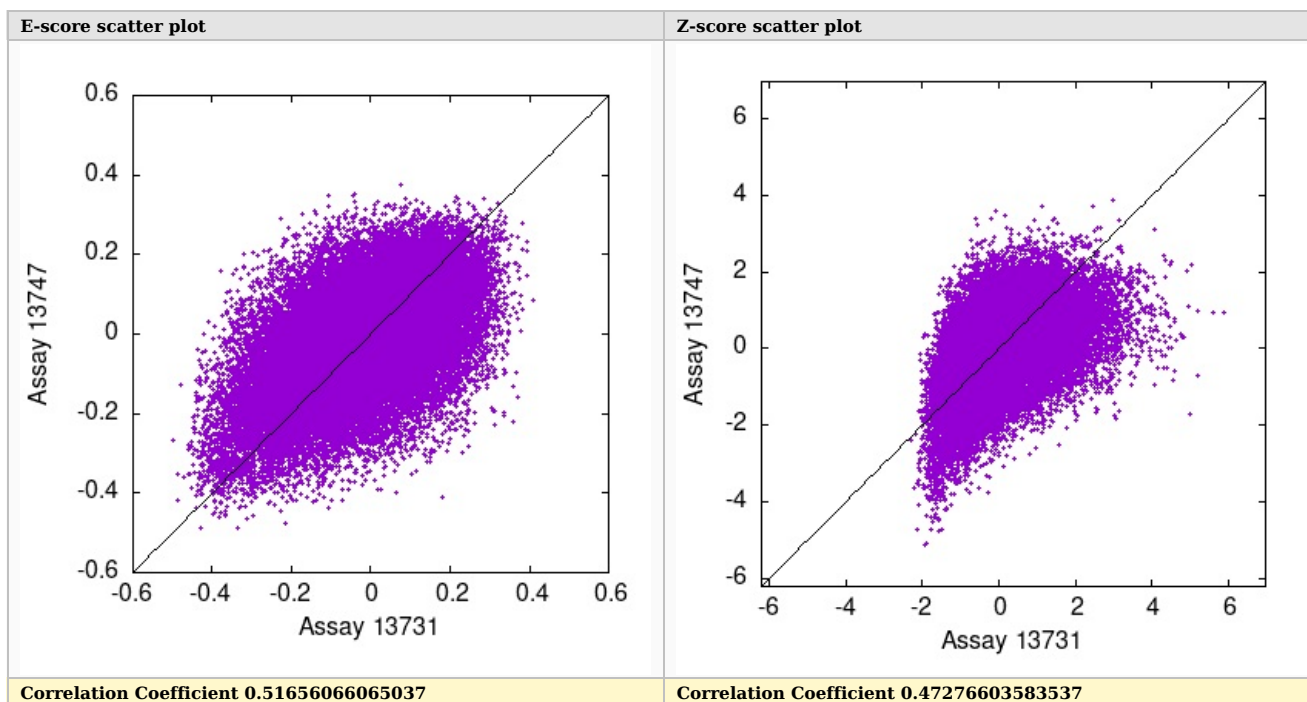


## QC report



### Top scoring motifs for Assay 13731

Protein ID: pTH14318.1 Gene: PREB.DBD Domain: Unknown Flag: Reject Array: 1M-ME

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

Forward:

Reverse:



#### Top 10

#### Scores

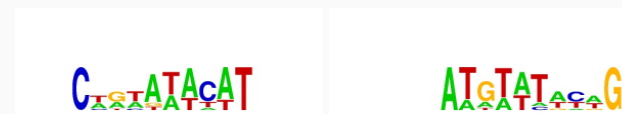
#### Alignment

ATGTACAT	0.40943	--ATGTACAT
TACAAACA	0.39401	-TACAAACA-
TAAATTTA	0.39386	-TAAATTTA-
GTATAATA	0.39243	GTATAATA--
TGTATACA	0.38232	-TGTATACA-
AATTTGTA	0.38214	-TACAAATT-
CATAATAC	0.38109	GTATTATG--
AACTGATA	0.38036	-AACTGATA--
ATCGATAC	0.37924	ATCGATAC--
ACAAACAT	0.37616	--ACAAACAT

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

Forward:

Reverse:



#### Top 10

#### Scores

#### Alignment

TAAATTTA	5.86176	-TAAATTTA----
ATGTACAT	5.58412	--ATGTACAT---
TGTATACA	5.20037	-TGTATACA----
AGAATTCT	5.17994	-AGAATTCT----
CTGTATAC	5.03320	CTGTATAC-----
AACATGTT	4.96826	-----AACATGTT
CATAATAC	4.96002	CATAATAC-----
TACAAACA	4.90707	-TACAAACA----
AGTAATAT	4.83296	-AGTAATAT----
CGTTAATA	4.78465	-CGTTAATA----

### Top scoring motifs for Assay 13747

Protein ID: pTH14318.2 Gene: PREB.DBD Domain: Unknown Flag: Reject Array: 1M-HK

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

Forward:

Reverse:



#### Top 10

#### Scores

#### Alignment

TAGTTGCA	0.37666	----TAGTTGCA--
CACTATAC	0.35120	--GTATAGTG----
CTCTGCTA	0.34761	----TAGCAGAG--
CGACGACG	0.34681	--CGACGACG----
ATATGTAC	0.34497	----ATATGTAC--
ATAATGTA	0.34057	----ATAATGTA--
CTTGTAAC	0.33997	-----CTTGTAAC
GATATGTA	0.33980	----GATATGTA--
ATACATTA	0.33506	----TAATGTAT--
ACCGATAA	0.33415	ACCGATAA-----

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

Forward:

Reverse:



#### Top 10

#### Scores

#### Alignment

ATAATGTA	3.88104	TACATTAT----
TAGTTGCA	3.71609	----TAGTTGCA
ATGTATTC	3.71030	---ATGTATTC--
CGACGACG	3.60674	--CGTCGTCG--
ACACAATC	3.48226	--GATTGTGT--
CACTATAC	3.40399	-GTATAGTG----
ATTGTTAC	3.39437	---ATTGTTAC-
GTAACCTA	3.37773	---TAAGTTAC-
GTATGTTA	3.36604	-GTATGTTA--
ACTAGTAC	3.35505	---ACTAGTAC-