Supplementary Table 1

			BROAD SPECTRUM PIPELINES				
			IgReC	**ImmunediveRsity**	**Immcantation Framework**	**IGGalaxy**	**VDJServer**
BASIC PROCESSING	**PREPROCESSING**	**Amplification methods supported**		▸ RACE	**pRESTO** ▸ Multiplex PCR ▸ RACE ▸ Can perform demultiplexing		▸ Access to pRESTO or VDJPipe
		Sequencing supported	▸ Single-end ▸ Paired-ends	▸ Single-end ▸ Paired-ends	▸ Single-end ▸ Paired-ends (overlapping or not)		
		Quality filtering		▸ Read quality	▸ Read quality		
		Amplification error correction	▸ UMI based correction ▸ Amplification correction without the need for UMI	▸ Amplification correction without the need for UMI	▸ UMI based correction		
	V/DJ ALIGNMENT	**V(D)J ALignment**	VJ	VJ	**TIgER** ▸ Takes already aligned reads and corrects it detecting new alleles	▸ Wraps IgBlast ▸ Wraps IMGT HighV-QUEST	▸ Wraps IgBlast
	CLONAL GROUPING	**Clonotype definition(s)**	▸ Grouping by Hamming graphs	▸ Unique antibodies	**Change-O** ▸ VJ + CDR3 (common ancestor) ▸ VJ + CDR3-AA	▸ VJ CDR-AA ▸ VJ CDR nucleotide	▸ Wraps Change-O and Alakazam
		Removes nonfunctional reads			✔	✔	
		Lineage Tree	▸ Lineage tree and Hamming graphs	▸ Network graphical representation	**Alakazam**		
REPERTOIRE CHARACTERIZATION AND ANALYSIS	**DIVERSITY**	**Basic Characterization**	**IgDiversityAnalyzer** ▸ Relative/absolute frequency of clonotypes		**Alakazam** ▸ Physicochemical properties of AA sequences ▸ V(D)J allele/ gene usage		▸ Wraps Alakazam
		Diversity Index	**IgDiversityAnalyzer** ▸ Simpson Index (SI) ▸ Clonal Simpson Index (CSI) ▸ Ratio SI/CSI	▸ Gini index ▸ Shannon Weiner index ▸ Shannon normalized	▸ Species richness ▸ Shannon Weiner ▸ Inverse simpson ▸ Berger Parker ▸ Total diversity estimation: Chao1		
		PLOTS	**IgDiversityAnalyzer** ▸ CDR3 length distribution ▸ CDR3 nucleotide content per position ▸ CDR3 aminoacid content ▸ VJ usage heatmap	▸ Histogram of CDR3 length distribution ▸ Proportion of AA in CDR3 ▸ AA distribution of CDR3 ▸ VJ use heatmap ▸ Rarefaction curve	▸ Clonal abundance distribution ▸ V(D)J allele/gene usage graphs ▸ Rarefaction curve	▸ VJ VD and DJ gene usage heatmaps	
	MUTATION ANALYSIS	**Mutation Analysis**	**IgDiversityAnalyzer** ▸ Identifies mutation type (substitution, insertion, deletion) ▸ V region mutation and AA change table ▸ Identifies synonym or stop codon mutations	▸ Identifies synonymous and non synonymous mutations	**SHazaM** ▸ Quantification of mutational load ▸ Statistical models of SHM targetting patterns ▸ Tools to build SHM targeting models from data ▸ Analysis of selection pressure using BASELINe		▸ Wraps SHazaM
		PLOTS	**IgDiversityAnalyzer** ▸ SHM vs relative position ▸ Number of reads vs SHM ▸ Distribution of indel SHMs positions ▸ Distribution of indel SHMs lengths ▸ Distribution of synonymous SHMs positions ▸ Heatmaps of amino acids, or nucleotide substitutions		▸ Mutability frequencies ▸ Visualization of SHM targeting model ▸ Probability density functions resulting from selection analysis ▸ Plot summary stastistics resulting from selection analysis		
	EVOLUTION	**Clonal dynamics**					
	CONVERGENCE	**Convergance of Repertoire**		✔	**RDI**		
	OTHER						

Supplementary Table 1. (continued)

			MiGEC	IMSEQ	MiXCR	LymAnalyzer	Partis	ImmuneDB	Vidjil
			MODULAR PIPELINES						
BASIC PROCESSING	**PREPROCESSING**	**Amplification methods supported**	▸ Multiplex PCR, RACE ▸ Can perform demultiplexing		▸ RACE ▸ RNA seq				
		Sequencing supported	▸ Paired-ends	▸ Single-end ▸ Paired-ends	▸ Single-end ▸ Paired-ends				
		Quality filtering	▸ Cluster average quality	▸ Read quality filtering ▸ Group quality filtering	✔				
		Amplification error correction	▸ UMI based correction	▸ Amplification correction without the need for UMI	▸ Amplification correction with and without UMI				
	VIDJ ALIGNMENT	**V(D)J ALignment**	✔	VJ	VDJ + C	VDJ	VDJ	VJ	VJ
	CLONAL GROUPING	**Clonotype definition(s)**	▸ Unique antibodies	▸ Unique antibodies	▸ Unique antibodies ▸ Can group by C		▸ Common ancestor	▸ VJ+ CDR3-AA	▸ Unique antibodies
		Removes nonfunctional reads		✔					
		Lineage Tree						✔	
REPERTOIRE CHARACTERIZATION AND ANALYSIS	**DIVERSITY**	**Basic Characterization**				▸ CDR3 extraction and characterization		▸ V length distribution ▸ CDR3 length distribution ▸ V, J usage	
		Diversity Index							▸ Shannon-Wiener ▸ Inverse Simpson
		PLOTS							
	MUTATION ANALYSIS	**Mutation Analysis**					▸ Mutation frequencies ▸ Identification of non-templated insertions		
		PLOTS				▸ Mutation tree (for each CDR3 one can visualize the hypermutation process)			
	EVOLUTION	**Clonal dynamics**							✔
	CONVERGENCE	**Convergance of Repertoire**							
	OTHER								

Supplementary Table 1. (continued)

			SONAR	TRiGS	IMEX	IRProfiler	VDJtools	DivE	BASELINe	AbSim
							SPECIALIZED PIPELINES			
BASIC PROCESSING	PREPROCESSING	Amplification methods supported	‣ Single-end							
		Sequencing supported	‣ Paired-ends							
		Quality filtering	✔				‣ Frequency based correction ‣ Frequency based filtering			
		Amplification error corrcetion								
	V(D)J ALIGNMENT	V(D)J ALignment				‣ Wraps IMGT HighV–QUEST ‣ 11 filtering criteria				
	CLONAL GROUPING	Clonotype definition(s)	‣ VJ + CDR3 (Common ancestor)	‣ VJ + CDR3 (Common ancestor) ‣ VJ + CDR3-AA	‣ VJ + CDR3 ‣ VJ + CDR3-AA		‣ VDJ + CDR3-AA ‣ VJ+ CDR3-AA ‣ V + CDR3-AA ‣ J + CDR3 ‣ CDR3			
		Removes nonfunctional reads			✔		✔			
		Lineage Tree		✔	✔			✔		
REPERTOIRE CHARACTERIZATION AND ANALYSIS	DIVERSITY	Basic Characterization			‣ Number of productive / unproductive reads ‣ VDJ gene total and relative frequencies	‣ Clonotype quantification ‣ V, J gene usage	‣ Read counts ‣ Mean clonotype sizes ‣ Non-functional reads ‣ Histogram of CDR3 nucleotide length			
		Diversity Index		‣ Gini index	‣ IMEX calculates sequence diversity using a more elaborated data mining approach.		‣ Shannon-Wiener ‣ Inverse Simpson ‣ D50 index, a recently developed immune diversity estimate ‣ Lower bound total diversity: Chao1 or Efron-Thisted estimate	‣ DiVE species richness estimate (fits different models and selects the top 5 model to estimate species richness)		
		PLOTS	‣ CDR3 length distribution	‣ CDR3 length distribution ‣ Histograms for VJ gene usage	‣ VDJ usage (heatmaps or histogram) ‣ Productive/ non productive pie charts ‣ Diversity curve		‣ V, J, VJ usage (heatmap and hierarchical clustering) ‣ Clonality plot (Plots a three-layer donut chart to visualize the repertoire clonality) ‣ Rarefaction plot	‣ Rarefaction plot		
	MUTATION ANALYSIS	Mutation Analysis	‣ V, J usage						‣ Identifies point and silent mutations ‣ Identifies and quantifies positive or negative selection ‣ Germline normalization for direct comparisson of different repertoires	
		PLOTS								
	EVOLUTION	Clonal dynamics					✔			
	CONVERGENCE	Convergance of Repertoire			✔	✔	✔			
	OTHER			‣ longitudinal phylogenetic "birthday" trees						Generates simulations of Ig reprrtoires with the desired characteristics