Supplemental Table 1

Mab Name	V-allele	D-allele	J-allele	CDR3 amino acid
8.9D Heavy chain	IGHV3-15*01	IGHD4-04*01	IGHJ4*02	T T V L T T D R A Y D A G S D Y
6.4C Heavy chain	IGHV3-15*01	IGHD4-04*01	IGHJ4*02	T T V L T T D R A Y D A G S D N
10.9D Heavy chain	IGHV3-15*01	IGHD5-12*01	IGHJ4*02	T T V L T T D S A Y D A G I G Y
6.1C Heavy chain	IGHV3-15*01	IGHD5-12*01	IGHJ4*02	T T V L T T D S A Y D A G I G Y
13.6A Heavy chain	IGHV3-15*01	IGHD5-12*01	IGHJ4*02	T T V L T T D S A Y D A G I G Y

[a] Non-templated nucleotides added at the DJ junction.

[b] The replacement to silent mutation ratio found in the framework regions.

[c] The replacement to silent mutation ratio found in the complementarity-determining

DJ n nucleotides[a]	DJ junction	Number of Mutations from Germline	Frequency of Mutations	R/S ratio FR[b]	R/S ratio CDR[c]
23	ATAGAGCCTACG ATGCAGGGAGC	26	8.84%	13/5	8/0
22	ATCGTGCCTACG ATGCAGGGAG	38	12.93%	13/12	10/3
11	GCAGGGATCGG	13	4.42%	4/4	5/0
11	GCAGGGATCGG	12	4.08%	3/4	5/0
11	GCAGGGATCGG	11	3.74%	4/2	5/0

regions.