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The Human Immunoglobulin Heavy Variable Genes

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Human genes · IMGT · Immunoglobulin · Heavy variable genes

Abstract
'Human Immunoglobulin Heavy Variable Genes', the fourth report of the 'IMGT Locus on Focus' section, comprises five tables entitled: (1) 'Number of human germline IGHV genes at 14q32.33 and potential repertoire'; (2) 'Human germline IGHV genes at 14q32.33'; (3) 'Human IGHV orphons on chromosome 15 (15q11.2)'; (4) 'Human IGHV orphons on chromosome 16 (16p11.2)', and (5) 'Human IGHV allele table'. These tables are available at the IMGT Marie-Paule page from IMGT, the international ImMunoGeneTics database (http://imgt.cnusc.fr:8104) created by Marie-Paule Lefranc, Université Montpellier II, CNRS, France.

Introduction

'Human Immunoglobulin Heavy Variable Genes' is the fourth report of the 'IMGT Locus on Focus' section launched in the April 1998 issue of *Experimental and Clinical Immunogenetics* [1], with the first report on the human immunoglobulin lambda variable (IGLV) genes and joining (IGLJ) segments [2], the second report on the human immunoglobulin kappa variable (IGKV) genes and joining (IGKJ) segments [3] and the third report on mouse *(Mus musculus)* IGKV genes and IGKJ segments [4]. This fourth report comprises five tables entitled: (1) 'Number of human germline IGHV genes at 14q32.33 and potential repertoire'; (2) 'Human germline IGHV genes at 14q32.33'; (3) 'Human IGHV orphons on chromosome 15 (15q11.2)'; (4) 'Human IGHV orphons on chromosome 16 (16p11.2)' and (5) 'Human IGHV allele table'. These tables 1–5 are available at the IMGT Marie-Paule page from IMGT, the international Immunogenetics da-

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Table 1. Number of human germline IGHV genes at 14q32.33 and potential repertoire

References

Matsuda et al. J. Exp. Med., 188, 1-15 (1998) and references in Table 2

123-129 IGHV genes belonging to 7 subgroups, on 900 kilobases :

39-45 FUNCTIONAL
4 ORF (Open Reading Frame)
78 PSEUDOGENE
1 ORF or PSEUDOGENE
1 FUNCTIONAL or PSEUDOGENE
5 Not sequenced

Potential repertoire : 39-45 FUNCTIONAL IGHV genes belonging to 6 or 7 subgroups

Subgroup	Functional	ORF	Pseudogene	Total
IGHV1	9	-	5	14
IGHV2	3	-	1	4
IGHV3	18-20**(+1)*	3(+1)*	24(+2)*	47-49**
IGHV4	7-10**	-	2	9-12**
IGHV5	1	-	1	2
IGHV6	1	-	-	1
IGHV7	0-1**	1	4	5-6**
IGHV(II)	-	-	22	22
IGHV(III)	-	-	18	18
IGHV(IV)	-	-	1	1
Total	39-45(+1)*	4(+1)*	78(+2)*	123-129**

* ORF or PSEUDOGENE (IGHV3-47)
* FUNCTIONAL or PSEUDOGENE (IGHV3-11)
** Allelic polymorphism by insertion/deletion :
- 50 kb insertion of 5 genes (3-30-5, 4-30-4, 3-30-3, 4-30-2, 4-30-1) in 45 % Caucaso des
- IGHV7-4-1

II, III, IV (in parentheses) refer to the clans, for the pseudogenes which could not be assigned to subgroups with functional genes. All these pseudogenes have truncations.
Clans comprise, respectively:
- clan I: IGHV1, IGHV5 and IGHV7 subgroup genes
- clan II: IGHV2, IGHV4 and IGHV6 subgroup genes, and pseudogenes IGHV(II)
- clan III: IGHV3 subgroup genes, and pseudognes IGHV(III)
- clan IV: one pseudogene IGHV(IV)-44

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tabase (http://imgt.cnusc.fr:8104) created by Marie-Paule Lefranc, Université Montpellier II, CNRS, France [5, 6]. Descriptions of functionality (functional, open reading frame, pseudogene) and of mutations [7] are according to the IMGT scientific chart, available at the IMGT Marie-Paule page. Nucleotide and amino acid numbering of the IGHV alleles is according to the IMGT unique numbering [6, 7].

Table 2. Human germline IGHV genes at 14q32.33

Fct : FUNCTIONALITY
F : Functional
P : Pseudogene
ORF : Open Reading Frame
R : Rearranged
T : Transcribed
Pr : Translated into protein
"+" or "-" indicates if the gene sequences have been found (+) or not been found (-) rearranged (R), transcribed (T), and/or translated into protein (Pr). Arbitrarily that information is shown on the first line of each gene when the data have been confirmed by several studies.
Sequences in bold have been mapped : "mapped" refers to sequences which have been obtained from clones (phages, cosmids, YACs...) either by subcloning or PCR, and does not apply to sequences obtained directly from genomic DNA.

IGHV subgroup	IGHV gene name	Fct	R	T	Pr	Reference sequences	Accession numbers	Sequences from the literature
1	**1-2**	F	+	+	+	**V35**[25]/**VI-2b**[37](1)	X07448	
		F	+			**VI-2**[37]	X62106	DP-75[Z14071] / hv1L1[X59704][27]
		F				**1-1**[5]	X92208	
		F	+			DP-8[39]	Z12310	
	1-3	F	+	+	+	**VI-3b**[37]	X62109	DP-25[Z12327][39]
		F				**VI-3**[37]	X62107	
	1-8	F	+	+	+	**V1-8**[26]	M99637	DP-15[Z12317][39]
	1-12	P	-	-	-	**22.1**[5] (2)	X92210	
		P				**V1-12P**[26] (2)	M99638	
	1-14	P	-	-	-	**V1-14P**[26] (3)	M99639	DP-16[Z12318][39]
	1-17	P	-	-	-	**V1-17P**[26] (4)	M99640	
		P				DP-6[39] (5)	Z12308	
	1-18	F	+	+	+	**V1-18**[26]	M99641	DP-14[Z12316][39]
		F				VH1GRR[52] (62)	X60503	
	1-24	F	+	+	+	**V1-24P**[26] (6)	M99642	DP-5[Z12307][39]
	1-45	F	+	+	+	**7-2**[5]	X92209	(**V1-45**[M99645][26] (7))
		F				DP-4[39]	Z12306	(**V1-45**[M99645][26] (7))
		F				**COS-5**	Z17391	
	1-46	F	+	+	+	**21-2**[5]	X92343	DP-7[Z12309][39] / **3-1**[X92207][5] / hv1f10[L06611][38] / **V1-46**[M99646][26] (60)
		F				**HG3**[30]	J00240	
		F				hv1f10t[38] (62)	L06612	
	1-58	F	+	+	+	**V71-5**[22] (6)	M29809	DP-2[Z12304][39]
	1-67	P	-	-	-	**8-2**[5] (8)	X92212	DP-11[Z12313][39]
		P				**YAC-8**[12] (8)	Z27507	
	1-68	P	-	-	-	**1-68 P** [61]		
	1-69	F	+	+	+	**YAC-7**[12]	L22582	DP-10[Z12312][39] / HULGLVH1[X92298][13] / **DA-6**[Z29982][12] / 10M28[34] / 13M28[34]
		F				hv1051[49]	Z27506	RR.VH1.1[X67902][41] (9) / 1M27[34] / 5M27[34] /
		F				57GTA8[19]	X92340	
		F				hv1263[53] (62)	M83132	
		F				RR.VH1.2[41] (62)	X67905	

IGHV subgroup	IGHV gene name	Fct	R	T	Pr	Reference sequences	Accession numbers	Sequences from the literature
	1-c	F				**COS-19**	Z18904	
	1-e	F				hv1051K[49]	L22583	7M27[34], DP-88[Z49804]
		F				**DA-2**[12]	Z29978	
	1-f	F				DP-3[39]	Z12305	
		F				**DA-1**[12]	Z29977	
	NL	P				V201[59]	M13911	
2	**2-5**	F	+	+	+	**VII-5**[37] (10)	X62111	
		F				DP-76	Z14072	**VII-5b**[X62108][37] (11)
		F				WAD4GL[44]	X93619	
		F				S12.2[2] (62)	L21963	
		F				S12.4[2] (62)	L21964	
		F				S12.6[2] (62)	L21966	
		F				S12.8[2] (62)	L21968	
		F				S12.12[2] (62)	L21971	
		F				S12.14[2] (62)	L21972	
	2-10	P	-	-	-	**V2-10P**[26] (12)	M99647	**COS-1**[Z17387]
	2-26	F	+	+	+	**V2-26**[26] (13)	M99648	DP-26[Z12328][39]
	2-70	F	+	+	+	S12-9[2]	L21969	DP-27[Z12329][39]
		F				VH2-MC2	X92241	VH2-MC2a[X92242][8] / VH2-MC2c[X92244] / VH2-MC2e[X92246][8]
		F	+			VH2-MC1[8]	X92238	VH2-MC1b[X92240] [8] (**DA-7**[Z29983][12])
		F				DP-28[39]	Z12330	(**DA-7**[Z29983][12])
		F				**YAC-3**[12]	Z27502	
		F				VH2-MC1a[8] (62)	X92239	
		F				VH2-MC2b[8] (62)	X92243	
		F				VH2-MC2d[8] (62)	X92245	
		F				S12-1[2] (62)	L21962	
		F				S12-5[2] (62)	L21965	
		F				S12-7[2] (62)	L21967	
		F				S12-10[2] (62)	L21970	
3	**3-6**	P	-	-	-	**V3-6P**[26] (14)	M99650	DP-60[Z12360][39]
	3-7	F	+	+	+	**V3-7**[26]	M99649	DP-54[Z12354][39] / HHG19[X62128][23]
		F				VH3-11[48] (62)	X92288	
	3-9	F	+	+	+	**V3-9**[26]	M99651	DP-31[Z12333][39] / A/B/C/D[47]
	3-11	F	+	+	+	**V3-11**[26]	M99652	DP-35[Z12337][39] / 22-2B[X92220][5]
		P	+			**hv3.3**[40] (15)	M15496	
		F				VH3-8[48] (62)	X92287	
	3-13	F	+	+	+	**13-2**[5]	X92217	DP-48[Z12348][39]
		F				**V3-13**[26]	M99653	
	3-15	F	+	+	+	**9-1**[5]	X92216	DP-38[Z12338][39] / LSG1.1[M99398][1] / LSG5.1[M99405][1]LSG7.1[M99407][1] / RCG1.1[M99411] / VHGL3.1[Z14216][14] (50)
		F	+			**V3-15**[26]	M99654	
		F				LSG8.1[1] (62)	M99408	LSG9.1[M99409][1] (62) /LSG10.1[M99399][1] (62)

(continued)

Table 2 (continued)

IGHV subgroup	IGHV gene name	Fct	R	T	Pr	Reference sequences	Accession numbers	Sequences from the literature
		F				LSG2.1[1] (62)	M99402	
		F				LSG3.1[1] (62)	M99403	
		F				LSG4.1[1] (62)	M99404	
		F				LSG6.1[1] (62)	M99406	
		F				LSG11.1[1] (62)	M99400	
	3-16	ORF	-	-	-	**V3-16P**[26] (16)	M99655	
	3-19	P	-	-	-	**V3-19P**[26] (17)	M99656	**COS-26**[Z27450]
	3-20	F	+	+	+	**V3-20**[26] (18)	M99657	DP-32[Z12334][39]
	3-21	F	+	+	+	DP-77	Z14073	WHG16[X62127][23]/HHG4[X62129][23] (62)
		F				**V3-21**[26]	M99658	
	3-22	P	-	-	-	**V3-22P**[26] (19)	M99659	
		P				**2-3**[5] (19)	X92221	DP-57[39][Z12357] / hv3033[9][M83135]
	3-23	F	+	+	+	**V3-23**[26]	M99660	DP-47[39][Z12347] / **VH26**[M83136][10] (20) / VH26-5.0[U29482][32]
		F				**VH26** (20)	J00236	
		F				VH26-3.7 [32]	U29481	
	3-25	P	-	-	-	**V3-25P[26]** (21)	M99661	
		P				DP-55[39] (21)	Z12355	
		P				DP-56[39] (21)	Z12356	
	3-29	P	-	-	-	**V3-29P**[26] (22)	M99662	**YAC-12**[Z49805]
	3-30	F	+	+	+	**hv3005**[9]	M83134	b36[M77325] / b42[X92318][28] / **3d24**[X92284][33]
		F				BHGH1[17]	L26401	**COS-3**[Z17389]
		F	+			**V3-30**[26]	M99663	
		F				hv3005f3[28]	L06615	b41[M77330] / f1[M77297][28] / **COS-8**[Z17394]
		F				b1-6[28] (23)	M77323	
		F				hv3019b18[28] (62)	L06617	b18[M77337][28] (62)
		F				hv3005b54[28] (62)	L06614	b54[M77332][28] (62)
		F				GL-SJ2[54] (62) (63)	M62737	
		F				f7[28] (62)	M77300	
		F				b25[28] (62)	M77326	
		F				b52[28] (62)	M77331	
		F				b26[28] (62)	M77338	
		F				b29[28] (62)	M77339	
		F				b32[28] (62)	M77324	
		F				b37[28] (62)	M77327	
		F				b43[28] (62)	M77328	
		F				b48[28] (62)	M77329	
	3-30-2	P	-	-	-	**3-30.2 P** [61]		
	3-30-3	F	+			**3d216**[33]	X92283	DP-46[Z12346][39]
		F				p2[28] (62)	M77302	
	3-30/3-30-5	F				1-9III[5]	X92214	DP-49[Z12349] / p3,4,7,8 (4 clones)[M77303][28] / p5[M77304][28]
		F				hv3019b13[28] (62)	L06616	b13[M77336][28] (62)
	3-32	P	-	-	-	**V3-32P**[26] (24)	M99664	

IGHV subgroup	IGHV gene name	Fct	R	T	Pr	Reference sequences	Accession numbers	Sequences from the literature
	3-33	F	+	+	+	hv3019b9[28]	L06618	DP-50[Z12350][39] / b9-12[M77333][28] / **3d277**[X92286][33]
		F	+			**V3-33**[26]	M99665	
		F				p6[28] (62)	M77305	
		F				b30[28] (62)	M77335	
		F				b28[28] (62)	M77334	
	3-33-2	P	-	-	-	**3-33.2 P** [61]		
	3-35	ORF	-	-	-	**V3-35**[26] (25)	M99666	DP-59[Z12359][39] / **VH19**[X92276][3]
	3-36	P	-	-	-	**V3-36P**[26] (26)	M99667	DP-83[Z15101]
	3-37	P	-	-	-	**V3-37P**[26] (27)	M99668	
		P				**VH4**[3]	X92277	**COS-7**[Z17393]
	3-38	ORF	-	-	-	**V3-38P**[26] (28)	M99669	
		ORF				**COS-23** (31)	Z27447	
	3-41	P	-	-	-	**V3-41P**[26] (29)	M99670	
	3-42	P	-	-	-	**V3-42P**[26] (30)	M99671	
		P				**VHBam**[4]	M12072	
	3-43	F	+	+	+	**V3-43**[26]	M99672	DP-33[Z12335][39]
		F				**COS-16**	Z18901	
	3-47	ORF	-	-	-	**COS-15**	Z18900	
		ORF				DP-52[39] (33)	Z12352	
		P				**V3-47P**[26] (32)	M99674	
	3-48	F	+	+	+	**V3-48**[26]	M99675	hv3d1[X92299][15] / WHG26[X62130][23]
		F	+			DP-51[39]	Z12351	
		F				DP-58[39] (62)	Z12358	hv3d1EG[U03893][15] (62)
	3-49	F	+	+	+	**V3-49**[26] (34)	M99676	
		F				LSG12.1[1] (62)	M99401	
		F				3-49RB [55] (62)	X87090	
	3-50	P	-	-	-	**V3-50P**[26] (35)	M99677	
	3-52	P	-	-	-	**V3-52P**[26] (36)	M99678	DP-43[Z12343][39] / **VH105**[X92280][18]
		P				**COS-2**	Z17388	
		P				**H16BR**[29] (36)	J00237	
	3-53	F	+	+	+	**V3-53**[26]	M99679	
		F	+			DP-42[39]	Z12342	
	3-54	P	-	-	-	**V3-54P**[26] (37)	M99680	
		P				**2-9III**[5] (37)	X92215	
		P				**COS-22**	Z27446	
	3-57	P	-	-	-	**V71-6**[22] (38)	M29815	
		P						**COS-10**[Z17396]
	3-60	P	-	-	-	**V71-3**[22] (39)	M29813	**COS-9**[Z17395]
	3-62	P	-	-	-	**V71-1**[22] (40)	M29814	DP-62[Z12362][39]
		P				**COS-28** (31)	Z27452	
	3-63	P	-	-	-	**V3-63P**[26] (41)	M99681	
		P				**DP-81** (41)	Z15099	

(continued)

Table 2 (continued)

IGHV subgroup	IGHV gene name	Fct	R	T	Pr	Reference sequences	Accession numbers	Sequences from the literature
	3-64	F	+	+	+	**V3-64**[26] (42)	M99682	**YAC-6**[Z27505][12]
		F	+			DP-61[39]	Z12361	
		F				f2 [28] (62)	M77298	
		F				f3[28] (62)	M77299	
		F				p1[28] (62)	M77301	
	3-65	P	-	-	-	**YAC-4**[12] (43)	Z27503	
		P						**DA-4**[Z29980][12]
	3-66	F	+	+	+	**8-1B**[5]	X92218	
		F	+			**YAC-5**[12]	Z27504	
		F				**DA-9**[12]	Z29984	DP-86[Z27455]
	3-71	P	-	-	-	**3-71 P** [61]		
	3-72	F	+	+	+	12-2[5] (44)	X92206	DP-29[Z12331][39]
		F				**DA-3**[12]	Z29979	
	3-73	F	+	+	+	**YAC-9**[12]	Z27508	MTGL[L15467][50] / **DA-11**[Z29986][12] / **COS-27**[Z27451]
	3-74	F	+	+	+	DP-53[39]	Z12353	hvm148[16] / 13G12[D16832][20](**DA-8**[Z30082][12])
		F	+			**COS-6**	Z17392	(**DA-8**[Z30082][12])
		F	+			**H11**[29]	J00239	
	3-75	P	-	-	-	**YAC-11**[12] (45)	Z27510	**COS-29**[Z27453]
	3-76	P	-	-	-	DP-41[39] (46)	Z12341	
		P				**COS-21**	Z27445	**DA-12**[Z30083][12]
	3-79	P	-	-	-	**3-79 P** [61]		
	3-d	F				**COS-12**	Z18898	
	3-g	P				DP-34[39] (47)	Z12336	**DA-10**[Z29985][12]
	3-h	F				**DA-5**[12]	Z29981	
4	**4-4**	F	+	+	+	**VIV-4**[37]	X62112	4.35[Z14240][45]
		F				4.38 [45] (62)	Z14243	
		F				**V79**[6] / **VIV-4b**[37]	X05713	VH4.19[X56363] (61)[31]
		F	+			4.41[45]	X92232	DP-70[Z12370][39] / 4d68[L10091][43] / VH4-GL15[Z75350][60](62)
		F				VH4-MC4[8]	X92252	
		F				VH4-MC4a[8] (62)	X92253	
		F				VH4-MC4b[8] (62)	X92254	
		F				VH4-GL3[60] (62)	Z75355	
	4-28	F	+	+		**V12G-1**[24]	X05714	1.9II[X92222][5] / DP-68[Z12368][39] / **3d28d**[L10096][33] / VH4.13[X56357][31] / H2[M95112][42] / VH4-GL5[Z75357][60](62)
		F				**hv4005**[11]	M83133	**3d24d**[L10099][33]
		F				4.42[45] (62)	X92233	
		F				VH4.14[45] (62)	X56358	
		F				VH4-MC7[8] (62)	X92260	
	4-30-1/4-31	F	+			4.33[45]	Z14237	DP-65[Z12365][39] / 3d75d[L10095][43] / VH4-MC9[X92269][8]
		F				H10[42] (62)	M95120	
		F				H11[42] (62)	M95121	

IGHV subgroup	IGHV gene name	Fct	R	T	Pr	Reference sequences	Accession numbers	Sequences from the literature
		F				VH4-MC9a[8] (62)	X92270	
		F				VH4-MC9b[8] (62)	X92271	
		F				VH4-MC9c[8] (62)	X92272	
		F				VH4-MC9d[8] (62)	X92273	
		F				4.32[45] (62)	Z14235	
	4-30-2	F	+			**3d216d**[33]	L10089	DP-64[Z12364][39] / VH4-GL12[Z75349][60][62]
		F				H12[42] (62)	M95122	
		F				4.31[45] (62)	X92229	
		F				VH4-GL17[60] (62)	Z75351	
	4-30-4	F				4.34[45]	Z14238	DP-78[Z14074][39] / **3d230d**[L10100][43]
		F				4.34.2[45] (62)	Z14239	
		F				VH4-MC9e[8] (62)	X92274	
		F				VH4-MC9f[8] (62)	X92275	
		ORF				VH4-GL2[60] (62)	Z75353	
		ORF				VH4-GL8[60] (62)	Z75360	
	4-31	F	+	+	+	**3d277d**[33]	L10098	
		F				**V4-31**[26]	M99683	VH4-GL6[Z75358][60](62)
	4-34	F	+	+	+	**VH5**[3]	X92278	**4d76**[L10090][43] / VH4.21[X56364][31] / DP-63[Z12363][39] / VH4-GL20[Z75354][60](62)
		F				**V4-34**[26]	M99684	
		F	+			VH4-MC5[8]	X92255	VH4-MC5b[X92257][8]
		F				4.44[45] (62)	X92236	
		F				4.44.3[45] (62)	X92237	
		F				VH4-MC5a[8] (62)	X92256	
		F				VH4-MC5c[8] (62)	X92258	
		F				H3[42] (62)	M95113	
		F				4.36[45] (62)	Z14241	
		F				4.37[45] (62)	Z14242	
		F				V58[24] (62)	X05716	
		F				TouVH4.21[56] (62)	X56591	
		F				VH4-GL4[60] (62)	Z75356	
	4-39	F	+	+	+	**4d154**[43]	L10094	DP-79[Z14075][39] / VH4.18[X56362][31] / MLH4-1[X54447][19] / VH4-GL19[Z75352][60](62)
		F				V2-1[31]	X05715	
		F	+			VH4-MC6[8]	X92259	
		F				G418[21]	X92297	
		F				H6[42] (62)	M95116	
		F				4.30[45] (62)	Z14236	
	4-55	P	-	-	-	**V4-55P**[26] (48)	M99685	DP-72[Z12372][39] / 4d64[L10092][43] / VH4-MC8a[X92262][8]
		P				**2.9II**[5]	X92223	VH4-MC8[X92261] / VH4MC8c[X92264][8]
		P				VH4-MC8b[8] (62)	X92263	
		P				VH4-MC8d[8] (62)	X92265	

(continued)

Table 2 (continued)

IGHV subgroup	IGHV gene name	Fct	R	T	Pr	Reference sequences	Accession numbers	Sequences from the literature
		P				VH4-MC8e[8] (62)	X92266	
		P				VH4-MC8f[8] (62)	X92267	
		P				VH4-MC8g[8] (62)	X92268	
		P				4.43[45] (62)	X92234	
		P				4.43.4[45] (62)	X92235	
	4-59	F	+	+	+	3d197d[43]	L10088	VH4-MC2[X92248][8] / DP-71[Z12371] / hv4c2[U03896][15] VH4.11[X56355] / VH4.15[X56359][31] (49) / G411[X92296][21]
		F				**V71.4**[22]	M29812	
		F				H4[42] (62)	M95114	
		F				H7[42] (62)	M95117	
		F				H8[42] (62)	M95118	
		F				H9[42] (62)	M95119	
		F				VH4.16[45] (62)	X56360	
		F				DP-71RB[55] (62)	X87091	
		F				VH4-GL7[60] (62)	Z75359	
	4-61	F	+	+	+	**V71-2**[22]	M29811	DP-66[Z12366][39] / H1[M95111][42] VH4-MC3[X92249] / VH4-MC3b[X92251][8] / VH4-GL1[Z75346][60](62)
		F				**3d279d**[43]	L10097	
		F				4.39[45] (62)	X92230	
		F				VH4-MC3a[8] (62)	X92250	
		F				VH4.12[45] (62)	X56356	
		ORF				VH4-GL10[60] (62)	Z75347	VH4-GL9[Z75361][60](62)
		F				VH4-GL11[60] (62)	Z75348	
	4-80	P	-	-	-	**4-80 P** [61]		
	4-b	F				DP-67[39]	Z12367	VH4-4B[X92289][48]
		F				VH4.22[31]	X56365	
5	**5-51**	F	+	+	+	**V5-51**[26]	M99686	DP-73[Z12373] / **VH251**[X92226][31](51) / VHVBLK[X56373][31]VHVAU[X56372] / VHVCH[X56370][31]VHVLB[X56369] / VHVTT[X56371][31]
		F	+			VH251[36] (51)	M18806	
		F	+			VHVCW[31]	X56368	**COS-24**[Z27448]
		F				VHVJB[31] (62)	X56367	
		F				**COS-25**	Z27449	
	5-78	P	-	-	-	**1-v**[5] (52)	X92213	**DP-80**[Z14076]
		P				**VH15**[18] (53)	X92281	
	5-a	F				VH32[31] (54)	X92227	
		P				**VH32**[18] (54)	X92279	
		F				VHVMW[31] (62)	X56375	VHVRG[X56374][31] (62)
		F				VHVBLK32[31] (62)	X56376	
6	**6-1**	F	+	+	+	**6-1G1**[5] / **VH6**[35]	X92224/J04097	DP-74[Z12374][39] / **VH-VI**[X92228][7] / VHVIBLK[X56382] / VHVICH[X56380] / VHVICW[X56381][31] VHVIIS[X56377] / VHVIJB[X56379] / VHIMW[X56383] / VHITE[X56378][31] / VH-VI[X14089] [7]

IGHV subgroup	IGHV gene name	Fct	R	T	Pr	Reference sequences	Accession numbers	Sequences from the literature
		F				VHGL6.3[8]	Z14223	
7	**7-4-1**	F	+			**4d275a**[46]	L10057	DP-21[Z12323][39]
		F	+			**VI-4.1b**[37] (55)	X62110	
		F				7A.4[57] (62)	X92290	
	7-27	P	-	-	-	**V1-27P**[26] (56)	M99643	DP-9[Z12311][39] / **1d292**[L10060][46]
	7-34-1	P	-	-	-	**7-34.1 P** [61]		
	7-40	P	-	-	-	**V1-40P**[26] (57)	M99644	
		P				2-20[47]		
		P				DP-18[39] (62)	Z12320	1d101[L10059][58] (62)
	7-56	P	-	-	-	**V71-7**[22] (58)	M29810	
		P				DP-13[39] (59)	Z12315	
	7-77	-				(64)		
	7-81	ORF	-	-	-	**YAC-10**[12] (31)	Z27509	**1d37**[L10058][46], **7-81** [61] (65)
	NL	P				7A.10[57]	X92291	
		P				7A.16[57]	X92292	
		P				7A.18[57]	X92293	
		P				7E.2[57]	X92294	
		P				7R.9[57]	X92295	

Pseudogenes not assigned to subgroups with functional genes. All these pseudogenes have truncations [61].

(II)-1-1	P	-	-	-	**4-1.1 P** [61]		
(II)-15-1	P	-	-	-	**4-15.1 P** [61]		
(II)-20-1	P	-	-	-	**4-20.1 P** [61]		
(II)-22-1	P	-	-	-	**4-22.1 P** [61]		
(II)-26-2	P	-	-	-	**4-26.2 P** [61]		
(II)-28-1	P	-	-	-	**4-28.1 P** [61]		
(II)-30-1	P	-	-	-	**4-30.1 P** [61]		
(II)-31-1	P	-	-	-	**4-31.1 P** [61]		
(II)-33-1	P	-	-	-	**4-33.1 P** [61]		
(II)-40-1	P	-	-	-	**4-40.1 P** [61]		
(II)-43-1	P	-	-	-	**4-43.1 P** [61]		
(II)-44-2	P	-	-	-	**4-44.2 P** [61]		
(II)-46-1	P	-	-	-	**4-46.1 P** [61]		
(II)-49-1	P	-	-	-	**4-49.1 P** [61]		
(II)-51-2	P	-	-	-	**4-51.2 P** [61]		
(II)-53-1	P	-	-	-	**4-53.1 P** [61]		
(II)-60-1	P	-	-	-	**4-60.1 P** [61]		
(II)-62-1	P	-	-	-	**4-62.1 P** [61]		
(II)-65-1	P	-	-	-	**4-65.1 P** [61]		
(II)-67-1	P	-	-	-	**4-67.1 P** [61]		
(II)-74-1	P	-	-	-	**4-74.1 P** [61]		
(II)-78-1	P	-	-	-	**4-78.1 P** [61]		
(III)-2-1	P	-	-	-	**3-2.1 P** [61]		

(continued)

Table 2 (continued)

(III)-5-1	P	-	-	-	**3-5.1 P** [61]		
(III)-5-2	P	-	-	-	**3-5.2 P** [61]		
(III)-11-1	P	-	-	-	**3-11.1 P** [61]		
(III)-13-1	P	-	-	-	**3-13.1 P** [61]		
(III)-16-1	P	-	-	-	**3-16.1 P** [61]		
(III)-22-2	P	-	-	-	**3-22.2 P** [61]		
(III)-25-1	P	-	-	-	**3-25.1 P** [61]		
(III)-26-1	P	-	-	-	**3-26.1 P** [61]		
(III)-38-1	P	-	-	-	**3-38.1 P** [61]		
(III)-44	P	-	-	-	**V3-44 P** [26]	M99673	
(III)-47-1	P	-	-	-	**3-47.1 P** [61]		
(III)-51-1	P	-	-	-	**3-51.1 P** [61]		
(III)-67-2	P	-	-	-	**3-67.2 P** [61]		
(III)-67-3	P	-	-	-	**3-67.3 P** [61]		
(III)-67-4	P	-	-	-	**3-67.4 P** [61]		
(III)-76-1	P	-	-	-	**3-76.1 P** [61]		
(III)-82	P	-	-	-	**3-82 P** [61]		
(IV)-44-1	P	-	-	-	**4-44.1 P** [61]		

IGHV genes are designated by a number for the subgroup, followed by a dash and a number for the localisation from 3' to 5' in the locus.
Eight genes which have been described as insertion polymorphism but which have not been precisely located are designated by a number for the subgroup, followed by a dash and a small letter: IGHV1-c, IGHV1-e, IGHV1-f, IGHV3-d, IGHV3-g, IGHV3-h, IGHV4-b, IGHV5-a.

Pseudogenes which could not be assigned to subgroups with functional genes are designated by a roman number between parentheses, corresponding to the clans [61], followed by a dash and a number for the localisation from 3' to 5' in the locus.
Clans comprise, respectively:
- clan I: IGHV1, IGHV5 and IGHV7 subgroup genes
- clan II: IGHV2, IGHV4 and IGHV6 subgroup genes, and pseudogenes IGHV(II)
- clan III: IGHV3 subgroup genes, and pseudogenes IGHV(III)
- clan IV: one pseudogene IGHV(IV)-44

Notes

(1) May be defective on structural grounds (Chothia et al. J. Mol. Biol., 227, 799-817 (1992)

(2) Truncated V-GENE with completely divergent 3' region

(3) Frameshifts in V-REGION

(4) INSERTION and DELETION of one nucleotide in FR1 and FR2 respectively

(5) DELETION of one nucleotide in FR2

(6) Absence of the conventional DONOR_SPLICE site (ngc instead of ngt) at the 5' end of the L-PART1, however this V-GENE has been seen rearranged in vivo

(7) The DELETION of nucleotides 208 to 248 in M99645 EMBL flat file is probably a typing error. This DELETION does not exist in the paper

(8) INSERTION of 4 nucleotides (tacc) between codons 28 and 29 in the FR1 leading to a frameshift

(9) The sequence described in the manuscript is different from the one submitted to the EMBL data library. We refer to the sequence published in the original manuscript

(10) Unusual V-HEPTAMER sequence (cacaaag instead of cacagtg) but this V-GENE has been seen rearranged

(11) Unusual V-HEPTAMER and V-NONAMER sequences (cacaaag and acaaaaccc instead of cacagtg and acaaaaacc). g100>del ,g107>del, g117>del may result from sequencing errors in X62108. The sequence is probably identical to allele *02 with CDR1-IMGT of 10 aminoacids

(12) In frame STOP-CODON and recombination signal sequences not conserved

(13) Unusual V-HEPTAMER sequence (cacagag instead of cacagtg) but this V-GENE has been seen rearranged

(14) DELETION of one nucleotide in FR1 and unusual V-HEPTAMER sequence (tacggta)

(15) Differs from the prototype sequence by DELETIONS

(16) Unusual V-HEPTAMER sequence : tcctgtg instead of cacagtg

(17) Unusual V-HEPTAMER sequence : cactgtg instead of cacagtg, ACCEPTOR_SPLICE site at the 5' side of the V-EXON and second part of the leader exon (L-PART2) are missing

(18) V-NONAMER sequence (acacaaacg) differs from the family consensus: acacaaacc but this V-GENE has been seen rearranged

(19) In frame STOP-CODON in CDR2, CONSERVED_TRP (tgg) residue at the beginning of FR2 is replaced by GLY (ggg)

(20) VH26 (J00236, Matthyssens and Rabbitts, P.N.A.S U.S.A, 77, 6561-6565, 1980) corrected by Chen et al. (M83136)

(21) In frame STOP-CODON, CONSERVED_TRP (tgg) residue at the beginning of FR2 is replaced by CYS (tgt)

(22) In frame STOP-CODON and unusual V-HEPTAMER and V-NONAMER sequences

(23) The sequence described in the manuscript is different from the one submitted to the EMBL data library. We refer to the sequence published in the original manuscript

(24) In frame STOP-CODON and unusual V-HEPTAMER and V-NONAMER sequences

(25) Unusual V-HEPTAMER sequence : cactgtg instead of cacagtg, may be defective on structural grounds (Chothia et al. J. Mol. Biol 227, 799-817 (1992))

(26) Translational frameshift in FR1 and STOP-CODON, no recombination signal sequences

(27) DELETION of 2 nucleotides in CDR2 leading to a frameshift after residue 61 and STOP-CODON

(28) Unusual V-HEPTAMER sequence: cacagag instead of cacagtg

(29) In frame STOP-CODON in FR2 and 1 bp DELETION leading to a frameshift after residue 70 in FR3

(30) One nucleotide INSERTION between codons 15, 16 in the FR1 leading to a frameshift and STOP-CODON

(31) Partial sequence whose functionality has been assigned by comparison to another sequence of the gene

(32) Missing translation initiation codon and frameshift after residue 80 in the FR3 due to one nucleotide DELETION

(33) May be defective on structural grounds (Chothia et al, J.Mol.Biol 227, 799-817 (1992))

(34) V-NONAMER sequence (acacagacc) differs from the subgroup consensus: acacaaacc

(35) In frame STOP-CODON in the leader exon and frameshift after residue 11 in the FR1

(36) In frame STOP-CODON in the FR1

(37) In frame STOP-CODON and unusual recombination signal sequences

(38) The sequence described in the manuscript is different from the one submitted to the EMBL data library. We refer to the sequence published in the original manuscript. Deleterious mutations throughout the V-GENE affecting translation initiation, RNA spicing

(39) The sequence described in the manuscript is different from the one submitted to the EMBL data library. We refer to the sequence published in the original manuscript. STOP-CODON at position 66 and mutation in the V-HEPTAMER recombination signal

(40) The sequence described in the manuscript is different from the one submitted to the EMBL data library. We refer to the sequence published in the original manuscript. STOP-CODON at position 46 and mutation in the V-HEPTAMER recombination signal

(41) In frame STOP-CODONs and not canonical recombination signal sequences

(42) V-NONAMER differs from the subgroup consensus: acacaaacc but this V-GENE has been seen rearranged

(43) Frameshift at the end of FR1

(continued)

Table 2 (continued)

(44) Unusual V-HEPTAMER recombination signal sequence : cacagcg instead of cacagtg this V-GENE has been seen rearranged
(45) Frameshifts in V-REGION
(46) In frame STOP-CODON and DELETION of 2 nucleotides at the end of FR2 leading to a translational frameshift
(47) In frame STOP-CODON in CDR2
(48) In frame STOP-CODON in CDR1 at position 35
(49) The sequence described in the manuscript is different from the one submitted to the EMBL data library. We refer to the sequence submitted to the EMBL data library (X56359)
(50) Germline transcript
(51) VH251 (M18806, Shen et al.) corrected by Sanz et al (X92226). The sequence (X92226) described in the manuscript is different from the one submitted to the EMBL data library: one nucleotide (g) inserted in the file compared to the publication. Correction
(52) 24 bp DELETION in the immediate 3' flank resulting in loss of the V-HEPTAMER and part of the spacer region (J. Exp. Med., 173, 1529-1535 (1991)) Incorrect translation frame due to the INSERTION of two nucleotides at the end of L-PART2
(53) One nucleotide INSERTION in L-PART1 and two nucleotides DELETIONS in CDR2 leading to a frameshift 24 bp DELETION resulting in loss of the V-HEPTAMER and part of the spacer region (J. Exp. Med., 173, 1529-1535(1991))
(54) VH32 (X92279, Humphries and al.) corrected by Sanz and al (X92227)
(55) Or VI-4.1b: extraordinary polymorphic allele (EMBO J., 10, 3641-3645 (1991)). V-NONAMER sequence differs from the subgroup consensus: tctaaaacc
(56) In frame STOP-CODON and 14 bp DELETION between codons 87 and 88 in the FR3
(57) Undetermined 5' region
(58) In frame STOP-CODON at position 27
(59) In frame STOP-CODON in FR1, 3 nucleotides DELETION in codon 52, 53 and 61 in CDR2 and one nucleotide INSERTION leading to translational frameshifts
(60) The INSERTION of one nucleotide between position 195 and 196 in M99646 EMBL flat file is probably a typing error. This insertion does not exist in the paper
(61) The substitutions of c46>t and a308>g in X56363 EMBL flat file are probably a typing error. These substitutions do not exist in the paper
(62) This sequence has been assigned by IMGT to a previously described gene by sequence alignment
(63) In EMBL/GenBank flat file, intron is missing. Request has been done by IMGT/LIGM-DB annotators for sequence correction
(64) Not found by Matsuda et al. J. Exp. Med. 188, 1-15 (1998)
(65) Unusual V-HEPTAMER (caccatg instead of cacagtg)

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Table 3. Human IGHV orphons on chromosome 15 (15q11.2)

Fct : FUNCTIONALITY
F : Functional
P : Pseudogene
ORF : Open Reading Frame

Sequences in bold have been mapped : "mapped" refers to sequences which have been obtained from clones (phages, cosmids, YACs...) either by subcloning or PCR, and does not apply to sequences obtained directly from genomic DNA. Note that "mapped" does not refer to the chromosomal assignment. ORPHON genes are designated by a number for the subgroup followed by a slash, OR (for ORPHON), the chromosome number, a dash and a specific gene number.

IGHV subgroup	IGHV gene name	Fct	Reference sequences	Accession numbers	Sequences from the literature
1	1/OR15-1	ORF	**HC15-1**[10]	Z29631	DP-1[Z12303][9]
	1/OR15-2	P	**V54**[6] (1)	L25543	**HC15-2**[Z29632][10] / DP-22[Z12324][9]
	1/OR15-3	P	**HC15-3**[10] (1)	Z29595	DP-19[Z12321][9]
		ORF	**COS-4**[10]	Z17390	
		P	HA2[7] (1)	J00238	
	1/OR15-4	P	**HC15-4**[10] (1)	Z29596	DP-23[Z12325][9]
	1/OR15-5	ORF	**HC15-5**[10]	Z29633	**COS-14**[Z18899][10]
		P	VH20[3] (2)	X92282	
		ORF	DP-12[9]	Z12314	
	1/OR15-6	P	**HC15-6**[10] (3)	Z29634	**COS-18**[Z18903][10]
		P	DP-24[9] (3)	Z12326	
	1/OR15-9	ORF	**V13C**[6] (4)	L25542	
3	3/OR15-7	ORF	**HC15-7**[10]	Z29597	
		ORF	**VHD26**[1]	M36530	
		ORF	DP-30[9]	Z12332	
		P	V3[5] (5)	X07449	
4	4/OR15-8	ORF	**HC15-8**[10]	Z29598	DP-69[Z12369][9] / 4d255[L10093][11] / VH4.17[X56361][8] VH4.23[X56366][8] / VH4MC1[X92247][2] H5[M95115][12] / 4.40[X92231][13]
		ORF	V11[4] (6)	X05712	

Notes

(1) STOP-CODON in frame.
(2) INSERTIONs of one nucleotide (a) leading to a frameshift.
(3) DELETIONs leading to a frameshift.
(4) Unusual V-HEPTAMER and V-NONAMER sequences.
(5) Frameshifts due to INSERTIONs and DELETIONs. The sequence described in the manuscript is different from the one submitted to the EMBL data library.
(6) Unusual V-HEPTAMER sequence: cacatga instead of cacagtg.

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Table 4. Human IGHV orphons on chromosome 16 (16p11.2)

Fct : FUNCTIONALITY
F : Functional
P : Pseudogene
ORF : Open Reading Frame

Sequences in bold have been mapped : "mapped" refers to sequences which have been obtained from clones (phages, cosmids, YACs...) either by subcloning or PCR, and does not apply to sequences obtained directly from genomic DNA. Note that "mapped" does not refer to the chromosomal assignment. ORPHON genes are designated by a number for the subgroup followed by a slash, OR (for ORPHON), the chromosome number, a dash and a specific gene number.

IGHV subgroup	IGHV gene name	Fct	Reference sequences	Accession numbers	Sequences from the literature	Related counterparts at 14q32.33
1	1/OR16-1	P	**HC16-1**[7](2)	Z29599	DP-17[Z12319][6]	1-14
	1/OR16-2	P	**HC16-2**[7](2)	Z29600	DP-20[Z12322][6] / 65-1[X55585][4]	1-14
	1/OR16-3	P	**HC16-3**[7](1)	Z29639	15-1[X92211][2]	1-12
	1/OR16-4	P	**COS-11**[7](1)	Z17397	65-3[X55586][4]	1-12
		P	**HC16-4**[7](1)	Z29601		1-12
2	2/OR16-5	ORF	**VF2-26**[5](7)	L25544	**YAC1**[Z18919][7] / **HC16-5**[Z29602][7]	2-26
3	3/OR16-6	P	**VF3-15P**[5](4)	L25545	**HC16-6**[Z29603][7] / DP-36[Z12602][6] / psiRC[M99410][1]	3-15
	3/OR16-7	P	**HC16-7**[7](4)	Z29604	DP-37[Z12603][6]	3-15
		P	**COS-20**[7]	Z18905		3-15
		P	**COS-30**[7]	Z29594		3-15
	3/OR16-8	ORF	**HC16-8**[7]	Z29605	DP-39[Z12339][6] / 65-4[X56164][4] (7)	3-11
	3/OR16-9	ORF	**HC16-9**[7]	Z29606	DP-40[Z12340][6] / 15-2B[X92219][2] (7)	3-11
	3/OR16-10	ORF	**HC16-10**[7]	Z29607	DP-44[Z12344][6] / 65-2[X56163][4]	3-13
		ORF			DP-45[Z12345][6]	3-13
	3/OR16-11	P	**HC16-11**[7](3)	Z29608	DP-85[Z27454][6]	3-13
	3/OR16-12	ORF	**HC16-12**[7]	Z29609	DP-84[Z27511][6]	3-11
	3/OR16-13	ORF	**HC16-13**[7]	Z29610	DP-87[Z27456][6]	3-74
	3/OR16-14	P	**HC16-14**[7](6)	Z29611	**COS-13**[Z18918][7]	3-74
	3/OR16-15	P	**VF3-16P**[5](6)	L25546	**YAC2**[Z27497][7]	3-16
		P	**HC16-15**[7](6)	Z29612	VHGL3.4[Z14217][3]	3-16
	3/OR16-16	P	**HC16-16**[7](5)	Z29613	{DP-82[Z15100]/VHGL3.5[Z14218][3] (8) / VHGL3.7[Z14220][3] (8)}	3-16

Notes

(1) Truncated V-GENE with completely divergent 3' region.
(2) DELETIONs in FR1 leading to a frameshift.
(3) DELETION of one nucleotide in FR1 leading to a frameshift.
(4) INSERTION of one nucleotide in FR1 leading to a frameshift.
(5) STOP-CODON in FR2.
(6) STOP-CODON in frame.
(7) Unusual V-HEPTAMER and V-NONAMER sequences.
(8) Germline transcript

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Table 5. Human IGHV allele table

Fct : FUNCTIONALITY
F : Functional
P : Pseudogene
ORF : Open Reading Frame

The IMGT allele table refers to the V-REGION polymorphism. It does not include polymorphisms in the other parts of the V-GENE.
V-REGION alleles are only described for genes which have at least one Functional or ORF allele.
The accession number of a reference sequence is given for each allele.

IGHV subgroup	IGHV gene name	Fct	IGHV allele name	Accession number	confirmed by genetics and/or data	Description of mutations
1	1-2	F	V1-2*01	X07448	+	c44 ,P15 |c163 ,R55 |a223 ,R75 |g233 ,t234 ,S78 |t299 ,V100 |
		F	V1-2*02	X62106	+	|c163>t,R55>W| |g233>t,t234>g,S78>M |t299>c,V100>A|
		F	V1-2*03	X92208		c44>t,P15>L |c163>t,R55>W| |g233>t,t234>g,S78>M |t299>c,V100>A|
		F	V1-2*04	Z12310		|c163>t,R55>W|a223>t,R75>W|g233>t,t234>g,S78>M |t299>c,V100>A|
	1-3	F	V1-3*01	X62109	+	c6 |t12 |t167 ,I56 |a208 ,K70 |a291 |c296 ,T99 |
		F	V1-3*02	X62107		c6>t|t12>g|t167>g,I56>S|a208>g,K70>E|a291>g|c296>t,T99>M|
	1-8	F	V1-8*01	M99637	+	
	1-18	F	V1-18*01	M99641	+	
		F	V1-18*02	X60503		(4)
	1-24	F	V1-24*01	M99642	+	
	1-45	F	V1-45*01	X92209		g139 ,G47 |t237 |
		F	V1-45*02	Z12306		|t237>c|
		F	V1-45*03	Z17391		g139>a,G47>R|t237>c|
	1-46	F	V1-46*01	X92343	+	c92 ,T31 |
		F	V1-46*02	J00240		c92>a,T31>N|
		F	V1-46*03	L06612		(4)
	1-58	F	V1-58*01	M29809	+	
	1-69 (3)	F	V1-69*01	L22582	+	g6 |g18 |g100 ,A34 |g163 ,G55 |t178 ,F60 |c185 ,T62 |g244 ,E82 |g291 ,E97 |
		F	V1-69*02	Z27506	+	g6>c|g18>a|g100>a,A34>T|g163>a,G55>R|t178>c,F60>I|c185>t, T62>I|g244>a,E82>K|
		F	V1-69*03	X92340		|g291>t,E97>D|
		F	V1-69*04	M83132		(4)
		F	V1-69*05	X67905		(4)
	1-c	F	V1-c*01	Z18904		
	1-e (3)	F	V1-e*01	L22583	+	g163 ,G55 |a244 ,K82 |
		F	V1-e*02	Z29978		g163>a,G55>R|a244>g,K82>E|
	1-f	F	V1-f*01	Z12305		c201 |
		F	V1-f*02	Z29977		c201>t|
2	2-5	F	V2-5*01	X62111		a175 ,N59 |c234 |

		F	V2-5*02	Z14072	+	a175>g,N59>D|
		F	V2-5*03	X93619		a175>g,N59>D|c234>t|
		F	V2-5*04	L21963		(4)
		F	V2-5*05	L21964		(4)
		F	V2-5*06	L21966		(4)
		F	V2-5*07	L21968		(4)
		F	V2-5*08	L21971		(4)
		F	V2-5*09	L21972		(4)
	2-26	F	V2-26*01	M99648	+	
	2-70	F	V2-70*01	L21969	+	g14 ,R14 |t106 ,C36 |t116 ,V39 |t164 ,I55 |a197 ,Y66 |a297 |a301 ,c302 ,T101 |
		F	V2-70*02	X92241	+	|a297>g|
		F	V2-70*03	X92238	+	g14>a,R14>K|t106>c,C36>R| |t164>g,I55>R|a197>t, Y66>F|a297>g|a301>g,c302>t,T101>V|
		F	V2-70*04	Z12330		g14>a,R14>K|t106>c,C36>R| |t164>g,I55>R|a197>t,Y66>F|
		F	V2-70*05	Z27502		|t106>c,C36>R|t116>c,V39>A|t164>g,I55>R|a197>t,Y66>F|
		F	V2-70*06	X92239		(4)
		F	V2-70*07	X92243		(4)
		F	V2-70*08	X92245		(4)
		F	V2-70*09	L21962		(4)
		F	V2-70*10	L21965		(4)
		F	V2-70*11	L21967		(4)
		F	V2-70*12	L21970		(4)
3	3-7	F	V3-7*01	M99649	+	
		F	V3-7*02	X92288		(4)
	3-9	F	V3-9*01	M99651	+	
	3-11	F	V3-11*01	M99652	+	|g32 ,G11 |g47 ,G16 |a206 ,D69 |c243 ,D81|
		P	V3-11*02	M15496		9^10>ins^t|g32>del#,G11>del#|g47>del#,G16>del#|a206>del#, D69>del#|c243>g,D81>E|(2)
		F	V3-11*03	X92287		(4)
	3-13	F	V3-13*01	X92217	+	g9 ,Q3 |t52 ,S18 |g95 ,S32 |t165 |t167 ,I56 |c222 |
		F	V3-13*02	M99653		g9>t,Q3>H|t52>g,S18>A|g95>a,S32>N|t165>c|t167>a,I56>N|c222>g|
	3-15	F	V3-15*01	X92216	+	g32 ,G11 |
		F	V3-15*02	M99654		g32>c,G11>A|
		F	V3-15*03	M99408		(4)
		F	V3-15*04	M99402		(4)
		F	V3-15*05	M99403		(4)
		F	V3-15*06	M99404		(4)
		F	V3-15*07	M99406		(4)
		F	V3-15*08	M99400		(4)
	3-16	ORF	V3-16*01	M99655		
	3-19	P	V3-19*01	M99656		
	3-20	F	V3-20*01	M99657	+	
	3-21	F	V3-21*01	Z14073	+	g9 |

(continued)

Table 5 (continued)

IGHV subgroup	IGHV gene name	Fct	IGHV allele name	Accession number	confirmed by genetics and/or data	Description of mutations
		F	V3-21*02	M99658		g9>a|
	3-23	F	V3-23*01	M99660	+	c164 ,A55 |a169 ,g170 ,S57 |g172 ,t174 ,G58 |a175 ,S59 |g181 ,G61 |c201 |c203 ,A68 |c237 |c243 |
		F	V3-23*02	J00236		|c203>g,A68>G|c237>a|
		F	V3-23*03	U29481		c164>t,A55>V|a169>t,g170>a,S57>Y|g172>a,t174>c,G58>S|a175>g, S59>G|g181>a,G61>S|c201>t| |c243>t|
	3-30	F	V3-30*01	M83134	+	a49 ,R17 |c75 |c101 ,t102 ,A34 |a150 |g163 ,V55 |t169 ,c170 ,a171 ,S57 |c201 |a293 ,D98 |
		F	V3-30*02	L26401	+	a49>g,R17>G|c75>g|c101>g,t102>c,A34>G|a150>g|g163>t,V55>F|t169>c, c170>g,a171>g,S57>R|c201>t|
		F	V3-30*03	M99663		|c101>g,t102>c,A34>G |a150>g| |c201>t|
		F	V3-30*04	L06615	+	|a150>g|
		F	V3-30*05	M77323		|c101>g,t102>c,A34>G| |a293>g,D98>G|
		F	V3-30*06	L06617		(4)
		F	V3-30*07	L06614		(4)
		F	V3-30*08	M62737 (5)		(4)
		F	V3-30*09	M77300		(4)
		F	V3-30*10	M77326		(4)
		F	V3-30*11	M77331		(4)
		F	V3-30*12	M77338		(4)
		F	V3-30*13	M77339		(4)
		F	V3-30*14	M77324		(4)
		F	V3-30*15	M77327		(4)
		F	V3-30*16	M77328		(4)
		F	V3-30*17	M77329		(4)
	3-30-3	F	V3-30-3*01	X92283	+	
		F	V3-30-3*02	M77302		(4)
	3-30/3-30-5	F	V3-30/3-30-5*01	X92214	+	
		F	V3-30/3-30-5*02	L06616		(4)
	3-33	F	V3-33*01	L06618	+	g6 |t212 ,V71 |a251 ,R84 |a263 ,Y88 |
		F	V3-33*02	M99665		g6>a|t212>c,V71>A|a251>c,R84>T|a263>t,Y88>F|
		F	V3-33*03	M77305		(4)
		F	V3-33*04	M77335		(4)
		F	V3-33*05	M77334		(4)
	3-35	ORF	V3-35*01	M99666	+	
	3-38	ORF	V3-38*01	M99669		c302 ,A121 |
		F	V3-38*02	Z27447		c302>t,A121>V|
	3-43	F	V3-43*01	M99672	+	t32 ,V11 |a100 ,T34 |g138 |t172 ,W58 |
		F	V3-43*02	Z18901		t32>g,V11>G|a100>g,T34>A|g138>a|t172>g,W58>G|

	3-47	ORF	V3-47*01	Z18900			c58 |c101 ,A34 |t149 ,I50 |t267 ,I89 |t270 ,H90 |t310 |
		ORF	V3-47*02	Z12352			c58>a |c101>t,A34>V|t149>c,I50>P| |t270>a,H90>Q|
		P	V3-47*03	M99674			c58>a |c101>t,A34>V|t149>c,I50>P|t267>del#,I89>del#|t270>a,H90>Q|t310>g|
	3-48	F	V3-48*01	M99675		+	c287 ,A96 |
		F	V3-48*02	Z12351			c287>a,A96>D|
		F	V3-48*03	Z12358		+	(4)
	3-49	F	V3-49*01	M99676			
		F	V3-49*02	M99401			(4)
		F	V3-49*03	X87090			(4)
	3-53	F	V3-53*01	M99679			t19 ,S7 |
		F	V3-53*02	Z12342			t19>a,S7>T|
	3-64	F	V3-64*01	M99682		+	a205 ,N69 |
		F	V3-64*02	Z12361			a205>g,N69>D|
		F	V3-64*03	M77298			(4)
		F	V3-64*04	M77299			(4)
		F	V3-64*05	M77301			(4)
	3-66	F	V3-66*01	X92218			g175 ,G59 |a75 |c288 |
		F	V3-66*02	Z27504			|a75>c|c288>t|
		F	V3-66*03	Z29984		+	g175>t,G59>C|
	3-72	F	V3-72*01	X92206		+	t186 |
		F	V3-72*02	Z29979			t186>c|
	3-73	F	V3-73*01	Z27508		+	
	3-74	F	V3-74*01	Z12353		+	c21 |g197 ,c198 ,S66 |
		F	V3-74*02	Z17392			c21>t|
		F	V3-74*03	J00239			|g197>c,c198>g,S66>T|
	3-d	F	V3-d*01	Z18898			
	3-h	F	V3-h*01	Z29981			
4	4-4	F	V4-4*01	X62112		+	(1)
		F	V4-4*02	Z14243			(4)
		F	V4-4*03	X05713		+	c46 ,F16 |g308 ,C103 |
		F	V4-4*04	X92232		+	c46>t,F16>S|g308>a,C103>Y|
		F	V4-4*05	X92252			|g308>a,C103>Y|
		F	V4-4*06	X92253			(4)
		F	V4-4*07	X92254			(4)
		F	V4-4*08	Z75355			(4)
	4-28	F	V4-28*01	X05714		+	g48 |g49 ,c51 ,D17 |c185 ,T62 |
		F	V4-28*02	M83133		+	g48>a|g49>c,c51>g,D17>Q|c185>t,T62>I|
		F	V4-28*03	X92233			(4)
		F	V4-28*04	X56358			(4)
		F	V4-28*05	X92260			(4)
	4-30-1/4-31	F	V4-30-1/4-31*01	Z14237		+	
		F	V4-30-1/4-31*02	M95120			(4)
		F	V4-30-1/4-31*03	M95121			(4)
		F	V4-30-1/4-31*04	X92270			(4)

(continued)

Table 5 (continued)

IGHV subgroup	IGHV gene name	Fct	IGHV allele name	Accession number	confirmed by genetics and/or data	Description of mutations
		F	V4-30-1/4-31*05	X92271		(4)
		F	V4-30-1/4-31*06	X92272		(4)
		F	V4-30-1/4-31*07	X92273		(4)
		F	V4-30-1/4-31*08	Z14235		(4)
	4-30-2	F	V4-30-2*01	L10089	+	
		F	V4-30-2*02	M95122		(4)
		F	V4-30-2*03	X92229		(4)
		F	V4-30-2*04	Z75351		(4)
	4-30-4	F	V4-30-4*01	Z14238	+	
		F	V4-30-4*02	Z14239		(4)
		F	V4-30-4*03	X92274		(4)
		F	V4-30-4*04	X92275		(4)
		ORF	V4-30-4*05	Z75353		(4)
		ORF	V4-30-4*06	Z75360		(4)
	4-31	F	V4-31*01	L10098		c69 |t224 ,i75 |
		F	V4-31*02	M99683	+	c69>t |t224>g,i75>R|
	4-34	F	V4-34*01	X92278	+	g15 |t300 |
		F	V4-34*02	M99684		g15>a|
		F	V4-34*03	X92255	+	|t300>c|
		F	V4-34*04	X92236		(4)
		F	V4-34*05	X92237		(4)
		F	V4-34*06	X92256		(4)
		F	V4-34*07	X92258		(4)
		F	V4-34*08	M95113		(4)
		F	V4-34*09	Z14241		(4)
		F	V4-34*10	X05716		(4)
		F	V4-34*11	X56591		(4)
		F	V4-34*12	Z75356		(4)
		F	V4-34*13	L10094		(4)
	4-39	F	V4-39*01	X05715	+	g258 ,G86 |a291 |t300 |c319 |
		F	V4-39*02	X92259		g258>c,G86>R| |c319>g|
		F	V4-39*03	X92297		|t300>c|
		F	V4-39*04	M95116		|a291>g|
		F	V4-39*05	Z14236		(4)
		F	V4-39*06	L10088		(4)
	4-59	F	V4-59*01	M29812	+	a94 ,I32 |
		F	V4-59*02	M95114		a94>g,I32>V|
		F	V4-59*03	M95117		(4)
		F	V4-59*04	M95118		(4)
		F	V4-59*05			(4)

		F	V4-59*06	M95119		(4)
		F	V4-59*07	X56360		(4)
		F	V4-59*08	X87091		(4)
		F	V4-59*09	Z75359		(4)
	4-61	F	V4-61*01	M29811	+	g48 |g49 ,E17 |g88 ,V30 |c136 ,a138 ,P46 |t163 ,a164 ,Y55 |t172 ,a173 ,Y58 |t288 |g291 |
		F	V4-61*02	L10097		g48>a|g49>c,E17>Q|g88>a,V30>I|c136>g,a138>c,P46>A|t163>c,a164>g, Y55>R|t172>a,a173>c,Y58>T|t288>c|g291>a|
		F	V4-61*03	X92230		(4)
		F	V4-61*04	X92250		(4)
		F	V4-61*05	X56356		(4)
		ORF	V4-61*06	Z75347		(4)
		F	V4-61*07	Z75348		(4)
	4-b	F	V4-b*01	Z12367	+	g70 ,A24 |
		F	V4-b*02	X56365		g70>a,A24>T|
5	5-51	F	V5-51*01	M99686	+	c45 |t116 ,I39 |g138 ,G47 |c148 |
		F	V5-51*02	M18806		|t116>c,I39>T| |c148>t|
		F	V5-51*03	X56368	+	c45>g|
		F	V5-51*04	X56367		(4)
		F	V5-51*05	Z27449		|g138>a,G47>R|
	5-a	F	V5-a*01	X92227		c148 |c288 ,A96 |
		P	V5-a*02	X92279		c148>t|c288>del#,A96>del#|
		F	V5-a*03	X56375		(4)
		F	V5-a*04	X56376		(4)
6	6-1	F	V6-1*01	X92224/J04097	+	a27 |
		F	V6-1*02	Z14223		a27>g|
7	7-4-1	F	V7-4-1*01	L10057	+	t274 ,C92 |
		F	V7-4-1*02	X62110		t274>a,C92>S|
		F	V7-4-1*03	X92290		(4)
	7-81	ORF	V7-81*01	Z27509	+	

Notes

(1) Given the high number of differences between IGHV4-4*01 and IGHV4-4*03, the mutations between these alleles are not described in this table. The alleles IGHV4-4*04, IGHV4-4*05, IGHV4-4*06 and IGHV4-4*07 are described by comparison to allele IGHV4-4*03.

(2) Differs from the prototype sequence by insertions and deletions.

(3) IGHV1-e and IGHV1-69 alleles are shown in the same alignment since IGHV1-e results from duplication of the IGHV1-69 gene. In the allele table, the description of the IGHV1-e and IGHV1-69 alleles is done by comparaison to the IGHV1-e*01 and IGHV1-69*01 alleles, respectively.

(4) Unmapped IGHV sequence: this sequence has been assigned by IMGT to a previously described gene by sequence alignment and is included in the allele alignment. Description of its mutations will be later included in the allele table.

(5) In EMBL/GenBank flat file, intron is missing. Request has been done by IMGT/LIGM-DB annotators for sequence correction.

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