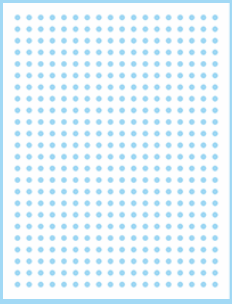
Analysis Report



Olink® Explore

PROJECT NAME	Q-01546_Neogi
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1. Project information

No. of samples	No. of plates	Normalization method
176	5	Intensity normalization

1.1 Sample type

EDTA Plasma

1.2 Project specific comments

Please note that data for FOLR3, PNLIPRP2 and TDGF1 have been PC normalized because these assays show a natural bimodal distribution. For more info see https://www.olink.com/faq-category/data/

The following Explore 384 Inflammation II assay did not meet Olink's batch release quality control criteria and is therefore not included in this project: KNG1. The following Explore 384 Oncology assays did not meet Olink's batch release quality control criteria and are therefore not included in this project: SMAD1 and ARHGAP25.

2. Quality control

Three internal controls are added to each sample, the Incubation control, the Extension Control and the Amplification control. The Extension Control is used for the generation of the NPX values. The Incubation Control and the Amplification Control are used to monitor the quality of assay performance, as well as the quality of individual samples.

Three external controls are included in each run, the Plate Control (healthy pooled plasma), Sample Control (healthy pooled plasma) and Negative Control. The Plate Control is used for data normalization, the Sample Control is used to assess potential variation between runs and plates, and the Negative Control is used to calculate Limit of Detection for each assay and to assess potential contamination of assays.

The following parameters are evaluated in the Quality Control (QC):

1. The average matched counts [1] for each sample. To pass QC, there should be at least 500 counts, otherwise the sample receives a QC warning status.

2. The deviation from the median value of the Incubation- and Amplification Controls for each individual sample. To pass QC, the deviation should not exceed +/-0.3 NPX for either of the internal controls, otherwise the sample will receive a QC warning status.

3. The deviation of the median value of the Negative Controls from a predefined value set for each assay. To pass QC, the deviation of the median of the Negative Controls must be ≤5 standard deviations from the set predefined value, otherwise the assay will receive a warning status.

[1] The number of reads for each specific combination of sample and assay

All samples included in the project are presented in the data output file. Samples that do not pass the QC are indicated with WARN in the column named QC_warning. Data points from samples that do not pass QC should be treated with caution. Manual QC warnings are indicated with MANUAL_WARN in the column named QC_warning. Section 2.1 reports the fraction of samples that pass QC for all assays per panel and the fraction of data points passing QC per panel. Samples with manual QC warning are counted as not passed QC. Assays that do not pass the QC are indicated with WARN in the column named Assay_warning. Data points from assays that do not pass QC should be treated with caution.

2.1 QC summary

Olink Panel	Samples passed QC	Samples passed QC (%)	Datapoints passed QC	Datapoints passed QC (%)
Explore 384 Cardiometabolic	171 / 176	97	64546 / 64944	99
Explore 384 Cardiometabolic II	164 / 176	93	63062 / 64592	98
Explore 384 Inflammation	166 / 176	94	63922 / 64768	99
Explore 384 Inflammation II	161 / 176	91	62879 / 64944	97
Explore 384 Neurology	153 / 176	87	62052 / 64592	96
Explore 384 Neurology II	152 / 176	86	61921 / 64592	96
Explore 384 Oncology	168 / 176	95	63376 / 64416	98
Explore 384 Oncology II	166 / 176	94	63663 / 64768	98

2.2 Intra- and Inter-assay Coefficient of Variance (%CV)

Intra- and inter-CVs are based on the Sample Controls (pooled plasma samples) included on each sample plate. Calculations are made for each assay using NPX-values. Average % CV for all assays on a panel is presented in section 2.2.1. The number of assays with CVs within defined intervals are presented in sections 2.2.2 and 2.2.3.

2.2.1 Average %CV

Olink Panel	Intra-assay %CV	Inter-assay %CV
Explore 384 Cardiometabolic	5	8
Explore 384 Cardiometabolic II	8	11
Explore 384 Inflammation	8	11
Explore 384 Inflammation II	7	10
Explore 384 Neurology	8	11
Explore 384 Neurology II	10	13
Explore 384 Oncology	7	10
Explore 384 Oncology II	10	14

2.2.2 Intra-assay %CV distribution

Olink Panel	<5%	≥5-<10%	≥10-<15%	≥15%	N/A*
Explore 384 Cardiometabolic	218	85	23	19	24
Explore 384 Cardiometabolic II	72	119	44	33	99
Explore 384 Inflammation	121	134	44	31	38
Explore 384 Inflammation II	136	84	32	28	89
Explore 384 Neurology	162	96	35	44	30
Explore 384 Neurology II	53	79	39	44	152
Explore 384 Oncology	159	92	41	29	45
Explore 384 Oncology II	52	63	39	38	176

*Assays where CV is not possible to calculate

2.2.3 Inter-assay %CV distribution

Olink Panel	<10%	≥10-<20%	≥20-<30%	≥30%	N/A*
Explore 384 Cardiometabolic	269	55	17	8	20
Explore 384 Cardiometabolic II	142	112	22	4	87
Explore 384 Inflammation	208	94	19	13	34

Explore 384 Inflammation II	196	66	17	9	81
Explore 384 Neurology	227	63	28	20	29
Explore 384 Neurology II	104	86	32	11	134
Explore 384 Oncology	215	80	24	8	39
Explore 384 Oncology II	83	78	29	15	163

*Assays where CV is not possible to calculate

3. Protein detection results

3.1 Number of proteins detected in >50% of the samples

Olink Panel	No. of detected proteins / Total no. of proteins	Detected proteins (%)	Expected detectability in EDTA plasma* (%)
Explore 384 Cardiometabolic	354 / 369	96	N/A
Explore 384 Cardiometabolic II	270 / 367	74	N/A
Explore 384 Inflammation	338 / 368	92	N/A
Explore 384 Inflammation II	297 / 369	80	N/A
Explore 384 Neurology	340 / 367	93	N/A
Explore 384 Neurology II	210 / 367	57	N/A
Explore 384 Oncology	343 / 366	94	N/A
Explore 384 Oncology II	203 / 368	55	N/A

*The expected detectability is based on EDTA plasma from healthy donors. These values are intended as guidelines only and protein levels are expected to vary depending on different pathological conditions, sample matrices, or sample preparation methods.

3.2 Data output

Data is presented as NPX (Normalized Protein eXpression) values. NPX is Olink's relative protein quantification unit on log2 scale. NPX values are calculated from the number of matched counts, using NGS (Next Generation Sequencing) as readout. The NPX values are presented in a separate results file delivered in the MyData cloud. Data values for measurements below limit of detection (LOD) are reported for all samples.