

## Introduction

Inflammation and disruptions in immune response represent key mechanisms in the development and treatment of many diseases. Detection and measurement of key immune related proteins provides critical information in the discovery and screening for biomarkers associated with disease progression or therapeutic response. The NULISAseq Inflammation Panel AQ measures the absolute concentrations of 150+ cytokines,

chemokines and inflammation-related human proteins present in biofluids such as plasma and serum. In addition, the panel measures the relative abundance of these proteins as well as 90+ additional proteins, covering the complete profile of the existing Inflammation RQ product. The analytical performance of the product has been carefully validated and the results are presented below.

## NULISA™ Technology

NULISAseq is a sandwich immunoassay in which 2 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 ARGO HT System and data is analyzed using the NULISA Analysis Software. More details on the assay protocol can be found [here](#).



## Data Normalization and Quantification Methods

For relative quantification (RQ) NULISA Protein Quantification (NPQ) units are log<sub>2</sub>-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 calibrator (CAL) samples on the plate. Data is then rescaled and log<sub>2</sub>-transformed to obtain the data in NPQ, which are approximately normally distributed values amenable to downstream statistical analysis.

For absolute quantification (AQ), data is normalized using the IC and CAL samples as described for RQ. Next, a run-specific 4PL curve is generated for each target by combining information from pre-determined master curve parameters, known CAL concentrations, and the CAL normalized counts using Alamar's AQ algorithm. These curves are then used to generate absolute concentrations in pg/mL and aM for the AQ targets in each sample.

## Dynamic Range

Dynamic range was determined using a set of 3 NULISaseq runs that included calibration standards comprising a mixture of recombinant antigens corresponding to each target in a dilution series extending to concentrations above and below each target's expected quantifiable range. Absolute quantification of standards was carried out using the pre-determined master curve parameters, known CAL concentrations, the CAL normalized counts, and Alamar's AQ algorithm. The AQ values were used to assess recovery of standards at various concentration levels. Precision was assessed using a precision profile model where intra-plate CV was modeled as a function of concentration. The dynamic range for each target was defined as the largest concentration range for which the intra-plate CV is below 30% and the mean recovery error is within 30%

of expected. The lower and upper limits of quantification (LLoQ and ULoQ) represent the lower and upper limits of the dynamic range, respectively. The log<sub>10</sub> range for each target is calculated as  $\log_{10}(\text{range}) = \log_{10}(\text{ULoQ}) - \log_{10}(\text{LLoQ})$ . (Table 2, Figure 1).

A sample is considered quantifiable for a given target if the sample's concentration falls within the target's dynamic range. To assess quantifiability, or percentage of quantifiable samples, for each AQ target, the concentration range of a set of 172 reference samples (57 healthy plasma, 62 disease plasma, 30 healthy serum, 23 disease serum) was measured using Alamar's AQ algorithm in 2 independent runs (Figure 1).

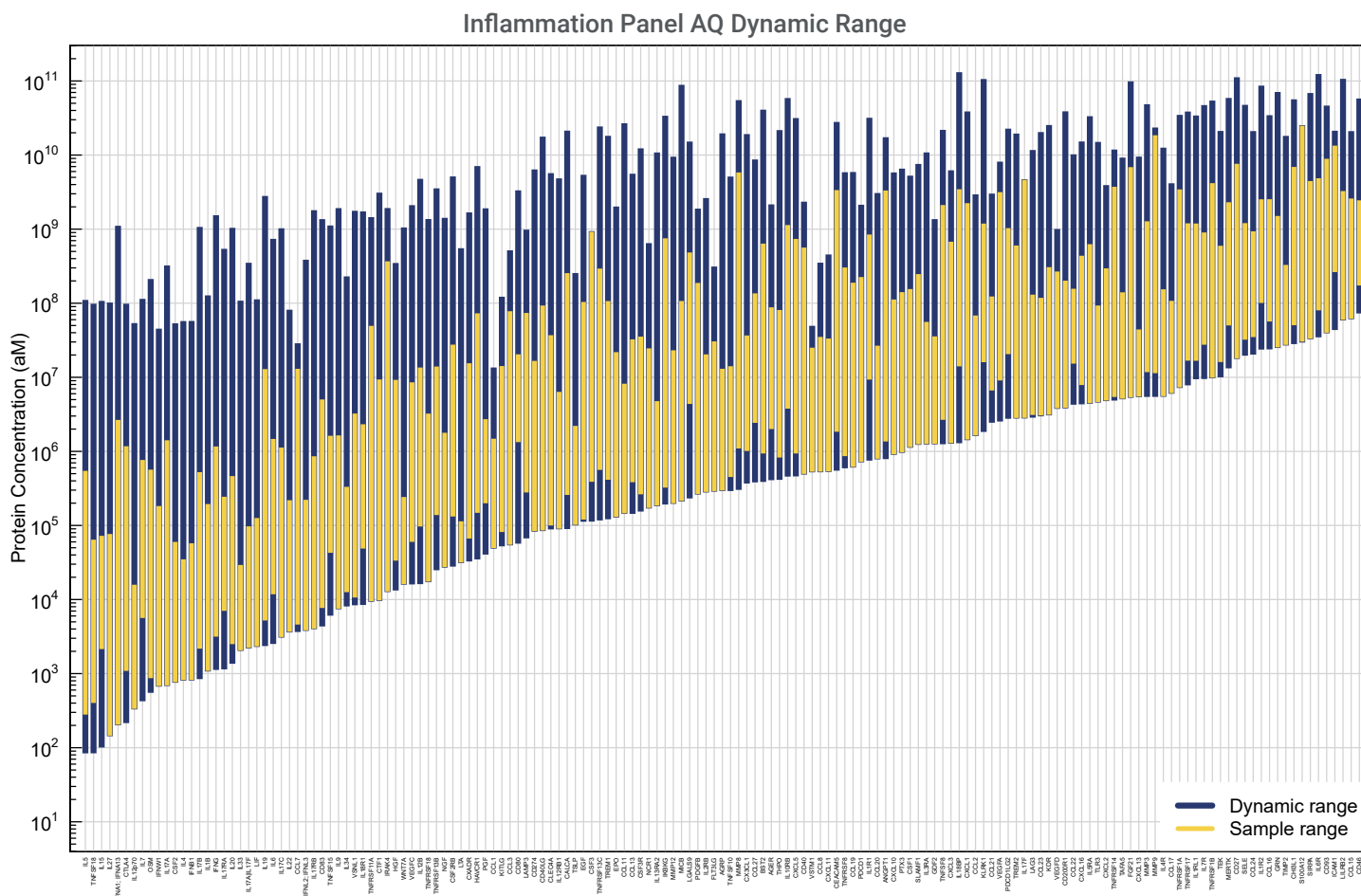


Figure 1. Dynamic range in aM for AQ targets with overlapping quantifiable concentration ranges for 119 plasma and 53 serum samples. Quantifiability, or whether a value falls within a target's dynamic range, was assessed for the 57 healthy and 62 disease plasma samples, and 94.9% of targets are now quantifiable in at least 50% of samples.

## Sensitivity & Quantifiability

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. A maximum of one outlier NC value may be omitted.

For AQ targets, LOD was determined in absolute concentration using a set of 3 additional runs. The mean plus three standard deviations of the 4 NC wells' normalized reads were converted to pg/mL using Alamar's proprietary algorithm (Table 2).

## Precision

For AQ targets, coefficient of variation (CV) was assessed using a set of 8 runs including 14 plasma samples with 3 technical replicates each. The plasma samples were spiked with different concentrations of recombinant antigen pools (13-point and 2-fold serial dilutions) and a sample diluent buffer. Data were quantified in absolute concentration using Alamar's AQ algorithm. Values outside of the dynamic range were excluded, and variance component models were then fit for each sample and target and included the factors reagent lot, instrument, inter-plate, and intra-plate. For each target, the estimated CV for each component was averaged across the 14 samples (Table 2). Table 1 shows across-target medians for each CV component.

Table 1: Across-target Median AQ Coefficients of Variation

CV component	Median CV (%), Plasma
Intra-plate	5.96
Inter-plate	3.07
Inter-Instrument	0.95
Inter-Reagent Lot	1.75
Total	8.35

## Dilutional Linearity

Dilutional linearity was assessed for each target using 13-point 2-fold dilutions of plasma samples with spiked-in recombinant antigen. Samples were quantified using Alamar's AQ algorithm, and values outside dynamic range were excluded. Recovery error was calculated by multiplying the measured concentration of the diluted samples by their dilution factor and dividing the result

by the measured concentration of the first dilution point below ULoQ times its own dilution factor. A <30% recovery error for at least 75% of samples within the dynamic range was required for each AQ target. Table 3 reports the average recovery error for all samples in the dynamic range for each target.

Inflammation Panel AQ Dilutional Linearity

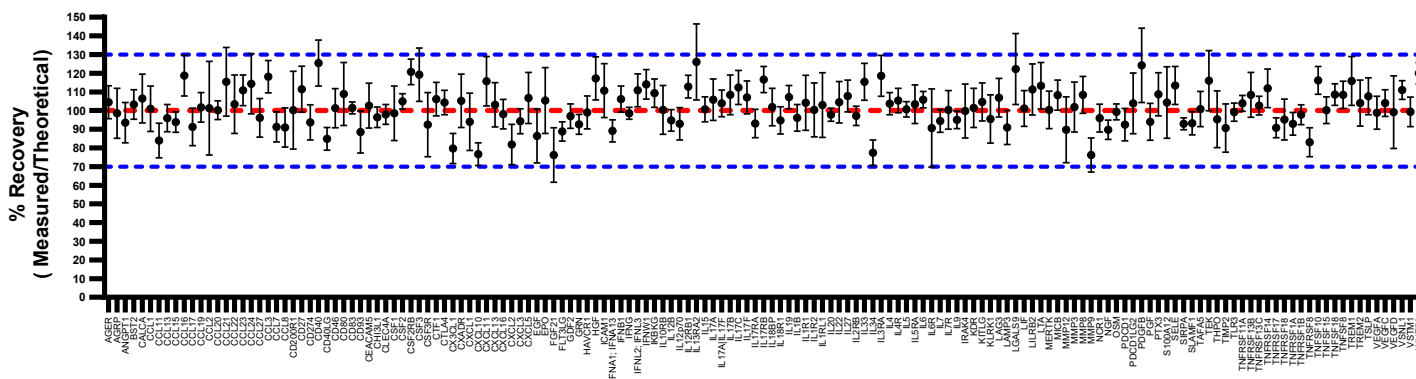


Table 2: Performance Validation Data by Target

Target	UniProt ID	Protein Name	Quantifiability (%)		AQ Precision (CV%)				LOD (pg/mL)	LLOQ (pg/mL)	ULOQ (pg/mL)	log10 Range	Dilution Linearity (%)
AQ Targets			Plasma		Plasma								
			Healthy n=57	Disease n=62	Intra	Inter	Lot	Total					
AGER	Q15109	Advanced glycosylation end product-specific receptor	100	100	4.5	3.7	1.3	7.3	0.82	19.19	84184	3.6	104
AGRP	O00253	Agouti-related protein	98	100	5.1	3.6	0.7	6.7	0.22	4.61	258244	4.7	98
ANGPT1	Q15389	Angiopoietin-1	100	100	5.0	2.3	2.2	6.8	30.66	49.60	912505	4.3	94
BST2	Q10589	Bone marrow stromal antigen 2	100	100	6.3	3.3	1.7	7.8	0.86	8.40	738248	4.9	103
CALCA	P01258	Calcitonin [Cleaved into: Calcitonin; Katalcalcin	100	100	6.0	2.0	1.0	7.2	0.26	1.52	301081	5.3	106
CCL1	P22362	C-C motif chemokine 1	96	100	4.0	2.0	4.1	7.5	0.01	0.59	136	2.4	101
CCL11	P51671	Eotaxin	98	100	5.2	2.9	0.2	6.3	0.28	1.69	262892	5.2	84
CCL13	Q99616	C-C motif chemokine 13	100	100	5.8	3.1	5.5	9.7	0.76	1.73	56020	4.5	96
CCL15	Q16663	C-C motif chemokine 15	100	100	5.9	2.6	7.8	12.0	171.93	816.14	234499	2.5	94
CCL16	O15467	C-C motif chemokine 16	100	100	8.1	2.0	0.9	9.1	n/a	355.18	427810	3.1	119
CCL17	Q92583	C-C motif chemokine 17	84	95	4.2	2.8	5.6	8.5	17.99	69.16	39828	2.8	91
CCL19	Q99731	C-C motif chemokine 19	100	98	5.5	6.3	0.8	10.4	1.60	7.29	59135	3.9	102
CCL2	P13500	C-C motif chemokine 2	98	100	5.6	4.9	8.1	12.8	3.57	19.44	29612	3.2	101
CCL20	P78556	C-C motif chemokine 20	32	40	8.0	5.1	2.4	11.1	3.89	9.22	30127	3.5	100
CCL21	O00585	C-C motif chemokine 21	100	100	4.7	2.8	1.4	6.5	2.92	39.16	40290	3.0	116
CCL22	O00626	C-C motif chemokine 22	100	100	6.5	3.8	5.0	11.1	10.46	49.75	99010	3.3	103
CCL23	P55773	C-C motif chemokine 23	100	100	7.5	3.5	4.0	10.7	0.49	43.84	250300	3.8	111
CCL24	O00175	C-C motif chemokine 24	100	100	5.2	3.3	2.1	7.4	196.78	291.76	252117	2.9	114
CCL27	Q9Y4X3	C-C motif chemokine 27	100	100	6.1	3.5	0.6	7.4	1.70	5.28	100215	4.3	96
CCL3	P10147	C-C motif chemokine 3	98	100	9.8	5.2	9.0	16.7	0.23	0.60	4758	3.9	118
CCL7	P80098	C-C motif chemokine 7	98	100	4.5	2.8	0.4	5.7	0.02	0.04	294	3.8	91
CCL8	P80075	C-C motif chemokine 8	88	97	5.7	4.2	23.9	27.2	0.93	6.44	3612	2.7	91
CD200R1	Q8TD46	Cell surface glycoprotein CD200 receptor 1	98	100	6.9	4.1	0.9	8.9	n/a	162.99	1385049	3.9	100
CD27	P26842	CD27 antigen	98	100	7.5	4.2	0.7	9.0	50.03	565.52	2982537	3.7	112
CD274	Q9NZQ7	Programmed cell death 1 ligand 1, PD-L1	98	100	6.4	3.2	2.4	8.2	0.78	3.00	193843	4.8	94
CD40	P25942	CD40 molecule	100	100	7.6	3.4	1.7	9.9	2.55	16.32	65513	3.6	125
CD40LG	P29965	CD40 ligand	89	100	4.2	3.6	2.3	6.4	0.13	2.70	472801	5.2	85
CD46	P15529	Membrane cofactor protein	98	100	6.0	1.5	1.6	7.3	663.66	3492.33	2312697	2.8	101
CD80	P33681	T-lymphocyte activation antigen CD80	100	100	6.0	2.2	2.1	7.5	0.49	2.06	100582	4.7	109
CD83	Q01151	CD83 antigen	100	100	4.2	6.4	0.5	9.1	0.07	0.11	28648	5.4	101
CD93	Q9NPY3	Complement component C1q receptor	98	100	6.9	2.0	0.5	8.0	163.08	2952.99	2906681	3.0	89
CEA-CAM5	P06731	Carcinoembryonic antigen related cell adhesion molecule 5	100	100	6.8	1.9	0.9	7.7	35.79	46.25	1958077	4.6	103
CHI3L1	P36222	Chitinase-3-like protein 1	100	100	7.8	2.1	2.2	9.2	245.49	1312.63	2195438	3.2	96
CLEC4A	Q9UMR7	C-type lectin domain family 4 member A	100	100	4.6	2.8	1.8	6.6	0.53	2.67	142916	4.7	98
CSF1	P09603	Macrophage colony-stimulating factor 1	98	100	7.5	5.8	8.9	15.3	20.43	73.90	288847	3.6	99
CSF2	P04141	Granulocyte-macrophage colony-stimulating factor	98	100	4.1	3.6	0.5	6.3	< 0.01	0.01	795	4.8	105
CSF2RB	P32927	Cytokine receptor common subunit beta	100	100	3.8	1.9	1.7	5.2	0.42	2.97	456414	5.2	121
CSF3	P09919	Granulocyte colony-stimulating factor, G-CSF	100	95	4.6	2.6	3.4	7.5	0.45	2.76	19100	3.8	119
CSF3R	Q99062	Granulocyte colony-stimulating factor receptor	100	100	5.3	2.8	0.1	6.6	1.24	15.58	1034743	4.8	92
CTF1	Q16619	Cardiotrophin-1	100	100	6.1	2.1	3.6	8.9	0.07	0.22	60124	5.4	106
CTLA4	P16410	Cytotoxic T-lymphocyte protein 4	100	100	4.1	3.2	0.7	5.6	0.01	0.01	2213	5.6	104
CX3CL1	P78423	Fractalkine	100	100	5.6	3.8	3.0	8.1	4.22	17.06	737633	4.6	80
CXADR	P78310	Coxsackievirus and adenovirus receptor	100	100	5.7	3.2	0.2	7.2	1.29	1.43	61372	4.6	105

Table 2: Performance Validation Data by Target (cont.)

Target	UniProt ID	Protein Name	Quantifiability (%)		AQ Precision (CV%)				LOD (pg/mL)	LLOQ (pg/mL)	ULOQ (pg/mL)	log10 Range	Dilution Linearity (%)
			Healthy n=57	Disease n=62	Intra	Inter	Lot	Total					
<b>AQ Targets</b>													
CXCL1	P09341	Growth-regulated alpha protein	82	100	7.7	4.3	2.3	10.5	10.55	17.57	399639	4.4	94
CXCL10	P02778	C-X-C motif chemokine 10	98	100	6.7	3.0	0.6	8.4	1.87	10.70	57738	3.7	77
CXCL11	O14625	C-X-C motif chemokine 11	91	100	4.9	4.7	15.1	18.7	1.14	5.99	4297	2.9	116
CXCL13	O43927	C-X-C motif chemokine 13	7	31	9.9	4.2	0.0	12.3	n/a	74.87	110041	3.2	103
CXCL16	Q9H2A7	C-X-C motif chemokine 16	100	100	6.1	2.4	4.2	9.2	10.73	130.65	383121	3.5	98
CXCL2	P19875	C-X-C motif chemokine ligand 2	61	65	6.2	3.9	2.2	8.6	3.39	59.60	40796	2.8	82
CXCL3	P19876	C-X-C motif chemokine ligand 3	100	98	7.3	1.2	5.1	10.1	4.55	15.80	64322	3.6	94
CXCL5	P42830	C-X-C motif chemokine 5	100	100	7.6	1.0	0.5	8.8	0.22	6.03	344308	4.8	107
EGF	P01133	Pro-epidermal growth factor	100	100	6.3	3.7	0.4	8.6	4.74	16.50	661236	4.6	86
EPO	P01588	Erythropoietin	98	100	6.5	3.6	1.4	8.9	1.84	2.99	39204	4.1	105
FGF21	Q9NSA1	Fibroblast growth factor 21	98	98	5.6	3.5	2.0	8.1	64.64	129.30	2008708	4.2	76
FLT3LG	P49771	Fms-related tyrosine kinase 3 ligand	98	100	7.0	11.0	12.7	18.8	0.92	8.28	7530	3.0	89
GDF2	Q9UK05	Growth/differentiation factor 2	98	100	7.9	2.8	4.4	12.3	29.89	64.63	58873	3.0	97
GRN	P28799	Progranulin	98	100	9.6	6.1	4.8	14.6	557.57	1734.37	4113406	3.4	93
HAVCR1	Q96D42	Hepatitis A virus cellular receptor 1	100	100	5.3	2.4	0.5	6.4	n/a	1.50	254043	5.2	99
HGF	P14210	Hepatocyte growth factor	100	100	9.0	3.9	1.1	12.0	0.39	1.21	26449	4.3	117
ICAM1	P05362	Intercellular adhesion molecule 1	100	100	7.4	1.7	2.1	9.0	601.06	2760.10	1122168	2.6	111
IFNA1; IFNA13	P01562; P01562	Interferon alpha-1; Interferon alpha-13	93	95	4.3	3.5	0.6	6.6	< 0.01	< 0.01	21989	6.7	89
IFNB1	P01574	Interferon beta	54	56	7.4	2.8	13.5	17.9	< 0.01	0.02	1170	4.8	106
IFNG	P01579	Interferon gamma	100	100	3.6	0.9	1.4	5.1	0.01	0.02	27162	6.1	98
IFNL2; IFNL3	Q8IZJ0; Q8IZI9	Interferon lambda-2; Interferon lambda-3	61	84	6.3	5.6	0.8	9.1	0.03	0.09	7745	4.9	111
IFNW1	P05000	Interferon omega-1	5	16	5.6	2.1	0.7	6.6	< 0.01	0.02	922	4.8	114
IKBKG	Q9Y6K9	Inhibitor of nuclear factor kappa B kinase subunit gamma	100	100	4.9	2.0	1.8	6.4	3.93	10.14	1490482	5.2	109
IL10RB	Q08334	Interleukin-10 receptor subunit beta	100	100	5.9	3.6	1.0	7.7	4.98	18.53	1983733	5.0	100
IL12B	P29460	Interleukin-12 subunit beta	100	100	4.9	1.6	0.3	5.9	0.39	0.66	161772	5.4	95
IL12p70	P29459  P29460	Interleukin-12 subunit beta Interleukin-12 subunit alpha	96	98	6.0	3.5	0.2	7.5	< 0.01	0.02	3046	5.1	93
IL12RB1	P42701	Interleukin-12 receptor subunit beta-1	96	100	5.1	1.6	1.2	6.4	5.38	7.12	322955	4.7	113
IL13RA2	Q14627	Interleukin 13 receptor subunit alpha 2	98	100	5.9	4.6	2.7	9.9	1.80	8.83	436350	4.7	126
IL15	P40933	Interleukin-15	100	100	4.2	2.6	2.5	6.2	< 0.01	< 0.01	1771	5.9	101
IL17A	Q16552	Interleukin-17A	96	100	5.8	2.5	2.9	7.8	0.01	0.01	5162	5.6	106
IL17A  IL17F	Q16552  Q96PD4	Interleukin-17A Interleukin-17F	81	77	7.6	4.5	1.2	9.6	0.01	0.09	11380	5.1	104
IL17B	Q9UHF5	Interleukin-17B	100	100	5.8	0.9	1.5	6.8	< 0.01	0.02	19968	6.0	108
IL17C	Q9P0M4	Interleukin-17C	100	100	6.9	2.6	5.0	10.4	0.02	0.07	20362	5.4	112
IL17F	Q96PD4	Interleukin-17F	79	74	7.1	9.5	0.0	14.1	17.26	55.05	77449	3.1	107
IL17RA	Q96F46	Interleukin-17 receptor A	100	100	5.5	3.1	0.8	7.3	0.06	0.12	47507	5.6	93
IL17RB	Q9NRM6	Interleukin-17 receptor B	98	100	4.2	1.8	0.2	5.4	0.10	0.24	91741	5.6	117
IL18BP	Q95998	Interleukin-18-binding protein	100	100	4.8	3.5	0.4	6.7	5.70	29.82	2524810	4.9	102
IL18R1	Q13478	Interleukin-18 receptor 1	100	100	5.1	2.0	1.9	6.5	0.23	0.58	98514	5.2	95
IL19	Q9UHD0	Interleukin-19	100	100	5.0	2.8	0.8	7.4	0.03	0.05	52257	6.0	107
IL1B	P01584	Interleukin-1 beta	46	29	9.9	3.9	7.4	15.1	0.01	0.04	3575	5.0	96
IL1R1	P14778	Interleukin-1 receptor type 1	100	100	4.8	2.3	1.4	6.3	7.43	53.85	1899090	4.5	104

Table 2: Performance Validation Data by Target (cont.)

Target	UniProt ID	Protein Name	Quantifiability (%)		AQ Precision (CV%)				LOD (pg/mL)	LLOQ (pg/mL)	ULOQ (pg/mL)	log10 Range	Dilution Linearity (%)
			Healthy n=57	Disease n=62	Intra	Inter	Lot	Total					
<b>AQ Targets</b>													
IL1R1	P14778	Interleukin-1 receptor type 1	100	100	4.8	2.3	1.4	6.3	4.270	30.956	1091798	4.5	104
IL1R2	P27930	Interleukin-1 receptor type 2	100	100	6.8	2.0	3.2	9.0	137.73	1179.23	3580906	3.5	100
IL1RL1	Q01638	Interleukin-1 receptor-like 1	100	100	8.7	5.1	5.7	13.4	n/a	654.72	1972632	3.5	103
IL20	Q9NYY1	Interleukin-20	100	100	4.9	2.1	2.0	6.7	0.01	0.03	19051	5.8	98
IL22	Q9GZX6	Interleukin-22	26	53	6.3	2.0	1.3	7.3	< 0.01	0.08	1489	4.3	104
IL27	Q8NEV9 Q14213	Interleukin 27 Interleukin-27 subunit beta	96	98	5.2	3.6	0.9	7.4	0.01	0.01	4919	5.8	108
IL2RB	P14784	Interleukin-2 receptor subunit beta	98	100	5.5	2.6	6.5	10.2	2.56	18.66	146319	3.9	97
IL33	O95760	Interleukin 33	95	100	7.2	2.8	0.2	8.3	0.01	0.07	3032	4.6	116
IL34	Q6ZMJ4	Interleukin-34	100	100	4.7	2.7	1.1	6.4	0.03	0.24	5766	4.4	77
IL3RA	P26951	Interleukin-3 receptor subunit alpha	98	100	5.7	2.2	2.5	7.7	6.00	59.06	428508	3.9	119
IL4	P05112	Interleukin-4	12	21	7.8	1.8	2.2	9.3	< 0.01	0.02	915	4.8	104
IL4R	P24394	Interleukin-4 receptor subunit alpha	98	100	7.3	4.4	0.9	9.4	28.45	536.86	1027452	3.3	105
IL5	P05113	Interleukin-5	100	100	4.2	2.5	0.7	5.7	< 0.01	< 0.01	1538	6.0	101
IL5RA	Q01344	Interleukin-5 receptor subunit alpha	98	100	7.3	2.1	0.4	8.3	13.14	229.55	1453409	3.8	103
IL6	P05231	Interleukin-6	98	100	6.2	6.2	2.0	9.6	0.03	0.07	15975	5.4	106
IL6R	P08887	Interleukin-6 receptor subunit alpha	100	100	8.3	4.7	1.8	10.9	n/a	1959.54	5832651	3.5	91
IL7	P13232	Interleukin-7	100	100	5.0	0.9	3.6	6.7	0.01	0.01	2106	5.4	94
IL7R	P16871	Interleukin-7 receptor subunit alpha	100	100	5.9	2.9	0.1	7.0	9.18	536.12	2220851	3.6	100
IL9	P15248	Interleukin-9	98	100	6.4	3.1	2.6	11.4	0.02	0.13	27863	5.3	95
IRAK4	Q9NWZ3	Interleukin-1 receptor-associated kinase 4	100	100	5.0	5.5	5.7	10.7	0.23	0.71	90469	5.1	100
KDR	P35968	Vascular endothelial growth factor receptor 2	98	98	7.0	1.0	1.1	7.8	33.77	508.83	3510551	3.8	101
KITLG	P21583	Kit ligand	98	100	6.3	7.0	20.3	22.7	1.57	1.77	3444	3.3	105
KLRK1	P26718	NKG2-D type II integral membrane protein	100	100	5.6	2.0	1.5	6.8	n/a	50.83	2451239	4.7	96
LAG3	P18627	Lymphocyte activation gene 3 protein	100	100	5.3	2.4	1.5	6.7	n/a	179.80	611992	3.5	107
LAMP3	Q9UQV4	Lysosomal associated membrane protein 3	98	100	6.5	2.4	4.7	9.3	3.26	3.26	39761	4.1	91
LGALS9	O00182	Galectin-9	100	100	4.6	2.1	0.7	5.8	2.25	10.04	547679	4.7	122
LIF	P15018	Leukemia inhibitory factor	96	100	5.5	2.3	1.2	6.9	0.01	0.06	2264	4.6	101
LILRB2	Q8N423	Leukocyte immunoglobulin-like receptor sub-family B member 2	98	100	6.5	2.4	0.0	7.5	237.45	4174.75	6329704	3.2	111
LTA	P01374	Lymphotoxin-alpha	67	87	8.8	0.8	17.2	20.0	0.18	0.76	11229	4.2	113
MERTK	Q12866	MER proto-oncogene, tyrosine kinase	100	100	6.3	4.7	0.1	8.1	601.24	1598.61	5927232	3.6	100
MICB	Q29980	MHC class I polypeptide-related sequence B	98	100	4.5	5.8	1.1	8.3	9.83	9.83	3442214	5.5	108
MMP12	P39900	Macrophage metalloelastase	98	100	7.0	2.5	0.6	8.3	5.05	11.60	467609	4.6	90
MMP3	P08254	Stromelysin-1	100	100	8.1	3.3	2.1	10.4	108.02	322.03	2386997	3.9	102
MMP8	P22894	Neutrophil collagenase	100	100	5.2	4.3	4.6	9.1	6.21	17.73	2683055	5.2	108
MMP9	P14780	Matrix metalloproteinase-9	100	100	5.8	3.0	11.4	15.0	75.31	468.57	1682732	3.6	76
NCR1	O76036	Natural cytotoxicity triggering receptor 1	98	100	5.7	1.6	7.2	11.2	4.17	6.41	20345	3.5	96
NGF	P01138	Beta-nerve growth factor	98	100	5.6	3.2	2.3	8.7	0.53	0.80	34919	4.6	90
OSM	P13725	Oncostatin-M	100	100	5.3	4.6	2.8	8.4	0.01	0.02	5508	5.5	99
PDCD1	Q15116	Programmed cell death protein 1	98	100	6.4	5.6	5.5	11.9	3.67	24.74	61520	3.4	92
PDC-D1LG2	Q9BQ51	Programmed cell death 1 ligand 2	100	100	6.0	2.2	2.0	7.6	13.60	93.61	640762	3.8	104
PDGFB	P01127	Platelet-derived growth factor subunit B	100	100	6.3	3.5	2.2	8.4	1.17	7.82	47031	3.8	124
PGF	P49763	Placenta growth factor	98	100	6.7	3.8	1.5	8.1	1.10	1.10	43142	4.6	94
PTX3	P26022	Pentraxin-related protein PTX3	98	100	6.4	4.2	7.7	12.7	3.36	44.00	250660	3.8	109

Table 2: Performance Validation Data by Target (cont.)

Target	UniProt ID	Protein Name	Quantifiability (%)		AQ Precision (CV%)				LOD (pg/mL)	LLOQ (pg/mL)	ULOQ (pg/mL)	log10 Range	Dilution Linearity (%)
			Plasma		Plasma								
			Healthy n=57	Disease n=62	Intra	Inter	Lot	Total					
<b>AQ Targets</b>													
S100A12	P80511	Protein S100-A12	95	92	7.0	9.1	8.7	17.6	40.27	341.51	243811	2.9	104
SELE	P16581	E-selectin	100	100	6.4	4.5	0.5	8.4	490.56	1431.09	2891740	3.3	113
SIRPA	P78324	Tyrosine-protein phosphatase non-receptor type substrate 1	98	100	6.1	2.6	1.6	7.6	685.40	1969.38	3445614	3.2	93
SLAMF1	Q13291	Signaling lymphocytic activation molecule	98	100	6.2	3.2	1.9	8.1	7.88	50.04	257346	3.7	93
TAFA5	Q7Z5A7	Chemokine-like protein TAFA-5	86	97	4.8	1.8	1.8	6.8	18.55	79.16	120425	3.2	101
TEK	Q02763	Angiopoietin-1 receptor	100	100	6.6	5.0	5.6	11.1	44.07	1380.94	2425819	3.2	116
THPO	P40225	Thrombopoietin	100	100	7.2	4.0	1.6	9.5	4.08	17.13	748745	4.6	95
TIMP2	P16035	Metalloproteinase inhibitor 2	4	5	8.7	1.0	23.0	25.1	57.76	719.19	403402	2.7	91
TLR3	O15455	Toll-like receptor 3	98	100	6.2	1.9	0.6	6.9	15.43	519.15	1424106	3.4	99
TNFRSF11A	Q9Y6Q6	TNF receptor superfamily member 11a	98	100	4.7	6.7	0.7	9.1	0.42	0.68	87348	5.1	104
TNFRSF13B	O14836	Tumor necrosis factor receptor superfamily member 13B	100	100	6.2	2.5	0.0	7.6	n/a	0.87	102992	5.1	108
TNFRSF13C	Q96RJ3	Tumor necrosis factor receptor superfamily member 13C	100	100	4.6	3.5	4.1	8.3	1.45	2.42	418219	5.2	103
TNFRSF14	Q92956	Tumor necrosis factor receptor superfamily member 14	100	100	6.9	3.9	0.0	8.7	10.66	161.78	328664	3.3	112
TNFRSF17	Q02223	Tumor necrosis factor receptor superfamily member 17	100	100	7.3	2.8	3.3	9.6	22.01	172.35	710323	3.6	91
TNFRSF18	Q9Y5U5	Tumor necrosis factor receptor superfamily member 18	98	100	4.9	2.6	2.3	6.8	0.12	0.49	32429	4.8	95
TNFRSF1A	P19438	Tumor necrosis factor receptor superfamily member 1A	98	100	7.3	1.6	2.4	8.9	195.96	397.07	1604445	3.6	93
TNFRSF1B	P20333	Tumor necrosis factor receptor superfamily member 1B	98	100	7.6	4.6	4.8	11.7	62.01	513.23	2392303	3.7	98
TNFRSF8	P28908	Tumor necrosis factor receptor superfamily member 8	100	100	6.2	1.3	0.8	8.5	6.45	41.37	340531	3.9	83
TNFSF10	P50591	Tumor necrosis factor ligand superfamily member 10	100	100	5.7	3.6	0.9	8.4	1.00	10.40	151847	4.2	116
TNFSF15	O95150	Tumor necrosis factor ligand superfamily member 15	100	100	6.1	5.1	1.9	8.7	< 0.01	0.19	28663	5.2	100
TNFSF18	Q9UNG2	Tumor necrosis factor ligand superfamily member 18	100	100	3.9	1.4	0.4	4.8	< 0.01	< 0.01	1821	6.0	109
TNFSF8	P32971	Tumor necrosis factor ligand superfamily member 8	100	100	5.1	4.9	1.1	7.8	n/a	35.63	518579	4.2	108
TREM1	Q9NP99	Triggering receptor expressed on myeloid cells 1	100	100	6.9	6.1	5.9	12.0	n/a	3.51	437232	5.1	116
TREM2	Q9NZC2	Triggering receptor expressed on myeloid cells 2	98	100	3.9	4.3	0.1	6.0	4.90	77.39	452161	3.8	104
TSLP	Q969D9	Thymic stromal lymphopoietin	81	100	4.9	3.9	0.2	6.7	0.61	1.99	4223	3.3	108
VEGFA	P15692	Vascular endothelial growth factor A	100	100	5.2	3.4	9.3	14.1	121.07	121.07	323760	3.4	99
VEGFC	P49767	Vascular endothelial growth factor C	100	100	4.8	2.4	0.8	6.2	0.46	0.82	90028	5.0	104
VEGFD	O43915	Vascular endothelial growth factor D	21	35	7.6	2.0	21.2	23.0	15.31	166.27	37024	2.3	99
VSNL1	P62760	Visinin-like protein 1	100	100	5.2	3.0	0.1	7.0	0.12	0.20	35667	5.2	111
VSTM1	Q6UX27	V-set and transmembrane domain containing 1	81	87	5.3	3.4	0.9	6.9	0.36	14.92	1178	1.9	99
WNT7A	O00755	Protein Wnt-7a	79	90	5.5	2.9	2.2	7.2	0.04	0.68	37470	4.7	120

## Ordering Information

### NULISAseq Assay Panels

Product Name	Plate Format	Sample Type	Catalog Number
NULISAseq Inflammation Panel AQ	96	plasma/serum	800154

### Consumables & Buffers

Product Name	Qty	Catalog Number
NULISA Wash Buffer (3L)	3L	801035

### Instrument

Product Name	Qty	Catalog Number
Alamar ARGO HT System	1	800101

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