



# Concordance Test Report

PROJECT NAME

Psomagen Concordance Test

STATISTICAL SERVICE

Generated by Olink® Concordance Test app (v. 2.0)

REPRESENTATIVE

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## Overview

An Olink® Concordance Test was performed to assess the performance between labs. The Olink® Concordance Test (batch B32104) comprised 31 samples, ran on Target 96 (Olink Inflammation) at both Psomagen and Analysis Service (AS) Boston. To assess the performance between the sites, Olink® Concordance Test compared detectability, CV, correlation and regression. After evaluation of the results, Psomagen **passed the Concordance Test**.

## QC Warning

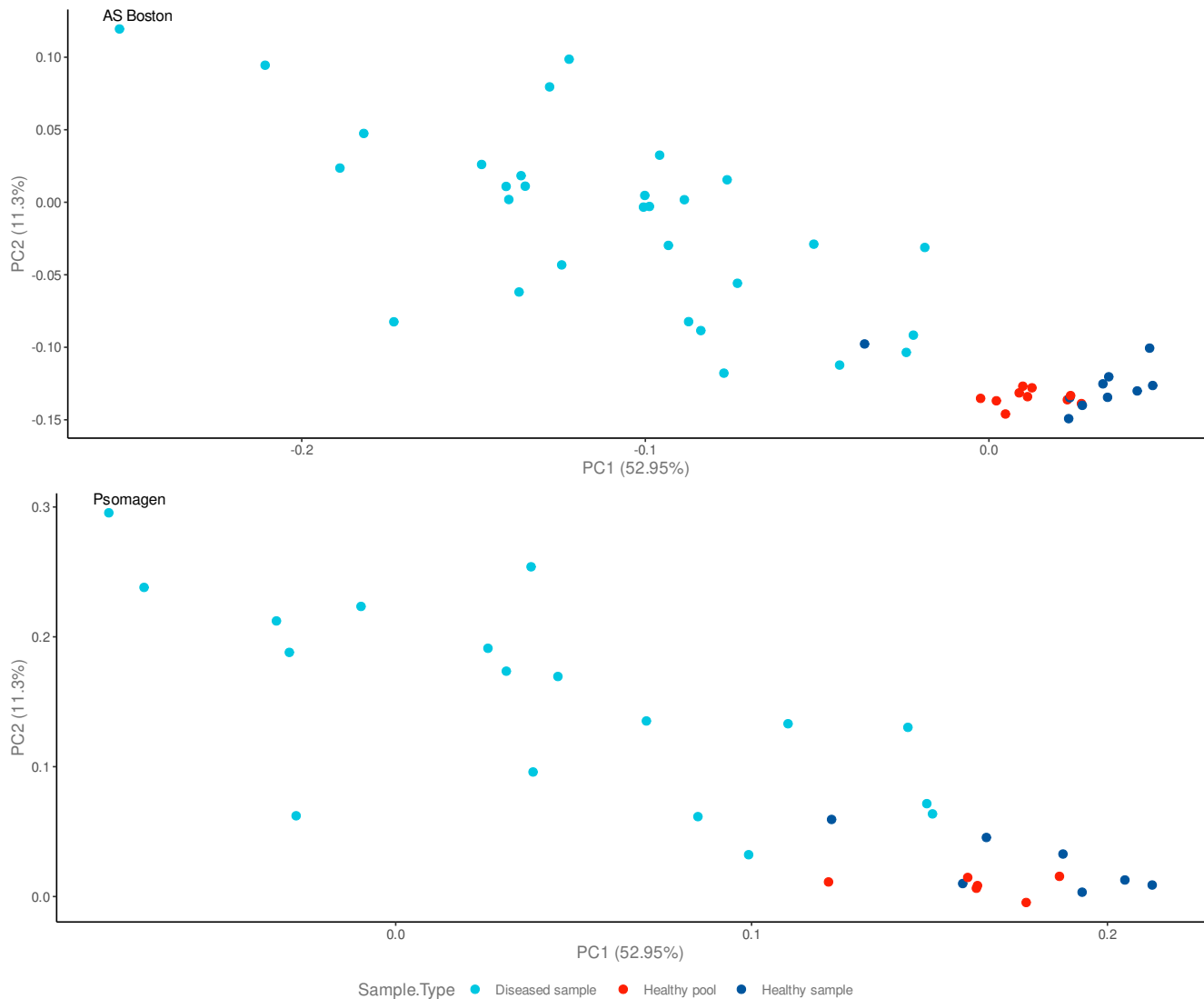
The number and percentage of samples with QC warning status was calculated and summarized in Table 1.

**Table 1:** The number and (percentage) of samples with a QC warning per site.

Site	Warnings
AS Boston	4 (8)
Psomagen	2 (6.5)

# PCA

Scatter plots along the first two principal components were generated to compare global data performance (Figure 1). Figure 1 displays PCA plots of AS Boston and Psomagen data separately.



**Figure 1:** Separated PCA plots of data from AS Boston and Psomagen, colored by sample type. Each point represents one sample. The position of the point is based on all measured protein values. The percentages displayed show the percentage of explained variance per principal component.

## Detectability

Detectability of each assay was calculated as the percentage of samples with results above the estimated limit of detection (LOD) (see Table 2).

```
## debug at <text>#2: params$detect_tbl %>% kbl(booktabs = T, caption = paste0("Average de
##   label = "detect_table", format = "pandoc") %>% kable_styling(bootstrap_options = c(
##   "hover", "condensed"), full_width = F, latex_options = "hold_position")
```

**Table 2:** Average detectability by site (%).

Panel	AS Boston	Psomagen
Olink Inflammation	89.5	87.9

## Coefficient of Variation

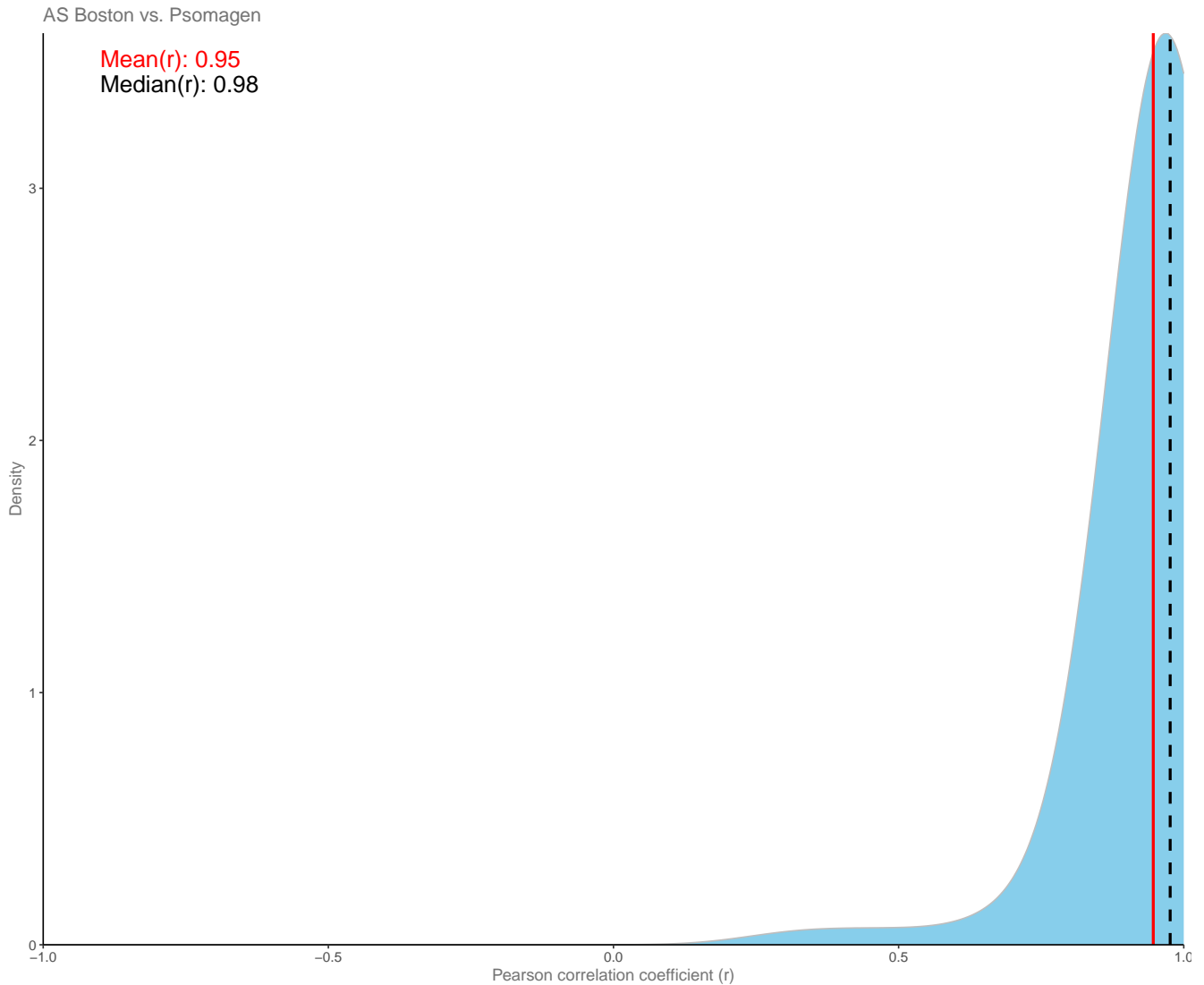
The coefficient of variance (CV) was calculated on a per assay basis, using the control samples that were included in each run (see Table 3). Intra CV less than 15.0% is preferred.

**Table 3:** Average intra CV by site (%).

Panel	AS Boston	Psomagen
Olink Inflammation	6.9	13

## Correlation

Correlation of NPX values between AS Boston and Psomagen were calculated on a per assay basis (healthy pools excluded, see Figure 2).

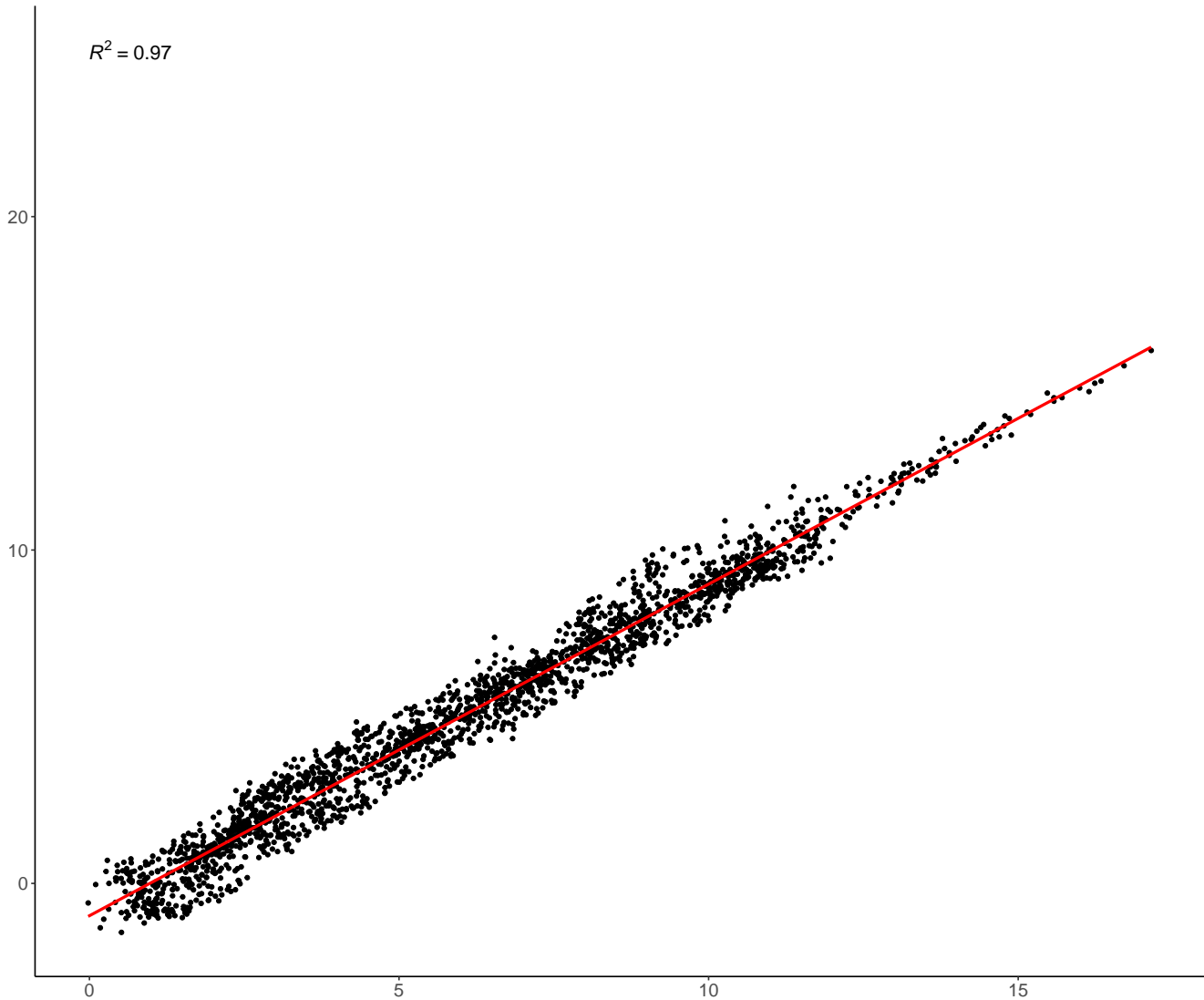


**Figure 2:** Density plot of Pearson correlation coefficients between two sites. The solid red line represents the mean of the correlation coefficients, serving as a central reference point, while the dashed black line indicates the median, providing insight into the distribution's central position. This figure provides a powerful tool for understanding complex interdependencies within the dataset, facilitating the identification of underlying patterns and trends in variable relationships.



## Regression

Figure 3 shows the NPX values from AS Boston on the x-axis and from Psomagen on the y-axis. The regression line is fitted using a linear model.



**Figure 3:** Scatter plot of data from both sites with a regression line fitted to present the linear relationship between two sites. In addition to the best-fit line, the figure includes the R-squared ( $R^2$ ) value, which quantifies the goodness of fit of the regression model.

## Summary

Detectability, CV, correlation and regression analysis were performed to compare the concordance of data generated with the same set of samples at AS Boston and Psomagen.

Psomagen had 6.5 % QC warnings (maximum 16 % allowed). Hence, **passing** the QC warning criteria.

Psomagen scored 87.9 % detectability (minimum 85.0 % allowed). Hence, **passing** the detectability criteria.

Psomagen scored 13.0 % intra CV (maximum 15.0 % allowed). Hence, **passing** the CV criteria.

Both mean (0.95) and median (0.98) correlation coefficient (r) of Psomagen vs. AS Boston scored more than the minimum allowed value (0.90). Hence, **passing** the correlation criteria.

Psomagen scored a coefficient of determination ( $R^2$ ) of 0.97 (minimum 0.90 allowed). Hence, **passing** the regression criteria.

In total, Psomagen failed 0 QC criterias (maximum 1 fail allowed). Hence, **passing the Concordance Test**.

# Appendix

## R Session Information

- R version 4.3.1 (2023-06-16), x86\_64-pc-linux-gnu
- Locale: LC\_CTYPE=en\_US.UTF-8, LC\_NUMERIC=C, LC\_TIME=en\_US.UTF-8, LC\_COLLATE=en\_US.UTF-8, LC\_MONETARY=en\_US.UTF-8, LC\_MESSAGES=en\_US.UTF-8, LC\_PAPER=en\_US.UTF-8, LC\_NAME=C, LC\_ADDRESS=C, LC\_TELEPHONE=C, LC\_MEASUREMENT=en\_US.UTF-8, LC\_IDENTIFICATION=C
- Time zone: America/New\_York
- TZcode source: system (glibc)
- Running under: Ubuntu 20.04.6 LTS
- Matrix products: default
- BLAS: /usr/lib/x86\_64-linux-gnu/blas/libblas.so.3.9.0
- LAPACK: /usr/lib/x86\_64-linux-gnu/lapack/liblapack.so.3.9.0
- Base packages: base, datasets, graphics, grDevices, methods, stats, utils
- Other packages: cicerone 1.0.4, Concordance 0.0.0.9000, dplyr 1.1.3, DT 0.30, extrafont 0.19, forcats 1.0.0, ggplot2 3.4.4, ggpubr 0.6.0, gtsummary 1.7.2, kableExtra 1.3.4, knitr 1.44, lubridate 1.9.3, OlinkAnalyze 3.6.0, plotly 4.10.3, purrr 1.0.2, readr 2.1.4, readxl 1.4.3, shiny 1.7.5.1, shinycssloaders 1.0.0, stringr 1.5.0, tibble 3.2.1, tidyr 1.3.0, tidyverse 2.0.0
- Loaded via a namespace (and not attached): abind 1.4-5, arrow 13.0.0.1, assertthat 0.2.1, attempt 0.3.1, backports 1.4.1, bit 4.0.5, bit64 4.0.5, boot 1.3-28.1, broom 1.0.5, broom.helpers 1.14.0, bslib 0.5.1, cachem 1.0.8, callr 3.7.3, car 3.1-2, carData 3.0-5, cellranger 1.1.0, cli 3.6.1, colorspace 2.1-0, compiler 4.3.1, config 0.3.2, cowplot 1.1.1, crayon 1.5.2, crosstalk 1.2.0, data.table 1.14.8, desc 1.4.2, digest 0.6.33, ellipsis 0.3.2, emmeans 1.8.9, estimability 1.4.1, evaluate 0.22, extrafontdb 1.0, fansi 1.0.5, farver 2.1.1, fastmap 1.1.1, fontawesome 0.5.2, fs 1.6.3, generics 0.1.3, ggrepel 0.9.4, ggsignif 0.6.4, glue 1.6.2, golem 0.4.1, grid 4.3.1, gridExtra 2.3, gt 0.10.0, gtable 0.3.4, hms 1.1.3, htmltools 0.5.6.1, htmlwidgets 1.6.2, httpuv 1.6.12, httr 1.4.7, jquerylib 0.1.4, jsonlite 1.8.7, labeling 0.4.3, later 1.3.1, lattice 0.22-5, lazyeval 0.2.2, lifecycle 1.0.3, lme4 1.1-34, lmerTest 3.1-3, magrittr 2.0.3, MASS 7.3-60, Matrix 1.6-1.1, memoise 2.0.1, mgcv 1.9-0, mime 0.12, minqa 1.2.6, munsell 0.5.0, mvtnorm 1.2-3, nlme 3.1-163, nloptr 2.0.3, numDeriv 2016.8-1.1, pillar 1.9.0, pkgbuild 1.4.2, pkgconfig 2.0.3, pkgload 1.3.3, plyr 1.8.9, polynom 1.4-1, prettyunits 1.2.0, processx 3.8.2, promises 1.2.1, ps 1.7.5, R6 2.5.1, Rcpp 1.0.11, rlang 1.1.1, rmarkdown 2.25, rprojroot 2.0.3, rstatix 0.7.2, rstudioapi 0.15.0, Rttf2pt1 1.3.12, rvest 1.0.3, sass 0.4.7, scales 1.2.1, shinyalert 3.0.0, shinyjs 2.1.0, shinythemes 1.2.0, shinyWidgets 0.8.0, splines 4.3.1, stringi 1.7.12, svglite 2.1.2, systemfonts 1.0.5, tidyselect 1.2.0, timechange 0.2.0, tinytex 0.48, tools 4.3.1, tzdb 0.4.0, utf8 1.2.4, uuid 1.1-1, vctrs 0.6.4, viridisLite 0.4.2, webshot 0.5.5, withr 2.5.1, xfun 0.40, xml2 1.3.5, xtable 1.8-4, yaml 2.3.7, zip 2.3.0