

This supplementary file includes examples of the Vδ1 and Vδ2 alignments obtained with IMGT.

IMGT/V-QUEST program version: 3.4.15; IMGT/V-QUEST reference directory release: 201851-4

Species:	Homo sapiens
Receptor type or locus:	TRD
IMGT directory reference set:	F+ORF+ in-frame P
Search for insertions and deletions:	no

Sequence: 13

Analysed sequence length:185.

Sequence analysis category: 1 (no indel search)

Sequence compared with the *Homo sapiens* (human) TR set from the IMGT reference directory

>3

```
tcaagaaagcagcgaatccgctgccttaaccattcagccttgagctagaagattcag  
caaagtactttgtgctcttggggccgaccccggaatccaccggtaaattcgtgttg  
gcacaagttccactgttactctgtccctgtaaatacagactcgtaactccttcggtt  
ttgtc
```

Result summary:	Productive TRD rearranged sequence: (no stop codon and in-frame junction)		
V-GENE and allele	Homsap TRDV1*01 F	score = 356	identity = 98.65% (73/74 nt)
J-GENE and allele	Homsap TRDJ1*01 F	score = 84	identity = 62.75% (32/51 nt)
D-GENE and allele by IMGT/JunctionAnalysis FR-IMGT lengths, CDR-IMGT lengths and AA JUNCTION	Homsap TRDD1*01 F [X.X.24.11]	 [X.X.14]	 CALGGRPRQSTGKFVF

V-REGION partial 5' missing nt nb: **199**

Sequence: 2 5

Analysed sequence length:185.

Sequence analysis category: 1 (no indel search)

Sequence compared with the *Homo sapiens* (human) TR set from the IMGT reference directory

>5

```
tcaagaaagcagcgaatccgtcgccttaaccattcagccttacagctagaagattcag  
caaagtactttgtgctcttgggggacggggtccggcgtacaccgataaactcatctttg  
gaaaaggaacccgtgtgactgtggaaccaa gaagtcagcctcataccaaccatccgtt  
ttgtc
```

Result summary:	Productive TRD rearranged sequence: (no stop codon and in-frame junction)		
V-GENE and allele	Homsap TRDV1*01 F	score = 365	identity = 100.00% (74/74 nt)
J-GENE and allele	Homsap TRDJ1*01 F	score = 255	identity = 100.00% (51/51 nt)
D-GENE and allele by IMGT/JunctionAnalysis FR-IMGT lengths, CDR-IMGT lengths and AA JUNCTION	Homsap TRDD3*01 F [X.X.24.11]	 [X.X.14]	 CALGGRGPAYTDKLIF

V-REGION partial 5' missing nt nb: **199**

Sequence: 39

Analysed sequence length:194.

Sequence analysis category: 1 (no indel search)

Sequence compared with the *Homo sapiens* (human) TR set from the IMGT reference directory

>9

```
ttagaagcagcgaatccgctgccttaaccattcagccttacagctagaagattcag  
caaagtacttctgtgctcttgggaactcctactattctactgggatacaccgataaac  
tcacctttgaaaaggaaccgtgtgactgtggaaccaaagaagtcagcctcataccaaac  
cttccgtttttgtc
```

Result summary:	Productive TRD rearranged sequence: (no stop codon and in-frame junction)		
V-GENE and allele	Homsap TRDV1*01 F	score = 347	identity = 97.30% (72/74 nt)
J-GENE and allele	Homsap TRDJ1*01 F	score = 255	identity = 100.00% (51/51 nt)
D-GENE and allele by IMGT/JunctionAnalysis	Homsap TRDD2*01 F and Homsap TRDD3*01 F		
FR-IMGT lengths, CDR-IMGT lengths and AA JUNCTION	[X.X.24.11]	[X.X.1 7]	CALGELLIFYWGYTDKLIF

V-REGION partial 5' missing nt nb: **199**

Sequence: 4 6

Analysed sequence length:195.

Sequence analysis category: 1 (no indel search)

Sequence compared with the *Homo sapiens* (human) TR set from the IMGT reference directory

>6

```
ttgcaaagcacctggctgtacttaagatactgcaccatcagagagatgaagggtct  
tactactgtcccgtgacactaagccagaagagaggggcctgtgtcctacaccgataaa  
ctcatcttgaaaaggaaccgtgtgactgtggaaccaagaaggcagcctcataccaa  
ccatcccgtttgtc
```

Result summary:	Productive TRD rearranged sequence: (no stop codon and in-frame junction)		
V-GENE and allele	Homsap TRDV2*01 F, or Homsap TRDV2*02 F or Homsap TRDV2*03 F	score = 322	identity = 97.10% (67/69 nt)
J-GENE and allele	Homsap TRDJ1*01 F	score = 255	identity = 100.00% (51/51 nt)
D-GENE and allele by IMGT/JunctionAnalysis	Homsap TRDD3*01 F		
FR-IMGT lengths, CDR- IMGT lengths and AA JUNCTION	[X.X.23.11]	[X.X.1 9]	CARDTKPEERGPVSYTDKLIF

V-REGION partial 5' missing nt nb: **207**

Sequence: 5 10

Analysed sequence length:191.

Sequence analysis category: 1 (no indel search)

Sequence compared with the *Homo sapiens* (human) TR set from the IMGT reference directory

>10

```
tcaagaaagcagcgaatccgtgccttaaccattcagccttacagctagaagattcag  
caaagtactttgtgctcttggggcaattgccgggggataccttacaccaataaactca  
tctttgaaaaggaaccgtgtgactgtggaaccaagaagtcagcctcataccaaacat  
ccgttttgc
```

Result summary:	Productive TRD rearranged sequence: (no stop codon and in-frame junction)		
V-GENE and allele	Homsap TRDV1*01 F	score = 356	identity = 98.65% (73/74 nt)
J-GENE and allele	Homsap TRDJ1*01 F	score = 246	identity = 98.04% (50/51 nt)
D-GENE and allele by IMGT/JunctionAnalysis FR-IMGT lengths, CDR-IMGT lengths and AA JUNCTION	Homsap TRDD3*01 F [X.X.24.11]	[X.X.16]	CALGAIARGIPYTNKLIF

V-REGION partial 5' missing nt nb: **199**

Sequence: 6 33

Analysed sequence length:180.

Sequence analysis category: 1 (no indel search)

Sequence compared with the *Homo sapiens* (human) TR set from the IMGT reference directory

>33

```
attgcaagaacctggctgtacttaagatactgcaccatcagagagatgaagggtct  
tactactgtgctgtgacctggaggggtcggaccaccgataaactcatcttgaaaa  
ggaacccgtgtgactgtggaaccaaagaagtcagcctcataccaaccatccgttttgc
```

Result summary:	Productive TRD rearranged sequence: (no stop codon and in-frame junction)		
V-GENE and allele	Homsap TRDV2*01 F, or Homsap TRDV2*02 F or Homsap TRDV2*03 F	score = 340	identity = 100.00% (69/69 nt)
J-GENE and allele	Homsap TRDJ1*01 F	score = 246	identity = 98.04% (50/51 nt)
D-GENE and allele by IMGT/JunctionAnalysis	Homsap TRDD3*01 F		
FR-IMGT lengths, CDR-IMGT lengths and AA JUNCTION	[X.X.23.11]	[X.X.14]	CACDTGGGRTTDKLIF

V-REGION partial 5' missing nt nb: **207**

Sequence: 7 46

Analysed sequence length:186.

Sequence analysis category: 1 (no indel search)

Sequence compared with the *Homo sapiens* (human) TR set from the IMGT reference directory

>46

```
attgcaaagaacctggctgtacttaagatactgcaccatcagagagatgaagggtct
tactactgtcctgtgacacccgtactggggacaccgaacgtacgataaactcatctt
ggaaaaggaaccgtgtgactgtggaaccaaagaagtcagcctcataccacccatccgtt
tttgc
```

Result summary:	Productive TRD rearranged sequence: (no stop codon and in-frame junction)		
V-GENE and allele	Homsap TRDV2*01 F, or Homsap TRDV2*02 F or Homsap TRDV2*03 F	score = 340	identity = 100.00% (69/69 nt)
J-GENE and allele	Homsap TRDJ1*01 F	score = 219	identity = 92.16% (47/51 nt)
D-GENE and allele by IMGT/JunctionAnalysis	Homsap TRDD3*01 F		
FR-IMGT lengths, CDR- IMGT lengths and AA JUNCTION	[X.X.23.11]	[X.X.1 6]	CACDTRTGGHRTYDKLIF

V-REGION partial 5' missing nt nb: 207

Sequence: 8 48

Analysed sequence length:174.

Sequence analysis category: 1 (no indel search)

Sequence compared with the *Homo sapiens* (human) TR set from the IMGT reference directory

>48

```
attgcaagaacctggctgtacttaagatacttgaccatcagagagatgaagggtct
tactactgtcctgtgacgccaagggtgacaccgataaactcatcttggaaaaggaacc
cgtgtgactgtggaaccaagaagtcagcctcatacacaacccatccgttttgtc
```

Result summary:	Productive TRD rearranged sequence: (no stop codon and in-frame junction)		
V-GENE and allele	Homsap TRDV2*01 F, or Homsap TRDV2*02 F or Homsap TRDV2*03 F	score = 340	identity = 100.00% (69/69 nt)
J-GENE and allele	Homsap TRDJ1*01 F	score = 255	identity = 100.00% (51/51 nt)
FR-IMGT lengths, CDR- IMGT lengths and AA JUNCTION	[X.X.23.11]	[X.X.1 2]	CACDAKVYTDKLIF

V-REGION partial 5' missing nt nb: **207**