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The Human Immunoglobulin Kappa Variable (IGKV) Genes and Joining (IGKJ) Segments

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Key Words
Human
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Abstract
'Human Immunoglobulin Kappa Variable (IGKV) Genes and Joining (IGKJ) Segments', second report of the 'IMGT Locus on Focus' section, comprises five tables entitled: (1) 'Number of human germline IGKV genes at 2p12 and potential repertoire'; (2) 'Human germline IGKV gene table'; (3) 'Human IGKV allele table'; (4) 'Human germline IGKJ table' and (5) 'Human IGKJ 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, CNRS, Université Montpellier II, Montpellier, France.

Introduction

'Human Immunoglobulin Kappa Variable (IGKV) Genes and Joining (IGKJ) Segments' is the second 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 IGLV genes and IGLJ segments [2]. This second report on human IGKV genes and IGKJ segments comprises five tables entitled: (1) 'Number of human germline IGKV genes at 2p12 and potential repertoire'; (2) 'Human germline IGKV gene table'; (3) 'Human IGKV allele table'; (4) 'Human germline IGKJ table' and (5) 'Human IGKJ 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, CNRS, Université Montpellier II, Montpellier, France [3, 4]. Description of functionality (FUNCTIONAL, ORF, PSEUDOGENE) and description of mutations [1] are according to the IMGT scientific chart available at the IMGT Marie-Paule page. Nucleotide and amino acid numbering of the IGKV alleles (table 3) is according to the IMGT unique numbering [1, 5].

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Table 1

Number of human germline IGKV genes at 2p12 and potential repertoire

Distal and proximal V-CLUSTERs (for the haplotypes with both clusters)

76 IGKV genes belonging to 7 subgroups, on 1 800 kilobases :

34 FUNCTIONAL
7 ORF (Open Reading Frame)
32 PSEUDOGENE
3 FUNCTIONAL or PSEUDOGENE

Potential repertoire : 34-37 FUNCTIONAL IGKV genes belonging to 5 subgroups

Subgroup	Functional	ORF	Pseudogene
IGKV1	17(+1)*	3	8(+1)*
IGKV2	9(+1)*	-	17(+1)*
IGKV3	6(+1)*	1	6(+1)*
IGKV4	1	-	-
IGKV5	1	-	-
IGKV6	-	3	-
IGKV7	-	-	1
Total	34(+3)*	7	32(+3)*

* FUNCTIONAL or PSEUDOGENE (IGKV1-39, IGKV2-29, IGKV3D-15)

Proximal V-CLUSTER (for the haplotypes without the distal V-CLUSTER)

40 IGKV genes belonging to 7 subgroups, on 600 kilobases :

18 FUNCTIONAL
3 ORF (Open Reading Frame)
17 PSEUDOGENE
2 FUNCTIONAL or PSEUDOGENE

Potential repertoire : 18-20 FUNCTIONAL IGKV genes belonging to 5 subgroups

Subgroup	Functional	ORF	Pseudogene
IGKV1	9(+1)*	1	4(+1)*
IGKV2	4(+1)*	-	9(+1)*
IGKV3	3	1	3
IGKV4	1	-	-
IGKV5	1	-	-
IGKV6	-	1	-
IGKV7	-	-	1
Total	18(+2)*	3	17(+2)*

* FUNCTIONAL or PSEUDOGENE (IGKV1-39, IGKV2-29)

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Human germline IGKV gene table

Fct : FUNCTIONALITY
F : Functional
P : Pseudogene
ORF : Open Reading Frame
R : Rearranged
T : Transcribed
P : Translated into protein

Part 1 - Sequences assigned to germline IGKV genes by sequence comparison

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.
NL : Not Localized

IGKV subgroup	IGKV gene name	Fct	R	T	P	Reference sequences ([12], unless indicated)	Accession numbers	Sequences from the literature
1	**1-5**	F				**L12**	Z00001 (V00559)	**HK102**[J00245][12]
		F				**V1[10]**	M23851	
		F	+	+	+	**L12a**	X72813	
	1-6	F		+		**L11**	M64858	**Vf**[12], DPK3[X93621][5]
	1-8	ORF (1)	+			**L9**	Z00014 (X00901/K02097)	**Ve**[12]
	1-9	F (2)	+	+		**L8**	Z00013 (X00902/K02096)	**Vd**[12], DPK8[X93626][5]
	1-12	F	+	+	+	**L5**	V01577 (X00898)	**Vb**[K02094][12], DPK5[X93623][5]
	1-12/1D-12	F	?	?		**L5/19a**	V01576 (X00899)	**Vb'**[8], **V4b**[12]
	1-13	P(3)				**L4**	Z00010 (X00903/K02093)	**Va**[12], DPK31[X93647][5]
	1-13/1D-13	F		?		**L4/18a**	Z00006 (X00900/K02098)	**Va'**[8], **V4a**[12]
	1-16	F		+	+	**L1**	J00248	**Q14**[12], **HK137**[12]
	1-17	F	+	+	+	**A30**	X72808	SG3[X92334][7]
	1-22	P (4)				**A25**	X71885	
	1-27	F (5)	+	+		**A20**	X63398	**Y2**[12], DPK4[X93622][5]
	1-32	P (6)				**A15**	X71883	DPK35(*)[X93651][5]
		P (6)				**A15a**	V00560	**HK100**[J00250 (J00251)][12], DPK35(*)
	1-33	F	+	+	+	**O18**	M64856	O18a[M64857][12], DPK1[X93620][5]
	1-35	P (7)				**O16**	X71890	**Q1**[12]

1-35/1D-35	P (7)				**O6/16a**	Z00005 (X00749/M23853)	**V55**[12]
1-37	F		+		**O14**	X59316	**Q5**[12]
1-37/1D-37	F		?		**O4/14a**	X70466	**DILp1**[12], DPK11(*) [X93629][5]
1-39	F	+	+	+	**O12**	X59315	DPK9(*) [X93627][5]
	P (8)				**O12a**	X59318	**V3b**[12]
1D-8	F	+	+		**L24**	Z00008 (X00750/M23850)	**Ve"**[12], **V13**[12], **Q3**[12], **L24a**[X72819][12], DPK10[X93628][5]
1D-12	F	?	?		**L19**	X17263	**Vb"**[12], DPK6[X93624][5]
1D-13	ORF (9)		?		**L18**	X17262	**Va"**[12]
1D-16	F				**L15**	K01323	**Q13**[12], **HK134**[X92329][12], **HK166**[2], DPK7[X93625][5]
	F				**L15a**	V00558 (J00244/J00246)	**HK101**[12], **HK146**[K01322][2], **HK189**[K01324][2]
1D-17	F	+			**L14**	X63392	**Q4**[12], DPK2[Z27498][5]
1D-22	P (4)				**A9**	X71887	
1D-27	P (10)				**A4**	Z00004 (X00748/M23848)	**A4a[12], V52**[12], DPK30 [X93646]
1D-32	P (11)				**O9**	X71896	
1D-33	F	?	?		**O8**	M64855	DPK1(*)
1D-35	P (7)				**O6**	X71894	
1D-37	F		?		**O4**	X71893	
1D-39	F	?	?		**O2**	X59312	DPK9(*)
1D-42	ORF (12)				**L22**	X72816	
1D-43	F				**L23**	X72817	**Q2**[12], **L23a**[X72818][12]
2-4	P (13)				**L13**	X72814	**Q6**[12]
2-10	P (14)				**L7**	Z00012 (X00904)	**Vc**[K02095][12]
2-14	P (15)				**L3**	X72810	**Q12**[12]
2-18	P (16)				**A29**	X63400	DPK27[X93643][5]
2-19	P (17)				**A28**	X12692	
2-23	P (18)				**A24**	X71885	
2-24	F	+	+		**A23**	X12684	DPK16[X93633][5]
2-26	P (19)				**A21**	X71884	
2-28	F	+	+	+	**A19**	X63397	**Q7** [12], DPK15(*) [X93632][5]
2-29	P (20)	+	+		**A18**	X63396	**A18a**[12], DPK28[X93644][5]
	F				A18b [1]	U41645	
2-30	F	+	+	+	**A17**	X63403	DPK18[X93635][5]
2-36	P (21)				**O15**	X71889	**Q8**[12]
2-38	P (22)				**O13**	X71888	
2-40	F		+	+	**O11**	X59314	DPK13(*)[X93631][5]
	F				**O11a**	X59317	**V3a**[12]
2D-10	P (14)				**L21**	X17265	**Vc"**[12]
2D-14	P (15)				**L17**	X72811	**Vz"**[8]
2D-18	P (16)				**A13**	X63395	

	2D-19	P (23)				**A12**	X71882		
	2D-23	P (24)				**A8**	X71887		
	2D-24	F				**A7**	X63401	DPK17[X93634][5]	
	2D-26	P (25)				**A5**	X12689		
	2D-28	F	?	?		**A3**	X12691	DPK15(*), RR25g][Z46616][5]	
	2D-29	F		+	+	**A2**	M31952	A2a[12], DPK12[X93630][5]	
		F (26)				A2c [1]	U41644	A2b[U41643][1]	
	2D-30	F		+		**A1**	X63402	DPK19[X93636][5]	
	2D-36	P (21)				**O5**	X71893		
	2D-38	P (22)				**O3**	X71892		
	2D-40	F		?		**O1**	X59311	DPK13(*)[5]	
	NL	F				DPK14	Z27499		
3	**3-7**	ORF (27)				**L10**	X02725	**kv3h**[3]	
		ORF (27)				**L10a**	X72812		
		ORF (27)				**Vh**	K02769		
	3-11	F	+	+		**L6**	X01668	**kv3g**[3], 38K/L6a[X92342][12],13K20/13K23[L37726][9]	
		F				**Vg**	K02768		
	3-15	F	+	+	+	**L2**	M23090	**O11**[12], **humkv328h5**[12], DPK21[X93638][5]	
	3-20	F	+	+	+	**A27**	X12686	**A27a**[M15038][12], **humkv325**[12], **humkv321**[M15039], VkRF[3], Tou kv325 [X56593][16], DPK22 [X93639][5]	
		F				13K18[9]	L37729		
	3-25	P (28)				**A22**	X06583 (X12685)	DPK29[X93645][5]	
	3-31	P (29)				**A16**	X71883		
		P (30)				**A16a**	M17765	**humkv301**[12]	
	3-31/3D-31	P (31)				**A16/O10b**	M17764	**humkv310**[12]	
	3-34	P (32)				**O17**	X71891		
	3D-7	F				**L25**	X72820	**V138**[12], **O9**[12], DPK23[Z27500][5]	
	3D-11	F	+			**L20**	X17264	**Vg"**[12], **kv3g"**[3], 13K11/13K12[L37725][9]	
	3D-15	F	?	?		**L16**	X72815	**O10**[12], **humkv328h2/L16a**[M23089][12], **humkv328/L16b**[M23088][12]/**humkv31es**[Y00640][4]	
		P (33)				**L16c**	M23091	**humkv329**[12]	
	3D-20	F	+			**A11**	X12687	**humkv305/A11a**[M14507][12], DPK20[X93637][5]	
	3D-25	P (28)				**A6**	X71886		
	3D-31	P (34)				**O10**	X71896		
	3D-34	P (35)				**O7**	X71895		
	NL	F				13K04[9]	L37728		
	NL	F				13K07/13K09[9]	L37727		
	NL	F				13K16/13K17[9]	L37730		
	NL	F				3A7[17]	L19271		
	NL	F				3A9[17]	L19272		

4	**4-1**	F	+	+	+	**B3**	Z00023	Vk IV, VkIV-GL [S56916][15], FSA10gl[Z46615][6], DPK24[X93640][5], HSIGKVZM[L33853]
5	**5-2**	F	+	+		**B2**	X02485	**EV15**[12]
6	**6-21**	ORF (36)		+		**A26**	X63399	DPK26(*) [X93642][5]
	6D-21	ORF (36)		?		**A10**	X12683	DPK26(*), HSIGKAU [M27750][14]
	6D-41	ORF (36)				**A14**	X12688	DPK25 [X93641][5], HSIGKAV [M27751][14]
7	**7-3**	P (37)				**B1**	X12682	

IGKV gene names 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. The IGKV genes of the distal duplicated V-CLUSTER are designated by the same number as the corresponding genes in the proximal V-CLUSTER, with the letter D added.

(*) As the DPK sequences only contain the V-REGION, some of them could be assigned neither to a gene or its duplicate, nor to any allele of the gene.
? Means that the rearrangement, transcript or protein could not be assigned to the gene in the proximal or distal cluster.

Accession numbers in parentheses correspond to secondary accession numbers.

Notes

(1) 21 bp DELETION starting at nucleotide 4 of DECANUCLEOTIDE [11].
(2) TTTGCTT instead of TTTGCAT in the core sequence of the DECANUCLEOTIDE element [11], but transcript found [8].
(3) CONSERVED_TRP replaced by a STOP-CODON in FR2, and non canonical V-HEPTAMER: CATAGTG instead of CACAGTG [11].
(4) STOP-CODONS in FR2, INSERTION of 4 bp at position 72 leading to a frameshift in FR3 [11].
(5) Non canonical V-HEPTAMER: CACTGTG instead of CACAGTG [3], but rearrangement product found [8].
(6) DELETION of 2 bp at position 17 and INSERTION of 1 bp at position 27/28, 1 bp at position 87/88, and 3 bp at position 85, leading to frameshifts [11].
(7) DELETION of nucleotide 4, and INSERTION of 1 bp at position 15/16. Defective DONOR_SPLICE [11].
(8) STOP-CODON in L-PART1 [11].
(9) Non canonical V-HEPTAMER: CATAGTG instead of CACAGTG [11].
(10) INSERTION of 1 bp at position 57 in FR3, leading to a frameshift [11].
(11) DELETION of 2 bp at position 17, INSERTION of 1 bp between codons 27/28, INSERTION of 3 bp in codon 85, INSERTION of 1 bp between codons 87/88 [11].
(12) TTTGCTT instead of TTTGCAT in the core sequence of the DECANUCLEOTIDE, and altered V-HEPTAMER: CACAGGG instead of CACAGTG [11].
(13) No INIT-CODON: ATG replaced by GTG [11].
(14) DELETION of 1 bp at position 74 leading to a frameshift, no INIT-CODON: ATG replaced by GTG, and non canonical ACCEPTOR_SPLICE [11].
(15) No INIT-CODON: ATG replaced by GTG , CT instead of GT in ACCEPTOR_SPLICE, and DELETION of 1 bp at position 4 leading to a frameshift, and non @ canonical V-HEPTAMER [11].
(16) No INIT-CODON: ATG replaced by ATA [11].
(17) No Vk-gene related sequence was found upstream of codon 12, 5' part of V-REGION truncated [11].
(18) V-EXON consists of 2 parts, separated by 180 bp that show no homology to Ig genes. STOP-CODON at position 35, and no INIT-CODON: ATG replaced by GTG [11].
(19) Frameshift in FR2 due to 1 bp INSERTION at position 39, and non canonical V-NONAMER [11].
(20) STOP-CODON at position 88 in FR3 [11].

(21) STOP-CODONS in V-REGION, V-REGION truncated: breakoff of homology before codon 15 and after codon 87[11].
(22) STOP-CODONS in V-REGION, and breakoff of homology before codon 21, and STOP-CODON in V-REGION [11].
(23) No Vk-gene related sequence was found upstream of codon 12, 5' part of V-REGION truncated [11].
(24) V-EXON consists of 2 parts, separated by 180 bp that show no homology to Ig genes, STOP-CODON in FR2, and no INIT-CODON [11].
(25) INSERTION of 1 bp in codon 39 leading to a frameshift in FR2, and DELETION of 1 bp in codon 45 [11], and frameshift in FR1 [13]
(26) A2c and A2b correspond to the same V-REGION allele. According to the IMGT functionality definition, A2b is ORF due to a non canonical V-HEPTAMER: CACAGAG instead of CACAGTG [1].
(27) GG instead of AG in the ACCEPTOR_SPLICE [11].
(28) Heavily mutated, insertion of 1.2 kb in V-INTRON. INSERTION of: 3 bp in codon -14/13, 7 bp in codon 81, and DELETION of: 2 bp in codon 27A, 24 bp from codon 56 to 65, 1 bp in codon 83 [11].
(29) STOP-CODON in L-PART1, and DELETION of 2 bp in codon 6 leading to a frameshift [11].
(30) DELETION of 2 bp in codon 5 leading to a frameshift [3].
(31) DELETION of 2 bp at position 6, leading to a frameshift [11].
(32) STOP-CODON in FR1 and FR2 at positions 23 and 38, INSERTION of 1 bp at position 85/86 [11].
(33) STOP-CODON in CDR3 in codon 94 [11].
(34) STOP-CODON in L-PART1, and 2 bp DELETION at position 6 leading to a frameshift [11].
(35) STOP-CODON in FR1 and FR2 at positions 23 and 38, INSERTION of 1 bp at position 85/86 [11].
(36) Non canonical V-HEPTAMER: CACTGTG instead of CACAGTG [11].
(37) No INIT-CODON: ATG replaced by ATA [11].

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Part 2 - Human IGKV orphons

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.

IGKV subgroup	IGKV gene name	Fct	Reference sequences	Accession number [8]	Localisation	Sequences from the literature
1	**1/OR-1**	P (1)	**Z1**	M23653	Outside chr2 [7]	[M20813]
	1/OR-2	P (2)	**Z2**	X64640 (S37418)	Outside chr2 [7]	DPK34 [X93650] [2]
	1/OR-3	P (3)	**Z3**	X64641 (S37419)	Outside chr2 [7]	DPK37 [Z27501] [2]
	1/OR-4	P (4)	**Z4**	X64642 (S37421)	Outside chr2 [7]	
	1/OR1-1	P (5)	**Chr1**	M20809 (M20708)	Chr1 [5]	
	1/OR2-0	ORF (21)	**Z0**	Y08392	Chr2 : 2p12, at, at least, 140 kb in 5' of IGKV3D-7 [1]	
	1/OR2-3	P (6)	**W3**	X05102	Long arm of chr2: 2q11-cen [9]	
	1/OR2-6	P (7)	**W6**	X05103	Long arm of chr2: 2q11-cen [9]	
	1/OR2-9	P (6)	**W9**	X51879	Long arm of chr2: 2q11-cen [9]	
	1/OR2-11	P (6)	**W11**	X51885	Long arm of chr2: 2q11-cen [9]	
	1/OR2-108	ORF	**V108**	X51887	Long arm of chr2 [8]: 2q12-14 [3]	
	1/OR2-118	P (9)	**V118**	M20812 (M20711)	Outside chr2 [7]	
	1/OR22-1	P (10)	**Chr22-1**	Z00040	Chr22 [5]	
	1/OR22-5	P (11)	**Chr22-5**	Z00003 (M23852/X00747)	Chr22 [5]	**V14**
	1/OR22-5a	P (11)	**Chr22-5a**	Z00002 (M23849/X00746)	Chr22 [5]	**V2b**[8]
2	**2/OR2-1**	P (8)	**W1**	X05101	Long arm of chr2: 2q11-cen [9]	
	2/OR2-1a	P (8)	**W1a**	X76074	Long arm of chr2: 2q11-cen [9]	
	2/OR2-2	P (12)	**W2**	X51884	Long arm of chr2: 2q11-cen [9]	DPK32[X93648] [2]
	2/OR2-4	P (13)	**W4**	X51883	Long arm of chr2: 2q11-cen [9]	
	2/OR2-7	P (14)	**W7**	X51881	Long arm of chr2: 2q11-cen [9]	
	2/OR2-8	P (15)	**W8**	X51880	Long arm of chr2: 2q11-cen [9]	DPK33 (*)[X93649] [2]
	2/OR2-10	P (16)	**W10**	X51886	Long arm of chr2: 2q11-cen [9]	DPK33 (*)
	2/OR22-3	P (17)	**Chr22-3**	Z00041	Chr22 [5]	
	2/OR22-4	P (18)	**Chr22-4**	M20707 (M20808)	Chr22 [5]	DPK36[X93652] [2]
3	**3/OR2-5**	P (19)	**W5**	X51882	Long arm of chr2: 2q11-cen [9]	
	3/OR2-268	ORF	**V268**	X74459	3' side of IGKC at 1.5Mb [8]	
	3/OR2-268a	ORF	**V268a**	X74460	3' side of IGKC at 1.5Mb [8]	
	3/OR22-2	P (20)	**Chr22-2**	Z00042	Chr22 [5]	

Accession numbers in parentheses correspond to secondary accession numbers.
(*) DPK33 could not be assigned to either 2/OR2-8 or 2/OR2-10 by the authors.

Notes

(1) No INIT-CODON: ATG replaced by ACG.
(2) No INIT-CODON: ATG replaced by ACG [7].

(3) No INIT-CODON: ATG replaced by AAG [7].
(4) No INIT-CODON: ATG replaced by ACA [7].
(5) No INIT-CODON: ATG replaced by ACA.
(6) STOP-CODON at position 87.
(7) STOP-CODONs at position -5 and 91, and 10 bp DELETION between codons 91/92 [6].
(8) STOP-CODONs at positions 35 and 36, and INSERTION of 2 bp in codon 87, leading to a frameshift [6].
(9) STOP-CODON at position 87, and no INIT-CODON: ATG replaced by ACA.
(10) INSERTION of 7 bp at position 1093 leading to a frameshift [4].
(11) STOP-CODON at position 71, and no INIT-CODON: ATG replaced by ACG [seq].
(12) 1 bp DELETION at position 740, 1 bp DELETION at position 935 leading to frameshifts, and STOP-CODON in L-PART1.
(13) 1 bp DELETION in L-PART1, STOP-CODON at position 36, and 2 bp INSERTION between positions 1046/1047 leading to a frameshift.
(14) STOP-CODON at position 36, INSERTION of 2 bp at position 957 leading to a frameshift.
(15) STOP-CODON in L-PART1, 1 bp DELETION at positions 731 and 925 leading to frameshifts.
(16) STOP-CODON in L-PART1, 1 bp DELETION at positions 744 and 938 leading to frameshifts.
(17) INSERTION of 3 bp between codons 22 and 23, DELETION of 1 bp at position 315 leading to a frameshift, and STOP-CODONs.
(18) STOP-CODON at position 81.
(19) No INIT-CODON: ATG replaced by ACG, 2 bp DELETIONs at positions 727, 831 and 833, 1 bp DELETION at position 747, leading to frameshifts.
(20) Breakoff of homology after codon 79, STOP-CODONs and DELETION [4].
(21) Defective DECANUCLEOTIDE, non canonical V-HEPTAMER and V-NONAMER [1].

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Table 3

Human IGKV 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.
Mutations affecting the same codon are separated by a vertical line.

IGKV subgroup	IGKV gene name	Fct	IGKV allele name	Accession number	Confirmed by genetics and/or data	Description of mutations
1	1-5	F	V1-5*01	**Z00001**	+	c65 ,T22 lg166 ,t168 ,D56 lc171 lc174 lg201 l
		F	V1-5*02	M23851		c65>t, T22>ll
		F	V1-5*03	X72813		lg166>a,t168>g,D56>Klc171>glc174>tlg201>al
	1-6	F	V1-6*01	**M64858**	+	
	1-8	ORF	V1-8*01	**Z00014**		
	1D-8	F	V1D-8*01	**Z00008**	+	
	1-9	F	V1-9*01	**Z00013**	+	
	1-12	F	V1-12*01	**V01577**	+	lc334 l
	1D-12	F	V1D-12*01	**X17263**	+	t30 lt270 lc334 l
	1-12/1D-12(1)	F	V1-12*02/1D-12*02	V01576		c334>tl (if IGKV1-12*02); t30>clt270>clc334>tl (if IGKV1D-12*02)
	1-13	P	V1-13*01	**Z00010**	+	a123, *41 la326, N109 l
	1D-13	ORF	V1D-13*01	**X17262**		la326, N109 l
	1-13/1D-13(1)	F	V1-13*02/1D-13*02	Z00006		a123>g,*41>Wla326>g,N109>Sl (if IGKV1-13*02); la326>g,N109>Sl (if IGKV1D-13*02)
	1-16	F	V1-16*01	**J00248**		
	1D-16	F	V1D-16*01	**K01323**	+	t78 ,S26 l
		F	V1D-16*02	V00558	+	t78>g,S26>Rl
	1-17	F	V1-17*01	**X72808**	+	
	1D-17	F	V1D-17*01	**X63392**		
	1-27	F	V1-27*01	**X63398**	+	
	1-33	F	V1-33*01	**M64856**	+	
	1D-33	F	V1D-33*01	**M64855**		
	1-37	F	V1-37*01	**X59316**		
	1D-37	F	V1D-37*01	**X71893**		
	1-39	F	V1-39*01	**X59315**	+	c29 ,S10 lc306 la315 lc316 ,a317 ,g318 ,Q106 la319 ,S107 lc330 l
		P	V1-39*02	X59318		c29>t,S10>Flc306>tla315>glc316>t,a317>g,g318>t,Q106>Cla319>g,S107>Glc330>al
	1D-39	F	V1D-39*01	**X59312**		
	1D-42	ORF	V1D-42*01	**X72816**		
	1D-43	F	V1D-43*01	**X72817**	+	
2	2-24	F	V2-24*01	**X12684**	+	
	2D-24	F	V2D-24*01	**X63401**	+	
	2-28	F	V2-28*01	**X63397**		
	2D-28	F	V2D-28*01	**X12691**	+	
	2-29	P	V2-29*01	**X63396**	+	g159 la312 ,*104 l
		F	V2-29*02	U41645		g159>ala312>c,*104>Cl
	2D-29	F	V2D-29*01	**M31952**	+	c145 ,P49 l
		F(2)	V2D-29*02	U41644		c145>t,P49>Sl
	2-30	F	V2-30*01	**X63403**	+	
	2D-30	F	V2D-30*01	**X63402**	+	

	2-40	F	V2-40*01	**X59314**		c120 Ig123 ,W41 Ig233 ,G78 I
		F	V2-40*02	X59317		c120>tIg123>t,W41>CIg233>a,G78>DI
	2D-40	F	V2D-40*01	**X59311**		
3	3-7	ORF	V3-7*01	**X02725**		a118 ,T40 It126 Ic141 Ig147 Ia208 ,S70 Ic322 ,H108 Ic571 ,T85 I
		ORF	V3-7*02	X72812		a118>t,T40>SIt126>cIc141>gIg147>tIa208>g,S70>GIc322>t,H108>YI
		ORF	V3-7*03	**K02769**		Ic571>g,T85>RI
	3D-7	F	V3D-7*01	**X72820**	+	
	3-11	F	V3-11*01	**X01668**	+	c568, T85 I
		F	V3-11*02	**K02768**	+	c568>g,T85>RI
	3D-11	F	V3D-11*01	**X17264**	+	
	3-15	F	V3-15*01	**M23090**	+	
	3D-15	F	V3D-15*01	**X72815**	+	c14 ,T5 Ig330 ,W110 I
		P	V3D-15*02	M23091		c14>t,T5>MIg330>a,W110>*I
	3-20	F	V3-20*01	**X12686**	+	g15 Ig26 ,G9 Ia221 ,c222 ,D74 Ig303 I
		F	V3-20*02	L37729		g15>aIg26>c,G9>AIa221>c,c222>a,D74>AIg303>tI
	3D-20	F	V3D-20*01	**X12687**	+	
4	4-1	F	V4-1*01	**Z00023**	+	
5	5-2	F	V5-2*01	**X02485**		
6	6-21	ORF	V6-21*01	**X63399**		
	6D-21	ORF	V6D-21*01	**X12683**	+	
	6D-41	ORF	V6D-41*01	**X12688**	+	

Notes

(1) Sequences which could not be assigned to the proximal or to the distal V-CLUSTER gene have been aligned with sequences of both genes. Both allele designation resulting from this alignment are given, separated by a dash, and mutation description is given by comparison to allele *01 of both genes.
Ex: Sequence Z00006 is designated as IGKV1-13*02/1D-13*02.

(2) An ORF sequence also exists for this V-REGION allele, due to a non-canonical heptamer.

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Human germline IGKJ table

All sequences in this table have been mapped
Fct: FUNCTIONALITY
F : Functional

IGKJ name	Fct	Reference sequences	Accession numbers	Sequences from the literature
IGKJ1	F	J1	J00242[1]	V00556[1][4], X61584[6], X67858[5]
IGKJ2	F	J2	J00242[1]	V00556[1][4], X63370[3], X61584[6], X67858[5]
IGKJ3	F	J3	J00242[1]	V00556[1][4], X63370[3], X61584[6], X67858[5]
IGKJ4	F	J4	J00242[1]	V00556[1][4], D90159[2], X61584[6], X67858[5]
IGKJ5	F	J5	J00242[1]	V00556[1][4], X61584[6], X67858[5]

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Table 5 **Human IGKJ allele table**

Fct : FUNCTIONALITY
F : Functional

The accession number of a reference sequence is given for each allele.
IMGT numbering and description of alleles for germline J-REGIONs start with the first nucleotide of the first codon.

IGKJ name	Fct	IGKJ Allele name	Accession number	confirmed by genetics and/or data	Description of mutations
IGKJ1	F	J1*01	**J00242**	+	
IGKJ2	F	J2*01	**J00242**	+	
IGKJ3	F	J3*01	**J00242**	+	
IGKJ4	F	J4*01	**J00242**	+	
IGKJ5	F	J5*01	**J00242**	+	

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