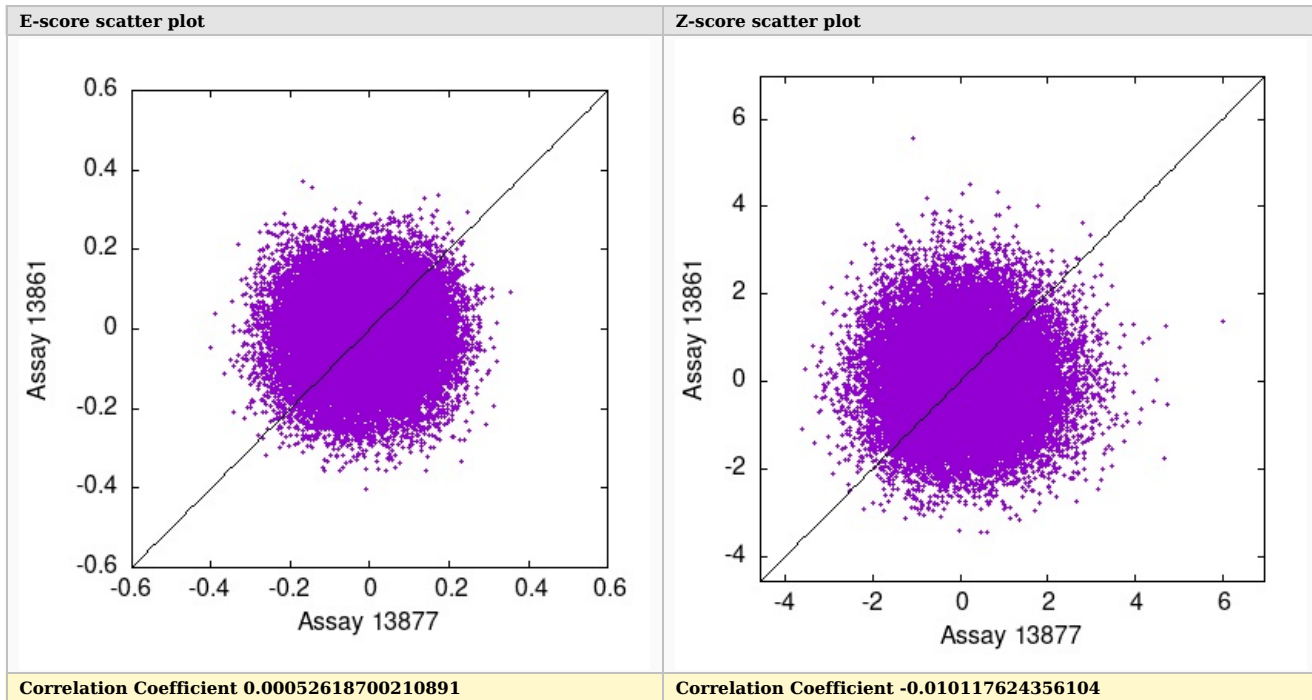


## QC report



### 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'			8 mer Z-scores for probeset 'all'		
Forward:		Reverse:	Forward:		Reverse:
Top 10	Scores	Alignment	Top 10	Scores	Alignment
CTCATGAG	0.35356	---CTCATGAG--	CTCATGAG	6.00830	--CTCATGAG----
CTTCGGAA	0.32218	---CTTCGGAA--	CTTCGGAA	4.74249	--TTCCGAAG----
CATCTTGC	0.32214	---GCAAGATG-	CAAAAGGA	4.69746	----CAAAAGGA--
AATATTGG	0.31373	---CCAATATT--	AATTAGCC	4.67654	-----GGCTAATT
ACCCGTAG	0.31128	CTACGGGT-----	ACCAACTA	4.49802	----TAGTTGGT---
AGTAGCAT	0.31051	AGTAGCAT-----	AATATTGG	4.43352	---AATATTGG----
GTCACCTA	0.30783	---GTCACCTA--	CCTGGGCG	4.32307	CGCCAGG-----
ACACCCCT	0.30506	ACACCCCT-----	CAACAACC	4.16905	-----GGTTGTTG--
AATTGCTG	0.29906	-----CAGCAATT	CAGGGGTC	4.14839	----CAGGGGTC---
CGCATGAA	0.29839	---CGCATGAA--	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'			8 mer Z-scores for probeset 'all'		
Forward:		Reverse:	Forward:		Reverse:
Top 10	Scores	Alignment	Top 10	Scores	Alignment
AAACTTAT	0.37245	AAACTTAT----	AAACTTAT	5.54689	---AAACTTAT---
ATGCGCGC	0.35595	---GCGCGCAT-	GCCCTTAA	4.48940	---TTAAGGGC----
GCGAACAA	0.33569	---GCGAACAA-	AACGGCTA	4.33806	-----AACGGCTA--
CGATACGA	0.33083	----CGATACGA	ATTAGCTA	4.30265	----ATTAGCTA--
TTAGCTAA	0.31901	----TTAGCTAA	CCGCTCAA	4.18952	-TTGAGCGG-----
GCCCTTAA	0.30129	-TTAAGGGC---	AGCATGCG	4.01414	-----CGCATGCT
ACCGAGCA	0.30036	--ACCGAGCA--	GAACAAGA	3.99308	---GAACAAGA---
GTAACCTA	0.29800	---TTGAGTAC-	CGTTTCAA	3.90977	TTGAAACG-----
ACGGAGCC	0.29524	---ACGGAGCC--	ACCGAGCA	3.85479	----ACCGAGCA--
CATGATAA	0.29469	-----TTATCATG	AATTCTAC	3.84324	-----AATTCTAC-