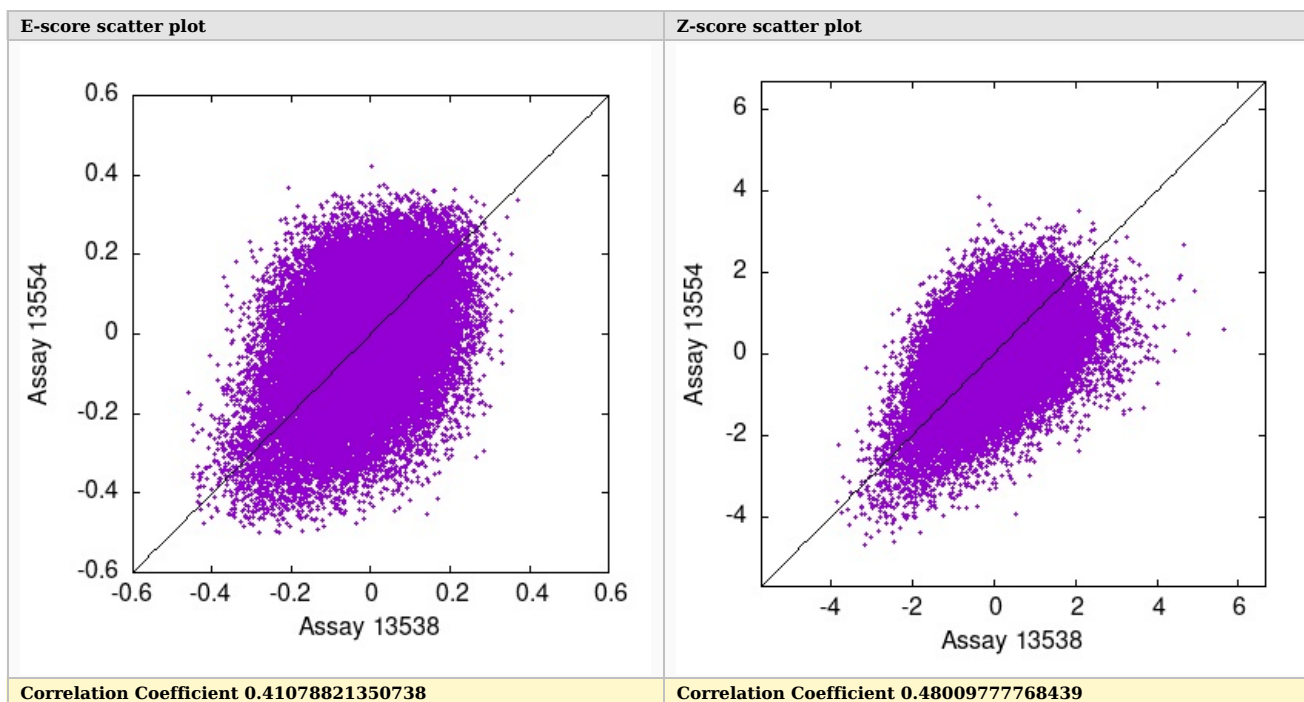


## QC report



### Top scoring motifs for Assay 13538

Protein ID: pTH14218.1 Gene: CAMTA1.DBD Domain: CG-1 Flag: Reject Array: 1M-ME

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

Forward:

Reverse:



##### Top 10

##### Scores

##### Alignment

TATACAAA	0.37200	-TTTGTATA-
GAGTGCTA	0.35570	-GAGTGCTA-
CCAACAAA	0.35350	--TTTGTGG
TACTATAA	0.35267	--TACTATAA
GTTGGTTA	0.34444	-GTTGGTTA-
CATCTTAA	0.33184	-CATCTTAA-
AACGAATT	0.33176	AATTCTTT--
ACTGCATA	0.32933	-ACTGCATA-
ACCGGTTA	0.32779	-ACCGGTTA-
CACGGTCA	0.32776	-CACGGTCA-

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

Forward:

Reverse:



##### Top 10

##### Scores

##### Alignment

ATATACCG	5.63382	ATATACCG----
CCAACAAA	4.91594	-CCAACAAA---
AATTGCGT	4.76352	--ACGCAATT--
TATACAAA	4.64763	-TATACAAA---
ATCGCGAT	4.60320	--ATCGCGAT--
ATATAGTA	4.55364	ATATAGTA----
ATCACTCA	4.42694	-ATCACTCA---
ACAAAACA	4.39723	----ACAAAACA
ACACCAGA	4.16468	--ACACCAGA--
TACTATAA	4.15156	TTATAGTA----

### Top scoring motifs for Assay 13554

Protein ID: pTH14218.2 Gene: CAMTA1.DBD Domain: CG-1 Flag: Reject Array: 1M-HK

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

Forward:

Reverse:



##### Top 10

##### Scores

##### Alignment

GATATGTA	0.42354	GATATGTA---
CATTATAG	0.37702	CATTATAG---
AACACAAT	0.37151	-ATTGTGTT--
CGTAACAA	0.36846	--TTGTTACG-
ATATCACA	0.36817	--ATATCACA-
TCTCGAGA	0.36273	--TCTCGAGA-
ATTATTAC	0.36095	-ATTATTAC--
CATTACAA	0.35958	---CATTACAA
GAATATTC	0.35811	GAATATTC---
GTAACAAA	0.35469	-TTTGTTAC--

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

Forward:

Reverse:



##### Top 10

##### Scores

##### Alignment

ATTATAAT	3.84405	-ATTATAAT---
GATATGTA	3.63652	GATATGTA----
GAATATTC	3.50837	GAATATTC----
ACTATTTG	3.31800	-ACTATTTG---
GAATTGTA	3.26066	GAATTGTA----
ATTATTAC	3.20627	-ATTATTAC---
ATTACGGA	3.17087	----ATTACGGA
CATAACAC	3.17018	--GTGTTATG--
ATATCACA	3.15348	--ATATCACA--
ATTACAAC	3.14635	-ATTACAAC---