

The working directory

/rds/project/jmmh2/rds-jmmh2-projects/olink_proteomics/scallop/NGS

Protein information

Results at work/ are according to the combination of,

- NGS panels – CARDIOMETABOLIC, INFLAMMATION, NEUROLOGY.
- qPCR panels – cvd2, cvd3, inf, neu.
- QC types:
 - raw – raw measurements
 - QC – NGS QC=PASS
 - LOD – set to be NA when < LOD
 - col1 – set to NA when 01

for a total of 16 NGS-Olink-QC combinations, with suffexes .dat for correlation and .pdf for scatter plots.

qPCR panel	Four combinations
cvd2	CARDIOMETABOLIC-cvd2 + [-col1, -LOD, -QC, -raw]
cvd3	CARDIOMETABOLIC-cvd3 + [-col1, -LOD, -QC, -raw]
inf	INFLAMMATION-inf + [-col1, -LOD, -QC, -raw]
neu	NEUROLOGY-neu + [-col1, -LOD, -QC, -raw]

The Olink NGS QC=PASS appears to have the highest correlation.

The corresponding density plots are shown in correlogram.pdf.

Genotype-protein association

plink2/ contains genotype-protein association results for $MAF \geq 0.05$, $INFO \geq 0.8$.

NGS.merge is contained for each of the following p value thresholds,

Directory	Description	Sentinels	Proteins
1e-5/	sentinel identification at $p=1e-5$	23,034	1,472
1e-6/	sentinel identification at $p=1e-6$	2,836	1,241
1e-7/	sentinel identification at $p=1e-7$	598	479

Note that the following three proteins appear on all four panels and should be treated specifically,

P01375 TNF P05231 IL6 P10145 CXCL8
see the Venn diagram.