UAMs and RSSs of genes in syntney block alginments

Group 2 with 1 units in hum and 1 units in org

Group 2 unit1 0 vs unit2 0 IGHJ3P

U9

```
HUM: G G G G T T T T T G G
ORG: A G G A T T T T T G G
```

U7

```
HUM: C C G T C T G
ORG: 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
ORG: 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
PI: 98.0
```

Group 2 with 1 units in hum and 1 units in org

Group 2 unit1 0 vs unit2 0 IGHJ5

U9

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

U7

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

```
Alignment stats:  'M': 48, 'I': 0, 'D': 0, 'X': 3
PI: 94.11764705882352
```

Group 2 with 1 units in hum and 1 units in org

Group 2 unit1 0 vs unit2 0 IGHJ4

U9

```
HUM: A G G T T T T T G T G
ORG: A G G T T T T T G T G
```

U7

```
HUM: C A A T G T G
ORG: 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
ORG: 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
PI: 95.83333333333334
```

Group 2 with 1 units in hum and 1 units in org

Group 2 unit1 0 vs unit2 0 IGHJ3

U9

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

U7

```
HUM: C C C T G T G
ORG: 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 C
ORG: 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 C
```

```
HUM: A G
ORG: A G
```

```
Alignment stats:  'M': 45, 'I': 2, 'D': 2, 'X': 3
PI: 86.53846153846155
```

Group 2 with 1 units in hum and 1 units in org

Group 2 unit1 0 vs unit2 0 IGHJ2P

U9

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

U7

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

```
Alignment stats:  'M': 59, 'I': 0, 'D': 0, 'X': 3
PI: 95.16129032258065
```

Group 2 with 1 units in hum and 1 units in org

Group 2 unit1 0 vs unit2 0 IGHJ2

U9

```
HUM: T G T G T T T T T G T
ORG: T G T G T T T T T G T
```

U7

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

```
Alignment stats:  'M': 51, 'I': 0, 'D': 0, 'X': 2
PI: 96.22641509433963
```

Group 2 with 1 units in hum and 1 units in org

Group 2 unit1 0 vs unit2 0 IGHJ1

U9

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

U7

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

Alignment stats: ’M’: 49, ’I’: 0, ’D’: 0, ’X’: 3
PI: 94.23076923076923

Group 2 with 1 units in hum and 1 units in org

Group 2 unit1 0 vs unit2 0 IGHD7-27

U9

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

U7

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

GENE ALIGN SEQ

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

D7

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

D9

HUM: T A C A A A A A C C A
ORG: T A C A A A A A C C A

```
Alignment stats:  'M': 11, 'I': 0, 'D': 0, 'X': 0
PI: 100.0
```

Group 2 with 1 units in hum and 1 units in org

Group 2 unit1 0 vs unit2 0 IGHJ1P

U9

```
HUM: C G C G T G T T T T G
ORG: C G T G T G T T T T G
```

U7

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

```
Alignment stats:  'M': 50, 'I': 0, 'D': 0, 'X': 4
PI: 92.5925925925926
```

Group 2 with 1 units in hum and 1 units in org

Group 2 unit1 0 vs unit2 0 IGHD1-26

U9

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

U7

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

D9

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

```
Alignment stats:  ’M’: 20, ’I’: 0, ’D’: 0, ’X’: 0
PI: 100.0
```

Group 2 with 1 units in hum and 1 units in org

Group 2 unit1 0 vs unit2 0 IGHD6-25

U9

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

U7

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

D9

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

```
Alignment stats:  'M': 17, 'I': 0, 'D': 0, 'X': 1
PI: 94.44444444444444
```

Group 3 with 4 units in hum and 5 units in org

Group 3 unit1 0 vs unit2 0 IGHD5-24

U9

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

U7

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

D9

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

```
Alignment stats:  'M': 19, 'I': 0, 'D': 0, 'X': 1
PI: 95.0
```

Group 3 with 4 units in hum and 5 units in org

Group 3 unit1 0 vs unit2 0 IGHD4-23

U9

```
HUM: G G C T T T T T G T G
ORG: G G C T T T T T G T G
```

U7

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

D9

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

```
Alignment stats:  'M': 19, 'I': 0, 'D': 0, 'X': 0
PI: 100.0
```

Group 3 with 4 units in hum and 5 units in org

Group 3 unit1 0 vs unit2 0 IGHD3-22

U9

```
HUM: A G G T T T G A A G T
ORG: A G G T T T G A A G T
```

U7

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

D9

```
HUM: A T C A A A A A C T C
ORG: A T C A A A A A C T C
```

```
Alignment stats:  'M': 24, 'I': 10, 'D': 4, 'X': 3
PI: 58.536585365853654
```

Group 3 with 4 units in hum and 5 units in org

Group 3 unit1 0 vs unit2 0 IGHD2-21

U9

```
HUM: A G G A T T T T G T G
ORG: A G G A T T T T G T G
```

U7

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

D9

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

```
Alignment stats:  ’M’: 23, ’I’: 4, ’D’: 1, ’X’: 4
PI: 71.875
```

Group 3 with 4 units in hum and 5 units in org

Group 3 unit1 0 vs unit2 0 IGHD1-20

U9

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

U7

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

D9

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

```
Alignment stats:  ’M’: 15, ’I’: 0, ’D’: 0, ’X’: 2
PI: 88.23529411764706
```

Group 3 with 4 units in hum and 5 units in org

Group 3 unit1 0 vs unit2 0 IGHD6-19

U9

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

U7

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

D9

```
HUM: G C C A G A A A C C C
ORG: G C C A G A A A C C C
```

```
Alignment stats:  'M': 19, 'I': 0, 'D': 0, 'X': 2
PI: 90.47619047619048
```

Group 3 with 4 units in hum and 5 units in org

Group 3 unit1 0 vs unit2 1 IGHD5-24

U9

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

U7

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

D9

```
HUM: A G C A G C A A C C A
ORG: A G C G G C A A C C A
```

```
Alignment stats:  'M': 13, 'I': 5, 'D': 3, 'X': 4
PI: 52.0
```

Group 3 with 4 units in hum and 5 units in org

Group 3 unit1 0 vs unit2 1 IGHD4-23

U9

```
HUM: G G C T T T T T G T G
ORG: G G C T T T T T G T G
```

U7

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

GENE ALIGN SEQ

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

D9

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

```
Alignment stats:  ’M’: 14, ’I’: 1, ’D’: 4, ’X’: 1
PI: 70.0
```

Group 3 with 4 units in hum and 5 units in org

Group 3 unit1 0 vs unit2 1 IGHD3-22

U9

```
HUM: A G G T T T G A A G T
ORG: A G G T T T G G G G T
```

U7

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

D7

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

D9

```
HUM: A T C A A A A A C T C
ORG: A T C A A A A A C C C
```

```
Alignment stats:  ’M’: 21, ’I’: 4, ’D’: 2, ’X’: 8
PI: 60.0
```

Group 3 with 4 units in hum and 5 units in org

Group 3 unit1 0 vs unit2 1 IGHD2-21

U9

```
HUM: A G G A T T T T G T G
ORG: A G G A T T T T G T G
```

U7

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

D9

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

```
Alignment stats:  ’M’: 23, ’I’: 4, ’D’: 1, ’X’: 4
PI: 71.875
```

Group 3 with 4 units in hum and 5 units in org

Group 3 unit1 0 vs unit2 1 IGHD1-20

U9

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

U7

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

D7

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

D9

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

```
Alignment stats:  ’M’: 15, ’I’: 0, ’D’: 0, ’X’: 2
PI: 88.23529411764706
```

Group 3 with 4 units in hum and 5 units in org

Group 3 unit1 0 vs unit2 1 IGHD6-19

U9

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

U7

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

D9

```
HUM: G C C A G A A A C C C
ORG: G C C A G A A A C C C
```

```
Alignment stats:  'M': 20, 'I': 4, 'D': 1, 'X': 0
PI: 80.0
```

Group 3 with 4 units in hum and 5 units in org

Group 3 unit1 0 vs unit2 2 IGHD5-24

U9

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

U7

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

D9

```
HUM: A G C A G C A A C C A
ORG: A G C A G C A A C C A
```

```
Alignment stats:  'M': 19, 'I': 0, 'D': 0, 'X': 1
PI: 95.0
```

Group 3 with 4 units in hum and 5 units in org

Group 3 unit1 0 vs unit2 2 IGHD4-23

U9

```
HUM: G G C T T T T T G T G
ORG: G G C T T T T T G T G
```

U7

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

GENE ALIGN SEQ

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

D7

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

D9

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

```
Alignment stats:  ’M’: 16, ’I’: 0, ’D’: 0, ’X’: 3
PI: 84.21052631578947
```

Group 3 with 4 units in hum and 5 units in org

Group 3 unit1 0 vs unit2 2 IGHD3-22

U9

```
HUM: A G G T T T G A A G T
ORG: A G G T T T G G G G T
```

U7

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

D9

```
HUM: A T C A A A A A C T C
ORG: A T C A A A A A C C C
```

```
Alignment stats:  'M': 24, 'I': 6, 'D': 6, 'X': 1
PI: 64.86486486486487
```

Group 3 with 4 units in hum and 5 units in org

Group 3 unit1 0 vs unit2 2 IGHD2-21

U9

```
HUM: A G G A T T T T G T G
ORG: A G G A T T T T G T G
```

U7

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

D9

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

```
Alignment stats:  'M': 23, 'I': 4, 'D': 1, 'X': 4
PI: 71.875
```

Group 3 with 4 units in hum and 5 units in org

Group 3 unit1 0 vs unit2 2 IGHD1-20

U9

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

U7

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

D7

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

D9

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

```
Alignment stats:  ’M’: 16, ’I’: 0, ’D’: 0, ’X’: 1
PI: 94.11764705882352
```

Group 3 with 4 units in hum and 5 units in org

Group 3 unit1 0 vs unit2 2 IGHD6-19

U9

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

U7

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

D9

```
HUM: G C C A G A A A C C C
ORG: G C C A G A A A C C C
```

```
Alignment stats:  'M': 17, 'I': 0, 'D': 3, 'X': 1
PI: 80.95238095238095
```

Group 3 with 4 units in hum and 5 units in org

Group 3 unit1 0 vs unit2 3 IGHD5-24

U9

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

U7

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

D9

```
HUM: A G C A G C A A C C A
ORG: A G C A G C A A C C A
```

```
Alignment stats:  'M': 15, 'I': 0, 'D': 0, 'X': 5
PI: 75.0
```

Group 3 with 4 units in hum and 5 units in org

Group 3 unit1 0 vs unit2 3 IGHD4-23

U9

```
HUM: G G C T T T T T G T G
ORG: G G C T T T T T G T G
```

U7

```
HUM: T G C T G T G
ORG: T G C T G T G
```

GENE ALIGN SEQ

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

D7

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

D9

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

```
Alignment stats:  'M': 15, 'I': 0, 'D': 3, 'X': 1
PI: 78.94736842105263
```

Group 3 with 4 units in hum and 5 units in org

Group 3 unit1 0 vs unit2 3 IGHD3-22

U9

```
HUM: A G G T T T G A A G T
ORG: A G G T T T G G G G T
```

U7

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

D7

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

D9

```
HUM: A T C A A A A A C T C
ORG: A T C A A A A A C C C
```

```
Alignment stats:  'M': 23, 'I': 0, 'D': 0, 'X': 8
PI: 74.19354838709677
```

Group 3 with 4 units in hum and 5 units in org

Group 3 unit1 0 vs unit2 3 IGHD2-21

U9

```
HUM: A G G A T T T T G T G
ORG: A G G A T T T T G T G
```

U7

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

D7

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

D9

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

```
Alignment stats:  ’M’: 24, ’I’: 4, ’D’: 1, ’X’: 3
PI: 75.0
```

Group 3 with 4 units in hum and 5 units in org

Group 3 unit1 0 vs unit2 3 IGHD1-20

U9

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

U7

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

D7

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

D9

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

Alignment stats: ’M’: 15, ’I’: 0, ’D’: 0, ’X’: 2
PI: 88.23529411764706

Group 3 with 4 units in hum and 5 units in org

Group 3 unit1 0 vs unit2 3 IGHD6-19

U9
HUM: A G G T T T C T G A A
ORG: A G G T T T C T G A A

U7
HUM: C A C A G T G
ORG: 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
ORG: G G A T A T A G C A G C G A C T G G T A C

D7
HUM: C A C A G T G
ORG: C A C

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

```
Alignment stats:  'M': 18, 'I': 0, 'D': 0, 'X': 3
PI: 85.71428571428571
```

Group 3 with 4 units in hum and 5 units in org

Group 3 unit1 0 vs unit2 4 IGHD5-24

U9

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

U7

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

D9

```
HUM: A G C A G C A A C C A
ORG: A G C A G C A A C C A
```

```
Alignment stats:  ’M’: 13, ’I’: 5, ’D’: 3, ’X’: 4
PI: 52.0
```

Group 3 with 4 units in hum and 5 units in org

Group 3 unit1 0 vs unit2 4 IGHD4-23

U9

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

U7

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

GENE ALIGN SEQ

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

D9

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

```
Alignment stats:  'M': 14, 'I': 1, 'D': 4, 'X': 1
PI: 70.0
```

Group 3 with 4 units in hum and 5 units in org

Group 3 unit1 0 vs unit2 4 IGHD3-22

U9

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

U7

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

D9

HUM: A T C A A A A A C T C
ORG: A T C A A A A A C C C

```
Alignment stats:  'M': 26, 'I': 0, 'D': 0, 'X': 5
PI: 83.87096774193549
```

Group 4 with 1 units in hum and 1 units in org

Group 4 unit1 0 vs unit2 0 IGHD1-1

U9

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

U7

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

D9

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

```
Alignment stats:  ’M’: 15, ’I’: 0, ’D’: 0, ’X’: 2
PI: 88.23529411764706
```

Group 4 with 1 units in hum and 1 units in org

Group 4 unit1 0 vs unit2 0 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
ORG: 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
ORG: 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
ORG: 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
ORG: 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
ORG: G A C A G C A
```

D9

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

```
Alignment stats:  'M': 171, 'I': 0, 'D': 1, 'X': 10
PI: 93.95604395604396
```

Group 10 with 1 units in hum and 1 units in org

Group 10 unit1 0 vs unit2 0 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
ORG: 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
ORG: 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
ORG: 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 G
ORG: 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 G

HUM: 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 G A
ORG: 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 G A

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

D9

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

```
Alignment stats:  'M': 273, 'I': 0, 'D': 1, 'X': 22
PI: 92.22972972972973
```

Group 10 with 1 units in hum and 1 units in org

Group 10 unit1 0 vs unit2 0 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
ORG: 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 -

HUM: G T 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
ORG: - T 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

HUM: G A 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
ORG: G A 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

HUM: T G 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
ORG: T G 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

HUM: A T 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
ORG: A T 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

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

D9

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

```
Alignment stats:  'M': 280, 'I': 3, 'D': 4, 'X': 7
PI: 95.23809523809523
```

Group 10 with 1 units in hum and 1 units in org

Group 10 unit1 0 vs unit2 0 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
ORG: 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
ORG: 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

HUM: T A T G C T A 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
ORG: T - - - - T A 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

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

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

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

HUM: A G A
ORG: A G A
```

D7

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

D9

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

```
Alignment stats:  'M': 276, 'I': 7, 'D': 7, 'X': 13
PI: 91.0891089108911
```

Group 12 with 1 units in hum and 1 units in org

Group 12 unit1 0 vs unit2 0 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 A C
ORG: 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 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 G G C T C C A T C A G C A G T A G T A A C T
ORG: 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 C T

HUM: 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 G G
ORG: 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 G G

HUM: 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 C G
ORG: 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 C G

HUM: 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 G A
ORG: 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 G A

HUM: 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
ORG: 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

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

D9

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

```
Alignment stats:  'M': 290, 'I': 0, 'D': 0, 'X': 6
PI: 97.97297297297297
```

Group 16 with 1 units in hum and 1 units in org

Group 16 unit1 0 vs unit2 0 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
ORG: 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
ORG: 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 T
ORG: 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 T

HUM: 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 G
ORG: 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 G

HUM: 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 A
ORG: 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 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 A C A G A
ORG: 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
ORG: C
```

D7

```
HUM: C A C A A A G
ORG: C A C A G A G
```

D9

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

```
Alignment stats:  'M': 291, 'I': 0, 'D': 0, 'X': 10
PI: 96.67774086378738
```

Group 16 with 1 units in hum and 1 units in org

Group 16 unit1 0 vs unit2 0 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
ORG: 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
ORG: 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
ORG: C G C A T G A
```

D9

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

```
Alignment stats:  'M': 98, 'I': 0, 'D': 0, 'X': 1
PI: 98.98989898989899
```

Group 16 with 1 units in hum and 1 units in org

Group 16 unit1 0 vs unit2 0 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
ORG: 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
ORG: 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
ORG: 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 C G A
ORG: 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 T G A

HUM: 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 G A A
ORG: 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 G A A

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

HUM: A
ORG: A
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D7

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HUM: T A C G G T A
ORG: C A T G G T A
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D9

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

```
Alignment stats:  ’M’: 267, ’I’: 6, ’D’: 5, ’X’: 23
PI: 88.70431893687709
```

Group 17 with 2 units in hum and 1 units in org

Group 17 unit1 0 vs unit2 0 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 C
ORG: 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 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 T A G C T A T T G G A
ORG: 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 A

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 G G C C A A C
ORG: 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 C

HUM: 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 G
ORG: 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 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
ORG: 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 A

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

D9

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

```
Alignment stats:  'M': 281, 'I': 0, 'D': 0, 'X': 15
PI: 94.93243243243244
```

Group 17 with 2 units in hum and 1 units in org

Group 17 unit1 1 vs unit2 0 IGHV3-21

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 C T G G T C A A G C C T G G G G G G T C
ORG: 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 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 A G C A
ORG: 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 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 C T C A T C C
ORG: 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 C

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

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

D9

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

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Alignment stats:  'M': 256, 'I': 0, 'D': 0, 'X': 40
PI: 86.48648648648648
```

Group 19 with 3 units in hum and 3 units in org

Group 19 unit1 0 vs unit2 0 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
ORG: 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
ORG: 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
ORG: 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
ORG: 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
ORG: 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
ORG: 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
ORG: 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
ORG: 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
ORG: 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
ORG: G A
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D7

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

```
Alignment stats:  'M': 433, 'I': 0, 'D': 0, 'X': 19
PI: 95.79646017699115
```

Group 19 with 3 units in hum and 3 units in org

Group 19 unit1 0 vs unit2 2 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
ORG: A T G G A G T T T G G G C T G A G C T G G G T T T T C C T T G T T G C T A T T T T T A A A G G T G 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
ORG: T A C A T G A G G A A A T A G A G A T A T T G A G T G T G A G T G G A C A T G A G T G A G A G A A A

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

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

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

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

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

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

HUM: C T T C 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
ORG: C T T C A 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

HUM: G A A A G - - A
ORG: A A A A G A C A
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D7

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

D9

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

```
Alignment stats:  'M': 414, 'I': 6, 'D': 0, 'X': 38
PI: 90.39301310043668
```

Group 19 with 3 units in hum and 3 units in org

Group 19 unit1 2 vs unit2 0 IGHV3-63

GENE ALIGN SEQ

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

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

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

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

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

D7

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

D9

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

```
Alignment stats:  'M': 281, 'I': 0, 'D': 0, 'X': 17
PI: 94.29530201342283
```

Group 19 with 3 units in hum and 3 units in org

Group 19 unit1 2 vs unit2 0 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
ORG: 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 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
ORG: C C T G A G A C T C T C C T G T G C A G C C T C T G G A T T C A C C T T C A G T A G C T A T G C T A

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

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

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

HUM: 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 G A G A
ORG: 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 G A
```

D7

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

D9

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

```
Alignment stats:  'M': 277, 'I': 0, 'D': 0, 'X': 19
PI: 93.58108108108108
```

Group 19 with 3 units in hum and 3 units in org

Group 19 unit1 2 vs unit2 1 IGHV3-63

GENE ALIGN SEQ

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

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

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

HUM: A T T C A C C A T C T C C A A A G A C A A T G C T A A G A A C T C A C C G T A T C T G C A A A C G A
ORG: 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 - - - - - - - - - - - - - - - - - - - - - -

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

D7

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

D9

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

```
Alignment stats:  'M': 211, 'I': 0, 'D': 70, 'X': 17
PI: 70.80536912751678
```

Group 19 with 3 units in hum and 3 units in org

Group 19 unit1 2 vs unit2 2 IGHV3-63

GENE ALIGN SEQ

```
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
ORG: 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 A A
ORG: 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 A A

HUM: 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 A T
ORG: 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 A T

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

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

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

D9

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

```
Alignment stats:  'M': 284, 'I': 0, 'D': 0, 'X': 14
PI: 95.30201342281879
```

Group 19 with 3 units in hum and 3 units in org

Group 19 unit1 2 vs unit2 2 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
ORG: 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
ORG: 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 A G C T
ORG: 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 A G T T

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

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

HUM: 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 G A G A
ORG: 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 G A C A
```

D7

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HUM: C A C A G T G
ORG: C A C A G T G
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D9

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

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Alignment stats:  'M': 270, 'I': 3, 'D': 1, 'X': 25
PI: 90.3010033444816
```

Group 20 with 1 units in hum and 1 units in org

Group 20 unit1 0 vs unit2 0 IGHV5-10-1

GENE ALIGN SEQ

```
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
ORG: 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
ORG: 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
ORG: 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 G C C A
ORG: 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 G C C A

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

D7

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

D9

```
HUM: T C T A A A A C C C T
ORG: T C A A A A A C C C T
```

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Alignment stats:  'M': 276, 'I': 0, 'D': 0, 'X': 20
PI: 93.24324324324324
```

Group 22 with 1 units in hum and 1 units in org

Group 22 unit1 0 vs unit2 0 IGHV3-11

GENE ALIGN SEQ

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

HUM: 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 C G
ORG: 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 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
ORG: 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 G A

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

D9

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

```
Alignment stats:  'M': 276, 'I': 0, 'D': 0, 'X': 20
PI: 93.24324324324324
```

Group 22 with 1 units in hum and 1 units in org

Group 22 unit1 0 vs unit2 0 IGHV1-12

GENE ALIGN SEQ

```
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
ORG: 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
ORG: 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
ORG: 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
ORG: 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 C T
ORG: 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 C T

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

D9

```
HUM: T A A C T C T A C T T
ORG: T A A C T C T A C T T
```

```
Alignment stats:  'M': 287, 'I': 0, 'D': 0, 'X': 9
PI: 96.95945945945947
```

Group 23 with 2 units in hum and 2 units in org

Group 23 unit1 0 vs unit2 0 IGHV3-13

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
ORG: 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 A
ORG: 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 A

HUM: 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 T
ORG: 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 T

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

HUM: 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 A
ORG: 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 A

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

D9

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

```
Alignment stats:  'M': 278, 'I': 0, 'D': 0, 'X': 15
PI: 94.88054607508532
```

Group 23 with 2 units in hum and 2 units in org

Group 23 unit1 0 vs unit2 0 IGHV(III)-13-1

GENE ALIGN SEQ

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

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

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

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

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

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

D7

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

D9

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

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Alignment stats:  'M': 290, 'I': 0, 'D': 0, 'X': 4
PI: 98.63945578231292
```

Group 23 with 2 units in hum and 2 units in org

Group 23 unit1 0 vs unit2 1 IGHV3-13

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
ORG: 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 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 A
ORG: 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 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 T
ORG: 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 C T G G T G A C C C A T A C T A T C C A G G C T C C G T G A A G G G C C G A T T
ORG: 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 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 A
ORG: 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 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
ORG: 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
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D7

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

D9

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

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Alignment stats:  'M': 264, 'I': 0, 'D': 0, 'X': 29
PI: 90.10238907849829
```

Group 23 with 2 units in hum and 2 units in org

Group 23 unit1 0 vs unit2 1 IGHV(III)-13-1

GENE ALIGN SEQ

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

HUM: A A T T C T G C - - - C T T T T C T G C 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
ORG: A A T T C T - 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

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

HUM: A A C A - - - - A T A A T T C A A A T A 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 A
ORG: A A C A T C A 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

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

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

HUM: A
ORG: A
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D7

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

D9

```
HUM: G A C A C C A A C C T
ORG: G A C A C A A A C C T G C C T G C A C G A A G A C A C A A A C C T
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```
Alignment stats:  'M': 266, 'I': 7, 'D': 2, 'X': 26
PI: 88.37209302325581
```

Group 23 with 2 units in hum and 2 units in org

Group 23 unit1 1 vs unit2 0 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
ORG: C A G G A G C A G C T G C A G G A G T C A G A C C T G G A C C T G A A G A G C C T G C A C T G C 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
ORG: C T C T G C A T C A C C T G C A C T 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
ORG: C T A C 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 G G A G G G G C T G C A A T G G A T
```

D7

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

D9

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

```
Alignment stats:  'M': 134, 'I': 0, 'D': 0, 'X': 13
PI: 91.15646258503402
```

Group 23 with 2 units in hum and 2 units in org

Group 23 unit1 1 vs unit2 1 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
ORG: 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
ORG: 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
ORG: 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
ORG: A A A A T G C
```

D9

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

```
Alignment stats:  'M': 141, 'I': 0, 'D': 0, 'X': 6
PI: 95.91836734693877
```

Group 24 with 1 units in hum and 1 units in org

Group 24 unit1 0 vs unit2 0 IGHV3-15

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 A A G C C T G G G G G G T C
ORG: 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
ORG: 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
ORG: 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
ORG: 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
ORG: 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 C A
ORG: 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 C A

HUM: G A
ORG: G A
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D7

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

```
Alignment stats:  'M': 291, 'I': 0, 'D': 0, 'X': 11
PI: 96.35761589403974
```

Group 24 with 1 units in hum and 1 units in org

Group 24 unit1 0 vs unit2 0 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
ORG: 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
ORG: 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
ORG: 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
ORG: 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 C A C
ORG: 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 C A C

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

D9

```
HUM: A C A C A A A C C T C
ORG: A C A C A A A C C T C
```

```
Alignment stats:  'M': 256, 'I': 0, 'D': 0, 'X': 15
PI: 94.4649446494465
```

Group 24 with 1 units in hum and 1 units in org

Group 24 unit1 0 vs unit2 0 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
ORG: 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
ORG: 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 G T
ORG: 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 G T

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

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

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

D7

```
HUM: T C C T G T G
ORG: T C C T G T G
```

D9

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

```
Alignment stats:  'M': 278, 'I': 0, 'D': 0, 'X': 18
PI: 93.91891891891892
```

Group 24 with 1 units in hum and 1 units in org

Group 24 unit1 0 vs unit2 0 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
ORG: 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

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

HUM: C C T T T 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
ORG: C C T T T 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

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

HUM: T C T C C 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
ORG: T C T C C 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

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

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

D7

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HUM: G A G A C A C
ORG: G A G A C A C
```

D9

```
HUM: G C C C A G A C A G A
ORG: G C C C A G A C A G A
```

```
Alignment stats:  'M': 290, 'I': 6, 'D': 5, 'X': 8
PI: 93.85113268608414
```

Group 24 with 1 units in hum and 1 units in org

Group 24 unit1 0 vs unit2 0 IGHV1-17

GENE ALIGN SEQ

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

D9

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

Alignment stats: 'M': 288, 'I': 0, 'D': 0, 'X': 7
PI: 97.6271186440678

Group 43 with 2 units in hum and 3 units in org

Group 43 unit1 0 vs unit2 0 IGHV1-24

GENE ALIGN SEQ

```
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
ORG: 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
ORG: 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
ORG: 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
ORG: 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
ORG: 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
ORG: 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

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HUM: C A C A G T G
ORG: C A C A G T G
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D9

```
HUM: G T C A G A A A C C C
ORG: 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
PI: 96.95945945945947
```

Group 44 with 1 units in hum and 1 units in org

Group 44 unit1 0 vs unit2 0 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 G T C
ORG: 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 G T C

HUM: 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 A C A
ORG: 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 A C A

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

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

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

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

D7

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

D9

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

```
Alignment stats:  'M': 276, 'I': 0, 'D': 0, 'X': 20
PI: 93.24324324324324
```

Group 44 with 1 units in hum and 1 units in org

Group 44 unit1 0 vs unit2 0 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
ORG: 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
ORG: 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
ORG: 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
ORG: 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
ORG: 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
ORG: 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
ORG: C A C A A T G
```

D9

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

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Alignment stats:  'M': 261, 'I': 0, 'D': 3, 'X': 16
PI: 93.21428571428572
```

Group 44 with 1 units in hum and 1 units in org

Group 44 unit1 0 vs unit2 0 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
ORG: 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
ORG: 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
ORG: 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
ORG: 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
ORG: 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 T A
ORG: 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 G A

HUM: C
ORG: G
```

D7

```
HUM: C A C A G A G
ORG: C A C A G A G
```

D9

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

```
Alignment stats:  'M': 293, 'I': 0, 'D': 0, 'X': 8
PI: 97.34219269102991
```

Group 44 with 1 units in hum and 1 units in org

Group 44 unit1 0 vs unit2 0 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 T
ORG: 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 T

HUM: 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 C
ORG: 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 C

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

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

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

HUM: 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 A
ORG: 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 A
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D7

```
HUM: C A C A G G G
ORG: C A C A G G A
```

D9

```
HUM: A G A C A C A A A A A
ORG: A G A C A C A A A A A
```

```
Alignment stats:  'M': 276, 'I': 0, 'D': 0, 'X': 20
PI: 93.24324324324324
```

Group 48 with 4 units in hum and 2 units in org

Group 48 unit1 0 vs unit2 0 IGHV4-28

GENE ALIGN SEQ

```
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
ORG: 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
ORG: 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
ORG: 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 T C G
ORG: 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 T C G

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

HUM: 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
ORG: 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

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

D9

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

```
Alignment stats:  'M': 276, 'I': 0, 'D': 0, 'X': 20
PI: 93.24324324324324
```

Group 48 with 4 units in hum and 2 units in org

Group 48 unit1 0 vs unit2 0 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
ORG: C A A C A A C T G T G T T T C G C A G T G C A C T T C T G G C T T C A G A C A T C C T C 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
ORG: 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
ORG: 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
ORG: 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
ORG: 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
ORG: T G A A C A C A C A A C T A T G C A T T T T T A A G C A A A A G A
```

D7

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

D9

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

```
Alignment stats:  'M': 263, 'I': 0, 'D': 7, 'X': 13
PI: 92.93286219081273
```

Group 48 with 4 units in hum and 2 units in org

Group 48 unit1 0 vs unit2 0 IGHV3-29

GENE ALIGN SEQ

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

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

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

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

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

D7

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

D9

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

```
Alignment stats:  'M': 283, 'I': 0, 'D': 0, 'X': 15
PI: 94.96644295302013
```

Group 48 with 4 units in hum and 2 units in org

Group 48 unit1 0 vs unit2 0 IGHV3-30

GENE ALIGN SEQ

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

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

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

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

D7

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

D9

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

```
Alignment stats:  'M': 283, 'I': 0, 'D': 0, 'X': 13
PI: 95.6081081081081
```

Group 48 with 4 units in hum and 2 units in org

Group 48 unit1 0 vs unit2 0 IGHV(II)-30-1

GENE ALIGN SEQ

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

HUM: C C T T C T G G A G C T G C A T C C A T C A G C G C C C C C A T G G G A G G T A C T G G A G T G G A
ORG: C C T G C T G G A G C T G C A T C C - T G C A G C G C C C C A C G G G A G G T A C T G G A G T G G A

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

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

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

HUM: A
ORG: A
```

D7

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

D9

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

```
Alignment stats:  ’M’: 279, ’I’: 0, ’D’: 1, ’X’: 21
PI: 92.69102990033223
```

Group 48 with 4 units in hum and 2 units in org

Group 48 unit1 0 vs unit2 0 IGHV3-30-2

GENE ALIGN SEQ

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

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

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

D9

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

```
Alignment stats:  'M': 275, 'I': 0, 'D': 0, 'X': 23
PI: 92.28187919463086
```

Group 48 with 4 units in hum and 2 units in org

Group 48 unit1 0 vs unit2 1 IGHV3-30-2

GENE ALIGN SEQ

```
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
ORG: G A G G T A C A G C T G G T G G A G T C T G A 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 G -

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

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

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

D7

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

D9

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

```
Alignment stats:  'M': 277, 'I': 2, 'D': 1, 'X': 20
PI: 92.33333333333333
```

Group 48 with 4 units in hum and 2 units in org

Group 48 unit1 1 vs unit2 0 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
ORG: 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 C T
ORG: 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 C T

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

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

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

HUM: 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 G
ORG: 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 G
```

D7

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

D9

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

```
Alignment stats:  'M': 276, 'I': 0, 'D': 0, 'X': 17
PI: 94.19795221843003
```

Group 48 with 4 units in hum and 2 units in org

Group 48 unit1 1 vs unit2 1 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
ORG: 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 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 C T
ORG: 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 C T

HUM: G G A G C T G G A T C C G C C A G C C C C C A G G G A A G G G G C T G G A G T G G A T T G G G G - A
ORG: 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 G A T T G G G G G -

HUM: 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 A G T
ORG: - - 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

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

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

D9

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

```
Alignment stats:  'M': 272, 'I': 5, 'D': 5, 'X': 16
PI: 91.2751677852349
```

Group 48 with 4 units in hum and 2 units in org

Group 48 unit1 2 vs unit2 1 IGHV7-56

GENE ALIGN SEQ

```
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
ORG: 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 A
ORG: 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 A

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

HUM: 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 T
ORG: 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 T

HUM: 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 C
ORG: 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 C

HUM: 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
ORG: 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
```

D7

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

D9

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

```
Alignment stats:  'M': 280, 'I': 0, 'D': 1, 'X': 13
PI: 95.23809523809523
```

Group 50 with 1 units in hum and 1 units in org

Group 50 unit1 0 vs unit2 0 IGHV7-34-1

GENE ALIGN SEQ

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

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

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

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

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

D9

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

```
Alignment stats:  'M': 281, 'I': 0, 'D': 0, 'X': 12
PI: 95.90443686006826
```

Group 51 with 1 units in hum and 1 units in org

Group 51 unit1 0 vs unit2 0 IGHV3-36

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 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
ORG: 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
ORG: 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
ORG: 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
ORG: 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
ORG: 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
ORG: 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
ORG: T G G
```

D7

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

D9

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

```
Alignment stats:  'M': 289, 'I': 2, 'D': 1, 'X': 11
PI: 95.37953795379538
```

Group 53 with 1 units in hum and 1 units in org

Group 53 unit1 0 vs unit2 0 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
ORG: 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
ORG: 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
ORG: 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 T
ORG: 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 T

HUM: 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 A
ORG: 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 A

HUM: 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
ORG: 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 C A
```

D7

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

D9

```
HUM: C A C A A A C C T C C
ORG: C A C A A A C C T C C
```

```
Alignment stats:  'M': 276, 'I': 3, 'D': 0, 'X': 16
PI: 93.55932203389831
```

Group 53 with 1 units in hum and 1 units in org

Group 53 unit1 0 vs unit2 0 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
ORG: 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
ORG: 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
ORG: 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
ORG: 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
ORG: 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
ORG: 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
ORG: G A C A G T G
```

D9

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

```
Alignment stats:  'M': 266, 'I': 2, 'D': 6, 'X': 10
PI: 93.66197183098592
```

Group 53 with 1 units in hum and 1 units in org

Group 53 unit1 0 vs unit2 0 IGHV4-39

GENE ALIGN SEQ

```
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
ORG: 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
ORG: 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
ORG: 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 A G
ORG: 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 A G

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

HUM: 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 A
ORG: 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 A
```

D7

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

D9

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

```
Alignment stats:  'M': 275, 'I': 0, 'D': 6, 'X': 18
PI: 91.9732441471572
```

Group 53 with 1 units in hum and 1 units in org

Group 53 unit1 0 vs unit2 0 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
ORG: 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 C A
ORG: 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 C C

HUM: 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 T G
ORG: 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 T G

HUM: 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 A G
ORG: 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 A G

HUM: A G A
ORG: A G A
```

D7

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

D9

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

```
Alignment stats:  'M': 190, 'I': 0, 'D': 0, 'X': 13
PI: 93.59605911330048
```

Group 53 with 1 units in hum and 1 units in org

Group 53 unit1 0 vs unit2 0 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
ORG: 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
ORG: 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
ORG: T A G G C A C
```

D9

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

```
Alignment stats:  'M': 73, 'I': 0, 'D': 0, 'X': 4
PI: 94.8051948051948
```

Group 55 with 1 units in hum and 1 units in org

Group 55 unit1 0 vs unit2 0 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
ORG: 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
ORG: 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
ORG: 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
ORG: 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
ORG: 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
ORG: 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
ORG: A G A G A
```

D7

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

D9

```
HUM: A C A C A A A T C T C
ORG: A C A C A A A T C T C
```

```
Alignment stats:  'M': 291, 'I': 2, 'D': 0, 'X': 12
PI: 95.40983606557377
```

Group 55 with 1 units in hum and 1 units in org

Group 55 unit1 0 vs unit2 0 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 T C
ORG: 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 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 G A T G A T T A T A C C A
ORG: 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 C A

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

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

HUM: 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 A T A
ORG: 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 A C A
```

D7

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

D9

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

```
Alignment stats:  'M': 282, 'I': 0, 'D': 0, 'X': 16
PI: 94.63087248322147
```

Group 55 with 1 units in hum and 1 units in org

Group 55 unit1 0 vs unit2 0 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
ORG: 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
ORG: 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
ORG: 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 G C
ORG: 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 G C

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

D7

```
HUM: T T G T T T T
ORG: T T A T T T
```

D9

```
HUM: G T G T G T G T T T T
ORG: T T T T T T T T T T T
```

```
Alignment stats:  'M': 198, 'I': 2, 'D': 1, 'X': 11
PI: 93.39622641509435
```

Group 57 with 1 units in hum and 1 units in org

Group 57 unit1 0 vs unit2 0 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
ORG: 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 G
ORG: 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 G

HUM: 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 G
ORG: 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 G

HUM: A T A T G G G T T A A G G G A A A C A C T A - - - - - A G C C C C A A C C T T C A G G G C A G A G C
ORG: 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 C

HUM: 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 A
ORG: 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 A

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

D9

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

```
Alignment stats:  'M': 279, 'I': 5, 'D': 2, 'X': 8
PI: 94.89795918367348
```

Group 57 with 1 units in hum and 1 units in org

Group 57 unit1 0 vs unit2 0 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
ORG: 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
ORG: 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
ORG: 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
ORG: 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
ORG: 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
ORG: A A C A G T G
```

D9

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

```
Alignment stats:  'M': 233, 'I': 0, 'D': 0, 'X': 4
PI: 98.31223628691983
```

Group 57 with 1 units in hum and 1 units in org

Group 57 unit1 0 vs unit2 0 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
ORG: 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
ORG: 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
ORG: 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
ORG: 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
ORG: 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
ORG: 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
ORG: C A C A G T G
```

D9

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

```
Alignment stats:  'M': 282, 'I': 1, 'D': 3, 'X': 11
PI: 94.94949494949495
```

Group 57 with 1 units in hum and 1 units in org

Group 57 unit1 0 vs unit2 0 IGHV1-46

GENE ALIGN SEQ

HUM: CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTC
ORG: CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTC

HUM: AGTGAAGGTTTCCTGCAAGGCATCTGGATACACCTTCACCAGCTACTATA
ORG: AGTGAAGGTTTCCTGCAAGGCTTCTGGTTACACCTTCACCAGCTGCTATA

HUM: TGCACTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGAATA
ORG: TGTACTGGGTGCAACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGAGTA

HUM: ATCAACCCTAGTGGTGGTAGCACAAGCTACGCACAGAAGTTCCAGGGCAG
ORG: ATCAACCCTAGTGATGGTAGCACAAGCTACGCACAGAAGTTCCAGGGCAG

HUM: AGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTACATGGAGCTGA
ORG: AGTCACCATGACCAGGGACACATCCACAAGCACAGTCTACATGGAGCTGA

HUM: GCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGA
ORG: GCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTATGCAAGAGA

D7

HUM: CACAGTG
ORG: CACAGTG

D9

HUM: GTCAGAAACCC
ORG: GTCAGAAACCC

```
Alignment stats:  ’M’: 285, ’I’: 0, ’D’: 0, ’X’: 11
PI: 96.28378378378379
```

Group 58 with 1 units in hum and 1 units in org

Group 58 unit1 0 vs unit2 0 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
ORG: 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
ORG: 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
ORG: 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
ORG: 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
ORG: 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
ORG: 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
ORG: C A C A G T G
```

D9

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

```
Alignment stats:  'M': 280, 'I': 0, 'D': 0, 'X': 16
PI: 94.5945945945946
```

Group 58 with 1 units in hum and 1 units in org

Group 58 unit1 0 vs unit2 0 IGHV3-49

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 A G G G C G G T C
ORG: 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 T C

HUM: 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 T A
ORG: 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 C A

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 A G G T T T C
ORG: 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 T C

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

HUM: G A
ORG: G A
```

D7

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

D9

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

```
Alignment stats:  ’M’: 294, ’I’: 0, ’D’: 0, ’X’: 8
PI: 97.35099337748345
```

Group 58 with 1 units in hum and 1 units in org

Group 58 unit1 0 vs unit2 0 IGHV(II)-49-1

GENE ALIGN SEQ

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

HUM: 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 G A
ORG: 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 G A
```

D7

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

D9

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

```
Alignment stats:  'M': 282, 'I': 1, 'D': 0, 'X': 16
PI: 94.31438127090301
```

Group 58 with 1 units in hum and 1 units in org

Group 58 unit1 0 vs unit2 0 IGHV3-50

GENE ALIGN SEQ

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

D7

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

D9

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

```
Alignment stats:  'M': 283, 'I': 0, 'D': 0, 'X': 14
PI: 95.28619528619528
```

Group 58 with 1 units in hum and 1 units in org

Group 58 unit1 0 vs unit2 0 IGHV5-51

GENE ALIGN SEQ

```
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
ORG: 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
ORG: 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
ORG: 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
ORG: 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
ORG: 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
ORG: 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
```

D7

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

D9

```
HUM: T C T A A A A C C C T
ORG: T C T A A A A C C C T
```

```
Alignment stats:  'M': 284, 'I': 0, 'D': 0, 'X': 12
PI: 95.94594594594594
```

Group 59 with 1 units in hum and 2 units in org

Group 59 unit1 0 vs unit2 0 IGHV(II)-51-2

GENE ALIGN SEQ

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

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

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

HUM: 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 C
ORG: 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 C

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

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

D7

```
HUM: A A C A G A A
ORG: A A C A G A G
```

D9

```
HUM: C A C A A A C T T C C
ORG: C A C A A A C T T C C
```

```
Alignment stats:  'M': 254, 'I': 0, 'D': 0, 'X': 9
PI: 96.57794676806084
```

Group 59 with 1 units in hum and 2 units in org

Group 59 unit1 0 vs unit2 1 IGHV(II)-51-2

GENE ALIGN SEQ

```
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 G
ORG: 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 G

HUM: 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 T
ORG: 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 T

HUM: 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 A
ORG: 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 A

HUM: 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 C
ORG: 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 C

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

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

D7

```
HUM: A A C A G A A
ORG: A A C A G A G
```

D9

```
HUM: C A C A A A C T T C C
ORG: C A C A A A C T T C C
```

```
Alignment stats:  'M': 255, 'I': 0, 'D': 0, 'X': 8
PI: 96.95817490494296
```

Group 60 with 1 units in hum and 1 units in org

Group 60 unit1 0 vs unit2 0 IGHV3-52

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

D9

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

```
Alignment stats:  'M': 286, 'I': 0, 'D': 0, 'X': 10
PI: 96.62162162162163
```

Group 60 with 1 units in hum and 1 units in org

Group 60 unit1 0 vs unit2 0 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
ORG: 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 C A
ORG: 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 C A

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 T T
ORG: 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 T A C

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

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

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

```
Alignment stats:  'M': 267, 'I': 0, 'D': 1, 'X': 25
PI: 91.12627986348123
```

Group 60 with 1 units in hum and 1 units in org

Group 60 unit1 0 vs unit2 0 IGHV(II)-53-1

GENE ALIGN SEQ

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

D9

```
HUM: C A C C C A A A C C T
ORG: C A T C C A A A C C T
```

```
Alignment stats:  'M': 257, 'I': 0, 'D': 1, 'X': 12
PI: 95.18518518518519
```

Group 61 with 1 units in hum and 1 units in org

Group 61 unit1 0 vs unit2 0 IGHV3-57

GENE ALIGN SEQ

```
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
ORG: 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
ORG: 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
ORG: 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 T A
ORG: 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 T A

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

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

D7

```
HUM: C A C A G G A
ORG: C A C A G G A
```

D9

```
HUM: A G A C A C A A A A A
ORG: A G A C A G A A A A A
```

```
Alignment stats:  'M': 273, 'I': 2, 'D': 2, 'X': 20
PI: 91.91919191919192
```

Group 62 with 1 units in hum and 6 units in org

Group 62 unit1 0 vs unit2 0 IGHV1-58

GENE ALIGN SEQ

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

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

D7

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

D9

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

```
Alignment stats:  'M': 273, 'I': 0, 'D': 0, 'X': 23
PI: 92.22972972972973
```

Group 62 with 1 units in hum and 6 units in org

Group 62 unit1 0 vs unit2 0 IGHV4-59

GENE ALIGN SEQ

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

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

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

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

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

D9

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

```
Alignment stats:  'M': 284, 'I': 0, 'D': 0, 'X': 9
PI: 96.9283276450512
```

Group 62 with 1 units in hum and 6 units in org

Group 62 unit1 0 vs unit2 0 IGHV3-60

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 A G T A A A G A C T G G A G G G - G
ORG: G A A G T G C A G C T G G T G G A G T C T G G G C G A C G C T T G G T A C A G C C T G G - - G G T G

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

HUM: 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 T C T C A G
ORG: T A T G - 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 G G A G T C G G T C T C A G

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

HUM: 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 G C A A A T
ORG: C G A T T C A C C A T C T C C A G A G A C A A T A C C C A G A A T T C A C T G T C 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 G C A C A G T T G T G T A C T A C T G T G T G A A A G A
ORG: G C 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 T G A A A G A
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D7

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

D9

```
HUM: A C A A A C C T C C T
ORG: A C A A A C C T C C C T
```

```
Alignment stats:  'M': 270, 'I': 1, 'D': 3, 'X': 24
PI: 90.60402684563759
```

Group 62 with 1 units in hum and 6 units in org

Group 62 unit1 0 vs unit2 1 IGHV1-58

GENE ALIGN SEQ

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

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

HUM: 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
ORG: 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 A G G C A G A
```

D7

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

D9

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

```
Alignment stats:  'M': 280, 'I': 0, 'D': 0, 'X': 16
PI: 94.5945945945946
```

Group 62 with 1 units in hum and 6 units in org

Group 62 unit1 0 vs unit2 1 IGHV4-59

GENE ALIGN SEQ

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

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

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

HUM: C T G T G A C C G C T G C G G A C A C G G C C G T G T A T T A C T G T G C G A G A G A
ORG: 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 T A
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D7

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

D9

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

```
Alignment stats:  'M': 283, 'I': 0, 'D': 0, 'X': 10
PI: 96.58703071672356
```

Group 62 with 1 units in hum and 6 units in org

Group 62 unit1 0 vs unit2 1 IGHV3-60

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 A G T A A A G A C T G G A G G G G T
ORG: G A A G T G C A G C T G G T G G A G T C T G G G C G A C G C T T G G T A C A G C C T G G - G G G G T

HUM: 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 C T C T G C T
ORG: 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 - - - - 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 T C T
ORG: A T G C T A T G 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 G G A G T G G G T C T

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

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

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

HUM: A
ORG: A
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D7

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

D9

```
HUM: A C A A A C C T C C T
ORG: A C A A A C C T C C C T
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```
Alignment stats:  'M': 270, 'I': 4, 'D': 6, 'X': 21
PI: 89.70099667774086
```

Group 62 with 1 units in hum and 6 units in org

Group 62 unit1 0 vs unit2 2 IGHV1-58

GENE ALIGN SEQ

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

HUM: A G T C A C C A T T A C C A G G G A C A T G T C C A C A A G C A C A G C C T A C A T G G A G C T G A
ORG: 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 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 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
ORG: 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 G G G T G C G G C A G A
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D7

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

D9

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

```
Alignment stats:  'M': 281, 'I': 0, 'D': 0, 'X': 15
PI: 94.93243243243244
```

Group 62 with 1 units in hum and 6 units in org

Group 62 unit1 0 vs unit2 2 IGHV4-59

GENE ALIGN SEQ

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

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

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

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

D7

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

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

```
Alignment stats:  'M': 282, 'I': 0, 'D': 0, 'X': 11
PI: 96.24573378839591
```

Group 62 with 1 units in hum and 6 units in org

Group 62 unit1 0 vs unit2 2 IGHV3-60

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 A G T A A A G A C T G G A G G G - G
ORG: G A A G T G C A G C T G G T G G A G T C T G G G C G A C G C T T G G T A C A G C C T G G - - G G T G

HUM: 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 C T C T G C
ORG: 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 T A C C T T C A G T A G C T - - - -

HUM: 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 T C
ORG: - A T G C T A T G 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 G G A G T C G G T C

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

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

HUM: G A
ORG: G A
```

D7

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

D9

```
HUM: A C A A A C C T C C T
ORG: A C A A A C C T C C C T
```

```
Alignment stats:  'M': 266, 'I': 5, 'D': 7, 'X': 24
PI: 88.0794701986755
```

Group 62 with 1 units in hum and 6 units in org

Group 62 unit1 0 vs unit2 3 IGHV1-58

GENE ALIGN SEQ

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

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

HUM: 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
ORG: 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
```

D7

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

D9

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

```
Alignment stats:  'M': 279, 'I': 0, 'D': 0, 'X': 17
PI: 94.25675675675676
```

Group 62 with 1 units in hum and 6 units in org

Group 62 unit1 0 vs unit2 3 IGHV4-59

GENE ALIGN SEQ

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

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

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

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

D7

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

D9

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

```
Alignment stats:  'M': 282, 'I': 0, 'D': 0, 'X': 11
PI: 96.24573378839591
```

Group 62 with 1 units in hum and 6 units in org

Group 62 unit1 0 vs unit2 3 IGHV3-60

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 A G T A A A G A C T G G A G G G - G
ORG: G A A G T G C A G C T G G T G G A G T C T G G G C G A C G C T T G G T A T A G C C T G G - - G G T G

HUM: 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 C T C T G C
ORG: 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 T A C C T T C A G T A G C T - - - -

HUM: 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 T C
ORG: - A T G C T A T G 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 G G A G T G G G T C

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

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

HUM: G A
ORG: G A
```

D7

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

D9

```
HUM: A C A A A C C T C C T
ORG: A C A A A C C T C C C T
```

```
Alignment stats:  'M': 267, 'I': 5, 'D': 7, 'X': 23
PI: 88.41059602649007
```

Group 62 with 1 units in hum and 6 units in org

Group 62 unit1 0 vs unit2 4 IGHV1-58

GENE ALIGN SEQ

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

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

HUM: 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
ORG: 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
```

D7

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

D9

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

```
Alignment stats:  'M': 279, 'I': 0, 'D': 0, 'X': 17
PI: 94.25675675675676
```

Group 62 with 1 units in hum and 6 units in org

Group 62 unit1 0 vs unit2 4 IGHV4-59

GENE ALIGN SEQ

```
HUM: CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGAC
ORG: CAAGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGAC

HUM: CCTGTCCCTCACCTGCACTGTCTCTGGTGGCTCCATCAG---TAGTTACT
ORG: CCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCCATCAGCAGTAGTAACT

HUM: ACTGGAGCTGGATCCGGCAGCCCCCAGGGAAGGGACTGGAGTGGATTGGG
ORG: GGTGGAGCTGGGTCCGCCAGCCCCCAGGGAAGGGCCTGGAGTGGATTGGA

HUM: TATATCTATTACAGTGGGAGCACCAACTACAACCCCTCCCTCAAGAGTCG
ORG: TATATCTATTACAGTGGGAGCACCAACTACAACCCCTCCCTCAAGAGTCG

HUM: AGTCACCATATCAGTAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGA
ORG: AGTCACCATGTCAGTAGACACGTCCAAGAACCAGTTCTCCCTGAAGTTGA

HUM: GCTCTGTGACCGCTGCGGACACGGCCGTGTATTACTGTGCGAGAGA
ORG: GCTCTGTGACCGCCGCGGACACAGCCGTGTATTACTGTGCGAGAGA
```

D7

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HUM: CACAGTG
ORG: CACAGTG
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D9

```
HUM: GACAAAAACCT
ORG: GACACAAACCT
```

```
Alignment stats:  'M': 280, 'I': 3, 'D': 0, 'X': 13
PI: 94.5945945945946
```

Group 62 with 1 units in hum and 6 units in org

Group 62 unit1 0 vs unit2 4 IGHV3-60

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 A G T A A A G A C T G G A G G G G T
ORG: 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 C G C T T G G T A C A G C C T G G - G G G G T

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

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

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

D7

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

D9

```
HUM: A C A A A C C T C C T
ORG: A C A A A C C T C C C T
```

```
Alignment stats:  'M': 266, 'I': 1, 'D': 1, 'X': 30
PI: 89.26174496644296
```

Group 62 with 1 units in hum and 6 units in org

Group 62 unit1 0 vs unit2 5 IGHV1-58

GENE ALIGN SEQ

```
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
ORG: 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
ORG: 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
ORG: 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
ORG: 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
ORG: 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
ORG: 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
```

D7

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

D9

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

```
Alignment stats:  'M': 276, 'I': 1, 'D': 3, 'X': 17
PI: 92.92929292929293
```

Group 62 with 1 units in hum and 6 units in org

Group 62 unit1 0 vs unit2 5 IGHV4-59

GENE ALIGN SEQ

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

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

HUM: 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 T
ORG: 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 T

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

D7

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

D9

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

```
Alignment stats:  'M': 280, 'I': 0, 'D': 0, 'X': 13
PI: 95.56313993174061
```

Group 62 with 1 units in hum and 6 units in org

Group 62 unit1 0 vs unit2 5 IGHV3-60

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 A G T A A A G A C T - - - - - - - G
ORG: 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
ORG: - - 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
ORG: 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
ORG: 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
ORG: 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 - T G
ORG: 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 C A A

HUM: A A A G A
ORG: G A G A G
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D7

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HUM: C G C A G T G
ORG: G C A G T G
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D9

```
HUM: A C A A A C C T C C T
ORG: A C A A A C C T C C C T
```

```
Alignment stats:  'M': 271, 'I': 8, 'D': 3, 'X': 23
PI: 88.85245901639345
```

Group 63 with 1 units in hum and 1 units in org

Group 63 unit1 0 vs unit2 0 IGHV(II)-60-1

GENE ALIGN SEQ

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

D9

```
HUM: C A C C C A A A C C T
ORG: C A C C C A A A C C T
```

```
Alignment stats:  'M': 260, 'I': 3, 'D': 1, 'X': 8
PI: 95.58823529411765
```

Group 64 with 1 units in hum and 1 units in org

Group 64 unit1 0 vs unit2 0 IGHV3-62

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
ORG: 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 C T G C T A
ORG: 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 A T C A G T A G C T A C G A C A

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

HUM: A T T A G T A C A A G T G G T G - - - - A T A C C G T A C T C T A C A C A G A C T C T G T G A A G G
ORG: A T T A G T A C T G G T G G T G G C A C A T A - - - - - - - C T A T G C A G A C T T T 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 G C C C A G A A T T C A C T G T A T C T G C A A
ORG: G C C G 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 G T A T C T G C A A

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

D7

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

D9

```
HUM: A C A A A C C T C C C
ORG: A C A A A C C T C C C
```

```
Alignment stats:  'M': 262, 'I': 4, 'D': 7, 'X': 27
PI: 87.33333333333333
```

Group 64 with 1 units in hum and 1 units in org

Group 64 unit1 0 vs unit2 0 IGHV(II)-62-1

GENE ALIGN SEQ

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

HUM: 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 T G
ORG: 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 T G

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

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

D9

```
HUM: C A C C A A A A C C T
ORG: C A C C A A A A C C T
```

```
Alignment stats:  'M': 258, 'I': 0, 'D': 2, 'X': 13
PI: 94.5054945054945
```

Group 67 with 1 units in hum and 1 units in org

Group 67 unit1 0 vs unit2 0 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
ORG: 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
ORG: 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 A
ORG: 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 A

HUM: 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 A
ORG: 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 A

HUM: 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 G
ORG: 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 G

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

D7

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

D9

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

```
Alignment stats:  'M': 285, 'I': 0, 'D': 1, 'X': 14
PI: 95.0
```

Group 67 with 1 units in hum and 1 units in org

Group 67 unit1 0 vs unit2 0 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
ORG: 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 A
ORG: 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 A

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 T T
ORG: 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 T A T A G C T G T G G T A G C A C A T A C T A C G C A G A C T C C G T G A A G G G C C G A T T
ORG: 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 A T T

HUM: 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 A
ORG: 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 A

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

D9

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

```
Alignment stats:  'M': 272, 'I': 0, 'D': 0, 'X': 21
PI: 92.83276450511946
```

Group 67 with 1 units in hum and 1 units in org

Group 67 unit1 0 vs unit2 0 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
ORG: 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
ORG: 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
ORG: 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
ORG: 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
ORG: 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
ORG: 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
ORG: G A

D7

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

D9

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

```
Alignment stats:  'M': 283, 'I': 2, 'D': 4, 'X': 13
PI: 93.70860927152319
```

Group 67 with 1 units in hum and 1 units in org

Group 67 unit1 0 vs unit2 0 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
ORG: 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
ORG: 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
ORG: 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
ORG: A A A A T G C
```

D9

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

```
Alignment stats:  'M': 136, 'I': 0, 'D': 0, 'X': 3
PI: 97.84172661870504
```

Group 67 with 1 units in hum and 1 units in org

Group 67 unit1 0 vs unit2 0 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
ORG: 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
ORG: 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
ORG: C A C A T G A
```

D9

```
HUM: A C A T A A A C C T C
ORG: A C A T C A A C C T C
```

```
Alignment stats:  'M': 95, 'I': 0, 'D': 0, 'X': 4
PI: 95.95959595959596
```

Group 68 with 2 units in hum and 3 units in org

Group 68 unit1 0 vs unit2 0 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
ORG: C A G G A C C A G A T G C A G C A G T C T G G G G C T G A G G T G A G G A A G C C T G G G A 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 - - - - - - -
ORG: A G T G A A G G T T T C T T G C A A G G T T T C T G G A T A T A C C T A A A G - C A G G T T A C G T

HUM: - - C A G C T A T G C T A 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
ORG: A T C A G C T A T C A T A T C A G 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 G C T T G A

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

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

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

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

D7

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

D9

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

```
Alignment stats:  'M': 259, 'I': 13, 'D': 1, 'X': 36
PI: 83.81877022653723
```

Group 68 with 2 units in hum and 3 units in org

Group 68 unit1 0 vs unit2 1 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
ORG: 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 G
ORG: 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 G

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

HUM: 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 A
ORG: 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 A

HUM: 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 G G
ORG: 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 A G

HUM: 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
ORG: 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
ORG: C A C A G C G
```

D9

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

```
Alignment stats:  'M': 258, 'I': 0, 'D': 4, 'X': 13
PI: 93.81818181818183
```

Group 68 with 2 units in hum and 3 units in org

Group 68 unit1 0 vs unit2 1 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
ORG: 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
ORG: 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
ORG: 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
ORG: 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
ORG: 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
ORG: 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
ORG: C A C A G G A
```

D9

```
HUM: A G A C A C A A A A A
ORG: A G A C A C A A A A A
```

```
Alignment stats:  'M': 283, 'I': 0, 'D': 0, 'X': 11
PI: 96.25850340136054
```

Group 68 with 2 units in hum and 3 units in org

Group 68 unit1 0 vs unit2 1 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
ORG: 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
ORG: 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
ORG: 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
ORG: 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
ORG: 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
ORG: 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
ORG: C A C A G T G
```

D9

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

```
Alignment stats:  'M': 281, 'I': 0, 'D': 0, 'X': 15
PI: 94.93243243243244
```

Group 68 with 2 units in hum and 3 units in org

Group 68 unit1 0 vs unit2 1 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
ORG: 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
ORG: 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
ORG: 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 G
ORG: 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 G

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

D9

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

```
Alignment stats:  'M': 280, 'I': 0, 'D': 0, 'X': 16
PI: 94.5945945945946
```

Group 68 with 2 units in hum and 3 units in org

Group 68 unit1 0 vs unit2 1 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
ORG: 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
ORG: 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
ORG: 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
ORG: 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
ORG: 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
ORG: 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
ORG: C
```

D7

```
HUM: C A C A G A G
ORG: C A C A G A G
```

D9

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

```
Alignment stats:  'M': 287, 'I': 0, 'D': 0, 'X': 14
PI: 95.34883720930233
```

Group 68 with 2 units in hum and 3 units in org

Group 68 unit1 0 vs unit2 2 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
ORG: 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
ORG: 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
ORG: 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 C A G
ORG: 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 C A G

HUM: 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 A
ORG: 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 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
ORG: 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 - - - - - -
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D7

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

D9

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

```
Alignment stats:  'M': 272, 'I': 0, 'D': 6, 'X': 18
PI: 91.8918918918919
```

Group 68 with 2 units in hum and 3 units in org

Group 68 unit1 0 vs unit2 2 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
ORG: 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
ORG: 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
ORG: 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
ORG: 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 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
ORG: 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
ORG: T G A C C A A C A T G G A C C C T G T G G A C A C A G C C A C A T A T T A C T G T G C A C G G A T A

HUM: C
ORG: C
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D7

```
HUM: C A C A G A G
ORG: C A C A G A G
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D9

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

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Alignment stats:  'M': 289, 'I': 0, 'D': 0, 'X': 12
PI: 96.01328903654485
```

Group 77 with 1 units in hum and 2 units in org

Group 77 unit1 0 vs unit2 0 IGHV3-72

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 A G G G T C
ORG: 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
ORG: 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
ORG: 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
ORG: 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
ORG: 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
ORG: 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
ORG: G A
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D7

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HUM: C A C A G C G
ORG: 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
ORG: 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
PI: 97.35099337748345
```

Group 77 with 1 units in hum and 2 units in org

Group 77 unit1 0 vs unit2 0 IGHV3-73

GENE ALIGN SEQ

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

HUM: A T T A G A A G C A A A G C T A A C A G T T A C G C G A C A G C A T A T G C T G C G T C G G T G A A
ORG: 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 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 G T T C A C C A T C T C C A G A G A T G A T T C A A A G A A C A C G G C G T A T C T G C
ORG: A G G C A G G T T C A C C A T C T C C A G A G A T G A T T C A A A G A A C A C G G C G T A T C T G 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 A C T - - A
ORG: 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 G T T A C T G T G C T A C A

HUM: G A C A
ORG: G A C A
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D7

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

D9

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

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Alignment stats:  'M': 283, 'I': 2, 'D': 0, 'X': 19
PI: 93.0921052631579
```

Group 77 with 1 units in hum and 2 units in org

Group 77 unit1 0 vs unit2 1 IGHV3-72

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 A G G G T C
ORG: 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 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
ORG: 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

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
ORG: 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 T T G G A G T G G G T T G G C T T 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
ORG: A T T A A A A A 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 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
ORG: 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 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
ORG: 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 A T A T A T T A C T G T G C T A G A

HUM: G A
ORG: G A
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D7

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

D9

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

```
Alignment stats:  'M': 277, 'I': 0, 'D': 0, 'X': 25
PI: 91.72185430463577
```

Group 77 with 1 units in hum and 2 units in org

Group 77 unit1 0 vs unit2 1 IGHV3-73

GENE ALIGN SEQ

```
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
ORG: 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 A
ORG: 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 A C C A G A

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

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

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

HUM: C A
ORG: T A
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D7

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HUM: C A C A G T G
ORG: C A C A G T G
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D9

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

```
Alignment stats:  'M': 271, 'I': 0, 'D': 0, 'X': 31
PI: 89.73509933774835
```

Group 78 with 1 units in hum and 1 units in org

Group 78 unit1 0 vs unit2 0 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
ORG: 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
ORG: 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 G T
ORG: 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 C T

HUM: 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 C G
ORG: 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 C A

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 A C G C T G T A T C T G C A A A T G A
ORG: 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 G A

HUM: A C A G T C T G A G A G C C G A G G A C A C G G C T G T G T A T T A C T G T G C A A G A G A
ORG: 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
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D7

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HUM: C A C A G T G
ORG: 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
ORG: G A C A C A A A C C T
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Alignment stats:  'M': 265, 'I': 0, 'D': 0, 'X': 31
PI: 89.52702702702703
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Group 78 with 1 units in hum and 1 units in org

Group 78 unit1 0 vs unit2 0 IGHV3-76

GENE ALIGN SEQ

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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
ORG: 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
ORG: 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
ORG: 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
ORG: 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
ORG: 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
ORG: 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
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D7

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

D9

```
HUM: G T C A C A A A C C T
ORG: 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
PI: 95.2054794520548
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Group 78 with 1 units in hum and 1 units in org

Group 78 unit1 0 vs unit2 0 IGHV(III)-76-1

GENE ALIGN SEQ

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

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

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

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

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

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

D7

```
HUM: C A C A G G A
ORG: C A C A G G A
```

D9

```
HUM: A C A G G G G A C A C
ORG: A C A G G A G A C A C
```

```
Alignment stats:  'M': 276, 'I': 0, 'D': 2, 'X': 10
PI: 95.83333333333334
```

Group 78 with 1 units in hum and 1 units in org

Group 78 unit1 0 vs unit2 0 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
ORG: 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
ORG: 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 C
ORG: 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 C

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

HUM: 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 A
ORG: 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 A

HUM: 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
ORG: 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

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HUM: G G G A C C A
ORG: C A G A C C A
```

D9

```
HUM: G T G C A G A G T G A
ORG: G T G C A G A G T G A
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```
Alignment stats:  'M': 280, 'I': 0, 'D': 0, 'X': 14
PI: 95.23809523809523
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Group 78 with 1 units in hum and 1 units in org

Group 78 unit1 0 vs unit2 0 IGHV(II)-78-1

GENE ALIGN SEQ

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

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HUM: C A C A G T G
ORG: C A C A G T G
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D9

```
HUM: C A C C C A A A C C T
ORG: 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
PI: 92.08633093525181
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