

# NULISAs<sup>TM</sup>eq Immune 340 Panel

DATA SHEET

## 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 NULISAs<sup>TM</sup>eq 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  $\mu$ L 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.

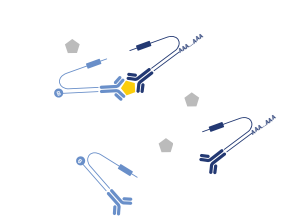


## NULISA<sup>TM</sup> Technology

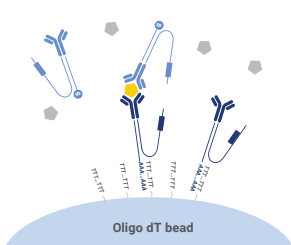
NULISA<sup>TM</sup>eq is a sandwich immunoassay in which two target specific antibodies, conjugated with unique oligonucleotide tags, bind and form a complex with the specific protein in solution. The resulting immunocomplex is purified in sequential capture and release steps to remove background and 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 ARGO<sup>TM</sup> HT System and data is analyzed using the NULISA Analysis Software. More details on the assay protocol can be found [here](#).

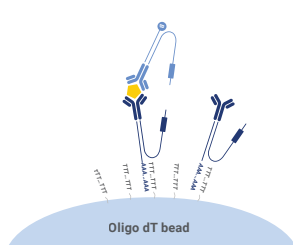
### 1. Immuno-complex formation



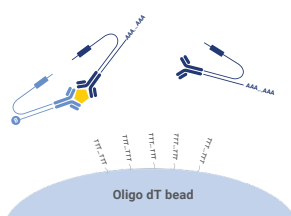
### 2. Capture 1



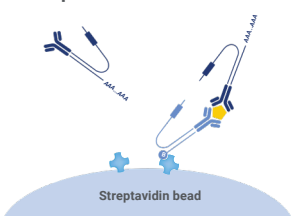
### 3. Wash 1



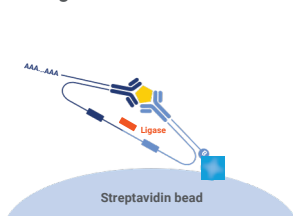
### 4. Release 1



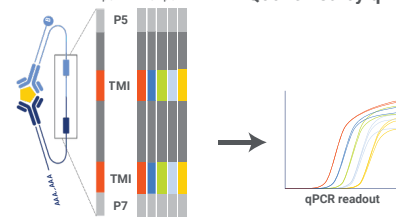
### 5. Capture 2 & Wash 2



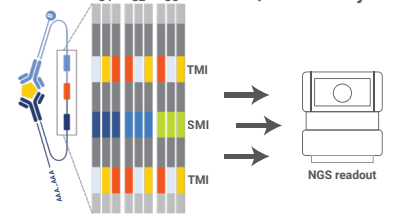
### 6. Ligation & Release 2



### 7a. Quantified by qPCR



### 7b. Quantified by NGS



## 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).

**Immune 340 Detectability: Healthy + Disease Serum Samples**

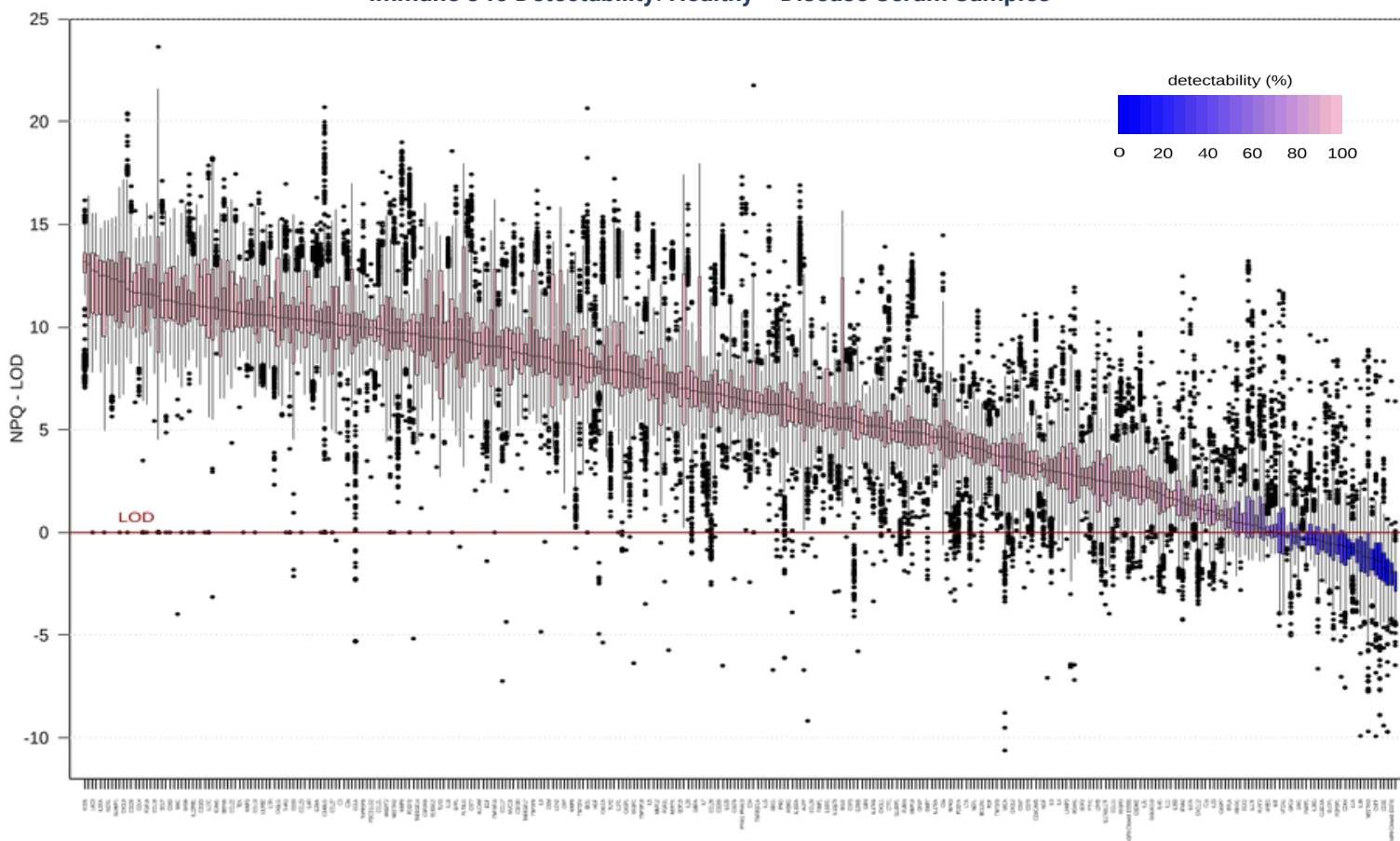


Figure 1. Detectability was assessed in a mix of healthy and diseased samples.

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 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 inter-plate controls (IPCs) 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.

## 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               |

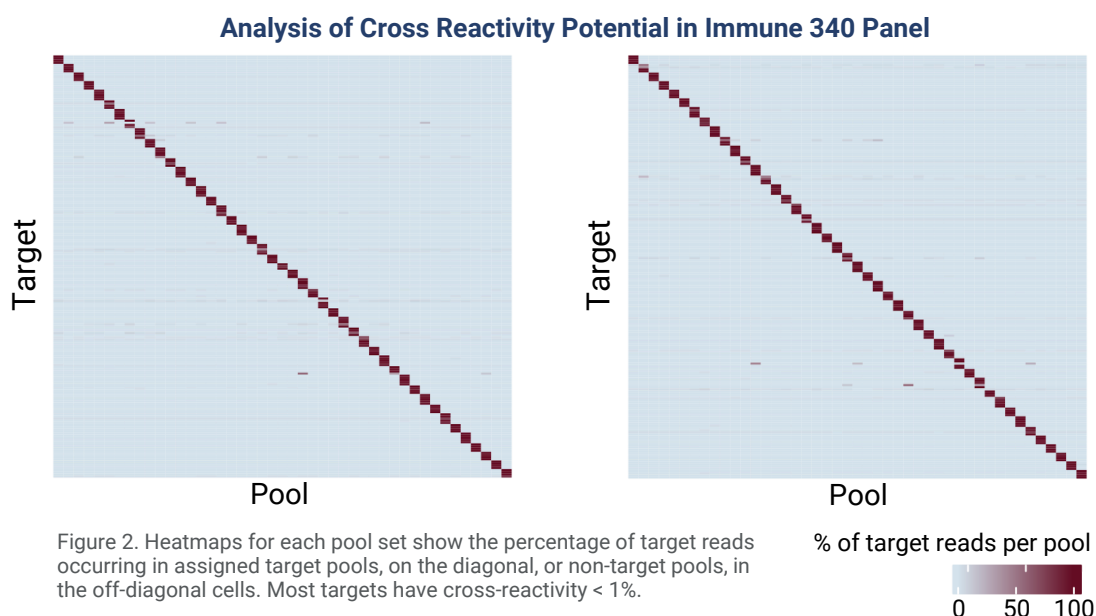
**Table 2: Percentage of Targets with CV Below 30%**

| 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).



# NULISAs<sup>seq</sup>™ Immune 340 Panel

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% <sup>a</sup>              |
| ANGPT1               | Q15389                       | Angiopoietin-1                                       | 92%               | 97%   | 10.1   | 8.2   | 11.1  | 12.1  | 11.0             | <1%                       | <1%                           |
| ANGPT2               | O15123                       | Angiopoietin-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/<br>P02746/<br>P02747 | C1Q complement                                       | N/A               | N/A   | 9.7    | 7.3   | 11.8  | 6.4   | N/A <sup>k</sup> | <1%                       | <1%                           |
| C3                   | P01024                       | Complement C3                                        | N/A               | N/A   | 6.3    | 7.5   | 5.5   | 8.2   | N/A <sup>k</sup> | <1%                       | <1%                           |
| C3A                  | P01024                       | Complement C3                                        | N/A               | N/A   | 5.7    | 3.8   | 5.7   | 4.2   | N/A <sup>k</sup> | <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% <sup>b</sup>              |
| CCL4                 | P13236                       | C-C motif chemokine 4                                | 100%              | 100%  | 9.2    | 6.0   | 9.2   | 8.3   | 5.5              | <1%                       | 315% <sup>c</sup>             |
| 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% <sup>d</sup>          | <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 <sup>k</sup> | <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% <sup>e</sup>                       |
| 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/<br>A0A087W-<br>WS6 | Interferon alpha-1/13                                   | 100%              | 100%  | 11.3   | 8.2   | 12.0  | 9.0   | 6.6       | <1%                       | 7.2%, 5.6%,<br>1.6%, 3.1% <sup>f</sup> |
| 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/<br>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%                                    |

# 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 |           |                           |                               |
| 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%                           |



# NULISAs<sup>seq</sup>™ 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/<br>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/<br>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 <sup>a</sup> | <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-<br>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% <sup>g</sup>               |
| 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<br>subfamily B member 1 | 100%              | 100%  | 8.0    | 10.0  | 6.3   | 10.7  | 0.4              | <1%                       | <1%                           |
| LILRB2 | Q8N423                                                                   | Leukocyte immunoglobulin-like receptor<br>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/<br>P13671/<br>P10643/<br>P07357/<br>P07358/<br>P07360/<br>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 <sup>a</sup> | <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% <sup>h</sup>             |
| SIRPA    | P78324     | Tyrosine-protein phosphatase non-receptor type substrate 1 | 100%              | 100%  | 5.8    | 8.6   | 4.8   | 9.1   | 6.0              | <1%                       | 7% <sup>i</sup>               |
| 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%                           |
| 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%                           |

<sup>a</sup>Cross-reactivity with ALPG, which has 98% homology with ALPP, ALPG is not in the Immune 340 Panel

<sup>b</sup>Cross-reactivity with CCL3L1, which has 95% homology with CCL3; CCL3L1 is not in the Immune 340 Panel

<sup>c</sup>Cross-reactivity with CCL4L1, which has 95% homology with CCL4; CCL4L1 is not in the Immune 340 Panel

<sup>d</sup>Cross-reactivity with NECTIN3, NECTIN3 is in the Immune 340 Panel

<sup>e</sup>Cross-reactivity with GZMH, which has 71% homology with GZMB; GZMH is not in the Immune 340 Panel

<sup>f</sup>Cross-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

<sup>g</sup>Cross-reactivity with LDHAL6B, which has 71% homology with LDHA, LDHAL6B is not in the Immune 340 Panel

<sup>h</sup>Cross-reactivity with SIGLEC11, which has 82% homology with SIGLEC10, SIGLEC11 is not in the Immune 340 Panel

<sup>i</sup>Cross-reactivity with SIRPB1, which has ~90% homology (extracellular domain) with SIRPA; SIRPB1 is not in the Immune 340 Panel

<sup>j</sup>Cross-reactivity with HPCAL4, which has 89% homology with VSNL1; HPCAL4 is not in the Immune 340 Panel

<sup>k</sup>Leverages a special algorithm for plasma and serum due to the high abundance of these analytes in these matrices. Not reported for other sample types.



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