

Supplementary Table 1. Rearrangeable IGHV genes from Stanford_S22 dataset as determined from analysis of iHMMune-align, IMGT/V-QUEST+JCTA and IgBLAST alignment results using the method described in (Boyd, et al., 2010). Where allelic variants represent identical coding region sequences when generated using FR2 primers, they are listed in the same cell. Putative alleles that have not been officially recognised include a 'p' in their allele name and a bracketed 'P' indicates a rearrangeable pseudogene.

Rearrangeable IGHV genes		
humIGHV181*p02 (partial) (P)	IGHV3-35*01	IGHV6-1*01/*02
IGHV1-18*01	IGHV3-43*01	IGHV7-4-1*02
IGHV1-2*p05(humIGHV071)	IGHV3-47*02(P)	IGHV7-81*01
IGHV1-24*01	IGHV3-48*02	
IGHV1-3*01	IGHV3-49*03/*02/*04/*05	
IGHV1-45*02/*03	IGHV3-53*01/02	
IGHV1-46*01/*02	IGHV3-64*01	
IGHV1-58*01/*02	IGHV3-64*02	
IGHV1-69*01/*12/*13	IGHV3-66*02	
IGHV1-69*10	IGHV3-66*03	
IGHV1-8*01	IGHV3-7*01	
IGHV2-26*01	IGHV3-7*02	
IGHV2-5*10/*02	IGHV3-71*01(P)	
IGHV2-5*p11/*08	IGHV3-72*01	
IGHV2-70*p16 (partial)	IGHV3-73*01/*02	
IGHV2-70*p17 (partial)	IGHV3-74*01/*02	
IGHV3-11*01	IGHV3-9*01	
IGHV3-13*01	IGHV4-31*02/*03/*04/*06/*07	
IGHV3-15*01/*02	IGHV4-34*01/*02/*08	
IGHV3-20*p02(humIGHV154)	IGHV4-39*01/*05	
IGHV3-21*01/*02	IGHV4-55*01/humIGHV222(P)	
IGHV3-23*01/*04	IGHV4-59*01/*02/*07/*09	
IGHV3-30*p21 (partial)	IGHV4-61*01/*07/*08	
IGHV3-33*01	IGHV5-51*01/*03/*05	