UAMs and RSSs of genes in syntney block alginments

Group 3 unit1 1 vs unit2 0 IGHD5-18

U9

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

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

U7

GENE: `G A C T G T G`

MAP : `G G C C A T G`

GENE ALIGN SEQ

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

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

D7

GENE: `C A C A G T G`

MAP : `C A C A G T G`

D9

GENE: `A G C A G C A A C C A`

MAP : `A G C A G C A A C C A`

Alignment stats: 'M': 14, 'I': 0, 'D': 0, 'X': 6
PI: 70.0

Group 3 unit1 1 vs unit2 0 IGHD4-17

U9
```
GENE: G G C T T T T T G T G
MAP : G G C T T T T T G T G
```

U7
```
GENE: T A C T G T G
MAP : T A C T G T T
```

GENE ALIGN SEQ
```
GENE: T G A C T A C G G T G - - - A C T A C
MAP : T G A C T A C G G T G G T A A C T C C
```

D7
```
GENE: C A C A G T G
MAP : T A C A G T G
```

D9
```
GENE: A G C A A A A A C T G
MAP : G G C A A A A A C T G
```

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

Group 3 unit1 1 vs unit2 0 IGHD3-16

U9

GENE: `A G G T T T G A A G T`

MAP : `A G G T T T G A A G T`

U7

GENE: `C A C T G T G`

MAP : `C A C T G T G`

GENE ALIGN SEQ

GENE: `G T A T T A T G A T T A C G - - - - - T T T G G G G G A G T T A T C G T T A T A C - - - - - - - - - C`

MAP : `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

GENE: `C A C A G C A`

MAP : `C A C A G T G`

D9

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

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

Alignment stats: 'M': 22, 'I': 12, 'D': 12, 'X': 3
PI: 44.89795918367347

Group 3 unit1 1 vs unit2 0

Group 3 unit1 1 vs unit2 0 IGHD2-15

U9
```
GENE: A G G A T T T T G T G
MAP : A G G A T T T T G T G
```

U7
```
GENE: C A C T G T G
MAP : C A C T G T G
```

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

D9
```
GENE: T T C C C A A A G C C
MAP : T T C C C A A A G C C
```

```
Alignment stats:  'M': 30, 'I': 0, 'D': 0, 'X': 1
PI: 96.7741935483871
```

Group 3 unit1 1 vs unit2 0 IGHD1-14

U9

```
GENE:  C G G A T T C C G A A
MAP :  C A G A T T C T G A A
```

U7

```
GENE:  C A C A G C G
MAP :  C A C A G T G
```

GENE ALIGN SEQ

```
GENE:  G G T A T A A C C G G A A C C A C
MAP :  G G T A T A A C T G G A A T G A T
```

D7

```
GENE:  C A C T G T C
MAP :  C A C T G T G
```

D9

```
GENE:  G T C A A A A A C T G
MAP :  A T C C A A A A C T G
```

```
Alignment stats:  'M': 13, 'I': 0, 'D': 0, 'X': 4
PI: 76.47058823529412
```

Group 3 unit1 1 vs unit2 0 IGHD6-13

U9

```
GENE: A G G T T T C T G A A
MAP : A G G T T T C T G A A
```

U7

```
GENE: C A C A G T G
MAP : C A C A G T G
```

GENE ALIGN SEQ

```
GENE: G G G T A T A G C A G C A G C T G G T A C
MAP : G G G T A T A G C A G C G G C T G G T C C
```

D7

```
GENE: C A C A G T G
MAP : C A C A G T G
```

D9

```
GENE: G C C A G A A A C C C
MAP : 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 unit1 1 vs unit2 1 IGHD5-18

U9

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

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

U7

GENE: `G A C T G T G`

MAP : `G A C T G T G`

GENE ALIGN SEQ

GENE: `G T G G A T A C A - - - G C T A T G G T T A C`

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

D7

GENE: `C A C A G T G`

MAP : `C A C A G T G`

D9

GENE: `A G C A G C A A C C A`

MAP : `A G C G G C A A C C A`

Alignment stats: 'M': 18, 'I': 3, 'D': 0, 'X': 2
PI: 78.26086956521739

Group 3 unit1 1 vs unit2 1 IGHD4-17

U9

```
GENE: G G C T T T T T G T G
MAP : G G C T T T T T G T G
```

U7

```
GENE: T A C T G T G
MAP : T A C T G T G
```

GENE ALIGN SEQ

```
GENE: T G A C T A C G G T G A C T A C
MAP : T G G C T A C A G T A A C T C C
```

D7

```
GENE: C A C A G T G
MAP : C A C A G T G
```

D9

```
GENE: A G C A A A A A C T G
MAP : G G G A A A A A C T G
```

```
Alignment stats:  'M': 12, 'I': 0, 'D': 0, 'X': 4
PI: 75.0
```

Group 3 unit1 1 vs unit2 1 IGHD3-16

U9

```
GENE: A G G T T T G A A G T
MAP : A G G T T T G G G G T
```

U7

```
GENE: C A C T G T G
MAP : C A C T G T G
```

GENE ALIGN SEQ

```
GENE: G T A T T A T G A T T A C G T T T G G G G G A G T T A T C G T T A T A C C
MAP : G T A T - - - G A T T A T G T T T G G G G A A G T T A T C G T T A T A C C
```

D7

```
GENE: C A C A G C A
MAP : C A C A G C A
```

D9

```
GENE: A T C A G A A A C C C
MAP : A T C A A A A A C C C
```

```
Alignment stats:  'M': 32, 'I': 0, 'D': 3, 'X': 2
PI: 86.48648648648648
```

Group 3 unit1 1 vs unit2 1

Group 3 unit1 1 vs unit2 1 IGHD2-15

U9
```
GENE: A G G A T T T T G T G
MAP : A G G A T T T T G T G
```

U7
```
GENE: C A C T G T G
MAP : C A C T G T G
```

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

D9
```
GENE: T T C C C A A A G C C
MAP : C T C C C A A A G C C
```

Alignment stats: 'M': 28, 'I': 0, 'D': 0, 'X': 3
PI: 90.32258064516128

Group 3 unit1 1 vs unit2 1 IGHD1-14

U9

```
GENE: C G G A T T C C G A A
MAP : C A G A T T C T G A A
```

U7

```
GENE: C A C A G C G
MAP : C A C A G T G
```

GENE ALIGN SEQ

```
GENE: G G T A T A A C C G G A A C C A C
MAP : G G T T T A A C T G G A A C T A C
```

D7

```
GENE: C A C T G T C
MAP : C A C T G T C
```

D9

```
GENE: G T C A A A A A C T G
MAP : G T C A A A A A C T G
```

```
Alignment stats:  'M': 14, 'I': 0, 'D': 0, 'X': 3
PI: 82.35294117647058
```

Group 3 unit1 1 vs unit2 1 IGHD6-13

U9

```
GENE: A G G T T T C T G A A
MAP : A A
```

U7

```
GENE: C A C A G T G
MAP : C A C A G T G
```

GENE ALIGN SEQ

```
GENE: G G G T A T A G C A G C A G C - - - T G G T A C
MAP : 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

```
GENE: C A C A G T G
MAP : C A C A G T G
```

D9

```
GENE: G C C A G A A A C C C
MAP : G C C A G A A A C C C
```

```
Alignment stats:  'M': 21, 'I': 3, 'D': 0, 'X': 0
PI: 87.5
```

Group 3 unit1 1 vs unit2 2 IGHD5-18

U9
```
GENE: T G G T T A T T G T C
MAP : T G G T T A T T G T C
```

U7
```
GENE: G A C T G T G
MAP : G G C C G T G
```

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

D7
```
GENE: C A C A G T G
MAP : C A C A G T G
```

D9
```
GENE: A G C A G C A A C C A
MAP : A G C A G C A A C C A
```

```
Alignment stats:  'M': 14, 'I': 0, 'D': 0, 'X': 6
PI: 70.0
```

Group 3 unit1 1 vs unit2 2

Group 3 unit1 1 vs unit2 2 IGHD4-17

U9
```
GENE: G G C T T T T T G T G
MAP : G G C T T T T T G T G
```

U7
```
GENE: T A C T G T G
MAP : T A C T G T G
```

GENE ALIGN SEQ
```
GENE: T G A C T A C G G T G - - - A C T A C
MAP : T G A C T A C A G T G C T A A C T A C
```

D7
```
GENE: C A C A G T G
MAP : C A C A G T G
```

D9
```
GENE: A G C A A A A A C T G
MAP : A G C A A A A A C T G
```

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

Group 3 unit1 1 vs unit2 2

Group 3 unit1 1 vs unit2 2 IGHD3-16

U9
```
GENE: A G G T T T G A A G T
MAP : A G G T T T G G G G T
```

U7
```
GENE: C A C T G T G
MAP : C A C T G T G
```

GENE ALIGN SEQ
```
GENE: G T A T T A - - - - - - - T G - - - - - - - - - - - A T T A C - - G T T T G G G G G A G T T A T C G T T A
MAP : 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 - - - - - - - - - - - - - - - - - - - - - - -
```

```
GENE: T A C C
MAP : - - - C
```

D7
```
GENE: C A C A G C A
MAP : C A C A G T G
```

D9
```
GENE: A T C A G A A A C C C
MAP : A T C A A A A A C C C
```

Alignment stats: 'M': 14, 'I': 17, 'D': 23, 'X': 0
PI: 25.925925925925924

Group 3 unit1 1 vs unit2 2

Group 3 unit1 1 vs unit2 2 IGHD2-15

U9

GENE: `A G G A T T T T G T G`

MAP : `A G G A T T T T G T G`

U7

GENE: `C A C T G T G`

MAP : `C A C T G T G`

GENE ALIGN SEQ

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

MAP : `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

GENE: `C A C A G T G`

MAP : `C A C A G T G`

D9

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

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

Alignment stats: 'M': 30, 'I': 0, 'D': 0, 'X': 1

PI: 96.7741935483871

Group 3 unit1 1 vs unit2 2 IGHD1-14

U9

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

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

U7

GENE: `C A C A G C G`

MAP : `C A C A G T G`

GENE ALIGN SEQ

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

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

D7

GENE: `C A C T G T C`

MAP : `C A C T G T G`

D9

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

MAP : `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 unit1 1 vs unit2 2 IGHD6-13

U9

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

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

U7

GENE: `C A C A G T G`

MAP : `C A C A G T G`

GENE ALIGN SEQ

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

MAP : `G A G T A T - - - A G C A G C T G G T A C`

D7

GENE: `C A C A G T G`

MAP : `C A C A G T G`

D9

GENE: `G C C A G A A A C C C`

MAP : `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 unit1 1 vs unit2 3 IGHD5-18

U9
GENE: `T G G T T A T T G T C`
MAP : `T G G T T A T T G T C`

U7
GENE: `G A C T G T G`
MAP : `G A C T G T G`

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

D7
GENE: `C A C A G T G`
MAP : `C A C A G T G`

D9
GENE: `A G C A G C A A C C A`
MAP : `A G C A G C A A C C A`

Alignment stats: 'M': 16, 'I': 0, 'D': 0, 'X': 4
PI: 80.0

Group 3 unit1 1 vs unit2 3 IGHD4-17

U9

```
GENE: G G C T T T T T G T G
MAP : G G C T T T T T G T G
```

U7

```
GENE: T A C T G T G
MAP : T G C T G T G
```

GENE ALIGN SEQ

```
GENE: T G A C T A C G G T G A C T A C
MAP : T G A C T A C G G T G A C T A C
```

D7

```
GENE: C A C A G T G
MAP : C A C A G T G
```

D9

```
GENE: A G C A A A A A C T G
MAP : G G C A A A A A C T A
```

```
Alignment stats:  'M': 16, 'I': 0, 'D': 0, 'X': 0
PI: 100.0
```

Group 3 unit1 1 vs unit2 3

Group 3 unit1 1 vs unit2 3 IGHD3-16

U9

GENE: `A G G T T T G A A G T`

MAP : `A G G T T T G G G G T`

U7

GENE: `C A C T G T G`

MAP : `C A C T G T G`

GENE ALIGN SEQ

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

MAP : `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

GENE: `C A C A G C A`

MAP : `C A C A G T G`

D9

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

MAP : `A T C A A A A A C C C`

```
Alignment stats:  'M': 27, 'I': 0, 'D': 6, 'X': 4
PI: 72.97297297297297
```

Group 3 unit1 1 vs unit2 3 IGHD2-15

U9

GENE: `AGGATTTTGTG`

MAP : `AGGATTTTGTG`

U7

GENE: `CACTGTG`

MAP : `CACTGTG`

GENE ALIGN SEQ

GENE: `AGGATATTGTAGTGGTGGTAGCTGCTACTCC`

MAP : `AGGATATTGTAGTGGTGGTAGCTGCTATACC`

D7

GENE: `CACAGTG`

MAP : `CACAGTG`

D9

GENE: `TTCCCAAAGCC`

MAP : `TTCCCAAAGCC`

Alignment stats: 'M': 29, 'I': 0, 'D': 0, 'X': 2
PI: 93.54838709677419

Group 3 unit1 1 vs unit2 3 IGHD1-14

U9

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

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

U7

GENE: `C A C A G C G`

MAP : `C A C A G T G`

GENE ALIGN SEQ

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

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

D7

GENE: `C A C T G T C`

MAP : `C A C T G T G`

D9

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

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

```
Alignment stats:  'M': 14, 'I': 0, 'D': 0, 'X': 3
PI: 82.35294117647058
```

Group 3 unit1 1 vs unit2 3 IGHD6-13

U9

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

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

U7

GENE: `C A C A G T G`

MAP : `C A C A G T G`

GENE ALIGN SEQ

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

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

D7

GENE: `C A C A G T G`

MAP : `C A C T G`

D9

GENE: `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 unit1 1 vs unit2 4 IGHD5-18

U9

```
GENE: T G G T T A T T G T C
MAP : T G G T T A T T G T C
```

U7

```
GENE: G A C T G T G
MAP : G A C T G T G
```

GENE ALIGN SEQ

```
GENE: G T G G A T A C A - - - G C T A T G G T T A C
MAP : G T G G A T A T A C T G G C T A C G G T T A C
```

D7

```
GENE: C A C A G T G
MAP : C A C A G T G
```

D9

```
GENE: A G C A G C A A C C A
MAP : A G C A G C A A C C A
```

```
Alignment stats:  'M': 18, 'I': 3, 'D': 0, 'X': 2
PI: 78.26086956521739
```

Group 3 unit1 1 vs unit2 4 IGHD4-17

U9

GENE: `G G C T T T T T G T G`

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

U7

GENE: `T A C T G T G`

MAP : `T A C T G T G`

GENE ALIGN SEQ

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

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

D7

GENE: `C A C A G T G`

MAP : `C A C A G T G`

D9

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

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

```
Alignment stats:  'M': 14, 'I': 0, 'D': 0, 'X': 2
PI: 87.5
```

Group 3 unit1 1 vs unit2 4 IGHD3-16

U9

GENE: `A G G T T T G A A G T`

MAP : `A G G T T T G G G G T`

U7

GENE: `C A C T G T G`

MAP : `C A C T G T G`

GENE ALIGN SEQ

GENE: `G T A T T A T G A T T A C G T T T G G - G G G A G T T A T C G T T A T A C C`

MAP : `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

GENE: `C A C A G C A`

MAP : `C A C A G T G`

D9

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

MAP : `A T C A A A A A C C C`

Alignment stats: 'M': 23, 'I': 1, 'D': 7, 'X': 7
PI: 60.526315789473685

Group 3 unit1 2 vs unit2 0 IGHD5-12

U9
```
GENE: T G G T T A T T G T C
MAP : T G G T T A T T G T C
```

U7
```
GENE: G A C T G T G
MAP : G G C C A T G
```

GENE ALIGN SEQ
```
GENE: G T G G A T A T A G - T G G C T A C G A T T A C
MAP : G T G G A - - - - G A T G G C T A C A A T T A C
```

D7
```
GENE: C A C A G T G
MAP : C A C A G T G
```

D9
```
GENE: A G C A G C A A C C A
MAP : A G C A G C A A C C A
```

```
Alignment stats:  'M': 18, 'I': 1, 'D': 4, 'X': 1
PI: 75.0
```

Group 3 unit1 2 vs unit2 0 IGHD4-11

U9

```
GENE: G G C T T T T T G T G
MAP : G G C T T T T T G T G
```

U7

```
GENE: T G C T G T G
MAP : T A C T G T T
```

GENE ALIGN SEQ

```
GENE: T G A C T A C - - - - A G T A A C T A C
MAP : T G A C T A C G G T G - G T A A C T C C
```

D7

```
GENE: C A T A G T G
MAP : T A C A G T G
```

D9

```
GENE: G G C A A A A A C T G
MAP : G G C A A A A A C T G
```

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

Group 3 unit1 2 vs unit2 0 IGHD3-10

U9

GENE: `A G G T T T G G G G T`

MAP : `A G G T T T G A A G T`

U7

GENE: `C A C T G T G`

MAP : `C A C T G T G`

GENE ALIGN SEQ

GENE: `G T A - - - - - - - - - - - - - - - - - - - - - - T T A C T A T G G T T C G G G G A G T T A T T A T A`

MAP : `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`

GENE: `A - - C`

MAP : `A A G C`

D7

GENE: `C A C A G T G`

MAP : `C A C A G T G`

D9

GENE: `A T C A A A A A C C C`

MAP : `A T C A A A A A C T C`

Alignment stats: 'M': 14, 'I': 23, 'D': 17, 'X': 0

PI: 25.925925925925924

Group 3 unit1 2 vs unit2 0 IGHD2-8

U9

```
GENE: A G G A T T T T G T G
MAP : A G G A T T T T G T G
```

U7

```
GENE: C A C T G T G
MAP : C A C T G T G
```

GENE ALIGN SEQ

```
GENE: A G G A T A T T G T A - C T A A T G G T G - T A - - T G C T A T A C C
MAP : 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

```
GENE: C A C A G T G
MAP : C A C A G T G
```

D9

```
GENE: T T C C C A A A G C C
MAP : T T C C C A A A G C C
```

Alignment stats: 'M': 25, 'I': 4, 'D': 4, 'X': 2
PI: 71.42857142857143

Group 3 unit1 2 vs unit2 0 IGHD1-7

U9

```
GENE: C G G A T T C T G A A
MAP : C A G A T T C T G A A
```

U7

```
GENE: C A C A G T G
MAP : C A C A G T G
```

GENE ALIGN SEQ

```
GENE: G G T A T A A C T G G A A C T A C
MAP : G G T A T A A C T G G A A T G A T
```

D7

```
GENE: C A C T G T G
MAP : C A C T G T G
```

D9

```
GENE: G T C C A A A A C G G
MAP : A T C C A A A A C T G
```

```
Alignment stats:  'M': 14, 'I': 0, 'D': 0, 'X': 3
PI: 82.35294117647058
```

Group 3 unit1 2 vs unit2 0 IGHD6-6

U9

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

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

U7

GENE: `C A C A G T G`

MAP : `C A C A G T G`

GENE ALIGN SEQ

GENE: `G A G T A T A G C A G C - - T C - - G T C C`

MAP : `G G G T A T A G C A G C G G - C T G G T C C`

D7

GENE: `C A C A G T G`

MAP : `C A C A G T G`

D9

GENE: `G C C A G A A A C C C`

MAP : `G C C A G A A A C C C`

```
Alignment stats:  'M': 16, 'I': 4, 'D': 1, 'X': 1
PI: 72.72727272727273
```

Group 3 unit1 2 vs unit2 1 IGHD5-12

U9

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

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

U7

GENE: `G A C T G T G`

MAP : `G A C T G T G`

GENE ALIGN SEQ

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

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

D7

GENE: `C A C A G T G`

MAP : `C A C A G T G`

D9

GENE: `A G C A G C A A C C A`

MAP : `A G C G G C A A C C A`

```
Alignment stats:  'M': 21, 'I': 0, 'D': 0, 'X': 2
PI: 91.30434782608695
```

Group 3 unit1 2 vs unit2 1 IGHD4-11

U9

```
GENE: G G C T T T T T G T G
MAP : G G C T T T T T G T G
```

U7

```
GENE: T G C T G T G
MAP : T A C T G T G
```

GENE ALIGN SEQ

```
GENE: T G A C T A C A G T A A C T A C
MAP : T G G C T A C A G T A A C T C C
```

D7

```
GENE: C A T A G T G
MAP : C A C A G T G
```

D9

```
GENE: G G C A A A A A C T G
MAP : G G G A A A A A C T G
```

```
Alignment stats:  'M': 14, 'I': 0, 'D': 0, 'X': 2
PI: 87.5
```

Group 3 unit1 2 vs unit2 1 IGHD3-10

U9

GENE: `A G G T T T G G G G T`

MAP : `A G G T T T G G G G T`

U7

GENE: `C A C T G T G`

MAP : `C A C T G T G`

GENE ALIGN SEQ

GENE: `G T A T T A C T A T G G T T C G G G G A G T T A T - - - T A T A A C`

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

D7

GENE: `C A C A G T G`

MAP : `C A C A G C A`

D9

GENE: `A T C A A A A A C C C`

MAP : `A T C A A A A A C C C`

```
Alignment stats:  'M': 25, 'I': 3, 'D': 0, 'X': 6
PI: 73.52941176470588
```

Group 3 unit1 2 vs unit2 1

Group 3 unit1 2 vs unit2 1 IGHD2-8

U9

GENE: `A G G A T T T T G T G`

MAP : `A G G A T T T T G T G`

U7

GENE: `C A C T G T G`

MAP : `C A C T G T G`

GENE ALIGN SEQ

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

MAP : `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

GENE: `C A C A G T G`

MAP : `C A C A G T G`

D9

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

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

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

Group 3 unit1 2 vs unit2 1 IGHD1-7

U9

```
GENE: C G G A T T C T G A A
MAP : C A G A T T C T G A A
```

U7

```
GENE: C A C A G T G
MAP : C A C A G T G
```

GENE ALIGN SEQ

```
GENE: G G T A T A A C T G G A A C T A C
MAP : G G T T T A A C T G G A A C T A C
```

D7

```
GENE: C A C T G T G
MAP : C A C T G T C
```

D9

```
GENE: G T C C A A A A C G G
MAP : G T C A A A A A C T G
```

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

Group 3 unit1 2 vs unit2 2 IGHD5-12

U9
```
GENE: T G G T T A T T G T C
MAP : T G G T T A T T G T C
```

U7
```
GENE: G A C T G T G
MAP : G G C C G T G
```

GENE ALIGN SEQ
```
GENE: G T G G A T A T A G - T G G C T A C G A T T A C
MAP : G T G G A - - - - G A T G G C T A C A A T T A C
```

D7
```
GENE: C A C A G T G
MAP : C A C A G T G
```

D9
```
GENE: A G C A G C A A C C A
MAP : A G C A G C A A C C A
```

Alignment stats: 'M': 18, 'I': 1, 'D': 4, 'X': 1
PI: 75.0

Group 3 unit1 2 vs unit2 2

Group 3 unit1 2 vs unit2 2 IGHD4-11

U9
```
GENE: G G C T T T T T G T G
MAP : G G C T T T T T G T G
```

U7
```
GENE: T G C T G T G
MAP : T A C T G T G
```

GENE ALIGN SEQ
```
GENE: T G A C T A C A G T - - - A A C T A C
MAP : T G A C T A C A G T G C T A A C T A C
```

D7
```
GENE: C A T A G T G
MAP : C A C A G T G
```

D9
```
GENE: G G C A A A A A C T G
MAP : A G C A A A A A C T G
```

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

Group 3 unit1 2 vs unit2 2

Group 3 unit1 2 vs unit2 2 IGHD3-10

U9
```
GENE: A G G T T T G G G G T
MAP : A G G T T T G G G G T
```

U7
```
GENE: C A C T G T G
MAP : C A C T G T G
```

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

D9
```
GENE: A T C A A A A A C C C
MAP : 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 unit1 2 vs unit2 2

Group 3 unit1 2 vs unit2 2 IGHD2-8

U9
```
GENE: A G G A T T T T G T G
MAP : A G G A T T T T G T G
```

U7
```
GENE: C A C T G T G
MAP : C A C T G T G
```

GENE ALIGN SEQ
```
GENE: A G G A T A T T G T A - C T A A T G G T G - T A - - T G C T A T A C C
MAP : 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
```
GENE: C A C A G T G
MAP : C A C A G T G
```

D9
```
GENE: T T C C C A A A G C C
MAP : T T C C C A A A G C C
```

Alignment stats: 'M': 25, 'I': 4, 'D': 4, 'X': 2
PI: 71.42857142857143

Group 3 unit1 2 vs unit2 2 IGHD1-7

U9

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

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

U7

GENE: `C A C A G T G`

MAP : `C A C A G T G`

GENE ALIGN SEQ

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

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

D7

GENE: `C A C T G T G`

MAP : `C A C T G T G`

D9

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

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

```
Alignment stats:  'M': 17, 'I': 0, 'D': 0, 'X': 0
PI: 100.0
```

Group 3 unit1 2 vs unit2 2 IGHD6-6

U9
```
GENE: A A G T T T C T G A A
MAP : A A G T T T C T G A A
```

U7
```
GENE: C A C A G T G
MAP : C A C A G T G
```

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

D7
```
GENE: C A C A G T G
MAP : C A C A G T G
```

D9
```
GENE: G C C A G A A A C C C
MAP : G C C A G A A A C C C
```

```
Alignment stats:  'M': 16, 'I': 0, 'D': 0, 'X': 2
PI: 88.88888888888889
```

Group 3 unit1 2 vs unit2 3 IGHD5-12

U9

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

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

U7

GENE: `G A C T G T G`

MAP : `G A C T G T G`

GENE ALIGN SEQ

GENE: `G T G - G A T A T A G T G G C T A C G A T T A C`

MAP : `G T G A - - - A T A - T G G C T A C G G T T A C`

D7

GENE: `C A C A G T G`

MAP : `C A C A G T G`

D9

GENE: `A G C A G C A A C C A`

MAP : `A G C A G C A A C C A`

```
Alignment stats:  'M': 18, 'I': 1, 'D': 4, 'X': 1
PI: 75.0
```

Group 3 unit1 2 vs unit2 3 IGHD4-11

U9

GENE: `G G C T T T T T G T G`

MAP : `G G C T T T T T G T G`

U7

GENE: `T G C T G T G`

MAP : `T G C T G T G`

GENE ALIGN SEQ

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

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

D7

GENE: `C A T A G T G`

MAP : `C A C A G T G`

D9

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

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

```
Alignment stats:  'M': 14, 'I': 0, 'D': 0, 'X': 2
PI: 87.5
```

Group 3 unit1 2 vs unit2 3 IGHD3-10

U9
```
GENE: A G G T T T G G G G T
MAP : A G G T T T G G G G T
```

U7
```
GENE: C A C T G T G
MAP : C A C T G T G
```

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

D9
```
GENE: A T C A A A A A C C C
MAP : A T C A A A A A C C C
```

```
Alignment stats:  'M': 28, 'I': 0, 'D': 0, 'X': 3
PI: 90.32258064516128
```

Group 3 unit1 2 vs unit2 3
Group 3 unit1 2 vs unit2 3 IGHD2-8

U9
GENE: `AGGATTTTGTG`
MAP : `AGGATTTTGTG`

U7
GENE: `CACTGTG`
MAP : `CACTGTG`

GENE ALIGN SEQ
GENE: `AGGATATTGTA-CTAATGGTG-TA--TGCTATACC`
MAP : `AGGATATTGTAG----TGGTGGTAGCTGCTATACC`

D7
GENE: `CACAGTG`
MAP : `CACAGTG`

D9
GENE: `TTCCCAAAGCC`
MAP : `TTCCCAAAGCC`

```
Alignment stats:  'M': 27, 'I': 4, 'D': 4, 'X': 0
PI: 77.14285714285715
```

49

Group 3 unit1 2 vs unit2 3 IGHD1-7

U9
```
GENE: C G G A T T C T G A A
MAP : T G G A T A C C A A A
```

U7
```
GENE: C A C A G T G
MAP : C A C A G T G
```

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

D7
```
GENE: C A C T G T G
MAP : C A C T G T G
```

D9
```
GENE: G T C C A A A A C G G
MAP : 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 unit1 2 vs unit2 4 IGHD5-12

U9
```
GENE: T G G T T A T T G T C
MAP : T G G T T A T T G T C
```

U7
```
GENE: G A C T G T G
MAP : G A C T G T G
```

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

D7
```
GENE: C A C A G T G
MAP : C A C A G T G
```

D9
```
GENE: A G C A G C A A C C A
MAP : A G C A G C A A C C A
```

```
Alignment stats:  'M': 21, 'I': 0, 'D': 0, 'X': 2
PI: 91.30434782608695
```

Group 3 unit1 2 vs unit2 4

Group 3 unit1 2 vs unit2 4 IGHD4-11

U9
```
GENE: G G C T T T T T G T G
MAP : G G A C T T T T T G T G
```

U7
```
GENE: T G C T G T G
MAP : T A C T G T G
```

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

D7
```
GENE: C A T A G T G
MAP : C A C A G T G
```

D9
```
GENE: G G C A A A A A C T G
MAP : G G A A A A A C T G
```

```
Alignment stats:  'M': 16, 'I': 0, 'D': 0, 'X': 0
PI: 100.0
```

Group 3 unit1 2 vs unit2 4 IGHD3-10

U9
```
GENE: A G G T T T G G G G T
MAP : A G G T T T G G G G T
```

U7
```
GENE: C A C T G T G
MAP : C A C T G T G
```

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

D9
```
GENE: A T C A A A A A C C C
MAP : A T C A A A A A C C C
```

```
Alignment stats:  'M': 24, 'I': 0, 'D': 0, 'X': 7
PI: 77.41935483870968
```

Group 3 unit1 3 vs unit2 0 IGHD5-5

U9

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

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

U7

GENE: `G A C T G T G`

MAP : `G G C C A T G`

GENE ALIGN SEQ

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

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

D7

GENE: `C A C A G T G`

MAP : `C A C A G T G`

D9

GENE: `A G C A G C A A C C A`

MAP : `A G C A G C A A C C A`

```
Alignment stats:  'M': 14, 'I': 0, 'D': 0, 'X': 6
PI: 70.0
```

Group 3 unit1 3 vs unit2 0 IGHD3-3

U9

```
GENE: A G G T T T G G G G T
MAP : A G G T T T G A A G T
```

U7

```
GENE: C A C T G T G
MAP : C A C T G T G
```

GENE ALIGN SEQ

```
GENE: G T A T T A C G A T T - - - - - - - - T T T G G A G T G G T T A T T A T A C C
MAP : 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

```
GENE: C A C A G T G
MAP : C A C A G T G
```

D9

```
GENE: A T C A A A A A C C C
MAP : A T C A A A A A C T C
```

Alignment stats: 'M': 23, 'I': 7, 'D': 1, 'X': 7
PI: 60.526315789473685

Group 3 unit1 3 vs unit2 0 IGHD2-2

U9

GENE: `A G G A T T T T G T G`

MAP : `A G G A T T T T G T G`

U7

GENE: `C A C T G T G`

MAP : `C A C T G T G`

GENE ALIGN SEQ

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

MAP : `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

GENE: `C A C A G T G`

MAP : `C A C A G T G`

D9

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

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

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

Group 3 unit1 3 vs unit2 1 IGHD5-5

U9

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

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

U7

GENE: `G A C T G T G`

MAP : `G A C T G T G`

GENE ALIGN SEQ

GENE: `G T G G A T A C A - - - G C T A T G G T T A C`

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

D7

GENE: `C A C A G T G`

MAP : `C A C A G T G`

D9

GENE: `A G C A G C A A C C A`

MAP : `A G C G G C A A C C A`

```
Alignment stats:  'M': 18, 'I': 3, 'D': 0, 'X': 2
PI: 78.26086956521739
```

Group 3 unit1 3 vs unit2 1 IGHD4-4

U9

GENE: `G G C T T T T T G T G`

MAP : `G G C T T T T T G T G`

U7

GENE: `T A C T G T G`

MAP : `T A C T G T G`

GENE ALIGN SEQ

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

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

D7

GENE: `C A C A G T G`

MAP : `C A C A G T G`

D9

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

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

Alignment stats: 'M': 14, 'I': 0, 'D': 0, 'X': 2
PI: 87.5

Group 3 unit1 3 vs unit2 1 IGHD3-3

U9
```
GENE: A G G T T T G G G G T
MAP : A G G T T T G G G G T
```

U7
```
GENE: C A C T G T G
MAP : C A C T G T G
```

GENE ALIGN SEQ
```
GENE: G T A T T A C G A T T T T T G G - - A - G T G G T T A T T A T A C C
MAP : G T A T G A T T A T G T T T G G G G A A G T T A T C G T T A T A C C
```

D7
```
GENE: C A C A G T G
MAP : C A C A G C A
```

D9
```
GENE: A T C A A A A A C C C
MAP : A T C A A A A A C C C
```

```
Alignment stats:  'M': 23, 'I': 3, 'D': 0, 'X': 8
PI: 67.64705882352942
```

Group 3 unit1 3 vs unit2 1 IGHD2-2

U9

GENE: `A G G A T T T T G T G`

MAP : `A G G A T T T T G T G`

U7

GENE: `C A C T G T G`

MAP : `C A C T G T G`

GENE ALIGN SEQ

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

MAP : `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

GENE: `C A C A G T G`

MAP : `C A C A G T G`

D9

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

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

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

Group 3 unit1 3 vs unit2 2 IGHD5-5

U9
```
GENE: T G G T T A T T G T C
MAP : T G G T T A T T G T C
```

U7
```
GENE: G A C T G T G
MAP : G G C C G T G
```

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

D7
```
GENE: C A C A G T G
MAP : C A C A G T G
```

D9
```
GENE: A G C A G C A A C C A
MAP : A G C A G C A A C C A
```

```
Alignment stats:  'M': 14, 'I': 0, 'D': 0, 'X': 6
PI: 70.0
```

Group 3 unit1 3 vs unit2 2 IGHD4-4

U9
```
GENE: G G C T T T T T G T G
MAP : G G C T T T T T G T G
```

U7
```
GENE: T A C T G T G
MAP : T A C T G T G
```

GENE ALIGN SEQ
```
GENE: T G A C T A C A G T - - - A A C T A C
MAP : T G A C T A C A G T G C T A A C T A C
```

D7
```
GENE: C A C A G T G
MAP : C A C A G T G
```

D9
```
GENE: A G C A A A A A C T G
MAP : A G C A A A A A C T G
```

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

Group 3 unit1 3 vs unit2 2 IGHD3-3

U9

GENE: `A G G T T T G G G G T`

MAP : `A G G T T T G G G G T`

U7

GENE: `C A C T G T G`

MAP : `C A C T G T G`

GENE ALIGN SEQ

GENE: `G T A T T A C G A T T T T T G G A G T G G T - - - - - - - T A T T A T A C C`

MAP : `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

GENE: `C A C A G T G`

MAP : `C A C A G T G`

D9

GENE: `A T C A A A A A C C C`

MAP : `A T C A A A A A C C C`

```
Alignment stats:  'M': 22, 'I': 6, 'D': 6, 'X': 3
PI: 59.45945945945946
```

Group 3 unit1 3 vs unit2 2 IGHD2-2

U9

```
GENE:  A G G A T T T T G T G
MAP :  A G G A T T T T G T G
```

U7

```
GENE:  C A C T G T G
MAP :  C A C T G T G
```

GENE ALIGN SEQ

```
GENE:  A G G A T A T T G T A G T A G T A C C A G C T G C T A T G C C
MAP :  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

```
GENE:  C A C A G T G
MAP :  C A C A G T G
```

D9

```
GENE:  T T C C C A A A G C C
MAP :  T T C C C A A A G C C
```

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

64

Group 3 unit1 3 vs unit2 3 IGHD5-5

U9

```
GENE: T G G T T A T T G T C
MAP : T G G T T A T T G T C
```

U7

```
GENE: G A C T G T G
MAP : G A C T G T G
```

GENE ALIGN SEQ

```
GENE: G T G G A T A C A G C T A T G G T T A C
MAP : G T G A A T A T G G C T A C G G T T A C
```

D7

```
GENE: C A C A G T G
MAP : C A C A G T G
```

D9

```
GENE: A G C A G C A A C C A
MAP : A G C A G C A A C C A
```

```
Alignment stats:  'M': 16, 'I': 0, 'D': 0, 'X': 4
PI: 80.0
```

Group 3 unit1 3 vs unit2 3 IGHD4-4

U9
```
GENE: G G C T T T T T G T G
MAP : G G C T T T T T G T G
```

U7
```
GENE: T A C T G T G
MAP : T G C T G T G
```

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

D7
```
GENE: C A C A G T G
MAP : C A C A G T G
```

D9
```
GENE: A G C A A A A A C T G
MAP : G G C A A A A A C T A
```

```
Alignment stats:  'M': 14, 'I': 0, 'D': 0, 'X': 2
PI: 87.5
```

Group 3 unit1 3 vs unit2 3 IGHD3-3

U9
```
GENE: A G G T T T G G G G T
MAP : A G G T T T G G G G T
```

U7
```
GENE: C A C T G T G
MAP : C A C T G T G
```

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

D9
```
GENE: A T C A A A A A C C C
MAP : A T C A A A A A C C C
```

```
Alignment stats:  'M': 25, 'I': 0, 'D': 0, 'X': 6
PI: 80.64516129032258
```

Group 3 unit1 3 vs unit2 3

Group 3 unit1 3 vs unit2 3 IGHD2-2

U9

```
GENE: A G G A T T T T G T G
MAP : A G G A T T T T G T G
```

U7

```
GENE: C A C T G T G
MAP : C A C T G T G
```

GENE ALIGN SEQ

```
GENE: A G G A T A T T G T A G T A G T A C C A G C T G C T A T G C C
MAP : 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

```
GENE: C A C A G T G
MAP : C A C A G T G
```

D9

```
GENE: T T C C C A A A G C C
MAP : T T C C C A A A G C C
```

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

68

Group 3 unit1 3 vs unit2 4 IGHD5-5

U9

```
GENE: T G G T T A T T G T C
MAP : T G G T T A T T G T C
```

U7

```
GENE: G A C T G T G
MAP : G A C T G T G
```

GENE ALIGN SEQ

```
GENE: G T G G A T A C A - - - G C T A T G G T T A C
MAP : G T G G A T A T A C T G G C T A C G G T T A C
```

D7

```
GENE: C A C A G T G
MAP : C A C A G T G
```

D9

```
GENE: A G C A G C A A C C A
MAP : A G C A G C A A C C A
```

```
Alignment stats:  'M': 18, 'I': 3, 'D': 0, 'X': 2
PI: 78.26086956521739
```

Group 3 unit1 3 vs unit2 4 IGHD4-4

U9
```
GENE: G G C T T T T T G T G
MAP : G A C T T T T T G T G
```

U7
```
GENE: T A C T G T G
MAP : T A C T G T G
```

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

D7
```
GENE: C A C A G T G
MAP : C A C A G T G
```

D9
```
GENE: A G C A A A A A C T G
MAP : G G A A A A A C T G
```

```
Alignment stats:  'M': 16, 'I': 0, 'D': 0, 'X': 0
PI: 100.0
```

Group 3 unit1 3 vs unit2 4 IGHD3-3

U9

GENE: `A G G T T T G G G G T`

MAP : `A G G T T T G G G G T`

U7

GENE: `C A C T G T G`

MAP : `C A C T G T G`

GENE ALIGN SEQ

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

MAP : `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

GENE: `C A C A G T G`

MAP : `C A C A G T G`

D9

GENE: `A T C A A A A A C C C`

MAP : `A T C A A A A A C C C`

Alignment stats: 'M': 25, 'I': 0, 'D': 0, 'X': 6
PI: 80.64516129032258

Group 23 unit1 1 vs unit2 0 IGHV3-47

GENE ALIGN SEQ

```
GENE: GAGGATCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTC
MAP : GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTC

GENE: CCTGCGACCCTCCTGTGCAGCCTCTGGATTCGCCTTCAGTAGCTATGCTC
MAP : CCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTGTCAGTAGCTACGACA

GENE: TGCACTGGGTTCGCCGGGGCTCCAGGGAAGGGTCTGGAGTGGGTATCAGCT
MAP : TGCACTGGGTTCGCCAGGCTCCAGGAAAAGGTCTGGAGTGGGTCTCAGCT

GENE: ATTGGTACTGGTGGTGATACATACTATGCAGACTCCGTGATGGGCCGATT
MAP : ATTGATACTGATGGTGACACATACTATGCAGACTCTGTGAAGGGCTGATT

GENE: CACCATCTCCAGAGACAACGCCAAGAAGTCCTTGTATCTTCATATGAACA
MAP : CACCATCTCCAGAGAAAATGCCAAGAACTCTTTGTATCTTCAAATGAACA

GENE: GCCTGATAGCTGAGGACATGGCTGTGTATTATTGTGCAAGAGA
MAP : GCCTGAGAGCCAAGGACACGGCTGTGTATTACTGTGCAAGAGA
```

D7

```
GENE: CACAGTG
MAP : CACAGTG
```

D9

```
GENE: GATACAAACTT
MAP : GACACAAACCT
```

```
Alignment stats:  'M': 262, 'I': 0, 'D': 0, 'X': 31
PI: 89.419795221843
```

Group 23 unit1 1 vs unit2 0
Group 23 unit1 1 vs unit2 0 IGHV(III)-47-1

GENE ALIGN SEQ

```
GENE: GAAGTTAATTACTGGAGTCTCTCAGAGAAATACTACAGACCAAGAATTCT
MAP : GAAGTTAACTAATGGAGTCAGACAGAGAAATACTACAGACCAGGAATTCT

GENE: CAGACTTTTCTGGAAACCCTGTGGATTCACTTTCACTGAAAACAGCATAA
MAP : --GCCTTTTCTGCAAAGCCTCTGGATTCACTTTCACTGAAAACAGCATAA

GENE: GCTTGGTCCAGCAGGCTTCATGACAGGGGTGGGTGTAGGTGATAACA-TC
MAP : GCTTGATCCAGCAGGCTTCATGACAGGGGTGGGTGTGGGTAATAACAA--

GENE: AGTAATTCAAGTGGAAGTTCTCAGTGGGACTCTCCTTGAGTACAAAGAAG
MAP : --TAATTCAAATGGAAGTTCTCAGTGGGACTCTCCTTCAGTAAAAAGATG

GENE: ATTAACAGTCCTCAGAGACACGCTTTTCAGATGATTCTCTCTTAAGATGA
MAP : AATAACAATCCTCAAATACACTCAGTTCAGGAGATTCTCTTTTAAGATGA

GENE: TTAACCTGAGAGCTCAGGAAAATTCCGTTTATTACTGTGAGGGA
MAP : TTAACCTGAAAGCTCAGGAAAAGTCCGTGTATTACTTTGAGGGA
```

D7
```
GENE: CACGGTG
MAP : CACAGTG
```

D9
```
GENE: GACACAAACCT
MAP : GACACCAACCT
```

```
Alignment stats:  'M': 256, 'I': 1, 'D': 6, 'X': 31
PI: 87.07482993197279
```

Group 23 unit1 1 vs unit2 1
Group 23 unit1 1 vs unit2 1 IGHV3-47

GENE ALIGN SEQ

```
GENE: G A G G A T C A G C T G G T G G A G T C T G G G G G A G G C T T G G T A C A G C C T G G G G G G G T C
MAP : 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 G T C

GENE: C C T G C G A C C C T C C T G T G C A G C C T C T G G A T T C G C C T T C A G T A G C T A T G C T C
MAP : 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

GENE: T G C A C T G 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
MAP : T G C A C T G 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

GENE: 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
MAP : 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

GENE: C A C C A T C T C C A G A G A C A A C G C C A A G A A G T C C T T G T A T C T T C A T A T G A A C A
MAP : 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

GENE: G C C T G A T A G C T G A G G A C A T G G C T G T G T A T T A T T G T G C A A G A G A
MAP : G C C T G A T A T C T G A G G A C A C G G C T G T G T A T T A C T G T G C A A G A G A
```

D7

```
GENE: C A C A G T G
MAP : C A C A G T G
```

D9

```
GENE: G A T A C A A A C T T
MAP : G A T A C A A A C T T
```

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

Group 23 unit1 1 vs unit2 1 IGHV(III)-47-1

GENE ALIGN SEQ

```
GENE: GAAGTTAATTACTGGAGTCTCTCAGAGAAATACTACAGACCAAGAATTCT
MAP : GAAGTTAATTAGTGGAGTCTCTCAGAGAAATACTACAGACCAAGAATTCT

GENE: CAGACTTTTCTGGAAACCCTGTGGATTCACTTTCACTGAAAACAGCATAA
MAP : CAGACTTTTCTGGAAAGCCTCTGGATTCACTTTCACTGAAAACAGCATAA

GENE: GCTTGGTCCAGCAGGCTTCATGACAGGGGTGGGTGTAGGTGATAACATCA
MAP : GCTTCGTCCAGCAGGCTTCATGACAGGGGTTGGTGTGGGTGATAACATCA

GENE: GTAATTCAAGTGGAAGTTCTCAGTGGGACTCTCCTTGAGTACAAAGAAGA
MAP : GTAATTCAAGTGGAAGTTCTCAGTGGGACTCTCCTTGACTACAAAGAAGA

GENE: TTAACAGTCCTCAGAGACACGCTTTTCAGATGATTCTCTCTTAAGATGAT
MAP : TTAACAGTCCTCAGAGACACTCTTTTCAGATGATTCTCTCTTTAAGATGAT

GENE: TAACCTGAGAGCTCAGGAAAATTCCGTTTATTACTGTGAGGGA
MAP : TAACCTGAGAGCTCAGGAAAATTCCGTTTATTACTGTGAGGGA
```

D7
```
GENE: CACGGTG
MAP : CACAGTG
```

D9
```
GENE: GACACAAACCT
MAP : GACACAAACCT
```

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

Group 48 unit1 1 vs unit2 0
Group 48 unit1 1 vs unit2 0 IGHV4-30-2

GENE ALIGN SEQ

```
GENE: CAGCTGCAGCTGCAGGAGTCCGGCTCAGGACTGGTGAAGCCTTCACAGAC
MAP : CAGGTGCAGCTGCAGGAGTCGGGCCCCAGGACTGGTGAAGCCTTCGGAGAC

GENE: CCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCCATCAGCAGTGGTGGTT
MAP : CCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCCATCAGCAGTGGT---T

GENE: ACTCCTGGAGCTGGATCCGGCAGCCACCAGGGAAGGGCCTGGAGTGGATT
MAP : ACTACTGGGGCTGGATCCGCCAGCCCCCAGGGAAGGGCCTGGAGTGGATT

GENE: GGGTACATCTATCATA--GTGGGAGCACCTACTACAACCCGTCCCTCAAG
MAP : GGG--CATATCAATTATGGTGGGAGCACCAGCTACAACCCATCCCTCAAG

GENE: AGTCGAGTCACCATATCAGTAGACAGGTCCAAGAACCAGTTCTCCCTGAA
MAP : AGTCGAGTCACCTTGTCAGTAGACACGTCCAAGAACCAGTTCTCCCTGAA

GENE: GCTGAGCTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGCCAGAG
MAP : GCTGAGCTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGCGAGAG

GENE: A
MAP : A
```

D7
```
GENE: CACAATG
MAP : CACAATG
```

D9
```
GENE: GACACAAACCT
MAP : GACAAAAACCT
```

Alignment stats: 'M': 273, 'I': 2, 'D': 5, 'X': 21
PI: 90.69767441860465

Group 48 unit1 1 vs unit2 0 IGHV(II)-30-21

GENE ALIGN SEQ

```
GENE: TCACAGACCCTCTCCCTCACCTGCACTGTCTCTGGATTCCCCATCATAAC
MAP : TCGCAGACCCTCTCCCTCACCTGCACTGTCTCTGGATTCCCCATCATAAC

GENE: CAGTGTTTCCTTCTAGAATTGTATCTGCTTGCCCCTAGAAGATGGACAGG
MAP : CAGTGTTTCCCACTAGAATTGTATCTGCTTGTCCCTAGAAGATGGACAGG

GENE: AGTGGATCAGGTGCATGGGTTGTGAAGGGAGCACAAATTACAACCCACTT
MAP : AGTGGATCAGGTGCATGGGTTGTGAAGGGAGCACAAATTACAACC-ACTT

GENE: CTCAAGAGTCCATATCCGGATCCAAGAAACAGTTCTTACAGCTGAGCTCT
MAP : CTCAAGAGTCCAT-------ATCCAAGAAACAGTTCTTACAGCTGAGCTCT

GENE: GTGCCCAGTGAACACACAACTACGCATTTTGAAGCAAAAGATGCAATGAA
MAP : GTGCCCAGTGAACACACAACTATGCATTTTTAAGCAAAAGAGGCAATGAG

GENE: GGGCCTT
MAP : AGGACTT
```

D7

```
GENE: CATTGTG
MAP : CATTATG
```

D9

```
GENE: CAGGGGTGAAT
MAP : CAGGGGTGCAT
```

```
Alignment stats:  'M': 240, 'I': 0, 'D': 7, 'X': 10
PI: 93.3852140077821
```

Group 48 unit1 1 vs unit2 0

Group 48 unit1 1 vs unit2 0 IGHV3-33-2

GENE ALIGN SEQ

GENE: GAGGTACAGCTCGTGGAGTCCGGAGAGGACCCAAGACAACCTGGGGGATC
MAP : GAGGTACAGCTAGTGGAGTCCGGAGAGGACCCAAGACAACCTGGGGGGTC

GENE: CTTGAGACTCTCCTGTGCAGACTCTGGATTAACCTTCAGTAGCTACTGAA
MAP : CGTGAGACTCTCCTGTGCAGACTCTGGATTAACCTTCAGTAGCTACTGAA

GENE: TGAGCTCGGTTTCCCAGGCTCCAGGGAAGGGGCTGGAGTGAGTAGTAGAT
MAP : TGAGCTCAGTTTCCCAGGCTCCAGGGAAGGGGCTGGAGTGAGTAGTAGAT

GENE: ATACAGTGTGATGGAAGTCAGATATGTTATGCCCAATCTGTGAAGAGCAA
MAP : AAATAGTACGATACAAGTCAGATATGTTATGCACAAACTGTGAAGAGCAG

GENE: ATTCACCATCTCCAAAGAAAATGCCAAGAACTCACTGTATTTGCAAATGA
MAP : ATTCACCATCTCCAAAGAAAATGCCAAGAACTCACTCCATTTGCAAATGA

GENE: ACAGTCTGAGAGCAGAGGGCACAGCTGTGTGTTACTGTATGTGAGGCA
MAP : ACGGTCTGAGAACAGAGGGCACAACTGTGTGTTACTGTATGTGAGGCA

D7
GENE: CCAGGTA
MAP : CCAGGTA

D9
GENE: GACACAGTTTC
MAP : GACACAGAATTTC

Alignment stats: 'M': 280, 'I': 0, 'D': 0, 'X': 18
PI: 93.95973154362416

Group 48 unit1 1 vs unit2 1
Group 48 unit1 1 vs unit2 1 IGHV3-33-2

GENE ALIGN SEQ

```
GENE: GAGGTACAGCTCGTGGAGTCCGGAGAGGACCCAAGACAACCTGGGGG--A
MAP : GAGGTACAGCTGGTGGAGTCTGAAGAGGACCCAAGACAACCTGGGGGGGG-

GENE: TCCTTGAGACTCTCCTGTGCAGACTCTGGATTAACCTTCAGTAGCTACTG
MAP : TCGCTGAGACTCTCCTGTGCAGCCTCTGGATTAACCTTCAGTAGCTACTG

GENE: AATGAGCTCGGTTTCCCAGGCTCCAGGGAAGGGGCTGGAGTGAGTAGTAG
MAP : AATGAGCTCGGTTTCCCAGGCTCCAGGGAAGGGGCTGGAGTGAGTAGTAG

GENE: ATATACAGTGTGATGGAAGTCAGATATGTTATGCCCAATCTGTGAAGAGC
MAP : ATAAATAGTACGATAGAAGTCAGATATGTTATGCACAATCTGTGAAGAGC

GENE: AAATTCACCATCTCCAAAGAAAATGCCAAGAACTCACTGTATTTGCAAAT
MAP : AGATTCACCATCTCCAAAGAAAATGCCAAGAACTCACTGTATTTGCAAAT

GENE: GAACAGTCTGAGAGCAGAGGGCACAGCTGTGTGTTACTGTATGTGAGGCA
MAP : GAACAGTCTGAGAGCAGAGGGCACCGCCGTGTATTACTGTATGTGAGGCA
```

D7

```
GENE: CCAGGTA
MAP : CCAGGTA
```

D9

```
GENE: GACACAGTTTC
MAP : GGTACAGAATTTC
```

```
Alignment stats:  'M': 281, 'I': 2, 'D': 1, 'X': 16
PI: 93.66666666666667
```

Group 48 unit1 2 vs unit2 0

Group 48 unit1 2 vs unit2 0 IGHV3-54

GENE ALIGN SEQ

```
GENE: GGATCCCTGAGACTCTCCTGTGCAGACTCTGGATTAACCTTCAGTAGCTA
MAP : GGGTCCGTGAGACTCTCCTGTGCAGACTCTGGATTAACCTTCAGTAGCTA

GENE: CTGAATGAGCTCAGATTCCCAGGCTCCAGGGAAGGGGCTGGAGTGAGTAG
MAP : CTGAATGAGCTCAGTTTCCCAGGCTCCAGGGAAGGGGCTGGAGTGAGTAG

GENE: TAGATATATAGTACGATAGAAGTCAGATATGTTATGCACAATCTGTGAAG
MAP : TAGATAAATAGTACGATACAAGTCAGATATGTTATGCACAAACTGTGAAG

GENE: AGCAGATTCACCATCTCCAAAGAAAATGCCAAGAACTCACTCTGTTTGCA
MAP : AGCAGATTCACCATCTCCAAAGAAAATGCCAAGAACTCACTCCATTTGCA

GENE: AATGAACAGTCTGAGAGCAGAGGGCACAGCTGTGTGTTACTGTATGTGAG
MAP : AATGAACGGTCTGAGAACAGAGGGCACAACTGTGTGTTACTGTATGTGAG
```

D7
```
GENE: GCACCAG
MAP : GCACCAG
```

D9
```
GENE: ACAGACACAGA
MAP : ACAGACACAGA
```

```
Alignment stats:  'M': 239, 'I': 0, 'D': 0, 'X': 11
PI: 95.6
```

Group 48 unit1 2 vs unit2 0

Group 48 unit1 2 vs unit2 0 IGHV4-55

GENE ALIGN SEQ

```
GENE: CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGAC
MAP : CAGGTGCAGCTACAGCAGTGGGGTGCAGGACTGGTGAAGCCTTCGGAGAC

GENE: CCTGTCCCTCATCTGCGCTGTCTCTGGTGACTCCATCAG----------CA
MAP : CCTGTCCCTCACCTGCGCTGTCTATGGTGGGTCCTTCAGTGATTATGGC-

GENE: GTGGTAACTGGTGAATCTGGGTCCGCCAGCCCCCCAGGGAAGGGGCTGGAG
MAP : -TGGAACTGGA-----------TCCGCCAGCCCCCCAGGGAAGGGGCTGGAG

GENE: TGGATTGGGGAAATCCATCATAGTGGGAGCACCTACTACAACCCGTCCCT
MAP : TGGATTGGGTACATCGTTAGTAGTGGGAGAACCAACTACAACCCGTCCCT

GENE: CAAGAGTCGAATCACCATGTCCGTAGACACGTCCAAGAACCAGTTCTACC
MAP : CAAGAGTCGAGTCACCATGTCAGTAGACACGTCCAAGAACCAGTTCTCCC

GENE: TGAAGCTGAGCTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGCG
MAP : TGAAGCTGAGCTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGCG

GENE: AGATA
MAP : AGAGG
```

D7

```
GENE: CACAGTG
MAP : CACAGTG
```

D9

```
GENE: GACACAAACCT
MAP : GATAAAAACCT
```

```
Alignment stats:  'M': 256, 'I': 9, 'D': 12, 'X': 28
PI: 83.93442622950819
```

Group 48 unit1 2 vs unit2 1

Group 48 unit1 2 vs unit2 1 IGHV3-54

GENE ALIGN SEQ

```
GENE: GG--ATCCCTGAGACTCTCCTGTGCAGACTCTGGATTAACCTTCAGTAGC
MAP : GGGG-TCGCTGAGACTCTCCTGTGCAGCCTCTGGATTAACCTTCAGTAGC

GENE: TACTGAATGAGCTCAGATTCCCAGGCTCCAGGGAAGGGGCTGGAGTGAGT
MAP : TACTGAATGAGCTCGGTTTCCCAGGCTCCAGGGAAGGGGCTGGAGTGAGT

GENE: AGTAGATATATAGTACGATAGAAGTCAGATATGTTATGCACAATCTGTGA
MAP : AGTAGATAAATAGTACGATAGAAGTCAGATATGTTATGCACAATCTGTGA

GENE: AGAGCAGATTCACCATCTCCAAAGAAAATGCCAAGAACTCACTCTGTTTG
MAP : AGAGCAGATTCACCATCTCCAAAGAAAATGCCAAGAACTCACTGTATTTG

GENE: CAAATGAACAGTCTGAGAGCAGAGGGCACAGCTGTGTGTTACTGTATGTG
MAP : CAAATGAACAGTCTGAGAGCAGAGGGCACCGCCGTGTATTACTGTATGTG

GENE: AG
MAP : AG
```

D7
```
GENE: GCACCAG
MAP : GCACCAG
```

D9
```
GENE: ACAGACACAGA
MAP : ACAGGTACAGA
```

Alignment stats: 'M': 239, 'I': 2, 'D': 1, 'X': 10
PI: 94.84126984126983

Group 48 unit1 2 vs unit2 1 IGHV4-55

GENE ALIGN SEQ

```
GENE: 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
MAP : 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

GENE: C C T G T C C C T C A T C T G C G C T G T C T C T G G T G A C T C C A T C A G C A G T G G T A A C T
MAP : 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

GENE: G G T G A A T C T G G G T C C G C C A G C C C C C 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
MAP : 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

GENE: G A A A T C C A T C A T A G T G G G A G C A C C T A C T A C A A C C C G T C C C T C A A G A G T C G
MAP : G G T A T C T A T T C C A G T G G G A G C A C C T A C T A C A A C C C G T C C C T C A A G A G T C G

GENE: A A T C A C C A T G T C C G T A G A C A C G T C C A A G A A C C A G T T C T A C C T G A A G C T G A
MAP : 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

GENE: 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 T A
MAP : 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

```
GENE: C A C A G T G
MAP : C A C A G T G
```

D9

```
GENE: G A C A C A A A C C T
MAP : G A C A A A A A C C T
```

```
Alignment stats:  'M': 270, 'I': 0, 'D': 3, 'X': 23
PI: 91.21621621621621
```

Group 48 unit1 3 vs unit2 0
Group 48 unit1 3 vs unit2 0 IGHV4-80

GENE ALIGN SEQ

```
GENE: GTGCAGCTGCAGGAGTGGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCT
MAP : GTGCAGCTACAGCAGTGGGGGTGCAGGACTGGTGAAGCCTTCGGAGACCCT

GENE: GTCCCTCACATGCGCTGTCT-CTGGTGACTCCATCAGCAGTGGTAACTGG
MAP : GTCCCTCACCTGCGCTGTCTA----------------------------TGG

GENE: TGG------------------AGCTGG-------GTCCGCCAGTCCCCAGG
MAP : TGGGTCCTTCAGTGATTATG-GCTGGAACTGGA-TCCGCCAGCCCCCAGG

GENE: GAAGGGGCTGGAATGGATTGGATACATCTATTATAGTGGGAGGAGCTACT
MAP : GAAGGGGCTGGAGTGGATTGGGTACATCGTTAGTAGTGGGAGAACCAACT

GENE: ACACCCCGTCCCTCAGGAGTTGAGTCACCATGTCAATAGAAACGTCCAAG
MAP : ACAACCCGTCCCTCAAGAGTCGAGTCACCATGTCAGTAGACACGTCCAAG

GENE: AACCAGTTTTTCCCTGAAGCTGAGCTCTGTGACCGCA
MAP : AACCAGTTCTCCCCTGAAGCTGAGCTCTGTGACCGC-
```

D7

```
GENE: GGGAGGC
```

D9

```
GENE: GCTCAGGACCA
```

Alignment stats: 'M': 211, 'I': 25, 'D': 29, 'X': 21
PI: 73.77622377622379

Group 48 unit1 3 vs unit2 1

Group 48 unit1 3 vs unit2 1 IGHV7-81

GENE ALIGN SEQ

```
GENE: CAGGTGCAGCTGGTGCAGTCTGGCCATGAGGTGAAGCAGCCTGGGG-CC-
MAP : CGAGTGCAGCTGGTGCAGTCTGGGCCTGAGGTGAAGCAGCCTGGGGACCG

GENE: TCAGTGAAGGTCTCCTGCAAGGCTTCTGGTTACAGTTTCACCACCTATGG
MAP : ---GTGAAGTTCTCCTGCAAGGCTTCTGGTTAAACTGTCATCACCTATGG

GENE: TATGAATTGGGTGCCACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGAT
MAP : TATGAATTGGATATGACAGACCCCAGGACAGGGGCTTGAGTGGATGGAAT

GENE: GGTTCAAC--ACCTACACTGG-GAACCCAACATATGCCCAGGGCTTCACA
MAP : GGATCATCCTACC----CTGGTGAACCCAACGTATGCCCACAGCTTCACA

GENE: -GGACGGTTTGTCTTCTCCATGGACACCTCTGCCAGCACAGCATACCTGC
MAP : C--ACGGTTTGTCTTCTCCATGGACACATCTGTCAGCATGGCAGATCTGC

GENE: AGATCAGCAGCCTAAAAGGCTGAGGACATGGCCATGTATTACTGTGCGAGA
MAP : AGACTAGCTGCCTGAAGACTGAGGATGCAGCCATTTATTACTGTGTGAGG

GENE: TA
MAP : TA
```

D7
```
GENE: CACCATG
MAP : CACCGTG
```

D9
```
GENE: GTCAGAAATCC
MAP : TTTAGAAACCC
```

Alignment stats: 'M': 247, 'I': 6, 'D': 9, 'X': 40
PI: 81.78807947019867

Group 68 unit1 1 vs unit2 0

Group 68 unit1 1 vs unit2 0 IGHV1-69D

GENE ALIGN SEQ

```
GENE: CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTC
MAP : CAGGACCAGATGCAGCAGTCTGGGGCTGAGGTGAGGAAGCCTGGGACCTC

GENE: GGTGAAGGTCTCCTGCAAGGCTTCTGGAGGCACCT-----TCAG--------
MAP : AGTGAAGGTTTCTTGCAAGGTTTCTGGATATACCTAAAG-CAGGTTACGT

GENE: --CAGCTATGCTATCAGCTGGGTGCGACAGGCCCCTGGACAAGGGCTTGA
MAP : ATCAGCTATCATATCAGCTGGGTGCGACAGGTCCCTGGACAAGGGCTTGA

GENE: GTGGATGGGAGGGATCATCCCTATCTTTGGTACAGCAAACTACGCACAGA
MAP : ATGGATGGGGATGGATCATCACTGGCAATGGTGACACAAACTATGCACAGA

GENE: AGTTCCAGGGCAGAGTCACGCGATTACCGCGGACGAATCCACGAGCACAGCC
MAP : AGTTCCAGGGCAGAGTCACCATGACCAGGGACACGTCCACAAGCACAGCC

GENE: TACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTG
MAP : TACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTG

GENE: TGCGAGAGA
MAP : TGCGAGAGA
```

D7
```
GENE: CACAGTG
MAP : CACAGTG
```

D9
```
GENE: GTCAGAAACCC
MAP : GTCAGAAACCC
```

```
Alignment stats:  'M': 258, 'I': 13, 'D': 1, 'X': 37
PI: 83.49514563106796
```

Group 68 unit1 1 vs unit2 1

Group 68 unit1 1 vs unit2 1 IGHV1-69D

GENE ALIGN SEQ

```
GENE: 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
MAP : 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

GENE: 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
MAP : 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

GENE: 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
MAP : 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

GENE: 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
MAP : 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

GENE: A G T C A C G A T T A C C G C G G A C G A A T C C A C G A G C A C A G C C T A C A T G G A G C T G A
MAP : 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

GENE: 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
MAP : 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

```
GENE: C A C A G T G
MAP : C A C A G T G
```

D9

```
GENE: G T C A G A A A C C C
MAP : 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 68 unit1 1 vs unit2 1

Group 68 unit1 1 vs unit2 1 IGHV2-70

GENE ALIGN SEQ

```
GENE: CAGGTCACCTTGAGGGAGTCTGGTCCTGCGCTGGTGAAACCCACACAGAC
MAP : CAGACCACCTTGAAGGAGTCTGGTCCTGCGCTGGTGAAATCCACACAGAC

GENE: CCTCACACTGACCTGCACCTTCTCTGGGTTCTCACTCAGCACTAGTGGAA
MAP : CCTCACGCTGACCTGCACCTTCTCTGGGTTCTCACTCAGCACTAGTGGAG

GENE: TGTGTGTGAGCTGGATCCGTCAGCCCCCAGGGAAGGCCCTGGAGTGGCTT
MAP : TGGGTGTGGGCTGGATCCGTCAGCCCCCAGGGAAGGCCCTGGAGTGGCTT

GENE: GCACTCATTGATTGGGATGATGATAAATACTACAGCACATCTCTGAAGAC
MAP : GCAAGCATTGATTGGGATGATGATAAATACTACAGCCCATCTCTGAAGAG

GENE: CAGGCTCACCATCTCCAAGGACACCTCCAAAAACCAGGTGGTCCTTACAA
MAP : CAGGCTCACCATCTCCAAGGACACCTCCAAAAACCAGGTGGTCGTTACAA

GENE: TGACCAACATGGACCCCTGTGGACACAGCCACGTATTACTGTGCACGGATA
MAP : TGACCAACATGGACCCCTGTGGACACAGCCACATATTACTGTGCACGGAGA

GENE: C
MAP : C
```

D7
```
GENE: CACAGAG
MAP : CACAGAG
```

D9
```
GENE: TACAAGAACCC
MAP : TACAAGAACTC
```

```
Alignment stats:  'M': 286, 'I': 0, 'D': 0, 'X': 15
PI: 95.01661129568106
```

Group 68 unit1 1 vs unit2 2
Group 68 unit1 1 vs unit2 2 IGHV1-69D

GENE ALIGN SEQ

```
GENE: CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTC
MAP : CAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTC

GENE: GGTGAAGGTCTCCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTA
MAP : AGTGAAGATCTCCTGCAAGGTTTCTGAAGACACCTTCAGCAGCTATGCTA

GENE: TCAGCTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGAGGG
MAP : TCAGCTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGAGTG

GENE: ATCATCCCTATCTTTGGTACAGCAAACTACGCACAGAAGTTCCAGGGCAG
MAP : ATCATTCCTGTTGCTGGTATAACAAACTACGCACAGAAGTTTCAGGGCAG

GENE: AGTCACGATTACCGCGGACGAATCCACGAGCACAGCCTACATGGAGCTGA
MAP : AGTCACGATTACTGCGGACACATCCACGAGCACAGCCCACATGGAGCTGA

GENE: GCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGA
MAP : GCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGC------
```

D7
```
GENE: CACAGTG
```

D9
```
GENE: GTCAGAAACCC
```

Alignment stats: 'M': 271, 'I': 0, 'D': 6, 'X': 19
PI: 91.55405405405406

Group 68 unit1 1 vs unit2 2 IGHV2-70

GENE ALIGN SEQ

```
GENE: CAGGTCACCTTGAGGGAGTCTGGTCCTGCGCTGGTGAAACCCACACAGAC
MAP : CAGGTCACCTTGAAGGAGTCTGGTCCTGCGTTGGTGAAACCCACACAGAC

GENE: CCTCACACTGACCTGCACCTTCTCTGGGTTCTCACTCAGCACTAGTGGAA
MAP : CCTCACGCTGACCTGCACCTTCTCTGGGTTCTCACTCAGCACTAGTGGAG

GENE: TGTGTGTGAGCTGGATCCGTCAGCCCCCAGGGAAGGCCCTGGAGTGGCTT
MAP : TGGGTGTGGGCTGGATCCGTCAGCCCCCAGGGAAGGCCCTGGAGTGGCTT

GENE: GCACTCATTGATTGGGATGATGATAAATACTACAGCACATCTCTGAAGAC
MAP : GCAAGAATTGATTGGGATGATGATAAATACTACAGCCCATCTCTGAAGAG

GENE: CAGGCTCACCATCTCTCCAAGGACACCTCCAAAAACCAGGTGGTCCTTACAA
MAP : CAGGCTCACCATCTCTCCAAGGACACCTCCAAAAACCAGGTGGTCGTTACAA

GENE: TGACCAACATGGACCCCTGTGGACACAGCCACGTATTACTGTGCACGGATA
MAP : TGACCAACATGGACCCCTGTGGACACAGCCACATATTACTGTGCACGGATA

GENE: C
MAP : C
```

D7
```
GENE: CACAGAG
MAP : CACAGAG
```

D9
```
GENE: TACAAGAACCC
MAP : TACAAGAACCC
```

```
Alignment stats:  'M': 288, 'I': 0, 'D': 0, 'X': 13
PI: 95.68106312292359
```