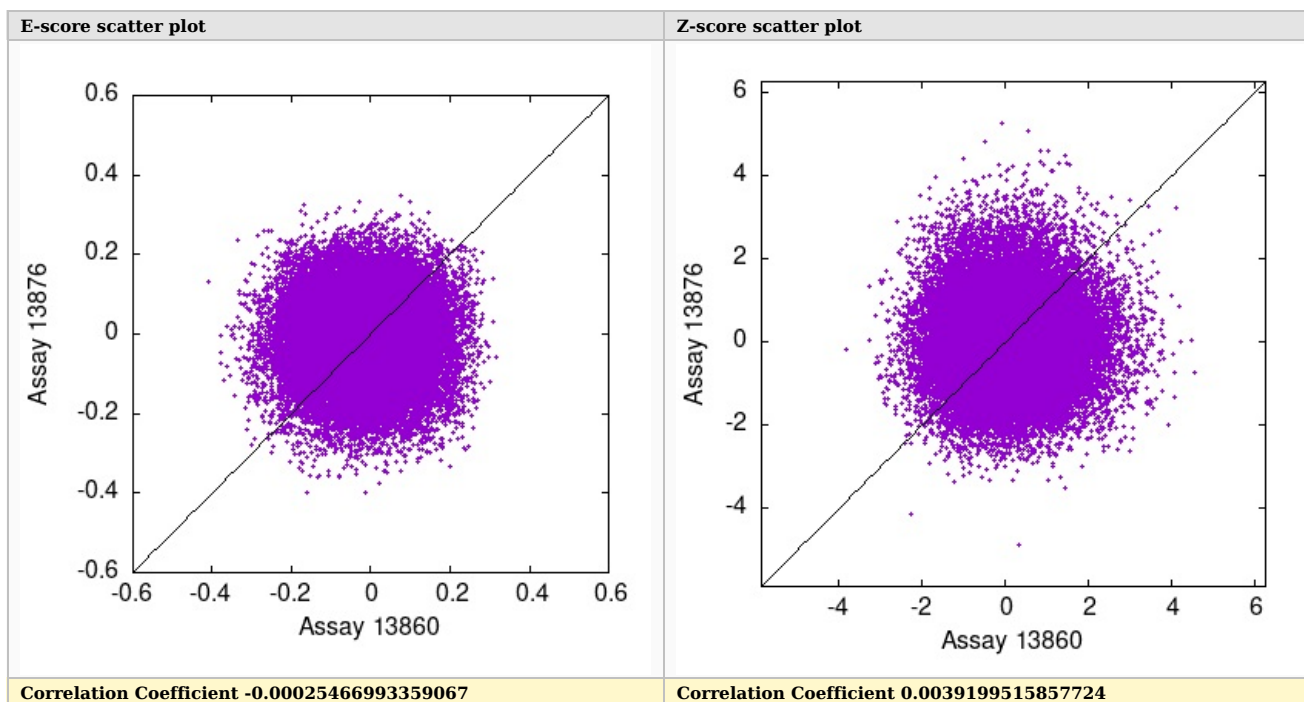


## QC report



Correlation Coefficient -0.00025466993359067

Correlation Coefficient 0.0039199515857724

### Top scoring motifs for Assay 13860

Protein ID: pTH14265.1 Gene: SETDB2.DBD Domain: MBD Flag: Reject Array: 1M-ME

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

Forward:

Reverse:

C A G T A C A G G A G G A C A A C A G T C C A A T C G T A A T T A A G C C G G G A A C T T C A G A T G A T C G G

#### Top 10

#### Scores

#### Alignment

CTGCTAGC	0.31586	----GCTAGCAG--
AAGTATCA	0.30972	---AAGTATCA---
AGACTATG	0.30829	-CATAGTCT-----
GAGAAAAA	0.30068	---GAGAAAAA---
GGGACAAC	0.29793	----GGGACAAC--
AGTCCAAT	0.29548	----AGTCCAAT--
CGTAATTA	0.29193	CGTAATTA-----
AGCCGGGA	0.28922	-----TCCCGGCT
AACTTCAG	0.28713	CTGAAGTT-----
ATGATCGG	0.28709	----ATGATCGG--

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

Forward:

Reverse:

A G C C A G C C A A G T C C A A T C G T A A T T A A G C C G G G A A C T T C A G A T G A T C G G

#### Top 10

#### Scores

#### Alignment

AACTAGTA	4.54383	---AACTAGTA--
AAGTATCA	4.46800	--AAGTATCA---
GGTACTTA	4.21375	--TAAGTACC---
AGCCGGGA	4.17264	--AGCCGGGA---
CTCTGTGC	4.09519	----GCACAGAG
ATTGTGCA	4.06398	----TGCACAAT--
CCGGCCGA	4.05389	----CCGGCCGA--
AAACGACA	4.02506	--AAACGACA---
TCAGGCGA	3.99994	TCAGGCGA-----
CGACGTCG	3.90850	--CGACGTCG---

### Top scoring motifs for Assay 13876

Protein ID: pTH14265.2 Gene: SETDB2.DBD Domain: MBD Flag: Reject Array: 1M-HK

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

Forward:

Reverse:

G A G T A C A G G A G G A C A A C A G T C C A A T C G T A A T T A A G C C G G G A A C T T C A G A T G A T C G G

#### Top 10

#### Scores

#### Alignment

AACTGATC	0.34822	-GATCAGTT--
CTCGGTAA	0.33458	---CTCGGTAA---
GCGGTGAC	0.33158	GTACACGC---
ATAGTTAG	0.32364	---ATAGTTAG---
TGAGATCA	0.31660	---TGAGATCA---
CGGGGGAG	0.31121	---CGGGGGAG---
GACTATAC	0.31099	---GACTATAC---
CACCCCAA	0.30867	---CACCCCAA---
ACAAGATA	0.30771	--ACAAGATA---
GGACAGGA	0.30477	GGACAGGA---

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

Forward:

Reverse:

A G C C A G C C A A G T C C A A T C G T A A T T A A G C C G G G A A C T T C A G A T G A T C G G

#### Top 10

#### Scores

#### Alignment

CGGGGGAG	5.23852	---CTCCCCCG---
GAATTCCA	5.06781	--GAATTCCA-----
CACCCCAA	4.81740	---CACCCCAA---
TCCATTAA	4.58757	--TCCATTAA-----
AACTGATC	4.58217	-AACTGATC-----
AATATGTC	4.46958	AATATGTC-----
TCTCACCA	4.39627	--TCTCACCA-----
CGCGAGCG	4.31418	-CGCTCGCG-----
CCATTTAA	4.29259	-----CCATTTAA
CTCGGTAA	4.29058	----TTACCGAG---