

# Supporting evidence for the inference of TRBV5-6\*01 T284G

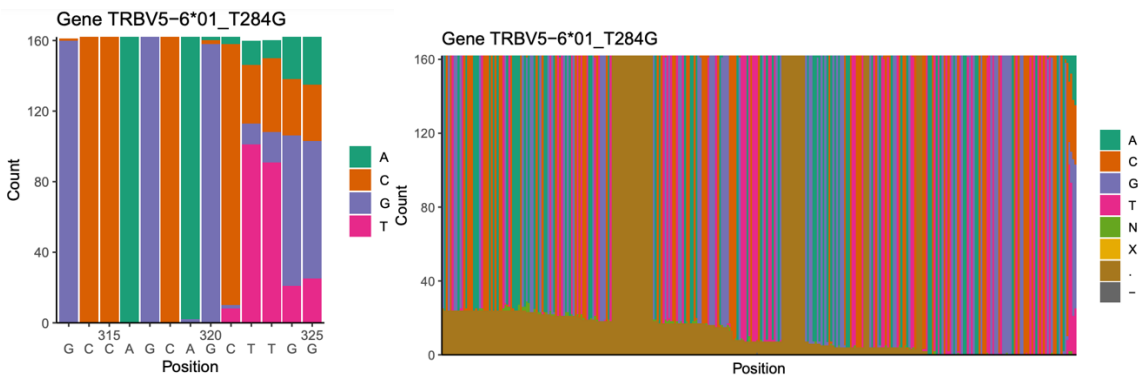
Inference based on VDJbase data set P4\_I12\_S1

Result summary: <b>TRBV5-6*01_T284G</b>		<b>No rearrangement found</b>	
V-GENE and allele	<a href="#">Homsap TRBV5-6*01 F</a>	score = 1356	identity = <b>99.63%</b> (272/273 nt)
FR-IMGT lengths, CDR-IMGT lengths	[5.6.X]		

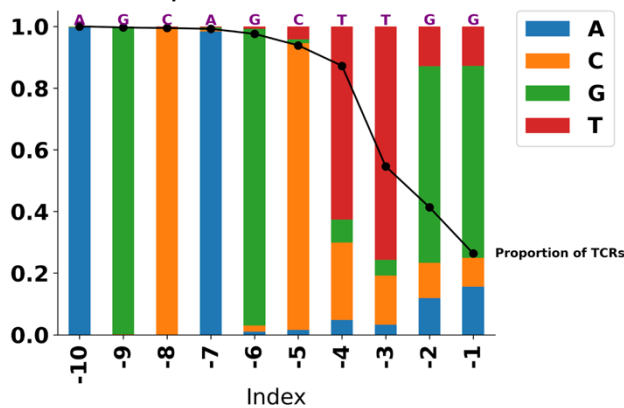
## 1. Alignment for V-GENE and allele identification

Closest V-REGIONS (evaluated from the V-REGION first nucleotide to the 2nd-CYS codon)

			Score	Identity
<a href="#">L36092</a>	Homsap	TRBV5-6*01 F	1356	99.63% (272/273 nt)
<a href="#">L36092</a>	Homsap	TRBV5-5*01 F	1212	93.77% (256/273 nt)
<a href="#">L36092</a>	Homsap	TRBV5-7*01 ORF	1212	93.77% (256/273 nt)
<a href="#">X57611</a>	Homsap	TRBV5-5*02 (F)	1203	93.41% (255/273 nt)
<a href="#">X58801</a>	Homsap	TRBV5-5*03 (F)	1203	93.41% (255/273 nt)

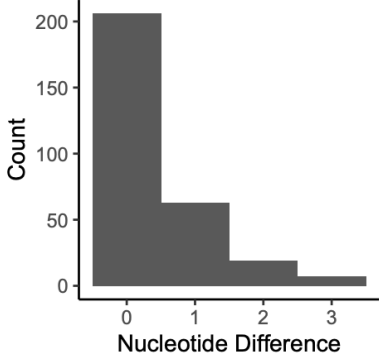


Consensus plot of 3'-end:



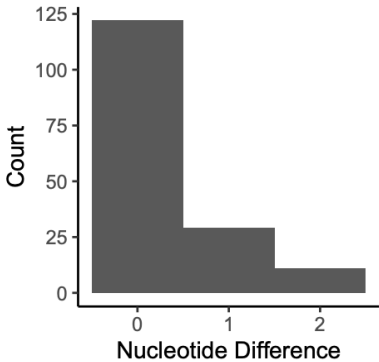
TRBV5-6\*01

295 sequences assigned  
206 (69.8%) exact matches, in which:  
197 unique CDR3  
13 unique J

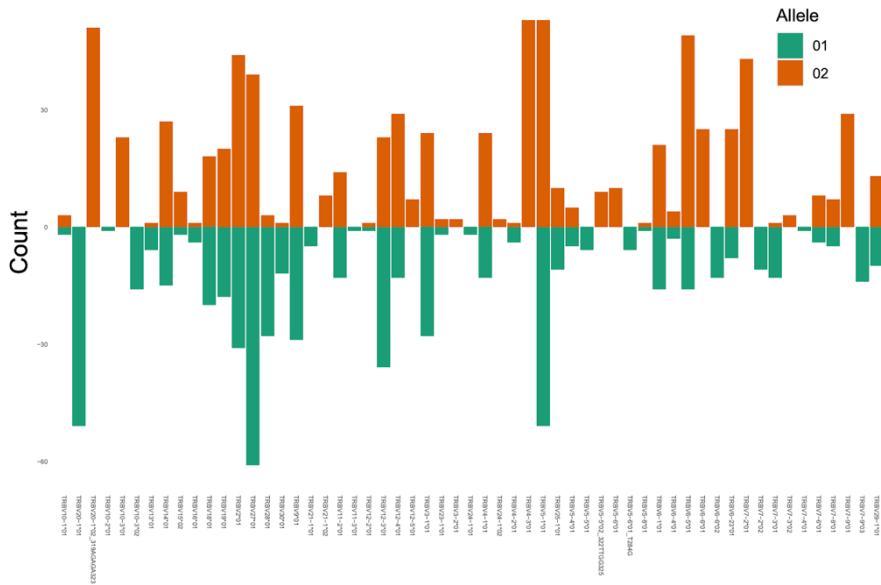
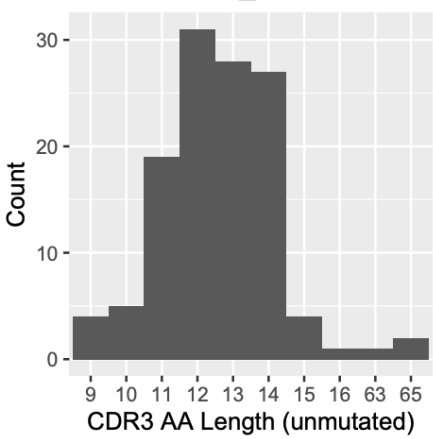


TRBV5-6\*01\_T284G

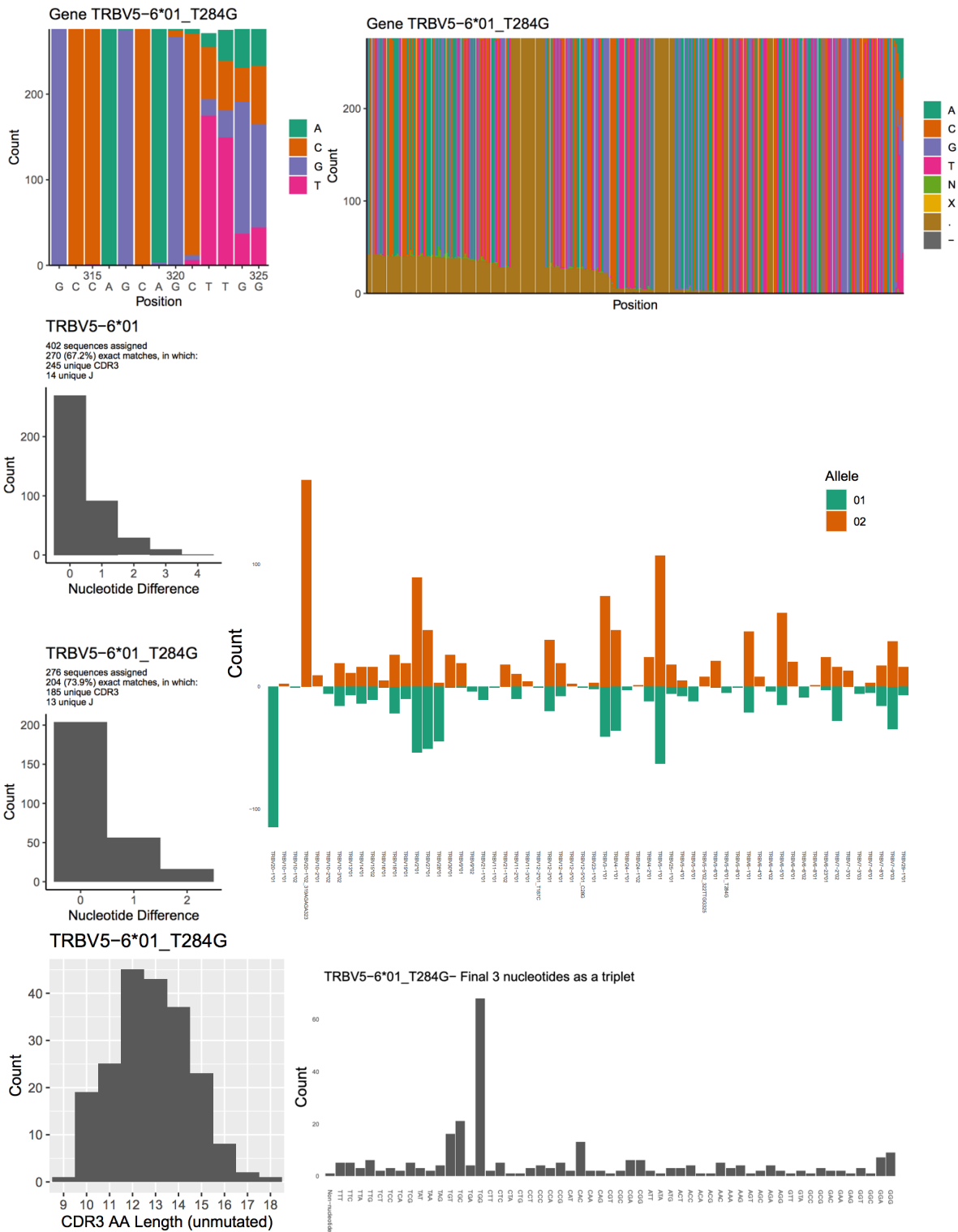
162 sequences assigned  
122 (75.3%) exact matches, in which:  
118 unique CDR3  
13 unique J



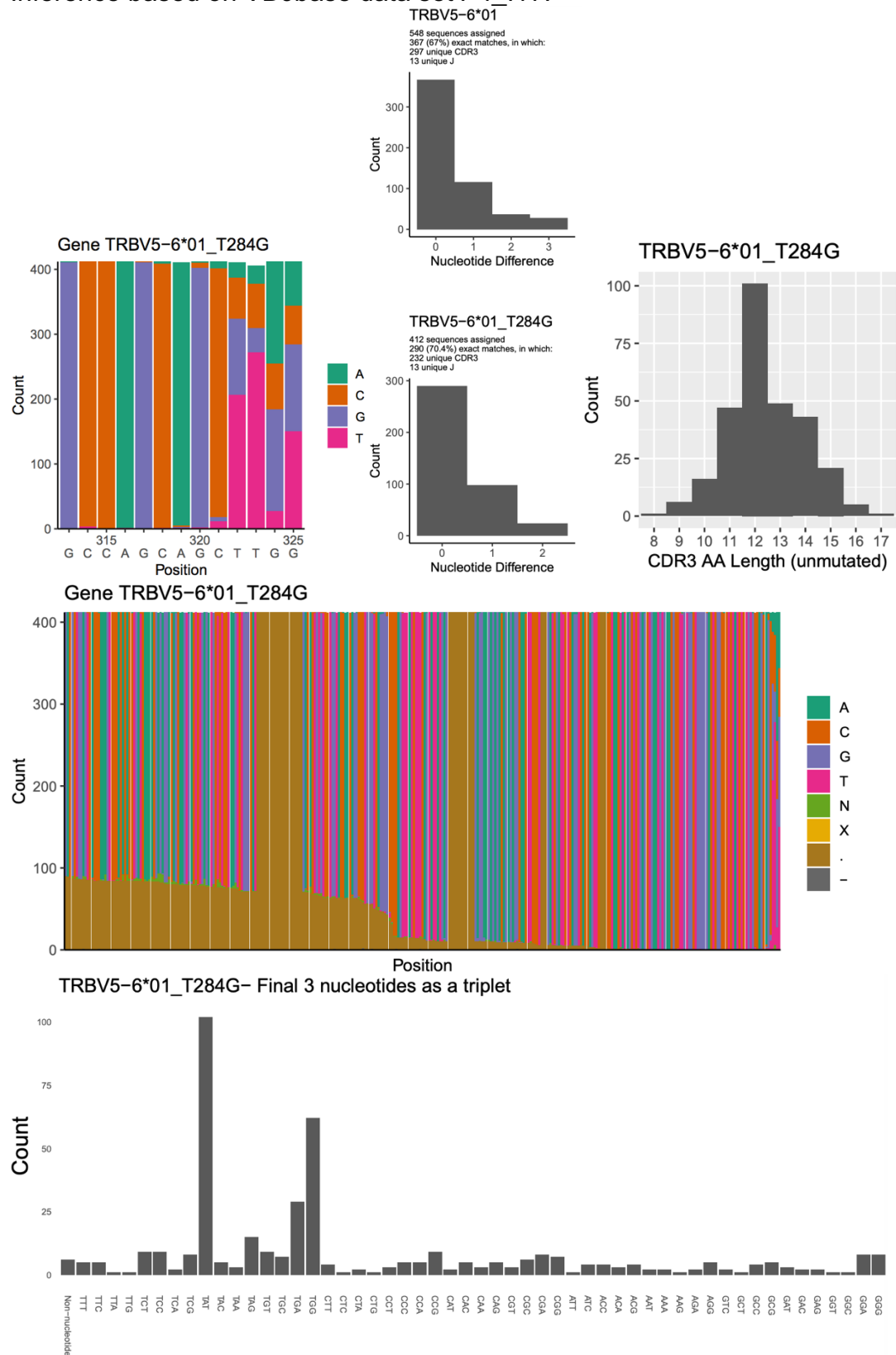
TRBV5-6\*01\_T284G



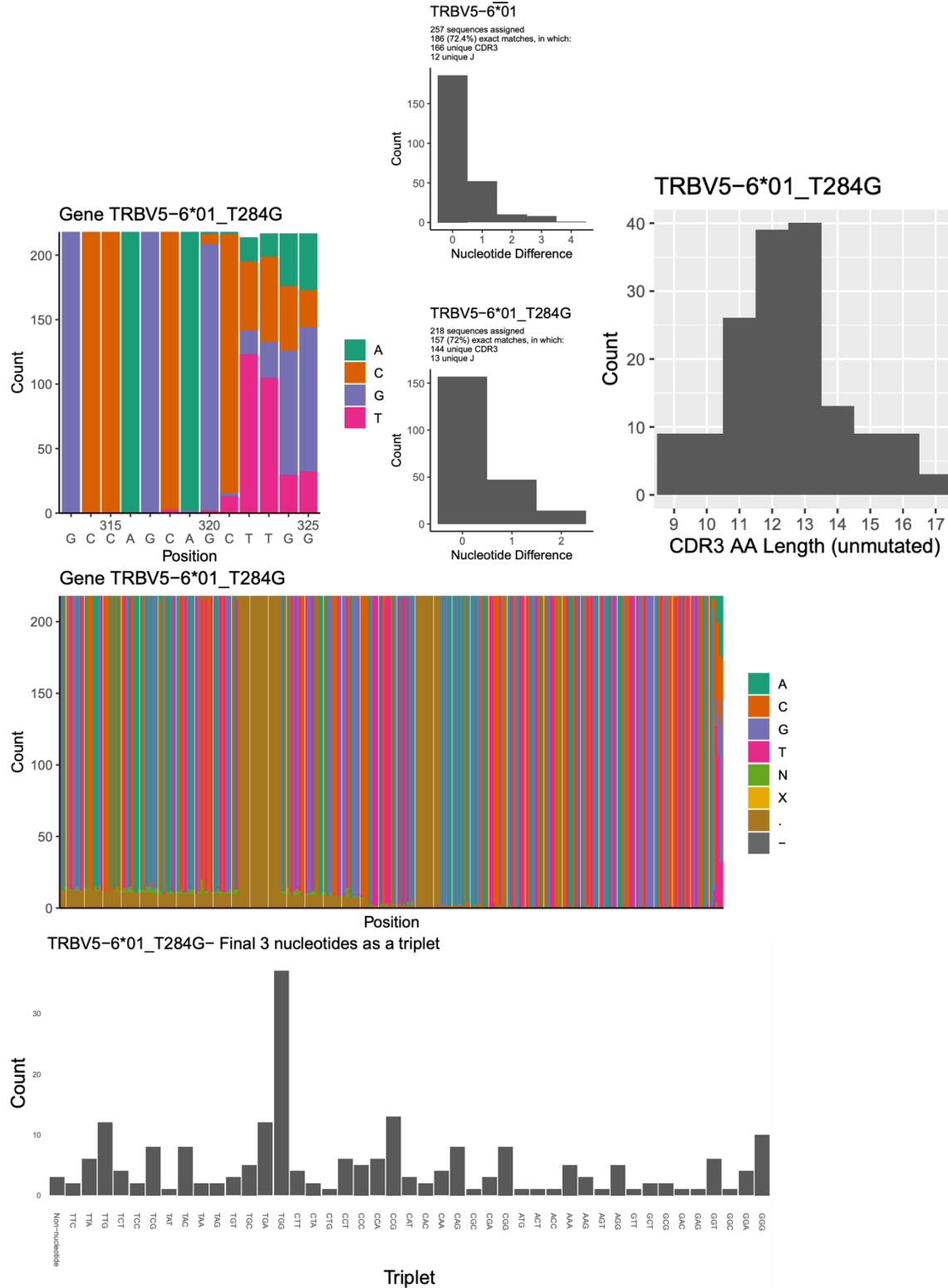
Other inferences:  
Inference based on VDJbase data set *P1\_I16*



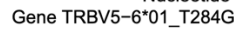
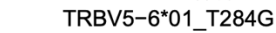
Inference based on VDJbase data set *P4\_I17*:



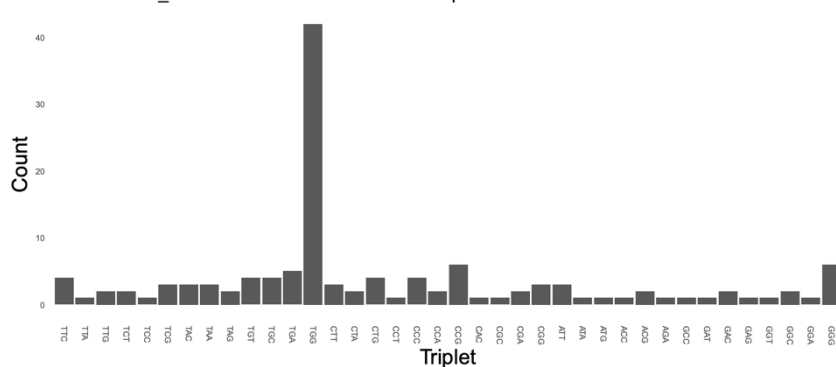
Inference based on VDJbase data set *P4\_128*:



Gene TRBV5-6\*01\_T284G



TRBV5-6\*01\_T284G- Final 3 nucleotides as a triplet



Sequence Count by TRBJ1-6 allele usage

