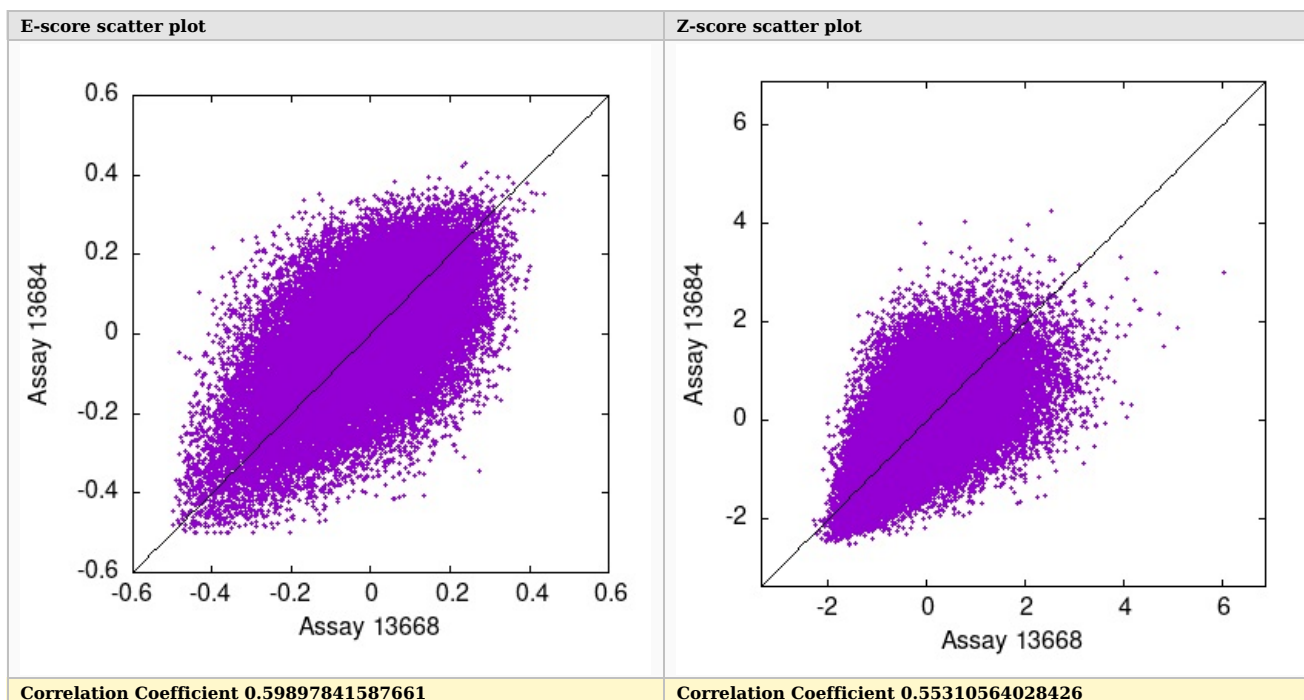


## QC report



### Top scoring motifs for Assay 13668

Protein ID: pTH14283.1 Gene: AEBP1.DBD Domain: Unknown Flag: Reject Array: 1M-ME

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

Forward:

Reverse:



#### Top 10

#### Scores

#### Alignment

AACATGTT	0.43528	-----AACATGTT
TAAATTTA	0.41826	-----TAAATTTA
TGTGCACA	0.40887	---TGTGCACA--
GTTGCAAC	0.40522	----GTTGCAAC--
ATGTACAT	0.40388	---ATGTACAT---
AGACGTCT	0.39820	----AGACGTCT--
CTGTATAC	0.39401	---CTGTATAC---
GTTTAAAC	0.39363	---GTTTAAAC---
ATCAGTTA	0.39155	ATCAGTTA-----
ACATACAA	0.38924	---ACATACAA---

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

Forward:

Reverse:



#### Top 10

#### Scores

#### Alignment

AACATGTT	6.02627	-----AACATGTT
ATGTACAT	5.08516	---ATGTACAT---
AGACGTCT	4.81583	----AGACGTCT--
TAAATTTA	4.70869	-----TAAATTTA
AACGCGTT	4.65937	---AACGCGTT---
TGTATACA	4.34447	----TGTATACA---
TTGTACAA	4.32097	---TTGTACAA---
TGTGCACA	4.21311	---TGTGCACA---
ATCAGTTA	4.14565	ATCAGTTA-----
AATGCATT	4.12151	----AATGCATT--

### Top scoring motifs for Assay 13684

Protein ID: pTH14283.2 Gene: AEBP1.DBD Domain: Unknown Flag: Reject Array: 1M-HK

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

Forward:

Reverse:



#### Top 10

#### Scores

#### Alignment

GATGCATC	0.43152	---GATGCATC---
TACTAGTA	0.42071	---TACTAGTA---
GTCATGAC	0.40525	---GTCATGAC---
TGTTAACA	0.39393	---TGTTAACA---
AGTCGACA	0.39376	---AGTCGACA---
TCTCGAGA	0.39360	---TCTCGAGA---
GTAATACA	0.39101	----GTAATACA---
CTGTATTA	0.39094	CTGTATTA-----
GTGTACAC	0.38474	---GTGTACAC---
AAACGTTT	0.38021	-----AAACGTTT

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

Forward:

Reverse:



#### Top 10

#### Scores

#### Alignment

GATGCATC	4.25727	-GATGCATC----
ATCTAGAT	4.02998	ATCTAGAT-----
GTGTACAC	4.00901	--GTGTACAC---
TGTTAACA	3.97301	-----TGTTAACA
GTCATGAC	3.65987	---GTCATGAC---
AATCGATT	3.59514	---AATCGATT---
CTGTATTA	3.50474	--CTGTATTA---
GAACGTTT	3.46689	--GAACGTTT---
ATCATACA	3.40832	---TGTATGAT---
TACTAGTA	3.36487	--TACTAGTA---