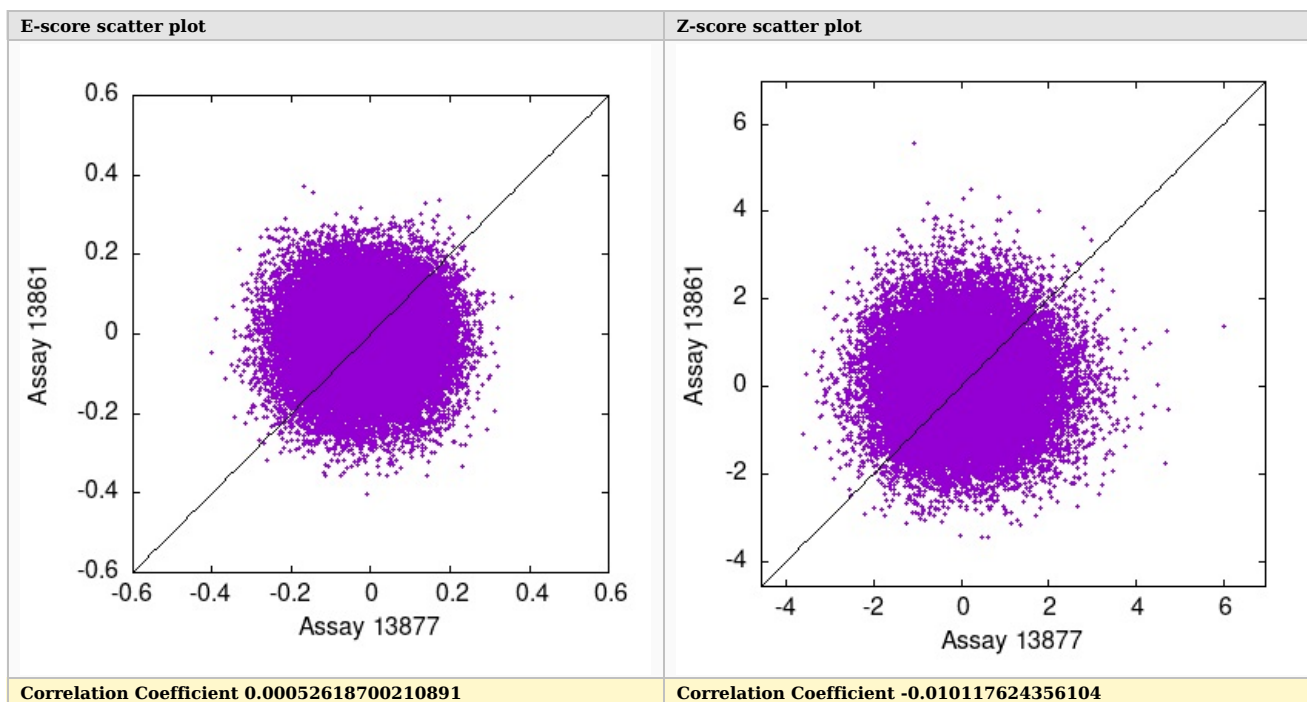


QC report



Top scoring motifs for Assay 13877

Protein ID: pTH14267.2 Gene: MTERF2.FL Domain: mTERF Flag: Reject Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:

Reverse:

A C C A A T A

T A T G G T T

8 mer Z-scores for probeset 'all'

Forward:

Reverse:

C A G G T

A C C C T G

Top 10

Scores

Alignment

CTCATGAG	0.35356	---CTCATGAG--
CTTCGGAA	0.32218	---CTTCGGAA--
CATCTTGC	0.32214	---GCAAGATG-
AATATTGG	0.31373	---CCAATATT-
ACCGGTAG	0.31128	CTACGGGT----
AGTAGCAT	0.31051	AGTAGCAT----
GTCACTTA	0.30783	---GTCACCTA--
ACACCCCT	0.30506	ACACCCCT----
AATTGCTG	0.29906	-----CAGCAATT
CGCATGAA	0.29839	---CGCATGAA--

Top 10

Scores

Alignment

CTCATGAG	6.00830	--CTCATGAG----
CTTCGGAA	4.74249	--TTCCGAAG----
CAAAAGGA	4.69746	-----CAAAAGGA--
AATTAGCC	4.67654	-----GGCTAATT
ACCAACTA	4.49802	----TAGTTGGT---
AATATTGG	4.43352	---AATATTGG----
CCTGGGCG	4.32307	CGCCAGG-----
CAACAACC	4.16905	-----GGTTGTTG--
CAGGGGTC	4.14839	----CAGGGGTC---
AGGGGTCC	4.11714	----AGGGGTCC---

Top scoring motifs for Assay 13861

Protein ID: pTH14267.1 Gene: MTERF2.FL Domain: mTERF Flag: Reject Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:

Reverse:

A G A C A A

T T G C T C T

Forward:

Reverse:

T A A C S T A C

G T A C C T A A

Top 10

Scores

Alignment

AAACTTAT	0.37245	AAACTTAT----
ATGCGCGC	0.35595	---GCGCGCAT-
GCGAACAA	0.33569	---GCGAACAA-
CGATACGA	0.33083	----CGATACGA
TTAGCTAA	0.31901	----TTAGCTAA
GCCCTTAA	0.30129	-TTAAGGGC---
ACCGAGCA	0.30036	--ACCGAGCA--
GTACTCAA	0.29800	---TTGAGTAC-
ACGAGGCC	0.29524	---ACGAGGCC--
CATGATAA	0.29469	-----TTATCATG

Top 10

Scores

Alignment

AAACTTAT	5.54689	---AAACTTAT---
GCCCTTAA	4.48940	---TTAAGGGC---
AACGGCTA	4.33806	-----AACGGCTA--
ATTAGCTA	4.30265	----ATTAGCTA--
CCGCTCAA	4.18952	---TTGAGCGG---
AGCATGCG	4.01414	-----CGCATGCT
GAACAAGA	3.99308	---GAACAAGA---
CGTTTCAA	3.90977	TTGAAACG-----
ACGAGCA	3.85479	-----ACGAGCA--
AATTCTAC	3.84324	-----AATTCTAC-