Human genes in HG38 (HUM) and their mappings (UAMs) in Chm13Terrt

IGHV(III)-82

GENE ALIGN SEQ HUM: A A G T C C T G T T G A A G C T T A C T G A A G C T T A C T G A T G G A G T C A G A G G G G A A A C A T T G T A C A G G G G G G G A A A C A T T G T A C A G G G G G G G G G G G G G G G G G
HUM: C C C A G C G G T T C T C A C A G A C T C T C T C T C T C T G T G T A C T C T C T G T A C T C T G T A C T C T G T A C T C T G T A C T T G T A C T A C T T G T A C T A C T T G T A C T C T C T C T C T C T C T C T C T
HUM: T G G C T A C A G C A T G A G C T T G G T C A G C T T G G T T G G T C C A G C T T C A G G A T T T G T G T UAM: T G G T A C A G G G A T T T G T G T G T C A G G C T T C A T G A C A G G G A T T T G T G T G T C A G G C T T C A T G A C A G G G A T T T G T G T G T G T G T G T
HUM: GGGGTGGCAACACAGTGAGTATATCAGGGTTAATCAGGTTAACTCAGGGTTAACTCAGGGTTAACTAGAGTAAGTA
HUM: T A A C A G T C C C A A G C A C C T T T C A A G T C C A G T T A A A A T G A C C UAM: T A A C A G T C A A G T C C A A G T C T A C C T T A A A A T G A C C UAM: T A A C A G T C A A G T C A A G T C A A G T C A A G T C A A G T C A A A T G A C C T T A A A A A T G A C C T T A A A A A T G A C C T T T A A A A A T G A C C T T T A A A A A T G A C C T T T A A A A A T G A C C T T T A A A A A T G A C C T T T A A A A A T G A C C T T T A A A A A T G A C C T T T A A A A A T G A C C T T T A A A A A T G A C C T T T A A A A A T G A C C T T T A A A A A T G A C C T T T A C C T T T A A A A A T G A C C T T T A C C T T T A C C T T T A A A A
HUM: A A T G T G A A A G C C A A G G A C A A G G A C A A G G A C A A G A G
D7 HUM: C A T A G G A UAM: C A T A G G A
D9 HUM: A G A C A A A A T UAM: A G A C A A A A A T
Alignment stats: 'M': 292, 'I': 0, 'D': 0, 'X': 0 Both human gene and its mapping are pseudogenes

IGHV7-81

GENE ALIGN SEQ
HUM: CAGGGCAGCTGAGCAGCTAGCAGCTAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCA
UAM: C A G G T G C A G C T G G T G C A G C T G C T G C C A G C C T C C C C C C C C C C C C C C C C
HUM: A G T G A A G G T C T C C T G C A A G G C T T C T A C A C C T A T G C T A
UAM: A G T G A A G G T C T C C T G C A A G G C T T C T G C A G T T A C A G T T T C A C C T A T G G T A
HUM: T G A A T T G G G T G C C A C A G G C C C T G G A G G C T T G A G T G G A T G G G G
UAM: TGAATTGGGGTGCCACACAGGCCCCTGGAAGGGCTTGGAGTGGATGGGATGG
HUM: TTCAACACACACAACAAAAAAAAAAAAAAAAAAAAAAA
UAM: TTCAACACATACACATACACAACAACAACATATATGCCCAAGGCACGCAGGGCCTTCAGGGACG
HUM: G T T T G T C T T C T C A T G A C A C A C A C A G C A G C A G C A T A C C T G A G A A G A A G A A C A A G C A A C A A C A C
UAM: G T T T G T C T T C T C C A T G G A C A C C T C T G C A G C A C A G C A T A C C T G C A G A T A C C T G C A G A T C A
HUM: GCAGCTAAAGGCTGAGGACATGATGGGCTGATGAGGAACATGGTATGTAT
UAM: G C A G C T A A A G G C T G A G G A C A T G G C C A T G T A T T A C T G T G C G A G A T A
D7
HUM: C A C C A T G
UAM: CACATG
D9
HUM: GTCAGAATCC
Alignment stats: 'M': 296, 'I': 0, 'D': 0, 'X': 0 Neither human gene nor its mapping is pseudogene
6 11 6 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

IGHV4-80

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GENE ALIGN SEQ
HUM: G T G C A G C T G C A G G A G T G G G G C C C A G G A C T G G T G A A G C C T T C G G A G A C C C T
                    CAGGAGTGGGGCCCAGGAC<mark>T</mark>GGTGAAGCCTT<mark>C</mark>GGAGACCCT
HUM: G T C C C T C A C A T G C G C T G T C T C T G G T G A C T C C A T C A G C A G T G G T A A C T G G T
UAM: G T C C C T C A C A T G C G C T G T C T C T G G T G A C T C A G C A G T G G T A A C T G G T
HUM: G G A G C T G G G T C C G C C A G T C C C A G G G G G G G C T G G A A T G G A T T G G A T
UAM: G G A G C T G G G T C C G C C A G T C C C A G G G G G G C T G G A A T G G A
HUM: A T C T A T T A T A G T G G G A G G A G C T A C T A C C C C G T C A G G A G T T G A G T
UAM: A T C T A T T A T A G T G G G A G G A G C T A C T A C C C G T C C G T C A G G A G T T G A G T
HUM: CACCATGAATAGAAACG<mark>T</mark>CAAAGAACG<mark>T</mark>CCAAGTTTTCCCCTGAAGC<mark>T</mark>GAAGC<mark>T</mark>
UAM: CACCATGAAATAGAAACGTCAAGAAGCAAGAAGCTT
HUM: C T G T G A C C G C A
UAM: C T G T G A C C G C A
D7
HUM: G G G A G G C
UAM: G G G A G G C
D9
HUM:
     G C T C A G G A C C A
UAM: G C T C A G G A C C A
Alignment stats: 'M': 261, 'I': 0, 'D': 0, 'X': 0
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IGHV(II)-78-1

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GENE ALIGN SEQ
HUM: T G G C C T G G T G A A G C C C T C A C A G A C C C T C T C C T T A C C T G C G C T G T G T G T C T G
UAM: T G G C C T G G T G A A G C C C T C A C A G A C C C T C T C C C C T T A C C T G C G
HUM: T G T T C C C C A T G A T A A C G A G G T C T T C C T G C T G A A G C T G G A T C C A T C A G C C C
UAM: T G T T C C C C G T G A T A A C G A G G T C T T C C T G C T G A A G C T G G A T C A T C A G C C C
HUM: CCCAGGGAAGGGAATGGAAGTGGAATTGGAATTGGGA<mark>TTGGGATTGGGGTGCATAGGGTCA</mark>
UAM: CCCAGGGAAGGAATGGAATGGAATTGGATTAGGATAGGTCATGAAGGGAG
HUM: T C C A A A A A A G C A G T T C T T C C T A C A G C T G A G C T A C A T G A G C A A C A A G C A C A
UAM: T C C A A A A A A G C A G T T C T T C C T A C A G C T G A G C T A C A T G A G C A A C A A G C A C A
HUM: T A G C C A T G T A T T T T A A G C C A A A G A
UAM: T A G C C A T G T A T T T T A A G C C A A A G A
D7
HUM: C A C A G T G
D9
HUM: CACCCAAACCT
UAM: CACCCAAACCT
Alignment stats: 'M': 274, 'I': 0, 'D': 0, 'X': 1
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IGHV5-78

GENE ALIGN SEQ
HUM: GAGGTGCAG <mark>CTGTTGCAGTTGCCAGTCAGCAGCAGGAGAGAAAAGACCC</mark> GGGGAG <mark>T</mark> C
UAM: GAGGTGCAG <mark>CTGTTGCAGTGCAGTGAGGAGGTGAAAAGACCC</mark> GGGGAG <mark>T</mark> C
HUM: T C T G A G G A T C T C C T G T A A G A C T T C T G G A T A C A G C T T T A C C A G C T A C T G G A
UAM: T C T G A G G A T C T C C T G T A A G A C T T C T G G A T A C A G C T T T A C C A G C T A C T G G A
HUM: TCCACTGGGTGCACACTGCAGACAAGAAAAAACAACTGAATGAA
UAM: TCCACTGGGTGCAGCTAGCAGAGAGAAGAAGAACTGGCAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA
HUM: A T C T A T C C T G G G A A C T C T G A T A C C A G A T A C A G C C C A T C C T T C C A A G G C C A
UAM: A T C T A T C C T G G G A A C T C T G A T A C C A G A T A C C A G C C A T C C T T C C A A G G C C A
HUM: CGTCACCATCAGCAGCCAGCAGCAGCAGCAGCAGCAGCACCGCCTACCAGAAAAAAAA
UAM: CGTCACCATCACAACAAACAAAAAAAAAAAAAAAAAAAA
HUM: GCAGCCTGAGGCCTCGGGACGCCTCGGGCCATGTTTATTATTGTGAGAGA
UAM: GCAGCCTGAAGCCTGAAGAAAAAAAAAAAAAAAAAAAAA
D7
HUM: G G G A C C A
UAM: G G G A C C A
D9
HUM: G T G C A G A G T G A
UAM: G T G C A G A G T G A
Alignment stats: 'M': 294, 'I': 0, 'D': 0, 'X': 0
Neither human gene nor its mapping is pseudogene

6

IGHV(III)-76-1

GENE ALIGN SEQ. HUM: CTGGTGGAATCTGGAAGAAATGAATACAGCCTAACTGATCAGAGAGCCT UAM: CTGGTGGAATCTGGAAGAGAAATGATACAGCCTAACTGTTCAGAGAGCCT HUM: T T T T T A C A A A G C C T C T G A A T T T A C C T T C A T T G A C T C T A G C A T G A G C T C A G UAM: T T T T T A C A A A G C C T C T G A A T T T A C C T T C A T T G A C T C T A G C A T G A G C T C A G HUM: CCCAGCAGCAGGATTCAAGGACAGGGTTGGG<mark>T</mark>GG<mark>T</mark>GGGGAGGCAAAAG<mark>C</mark>GAGGGAAGAAAG<mark>C</mark> HUM: T C A A G T G G A A T T T G T T A G T G G T A C C C T C C A T C A A T A C A A A G A A A A A T C A T HUM: A A T C C T C A G G G A C A C C C T T G T C A G C A C C T T C A A A T G A C C UAM: A A T C C T C A G G G A C A C C C T T G T C A G C A C A G T C T C C C T C A A A A T G A C C A A C C HUM: T G A G A G C C G A G G A G A A G G C C A T G T A T T A C T G T G A G A G A D7HUM: C A C A G G A UAM: C A C A G G A D9HUM: A C A G G G G A C A C UAM: A C A G G G G A C A C Alignment stats: 'M': 288, 'I': 0, 'D': 0, 'X': 0

7

GENE ALIGN SEQ. UAM: GAAGTGTAGCTGGTAGAGTCTGGGGGGAGG<mark>CTT</mark>GGTACAG<mark>CTT</mark>GGGGGGGT<mark>C</mark> HUM: CATGTGACTCCTGTGCGGGCTCTCTGAGCACTTATCAGTAACTTATGGGCA UAM: C A T G T G A C T C T C T G T G C A G C C T C T C T C A G C A C T C T C A G T A T C A G T A A C T A T G G C A UAM: TGCACTAGGACTAGGACCAAGCCAAGGCTCCAAGGGAAGTGGGTCTAACAT HUM: TAATGCTAGTGGAGGGCATATATACTACTCAGAGTGAAGGGCCGGT UAM: TGACCATCTCAGAGAAAACACCAAGAACTCACTGTATCTGCAAATAAAC HUM: A G T T T C A T T G C T G A C A C C A T G G C C G T C T A T T A C T G T A A G A G A D7HUM: C A C A G T G D9HUM: G T C A C A A A C C T UAM: G T C A C A A A C C T Alignment stats: 'M': 292, 'I': 0, 'D': 0, 'X': 0

8

GENE ALIGN SEQ. HUM: GAGGTGCAGCTGGAGTCCGGGGGGGGGGTC CTGGTGGAGTCCGGGGGGGC<mark>TTAGTT</mark>CAGCCTGGGGGG<mark>T</mark>C HUM: TGCACTGGGTCAAGGCTCAAGGCTCAAGGCTCAAGGCTCAAGGGGAAGGGGCTGGTGTCACACGT UAM: TGCACTGGGTCAAGGCTGGGGTCAAGGCTCAAGGGGAAGGGGCTGGTGTCACGT HUM: A T T A A T A G T G A T G G G A G T A G C A A G C T A C G C G G A C T C C G T G A A G G C C G UAM: A T T A A T A G T G A T G G G A G T A G C A A G C T A C G C G A C T C C G T G A A G C C G HUM: A C A G T C T G A G A G C C G A G G A C A C G G C T G T G T A T T A C T G T G C A A G A G A D7HUM: C A C A G T G D9HUM: GACACAAACCT UAM: G A C A C A A A C C T Alignment stats: 'M': 296, 'I': 0, 'D': 0, 'X': 0

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GENE ALIGN SEQ.
HUM: GAGGTGCAGCTGGAGTCCGGGGGGGGGGTC
                 CTGGTGGAGTCCGGGGGGC<mark>TTGGTCCAGCCT</mark>GGGGGG<mark>T</mark>C
UAM: CCTGAAACTCTCTGTGTGTGCTGCTGCTGCTGCTA
HUM: TGCACTGGGTCCGCCTCGCCAGGCTTCCGGGAAAGGGCTTGGGAGTTGGGCCGT
    T G C A C T G G G T C C G C C A G G C T T C C G G G A A A G G G C T G G A G T G G G T T G G C C G T
UAM:
HUM: A T T A G A A G C A A A G C T A A C A G T T A C G C G A C A G C A T A T
UAM: A T T A G A A G C A A A G C T A A C A G T T A C G C G A C A C
HUM: A G G C A G G T T C A C C A T C T C C A G A G A T G A T T C A A A G A A C A C G G C G T A T C T G
UAM: A G G C A G G T T C A C C A T C T C C A G A G A T T C A A A G A A C A C G G
HUM: A A A T G A A C A G C C T G A A A A C C G A G G A C A C G G C C G T G T A T T A C T G T A C T A G A
UAM: A A A T G A A C A G C C T G A A A C C G A G G A C A C G G C C G T G T A T T A C T G T A C T A G A
HUM: C A
UAM: C A
D7
HUM:
   C A C A G T G
UAM:
D9
HUM: G A C A C A A A C C T
UAM: GACAGAAACCT
Alignment stats: 'M': 302, 'I': 0, 'D': 0, 'X': 0
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GENE ALIGN SEQ.
CTGGTGGAGTCTGGGGGGAGG<mark>CTTGGT</mark>CCAGCCTGGAGGGT<mark>C</mark>
UAM: C C T G A G A C T C T C T G T G C A G C C T G T A C A G C C T C T C T C A C C T T C A C T T C A C T A C A
HUM: TGGACTGGGTCCAGGCTCAAGGGAAGGGGCTCAAGGGCCTCAAGGGGAAGTGGGG<mark>CTGGAAGT</mark>GGG<mark>CCGG</mark>T
UAM: T G G A C T G G G T C C G C C A G G C T C C A G G G A A G G G G C T G G A G T G G G T T G G C C G T
HUM: A C T A G A A A C A A A G C T A A C A G T T A C A C C A C A G A A T A C G C C G C G T C T G T G A A
UAM: A C T A G A A A C A A A G C T A A C A G T T A C A C C A C A G A A T A C G
HUM: A G G C A G A T T C A C C A T C T C A A G A G A T T C A A A G A A C T C A C T G T A T C T G
UAM: A G G C A G A T T C A C C A T C T C A A G A G A T T C A A A A A A A C T C A C T G T
HUM: A A A T G A A C A G C C T G A A A A C C G A G G A C A C G G C C G T G T A T T A C T G T G C T A G A
UAM: A A A T G A A C A G C C T G A A A A C C G A G G A C A C G G C C G T G T A T T A C T G T G C T A G A
HUM:
UAM:
D7
HUM:
   C A C A G C G
UAM:
D9
HUM: G A C A C A A A C C T
UAM: GACAGAAACCT
Alignment stats: 'M': 302, 'I': 0, 'D': 0, 'X': 0
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GENE ALIGN SEQ.
HUM: GAGGTGCAGCTGGAGTCCGGGGGGGGGGTC
                 CTGGTGGAGTCCGGGGGGC<mark>TTGGTCCAGCCT</mark>GGGGGG<mark>T</mark>C
HUM: CCTGAGACTCTCTGTGCAGCTTCTACACCTTCACCTTCACCTTCACACCTTCACTACACCTACAC
UAM: C C T G A G A C T C T C T G T G C T G T G T G T A G A G C C T C T G A G C C T C T C A C C T T C A G T G A C T A C T A C A
HUM: TGAGCTGGGTCCAGGCTCCGGCAGGCTCCCGGGAAGGCTGGAAGGTGGGTTAGGGTTTTC
UAM: TGAGCTGGGTCCAGGCTCCCGGGAAGGGCTGGAGTAGGTTTC
HUM: A T T A G A A A C A A A G C T A A T G G T G G G A C A A C A G A A T A G A C C A C G T C T G T G A A
UAM: A T T A G A A A C A A A G C T A A T G G T G G G A C A A C A G A A T A G A C C A C G T C T G T G A A
HUM: A G G C A G A T T C A C A A T C T C A G A G A T G A T T C C A A A A G C A T C A C C T A T C T G
UAM: A G G C A G A T T C A C A A T C T C A A G A G A T T C C A A A A G C A T C A C C T A T C T G C
HUM: A A A T G A A C A G C C T G A G A G C C G A G G A C A C G G C C G T G T A T T A C T G T G C G A G A
HUM:
UAM:
D7
HUM:
   C A C A G T G
UAM:
D9
HUM: G A C A C A A A C C T
UAM: GACAGAAACCT
Alignment stats: 'M': 302, 'I': 0, 'D': 0, 'X': 0
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IGHV2-70

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GENE ALIGN SEQ.
HUM: CAGGTCACCTTGAGGGAGTCTGGCCGCTGGTGAAACCCAACAGAC
UAM: CAGGTCACCTTGAGGGAGTCTGGTCTGGTGTGAAACCCAACACAGAGAC
T G T G T G T G A G C T G G A T C C G T C A G C C C C C A G G G A A G G C C C T G G A G T G G C T T
HUM:
   T G T G T G T G A G C T G G A T C C G T C A G C C C C A G G G A A G G C C C T G G A G T G G C T T
UAM:
   CACTCATTGATTGGGGATGATAAATACTACAGCAGCATCTGAAGAC
HUM:
HUM: CAGGCTCACCATCTCCAAGGACACCTCCAAAAACCAGGTCCTTACAA
HUM: TGACCAACATGGACCCTGTGTGGACACAGCGTATTACTGTGTGGATA
UAM: T G A C C A A C A T G G A C C C T G T G G A C A C A C A C G T A T T A C T G T G C A C G G A T A
HUM: C
UAM: C
D7
HUM:
  C A C A G A G
UAM:
D9
HUM: T A C A A G A A C C C
UAM: T A C A A G A A C C C
Alignment stats: 'M': 301, 'I': 0, 'D': 0, 'X': 0
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IGHV1-68

GENE ALIGN SEQ	
HUM: CAGGTGCAGCTGGGGCTGAGTCTGAGGCTGAAAG <mark>CCT</mark> GAGG <mark>T</mark> AAAGAAG <mark>CCT</mark> GGGG <mark>CC</mark> T	
UAM: CAGG <mark>TGCAGCT</mark> GGGG <mark>CAGTCTGAGGCTGAGGCT</mark> AAAG <mark>CCT</mark> GGGG <mark>C</mark> T	C
HUM: A G T G A A G G T C T C C T G C A A G G C T T C C G G A T A C A C C T T C A C T T G C T G C T C C	Т
UAM: A G T G A A G G T C T C C T G C A A G G C T T C C G G A T A C A C C T T C A C T T G C T C C T	Т
HUM: T G C A C T G G T T G C A A C A G G C C C C T G G A A G G G C T T G A A A G G A T G A G A T G A G A T G A G G A T G A G A	; G
UAM: T G C A C T G G T T G C A A C A G G C C C C T G G A C A A G G G C T T G A A A G G A T G A G A T G	G
HUM: A T C A C A C T T T A C A A T G G T A A C A A C A C A A C A A C A A C A A G A A G T T C C A G G G C A	
UAM: A T C A C A C T T T A C A A T G G T A A C A A C A A C T A T G C A A A G A A G T T C C A G G G C A	A G
HUM: A G T C A C C A T T A C C A G G G A C A T G T C C C T G A G G A C A G C T A C A T A G A G C T	A
UAM: A G T C A C C A T T A C C A G G A C A T T A C C C A G C C A T G T C C T G A G G A C A G C T A C A T A G A G C T	A
HUM: GCAGCCTGAGATCTGAGGACTCGGCTGTGTATTACTGGGGAAGATA	
UAM: G C A G C C T G A G A T C T G A G G A C T C G G C T G T G T A T T A C T G G G C A A G A T A	
OHN. GOAGOOIGAGATOIGAGGACIOGGIGIAIIAOIGGGAAGAIA	
D7	
HUM: CACGGTG	
UAM: C A C G G T G	
D9	
HUM: G T C A G G A A C C C	
UAM: G T C A G G A A C C C	
Alignment stats: 'M': 296, 'I': 0, 'D': 0, 'X': 0	
Neither human gene nor its mapping is pseudogene	

IGHV(III)-67-4

GENE ALIGN SEQ
HUM: A A G T T C A G T G G T G G A G T C A G A G T C A G A G G G G T A A A C G T A G T A C A G C C C A G T G G T T C
UAM: A A G T T C A G T G G T G G A G T C A G A G T C A G A G T C A G G G G G T A A A C G T A G T A C A G C C C A G T G G T T C
HUM: A C T G A G A C T T T C T T G C A A A G C G T C T G C A C C T T T T C T G G C A A C A G C C
UAM: A C T G A G A C T T T C T T G C A A A G C G T C T G C A C C T T T T C T G G A G C C
HUM: TGAGG <mark>TTGGGTCCAGCCTTCACAC</mark> AAGCAAC <mark>TTCACAACAACAACAACAATTGTGGTGGCT</mark> GG <mark>CAAC</mark> AA
UAM: T G A G G T T G G T C C A G C A G G C T T C A C A A C A G G G A T T G T G G T G G C T G G C A A C A
HUM: G T G A G T C A A C A A G T G G G A G T G C T C A G G T T T A C T C A T G A G T A C A A T A
UAM: G T G A G T C A A C A A G T G G G A G T G C T C A G G T T T A C T C T T C A T G A G T A C A A T A
HUM: A A T T A A C T G G T C C A G C G A C C C T T T C A C G T C T A C C T T A C A A T G A
UAM: A A T T A A C T G G T C C A G C G A C C C T T T C A C G T C T A C C T T A C A A T G A
HUM: C T A A C C T G A A A G C C A A G G A C A A G G T T G T A A T A C T G T G A G C T T
UAM: C T A A C C T G A A A G C C A A G G A C A A G G T T G T A A T A C T G T G A G C T T
D7
HUM: C A C A G G A UAM: C A C A G G A
OAM. CAGAGGA
D9
HUM: A G A C A C A A A A A UAM: A G A C A C A A A A A
Alignment stats: 'M': 294, 'I': 0, 'D': 0, 'X': 0
Both human gene and its mapping are pseudogenes

IGHV(III)-67-3

GENE ALIGN SEQ
HUM: CAGCCTGGCTGTCTCTCTACCTCTTAGCTTCTTAGCAAAGCATCAAGCTTTTTGCAAGAAGCATTCAAGCTTT
UAM: CAGCCTGGTTCTTAGCTTCTTAGCTTTTTGCAAGCATTCTT
HUM: CACTGACTACAGCATAAAATTGAGCCCAGA <mark>T</mark> GGGGGACAGAGG <mark>CT</mark> GG
UAM: C A C T G A C T A C A G A A T A A A T T G A G C C A G C A G C A G C T G G G A C A G A G G C T G G
HUM: A G T G G G T G G T A A C A G T G A T T G A T T C A A G T G G A A G T T C T C A G T G A T A T T C T
UAM: A G T G G G T G G T A A C A G T G A T T G A T T C A A G T G G A A G T T C A G T G A T A T T C T
HUM: G C A T C A G C A T A A T G A A G A T T C A G A T A A T G A A G A T T C A C A A T T C C C A G G G A C A C C A A T T A C C A G C A G C A G C A C A C C A A T T A C C A G C A G C A C C A A T T A C C A G C A C C A C C A A T T A C C A G C A C C C A C C C C A C C C A C
OAM. GOATORGOATARIGAAGATIOACAATI
HUM: CAGTCT CCTAAAAAATAAATAAATAAATAAATAAAAAAAAAA
UAM: CAGTCTCTAAAATTAAATTAATCTAGGAGGCTCTCAC
HUM: G T A G G C A G T G T A T T A C T G T G A G A
UAM: G T A G G C A G T G T A T T A C T G A G A G A
D7
HUM: CACAGCG
UAM: CACAGC
D9
HUM: ACAGAAACCTC
UAM: A C A G A A A C C T C
Alignment stats: 'M': 275, 'I': 0, 'D': 0, 'X': 0

IGHV(III)-67-2

GENE ALIGN SEQ

D7

HUM: C A C A T G A
UAM: C A C A T G A

D9

HUM: A C A T A A A C C T C
UAM: A C A T A A A C C T C

Alignment stats: 'M': 99, 'I': 0, 'D': 0, 'X': 0 Neither human gene nor its mapping is pseudogene

IGHV(II)-67-1

GENE ALIGN SEQ HUM: A G G A G C A G C T A C A G C A G T C A T G C C T A G G T G A A G A T C A C A C T G A C T G A C T UAM: A G G A G C A C CAGTCATGCCTAGGTGAAGAT HUM: CACCCATGCTCTGGCCACTTCACTCACACCAACCAATGCTTAATATTGGA HUM: C G T G G A T C T G C C A G T C C C C G G G G A A T G G G T T G A A T UAM: C G T G G A T C T G C C A G T C C C G G G A A T G G T T G A A D7HUM: A A A A T G C UAM: D9HUM: C A T T C C T A C T G T T C C T A C T G UAM: C A Alignment stats: 'M': 139, 'I': 0, 'D': 0, 'X': 0

IGHV1-67

HUM: C A G G T G C A G C T G G T G C A G T C T G G T G C A G T C T G G G G G A T G A T G A G A T G A G A
HUM: A G T G A A A G T C T C C T G C A A G A C T T G T G C A T G C A A G A C T T A C A T G T G T A C C T T C A C C A G T T A C UAM: A G T G T A T G T G T A T G T G T A T G T G
HUM: A A A G T G A A A G T C T C T C T C T G C A G T G C A G A G A G T G C A G G C C A G C C C A G C A G C C A G C A G C A G C A G C
HUM: A A A G T G A A A G T C T C T C T C T G C A G T G C A G A G A G T G C A G G C C A G C C C A G C A G C C A G C A G C A G C A G C
HUM: T C T A T G C A C T A G C
HUM: A A G C A G C T G C A G C
HUM: A A G G A T G T G C C T A G T G T G C C T A G T G A T G A T G A T G A T G A T G A T G A T G A T G A T G A T G A T G A T G A G C A T A A G C A T A A G C T A G G A A G T T C A G G C A G A G A A G T T C A G G C A G A G A A G T T C A G G C A G A G A G A A G T T C C A G G C A G A G A G A A G T T C C A G G C A G A G A G A A G T T C C A G G C A G A G A G A A G T T C C A G G C A G A G A G A A G T T C C A G G C A G A G C A G A G A G A A G T C A G C A G A G C A G A G A G A A G T C A G C A G C A G C A G A G C A G A G C A G A G
HUM: G C A G C A C C C A C
HUM: G C A G C A C C C A C
HUM: G C A G A G T C A T G A C C A T G A C C A T G A C C A T G A C C A T G A G G G A C A T C C A T C C A T C C A C A C A C
UAM: G C A G A G T C A C C A T G A C C A G G G A C A C A C A C A C A C
UAM: G C A G A G T C A C C A T G A C C A G G G A C A C A C A C A C A C
UAM: C T G A G C A G C T G A G T C T A A G A T C T G A A G A C A C G G C A T G T A T T A C T G T G G A G A G A
D7
HUM: CACAGTG
UAM: CACAGTG
HUM: G T C A G T A A C C C UAM: G T C A G T A A C C C
OAM. GILORGIA A CCC
Alignment stats: 'M': 300, 'I': 0, 'D': 0, 'X': 0

GENE ALIGN SEQ
HUM: GAGGTGAGCTGGTGAGTGGAGTCTGAGTCTGAGGAGTCTGAGGAGGAGGAGGAGGAGGGTTC
UAM: GAGGTGCAGCTGGAGTCTGGAGGTCTGGAGGAGGAGGCTTGAGCCTGGGGGGTC
HUM: C C T G A G A C T C T C T G T G C A G C T C T G T A G C A G C C T C T C T C C A C C G T C A G T A G C A A C T A C A
UAM: CCTGAGACTCTCTGTGTGCTGTCTTCTTCTTCTTCTTCTTCTTCTTC
HUM: T G A G C T G G G T C C G C C A G G C T C C A G G G G G G G C T G G A G T G G G T C T C A G T T
UAM: T G A G C T G G G T C C G C C A G G C T C C A G G G A A G G G G C T G G A G T C T C A G T T
HUM: A T T T A T A G C T G T G G T A G C A G A C T A C G C A G A G A G G G C G A T T
UAM: A T T T A T A G C T G T G G T A G C A C A T A C T A C G C A G A C T C C G T G A A G G G C C G A T T
HUM: C A C C A T C T C C A G A G A C A T T C C A A G A G A T T C C A A G A A C A C G C T G T A T C T T C A A A T G A A C A
UAM: C A C C A T C T C C A G A G A C A A T T C C A A G A A C A C G C T G T A T C A A A T G A A C A
HUM: GCCTGAGAGAGAGAGAGACACACTA
UAM: G C C T G A G A G C T G A G G A C A C G G C T G T A T T A C T G T G C A G A G A
D7
HUM: CACAGTG
UAM: CACAGTG
D9
HUM: GACAAACCT
UAM: GACAAACCT
Alignment stats: 'M': 293, 'I': 0, 'D': 0, 'X': 0
Neither human gene nor its mapping is pseudogene

IGHV(II)-65-1

GENE ALIGN SEQ
HUM: C A A C A A C T G T G T T C T C T G C T G T G T T T C T C
UAM: CAACAACTGTGTTCTCTCCTCTTCTTCTTCTTCTTCTTCTTCTTCT
HUM: C C T C T C T C T C T C A C C T G T G T G T G T G T G T G T G T G
UAM: CCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC
HUM: C C T G C T G G A G C T G C A T C C A T C C A T C C C C C C C C G A A G G A A G G A C T G G A G C G A A
UAM: CCTGGAGCTGATCATCATCATCATCACCCCCCGAAGGGAAGCTGAAGAAAAAAAA
HUM: TCAGGTGCAGGTCATGATGATGAGGGAGGTGATGATGAGGAGGAGTGCATCAT
UAM: TCAGGTGCACAGGTCATGAGGGTGAGTGCAACCCACTCAAGA
HUM: G T C C A G T C A C T A T C A C T A T C A C T A T C T C
UAM: G T C C A G T C A C T A T C T C C A G A T C C A A A A A A A C A G T T T C C T G T A G
HUM: C T G A G C T A C C T G A G C A A C A A G T A C A A G A A C A A G A A C A A C A A C A A C A A C A A C A A C A A C A
UAM: C T G A G C T A C C T G A G C A A C A A G T A C A A G A A C A A G A A C A A C C A T G A A T T T T A A T A C A A A G A
D7
HUM: C A C A A C G
UAM: CACAACG
D9
HUM: G A T A C A A A C C T UAM: G A T A C A A C C T
Alignment stats: 'M': 300, 'I': 0, 'D': 0, 'X': 0
Both human gene and its mapping are pseudogenes

GENE ALIGN SEQ
HUM: G A G G T G C A G C T G G T G G A G T C T G G A G T C T C G G G G A A G G C T T G G T C C A G C C T G G G G G G T C
UAM: GAGGTGAGCTGGAGTGGAGTGGAGTGGAGTGGAGGGGGGGG
HUM: C C T G A G A C T C T C C T G T G C A G C C T C T G G A T T C A C C T T C A G T A G C T A T G C T A
UAM: C C T G A G A C T C T C C T G T G C A G C C T C T G G A T T C A C C T T C A G T A G C T A T G C T A
HUM: T G C A C T G G G T C C G C C A G G C T C C A G G C T C C A G G G A A G G G A C T G G A A T A T G T T T C A G C T
UAM: T G C A C T G G G T C C G C C A G G C T C C A G G G T C C A G G G A A G G G A C T G G A A T A T G T T T C A G C T
HUM: A T T A G T A A T G G G G G T A G C A C A T A T G C A C A C A C A C A C A C A C A C A C
UAM: A T T A G T A G T A A T G G G G G T A G C A C A T A T G C A G A C T C T G T G A A G G G C A G
HUM: A T T C A C C A T C T C C A G A G A C A A T T C C A A G A A C A C G C T G T A T C T T C A A A T G G
UAM: A T T C A C C A T C T C C A G A G A C A A T T C C A A G A A C A C G C T G T A T C T T C A A A T G G
OAM: A I I C A C C A I C I C C A G A G A C A A I I C C A A G A A C A C G C I G I A I C I I C A A A I G G
HUM: G C A G C T G A G A G C T G A G G A C A T G G C T G T A T T A C T G T G C A G A G A
UAM: G C A G C T G A G A G C T G A G G A C A T G G C T G T G T A T T A C T G T G C G A G A G A
D7
HUM: CACACACT G
UAM: C A C A G T G
D9
HUM: TGCAGAAACCT
UAM: T G C A G A A A C C T
Alignment stats: 'M': 296, 'I': 0, 'D': 0, 'X': 0
Neither human gene nor its mapping is pseudogene

GENE ALIGN SEQ. HUM: GAGGTGGAGCTGATAGAGTCCATAGAGGGG<mark>CCTGAGACTT</mark>GGGAAG<mark>T</mark>T UAM: GAGGTGGAGCTGATAGAGTCCATAGAGGGG<mark>CCT</mark>GAGACTTGGGGAAGTT HUM: CCTGAGACTCTCTGTGTGTGTGTAGCCTCTGAATTCACCTTCAGCTACTGAA UAM: C C T G A G A C T C T C T G T G T G T G T A G C C T A G T A G C C T C T C T G A C C T T C A C C T T C A G C T A G C T A C T A C T G A A UAM: T G A G C T G G G T C A A T G A G A C T C T A G G G A A G G G G C T G G A G G G A A T A A T HUM: G T A A A A T A T G A T G G A A G T C A G A T A T A C C A T G C A G A C T C T G T G A A G G G C A G UAM: G T A A A A T A T G A T G G A A G T C A G A T A T A C C A T G C A G A C T C T G T G A A G G G C A G HUM: A T T C A C C A T C T C C A A A G A C A A T G C T A A G A A C T C A C C G T A T C T G C A A A C G A UAM: A T T C A C C A T C T C C A A A G A C A A T G C T A A G A A C T C A C C G T A T C T G C A A A C G A HUM: A C A G T C T G A G A G C T G A G G A C A T G A C C A T G C A T G G C T G T A C A T A A G G T T UAM: A C A G T C T G A G C T G A G C T G A G G T G A G G T G A C A T G A C C A T G C A T G G C T G T A C A T A A G G T T D7HUM: C C A A G T G UAM: C C A A G T G D9HUM: G A C A C A A A A T T G A C A C A A A A T T UAM: Alignment stats: 'M': 298, 'I': 0, 'D': 0, 'X': 0

IGHV(II)-62-1

GENE ALIGN SEQ
HUM: G G G C C T G G T G A A G C C C T C A C A G A C C C T C A C A G A C C C T C A T C A T G T G T G T C A T C T G C UAM: G G C C T G A C A G A C C C T C T C T C A T G T G T G T C A T C T G C
HUM: A T T C T C A T C A A C A A C C A G T C C A G C A G C A G C C C C C C C C C C
HUM: T C T C T G G G A A T G G A A T G G A G A A T G A A T G A A T G A A T A A A A
HUM: C A C A T T A C T C C C T T T C C T C A A G A G T C C A G T C A C A T C C A T C A T C C A T C A T C C A T C A T C C A T C C A T C A T C C A T C A T C C A T C A T C C A T C A T C C A T C C A T C A T C C C A T C C A T C C A T C C A T C C A T C C A T C C A T C C A T C C C A T C C A T C C C A T C C A T C C C A T C C C A T C C C A T C C C A T C C C A T C C C A T C C C A T C C C A T C C C A T C C C A T C C C A T C C C A T C C C A T C C C A T C C C C
HUM: T C C A A A A A C A G T T C T T C C T A C A G C T A C A G C T A C A G C T A C A G C T A C A T G A G C A A C A A T C A T A C A T A C A T A C A T A C A T A C A T C A C A
HUM: G C C A T A T
D7 HUM: C A C A G T G UAM: C A C A G T G
D9 HUM: C A C C A A A A C C T UAM: C A C C A A A A C C T
Alignment stats: 'M': 273, 'I': 0, 'D': 0, 'X': 0 Both human gene and its mapping are pseudogenes

GENE ALIGN SEQ
HUM: G A G G T G C A G C T G G T G G A G T G G T G G T G G T G G T G G T G G G G G T C T G G G G
HUM: C C T G A G A C T C T C T G A G A C T C T C T C T C T G T G T G T G T G T
HUM: T G C A C T G G G T C C A G G C A G G C A G G C T C A G G C T C A A G A A G G G T T T G T A G T G G G T C A G T T T A G T A G T C A G T T T T T T T T T T T T T T T T T T
HUM: A T T A G T A C A A G T G G T G A T A C C G T A C G T G G T G G T G G T G A T A C C G T A C T C T A C A C A C A C A C A C A C
HUM: A T T C A C C A T C A G A G A G A A T C A A A T C A A A A T A A A T A A A T A A A T A A A T A A A A T A
HUM: A C A G C T G A G C C T G A G C C G A G C G A C A T G G T G T A T A C T G T G T G A A A G A UAM: A C A G C C T G A G C C G A C A T G G C T G T G T A T A C T G T G T G A A A G A
D7 HUM: C G C A G T G UAM: C G C A G T G
D9 HUM: A C A A A C C T C C C UAM: A C A A A C C T C C
Alignment stats: 'M': 296, 'I': 0, 'D': 0, 'X': 0 Both human gene and its mapping are pseudogenes

IGHV4-61

GENE ALIGN SEQ				
HUM: CAGGTGCAGCTGCAGCTGCAGGAGGCCCCAGGGCCCAGGGCCCAGGCCCAGGCCCAGGCCCTCCGGAGACC				
UAM: CAGGTGCAGCTGCAGGAGGCGGCGGCCCAGGGACTGAAG <mark>CCT</mark> GAAG <mark>CCTT</mark> GAAG				
HUM: CCTGTCCCTCACCTGCACTGTCTGTCTGGTCCGCTCAGCAGTGGTT				
UAM: C C T G T C C C T C A C C T G C A C T G T C T C T G G T G C T C C G T C A G C A G T G G T T T				
HUM: A C T A C T G G A G C T G G A T C C G G C A G C C C C A G G G A A G G G A C T G G A G T G G A T T				
UAM: A C T A C T G G A G C T G G A T C C G G C A G C A G C A G C A G C C C C				
HUM: G G G T A T A T C T A T T A C A G T G G A G C A C A C T A C A C C C T C C T C A A G A G A G A G A G A G A G A G A G				
UAM: G G G T A T A T C T A T T A C A G T G G G A G C A A C T A C A A C C C T C A A G A G A G				
HUM: TCGAGTCACATATATCAGTAGTAGCAGTAGAGGCAGGTCCAAGTTCCTCAAGCAAG				
UAM: T C G A G T C A C C A T A T C A G T A G A C A C G T C C A A G A A C C A G T T C T C C C T G A A G C				
HUM: TGAGCTCTCTGTGACCCCCCCCCCCCCCCCCCCCCCCCC				
UAM: TGAG <mark>CTCTGTGACCGCTGCTGCGCTGC</mark> GCTGCGGCCGCTGTGTACTACTGCGAGA				
D7				
HUM: CACAGTG				
UAM: CACAGTG				
D9				
HUM: GACACAAACCT				
UAM: GACACA CT				
Alignment stats: 'M': 299, 'I': 0, 'D': 0, 'X': 0				
Naithan buman mana nan ita manning ia naandanan				

IGHV(II)-60-1

GENE ALIGN SEQ
HUM: GGCCTGGTGGAGCCCTCGTCGCAGAGACCCTCAACAAAAAAAA
UAM: G G C C T G G T G G A G C C C T C G C A G A C C C T C T C C T C A C C T G T G T G T C T C T G G
HUM: A T T T T C C A T C A C A A C C A G T G T T T C C T G C T G G A G C T G G A T C C A C G A G T C C A
UAM: A T T T T C C A T C A C A A C C A G T G T T T C C T G C T G G A G C T G G A T C C A C G A G T C C A C G A
OHI. HITTIOORIORORUOTUITIOOTUURUOTUURIOOROURUU
HUM: CATGGAAGGAAGGAAGTAGAGGAG <mark>T</mark> GGAACAGG <mark>CGCACACGT</mark> CATGAAGGGAAGAA
UAM: CATGGAAGGACTGGAG <mark>T</mark> GGAG <mark>T</mark> GGAG <mark>TGGAGGGGGGGGGAGGAAGGGAAG</mark>
HUM: A A T T C C C A C C C A C T C C T T A T G A A T C C A G T C A C C A T C T C A A A T T C G G G T C
UAM: A A T T C C C A C C A C T C C T T A T G A A T C C A G T C A C C A T C T C C A A A T T C G G G T C
HUM: CAAAAAACACTT GTTTT TACAGT GAGCT ATGT GAGCAAGCT CACAG
UAM: C A A A A A C A C T T G T T T T T A C A G T G G A G C T A T G T G A G C A A C A A G C T C A C A G
OAN. CHARRACACTION TO A CHORCACTOR CARCACTOR C
HUM: CCATTTTAAAGAGAGA
UAM: CCATGTTTAAAAGAAGAAAAAAAAAAAAAAAAAAAAAAA
D7
HUM: C A G A G T G
UAM: C A G A G T G
D9
HUM: CACCAAACCT
UAM: CACCAAAACCT
Alignment stats: 'M': 269, 'I': 0, 'D': 0, 'X': 0

GENE ALIGN SEQ
HUM: GAGG <mark>TGCAGCTGGAGGT</mark> GGAG <mark>T</mark> CGGAG <mark>TCTGGGGGGGAGG<mark>CTT</mark>AG<mark>T</mark>AAA<mark>GACT</mark>GGAGGG<mark>T</mark></mark>
UAM: GAGG <mark>TGCAG<mark>C</mark>TGGTGGAG<mark>T</mark>CTGGGGGGG<mark>TTTAG<mark>T</mark>AAAG<mark>T</mark>AAAGG<mark>T</mark>GGGGG<mark>T</mark></mark></mark>
HUM: CTCTCTGAGAGACTCTGAGAGACTCTGTGAGCAGCTTCTCTGAGAGCCTTCTGAGACCTTCAGGAATTCAAGTAGCTCTGCT
UAM: CTCTGAGAGACTCTGCAGTGCAGCAGCAGCAGCAGCAGAGCAGAGAAAAAAAA
HUM: ATGCACTGGGTCACCACCACCAGGCTCCAGGGAAAGGGTTTGGGAGTGGGTCTCAGT
UAM: A T G C A C T G G G T C C A C C A G G C T C C A G G G A A A G G G T T T G G A G T G G G T C T C A G T
HUM: TATTAGTACAAGTGAGTGATGGTGATACCGTACACAGACACAGACTGTCT
UAM: TATTAGTACAAGTGATACCTTTACACACAGACTCTTTTACTTTTTACTTTTTTTT
HUM: GATTCACACCATCAAAATGAAATGCAATGCAATGCAATG
UAM: GATTCACCATCTAAGAGACAATGCCAATGCAATGCCAATGCACTGCTGCACTGCTGCAAATG
HUM: A A C A G C C T G A G C C G A G G G C A C A G T T G T A C T A C T G T G A A A G A
UAM: A A C A G C C T G A G A G C C G A G G G C A C A G T T G T G T A C T A C T G T G T G A A A G A
D7
HUM: CGCAGTG UAM: CGCAGTG
D9
HUM: ACAAACCTCCT
UAM: A C A A A C C T C C T
Alignment stats: 'M': 297, 'I': 0, 'D': 0, 'X': 0
Both human gene and its mapping are pseudogenes

IGHV4-59

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GENE ALIGN SEQ.
HUM: CAGGTGCAGCTGCAGGGAGTCGGGGCCAGGACTGGAAGCCTTCGGAAGC
              CTGCAGGAGTCGGGCCCAGGAC<mark>T</mark>GGTGAAGCCTT<mark>C</mark>GGAGAC
HUM: G G A G C T G G A T C C G G C A G C C C C C A G G G A A G G G A C T G G A G T G G A T T G G G T
   G G A G C T G G A T C C G G C A G C C C C A G G G A A G G G A C T G G A G T G G A T T G G G T A T
UAM:
HUM: A T C T A T T A C A G T G G G A G C A C C A A C T A C A A C C C T C C A A G A G T C G A G T
UAM: A T C T A T T A C A G T G G G A G C A C C A A C T A C A A C C C T C C T C A A G A G T C G A G T
UAM: CACCATATCAGTAGACACGTCCAAGATCTCTCCTGAAGCT
HUM: C T G T G A C C G C T G C G G A C A C G G C C G T G T A T T A C T G T G C G A G A G A
UAM: C T G T G A C C G C T G C G G A C A C G G C C G T G T A T T A C T G T G C G A G A G A
D7
HUM: C A C A G T G
UAM:
D9
HUM: GACAAAACCT
UAM: GACAAAACCT
Alignment stats: 'M': 293, 'I': 0, 'D': 0, 'X': 0
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IGHV1-58

GENE ALIGN SEQ					
HUM: CAAATGCAGCTGGTGGTGCAG <mark>TCT</mark> GGCAG <mark>TCT</mark> GGGCCTGAGG <mark>T</mark> GAAGAAG <mark>CCT</mark> GGGACC					
JAM: CAAATGCAG <mark>CTGGTGCAGTCTGGGGCCTGAGGTGAAGAAG</mark> CC <mark>T</mark> GGG <mark>CC</mark> TGAGG <mark>TGAAGAAG</mark> CCT	T C				
HUM: A G T G A A G G T C T C C T G C A A G G C T T C T G G A T T C A C C T T T A C T A G C T C T G C	T G				
JAM: A G T G A A G G T C T C C T G C A A G G C T T C T G G A T T C A C C T T T A C T A G C T C T G C					
HUM: TGCAGTGGGTGCAGGTGCGAGGCTGGCAGGCTCGAGGCTGGAGGGGAGGGGAGGGGAGGGGAGGGGAGGGGAGGGGAGGGG	G G				
JAM: TGCAGTGGGTGCAGGCTGCTCGTGGACAGGTTGGAGTAGGATAGGAT					
HUM: A T C G T C G T T G G C A G T G G T A A C A C A A C T A C G C A C A G T T C C A G G A A					
JAM: A T C G T C G T T G G C A G T G G T A A C A A A C T A C G C A C A G A A G T T C C A G G A A					
HUM: A G T C A C C A T T A C C A G G G A C A T G T C C A C A A G C A C A G C C T A C A T G C T					
JAM: A G T C A C C A T T A C C A G G G A C A T G T C C A G C A G C A G C T A C A T G G A G C T	G A				
HUM: GCAGCCTGAGAGAGAAGAGGAGGAGGACGACGG <mark>CCGTGTATTACTGC</mark> GGAGAGA					
JAM: GCAG <mark>CCTGAGATCCGAGGACGCCGTGTATTACTGC</mark> GGCAGA					
D7					
HUM: C A C A G T G					
JAM: CACAGTG					
D9					
HUM: G T C A G A A A C G C					
JAM: GTCAGAAACCC					
Alignment stats: 'M': 296, 'I': 0, 'D': 0, 'X': 0 Neither human gene nor its mapping is pseudogene					
neroner namen Bene nor 100 maphing 19 beendogene					

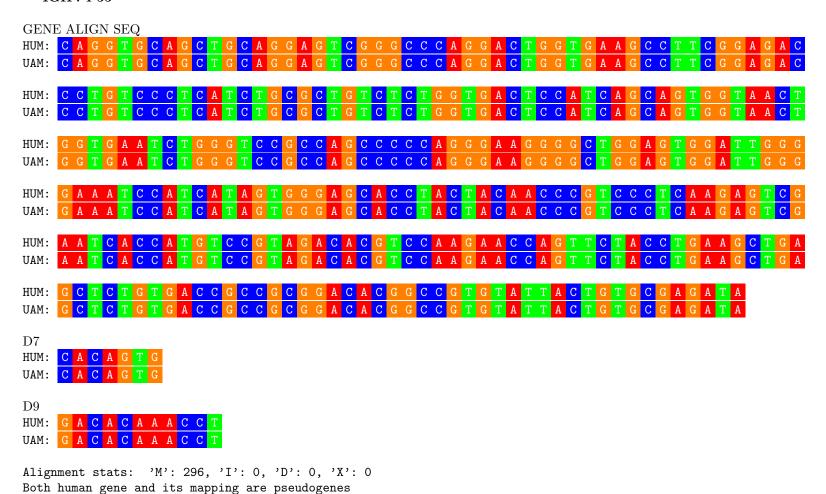
GENE ALIGN SEQ HUM: GAAGTTTAATTGAATGAAGAGAGAGAAAAAATTGAAGCCAAG<mark>T</mark>GGATT<mark>C</mark> UAM: G A A G T T T A T T G A T G G A G T C A G A G G C A G A A A A T T G T A C A G C C C A G T G G T T C HUM: A C T G A G A C T C T C C T G C A A A G C C T C T G A T T T C A C C T T T A C T G G C T A C A G C A UAM: A C T G A G A C T C T C C T G C A A A G C C T C T G A T T T C A C T T T A C T G G C T A C A G C A UAM: T G A G C T T G G T C C A G C A G G C T T C A T G A C A G G G A T T G G T G T G G G A A A C A HUM: G T G A G T G A A G T G G G A G T T C T C A G A G T T C T C C A T G A G T A C A A A T A UAM: G T G A G T G A T C A A G T G G G A G T T C T C A G G T T C T C A G G T T A C T C T C A T G A G T A C A A A T A HUM: A A T T A A C A G T C C C A A G C G A C C T T T T C A T G T G C A G T C T A C C T T A C A A T G UAM: A A T T A A C A G T C C C A A G C G A C A C C T T T T C A T G T G C A G T C T A C C T T A C A A T G HUM: A C C A A C C T G A A A G C C A A G G A C A A G G C T G T G T A T T A C T G T G A G G G A UAM: A C C A A C C T G A A A G C C A A G G A A A G G A A A G G A A A G G A C A A G G C T G T A T T A C T G T G A G G G A D7HUM: C A C A G G A UAM: C A C A G G A D9HUM: A G A C A C A A A A UAM: A G A C A C A A A A

Alignment stats: 'M': 295, 'I': 0, 'D': 0, 'X': 0 Both human gene and its mapping are pseudogenes

IGHV7-56

GENE ALIGN SEQ				
HUM: C G A G T G C A G C T G G T G C A G C T G C A G T C T G G G C C T G A G G T G A A G C A G C C T G G G C C T C				
UAM: C G A G T G C A G C T G G T G C A G T C T G G G C C T G A G C A G C C T G G G C C T C				
HUM: GGCGAAGGTCTGAAGGTTGCTAAGGTTGTGTAAACTTGTAAACCTGTCACCTAATGTA				
UAM: G G C G A A G G T C T C C T G C A A G G T C T G C A A G G T G T C T G G T T A A A C T G T C A T C A C C T A T G G T A				
HUM: T G A A T T G G A T A C G A C A G A C C C C A G G A C A G G G G				
UAM: T G A A T T G G A T A C G A C A G A C C C C A G G A C A G G G G				
HUM: A T C A T C C T A C C T G G T G A A C C C A A T G T A C C C A A T G T T C A C A C A C A C A C A C A C A C A				
UAM: A T C A T C C T A C C C T G G T G A A C C C A A T G T A T G C C C A C A G A T T C A C A C G G T				
HUM: TTGTGTCTTCTCATCATCATCATACATACATACATACATA				
UAM: TTGTCTTCTCATCTTCTTCTTCTTCTTCTCTTCTCTTCT				
HUM: T G C C T A A A G A C T G A G G A T G C A G C A T T T A T T A C T G T G T G A G G T A				
UAM: T G C C T A A A G A C T G A G G A T G C A G C A T T T A T T A C T G T G T G A G G T A				
D7				
HUM: CACCGTG				
UAM: CACGT GACCG				
D9				
HUM: TTTAAGAAACCC UAM: TTTAAGAAACCC				
Alignment stats: 'M': 294, 'I': 0, 'D': 0, 'X': 0				
Both human gene and its mapping are pseudogenes				

IGHV4-55



GENE ALIGN SEQ HUM: G G A T C C C T G A G A C T C T C C T G T G C A G A C T C T G G A T T A A C C T T C A G T A G C T A UAM: G G A T C C C T G A G A C T C T C C T G T G C A G A C T C T G G A T T A A C C T HUM: C T G A A T G A G C T C A G A T T C C C A G G C T C A G G G G G G G T G G A G T G A G T A G UAM: C T G A A T G A G C T C A G A T T C C C A G G C T C A G G T G A G T A G HUM: T A G A T A T A T A G T A C G A T A G A G A G A G T C A G A T A T C A G A G T C A G A T A T C T G T G A A T C T G T G A A G G A G A G G A G A G G A T A T A G T A G G A T A G A A G T C A G C T HUM: A G C A G A T T C A C C A T C T C C A A A G A A A A T G C C A A G A A C T C A C T C T G T T T G UAM: A G C A G A T T C A C C A T C T C C A A G A A A G A A A A T G C C A A G A A C T C A C T C T G T T T G HUM: A A T G A A C A G T C T G A G A G C A G A G C A G A G C A G C A G T G T G T A C T G T A T G T G A G UAM: A A T G A A C A G T C T G A G A G C A G A G G G G C C G T G T A T T A C T G T A T G T G A G D7G C A C C A G HUM: T C A C C A G UAM: D9HUM: A C A G A C A C A G A A C A G A C A C A G A

Alignment stats: 'M': 245, 'I': 0, 'D': 0, 'X': 5 Both human gene and its mapping are pseudogenes

IGHV(II)-53-1

GENE ALIGN SEQ	
HUM: G G C C T G G T G A A G C C C T C A C A G A C C C T C T C C T A	
UAM: G G C C T G G T G A A G C C C T C A C A G A C C C T C T C A	C C T G T G C T G T C T G G
HUM: A T T C C C C A T C A C A A C C A G T G C T T C C T G C T G T A G C	
UAM: A T T C C C C A T C A C A A C C A G T G C T T C C T G C T G T A G C	
HUM: CCAAGAACGAACTO ACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	
UAM: CCAGAGGAACGACACACACACACACACACACACACACAC	T C A T G A G G G A G T G C A C
HUM: A T T C C A A C C C A C T C C T C A A G A G T C C A G T C A C A T UAM: A T T C C A A C C C A C T C A C A C T C A A C C A T	
UAM: A T T C C A A C C C A C T C C A A G A G T C C A G T C A C C A T	
HUM: A A A A A G C A G T T C T T C C T A C A G C C G A G C T A A G T G A	G C C G C A A G C A C A C A G C
UAM: A A A A A G C A G T T C T T C C T A C A G C C G A G C T A A G T G A	
HUM: CATGTATTTAACAAAAGA	
UAM: CATGTATTTAACCAAAAGA	
D7	
HUM: CACAGTA	
UAM: CACAGTA	
—	
HUM: CACCAAAACCT UAM: CACCAAAACCT	
OAM. CACAAACCI	
Alignment stats: 'M': 267, 'I': 0, 'D': 0, 'X': 3	

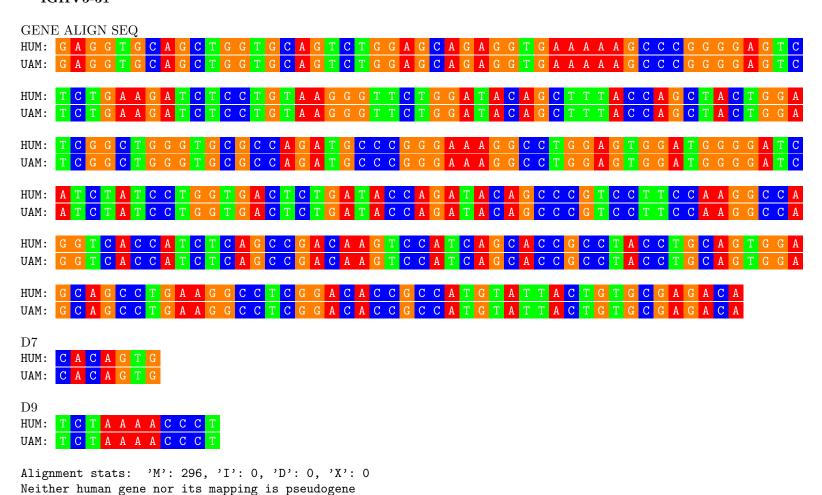
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GENE ALIGN SEQ.
HUM: GAGGTGCAGCTGGAGACTGGAGGGGGTC
               CTGGTGGAGTCTGGAGGAGG<mark>CTTGAT</mark>CCAGCCTGGGGGG<mark>T</mark>C
HUM: CCTGAGACTCTCTGTGCAGCTCTCTCTCTCACCTGTCACCTACACCG
UAM: C C T G A G A C T C T C T G T G C A G C T C T A G A C T C T A C A C C T A C A C C A A C T A C A
UAM: TGAGCTGGGTCAGGCTCAGGCTCAGGGAAGGTGGGTTCAGGTT
HUM: A T T T A T A G C G G T G G T A G C A C A T A C T A C G C A G A C T C C G T G A A G G G C C G A T T
UAM: A T T T A T A G C G G T G G T A G C A C A T A C T A C G C A G A C T C C G T G A A G G G C C G A T T
HUM: CACCATCT CCAGAGAGACAATT CCAAGAACACGCTGT AT CTAAATGAACA
UAM: CACCATCTCAGAGAGACAATTCCAAGAACACGCTGTATCAAATGAACA
HUM: G C C T G A G A G C C G A G G A C A C G G C C G T G T A T T A C T G T G C G A G A G A
UAM: G C C T G A G A G C C G A G G A C A C G G G C C G T G T A T T A C T G T G C G A G A G A
D7
HUM: C A C A G T G
UAM:
D9
HUM: GACACAAACCT
UAM: GACACAAACCT
Alignment stats: 'M': 292, 'I': 0, 'D': 0, 'X': 1
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GENE ALIGN SEQ	
HUM: GAGGTGCAGCTGGAGTGGAGTGAGTGAGGTGAGGCTTGACAGCCTGGAGG	
UAM: GAGG <mark>TGCAGCT</mark> GG <mark>TGGTGGAGT</mark> GGAG <mark>TCT</mark> GGGG <mark>T</mark> GAGG <mark>CTT</mark> GG <mark>TAC</mark> AG <mark>CCT</mark> GGAGG	G T C
HUM: CCTGAGACTCTCCTGTGCCAGCCTCTGAGCTTCACCTTCAGTAGCTCT	G G A
UAM: CCTGAGACTCTCAGTGCAGCATCTCAGAGCCTCTGAATCAGTAGCTCT	
HUM: TGCACTGGGTCTGCCACCACACACACACACACACACAAAAAAAA	
UAM: TGCACTGGGTCTGCCAGGCTCGGAGAGAAGGGGGCTGGAGTGGCCC	G A C
HUM: A T A A A G T G T G A C G G A A G T G A G A A A T A C T A T G T A G A C T C T G T G A A G G G G	C C C
UAM: A T A A A G T G T G A C G G A A G T G A G A A A T A C T A T G T A G A C T C T G T G A A G G G G	
OAM. A I A A A G I G I G A G I G A G I G A G I A I A	
HUM: A T T G A C C A T C T C C A G A G A C A A T G C C A A G A A C T C C C T C T A T C T G C A A G	T G A
UAM: A T T G A C C A T C T C C A G A G A C A A T G C A A G A G C C A C T C T A T C T G C A A G	r G A
HUM: A C A G C C T G A G C T G A G C T G A G G G A G G G A C A T G A C C G T G T A T T A C T G T G T G A G A G G	
UAM: A C A G C C T G A G C T G A G G A G C A G G A C A T G A C C G T G T A T T A C T G T G T G A G A G G	
D7	
HUM: CACAGTG	
UAM: CACAGTG	
D9	
HUM: G A C A A A C C T	
UAM: GACACACT	
Alignment stats: 'M': 296, 'I': 0, 'D': 0, 'X': 0	
Both human gene and its mapping are pseudogenes	

IGHV(II)-51-2

GENE ALIGN SEQ
HUM: G G C C T G G T G A G G C C T C A C A C A C C C C T C A C C T C A C T G T G T C T C T C T C T C T C T C T
UAM: G G C C T G G T G A G G C C T C A C A G A C C C C T C A C C T C A C C T G T G T G T C T G G
HUM: A T T C T C C A T C A C A A C T A G T C C T T C C T G G A G C T C G C A G T C C T C T C T C
UAM: A T T C T C C A T C A C A A C T A G T C C T T C C T G C T G G A G C T T G C T T G C T T G C T G C T G C T G C T G C T G C T G C T G C T G C T G C T G C
HUM: C A G T C A A G G G A G T C A A G G G A G T G A T C A G G G C A T C A G G G C A T A G G T C A C A A A T T C T A
UAM: CAGTCAAGGGAAGTGAATCAGGGCATAATCAAGGGTAAGGGAGCAAATTCTA
HUM: A C C C A C T C T C A T G A G C T C A T G A G C T C A G T C A G T C A G T C A G T C A G A T C C A G A T C C A C G T C C A A G A A C
UAM: A C C C A C T C C T C A T G A G C T C A G T C A G T C A G T C A G T C C A G A T C C A G A T C C A C G T C C A A G A A C
HUM: C A A A T T T T C T T T T A G C T G A G T T C T G A G C A C A A T G C A A C A A C T G T A
UAM: C A A A T T T T C T T T T A G C T G A G T T C T G A G C A A C A A T G C A A C A A C T T G T A
HUM: T T A C T G T G A G A G G UAM: T T A C T G A G A G G
D7 HUM: A A C A G A A
UAM: A A C A G A A
D9
HUM: C A C A A A C T T C C UAM: C A C A A A C T T C C
Alignment stats: 'M': 263, 'I': 0, 'D': 0, 'X': 0 Both human gene and its mapping are pseudogenes

IGHV5-51



GENE ALIGN SEQ. HUM: G G G G T G C A G A T G G T G G A G T C T T G G G G A G A G T T G G C A C A A G C T G A A T G T G UAM: G G G G T G C A G A T G G T G G A G T C T T G G G G A G A G T T G G C A C A A G C T G A A HUM: C T G A G A C T C T G C C G T G C A T C C T G A A T C C A C C T T C T G T A G C T A C T A G A T UAM: C A G C T G A A T C T G C C A G G C T C C A G G G A A A G G G G C T G C A G T TTCACCATCTAAAGACAATGCAAAGCAAGCAAGGTTGTATCTGCAAATGAA HUM: HUM: CAGTCTGAGAGAGATATAGGCTCTGAGATATAGGCTCAAAGGTA UAM: C A G T C T G A G C T G A G A T A T A T G G C T C T G A T A A T A A T A T A T T A T T G A G T C A A A G G T A D7HUM: C C A A A T G UAM: C C A A A T G D9HUM: G A C A C A A A A T T G A C A C A A A A T T UAM: Alignment stats: 'M': 297, 'I': 0, 'D': 0, 'X': 0

IGHV(II)-49-1

GENE ALIGN SEQ	
HUM: C G A C A T C T G T A T T T C T C G T G C G T T C T T G G C C	
UAM: CGACATCTGTATTCTCGGCGTTCTTGGCC	T G G C G A A G C C C T C A C A G A C
HUM: CCTCTCCTCATCTGTGCTGTCTCTCTTCT	C C A T C A C A A C C A C T C C T T C
UAM: C C T C T C C C T C A T C T G T G C T C T C T C C T C T C T C	
HUM: C T G C T G G A G C T G G A T C C C T C A G C T C C C A G G	GAAGGGA <mark>CT</mark> GGAG <mark>T</mark> GAA <mark>TC</mark>
UAM: C T G C T G G A G C T G G A T C C T C A G C T C C C A G G	GAAGGGA <mark>C</mark> TGGAG <mark>T</mark> GAA <mark>TC</mark>
HUM: A G G T G C A C A G G T C A T G A G G G A A C A C A A C G	
UAM: A G G T G C A C A G G T C A T G A G G G A G A A C A C A A C G G	C A A C C C A C G C C T C A A G A G T
HUM: CCAGTCACCATCTCAGATCCAATCAAAA	
UAM: C C A G T C A C C A T C T C C A G A T C C A C A T C C A A A A A	
HUM: GAGCTACATGAGCAACGAACATGA	
UAM: G A G C T A C C T G A G C A A C G A G T A C A C C A A C C A T G A	A A <mark>T T T T T</mark> A <mark>C A C</mark> A A A A G A
D7	
HUM: T A C A G C A	
UAM: T A C A G C A	
D9	
HUM: GAAACAAACT	
UAM: GAAACAAACT	
Alignment stats: 'M': 298, 'I': 0, 'D': 0, 'X': 0	
Both human gene and its mapping are pseudogenes	

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GENE ALIGN SEQ.
HUM: GAGGTGCAGGTGGAGTCTGGGGGGGAGG<mark>CTTGGGGGGG</mark>
                 CTGGTGGAGTCTGGGGGGAGG<mark>CTTGGTAAAGCCA</mark>GGG<mark>C</mark>GG<mark>T</mark>C
HUM: CCTGAGACTCTCTGTACAGCTTCTTCTACACCTTTCTAGGTATTACTACTA
HUM: TGAGCTGGGTCCAGGCTCAAGGCTCAAGGGCTCAAGGGCTCAAGGGGAAGTGGGAGTAAGGTTAC
UAM: TGAGCTGGTTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTAGGTTTC
HUM: A T T A G A A G C A A A G C T T A T G G T G G G A C A A C A G A A T A C G C C G C G T C T G T G A A
UAM: A T T A G A A G C A A A G C T T A T G G T G G G A C A A C A G A A T A C G
HUM: A G G C A G A T T C A C C A T C T C A A G A G A T T C C A A A A G C A T C G C C T A T C T G
UAM: A G G C A G A T T C A C C A T C T C A A G A G A T T A A A A A A A G C A T C G C C T
HUM: A A A T G A A C A G C C T G A A A A C C G A G G A C A C A G C C G T G T A T T A C T G T A C T A G A
UAM: A A A T G A A C A G C C T G A A A A C C G A G G A C A G C C G T G T A T T A C T G T A C T A G A
HUM:
UAM:
D7
HUM:
   C A C A G T G
UAM:
D9
HUM: G A C A C A A A C C T
UAM: GACAGAAACCT
Alignment stats: 'M': 300, 'I': 0, 'D': 0, 'X': 2
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GENE ALIGN SEQ	
HUM: GAGG <mark>TGCAGCTGGAGTCT</mark> GGAG <mark>TCTGGGGGGGGCTTGGTACAGCCT</mark> GGAGGG <mark>T</mark> C	
UAM: GAGG <mark>TGCAGCT</mark> GGAG <mark>TCT</mark> GGAG <mark>TCT</mark> GGGGGG <mark>TTTGGTACAGCCT</mark> GGGG	l
HUM: CCTGAGACTCTCTGTGCAGCCTCTCACCTTCACTTCACT	1
UAM: C C T G A G A C T C T C C T G T G C A G C C T C T G A G C C T T C A C C T T C A G C T A T A G C -	•
HUM: A A T G A A <mark>C T</mark> G G G <mark>T C C</mark> G <mark>C C A G G C T</mark> C C A G G G G A A G G G G <mark>C T</mark> G G A G <mark>T G G G T T T C A T</mark>	
UAM: - A T G A A C T G G G T C C G C C A G G C T C C A G G G G G G G C T G G A G T G G G T T T C A T	
HUM: A C A T T A G T A G T A G T A G T A G T A G T A G T A G T A G T A G T A C C A T A C T A C T A C G C A G A C T C T G T G A A G G G C UAM: A C A T T A G T A G T A G T A G T A C C A T A C C A T A C C A T A C C A G A C T C T G T G A A G G G C	
UAM: A CATTAGIA GIA GIA GIA GIA CCATATACA CA CACACI GIGA A GGC	ı
HUM: CGATTCACCATCAGAGAGACAACGAAGAACTAACTAACTA	ı
UAM: CGATTCACAAATCAAATCAAATGAAATGCAAATGCAAAAT	
	•
HUM: G A A C A G C C T G A G C C G A G G A C A C G G T G T T A C T G T G A G A G A G A	
UAM: GAACAG <mark>CCT</mark> GAGAGAGAGAGGGGGG <mark>CTGTGTATACTGC</mark> GAAGAAA	
D7	
HUM: CACAGTG	
UAM: CACAGTG	
D9	
HUM: GACAAACCT	
UAM: GACAACT	
Alignment stats: 'M': 288, 'I': 2, 'D': 2, 'X': 6	
No. the name of the second of	

IGHV(III)-47-1

GENE ALIGN SEQ
HUM: G A A G T T A A T T A C T G G A G T C T C T C A G A A A T A C T A C A G A C C A A G A A T C T
UAM: GAAG <mark>TTAATTACT</mark> GGAG <mark>TCTCTC</mark> AGAGAA <mark>TACT</mark> A <mark>CTACAGAAGAA</mark> TT
HUM: CAGACTTTTCTCAGAAACCCTGTGTGTGATTCACTGACTG
UAM: CAGACTTTTCTCTGAAACCCTTGTGTGACTTCACTTCAC
HUM: G C T T G G T C A G C A G C T T C A T G A C A G G T T C A T A C A G G G G G T G T A G G T A A C A T C A
UAM: G C T T G G T C C A G C A G G T T C A T G A C A G G G G T G T A G G T A A C A T C A
HUM: G T A A T T C A A G T G G A A G T T C T C A G T G G A T T C A G T G G G A C T C T C T T G A G T A C A A A G A A G A
UAM: G T A A T T C A A G T G G A A G T T C T C A G T G G G A C T C T C C T T G A G T A C A A G A A G A
HUM: TT TAAACAGT CCTCAGAACACACACACACACACACACACACACACACACA
UAM: TTAAACAGTCCTCAGAGACACGCTTTTTCAGATTGATTCTCTCTTTAAAGATGAT
HUM: T A A C C T G A G A G C T C A G G A A A T T C C G T T T A T T A C T G T G A G G G A
UAM: TAACCTGAGAGCTCAAAATTCCGGTTTATAACTGAAAAAAAA
HUM: C A C G G T G UAM: C A C G G T G
D9
HUM: GACAAACCT
UAM: GACAAACCT
Alignment stats: 'M': 293, 'I': 0, 'D': 0, 'X': 0
Both human gene and its mapping are pseudogenes

GENE ALIGN SEQ HUM: GAGGATCAGCTGGAGTCTGGGGGGGGGTC UAM: GAGGATCAGCTGGAGTCTGGGGGGGAGGCTTGGGGGGGTC UAM: C C T G A G A C C C T C C T G T G C A G C C T C T G T G T G T G C A G C C T C T C T G G A T T C G C C T T C A G T A G C T A T G T T C HUM: TGCACTGGGTTCGGGCTACGGGGCTCCAGGGGAAGGGTCTGGGAGTGATCAG HUM: A T T G G T A C T G G T G G T G A T A C A T A C T A T G C A G A C T C C G T G A T G G C C G A T T UAM: A T T G G T A C T G G T G G T G A T A C A T A C T A T G C A G A C T C C G T G A T G G C C G A T T HUM: CACCATCT CCAGAGAGACAACGCAAGAAGTCCTTGTATCATAATGAACA UAM: CACCATCTCAGAGAGACAACGCCAAGAAGTCCTTGTATCTTCAAATGAACA G C C T G A T A G C T G A G G A C A T G G C T G T G T A T T A T T G T G C A A G A G A D7HUM: C A C A G T G UAM: D9HUM: G A T A C A A A C T T G A T A C A A A C T T UAM: Alignment stats: 'M': 289, 'I': 0, 'D': 0, 'X': 4

IGHV(II)-46-1

GEN	E AI	IGN	SEQ)																																				
HUM:	C	A G	G A	G C	A	G	C	T	G	C A	A G	G	Α	G	T	A	G	C	C (T	G	G	A (C	Т	G	A A	T	Α	G	C .	A (CA	C	Α	С	ТТ	Α	С	C
UAM:	C	A G	G A	G	A	G	C	T	G	C A	A G	G	Α	G	T	A	G	C	C (Т	G	G	A (C	Т	G	A /	T	Α	G	C .	A (CA	C	Α	С	ТТ	A	C	C
			T G (_					C C			
UAM:	C	C C	T G	C C	T	C	Α	C	C	T A	A C	Α	C	T	G 1	T	A	C	T (G G	C	C	A (T	C	C	G 7	C	Α	C	Α .	A (C	Α	G	T	C C	Τ	T	Α
HUM:			G T (A T			
UAM:	C	A	G T	G G	A	C	C	T	G (G A	T	C	Т	G	C C	G	G	C	T (T	C	Α	G (G G	Α	G	G (G	C	T	G	C I	A A	T	G	G	A T			
D7 HUM: UAM:			A T (
D9 HUM: UAM:			T T																																					
Align	nmen	t st	ats:	,	м':	14	47,	, ,	I':	: 0	, ,	D,	: 0),	,х,	: 0)																							

IGHV1-46

GENE ALIGN SEQ
HUM: CAGGTGAGAGCTAGCAGCTAGCTAGCTAGCTAGCTAGCTA
UAM: CAGGTGCAGCTGGTGCAGTCTGGGGGGCTGAGGGGCTGAGGGGCCTC
HUM: A G T G A A G G T T T C C T G C A A G G C A T C T G C A G C A T C T G G A T A C A C C T T C A C C A G C T A C T A T A
UAM: A G T G A A G G T T T C C T G C A A G G C A T C T G C A T C T G C A C C T T C A C C A G C T A C T A T A
HUM: T G C A C T G G G T G C G A C A G G C C C T G G A C A G G C T T G A G T G G A T G G G A T A T A
UAM: T G C A C T G G G T G C G A C A G G C C C C T G G A C A G G C T T G A G T G G A T G G G A T A
HUM: A T C A A C C C T A G T G G T G G T A G C A C A G C A C A G A G T T C C A G G C A G
UAM: A T C A A C C C T A G T G G T A G C A C A A G C T A C G C A C A G A A G T T C C A G G G C A G
HUM: A G T C A C C A T G A C C A G G G A C A C G T C A C G T C A C A C A C A C A C A C A C A C A C
UAM: A G T C A C C A T G A C C A G G G A C A C G T C C A C G T C A C A G T C T A C A T G G A G C T G A
HUM: GCAGCCTGAGAGACGAGACGGGCCGTGTACTGAGAGAAAAAAAA
UAM: GCAGCCTGAGAGAGAGAGAGACACGGCCGTGTATTACTGCGAGAGA
D7
HUM: C A C A G T G
UAM: CACACACAC
D9
HUM: G T C A G A A A C C C
UAM: G T C A G A A A C C C
Alignment stats: 'M': 296, 'I': 0, 'D': 0, 'X': 0
Neither human gene nor its mapping is pseudogene

IGHV1-45

GENE ALIGN SEQ CTGGTGCAGTCTGGGGCTGAGGTGAAGAAGACTGGGTCCTC HUM: A G T G A A G G T T T C C T G C A A G G C T T C C G G A T A C A C C T T C A C C T A C C G C T A C C UAM: A G T G A A G G T T T C C T G C A A G G C T T C C G G A T A C A C C T T C A C C T A C C G C T A C C HUM: TGCACTGGGTGGCACCCCCCCGGACAAGCCTTGAGTGGAATGGGATGGGATGGGATGGGATGG UAM: T G C A C T G G G T G C G A C A G G C C C C G G A C A A G C HUM: A T C A C A C C T T T C A A T G G T A A C A C T A C G C A C A G A A T T C C A G G A C A G UAM: A T C A C A C C T T T C A A T G G T A A C A C C A A C T A C G C A G A A T T C C A G G A C A G HUM: A G T C A C C A T T A C C A G G G A C A G G T C T A T G A G C A C A G C C T A C A T G G A G C T G A UAM: A G T C A C C A T T A C C A G G G A C A G G T C T A T G A G C A C A G C C T A C A T G G A G C T G A HUM: G C A G C C T G A G A T C T G A G G A C A C A G C C A T G T A T T A C T G T G C A A G A T A UAM: G C A G C C T G A G A T C T G A G G A C A C A C A G C C A T G T A T T A C T G T G C A A G A T A D7HUM: C A C A G T G UAM: D9HUM: G T C A G A A A C C C UAM: G T C A G A A A C C C Alignment stats: 'M': 296, 'I': 0, 'D': 0, 'X': 0

IGHV(II)-44-2

HUM: C T C T T C C T C A A C A T G C C A T T A C A T A C A T A C A T A A C A C A
HUM: C T G C T G G A G C T G A A T C C A C T A G C C C G C T T C C A T G G G C T G T C A G G A A C A C A
UAM: CTGCTGGAGCTGAATCCACTAGCCGGCTTGGGGCTGTCAGGAACACA
HUM: TTTGCAAAGGAACACACACACACACACACACACACACACA
UAM: TTGCAAGGGTGACACACACACACACACATGATCCTCTGCAGAGCCAACTCT
HUM: T C T C C A G A G A T T C A T C C A A G A A A C A A T T T T G A C T A T A C C T G A G C T C T G T G T G
UAM: T C T C C A G A G A T T C A T C C A A G A A C A A T T T T G A C T A T A C C T G A G T G T G T G
HUM: A C A T C T G A G G A C A T G G T T T G T A T T A C T G T G C A A G A C A
UAM: A C A T C T G A G G A C A T G G T T T G T A T T G C T G T G T G C A A G A C A
D7
HUM: A A C A G T G
UAM: A A C A G T G
Ohn. A h o h o h o h
D9
HUM: GACATAAACCT
UAM: GACATAAACCT
Alignment stats: 'M': 237, 'I': 0, 'D': 0, 'X': 0
Both human gene and its mapping are pseudogenes

IGHV(IV)-44-1

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GENE ALIGN SEQ
HUM: GAGGACCACCTTGGTGCAATGGGAAGGAAGTAG<mark>T</mark>GGTCCCCTTTGG<mark>T</mark>CA<mark>T</mark>
G C T C A G C C T C A C C T A T G C C G C C T A T G C A C A T T C A A T T T C T G A A C A T T C T G
   GCTCAGCCTCAACCTATGCCGCCTATTGCCTATTCTCTAATGCTG
HUM: TTTCCTGGGATCCATCATCATATCAAAAAGGTCTTCAAGTGTGTTGTT
HUM: A T A T G G G T T A A G G G A A A C A C T A A G C C C C A A C C T T C A G G G C A G A G C T A G
UAM: A T A T G G G T T A A G G G A A A C A C T A A G C C C A A C C T T C A G G G C A G A G C T A G
   T C T C C A G A A C A C A T A G T A A A A A A C A A G A A A C T T A C A G C T G A G A A G T G T
HUM:
UAM: T C T C C A G A A A C A C A T A G T A A A A A A A C A A C T T A C A G C T G A G A G T G T
HUM: GATGGCTGGGGGAGGCAGGCGTGTATTACTGTGCAAGG
D7
HUM:
  C A C T G T G
UAM:
D9
HUM: G A C A C A A A C C T
UAM: GACACAAACCT
Alignment stats: 'M': 288, 'I': 0, 'D': 0, 'X': 1
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IGHV(II)-43-1

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GENE ALIGN SEQ
HUM: T C T G G A T T C C C C A A C A G A A C C A G T G C T T C C T G C T G G A G C T G G A T C C A T C A
UAM: T C T G G A T T C C C C A A C A G A A C C A G T G C T T C C T G
       G <mark>C C C C A G G G A A G G G A <mark>C T</mark> G G A G <mark>T</mark> G G G <mark>T C A G G <mark>T G C A C A G G <mark>T C</mark> A <mark>T</mark> G A A G G G A</mark></mark></mark>
HUM:
       G <mark>C C C C A</mark> G G G A A G G G A <mark>C T</mark> G G A G <mark>T</mark> G G G <mark>T C A G G <mark>T G C A C A G G <mark>T C</mark> A <mark>T</mark> G A A G G G A</mark></mark>
UAM:
HUM:
        CACAAA<mark>TTCT</mark>AACCCAC<mark>T</mark>CCAGAG<mark>T</mark>CAAGAG<mark>T</mark>CAAC<mark>T</mark>CAAGA<mark>T</mark>CA
       G C A C A A T T C T A A C C C A C T C C T C A A G A G T C C A G T C A C C T C C A G A T C T
UAM:
HUM: A T G T C C A A A A A C A G C T C T T C G T A T G G C T G A G T G A C A T T A G C A A C A A G C A C
UAM: A T G T C C A A A A C A G C T C T T C G T A T G G C T G A G C A T T A G C A A C A A G C A C C
HUM: A C A G C C A T G T
UAM: A C A G C C A T G T
D7
HUM:
UAM:
D9
HUM: G T G T G T G T T T
UAM:
Alignment stats: 'M': 210, 'I': 0, 'D': 0, 'X': 0
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GENE ALIGN SEQ
HUM: G A A G T G C A G C T G G T G G A G T C T G G G G G G T C G T G G T A C A G C C T G G G G G T C
UAM: GAAG <mark>TGCAGCT</mark> GGAG <mark>TCT</mark> GGAG <mark>TCT</mark> GGGGGGG <mark>TCGT</mark> GGGGGG <mark>TCGT</mark> GG <mark>T</mark> ACAG <mark>CCT</mark> GGGGG <mark>T</mark> C
HUM: CCTGAGAGTCTCTGTGTGCAGCTTCTGACCTTCTAGATTCACCTTTTGATATACA
UAM: CCTGAGAGACTCTGAGTGCTGTGTGCTTCTCTGATTGATT
HUM: TGCACTGGGTCGGTCAGGCAGGCGGGGAAGGCTCTT
UAM: TGCACTGGTCAGCGCAGGCAGGCGAAGGGGAAGGGTCTCTT
HUM: A T T A G T T G G G A T G G T A G C A C A T A C T A T G C A G A C T C T G T G A A G G G C C G
UAM: A T T A G T T G G G A T G G T A G C A C A T A C T A T G C A G A C T C T G T G A A G G G C C G
HUM: A T T C A C C A T C T C C A G A C A A C A A C A A A A C T C C T G T A T C T G C A A A A T G A
UAM: A T T C A C C A T C T C C A G A G A C A A C A C A A A A C T C C T G T A T C T G C A A A T G A
HUM: A C A G T C T G A G A C T G A G G A C T G A G G A C C G C C T T G T A T T A C T G T G C A A A A G A T A UAM: A C A G T C T G A G A A C T G A G G A C C C C C T T G T A T T A C T G T G C A A A A G A T A
OAM. A CAGICIGAGAACIGAGGACACCGCCIIGIATIACIGIGCAAAAGAIA
D7
HUM: CACAGTG
UAM: CACAGTG
D9
HUM: GACAAAACCT
UAM: G A C A A A A A C C T
Alignment stats: 'M': 298, 'I': 0, 'D': 0, 'X': 0

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GENE ALIGN SEQ.
HUM: GAGGCGCAGCTGGAGTCTGGGGGGAGGCTTGGGCTGGGGT
                 CTGGTGGAGTCTGGGGAGG<mark>CTTGGTACAGCCT</mark>GGGT
UAM: CCCCGAGACTCTCATTTGCAGCTTCTAGACCTTCACTAGACCTTCAACTTGA
HUM: A T G C A C T G G A T C C G C C A G G C T T C T G G G A A A G G G C T G G A G T G G G T T G G C C G
UAM: A T G C A C T G G A T C C G C C A G G C T T C T G G G A A A G G G C T G G A G T G G G T
    TATTAGAACCAAACGTAACAGTTACACGAAAT
    T A T T A G A A C C A A A C G T A A C A G T T A C A C G A C A G A A T G
HUM: A A G G C A G G T T C A C C A T C T C A A G A G A T G A T T C A A A A A A C A C A C T G T A T C T G
UAM: A A G G C A G G T T C A C C A T C T C A A G A G A T G A T T C A A A A A A C A C A C T G T A T C T G
HUM: CAAGTGAATACCCTTGAAAACCGAAGTACACGGCCATTCTACTGTACT
UAM: C A A G T G A A T A C C C T G A A A A C C G A G T A C A C G G C C A T C T A T T A C T G T A C T A G
HUM: A G A
UAM: A G A
D7
HUM: C A G T G A G
UAM:
D9
HUM: A C A C A A A T C T C
UAM: A C A C A A A T C T C
Alignment stats: 'M': 303, 'I': 0, 'D': 0, 'X': 0
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GENE ALIGN SEQ.
HUM: GAGGTGCAGCTGGAGTCTGGGGGGGGGTC
              C T G G T G G A G T C T G G G G G A G G C T T G G T C C A G C C T G G G G G T C
HUM: A T C T G G A A T G A T G G A A G T C A G A A T A C T A T G C A G A C T C T G T G A A G G G C C G
UAM: A T C T G G A A T G A T G G A A G T C A G A A A T A C T A T G C A G A C T C T G T G A A G G G C C G
HUM: A T T C A C A A T C T C C A G A G A C A A T T C T A A G A G C A T G C T A T C T G C A A A T G G
UAM: A T T C A C A A T C T C C - G A G A C A A T T C T A A G A G C A T G C T A T C T G C A A A T G G
HUM: A C A G T C T G A A A G C T A A G G A C A C G G C C A T G T A T T A C T G T A C C A G A
UAM: A C A G T C T G A A A G C T A A G G A C A C G G C C A T G T A T T A C T G T A C C A G A
D7
HUM: C A C A G T G
D9
HUM: G A C A C A A A C C T
UAM: GACACAAACCT
Alignment stats: 'M': 292, 'I': 0, 'D': 1, 'X': 1
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IGHV(II)-40-1

IGHV7-40

GENE ALIGN SEQ
HUM: TATGGTATGAATTCAGTGAGTGAGTGAGCCAGCCCTGGAAGGGGCTTGAAGGGACTATGAAGT
UAM: TATGGTATGAATTCAGTGAGTGACCAGCCCTGGAAGGGG <mark>CTT</mark> GAAGTAA
HUM: G G G G A T G G A T C A T C A C T A C A C T A C A C T A C A C
HUM: C A G G A C G G T T T C T A T T C T C T A T T C T C T C
HUM: CAGAGACTGAGCAGCCTAAAAGGCTAGAGGACACGG <mark>CCGTGTAT</mark> GACTGAT
UAM: CAGAGATCAGCAGCTAAAGGC <mark>CT</mark> AAAGGG <mark>CTGAGGAGGGACGGCGTGTAT</mark> ATGA <mark>TGAT</mark> GAATGAG
HUM: A G A UAM: A G A
D7 HUM: C A C A G T G UAM: C A C A G T G
D9 HUM: G T C A G A A A C C C UAM: G T C A G A A A C C C
Alignment stats: 'M': 203, 'I': 0, 'D': 0, 'X': 0 Both human gene and its mapping are pseudogenes

IGHV4-39

GENE ALIGN SEQ
HUM: CAGCTGAGCAGCAGGAGGAGGCAGGAGAGTCAGAGAGTAGAAGCTAGAAGCTAGAAGCAAGAAG
UAM: CAGCTGCAGGAGTCGAGGAGTCGGGGCCCAGGACTGAGGAGCTGAGGAGAGAGA
HUM: C C T G T C C C T C A C C T G C A C T G T C T G T C T C T C T C T C T C T
UAM: C C T G T C C C T C A C C T G C A C T G T G T C T C T C T C T C T G C T C C A T C A G C A G T A G T T C
HUM: A C T A C T G G G G C T G G A T C C G C C A G C C C C A G G G G G C T G G A G T G G A T T
UAM: A C T A C T G G G G C T G G A T C C G C C A G C C C C A G G G G A A G G G G
HUM: G G G A G T A T C T A T T A T A T G G G A G C A C C T A C A C C C G T C A A G A G A G A G A G A G A G A G A G
UAM: G G G A G T A T C T A T T A T A G T G G G A G C A C C T A C A A C C C G T C C A A G A G A G
HUM: TCGAGTCACACATATCCGATACACATACATACATACAACAACAAAAAAAA
UAM: TCGAGTCACATATCCGTACACATATCCCGTAGTCCAAGATCCAGTCCAAGTTCCTCCTAAGCAAGC
HUM: T G A G C T C T G T G A C C G C C G C A G A C G C T G T G T A C T G T G T G T A C T G T G T G T G T G T G T G T G T G T
UAM: T G A G C T C T G T G A C C G C C G C A G A C A C G C T G T A T T A C T G T G C A G A C A
D7
HUM: CACAGTG
UAM: CACAGTG
D9
HUM: GACAAAACCT
UAM: GACAAAACCT
Alignment stats: 'M': 299, 'I': 0, 'D': 0, 'X': 0 Neither human gene nor its mapping is pseudogene
neroner namen gene ner rob mapping ib phendogene

IGHV(III)-38-1

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GENE ALIGN SEQ
HUM: GAAGTTAAACTAGGGAGTCAGAGACAGACTCATAGAAATACTACAGACCAAAGAATTCT
UAM: C A G A C T G T T C T G C A A A G C C C T G G A T T C A C T G A A A A A A A C C A A G T T G G
HUM: T C C A G C A G G A T T C A T G G C A A G T G G C A A G T G G T G A G G G A G A T A A C A G T A A T T C A A
HUM: G T G G A A G T T C T C A A T G G G A C T C G C C T T C A G T A C A A G A A G A T T A A C A G T C
UAM: G T G G A A G T T C T C A A T G G G A C T C G C C T T C A G T A C A A A G A A G A T T A A C A G T C
HUM: CTCAGAGAGACTGTTCAGAAGATTCTTTTAAAGATAAAACTGAGAGAG
UAM: C T C A G A G A C A C T G T T C A G A A G A T T C T C T T T T A A G A T A A A A C T G A G A G
HUM: CCCAAGACAAGTCTGTGTATTACTGTGAGGGA
UAM: CCCAAAGACAGTCTGTGTATTACTGTGAGGAA
D7
HUM: C A C A G T G
UAM: C A C A G T G
D9
HUM: G A C A C A A A A G T
UAM: GACACAAAAGT
Alignment stats: 'M': 282, 'I': 0, 'D': 0, 'X': 0
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GENE ALIGN SEQ
HUM: GAGGTGCAGCTGGAGTCTGGAGTCTGGGGGGGTTGGGGGGGT
UAM: GAGG <mark>TGCAGCTGGAGTGGAGTGGAGGGGGGGTT</mark> GGG <mark>TGGGGGG</mark> TGGGGG <mark>CTT</mark> AGG <mark>CCT</mark> AGGGGG <mark>T</mark> C
HUM: CCTGAGACTCTGAGACTCTGAGCAGCCTTTTCTGACCGTCAG <mark>TAGCAAT</mark> GAGA
UAM: C C T G A G A C T C T C T G A G A C A C T C T C T C T G T G C A G C C T C T C T C T C T C A C C G T C A G T A G C A A T G A G A
HUM: T G A G C T G G A T C C G C C A G G C T C C A G G G G A A G G G G C T G G A G T G G G T C T C A T C C
UAM: T G A G C T G G A T C C G C C A G G C T C C A G G G A A G G G G C T G G A G T G G G T C T C A T C C
HUM: A T T A G T G G T G G T A G C A C A T A C T A C G C A G A C A G G A A G G G C A G A C T C C A G G A A G G G C A G A T T C A C
UAM: A TTAGTGGTGGTAGCACATACTACGCACACATACCTACGAGAGGGAAGGGAAGACTCCAAGGAAGG
HUM: CATCTCAGAGAGACAATTCAAAGAACACGCTGTATCAAA <mark>T</mark> GAA <mark>C</mark> AACC
UAM: C A T C T C A G A G A G A C A A T T C A A G A G A C A A T T C C A A G A C A C A C A C A C C C C T C T C A A T C A A A T G A A C A C C
HUM: TGAGAGCTGAGGGCCCGTGTATTACTGCCAGATA
UAM: T G A G A G C T G A G G G C A C G G C C G T G T A T T A C T G T G C C A G A T A T A
D7
HUM: C A C A G A G UAM: C A C A G A G
D9
HUM: CACAAACC <mark>TCC</mark> UAM: CAAAACCTCC
Alignment stats: 'M': 292, 'I': 0, 'D': 0, 'X': 0
Neither human gene nor its mapping is pseudogene

GENE ALIGN SEQ
HUM: GAGGTGAGCTGGTAGGTAGGTAGGTGGGGGGGGAGACTTGGGTGGG
UAM: G A G G T G C A G C T G G T A G A G T G G T G G G G G G G G
HUM: TTGGGGGTGTCTGAGAGACTCTCTCATGAGAGACTCTATGTGTGCAGCCTGCGGATTCATGAGA
UAM: TTGGGGGTGTGTGAGAGACTCATCATCATCATCATCATCATCATCATCATCATCAT
HUM: A G C A A T G A C A T G A A C T G G G C C A C C G G G C T T C A A G A A A G G G C T G G A A T G
UAM: A G C A A T G A C A T G A A C T G G G C C C A C C G G G C T T C A A G A A A G G G G C T G G A A T G
HUM: G G T C T C A T A C A T T A G T G C T A G T G G T G G T G G T G G T A G C T A T A C T A T G C A G A C A C T G
UAM: G G T C T C A T A C A T T A G T G C T A G T G C T A G T G C T A G T G C T A G T G C T A T A C T A T G C A G A C A C T G
HUM: A A G G G T A G A T T C A C C A T C T A G A G A G A T G C T A G A G A G A C A T G T T
UAM: A A G G G T A G A T T C A C C A T C T A G A G A T G C A A G A A C A T G C T T
HUM: GCAAATGAACACAGTCTGAGAGAGAGAGAGA <mark>TGAGGGAGTGT</mark> CGG <mark>CTGTGTGTGAGAGA</mark>
UAM: GCAAATGAACAGICIGAGAGAGAGAGAGAGAGAGA
D7
HUM: CATGGTG
UAM: C A T G G T G
D9
HUM: G C C A G A A A C C T
UAM: G C C A G A A A C C T
Alignment stats: 'M': 294, 'I': 0, 'D': 0, 'X': 0
Both human gene and its mapping are pseudogenes

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GENE ALIGN SEQ.
HUM: GAGGTGCAGCTGGAGTCTTTGGGAGGCTTGTATAGCCCTGGGGGTCC
                    CTGGTGGAGTCTTTGGGAGGCTTGTTATAGCCTGGGGGTCC
HUM: C T G A G A C T T T C T T T T G C A G C C T C T G G A T T C A C C T T T A G T A C C T T T A T T A G
UAM: C T G A G A C T T T C T T T T G C A G C T C T C T G A T T T A G C A G C C T C T C T G G A T T C A C C T T T A G T A C C T T T A G T T A G
     G T A C T G G A T G A G C T G G G T C C A T C A G G C T G G G A A A G G G C T G G A G T A G G
HUM:
     G T A C T G G A T G A G C T G G G T C C A T C A G G C T C C T G G G A A A G G G C T G G A G T A G G
UAM:
     TCTCATTATGAGTTGTGTGTAGCAAGCTATGCAAGCTATGCAAACTCTGTG
HUM:
HUM: A A G G G T C G A T T C A C C C T C T C C A G A G A T G C C A A G A A T C A C T G T A T C T
UAM: A A G G G T C G A T T C A C C C T C T C C A G A G A T G C C A A G A A A T C A C T G T A T C T
     G C A A A T G A A C A G C G T C A G A G C C G A G G A T A G G T C T G T A T T A C T G T G G T G
     G C A A A T G A A C A G C G T C A G A G C C G A G G G T A T A G G T C T G T G T A T T A C T G T G T G
HUM:
UAM:
D7
HUM:
UAM:
D9
HUM: G C A G A G A T G C T
    G C A G A G A T G C T
Alignment stats: 'M': 301, 'I': 0, 'D': 0, 'X': 0
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GENE ALIGN SEQ
HUM: GAGGTGCAGCTGGAGTGGAGTGGAGTCTGGGGGGGGGGG
UAM: GAGG <mark>TGAGCT</mark> GGTGGAG <mark>TCT</mark> GGAG <mark>TCT</mark> GGGGGGGGAGG <mark>CTTGGGAGCCT</mark> GGGGA <mark>T</mark> C
HUM: CCTGAGACTCTCTGTGCAGCAGCTCACACCTTCACAGTAACAGTGACA
UAM: C C T G A G A C T C T C C T G T G C A G C C T C T C T G A G A T T C A C T T C A G T A A C A G T G A C A
HUM: T G A A C T G G G T C C A T C A G G C T C C A G G G G G C T G G A G T G G G T A T C G G G T
UAM: T G A A C T G G G T C C A T C A G G C T C C A G G A A A G G G G C T G G A G T G G G T A T C G G G T
HUM: G T T A G T T G G A A T G G C A G T A G G A C G C A C T A T G C A G A C T C T G T G A A G G G C C G
UAM: G T T A G T T G G A A T G G C A G T A G G A C G C A C T A T G C A G A C T C T G T G A A G G G C C G
HUM: A T T C A T C A T C A G C A G A C A A T C A G A G A C A A T T C C A G G A A C A C C T G T A T C T G C A A C G A
UAM: A T T C A T C A T C T C A G A G A C A A T T C C A G A C A A T T C C A G G A A C A C C T G T A T C T G C A A A C G A
HUM: A T A G C C T G A G G C C G A G G A C A C G G T G T G T A T T A C T G T G A G A A A UAM: A T A G C C T G A G G C C G A G G A C A C G G C T G T G T A T T A C T G T G A G A A A
OAM. A TAGOCIGA GGCOGA GGA GGA CAGGIGI GI A TITA CIGIGI GA GA A A
D7
HUM: C A C T G T G
UAM: CACTGTG
D9
HUM: GACAAACCT
UAM: GACAAACCT
Alignment stats: 'M': 296, 'I': 0, 'D': 0, 'X': 0

IGHV7-34-1

GENE ALIGN SEQ
HUM: C T G C A G C T G G T G C A G T C T G G G G C C T G A G G T G A A G C C T G G G G C C T C A G T
UAM: CTGCAGCTGGTGCAGTCAGTGAGTCTTGAGGAGAAGCCTTGAGT
HUM: GAAGG <mark>TCTCTATATAAGTCTTCTTCTTACACTTC</mark> TACCTCTTACACCTTCACATCTATGGTATGA
UAM: G A A G G T C T C T A T A A G T C T T C T G G T T A C A C C T T C A C C A T C T A T G G T A T G A
HUM: A T T G G G T A T G A T A G A C C C C T G G A C A G G G C T T T G A G T G G A T G T G A T G G A T C
UAM: A T T G G G T A T G A T A G A C C C C T G G A C A G G G C T T T G A G T G G A T G T G A T G G A T C
HUM: A T C A C C T A C A C T G G G A A C C C A A C G T A T A C C C A C G G C T T C A C A G G A T G G T T
UAM: A T C A C C T A C A C T G G G A A C C C A A C G T A C G G G C T T C A C A G G A T G G T T
HUM: T G T C T T C T C C A T G G A C A C G T C T G A G C A C G T C T G T C A G C G G C G T G T C T T C A G A T C A G C A
UAM: T G T C T T C T C C A T G G A C A C G T C T G T C A G C A C G T G T C T G T C A G C A C G G T G T C T T C A G A T C A G C A
HUM: G C C T A A A G G C T G A G G A C A C G G C C G A G T A T T A C T G T G C G A A G T A
UAM: G C C T A A A G G C T G A G G A C A C G G C C G A G T A T T A C T G T G C G A A G T A
HUM: CACAGTG UAM: CACAGTG
D9
HUM: TTCAGAAAGCC UAM: TTCAGAAAGCC
OAM. TITORGRAAG CC
Alignment stats: 'M': 293, 'I': 0, 'D': 0, 'X': 0
Both human gene and its mapping are pseudogenes

IGHV4-34

GENE ALIGN SEQ
HUM: CAGGTGCAGCTACAGCAGCAGTGGGGCGCAGTGGGGCGCAGGACTGGTTGAAGCCTTCGAAGCAGAGACA
UAM: CAGGTGCAGCTACAGCAGCAGTGGGGCGCAGGACTGAAGCCTTGAAGCAGAAGCAGAAGA
HUM: CCTGTCCCTCACCTGCCTCTCTCTCTCTCTATCTTCTTCACTTCTTCTTCTTCTT
UAM: CCTGTCCCTCACCTGCTCACCTGCCTCTCTCTCTATCTAT
HUM: G G A G C T G G A T C C G C C A G C C C C C A G G G G G C T G G A G T T G G G G A A
UAM: G G A G C T G G A T C C G C C A G C C C C A G G G G A A G G G G
HUM: A T C A A T C A T A G T G G A A G C A C C A A C T A C A A C C C G T C C A A G A G T C G A G T
UAM: A T C A A T C A T A G T G G A A G C A C C A A C T A C A A C C G T C A A G A G T C G A G T
HUM: CACAATATATATATATATATATATATATATATATATATA
UAM: CACATATATCAGTAGAGTAGACACACAAAAAACAAGAACAAGTAAGAAGAAGCAAGTAAAGCAAAGTAAAGCTA
HUM: CTGTGACCGCGCGGACACGCTGTGTATTACTGTGCGAGAGG
UAM: CTGTGACCGCGCGGACACGCTGTGTATTACTGTGCGAGAGAGG
D7
HUM: C A C A G T G
UAM: C A C A G T G
D9
HUM: GACAAAA CCT
UAM: G A C A A A A C C T
Alignment stats: 'M': 293, 'I': 0, 'D': 0, 'X': 0 Neither human gene nor its mapping is pseudogene
October 101 102 makking to kanadagana

IGHV3-33-2

	IE ALIGN SEQ																										
	G A G G T A C																										
UAM:	G A G G T A C	A G	C T (C G T	G G	A	G T	C C	G (A	G A	G	G A	C C	C	A A	G	A C	A .	A C	C	T G	G	G G	G	A T	C
LITIM .	C T T G A G A	СТ	C T /	C C T		. .	<u> </u>	C A	C T	r C	T C	C	Λ <u>T</u>	T A	Λ	C C	Tr. T	r C	٨	<u>т</u>	۸	C C	T	A C	T	~ A	Λ
	C T T G A G A																										
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HUM:	T G A G C T (G G	T T :	T C C	C	A G	G C	T C	C A	A G	G G	A	A G	G G	G	C T	G (G A	G	T G	A	G T	A	G T	A	G A	T
	T G A G C T (
														and the same													
HUM:																											
UAM:	A T A C A G	G T	G A	T G G	A A	A G	T C	A G	A	A	T G	Τ	T A	T G	С	C C	A A	A T	C	Γ G	T	G A	A	G A	G	C A	Α
ним.	A T T C A C	AT	C T (C C A	Α Δ	A G	Α Α	Α Α	Т (: C	C A	Δ	G A	A C	Т	C A	C '	r G	Т	А Т	Т	T G	С	Α Α	Α	r G	Α
	A T T C A C																										
HUM:	A C A G T C	G A	G A	G <mark>C</mark> A	G A	A G	G G	C A	C	A G	C T	G	T G	T G	Т	T A	C	r G	T	A T	G	T G	A	G G	C	A	
UAM:	A C A G T C 1	G A	G A	G <mark>C</mark> A	G A	A G	G G	C A	C A	A G	C T	G	T G	T G	Т	T A	C	G G	Τ.	A T	G	T G	A	G G	C	A	
D.=																											
D7	C C A G G T																										
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OAII.	C C A G G I	1																									
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HUM:																											
UAM:	G A C A C A C	TT	T C																								
47:		M1. 00		T1. ^	10	1. ^	, , , ,	71. /	`																		
_	nment stats: '								J																		

IGHV(II)-30-21

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GENE ALIGN SEQ
HUM: T C A C A G A C C C T C T C C C T C A C C T G C A C T G T C T C T G C A T C A T A A C
UAM: T C A C A G A C C C T C T C C C T C A C C T G C A C T G T C T C T G G A T
                                                             TCCCCATCA
HUM: CAGTGTTTCCTAGAATTGTATCTTAGAATTGGTATCTTGCTAGCCCCTAGAAATTGGAGA
HUM: A G T G G A T C A G G T G C A T G G G T T G T G A A G G G A G C A A A T T A C A A C C C A C T T
UAM: A G T G G A T C A G G T G C A T G G G T T G T G A A G G G A G C A A A T
HUM: C T C A A G A G T C C A T A T C C G G A T C C A A G A A C A G T T C T T A C A G C T G A G C T C T
UAM: C T C A A G A G T C C A T A T C C G G A T C C A A G A A C A G T T C T T A C A G C T G A G C T C T
UAM: G T G C C C A G T G A A C A C A C A C A C A C A A C T A C G C A T T T T G A A G C A A A A G A T G C A A T G A A
HUM: G G G C C T T
UAM: G G G C C T T
D7
HUM:
UAM:
D9
HUM: C A G G G G T G A A
UAM: C A G G G G T G A A T
Alignment stats: 'M': 257, 'I': 0, 'D': 0, 'X': 0
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IGHV4-30-2

GENE ALIGN SEQ HUM: CAGCTGCAGCTGCAGGAGTCCGGCTCAGGGCTGAAGCCTTCACAAGAC CTGCAGGAGTCCGGCTCAGGACTGGTGAAGCCTTCACAGAC HUM: CCTGTCCCTCACCTGCGCTCTCTCTCTCTCCTGCTCTCACCACCAGTGGTT HUM: A C T C C T G G A G C T G G A T C C G G C A G C C A G G G A A G G G C C T G G A G T G G A T T UAM: A C T C C T G G A G C T G G A T C C G G C A G C C A G G G A A G G G C C T G G A G T G G A T T HUM: G G G T A C A T C T A T C A T A G T G G G A G C A C C T A C T A C A C C G T C C T C A A G A G A G A G A G UAM: G G G T A C A T C T A T C A T A G T G G A G C A C C T A C T A C A A C C C G T C C T C A A G A G A G HUM: T C G A G T C A C C A T A T C A G T A G A C A G G T C C A A G A A C C A G T T C T C C C T G A A G C UAM: T C G A G T C A C C A T A T C A G T A G A C A G A A C C A G T T C T C C C T G A A G C UAM: T G A G C T C T G T G A C C G C C G C G G G C C G T G T A T T A C T G T G C C A G A G A D7HUM: C A C A A T G UAM: CACAATG D9HUM: GACACAAACCT UAM: GACACAAACCT Alignment stats: 'M': 299, 'I': 0, 'D': 0, 'X': 0

IGHV3-30-2

GENE ALIGN SEQ	
HUM: GAGG <mark>TACAGCTCGTGGAGTCCGT</mark> CGTGAGGAG <mark>TCCG</mark> GAAGACCCAAGA <mark>CCT</mark> GGG	
UAM: GAGG <mark>TACAGCTCGTGGAGTCCGGAGGAGAGGACCCAAGACCT</mark> GGG	G G A T C
HUM: C C T G A G A C T C T C T G T G T G T G T G T G T A G A C T T A A C C T T C A G T A G C T A	C T G A A
UAM: C C T G A G A C T C T C T G T G C A G A C T C T A G C A C T C T A G C T T C A G T A G C T A	
HUM: G G A A C T C G G T T T C C C A G G C T C C A G G G G A A G G G G C T G G A G T G A G T A G	
UAM: G G A A C T C G G T T T C C C A G G C T C C A G G G A A G G G G T G A G T A G	
HUM: A T A C A G T G T G A T G G A A G T C A G A T A T G T T A T G C A T A A T C T T T G A A G	
UAM: A T A C A G T G T G A T G G A A G T C A G A T A T G T T A T G C A T A A T C T T T G A A G	
HUM: A T T C A C C A T C T C A A A G A A A T G C A A A G T G C C A A G A A C T C A C T G T A T T T G C T	
UAM: A T T C A C C A T C T C C A A A G A A A A T G C C A A G A A C T C A C T G T A T T T G C T	
HUM: A C A G T C T G A G C A G C G G G C A C A G C T G T G T A C T G T A T G T G A G C A G	
UAM: A C A G T C T G A G A G C A G C G G G C A C A G C T G T G T A C T G T A T G T G A G	G C A
D7	
HUM: CCAGGTA	
UAM: CCAGGTA	
D9	
HUM: GACAGTTTCC UAM: GACAGTTTCC	
Alignment stats: 'M': 298, 'I': 0, 'D': 0, 'X': 0	
Both human gene and its mapping are pseudogenes	

IGHV(II)-30-1

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GENE ALIGN SEQ
HUM: A A C A A C T G T A T T T C T C G G T G C A C T C T T G G C C T G G T G A A G C C T T C A C A G A A
                                          CCTGGTGAAGCCTTCACAGAA
UAM: CCTCTCCCTCACCTGTGCCATCTCTCTCTCTCATCACAACCAGTGTTT
UAM: CCTTCTGGAGCTG
                    CATCCATCAGCGCCCCATGGAGTACTGGAGTGGA
   HUM:
   T C G G G T G C A T A G G T C A T G G A G G G A G C A C A A A T T A C T C C C C T C T
HUM: A G T C C A G T C A C C A T C T C C A G A T C C A T G T C C A A A A A G T A G T T C T T C T T A C A
UAM: A G T C C A G T C A C C A T C T C C A G A T C C A T G T C C A A A A A G T A G T T C T T C T T A C A
   G C T G A A C T A T G T G A G G A A C A A A C A C A T A G C C A T G T A T T T T A G A G C A A A G
UAM: G C T G A A C T A T G T G A G G A A C A A A C A A A C A A G C C A T A G T A T T T A G A G C A A A A G
HUM: A
UAM: A
D7
HUM:
   C A C A G T G
UAM:
D9
HUM: T A C C C A A G C C T
UAM: TACCCAAGCCT
Alignment stats: 'M': 301, 'I': 0, 'D': 0, 'X': 0
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HUM: CAGG <mark>TGCAGCT</mark> GG <mark>TGGAGTCT</mark> GGAG <mark>TCT</mark> GGGGGGG <mark>TGG<mark>T</mark>GG<mark>TCCAGCCT</mark>GGGAGG<mark>T</mark>C</mark>
UAM: CAGGTGAGCTGAGTGAGTGAGTGAGTGAGTGAGTGAGGGGGAGG <mark>TGGTGGTGGTGGTGGGTG</mark>
HUM: CCTGAGACTCTCACTGCTGCAGCATCACACCTTCACACCTTCACACCTAGGCATAGCCA
UAM: C C T G A G A C T C T C T G T G C A G C C T C T C T G A G C A G C A C C T C A C C T T C A G T A G C T A T G G C A
HUM: T G C A C T G G G T C C G C C A G G C T C C A G G C T G G G G C T G G A G T G G G T G G C A G T T
UAM: T G C A C T G G G T C C G C C A G G C T C C A G G C T G G G G C T G G A G T G G G T G G C A G T T
HUM: A T A T C A T A T G A A G T A A T A A T A A T A A T A A T A A T A A T A A T A C T A T G C A G A C T C C G T G A A G G G C C G UAM: A T A T A T A T A T A T A T A T A T A
OAM. A TATO A TATO A TO GAAGTAATAA TACTATO CAGACTO COTO A A GGO CO
HUM: A T T C A C C A T C T C C A G A G A C A A T T C C A A G A A C A C G C T G T A T C T G C A A A T G A
UAM: A T T C A C C A T C T C A G A G A G A T C T A G A G A G A C A A T T C C A A G A A C A C G C T G T A T C T G C A A A T G A
HUM: A C A G C C T G A G C T G A G G A G C T G A G G A C A C G G C T G T G T A T T A C T G T G C G A A A G A
UAM: A C A G C C T G A G C T G A G G A C A C G G C T G T G T G T G T A T T A C T G T G C G A A A G A
D7
HUM: CACAGTG
UAM: CACAGTG
D9
HUM: G A C A A A C C T
UAM: GACAACT
Alignment stats: 'M': 296, 'I': 0, 'D': 0, 'X': 0
Neither human gene nor its mapping is pseudogene

GENE ALIGN SEQ. HUM: GAGGTGGAGCTGATAGAGCCCACAGAGAGGCCTGAGACCTGGGGAAG<mark>TT</mark> UAM: GAGGTGGAGCTGATAGAGCCCACAGAGGGC<mark>T</mark>GAGACCTGGGGAAGTT HUM: CCTGAGACTCTCTGTGTGTAGCCTCTAGAGACTTCAGACTTCAGAATTC UAM: C C T G A G A C T C T C T G T G T G T G T A G C C T C T C T A G C C T C T A G A T T C G C C T T C A G T A G C T T C T A A HUM: TGAGCCCAGTTCACAGTCAGCAGTCAGCAGTCAGCAGGCAAGGTAAAT UAM: TGAGCCCAGTTCACAGTCAGCAGTCAGCAAGGCAAGGGCAAGTAA HUM: A T A A A A G A T G A T G G A A G T C A G A T A C A C C A T G C A G A C T C T G T G A A G G G C A G UAM: A T A A A A G A T G A T G G A A G T C A G A T A C A T C A G A T G C A G A C T C T G T G A A G G G C A G HUM: A T T C T C C A T C T C C A A A G A C A A T G C T A A G A A C T C T C T G T A T C T G C A A A T G A UAM: A T T C T C C A T C T C C A A A G A C A A T G C T A A G A A C T C T C T G T A T C T G C A A A T G A HUM: A C A G T C A G A G A A C T G A G G A C A T G G C T G T G T A T G G C T G T A C A T A A G G T T D7HUM: C C A A G T G UAM: C C A A G T G D9HUM: G A C A C A A A A T T UAM: G A C A C A A A A T T Alignment stats: 'M': 297, 'I': 0, 'D': 0, 'X': 1

IGHV(II)-28-1

GENE ALIGN SEQ
HUM: CAACAACTATGTTTCTCAGCACACTTCTGAGCACTTCAGACTTCCTGAGACGTCCTTGAAACG
JAM: CAACAACTATGTTTCTCAGCACTTCTCAGCACTTCAGCTTCAGAGACGTCCTTGAGACG
HUM: CCTCTCTCTCACCTCACTCACTTCTTCTCTCTCTCTCTC
JAM: CCTCTCTCACCTCACCTGCACTGTCTCTCCCCATCATAACCAGTGTTT
HUM: CCTGCTGCTAGAATTGTATGCTATGCTGCTTAGCAAGAAAAAAAA
JAM: CCTGCTAAATTGTATCTGCTAACATTGAATCTGCTAAAAAAAA
HUM: A G G T G C A T G G G T T G T A A G G G A G C A C A C A A C C C A C T G C T A A G A G A G A G C A C A C T C A A G A G A G A G A G A G A G A G A G
JAM: A G G T G C A T G G G T T G T G A A G G G A G C A C A A A T T A C A A C C C A C T G C T C A A G A G
HUM: TCCATATATCCAGAGATCAAGAAGAAGAAGAATCAGTTTCTTACACAGCTGAGCTCTGTGAGCCCAG
JAM: TCCATACAAAACAACTTACAAGAAACAACTTACTTACAAGCAGCTGAG
HUM: TGAACACACAACTACACTACACTACACTACACACTACACACACAACA
JAM: TGAACACAACAACTACAACTACATTATTAAGCAAAAGA
D7
HUM: C G C A A T G
JAM: CGCAATG
D9
HUM: GACACACCT
JAM: GACACAC <mark>T</mark>
Alignment stats: 'M': 282, 'I': 0, 'D': 0, 'X': 1
Soth human gene and its mapping are pseudogenes

IGHV4-28

GENE ALIGN SEQ
HUM: CAGGTACAGCTGAGCAGGAGGAGTCAGGAGGAGTCAGGAGGACAGGAGGAGAAGCCAAGGAAG
UAM: CAGGTACAGCAGGAGGAGTCGGGGCCCAGGACTGGAAGCCTTGGAAGCCTTCGACACAC
HUM: CCTGTGTCCTTCACTTCTTTTTTTTTTTTTTTTTTTTTT
UAM: CCTGTCCTCACCTCACCTGCCTCTCTCTCTCTCTCCTCACCACCAGTAGTAACT
HUM: G G T G G G G C T G G A T C C G G C A G C C C C A G G G A A G G G A C T G G A G T T G G A T T G G G
UAM: G G T G G G C T G G A T C C G G C A G C C C C A G G G A A G G G A C T G G A G T G G A G T T G G G
HUM: TACATOTATATATATATATATATATATATATATATATATA
UAM: TACATCTATATAGTGGGGAGCACTACTACCGTCCCTCAAGACCCCGTCAAGACC
HUM: A G T C A C C A T G T C A G T A G A C A C G T C C A A G T C C A G T T C T C C T G A A G C T G A
UAM: A G T C A C C A T G T C A G T A G A C A C G T C C A A G A A C C A G T T C T C C C T G A A G C T G A
HUM: GCTCTGTGTGACCGCCGTCCGTGGGACCGTGGGGCCGTGGCCGTGTGTATTACTTGCCGAAAA
UAM: GCTCTGTGACCGCGTGGACACGTGGTACACGTTTTACTGTGAAA
HUM: C A C A G T G UAM: C A C A G T G
D9
HUM: GACACACT
UAM: GACACCT
Alignment stats: 'M': 296, 'I': 0, 'D': 0, 'X': 0
Neither human gene nor its mapping is pseudogene

IGHV7-27

GENE ALIGN SEQ	
HUM: CAGG <mark>TGCAGCTGGTGCAGCTGCCT</mark> GGG <mark>CCT</mark> GGG <mark>CCT</mark> GAG <mark>TCAGGCCT</mark>	
UAM: CAGGTGAGCAGCTGAGTGAGCAGTCTGAGAGAGAGCTT	C
HUM: A T T G A A G G T T T C C T G C A A G G C T T C T G G A T A C A C C T T C A C A A G C T A T G C T	Δ
UAM: A T T G A A G G T T T C C T G C A A G G C T T C T G G A T A C A C C T T C A C A A G C T A T G C T	A
HUM: TCAGCTGGGTACACAT	
UAM: TCAGCTGGGTACAGCAGGCCCATGGACAAGGGCCTTGAAATGGAGAAATGGAAAT	G
	α
HUM: A T C A A C A C C A A C A C T G G G A A C T A C T G G G A C C T A A C G T A T G C C C A G G G T T C A C A G G A C UAM: A T C A A C A C A C A C A C A C A C A C	
	G
HUM: G T T T G T C T T C T C C A T G G A C A C C T C C G T C A G C A T G G C A T A T C T T C A T A T C	Α
	Α
HUM: G C A G C T A A A G G C T G A G G A C A C G T G A G G A C A C G T G C A A G A G G	
UAM: G C A G C C T A A A G G C T G A G G A C A C G T G A G A G A G G	
D7	
HUM: CACAGTG	
UAM: CACAGTG	
D9	
HUM: A C C A G A A A T C C	
UAM: A C C A G A A A T C C	
Alignment stats: 'M': 282, 'I': 0, 'D': 0, 'X': 0	
Both human gene and its mapping are pseudogenes	

IGHV(II)-26-2

GENE ALIGN SEQ
HUM: CAGGTGAGAGCAGAGAAGAAAAAAAAAAAAAAAAAAAAA
UAM: C A G G T G C A G C T G C A G G T C A G G T C A G G T C A G G T C C A G G A C C C A T G A G G C C C T C A G A C A C
HUM: T G C C C T C T G C C T G T G T G T T G T G
UAM: TGCCCTCTGTGTGTTTTTTTTACCATGATA
HUM: TTTGAGAGAA <mark>TGAATCCACACC</mark> A <mark>TCCCGT</mark> CCACCACCACCGTGTGGGCAACAGGCTGGAA <mark>T</mark> GG <mark>CT</mark> GGGG <mark>C</mark>
UAM: TTTGAGAATGAA <mark>TCCACCGTCCGCGTGGGAACACAGGCT</mark> GGAA <mark>TCCCC</mark> C
HUM: A C A G T T A C T A G A C T G G A T C A T C A A G G A A T A C A C A T C A T G C A C C T C C A C C
UAM: A C A G T T A C T A G A C T G G A T C A T C A T C A T C A T C A A G G A A T C A T C A T C A T C A T C A T C A T C A T C A T C A T C A T C A T C A T C A T C A T C C T C C A C C
HUM: CAGGTCCATGTCAACAGTCAACAGTCAACAGTCAAGAGAGTTCTTTT
UAM: CAGGTCCATGTCCCCATCAACAGTGACTCAACCAAGTTCTCTCTGT
HUM: G A A G C T C A G C T C A T G A C C A T G A C C A C C T A G G A C G G C T G A G T A T T A C T G T G A A A
UAM: GAAG <mark>CTCAGTCAGTCAT</mark> GACCATGACCATGAGGGAGGTAGGAGTAGAAA
HUM: G A
UAM: GA
D7 HUM: CTCAGTG
UAM: C T C A G T G
D9
HUM: GACAAACCT UAM: GACAAACCT
Only of the orange of the oran
Alignment stats: 'M': 302, 'I': 0, 'D': 0, 'X': 0

Both human gene and its mapping are pseudogenes

IGHV(III)-26-1

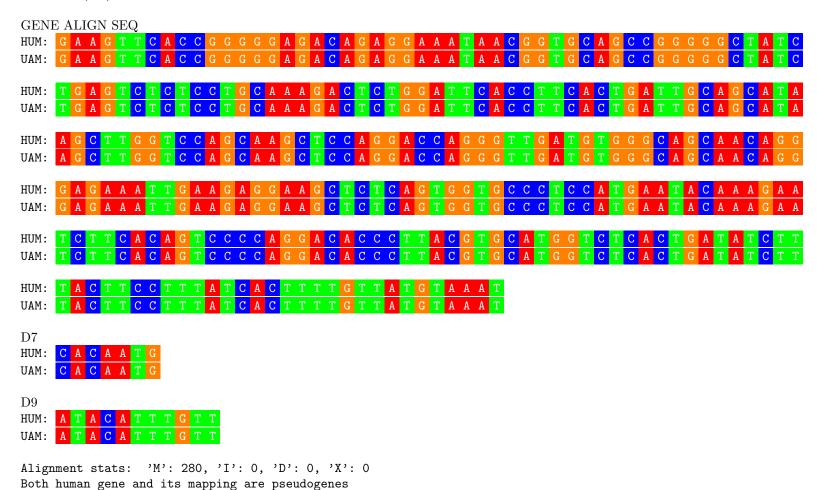
GENE ALIGN SEQ
HUM: G A T G T T T A C T G A T G G A G T C A G A A G A A A A A A A T T T A A C A G C C C A G C A G T T
UAM: G A T G T T T A C T G A T G G A G T C A G A A G G A A A A A A T T T A A C A G C C C A G C A G T T
HUM: CACTGAGAGACTGAAGCCACTGAAAGCCTCTCTCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCT
UAM: CACTGAGAGACTGTGAAAGCCTCTCTGGTGGTTTTCGGGTTTTACTGGGGTGCAGC
HUM: A T G A G C T T G G T C C A G C A C T T C A C A G C A C T T C A C A A C A G G A A T T G G T G G G T A G C A A C
UAM: A T G A G C T T G G T C C A G C A C A C T T C A C A A C A G G A A T T G G T G G T A G C A A C
HUM: A G T G A G A G A T C A T A T G G G A G T T A A G G G T T A C T C T A G G A T G A G T A C A G A T G A G T A C A G A T
UAM: A G T G A G A T C A T A T G G G A G T T C T A A G G G T T A C T C C A T G A G T A C A G A T
HUM: A A A T C A A C A T T C C C A A G T G A C C C T T T C A A G T G C A G T C T A C C T T A C A A G
UAM: A A A T C A A C A T T C C C A A G T G A C C C T T T C A A G T G C A G T C T A C C T T A C A A G
HUM: G A C C A A C C T G A A A G C C A A G C C A A G G G C A A G G G C C A A G G C C G T A T A T A C A G T G A G G G A
UAM: G A C C A A C C T G A A A G C C A A G G G C A A G G G C C G T A T A T A C A G T G A G G G A
D7
HUM: C A C A G G G
UAM: CACAGGG
D9
HUM: A G A C A C A A A A A
UAM: A G A C A C A A A A A
Alignment stats: 'M': 296, 'I': 0, 'D': 0, 'X': 0
Both human gene and its mapping are pseudogenes

IGHV2-26

```
GENE ALIGN SEQ
HUM: CAGGTCACCTTGAAGGAGTCTGGTCCTGTGTGTGCTGAAACCCAAGAGAGAC
UAM: CAGGTCACCTTGAAGGAGTCTGGTCTGGTGCTGGTGAAACCCAACAGAGACA
UAM: C C T C A C G C T G A C C T G C A C C T G C A C C G T C T C T C T C T C T C T C A C T C A G C A A T G C T A G A A
HUM: TGGGTGTGAGGTGAGGTGAGTGGATCCGTCAAGGCCCCAAGGGAAGGCCCTGGAAGTGGCTT
UAM: T G G G T G T G A G C T G G A T C C G T C A G C C C C A G G G A A G G C C C T G G A G T G G C T T
    CACACAGATTTTTCGAATGAAAAAATCCTACAGCAATCTGAAGAAGAGA
    HUM: CAGGCTCACCATCTCAAGGACAAGGACACCTAAAAGCCAGGTGGTTACCA
UAM: CAGGCTCACCATCTACCAAGGACACCAAAAAGCCAAGGTGCTAACCA
HUM: TGACCAACATGGACCCTTGTGGACACACATATTACTGTGGATA
UAM: T G A C C A A C A T G G A C C C T G T G G A C A C A G C C A C A T A T T A C T G T G C A C G G A T A
HUM: C
UAM: C
D7
HUM:
  C A C A G A G
UAM:
D9
HUM: T A C A A G A A C C T
UAM: TACAAGAACCT
Alignment stats: 'M': 301, 'I': 0, 'D': 0, 'X': 0
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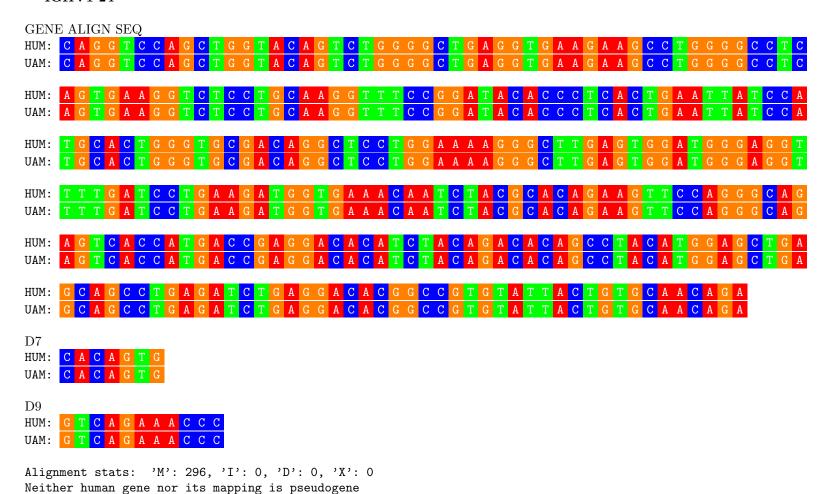
Neither human gene nor its mapping is pseudogene

IGHV(III)-25-1



GENE ALIGN SEQ	
HUM: GAGAGATGCAGCTGAGTGGAGTGGAGTGGAGGGGGGGGGG	
UAM: G A G A T G C A G C T G G T G G A G T C T G G G G G G G G G G G G G G G G	G T C
HUM: C C C G A G A C T C T C T G T G C A G C C T C T C A A T T C A C C T T C A G T A G C T A C T	A C A
UAM: C C C G A G A C T C T C T G T G C A G C C T C T C A G T C T C A G T A G C T A C T C A G T A G C T A C T C T C A G T A G C T A C T C T C A G T A G C T A C T C T C A G T A G C T A C T C T C A G T A C T C T C T C T C T C T C T C T C T	A C A
HUM: T G A A C T G T G T C C G C C A G G C T C C A G G G A A T G G G C T G G A G T T G G T T G G A G T T G G T T G G A G T T G G T T G G A G T T G G T T G G A G T T G G T T G G A G T T G G T T G G T T G G A G T T G G T T G G A G T T G G T T G G A G T T G G T T G G A G T T G G T T G G A G T T G G T T G G A G T T G G T T G G T T G G A G T T G G T T G G A G T T G T T G G T T G T T G G T T G T T G G T T G T T G T T G T T G T T G T T G T T G T T G T T G T T G T T G T T G T T G T T G T T G T T G T T G T T T G T T T G T T T G T T G T T T G T T T G T T T G T T T G T T T G T T T G T T T G T T T G T T T G T T T G T T T G T T T G T T T T G T T T T G T T T T G T T T T G T	C A A
UAM: T G A A C T G T G T C C G C C A G G C T C C A G G G G A A T G G G C T G G A G T T G G A G T T T G A	C A A
HUM: G T T A A T C C T A A T G G G G G T A G C A C A T A C C T C A T A G A C T C C G G T A A G G G	C C G
UAM: G T T A A T C C T A A T G G G G G T A G C A C A T A C C T C A T A G A C T C C G G T A A G G A	
HUM: A T T C A A T A C C T C C A G A G A T A A C G C C A A G A C A C A C T T C A T C T G C A A A	
UAM: A TTCAATCAATACCTCAAAAACAACAACACACTCATCAAAAAA	T G A
HUM: A C A G C C T G A A A A C C G A G G A C A C G G C C T G T A T T A G T G T A C C A G A G A	
UAM: A C A G C C T G A A A A C C G A G G A C A C G G C C T C T A T T A G T G T A C C A G A G A	
HUM: C A C A G T G UAM: C A C A G T G	
UAII. C R C R G I G	
D9	
HUM: GACAAACCT	
UAM: G A C A A A C C T	
Alignment stats: 'M': 294, 'I': 0, 'D': 0, 'X': 2	
Both human gene and its mapping are pseudogenes	

IGHV1-24



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GENE ALIGN SEQ.
HUM: GAGGTGCAGCTGGAGTCTGGGGGGGGGGTC
                 CTGTTGGAGTCTGGGGGGAGG<mark>CTTGGTACAGCCT</mark>GGGGGG<mark>T</mark>C
HUM: CCTGAGACTCTCTGTGCAGCTTCTAGCAGCCTCAGCAGCTATGCACCTTTAGGAGCTATGCA
UAM: C C T G A G A C T C T C T G T C T C T G T C T G T G C A G C C T C T C T G A C C T T T A G C A G C T A T G C A
HUM: TGAGCTGGGTCAGGCTCAGGCTCAGGGAAGGGCTCAGGCTCAGGGAAGGTGGGTCAGGCT
UAM: TGAGCTGGGTCCAGGCTCAAGGGAAGGGGCTGAAGGGAAGTGGGTCTCAAG
HUM: A T T A G T G G T A G T G G T G G T A G C A G A C A T A C T A C G C A G A C T C C G T G A A G G G C C G
UAM: A T T A G T G G T A G T G G T A G T G G T A G C A C A T A C T A C G C A G A C T C C G T G A A G G G C C G
HUM: G T T C A C C A T C T C C A G A G A C A A T T C C A A G A A C A C G C T G T A T C T G C A A A T G A
UAM: G T T C A C C A T C T C C A G A G A C A A T T C C A A G A A C A C G C T G T A T C T G C A A A T G A
HUM: A C A G C C T G A G A G C C G A G G A C A C G G C C G T A T A T T A C T G T G C G A A A G A
D7
HUM: C A C A G T G
UAM:
D9
HUM: GACACAAACCT
UAM: GACACAAACCT
Alignment stats: 'M': 295, 'I': 0, 'D': 0, 'X': 1
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Neither human gene nor its mapping is pseudogene

IGHV(III)-22-2

GENE ALIGN SEQ

D7

HUM: A C A A G A G UAM: A C A A G A G

D9

HUM: G G G T G A G G T G

UAM: G G G T G A G G T G

Alignment stats: 'M': 30, 'I': 0, 'D': 0, 'X': 0 Neither human gene nor its mapping is pseudogene

IGHV(II)-22-1

GENE ALIGN SEQ
HUM: G G C C T G G T G A A G C C C T C A C A G A T C C C C C C C C C C T G T G C C A T C T C C C C C C C C C C C C C C
UAM: G G C C T G G T G A A G C C C T C A C A G A T C C C C C T G C C C T G T G C A T C T G C
HUM: TTCTCCATTACAACCAGTGCTTCCTGCAGCTGGAGCTGGATCCGTCACCCCC
UAM: TTCTCTCATACATACATACATACATACATACATACATAC
HUM: G G G G A A G G G A <mark>C T</mark> G G A G <mark>C</mark> G A A <mark>T C</mark> A G G <mark>T G C A C A G G T C A <mark>T</mark> G A G G G A G <mark>T</mark> G C A <mark>C</mark> A</mark>
UAM: G G G G A A G G G A C T G G A G C G A A T C A G G T G C A C A G G T C A T G A G G G G A G T G C A C A
HUM: A T C C A A C C C A C T C C T C A A G A G T C C A G T C A G T C C A G T C A G T C A G A T C C A G A T C C A C A T C A C A T C A C A T C A T C C A C A
OAM. A I C C A A C C C A C I C C A G A G A G I C A G I C A I C I C A G A I C C A I C C
HUM: A A A A A C A G T T T C T C C T A C A G C T G A G C T A C C T T A C A A C A A G G A G T A C A A C C
UAM: A A A A A C A G T T T C T C C T A C A G C T G A G C T A C C T T A A C A A G G A G T A C A A C C
HUM: A T G A T T T T A T A C A A A A G A
UAM: A T G A T T T T A T A C A A A A G A
D7
HUM: CACAGCG
UAM: C A C C G
D9
HUM: GAACT ACTACT
UAM: GAACACT ACTAC
Alignment stats: 'M': 269, 'I': 0, 'D': 0, 'X': 0

Both human gene and its mapping are pseudogenes

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GENE ALIGN SEQ.
HUM: GAGGTGCAGCTGGAGTCTGGGGGGGGGGTC
                  CTGGTGGAGTCTGGGGGGTCTTGGTACAGCCTGGGGGGT
UAM: C C T G A G A C T C T C T G T G C T G T G T G T G A G C C T C T C T C T C T C T C A C C T T C A C C T T C A C T A C T A C T A C T A C A
HUM: TGAGGGGGTCCGGCCAGGCTCCGGGAAGGGCTCCGGGGAAGGGCTGGGAATGGGGTAAGGGTTTC
UAM: T G A G C G G G T C C G C C A G G C T C C C G G G A A G G G C T G G A A T G G G T A G G T T T C
HUM: A T T A G A A A C A A A G C T A A T G G T G G G A C A A C A G A A T A G A C C A C G T C T G T G A A
UAM: A T T A G A A A C A A A G C T A A T G G T G G G A C A A C A G A A T A G A C C A C G T C T G T G A A
HUM: A G G C A G A T T C A C A A T C T C A G A G A T G A T T C C A A A A G C A T C A C C T A T C T G
UAM: A G G C A G A T T C A C A A T C T C A A G A G A T T C C A A A A G C A T C A C C T A T C T G C
HUM: A A A T G A A G A G C C T G A A A A C C G A G G A C A C G G C C G T G T A T T A C T G T T C C A G A
UAM: A A A T G A A G A G C C T G A A A C C G A G G A C A C G G C C G T G T A T T A C T G T T C C A G A
HUM:
UAM:
D7
HUM:
   C A C A G T G
UAM:
D9
HUM: G A C A C A A A C C T
UAM: GACAGAAACCT
Alignment stats: 'M': 302, 'I': 0, 'D': 0, 'X': 0
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Both human gene and its mapping are pseudogenes

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GENE ALIGN SEQ.
HUM: GAGGTGCAGCTGGAGTCTGGGGGGGGGGGTC
               CTGGTGGAGTCTGGGGGGG<mark>CCT</mark>GGT<mark>CAAGCCT</mark>GGGGGG<mark>T</mark>C
UAM: C C T G A G A C T C T C T G T G C A G C C T C T C A G C A G C C A C C T C A C C T T C A G T A G C T A T A G C A
UAM: TGAACTGGGTCCAGGCTCAAGGGAAGGGGAAGTGGGAAGTCATCA
HUM: A T T A G T A G T A G T A G T A G T T A G T T A C A T A T A C T A C G C A G A C T C A G T G A A G G G C C G
UAM: A T T A G T A G T A G T A G T A G T A G T T A C A T A T A C T A C G C A G A C T C A G T G A A G G G C C G
HUM: A T T C A C C A T C T C C A G A G A C A C G C C A A G A A C T C A C T G T A T C T G C A A A T G A
UAM: A T T C A C C A T C T C C A G A G A C A A C G C C A A G A A C T C A C T G T A T C T G C A A A T G A
HUM: A C A G C C T G A G A G C C G A G G A C A C G G C T G T G T A T T A C T G T G C G A G A G A
D7
HUM: C A C A G T G
D9
HUM: GACACAAACCT
UAM: GACACAAACCT
Alignment stats: 'M': 296, 'I': 0, 'D': 0, 'X': 0
```

Neither human gene nor its mapping is pseudogene

GENE ALIGN SEQ
HUM: GAGG <mark>TGAGGT</mark> GGAG <mark>CTGGAGGTGGAGGGGGGGGGGTGTGTACGGGGG</mark>
UAM: GAGGTGAGCAGCTGAGTGGAGTGGAGTGGAGGGGGGGGGG
HUM: CCTGAGACTCTCTTGCAGCCTTCTGGATTGATGATTGGCA
UAM: CCTGAGACTCTCTTGAGCAGCCTCTGGATTCACCTTTTGATGATTATGGCA
HUM: T G A G C T G G G T C C G C C A A G C T C C A G G G G G G C T G G A G T G G G T C T C T G G T
UAM: T G A G C T G G G T C C G C C A A G C T C C A G G G G G G G C T G G A G T G G G T C T C T G G T
HUM: A T T A A T T G G A A T G G T G G T A G C A G G T T A T G C A G A C T C T G T G A A G G G C C G
UAM: A T T A A T T G G A A T G G T G G T A G C A G G T T A T G C A G A C T C T G T G A A G G G C C G
HUM: A T T C A C C A T C T C C A G A G A C A A C G C C A A G A A C T C C T G T A T C T G C A A A T G A
UAM: A T T C A C C A T C T C C A G A G A C A A C G C C A A G A A C T C C T G T A T C T G C A A A T G A
HUM: A C A G T C T G A G A G C C G A G G A C A C G G C C T T G T A T C A C T G T G C G A G A G A
UAM: A C A G T C T G A G A G C C G A G G A C A C G G C C T T G T A T C A C T G T G C G A G A G A
D7
HUM: CACAGTG
UAM: C A C A G T G
D9
HUM: GACAAACGT
UAM: GACACACGT
Alignment stats: 'M': 295, 'I': 0, 'D': 0, 'X': 1
Neither human gene nor its mapping is pseudogene

GENE ALIGN SEQ
HUM: A C A G T G C A G C T G G T G G T G G T G G T G G T G G T G
UAM: A C A G T G C A G C T G G T G G A G T C T G G G G G G G G G T T G G T A G A G C C T G G G G G T C
HUM: C C T G A G A C T C T G T G T G C A G C T C T G T A G C A C C T C T C A C C T T C A G T A A C A G T G A C A
UAM: C C T G A G A C T C T C T G T G C A G C A G C A G C C T C T G A G C A G C A C C T T C A G T A A C A G T G A C A
HUM: TGAACTGGG <mark>TCCGCCAGGCTA</mark> GGCT <mark>CCAGGGAAAGGGGCTGGAGTGGGTATC</mark> GGG <mark>T</mark>
UAM: TGAACTGGGTCCAGCCAGCCACGCACGCACCACCACCACCACCACCACCA
HUM: G T T A G T T G G A A T G G C A G T A G G A C G C A C T A T G C A G A C T C T G T G A A G G G C C G
UAM: G T T A G T T G G A A T G G C A G T A G G A C G C A C T A T G C A G T C T G T G A A G G G C C G
HUM: A T T C A T C A T C T C C A G A G A C A A T T C C A G G A A C T T C C T G T A T C A G C A A A T G A
UAM: A T T C A T C A T C T C C A G A G A C A A T T C C A G G A A C T T C C T G T A T C A G C A A A T G A
HUM: A C A G C C T G A G G C C C G A G G A C A T G G C T G T A T T A C T G T G T G A G A A A UAM: A C A G C C T G A G G C C C G A G G A C A T G G C T G T G T A T T A C T G T G T G A G A A A
D7 HUM: CACTGTG
UAM: C A C T G T G
D9 HUM: <mark>G A C A A A C C T</mark>
UAM: GACAAACCT
Alignment stats: 'M': 296, 'I': 0, 'D': 0, 'X': 0
Neither human gene nor its mapping is pseudogene

IGHV1-18

GENE ALIGN SEQ
HUM: CAGGTTCAGCTGAGTGAGTGAGTCTGAGTCTGAGGTGAGGTGAAGAAGAAGCATGAAG
UAM: CAGGTTCAGCTGATGATGATGATA
HUM: A G T G A A G G T C T C C T G C A A G G C T T C T G G T T A C A C C T T T A C C A G C T A C G G T A
UAM: A G T G A A G G T C T C C T G C A A G G C T T C T G C A A G G C T T C T G G T T A C A C C T T T A C C A G C T A T G G T A
HUM: TCAGCTGGGTGGCACAGGCCCCTGGACAAGGGCCTTGGAAGGGCTTGAAGGGGCTTGGAGTGGAATGG
UAM: TCAGCTGGGTGCGACAGGCCCCTGGACAAGGGC <mark>TT</mark> GAG <mark>TGGAT</mark> GGA
HUM: A T C A G C G C T T A C A A T G G T A A C A A C A C A A T G G C A A A C A C A A A C T A T G C A G A A G C T C C A G G G C A G UAM: A T C A G C A G C A G A A G C T C C A G G G C A G
OAM. RICAGOGOTTA CARIGOTA A CACA A A CIATOTA I GOA CAGA A A GOI COA GAGA GAGA GAGA GAGA GAGA GAGA GAGA
HUM: A G T C A C C A T G A C C A C A G A C A C A T C C A C A G C A C A G C T A C A T G G A G C T A A
UAM: A G T C A C C A T G A C C A C A G A C A C A C A C A G A A C A A C A A C A C
HUM: GGAG <mark>CCTGAGAGACGACGGCGCCGTGTATTACTGCGAGAGA</mark>
UAM: G G A G C C T G A G A T C T G A C A C G C G C C G T G T A T T A C T G T G C A G A G A
D7
HUM: CACAGTG
UAM: C A C A G T G
D9
HUM: TTCAGAAACCC
UAM: TTCAGACCC
Alignment stats: 'M': 295, 'I': 0, 'D': 0, 'X': 1
Neither human gene nor its mapping is pseudogene

IGHV1-17

GENE ALIGN SEQ
HUM: CAGGTTCAGCAGCTGAGCAGCTGAGCAGCTGAGCAGCTGAGCAGAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAA
UAM: C A G G T T C A G C T G T T G C A G C T G T T G C A G C T G G G G C T G A G G T G A A G A A G C C T G C T C
HUM: A G T G A A G G T C T C C T G C C A G G C T T C C A G A G C T T C C A G A C C T T C A C C A A A T A C T T T A
UAM: A G T G A A G G T C T C C T G C C A G G C T T C C A G A T A C A C C T T C A A A T A C T T T A
HUM: C A C A G T G G T T G C A C A G T G C A C A C A C A C A C A C A C A C A C
UAM: CACAGTGGGACAGACAGGGCCTGGAAGGGGCCTTGGAAGGGGTTGGGATGCA
HUM: TCAACCCTTACATACATACATAACAATAACAATAAAAAAA
UAM: TCAACCCTTACAATACAATAACAACACACACACACACAC
HUM: G T C A C C A T T A C C A G T G A G T G A G T G A G T G A G T G A G G T C C G T G A G C A G C A G C T A C A T G G A G C T G A G
UAM: G T C A C C A T T A C C A G T G A G T C G T G A G C A G C T A C A T G G A G C T G A G
HUM: C A G C C T G A G A T C T G A A G A C A T C T G A A G A C A T G G T C G T G T C C T G T G A G A G A
UAM: CAGCCTGAGAGAAGAAGACATCGTGAAGATGGTTCGTGTGTGT
D7
HUM: C A C A G T G
UAM: C A C A G T G
D9
HUM: G T C A G A A A C C C UAM: G T C A G A A A C C C
Onl. Old R. R. R. O. O. O.
Alignment stats: 'M': 295, 'I': 0, 'D': 0, 'X': 0
Both human gene and its mapping are pseudogenes

IGHV(III)-16-1

```
GENE ALIGN SEQ
HUM: GAAGTCCTGTGTGAAATTTTACTGATAGAGTCAGGGGGGAAAAA<mark>TTTGT</mark>ACA
UAM: GAAGTCCTGTGAAATTTACTGAATAGAGTCAGGGGGAA-ATTTACTTACT
     G C C C A G T G G T T C A C T G A G A C T C T C A T G C A A A G C C T C T G A T T T C A C C T T T A
     G C C C A G T G G T T C A C T G A G A C T C T C A T G C A A A G C C T C T G A T T T C A C C T T T A
HUM: C T G G C T A C A G C A T G A G C T T G G T C C A G C A G G C T T C A T G A C A G G G A T T G G T G
                     CATGAGCTTGGTCCAGCAGGCTTCATGACAGGGA
UAM: C T G G
HUM: T G G G T G G A A A C A G T G A G T G A G T C A A G T G G G A G T T C T C A G A G T T A C T C T C A
UAM: T G G G T G G A A A C A G T G A G T G A G T C A A G T G G G A G T T C T C A G A G T T A C T C T C A
HUM: T G A G T A C A A A T A A A T T A A C A G T C C C A A G T G A C A C C T T T T C A T G T G C A G T C
UAM: T G A G T A C A A A T A A A T T A A C A G T C C C A A G C G A C A C C T T T T C A T G T G C A G T C
HUM: TACCTTAAAGGGACCAAACTGAAAGTCAAGGACAAGGCCTTGTAATACTG
UAM: TACCTTAAAAGGAAACTGAAAGTGAAAGTCAAAGGAAAGGAAAGTGAAAGTAAATACTG
HUM:
UAM:
D7
HUM:
     G A G A C A C
UAM:
D9
HUM: G C C C A G A C A G A
UAM: G C C C A G A C A G A
Alignment stats: 'M': 301, 'I': 0, 'D': 1, 'X': 1
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Both human gene and its mapping are pseudogenes

GENE ALIGN SEQ
HUM: GAGGTGCAG <mark>CT</mark> GGTGGAG <mark>TCT</mark> GGAG <mark>TCT</mark> GGGGGGG <mark>CTTGGGTACCT</mark> GGGGGG <mark>C</mark> T
UAM: GAGG <mark>TGCAGCT</mark> GG <mark>TGGAGT</mark> GGAG <mark>TCT</mark> GGGGGG <mark>CTTGGGTACAGCCT</mark> GGGGG <mark>T</mark> C
HUM: CCTGAGACTCTCTGTGCAGCCTCTGGATTCACTTAACAGTGACA
UAM: CCTGAGAGACTCTGAGAGCTGAGCTTCTGAGATTCACTTCAGTAACAGTGACA
HUM: TGAACTGGGCCCGGCAAGGCAAGGGCAAGGGGGG <mark>CT</mark> GGA <mark>T</mark> GGG <mark>T</mark> ATCGGG <mark>T</mark>
UAM: TGAACTGGGCCCGCAAGGCAAGGGCAAGGG <mark>CTCCAAGGGGGCT</mark> GGA <mark>T</mark> GGG <mark>T</mark> ATCGGG <mark>T</mark> A
HUM: G T T A G T T G G A A T G G C A G T A G G A C G C A C T A T G T G G A C T C C G T G A A G C G C C G
UAM: G T T A G T T G G A A T G G C A G T A G G A C G C A C T A T G T G G A C T C C G T G A A G C G C C G
HUM: A T T C A T C A T C A C T C C A G A G A C A A T T C C A G G A A C T C C T G T A T C T G C A A A A G A
UAM: A T T C A T C A T C T C C A G A G A C A A T T C C A G G A A C T C C T G T A T C T G C A A A A G A
HUM: A C A G A C G G A G A G C C G A G G A C A T G G C T G T A T T A C T G T G A G A A A
UAM: A C A G A C G G A G A G C C G A G G A C A T G G C T G T G T A T T A C T G T G T G A G A A A
D7
HUM: T C C T G T G
UAM: T C C T G T G
D9
HUM: GACAACT
UAM: GACAAACCT
Alignment stats: 'M': 296, 'I': 0, 'D': 0, 'X': 0 Neither human gene nor its mapping is pseudogene
werener namen Sene nor res mabbing is beencoSene

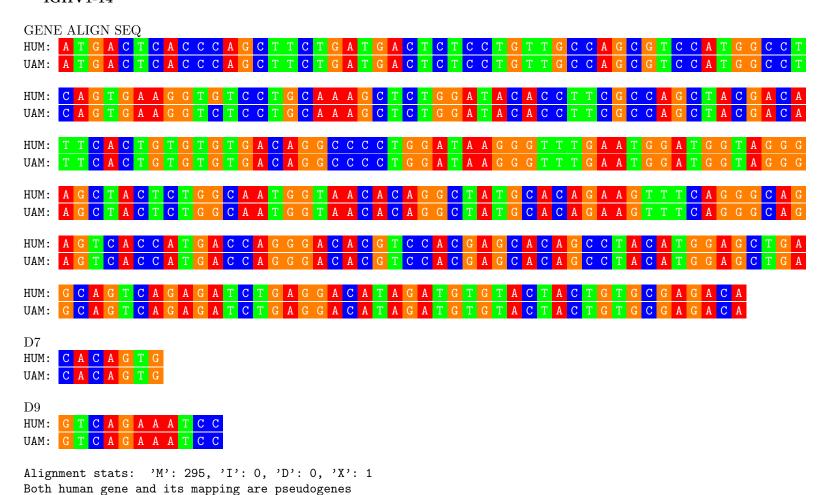
IGHV(II)-15-1

GENE ALIGN SEQ
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UAM: G T T C T A G T A A A G C C C T C A G A C C C T C T C T C T C T C T C T C T C
HUM: A T T T C C A A T C A T A A C C A G T A C T T C C T G G A G C T G T A T C T G C C A G C C C
UAM: A T T T C C A A T C A T A A C C A G T A C T T C C T C C T G G A G C T G T A T C T G C C A G C C C C
HUM: CAGGGAAGAAGAAGTO AAG <mark>CT</mark> GAAG <mark>T</mark> GGG <mark>T</mark> CAGG <mark>TGT</mark> AGG <mark>T</mark> AGG <mark>T</mark> AGG <mark>T</mark> AGGAAACACA
UAM: CAGGGAAGAAG <mark>CT</mark> GAAG <mark>T</mark> CGG <mark>T</mark> CAGG <mark>T</mark> CAGG <mark>T</mark> CAGG <mark>T</mark> CAGG <mark>T</mark> CAGGG <mark>TCACGAGGAAACA</mark> CA
HUM: A G T G C A A C C C G C T T C T C A A G A G T C C A G T C C A G T C C A G T C C A G A T C C A C A T T C C A C A T T C C A C A
UAM: A G T G C A A C C C G C T T C T C A A G A G T C C A G T C A C C T C C A G A T C A C A T T C
HUM: A G A A A A C A G T T T T T C C T A C A G C T G A G C T A C C C G C A C A A T G A G T A A A C C A C
UAM: A G A A A A C A G T T T T T C C T A C A G C T G A G C T A C C C G C A C A A T G A G T A A A C C A C
HUM: CATGGAATTTTAATAGAAAGA
UAM: C A T G G A T T T T T A C A A A G A
D7
HUM: CACAGAA
UAM: C A C A G A A
D9
HUM: ACACACCTC
UAM: A C A C A A A C C T C
Alignment stats: 'M': 271, 'I': 0, 'D': 0, 'X': 0
Both human gene and its mapping are pseudogenes

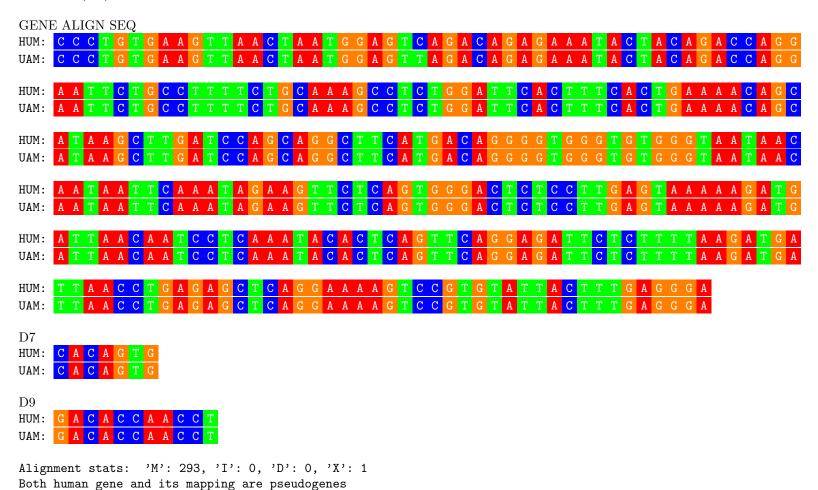
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GENE ALIGN SEQ.
HUM: GAGGTGCAGCTGGAGTCTGGGGGGGGGTC
                 CTGGTGGAGTCTGGGGGGTCTTGGTAAAGCCTTGGGG
HUM: CCTTAGGACTCTCTGTGCAGCTTCTCAGTAACGCCTGAGA
UAM: C C T T A G A C T C T C T G T G C A G C C T C T C T G A G C A A G C C T C T C A G T T T C A G T A A C G C C T G A
HUM: TGAGCTGGGTCCAGGCTCAAGGGCTCAAGGGCTCAAGGGCCTGGAAGGCGCTGGAAGTGGGCCGT
UAM: T G A G C T G G G T C C G C C A G G C T C C A G G G A A G G G G C T G G A G T G G G T T G G C C G T
UAM: A T T A A A A G C A A A A C T G A T G G T G G A C A A C A G A C T A C G C T G
HUM: A G G C A G A T T C A C C A T C T C A A G A G A T G A T T C A A A A A A C A C G C T G T A T C T G
UAM: A G G C A G A T T C A C C A T C T C A A G A G A T G A T T C A A A A A A C A C G
HUM: A A A T G A A C A G C C T G A A A A C C G A G G A C A C A G C C G T G T A T T A C T G T A C C A C A
UAM: A A A T G A A C A G C C T G A A A A C C G A G G A C A G C C G T G T A T T A C T G T A C C A C A
HUM:
UAM:
D7
HUM:
   C A C A G T G
UAM:
D9
HUM: GACACAAACCT
UAM: GACAGAAACCT
Alignment stats: 'M': 302, 'I': 0, 'D': 0, 'X': 0
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Neither human gene nor its mapping is pseudogene

IGHV1-14



IGHV(III)-13-1



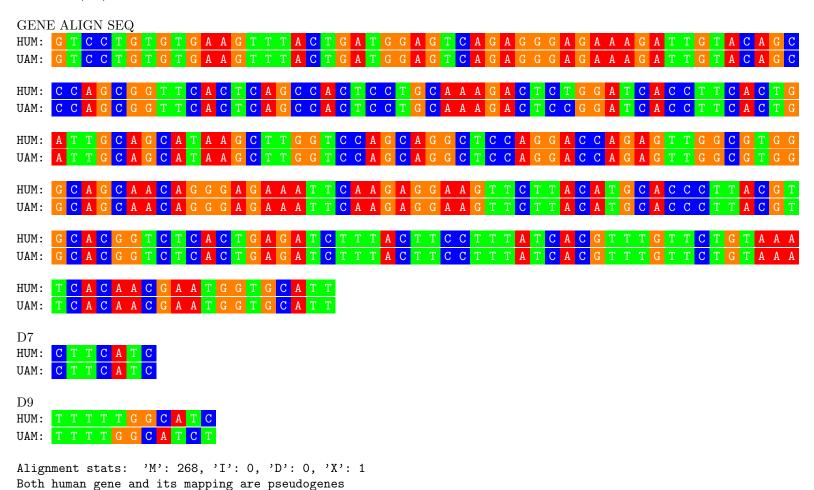
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GENE ALIGN SEQ.
HUM: GAGGTGCAGCTGGAGTCTGGGGGGGGGTC
                CTGGTGGAGTCTGGGGGGTCTTGGTACAGCCTGGGGGGT
HUM: CCTGAGACTCTCTGTGCAGCTGAGCAGCAGCATCAGAACTTCAACTTAAGCTAACGACA
UAM: C C T G A G A C T C T C T G T G C T G T G T G T G T A G C T C T A C C T A C C T C A C C T T C A C C T T C A G C T A C C A C A
UAM: TGCACTGGGTCCAAGCTAAGCAGGAAAAGGTCTACAGGAAAAGGTCTGGGAGTCTCAG
HUM: A T T G G T A C T G C T G G T G A C C C A T A C T A T C C A G G C T C C G T G A A G G G C C G A T T
UAM: A T T G G T A C T G C T G G T G A C A C A C A T A C T A T C C A G G C T C C G T G A A G G G C C G A T T
HUM: CACCATCT CCAGAGAAAATGCCAAGAACTCCTTGTATCAAATGAACA
UAM: CACCATCTCAGAGAGAAATGCCAAGAACTCCTTGTATCAAATGAACA
   G C C T G A G A G C C G G G G A C A C G G C T G T G T A T T A C T G T G C A A G A G A
UAM: G C C T G A G A G C C G G G G A C A C G G G T G T G T A T A C T G T G A G A G A G A
D7
HUM: C A C A G T G
UAM:
D9
HUM: GACACAAACCT
UAM: GACACAAACCT
Alignment stats: 'M': 292, 'I': 0, 'D': 0, 'X': 1
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Neither human gene nor its mapping is pseudogene

IGHV1-12

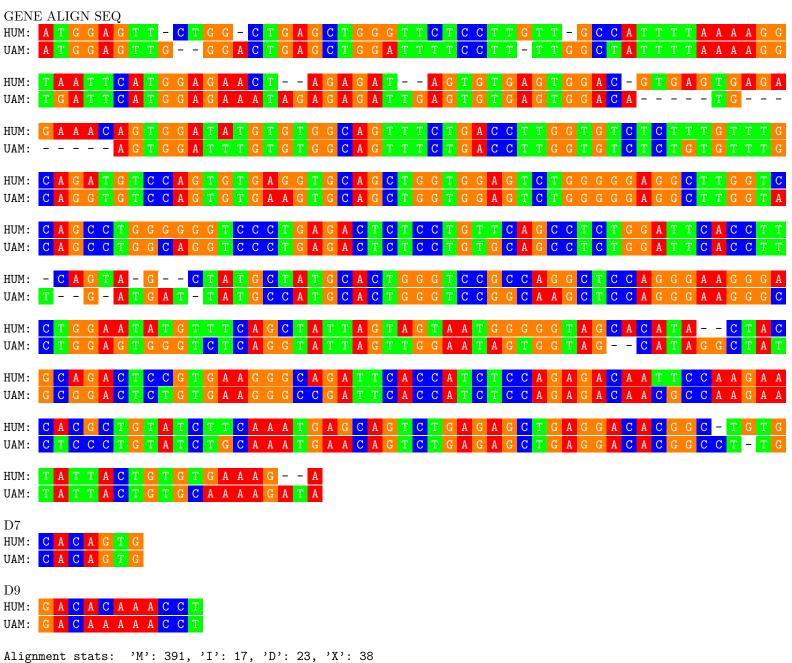
GENE ALIGN SEQ
HUM: CAGGTGAGCAGCTGAATCTGAATCTGGGGGCTGAAGAAGAAGCCT
UAM: CAGG <mark>TGAGCTGAT</mark> GGTGCAA <mark>TCT</mark> GGGGG <mark>TGAGGTGAAGAAGCT</mark> GGGG <mark>T</mark> GAAGAAG <mark>CCT</mark> GGGG <mark>T</mark> C
HUM: A G T G A A G G T C T C C T G C A A G G C T T C T G G A T A C A C C T T C A C C T A C T G C T A C T
UAM: A G T G A A G G T C T C C T G C A A G G C T T C T G G A T A C A C C T T C A C C T A C T G C T A C T
HUM: T G C A C T G G G T A T G A C A G G C C C C T G G A C A A G G C T T G A A T G G A C A G G A T T T
UAM: T G C A C T G G G T A T G A C A G G C C C C T G G A C A A G G G C T T G A A T G G A C A G G A T T T
HUM: TAGTTATTGAGAGAGATTTTCATACAACAACATTTATTCTCATACAACATTTCTC
UAM: TAGTTATTTGAGAGAGTTTTTCATACAACATTTTATTCTGTAAGCAAATTTCC
HUM: A G G G A T T G T A G A A T G A A T C A T A T A A C A A T C T G A C A G A A C T T C T C T
UAM: A G G G A T T G T A G A A T G A A T C A T A T T A A C A A T C A G A C A G A A C T T C T C T
HUM: GAATCAATCTAATTTTTTTTTTTTTTTTTTTTTTTTTTT
UAM: GAATCAATCTTACTAAACATCAATCATACAATTCAAATCAATA
$\mathrm{D}7$
HUM: TTTCAGAGA
UAM: TTTCAGAGA
Do.
D9 HUM: <mark>T A A C T C T A C T T</mark>
UAM: TAACTCTACTT
Alignment stats: 'M': 296, 'I': 0, 'D': 0, 'X': 0
Both human gene and its mapping are pseudogenes

IGHV(III)-11-1



GENE ALIGN SEQ	
HUM: CAGGTGCAGCTGGTGGTGGAGTCTGGAGTCT	
UAM: CAGGTGAGCTGATGTTGGTGATGAGTGTAGGTGTGAAG <mark>CTT</mark> GGGAGG <mark>CTT</mark> GG <mark>TC</mark> AAG <mark>CC</mark> TGGAA	G G G T C
HUM: CCTGAGACTCTCTGTGCCTCTGGATTCACTTAC	C T A C A
UAM: C C T G A G A C T C T C C T G T G C A G C C T C T G G A T T C A C C T T C A G T G A C T A G	
HUM: T G A G C T G G A T C C G C C A G G C T C C A G G G G G C T G G A G T G G G T T T T	
UAM: TGAGCTGGATCCGCCAGGCTCCAGGGAAGGGGCTGGAG <mark>T</mark> GGG <mark>TTTT</mark>	C A T A C
HUM: A T T A G T A G T A G T A G T A G T A G T A G T A G T A G T T A C A C A A C T A C G C A G A C T C T G T G A A G C UAM: A T T A G T A	
UAM: A T T A G T A G T A G T G G T A G T A G T A G C A T A C T A C G C A G A C T C T G T G A A G G	G G G G
HUM: A T T C A C C A T C T C C A G A G A C A A C G C C A A G A A C T C A C T G T A T C T G C A A	A A T G A
UAM: A T T C A C C A T C T C C A G G G A C A A C G C C A A G A A C T C A C T G T A T C T G C A A	
HUM: A C A G C C T G A G C C G A G C C G A G G A C A C G G C T G T A T T A C T G T G C G A G A G A	
UAM: A C A G C C T G A G A G C C G A G G A C A C G G C C G T G T A T T A C T G T G C G A G A G A	A
D7	
HUM: CACAGTG	
UAM: C A C A G T G	
D9	
HUM: GACACAAC <mark>T</mark>	
UAM: GACAAACCT	
Alignment stats: 'M': 289, 'I': 0, 'D': 0, 'X': 7	
Neither human gene nor its mapping is pseudogene	

IGHV3-64D



Both human gene and its mapping are pseudogenes

GENE ALIGN SEQ
HUM: GAGGTGAGGTGGAGGTGAGGTGGAGGTGGAGGGGGGGGG
UAM: GAGG <mark>TGCAGCTGGAGTCT</mark> GGAGTGGAGTCTGGGGGGG <mark>TCTTGGTCCAGCCT</mark> GGGGGG <mark>TC</mark>
HUM: CCTGAGACTCTCTGTGCAGCCTCTCACCTTAAGTAGCTATGGA
UAM: C C T G A G A C T C T C C T G T G C A G C C T C T G G A T T C A C C T T T A G T A G C T A T T G G A
HUM: TGAGCTGGGTCCAGGCTCAAGGGAAGGGG <mark>CT</mark> GGG <mark>CCAA</mark> GGGGAAGGGG <mark>CT</mark> GGAG <mark>T</mark> GGG <mark>CCAA</mark> C
UAM: TGAGGTGGGTCAAGGCAAGGCAAGGCAAGGCAAGGGAAGGGAAAGGGGCTGGAAGTGGGCAAC
HUM: A T A A A G C A A G A T G G A A G T G A A A T A C T A T G T G A C T C T G T G A A G G G C C G
UAM: A T A A A G C A A G A T G G A A G T G A A G T G A G G A A T A C T A T G T G G A C T C T G T G A A G G G C C G
HUM: A T T C A C C A T C T C C A G A G A C A A C G C C A A G A A C T C A C T G T A T C T G C A A A T G A
UAM: A T T C A C C A T C T C C A G A G A C A A C G C C A A G A A C T C A C T G T A T C T G C A A A T G A
HUM: A C A G C C T G A G C C G A G G A C A C G G C C G T G T A T T A C T G T G C G A G A G A
UAM: A C A G C C T G A G C C G A G G A C A C G G T G T G T A T T A C T G C G A G A G A
$\mathrm{D}7$
HUM: CACAGTG
UAM: CACAGTG
D9
HUM: GACAAACCT
UAM: GACACACT
Alignment stats: 'M': 295, 'I': 0, 'D': 0, 'X': 1
Noith an haman and the manning is a soul and

Neither human gene nor its mapping is pseudogene

GENE ALIGN SEQ
HUM: GAGATGCAGCTGGTAGCTGCTGCTGCTGCTGGAGCAAAG <mark>CCT</mark> GGGAGCAAAG <mark>CCT</mark> GGGG <mark>TGCC</mark>
UAM: GAGA <mark>T</mark> GCAG <mark>CT</mark> GG <mark>T</mark> AGAG <mark>T</mark> CTGAAG <mark>CT</mark> GAAA <mark>CTT</mark> GAAAG <mark>CCT</mark> GGG <mark>T</mark> CC
HUM: CAGAGACTCTCTCTCTTCTCACTCACTCACCTCTCTCTCACCTTCACCTTCACCTTCACCAC
UAM: C T G A G A C T C T C T G T G C A G C C T C T C T C A G C A T A G C A T A G C A T A G C A C A C A C A C A C A C A C A C A
HUM: G C A C T G G G T C C C C A G G C T C C A G G G T C T G G G T C T G C A G T G C C A G T T A
UAM: G C A C T G G G T C C C C A G G C T C C A G G G T C T G G G T C T G C A G T G C C A G T T A
HUM: TTAGTGGTAGTGGTAGTAGTACCATGTACGCATGT
UAM: T T A G T G G T A G T A G T A C C A T G T A C T A C G C A G A C T C T G T G A A G G G C C G A
HUM: TTCACATTTCAAATTCAAATACAATAATAAAAAAACTCACTAATAA
UAM: TTCACAATTCAAATTCAAATAATAAAAAAAACTCAAATAAAAAA
HUM: CAGAGACTGAGGGCAGAGGGCAGGGCAGGGA <mark>TGCAGCTGCATGCTGCTGCTGTGTGTGTGAGAGAGAGAGA</mark>
UAM: CAGACTGAGAGAGAGAATGCAGCAG <mark>CAGCTGCATGATGATGAGAGA</mark>
$\mathrm{D}7$
HUM: TACGTA
UAM: T A C G G T A
Do.
D9 HUM: <mark>GACAAACCT</mark>
UAM: GACACAACT
Alignment stats: 'M': 293, 'I': 0, 'D': 0, 'X': 2
Both human gene and its mapping are pseudogenes

IGHV(III)-5-1

GENE ALIGN SEQ

D7

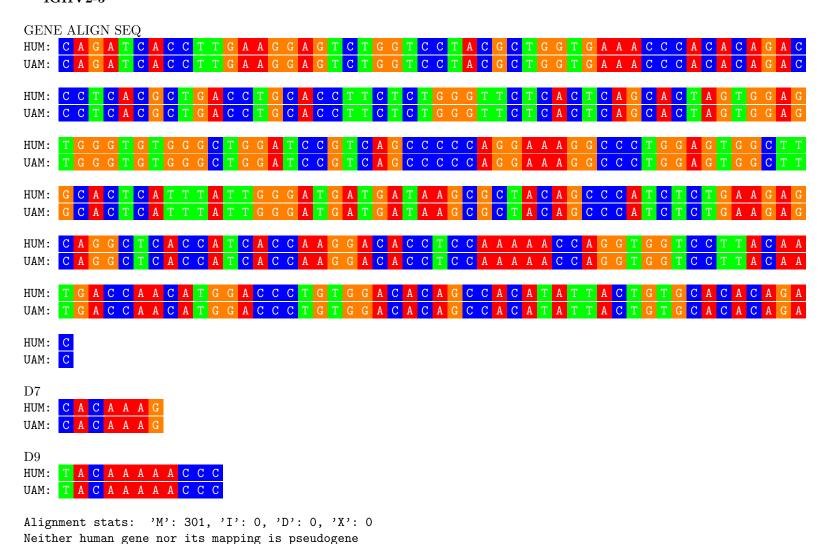
HUM: C A C A T G A
UAM: C A C A T G A

D9

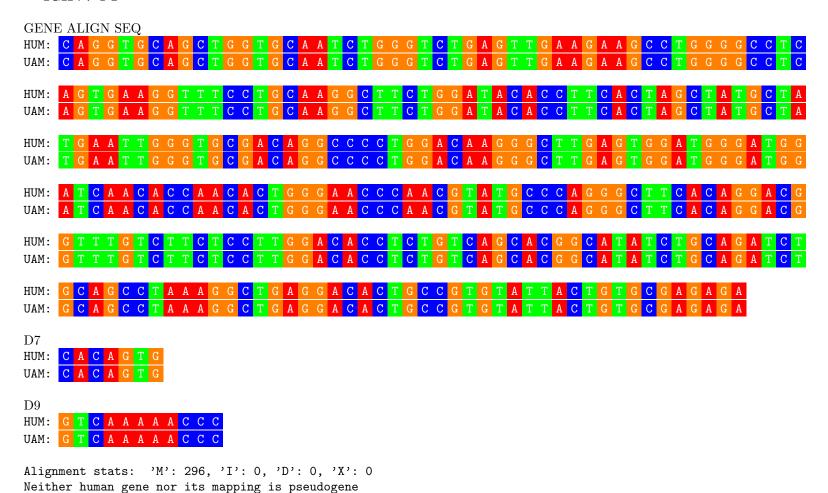
HUM: A A C C T C C A G G A UAM: A A C C T C C A G G A

Alignment stats: 'M': 99, 'I': 0, 'D': 0, 'X': 0 Neither human gene nor its mapping is pseudogene

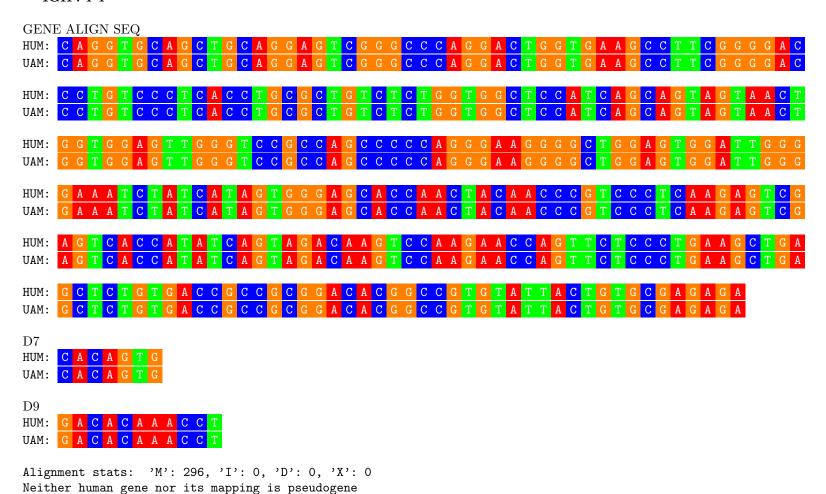
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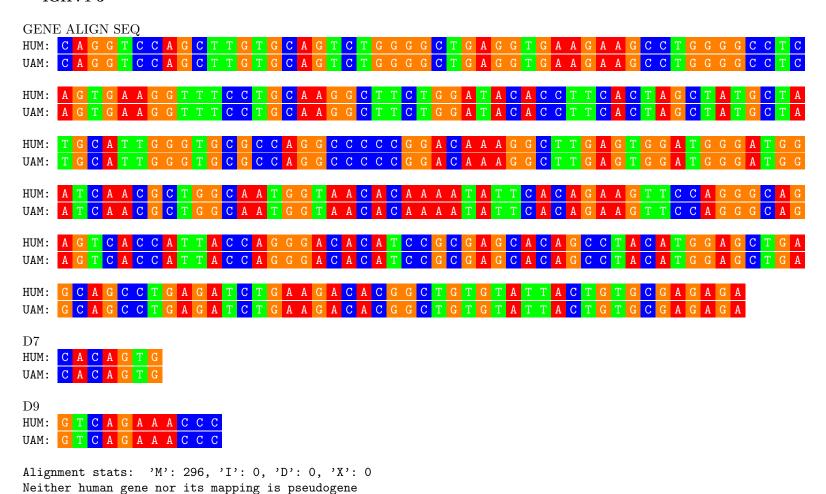
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IGHV4-4



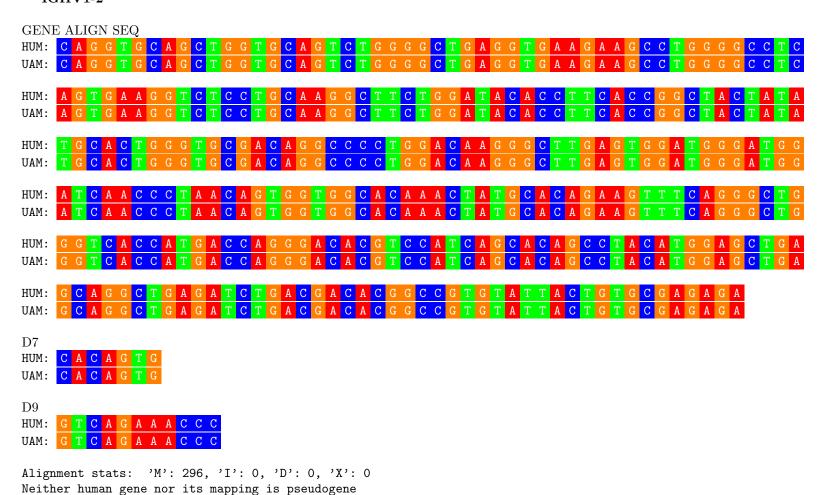
IGHV1-3



IGHV(III)-2-1

GENE ALIGN SEQ
HUM: GAAGTTTACTGATGAGTGAGTCAGAGGGGGAAAAATTTTTACAGAGCCCAGTGGTG
UAM: G A A G T T T A C T G A T G G A G T C A G A G G G G A A A A A T T T T A C A G C C C A G T G G T G
HUM: A G A C T C T C T G C A A A G C C T C T G C A A A G C C T C T G G T T T C A C C T T T A C T G G T T A C A G C A T G A G
UAM: A G A C T C T C C T G C A A A G C C T C T G G T T T C A C C T T T A C T G G T T A C A G C A T G A G
HUM: C T T G G T C A G C A T G C T T C A C A A C A G G G A T A G G T G T G C A A C A G T A A C A A C A A C A G T G A
UAM: C T T G G T C C A G C A T G C T T C A C A A C A G G G A T A G G T G T G G G T G C C A A C A G T G A
HUM: G T G A T C A A G T A T G A A T T C T C A G G G T T A C T C T C C A T G A G T A C A A A T A A A T T
UAM: G T G A T C A A G T A T G A A T T C T C A G G G T T A C T C C A T G A G T A C A A A T A A A T T
HUM: A A C A A T C T C A A G C A A C A C C C T T T T A A G T G C A G T C T T A C A A T G A C C A
UAM: A A C A A T C T C A A G C A A C A C C C T T T T A A G T G C A G T C T G C C T T A C A A T G A C C A
HUM: A T C T G A A A G C C A A G G A C A A G G T C A T G T A T T A C T G T G A G T G A
UAM: A T C T G A A A G C C A A G G A C A A G G T C A T G T A T T A C T G T G A G T G A
D7 HUM: <mark>C A C A G T G</mark>
UAM: C A C A G T G
D9 HUM: <mark>GACAAAGCT</mark>
UAM: GACACAAAGCT
Alignment stats: 'M': 291, 'I': 0, 'D': 0, 'X': 0
Both human gene and its mapping are pseudogenes

IGHV1-2



IGHV(II)-1-1

```
GENE ALIGN SEQ
HUM: CTGGGCCTGGACCCAGCAGCTCTCTGGGGAAGGCCGCTGGAACCTCAGCT
UAM: C T G G G C C T G G A C C C A G C C C T C T G G G A A G G
HUM: CCAGGGGCAGCACACTTCAGCCCAGCCTTTCCTGGGCCAACTCATC
HUM: T G T A G A G A C A C A T C C A A G G C C C A G T T A T C C C T C
UAM:
   T G T A G A G A C A C A T C C A A G G C C C A G T T A T C C C T G
D7
HUM:
   G A C A G A A
UAM:
D9
HUM:
   GACACAAACC<mark>T</mark>
UAM:
   G A C A C A A A C C T
Alignment stats: 'M': 182, 'I': 0, 'D': 0, 'X': 0
```

IGHV6-1

```
GENE ALIGN SEQ.
CTGCAGCAGTCAGGTCCAGGACTGGTGAAGCCCTCGCAGAC
HUM: CCTCTCACTCACCTGTGCCATCACATGTGCCACATCTCAGGTGTCTCTAGCAACAGTG
HUM: C T G C T T G G A A C T G G A T C A G G C A G T C C C C A T C G A G G C C T T G A G T G G C T
UAM: CTGCTTGGAACTGGATCAGGCAGTCCCCATCGAGAGG
HUM: G G A A G G A C A T A C T A C A G G T C C A A G T G G T A A A T
   G G A A G G A C A T A C T A C A G G T C C A A G T G G T
HUM: GAAAAG<mark>T</mark>CGAA<mark>T</mark>AACCA<mark>T</mark>CAACCCAGACA<mark>T</mark>CCAAGACCAAGACCAG<mark>TT</mark>CCC
UAM: GAAAAG<mark>T</mark>CGAATAACCA<mark>T</mark>CAACCCAGACA<mark>T</mark>CCAAGACCAAGACCAG<mark>TTC</mark>CC
HUM: TGCAGCTGAACTCTGTGACCCGAGGGACGGCTGTGTATTACTGTGCA
UAM: TGCAGCTGAACTCTGTGACTCCCGAGGACACGGCTGTGTATTACTGTGCA
HUM: A G A G A
UAM: A G A G A
D7
HUM: C A C A G T G
D9
HUM: G A C A C A A A C C T
UAM: GACAGAAACCT
Alignment stats: 'M': 305, 'I': 0, 'D': 0, 'X': 0
```

IGHD1-1

```
U9
HUM: C A G A T T C T G A A
UAM: C A G A T T C T G A A
U7
HUM: C A C G G T G
UAM: C A C G G T G
GENE ALIGN SEQ
HUM: G G T A C A A C T G G A A C G A C
UAM: G G T A C A A C T G G A A C G A C
D7
HUM: C A C C G T G
UAM: C A C C G T G
D9
HUM: G T C C A A A A C T C
UAM: G T C C A A A A C T G
Alignment stats: 'M': 17, 'I': 0, 'D': 0, 'X': 0
```

IGHD2-2

U9HUM: A G G A T T T T G T G UAM: A G G A T T T T G T G U7HUM: C A C T G T G UAM: C A C T G T G GENE ALIGN SEQ HUM: A G G A T A T T G T A G T A G T A G C A G C T G C T A T G C C UAM: A G G A T A T T G T A G T A G T A G T G C T G C T A T G C C D7HUM: C A C A G T G UAM: C A C A G T G D9HUM: TTCCCAAAGCC UAM: T T C C C A A A G C C Alignment stats: 'M': 31, 'I': 0, 'D': 0, 'X': 0

IGHD3-3

U9HUM: A G G T T T G G G G T UAM: A G G T T T G G G G T U7HUM: C A C T G T G UAM: C A C T G T G GENE ALIGN SEQ UAM: G T A T T A C G A T T T T G G A G T G G T T A T T A T G C D7HUM: C A C A G T G UAM: C A C A G T G D9HUM: A T C A A A A A C C C UAM: A T C A A A A A C C C Alignment stats: 'M': 31, 'I': 0, 'D': 0, 'X': 0

IGHD4-4

```
U9
HUM: G G C T T T T T G T G
UAM: G G C T T T T G T G
U7
HUM: T A C T G T G
UAM: T A C T G T G
GENE ALIGN SEQ
HUM: T G A C T A C A G T A A C T A C
UAM: T G A C T A C A G T A A C T A C
D7
HUM: C A C A G T G
UAM: C A C A G T G
D9
HUM: A G C A A A A A C T G
UAM: A G C A A A A A C T G
Alignment stats: 'M': 16, 'I': 0, 'D': 0, 'X': 0
```

IGHD5-5

U9HUM: T G G T T A T T G T C UAM: T G G T T A U7HUM: G A C T G T G UAM: G A C T G T G GENE ALIGN SEQ HUM: G T G G A T A C A G C T A T G G T T A C UAM: G T G G A T A C A G C T A T G G T T A C D7HUM: C A C A G T G UAM: C A C A G T G D9HUM: A G C A G C A A C C A UAM: A G C A G C A A C C A Alignment stats: 'M': 20, 'I': 0, 'D': 0, 'X': 0

IGHD6-6

U9HUM: A A G T T T C T G A A UAM: A A G T T T C T G A A U7HUM: C A C A G T G UAM: C A C A G T G GENE ALIGN SEQ HUM: G A G T A T A G C A G C T C G T C C UAM: G A G T A T A G C A G C T C G T C C D7HUM: C A C A G T G UAM: C A C A G T G D9HUM: C C A G A A A C C C UAM: G C C A G A A A C C C Alignment stats: 'M': 18, 'I': 0, 'D': 0, 'X': 0 Neither human gene nor its mapping is pseudogene

IGHD1-7

U9
HUM: C G G A T T C T G A A
UAM: C G G A T T C T G A A

UAM: C A C A G T G
UAM: C A C A G T G
UAM: C A C A G T G

UAM: C A C A G T G

UAM: C A C A G T G

UAM: C A C A G T G

UAM: C A C T A T A A C T G G A A C T A C

UAM: C A C T G T G

Alignment stats: 'M': 17, 'I': 0, 'D': 0, 'X': 0 Neither human gene nor its mapping is pseudogene

IGHD2-8

U9HUM: A G G A T T T T G T G UAM: A G G A T T T T G T G U7HUM: C A C T G T G UAM: C A C T G T G GENE ALIGN SEQ HUM: A G G A T A T T G T A C T A A T G G T G T A T G C T A T C C UAM: A G G A T A T T G T A C T G G T G T G T A T G C T A C C D7HUM: C A C A G T G UAM: C A C A G T G D9HUM: TTCCCAAAGCC UAM: T T C C C A A A G C C Alignment stats: 'M': 29, 'I': 0, 'D': 0, 'X': 2

IGHD3-9

U9HUM: A G G T T T A G A A UAM: A G G T T T A G A A T U7HUM: C A C T G T G UAM: C A C T G T G GENE ALIGN SEQ HUM: G T A T T A C G A T A T T T G A C T G G T T A T A T A A C UAM: G T A T T A C G A T A T T T T G A C T G G T T A T T A T A A C D7HUM: C A C A G T G UAM: C A C A G T G D9HUM: A T C A A A A A C C C UAM: A T C A A A A A C C C Alignment stats: 'M': 31, 'I': 0, 'D': 0, 'X': 0

IGHD3-10

```
U9
HUM: A G G T T T G G G G T
UAM: A G G T T T G G G G T
U7
HUM: C A C T G T G
UAM: C A C T G T G
GENE ALIGN SEQ
HUM: G T A T T A C T A T G G T T C G G G G G A G T T A T A T A A C
UAM: G T A T T A C T A T G G T T C A G G G A G T T A T T A T A A C
D7
HUM: C A C A G T G
UAM: C A C A G T G
D9
HUM: A T C A A A A A C C C
UAM: A T C A A A A A C C C
Alignment stats: 'M': 30, 'I': 0, 'D': 0, 'X': 1
```

IGHD4-11

```
U9
HUM: G G C T T T T T G T G
UAM: G G C T T T T T G T G
UAM: T G C T G T G
UAM: T G C T G T G
UAM: T G A C T A C A G T A A C T A C
UAM: T G A C T A C A G T A A C T A C
UAM: T G A C T A C A G T A A C T A C
UAM: T G A C T A C A G T A A C T A C
UAM: T G A C T A C A G T A A C T A C
UAM: T G A C T A C A G T A A C T A C
UAM: C A T A G T G
UAM: C A T A G T G
UAM: C A T A G T G
UAM: G G C A A A A A C T G
```

IGHD5-12

U9HUM: T G G T T A T T G T C UAM: T G G T T A U7HUM: G A C T G T G UAM: G A C T G T G GENE ALIGN SEQ HUM: G T G G A T A T A G T G G C T A C G A T T A C UAM: G T G G A T A T A G T G G C T A C G A T T A C D7HUM: C A C A G T G UAM: C A C A G T G D9HUM: A G C A G C A A C C A UAM: A G C A G C A A C C A Alignment stats: 'M': 23, 'I': 0, 'D': 0, 'X': 0

IGHD6-13

U9HUM: A G G T T T C T G A A UAM: A G G T T T C T G A A U7HUM: C A C A G T G UAM: C A C A G T G GENE ALIGN SEQ HUM: G G G T A T A G C A G C A G C T G T A C
UAM: G G G T A T A G C A G C A G C T G G T A C D7HUM: C A C A G T G UAM: C A C A G T G D9HUM: C C A G A A A C C C UAM: G C C A G A A A C C C Alignment stats: 'M': 21, 'I': 0, 'D': 0, 'X': 0

IGHD1-14

U9
HUM: C G G A T T C C G A A
UAM: C G G A T T C C G A A

UAM: C A C A G C G
UAM: C A C A G C G
UAM: C A C A G C G

UAM: C A C A G C G

HUM: G T A T A A C C G G A A C C A C

UAM: C A C T G T C

Alignment stats: 'M': 17, 'I': 0, 'D': 0, 'X': 0 Neither human gene nor its mapping is pseudogene

IGHD2-15

U9HUM: A G G A T T T T G T G UAM: A G G A T T T T G T G U7HUM: C A C T G T G UAM: C A C T G T G GENE ALIGN SEQ HUM: A G G A T A T T G T A G T G G T G G T A G C T G C T A C T C C UAM: A G G A T A T T G T A G T G G T G G T A G C T G C T A C T C C D7HUM: C A C A G T G UAM: C A C A G T G D9HUM: T T C C C A A A G C C UAM: T T C C C A A A G C C Alignment stats: 'M': 31, 'I': 0, 'D': 0, 'X': 0

IGHD3-16

U9HUM: A G G T T T G A A G T UAM: A G G T T T G A A G T U7HUM: C A C T G T G UAM: C A C T G T G GENE ALIGN SEQ HUM: G T A T T A T G A T T A C G T T T G G G G G A G T T A T C G T T A T C C UAM: G T A T T A T G A T T A C A T T T G G G G G A G T T A T C G T T A C C D7HUM: C A C A G C A UAM: C A C A G C A D9HUM: A T C A G A A A C C C UAM: A T C A G A A A C C C Alignment stats: 'M': 36, 'I': 0, 'D': 0, 'X': 1

IGHD4-17

```
U9
HUM: G G C T T T T T G T G
UAM: G G C T T T T T G T G
UAM: T A C T G T G
UAM: T A C T G T G
UAM: T A C T G T G
UAM: T G A C T A C G G T G A C T A C
UAM: T G A C T A C G G T G A C T A C
UAM: T G A C T A C G T G T G
UAM: C A C A G T G
UAM: C A C A G T G
UAM: C A C A G T G
UAM: A G C A A A A A C T G
UAM: A G C A A A A A C T G
```

Alignment stats: 'M': 16, 'I': 0, 'D': 0, 'X': 0 Both human gene and its mapping are pseudogenes

IGHD5-18

```
U9
HUM: T G G T T A T T G T C
UAM: T G G T T A T C G T C
U7
HUM: G A C T G T G
UAM: G A C T G T G
GENE ALIGN SEQ
HUM: G T G - - - G A T A - - - C A G C T A T G G T T A C
UAM: G T G A A T - A T A G T G - - G C T A C G A T T A C
D7
HUM: C A C A G T G
UAM: C A C A G T G
D9
HUM: A G C A G C A A C C A
UAM: A G C A G C A A C C A
Alignment stats: 'M': 15, 'I': 6, 'D': 3, 'X': 2
```

IGHD6-19

U9HUM: A G G T T T C T G A A UAM: A G G T T T C T G A A U7HUM: C A C A G T G UAM: C A C A G T G GENE ALIGN SEQ HUM: G G G T A T A G C A G T G G C T G G T A C UAM: G G G T A T A G C A G T G G C T G G T A C D7HUM: C A C A G T G UAM: C A C A G T G D9HUM: C C A G A A A C C C UAM: G C C A G A A A C C C Alignment stats: 'M': 21, 'I': 0, 'D': 0, 'X': 0

IGHD1-20

```
U9
HUM: C G G A T T C T G A A
UAM: C G G A T T C T G A A
U7
HUM: C A C A G T G
UAM: C A C A G T G
GENE ALIGN SEQ
HUM: G G T A T A A C T G G A A C G A C
UAM: G G T A T A A C T G G A A C G A C
D7
HUM: C A C C G T G
UAM: C A C C G T G
D9
HUM: G T C C A A A A C T G
UAM: G T C C A A A A C T G
Alignment stats: 'M': 17, 'I': 0, 'D': 0, 'X': 0
```

IGHD2-21

```
U9
HUM: A G G A T T T T G T G
UAM: A G G A T T T T G T G
U7
HUM: C A C T G T G
UAM: C A C T G T G
GENE ALIGN SEQ
HUM: A G C A T A T T G T G G T G G T G A C T G C T A T T C C
UAM: A G C A T A T T G T G G T G G T G A T T G C T A T T C C
D7
HUM: C A C A G T G
UAM: C A C A G T G
D9
HUM:
     T T C C T A A A G C C
UAM: T T C C T A A A G C C
Alignment stats: 'M': 27, 'I': 0, 'D': 0, 'X': 1
Both human gene and its mapping are pseudogenes
```

IGHD3-22

U9
HUM: A G G T T T G A A G T
UAM: A G G T T T G A A G T

U7
HUM: C A C T G T G
UAM: C A C T G T G
UAM: C A C T G T G
UAM: C A C T G T G

HUM: G T A T T A C T A T G A T G T G
UAM: G T A T T A C T A T G A T A G T A G T G T T A T T A C T A C
UAM: G T A T T A C T A T G A T A G T A G T G G T T A T T A C T A C

D7
HUM: C A C A G T G
UAM: C A C A G T G
UAM: C A C A G T G

Alignment stats: 'M': 31, 'I': 0, 'D': 0, 'X': 0

IGHD4-23

```
U9
HUM: G G C T T T T T G T G
UAM: G G C T T T T T G T G
UAM: T G C T G T G
UAM: T G C T G T G
UAM: T G C T G T G
UAM: T G A C T A C G G T G T A A C T C C
UAM: T G A C T A C G G T G T A C C
UAM: T G A C T A C G G T G T A C C
UAM: T G A C T A C G G T G T A C C
UAM: T G A C T A C G G T G G T A A C T C C

D7
HUM: C A C A G T G
UAM: C A C A G T G
UAM: C A C A G T G
UAM: A G C A A A A A A C T G
UAM: A G C A A A A A A C T G
```

Alignment stats: 'M': 19, 'I': 0, 'D': 0, 'X': 0 Both human gene and its mapping are pseudogenes

IGHD5-24

U9
HUM: T G G T T A T T G T C
UAM: T G G T T A T T G T C
UAM: T G G T T A T T G T C

UAM: G G C C G T G

UAM: G T A G A G A T G C T A C A A T T A C

UAM: G T A G A G T G

UAM: C A C A G T G

Alignment stats: 'M': 20, 'I': 0, 'D': 0, 'X': 0 Neither human gene nor its mapping is pseudogene

IGHD6-25

U9
HUM: A G G T T T C T G A A
UAM: A G G T T T C T G A A

UAM: A G G T T T C T G A A

UAM: C A C A G T C

UAM: C G C A G T C

UAM: G G G T A T A G C A G C G C T A C

UAM: G A C A A T G

UAM: C A C A A T G

D9
HUM: G A C A G A A T C C C
UAM: C A C A G A A T C C C
UAM: C A C A G A A T C C C

Alignment stats: 'M': 18, 'I': 0, 'D': 0, 'X': 0 Neither human gene nor its mapping is pseudogene

IGHD1-26

U9
HUM: T G G A T T C T G A A
UAM: T G G A T T C T G A A

UAM: T G G A T T C T G A A

UAM: C A C G G T G

UAM: C A C G G T G

UAM: G G T A T A G T G G A G C T A C T A C

UAM: G G T A T A G T G G G A G C T A C T A C

UAM: C A C T G T G

Alignment stats: 'M': 20, 'I': 0, 'D': 0, 'X': 0 Neither human gene nor its mapping is pseudogene

IGHJ1P

U9

HUM: C G C G T G T T T T G

UAM: C A C G T G T T T T T G

U7

HUM: C A C T G G C
UAM: C A C T G G C

GENE ALIGN SEQ

HUM: A T C A
UAM: A T C A

Alignment stats: 'M': 54, 'I': 0, 'D': 0, 'X': 0 Neither human gene nor its mapping is pseudogene

IGHD7-27

U9

HUM: T G G G T T T C T G T UAM: T G G G T T T C T C T G T

U7

HUM: C A C C G T G
UAM: C A C C G T G

GENE ALIGN SEQ

HUM: A G
UAM: A G

Alignment stats: 'M': 52, 'I': 0, 'D': 0, 'X': 0 Neither human gene nor its mapping is pseudogene

U9

HUM: T G T G T T T T G T UAM: T G T G T T T T T G T

U7

HUM: G G C T G T G
UAM: G G C T G T G

GENE ALIGN SEQ

HUM: C A G
UAM: C A G

Alignment stats: 'M': 53, 'I': 0, 'D': 0, 'X': 0 Neither human gene nor its mapping is pseudogene

IGHJ2P

U9

HUM: G C T G T T C A T G T UAM: G C T G T T C A T G T

U7

HUM: T A G T G T G
UAM: T A G T G T G

GENE ALIGN SEQ

HUM: C T G G G A A C G T C A

UAM: C T G G G A A C G T C A

Alignment stats: 'M': 62, 'I': 0, 'D': 0, 'X': 0 Neither human gene nor its mapping is pseudogene

U9
HUM: A G G T T T A T G T C
UAM: A G G T T T C C

U7

HUM: C C C T G T G
UAM: C C C T G T G

GENE ALIGN SEQ

Alignment stats: 'M': 50, 'I': 0, 'D': 0, 'X': 0 Both human gene and its mapping are pseudogenes

U9

HUM: A G G T T T T T G T G UAM: A G G T T T T T G T G

U7

HUM: C A A T G T G
UAM: C A A T G T G

GENE ALIGN SEQ

HUM: A C T A C T T T G A C T A

Alignment stats: 'M': 48, 'I': 0, 'D': 0, 'X': 0 Neither human gene nor its mapping is pseudogene

U9

HUM: C A G T T C T G C C

UAM: C A G T T C T C C C

U7

HUM: C A A T G T G
UAM: C A A T G T G

GENE ALIGN SEQ

HUM: A C A A C T G G T T C G A C C C T G G T T C G A C C C T G G G C C A G G G A A C C C T G G T C A C C C T C A C C T C A C C T C A C C T C A C C T C A C C T C A C C C T C A C C C T C A C C C T C A C C C T C A C C C T C A C C C T C A C C C T C A C C C T C A C C C T C A C C C T C A C C C T C C T C A C C C T C A C C C T C A C C C T C A C C C T C A C C C T C C T C A C C C T C A C C C T C A C C C T C C T C C T C A C C C T C T C C T C C T C C T C T C C T C T C C T C T C C T C T C C T C T C C T C T C C T C T C C T C T C C T C T C C T C T C C T C T C C T C T C C T

HUM: G UAM: G

Alignment stats: 'M': 51, 'I': 0, 'D': 0, 'X': 0 Neither human gene nor its mapping is pseudogene

IGHJ3P

U9

HUM: G G G G T T T T T G G

UAM: G G G G T T T T T G G

U7

HUM: C C G T C T G
UAM: C C G T C T G

GENE ALIGN SEQ

Alignment stats: 'M': 50, 'I': 0, 'D': 0, 'X': 0 Neither human gene nor its mapping is pseudogene

U9
HUM: T G G G T T T T T G T
UAM: T G G G T T T T T G T

HUM: C A T T G T G
UAM: C A T T G T G

GENE ALIGN SEQ

HUM: A T T A C T A

HUM: T C A C C G T C T C T C A G
UAM: T C A C C G T C T C T C A G

Alignment stats: 'M': 60, 'I': 2, 'D': 2, 'X': 1 Neither human gene nor its mapping is pseudogene