTGTGTGGTGGGACATGAAGCGATTTCCTTTGAAGATCATCAACAGAACCCTGGATAAATCCAGCG 1557
 G4E2 TGTACAGCCTATTGTCCATTGCTGCGGAGGAGTGGGCCAGCGGTGCTTCTTACTCCTGTGTGGTGGGACATGAAGCGATTTCCTTTGAAGATCATCAACAGAACCCTGGATAAATCCAGCG 1557
 G4S5 TGTACAGCCTATTGTCCATTGCTGCGGAGGAGTGGGCCAGCGGTGCTTCTTACTCCTGTGTGGTGGGACATGAAGCGATTTCCTTTGAAGATCATCAACAGAACCCTGGATAAATCCAGCG 1557
 G3 TGTACAGCCTATTATCCATTGCTGCGGAGGAGTGGGCCAGCGGTGCTTCTTACTCCTGTGTGGTGGGACATGAAGCGATTTCCTTTGAAGATCATCAACAGAACCCTGGATAAATCCAGTG 1557
 G2A TGTACAGCCTGTTATCCATTGCGAGCGGAGGAGTGGGCCAGCGGTGCTTCTTACTCCTGTGTGGTGGGACATGAAGCGATTTCATTGAAGATCATCAACAGAACCCTGGATAAATCCAGCG 1557
 G2B TGTACAGCCTGTTATCCATTGCGAGCGGAGGAGTGGGCCAGCGGTGCTTCTTACTCCTGTGTGGTGGGACATGAAGCGATTTCATTGAAGATCATCAACAGAACCCTGGATAAATCCAGCG 1557
 G5 TGTACAGCCTGTTATCCATTGCGAGCGGAGGAGTGGGCCAGCGGTGCTTCTTACTCCTGTGTGGTGGGACATGAAGCGATTTCATTGAAGATCATCAACAGAACCCTGGATAAATCCAGCG 1551
 G1 TGTACAGCCTGTTATCCATTGCTGCGGAGGAGTGGGCCAGCGGTGCTTCTTACTCCTGTGTGGTGGGACATGAAGCGATTTCATTGAAGATCATTAACAGAACCCTGGATAAATCCAGCG 1554

Tailpiece

G4B3 GTAAACCGAGTTTTGTGAATATTTCACTTGCCTGATGGACACCATTAATTCATGCCAA 1613
 G4B2 GTAAACCGAGTTTTGTGAATATTTCACTTGCCTGATGGACACCATTAATTCATGCCAA 1616
 G4E2 GTAAACCGAGTTTTGTGAATATTTCACTTGCCTGATGGACACCATTAATTCATGCCAA 1616
 G4S5 GTAAACCGAGTTTTGTGAATATTTCACTTGCCTGATGGACACCATTAATTCATGCCAA 1616
 G3 GTAAACCGAGTTTTGTGAATATTTGCTTGCCTGATGGACACCATTAATTCATGCCAA 1616
 G2A GTAAACCGAGTTTTGTGAATATTTCACTTGCCTGATGGACACCATTAATTCATGCCAA 1616
 G2B GTAAACCGAGTTTTGTGAATATTTCACTTGCCTGATGGACACCATTAATTCATGCCAA 1616
 G5 GTAAACCGAGTTTTGTGAATATTTCACTTGCCTGATGGACACCATTAATTCATGCCAA 1610
 G1 GTAAACCAAGTTTTGTGAACATTTCACTTGCCTGATGGACACCATTAATTCATGCCAA 1613

