SOMAScan Quality Statement

Client: WUS
Date: March 23, 2018

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	48
		FLAG	0
		TOTAL	48

Plate Scale Factor	Acceptance Criteria	PltCheck	Value
Set 001	0.4-2.5	FLAG	0.372
Set 002	0.4-2.5	FLAG	0.361

SOMAmer	Acceptance Criteria	ColCheck	Count
Calibration	median +/- 0.4	PASS	1182
		FLAG	123
		TOTAL	1305

Plate Median SF	Acceptance Criteria	PltCheck	Value
Set 001	0.8-1.2	PASS	0.997
Set 002	0.8-1.2	PASS	1.0

Plate tail test	Acceptance Criteria	PltCheck	Percent
Set 001	less than 10%	PASS	8.05
Set 002	less than 10%	PASS	8.66

2. Sample Appearance

All samples were consistent with typical appearance for this matrix.

3. Calibrator CVs

Quantiles for the distribution of calibrator CVs on each plate is shown below. At least 50% of SOMAmer reagents should have CVs less than 0.1 and 95% should have CVs below 0.2.

Plate	Samples	5%	50%	95%
Set 001	5	0.009	0.026	0.094
Set 002	5	0.011	0.038	0.199

4. QC CVs

SampleId	Samples	5%	50%	95%
170255	4	0.008	0.023	0.085

5. Generated ADats

WUS-18-007.hybNorm.plateScale.medNorm.calibrate.20180323.adat
WUS-18-007.hybNorm.plateScale.medNorm.20180323.adat
WUS-18-007.hybNorm.plateScale.20180323.adat
WUS-18-007.hybNorm.20180323.adat
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