

Introduction

Immune biology is too interconnected to profile one pathway at a time. The immune system is a dynamic network implicated in nearly every major disease area—cancer, autoimmunity, neurodegeneration, metabolic disease, infection. Any given immune response reflects the sum of multiple protein signals: cytokines, chemokines, checkpoint molecules, complement. Disease phenotypes emerge from their interaction, not from any single protein in isolation.

The NULISAseq™ Immune 340 Panel captures this complexity in a single run. Spanning innate and adaptive immunity, cytokines, chemokines, checkpoints, and cell-death pathways, it simultaneously measures ~340 immune mediators from just 25 µL of plasma or serum. Attomolar sensitivity and broad dynamic range resolve low-abundance signals often missed by conventional platforms—delivering the deep, comprehensive immune profiling for translational research and exploratory studies of biological heterogeneity and underlying mechanisms.

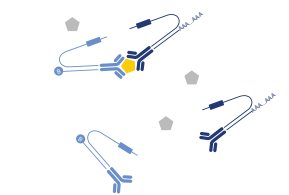


NULISA™ Technology

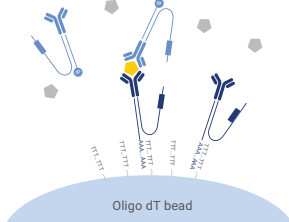
NULISAseq is a sandwich immunoassay in which two target specific antibodies, conjugated with unique oligonucleotide tags, bind and form a complex with the specific protein in solution. The resulting immunocomplex is purified in sequential capture and release steps to remove background and unbound antibodies. Successful formation of the immunocomplex brings the two oligonucleotide tags into proximity

for a ligation reaction and amplification. The resulting unique oligonucleotide reporters containing both target and sample information are then pooled to a library for analysis on an NGS sequencer. The assay protocol is fully automated on the ARGOTM HT System and data is analyzed using the NULISA Analysis Software. More details on the assay protocol can be found [here](#).

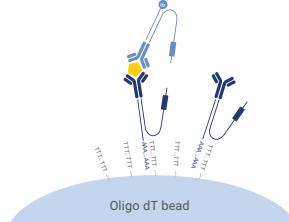
1. Immuno-complex formation



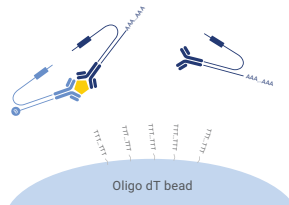
2. Capture 1



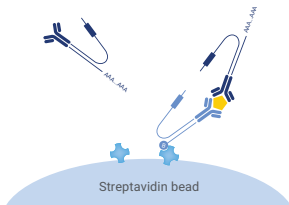
3. Wash 1



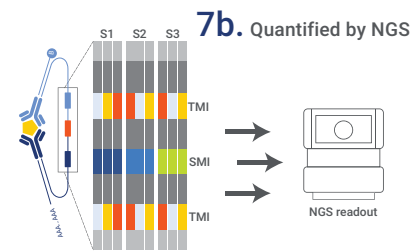
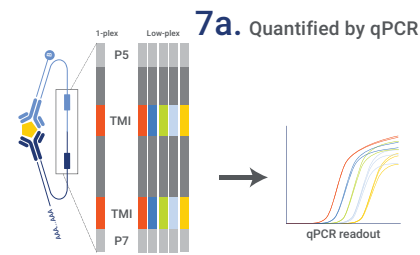
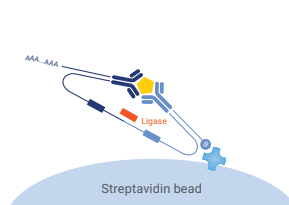
4. Release 1



5. Capture 2 & Wash 2



6. Ligation & Release 2



Sensitivity & Detectability

The limit of detection (LOD), or the lowest concentration of the analyte that can be distinguished from the background signal of the assay, is calculated for each target as the mean plus three standard deviations of the 4 negative control (NC) wells' normalized reads. These values are rescaled and log-transformed to obtain LOD in NPQ. A maximum of one outlier NC value may be omitted.

Validation data LOD median and interquartile ranges (IQR) summarize LODs generated across 37 runs (Table 3). Target detectability is the percentage of samples above LOD. Detectability was assessed using 426 EDTA plasma samples and 530 Serum samples. More than 90% of targets were detectable in at least 50% of samples (Table 3, Figure 1).

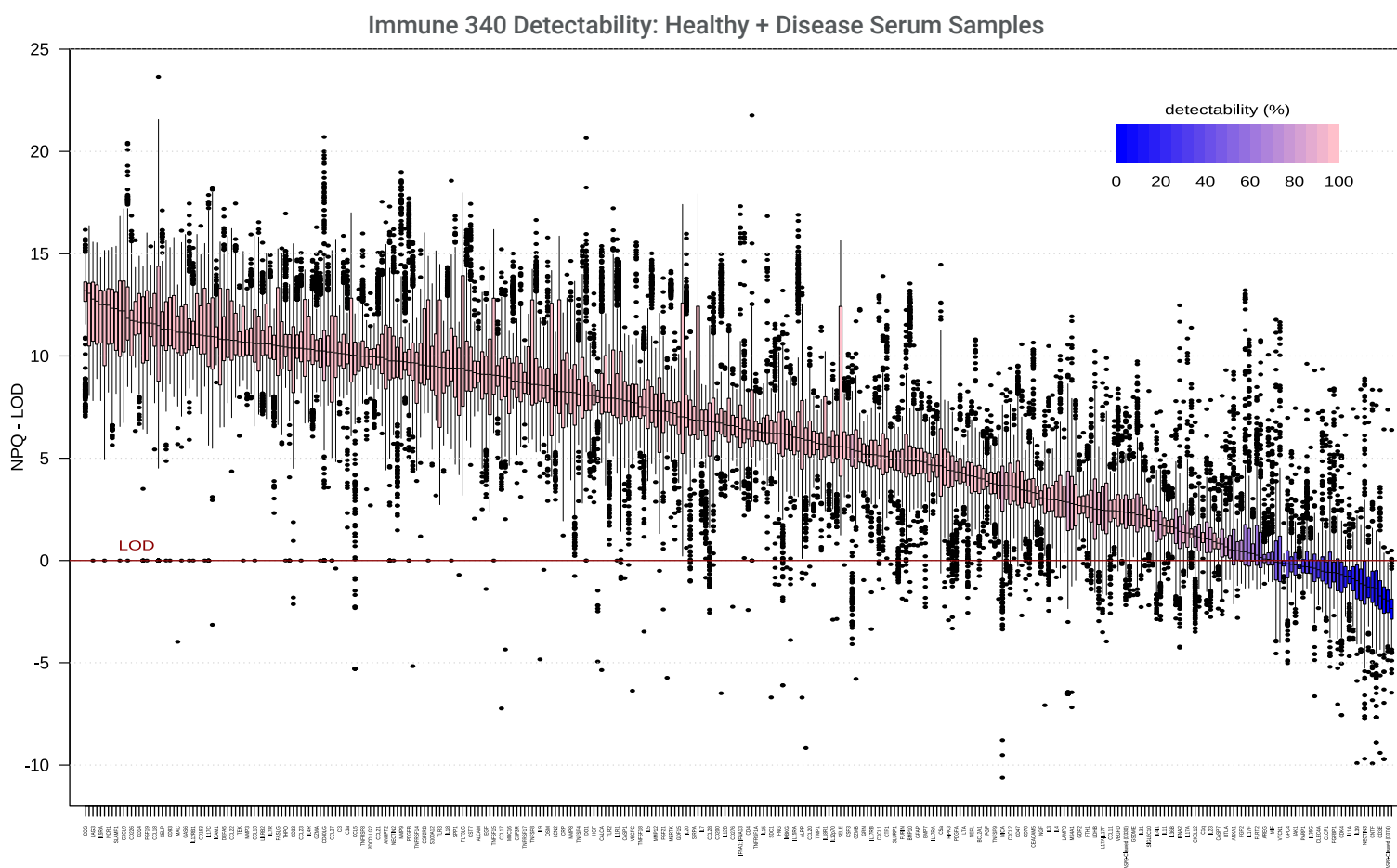


Figure 1. Detectability was assessed in a mix of healthy and diseased samples.

More than 90% of targets were detectable in at least 50% of samples.

*All targets are represented in the chart; however, labels are displayed at intervals to maintain readability. Full target names and performance can be referenced in the accompanying data table.

Data Normalization & Calculation of NULISA Protein Quantification (NPQ) Values

NULISA Protein Quantification (NPQ) units are log₂-scale values used to quantify relative protein abundances. NPQ is derived from the raw sequencing reads using the following normalization and transformation steps. First, to control for intra-plate well-to-well variation, the raw sequencing read count for each analyte for a given sample well is divided by that well's internal control (IC)

raw count. Second, to control for plate-to-plate variation, the IC-normalized values for each analyte are divided by the analyte-specific median IC-normalized counts from the 3 inter-plate controls (IPCs) on the plate. Data is then rescaled and log₂-transformed to obtain the data in NPQ, which are approximately normally distributed values amenable to downstream statistical analysis.

Precision

Intra- and Inter-assay precision was measured to assess the variation in technical replicates; this is reported in Tables 1-3 as intra-plate and inter-plate coefficient of variation (CV).

For each target, CV was determined using a variance component analysis model to assess the contribution of various factors to the total CV of the normalized reads. Six plasma samples and five serum samples with 3 technical replicates each were measured across a set of 19 runs which included 2 reagent lots and 2 instruments across 5 days.

Variance component analysis models were fit for each sample and target and included the factors reagent lot, instrument, instrument bay, inter-plate, and intra-plate (Tables 1-3).

Table 1: Across-target Median Coefficients of Variation

CV component	Plasma Median CV (%)	Serum Median CV (%)
Intra-plate	8.14	8.91
Inter-plate	8.45	8.67
Inter-bay	1.02	0.6
Instrument	0.31	0.24
Reagent Lot	1.85	1.32
Total	13.76	14.26

Table 2: Percentage of Targets with CV Below 30%

CV component	% targets < 30%, Plasma	% targets < 30%, Serum
Intra-plate	98.8	99.1
Inter-plate	96.5	96.5
Total	88.5	86.7

Cross-Reactivity

To assess cross-reactivity, targets were randomly assigned to two sets of 57 pools containing either six or seven targets each, such that no two targets shared a pool for both sets. Counts were normalized using an internal control. Cross-reactivity for each target was quantified as (maximum non-target pool count – background)/(average

target pool counts – background) * 100, where the background was calculated as the median count across nontarget pools. Cross-reactivity was only assessed for targets with commercially available recombinant antigen (Table 3, Figure 2).

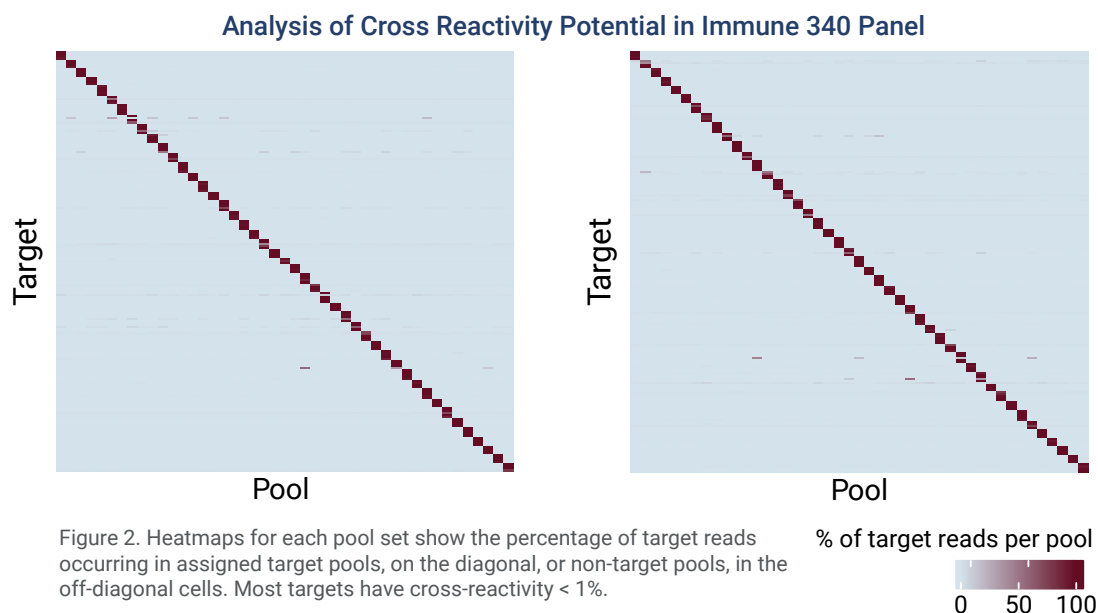


Table 3: Performance Validation Data by Target

Target	UniProt ID	Protein Name	Detectability (%)		CV (%)				LOD (NPQ)	In Panel Cross Reactivity	Out of Panel Cross Reactivity
			Plasma	Serum	Plasma		Serum				
					Intra	Inter	Intra	Inter			
AGER	Q15109	Advanced glycosylation end product-specific receptor	100%	100%	10.2	9.0	9.9	9.9	0.4	<1%	<1%
AGRP	O00253	Agouti-related protein	100%	100%	7.3	5.8	7.2	9.6	6.8	<1%	<1%
ALCAM	Q13740	CD166 antigen	100%	100%	6.2	10.4	5.0	10.1	4.2	<1%	<1%
ALPP	P05187	Alkaline phosphatase, placental type	100%	99%	8.9	5.4	11.4	5.5	5.2	<1%	14% ^a
ANGPT1	Q15389	Angiopietin-1	92%	97%	10.1	8.2	11.1	12.1	11.0	<1%	<1%
ANGPT2	O15123	Angiopietin-2	100%	100%	7.0	8.7	7.1	10.5	1.4	<1%	<1%
ANXA1	P04083	Annexin A1	49%	68%	13.6	5.9	16.6	5.5	10.2	<1%	<1%
AREG	P15514	Amphiregulin	63%	60%	5.9	4.2	5.2	4.0	11.8	<1%	<1%
AXL	P30530	Tyrosine-protein kinase receptor UFO	100%	100%	7.4	10.3	6.0	10.6	0.1	<1%	<1%
BCL2A1	Q16548	Bcl-2-related protein A1	100%	99%	5.6	6.3	7.7	5.7	9.8	<1%	<1%
BCL2L11	O43521	Bcl-2-like protein 11	4%	9%	5.4	4.9	5.7	4.8	11.3	<1%	<1%
BDNF	P23560	Brain-derived neurotrophic factor	100%	100%	8.7	9.9	11.7	5.5	6.4	<1%	<1%
BMP10	O95393	Bone morphogenetic protein 7	87%	100%	9.8	4.1	11.6	5.1	6.7	<1%	<1%
BMP7	P18075	Bone morphogenetic protein 10	100%	99%	21.4	11.8	13.4	12.2	7.7	<1%	<1%
BST2	Q10589	Bone marrow stromal antigen 2	100%	100%	8.7	8.1	8.9	7.1	0.8	<1%	<1%
BTLA	Q7Z6A9	B- and T-lymphocyte attenuator	55%	86%	15.2	15.4	15.0	16.2	10.1	<1%	<1%
C1Q	P02745/ P02746/ P02747	C1Q complement	N/A	N/A	9.7	7.3	11.8	6.4	N/A ^k	<1%	<1%
C3	P01024	Complement C3	N/A	N/A	6.3	7.5	5.5	8.2	N/A ^k	<1%	<1%
C3A	P01024	Complement C3	N/A	N/A	5.7	3.8	5.7	4.2	N/A ^k	<1%	<1%
C5	P01031	Complement C5	100%	100%	7.3	4.2	5.7	4.8	0.3	<1%	<1%
C5A	P01031	Complement C5	23%	99%	16.1	15.8	7.6	18.3	7.2	<1%	<1%
CALCA	P01258	Calcitonin	100%	100%	7.4	6.9	7.5	7.8	3.2	<1%	<1%
Casp1	P29466	Caspase-1	100%	100%	5.1	5.9	7.0	6.4	6.3	<1%	<1%
CASP1-Cleaved (D297)	P29466	Caspase-1, cleaved at D297	99%	100%	7.2	6.8	10.3	6.0	6.9	<1%	<1%
CASP7	P55210	Caspase-7	98%	96%	11.4	4.7	9.9	3.4	11.9	<1%	<1%
CASP7-Cleaved (D198)	P55210	Caspase-7, cleaved at D198	95%	72%	6.7	7.3	8.5	6.5	11.5	<1%	<1%
CASP8	Q14790	Caspase-8	2%	1%	17.8	17.7	N/A	N/A	11.4	<1%	<1%
CASP8-Cleaved (D374)	Q14790	Caspase-8, cleaved at D374	1%	0%	16.0	14.1	23.7	54.7	9.5	<1%	<1%
CASP9	P55211	Caspase-9	100%	98%	8.2	9.0	17.5	8.1	5.7	<1%	<1%
CASP9-Cleaved (D315)	P55211	Caspase-9, cleaved at D315	100%	100%	6.3	8.6	9.9	8.9	7.7	<1%	<1%
CASP9-Cleaved (D330)	P55211	Caspase-9, cleaved at D330	94%	93%	6.0	10.9	10.6	14.4	10.6	<1%	<1%
CCL1	P22362	C-C motif chemokine 1	100%	100%	6.9	11.2	6.8	10.9	4.8	<1%	<1%
CCL2	P13500	C-C motif chemokine 2	100%	100%	9.3	9.7	8.9	10.5	2.3	<1%	<1%
CCL3	P10147	C-C motif chemokine 3	100%	100%	10.2	8.3	13.2	6.4	5.4	<1%	10% ^b
CCL4	P13236	C-C motif chemokine 4	100%	100%	9.2	6.0	9.2	8.3	5.5	<1%	315% ^c
CCL5	P13501	C-C motif chemokine 5	100%	98%	10.2	7.2	14.5	9.7	1.6	<1%	<1%
CCL7	P80098	C-C motif chemokine 7	100%	99%	9.7	7.3	11.3	6.9	9.5	<1%	<1%
CCL8	P80075	C-C motif chemokine 8	100%	100%	7.9	14.1	12.3	13.4	0.8	<1%	<1%
CCL11	P51671	Eotaxin	100%	97%	12.6	12.0	20.3	14.8	8.1	<1%	<1%
CCL13	Q99616	C-C motif chemokine 13	100%	100%	7.8	8.4	10.5	7.7	0.7	<1%	<1%
CCL14	Q16627	C-C motif chemokine 14	100%	100%	8.3	5.3	8.0	7.0	0.1	<1%	<1%

Table 3: Performance Validation Data by Target (cont.)

Target	UniProt ID	Protein Name	Detectability (%)		CV (%)				LOD (NPQ)	In Panel Cross Reactivity	Out of Panel Cross Reactivity
			Plasma	Serum	Plasma		Serum				
					Intra	Inter	Intra	Inter			
CCL15	Q16663	C-C motif chemokine 15	100%	100%	7.8	7.8	8.9	11.9	0.3	<1%	<1%
CCL16	O15467	C-C motif chemokine 16	100%	100%	8.6	4.9	7.1	5.7	0.3	<1%	<1%
CCL17	Q92583	C-C motif chemokine 17	100%	100%	7.5	12.2	9.8	10.7	4.3	<1%	<1%
CCL18	P55774	C-C motif chemokine 18	100%	100%	8.3	8.0	9.6	10.2	0.0	<1%	<1%
CCL19	Q99731	C-C motif chemokine 19	100%	100%	8.2	7.2	13.2	5.8	0.1	<1%	<1%
CCL20	P78556	C-C motif chemokine 20	100%	100%	6.3	5.4	6.5	5.4	6.5	<1%	<1%
CCL21	O00585	C-C motif chemokine 21	100%	100%	6.6	5.6	7.2	5.6	0.4	<1%	<1%
CCL22	O00626	C-C motif chemokine 22	100%	100%	9.8	15.0	8.3	16.3	0.0	<1%	<1%
CCL23	P55773	C-C motif chemokine 23	100%	100%	6.7	7.9	7.6	8.3	0.2	<1%	<1%
CCL24	O00175	C-C motif chemokine 24	100%	100%	10.3	9.4	7.4	11.1	0.4	<1%	<1%
CCL25	O15444	C-C motif chemokine 25	100%	99%	8.4	6.3	10.4	5.3	4.2	<1%	<1%
CCL26	Q9Y258	C-C motif chemokine 26	100%	100%	9.1	9.0	16.8	5.2	4.5	<1%	<1%
CCL27	Q9Y4X3	C-C motif chemokine 27	100%	100%	8.4	10.4	13.1	9.0	0.2	<1%	<1%
CCL28	Q9NRJ3	C-C motif chemokine 28	100%	95%	8.3	8.5	13.5	18.3	8.7	<1%	<1%
CD163	Q86VB7	Scavenger receptor cysteine-rich type 1 protein M130	100%	100%	19.1	11.8	15.3	25.3	0.5	<1%	<1%
CD3E	P07766	T-cell surface glycoprotein CD3 epsilon chain	5%	10%	7.7	11.4	8.8	9.9	9.7	<1%	<1%
CD4	P01730	T-cell surface glycoprotein CD4	100%	100%	24.8	30.1	21.1	32.0	6.6	<1%	<1%
CD6	P30203	T-cell differentiation antigen CD6	19%	36%	9.6	13.2	12.9	11.8	8.6	<1%	<1%
CD24	P25063	Signal transducer CD24	99%	99%	7.6	10.5	7.2	10.7	10.8	<1%	<1%
CD27	P26842	CD27 antigen	100%	100%	7.0	7.6	7.5	6.8	2.3	<1%	<1%
CD28	P10747	T-cell-specific surface glycoprotein CD28	100%	100%	7.3	10.2	8.9	6.9	2.3	<1%	<1%
CD33	P20138	Myeloid cell surface antigen CD33	100%	100%	6.4	7.8	6.8	8.5	3.7	<1%	<1%
CD40	P25942	Tumor necrosis factor receptor superfamily member 5	100%	100%	9.4	13.9	6.3	14.0	5.8	<1%	<1%
CD40LG	P29965	CD40 ligand	100%	100%	7.2	11.3	6.2	11.2	0.0	<1%	<1%
CD46	P15529	Membrane cofactor protein	100%	100%	17.8	8.3	19.6	12.5	6.5	<1%	<1%
CD47	Q08722	Leukocyte surface antigen CD47	99%	99%	11.6	7.6	8.5	9.1	7.3	<1%	<1%
CD70	P32970	CD70 antigen	95%	100%	7.3	8.2	6.9	8.3	11.4	<1%	<1%
CD80	P33681	T-lymphocyte activation antigen CD80	100%	100%	8.9	9.2	10.6	7.3	1.6	<1%	<1%
CD83	Q01151	CD83 antigen	100%	100%	7.0	7.0	7.6	6.9	6.6	<1%	<1%
CD86	P42081	T-lymphocyte activation antigen CD86	100%	100%	6.9	10.6	6.5	11.5	0.0	<1%	<1%
CD93	Q9NPY3	Complement component C1q receptor	100%	100%	8.3	8.3	7.3	9.7	0.1	<1%	<1%
CD200	P41217	OX-2 membrane glycoprotein	100%	100%	7.1	9.1	6.3	10.2	6.8	<1%	<1%
CD200R1	Q8TD46	Cell surface glycoprotein CD200 receptor 1	100%	100%	8.5	9.7	7.6	9.5	0.8	<1%	<1%
CD226	Q15762	CD226 antigen	100%	100%	10.9	5.0	8.9	7.3	0.2	<1% ^d	<1%
CD274	Q9NZQ7	Programmed cell death 1 ligand 1	100%	100%	6.1	8.3	7.0	8.2	8.5	<1%	<1%
CD276	Q5ZPR3	CD276 antigen	100%	100%	6.9	6.6	7.0	7.0	7.4	<1%	<1%
CDK4	P11802	Cyclin-dependent kinase 4	20%	22%	19.9	56.6	32.1	28.3	9.1	<1%	<1%
CDK6	Q00534	Cyclin-dependent kinase 6	80%	76%	13.5	11.9	11.6	11.8	12.4	<1%	<1%
CEACAM1	P13688	Carcinoembryonic antigen-related cell adhesion molecule 1	100%	100%	9.0	11.4	8.9	11.9	2.1	<1%	<1%
CEACAM5	P06731	Carcinoembryonic antigen-related cell adhesion molecule 5	100%	100%	7.5	7.4	7.3	8.8	10.2	<1%	<1%
CHI3L1	P36222	Chitinase-3-like protein 1	100%	100%	9.3	7.8	10.3	8.0	1.0	<1%	<1%
CLCF1	Q9UBD9	Cardiotrophin-like cytokine factor 1	35%	22%	17.1	27.1	15.0	26.4	11.8	<1%	<1%
CLEC4A	Q9UMR7	C-type lectin domain family 4 member A	9%	26%	11.1	12.9	17.9	15.1	12.1	<1%	<1%

Table 3: Performance Validation Data by Target (cont.)

Target	UniProt ID	Protein Name	Detectability (%)		CV (%)				LOD (NPQ)	In Panel Cross Reactivity	Out of Panel Cross Reactivity
			Plasma	Serum	Plasma		Serum				
					Intra	Inter	Intra	Inter			
CNTF	P26441	Ciliary neurotrophic factor	9%	14%	32.9	44.2	21.1	58.7	10.0	<1%	<1%
CRP	P02741	C-reactive protein	N/A	N/A	8.9	8.5	6.3	5.8	N/A ^k	<1%	<1%
CSF1	P09603	Macrophage colony-stimulating factor 1	100%	100%	8.0	8.7	8.9	8.6	8.0	<1%	<1%
CSF1R	P07333	Macrophage colony-stimulating factor 1 receptor	100%	100%	9.1	10.4	7.8	11.2	0.1	<1%	<1%
CSF2	P04141	Granulocyte-macrophage colony-stimulating factor	99%	100%	6.5	6.3	6.4	7.2	9.8	<1%	<1%
CSF2RB	P32927	Cytokine receptor common subunit beta	100%	100%	7.8	9.3	8.3	7.6	0.9	<1%	<1%
CSF3	P09919	Granulocyte colony-stimulating factor	100%	100%	5.6	5.2	6.0	6.9	8.5	<1%	<1%
CSF3R	Q99062	Granulocyte colony-stimulating factor receptor	100%	100%	5.9	7.6	6.3	7.2	3.6	<1%	<1%
CST7	O76096	Cystatin-F	100%	100%	10.0	9.7	14.1	9.6	0.0	<1%	<1%
CTF1	Q16619	Cardiotrophin-1	100%	100%	7.4	8.0	12.3	7.9	7.3	<1%	<1%
CTLA4	P16410	Cytotoxic T-lymphocyte protein 4	100%	100%	6.8	9.2	6.3	9.9	11.1	<1%	<1%
CTSS	P25774	Cathepsin S	100%	100%	9.0	15.2	12.9	14.4	0.1	<1%	<1%
CX3CL1	P78423	Fractalkine	100%	100%	6.4	8.6	6.5	8.2	6.1	<1%	<1%
CXADR	P78310	Coxsackievirus and adenovirus receptor	100%	100%	10.5	5.6	10.1	7.6	8.4	<1%	<1%
CXCL1	P09341	Growth-regulated alpha protein	100%	99%	9.0	4.6	8.0	5.6	9.0	<1%	<1%
CXCL10	P02778	C-X-C motif chemokine 10	100%	100%	10.8	9.0	11.4	10.6	2.9	<1%	<1%
CXCL11	O14625	C-X-C motif chemokine 11	100%	100%	6.4	7.6	9.4	8.5	0.0	<1%	<1%
CXCL12	P48061	Stromal cell-derived factor 1	42%	85%	6.5	7.0	7.2	7.6	12.1	<1%	<1%
CXCL13	O43927	C-X-C motif chemokine 13	100%	100%	9.2	8.4	11.4	10.0	0.8	<1%	<1%
CXCL16	Q9H2A7	C-X-C motif chemokine 16	100%	100%	6.1	8.2	6.9	8.3	0.3	<1%	<1%
CXCL2	P19875	C-X-C motif chemokine 2	92%	97%	9.7	9.0	14.8	8.2	10.6	<1%	<1%
CXCL3	P19876	C-X-C motif chemokine 3	100%	100%	7.3	10.6	10.1	11.2	5.7	<1%	<1%
CXCL5	P42830	C-X-C motif chemokine 5	100%	100%	11.2	12.3	12.2	13.1	0.9	<1%	<1%
CXCL6	P80162	C-X-C motif chemokine 6	100%	98%	8.5	10.4	15.3	25.3	10.1	<1%	<1%
CXCL8	P10145	Interleukin-8	100%	100%	6.9	7.4	12.3	10.2	7.6	<1%	<1%
CXCL9	Q07325	C-X-C motif chemokine 9	100%	100%	7.0	6.4	6.9	8.0	1.1	<1%	<1%
DEFA5	Q01523	Defensin alpha 5	100%	100%	5.8	6.6	6.7	7.3	0.4	<1%	<1%
EGF	P01133	Pro-epidermal growth factor	100%	100%	8.6	7.1	7.7	9.7	4.2	<1%	<1%
EGFR	P00533	Epidermal growth factor receptor	100%	100%	8.3	9.9	6.8	10.5	2.2	<1%	<1%
EPO	P01588	Erythropoietin	100%	100%	6.3	6.4	6.7	6.8	8.4	<1%	<1%
ERBB2	P04626	Receptor tyrosine-protein kinase erbB-2	100%	100%	10.9	7.6	8.5	7.3	2.9	<1%	<1%
ERBB4	Q15303	Receptor tyrosine-protein kinase erbB-4	100%	99%	7.1	11.1	6.7	12.0	8.2	<1%	<1%
FAM3C	Q92520	Protein FAM3C	100%	100%	5.2	9.5	6.2	7.8	9.7	<1%	<1%
FAS	P25445	Tumor necrosis factor receptor superfamily member 6	100%	100%	6.7	9.9	8.2	9.8	6.9	<1%	<1%
FASLG	P48023	Tumor necrosis factor ligand superfamily member 6	100%	100%	6.5	7.7	7.3	8.1	0.2	<1%	<1%
FGF19	O95750	Fibroblast growth factor 19	100%	100%	6.8	7.0	7.2	4.3	0.4	<1%	<1%
FGF2	P09038	Fibroblast growth factor 2	76%	75%	12.1	10.0	13.2	9.6	10.6	<1%	<1%
FGF21	Q9NSA1	Fibroblast growth factor 21	100%	100%	6.4	7.5	8.4	8.0	4.8	<1%	<1%
FGF23	Q9GZV9	Fibroblast growth factor 23	93%	85%	9.7	10.5	12.4	19.4	11.0	<1%	<1%
FLRT2	O43155	Leucine-rich repeat transmembrane protein FLRT2	57%	62%	6.7	4.9	10.3	10.2	10.6	<1%	<1%
FLT1	P17948	Vascular endothelial growth factor receptor 1	100%	100%	8.2	9.3	9.7	9.2	11.0	<1%	<1%
FLT3LG	P49771	Fms-related tyrosine kinase 3 ligand	100%	100%	12.5	7.8	10.4	7.4	2.9	<1%	<1%

Table 3: Performance Validation Data by Target (cont.)

Target	UniProt ID	Protein Name	Detectability (%)		CV (%)				LOD (NPQ)	In Panel Cross Reactivity	Out of Panel Cross Reactivity
			Plasma	Serum	Plasma		Serum				
					Intra	Inter	Intra	Inter			
FLT4	P35916	Vascular endothelial growth factor receptor 3	100%	100%	9.4	7.6	9.6	8.2	0.5	<1%	<1%
FST	P19883	Follistatin	100%	99%	7.3	14.4	11.6	12.9	7.2	<1%	<1%
FBTH1	P02794	Ferritin heavy chain	100%	99%	6.8	7.2	8.9	5.9	10.0	<1%	<1%
FURIN	P09958	Furin	100%	99%	11.4	12.3	10.6	11.6	8.5	<1%	<1%
GAS6	Q14393	Growth arrest-specific protein 6	100%	100%	13.1	12.3	6.3	15.4	0.3	<1%	<1%
GDF15	Q99988	Growth/differentiation factor 15	100%	100%	13.9	4.8	11.9	5.8	8.4	<1%	<1%
GDF2	Q9UK05	Growth/differentiation factor 2	99%	100%	7.5	7.7	8.9	9.2	9.2	<1%	<1%
GFAP	P14136	Glial fibrillary acidic protein	100%	100%	6.6	7.5	6.8	7.8	9.7	<1%	<1%
GNLY	P22749	Granulysin	100%	100%	7.1	8.3	13.2	6.6	0.6	<1%	<1%
GPC4	O75487	Glypican-4	26%	43%	30.2	9.8	29.6	12.0	8.2	<1%	<1%
GRN	P28799	Progranulin	100%	100%	7.4	7.8	6.2	8.2	7.9	<1%	<1%
GSDMD	P57764	Gasdermin-D	32%	35%	6.0	4.7	6.0	3.3	11.6	<1%	<1%
GSDME	O60443	Gasdermin-E	82%	100%	8.6	9.6	12.0	12.2	10.8	<1%	<1%
GZMA	P12544	Granzyme A	100%	100%	9.3	7.5	10.0	6.5	1.0	<1%	<1%
GZMB	P10144	Granzyme B	100%	100%	11.7	7.7	22.5	3.5	5.1	<1%	10% ^e
GZMK	P49863	Granzyme K	100%	100%	6.4	8.3	9.0	7.4	4.7	<1%	<1%
HAVCR1	Q96D42	Hepatitis A virus cellular receptor 1	100%	100%	7.3	6.7	8.4	7.4	0.3	<1%	<1%
HAVCR2	Q8TDQ0	Hepatitis A virus cellular receptor 2	100%	100%	7.9	8.1	8.3	8.3	7.1	<1%	<1%
HDAC1	Q13547	Histone deacetylase 1	38%	88%	19.1	23.6	18.0	20.2	8.7	<1%	<1%
HGF	P14210	Hepatocyte growth factor	100%	100%	7.2	12.4	9.8	12.0	6.9	<1%	<1%
HLA-DRA	P01903	HLA class II histocompatibility antigen, DR alpha chain	100%	100%	9.5	6.3	9.1	8.2	7.9	<1%	<1%
ICAM1	P05362	Intercellular adhesion molecule 1	100%	100%	7.1	5.4	7.1	5.4	1.1	<1%	<1%
ICOS	Q9Y6W8	Inducible T-cell costimulator	100%	100%	10.3	12.1	9.4	12.6	2.7	<1%	<1%
ICOSLG	O75144	ICOS ligand	100%	100%	20.5	7.8	16.0	11.7	0.0	<1%	<1%
IDO1	P14902	Indoleamine 2,3-dioxygenase 1	100%	100%	5.6	8.0	11.1	8.9	6.7	<1%	<1%
IFNA1; IFNA13	P0DY56/ A0A087W- WS6	Interferon alpha-1/13	100%	100%	11.3	8.2	12.0	9.0	6.6	<1%	7.2%, 5.6%, 1.6%, 3.1% ^f
IFNA2	P01563	Interferon alpha-2	86%	87%	15.1	7.6	18.7	30.4	6.8	<1%	<1%
IFNB1	P01574	Interferon beta	97%	94%	10.5	5.9	12.0	27.7	9.0	<1%	<1%
IFNG	P01579	Interferon gamma	100%	100%	7.8	10.2	9.8	9.7	7.9	<1%	<1%
IFNL1	Q8IU54	Interferon lambda-1	100%	100%	7.1	9.1	7.9	8.7	7.7	<1%	<1%
IFNL2; IFNL3	Q8IZJ0/ Q8IZI9	Interferon lambda-2_Interferon lambda-3	95%	92%	12.9	6.3	15.8	13.5	9.2	<1%	<1%
IFNW1	P05000	Interferon omega-1	33%	47%	17.7	30.2	21.2	27.8	8.1	<1%	<1%
IKBKG	Q9Y6K9	NF-kappa-B essential modulator	100%	100%	7.7	5.4	6.6	7.2	5.8	<1%	<1%
IL1A	P01583	Interleukin-1 alpha	32%	9%	11.7	22.1	11.8	20.3	11.7	<1%	<1%
IL1B	P01584	Interleukin-1 beta	50%	55%	8.6	18.5	10.0	24.2	10.5	<1%	<1%
IL1R1	P14778	Interleukin-1 receptor type 1	100%	100%	7.7	9.9	6.6	10.2	5.0	<1%	<1%
IL1R2	P27930	Interleukin-1 receptor type 2	100%	100%	8.2	9.5	7.0	9.3	0.5	<1%	<1%
IL1RL1	Q01638	Interleukin-1 receptor-like 1	100%	100%	6.4	6.4	6.7	7.1	0.1	<1%	<1%
IL1RN	P18510	Interleukin-1 receptor antagonist protein	100%	100%	6.6	9.3	9.4	8.4	8.6	<1%	<1%
IL2	P60568	Interleukin-2	100%	100%	9.3	7.0	12.2	7.6	10.0	<1%	<1%
IL2RA	P01589	Interleukin-2 receptor subunit alpha	100%	100%	7.2	7.3	7.5	6.8	0.3	<1%	<1%
IL2RB	P14784	Interleukin-2 receptor subunit beta	100%	100%	11.2	10.0	11.7	7.8	0.2	<1%	<1%
IL3	P08700	Interleukin-3	86%	96%	8.6	7.9	10.1	8.2	11.4	<1%	<1%

Table 3: Performance Validation Data by Target (cont.)

Target	UniProt ID	Protein Name	Detectability (%)		CV (%)				LOD (NPQ)	In Panel Cross Reactivity	Out of Panel Cross Reactivity
			Plasma	Serum	Plasma		Serum				
					Intra	Inter	Intra	Inter			
IL3RA	P26951	Interleukin-3 receptor subunit alpha	100%	100%	6.1	7.5	5.6	7.7	1.8	<1%	<1%
IL4	P05112	Interleukin-4	82%	100%	13.9	7.1	14.1	13.9	8.5	<1%	<1%
IL4I1	Q96RQ9	L-amino-acid oxidase	59%	88%	14.3	10.6	18.3	25.4	8.7	<1%	<1%
IL4R	P24394	Interleukin-4 receptor subunit alpha	100%	100%	6.7	12.6	5.1	13.0	1.8	<1%	<1%
IL5	P05113	Interleukin-5	98%	100%	6.9	6.7	6.9	7.2	5.6	<1%	<1%
IL5RA	Q01344	Interleukin-5 receptor subunit alpha	100%	100%	10.8	8.3	11.5	8.1	0.0	<1%	<1%
IL6	P05231	Interleukin-6	99%	100%	10.6	10.4	10.4	10.5	10.1	<1%	<1%
IL6R	P08887	Interleukin-6 receptor subunit alpha	100%	100%	11.4	10.9	10.7	12.0	0.5	<1%	<1%
IL6ST	P40189	Interleukin-6 receptor subunit beta	100%	100%	7.0	5.8	6.4	6.2	1.7	<1%	<1%
IL7	P13232	Interleukin-7	100%	100%	7.4	10.2	9.5	8.4	8.7	<1%	<1%
IL7R	P16871	Interleukin-7 receptor subunit alpha	100%	100%	7.1	8.2	7.0	8.5	0.1	<1%	<1%
IL9	P15248	Interleukin-9	100%	100%	5.9	8.6	5.5	8.9	5.4	<1%	<1%
IL10	P22301	Interleukin-10	100%	100%	13.8	6.5	15.2	4.6	6.3	<1%	<1%
IL10RB	Q08334	Interleukin-10 receptor subunit beta	100%	100%	6.6	9.7	7.1	8.8	3.5	<1%	<1%
IL11	P20809	Interleukin-11	100%	99%	5.7	5.6	6.5	9.8	12.5	<1%	<1%
IL12B	P29460	Interleukin-12 subunit beta	100%	100%	6.4	6.9	5.9	8.5	6.7	<1%	<1%
IL12p70	P29459_P29460	Interleukin-12 p70 heterocomplex	100%	100%	7.4	7.3	6.7	7.9	8.4	<1%	<1%
IL12RB1	P42701	Interleukin-12 receptor subunit beta-1	100%	100%	6.4	6.8	7.7	8.3	0.6	<1%	<1%
IL13	P35225	Interleukin-13	100%	100%	6.1	5.2	5.2	6.2	10.4	<1%	<1%
IL13RA2	Q14627	Interleukin-13 receptor subunit alpha-2	86%	95%	14.8	13.8	14.4	14.0	9.4	<1%	<1%
IL15	P40933	Interleukin-15	100%	100%	6.5	7.8	6.8	8.3	7.7	<1%	<1%
IL15RA	Q13261	Interleukin-15 receptor subunit alpha	100%	100%	9.4	10.1	10.4	10.2	7.2	<1%	<1%
IL16	Q14005	Pro-interleukin-16	100%	100%	8.0	9.5	9.2	8.9	2.3	<1%	<1%
IL17A	Q16552	Interleukin-17A	84%	93%	8.2	7.5	10.4	6.3	11.0	<1%	<1%
IL17A IL17F	Q16552/Q96PD4	Interleukin-17A F heterocomplex	78%	93%	13.2	5.1	17.0	8.7	8.4	<1%	<1%
IL17B	Q9UHF5	Interleukin-17B	100%	100%	8.3	9.3	13.5	9.5	1.3	<1%	<1%
IL17C	Q9P0M4	Interleukin-17C	100%	100%	9.3	9.2	14.9	8.7	1.2	<1%	<1%
IL17D	Q8TAD2	Interleukin-17D	50%	57%	7.7	5.6	7.1	5.8	10.8	<1%	<1%
IL17F	Q96PD4	Interleukin-17F	53%	62%	9.8	2.4	5.6	5.3	9.4	<1%	<1%
IL17RA	Q96F46	Interleukin-17 receptor A	100%	100%	7.2	8.9	9.8	7.3	9.3	<1%	<1%
IL17RB	Q9NRM6	Interleukin-17 receptor B	100%	100%	8.1	7.6	10.8	6.6	8.2	<1%	<1%
IL18	Q14116	Interleukin-18	100%	100%	6.2	8.8	7.6	8.0	0.4	<1%	<1%
IL18BP	O95998	Interleukin-18-binding protein	100%	100%	6.4	12.0	7.9	10.8	5.7	<1%	<1%
IL18R1	Q13478	Interleukin-18 receptor 1	100%	100%	12.3	10.9	10.8	12.2	7.0	<1%	<1%
IL19	Q9UHD0	Interleukin-19	100%	100%	9.5	6.1	9.0	5.7	9.0	<1%	<1%
IL20	Q9NYY1	Interleukin-20	100%	100%	7.1	7.6	7.2	7.7	4.6	<1%	<1%
IL21	Q9HBE4	Interleukin-21	21%	36%	34.4	54.0	24.4	43.3	8.3	<1%	<1%
IL22	Q9GZX6	Interleukin-22	81%	96%	12.8	9.9	12.7	6.5	8.2	<1%	<1%
IL23	Q9NPF7/P29460	Interleukin-23 heterocomplex	77%	84%	16.8	13.4	13.5	16.8	10.0	<1%	<1%
IL25	Q9H293	Interleukin-25	6%	12%	26.0	49.8	21.3	7.8	8.9	<1%	<1%
IL27	Q8NEV9	Interleukin-27 heterocomplex	80%	91%	11.5	16.4	20.6	19.7	11.6	<1%	<1%
IL31	Q6EBC2	Interleukin-31	96%	98%	9.1	7.7	12.7	5.9	9.5	<1%	<1%
IL32	P24001	Interleukin-32	71%	88%	15.1	28.6	18.8	17.1	10.8	<1%	<1%

NULISaseq™ Immune 340 Panel

Table 3: Performance Validation Data by Target (cont.)

Target	UniProt ID	Protein Name	Detectability (%)		CV (%)				LOD (NPQ)	In Panel Cross Reactivity	Out of Panel Cross Reactivity
			Plasma	Serum	Plasma		Serum				
					Intra	Inter	Intra	Inter			
IL33	O95760	Interleukin-33	88%	99%	12.0	8.1	12.1	10.9	9.2	<1%	<1%
IL34	Q6ZMJ4	Interleukin-34	100%	99%	7.1	5.9	6.9	6.9	7.4	<1%	<1%
IL35	P29459/ Q14213	Interleukin-35 heterocomplex	3%	3%	20.1	11.1	32.8	35.8	10.3	<1%	<1%
IL36A	Q9UHA7	Interleukin-36 alpha	100%	100%	6.3	7.9	5.2	8.2	5.0	<1%	<1%
IL36B	Q9NZH7	Interleukin-36 beta	97%	100%	14.2	21.9	8.5	20.0	12.0	<1%	<1%
IL36G	Q9NZH8	Interleukin-36 gamma	27%	28%	11.2	30.7	8.9	30.8	12.2	<1%	<1%
IL37	Q9NZH6	Interleukin-37	11%	6%	24.5	42.2	21.2	48.4	11.3	<1%	<1%
IL39	Q9NPF7/ Q14213	Interleukin-39 heterocomplex	7%	18%	19.2	23.5	20.5	39.5	10.3	<1%	<1%
IRAK4	Q9NWZ3	Interleukin-1 receptor-associated kinase 4	90%	90%	9.3	11.6	19.2	9.2	7.4	<1%	<1%
JAK1	P23458	Tyrosine-protein kinase JAK1	51%	41%	9.9	9.4	16.4	13.7	11.3	<1%	<1%
KDR	P35968	Vascular endothelial growth factor receptor 2	100%	100%	11.9	5.0	8.0	8.1	0.9	<1%	<1%
KITLG	P21583	Kit ligand	99%	96%	5.1	6.5	6.0	6.4	11.6	<1%	<1%
KLRK1	P26718	NKG2-D type II integral membrane protein	100%	100%	7.0	8.4	7.3	6.6	0.5	<1%	<1%
KNG1	P01042	Kininogen-1	N/A	N/A	6.1	10.1	5.6	11.2	N/A ^h	<1%	<1%
LAG3	P18627	Lymphocyte activation gene 3 protein	100%	100%	7.7	8.5	9.8	7.7	0.1	<1%	<1%
LAMP3	Q9UQV4	Lysosome-associated membrane glycopro- tein 3	99%	100%	9.5	8.7	10.0	6.8	11.1	<1%	<1%
LCN2	P80188	Neutrophil gelatinase-associated lipocalin	100%	100%	7.3	6.1	6.7	8.5	5.8	<1%	<1%
LDHA	P00338	L-lactate dehydrogenase A chain	79%	81%	7.0	32.4	9.5	24.5	10.3	<1%	4% ^g
LDHB	P07195	L-lactate dehydrogenase B chain	99%	93%	5.4	38.9	8.4	25.5	8.0	<1%	<1%
LGALS9	O00182	Galectin-9	100%	100%	6.2	6.9	6.7	7.9	1.3	<1%	<1%
LIF	P15018	Leukemia inhibitory factor	73%	96%	11.8	7.9	14.4	10.8	9.8	<1%	<1%
LILRB1	Q8NHL6	Leukocyte immunoglobulin-like receptor subfamily B member 1	100%	100%	8.0	10.0	6.3	10.7	0.4	<1%	<1%
LILRB2	Q8N423	Leukocyte immunoglobulin-like receptor subfamily B member 2	100%	100%	6.6	6.1	7.2	6.2	0.2	<1%	<1%
LTA	P01374	Lymphotoxin-alpha	100%	100%	8.2	7.0	7.9	7.5	9.2	<1%	<1%
MAC	P01031/ P13671/ P10643/ P07357/ P07358/ P07360/ P02748	Membrane Attack Complex	100%	100%	8.9	9.1	8.0	6.0	0.5	<1%	<1%
MDK	P21741	Midkine	89%	98%	7.6	10.1	6.9	6.3	12.6	<1%	<1%
MERTK	Q12866	Tyrosine-protein kinase Mer	100%	100%	9.9	4.1	8.9	7.5	4.5	<1%	<1%
MICA	Q29983	MHC class I polypeptide-related sequence A	96%	92%	11.6	9.0	13.2	6.3	9.3	<1%	<1%
MICB	Q29980	MHC class I polypeptide-related sequence B	97%	95%	10.3	9.5	9.7	11.7	11.3	<1%	<1%
MIF	P14174	Macrophage migration inhibitory factor	78%	52%	5.7	8.8	6.4	2.1	12.4	<1%	<1%
MMP1	P03956	Interstitial collagenase	99%	100%	13.7	15.3	15.1	9.0	9.8	<1%	<1%
MMP2	P08253	72 kDa type IV collagenase	100%	100%	10.7	7.8	6.9	9.3	0.2	<1%	<1%
MMP3	P08254	Stromelysin-1	100%	100%	6.2	5.1	6.2	5.7	0.5	<1%	<1%
MMP8	P22894	Neutrophil collagenase	100%	100%	6.1	9.4	6.7	9.6	6.3	<1%	<1%
MMP9	P14780	Matrix metalloproteinase-9	100%	100%	6.3	8.4	7.6	10.0	3.1	<1%	<1%
MMP10	P09238	Stromelysin-2	100%	100%	6.7	9.5	7.2	8.3	6.8	<1%	<1%
MMP12	P39900	Macrophage metalloelastase	100%	100%	8.1	6.4	9.8	7.3	6.8	<1%	<1%
MPO	P05164	Myeloperoxidase	100%	99%	7.6	5.4	6.2	6.4	5.4	<1%	<1%
MRC1	P22897	Macrophage mannose receptor 1	100%	100%	6.2	7.2	5.2	8.7	0.2	<1%	<1%

Table 3: Performance Validation Data by Target (cont.)

Target	UniProt ID	Protein Name	Detectability (%)		CV (%)				LOD (NPQ)	In Panel Cross Reactivity	Out of Panel Cross Reactivity
			Plasma	Serum	Plasma		Serum				
					Intra	Inter	Intra	Inter			
MS4A1	P11836	B-lymphocyte antigen CD20	81%	95%	23.8	3.2	18.6	8.7	6.5	<1%	<1%
MUC16	Q8WXI7	Mucin-16	100%	100%	8.6	8.5	8.8	7.2	6.6	<1%	<1%
NAMPT	P43490	Nicotinamide phosphoribosyltransferase	100%	100%	6.3	10.4	9.9	7.9	10.7	<1%	<1%
NCR1	O76036	Natural cytotoxicity triggering receptor 1	100%	100%	7.5	10.0	9.0	9.5	0.0	<1%	<1%
NCR3LG1	Q68D85	Natural cytotoxicity triggering receptor 3 ligand 1	100%	100%	7.3	9.2	8.0	9.2	9.1	<1%	<1%
NECTIN2	Q92692	Nectin-2	100%	100%	10.7	9.9	12.4	13.0	0.1	<1%	<1%
NECTIN3	Q9NQS3	Nectin-3	25%	25%	17.3	43.2	31.8	34.1	9.0	<1%	<1%
NEFL	P07196	Neurofilament light polypeptide	100%	100%	5.5	7.8	5.6	7.4	10.8	<1%	<1%
NGF	P01138	Beta-nerve growth factor	100%	98%	7.0	7.2	8.6	8.0	10.5	<1%	<1%
NTF3	P20783	Neurotrophin-3	29%	36%	8.8	8.6	9.5	11.0	12.9	<1%	<1%
OSM	P13725	Oncostatin-M	100%	100%	3.9	8.4	5.9	8.5	7.1	<1%	<1%
OSMR	Q99650	Oncostatin-M-specific receptor subunit beta	100%	100%	8.2	5.4	9.2	6.3	2.8	<1%	<1%
PARP1	P09874	Poly [ADP-ribose] polymerase 1	11%	27%	10.3	4.1	9.7	4.8	10.1	<1%	<1%
PDCD1	Q15116	Programmed cell death protein 1	100%	100%	6.8	8.6	6.1	8.1	3.1	<1%	<1%
PDCD1LG2	Q9BQ51	Programmed cell death 1 ligand 2	100%	100%	6.7	7.9	5.6	8.7	0.2	<1%	<1%
PDGFA	P04085	Platelet-derived growth factor subunit A	98%	98%	9.0	5.4	10.8	7.2	10.8	<1%	<1%
PDGFB	P01127	Platelet-derived growth factor subunit B	100%	100%	6.6	10.4	15.0	10.7	0.5	<1%	<1%
PGF	P49763	Placenta growth factor	100%	100%	6.1	5.4	5.2	6.0	10.1	<1%	<1%
PRF1	P14222	Perforin-1	100%	100%	11.2	11.8	11.0	12.8	0.6	<1%	<1%
PROS1	P07225	Vitamin K-dependent protein S	N/A	N/A	5.3	5.9	6.0	6.4	N/A ^a	<1%	<1%
PTX3	P26022	Pentraxin-related protein PTX3	100%	98%	6.0	6.6	10.0	5.9	9.4	<1%	<1%
PVR	P15151	Poliovirus receptor	100%	100%	6.1	7.7	6.2	8.0	9.1	<1%	<1%
RIPK3	Q9Y572	Receptor-interacting serine/threonine-protein kinase 3	100%	100%	6.5	10.5	7.2	9.1	10.6	<1%	<1%
S100A12	P80511	Protein S100-A12	100%	100%	4.5	10.9	7.8	11.1	4.6	<1%	<1%
S100A9	P06702	Protein S100-A9	98%	99%	6.4	12.8	7.7	12.7	11.1	<1%	<1%
SCG2	P13521	Secretogranin-2	95%	82%	14.5	9.0	16.6	20.6	10.2	<1%	<1%
SDC1	P18827	Syndecan-1	100%	100%	10.1	8.8	9.4	9.4	6.7	<1%	<1%
SELE	P16581	E-selectin	100%	100%	14.1	7.9	12.8	5.8	8.1	<1%	<1%
SELP	P16109	P-selectin	100%	100%	8.0	5.8	6.8	8.0	0.2	<1%	<1%
SIGLEC10	Q96LC7	Sialic acid-binding Ig-like lectin 10	96%	100%	16.4	11.5	18.5	13.4	7.6	<1%	133% ^h
SIRPA	P78324	Tyrosine-protein phosphatase non-receptor type substrate 1	100%	100%	5.8	8.6	4.8	9.1	6.0	<1%	7% ⁱ
SLAMF1	Q13291	Signaling lymphocytic activation molecule	100%	100%	8.1	8.8	8.8	8.9	0.2	<1%	<1%
SLURP1	P55000	Secreted Ly-6/uPAR-related protein 1	100%	100%	8.0	8.3	9.4	9.4	9.2	<1%	<1%
SPP1	P10451	Osteopontin	100%	100%	9.3	14.6	11.9	15.3	2.4	<1%	<1%
STAT3	P40763	Signal transducer and activator of transcription 3	54%	64%	9.6	6.4	9.0	5.1	8.5	<1%	<1%
TEK	Q02763	Angiopoietin-1 receptor	100%	100%	6.6	11.6	5.8	12.1	0.7	<1%	<1%
TGFB1	P01137	Transforming growth factor beta-1 proprotein	100%	100%	5.1	8.8	7.0	7.0	10.7	<1%	<1%
TGFB3	P10600	Transforming growth factor beta-3 proprotein	21%	29%	21.9	12.6	25.5	29.0	9.5	<1%	<1%
THBS2	P35442	Thrombospondin-2	100%	100%	10.4	11.8	8.2	11.5	8.7	<1%	<1%
THPO	P40225	Thrombopoietin	100%	100%	7.6	9.7	7.7	8.3	1.0	<1%	<1%
TIGIT	Q495A1	T-cell immunoreceptor with Ig and ITIM domains	100%	100%	7.3	11.0	9.2	9.7	6.2	<1%	<1%
TIMP1	P01033	Metalloproteinase inhibitor 1	100%	100%	7.2	5.9	7.8	6.8	7.7	<1%	<1%

Table 3: Performance Validation Data by Target (cont.)

Target	UniProt ID	Protein Name	Detectability (%)		CV (%)				LOD (NPQ)	In Panel Cross Reactivity	Out of Panel Cross Reactivity
			Plasma	Serum	Plasma		Serum				
					Intra	Inter	Intra	Inter			
TIMP2	P16035	Metalloproteinase inhibitor 2	99%	99%	10.9	9.4	10.8	10.8	12.3	<1%	<1%
TLR2	O60603	Toll-like receptor 2	100%	100%	8.6	5.3	9.9	9.3	7.2	<1%	<1%
TLR3	O15455	Toll-like receptor 3	100%	100%	12.4	6.9	10.7	8.7	3.5	<1%	<1%
TNF	P01375	Tumor necrosis factor	25%	25%	4.0	3.3	3.7	4.1	12.7	<1%	<1%
TNFRSF1A	P19438	Tumor necrosis factor receptor superfamily member 1A	100%	100%	6.3	7.2	6.2	8.0	7.2	<1%	<1%
TNFRSF1B	P20333	Tumor necrosis factor receptor superfamily member 1B	100%	100%	7.8	8.8	7.9	10.0	0.8	<1%	<1%
TNFRSF4	P43489	Tumor necrosis factor receptor superfamily member 4	100%	100%	5.3	9.4	6.4	9.9	5.8	<1%	<1%
TNFRSF8	P28908	Tumor necrosis factor receptor superfamily member 8	100%	100%	10.3	12.5	9.2	14.4	0.9	<1%	<1%
TNFRSF9	Q07011	Tumor necrosis factor receptor superfamily member 9	100%	100%	9.1	10.5	10.1	11.0	11.5	<1%	<1%
TNFRSF11A	Q9Y6Q6	Tumor necrosis factor receptor superfamily member 11A	100%	100%	8.7	11.6	9.8	7.5	10.6	<1%	<1%
TNFRSF11B	O00300	Tumor necrosis factor receptor superfamily member 11B	100%	100%	7.2	6.9	6.9	9.1	3.5	<1%	<1%
TNFRSF13B	O14836	Tumor necrosis factor receptor superfamily member 13B	100%	100%	7.9	4.5	7.7	6.0	0.9	<1%	<1%
TNFRSF13C	Q96RJ3	Tumor necrosis factor receptor superfamily member 13C	100%	100%	7.7	6.9	8.9	8.3	6.8	<1%	<1%
TNFRSF14	Q92956	Tumor necrosis factor receptor superfamily member 14	100%	100%	6.8	11.3	8.4	10.4	4.0	<1%	<1%
TNFRSF17	Q02223	Tumor necrosis factor receptor superfamily member 17	100%	100%	7.0	10.4	6.4	11.3	4.4	<1%	<1%
TNFRSF18	Q9Y5U5	Tumor necrosis factor receptor superfamily member 18	100%	100%	6.2	6.6	7.9	5.0	9.1	<1%	<1%
TNFRSF21	O75509	Tumor necrosis factor receptor superfamily member 21	14%	13%	15.9	12.3	16.8	6.2	9.0	<1%	<1%
TNFSF4	P23510	Tumor necrosis factor ligand superfamily member 4	100%	100%	6.7	9.1	7.5	8.0	6.1	<1%	<1%
TNFSF8	P32971	Tumor necrosis factor ligand superfamily member 8	100%	100%	6.7	9.2	6.6	9.9	4.0	<1%	<1%
TNFSF9	P41273	Tumor necrosis factor ligand superfamily member 9	100%	100%	8.6	8.1	8.5	8.5	9.6	<1%	<1%
TNFSF10	P50591	Tumor necrosis factor ligand superfamily member 10	100%	100%	7.3	6.5	7.1	8.4	3.9	<1%	<1%
TNFSF11	O14788	Tumor necrosis factor ligand superfamily member 11	100%	100%	7.1	7.4	5.8	7.4	6.9	<1%	<1%
TNFSF12	O43508	Tumor necrosis factor ligand superfamily member 12	100%	100%	10.7	9.6	9.3	9.7	2.0	<1%	<1%
TNFSF13	O75888	Tumor necrosis factor ligand superfamily member 13	93%	95%	7.3	13.7	10.4	10.8	11.2	<1%	<1%
TNFSF13B	Q9Y275	Tumor necrosis factor ligand superfamily member 13B	100%	100%	7.9	7.9	7.6	7.1	0.3	<1%	<1%
TNFSF14	O43557	Tumor necrosis factor ligand superfamily member 14	100%	100%	8.2	9.0	9.1	9.3	1.5	<1%	<1%
TNFSF15	O95150	Tumor necrosis factor ligand superfamily member 15	100%	100%	8.6	6.8	8.2	6.8	3.6	<1%	<1%
TNFSF18	Q9UNG2	Tumor necrosis factor ligand superfamily member 18	100%	100%	6.5	8.0	6.8	6.5	7.0	<1%	<1%
TP53	P04637	Cellular tumor antigen p53	4%	14%	21.5	9.8	17.9	15.8	10.7	<1%	<1%
TPO	P07202	Thyroid peroxidase	89%	96%	8.2	9.5	10.8	9.3	11.6	<1%	<1%

NULISaseq™ Immune 340 Panel

Table 3: Performance Validation Data by Target (cont.)

Target	UniProt ID	Protein Name	Detectability (%)		CV (%)				LOD (NPQ)	In Panel Cross Reactivity	Out of Panel Cross Reactivity
			Plasma	Serum	Plasma		Serum				
					Intra	Inter	Intra	Inter			
TREM1	Q9NP99	Triggering receptor expressed on myeloid cells 1	100%	100%	7.6	8.9	7.7	9.1	5.9	<1%	<1%
TREM2	Q9NZC2	Triggering receptor expressed on myeloid cells 2	100%	100%	9.1	10.3	9.0	9.0	0.4	<1%	<1%
TSLP	Q969D9	Thymic stromal lymphopoietin	100%	100%	7.7	7.5	8.5	6.4	10.6	<1%	<1%
VCAM1	P19320	Vascular cell adhesion protein 1	100%	100%	6.5	2.8	6.7	4.4	0.2	<1%	<1%
VEGFA	P15692	Vascular endothelial growth factor A, long form	100%	100%	6.8	7.1	8.6	9.0	9.3	<1%	<1%
VEGFC	P49767	Vascular endothelial growth factor C	100%	100%	5.5	6.5	6.3	5.9	6.3	<1%	<1%
VEGFD	O43915	Vascular endothelial growth factor D	97%	99%	12.1	10.7	7.1	10.4	10.8	<1%	<1%
VSNL1	P62760	Visinin-like protein 1	100%	100%	8.8	7.9	7.9	6.1	9.1	<1%	75% ^j
VSTM1	Q6UX27	V-set and transmembrane domain-containing protein 1	92%	100%	10.3	4.8	12.4	6.9	7.3	<1%	<1%
VTCN1	Q7Z7D3	V-set domain-containing T-cell activation inhibitor 1	13%	48%	16.5	21.1	23.5	54.9	9.6	<1%	<1%
WNT16	Q9UBV4	Protein Wnt-16	100%	100%	10.4	11.7	10.3	11.8	8.6	<1%	<1%
WNT7A	O00755	Protein Wnt-7a	99%	99%	8.7	5.4	8.3	7.5	11.7	<1%	<1%
XCL1	P47992	Lymphotactin	15%	13%	38.5	50.8	26.6	58.4	4.7	<1%	<1%

^aCross-reactivity with ALPG, which has 98% homology with ALPP; ALPG is not in the Immune 340 Panel

^bCross-reactivity with CCL3L1, which has 95% homology with CCL3; CCL3L1 is not in the Immune 340 Panel

^cCross-reactivity with CCL4L1, which has 95% homology with CCL4; CCL4L1 is not in the Immune 340 Panel

^dCross-reactivity with NECTIN3, NECTIN3 is in the Immune 340 Panel

^eCross-reactivity with GZMH, which has 71% homology with GZMB; GZMH is not in the Immune 340 Panel

^fCross-reactivity with IFNA17 (7.2%), IFNA7 (5.6%), IFNA10 (1.6%), IFNA5 (3.1%) (out-of-panel IFN-alpha subtype homologs; human IFN-alpha subtypes share 75-99% homology); not in the Immune 340 Panel

^gCross-reactivity with LDHAL6B, which has 71% homology with LDHA, LDHAL6B is not in the Immune 340 Panel

^hCross-reactivity with SIGLEC11, which has 82% homology with SIGLEC10, SIGLEC11 is not in the Immune 340 Panel

ⁱCross-reactivity with SIRPB1, which has ~90% homology (extracellular domain) with SIRPA; SIRPB1 is not in the Immune 340 Panel

^jCross-reactivity with HPCAL4, which has 89% homology with VSNL1; HPCAL4 is not in the Immune 340 Panel

^kLeverages a special algorithm for plasma and serum due to the high abundance of these analytes in these matrices. Not reported for other sample types.

Ordering Information

NULISaseq Panel

Product Name	Plate Format	Sample Type	Catalog Number
NULISaseq™ Immune 340 Panel	96	plasma/serum	800472

Consumables & Buffers

Product Name	Qty	Catalog Number
NULISA™ 10X Wash Buffer	1L	801056

Instrument

Product Name	Qty	Catalog Number
Alamar ARGO™ HT System	1	800101

Alamar Biosciences, Inc.
47071 Bayside Parkway
Fremont, CA 94538
T +1 (510) 626-9888
E info@alamarbio.com

Visit [AlamarBio.com](https://www.alamarbio.com) to learn more.

FOR RESEARCH USE ONLY. Not for use in diagnostic procedures.
©2026 Alamar Biosciences, Inc. All rights reserved. Alamar, NULISA, NULISaseq and ARGO are trademarks of Alamar Biosciences, Inc. All other trademarks and/or service marks not owned by Alamar that appear are the property of their respective owners.
M1047-0726.1

