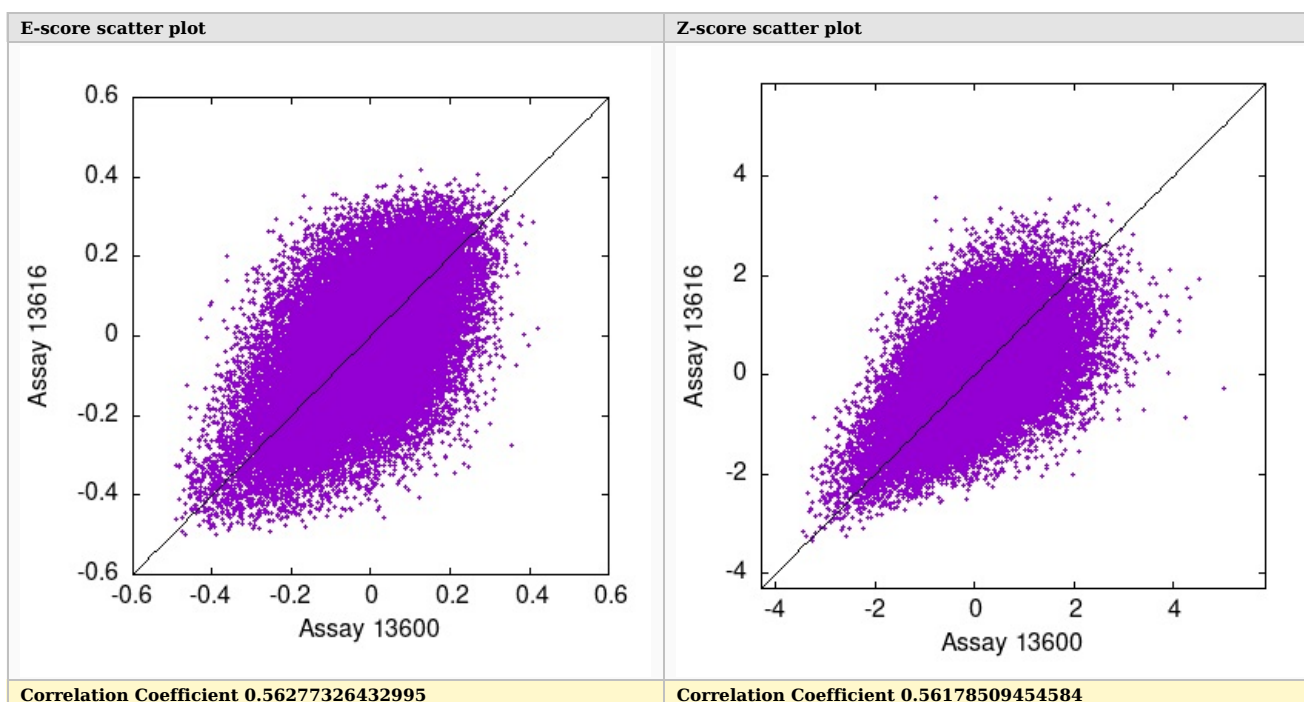


## QC report



Correlation Coefficient 0.56277326432995

Correlation Coefficient 0.56178509454584

### Top scoring motifs for Assay 13600

Protein ID: pTH14297.1 Gene: DACH1.DBD Domain: Unknown Flag: Reject Array: 1M-ME

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

Forward:

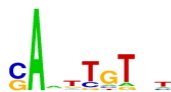
Reverse:



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

Forward:

Reverse:



#### Top 10

#### Scores

#### Alignment

TATATATA	0.42159	--TATATATA--
ATTGTACA	0.41080	---ATTGTACA-
ATATATAT	0.39781	---ATATATAT--
CAATTGTA	0.39222	---CAATTGTA--
GAATTCGA	0.38696	--GAATTCGA--
AATTAATT	0.38270	---AATTAATT--
ATTTGTAC	0.38000	---ATTTGTAC--
CAATTGCG	0.37531	CGCAATTG----
TTGTACAA	0.36931	-----TTGTACAA
AGACGTCT	0.36811	---AGACGTCT--

#### Top 10

#### Scores

#### Alignment

AGACGTCT	5.00740	---AGACGTCT--
CAATTGCG	4.50598	CGCAATTG----
CAATTGTA	4.33494	---CAATTGTA--
AATTAATT	4.26956	---AATTAATT--
GACGCGTC	4.22760	--GACGCGTC--
TTGTACAA	4.11827	-----TTGTACAA
ATACACAT	4.11163	---ATGTGTAT--
CAACGTTG	3.91662	--CAACGTTG--
GAATTCGA	3.90439	--GAATTCGA--
ATGACAAC	3.87007	---GTTGTCAT--

### Top scoring motifs for Assay 13616

Protein ID: pTH14297.2 Gene: DACH1.DBD Domain: Unknown Flag: Reject Array: 1M-HK

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

Forward:

Reverse:



Forward:

Reverse:



#### Top 10

#### Scores

#### Alignment

GAATATTC	0.41638	----GAATATTC--
GTCATGAC	0.40486	---GTCATGAC---
AAACGTTT	0.40232	----AAACGTTT--
ACTATTGA	0.39538	TCAATAGT-----
AAATCGAT	0.38402	----AAATCGAT--
ATAAATTA	0.38305	----TAATTATAT--
ATAATGTA	0.38012	---ATAATGTA---
AATGTACA	0.37894	-----AATGTACA-
ATTATTAG	0.37851	CTAATAAT-----
ACATATAT	0.37775	-----ATATATGT

#### Top 10

#### Scores

#### Alignment

ATGTATAG	3.56079	ATGTATAG---
CATATATG	3.52825	-CATATATG---
ACATATAT	3.43676	ACATATAT---
AAAATTTT	3.39963	AAAATTTT---
AATGTACA	3.38852	-AATGTACA---
AAACGTTT	3.33524	AAACGTTT---
CGCGCGCG	3.32208	-CGCGCGCG---
ATTATAAT	3.31819	-ATTATAAT---
AAATCGAT	3.26072	AAATCGAT---
ATAATGTA	3.25588	---TACATTAT