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

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HUM: C A T A G G A
UAM: C A C A G G A
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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
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Alignment stats:  'M': 275, 'I': 1, 'D': 1, 'X': 16
Both human gene and its mapping are pseudogenes
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IGHV7-81

GENE ALIGN SEQ

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

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

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

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

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

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

D7

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

D9

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

```
Alignment stats:  ’M’: 287, ’I’: 0, ’D’: 0, ’X’: 9
Neither human gene nor its mapping is pseudogene
```

IGHV(II)-78-1

GENE ALIGN SEQ

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

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

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

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

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

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

D7

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

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Alignment stats:  'M': 256, 'I': 3, 'D': 5, 'X': 14
Human gene gained functionality in primate
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IGHV5-78

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

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

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

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

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

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

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

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

```
Alignment stats:  'M': 281, 'I': 3, 'D': 3, 'X': 10
Neither human gene nor its mapping is pseudogene
```

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
Both human gene and its mapping are pseudogenes

IGHV3-76

GENE ALIGN SEQ

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

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

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

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

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

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

D7

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

```
HUM: G T C A C A A A C C T
UAM: G T A A C A A A C C T
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Alignment stats:  'M': 278, 'I': 0, 'D': 0, 'X': 14
Both human gene and its mapping are pseudogenes
```

IGHV3-74

GENE ALIGN SEQ

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

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

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

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

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

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

D7

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

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HUM: G A C A C A A A C C T
UAM: G A C A C A A A C C T
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Alignment stats:  'M': 266, 'I': 4, 'D': 4, 'X': 26
Neither human gene nor its mapping is pseudogene
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IGHV3-73

GENE ALIGN SEQ

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

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

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

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

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

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

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

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

D9

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HUM: G A C A C A A A C C T
UAM: G A T A C A A A C C T
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Alignment stats:  'M': 271, 'I': 6, 'D': 6, 'X': 25
Neither human gene nor its mapping is pseudogene
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IGHV3-72

GENE ALIGN SEQ

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

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

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

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

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

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

HUM: G A
UAM: G A
```

D7

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

D9

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

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Alignment stats:  'M': 294, 'I': 0, 'D': 0, 'X': 8
Neither human gene nor its mapping is pseudogene
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IGHV2-70

GENE ALIGN SEQ

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

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

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

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

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

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

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

D7

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

D9

```
HUM: T A C A A G A A C C C
UAM: T A C A A G A A C C C
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Alignment stats:  'M': 288, 'I': 2, 'D': 2, 'X': 11
Neither human gene nor its mapping is pseudogene
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IGHV1-69D

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

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

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

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

```
Alignment stats:  'M': 277, 'I': 6, 'D': 6, 'X': 13
Neither human gene nor its mapping is pseudogene
```

IGHV2-70D

GENE ALIGN SEQ

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

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

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

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

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

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

HUM: C
UAM: C
```

D7

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

D9

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

```
Alignment stats:  'M': 287, 'I': 0, 'D': 0, 'X': 14
Neither human gene nor its mapping is pseudogene
```

IGHV1-69

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

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

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

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

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

D7

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

D9

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

```
Alignment stats:  'M': 281, 'I': 3, 'D': 3, 'X': 12
Neither human gene nor its mapping is pseudogene
```

IGHV1-68

GENE ALIGN SEQ

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

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

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

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

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

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

D7

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

D9

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

```
Alignment stats:  'M': 281, 'I': 0, 'D': 0, 'X': 15
Human gene lost functionality in primate
```

IGHV(III)-67-4

GENE ALIGN SEQ

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

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

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

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

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

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

D7

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

D9

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

```
Alignment stats:  'M': 283, 'I': 0, 'D': 0, 'X': 11
Both human gene and its mapping are pseudogenes
```

IGHV(III)-67-3

GENE ALIGN SEQ

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

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

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

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

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

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

D7

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

D9

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

```
Alignment stats:  'M': 260, 'I': 2, 'D': 6, 'X': 9
Both human gene and its mapping are pseudogenes
```

IGHV(III)-67-2

GENE ALIGN SEQ

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

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

D7

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

D9

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

```
Alignment stats:  ’M’: 95, ’I’: 0, ’D’: 0, ’X’: 4
Neither human gene nor its mapping is pseudogene
```

IGHV(II)-67-1

GENE ALIGN SEQ

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

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

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

D7

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

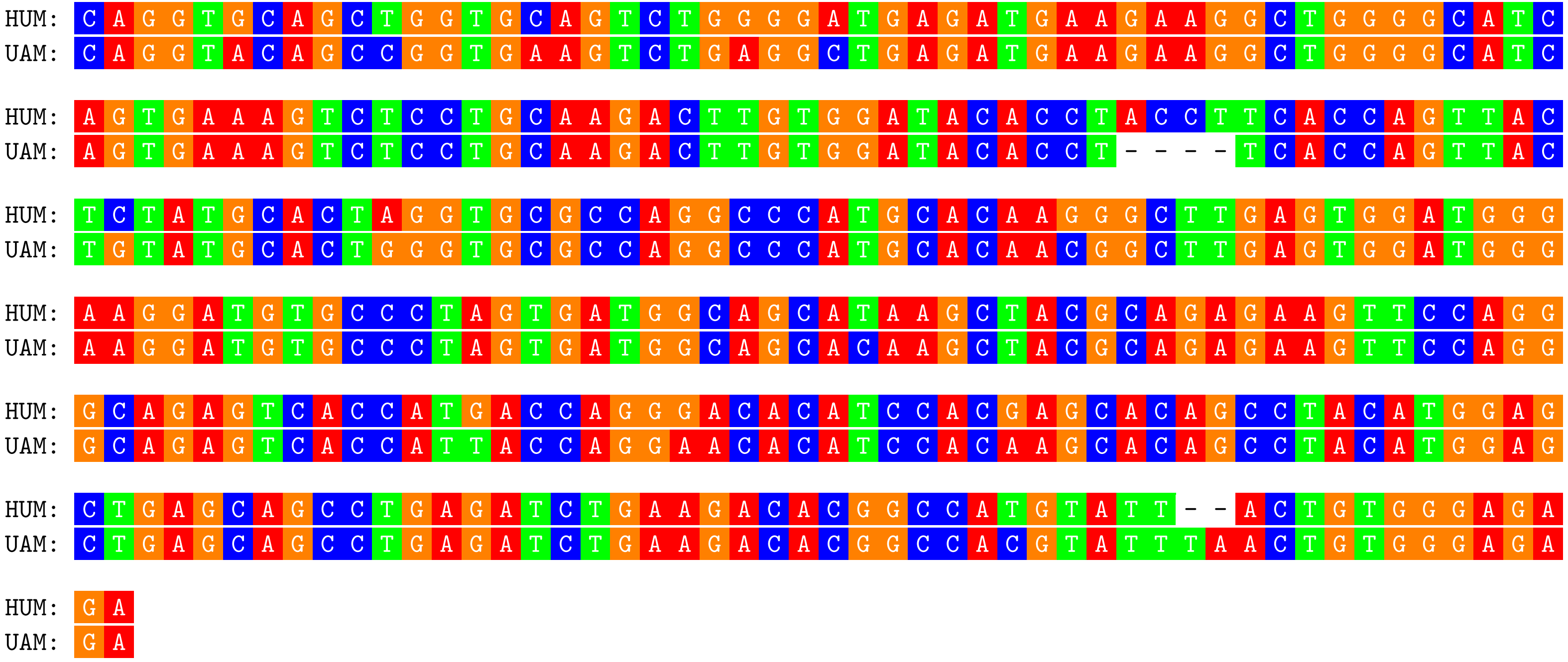
D9

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

```
Alignment stats:  'M': 136, 'I': 0, 'D': 0, 'X': 3
Both human gene and its mapping are pseudogenes
```

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

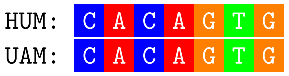
HUM: A A G G A T G T G C C C T A G T G A T G G C A G C A T A A G C T A C G C A G A G A A G T T C C A G G
UAM: A A G G A T G T G C C C T A G T G A T G G C A G C A C A A G C T A C G C A G A G A A G T T C C A G G

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

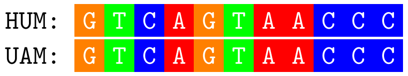
HUM: G A
UAM: G A

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`
`Human gene gained functionality in primate`

IGHV3-66

GENE ALIGN SEQ

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

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

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

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

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

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

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

```
Alignment stats:  'M': 276, 'I': 3, 'D': 3, 'X': 14
Neither human gene nor its mapping is pseudogene
```

IGHV(II)-65-1

GENE ALIGN SEQ

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

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

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

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

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

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

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

D7

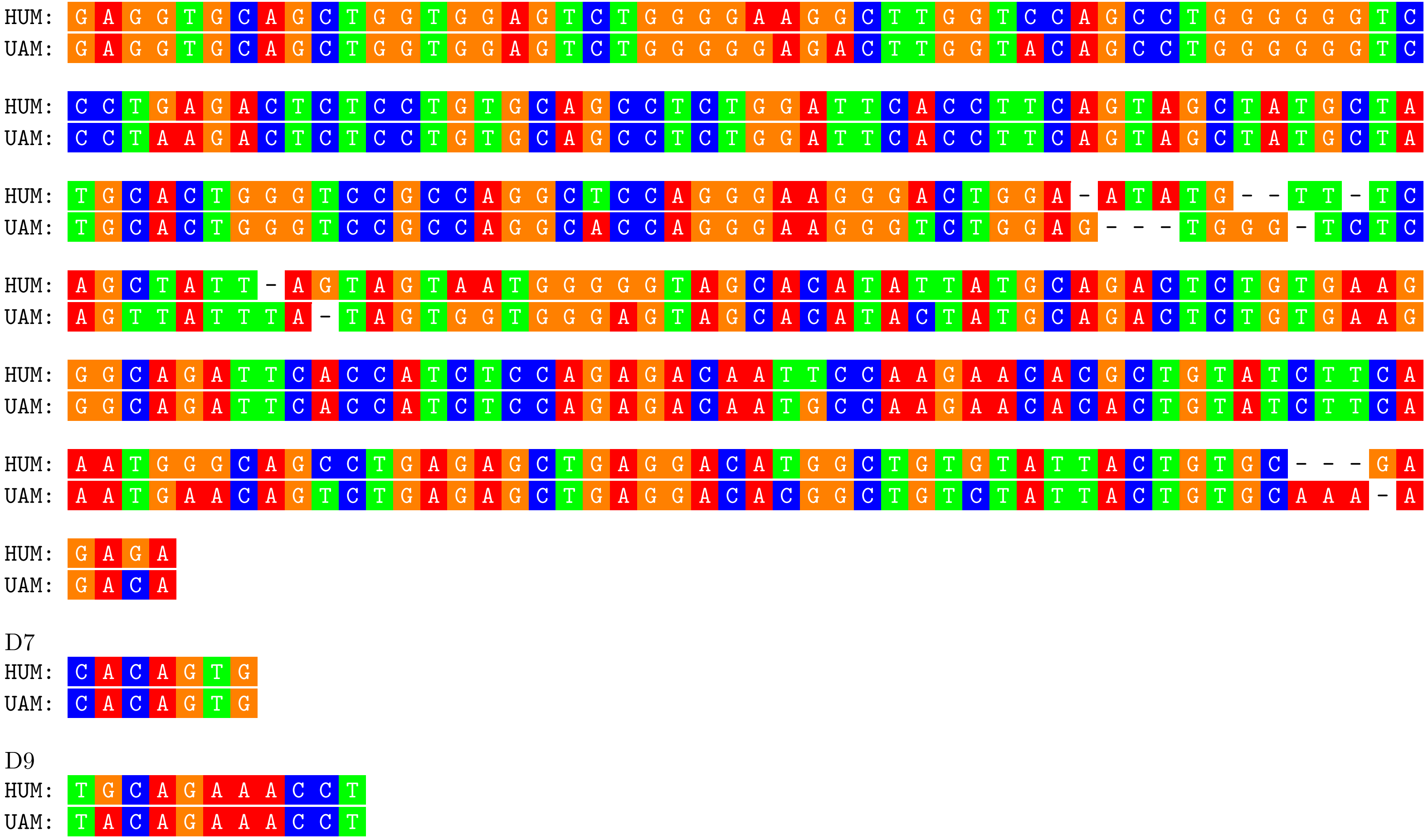
```
HUM: C A C A A C G
UAM: T A C A G C G
```

D9

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

```
Alignment stats:  'M': 286, 'I': 3, 'D': 4, 'X': 10
Both human gene and its mapping are pseudogenes
```

IGHV3-64



GENE ALIGN SEQ

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

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

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

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

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

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

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

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

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HUM: T G C A G A A A C C T
UAM: T A C A G A A A C C T
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Alignment stats:  'M': 271, 'I': 8, 'D': 6, 'X': 19
Human gene lost functionality in primate
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IGHV3-63

GENE ALIGN SEQ

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

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

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

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

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

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

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

```
HUM: G A C A C A A A A T T
UAM: G A C A C A A A A T T
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Alignment stats:  'M': 285, 'I': 2, 'D': 2, 'X': 11
Both human gene and its mapping are pseudogenes
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IGHV(II)-62-1

GENE ALIGN SEQ

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

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

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

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

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

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

D7

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

D9

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

```
Alignment stats:  'M': 257, 'I': 2, 'D': 4, 'X': 12
Both human gene and its mapping are pseudogenes
```

IGHV(II)-60-1

GENE ALIGN SEQ

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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
```

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Alignment stats:  'M': 260, 'I': 3, 'D': 1, 'X': 8
Both human gene and its mapping are pseudogenes
```

IGHV3-60

GENE ALIGN SEQ

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

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

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

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

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

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

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

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

D9

```
HUM: A C A A A C C T C C T
UAM: A C A C A A A C C T C
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Alignment stats:  'M': 274, 'I': 11, 'D': 9, 'X': 14
Both human gene and its mapping are pseudogenes
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IGHV4-59

GENE ALIGN SEQ

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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 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

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

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

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

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

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

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

D9

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

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Alignment stats:  'M': 282, 'I': 2, 'D': 2, 'X': 9
Neither human gene nor its mapping is pseudogene
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IGHV1-58

GENE ALIGN SEQ

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

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

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

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

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

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

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

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HUM: G T C A G A A A C G C
UAM: G T C A G A A A C C C
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Alignment stats:  'M': 276, 'I': 1, 'D': 3, 'X': 17
Human gene lost functionality in primate
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IGHV3-57

GENE ALIGN SEQ

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

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

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

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

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

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

D7

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

D9

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

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Alignment stats:  'M': 275, 'I': 5, 'D': 5, 'X': 15
Both human gene and its mapping are pseudogenes
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IGHV7-56

GENE ALIGN SEQ

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

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

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

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

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

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

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

D9

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

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Alignment stats:  'M': 281, 'I': 1, 'D': 2, 'X': 11
Both human gene and its mapping are pseudogenes
```

IGHV4-55

GENE ALIGN SEQ

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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 G T G C A G T 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

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

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

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

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

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

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

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Alignment stats:  'M': 269, 'I': 13, 'D': 16, 'X': 11
Both human gene and its mapping are pseudogenes
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IGHV3-54

GENE ALIGN SEQ

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HUM: G G - - A T C C C T G A G A C T C T C C T G T G C A G A C T C T G G A T T A A C C T T C A G T A G C
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
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D7

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

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HUM: A C A G A C A C A G A
UAM: A C A G G T A C A G A
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Alignment stats:  'M': 239, 'I': 6, 'D': 5, 'X': 6
Both human gene and its mapping are pseudogenes
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IGHV(II)-53-1

GENE ALIGN SEQ

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

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

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

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

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

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

D7

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

D9

```
HUM: C A C C C A A A C C T
UAM: C A T C C A A A C C T
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Alignment stats:  'M': 257, 'I': 0, 'D': 1, 'X': 12
Human gene gained functionality in primate
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IGHV3-53

GENE ALIGN SEQ

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

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

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

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

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

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

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

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

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Alignment stats:  'M': 272, 'I': 7, 'D': 8, 'X': 13
Human gene lost functionality in primate
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IGHV3-52

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

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

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

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

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

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

Alignment stats:  'M': 286, 'I': 0, 'D': 0, 'X': 10
Both human gene and its mapping are pseudogenes
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IGHV(II)-51-2

GENE ALIGN SEQ

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

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

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

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

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

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

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

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HUM: C A C A A A C T T C C
UAM: C A C A A A C T T C C
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Alignment stats:  'M': 256, 'I': 1, 'D': 1, 'X': 6
Both human gene and its mapping are pseudogenes
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IGHV5-51

GENE ALIGN SEQ

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

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

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

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

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

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

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

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

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Alignment stats:  'M': 284, 'I': 3, 'D': 3, 'X': 9
Neither human gene nor its mapping is pseudogene
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IGHV3-50

GENE ALIGN SEQ

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

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

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

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

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

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

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

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HUM: G A C A C A A A A T T
UAM: G A C A C A A A A T T
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Alignment stats:  'M': 283, 'I': 0, 'D': 0, 'X': 14
Both human gene and its mapping are pseudogenes
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IGHV(II)-49-1

GENE ALIGN SEQ

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

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

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

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

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

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

HUM: G A
UAM: G A
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D7

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

D9

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

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Alignment stats:  'M': 282, 'I': 4, 'D': 3, 'X': 13
Both human gene and its mapping are pseudogenes
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IGHV3-49

GENE ALIGN SEQ

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

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

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

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

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

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

HUM: G A G A
UAM: G A G A
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D7

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

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

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Alignment stats:  'M': 294, 'I': 2, 'D': 2, 'X': 6
Neither human gene nor its mapping is pseudogene
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IGHV3-48

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

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

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

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

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

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

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

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

`Alignment stats: 'M': 280, 'I': 0, 'D': 0, 'X': 16`
`Neither human gene nor its mapping is pseudogene`

IGHV(III)-47-1

GENE ALIGN SEQ

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

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

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

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

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

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

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

```
Alignment stats:  'M': 284, 'I': 0, 'D': 0, 'X': 9
Both human gene and its mapping are pseudogenes
```

IGHV3-47

GENE ALIGN SEQ

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

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

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

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

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

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

```
Alignment stats:  'M': 284, 'I': 0, 'D': 0, 'X': 9
Neither human gene nor its mapping is pseudogene
```

IGHV(II)-46-1

GENE ALIGN SEQ

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

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

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

D7

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

D9

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

```
Alignment stats:  'M': 141, 'I': 0, 'D': 0, 'X': 6
Neither human gene nor its mapping is pseudogene
```

IGHV1-46

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

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

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

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

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

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

```
Alignment stats:  'M': 285, 'I': 0, 'D': 0, 'X': 11
Neither human gene nor its mapping is pseudogene
```

IGHV1-45

GENE ALIGN SEQ

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

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

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

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

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

D7

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

D9

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

```
Alignment stats:  'M': 282, 'I': 1, 'D': 3, 'X': 11
Human gene lost functionality in primate
```

IGHV(II)-44-2

GENE ALIGN SEQ

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

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

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

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

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

D7

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

D9

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

```
Alignment stats:  'M': 233, 'I': 0, 'D': 0, 'X': 4
Both human gene and its mapping are pseudogenes
```

IGHV(IV)-44-1

GENE ALIGN SEQ

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

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

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

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

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

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

D7

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

D9

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

```
Alignment stats:  'M': 280, 'I': 6, 'D': 3, 'X': 6
Both human gene and its mapping are pseudogenes
```

IGHV(II)-43-1

GENE ALIGN SEQ

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

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

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

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

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

D7

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

D9

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

```
Alignment stats:  'M': 199, 'I': 11, 'D': 3, 'X': 8
Both human gene and its mapping are pseudogenes
```

IGHV3-43

GENE ALIGN SEQ

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

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

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

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

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

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

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

D7

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

D9

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

```
Alignment stats:  'M': 282, 'I': 5, 'D': 5, 'X': 11
Neither human gene nor its mapping is pseudogene
```

IGHV3-42

GENE ALIGN SEQ

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

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

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

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

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

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

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

D7

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

D9

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

```
Alignment stats:  'M': 291, 'I': 2, 'D': 0, 'X': 12
Human gene gained functionality in primate
```

IGHV3-41

GENE ALIGN SEQ

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

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

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

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

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

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

D7

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

D9

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

```
Alignment stats:  'M': 274, 'I': 5, 'D': 5, 'X': 15
Both human gene and its mapping are pseudogenes
```

IGHV(II)-40-1

GENE ALIGN SEQ

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

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

D7

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

D9

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

```
Alignment stats:  'M': 73, 'I': 0, 'D': 0, 'X': 4
Neither human gene nor its mapping is pseudogene
```

IGHV7-40

GENE ALIGN SEQ

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

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

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

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

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

```
Alignment stats:  'M': 190, 'I': 2, 'D': 2, 'X': 11
Both human gene and its mapping are pseudogenes
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IGHV4-39

GENE ALIGN SEQ

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HUM: C A G C 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 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

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

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

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

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

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

HUM: A
UAM: A
```

D7

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

D9

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

```
Alignment stats:  'M': 277, 'I': 2, 'D': 8, 'X': 14
Neither human gene nor its mapping is pseudogene
```

IGHV(III)-38-1

GENE ALIGN SEQ

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

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

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

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

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

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

D7

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

D9

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

```
Alignment stats:  'M': 266, 'I': 2, 'D': 6, 'X': 10
Both human gene and its mapping are pseudogenes
```

IGHV3-38

GENE ALIGN SEQ

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

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

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

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

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

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

D7

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

D9

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

```
Alignment stats:  'M': 277, 'I': 6, 'D': 5, 'X': 10
Human gene lost functionality in primate
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IGHV3-37

GENE ALIGN SEQ

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

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

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

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

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

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

D7

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

D9

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

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Alignment stats:  'M': 281, 'I': 0, 'D': 0, 'X': 13
Both human gene and its mapping are pseudogenes
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IGHV3-36

GENE ALIGN SEQ

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

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

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

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

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

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

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

D7

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

D9

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

```
Alignment stats:  'M': 289, 'I': 2, 'D': 1, 'X': 11
Both human gene and its mapping are pseudogenes
```

IGHV3-35

GENE ALIGN SEQ

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

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

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

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

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

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

D7

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

D9

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

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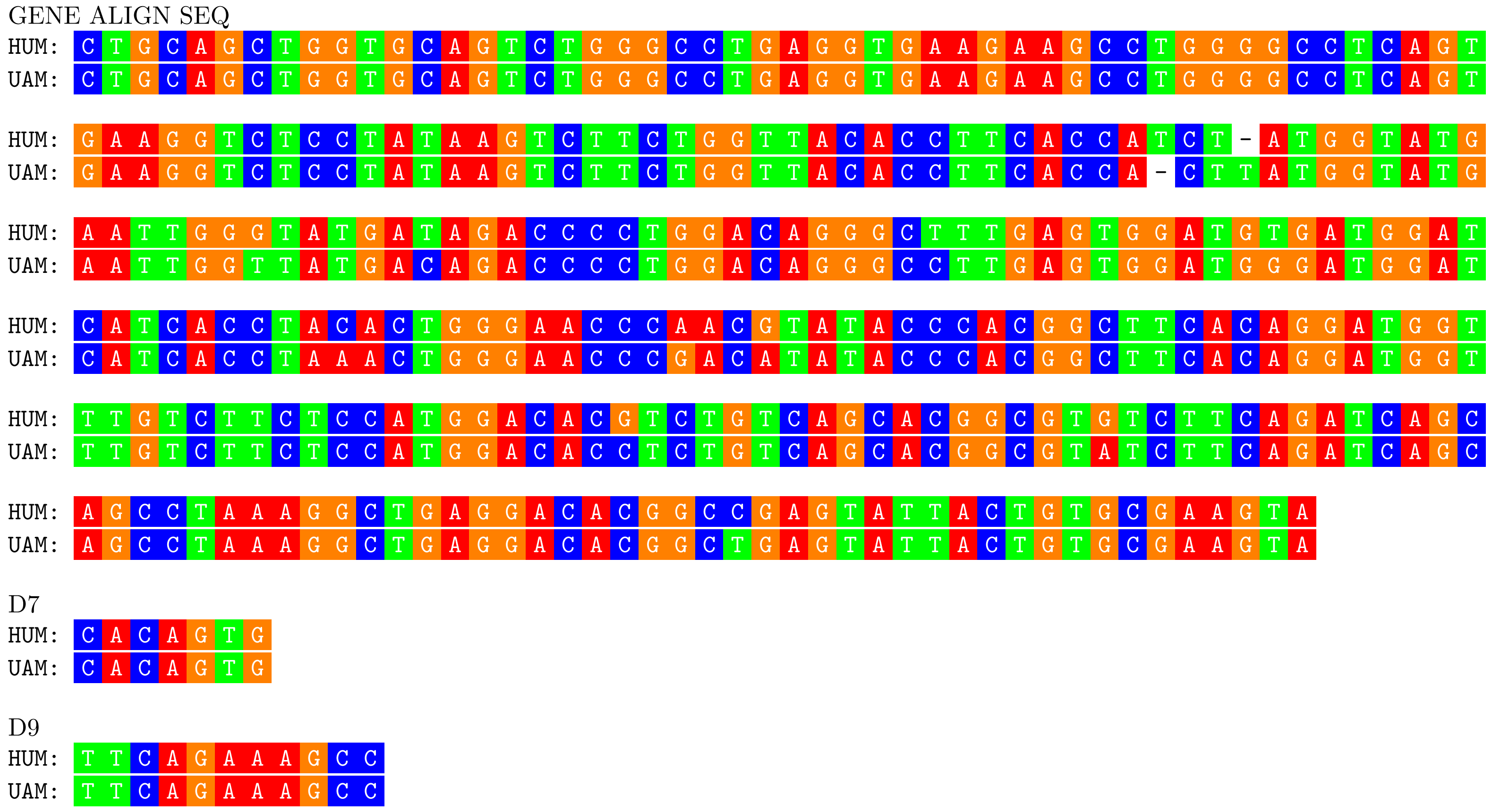
Alignment stats:  'M': 280, 'I': 2, 'D': 2, 'X': 14
Neither human gene nor its mapping is pseudogene
```

IGHV7-34-1



GENE ALIGN SEQ

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

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

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

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

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

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

D7

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

D9

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

```
Alignment stats:  'M': 282, 'I': 1, 'D': 1, 'X': 10
Both human gene and its mapping are pseudogenes
```

IGHV4-34

GENE ALIGN SEQ

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

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

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

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

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

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

HUM: G
UAM: G
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D7

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

D9

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

```
Alignment stats:  ’M’: 277, ’I’: 8, ’D’: 8, ’X’: 8
Neither human gene nor its mapping is pseudogene
```

IGHV3-33-2

GENE ALIGN SEQ

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

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

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

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

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

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

D7

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

D9

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

```
Alignment stats:  'M': 280, 'I': 2, 'D': 2, 'X': 16
Both human gene and its mapping are pseudogenes
```

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
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D7

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

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

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Alignment stats:  'M': 226, 'I': 0, 'D': 51, 'X': 6
Both human gene and its mapping are pseudogenes
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IGHV4-28

GENE ALIGN SEQ

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

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

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

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

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

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

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

D9

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

```
Alignment stats:  'M': 277, 'I': 3, 'D': 3, 'X': 16
Neither human gene nor its mapping is pseudogene
```

IGHV7-27

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

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

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

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

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

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

HUM: G
UAM: A
```

D7

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

D9

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

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Alignment stats:  'M': 249, 'I': 19, 'D': 5, 'X': 28
Human gene gained functionality in primate
```

IGHV(III)-26-1

GENE ALIGN SEQ

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

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

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

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

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

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

HUM: A
UAM: A
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D7

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

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

```
Alignment stats:  'M': 277, 'I': 5, 'D': 5, 'X': 14
Both human gene and its mapping are pseudogenes
```

IGHV2-26

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

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

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

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

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

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

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

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

```
Alignment stats:  ’M’: 293, ’I’: 2, ’D’: 2, ’X’: 6
Neither human gene nor its mapping is pseudogene
```

IGHV(III)-25-1

GENE ALIGN SEQ

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

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

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

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

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

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

D7

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

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

```
Alignment stats:  'M': 261, 'I': 0, 'D': 3, 'X': 16
Both human gene and its mapping are pseudogenes
```

IGHV3-25

GENE ALIGN SEQ

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

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

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

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

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

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

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

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Alignment stats:  'M': 277, 'I': 3, 'D': 3, 'X': 16
Both human gene and its mapping are pseudogenes
```

IGHV1-24

GENE ALIGN SEQ

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

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

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

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

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

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

D7

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

D9

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

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Alignment stats:  'M': 287, 'I': 0, 'D': 0, 'X': 9
Neither human gene nor its mapping is pseudogene
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IGHV3-23

GENE ALIGN SEQ

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

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

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

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

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

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

```
Alignment stats:  'M': 271, 'I': 6, 'D': 3, 'X': 22
Neither human gene nor its mapping is pseudogene
```

IGHV(III)-22-2

GENE ALIGN SEQ

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

D7

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

D9

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

```
Alignment stats:  'M': 28, 'I': 0, 'D': 0, 'X': 2
Neither human gene nor its mapping is pseudogene
```

IGHV(II)-22-1

GENE ALIGN SEQ

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

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

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

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

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

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

D7

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

D9

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

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Alignment stats:  'M': 247, 'I': 4, 'D': 2, 'X': 20
Both human gene and its mapping are pseudogenes
```

IGHV3-22

GENE ALIGN SEQ

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

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

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

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

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

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

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

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

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

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Alignment stats:  'M': 285, 'I': 8, 'D': 8, 'X': 9
Both human gene and its mapping are pseudogenes
```

IGHV1-17

GENE ALIGN SEQ

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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
Both human gene and its mapping are pseudogenes
```

IGHV(III)-16-1

GENE ALIGN SEQ

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

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

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

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

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

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

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

D7

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

D9

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

```
Alignment stats:  'M': 293, 'I': 1, 'D': 0, 'X': 10
Both human gene and its mapping are pseudogenes
```

IGHV3-16

GENE ALIGN SEQ

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

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

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

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

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

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

HUM: A
UAM: A
```

D7

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

D9

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

```
Alignment stats:  'M': 279, 'I': 5, 'D': 5, 'X': 12
Neither human gene nor its mapping is pseudogene
```

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 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
Both human gene and its mapping are pseudogenes
```

IGHV3-15

GENE ALIGN SEQ

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

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

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

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

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

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

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

```
Alignment stats:  'M': 291, 'I': 2, 'D': 2, 'X': 9
Neither human gene nor its mapping is pseudogene
```

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
Both human gene and its mapping are pseudogenes
```

IGHV3-13

GENE ALIGN SEQ

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

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

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

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

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

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

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

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Alignment stats:  'M': 279, 'I': 1, 'D': 1, 'X': 13
Human gene lost functionality in primate
```

IGHV1-12

GENE ALIGN SEQ

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

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

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

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

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

D7

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

D9

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

```
Alignment stats:  ’M’: 287, ’I’: 2, ’D’: 2, ’X’: 7
Both human gene and its mapping are pseudogenes
```

IGHV3-11

GENE ALIGN SEQ

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

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

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

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

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

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

```
Alignment stats:  'M': 278, 'I': 2, 'D': 2, 'X': 16
Neither human gene nor its mapping is pseudogene
```

IGHV5-10-1

GENE ALIGN SEQ

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

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

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

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

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

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

D7

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

D9

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

```
Alignment stats:  'M': 275, 'I': 4, 'D': 6, 'X': 15
Human gene lost functionality in primate
```

IGHV3-64D

GENE ALIGN SEQ

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

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

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

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

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

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

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

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

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

```
Alignment stats:  'M': 433, 'I': 0, 'D': 0, 'X': 19
Both human gene and its mapping are pseudogenes
```

IGHV3-7

GENE ALIGN SEQ

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

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

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

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

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

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

```
Alignment stats:  'M': 282, 'I': 4, 'D': 4, 'X': 10
Human gene lost functionality in primate
```

IGHV3-6

GENE ALIGN SEQ

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

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

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

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

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

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

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

D7

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

D9

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

```
Alignment stats:  'M': 269, 'I': 12, 'D': 11, 'X': 15
Both human gene and its mapping are pseudogenes
```

IGHV(III)-5-1

GENE ALIGN SEQ

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

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

D7

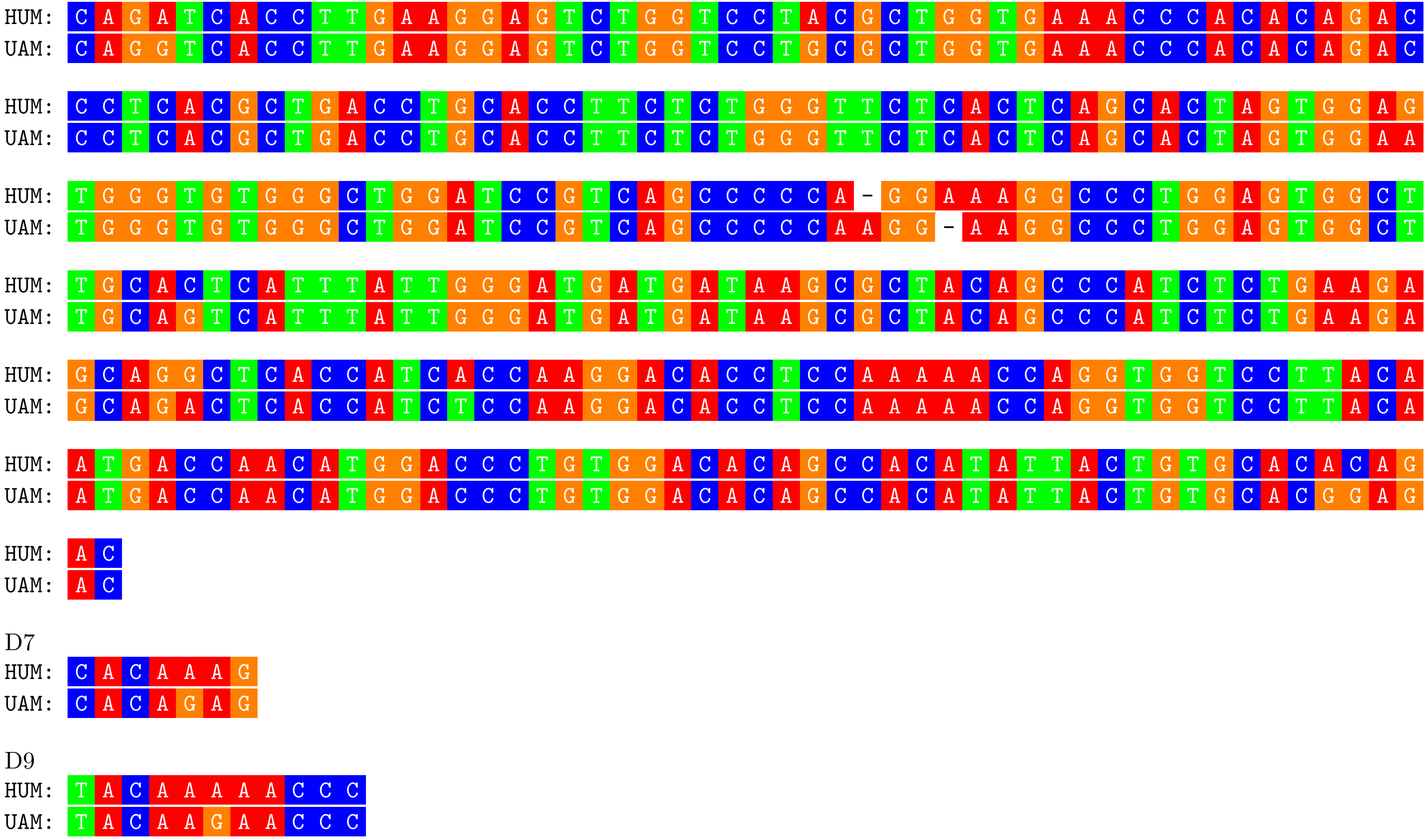
```
HUM: C A C A T G A
UAM: C G C A T G A
```

D9

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

```
Alignment stats:  'M': 98, 'I': 0, 'D': 0, 'X': 1
Neither human gene nor its mapping is pseudogene
```

IGHV2-5



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

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

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

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

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

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

HUM: A C
UAM: A C

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

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

```
Alignment stats:  'M': 292, 'I': 1, 'D': 1, 'X': 8
Neither human gene nor its mapping is pseudogene
```

IGHV4-4

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

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

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

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

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

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

D7

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

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

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Alignment stats:  'M': 290, 'I': 2, 'D': 2, 'X': 4
Neither human gene nor its mapping is pseudogene
```

IGHV1-3

GENE ALIGN SEQ

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

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

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

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

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

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

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Alignment stats:  ’M’: 278, ’I’: 0, ’D’: 0, ’X’: 18
Neither human gene nor its mapping is pseudogene
```

IGHV(III)-2-1

GENE ALIGN SEQ

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

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

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

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

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

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

```
Alignment stats:  'M': 281, 'I': 1, 'D': 2, 'X': 8
Both human gene and its mapping are pseudogenes
```

IGHV1-2

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

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

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

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

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

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

```
Alignment stats:  'M': 273, 'I': 2, 'D': 3, 'X': 20
Human gene lost functionality in primate
```

IGHV(II)-1-1

GENE ALIGN SEQ

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

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

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

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

D7

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

D9

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

```
Alignment stats:  'M': 171, 'I': 0, 'D': 1, 'X': 10
Human gene gained functionality in primate
```

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
Neither human gene nor its mapping is pseudogene
```

IGHD3-3

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

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

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

Alignment stats: ’M’: 26, ’I’: 3, ’D’: 3, ’X’: 2
Human gene lost functionality in primate

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
Both human gene and its mapping are pseudogenes
```

IGHD5-5

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

```
Alignment stats:  'M': 16, 'I': 0, 'D': 0, 'X': 4
Neither human gene nor its mapping is pseudogene
```

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
Neither human gene nor its mapping is pseudogene
```

IGHD1-7

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

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

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

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

IGHD2-8

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

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

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

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

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

Alignment stats: ’M’: 25, ’I’: 4, ’D’: 4, ’X’: 2
Both human gene and its mapping are pseudogenes

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
Both human gene and its mapping are pseudogenes
```

IGHD4-11

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

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

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

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

```
Alignment stats:  'M': 16, 'I': 3, 'D': 0, 'X': 0
Both human gene and its mapping are pseudogenes
```

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
Neither human gene nor its mapping is pseudogene
```

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
Neither human gene nor its mapping is pseudogene
```

IGHD1-14

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

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

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

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

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

Alignment stats: ’M’: 14, ’I’: 0, ’D’: 0, ’X’: 3
Neither human gene nor its mapping is pseudogene

IGHD2-15

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

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

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

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

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

```
Alignment stats:  'M': 28, 'I': 0, 'D': 0, 'X': 3
Both human gene and its mapping are pseudogenes
```

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
Both human gene and its mapping are pseudogenes
```

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 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
Both human gene and its mapping are pseudogenes
```

IGHD5-18

U9
HUM: T G G T T A T T G T C
UAM: T G G T T A T 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
Neither human gene nor its mapping is pseudogene
```

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
Neither human gene nor its mapping is pseudogene
```

IGHD1-20

U9

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

GENE ALIGN SEQ

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

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

```
Alignment stats:  'M': 15, 'I': 0, 'D': 0, 'X': 2
Neither human gene nor its mapping is pseudogene
```

IGHD2-21

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

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

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

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

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

```
Alignment stats:  'M': 24, 'I': 4, 'D': 1, 'X': 3
Both human gene and its mapping are pseudogenes
```

IGHD3-22

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

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

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

```
Alignment stats:  'M': 24, 'I': 12, 'D': 6, 'X': 1
Both human gene and its mapping are pseudogenes
```

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

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

IGHD5-24

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

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
Neither human gene nor its mapping is pseudogene
```

IGHD6-25

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

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

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

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

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

```
Alignment stats:  'M': 17, 'I': 0, 'D': 0, 'X': 1
Neither human gene nor its mapping is pseudogene
```

IGHD1-26

U9

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

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
Neither human gene nor its mapping is pseudogene
```

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

Human gene lost functionality in primate

IGHD7-27

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

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

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

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

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

```
Alignment stats:  'M': 11, 'I': 0, 'D': 0, 'X': 0
Neither human gene nor its mapping is pseudogene
```

IGHJ1

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

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

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

HUM: A G
UAM: A G

```
Alignment stats:  'M': 49, 'I': 0, 'D': 0, 'X': 3
Neither human gene nor its mapping is pseudogene
```

IGHJ2

U9

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

U7

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

GENE ALIGN SEQ

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

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

```
Alignment stats:  'M': 51, 'I': 0, 'D': 0, 'X': 2
Neither human gene nor its mapping is pseudogene
```

IGHJ2P

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

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

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

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

```
Alignment stats:  'M': 59, 'I': 0, 'D': 0, 'X': 3
Neither human gene nor its mapping is pseudogene
```

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

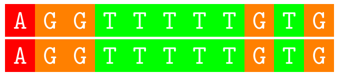
```
HUM: T G A T G C T T T T G A T A T C T G G G G C C A A G G G - - A C - A A T G G T C A C C G T C T C T T
UAM: T G A T G C T T T T G A T A T C T G G G G C C T A G G G G T - C G - - T G G T C A C C G T C T C T T
```

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

```
Alignment stats:  'M': 46, 'I': 3, 'D': 3, 'X': 1
Both human gene and its mapping are pseudogenes
```

IGHJ4

U9



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

U7

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

GENE ALIGN SEQ

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

```
Alignment stats:  'M': 46, 'I': 0, 'D': 0, 'X': 2
Neither human gene nor its mapping is pseudogene
```

IGHJ5

U9

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

U7

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

GENE ALIGN SEQ

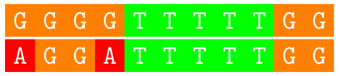
```
HUM: A C A A C T G G T T C G A C C C C T G G G G C C A G G G A A C C C T G G T C A C C G T C T C C T C A
UAM: A C A A C C A G T T C G A C C C C T G G G G C C A G G G A A C C C T G G T C A C C G T C T C C C C A

HUM: G
UAM: G
```

```
Alignment stats:  'M': 48, 'I': 0, 'D': 0, 'X': 3
Neither human gene nor its mapping is pseudogene
```

IGHJ3P

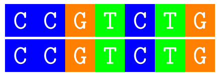
U9



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

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

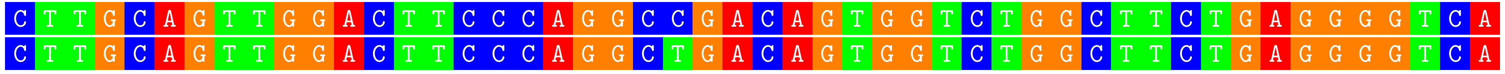
U7



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
Neither human gene nor its mapping is pseudogene
```

IGHJ6

U9

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

U7

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

GENE ALIGN SEQ

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

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

```
Alignment stats:  'M': 47, 'I': 5, 'D': 14, 'X': 2
Neither human gene nor its mapping is pseudogene
```