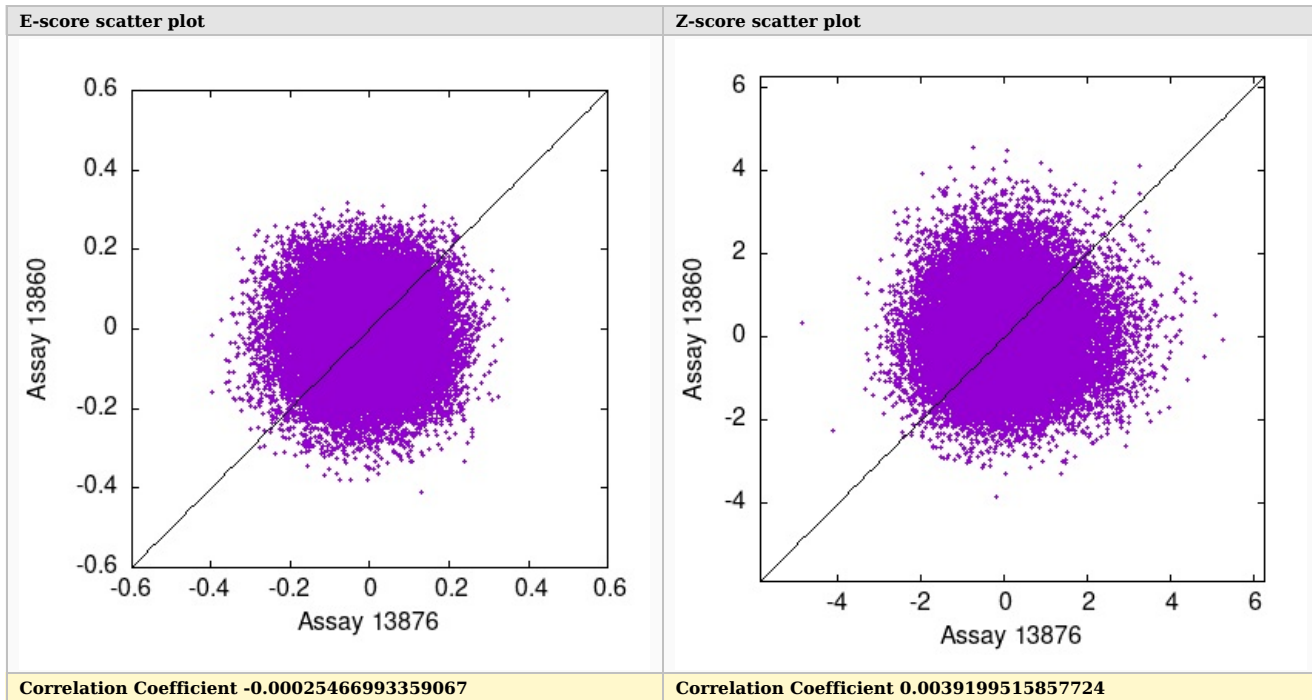


## QC report



### 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'			8 mer Z-scores for probeset 'all'		
Forward:		Reverse:	Forward:		Reverse:
Top 10	Scores	Alignment	Top 10	Scores	Alignment
AACTGATC	0.34822	-GATCAGTT--	CGGGGGAG	5.23852	---CTCCCCG---
CTCGGTAA	0.33458	---CTCGGTAA	GAATTCCA	5.06781	--GAATTCCA----
GCGGTAC	0.33158	GTACACGC---	CACCCCAA	4.81740	---CACCCCAA----
ATAGTTAG	0.32364	---ATAGTTAG	TCCATTAA	4.58757	--TCCATTAA----
TGAGATCA	0.31660	---TGAGATCA	AACTGATC	4.58217	-AACTGATC-----
CGGGGGAG	0.31121	---CGGGGGAG	AATATGTC	4.46958	AATATGTC-----
GACTATAC	0.31099	---GACTATAC	TCTCACCA	4.39627	--TCTCACCA----
CACCCCAA	0.30867	---CACCCCAA	CGCGAGCG	4.31418	-CGCTCGCG-----
ACAAGATA	0.30771	--ACAAGATA-	CCATTTAA	4.29259	-----CCATTTAA
GGACAGGA	0.30477	GGACAGGA---	CTCGGTAA	4.29058	----TTACCGAG---

### 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'			8 mer Z-scores for probeset 'all'		
Forward:		Reverse:	Forward:		Reverse:
Top 10	Scores	Alignment	Top 10	Scores	Alignment
CTGCTAGC	0.31586	----GCTAGCAG--	AACTAGTA	4.54383	---AACTAGTA--
AAGTATCA	0.30972	---AAGTATCA---	AAGTATCA	4.46800	--AAGTATCA---
AGACTATG	0.30829	-CATAGTCT-----	GGTACTTA	4.21375	--TAAGTACC---
GAGAAAAA	0.30068	---GAGAAAAA---	AGCCGGGA	4.17264	-AGCCGGGA---
GGGACAAC	0.29793	----GGGACAAC--	CTCTGTGC	4.09519	----GCACAGAG
AGTCCAAT	0.29548	---AGTCCAAT---	ATTGTGCA	4.06398	----TGCACAAT--
CGTAATTA	0.29193	CGTAATTA-----	CCGGCCGA	4.05389	----CCGGCCGA-
AGCCGGGA	0.28922	-----TCCCGGCT	AAACGACA	4.02506	--AAACGACA---
AACTTCAG	0.28713	CTGAAGTT-----	TCAGGCGA	3.99994	TCAGGCGA----
ATGATCGG	0.28709	----ATGATCGG--	CGACGTCG	3.90850	--CGACGTCG---