Table S3. Simulated Data with 0.5% sequencing error (TRA/IGK/IGL) and 4% hyper-mutation for IGK/IGL

Gene	Mismatch Rate	Hyper-Mutation Rate	Software	V-Gene(%)	J-Gene(%)	V-allele(%)	J-allele(%)
IGK	0.50%	4.00%	**IMMonitor**	93.57	99.99	86.91	92.70
			HighV-QUST	73.13	99.97	64.94	93.19
			IgBLAST	91.53	100.00	85.46	92.94
IGL	0.50%	4.00%	**IMMonitor**	100.00	99.57	77.24	98.79
			HighV-QUST	98.82	97.54	76.85	97.26
			IgBLAST	100.00	99.67	78.25	99.53
TRA	0.50%	0.00%	**IMMonitor**	98.35	100.00	86.75	99.39
			HighV-QUST	100.00	94.12	83.31	93.85
			IgBLAST	100.00	100.00	85.32	99.93
			Decombinator	68.36	72.83	-	-