Table S1. Simulated TRB with 0.1%, 0.5% and 2% sequencing error.

Mismatch Rate	Hyper-Mutation Rate	Software	TRBV-Gene(%)	TRBD-Gene(%)	TRBJ-Gene(%)	TRBV-allele(%)	TRBD-allele(%)	TRBJ-allele(%)
0.10%	0.00%	**IMMonitor**	98.25	77.04	100.00	82.95	72.13	99.98
		HighV-QUST	91.46	86.31	99.24	65.94	81.69	99.23
		IgBLAST	97.87	80.55	99.20	72.46	76.33	99.19
		Decombinator	70.28	-	80.76	29.53	-	70.17
0.50%	0.00%	**IMMonitor**	98.18	76.90	100.00	82.34	71.60	99.83
		HighV-QUST	91.44	85.77	99.24	66.04	80.75	99.14
		IgBLAST	97.80	79.32	99.02	72.58	74.95	98.92
		Decombinator	68.33	-	78.64	-	-	-
2%	0.00%	**IMMonitor**	98.13	77.82	100.00	80.01	70.77	99.42
		HighV-QUST	91.59	83.89	99.30	65.39	77.27	98.96
		IgBLAST	97.83	75.13	98.61	71.82	70.07	98.27
		Decombinator	59.58	-	68.45	24.85	-	60.18