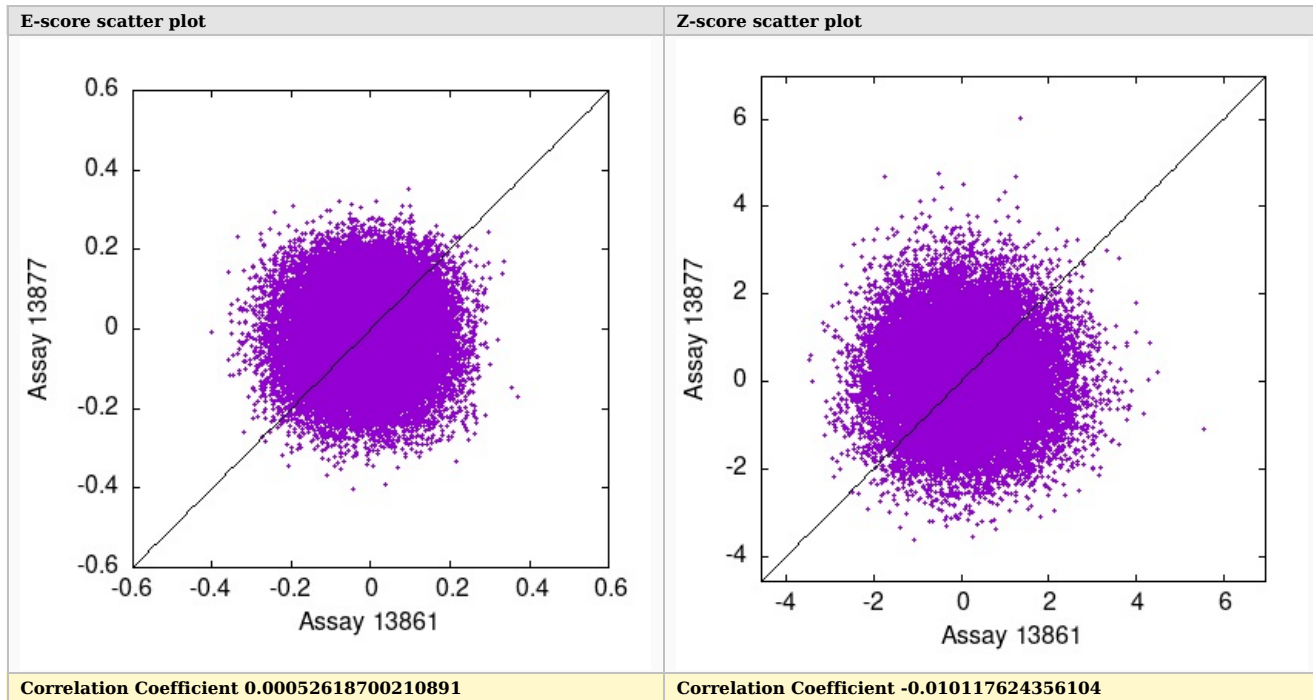


## QC report



### 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:



#### 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--
GTAACCAA	0.29800	---TTGAGTAC--
ACGGAGCC	0.29524	--ACGGAGCC--
CATGATAA	0.29469	----TTATCATG

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

Forward:

Reverse:



#### 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-----
ACCGAGCA	3.85479	----ACCGAGCA--
AATTCTAC	3.84324	----AATTCTAC--

### 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:



#### Top 10

#### Scores

#### Alignment

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

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

Forward:

Reverse:



#### 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	CGCCCAAG-----
CAACAACC	4.16905	-----GGTTGTTG--
CAGGGGTC	4.14839	----CAGGGGTC---
AGGGGTCC	4.11714	-----AGGGGTCC--