Immune Repertoire Profiling Service

DESCRIPTION

Immune repertoire often represents an individual's current immunological status; whether the person is healthy, vaccinated, diseased, or infected. Only high-throughput NGS analysis can comprehensively profile an individual's immune repertoire. The Immune Repertoire Profiling Service provides effective data acquisition, integration, and interpretation for the customers.

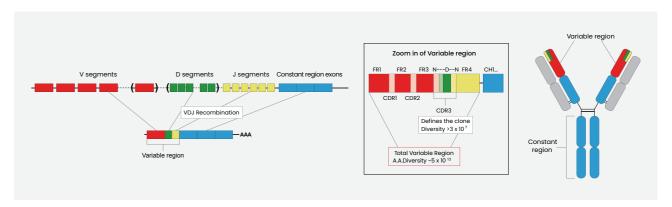
KEY FEATURES

1. Quantitative analysis of library diversity	 NGS-based analysis of complex antibody library consisting of millions (10⁶~10¹²) of sequences in a single experiment Analysis of immunoglobulin and T-cell receptor repertoire; analysis of BCR/TCR for each clone Frequency analysis of individual antibody clones within the library, identifying major and minor clones
Tracking of clonal frequencies for each sample	 For antibody discovery, analysis of library diversity according to its panning degree enabling monitoring changes in clonal frequency Minimized omission of potentially significant antibody clones Analysis of immune repertoire characteristics from blood sample and monitoring of each clone
Various analysis options for immune system studies	Perform the experiment with drastically reduced time and cost enabled by the advanced technology of MSSIC developed by Celemics

REQUIREMENTS

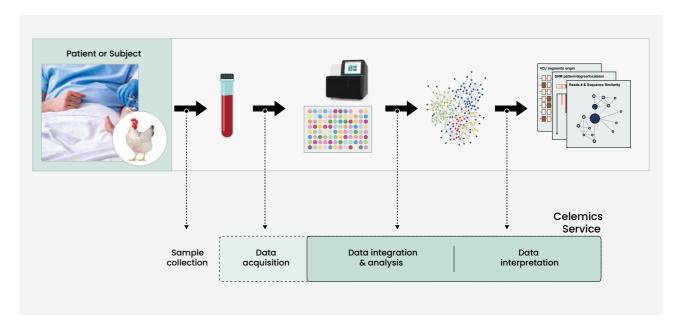
Sample type	Total RNA from B-Cell or/and T-Cell, DNA from B-Cell or/and T-Cell, DNA/RNA Amplicons
Concentration	100 ng/μl
Amount	1 µg
Turnaround time	Within 4-6 business weeks from sample collection
Temperature	RT for storage and shipment

DIVERSITY OF ANTIBODY



The antibody genes are composed of many different segments. The antibodies are presented in B cells with great diversity of 10¹³ repertoires.

GENERAL WORKFLOW



Celemics provides service for data acquisition, integration, and analysis, and interpretation.



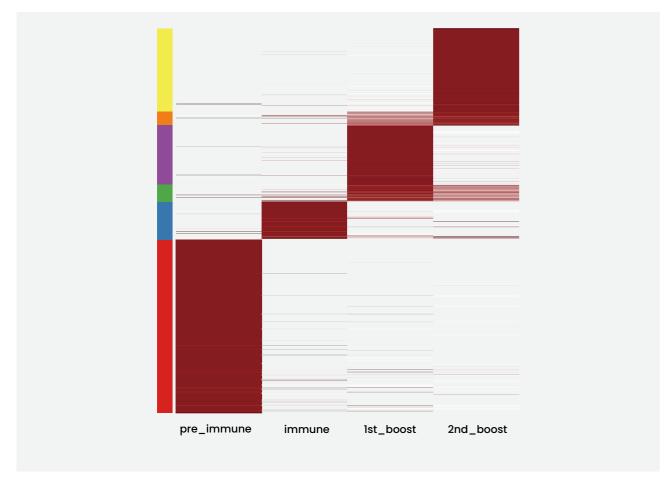
IMMUNE PROFILING EXAMPLES

Example 1 - Discovery of candidate antibodies from actively immunized chickens

CDR3 sorting results

CDR3 ID	CDR3 AA	p_pre-immune	p_immune	p_lst_boost	p_2nd_boost	p_tissue	p_BM_2nd
CDR3sample_1	GSRDSSASTI	2433	773	31	0	2	461
CDR3sample_2	GSYDSSYVGI	1756	1444	2269	895	1058	789
CDR3sample_3	GSIDSSYVGI	1019	402	876	938	541	346
CDR3sample_4	ANFDSSSGAGI	46	25	338	483	1707	345
CDR3sample_5	GGYDSSAGI	231	268	934	207	966	7770
CDR3sample_6	GSFDSSTYAGI	3678	1034	425	290	547	431
CDR3sample_7	GSRDSSASTI	2433	773	31	0	2	461
CDR3sample_8	GSRDSSYVGI	6427	6370	10151	5756	10089	2680
CDR3sample_9	GGYDGSTYVGI	279	211	2047	178	271	88
CDR3sample_10	GSRDSNYVGI	407	567	974	749	868	224
CDR3sample_11	GSSSGTGI	1563	2580	899	1999	114	24702
CDR3sample_12	GSYDSSAGI	1195	875	1342	743	746	288
CDR3sample_13	GSRDSTYVGI	461	795	1355	998	983	136
CDR3sample_14	GGYDSSTDAGI	1167	1129	1353	1617	892	405

Sequence abundance clustering result



Example 2 - Discovery of novel drug candidates with antibody analysis from respiratory infection patient samples

CDR3 similarity analysis

								Hor	nolo	gy																	Т									PTN	Cou	nt (CD	R3)						
Clone ID	CDR	Homology	CDR3 NT	CDR3 AA	=			*	*	А	в	0	E	F	G	н	1 4	к	L	м	N	0 P	Q	R	s	T L		2	diff	NT dif	faa I	binder	reads	S2 rea	dsdea	n apa	rt apo	artN_gi	lycœl	eavao	xidati	free_	sulfa	t sulfa	atmethy
CRD3sample_1	15	1	GATGAGGGG	DEGSHATILTGYF	D	E (3 S	н	А	Т	1 1	. 1	G	Υ	F		\top	Т		П		\top	\top	П	\neg	\neg	D	S	3		2	1411			0	1	1	0		0	0	0	1	1	0
CRD3sample_2	16	1	вение	GPWKWYGGN	G	P N	N K	w	Υ	G	G I	N S	Е	N	Υ	Е	\neg	Т	Т	П		\neg	Т	П		Т	D	С			0	S2	1545	2	1	0	0	0		1	2	0	2	2	1
CRD3sample_3	10	2	AGACGGGGA	RRGSSSGLD	R	R (3 S	s	S	G	L		Т	Т			\neg	Т	Т	П		\top	Т	П		\neg	D	S			0	S2	1231	4	0	- 1	- 1	0		0	0	0	0	0	2
CRD3sample_4	15	1	GATGAGGGG	DEGSHGGID	D	E (3 S	н	G	G	1 1	. 1	G	Υ	F		\neg	Т	Т	П	П	\top	Т	П		\neg	D	S			0	S2	7183	44	0	- 1	- 1	0		0	0	0	1	1	0
CRD3sample_5	14	2	CATATATCA	HISQLEGSK	н	1 8	s Q	L	Е	G	S	K	G	F		П	\neg	Т	Т	П	П	\top	Т	П		\neg	D	F			0		877		0	0	0	0		0	0	0	0	0	2
CRD3sample_6	13	1	CTGGGTCCT	LGPCGRDCY	L	G F	РС	G	R	D	C 1	Y S	F	Т		П	\neg	Т	Т	П	П	\top	Т	П	\neg	\neg	D	Υ			0		814	0	0	0	0	0		0	0	0	2	2	- 1
CRD3sample_7	17	1	CTTACGGGG	LTGLPATRDYYY	L	T (B L	Р	Α	Т	R I) Y	Y	Y	н	Р	L	Т	Т	П	П	\top	Т	П	\neg	\neg	D	1			0		1275		0	0	0	0		0	0	0	3	3	- 1
CRD3sample_8	14	1	ACAACCAAC	TTNAGYSSG	т	T I	N A	G	Υ	s	S (3 W	w	G		П	\neg	Т	Т	П	П	Т	Т	П	П	\neg	D	Υ			0		1005		0	0	0	0		0	2	0	2	2	0
CRD3sample_9	15	1	GATGAGGGG	DEGSHGGFD	D	E (3 S	н	G	G	F I	. 1	G	Y	F	П	Т	Т	Т	П	П	Т	Т	П	\neg	Т	D	s	1		1	S2	507	6	0	- 1	- 1	0		0	0	0	1	1	0
CRD3sample_10	18	1	ATATTTTGT	IFCSGGSCY	1	F (c s	G	G	s	C 1	Y C	К	G	Q	D	W F		Т	П	П	\top	\top	П		\neg	D	Р			0	S2	32989	1343	0	0	0	0		0	1	0	1	1	- 1
CRD3sample_11	12	1	ATAATTGAG	HEGSTSTA	1	1 8	E G	s	Т	s	т /	A F	Т				\neg	\top	Т	П		\top	\top	П		\neg	D	1			0		841	0	0	0	0	0		0	0	0	0	0	0
CRD3sample_12	15	1	GATGAGGGG	DEGSHDGFD	D	E (3 S	н	D	G	F I	. 1	G	Υ	F		\neg	\top	Т	П		\top	\top	П		\neg	D	s	2		2	S2	542	2	0	2	2	0		1	0	0	1	- 1	0
CRD3sample_13	9	2	TGGGAAACT	WETSYNLDI	w	E 1	T S	Υ	N	L			Т				\neg	\top	Т	П		\neg	\top	П		\neg	D	1			0		560		0	0	0	0		0	1	0	- 1	- 1	0
CRD3sample_14	6	1	GGCAACTGG	GNWFDP	G	N I	N F			П		Т	Т	Т	П		\neg	\top		П		\neg	\top	П			D	Р			0		619		0	0	0	0		0	1	0	0	0	0
CRD3sample_15	1	1	TATTTTGGT	TFGSGSGNE	Υ	F (3 S	G	s	G	N E	F															D	Υ)	0		3709		0	0	0	0		0	0	0	2	2	0
CRD3sample_16	1	2	AAAAAAGAT	KKDNRGSIE	К	K I	D N	R	G	s	1 8	F					\neg			П				П			D	Υ)	0	S2	2888	8	0	0	0	0	_	1	0	0	1	- 1	3

Network Analysis Between Antibody Sequences

