Table S2. Simulated IGH with 0.1%, 0.5% and 2% sequencing error and 0.1% hyper-mutation

Mismatch Rate	Hyper-Mutation Rate	Software	IGHV-Gene(%)	IGHD-Gene(%)	IGHJ-Gene(%)	IGHV-allele(%)	IGHD-allele(%)	IGHJ-allele(%)
0.10%	0.10%	**IMonitor**	98.30	83.97	99.98	81.48	81.41	99.88
		HighV-QUST	87.97	72.90	98.60	69.38	70.81	97.21
		IgBLAST	98.76	75.68	99.83	80.74	73.7	99.73
0.50%	0.10%	**IMonitor**	98.19	83.86	99.98	81.3	81.28	99.66
		HighV-QUST	87.51	72.73	98.61	68.96	70.66	97.01
		IgBLAST	98.63	75.47	99.83	80.63	73.52	99.5
2%	0.10%	**IMonitor**	98.02	83.79	99.96	80.46	81.01	98.68
		HighV-QUST	87.72	72.33	98.59	68.43	70.04	96.17
		IgBLAST	98.52	74.61	99.79	79.63	72.22	98.55