SOMAscan™ Quality Statement

SomaLogic, Inc.
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Client: Emory
Study: EMO-16-197
Date: October 25, 2016

Overview: Quality summary of results from the analysis of clinical samples with the SOMAscan proteomic discovery platform performed by SomaLogic, Inc.

1 Standardization

Sample data is first normalized to remove hybridization variation within a run followed by median normalization across all samples to remove other assay biases within the run and finally calibrated to remove assay differences between runs. Acceptance criteria are shown below. Non-standard matrices are often not subject to all normalization procedures.

Sample	Acceptance Criteria	RowCheck	Count
Normalization	0.4-2.5	PASS	29
		FLAG	1
		TOTAL	30

2 Sample Appearance

The assay execution team made the following notes regarding sample appearance at the time of processing. Samples from your study corresponding to notes seen below can be found using the "SampleNotes" column in the .adat data file.

Sample Notes	Count
short transfer volume corrected by hand for 30% sample plate	1

3 Delivered Adats

The following adat data files were delivered:

EMO_16-194.hybNorm.20161025.adat
EMO_16-194.hybNorm.medNorm.20161025.adat

Bioinformatics Notes:
Two adats are delivered due to median normalization potentially introducing a subtle artificial bias into the data. For example, when comparing the median normalization scale factors by time points (see below plot), there is the possibility that median normalization is removing something significant other than nuisance differences in overall protein concentration (what it is meant for).