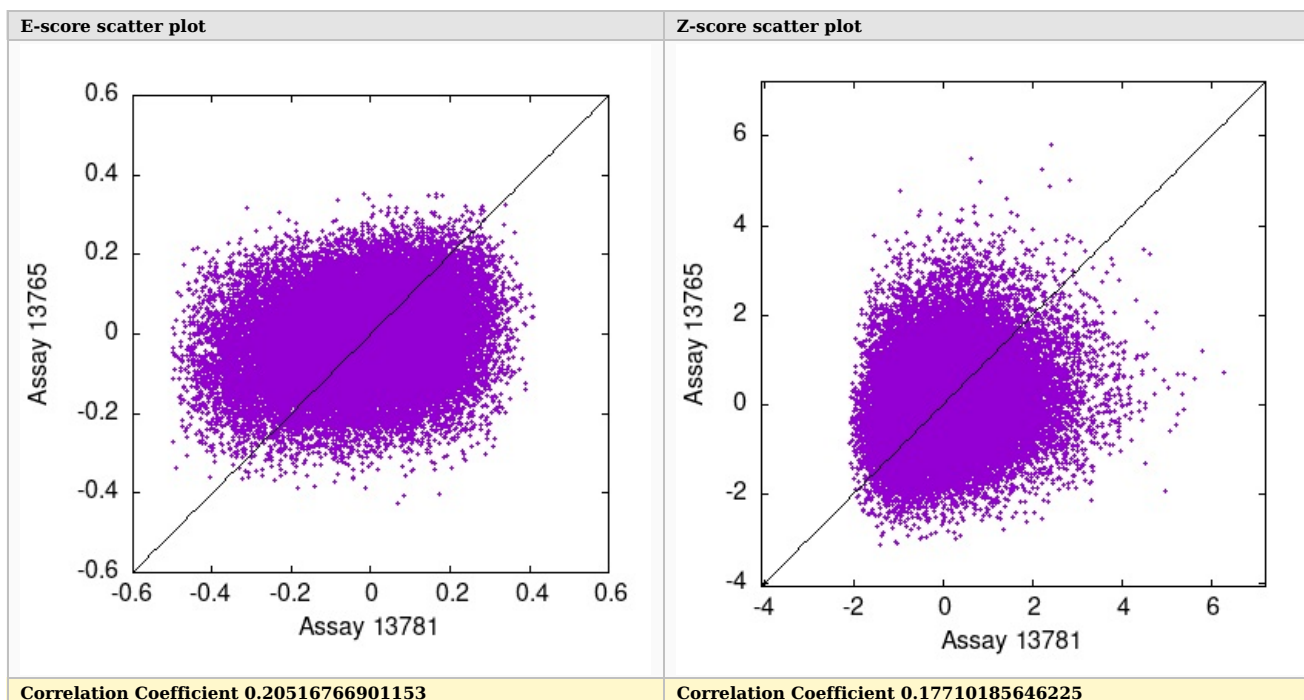


## QC report



### Top scoring motifs for Assay 13781

Protein ID: pTH14303.2 Gene: GPBP1.FL Domain: Unknown Flag: Reject Array: 1M-HK

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

Forward:

Reverse:



#### Top 10

#### Scores

#### Alignment

GATGCATC	0.41159	GATGCATC-----
AGTATACT	0.40843	AGTATACT-----
ATGCATCA	0.40548	-ATGCATCA----
TCTCGAGA	0.40045	-TCTCGAGA----
ATGCGCAT	0.39064	-ATGCGCAT----
ATACATTA	0.38967	-ATACATTA----
GTTTAAAC	0.38914	----GTTTAAAC-
TAACGTAA	0.38907	-TTACGTTA----
ATTATAAT	0.38593	-----ATTATAAT
GTACAACA	0.38424	-GTACAACA----

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

Forward:

Reverse:



#### Top 10

#### Scores

#### Alignment

TGTTAACA	6.27951	TGTTAACA-----
TCTCGAGA	5.78811	---TCTCGAGA--
TAACGTAA	5.64109	---TAACGTAA--
ATAACGTA	5.38745	--ATAACGTA---
ATGCATCA	5.38331	---TGATGCAT--
GCATATGC	5.35124	-----GCATATGC
GATGCATC	5.26041	-----GATGCATC
AAGTTAGT	5.24209	-ACTAATCT----
CTGTATTA	5.21009	---TAATACAG--
AACAAATC	5.06531	---AACAAATC--

### Top scoring motifs for Assay 13765

Protein ID: pTH14303.1 Gene: GPBP1.FL Domain: Unknown Flag: Reject Array: 1M-ME

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

Forward:

Reverse:



#### Top 10

#### Scores

#### Alignment

CGTAACAC	0.35417	-CGTAACAC---
TATATGGA	0.35212	TCCATATA----
ATAAATAA	0.34960	-ATAAATAA----
ATAGTCTG	0.34850	---ATAGTCTG-
CAAATACA	0.34719	--CAAATACA--
ACAACATC	0.34630	----ACAACATC
TCCCAACA	0.34041	TCCCAACA----
GTGGGTGA	0.33860	---TAACCCAC-
ATATAAAC	0.32326	---ATATAAAC-
AATAATAG	0.32129	---AATAATAG-

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

Forward:

Reverse:



#### Top 10

#### Scores

#### Alignment

CTAGTGTA	5.82198	----TACACTAG
TCCCAACA	5.49679	TCCCAACA----
AATAATAG	5.24246	-AATAATAG---
TATGTGAA	5.00282	--TTCACATA--
GGTAATAC	4.99865	-GGTAATAC---
ATCGATCA	4.86525	ATCGATCA----
GTGGGTGA	4.77531	---TAACCCAC-
CGTAACAC	4.59936	-CGTAACAC---
AAATAATA	4.44144	AAATAATA----
CAACCTGA	4.35566	---CAACCTGA-