

# The Human T Cell Receptor Alpha Variable (TRAV) Genes

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## Key Words

Human genes · IMGT · T cell receptor ·  
Alpha variable genes

## Abstract

'Human T Cell Receptor Alpha Variable (TRAV) Genes', the eighth report of the 'IMGT Locus in Focus' section, comprises four tables: (1) 'Number of human germline TRAV genes at 14q11 and potential repertoire'; (2) 'Human germline TRAV genes at 14q11'; (3) 'Human TRAV allele table', and (4) 'Correspondence between the different human TRAV gene nomenclatures'. These tables are available at the IMGT Marie-Paule page of **IMGT**, the international ImMunoGeneTics database (<http://imgt.cines.fr:8104>) created by Marie-Paule Lefranc, Université Montpellier II, CNRS, France.

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## Introduction

'Human T Cell Receptor Alpha Variable (TRAV) Genes' is the eighth report of the 'IMGT Locus in Focus' section, launched in

the April 1998 issue of *Experimental and Clinical Immunogenetics* [1]. We have previously reported the complete repertoire of the human germline IGH, IGK and IGL genes [2–6], and that of the human germline TRBV genes [7]. This eighth report on the human T cell receptor alpha variable genes comprises four tables: (1) 'Number of human germline TRAV genes at 14q11 and potential repertoire'; (2) 'Human germline TRAV genes at 14q11'; (3) 'Human TRAV allele table', and (4) 'Correspondence between the different human TRAV gene nomenclatures'. These tables are available at the IMGT Marie-Paule page of **IMGT**, the international ImMunoGeneTics database (<http://imgt.cines.fr:8104>) created by Marie-Paule Lefranc, Université Montpellier II, CNRS, France [8–10]. Descriptions of functionality (functional, open reading frame, pseudogene) and mutations are in accordance with the IMGT Scientific chart [10], available at the IMGT Marie-Paule page. Nucleotide and amino acid numbering of the V-REGION is in accordance with the unique IMGT numbering system [9, 11, 12].

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**Table 1**

**Number of human germline TRAV genes at 14q11.2  
and potential repertoire**

IMGT TRAV subgroups are according to Boysen, C. et al., unpublished (AE000658 - AE000661).

54 TRAV genes belonging to 41 subgroups, on 700 kilobases :  
 45 FUNCTIONAL  
 7 PSEUDOGENE  
 2 FUNCTIONAL or PSEUDOGENE

Potential repertoire : 45-47 FUNCTIONAL TRAV genes belonging to 41 subgroups

Subgroup	Functional	ORF	Pseudogene	Total
TRAV1	2	-	-	2
TRAV2	1	-	-	1
TRAV3	(1*)	-	(1*)	1
TRAV4	1	-	-	1
TRAV5	1	-	-	1
TRAV6	1	-	-	1
TRAV7	1	-	-	1
TRAV8	6	-	1	7
TRAV9	2	-	-	2
TRAV10	1	-	-	1
TRAV11	1	-	-	1
TRAV12	3	-	-	3
TRAV13	2	-	-	2
TRAV14/DV4	1	-	-	1
TRAV15	-	-	1	1
TRAV16	1	-	-	1
TRAV17	1	-	-	1
TRAV18	1	-	-	1
TRAV19	1	-	-	1
TRAV20	1	-	-	1
TRAV21	1	-	-	1
TRAV22	1	-	-	1
TRAV23/DV6	1	-	-	1
TRAV24	1	-	-	1
TRAV25	1	-	-	1
TRAV26	2	-	-	2
TRAV27	1	-	-	1
TRAV28	-	-	1	1
TRAV29/DV5	(1)*	-	(1)*	1
TRAV30	1	-	-	1
TRAV31	-	-	1	1
TRAV32	-	-	1	1
TRAV33	-	-	1	1
TRAV34	1	-	-	1
TRAV35	1	-	-	1
TRAV36/DV7	1	-	-	1
TRAV37	-	-	1	1
TRAV38/DV8	2	-	-	2
TRAV39	1	-	-	1
TRAV40	1	-	-	1
TRAV41	1	-	-	1
Total	45(+2)*	0	7(+2)*	54

\* FUNCTIONAL or PSEUDOGENE (TRAV3, TRAV29/DV5)

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**Table 2. Human germline TRAV genes at 14q11.2**

Fct: FUNCTIONALITY  
 F: Functional  
 P: Pseudogene  
 ORF: Open Reading Frame  
 vg: Vestigial  
 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.

Functionality is shown between:

- parentheses when the accession number refers to rearranged genomic DNA or cDNA and the corresponding germline gene has not yet been isolated.

- brackets when the accession number refers to genomic DNA, but not known as being germline or rearranged.

Sequences assigned to germline TRAV genes at 14q11 by sequence comparison.

**Reference 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.

Since the TRD locus is embedded in the TRA locus, five V-GENES have been found rearranged to both (DV) segments of the TRD locus and TRAJ segments.

These genes are designated as TRAV14/DV4, TRAV23/DV6, TRAV29/DV5, TRAV36/DV7 and TRAV38-2/DV8.

TRAV subgroup	TRAV gene name	Fct	Reference sequences						Accession numbers	Sequences from the literature
			R	T	P	R	T	P		
1	1-1	F	+	+					<b>V1S1</b> AE000658 [40]	[M12070][21]#hg
		(F)	+	+					Valpha7.1 X04939 [1]#c	AV7S1[U11161]35 (12)°
1-2	F	+	+						<b>V1S2</b> AE000658 [40]	Valpha7[X58744][15](3)#c
		[F]							AV7S2 U32544 [38](29)°	
2	2	F	+	+					<b>V2S1</b> AE000658 [40]	Valpha11.1[X04936][1]#c, AV11S1[U32522]38 (17)°
									(F) +	
3	3	F	+	+					<b>Valpha11.1</b> M17659 [7]#c AE000658 [40]	Valpha1.6[M117651][7]#c, AV16S1[U32525]38 (22)°
									(P)(1) +	
									<b>Valpha16.1</b> M27377 [13]#c	

4	4	F	+ +	V4S1	AE0006558 [40]	Valpha16.1[M17663][7]#c, AV20S1[U32529][38](27)°
5	5	F	+ +	V5S1	AE0006559 [40]	Valpha15.1[M27376][13]#c
6	6	F	+ +	V6S1	AE0006559 [40]	
		(F)	+ +	Valpha5	X58747[15](3)##c	
		(F)	+ +	<b>AV5S1</b>	Z49060 [16](7)°	
		(F)	+ +	AV5S1	Y10409 [17](7)°	
		(F)	+ +	AV5S1	Y10410 [17](7)°	
		[F]		AV5S1	U32542 [38](28)°	
7	7	F	+ +	<b>V7S1</b>	AE0006559 [40]	
8	8-1	F	+ +	V8S1	AE0006559 [40]	Valpha1.1[X04949][1]#c
		[F]		AV1S1	U32520 [38](15)°	
8-2		F	+ +	<b>V8S2</b>	AE0006559 [40]	
		(F)	+ +	Valpha1.5	M17650 [7]#c	
				V8S3	AE0006559 [40]	
8-3		F	+ +	<b>Valpha1.4</b>	M35617[10]#g	
		(F)	+ +	Valpha1.n1	L06885 [11](3)##c	
		(F)	+ +	<b>V8S4</b>	AE0006559 [40]	[X02592][2]#c
8-4		F	+ +		M12423 [3]#c	
		(F)	+ +		D13077 [4](3)##c	
		(F)	+ +	AV1.2a		
		(F)	+ +		M12959 [2]#c	
		(F)	+ +	Valpha1.2	X63455 [5]#c	
		(F)	+ +		K02777 [6](4)##c	
		(F)	+ +	<b>Valpha1.2</b>	M17665 [7](5)##c	
8-5	P			<b>V8S5</b>	AE0006559 [40]	
8-6		F	+ +	2	X02850 [8]	
		F	+ +	<b>V8S6</b>	AE0006559 [40]	Valpha1.3[M86361][9]#c
8-7		F	+ +	<b>V8S7</b>	AE0006660 [40]	
9	9-1	F	+ +	<b>V9S1</b>	AE0006559 [40]	
				<b>V9S2</b>	AE0006559 [40]	AV22.1a[D13072][4]#c
	9-2	F	+ +	Valpha22	X58745[15](3)##c	AV22S1[U32530][38](19)°
		(F)	+ +	Valpha22n1	L06881 [11](3)##c	
		(F)	+ +	Valpha22n2	L06882 [11](3)##c	

10	10	F	++	V10S1	AE000659 [40]	Valphaw24[X58737][15](3)#c, AV24S1[U32532][38](23)°
11	11	F	++	V11S1	AE000659 [40]	
12	12-1	F	++	V12S1	AE000659 [40]	AV2.5a[D13078][4](3)#c
	(F)	++		Valpha2.3	M17657 [7]#c	
	12-2	F	++	V12S2	AE000659 [40]	Valpha2.2[M27369][13](6)#c
	(F)	++		Valpha2.1	M81774 [12]#c	AV2S1[L11159][35](11)°
	(F)	++		Valpha2.1	X04946 [1](6) #c	
	12-3	F	++		X06193 [14]	V12S3[AE000659][40], AV2S4[U32538][38](25)°
		(F)	++	Valpha2.2	M17656 [7]#c	
13	13-1	F	++	V13S1	AE000659 [40]	AV8.1a[D13079][4](3)#c, [M99570][37](14)
		(F)	++	Valpha8.1	X04954 [1]#c	
				[F]	AV8S1	L11162 [35](24)°
					V13S2	AE000659 [40]
					Valpha8.2	AV8S2[U32545][38](11)°
				(F)	M17658 [7]#c	
14	14/DV4	F	++		M21626 [18]	
		F	++		hADV14S1	AE000659 [40]
		(F)	++		M21624 [18]#c	[S51029][20](8) #c
				[F]	AV06S1	L09758 [19]°
15	15	P(31)		V15S1	AE000659 [40]	
16	16	F	++	V16S1	AE000659 [40]	Valpha9.1[X04942][1]#c, AV9S1[U32546][38](20)°
17	17	F	++	V17S1	AE000660 [40]	Valpha3.1[X04955][1]#c, AV3S1[U32540][38](26)°
18	18	F	++	V18S1	AE000660 [40]	
19	19	F	++	V19S1	AE000660 [40]	[X01403][22]#c
20	20	F	++	V20S1	AE000660 [40]	X68696 [2](3) #c
		(F)	++			S60789 [33](10) #c
		(F)	++			Valpha28.2
		(F)	++			Valphaw30 X70305 [26](3) #c

					V21S1	AE0000660 [40]	
21	21	F	(F)	+	Valphaw23	X58736 [15](3)#c	
22	22	F	F	+	V22S1	AE0000660 [40]	
23	23/DV6	F	F	+	hADV23S1	AE0000660 [40]	
						Valpha17b[X70309](26)(13)*, Valpha13.1[M27374](13)*c, Valpha13.1[M22936](36)(13)*, AV7S1[U32526](38)(30)°, Valpha13.1[M22936](36)(13)*	
						Valpha13.1 M17660 [7]#c AV7S1[Z49057](16)(9)°	
						Valpha17.1-V M97704 (27)#[c]	
			[F]	+		Y10411 [17](9)°	
24	24	F	F	+	V24S1	AE0000660 [40]	
25	25	F	F	+	V25S1	AE0000660 [40]	
26	26-1	F	F	+	V26S1	AE0000660 [40]	
		(F)	(F)	+	Valpha4.2	M27371 [13]#c AV4S2[U32541](38)(27)°	
						Valpha4.n1 L06886 [11](3)#c	
						Valpha2	AE0000660 [40]
						Valpha4.1[X04937](1)#[c]	
						AV4S1 L11160 (35)(11)°	
27	27	F	F	+	V27S1	AE0000660 [40]	
		(F)	(F)	+		AV10S2[L09760](19)(9)°, AV10S1[U32521](38)(16)°*	
						X04957 [1]#c	
						D13075 [4](3)#c AV10S1[U32521](38)(16)°*, AV10S2[L09759](19)(9)°	
28	28	P(32)			V28S1	AE0000660 [40]	
29	29/DV5	F	F	+	hADV29S1	AE0000660 [40]	
		(F)	(F)	+	Valpha21a	S81645 [28]#[c]	
			P(2)		Valpha21c	[28]	
30	30	F	F	+	V30S1	AE0000660 [40]	
		(F)	(F)	+		[S633879](30)#[g]	
						Valphaw29 X58768 [15](3)#c	
						L06883 [11](3)#c	
						1	
						AV29S1 U32537 (38)(24)°	
31	31	P(31)			V31S1	AE0000660 [40]	
32	32	P(31)			V32S1	AE0000660 [40]	
33	33	P(33)			V33S1	AE0000660 [40]	
34	34	F		+	V34S1	AE0000660 [40]	
						Valphaw26[X58739](15)(3)#c, AV26S1[U32534](38)(23)°	

35	35	F		V35S1	AE0000660 [40]
	(F)	+	+	Valphaw25	X58738 [15](3#C AV25S1[U32533][38](20)°
36	36/DV7	F		<b>hADV36S1</b>	AE0000660 [40]
	(F)	+	+	Valphaw28	X61070[15]#C
	(F)	+	+	Valphaw28	X58767 [15](3#C
	(F)	+	+	Vdelta7	Z46643 [29]#C AV28S1[U32536][38](19)°
37	37	P(34)		<b>V37S1</b>	AE0000661 [40]
38	38-1	F	+	<b>V38S1</b>	AE0000661 [40] Valpha14.1a[D13074][4](3) #C
	(F)	+	+	VA14.2	M64355 [24]#C
	(F)	+	+	M95394 [25]#C	
	(F)	+	+	Valpha14.n1	L06880 [11](3) #C
38-2/DV8		F	+	<b>hADV38S2</b>	AE0000661 [40] Valpha14.1[Z29614][23]#C, Valpha8[Z46644][29]#g, AV14S1[U32524][38](18)°, Valpha14.2[X58158][39](30)
39	39	F	+	<b>V39S1</b>	AE0000661 [40] Valphaw27[X58740][15](3) #C
40	40	F		Valpha31	X73521 [34] <b>V40S1</b> [AE000661][40]
41	41	F	+	<b>V41S1</b>	AE0000661 [40] Valpha15.1[M17662][7]#C, AV19S1[U32528][38](21)°

#c: rearranged cDNA, #g: rearranged genomic DNA.

° DNA genomic sequence, but not known to be rearranged or germline.

\* Partial sequences which could not be assigned to a given allele.

IMGT notes:

- (1) DELETION of one nucleotide in FR1-IMGT (c20>del#), leading to a frameshift.
- (2) DELETION of one nucleotide leading to a frameshift.
- (3) CDR3-IMGT is partial: only amino acid 105 is present.
- (4) Due to several sequencing errors between nucleotides 1 and 30, this part of the sequence is not annotated and FR1-IMGT and CDR1-IMGT have not been assigned. As a consequence, V-REGION is partial.
- (5) V-REGION is partial: AA 1 to 29 are missing (no FR1-IMGT, and partial CDR1-IMGT).
- (6) V-REGION is partial: AA 1 to 8 are missing (partial FR1-IMGT).
- (7) V-REGION is partial: AA 1 to 8 are missing (partial FR1-IMGT), and only amino acid 105 is present ( partial CDR3-IMGT).
- (8) Rearranged CDR3-IMGT is partial.
- (9) V-REGION is partial: AA 1 is missing (partial FR1-IMGT), and no CDR3-IMGT.
- (10) V-REGION is partial: no CDR3-IMGT.
- (11) V-REGION is partial: AA 89 to 104 are missing (partial FR3-IMGT), and no CDR3-IMGT.
- (12) V-REGION is partial: AA 96 to 104 are missing (partial FR3-IMGT), and no CDR3-IMGT.
- (13) V-REGION is partial: AA 1 to 42 are missing (partial FR2-IMGT), and no FR1-IMGT.
- (14) V-REGION is partial: AA 1 is missing (partial FR1-IMGT), and only amino acid 105 is present (CDR3-IMGT partial).
- (15) V-REGION is partial: AA 99 to 104 are missing (partial FR3-IMGT), and no CDR3-IMGT.
- (16) V-REGION is partial: AA 79 to 104 are missing (partial FR3-IMGT), and no CDR3-IMGT.
- (17) V-REGION is partial: AA 71 to 104 are missing (partial FR3-IMGT), and no CDR3-IMGT.
- (18) V-REGION is partial: only one nucleotide in FR3-IMGT, and no CDR3-IMGT.
- (19) V-REGION is partial: AA 100 to 104 are missing (partial FR3-IMGT), and no CDR3-IMGT.
- (20) V-REGION is partial: AA 97 to 104 are missing (partial FR3-IMGT), and no CDR3-IMGT.
- (21) V-REGION is partial: AA 85 to 104 are missing (partial FR3-IMGT), and no CDR3-IMGT.
- (22) V-REGION is partial: AA 101 to 104 are missing (partial FR3-IMGT), and no CDR3-IMGT.
- (23) V-REGION is partial: AA 94 to 104 are missing (partial FR3-IMGT), and no CDR3-IMGT.
- (24) V-REGION is partial: AA 93 to 104 are missing (partial FR3-IMGT), and no CDR3-IMGT.
- (25) V-REGION is partial: AA 81 to 104 are missing (partial FR3-IMGT), and no CDR3-IMGT.
- (26) V-REGION is partial: AA 78 to 104 are missing (partial FR3-IMGT), and no CDR3-IMGT.
- (27) V-REGION is partial: AA 84 to 104 are missing (partial FR3-IMGT), and no CDR3-IMGT.
- (28) V-REGION is partial: AA 87 to 104 are missing (partial FR3-IMGT), and no CDR3-IMGT.
- (29) V-REGION is partial: AA 75 to 104 are missing (partial FR3-IMGT), and no CDR3-IMGT.
- (30) V-REGION is partial: AA 59 to 104 are missing (partial CDR2-IMGT), no FR3-IMGT, and no CDR3-IMGT.
- (31) Frameshifts in V-REGION.
- (32) Frameshift in FR3-IMGT.
- (33) STOP-CODON in V-REGION.
- (34) Frameshift in CDR1-IMGT.

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**Table 3. Human TRAV allele table**

Fct: FUNCTIONALITY  
 F: Functional  
 P: Pseudogene  
 ORF: Open Reading Frame  
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Functionality is shown below:

- Parentheses when the accession number refers to rearranged genomic DNA or cDNA and the corresponding germline gene has not yet been isolated.
- Brackets when the accession number refers to genomic DNA, but not known as being germline or rearranged.

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.  
 Nucleotide mutations and amino acid changes in CDR3-IMGT of rearranged sequences, are not taken into account for the description of polymorphism.

TRAV sub-group	TRAV gene name	Fct	TRAV allele name	Accession number	Confirmed by genetics and/or data	Description of mutations
1	1-1	F	V1*1*01	AE000658	+	c170>A57
		(F)	V1*1*02	X04639	+	c170>g A57>G
1-2	F		V1*2*01	AE000658	+	t205
		(F)	V1*2*02	U232544		t205>c
2	2	F	V2*1*01	AE000658	+	t114>Y42
		(F)	V2*1*02	M17659		t124>c Y42>H
3	3	F	V3*01	AE000658	+	c20
		(P)	V3*02	M27377		c20>del#
4	4	F	V4*01	AE000658	+	
5	5	F	V5*01	AE000659	+	
6	6	F	V6*01	AE000659		a78 c87 c165 a255 K85 a271 .191
		(F)	V6*02	X58747		c87>t c165>t
		(F)	V6*03	Z49060		c87>t c165>t
		(F)	V6*04	Y10409		a271>g 191>t
		(F)	V6*05	Y10410		a78>g c87>t
		(F)	V6*06	U32542		a255>c K85>N



22	22	F	V22*01	AE000660	+		
23	23/DV6	F	V23*01	AE000660	+	t <sub>55</sub> ,S19   a129   a132	
	(F)		V23*02	M17660	+	t <sub>55</sub> >c, S19>p	
	(F)		V23*03	M97704	+		
	(F)		V23*04	Y10411		a132>g	
24	24	F	V24*01	AE000660	+		
25	25	F	V25*01	AE000660	+		
26	26-1	F	V26-1*01	AE000660	+	c25 ,P9   t154 ,y52	
	(F)		V26-1*02	M27371	+	c25>a, P9>t	
	(F)		V26-1*03	L06886		c25>a, P9>t   t154>a, Y52>n	
26-2	26-2	F	V26-2*01	AE000660	+	c210 ,s77   c232 ,l79	
27	27	F	V26-2*02	L11160		c210>s, s77>c   c232>g, l79>y	
	(F)		V27*01	AE000660	+	a119 ,a2179   c236 ,p96   t302 ,l101	
	(F)		V27*02	X04957		a119>q, a2179>q   t302>a, l101>h	
29	29/DV5	F	V27*03	D13075	+	a119>q, a2179>q   c236>s, p96>t   t302>a, l101>h	
	(F)		V29*01	AE000660	+	c126   c234	
	P		V29*02	S81645		c234>t	
30	30	F	V29*03	[1]		c126>d#	
	(F)		V30*01	AE000660	+	t <sub>62</sub> ,t <sub>21</sub>   a209 ,x70   g211 ,g71   a215 ,h72   a254 ,q35	
	(F)		V30*02	X58768		t <sub>62</sub> >c, t <sub>21</sub> >t, a209>t, x70>m, g211>c, g71>r   a215>q, h72>r	
	(F)		V30*03	L06883		a254>q, q35>r	
34	34	F	V34*04	U32537			
35	35	F	V35*01	AE000660	+		
	(F)		V35*02	X58738		a115 ,c ,b44>d	
36	36/DV7	F	V35*01	AE000660	+	t <sub>26</sub> ,l9   c54   t <sub>62</sub> ,l21   g79   t119 ,l40   c257 ,s86   a301 ,l101	
	(F)		V35*02	X61070		t <sub>26</sub> >a, l9>q, c54>t	
	(F)		V35*03	X58767		c54>t, t <sub>62</sub> >c, l21>p	
	(F)		V35*04	Z46643	+	c54>t	
38	38-1	F	V38-1*01	AE000661	+	t <sub>21</sub>   a24   a89 ,n70   a91 ,n31   g129	
	(F)		V38-1*02	M64355		a91>g, n31>d	
	(F)		V38-1*03	M85394		a89>q, n70>g   g129>a	
	(F)		V38-1*04	L06880		t <sub>21</sub> >c, a24>g	
	38-	2(DV8	F	V38-2*01	AE000661	+	
39	39	F	V39*01	AE000661	+		
40	40	F	V40*01	X73521	+		
41	41	F	V41*01	AE000661	+		

Reference:  
[1] Wright, J.A. et al, Hum. Immunol., 32, 277-283 (1991).

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**Table 4****Correspondence between the different human TRAV gene nomenclatures**

TRAV genes are listed from 3' (top of the table) to 5' (bottom of the table).

IMGT TRAV gene name	Boysen et al. [1]	Arden et al. [2]
TRAV41	41S1	19S1
TRAV40	40S1	31S1
TRAV39	39S1	27S1
TRAV38-2/DV8	hADV38S2	14S1-ADV14S1
TRAV38-1	38S1	14S2
TRAV37	37S1	
TRAV36/DV7	hADV36S1	28S1-DV28S1
TRAV35	35S1	25S1
TRAV34	34S1	26S1
TRAV26-2	26S2	4S1
TRAV33	33S1	
TRAV32	32S1	
TRAV31	31S1	
TRAV30	30S1	29S1
TRAV29/DV5	hADV29S1	21S1-ADV21S1
TRAV28	28S1	
TRAV27	27S1	10S1
TRAV8-7	8S7	
TRAV26-1	26S1	4S2
TRAV25	25S1	32S1
TRAV24	24S1	18S1
TRAV23/DV6	hADV23S1	17S1-ADV17S1
TRAV22	22S1	13S1
TRAV21	21S1	23S1
TRAV20	20S1	30S1
TRAV19	19S1	12S1
TRAV18	18S1	
TRAV17	17S1	3S1
TRAV16	16S1	9S1
TRAV8-6	8S6	1S3
TRAV12-3	12S3	2S2
TRAV15	15S1	
TRAV9-2	9S2	22S1
TRAV14/DV4	hADV14S1	6S1-ADV6S1
TRAV13-2	13S2	8S2
TRAV8-5	8S5	
TRAV8-4	8S4	1S2
TRAV12-2	12S2	2S1
TRAV13-1	13S1	8S1
TRAV8-3	8S3	1S4
TRAV8-2	8S2	1S5
TRAV12-1	12S1	2S3
TRAV11	11S1	
TRAV10	10S1	24S1
TRAV9-1	9S1	
TRAV8-1	8S1	1S1
TRAV7	7S1	
TRAV6	6S1	5S1
TRAV5	5S1	15S1
TRAV4	4S1	20S1
TRAV3	3S1	16S1
TRAV2	2S1	11S1
TRAV1-2	1S2	7S2
TRAV1-1	1S1	7S1

**IMGT note:**

TRAV genes are designated by a number for the subgroup [1] followed, whenever there are several genes belonging to the same subgroup, by a dash and a number for their relative localisation in the locus.

**References:**

- [1] Boysen, C. et al., unpublished (AE000658-AE000661).  
[2] Arden, B. et al., Immunogenetics, 42, 455-500 (1995).

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