

UAMs and RSSs of genes in syntney block alginments

Group 3 with 4 units in hum and 5 units in org
Group 3 unit1 1 vs unit2 0 IGHD5-18

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

GENE ALIGN SEQ
HUM: G T G G A T A C A G C T A T G G T T A C
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': 14, 'I': 0, 'D': 0, 'X': 6
PI: 70.0

Group 3 with 4 units in hum and 5 units in org
Group 3 unit1 1 vs unit2 0 IGHD4-17

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 A 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 - - - A C T A 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': 15, 'I': 3, 'D': 0, 'X': 1
PI: 78.94736842105263

Group 3 with 4 units in hum and 5 units in org
Group 3 unit1 1 vs unit2 0 IGHD3-16

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 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
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 C A
ORG: C A C A G T G

D9
HUM: A T C A G A A A C C C
ORG: 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 with 4 units in hum and 5 units in org
Group 3 unit1 1 vs unit2 0 IGHD2-15

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 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
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 C A A A G C C
ORG: 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 with 4 units in hum and 5 units in org
Group 3 unit1 1 vs unit2 0 IGHD1-14

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

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

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

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

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

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

Group 3 with 4 units in hum and 5 units in org
Group 3 unit1 1 vs unit2 0 IGHD6-13

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 C A 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 1 vs unit2 1 IGHD5-18

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

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

D7
HUM: C A C A G T G
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': 18, 'I': 3, 'D': 0, 'X': 2
PI: 78.26086956521739

Group 3 with 4 units in hum and 5 units in org
Group 3 unit1 1 vs unit2 1 IGHD4-17

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 A 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 A C T A 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': 12, 'I': 0, 'D': 0, 'X': 4
PI: 75.0

Group 3 with 4 units in hum and 5 units in org
Group 3 unit1 1 vs unit2 1 IGHD3-16

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 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
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 C

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

D9
HUM: A T C A G A A A C C C
ORG: 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 with 4 units in hum and 5 units in org
Group 3 unit1 1 vs unit2 1 IGHD2-15

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 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
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 C A A A G C C
ORG: 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 with 4 units in hum and 5 units in org
Group 3 unit1 1 vs unit2 1 IGHD1-14

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

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

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

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

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

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

Group 3 with 4 units in hum and 5 units in org
Group 3 unit1 1 vs unit2 1 IGHD6-13

U9
HUM: A G G T T T C T G A A
ORG: 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 C A 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': 21, 'I': 3, 'D': 0, 'X': 0
PI: 87.5

Group 3 with 4 units in hum and 5 units in org
Group 3 unit1 1 vs unit2 2 IGHD5-18

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

GENE ALIGN SEQ

HUM: G T G G A T A C A G C T A T G G T T A C
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': 14, 'I': 0, 'D': 0, 'X': 6
PI: 70.0

Group 3 with 4 units in hum and 5 units in org
Group 3 unit1 1 vs unit2 2 IGHD4-17

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 A 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 - - - A C T A 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': 15, 'I': 3, 'D': 0, 'X': 1
PI: 78.94736842105263

Group 3 with 4 units in hum and 5 units in org
Group 3 unit1 1 vs unit2 2 IGHD3-16

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 - - - - - 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
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 -

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

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

D9
HUM: A T C A G A A A C C C
ORG: 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 with 4 units in hum and 5 units in org
Group 3 unit1 1 vs unit2 2 IGHD2-15

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 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
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 C A A A G C C
ORG: 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 with 4 units in hum and 5 units in org
Group 3 unit1 1 vs unit2 2 IGHD1-14

U9

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

U7

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

GENE ALIGN SEQ

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

D7

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

D9

HUM: G T C A A A A C T G
ORG: G T C C 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 1 vs unit2 2 IGHD6-13

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 C A 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 1 vs unit2 3 IGHD5-18

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

GENE ALIGN SEQ
HUM: G T G G A T A C A G C T A T G G T T A C
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': 16, 'I': 0, 'D': 0, 'X': 4
PI: 80.0

Group 3 with 4 units in hum and 5 units in org
Group 3 unit1 1 vs unit2 3 IGHD4-17

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 A 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 A C T A 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': 16, 'I': 0, 'D': 0, 'X': 0
PI: 100.0

Group 3 with 4 units in hum and 5 units in org
Group 3 unit1 1 vs unit2 3 IGHD3-16

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 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
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 C A
ORG: C A C A G T G

D9
HUM: A T C A G A A A C C C
ORG: 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 with 4 units in hum and 5 units in org
Group 3 unit1 1 vs unit2 3 IGHD2-15

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

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

Group 3 with 4 units in hum and 5 units in org
Group 3 unit1 1 vs unit2 3 IGHD1-14

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

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

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

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

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

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

Group 3 with 4 units in hum and 5 units in org
Group 3 unit1 1 vs unit2 3 IGHD6-13

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 C A 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 T G

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 1 vs unit2 4 IGHD5-18

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

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

D7
HUM: C A C A G T G
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': 18, 'I': 3, 'D': 0, 'X': 2
PI: 78.26086956521739

Group 3 with 4 units in hum and 5 units in org
Group 3 unit1 1 vs unit2 4 IGHD4-17

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 A 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 A C T A 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': 0, 'D': 0, 'X': 2
PI: 87.5

Group 3 with 4 units in hum and 5 units in org
Group 3 unit1 1 vs unit2 4 IGHD3-16

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 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
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 C A
ORG: C A C A G T G

D9
HUM: A T C A G A A A C C C
ORG: 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 with 4 units in hum and 5 units in org
Group 3 unit1 2 vs unit2 0 IGHD5-12

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

GENE ALIGN SEQ
HUM: G T G G A T A T A G - T G G C T A C G A T T A C
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': 18, 'I': 1, 'D': 4, 'X': 1
PI: 75.0

Group 3 with 4 units in hum and 5 units in org
Group 3 unit1 2 vs unit2 0 IGHD4-11

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

D9
HUM: G 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': 14, 'I': 4, 'D': 1, 'X': 1
PI: 70.0

Group 3 with 4 units in hum and 5 units in org
Group 3 unit1 2 vs unit2 0 IGHD3-10

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

HUM: A - - C
ORG: 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 C C
ORG: 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 with 4 units in hum and 5 units in org
Group 3 unit1 2 vs unit2 0 IGHD2-8

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 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
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 C A A A G C C
ORG: 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 with 4 units in hum and 5 units in org
Group 3 unit1 2 vs unit2 0 IGHD1-7

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

D9
HUM: G T C C A A A A C G G
ORG: 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 with 4 units in hum and 5 units in org
Group 3 unit1 2 vs unit2 0 IGHD6-6

U9
HUM: A A 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 A G T A T A G C A G C - - T C - - G T C 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': 16, 'I': 4, 'D': 1, 'X': 1
PI: 72.72727272727273

Group 3 with 4 units in hum and 5 units in org
Group 3 unit1 2 vs unit2 1 IGHD5-12

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

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

D7
HUM: C A C A G T G
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': 21, 'I': 0, 'D': 0, 'X': 2
PI: 91.30434782608695

Group 3 with 4 units in hum and 5 units in org
Group 3 unit1 2 vs unit2 1 IGHD4-11

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

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

D9
HUM: G 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': 0, 'D': 0, 'X': 2
PI: 87.5

Group 3 with 4 units in hum and 5 units in org
Group 3 unit1 2 vs unit2 1 IGHD3-10

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

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

D9
HUM: A T C A A A A A C C C
ORG: 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 with 4 units in hum and 5 units in org
Group 3 unit1 2 vs unit2 1 IGHD2-8

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 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
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 C A A A G C C
ORG: 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 with 4 units in hum and 5 units in org
Group 3 unit1 2 vs unit2 1 IGHD1-7

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

D9
HUM: G T C C A A A A C G G
ORG: 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 with 4 units in hum and 5 units in org
Group 3 unit1 2 vs unit2 2 IGHD5-12

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

GENE ALIGN SEQ
HUM: G T G G A T A T A G - T G G C T A C G A T T A C
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': 18, 'I': 1, 'D': 4, 'X': 1
PI: 75.0

Group 3 with 4 units in hum and 5 units in org
Group 3 unit1 2 vs unit2 2 IGHD4-11

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

D9
HUM: G 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': 3, 'D': 0, 'X': 0
PI: 84.21052631578947

Group 3 with 4 units in hum and 5 units in org
Group 3 unit1 2 vs unit2 2 IGHD3-10

U9
HUM: A G G T T T G G G 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 G T T C G G G G A G T T A T T A T A 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 C 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 2 vs unit2 2 IGHD2-8

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 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
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 C A A A G C C
ORG: 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 with 4 units in hum and 5 units in org
Group 3 unit1 2 vs unit2 2 IGHD1-7

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

D9
HUM: G T C C A A A A C G G
ORG: 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 with 4 units in hum and 5 units in org
Group 3 unit1 2 vs unit2 2 IGHD6-6

U9
HUM: A A 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 A G T A T A G C A G C T C G T C 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': 16, 'I': 0, 'D': 0, 'X': 2
PI: 88.88888888888889

Group 3 with 4 units in hum and 5 units in org
Group 3 unit1 2 vs unit2 3 IGHD5-12

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

GENE ALIGN SEQ

HUM: G T G - G A T A T A G T G G C T A C G A T T A C
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': 18, 'I': 1, 'D': 4, 'X': 1
PI: 75.0

Group 3 with 4 units in hum and 5 units in org
Group 3 unit1 2 vs unit2 3 IGHD4-11

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

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

D9
HUM: G 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': 14, 'I': 0, 'D': 0, 'X': 2
PI: 87.5

Group 3 with 4 units in hum and 5 units in org
Group 3 unit1 2 vs unit2 3 IGHD3-10

U9
HUM: A G G T T T G G G 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 G T T C G G G G A G T T A T T A T A 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 C C
ORG: 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 with 4 units in hum and 5 units in org
Group 3 unit1 2 vs unit2 3 IGHD2-8

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

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

Group 3 with 4 units in hum and 5 units in org
Group 3 unit1 2 vs unit2 3 IGHD1-7

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

D9
HUM: G T C C A A A A C G 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 2 vs unit2 4 IGHD5-12

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

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

D7
HUM: C A C A G T G
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': 21, 'I': 0, 'D': 0, 'X': 2
PI: 91.30434782608695

Group 3 with 4 units in hum and 5 units in org
Group 3 unit1 2 vs unit2 4 IGHD4-11

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

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

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

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

Group 3 with 4 units in hum and 5 units in org
Group 3 unit1 2 vs unit2 4 IGHD3-10

U9
HUM: A G G T T T G G G 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 G T T C G G G G A G T T A T T A T A 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 C C
ORG: 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 with 4 units in hum and 5 units in org
Group 3 unit1 3 vs unit2 0 IGHD5-5

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

GENE ALIGN SEQ
HUM: G T G G A T A C A G C T A T G G T T A C
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': 14, 'I': 0, 'D': 0, 'X': 6
PI: 70.0

Group 3 with 4 units in hum and 5 units in org
Group 3 unit1 3 vs unit2 0 IGHD3-3

U9
HUM: A G G T T T G G G 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 G A T T - - - - - T T T G G A G T G G T T A T T A T A C 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 C C
ORG: 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 with 4 units in hum and 5 units in org
Group 3 unit1 3 vs unit2 0 IGHD2-2

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 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
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 C A A A G C C
ORG: 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 with 4 units in hum and 5 units in org
Group 3 unit1 3 vs unit2 1 IGHD5-5

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

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

D7
HUM: C A C A G T G
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': 18, 'I': 3, 'D': 0, 'X': 2
PI: 78.26086956521739

Group 3 with 4 units in hum and 5 units in org
Group 3 unit1 3 vs unit2 1 IGHD4-4

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

GENE ALIGN SEQ
HUM: T G A C T A C A G T A A C T A C
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': 0, 'D': 0, 'X': 2
PI: 87.5

Group 3 with 4 units in hum and 5 units in org
Group 3 unit1 3 vs unit2 1 IGHD3-3

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

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

D9
HUM: A T C A A A A A C C C
ORG: 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 with 4 units in hum and 5 units in org
Group 3 unit1 3 vs unit2 1 IGHD2-2

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 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
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 C A A A G C C
ORG: 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 with 4 units in hum and 5 units in org
Group 3 unit1 3 vs unit2 2 IGHD5-5

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

GENE ALIGN SEQ
HUM: G T G G A T A C A G C T A T G G T T A C
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': 14, 'I': 0, 'D': 0, 'X': 6
PI: 70.0

Group 3 with 4 units in hum and 5 units in org
Group 3 unit1 3 vs unit2 2 IGHD4-4

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

GENE ALIGN SEQ
HUM: T G A C T A C A G T - - - A A C T A C
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': 3, 'D': 0, 'X': 0
PI: 84.21052631578947

Group 3 with 4 units in hum and 5 units in org
Group 3 unit1 3 vs unit2 2 IGHD3-3

U9
HUM: A G G T T T G G G 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 G A T T T T T G G A G T G G T - - - - - T A T T A T A C 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 C C
ORG: 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 with 4 units in hum and 5 units in org
Group 3 unit1 3 vs unit2 2 IGHD2-2

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 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
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 C A A A G C C
ORG: 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 with 4 units in hum and 5 units in org
Group 3 unit1 3 vs unit2 3 IGHD5-5

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

GENE ALIGN SEQ
HUM: G T G G A T A C A G C T A T G G T T A C
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': 16, 'I': 0, 'D': 0, 'X': 4
PI: 80.0

Group 3 with 4 units in hum and 5 units in org
Group 3 unit1 3 vs unit2 3 IGHD4-4

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

GENE ALIGN SEQ

HUM:	T	G	A	C	T	A	C	A	G	T	A	A	C	T	A	C
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': 14, 'I': 0, 'D': 0, 'X': 2
PI: 87.5

Group 3 with 4 units in hum and 5 units in org
Group 3 unit1 3 vs unit2 3 IGHD3-3

U9
HUM: A G G T T T G G G 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 G A T T T T T G G A G T G G T T A T T A T A C 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 C C
ORG: 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 with 4 units in hum and 5 units in org
Group 3 unit1 3 vs unit2 3 IGHD2-2

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 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
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 C A A A G C C
ORG: 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 with 4 units in hum and 5 units in org
Group 3 unit1 3 vs unit2 4 IGHD5-5

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

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

D7
HUM: C A C A G T G
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': 18, 'I': 3, 'D': 0, 'X': 2
PI: 78.26086956521739

Group 3 with 4 units in hum and 5 units in org
Group 3 unit1 3 vs unit2 4 IGHD4-4

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

GENE ALIGN SEQ
HUM: T G A C T A C A G T A A C T A C
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': 16, 'I': 0, 'D': 0, 'X': 0
PI: 100.0

Group 3 with 4 units in hum and 5 units in org
Group 3 unit1 3 vs unit2 4 IGHD3-3

U9
HUM: A G G T T T G G G 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 G A T T T T T G G A G T G G T T A T T A T A C 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 C C
ORG: 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 with 2 units in hum and 2 units in org
Group 23 unit1 1 vs unit2 0 IGHV3-47

GENE ALIGN SEQ

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

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

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

Group 23 with 2 units in hum and 2 units in org
Group 23 unit1 1 vs unit2 0 IGHV(III)-47-1

GENE ALIGN SEQ

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

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

Group 23 with 2 units in hum and 2 units in org
Group 23 unit1 1 vs unit2 1 IGHV3-47

GENE ALIGN SEQ

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

D7

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

D9

HUM:	G	A	T	A	C	A	A	A	C	T	T
ORG:	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 with 2 units in hum and 2 units in org
Group 23 unit1 1 vs unit2 1 IGHV(III)-47-1

GENE ALIGN SEQ

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

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

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

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

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

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

D7

HUM: C A C G 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': 284, 'I': 0, 'D': 0, 'X': 9
PI: 96.9283276450512

Group 48 with 4 units in hum and 2 units in org
Group 48 unit1 1 vs unit2 0 IGHV4-30-2

GENE ALIGN SEQ

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

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

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

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

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

HUM: A
ORG: A

D7

HUM: C A C A A 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': 273, 'I': 2, 'D': 5, 'X': 21
PI: 90.69767441860465

Group 48 with 4 units in hum and 2 units in org
Group 48 unit1 1 vs unit2 0 IGHV(II)-30-21

GENE ALIGN SEQ

HUM:	T	C	A	C	A	G	A	C	C	C	T	C	T	C	C	C	T	C	A	C	C	T	G	C	A	C	T	G	T	C	T	C	T	G	G	A	T	T	C	C	C	C	A	T	C	A	T	A	A	C
ORG:	T	C	G	C	A	G	A	C	C	C	T	C	T	C	C	C	T	C	A	C	C	T	G	C	A	C	T	G	T	C	T	C	T	G	G	A	T	T	C	C	C	C	A	T	C	A	T	A	A	C
HUM:	C	A	G	T	G	T	T	T	C	C	T	T	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
ORG:	C	A	G	T	G	T	T	T	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
HUM:	A	G	T	G	G	A	T	C	A	G	G	T	G	C	A	T	G	G	G	T	T	G	T	G	A	A	G	G	G	A	G	C	A	C	A	A	A	T	T	A	C	A	A	C	C	C	A	C	T	T
ORG:	A	G	T	G	G	A	T	C	A	G	G	T	G	C	A	T	G	G	G	T	T	G	T	G	A	A	G	G	G	A	G	C	A	C	A	A	A	T	T	A	C	A	A	C	C	-	A	C	T	T
HUM:	C	T	C	A	A	G	A	G	T	C	C	A	T	A	T	C	C	G	G	A	T	C	C	A	A	G	A	A	A	C	A	G	T	T	C	T	T	A	C	A	G	C	T	G	A	G	C	T	C	T
ORG:	C	T	C	A	A	G	A	G	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
HUM:	G	T	G	C	C	C	A	G	T	G	A	A	C	A	C	A	C	A	A	C	T	A	C	G	C	A	T	T	T	T	G	A	A	G	C	A	A	A	A	G	A	T	G	C	A	A	T	G	A	A
ORG:	G	T	G	C	C	C	A	G	T	G	A	A	C	A	C	A	C	A	A	C	T	A	T	G	C	A	T	T	T	T	A	A	G	C	A	A	A	A	G	A	G	G	C	A	A	T	G	A	G	
HUM:	G	G	G	C	C	T	T																																											
ORG:	A	G	G	A	C	T	T																																											
D7																																																		
HUM:	C	A	T	T	G	T	G																																											
ORG:	C	A	T	T	A	T	G																																											
D9																																																		
HUM:	C	A	G	G	G	G	T	G	A	A	T																																							
ORG:	C	A	G	G	G	G	T	G	C	A	T																																							

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

Group 48 with 4 units in hum and 2 units in org
Group 48 unit1 1 vs unit2 0 IGHV3-33-2

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 T C

HUM: C T T G A G A C T C T C C T G T G C A G A C T C T G G A T T A A C C T T C A G T A G C T A C T G A A
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: T G A G C T C G G T T T C C C A G G C T C C A G G G A A G G G G C T G G A G T G A G T A G T A G A T
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 C C A A T C T G 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 A 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 A G G G C A C A G C T G T G T G T T A C T G T A T G T G A G G C A
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': 280, 'I': 0, 'D': 0, 'X': 18
PI: 93.95973154362416

Group 48 with 4 units in hum and 2 units in org
Group 48 unit1 1 vs unit2 1 IGHV3-33-2

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 T T G A G A C T C T C C T G T G C A G A C T C T G G A T T A A C C T T C A G T A G C T A C T G
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 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
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 C C A A T C T G 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 A 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 A G G G C A C A G C T G T G T G T T A C T G T A T G T G A G G C A
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': 281, 'I': 2, 'D': 1, 'X': 16
PI: 93.66666666666667

Group 48 with 4 units in hum and 2 units in org
Group 48 unit1 2 vs unit2 0 IGHV3-54

GENE ALIGN SEQ

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

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

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

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

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

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

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

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

Group 48 with 4 units in hum and 2 units in org
Group 48 unit1 2 vs unit2 0 IGHV4-55

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 A C A G C A G T 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 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
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 -

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

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

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

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

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

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

Group 48 with 4 units in hum and 2 units in org
Group 48 unit1 2 vs unit2 1 IGHV3-54

GENE ALIGN SEQ

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

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

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

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

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

HUM: A G
ORG: A G

D7

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

D9

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

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

Group 48 with 4 units in hum and 2 units in org
Group 48 unit1 2 vs unit2 1 IGHV4-55

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

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

HUM: 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
ORG: 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

HUM: 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
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 T 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 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 with 4 units in hum and 2 units in org
Group 48 unit1 3 vs unit2 0 IGHV4-80

GENE ALIGN SEQ

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

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

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

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

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

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

D7
HUM: G G G A G G C

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

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

Group 48 with 4 units in hum and 2 units in org
Group 48 unit1 3 vs unit2 1 IGHV7-81

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

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

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

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

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

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

HUM: T A
ORG: T A

D7

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

D9

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

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

Group 68 with 2 units in hum and 3 units in org
Group 68 unit1 1 vs unit2 0 IGHV1-69D

GENE ALIGN SEQ

HUM:	C	A	G	G	T	G	C	A	G	C	T	G	G	T	G	C	A	G	T	C	T	G	G	G	G	C	T	G	A	G	G	T	G	A	A	G	A	A	G	C	C	T	G	G	G	T	C	C	T	C	
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	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	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	G	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': 258, 'I': 13, 'D': 1, 'X': 37
PI: 83.49514563106796

Group 68 with 2 units in hum and 3 units in org
Group 68 unit1 1 vs unit2 1 IGHV1-69D

GENE ALIGN SEQ

HUM: C A G G T G C A G C T G G T G C A G T C T G G G G C T G A G G T G A A G A A G C C T G G G T C C T C
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 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
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': 279, 'I': 0, 'D': 0, 'X': 17
PI: 94.25675675675676

Group 68 with 2 units in hum and 3 units in org
Group 68 unit1 1 vs unit2 1 IGHV2-70

GENE ALIGN SEQ

HUM:	C	A	G	G	T	C	A	C	C	T	T	G	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	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	T	G	T	G	T	G	A	G	C	T	G	G	A	T	C	C	G	T	C	A	G	C	C	C	C	C	A	G	G	G	A	A	G	G	C	C	C	T	G	G	A	G	T	G	G	C	T	T
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	T	C	A	T	T	G	A	T	T	G	G	G	A	T	G	A	T	G	A	T	A	A	A	T	A	C	T	A	C	A	G	C	A	C	A	T	C	T	C	T	G	A	A	G	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	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	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': 286, 'I': 0, 'D': 0, 'X': 15
PI: 95.01661129568106

Group 68 with 2 units in hum and 3 units in org
Group 68 unit1 1 vs unit2 2 IGHV1-69D

GENE ALIGN SEQ

HUM:	C	A	G	G	T	G	C	A	G	C	T	G	G	T	G	C	A	G	T	C	T	G	G	G	G	C	T	G	A	G	G	T	G	A	A	G	A	A	G	C	C	T	G	G	G	T	C	C	T	C	
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	O	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	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	
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	-	-	-	-	-	-					

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

Group 68 with 2 units in hum and 3 units in org
Group 68 unit1 1 vs unit2 2 IGHV2-70

GENE ALIGN SEQ

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

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	C	C

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