## 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>=0.05, INFO>=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 |