V genes pairwise similarity distribution

Family	% Iden	Len. Av.	# Seq	# Var. Pos.
IGHV1	0.85	291.1	42	43.7
IGHV1/OR15	0.88	292.7	14	35.1
IGHV1/OR21	None	296 *	1	-
IGHV2	0.90	291.6	25	29.2
IGHV2/OR16	None	301*	1	-
IGHV3	0.83	295.5	139	50.2
IGHV3/OR15	0.98	300.5	4	6.0
IGHV3/OR16	0.84	294.4	13	47.1
IGHV4	0.87	285.9	87	37.2
IGHV4/OR15	0.99	296 *	3	2.9
IGHV5	0.92	289.6	10	23.2
IGHV6	0.99	*305 *	2	3.0
IGHV7	0.86	292.7	9	40.9

Number of sequences : 350
Number of pairwise alignements : 61075
Alignement : Needleman-Wunsch
Gap penalty : -4
Substitution weight : -2

Len. Av. : Sequence Length average
Seq : Number of sequence in family
Var. Pos. : Number of variable position [(1-%Iden)* Len. Av.]

D genes pairwise similarity distribution
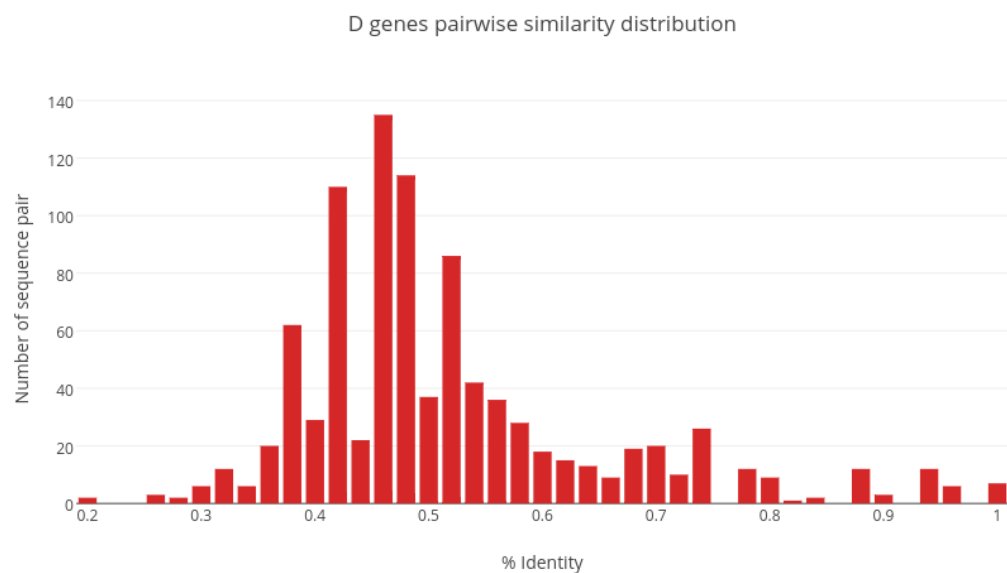
Family	% Iden	Len. Av.	# Seq	# Var. Pos.
IGHD1	0.79	17.6	5	3.7
IGHD1/OR15	1.0	17 *	2	0
IGHD2	0.77	30.2	8	6.9
IGHD2/OR15	1.0	31*	2	0
IGHD3	0.74	32.4	8	8.4
IGHD3/OR15	1.0	31*	2	0
IGHD4	0.83	16.7	4	2.8
IGHD4/OR15	1.0	19*	2	0
IGHD5	0.75	20.7	4	5.2
IGHD5/OR15	1.0	23*	2	0
IGHD6	0.78	19.5	4	4.3
IGHD7	None	11*	1	-

Number of sequences : 44
Number of pairwise alignements : 946
Alignement : Needleman-Wunsch
Gap penalty : -4
Substitution weight : -2

Len. Av. : Sequence Length average
Seq : Number of sequence in family
Var. Pos. : Number of variable position [(1-%Iden)* Len. Av.]

J genes pairwise similarity distribution
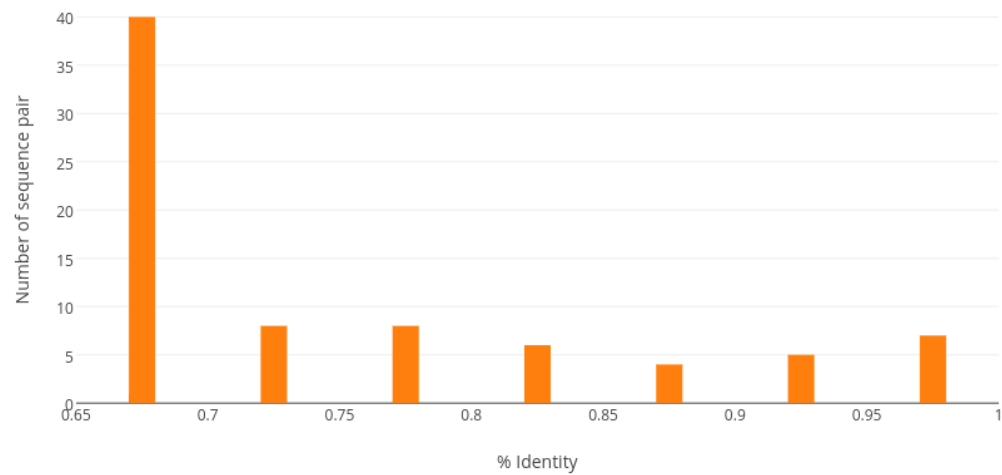
Family	% Iden	Len. Av.	# Seq	# Var. Pos.
IGHJ1	None	52 *	1	-
IGHJ2	None	53 *	1	-
IGHJ3	0.98	50 *	2	1
IGHJ4	0.95	48 *	3	2.4
IGHJ5	0.96	51 *	2	2.0
IGHJ6	0.94	62.5	4	3.7

Number of sequences : 13
Number of pairwise alignements : 78
Alignement : Needleman-Wunsch
Gap penalty : -4
Substitution weight : -2

Len. Av. : Sequence Length average
Seq : Number of sequence in family
Var. Pos. : Number of variable position [(1-%Iden)* Len. Av.]