

**A**

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IGHV4-n*03|AR212      CAGGTGCAGCTGCAGGAGTCGGGCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCGCTGTCTCTGGTTACTCCATCAGCAGTGGTTACT
DH846.1 VH           ...C.....GT.....A.....GT.....CAA...TG
DH846.2 VH           .....GAG.....GT..AA...TG

IGHV4-n*03|AR212      ACTGGGGCTGGATCCGTCAGCCCCAGGGAAGGGACTGGAGTATATTGGGTATATCAGTGGTAGTAGTGGGAGCACCTACTACAACCCCTCCCTCAAGAG
DH846.1 VH           G.....C.....T.....C.GG...T.AC...TA..CG..CG..A.A.....GC...T.....G..G.
DH846.2 VH           G.....C.....G.....GG...T.AC...TA..G..CG..A.....G.....G

IGHV4-n*03|AR212      TCGAGTCACCATTTCAAAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACC GCCGGACAGGCCGTGATTACTGTGCGAGA
DH846.1 VH           .....TG.....G.A.....G.....A.....A.....A.....A.....T.....G
DH846.2 VH           .....C.....G.A.....C.....A.....A.....A.....A.....A.....G

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**B**

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IGHV4-e*01|AR194      CAGGTGCAGCTGCAGGAGTCGGGCCAGGACTGGTGAAGCCTTCGGAGACCCTGCCCTCACCTGCGCTGTCTCTGGTGCCTCCATCAGCAGTAACTAA--
DH846.1 VH           ...C.....T.....A.....T.....C...T...TG
DH846.2 VH           .....T.....GAG.....GT..T...TG

IGHV4-e*01|AR194      CTGGAGCTGGATCCGCCAGCCCCAGGGAAGGGACTGGAGTGGATTGGGTATATCTATGGTGGTAGTGGGAGCACCTACTACAACCCCTCCCTCAAGAG
DH846.1 VH           G...G.....T.....C.....T.AC.....C...CG..A.A...TA...GC...T.....G..G.
DH846.2 VH           G...G.....G.....T.AC.....CG..A...TA...G.....G

IGHV4-e*01|AR194      TCGAGTCACCATTTCAAAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACC GCCGGACACGGTCGTGATTACTGTGCGAGA
DH846.1 VH           .....TG.....A.....G.A.....G.....A.....A.....A.....C...A.....T.....G
DH846.2 VH           .....C...A.....G.A.....C.....A.....A.....A.....A.....C.....G

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**C**

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IGHV4-f*03|AR197      CAGGTGCAGCTGCAGGAGTCGGGCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCGCTGTCTCTGGTGGTCCATCAGCGATTACTACT
DH846.1 VH           ...C.....A.....A.....T.....AGCA...T...TG
DH846.2 VH           .....GA.....T.A...T...TG

IGHV4-f*03|AR197      ACTGGAACTGGATCCGCCAACCCCCAGGGAAGGGGCTGGAGTGGATTGGGAATATCTATGGTAAATAGTCCGAGCACCTACTACAACCCCTCCCTCAAGAG
DH846.1 VH           G...GG.....G.....T.....A.....C.....T..C.....CGG..CG..GA.A.....GC...T.....G..G.
DH846.2 VH           G...GG.....G.....T..C.....GG..CG..G..A.....G.....G

IGHV4-f*03|AR197      TCGAGTCACCATTTCAAAGACACGTCCAAGAACCAGTTCTCCTGAAGCTGAGCTCTGTGACC GCCGGACACCGCCGCTGATTACTGTGCGAGA
DH846.1 VH           .....TG.....G.A.....C.....G.....A.....A.....A.....G.....A.....T.....G
DH846.2 VH           .....C.....G.A.....C.....C.....A.....A.....A.....G.....G

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**D**

| Reference VH gene segment comparison with DH846.1 and DH846.2 |                               |                   |         |        |
|---|-------------------------------|-------------------|---------|--------|
| VH  | Mismatches with DH840.1 and 2 | VH divergence (%) |         | Indels |
|   |                               | DH846.1           | DH846.2 |        |
| IGHV4-n   | 21                            | 13.7              | 10      | 0      |
| IGHV4-e   | 20                            | 13.1              | 9.6     | 3      |
| IGHV4-f   | 22                            | 14.8              | 9.3     | 0      |

**S12 Fig. Comparison of DH846.1 and DH846.2 nucleotide sequence with putative rhesus macaque germline V gene segments. (A-C) Nucleotide alignments for the three rhesus macaque germline V gene segments with highest sequence identity to DH846.1 and DH846.2. HCDRs are bolded. Nucleotides that are the same in DH846.1 and DH846.2, but different in the reference gene segment are highlighted yellow, and the total number of these differences is shown in (D). IGHV4-e, but not the other two reference V gene segments, contained a 3 nucleotide insertion (indels) in HCDR2 compared to DH846.1 and DH846.2 antibodies.**