Human genes (HUM) and their mappings (UAMs) in Orangutans

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

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

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

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

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

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

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

Alignment stats: 'M': 275, 'I': 1, 'D': 1, 'X': 16

IGHV7-81

GENE ALIGN SEQ

```
HUM: CAGGTGCAGCTGGTGCAGTCTGGCCATGAGGTGAAGCAGCCTGGGGCCTC
UAM: CAGGTGCAGTTGGTGCAGTCTGGTCATGAGGTGAAGCAGCCTGGGGCCTC

HUM: AGTGAAGGTCTCCTGCAAGGCTTCTGGTTACAGTTTCACCACCTATGGTA
UAM: AGTGAAGGTCTCCTGCAAGGATTCTGGTTACAGTTTCACCACCTATGGTA

HUM: TGAATTGGGTGCCACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGATGG
UAM: TGAATTGGGTGCAACAGGCCCCTGAACAAGGGCTTGAGTGGATGGGATGG

HUM: TTCAACACCTACACTGGGAACCCAACATATGCCCAGGGCTTCACAGGACG
UAM: TTCAACACCGACACTGGGAACCCAACATATGCCCAGGGCTTCACAGGATG

HUM: GTTTGTCTTCTCCATGGACACCTCTGCCAGCACAGCATACCTGCAGATCA
UAM: GTTTGTCTTCTCCATGGACACCTCTGTCAGCACAGCATACCTGCAGATCA

HUM: GCAGCCTAAAGGCTGAGGACATGGCCATGTATTACTGTGCGAGATA
UAM: GCAGCCTAAAGGCTGAGGACACGGCCATGTATTACTGTGCGAGATA
```

D7
```
HUM: CACCATG
UAM: CACCATG
```

D9
```
HUM: GTCAGAAATCC
UAM: GTCAGAAACCC
```

Alignment stats: 'M': 287, 'I': 0, 'D': 0, 'X': 9

IGHV4-80

GENE ALIGN SEQ

```
HUM: GTGCAGCTGCAGGAGTGGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCT
UAM: GTGCAGCTGCAGGAGTGGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCT

HUM: GTCCCTCACATGCGCTGTCTCTGGTGACTCCATCAGCAGTGGTAACTGGT
UAM: GTCCCTCACCTGCGCTGTCTCTGATGACTCCATCAGCAGTGGAAACTGGT

HUM: GGAGCTGGGTCCGCCAGTCCC-CAGGGAAGGGGCTGGAATGGATTGGATA
UAM: GGATCTGAGTCCGCCAG-CCCTCAGGGAAGGGGCTGGAATGCATTGGGTA

HUM: CATCTATTATAGTGGGAGGAGCTACTACACCCCGTCCCTCAGGAGTTGAG
UAM: CATTTATTATAGTGGGAGCAGCTACTACACCCCGTCCCTCAGGAGTTGAG

HUM: TCACCATGTCAATAGAAACGTCCAAGAACCAGTTTTCCCTGAAGCTGAGC
UAM: TCACCGTGTCAGTAGACACGTCCAAGAACCAGTTTTCCCTGAAGCTGAGC

HUM: TCTGTGACCGC---------------------------------------
UAM: TCTGTGACCGCCGCTGACACCGCCGTGTATTACTGTGCGAGAGACACAGT

HUM: ---------------------------------------------A
UAM: GAGGGGACGTGAGTGTGAGCTCAGACACAAACATCCCTGCAA-
```

D7
```
HUM: GGGAGGC
UAM: GGAGGCG
```

D9
```
HUM: GCTCAGGACCA
UAM: CTCAGGACCAG
```

Alignment stats: 'M': 247, 'I': 82, 'D': 2, 'X': 12

4

IGHV(II)-78-1

GENE ALIGN SEQ

```
HUM: TGGCCTGGTGAAGCCCTCACAGACCCTCTCCCTTACCTGCGCTGTGTCTG
UAM: TGGCCTGGTGAAGCCCTCACAGACCCTCTCCCTCACCTGTGCTGTGTCTG

HUM: TGTTCCCCATGATAACGAGGTCTTCCTGCTGAAGCTGGATCCATCAGCCC
UAM: TGTTCCCCAT---AATGAGGTCTTCCTGCTGAAGCTGGATACATCAGCCC

HUM: CCC---AGGGAAGGGAATGGAGTGGATTGGGGTGCATAGGTCATGAAGGGA
UAM: CCCTCT-GGG-AGGGAATGGAGTGGATCGGGGTGCATAGGTCATGAAGGGA

HUM: GCACACATTACCACCCACTCCTCAAGTGTCCAGTCACCATCCCCAGATCC
UAM: GCACACGTTACCACCCGCTTCTCAAGAGTCCAGTCACCATCCCCAGATCC

HUM: GTGTCCAAAAAAGCAGTTCTTCCTACAGCTGAGCTACATGAGCAACAAGC
UAM: ATGTCCAAAAAAACAGTTCTTCCTACAGCTGAGCTGCGTGAGCAACAAGC

HUM: ACATAGCCATGTATTTTTTAAGCCAAAAGA
UAM: ACATAGCCATGTATTTTTTAAGCCTAAGA
```

D7
```
HUM: CACAGTG
UAM: CACAGTG
```

D9
```
HUM: CACCCAAACCT
UAM: CACCCAAACCT
```

Alignment stats: 'M': 256, 'I': 3, 'D': 5, 'X': 14

IGHV5-78

GENE ALIGN SEQ
```
HUM: GAGGTGCAGCTGTTGCAGTCTGCAGCAGAGGTGAAAAGACCCGGGGAGTC
UAM: GAGGTGCAGCTGGTGCAGTCTGCAGCAGAGGTGAAAAGGCCCGGGGAGTC

HUM: TCTGAGGATCTCCTGTAAGACTTCTGGATACAGCTTTACCAGCTACTGGA
UAM: TCTGAGGATCTCCTGTAAGACTTCTGGATACAGCTTTACCAGCTACTGGA

HUM: TCCACTGGGTGCGCCAGATGCCCGGGAAAGAACTGGAGTGGAT-GGGGAG
UAM: TCCACTGGGTGTGCCAGGTGCCCGAGAAAGAACTGGAGTGGATAGGGG-G

HUM: CATCTATCCTGGGAACTCTGATACCAGATACAGCCCATCCTTCCAAGGCC
UAM: CATCTATCCTGGGAACTCTGATACCAGATACAGCCCATCCTTCCAAGCCC

HUM: ACGTCACCATCTCAGCCGACAGCTCCAGCAGCACCGCCTACCTGCAGTGG
UAM: ATGTCACCATCTCAGCCGACAGCTCTATCAGCACCACCTACCTGCAGTGG

HUM: AGCAGCCTGAAGGCCTCGGAC-GCC-GCCATGTATTATTGTGTGAGA
UAM: AGCAGCCTGAAGGCCTCGGACA--CTGCCATGTATTATTGTGTGAGA
```

D7
```
HUM: GGGACCA
UAM: CAGACCA
```

D9
```
HUM: GTGCAGAGTGA
UAM: GTGCAGAGTGA
```

Alignment stats: 'M': 281, 'I': 3, 'D': 3, 'X': 10
```
```

IGHV(III)-76-1

GENE ALIGN SEQ

```
HUM: CTGGTGGAATCTGGAAGAGAAATGATACAGCCTAACTGTTCTCAGAGCCT
UAM: CTGGTGGAATCTGGAAGAGAAATGGTACAGCCCAACAATTCTCAGAGCCT

HUM: TTTTTACAAAGCCTCTGAATTTACCTTCATTGACTCTAGCATGAGCTCAG
UAM: TTTTTACAAAGCCTCTGAATTTACCTTCATTGACTCTAGCATGAGCTCAG

HUM: CCCAGCAGGCTTCAGGACAGGGGTTGGTGTGGGAGGCAAAAGCGAGGGAT
UAM: CCCAGCAGGCTTCAGGACAGGGGTTGTTGTGGGAGGCAACAGCAAGTGAT

HUM: TCAAGTGGAATTTGTTAGTGGTACCCTCCATCAATACAAAGAAAAATCAT
UAM: TCAAGTGGAATTTGTTAGTGGTACCCTCCATCAATACAAAGAAAAATCAT

HUM: AATCCTCAGGGACACCCTTGTCAGCACAGTCTCCCTCAAAATGACCAACC
UAM: AATCTTCAGGGACACCCTTGTCAGCACAGTCTCCCTCAAAATGACCAACC

HUM: TGAGAGCCGAGGAGAAGGCCATGTATTACTGTGAGAGA
UAM: TGAGAGCCGAGCAGAAGGCCATGTATTAC--TGAGAGA
```

D7
```
HUM: CACAGGA
UAM: CACAGGA
```

D9
```
HUM: ACAGGGGACAC
UAM: ACAGGAGACAC
```

Alignment stats: 'M': 276, 'I': 0, 'D': 2, 'X': 10

IGHV3-76

GENE ALIGN SEQ

HUM: GAAGTGTAGCTGGTAGAGTCTGGGGGAGGCTTGGTACAGCTTGGGGGGTC
UAM: GAAGTGTAGCTGTTAGAGTCTGGGGGAGGCTTGGTAAAGCCTGGGGGGTC

HUM: CATGTGACTCTCCTGTGCAGCCTCTGGATACACTTTCAGTAACTATGGCA
UAM: CATGTGACTCTCCTGTGCAGCCTCTGGATACACCTTCAGTAGCTATGGCA

HUM: TGCACTAGGTGGACCAAGCTCCAGGGAAGGGACTGGAGTGGGTCTTACAT
UAM: TGCACTAGGTGGACCAAACTCCAAGGAAGGGACTGGAGTGGGTCTTACAT

HUM: TAATGCTAGTGGTGGAGGCATATACTACTCAGACTCTGTGAAGGGCCGGT
UAM: TAATGCTAGTGGTGGAAGCACATACTACTCAGACTCTTTGAAGGGCCGAT

HUM: TGACCATCTCCAGAGAAAACACCAAGAACTCACTGTATCTGCAAATAAAC
UAM: TCACCATCTCCAGAGAAAACACCAAGAACTCACTGTATCTGCAAATAAAC

HUM: AGTTTCATTGCTGACACCATGGCCGTCTATTACTGTAAGAGA
UAM: AGTTTGATTGCTGACACCATGGCTGTCTATTACTGTAAGAGA

D7
HUM: CACAGTG
UAM: CACAGTG

D9
HUM: GTCACAAACCT
UAM: GTAACAAACCT

Alignment stats: 'M': 278, 'I': 0, 'D': 0, 'X': 14

8

IGHV3-74

GENE ALIGN SEQ

HUM: GAGGTGCAGCTGGTGGAGTCCGGGGGAGGCTTAGTTCAGCCTGGGGGGTC
UAM: GAGGTGCAGCTGTTGGAGTCAGGGGGAGGCTTGGTACAGCCTGAGGGGTC

HUM: CCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTACTGGA
UAM: CCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAACTACTACA

HUM: TGCACTGGGTCCGCCAAGCTC-CAGG-GAAGGGGCTGGTGTGGGTCTCAC
UAM: TGAACTGGGTCTGCCAGGCTCT--GGAGAAGGGGTTGGAGTGGTTCTCAC

HUM: GTATTAATAGTGATGGGAGTAGCACAAGCTACGCGGACTCCGTGAAGGGC
UAM: CTATTAATAGAGATGGGAGTAGCATAAGCTATGCAGACTCCATGAAGGGC

HUM: CGATTCACCATCTCCAGAGACAACGCCAAGAACACGCTGTATCTGCAAAT
UAM: CAATTTACCATCTCCAGAGACAACGCCAAGAACACGCTATATCTGCGAAT

HUM: GAACAGTCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCA--AGAGA
UAM: GAACAGTCTGAGAGCCGAGAACACGACTGTGTATTACTGT--ACTAGAGA

D7
HUM: CACAGTG
UAM: CGCAGTG

D9
HUM: GACACAAACCT
UAM: GACACAAACCT

Alignment stats: 'M': 266, 'I': 4, 'D': 4, 'X': 26

9

IGHV3-73

GENE ALIGN SEQ

```
HUM: GAGGTGCAGCTGGTGGAGTCCGGGGGAGGCTTGGTCCAGCCTGGGGGGTC
UAM: GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTAGTCCAGCCTGGCGGGTC

HUM: CCTGAAACTCTCCTGTGCAGCCTCTGGGTTCACCTTCAGTG-GCTCTGCT
UAM: CCTGAGACTCTCCTGTGCTGCCTCTGGATTCACCTCCAGTGA------CT

HUM: A------TGCACTGGGTCCGCCAGGCTTCCGGGAAAGGGCTGGAGTGGGTT
UAM: ACCAGATGTACTGGGTGCGCCAGGCTTCTGGGAAAGGACCGGAGTGGGTT

HUM: GGCCGTATTAGAAGCAAAGCTAACAGTTACGCGACAGCATATGCTGCGTC
UAM: GGCTATATTGGAAGCAAATCTAACAGTTATGCGACAGCATACGCTGCGTC

HUM: GGTGAAAGGCAGGTTCACCATCTCCAGAGATGATTCAAAGAACACGGCGT
UAM: TGTGAAAGGCAGGTTCACCATCTCAAGAGATGATTCAAAGAACACACCGT

HUM: ATCTGCAAATGAACAGCCTGAAAAACCGAGGACACGGCCGTGTATTACTGT
UAM: ATCTGCAAATGAACAGCCTGAAAAACCGAGGACACGGCCCTGTATTACTGT

HUM: ACTAGACA
UAM: GCTAGATA
```

D7
```
HUM: CACAGTG
UAM: CACAGTG
```

D9
```
HUM: GACACAAACCT
UAM: GATACAAACCT
```

Alignment stats: 'M': 271, 'I': 6, 'D': 6, 'X': 25

IGHV3-72

GENE ALIGN SEQ

```
HUM: GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGAGGGTC
UAM: GAGGTGCAGCTGGTGGAGTCTGGGGGTAGGCTTGGTCCAGCCTGGGGGGTC

HUM: CCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTGACCACTACA
UAM: CCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTGACCACTACA

HUM: TGGACTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGGTTGGCCGT
UAM: TGGACTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGGTTGCCCGT

HUM: ACTAGAAACAAAGCTAACAGTTACACCACAGAATACGCCGCGTCTGTGAA
UAM: ATTAGAAACAAAGCTAACAGTTACACCACAGAATACGCCGCGTCTGTGAA

HUM: AGGCAGATTCACCATCTCAAGAGATGATTCAAAGAACTCACTGTATCTGC
UAM: AGGAAGATTTACCATCTCAAGAGATGATTCAAAGAACACACTGTATCTGC

HUM: AAATGAACAGCCTGAAAACCGAGGACACGGCCGTGTATTACTGTGCTAGA
UAM: AAATGAGCAGCCTGAAAACCGAGGACACGGCCGTGTATTACTGTGCTAGA

HUM: GA
UAM: GA
```

D7
```
HUM: CACAGCG
UAM: CACAGTG
```

D9
```
HUM: GACACAAACCT
UAM: GACACAAACCT
```

Alignment stats: 'M': 294, 'I': 0, 'D': 0, 'X': 8

IGHV2-70

GENE ALIGN SEQ

```
HUM: CAGGTCACCTTGAGGGAGTCTGGTCCTGCGCTGGTGAAACCCACACAGAC
UAM: CAGGTCACCTTGAAGGAGTCTGGTCCTGCGCGTTGGTGAAACCCACACAGAC

HUM: CCTCACACTGACCTGCACCTTCTCTGGGTTCTCACTCAGCACTAGTGGAA
UAM: CCTCACGCTGACCTGCACCTTCTCTGGGTTCTCACTCAGCACTAGTGGA-

HUM: TGT--GTGTGAGCTGGATCCGTCAGCCCCCAGGGAAGGCCCTGGAGTGGC
UAM: -GTGGGTGTGGGCTGGATCCGTCAGCCCCCAGGGAAGGCCCTGGAGTGGC

HUM: TTGCACTCATTGATTGGGATGATGATAAATACTACAGCACATCTCTGAAG
UAM: TTGCAAGAATTGATTGGGATGATGATAAATACTACAGCCCATCTCTGAAG

HUM: ACCAGGCTCACCATCTCCAAGGACACCTCCAAAAACCAGGTGGTCCTTAC
UAM: AGCAGGCTCACCATCTCCAAGGACACCTCCAAAAACCAGGTGGTCGTTAC

HUM: AATGACCAACATGGACCCTGTGGACACAGCCACGTATTACTGTGCACGGA
UAM: AATGACCAACATGGACCCTGTGGACACAGCCACATATTACTGTGCACGGA

HUM: TAC
UAM: TAC
```

D7
```
HUM: CACAGAG
UAM: CACAGAG
```

D9
```
HUM: TACAAGAACCC
UAM: TACAAGAACCC
```

Alignment stats: 'M': 288, 'I': 2, 'D': 2, 'X': 11

IGHV1-69D

GENE ALIGN SEQ

```
HUM: CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTC
UAM: CAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTC

HUM: GGTGAAGGTCTCCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTA
UAM: AGTGAAGATCTCCTGCAAGGTTTCTGAAGACACCTTCAGCAGCTATGCTA

HUM: TCAGCTGGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGAGGG
UAM: TCAGCTGGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGAGTG

HUM: ATCA-TCCCTATCTT--TGGTACAGCAAACTACGCACAGAAGTTCCAGGG
UAM: ATCATTCC---TGTTGCTGGTATAACAAACTACGCACAGAAGTTTCAGGG

HUM: CAGAGTCACGATTACCGCGGACGA-ATCCACGAGCACAGCCTACATGGAG
UAM: CAGAGTCACGATTACTGCGGAC-ACATCCACGAGCACAGCCCACATGGAG

HUM: CTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGA--GA
UAM: CTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGC-AAC-A

HUM: GA
UAM: GA
```

D7
```
HUM: CACAGTG
UAM: CACAGTG
```

D9
```
HUM: GTCAGAAACCC
UAM: GTCAGAAACCC
```

Alignment stats: 'M': 277, 'I': 6, 'D': 6, 'X': 13

IGHV2-70D

GENE ALIGN SEQ

HUM: CAGGTCACCTTGAAGGAGTCTGGTCCTGCGCTGGTGAAACCCACACAGAC
UAM: CAGACCACCTTGAAGGAGTCTGGTCCTGCGCTGGTGAAATCCACACAGAC

HUM: CCTCACACTGACCTGCACCTTCTCTGGGGTTCTCACTCAGCACTAGTGGAA
UAM: CCTCACGCTGACCTGCACCTTCTCTGGGGTTCTCACTCAGCACTAGTGGAG

HUM: TGCGTGTGAGCTGGATCCGTCAGCCCCCAGGGAAGGCCCTGGAGTGGCTT
UAM: TGGGTGTGGGCTGGATCCGTCAGCCCCCCAGGGAAGGCCCTGGAGTGGCTT

HUM: GCACGCATTGATTGGGATGATGATAAATTCTACAGCACACATCTCTGAAGAC
UAM: GCAAGCATTGATTGGGATGATGATAAATACTACAGCCCATCTCTGAAGAG

HUM: CAGGCTCACCATCTCCAAGGACACCTCCAAAAACCAGGTGGTCCTTACAA
UAM: CAGGCTCACCATCTCCAAGGACACCTCCAAAAACCAGGTGGTCGTTACAA

HUM: TGACCAACATGGACCCCTGTGGACACAGCCACGTATTACTGTGCACGGATA
UAM: TGACCAACATGGACCCCTGTGGACACAGCCACATATTACTGTGCACGGAGA

HUM: C
UAM: C

D7
HUM: CACAGAG
UAM: CACAGAG

D9
HUM: TACAAGAACCC
UAM: TACAAGAACTC

Alignment stats: 'M': 287, 'I': 0, 'D': 0, 'X': 14

14

IGHV1-69

GENE ALIGN SEQ

```
HUM: CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTC
UAM: CAGGTCCAGCTGGTGCAGTCGGGGGCTGAGGTGAAGAAGCCTGGGTCCTC

HUM: GGTGAAGGTCTCCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTA
UAM: AGTGAAGATCTCCTGCAAGGTTTCTGAAGACACCTTCAGCAGCTATGCTA

HUM: TCAGCTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGAGGG
UAM: TCAGCTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGAGGG

HUM: ATCATCCCTAT-CTTTGGTACAGCAAACTACGCACAGAAGTTCCAGGGCA
UAM: ATCATCCCTGTGC-TTGGTACAGCAGACTATGCACAGAAGTTCCAGGGCA

HUM: GAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACATGGAGCTG
UAM: GAGTCACGATTACCGCGGACACATCAACGAGCACAGCCTACATGGAGCTG

HUM: AGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGA--GAGA
UAM: AGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGC-AAC-AGA
```

D7
```
HUM: CACAGTG
UAM: CACAGTG
```

D9
```
HUM: GTCAGAAACCC
UAM: GTCAGAAACCC
```

Alignment stats: 'M': 281, 'I': 3, 'D': 3, 'X': 12

IGHV1-68

GENE ALIGN SEQ

```
HUM: CAGGTGCAGCTGGGGCAGTCTGAGGCTGAGGTAAAGAAGCCTGGGGCCTC
UAM: CAGGTGCAGCTGGGGCAGTCTGAGGCTGAGGTGAAGAAGCCTGGGGCCTC

HUM: AGTGAAGGTCTCCTGCAAGGCTTCCGGATACACCTTCACTTGCTGCTCCT
UAM: AGTGAAGGTCTCCTGCAAGGCTTCCGGATACACCTTCACCTACTGCTACT

HUM: TGCACTGGTTGCAACAGGCCCCTGGACAAGGGCTTGAAAGGATGAGATGG
UAM: TGCACTGGGTGTGACAGGCCCCTGGACAAGGGCTTGAATGGATGAGATGG

HUM: ATCACACTTTACAATGGTAACACCAACTATGCAAAGAAGTTCCAGGGCAG
UAM: ATCACACTTTGCAATGGTAACGCCAACTGCGCACAGAAGTTCCAGGGCAG

HUM: AGTCACCATTACCAGGGACATGTCCCTGAGGACAGCCTACATAGAGCTGA
UAM: AGTCACCATTACCAGGGACATGTCCCTGAGGACAGCCTACATGGAGCTGA

HUM: GCAGCCTGAGATCTGAGGACTCGGCTGTGTATTACTGGGCAAGATA
UAM: GTAGCCTGAGATCTGAGGACTCGGCTGTGTATTACTGGGCAAGATA
```

D7
```
HUM: CACGGTG
UAM: CACAGTG
```

D9
```
HUM: GTCAGGAACCC
UAM: GTCAGAAACCC
```

Alignment stats: 'M': 281, 'I': 0, 'D': 0, 'X': 15

16

IGHV(III)-67-4

GENE ALIGN SEQ

HUM: AAGTTCAGTGGTGGAGTCAGAGGGGTAAACGTAGTACAGCCCAGTGGTTC
UAM: AAGTTCAGTGGTGGAGTCAGAGGGGTAAACGTTGTACAGCCCAGTGGTTC

HUM: ACTGAGACTTTCTTGCAAAGCGTCTGGATTCACCTTTTCTGGCAACAGCC
UAM: ACTGAGACTTTCTTGCAAAGCGTCTGGATTCACCTTTGCTGGCAACAGCC

HUM: TGAGGTTGGTCCAGCAGGCTTCACAACAGGGATTGTGGTGGCTGGCAACA
UAM: TGAGGTTGGTCCAGCAGGCTTCACAACAGGGACTGTTGTGGCTGGCAATA

HUM: GTGAGTCAACAAGTGGGAGTGCTCAGGTTTACTCTTCATGAGTACAAATA
UAM: GTGAGTCATCAAGTGGGAGTGCTCAGGGTTACTCTTCATGAGTACAAATA

HUM: AATTAACTGGTCCAGCGACACCCTTTCACGTGCACTCTACCTTACAATGA
UAM: AATTAACTGGTCCAGTGACACCCTTTCACGTGCAGTCTACCTTACAATGA

HUM: CTAACCTGAAAGCCAAGGACAAGGTTGTGTAATACTGTGAGCTT
UAM: CTAACCTGAAAGCCAAGGACAAGGTTGTGTAATACTGTGGGGTT

D7

HUM: CACAGGA
UAM: CACAGGA

D9

HUM: AGACACAAAAA
UAM: AGACACAAAAA

Alignment stats: 'M': 283, 'I': 0, 'D': 0, 'X': 11

17

IGHV(III)-67-3

GENE ALIGN SEQ

HUM: CAGCCTGGCTGTTCTCTTAGCCTCTTTTGCAAAGCATCAAGATTCACCTT
UAM: CAGCCTGGCTGTTCTCTTAGCCTCTTCTGCAAAGCATCAAGATTCGCCTT

HUM: CACTGACTACAGCATA-AATTGAGCCCAGATGGCTGGGGGACAGAGGCTG
UAM: CACTGACTACAGCA-AGAATTGAGCCCAGATGGCTGGAGGAGAGAGGCTG

HUM: GAGTGGGTGGTAACAGTGATTGATTCAAGTGGAAGTTCTCAGTGATATTC
UAM: GAGTGGGTGGTAACAGTGATTGATTCAAGTGTAAGTTCTCAGTGATACTC

HUM: TGCATCAGCATAATGAAGATTCACAATTCCCAGGGACACCAATTACCAGC
UAM: TGCATCAGCACAATGAAGATTCACAATTCCCAGGGACACCAATTACCAGC

HUM: ACAGTCTCCCTTAAAATAATCTAC-TTGGAAGCTGAGGGGGCTCTCACAG
UAM: ACAGTCTCCCTTAAAATAATCT-CTTTGCAAGCTGAGGGGGCTCTCACAG

HUM: GGGTAGGCAGTGTATTACTGTGAGAGA
UAM: AGGTAGGCAGTGTATTACT----GAGA

D7
HUM: CACAGCG
UAM: CACAGCG

D9
HUM: ACAGAAACCTC
UAM: ACAGAAACCTT

Alignment stats: 'M': 260, 'I': 2, 'D': 6, 'X': 9

IGHV(III)-67-2

GENE ALIGN SEQ

HUM: GATTTATTGTCTCCAGAGACAATGTCAAGAATATGCTATATCTGCAAATG

UAM: GATTTATCATCTCCAGAGACAATGTCAAGAATATGCTGTATCTGCAAATG

HUM: GGCGATCTGTAAACCAAGAACACATCAGTATATCACTGTGCAAGAGGAG

UAM: GGCAATCTGTAAACCAAGAACACATCAGTATATCACTGTGCAAGAGGAG

D7

HUM: CACATGA

UAM: CACATGA

D9

HUM: ACATAAACCTC

UAM: ACATCAACCTC

Alignment stats: 'M': 95, 'I': 0, 'D': 0, 'X': 4

19

IGHV(II)-67-1

GENE ALIGN SEQ

```
HUM:  AGGAGCAGCTACAGCAGTCATGCCTAGGTGTGAAGATCACACACTGACCT
UAM:  AGGAGCAGCTACAGCAGTCATGCCTAGATGTGAAGATCACACACTGACCT

HUM:  CACCCATGCTGTCTCTGGCCACTTCATCACAACCAATGCTTAATATTGGA
UAM:  CACCCATGCTGTCTCTGGCCACTTCATCACAACCAATGCTTAATACTGGA

HUM:  CGTGGATCTGCCAGTCCCCGGGGAATGGGTTGAATGGAT
UAM:  CGTGGATCTGCCAGTCCCCAGGGAATGGGTTGAATGGAT
```

D7

```
HUM:  AAAATGC
UAM:  AAAATGC
```

D9

```
HUM:  CATTCCTACTG
UAM:  CAGTCCTACTG
```

Alignment stats: 'M': 136, 'I': 0, 'D': 0, 'X': 3

IGHV1-67

GENE ALIGN SEQ

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

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

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

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

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

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

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

Alignment stats: 'M': 283, 'I': 2, 'D': 4, 'X': 13

IGHV3-66

GENE ALIGN SEQ

```
HUM: GAGGTGCAGCTGGTGGAGTCTGGAGGAGGCTTGATCCAGCCTGGGGGGTC
UAM: GAGGTGCAGCTGGTGGAGTCTGGGGGGAGGCTTGGTACAGCCTGGGGGGTC

HUM: CCTGAGACTCTCCTGTGCAGCCTCTGGGTTCACCGTCAGTAGCAACT-AC
UAM: CCTCAGACTCTCCTGTGCAGCCTCTGGATTCACCGTCAGTAGCAA-TGAG

HUM: ATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCAGT
UAM: ATGAGCTGGATCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCAAC

HUM: TATT--TATAGCTGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCG
UAM: CATTAGTATAG--GTGGTAGCACATACTACACAGACTCCGTGAAGGGCAG

HUM: ATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTTCAAATGA
UAM: ATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTTCAAATGA

HUM: ACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAGA
UAM: ACAGCCTGAGGGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGA
```

D7
```
HUM: CACAGTG
UAM: CACAGTG
```

D9
```
HUM: GACACAAACCT
UAM: GACACAAACCT
```

Alignment stats: 'M': 276, 'I': 3, 'D': 3, 'X': 14

IGHV(II)-65-1

GENE ALIGN SEQ

```
HUM: CAACAACTGTGTTTCTCCTGCACTCTTGGGCTAGTGAAGCTCTCACAGAC
UAM: CAACAACTGTGTTTCTTCTGCACTCTTGGGCTAGTGAAGCTCTCACCGAC

HUM: CCTCTCTCTCACCTGTGCTGTCTCTGCATTCTCCATCACAACCAGTGCTT
UAM: CCTCTCTCTCACCTGTGCTGTCTCTGCATTCTCCATCACAACCAGTG-TT

HUM: CCTGCTGGAGCTGCATCCATCA-CCCCCCGCAAGGAAGGGACTGGAGCGA
UAM: CCTGCTGGAACTGCATCCATCAGCCCCCC-CAAGGAAGGGACTGGAGTGA

HUM: ATCAGGTGCACAGGTCATGAGGGAGTGCACATTCCAACCCACTCCTCAAG
UAM: ATCAGGTGCACAGGTCATGAGGGAGTGCACAATCCAACCCACTCCTCAAG

HUM: AGTCCAGTCACTATCTCCAGATCCACATCCAAAAAACAGTGTTTCCTGTA
UAM: AGTCCAGTCACCATCTCCAGATCCACATCCAAAAAACAGTGTTTCCTACA

HUM: GCTGAGCTACCTGAGCAACAAGTACACAACCATGA--ATTTTAATACAAA
UAM: GCTGAGCTACCTGAACAACGAGTACACAACCATGAGT-TTTTA-TACAAA

HUM: AGA
UAM: AGA
```

D7
```
HUM: CACAACG
UAM: TACAGCG
```

D9
```
HUM: GATACAAACCT
UAM: GATACAAACCT
```

Alignment stats: 'M': 286, 'I': 3, 'D': 4, 'X': 10

23

IGHV3-64

GENE ALIGN SEQ

HUM: GAGGTGCAGCTGGTGGAGTCTGGGGAAGGCTTGGTCCAGCCTGGGGGGTC
UAM: GAGGTGCAGCTGGTGGAGTCTGGGGGAGACTTGGTACAGCCTGGGGGGTC

HUM: CCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGCTA
UAM: CCTAAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGCTA

HUM: TGCACTGGGTCCGCCAGGCTCCAGGGAAGGGACTGGA-ATATG--TT-TC
UAM: TGCACTGGGTCCGCCAGGCACCAGGGAAGGGTCTGGAG---TGGG-TCTC

HUM: AGCTATT-AGTAGTAATGGGGGTAGCACATATTATGCAGACTCTGTGAAG
UAM: AGTTATTTA-TAGTGGTGGGAGTAGCACATACTATGCAGACTCTGTGAAG

HUM: GGCAGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTTCA
UAM: GGCAGATTCACCATCTCCAGAGACAATGCCAAGAACACACTGTATCTTCA

HUM: AATGGGCAGCCTGAGAGCTGAGGACATGGCTGTGTATTACTGTGC---GA
UAM: AATGAACAGTCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCAAA-A

HUM: GAGA
UAM: GACA

D7
HUM: CACAGTG
UAM: CACAGTG

D9
HUM: TGCAGAAACCT
UAM: TACAGAAACCT

Alignment stats: 'M': 271, 'I': 8, 'D': 6, 'X': 19

IGHV3-63

GENE ALIGN SEQ

HUM: GAGGTGGAGCTGATAGAGTCCATAGAGGGCCTGAGACAACTTGGGAAGTT
UAM: GAGGTGCAGCTGATAGAGTCCATAGAGGACCTGAGACAACCTGGGAAGTT

HUM: CCTGAGACTCTCCTGTGTAGCCT-C-TGGATTCACCTTCAGTAGCTACTG
UAM: CCTGAGACTCTCCTGTGTAGCCTACA--GATTCACCTTCAGTAACTACTG

HUM: AATGAGCTGGGTCAATGAGACTCTAGGGAAGGGGCTGGAGGGAGTAATAG
UAM: AATGAGCTGGATCAATGAGACTCTAGGGAAGGGGCTGGAGGGAGTAATAG

HUM: ATGTAAAATATGATGGAAGTCAGATATACCATGCAGACTCTGTGAAGGGC
UAM: ATGTAAAATACGATGGAAGTCAGATATACCATGCAGACTCTGTGAAGGGC

HUM: AGATTCACCATCTCCAAAGACAATGCTAAGAACTCACCGTATCTGCAAAC
UAM: AGATTCACCATCTCCAAAGAAAATGCTAAGAACTCGCCGTAACTGCAAAC

HUM: GAACAGTCTGAGAGCTGAGGACATGACCATGCATGGCTGTACATAAGGTT
UAM: GAACAGTCTGAGAGCTGAGGACATGGCCATGCACGGCTGTACATAAGGTT

D7
HUM: CCAAGTG
UAM: CCAAGTG

D9
HUM: GACACAAAATT
UAM: GACACAAAATT

Alignment stats: 'M': 285, 'I': 2, 'D': 2, 'X': 11

IGHV(II)-62-1

GENE ALIGN SEQ
```
HUM: GGCCTGGTGAAGCCCTCACAGACCCTCTCCCTCATGTGTGTCATCTCTGC
UAM: GGCCTGGTGAAGCCCTCACAGACCCTCTCCCTCCTGTGTGCCATCTCTGC

HUM: ATTCTCCATCACAACCAGTGCTTCCTCCTGGAGCTGCATCCATCAGCCCC
UAM: ATTCTCCATCACAACCAGTGTTTCCTCCTGGAGCTGCATCCCTCAGCCC-

HUM: TCTC--TGGGAGGGAATGGAGTGGATTGGGTGCATAGGTCATGAAGGGAG
UAM: --TCAC-GGGAGGGAATGGAGTGGATCGGGTGCATAGGTCACGGAGGGAG

HUM: CACACATTACTCCCCTTTCCTCAAGAGTCCAGTCACCATCCCCAGATCCA
UAM: CACACATTACTCCCCTCTCCTCAAGAGTCCAGTCACCATCCCCTGATCCA

HUM: TGTCCAAAAACAGTTCTTCCTACAGCTGAGCTACATGAGCAACAATCACA
UAM: TGTCCAAAAACAGTTCTTCCTACAGCTGAGCTACATGAGCAATAATCACA

HUM: TAGCCATATATTTTTAAGCAAAAGA
UAM: TAGCCACGTATTTTTAAGCAAAAGA
```

D7
```
HUM: CACAGTG
UAM: CACAGTG
```

D9
```
HUM: CACCAAAACCT
UAM: CACCAAAACCT
```

Alignment stats: 'M': 257, 'I': 2, 'D': 4, 'X': 12

IGHV4-61

GENE ALIGN SEQ

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

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

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

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

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

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

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

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

HUM: A - - G A
UAM: A T A - A
```

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

Alignment stats: 'M': 93, 'I': 106, 'D': 201, 'X': 5

IGHV(II)-60-1

GENE ALIGN SEQ

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

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

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

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

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

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

D9
```
HUM:  C A C C C A A A C C T
UAM:  C A C C C A A A C C T
```

Alignment stats: 'M': 260, 'I': 3, 'D': 1, 'X': 8

IGHV3-60

GENE ALIGN SEQ

```
HUM: GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTAGTAAAGACT--------G
UAM: GAGGTGCAGCTGGTGGAGTCTAGGGGAGGCTTAGTAAAGACTTGGGGGC-

HUM: GAGGGGTCTCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAG
UAM: --GGGGTCTCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAG

HUM: CTCTGCTATGCACTGGGTCCACCAGGCTCCAGGAAAGGGTTTGGAGTGGG
UAM: CTATGCTATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTCGAGTGGG

HUM: TCTCAGTTATTAGTACAAGTGGTGATACCGTACTCTACACAGACTCTGTG
UAM: TCTCAGTTATTAGTACAAGTGGTGGTACCAAACTCTACACAGACTCTGTG

HUM: AAGGGCTGATTCACCATCTCTAGAGACAATGCCCAGAATTCACTGTCTCT
UAM: AAGGGCCGATTCACCATCTCCAGAGACAATGTCCAGAACTCACTGTATCT

HUM: GCAAATGAACAGCCTGAGAGCCGAGGGCACA-G--TTGTGTACTACTGTG
UAM: GCAAATGAACAGCCTGAGAGCCGAGG--ACACGGC-TGTGTATTACTGTG

HUM: -TGAAAGA
UAM: C---AAGA
```

D7
```
HUM: CGCAGTG
UAM: GAGGCAG
```

D9
```
HUM: ACAAACCTCCT
UAM: ACACAAACCTC
```

Alignment stats: 'M': 274, 'I': 11, 'D': 9, 'X': 14

IGHV4-59

GENE ALIGN SEQ

```
HUM: CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGAC
UAM: CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGAC

HUM: CCTGTCCCTCACCTGCACTGTCTCTGGTGGCTCCATCAGTAGTTACTACT
UAM: CCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCCATCAGTAGTAACTACT

HUM: GGAGCTGGATCCGGCAGCCCCCAGGGAAGGGACTGGAGTGGATTGGGTA-
UAM: GGAGCTGGATCCGGCAGCCACCAGGGAAGAGACTGGAGTGGATTGGG-AG

HUM: TATCTATTACAGTGGGAGCACCAACTACAACCCCCTCCCTCAAGAGTCGAG
UAM: TATCTATTCCAGTGGGAGCACCTACTACAACCCGTCCCTCAAGAGTCGAG

HUM: TCACCATATCAGTAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGC
UAM: TCACCATATCAATAGACTCGTCCAAGAACCAGTTCTCCCTGAAGCTGAGC

HUM: TCTGTGACCGC-TGCGGACACGGCCGTGTATTACTGTGCGAGAGA
UAM: TCTGTGACCGCCT-CGGACACGGCCGTGTATTACTGTGCGAGAGA
```

D7
```
HUM: CACAGTG
UAM: CACAGTG
```

D9
```
HUM: GACAAAAACCT
UAM: GACAAAAACCT
```

Alignment stats: 'M': 282, 'I': 2, 'D': 2, 'X': 9

IGHV1-58

GENE ALIGN SEQ
```
HUM: CAAATGCAGCTGGTGCAGTCTGGGCCTGAGGTGAAGAAGCCTGGGACCTC
UAM: CAAATGCAGCTTGTGCAATCTGGGCCTGAGGTTAAGAAGCCTGGGGCCTC

HUM: AGTGAAGGTCTCCTGCAAGGCTTCTGGATTCACCTTTACTAGCTCTGCTG
UAM: AGTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTTACTAGCTCTGCTA

HUM: TGCAGTGGGTGCGACAGGCTCGTGGACAACGCCTTGAGTGGATAGGATGG
UAM: TGCAGTGGGTGTGACAGGCTCCTGGACAAGGCCTTGAGTGGATAGAATGG

HUM: ATCGTCGTTGGCAGTGGTAACACAAACTACGCACAGAAGTTCCAGGAAAG
UAM: ATCATCGTTGGCAGTGGTAACGCAAACTACGCACAGAAGTTCCAGG---G

HUM: -AGTCACCATTACCAGGGACATGTCCACAAGCACAGCCTACATGGAGCTG
UAM: CAGTCACCAATACCAGGGACACGTCCACGAGCACAGCCTACATGGAGCTG

HUM: AGCAGCCTGAGATCCGAGGACACGGCCGTGTATTACTGTGCGGCAGA
UAM: AGCAGCCTGAGATCCAAGGACATGGCCGTGTATTACTGTGCGGCAGA
```

D7
```
HUM: CACAGTG
UAM: CACAGTG
```

D9
```
HUM: GTCAGAAACGC
UAM: GTCAGAAACCC
```

Alignment stats: 'M': 276, 'I': 1, 'D': 3, 'X': 17
```

**IGHV3-57**

GENE ALIGN SEQ

HUM: GAAGTTTATTGATGGAGTCAGAGGCAGAAAATTGTACAGCCCAGTGGTTC
UAM: GAAGTTTATTGATGGAGTCAGAGGGGGAAAATTGTACAGTGCAGGGGTTC

HUM: ACTGAGACTCTCCTGCAAAGCCTCTGATTTCACCTTTACTGGCTACAGCA
UAM: ACTGAGACTCTCCTGCAAAGCCTCTGATGTCACCTTCACTGGCTACAGCA

HUM: TGAGCTTGGTCCAGCAGGCTTCATGACAGGGATTGGTGTGGGTGGAAACA
UAM: TGACCTTGGTCCATCAGGCTTCATGACAGAGATTGGTGTGGGTGGAAACA

HUM: GTGAGTGATCAAGT--GGGAGTTCTCAGAGTTACTCTCCATGAGTACAAA
UAM: GTGAGTGATCA--TGCGGGAGTTCTCAGAGTTACTCTCCTTGAGTACAAA

HUM: TAAATTAACAGTCCCAAGCGACACCTTTTCATGTGCAGTCTACCTTACAA
UAM: TAAATTAACAGTTCCAAGCGACGCCTTTTCATGTGCAGTCTACCTTACAA

HUM: TGACCAACCTGAAAGCCAAGGACAAGGC--TGTGTA-TTACTGTGAGGGA
UAM: TGACCAACCTGAAAGTCAAGGGCAAGGCCTTGT-TAG--ACTGTGAGGGA

D7
HUM: CACAGGA
UAM: CACAGGA

D9
HUM: AGACACAAAAA
UAM: AGACAGAAAAA

Alignment stats: 'M': 275, 'I': 5, 'D': 5, 'X': 15

**IGHV7-56**

GENE ALIGN SEQ

```
HUM:  CGAGTGCAGCTGGTGCAGTCTGGGCCTGAGGTGAAGCAGCCTGGGGCCTC
UAM:  CGAGTGCAGCTGGTGCAGTCTGGGCCTGAGGTGAAGCAGCCTGGGGAC-C

HUM:  GGCGAAGGTCTCCTGCAAGG-TGTCTGGTTAAACTGTCATCACCTATGGT
UAM:  GGTGAAGTTCTCCTGCAAGGCT-TCTGGTTAAACTGTCATCACCTATGGT

HUM:  ATGAATTGGATACGACAGACCCCAGGACAGGGGCTTGAGTGGATGGGATG
UAM:  ATGAATTGGATATGACAGACCCCAGGACAGGGGCTTGAGTGGATGGAATG

HUM:  GATCATCCTACCCTGGTGAACCCAATGTATGCCCACAGATTCACACACGG
UAM:  GATCATCCTACCCTGGTGAACCCAACGTATGCCCACAGCTTCACACACGG

HUM:  TTTGTCTTCTCCATGGACACCTCTGTCAGCACGGCGGATCTGCAGACTAG
UAM:  TTTGTCTTCTCCATGGACACATCTGTCAGCATGGCAGATCTGCAGACTAG

HUM:  CTGCCTAAAGACTGAGGATGCAGCCATTTATTACTGTGTGAGGTA
UAM:  CTGCCTGAAGACTGAGGATGCAGCCATTTATTACTGTGTGAGGTA
```

D7
```
HUM:  CACCGTG
UAM:  CACCGTG
```

D9
```
HUM:  TTTAGAAACCC
UAM:  TTTAGAAACCC
```

Alignment stats: 'M': 281, 'I': 1, 'D': 2, 'X': 11

IGHV4-55

GENE ALIGN SEQ

```
HUM: CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGAC
UAM: CAGGTGCAGTTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGAC

HUM: CCTGTCCCTCATCTGCGCTGTCTCTGGTGACTCCATCAGCAGTGGTA--A
UAM: CCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCCATCAGTAGT--TACTA

HUM: CTGGTGA------ATCTGGGTCCGCCAGCCCCCAGGGAAGGGGCTGGAGTG
UAM: CTGG--AGCTGGAT-------CCGGCAGCCACCAGGGAAGGGGCTGGAGTG

HUM: GATTGGGG--AA---A-TCCATCATAGTGGGAGCACCTACTACAACCCGT
UAM: GATTGGGGGT-ATCTATTCC-----AGTGGGAGCACCTACTACAACCCGT

HUM: CCCTCAAGAGTCGAATCACCATGTCCGTAGACACGTCCAAGAACCAGTTC
UAM: CCCTCAAGAGTCGAGTCACCATATCAGTAGACACGTCCAAGAACCAGTTC

HUM: TACCTGAAGCTGAGCTCTGTGACCGCCGCGGACACGGCCGTGTATTACTG
UAM: TCCCTGAAGCTGAGCTCTGTGACCGCCGCGGACACGGCCGTGTATTACTG

HUM: TGCGAGATA
UAM: TGCGAGAGA
```

D7
```
HUM: CACAGTG
UAM: CACAGTG
```

D9
```
HUM: GACACAAACCT
UAM: GACAAAAACCT
```

Alignment stats: 'M': 269, 'I': 13, 'D': 16, 'X': 11

IGHV3-54

GENE ALIGN SEQ

```
HUM:  GG - - 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
UAM:  G G G G - T C G 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 A A C C T T C A G T A G C

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

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

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

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

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

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

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

Alignment stats: 'M': 239, 'I': 6, 'D': 5, 'X': 6

IGHV(II)-53-1

GENE ALIGN SEQ

```
HUM: GGCCTGGTGAAGCCCTCACAGACCCTCTCCCTCACCTGTGCTGTCTCTGG
UAM: GGCCTGGTGAAGCCCTCACAGACCCTCTCCATTACCTGTGCCGTCTCTGG

HUM: ATTCCCCATCACAACCAGTGCTTCCTGCTGTAGCTGCATTCATAAACCCC
UAM: ATTCCCCATCACAACCAGTGTTTCCTGCTGGAGCTGCA-TCATAAATCCC

HUM: CCAGGAAGGGACTGGAGTGAATCCGGTGCACAGGTCATGAGGGAGTGCAC
UAM: CCAGGAAGGGACTGGAGTGAATCCACTGCACAGGTCATGAGGGAGTGCAC

HUM: ATTCCAACCCCACTCCTCAAGAGTCCAGTCACCATCTCCAGATCCATGTCC
UAM: ATTCCAACCTACTCCTCAAGAGTCCAGTCACCATCTCCAGATCCATGTCC

HUM: AAAAAGCAGTTCTTCCTACAGCCGAGCTAAGTGAGCCGCAAGCACACAGC
UAM: AAAAAGCAGTTCTTCCTACAGCTGAGCTAAGTGAGTCGCAAGCACATAGC

HUM: CATGTATTTTTTAACAAAAGA
UAM: CATGTATTTTTTAACAAAAGA
```

D7
```
HUM: CACAGTA
UAM: CACAGTG
```

D9
```
HUM: CACCCAAACCT
UAM: CATCCAAACCT
```

Alignment stats: 'M': 257, 'I': 0, 'D': 1, 'X': 12

IGHV3-53

GENE ALIGN SEQ

HUM: GAGGTGCAGCTGGTGGAGACTGGAGGAGGCTTGATCCAGCCTGGGGGGTC
UAM: GAGGTGCAGCTGGTGGAGTCTGGAGGAGGCTTGGTACAGCCTGGGGGGTC

HUM: CCTGAGACTCTCCTGTGCAGCCTCTGGGTTCACCGTCAGTAGC-AACTA-
UAM: CCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCGTCAGTAGCT--CTAG

HUM: CATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCAG
UAM: CATGATCTGGGTCTGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCA-

HUM: TT--ATTTA-TAG-CGG-TGGTAGCACATACTACGCAGACTCCGTGAAGG
UAM: -TACATT-AGTAGT--GATGGTAGCGCATACTACGCAGACTCCGTGAAGG

HUM: GCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTTCAA
UAM: GTAGATTCACCGTCTCCAGAGACAATTCCAAGAACACGCTGTATCTTCAA

HUM: ATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGA
UAM: ATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTA-TACTGTGCGAAAGA

D7
HUM: CACAGTG
UAM: CACAGGG

D9
HUM: GACACAAACCT
UAM: GACACAAACCT

Alignment stats: 'M': 272, 'I': 7, 'D': 8, 'X': 13

IGHV3-52

GENE ALIGN SEQ

HUM: GAGGTGCAGCTGGTGGAGTCTGGGTGAGGCTTGGTACAGCCTGGAGGGTC
UAM: GAGGTGCAGCTGGTGGAGTCTGGGTGAGGCTTGGTACAGCCTGGAGGGTC

HUM: CCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTCCTGGA
UAM: CCTGAGACTCTCCTTTGCAGCCTCTGGATTCACCTTCAGTAGCTCCTGGA

HUM: TGCACTGGGTCTGCCAGGCTCCGGAGAAGGGGCTGGAGTGGGTGGCCGAC
UAM: TGCACTGGGTCTGCCAGGCTCCAGAGAAGGGGCTGGAGAGGGTGGCCAAC

HUM: ATAAAGTGTGACGGAAGTGAGAAATACTATGTAGACTCTGTGAAGGGCCG
UAM: ATAAAGTGTGATGGAAGTGAGAAATACTATGCAGACTCTGTGAAGGGCCG

HUM: ATTGACCATCTCCAGAGACAATGCCAAGAACTCCCTCTATCTGCAAGTGA
UAM: ATTGACCATCTCCAGAGACAATGCCAAGAACTCTCTCTATCTGCAAATGA

HUM: ACAGCCTGAGAGCTGAGGACATGACCGTGTATTACTGTGTGAGAGG
UAM: ACAGCCTGAGAGCTGAGGACATGGCCGTGTATTACTGTGTGAGAGA

D7
HUM: CACAGTG
UAM: CACAGTG

D9
HUM: GACACAAACCT
UAM: GACACAAACCT

Alignment stats: 'M': 286, 'I': 0, 'D': 0, 'X': 10

IGHV(II)-51-2

GENE ALIGN SEQ

```
HUM: GGCCTGGTGAGGCCCTCAC-AGACCCCCTCCCTCACCTGTGCTGTCTCTG
UAM: GGCCTGGTGAGGCCCTC-CGAGACCCCCTCCCTCACCTGTGCTGTCTCTG

HUM: GATTCTCCATCACAACTAGTGCTTCCTGCTGGAGCTGGATCCGCCAGTCC
UAM: GATTCTCCATCACAACCAGCGCTTCCTGCTGGAGCTGGATCCGCCAGTCC

HUM: TCAGTCAAGGGAGTGGATCAGGGCATAGGTCACGAGGGAGCACAAATTCT
UAM: TCAGTCAAGGAAGTGGATCAGGGCATAGGTAACGAGGGAGCACAAATTCT

HUM: AACCCACTCCTCATGAGCTCAGTCACCATCTCCAGATCCACGTCCAAGAA
UAM: AACCCACTCCTCATGAGCTCAGTCACCATCTCCAGGTCCACGTCCAAGAA

HUM: CCAAATTTTCTTTTAGCTGAGTTCTGTGACCAACAATGCCACAACCTTGT
UAM: CCAAATTTTCTTTTAGCTGAGTTCTGTGACCAACAACGCCACAACCTTGT

HUM: ATTACTGTGAGAGG
UAM: ATTACTGTGAGAGG
```

D7
```
HUM: AACAGAA
UAM: AACAGAG
```

D9
```
HUM: CACAAACTTCC
UAM: CACAAACTTCC
```

Alignment stats: 'M': 256, 'I': 1, 'D': 1, 'X': 6

IGHV5-51

GENE ALIGN SEQ

```
HUM: GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGGAGTC
UAM: GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGGCCCGGGGAGTC

HUM: TCTGAAGATCTCCTGTAAGGGGTTCTGGATACAGCTTTACCAGCTACTGGA
UAM: TCTGAGGATCTCCTGTAAGACTTCTGGATACAGCTTTACCAGCTACTGGA

HUM: TCGGCTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGTGGATGGGGATC
UAM: TCAGCTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGTGGATGGGGAGC

HUM: ATCTATCCTGGTGACTCTGATACCAGATACAGCCCGTCCTTCCAAGGCCA
UAM: ATCTATCCTGGTGACTCTGATACCAGATACAGCCCATCCTTCCAAGGCCA

HUM: GGTCACCATCTCAGCCGACAAGTCCATCAGCACCGCCTACCTGCAGTGGA
UAM: CGTCACCATCTCAGCCGACAAGTCCATCAGCACCACCTACCTGCAGTGGA

HUM: GCAGCCTGAAGGCCTCGGACACCGCCATGTATTACTGTGC---GAGACA
UAM: GCAGCCTGAAGGCCTCGGACACCGCCATGTATTACTGTGCAAA-AG--A
```

D7
```
HUM: CACAGTG
UAM: CACAGTG
```

D9
```
HUM: TCTAAAACCCT
UAM: TCTAAAACCCT
```

Alignment stats: 'M': 284, 'I': 3, 'D': 3, 'X': 9

IGHV3-50

GENE ALIGN SEQ

```
HUM: GGGGTGCAGATGGTGGAGTCTTGGGGAGAGTTGGCACAAGCTGAATGTGC
UAM: GAGGTGCAGGTGGTGGAGTCTTGGGGAGAGTTGGCACAAGCTGGATGTGC

HUM: CTGAGACTCTGCCGTGCATCCTCTGAATCCACCTTCTGTAGCTACTAGAT
UAM: CTGAGACTCTGCTGTGCAGCCTCTGAATCCACCTTCCGTAGCTACTAGAT

HUM: CAGCTGAATCTGCCAGGCTCCAGGAAAGGGGCTGCAGTGAGTAGTAGATA
UAM: CAGCTGAACCTGCCAGGCTTCAGGGAAGGGGCTGCAGTGAATAGTAGATA

HUM: TAATGTACGATGGAAGTCAGACATAATATGCAGACTCTGTGAAGGTCAGA
UAM: TAATGTACGGTGGAAGTCAGACAAAATATGCAGACTCTGTGAAGGTCAGA

HUM: TTCACCATCTCCAAAGACAATGCCAAGCACAGGTTGTATCTGCAAATGAA
UAM: TTCACCATCTCCAAAGACAATGCCAAGCACACGTTGTATCTGCAAATGAA

HUM: CAGTCTGAGAGCTGAGAATATGGCTCTGTATTATTGAGTCAAAGGTA
UAM: CAGTCTGAGAGCTGAGAATATGGCTCTGTATTATTGAGACAAAGGTA
```

D7
```
HUM: CCAAATG
UAM: CCAAATG
```

D9
```
HUM: GACACAAAATT
UAM: GACACAAAATT
```

Alignment stats: 'M': 283, 'I': 0, 'D': 0, 'X': 14

IGHV(II)-49-1

GENE ALIGN SEQ

```
HUM: CGACATCTGTATTTCTCGTGCGTTCTTGGCCTGGCGAAGCCCTCACAGAC
UAM: CGACATCTGTGTTTCTCGTGCATTCTTGGCCTGGCGAAGCCCTCACAGAC

HUM: CCTCTCCCTCATCTGTGCTGTCTCTGC-TTCTCCATCACAACCAGTGCTT
UAM: CCTCTCCCCCATCTGTGCTGTCTCTGCATTCTCCATTTCAAACAGTGCTT

HUM: CCTGCTGGAGCTGGATCCCTCAGCTCCCCAGGGAAGGGACTGGAGTGAAT
UAM: CCTGCTGGAGCTGGATCCATCAGCTCCCCAGGGAAGGGACTGGAGCGAAT

HUM: CAGGTGCACAGGTCATGAGGGAGAACACAACGCAACCCACGCCTCAAGAG
UAM: CAGGTGCACAGGTCATGAGGGAGAGCACAACGCAACCCACTCCTCAAGAG

HUM: TCCAGTCACCATCTCCAGATCCACATCCAAAACACAG--TTTC-TTCTAC
UAM: TCCAGTCACCATCTCCAGATCCACACCCAAAAAACTGTTTTTCG---TAC

HUM: AGCTGAGCTACCTGAGCAACGAGTACACAACCATGAATTTTTACACAAAA
UAM: AGCTGAGCTACCTGAGCAACGAGTACACAACCATGAATTTTTACACAAAA

HUM: GA
UAM: GA
```

D7
```
HUM: TACAGCA
UAM: TACAGCG
```

D9
```
HUM: GAAACAAACCT
UAM: GAAACAAATCC
```

Alignment stats: 'M': 282, 'I': 4, 'D': 3, 'X': 13

IGHV3-49

GENE ALIGN SEQ

HUM: GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGT--ACAGCCAGGGCGG
UAM: GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAC--CCAGGGGGG

HUM: TCCCTGAGACTCTCCTGTACAGCTTCTGGATTCACCTTTGGTGATTATGC
UAM: TCCCTGAGACTCTCCTGTACAGCTTCTGGATTCACCTTTGGTGATTATGC

HUM: TATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTAGGTT
UAM: CATGAGGTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTAGGTT

HUM: TCATTAGAAGCAAAGCTTATGGTGGGGACAACAGAATACGCCGCGTCTGTG
UAM: TCATTAGAAGCAAAGCTTATGGTGGGGACAACAGAATACGCTGCGTCTGTG

HUM: AAAGGCAGATTCACCATCTCAAGAGATGATTCCAAAAGCATCGCCTATCT
UAM: AAAGGCAGATTCACCATCTCAAGAGATGATTCCAAAAGCATCGCCTATCT

HUM: GCAAATGAACAGCCTGAAAACCGAGGACACAGCCGTGTATTACTGTACTA
UAM: GCAAATGAACAGCCTGAAAACCGAGGACACGGCCGTGTATTACTGTGCTA

HUM: GAGA
UAM: GAGA

D7
HUM: CACAGTG
UAM: CACAGTG

D9
HUM: GACACAAACCT
UAM: GACACAAACCT

Alignment stats: 'M': 294, 'I': 2, 'D': 2, 'X': 6

IGHV3-48

GENE ALIGN SEQ

```
HUM: GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGAGGGTC
UAM: GAGGTGCAGCTGGTGGAGTCTGGAGGAGGCTTGGTACAGCCTGGGGGGTC

HUM: CCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGTTATGAAA
UAM: CCTGAGACTCTCCTGTGCAGCCTCTGAATTCACCTTCAGTAGTAATGACA

HUM: TGAACTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTTTCATAC
UAM: TGAGCTGGGTCCACCAGGCTCCAGGGAAGGGACTGGAGTGGGTCTCATAC

HUM: ATTAGTAGTAGTGGTAGTACCATATACTACGCAGACTCTGTGAAGGGCCG
UAM: ATTAGTAACAGTGGTAGAACCACATACTATGCAGACTCCGTGAAGGGCCG

HUM: ATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGA
UAM: ATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGA

HUM: ACAGCCTGAGAGCCGAGGACACGGCTGTGTTTATTACTGTGCGAGAGA
UAM: ACAGCCTGAGAGCCGAGGACACAGCTGTGTTTATTACTGTGCGAGAGA
```

D7

```
HUM: CACAGTG
UAM: CACAGTG
```

D9

```
HUM: GACACAAACCT
UAM: GACACAAACCT
```

Alignment stats: 'M': 280, 'I': 0, 'D': 0, 'X': 16

IGHV(III)-47-1

GENE ALIGN SEQ

```
HUM: GAAGTTAATTACTGGAGTCTCTCAGAGAAATACTACAGACCAAGAATTCT
UAM: GAAGTTAATTAGTGGAGTCTCTCAGAGAAATACTACAGACCAAGAATTCT

HUM: CAGACTTTTCTGGAAACCCTGTGGATTCACTTTCACTGAAAACAGCATAA
UAM: CAGACTTTTCTGGAAAGCCTCTGGATTCACTTTCACTGAAAACAGCATAA

HUM: GCTTGGTCCAGCAGGCTTCATGACAGGGGTGGGTGTAGGTGATAACATCA
UAM: GCTTCGTCCAGCAGGCTTCATGACAGGGGTTGGTGTGGGTGATAACATCA

HUM: GTAATTCAAGTGGAAGTTCTCAGTGGGACTCTCCTTGAGTACAAAGAAGA
UAM: GTAATTCAAGTGGAAGTTCTCAGTGGGACTCTCCTTGACTACAAAGAAGA

HUM: TTAACAGTCCTCAGAGACACGCTTTTCAGATGATTCTCTCTTAAGATGAT
UAM: TTAACAGTCCTCAGAGACACTCTTTTCAGATGATTCTCTCTTTTAAGATGAT

HUM: TAACCTGAGAGCTCAGGAAAATTCCGTTTATTACTGTGAGGGA
UAM: TAACCTGAGAGCTCAGGAAAATTCCGTTTATTACTGTGAGGGA
```

D7
```
HUM: CACGGTG
UAM: CACAGTG
```

D9
```
HUM: GACACAAACCT
UAM: GACACAAACCT
```

Alignment stats: 'M': 284, 'I': 0, 'D': 0, 'X': 9

IGHV3-47

GENE ALIGN SEQ

```
HUM: GAGGATCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTC
UAM: GAGGATCAGCTGGTGGTGTCTGCGGGAGGCTTGGTACAGCCTGGGGGGTC

HUM: CCTGCGACCCTCCTGTGCAGCCTCTGGATTCGCCTTCAGTAGCTATGCTC
UAM: CCTGAGACCCTCCTGTGCAGCCTCTGGATTCGCCTTCAGTAGCTATGTTC

HUM: TGCACTGGGTTCGCCGGGCTCCAGGGAAGGGTCTGGAGTGGGTATCAGCT
UAM: TGCACTGGGTTCGCCGGGCTCCAGGGAAGGGTCTGGAGTGGGTATCAGCT

HUM: ATTGGTACTGGTGGTGATACATACTATGCAGACTCCGTGATGGGCCGATT
UAM: ATTGGTACTGGTGGTGATACATACTATGCAGACTCCGTGATGGGCCGATT

HUM: CACCATCTCCAGAGACAACGCCAAGAAGTCCTTGTATCTTCATATGAACA
UAM: CACCATCTCCAGAGACAATGCCAAGAAGTCCTTGTATCTTCAAATGAACA

HUM: GCCTGATAGCTGAGGACATGGCTGTGTATTATTGTGCAAGAGA
UAM: GCCTGATATCTGAGGACACGGCTGTGTATTACTGTGCAAGAGA
```

D7
```
HUM: CACAGTG
UAM: CACAGTG
```

D9
```
HUM: GATACAAACTT
UAM: GATACAAACTT
```

Alignment stats: 'M': 284, 'I': 0, 'D': 0, 'X': 9

46

IGHV(II)-46-1

GENE ALIGN SEQ

```
HUM: CAGGAGCAGCTGCAGGAGTCAGCCCTGGACCTGAATAGCACACACTTACC
UAM: CAGGAGCAGCTGCAGGAGTCAGCCCTGGACCTGAATAGCACACACTTACC

HUM: CTCTGCCTCACCTACACTGTTACTGGCCACTCCGTCACAACCAGTCCTTA
UAM: CTCTGCCTCACCTACACCGTTTCTGGCCACTCCATCACAACCAGTCCTTA

HUM: CTAGTGGACCTGGATCTGCCGGCTCTCAGGGAGGGGCTGCAATGGAT
UAM: CTAGTGGACCTGGATCTGCCAGCTCTCAGAGAGGGGCTGAAATGGAT
```

D7

```
HUM: AAAATCC
UAM: AAAATGC
```

D9

```
HUM: CATTTGTCTTG
UAM: CACTGGTCTTG
```

Alignment stats: 'M': 141, 'I': 0, 'D': 0, 'X': 6

47

IGHV1-46

GENE ALIGN SEQ

```
HUM: CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTC
UAM: CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTC

HUM: AGTGAAGGTTTCCTGCAAGGCATCTGGATACACCTTCACCAGCTACTATA
UAM: AGTGAAGGTTTCCTGCAAGGCTTCTGGTTACACCTTCACCAGCTGCTATA

HUM: TGCACTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGAATA
UAM: TGTACTGGGTGCAACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGAGTA

HUM: ATCAACCCTAGTGGTGGTAGCACAAGCTACGCACAGAAGTTCCAGGGCAG
UAM: ATCAACCCTAGTGATGGTAGCACAAGCTACGCACAGAAGTTCCAGGGCAG

HUM: AGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTACATGGAGCTGA
UAM: AGTCACCATGACCAGGGACACATCCACAAGCACAGTCTACATGGAGCTGA

HUM: GCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGA
UAM: GCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTATGCAAGAGA
```

D7
```
HUM: CACAGTG
UAM: CACAGTG
```

D9
```
HUM: GTCAGAAACCC
UAM: GTCAGAAACCC
```

Alignment stats: 'M': 285, 'I': 0, 'D': 0, 'X': 11

48

IGHV1-45

GENE ALIGN SEQ

HUM: CAGATGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGACTGGGTCCTC

UAM: CAGATGCAGCTGGTGCAGTCTGGGGCTGAGATGAAGAAGCCTGGGTCCTC

HUM: AGTGAAGGTTTCCTGCAAGGCTTCCGGATACACCTTCACCTACCGCTACC

UAM: AGTGAAGGTTTCCTGCAAGGCTTCTGGATACACCTTCACCGACCGCTACC

HUM: TGCACTGGGTGCGACAGGCC-CCCGGACAAGCGCTTGAGTGGATGGGATG

UAM: TGCACTGGGTGCGACAGGCCT---GGACAAGAGCTTGAGTGGATGGGATG

HUM: GATCACACCTTTCAATGGTAACACCAACTACGCACAGAAATTCCAGGACA

UAM: GATCACACCTTACAATGGTAACACCAACTATGCACAGAAGTTCTAGGACA

HUM: GAGTCACCATTACCAGGGACAGGTCTATGAGCACAGCCTACATGGAGCTG

UAM: GAGTCACCATTACCAGGGACAGGTCTATGAGCACAGCCTACATGGAGCTG

HUM: AGCAGCCTGAGATCTGAGGACACAGCCATGTATTACTGTGCAAGATA

UAM: AGCAGCCTGAGACCTGAGGACACAGCCGTGTATTACTGTGCAAGATA

D7

HUM: CACAGTG

UAM: CACAGTG

D9

HUM: GTCAGAAACCC

UAM: GTCAGAAACCC

Alignment stats: 'M': 282, 'I': 1, 'D': 3, 'X': 11

IGHV(II)-44-2

GENE ALIGN SEQ

HUM: CTCTTCCTCACATGCCCCATTTCTGGGTTGTCCATCCCAACCAACAGTTA
UAM: CTGTTCCTCACATGCCCCATTTCTGGGTTGTCCATCCCAACCAACAGTTA

HUM: CTGCTGGAGCTGAATCCACTAGCCCGCTTCCATGGGCTGTCAGGAACACA
UAM: CTGCTGGAGCTGCATCCACTAGCCCGCTTCCATGGGCTGTCAGGAACACA

HUM: TTGCAAGGGTGACACACACGATGATCCATCTCTGCAGAGCCAACTCTCCT
UAM: TTGCAAGGGTGACACACGCGATGATCCATCTCTGCAGAGCCAACTCTCCT

HUM: TCTCCAGAGATTCATCCAAGAAACAATTTTGACTATACCTGAGCTCTGTG
UAM: TCTCCAGAGATTCATCCAAGAAACAATTTTGACTATACCTGAGCTCTGTG

HUM: ACATCTGAGGACATGGTTTGTATTACTGTGCAAGACA
UAM: ACATCTGAGGACATGGTTTGTATTACTGTGCAAGATA

D7

HUM: AACAGTG
UAM: AACAGTG

D9

HUM: GACATAAACCT
UAM: GACATAAACCT

Alignment stats: 'M': 233, 'I': 0, 'D': 0, 'X': 4

IGHV(IV)-44-1

GENE ALIGN SEQ

```
HUM: GAGGACCACCTTGTGCAATGGGAGGAAGAAGTAGTGGTCCCCTTGGTCAT
UAM: GAGGACCACCTTGTGCAATGGGAGGAAGAAGTAGTGGTCCCCTTGGTCAT

HUM: GCTCAGCCTCACCTA-TGCCGCCTATGCACATTCAATTTCTGAACATTCT
UAM: GCTCAGCCTCACC-AGTGCCGCCTACGCACATTCAATTTCTGAACAT--T

HUM: GTTTCCTGGATCCACCATCTCCCATCAAAAGGTCTTCAGTGTGTGTTGGTGT
UAM: GTTTCCTGGATCCACCATCTCCCATCAAAAGGTCTTGAGTGTGTGTTGGTGT

HUM: GATATGGGTTAAGGGAAACACTA------AGCCCCAACCTTCAGGGCAGAG
UAM: GATATGGGTTAAGGGAAACACTAACTGCAGCCCCAACCTTCAGGGCAGAG

HUM: CTAGCATCTCCAGAAACACATAGTAAAAAACAAGAAAACTTACAGCTGAG
UAM: CTAGCATCTCCAGAAACACATAGTGAAAAACAAGAAAACTTACAGCTGAG

HUM: AAGTGTGATGGCTGGGGAGGCAGGCGTGTATTACTGTGCTCAAGG
UAM: AAGTGTGATGGCTGAGGATGCAGGCGTGTATTACTTTGCTCAAGG
```

D7

```
HUM: CACTGTG
UAM: CACTGTG
```

D9

```
HUM: GACACAAACCT
UAM: GACACAAACCT
```

Alignment stats: 'M': 280, 'I': 6, 'D': 3, 'X': 6

IGHV(II)-43-1

GENE ALIGN SEQ
```
HUM: TCTGGATTCCCCAACAGAACCAGTGCTTCCTGCTGGAGCTGGATCCATCA
UAM: GCTGGATTCCCCAACACAAAACCAGTGCTTCCTGCTGGAGCTGGATCCATCA

HUM: GCCCCCAGGGAAGGGACTGGAGTGGGTCAGGTGCACAGGTCATGAAGGGA
UAM: GCCCCCAGGGAAGGGATTGGAGTGGGTCGGGTGCACAGGTCATGAAAGGA

HUM: GCACAAATTCTAACCCACTCCTCAAGAGTCCAGTCACCACCTCCAGATCT
UAM: GCACAAATTCCAACCCACTCCTCAAGAGTCCAGTCACCACCTCCAGATCT

HUM: ATGTCCAAAAA--CAGCTCTTCGTATGGCTGAGTGACAT-T-AGCAACAA
UAM: ATGTCCAAAAAAT-AGCTCTTCCTATGGCTGAGTGA--TGTGAGCAACAA

HUM: GCACACAGCCATG-------T
UAM: GCACACAACCATGTTTATTTT
```

D7
```
HUM: TTGTTTT
UAM: TTGTTTT
```

D9
```
HUM: GTGTGTGTTTT
UAM: TTTTGATAGAG
```

Alignment stats: 'M': 199, 'I': 11, 'D': 3, 'X': 8

IGHV3-43

GENE ALIGN SEQ

HUM: GAAGTGCAGCTGGTGGAGTCTGGGGGAGTCG--TGGTACAGCCTGGGGGG
UAM: GAAGTGCAGCTGGTGGAGTCTGAGGGAG--GCTTGGTACAGCCTGGGGGGT

HUM: TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGATGATTATAC
UAM: TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGC

HUM: CATGCACTGGGTCCGTCAAGCTCCGGGGAAGGGTCTGGAGTGGGT-CTCT
UAM: CATGCACTGGGTCCGTCAAGCTCCAGGGAAGGGTCTGAAGTGGGTT---T

HUM: CT--TATTAGTTGGGATGGTGGTAGCACATACTATGCAGACTCTGTGAAG
UAM: CTGGTATTAATTGGAATGGTGGTAGCACATACTATGCAGATTCTGTGAAG

HUM: GGCCGATTCACCATCTCCAGAGACAACAGCAAAAACTCCCTGTATCTGCA
UAM: GGCCGATTCACCATCTCCAGAGACAACAGCAAAAACTCCCTGTATCTGCA

HUM: AATGAACAGTCTGAGAACTGAGGACACCGCCTTGTATTACTGTGCAAAAG
UAM: AATGAACAGTCTGAGAGCTGAGGACACGGCCTTGTATTACTGTGCAAAAG

HUM: ATA
UAM: ACA

D7
HUM: CACAGTG
UAM: CACAGTG

D9
HUM: GACAAAAACCT
UAM: GACAAAAACCT

Alignment stats: 'M': 282, 'I': 5, 'D': 5, 'X': 11

IGHV3-42

GENE ALIGN SEQ

```
HUM: GAGGCGCAGCTGGTGGAGTCTGGGGGAGGCTTGG--TACAGCCTGGGTGG
UAM: GAGGCACAGCTGGTGGAGTCTGGGGGAGGCTTGGTATACAGCCTGGGTGG

HUM: GTCCCCGAGACTCTCATTTGCAGCTTCTAGATTCACCTTCAGTGACTTCT
UAM: GTCCCTGAGACTCTCATTTGCAGCCTCTGGATTCACCTTCAGTGACTTCT

HUM: GAATGCACTGGATCCGCCAGGCTTCTGGGAAAGGGCTGGAGTGGGGTTGGC
UAM: GGATGCACTGGATCCGCCAGGCTTCTGGCAAAGGGCTGGAGTGGGGTTGGC

HUM: CGTATTAGAACCAAACGTAACAGTTACACGACAGAATGCGCTGCATCTGT
UAM: CGTATTAGAACCAAACGTAACAGTTACGTGACAGAATGCGCTGCATCTGT

HUM: GAAAGGCAGGTTCACCATCTCAAGAGATGATTCAAAGAACACACTGTATC
UAM: GAAAGGCAGGTTCACCATCTCAAGAGATGATTCAAAGAACACACTGTATA

HUM: TGCAAGTGAATACCCTGAAAAACCGAGTACACGGCCATCTATTACTGTACT
UAM: TGCAAATGAATACCCTGAAAAACTGAGGACACGGCCATCTATTACTGTACT

HUM: AGAGA
UAM: AGAGA
```

D7
```
HUM: CAGTGAG
UAM: CACAGTG
```

D9
```
HUM: ACACAAATCTC
UAM: TACACAAATCT
```

Alignment stats: 'M': 291, 'I': 2, 'D': 0, 'X': 12

IGHV3-41

GENE ALIGN SEQ

HUM: GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTC
UAM: GAGGTGCAGCTGATGGAATCTGGGGGAGGTTTGGTACAGCCTGGGGGGTC

HUM: CCTG----AGACTCTCCTGTGCAGCCTCAGGATTCTCCTTTAGTAGCTAT
UAM: --TGTAAA--ACTCTCTTGTGCAGCCTCAGGATTCACCTTTAGTAGCTAT

HUM: GGCATGAG-CTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGACTGAGTGG
UAM: GGCATG-GACTGGGTCTGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGG

HUM: CACATATCTGGAATGATGGAAGTCAGAAATACTATGCAGACTCTGTGAAG
UAM: TACATATATGGAATGATGGAAGTCAGAAATACTATGCAGACTCTGTGAAG

HUM: GGCCGATTCACAATCTCCAGAGACAATTCTAAGAGCATGCTCTATCTGCA
UAM: GGCCAATTCACGATCTCCAGAGACAATTCTAAGAGCATGCTCTATCTGCA

HUM: AATGGACAGTCTGAAAGCTAAGGACACGGCCATGTATTACTGTACCAGA
UAM: AATGGACAGTCTGAAAGCTGAGGACACGGCCATGTATTACTGTACCAGA

D7

HUM: CACAGTG
UAM: CAGAGTG

D9

HUM: GACACAAACCT
UAM: GACACAAACTT

Alignment stats: 'M': 274, 'I': 5, 'D': 5, 'X': 15

IGHV(II)-40-1

GENE ALIGN SEQ

HUM: `AGCCTGGTGAAGCCCTTGCAAACCCCCTCACTCACCTGTGCTGCCTCTGG`
UAM: `AGCCTAGTGAAGCCCTTGCAAACCCCCCTCACTCACCTGTGCTGCCTGTGG`

HUM: `ATTCTCTGTCACAATCAGTGCTTCCTG`
UAM: `ATTCTCCATCACAATCAGTGCTTCCTG`

D7

HUM: `TAGGCAC`
UAM: `TAGGCAC`

D9

HUM: `GTCAGGTGCAT`
UAM: `GTCAGGTGCAT`

Alignment stats: 'M': 73, 'I': 0, 'D': 0, 'X': 4

IGHV7-40

GENE ALIGN SEQ

```
HUM: TATGGTATGAATTCAGTGTGACCAGCCCCTGGACAAGGGCTTGAGTGGAT
UAM: TATGGTATGAATTCGGTGTGACCGGCCCCTGGACAAGGGCTTGAGTGGAT

HUM: GGGATGGATCATCACCTACACTGGGAACCCAACATATATACCAAC--GGCTT
UAM: GGGATGGATCATCACCTACACTGGGAACCCAAGGTATACC--CATGGCTT

HUM: CACAGGACGGTTTCTATTCTCCATGGACACCTCTGTCAGCATGGCGTATC
UAM: CCCAGGACGGTTTGTCTTCTCCATGGAGACCTCTGTCAGCATGGCATATC

HUM: TGCAGATCAGCAGCCTAAAGGCTGAGGACACGGCCGTGTATGACTGTATG
UAM: TGCAGATCAGCAGCCTAAAGGCTGAGGACATGGCCATGTATGACTGTATG

HUM: AGAGA
UAM: AGAGA
```

D7
```
HUM: CACAGTG
UAM: CACAGTG
```

D9
```
HUM: GTCAGAAACCC
UAM: GTCAGAAACCC
```

Alignment stats: 'M': 190, 'I': 2, 'D': 2, 'X': 11
```

IGHV4-39

GENE ALIGN SEQ

```
HUM: CAGCTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGAC
UAM: CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGAC

HUM: CCTGTCCCTCACCTGCACTGTCTCTGGTGGCTCCATCAGCAGTAGTAGTT
UAM: CCTGTCCCTCACCTGCGCGCTGTCTCTGGTGGCTCCATCAG---TAGTA---

HUM: ACTACTGGGGCTGGATCCGCCAGCCCCCAGGGAAGGGGCTGGAGTGGATT
UAM: ACTACTGGAGCTGGATCCGGCAACCACCAGGGAAGGGGCTGGAGTGGATT

HUM: GGG-AGTATCTATTATAGTGGGAGCACCTAC-TACAACCCGTCCCTCAAG
UAM: GGGCA-TATCCATTATGGTGGTAGCAACTACCT-CAACCCGTCCCTCAAG

HUM: AGTCGAGTCACCATATCCGTAGACACGTCCAAGAACCAGTTCTCCCTGAA
UAM: AGTCGAGTCACCATATCAGTAGACACGTCCAAGAACCAGTTCTCCCTGAA

HUM: GCTGAGCTCTGTGACCGCCGCAGACACGGCTGTGTATTACTGTGCGAGAC
UAM: GCTGAGCTCTGTGACCGCCGCAGACACAGCCGTGTATTACTGTGCGAGAG

HUM: A
UAM: A
```

D7
```
HUM: CACAGTG
UAM: CACAGTG
```

D9
```
HUM: GACAAAAACCT
UAM: GACACAAACTT
```

Alignment stats: 'M': 277, 'I': 2, 'D': 8, 'X': 14

IGHV(III)-38-1

GENE ALIGN SEQ

```
HUM: GAAGTTAACTAGTGGAGTCAGACAGG--AAAATACTACAGACCAAGAATT
UAM: GAAGTTAACTAGTGGAGTCAGACAGGGC-------CTACAGACGAAGAATT

HUM: CTCAGACTGTTCTGCAAAGCCCCTGGATTCACTGAAAAAAGAACAAGTTT
UAM: CTCAGACTGTTCTGCAAAGCCCCTAGATTCACTGAAAACAGAACAAGTTT

HUM: GGTCCAGCAGGATTCATGGCAAGTGTTGGTGAGGGAGATAACAGTAATTC
UAM: GGTCCAGCAGGATTCATGACAAGGGTTGGTGTGGGAGATAACAGTAATTC

HUM: AAGTGGAAGTTCTCAATGGGACTCGCCTTCAGTACAAAGAAGATTAACAG
UAM: AAGTGGAAGTTCTCAATGGGACTCTCCTTCAGTACAAAGAAGATTAACAG

HUM: TCCTCAGAGACACTGTTCAGAAGATTCTCTTTTAAGATAATAAAACTGAG
UAM: TCCTCAGAGACACTGTTCAGAAGATTCTCTTTTAAGATAATTAAACTGAG

HUM: AGCCCAAGACAAGTCTGTGTATTACTGTGAGGGA
UAM: AGCCCAGGACAAGTCCGTGTATTACTGTGAGGGA
```

D7
```
HUM: CACAGTG
UAM: GACAGTG
```

D9
```
HUM: GACACAAAAGT
UAM: GACACAAAACT
```

Alignment stats: 'M': 266, 'I': 2, 'D': 6, 'X': 10

59

IGHV3-38

GENE ALIGN SEQ

HUM: GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTAGGGGGTC
UAM: GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTC

HUM: CCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCGTCAGTAGCAATGAGA
UAM: CCTCAGACTCTCCTATGCAGCCTCTGGATTCACTGTCAGTAGCAATGAGA

HUM: TGAGCTGGATCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCATCC
UAM: TGAGCTGGATCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCAACC

HUM: ATTAGT---GGTGGTAGCACATACTACGCAGACTCCAG-GAAGGGCAGAT
UAM: ATTAGTAGAGGTGGTAGCACATACTACACAGACTCC-GTGAAGGGCAGAT

HUM: TCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTTCAAATGAAC
UAM: TCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTTCAAATGAAC

HUM: AACCTGAGAGCT-GAGGGCACGGCCGTGTATTACTGTGCCAGA-TATA
UAM: AGCCTGAGAG-TGGAGGACACGGCTGTGTATTACTGTGCGAGAG---A

D7
HUM: CACAGAG
UAM: CACAGTG

D9
HUM: CACAAACCTCC
UAM: AACACAAACCT

Alignment stats: 'M': 277, 'I': 6, 'D': 5, 'X': 10

60

IGHV3-37

GENE ALIGN SEQ
```
HUM:  GAGGTGCAGCTGGTAGAGTCTGGGGGAGACTTGGTACAGCTGTGGTGGGG
UAM:  GAGGTGCAGCTGGTAGAGTCTGGGGGAGACTTGGTACAGCTGTGGCGGGG

HUM:  TTGGGGGTGTCCTGAGACTCTCATGTGCAGCCTGCGGATTCATCTTGAGA
UAM:  TTGGGGGTGTCCTGAGACTTTCCTGTGCAGCCTGTGGATTCACCTTGAGA

HUM:  AGCAATGACATGAACTGGGCCCACCGGGCTTCAAGAAAGGGGCTGGAATG
UAM:  AGCAATGACATGAACTGGGTCCACCGGGCTTCAAGAAAGGGGCTGGAGTG

HUM:  GGTCTCATACATTAGTGCTAGTGGTGGTAGCCTATACTATGCAGACACTG
UAM:  AGTCTCATACATTAGTGCTAGTGGTGGTAGCCTATACTATGCAGACACTG

HUM:  AAGGGTAGATTCACCATCTCTAGAGACAATGGCAAGAACATGCTGTACTT
UAM:  AAGGGTAGATTCGCCATCTGTAGAGACAATGGCAAGAGCATGCTGTACTT

HUM:  GCAAATGAACAGTCTGAGAGATGAGGACTCGGCTGTGTGAGAGA
UAM:  GCAAATGCACAGTCTGAGAGATGAGGACTCGGCCGTGTGAGAGA
```

D7
```
HUM:  CATGGTG
UAM:  CATGGTG
```

D9
```
HUM:  GCCAGAAACCT
UAM:  GCCAGAAACCT
```

Alignment stats: 'M': 281, 'I': 0, 'D': 0, 'X': 13

61

IGHV3-36

GENE ALIGN SEQ

```
HUM: GAGGTGCAGCTGGTGGAGTCTTTGGGAGGCTTGTTATAGCCTGGGGGTCC
UAM: GAGGTGCTTCTGGTGGAGTCTTTGGGAGGCTTGTTATATCCTGGGGGTCC

HUM: CTGAGACTTTCTTTTGCAGCCTCTGGATTCACCTTTAGTACCTTTATTAG
UAM: CTGAGACTTTCTTTTGCAGCCTCTGGATTCACCTTTAGTACCTTTAGTAG

HUM: GTACTGGATGAGCTG--GGTCCATCAGGCTCCTGGGAAAGGGCTGGAGTA
UAM: GTACTGGATGAGCTGCC-GTCCATCAAGCTCCTGGGAAAGGGCTGCAGTA

HUM: GGTCTCATTTATGAGTTGTTGTGTAGGTAGCACAAGCTATGCAGACTCTG
UAM: GGTCTCATTTATGAGTTGTTGTGTAGGTAGCACAAACTATGCAGACTCTG

HUM: TGAAGGGTCGATTCACCCTCTCCAGAGATGATGCCAAGAAATCACTGTAT
UAM: TGAAGGGTCGATTCACCGTCTCCAGAGATGATGCCAAGAAATCACTGTAT

HUM: CTGCAAATGAACAGCGTCAGAGCCGAGGATAGGTCTGTGTATTACTGTGG
UAM: CTGCAAATGAACAGCGTGAGAGCCTAGGATAGGTCTGTGTATTACTGTAG

HUM: TGG
UAM: TGG
```

D7
```
HUM: CATTGTG
UAM: CATTCTG
```

D9
```
HUM: GCAGAGATGCT
UAM: GCAGAGATGCT
```

Alignment stats: 'M': 289, 'I': 2, 'D': 1, 'X': 11

IGHV3-35

GENE ALIGN SEQ

```
HUM: GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGATC
UAM: GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGAGATC

HUM: CCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAACAGTGACA
UAM: CCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAACACTGACA

HUM: TGAACTGGGTCCATCAGGCTCCAGGAAAGGGGCTGGAGTGGGTATC--GG
UAM: TGAACTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGT--CTTGG

HUM: GTGTTAGTTGGAATGGCAGTAGGACGCACTATGCAGACTCTGTGAAGGGC
UAM: GTATTAGTTGGAATGGTGGGTAGGATGCACTATGCGGACTCCGTGAAGGGC

HUM: CGATTCATCATCTCCAGAGACAATTCCAGGAACACCCTGTATCTGCAAAC
UAM: CGATTCATCATCTCCAGAGACAATTCCAGGAACTTCCTGTATCTGCAAAC

HUM: GAATAGCCTGAGGGCCGAGGACACGGCTGTGTATTACTGTGTGAGAAA
UAM: GAATAGCCTGAGGGCCGAGGACACAGCTGTGTATTACTGTGTGAGAAA
```

D7
```
HUM: CACTGTG
UAM: CACTGTG
```

D9
```
HUM: GACACAAACCT
UAM: GACACAAACCT
```

Alignment stats: 'M': 280, 'I': 2, 'D': 2, 'X': 14

IGHV7-34-1

GENE ALIGN SEQ

```
HUM:  CTGCAGCTGGTGCAGTCTGGGCCTGAGGTGAAGAAGCCTGGGGCCTCAGT
UAM:  CTGCAGCTGGTGCAGTCTGGGCCTGAGGTGAAGAAGCCTGGGGCCTCAGT

HUM:  GAAGGTCTCCTATAAGTCTTCTGGTTACACCTTCACCATCT-ATGGTATG
UAM:  GAAGGTCTCCTATAAGTCTTCTGGTTACACCTTCACCA-CTTATGGTATG

HUM:  AATTGGGTATGATAGACCCCTGGACAGGGCTTTGAGTGGATGTGATGGAT
UAM:  AATTGGTTATGACAGACCCCTGGACAGGGCCTTGAGTGGATGGGATGGAT

HUM:  CATCACCTACACTGGGAACCCAACGTATACCCACGGCTTCACAGGATGGT
UAM:  CATCACCTAAACTGGGAACCCGACATATACCCACGGCTTCACAGGATGGT

HUM:  TTGTCTTCTCCATGGACACGTCTGTCAGCACGGCGTGTCTTCAGATCAGC
UAM:  TTGTCTTCTCCATGGACACCTCTGTCAGCACGGCGTATCTTCAGATCAGC

HUM:  AGCCTAAAGGCTGAGGACACGGCCGAGTATTACTGTGCGAAGTA
UAM:  AGCCTAAAGGCTGAGGACACGGCTGAGTATTACTGTGCGAAGTA
```

D7
```
HUM:  CACAGTG
UAM:  CACAGTG
```

D9
```
HUM:  TTCAGAAAGCC
UAM:  TTCAGAAAGCC
```

Alignment stats: 'M': 282, 'I': 1, 'D': 1, 'X': 10

IGHV4-34

GENE ALIGN SEQ

```
HUM: CAGGTGCAGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGAC
UAM: CAGGTGCAGCTACAGCAGTGGGGGTGCAGGACTGGTGAAGCCTTCGGAGAC

HUM: CCTGTCCCTCACCTGCGCTGTCTATGGTGGGTCCTTCAGTGGTTACT--A
UAM: CCTGTCCCTCACCTGCGCTGTCTATGGTGGGTCCTTCAGTGATTA-TGG-

HUM: CTGGAGCTGGATCCGCCAGCCCCCAGGGAAGGGGCTGGAGTGGATTGGGG
UAM: CTGGAACTGGATCCGCCAGCCCCCAGGGAAGGGGCTGGAGTGGATTGGG-

HUM: AAAT-CAATC-----ATAGTGGAAGCACCAACTACAACCCGTCCCTCAAG
UAM: ---TAC-ATCGTTAG-TAGTGGGAGAACCAACTACAACCCGTCCCTCAAG

HUM: AGTCGAGTCACCATATCAGTAGACACGTCCAAGAACCAGTTCTCCCTGAA
UAM: AGTCGAGTCACCATGTCAGTAGACACGTCCAAGAACCAGTTCTCCCTGAA

HUM: GCTGAGCTCTGTGACCGCCGCGGACACGGCTGTGTGTATTACTGTGCGAGAG
UAM: GCTGAGCTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGCGAGAG

HUM: G
UAM: G
```

D7
```
HUM: CACAGTG
UAM: CACAGTG
```

D9
```
HUM: GACAAAAACCT
UAM: GATAAAAACCT
```

Alignment stats: 'M': 277, 'I': 8, 'D': 8, 'X': 8

IGHV3-33-2

GENE ALIGN SEQ

```
HUM: GAGGTACAGCTCGTGGAGTCCGGAGAGGACCCAAGACAACCTGGGGGATC
UAM: GAGGTACAGCTAGTGGAGTCCGGAGAGGACCCAAGACAACCTGGGGGGTC

HUM: CTTGAGACTCTCCTGTGCAGACTCTGGATTAACCTTCAGTAGCTACTGAA
UAM: CGTGAGACTCTCCTGTGCAGACTCTGGATTAACCTTCAGTAGCTACTGAA

HUM: TGAGCTCGGTTTCCCAGGCTCCAGGGAAGGGGCTGGAGTGAGTAGTAGAT
UAM: TGAGCTCAGTTTCCCAGGCTCCAGGGAAGGGGCTGGAGTGAGTAGTAGAT

HUM: A--TACAGTGTGATGGAAGTCAGATATGTTATGCCCAATCTGTGAAGAGC
UAM: AAAT--AGTACGATACAAGTCAGATATGTTATGCACAAACTGTGAAGAGC

HUM: AAATTCACCATCTCCAAAGAAAATGCCAAGAACTCACTGTATTTGCAAAT
UAM: AGATTCACCATCTCCAAAGAAAATGCCAAGAACTCACTCCATTTGCAAAT

HUM: GAACAGTCTGAGAGCAGAGGGCACAGCTGTGTGTTACTGTATGTGAGGCA
UAM: GAACGGTCTGAGAACAGAGGGCACAACTGTGTGTTACTGTATGTGAGGCA
```

D7
```
HUM: CCAGGTA
UAM: CCAGGTA
```

D9
```
HUM: GACACAGTTTC
UAM: GACACAGAATT
```

Alignment stats: 'M': 280, 'I': 2, 'D': 2, 'X': 16
```

**IGHV(II)-28-1**

GENE ALIGN SEQ

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

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

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

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

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

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

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

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

Alignment stats: 'M': 226, 'I': 0, 'D': 51, 'X': 6

IGHV4-28

GENE ALIGN SEQ

```
HUM: CAGGTACAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGACAC
UAM: CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGAC

HUM: CCTGTCCCTCACCTGCGCTGTCTCTGGTTACTCCATCAGCAGTAGTAACT
UAM: CCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCCATCAGCAGTGGTTACT

HUM: GGTGGGGCTGGATCCGGCAGCCCCCAGGGAAGGGACTGGAGTGGATTGGG
UAM: ACTGGGGCTGGATCCGCCAGCCCCCAGGGAAGGGCCTGGAGTGGATTGGG

HUM: --TACATCTATTATAGTGGGAGCACCTA-CTACAACCCGTCCCTCAAGAG
UAM: CATA--TCAATTATGGTGGGAGCACC-AGCTACAACCCATCCCTCAAGAG

HUM: TCGAGTCACCATGTCAGTAGACACGTCCAAGAACCAGTTCTCCCTGAAGC
UAM: TCGAGTCACCTTGTCAGTAGACACGTCCAAGAACCAGTTCTCCCTGAAGC

HUM: TGAGCTCTGTGACCGCCGTGGACACGGCCGTGTATTACTGTGCGAGAAA
UAM: TGAGCTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGCGAGAGA
```

D7
```
HUM: CACAGTG
UAM: CACAATG
```

D9
```
HUM: GACACAAACCT
UAM: GACAAAAACCT
```

Alignment stats: 'M': 277, 'I': 3, 'D': 3, 'X': 16
```

IGHV7-27

GENE ALIGN SEQ

HUM: CAGGTGCAGCTGGTGCAGTCTGGGCCTGAGGTGAAGAAGCCTGGAGCCTC
UAM: CAGGTGCAGCTGGTGCAGTCTGAGCCTGAGATGAAGCAGCCTGGGGCCTC

HUM: ATTGAAGGTT-TCCTGCAAGGCTTCTGGATACACCTTCACAAGCTATGCT
UAM: AGTGAAG-TTCTCCTGCAAGGCTACTGGTTACACCTTCACTAGCTATGTT

HUM: ATCAG--CTGGGTATGACAGGCCCCATGGACAAGGGCTTGAGGAAATGGGA
UAM: AT--GAACTGGGTGCGACAGGCCCCCTGGACAAGGGCTTGAGTGGGTGGGA

HUM: TGGATCAACACCAACACTGGGAACCTAACGTATGCCCAGGGCTTCACAGG
UAM: TGGATCAACACCAACACTGGGAACCCAATGTATGCCCAGGGCTTCACAGG

HUM: ACGGTTTGTCTTCTCCATGGACACCTCCGTCAGCATGGCATATCTTCATA
UAM: ACAGTTTGTCTTCTCCATGGACACCTCTGTCAGTACAGTATATCTGCAGA

HUM: TCAGCAGCCTAAAAGGCTGAGGACA-----CGTG-----C-------AAGAG
UAM: TCAGTAGCCTAAAAGGCTGAGGACATGGCT-GTGTATTACTGTTTG-AGAG

HUM: G
UAM: A

D7
HUM: CACAGTG
UAM: CACAGTG

D9
HUM: ACCAGAAATCC
UAM: GTCAGAAACCC

Alignment stats: 'M': 249, 'I': 19, 'D': 5, 'X': 28

IGHV(III)-26-1

GENE ALIGN SEQ

HUM: GATGTTTACTGATGGAGTCAGAAGGAGAAAAATT-TAACAGCCCAGCAGT
UAM: GATGTTTACTGATGGAGTCAGAAGGGGAAAAATTGT-ACAGCCCAGCGGT

HUM: TCACTGAGACTGTCCTGCAAAGCCTCTGGTTTCGGGTTTACTGGGTGCAG
UAM: TCACTGAGACTGTCCTGCAAAACCTCTGGTTTCGGGTTTACTGGGTACAG

HUM: CATGAGCTTGGTCCAGC-ACACT---TCACAACAGGAATTGGTGTGGGTA
UAM: CATGAGCTTGGTCCAGCG----TGCGTCACAACAGGAATTGGTGTGGATA

HUM: GCAACAGTGAGAGATCATATGGGAGTTCTAAGGGTTACTCTCCATGAGTA
UAM: GCAACGGTGAGAGATCATATGGGAGTTCTCAGGGTTACTCTCCATGAGTA

HUM: CAGATAAATCAACATTCCCAAGTGACACCCTTTCAAGTGCAGTCTACCTT
UAM: CAAATAAGTTAACATTCCCAAGCGACACCCTTTCAAGTGCAGTCTACCTT

HUM: ACAAGGACCAACCTGAAAGCCAAGGGCAAGGCCGTATATTACAGTGAGGG
UAM: ACAATGACCAACCTGAAAGCCAAGGGCAAGGCCGTGTATCACAGTGAGGG

HUM: A
UAM: A

D7
HUM: CACAGGG
UAM: CACAGGA

D9
HUM: AGACACAAAAA
UAM: AGACACAAAAA

Alignment stats: 'M': 277, 'I': 5, 'D': 5, 'X': 14

IGHV2-26

GENE ALIGN SEQ

```
HUM:  CAGGTCACCTTGAAGGAGTCTGGTCCTGTGCTGGTGAAACCCACAGAGAC
UAM:  CAGGTCACCTTGAAGGAGTCTGGTCCTGCGCTGGTGAAACCCACAGAGAC

HUM:  CCTCACGCTGACCTGCACCGTCTCTGGGGTTCTCACTCAGCAATGCTAGAA
UAM:  CCTCACGCTGACCTGCACCGTCTCTGGGGTTCTCACTCAGCAATTCTAAAA

HUM:  TGGGTGTGAGCTGGATCCGTCAGCCCCCCAGGGAAGGCCCTGGAGTGGCTT
UAM:  TGGGTGTGAGCTGGATCCGTCAGCCCCCCAGGGAAGGCCCTGGAGTGGCTT

HUM:  GCACACATTTTTTTCGAATGACGAAAAATCCTACAGCACATCTCTGAAGAG
UAM:  GCACACATTTTTTTCGAATGACGAAAAATCCTACAGCACATCTCTGAAGAG

HUM:  CAGGCTCACCATCTCCAAGGACACCTCCAAAAGCCAGGTGGTCCTTACCA
UAM:  CAGGCTCACCATCTCCAAGGACACCTCCAAAAGCCAGGTGGTCCTTACCA

HUM:  TGACCAACATGGACCCTGTGGACACAGCCACATATTACTGTGC--ACGGA
UAM:  TGACCAACATGGACCCTGTGGACACAGCCACGTATTACT--GCACACGGA

HUM:  TAC
UAM:  GAG
```

D7
```
HUM:  CACAGAG
UAM:  CACAGAG
```

D9
```
HUM:  TACAAGAACCT
UAM:  TACAAGAACCC
```

Alignment stats: 'M': 293, 'I': 2, 'D': 2, 'X': 6

IGHV(III)-25-1

GENE ALIGN SEQ
```
HUM: GAAGTTCACCGGGGGAGACAGAGGAAATAACGGTGCAGCCGGGGGCTATC
UAM: GAAGTTCACTGGCGGAGACAGAGGAAATAATGGTACAGCTGGGGGCTATC

HUM: TGAGTCTCTCCTGCAAAGACTCTGGATTCACCTTCACTGATTGCAGCATA
UAM: TGAGTCTCTCCTGCAAAGACGCTGGATTCACCTTCACTGATTGCAGCCTA

HUM: AGCTTGGTCCAGCAAGCTCCAGGACCAGGGGTTGATGTGGGGCAGCAACAGG
UAM: AGCTTGGTCCAGCAGGCTTCAGGACCAGGGGTTGATGTAGGCAGCAACGGG

HUM: GAGAAATTGAAGAGGAAGCTCTCAGTGGTGCCCTCCATGAATACAAAGAA
UAM: GAGAAATTGAAGA---AGTTCCCAGTGGTGCCCTCCATGAATACAAAGAA

HUM: TCTTCACAGTCCCCAGGACACCCCTTACGTGCATGGTCTCACTGATATCTT
UAM: TCTTCACAGTCCCCAGGACACCCCTTACTTGCATGGTCTCACTGACATCTT

HUM: TACTTCCTTTATCACTTTTGTTATGTAAAT
UAM: TACTTCCTTTATCACTTTTGTTCTGTAAAT
```

D7
```
HUM: CACAATG
UAM: CACAATG
```

D9
```
HUM: ATACATTTGTT
UAM: ATATATTTGTT
```

Alignment stats: 'M': 261, 'I': 0, 'D': 3, 'X': 16

IGHV3-25

GENE ALIGN SEQ

```
HUM: GAGA-TGCAGCTGGTGGAGTC-TGGGG-GAGGCTTGGCAAAGCCTGCGTG
UAM: GA-AGTGTAGCTGGTGGAGACC--GGGCGAGGCTTGGCAAAGCCTGGGTG

HUM: GTCCCCGAGACTCTCCTGTGCAGCCTCTCAATTCACCTTCAGTAGCTACT
UAM: GTCCCCGAGACTCTCCTGTGCCGCCTCTCGATTCACCTTCAGTAGCTACT

HUM: ACATGAACTGTGTCCGCCAGGCTCCAGGGAATGGGCTGGAGTTGGTTGGA
UAM: ACATGAACTGTGTCTGCCAGGCTCCAGGGAATAGGCTGGAGTTGGTTGGA

HUM: CAAGTTAATCCTAATGGGGGTAGCACATACCTCATAGACTCCGGTAAGGA
UAM: CAAGTTAATCCTAATGGGGGTAGCACATACCTCATAGACTCTGGGAAGGG

HUM: CCGATTCAATACCTCCAGAGATAACGCCAAGAACACACTTCATCTGCAAA
UAM: CCAATTCACTACCTCCAGAGATAACGCCAAGAACACTCTTCATCTGCAAA

HUM: TGAACAGCCTGAAAACCGAGGACACGGCCCTGTATTAGTGTACCAGAGA
UAM: TGAACAACCTGAAAACCGAGGACATGGCCCTGTATTAGTGTACTAGAGA
```

D7
```
HUM: CACAGTG
UAM: CACAGTG
```

D9
```
HUM: GACACAAACCT
UAM: GACACAAACCT
```

Alignment stats: 'M': 277, 'I': 3, 'D': 3, 'X': 16

73

IGHV1-24

GENE ALIGN SEQ

```
HUM:  CAGGTCCAGCTGGTACAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTC
UAM:  GAGGTCCAGCTGGTACAGTCCGGGGCTGAGGTGAAGAAGCCTGGGGCCTC

HUM:  AGTGAAGGTCTCCTGCAAGGTTTCCGGATACACCCTCACTGAATTATCCA
UAM:  AGTGAAGTTCTCCTGCAAGGTTTCTGGATACACCTTCACCGAATTATCCA

HUM:  TGCACTGGGGTGCGACAGGCTCCTGGAAAAGGGCTTGAGTGGATGGGAGGT
UAM:  TGCACTGGGGTGCGACAGGCTCCTGGAAAAGGGCTTGAGTGGATGGGAGGT

HUM:  TTTGATCCTGAAGATGGTGAAACAATCTACGCACAGAAGTTCCAGGGCAG
UAM:  TTTGATCCTGATGATGGTGAAACAATCTACGCACAGAAGTTCCAGGGCAG

HUM:  AGTCACCATGACCGAGGACACATCTACAGACACAGCCTACATGGAGCTGA
UAM:  AGTCACCATGACCGAGGACACGTCTACAGACACAGCCTACATGGAGCTGA

HUM:  GCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCAACAGA
UAM:  GCAGCCTGAGATCTGAGGACACGGCCATGTATTACTGTGCAACAGA
```

D7
```
HUM:  CACAGTG
UAM:  CACAGTG
```

D9
```
HUM:  GTCAGAAACCC
UAM:  GTCAGAAACCC
```

Alignment stats: 'M': 287, 'I': 0, 'D': 0, 'X': 9

74

IGHV3-23

GENE ALIGN SEQ

```
HUM: GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTC
UAM: GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTC

HUM: CCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTAGCAGCTATGCCA
UAM: CCTGAGACTCTCCTGTGCAGCCTCTGGATTCACGTTCACTAACTACTACC

HUM: TGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCAGC-
UAM: TGCACTGGGTTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTC---GCA

HUM: TAT------TAGTGGTAGTGGTGGGTAGCACATACTACGCAGACTCCGTGAA
UAM: TATATTAGTAGTGGTAGTGGTGGGTAGCACAAACTACCCAGATTCTGTGAA

HUM: GGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGC
UAM: GGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACACGCTGTATCTGC

HUM: AAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAAA
UAM: AAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGA

HUM: GA
UAM: GA
```

D7
```
HUM: CACAGTG
UAM: CACAGTG
```

D9
```
HUM: GACACAAACCT
UAM: GACACAAACCT
```

Alignment stats: 'M': 271, 'I': 6, 'D': 3, 'X': 22

IGHV(III)-22-2

GENE ALIGN SEQ
HUM: GAGGTGCAGGTGGTGGAGTGTAGGGGAGAG
UAM: GAGGTGCAGGTGGTGGAGTCTCGGGGAGAG

D7
HUM: ACAAGAG
UAM: GCAAGAG

D9
HUM: GGGTGAGGCTG
UAM: GGGTGAGCTGT

Alignment stats: 'M': 28, 'I': 0, 'D': 0, 'X': 2

IGHV(II)-22-1

GENE ALIGN SEQ

```
HUM: GGCCTGGTGAAGCCCTCACAGATCCTCCCCCTGGCCTGTGGCATCTCTGC
UAM: GGCCTGGTGAAGCCCTCACAGATCCTCCCCCTCGCCTGTGCCATCTCTGC

HUM: TTCTCCATTACAACCAGTGCTTCCTGCTGGAGCTGGATCCGTCA-CCCCC
UAM: CTCTCCATTACAACCAGTGCTTCCTGCTGTAGCTAGATCCATCAGCCCCC

HUM: CGGGGAAGGGACTGGAGCGAATCAGGTGCACA-GGT-CATGAGGGAGTGC
UAM: CAGGGAAGGGACGGGGAGTGAAACAGGTGCACAA--TACATGAGAGAGTGC

HUM: ACAATCCAACCCACTCCTCAAGAGTCCAGTCACCATCTCCAGATCCACAT
UAM: ACAATCCAACCCACTCCTCAAGAGTCCAGTCGCCATCTCCAGATCCACAT

HUM: CCAAAAAACAGTTTCTCCTACAGCTGAGCTACCTTAACAAGGAGTACACA
UAM: CCAAAAAGCTGTTTTTCCTACAGCTGAGCTAACTGAGCAACGAGTACACA

HUM: ACCATGA-TTTTTATACAAAAGA
UAM: ACCATGAATTTTTACACAAAAGA
```

D7
```
HUM: CACAGCG
UAM: CAGGGTA
```

D9
```
HUM: GAACACTCTAC
UAM: GTCACAAACCT
```

Alignment stats: 'M': 247, 'I': 4, 'D': 2, 'X': 20

IGHV3-22

GENE ALIGN SEQ

```
HUM: GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTC
UAM: GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGATC

HUM: CCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTTACTACTACA
UAM: CCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAACTACTACA

HUM: TGAGC---GGGGTCCGCCAGGCTCC-CGGG-AAGGGGCTGGAATGGGTAG
UAM: TG--CATT-GGGTCCGCCAGGCTCCA--GGAAAGGGGCTGGAATGGGTAG

HUM: GTTTCATTAGAAACAAAGCTAATGGTGGGACAACAGAATA-GACCACGTC
UAM: GTTTCATTAGAACCAAAGCTAAAGGTGGGACAACAGAATACG-CCGCGTC

HUM: TGTGAAAGGCAGATTCACAATCTCAAGAGATGATTCCAAAAGCATCACCT
UAM: TGTGAAAGGCAGATTCACCATCTCAAGAGATGATTCCAAAAGCATCGCCT

HUM: ATCTGCAAATGAAGAGCCTGAAAAACCGAGGACACGGCCGTGTATTACTGT
UAM: ATCTGCAAATGAACAGCCTGAAAAACCGAGGACACGGCTGTGTATTACTGT

HUM: --TCCAGAGA
UAM: ACT--AGAGA
```

D7
```
HUM: CACAGTG
UAM: CACAGTG
```

D9
```
HUM: GACACAAACCT
UAM: GACACAAACCT
```

Alignment stats: 'M': 285, 'I': 8, 'D': 8, 'X': 9

IGHV1-17

GENE ALIGN SEQ

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

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

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

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

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

Alignment stats: 'M': 288, 'I': 0, 'D': 0, 'X': 7

79

IGHV(III)-16-1

GENE ALIGN SEQ

```
HUM: GAAGTCCTGTGTGTGAAATTTACTGATAGAGTCAG-GGGGGAAAAATTGTAC
UAM: GAAGTCCTGTGTGTAAAATTTATTGATGGATTCAGAGGGGGAAAAATTGTAC

HUM: AGCCCAGTGGTTCACTGAGACTCTCATGCAAAGCCTCTGATTTCACCTTT
UAM: AGCCCAGTGGTTCACTGAGACTCTCATGCAAAGCCTCTGATTTCACCTTT

HUM: ACTGGCTACAGCATGAGCTTGGTCCAGCAGGCTTCATGACAGGGATTGGT
UAM: ACTGGCTACAGCATGAGCTTGCTCCAGCCGGCTTCATGACAGGGATTTGT

HUM: GTGGGTGGAAACAGTGAGTGATCAAGTGGGAGTTCTCAGAGTTACTCTCC
UAM: GTGGGTGGAAACAGTGAGTGATCAAGTGGGAGTTCTCAGAGTTACTCTCC

HUM: ATGAGTACAAATAAATTAACAGTCCCAAGTGACACCTTTTCATGTGCAGT
UAM: ATGAGTACAAATAAATTAACAGTCCCAAGCGACACCTTTTAATATGCAGT

HUM: CTACCTTAAAGGGACCAAACTGAAAGTCAAGGACAAGGCCTTGTAATACT
UAM: CTACCTTAAAGGGACCAAACTGAAAGTCAAGGACAAGGCCTTGTAATACT

HUM: GTGA
UAM: GTGA
```

D7
```
HUM: GAGACAC
UAM: GAGACAC
```

D9
```
HUM: GCCCAGACAGA
UAM: GCCCAGACAGA
```

Alignment stats: 'M': 293, 'I': 1, 'D': 0, 'X': 10

IGHV3-16

GENE ALIGN SEQ

HUM: GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTC
UAM: GAGGTGCAGCTGGTGGAGTCTGGGGGAGGGGTTGGTACAGCCTGGGGGGTC

HUM: CCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAACAGTGACA
UAM: CCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAACACTGACA

HUM: TGAACTGGGCCCGCAAGGCTCCAGGAAAGGGGCTGGAGTGGGTATC--GG
UAM: TGAACTGGGTCCGCGAGGCTTCAGGAAAGGGGCTGGAGTGGGT--CTTGG

HUM: GTGTTAGTTGGAATGGCAGTAGGACGCACTATGTGGACTCCGTGAAGCGC
UAM: GTATTAGTTGGAATGGTGGGTAGGATGCACTATGCGGACTCCGTGAAGGGC

HUM: CGATTCAT--CATCTCCAGAGACAATTCCAGGAA-CTCCCTGTATCTGCA
UAM: CGATT--TACCATCTCCAGAGACAATTCCAGGAAGC-CCCTGTATCTGCA

HUM: AAAGAACAGACGGAGAGCCGAGGACATGGCTGTGTATTACTGTGTGAGA
UAM: AAAGAACAGACGGAGAGCCGAGGACATGGCCGTGTATTACTGTGTGAGAA

HUM: A
UAM: A

D7

HUM: TCCTGTG
UAM: TCCTGTG

D9

HUM: GACACAAACCT
UAM: GACACAAACCT

Alignment stats: 'M': 279, 'I': 5, 'D': 5, 'X': 12

IGHV(II)-15-1

GENE ALIGN SEQ

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

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

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

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

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

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

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

D9
```
HUM:  A C A C A A A C C T C
UAM:  A C A C A A A C C T C
```

Alignment stats: 'M': 257, 'I': 3, 'D': 3, 'X': 11

IGHV3-15

GENE ALIGN SEQ

```
HUM: GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTAAAGCCTGGGGGGTC
UAM: GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTC

HUM: CCTTAGACTCTCCTGTGCAGCCTCTGGATTCACTTTCAGTAACGCCTGGA
UAM: CCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTCAGTAACGCCTGGT

HUM: TGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTTGGCCGT
UAM: TGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTTGGCCGT

HUM: ATTAAAAGCAAAACTGATGGTGGGACAACAGACTACGCTGCACCCGTGAA
UAM: ATTAAAAGCAAAGCTGATGGTGGGACAACAGACTACGCTGCACCTGTGAA

HUM: AGGCAGATTCACCATCTCAAGAGATGATTCAAAAAACACGCTGTATCTGC
UAM: AGGCAGATTCACCATCTCAAGAGATGATTCAAAAAACACTTTGTATCTGC

HUM: AAATGAACAGCCTGAAAACCGAGGACACAGCCGTGTATTACTGT-ACC-A
UAM: AAATGAACAGCCTGAAAACCGAGGACACGGCCGTGTATTACTGTG--CTA

HUM: CAGA
UAM: CAGA
```

D7
```
HUM: CACAGTG
UAM: CACAGTG
```

D9
```
HUM: GACACAAACCT
UAM: GACACAAACCT
```

Alignment stats: 'M': 291, 'I': 2, 'D': 2, 'X': 9

IGHV(III)-13-1

GENE ALIGN SEQ

```
HUM: CCCTGTGAAGTTAACTAATGGAGTCAGACAGAGAAATACTACAGACCAGG
UAM: CCCTGTGAAGTTAACTAATGGAGTCAGACAGAGAAATACTACAGACCAGG

HUM: AATTCTGCCTTTTCTGCAAAGCCTCTGGATTCACTTTCACTGAAAACAGC
UAM: AATTCTGCCTTTTCTGCAAAGCCTCTGGATTCACTTTCACTGAAAACAGC

HUM: ATAAGCTTGATCCAGCAGGCTTCATGACAGGGGTGGGTGTGGGTAATAAC
UAM: ATAAGCTTGATCCAGCAGGCTTCATGACAGGGGTGGGTGTGGGTAATAAC

HUM: AATAATTCAAATAGAAGTTCTCAGTGGGACTCTCCTTGAGTAAAAAGATG
UAM: AATAATTCAAATGGAAGTTCTCAGTGGGACTCTCCTTCAGTAAAAAGATG

HUM: ATTAACAATCCTCAAATACACTCAGTTCAGGAGATTCTCTTTTAAGATGA
UAM: AATAACAATCCTCAAATACACTCAGTTCAGGAGATTCTCTTTTAAGATGA

HUM: TTAACCTGAGAGCTCAGGAAAAGTCCGTGTATTACTTTGAGGGA
UAM: TTAACCTGAAAGCTCAGGAAAAGTCCGTGTATTACTTTGAGGGA
```

D7
```
HUM: CACAGTG
UAM: CACAGTG
```

D9
```
HUM: GACACCAACCT
UAM: GACACCAACCT
```

Alignment stats: 'M': 290, 'I': 0, 'D': 0, 'X': 4

IGHV3-13

GENE ALIGN SEQ

HUM: GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTC
UAM: GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTC

HUM: CCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCT-TCAGTAGCTACGAC
UAM: CCTGAGACTCTCCTGTGCAGCCTCTGGATTCAC-TGTCAGTAGCTACGAC

HUM: ATGCACTGGGTCCGCCAAGCTACAGGAAAAGGTCTGGAGTGGGTCTCAGC
UAM: ATGCACTGGGTTCGCCAGGCTCCAGGAAAAGGTCTGGAGTGGGTCTCAGC

HUM: TATTGGTACTGCTGGTGACCCCATACTATCCAGGCTCCGTGAAGGGCCGAT
UAM: TATTGATACTGATGGTGACACATACTATGCAGACTCTGTGAAGGGCTGAT

HUM: TCACCATCTCCAGAGAAAATGCCAAGAACTCCTTGTATCTTCAAATGAAC
UAM: TCACCATCTCCAGAGAAAATGCCAAGAACTCTTTGTATCTTCAAATGAAC

HUM: AGCCTGAGAGCCGGGGACACGGCTGTGTATTACTGTGCAAGAGA
UAM: AGCCTGAGAGCCAAGGACACGGCTGTGTATTACTGTGCAAGAGA

D7

HUM: CACAGTG
UAM: CACAGTG

D9

HUM: GACACAAACCT
UAM: GACACAAACCT

Alignment stats: 'M': 279, 'I': 1, 'D': 1, 'X': 13

IGHV1-12

GENE ALIGN SEQ

```
HUM: CAGGTGCAGCTGGTGCAATCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTC
UAM: CAGGTGCAGCTGGTGCAATCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTC

HUM: AGTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCTACTGCTACT
UAM: AGTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCTACTGCTACT

HUM: TGCACTGGGTATGACAGGCCCCTGGACAAGGGCTTGAATGGACAGGATTT
UAM: TGCACTGGGTGCGACAGGTCCCTGGACAAGGACTTGAGTGGACAGGATTT

HUM: TAGTTATTTGAGAGATTTTTCATACAACATTTATTCTGTAAGCAAATTTC
UAM: TAGTTATTTGAGAGATTTTTCATACAACATTTATTCTGTAAGCAAATTTC

HUM: AGGGATTGTAGAATGAATCAT--ATTAACAAATCTGACACAGAACTTCCT
UAM: AGGGATTGTAGAATGAAT--TACATTAACAAATCTGATACAGAACTTCCT

HUM: CTGAATCAATCTTTGTAAACATCAATTTCTGAATCAATGTTGTAAATA
UAM: CTGAATCAATCTTTGTAAACATCAATTTCTGAATCAATGTTGTAAATA
```

D7
```
HUM: TTTCAGA
UAM: TTTCAGA
```

D9
```
HUM: TAACTCTACTT
UAM: TAACTCTACTT
```

Alignment stats: 'M': 287, 'I': 2, 'D': 2, 'X': 7

IGHV3-11

GENE ALIGN SEQ

```
HUM: CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCA-AGCCTGGAGGGT
UAM: GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGT-ACAGCCTGGGGGGT

HUM: CCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTGACTACTAC
UAM: CCCTGAGACTCTCCTGTGCAGCCTCTGGAATCACCTTCAGTAACCAATAC

HUM: ATGAGCTGGATCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTTTCATA
UAM: ATGAGCTGGGTCCGCCAGGCTACAGGGAAGGGACTGGAGTGGGTTTCATA

HUM: CATTAGTAGTAG-TAGTAGTTACACAAACTACGCAGACTCTGTGAAGGGC
UAM: CATTAGTGGT-GATAGTAGTTACACAAGCTACGCAGACTCTGTGAAGGGC

HUM: CGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAAT
UAM: CGATTCACCATCTCCAGGGACAACGCCAAGAACTCACTGTATCTGCAAAT

HUM: GAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGA
UAM: GAACAGCCTGAGAGTCGAGGACACGGCTGTGTATTACTGTGTGAAACA
```

D7
```
HUM: CACAGTG
UAM: CACAGTG
```

D9
```
HUM: GACACAAACCT
UAM: GACACAAACCT
```

Alignment stats: 'M': 278, 'I': 2, 'D': 2, 'X': 16

IGHV5-10-1

GENE ALIGN SEQ

```
HUM: GAAGTGCAGCTGGTGCAGTCCGGAGCAGAGGTGAAAAAGCCCGGGGAGTC
UAM: GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAGGCCCGGGGAGTC

HUM: TCTGAGGATCTCCTGTAAGGGGTTCTGGATACAGCTTTACCAGCTACTGGA
UAM: TCTGAGGATCTCCTGTAAGGGGTTCTGGATACAGCTTTACCAGCTACTGGA

HUM: TCAGCTGGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGTGGATGGGGAGG
UAM: TAAGCTGGGGTGCGCCAGATGCCTGGGAAAGGCTTGGAGTTGATGCGGATA

HUM: ATTGATCCTAGTGACTCTT---ATACCA-ACTACAGCCCGTCCTTCCAAG
UAM: ATTGATCCTAGTGA---TTCCGATACCAGA-TACAGCCCATCCTTCCAAG

HUM: GCCACGTCACCATCTCAGCTGACAAGTCCATCAGCACTGCCTACCTGCAG
UAM: GCCACATCACCATCTCAGCCGACAAGTCCATCAGCACCGCCTACCTGCAG

HUM: TGGAGCAGCCTGAAGGCCTCGGACACCGCCATGTATTACTGTGCGAGACA
UAM: TGGACCAGCCTGAAGGCCTCGGACACCGCCATGTATTACTGTGCGAG--A
```

D7
```
HUM: CACAGTG
UAM: CACAGTG
```

D9
```
HUM: TCTAAAACCCT
UAM: TCAAAAACCCT
```

Alignment stats: 'M': 275, 'I': 4, 'D': 6, 'X': 15

IGHV3-64D

GENE ALIGN SEQ

HUM: ATGGAGTTCTGGCTGAGCTGGGTTCTCCTTGTTGCCATTTTAAAAGGTAA
UAM: ATGGAGTTCGGGCTGAGCTGGGTTCTCCTTGTTGCCATTTTAAAAGGTAA

HUM: TTCATGGAGAACTAGAGATAGTGTGAGTGGACGTGAGTGAGAGAAACAGT
UAM: TTCATGGAGAACTAGAGATAGTGTGAGGGGATGTGAGTGAGAGAAACAGT

HUM: GGATATGTGTGGCAGTTTCTGACCTTGGTGTCTCTTTGTTTGCAGATGTC
UAM: GGATATGTGTGGCAGTTTCTGACCTTGGTGTCTCTTTGTTTGCAGGTGTC

HUM: CAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGG
UAM: CAGTGTGAGGTGCAGCTTGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGG

HUM: GGGGTCCCTGAGACTCTCCTGTTCAGCCTCTGGATTCACCTTCAGTAGCT
UAM: GGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCT

HUM: ATGCTATGCACTGGGTCCGCCAGGCTCCAGGGAAGGGACTGGAATATGTT
UAM: ATGCTATGCACTGGGTCCGCCAGGCTCCAGGGAAGGGACTGGAATGGGTA

HUM: TCAGCTATTAGTAGTAATGGGGGTAGCACATACTACGCAGACTCCGTGAA
UAM: TCAGCTATTAATAGTGGTGGGGGTAGCACATACTATGCAGACTCCGTGAA

HUM: GGGCAGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTTC
UAM: GGGCAGATTCACCATCTCCAGAGAAAATGCCAAGAACACACTGTATCTTC

HUM: AAATGAGCAGTCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGTGAAA
UAM: AAATGAGCAGTCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCAAAA

HUM: GA
UAM: GA

D7
HUM: CACAGTG
UAM: CACAGTG

D9
HUM: GACACAAACCT
UAM: TACAGAAACCT

Alignment stats: 'M': 433, 'I': 0, 'D': 0, 'X': 19

89

IGHV3-7

GENE ALIGN SEQ

HUM: GAGGTGCAGCTGGTG-GAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGT
UAM: GAGGTGCAGCTGGTGCG-GTCTGGGGGAGGCTTGGTACAGCCTGGGGGGT

HUM: CCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTAGTAGCTATTGG
UAM: CCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTAGTAGCTACTGG

HUM: ATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGGTGGCCAA
UAM: ATGAGCTGGGTCCGCCAGGCTCCAGGGAAAGGGCTGGAGTGGGGTGGCCAA

HUM: CATAAAGCAAGATGGAAGTGAGAAATACTATGTGGACTCTGTGAAGGGCC
UAM: CATAAAGCAAGATGGAAGTGAGAAATACTATGTAGACTCTGTGAAGGGCC

HUM: GATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATG
UAM: GATTCACTATCTCCGGAGACAGCGCCAAGAACTCGCTGTATCTGCAAATG

HUM: AACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGC---GAGAGA
UAM: AACAGCCTGAGAGCCTAGGACACGGCTGTGTATTACT---CTATGAGAGA

D7
HUM: CACAGTG
UAM: CACAGTG

D9
HUM: GACACAAACCT
UAM: GACACAAACCT

Alignment stats: 'M': 282, 'I': 4, 'D': 4, 'X': 10

90

IGHV3-6

GENE ALIGN SEQ

```
HUM: GAGATGCAGCTGGTAGAGTCTGGAGCAAACTTGACAAAGCCTGGGTGTCC
UAM: GAGATGCAGCTGGTAGAGTCTGGAGGAAACTTGACAAAGCCTGGGTGTCT

HUM: CAGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCCATAGCAC
UAM: CTGAGACGCTCCTGTGCAGCCTCTGTATTCACCTTCAGTAGCCATAGCAC

HUM: GCACTGGGTCCCCCAGGCTCCAGGGAAGGGTCTGCAGTGGGTCCCAGTTA
UAM: GCACTGGTTCCCCCAGGCTCCAGGGAAGGGTCTGCAGTGGGTCTCAGTTA

HUM: TTAGTGGTAGTGGT-AGTACCATGTA--CTACGCAGACTCTGTGAAGGGC
UAM: TTAGTAGTAGTGGTTA-TACCAT--ATTCTACGCAGACTCTGTGAAGGGC

HUM: CGATTCACCATTTCCAGAGACAATACGAAAAACTCACTGTATCTGCAAAT
UAM: TGATTCACCATTTCCAGAGACAATACCAAAAACTCACAGTATCTGCAAAT

HUM: GAACAG-----------ACTGAGGGCAGAGGATGCAGCTGCATATGACTCTG
UAM: GAACAGCCTGAGAGC-CTGAGGAC-----ATG--GCTGTGTATTACTCTG

HUM: TGAGAGA
UAM: TGAGAGA
```

D7
```
HUM: TACGGTA
UAM: CATGGTA
```

D9
```
HUM: GACACAAACCT
UAM: ACAAACCTCCC
```

Alignment stats: 'M': 269, 'I': 12, 'D': 11, 'X': 15

IGHV(III)-5-1

GENE ALIGN SEQ

HUM: GATTTATCATCTCAAGAGACAATGTCAAGAAGATGCTGTTTCTGCAAATG
UAM: GATTTATCATCTCAAGAGACAATGTCAAGAAGATGCTGTTTCTGCAAATG

HUM: GGCAATCTGCAAACCAAGGACACGTCACTACATTACTGTGCAAGAGAAG
UAM: GGCAATCTGCAAACCAAGGACACGTCACTATATTACTGTGCAAGAGAAG

D7

HUM: CACATGA
UAM: CGCATGA

D9

HUM: AACCTCCAGGA
UAM: AAACTCCAGGG

Alignment stats: 'M': 98, 'I': 0, 'D': 0, 'X': 1

92

IGHV2-5

GENE ALIGN SEQ

HUM: CAGATCACCTTGAAGGAGTCTGGTCCTACGCTGGTGAAACCCACACAGAC
UAM: CAGGTCACCTTGAAGGAGTCTGGTCCTGCGCTGGTGAAACCCACACAGAC

HUM: CCTCACGCTGACCTGCACCTTCTCTGGGGTTCTCACTCAGCACTAGTGGAG
UAM: CCTCACGCTGACCTGCACCTTCTCTGGGGTTCTCACTCAGCACTAGTGGAA

HUM: TGGGTGTGGGCTGGATCCGTCAGCCCCCCA-GGAAAGGCCCTGGAGTGGCT
UAM: TGGGTGTGGGCTGGATCCGTCAGCCCCCCAAGG-AAGGCCCTGGAGTGGCT

HUM: TGCACTCATTTATTGGGATGATGATAAGCGCTACAGCCCATCTCTGAAGA
UAM: TGCAGTCATTTATTGGGATGATGATAAGCGCTACAGCCCATCTCTGAAGA

HUM: GCAGGCTCACCATCACCAAGGACACCTCCAAAAACCAGGTGGTCCTTACA
UAM: GCAGACTCACCATCTCCAAGGACACCTCCAAAAACCAGGTGGTCCTTACA

HUM: ATGACCAACATGGACCCTGTGGACACAGCCACATATTACTGTGCACACAG
UAM: ATGACCAACATGGACCCTGTGGACACAGCCACATATTACTGTGCACGGAG

HUM: AC
UAM: AC

D7
HUM: CACAAAG
UAM: CACAGAG

D9
HUM: TACAAAAACCC
UAM: TACAAGAACCC

Alignment stats: 'M': 292, 'I': 1, 'D': 1, 'X': 8

93

IGHV4-4

GENE ALIGN SEQ

```
HUM: CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTT-CGGG-G
UAM: CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTT--GGAG

HUM: ACCCTGTCCCTCACCTGCGGCTGTCTCTGGTGGCTCCATCAGCAGTAGTAA
UAM: ACCCTGTCCCTCACCTGCGGCTGTCTCTGGTGGCTCCATCAGCAGTAGTAA

HUM: CTGGTGGAGTTGGGTCCGCCAGCCCCCCAGGGAAGGGGCTGGAGTGGATTG
UAM: CTGGTGGAGCTGGGTCCGCCAGCCCCCCAGGGAAGGGCCTGGAGTGGATTG

HUM: GGGAAATCTATCATAGTGGGAGCACCAACTACAACCCGTCCCTCAAGAGT
UAM: GGGAAATCTATCAAAGTGGGAGCACCAACTACAACCCGTCCCTCAAGAGT

HUM: CGAGTCACCATATCAGTAGACAAGTCCAAGAACCAGTTCTCCCTGAAGCT
UAM: CGAGTCACCATATCAGTAGACACGTCCAAGAACCAGTTCTCCCTGAAGCT

HUM: GAGCTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGCGAGAGA
UAM: GAGCTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGCGAGAGA
```

D7
```
HUM: CACAGTG
UAM: CACAGTG
```

D9
```
HUM: GACACAAACCT
UAM: GTCACAAACCT
```

Alignment stats: 'M': 290, 'I': 2, 'D': 2, 'X': 4

IGHV1-3

GENE ALIGN SEQ

```
HUM: CAGGTCCAGCTTGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTC
UAM: CAGGTCCAGCTCGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTC

HUM: AGTGAAGGTTTCCTGCAAGGCTTCTGGATACACCTTCACTAGCTATGCTA
UAM: AGTGAAGGTCTCCTGCAAGGCTTCTGGATATACCTTCACCGACTACTTTA

HUM: TGCATTGGGTGCGCCAGGCCCCCGGACAAAGGCTTGAGTGGATGGGATGG
UAM: TGCACTGGATGCTCCAGGCCCCTGGACAAAGGCTTGAGTGGATGGGATGG

HUM: ATCAACGCTGGCAATGGTAACACAAAATATTCACAGAAGTTCCAGGGCAG
UAM: ATCAGCGCTGGCAATGGTAACACAAAATATTCACAGAAGTTCCAGGGCAG

HUM: AGTCACCATTACCAGGGACACATCCGCGAGCACAGCCTACATGGAGCTGA
UAM: AGTCACCATTACCAGAGACACGTCCGCGAGCACAGCCTACATGGAGCTGA

HUM: GCAGCCTGAGATCTGAAGACACGGCTGTGTATTACTGTGCGAGAGA
UAM: GCAGCCTGAGATCTGAGGACACGGCTGTGTATTACTGTGTGAGAGA
```

D7
```
HUM: CACAGTG
UAM: CACAGTG
```

D9
```
HUM: GTCAGAAACCC
UAM: GTCAGAAACCC
```

Alignment stats: 'M': 278, 'I': 0, 'D': 0, 'X': 18

IGHV(III)-2-1

GENE ALIGN SEQ

```
HUM:  GAAGTTTACTGATGGAGTCAGAGGGGGAAAAATTTTACAGCCCAGTGG-T
UAM:  GAAGTTTACTGATGGAGTCAGAGGGAGAAAAATTTTACAGCCTAGCGGTT

HUM:  GAGACTCTCCTGCAAAGCCTCTGGTTTCACCTTTACTGGTTACAGCATGA
UAM:  GAGACTCTCCCGCAAAGCCTCTGGTTTCACCTTTACTGGCTACCGCATGA

HUM:  GCTTGGTCCAGCATGCTTCACAACAGGGATAGGTGTGGGTGCCAACAGTG
UAM:  GCTTGGTCCAGCATGCTTCACAACAGGGATAGGTGTGGGTGCCAACAGTG

HUM:  AGTGATCAAGTATGAATTCTCAGGGTTACTCTCCATGAGTACAAATAAAT
UAM:  AGTGATCAAGTATGAATTCTCAGGGTTACTCTCCATGAGTACAAATAAAT

HUM:  TAACAATCTCAAGCAACACCCCTTTTAAGTGCAGTCTGCCTTACAATGACC
UAM:  TAACAATCTCAAGCAACACCCCTTTCAAGTGCAGTCTGCCTTACAATGACC

HUM:  AATCTGAAAGCCAAGGACAAGGTCATGTATTACTGTGAGTGA
UAM:  AATCTGAAAGCCAAGGACAAGGCCATGTATTAC--TGAGTGA
```

D7
```
HUM:  CACAGTG
UAM:  CACAGTG
```

D9
```
HUM:  GACACAAAGCT
UAM:  GACACAAAGCT
```

Alignment stats: 'M': 281, 'I': 1, 'D': 2, 'X': 8

IGHV1-2

GENE ALIGN SEQ
```
HUM: CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTC
UAM: CAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAACCTGGGACCTC

HUM: AGTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCGGCTACTATA
UAM: AGTGAAGATCTCCTGCAAGGCTTCTGGTTACACCTTCACCAGCTACTATA

HUM: TGCACTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGATGG
UAM: TGCACTGGGTGCGACAGGCCCCTGGACAGGGGCTTGAGTGGATTGGACGG

HUM: ATCAACCCTAACAGTGGTGGCACAAACTATGCACAGAAGTTTCAGGGC-T
UAM: ATCAACCCTAACAGTGGTAACACAAACTACGCACAGAAGTTTCAGGGCA-

HUM: GG-GTCACCATGACCAGGGACACGTCCATCAGCACAGCCTACATGGAGCT
UAM: -GAGTCGCCATGACCAGGGACACGTCCATCAGCACAGCCTACATGGAGCT

HUM: GAGCAGGCTGAGATCTGACGACACGGCCGTGTATTACTGTGCGAGAGA
UAM: GAGAAGCCTGAGATCTGAGGACACAGCCACCTATTACTGTG-GAGAGA
```

D7
```
HUM: CACAGTG
UAM: CACAGTG
```

D9
```
HUM: GTCAGAAACCC
UAM: GTCAGAAACCC
```

Alignment stats: 'M': 273, 'I': 2, 'D': 3, 'X': 20

97

IGHV(II)-1-1

GENE ALIGN SEQ

```
HUM: CTGGGCCTGGACCCAGCAGCCCTCTGGGAAGGCGCTGGGGCACCTCAGCT
UAM: CTGGGCCTGGACCCAGCAGCACTCTGGGAAGGCGCTGGGGCACCTCAGCT

HUM: CCAGGGGCAGCACACACTTCAGCCCAGCCTTTCTGGGCCAACTCTCCATC
UAM: CCAGGGGCAGCACACACTTCAGCCCA-CCCTTCTGGGCCAACTGTCCATC

HUM: TGTAGAGACACATCCAAGGCCCAGTTATCCCTGCAGCTGAGCTCCGTGAT
UAM: TGCAGAGACACATCCAAGGCCCAGTTATCTCTGCAGCTGAGCTCCGTGAC

HUM: GGCCAAGGGCAGGGCCGCACACATTCCCGTGGGA
UAM: GGCCACGGGCAGGGCCACACACATTCCCATGGAA
```

D7
```
HUM: GACAGAA
UAM: GACAGCA
```

D9
```
HUM: GACACAAACCT
UAM: GACACAAATCT
```

Alignment stats: 'M': 171, 'I': 0, 'D': 1, 'X': 10

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 A 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 T A A C T G G A A T G A C

D7
HUM: C A C C G T G
UAM: C A C T 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': 15, 'I': 0, 'D': 0, 'X': 2

99

IGHD3-3

U9
HUM: `AGGTTTGGGGT`
UAM: `AGGTTTGGGGT`

U7
HUM: `CACTGTG`
UAM: `CACTGTG`

GENE ALIGN SEQ
HUM: `GTATTACGAT--TTTTGG-AGTGGTTATTATACC`
UAM: `GTATTACTATAG---TGGTAGTGGTTATTATAAC`

D7
HUM: `CACAGTG`
UAM: `CACAGTG`

D9
HUM: `ATCAAAAACCC`
UAM: `ATCAAAAACCC`

Alignment stats: 'M': 26, 'I': 3, 'D': 3, 'X': 2

IGHD4-4

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

Alignment stats: 'M': 16, 'I': 0, 'D': 0, 'X': 0

IGHD5-5

U9
HUM: `TGGTTATTGTC`
UAM: `TGGTTATTGTC`

U7
HUM: `GACTGTG`
UAM: `GACTGTG`

GENE ALIGN SEQ
HUM: `GTGGATACAGCTATGGTTAC`
UAM: `GTGAATATGGCTACGGTTAC`

D7
HUM: `CACAGTG`
UAM: `CACAGTG`

D9
HUM: `AGCAGCAACCA`
UAM: `AGCAGCAACCA`

Alignment stats: 'M': 16, 'I': 0, 'D': 0, 'X': 4

IGHD6-6

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

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

D9
HUM: G 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': 16, 'I': 0, 'D': 0, 'X': 2

IGHD1-7

U9
HUM: `CGGATTCTGAA`
UAM: `CGGATTCTGAA`

U7
HUM: `CACAGTG`
UAM: `CACAGTG`

GENE ALIGN SEQ
HUM: `GGTATAACTGGAACTAC`
UAM: `GGTATAACTGGAACTAC`

D7
HUM: `CACTGTG`
UAM: `CACTGTG`

D9
HUM: `GTCCAAAACGG`
UAM: `GTCCAAAACTG`

Alignment stats: 'M': 17, 'I': 0, 'D': 0, 'X': 0

IGHD2-8

U9
HUM: `AGGATTTTGTG`
UAM: `AGGATTTTGTG`

U7
HUM: `CACTGTG`
UAM: `CACTGTG`

GENE ALIGN SEQ
HUM: `AGGATATTGTA-CTAATGGTG-TA--TGCTATACC`
UAM: `AGGATATTGTAG----TGGTGGTAGCTGCTACGCC`

D7
HUM: `CACAGTG`
UAM: `CACAGTG`

D9
HUM: `TTCCCAAAGCC`
UAM: `TTCCCAAAGCC`

Alignment stats: 'M': 25, 'I': 4, 'D': 4, 'X': 2

105

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 A G T T A T T A T A A C
UAM:  G T A T T A C T A T A G T G G T G G T A C C T A T T A C 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': 23, 'I': 0, 'D': 0, 'X': 8

IGHD4-11

U9
HUM: GGCTTTTTGTG
UAM: GGCTTTTTGTG

U7
HUM: TGCTGTG
UAM: TACTGTG

GENE ALIGN SEQ
HUM: TGACTACAGT---AACTAC
UAM: TGACTACAGTGCTAACTAC

D7
HUM: CATAGTG
UAM: CACAGTG

D9
HUM: GGCAAAAACTG
UAM: AGCAAAAACTG

Alignment stats: 'M': 16, 'I': 3, 'D': 0, 'X': 0

IGHD5-12

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
```

U7
```
HUM: G A C T G T G
UAM: G G C C 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 - - - - G A T G G C T A C A 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': 18, 'I': 1, 'D': 4, 'X': 1

IGHD6-13

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
```

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

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

D9
```
HUM: G 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': 3, 'D': 0, 'X': 0

IGHD1-14

U9
HUM: `CGGATTCCGAA`
UAM: `CAGATTCTGAA`

U7
HUM: `CACAGCG`
UAM: `CACAGTG`

GENE ALIGN SEQ
HUM: `GGTATAACCGGAACCAC`
UAM: `GGTTTAACTGGAACTAC`

D7
HUM: `CACTGTC`
UAM: `CACTGTC`

D9
HUM: `GTCAAAAACTG`
UAM: `GTCAAAAACTG`

Alignment stats: 'M': 14, 'I': 0, 'D': 0, 'X': 3

IGHD2-15

U9
```
HUM: AGGATTTTGTG
UAM: AGGATTTTGTG
```

U7
```
HUM: CACTGTG
UAM: CACTGTG
```

GENE ALIGN SEQ
```
HUM: AGGATATTGTAGTGGTGGTAGCTGCTACTCC
UAM: AGGATATTGTAGTGGTAGTGGCTGCTACGCC
```

D7
```
HUM: CACAGTG
UAM: CACAGTG
```

D9
```
HUM: TTCCCAAAGCC
UAM: CTCCCAAAGCC
```

Alignment stats: 'M': 28, 'I': 0, 'D': 0, 'X': 3

IGHD3-16

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

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

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

Alignment stats: 'M': 32, 'I': 0, 'D': 3, 'X': 2

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

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

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

Alignment stats: 'M': 12, 'I': 0, 'D': 0, 'X': 4

IGHD5-18

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
```

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 G A T A T A C T G G C T A C G G 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 G G C A A C C A
```

Alignment stats: 'M': 18, 'I': 3, 'D': 0, 'X': 2

IGHD6-19

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`

U7
HUM: `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 C G G C T G G T C C`

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

D9
HUM: `G 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': 19, 'I': 0, 'D': 0, 'X': 2

IGHD1-20

U9
HUM: `CGGATTCTGAA`
UAM: `CAGATTCTGAA`

U7
HUM: `CACAGTG`
UAM: `CACAGTG`

GENE ALIGN SEQ
HUM: `GGTATAACTGGAACGAC`
UAM: `GGTATAACTGGAATGAT`

D7
HUM: `CACCGTG`
UAM: `CACTGTG`

D9
HUM: `GTCCAAAACTG`
UAM: `ATCCAAAACTG`

Alignment stats: 'M': 15, 'I': 0, 'D': 0, 'X': 2

IGHD2-21

U9
```
HUM: AGGATTTTGTG
UAM: AGGATTTTGTG
```

U7
```
HUM: CACTGTG
UAM: CACTGTG
```

GENE ALIGN SEQ
```
HUM: AGCATATTG---TGGTGGTGA-CTGCTATTCC
UAM: AGGATATTGTAGTGGTGGT-AGCTGCTACGCC
```

D7
```
HUM: CACAGTG
UAM: CACAGTG
```

D9
```
HUM: TTCCTAAAGCC
UAM: TTCCCAAAGCC
```

Alignment stats: 'M': 24, 'I': 4, 'D': 1, 'X': 3

IGHD3-22

U9
HUM: AGGTTTGAAGT
UAM: AGGTTTGAAGT

U7
HUM: CACTGTG
UAM: CACTGTG

GENE ALIGN SEQ
HUM: GTATTA-----CTATGATAGTAGTGG--TTATTACTA-------C
UAM: GTATTATGAT-TATGATACT--TGGGG---TTACTATTAAAGC

D7
HUM: CACAGTG
UAM: CACAGTG

D9
HUM: ATCAAAAACTC
UAM: ATCAAAAACTC

Alignment stats: 'M': 24, 'I': 12, 'D': 6, 'X': 1

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
```

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

GENE ALIGN SEQ
```
HUM:  T G A C T A C G G T G G T A A C T 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:  T A C A G T G
```

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

Alignment stats: 'M': 19, 'I': 0, 'D': 0, 'X': 0

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`

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

GENE ALIGN SEQ
HUM: `G T A G A G A T G G C T A C A A T T A C`
UAM: `G T G G A G A T G G C T A C A 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': 19, 'I': 0, 'D': 0, 'X': 1

IGHD6-25

U9
HUM: `AGGTTTCTGAA`
UAM: `AGGTTTCCGAA`

U7
HUM: `CACAGTC`
UAM: `CACAGTG`

GENE ALIGN SEQ
HUM: `GGGTATAGCAGCGGCTAC`
UAM: `GGGTATAGCAGTGGCTAC`

D7
HUM: `CACAATG`
UAM: `CACAATG`

D9
HUM: `GACAGAAACCC`
UAM: `GACAGAAACCC`

Alignment stats: 'M': 17, 'I': 0, 'D': 0, 'X': 1

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
```

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

GENE ALIGN SEQ
```
HUM: G G T A T A G T G 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
```

D7
```
HUM: C A C T G T G
UAM: C A C T 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': 20, 'I': 0, 'D': 0, 'X': 0

IGHJ1P

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

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

Alignment stats: 'M': 50, 'I': 0, 'D': 0, 'X': 4

123

IGHD7-27

U9
HUM: `GGGTTTTGGCT`
UAM: `GGGTTTTGGCT`

U7
HUM: `CACTGTG`
UAM: `CACCGTG`

GENE ALIGN SEQ
HUM: `CTAACTGGGGA`
UAM: `CTAACTGGGGA`

D7
HUM: `CACAGTG`
UAM: `CAGAGTG`

D9
HUM: `TACAAAAACCA`
UAM: `TACAAAAACCA`

Alignment stats: 'M': 11, 'I': 0, 'D': 0, 'X': 0

IGHJ1

U9
HUM: `TGGGTTTCTGT`
UAM: `TGGGTTTCTGC`

U7
HUM: `CACCGTG`
UAM: `CACCGTG`

GENE ALIGN SEQ
HUM: `GCTGAATACTTCCAGCACTGGGGCCAGGGCACCCTGGTCACCGTCTCCTC`
UAM: `GCCGAATACTTCAAGCACTGGGGCCAGGGCATCCTGGTCACCGTCTCCTC`

HUM: `AG`
UAM: `AG`

Alignment stats: 'M': 49, 'I': 0, 'D': 0, 'X': 3

IGHJ2

U9
HUM: `TGTGTTTTTGT`
UAM: `TGTGTTTTTGT`

U7
HUM: `GGCTGTG`
UAM: `GGCTGTG`

GENE ALIGN SEQ
HUM: `CTACTGGTACTTCGATCTCTGGGGCCGTGGCACCCTGGTCACTGTCTCCT`
UAM: `CTACTTGTACTTCGATCTCTGGGGCCGTGGCACCCTGGTCACCGTCTCCT`

HUM: `CAG`
UAM: `CAG`

Alignment stats: 'M': 51, 'I': 0, 'D': 0, 'X': 2

IGHJ2P

U9
HUM: `GCTGTTCATGT`
UAM: `GCTGTTCATGT`

U7
HUM: `TAGTGTG`
UAM: `TAGTGTG`

GENE ALIGN SEQ
HUM: `GCTACAAGTGCTTGGAGCACTGGGGCCAGGGCAGCCCGGCCACCGTCTCC`
UAM: `GCTACAAGTACTTGGAGCACTGGGTCCAGGGCAGCCCGGCCACCGTCTCC`

HUM: `CTGGGAACGTCA`
UAM: `CTGGGAACTTCA`

Alignment stats: 'M': 59, 'I': 0, 'D': 0, 'X': 3

IGHJ3

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

U7
```
HUM:  C C C T G T G
UAM:  C C C T G T G
```

GENE ALIGN SEQ
```
HUM:  T G A T G C T T T T G A T A T C T G G G G C C A A G G G - - A C - A A T G G T C A C C G T C T C T T
UAM:  T G A T G C T T T T G A T A T C T G G G G C C T A G G G G T - C G - - T G G T C A C C G T C T C T T
```

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

Alignment stats: 'M': 46, 'I': 3, 'D': 3, 'X': 1

IGHJ4

U9
HUM: AGGTTTTTGTG
UAM: AGGTTTTTGTG

U7
HUM: CAATGTG
UAM: CAATGTG

GENE ALIGN SEQ
HUM: ACTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
UAM: ACTACTTTGAGTACTGGGGCCAGGGAACCCTGCTCACCGTCTCCTCAG

Alignment stats: 'M': 46, 'I': 0, 'D': 0, 'X': 2

IGHJ5

U9
HUM: `CAGTTCTTGCC`
UAM: `CAGTTCTTGCC`

U7
HUM: `CAATGTG`
UAM: `CAATGTG`

GENE ALIGN SEQ
HUM: `ACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA`
UAM: `ACAACCAGTTCGACCCCTGGGGCCAGGGAACCCTGGTCACCGTCTCCCCA`

HUM: `G`
UAM: `G`

Alignment stats: 'M': 48, 'I': 0, 'D': 0, 'X': 3

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IGHJ3P

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

Alignment stats: 'M': 49, 'I': 0, 'D': 0, 'X': 1

IGHJ6

U9
HUM: `TGGGTTTTTGT`
UAM: `TGGGTTTTTGT`

U7
HUM: `CATTGTG`
UAM: `CATTGTG`

GENE ALIGN SEQ
HUM: `ATTACTAC---TACTACTACTACATGGACGTCTGGGGCA--AAGGGACCA`
UAM: `ATTACTACGGT--------------ATGGACTTCTGGG--ACTAAGGGACCA`

HUM: `CGGTCACCGTCTCCTCAG`
UAM: `TGGTCACCGTCTCCTCAG`

Alignment stats: 'M': 47, 'I': 5, 'D': 14, 'X': 2