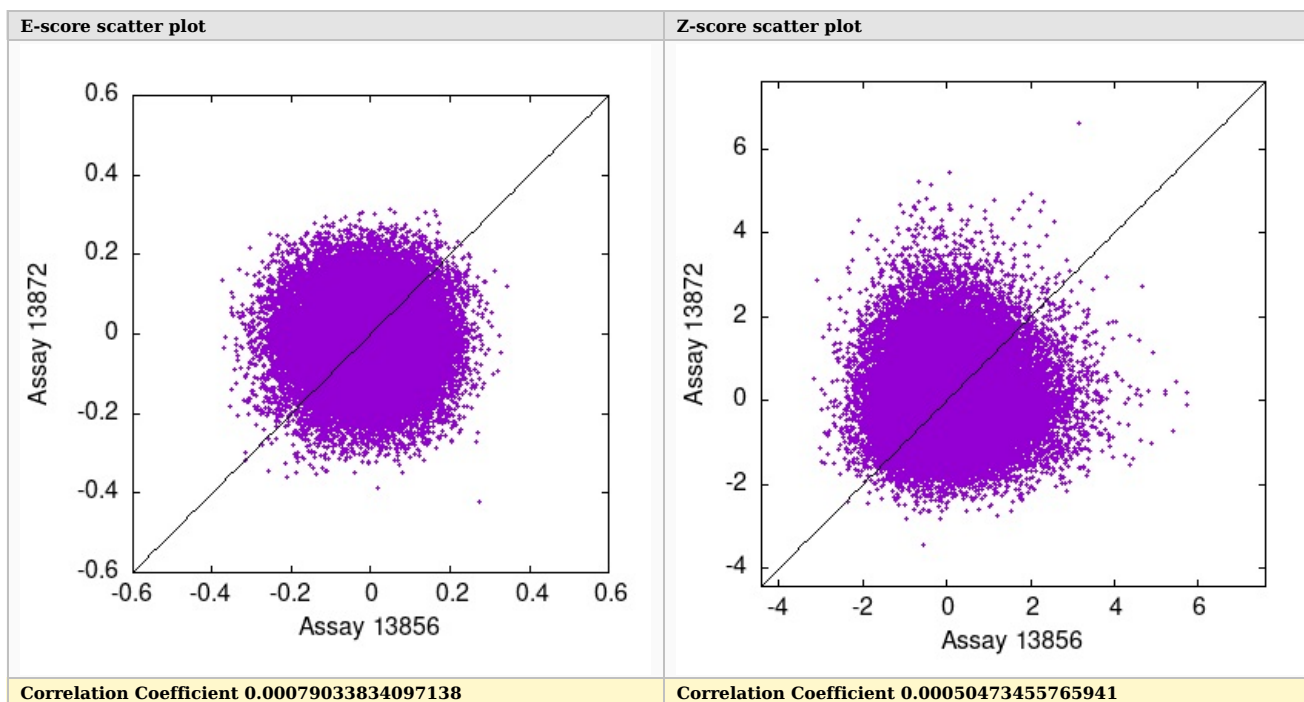


QC report



Top scoring motifs for Assay 13856

Protein ID: pTH14260.1 Gene: MBD3.FL Domain: MBD Flag: Reject Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:

Reverse:

C C A T T G A

T A C A A T G G

8 mer Z-scores for probeset 'all'

Forward:

Reverse:

A C G T T G A

T A C A A T G G

Top 10

Scores

Alignment

CGATGAGA	0.34550	---CGATGAGA
CAGTGGCG	0.32714	-CGCCACTG--
ACAATCCA	0.32586	--TGGATTGT-
CGCGATTA	0.31973	-CGCGATTA--
AAGTGAGG	0.31356	CCTCACTT---
CAACTGGA	0.30805	---CAACTGGA
CTGATGTA	0.30440	--TACATCAG-
ACGACTCT	0.30352	--ACGACTCT-
ACGAATTG	0.29744	---CAATTCGT
ACAAACGC	0.29617	--GCGTTTGT-

Top 10

Scores

Alignment

CTGATGTA	5.74629	TACATCAG----
AAACGTAA	5.71550	--AAACGTAA---
CCTGTGGC	5.45852	---CCTGTGGC-
CGCGATTA	5.38561	-TAATCGCG----
ATCTTTGA	5.23073	---ATCTTTGA--
CGATGAGA	5.21234	-CGATGAGA----
ATGTTCTG	4.90638	-----CAGAACAT
AAATTCCT	4.88738	-AAATTCCT----
AATCAGTA	4.79962	--AATCAGTA---
ACGCCCG	4.65679	-CGGGCGGT----

Top scoring motifs for Assay 13872

Protein ID: pTH14260.2 Gene: MBD3.FL Domain: MBD Flag: Reject Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:

Reverse:

G A C C C G G

C C A A G A G T C

8 mer Z-scores for probeset 'all'

Forward:

Reverse:

C G T T T

A A C G G

Top 10

Scores

Alignment

GAGTGAAC	0.31186	--GTTCACTC----
CCAAGAAC	0.30803	-----GTTCTTGG
TACCGGCA	0.30748	---TACCGGCA---
AAGAACCC	0.30509	AAGAACCC-----
CATCATGG	0.30420	-----CATCATGG
GACGCTCC	0.30371	---GACGCTCC---
GTACCTTA	0.30214	--GTACCTTA----
AGTCGGTG	0.30027	---CACCGACT---
ATCGGGTG	0.29699	---CACCGGAT---
ACCCTCTA	0.29387	----ACCCTCTA--

Top 10

Scores

Alignment

CCAAGAAC	6.60233	-----GTTCTTGG
CGTTAGTA	5.43294	----CGTTAGTA--
ACGATTCTG	5.21169	---ACGATTCTG--
GCGTTGAC	5.15221	---GCGTTGAC---
ATCGGGTG	4.91146	CACCCGAT-----
TATCGGAA	4.82993	-TTCCGATA-----
ACTAATGA	4.78541	---TCATTAGT---
TACCGGCA	4.75457	---TGCCGGTA---
CACCTTAG	4.75289	---CACTTTAG---
CGGGAATC	4.74105	----CGGGAATC-