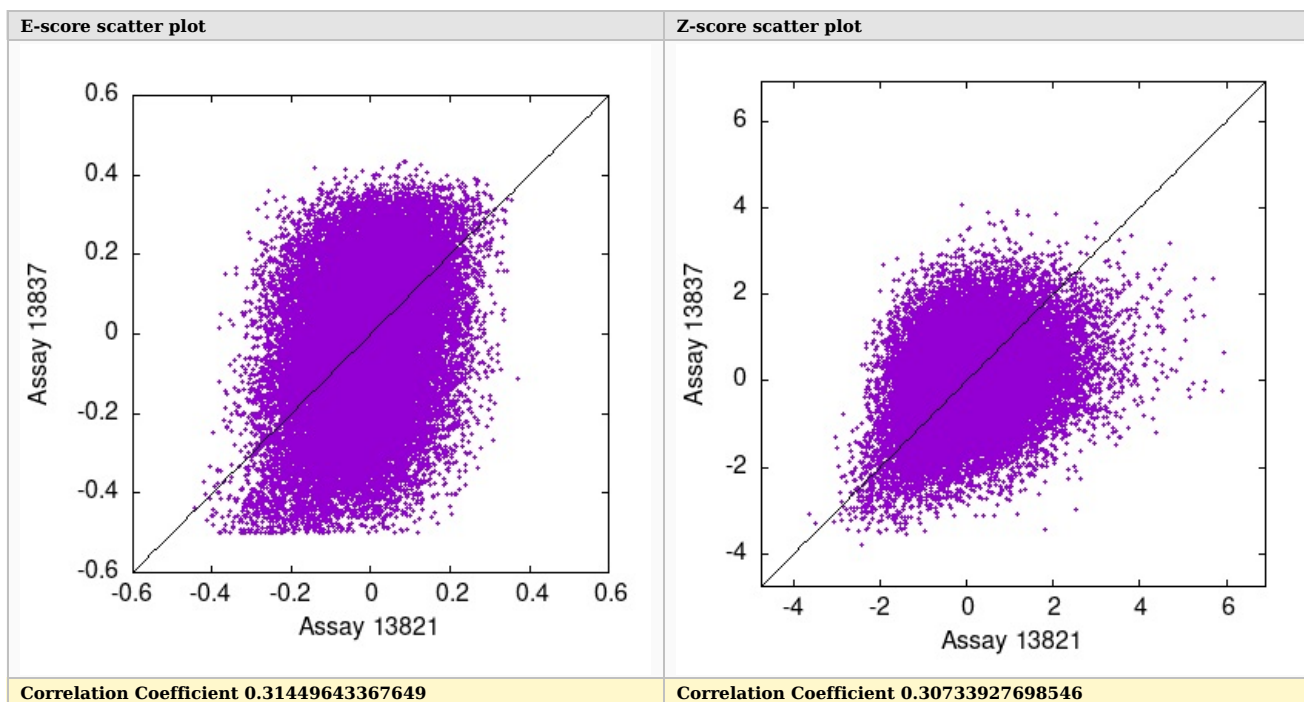


## QC report



### Top scoring motifs for Assay 13821

Protein ID: pTH13922.1 Gene: SCML4.DBD Domain: AT\_hook Flag: Reject Array: 1M-ME

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

Forward:

Reverse:



#### Top 10

#### Scores

#### Alignment

ACACACAC	0.37235	--GTGTGTGT--
AATTTGTA	0.35407	--AATTTGTA--
AATTAATT	0.34265	--AATTAATT--
ATTAATTA	0.34249	TAATTAAT---
CATATAAC	0.33948	---GTTATATG
AATATCAC	0.33820	--AATATCAC--
GTGTGGTA	0.33676	--GTGTGGTA--
CCAACACA	0.33665	---TGTGTTGG
GTATAATA	0.33634	--TATTATAC--
ATATTATA	0.33444	--ATATTATA--

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

Forward:

Reverse:



#### Top 10

#### Scores

#### Alignment

CCAACACA	5.93516	--TGTGTTGG--
CAGCAACC	5.92351	--GGTTGCTG--
CTATATTA	5.68917	--CTATATTA--
ACACACAC	5.53141	--GTGTGTGT--
AATATCAC	5.48571	---GTGATATT
ATCCACAC	5.47055	--GTGTGGAT--
AATTTGTA	5.27062	--AATTTGTA--
TATAAATA	5.23456	--TATTTATA--
GTGTGGTA	5.22243	--GTGTGGTA--
ACAACACC	5.19517	GGTGTGTT--

### Top scoring motifs for Assay 13837

Protein ID: pTH13922.2 Gene: SCML4.DBD Domain: AT\_hook Flag: Reject Array: 1M-HK

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

Forward:

Reverse:



#### Top 10

#### Scores

#### Alignment

ATAGTAAT	0.43463	--ATAGTAAT--
ACAAAATA	0.43437	ACAAAATA---
CTGTATTA	0.42534	---CTGTATTA
AATAAATT	0.42515	--AATAAATT--
AATATATT	0.41881	--AATATATT--
ATCTAGAT	0.41765	---ATCTAGAT
AGAAATAT	0.41617	--AGAAATAT--
ATAATGTA	0.41515	ATAATGTA---
GATATGTA	0.41445	--GATATGTA--
AGATATCT	0.41155	---AGATATCT

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

Forward:

Reverse:



#### Top 10

#### Scores

#### Alignment

GATATGTA	4.07819	--GATATGTA--
AATATATT	3.92110	--AATATATT--
CACATATA	3.88521	--CACATATA--
AATAAATT	3.86519	--AATAAATT--
ACAAAATA	3.85148	ACAAAATA---
ATAATGTA	3.79979	ATAATGTA---
ATAGTAAT	3.68101	--ATAGTAAT--
TATTAATA	3.63313	--TATTAATA--
AGATATCT	3.62515	---AGATATCT
AATTTAAA	3.58852	--AATTTAAA--