

## SOMAScan Quality Statement

Client: UFL

Date: April 11, 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	69
		FLAG	3
		TOTAL	72

Plate Scale Factor	Acceptance Criteria	PltCheck	Value
Set 001	0.4-2.5	PASS	0.558
Set 002	0.4-2.5	PASS	0.862
Set 003	0.4-2.5	PASS	0.679

SOMAmer	Acceptance Criteria	ColCheck	Count
Calibration	median +/- 0.4	PASS	663
		FLAG	642
		TOTAL	1305

Plate Median SF	Acceptance Criteria	PltCheck	Value
Set 001	0.8-1.2	PASS	0.999
Set 002	0.8-1.2	PASS	1.008
Set 003	0.8-1.2	PASS	0.999

Plate tail test	Acceptance Criteria	PltCheck	Percent
Set 001	less than 10%	PASS	4.37
Set 002	less than 10%	FLAG	47.97
Set 003	less than 10%	PASS	3.6

### 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	0.013	0.032	0.082
Set 002	5	0.011	0.035	0.141
Set 003	5	0.013	0.031	0.074

### 4. QC CVs

SampleId	Samples	5%	50%	95%
160384	9	0.071	0.105	0.254

### 5. Generated ADats

UFL-17-005.hybNorm.plateScale.medNorm.calibrate.20180411.adat  
UFL-17-005.hybNorm.plateScale.medNorm.20180411.adat  
UFL-17-005.hybNorm.plateScale.20180411.adat  
UFL-17-005.hybNorm.20180411.adat  
UFL-17-005.20180411.adat