SOMAscan™ Quality Statement
Client Name

SomaLogic, Inc.
2945 Wilderness Drive
Boulder, CO 80301

Sponsor:
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Description: Quality summary of results from the analysis of Matrix Name samples with the SOMAscan proteomic discovery platform performed by SomaLogic, Inc.

1 Overview

A total of XX Matrix Name samples were assayed in the Version 3.0 SOMAscan™ assay in Sets, along with X Matrix Name calibrator samples, X quality control samples, and X. Run qualification standards were derived from metrics on the SOMAscan™ discovery platform of 1200^{+} SOMAmers™. Results, quantified in relative florescence units (RFU), are reported for XX Matrix Name samples and XX SOMAmers.

2 Assay Background

Sample data is first normalized to remove hybridization artifacts within a run followed by median normalization to remove other assay biases within the run and finally calibrated to remove assay differences between runs.

Hybridization control and median normalization scale factors are expected to be in the range of $0.4-2.5$ (± 1.32 on $\log_2$ scale). The median of the calibration scale factors is expected to be in the range $0.8-1.2$ and a minimum of 95% of individual SOMAmer™ reagents in the total array must be within $\pm$ 0.4 of the median (i.e. less than 5% in the tails of the distribution). Gaussian distributions of scale factors are expected.

2.1 Hybridization Control Normalized Data

Each set of measurements was normalized to remove intra-run hybridization variation using the hybridization reference standard. The distribution of these scale factors are displayed below in Figure **??** and summarized in Table **??**.

Figure 1: Boxplot of the hybridization scale factors grouped by run. The acceptance criteria for scale factors are indicated with dashed lines.

Table 1: Summary of $\log_2$ hybridization scale factor distribution.

All samples in the run had hybridization scale factors within the acceptable range.

2.2 Median Normalized Data

Hybridization normalized data were subsequently median normalized by SOMAmer™ dilution mix. Median normalization is performed separately for clinical samples and assay calibrators within each run. Clinical samples were median normalized how was the data normalized, by group, across groups, etc. After data delivery the samples will be unblinded and the topic of normalization grouping may be revisited. The distributions of median normalization scale factors are displayed below in Figure **??** and summarized in Table **??**.

Figure 2: Boxplot of the median normalization scale factors by set and dilution. The acceptance criteria for scale factors are indicated with dashed lines.

Table 2: Summary of $\log_2$ median normalization scale factor distributions.

All samples in the run had median normalization scale factors within the acceptable range.

2.3 Calibrated Data

For each SOMAmer, the ratio of the calibration reference standard to the median calibrator signal in the run was calculated and resulting scale factor was applied to reduce inter-run variation. The distribution of the calibration scale factors are displayed below in Figure **??** and summarized in Table **??**.

Figure 3: Distribution of the calibration scale factors grouped by run. The median of each calibration scale factor distribution must be between 0.8 and 1.2 (left panel). Additionally, 95% of the scale factors for each distribution must be within 0.6 and 1.4 of the median for that run (right panel).

Table 3: Summary of the calibration scale factor distribution.

Plate failures are not handled by the auto-sqs, you'll need to add your own text here. Choose from: All runs passed the run acceptance criteria based on location and tail weight of the calibration scale factor distribution. All runs also passed the criterion that 95% of the scale factors must be within 0.6 and 1.4

All samples in the run had calibration scale factors within the acceptable range.

2.4 Sample Appearance

Sample appearance was consistent with typical Matrix Name samples and no hemolyzed or lipemic samples were noted.