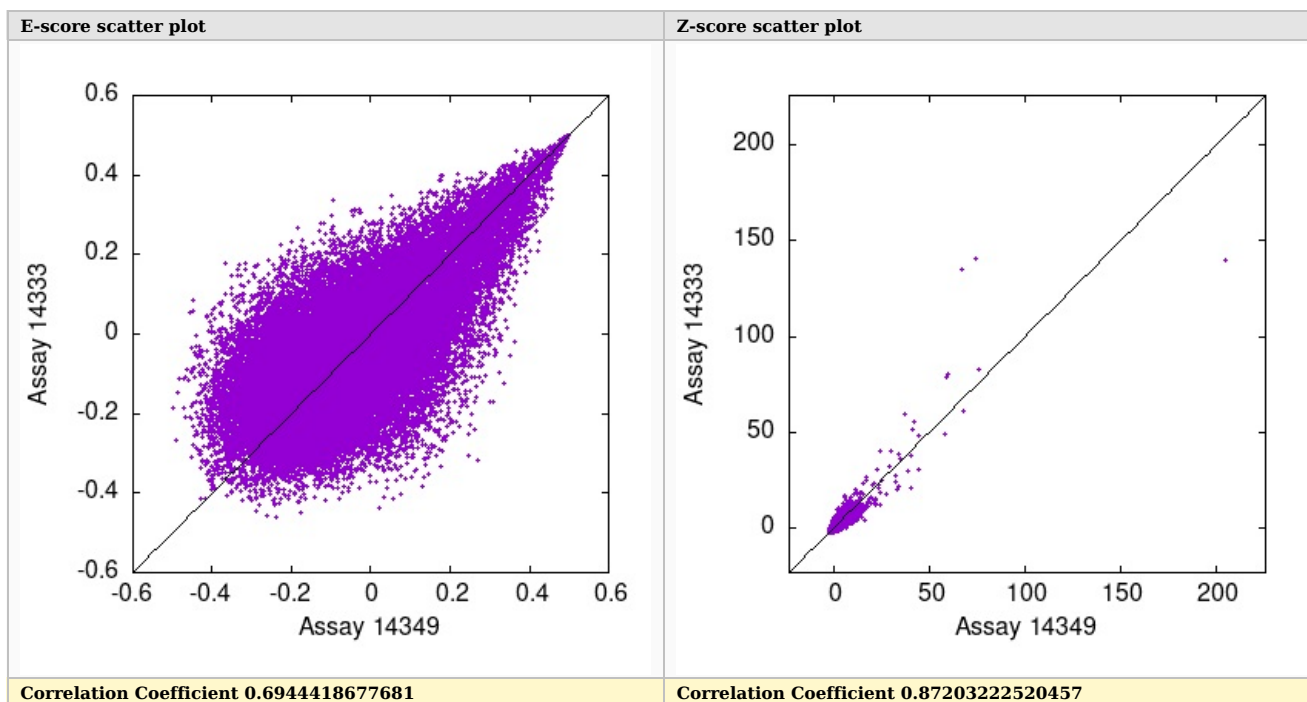


## QC report



Correlation Coefficient 0.6944418677681

Correlation Coefficient 0.87203222520457

### Top scoring motifs for Assay 14349

Protein ID: pTH15532.2 Gene: LEF1 Domain: HMG\_box Flag: Pass matched\_pair Array: 1M-HK

#### 8 mer E-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

CTTTGATC	0.49909	-CTTTGATC-
ACATCAAA	0.49597	--TTTGATGT
AGATCAAA	0.49558	--TTTGATCT
CATCAAA	0.49533	-CTTTGATG-
ATCAAAGA	0.49512	TCTTTGAT--
ATCAAAGG	0.49416	CCTTTGAT--
CTTCAAA	0.49390	-CTTTGAAG-
ATCAAAGC	0.49346	GCTTTGAT--
TGATCAAA	0.49274	--TTTGATCA
ACTTTGAT	0.49225	ACTTTGAT--

#### 8 mer Z-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

CTTTGATC	205.02798	-CTTTGATC-
CTTCAAA	76.15573	-CTTTGAAG-
AGATCAAA	74.56111	--TTTGATCT
ACATCAAA	68.01338	--TTTGATGT
CATCAAA	67.32372	-CTTTGATG-
ATCAAAGA	59.39198	TCTTTGAT--
ATCAAAGC	59.06268	GCTTTGAT--
ATCAAAGG	58.23706	CCTTTGAT--
CCTTTGAA	44.71681	CCTTTGAA--
TGATCAAA	44.62768	--TTTGATCA

### Top scoring motifs for Assay 14333

Protein ID: pTH15532.1 Gene: LEF1 Domain: HMG\_box Flag: Pass matched\_pair Array: 1M-ME

#### 8 mer E-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

CTTTGATC	0.49813	-GATCAAAG-
AGATCAAA	0.49809	AGATCAAA--
CATCAAA	0.49723	-CATCAAAG-
CTTCAAA	0.49585	-CTTCAAAG-
ATCAAAGA	0.49561	--ATCAAAGA
ACATCAAA	0.49550	ACATCAAA--
ACTTCAAA	0.49478	ACTTCAAA--
ATCAAAGC	0.49476	--ATCAAAGC
ATCAAAGG	0.49335	--ATCAAAGG
GATCAAAC	0.49182	-GATCAAAC-

#### 8 mer Z-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

AGATCAAA	140.57156	AGATCAAA--
CTTTGATC	139.90488	-GATCAAAG-
CATCAAA	134.65813	-CATCAAAG-
CTTCAAA	82.95967	-CTTCAAAG-
ATCAAAGA	80.25107	--ATCAAAGA
ATCAAAGC	79.05008	--ATCAAAGC
ACATCAAA	61.43737	ACATCAAA--
ACTTCAAA	59.17107	ACTTCAAA--
GATCAAAC	55.58047	-GATCAAAC-
ATCAAACG	51.16477	--ATCAAACG