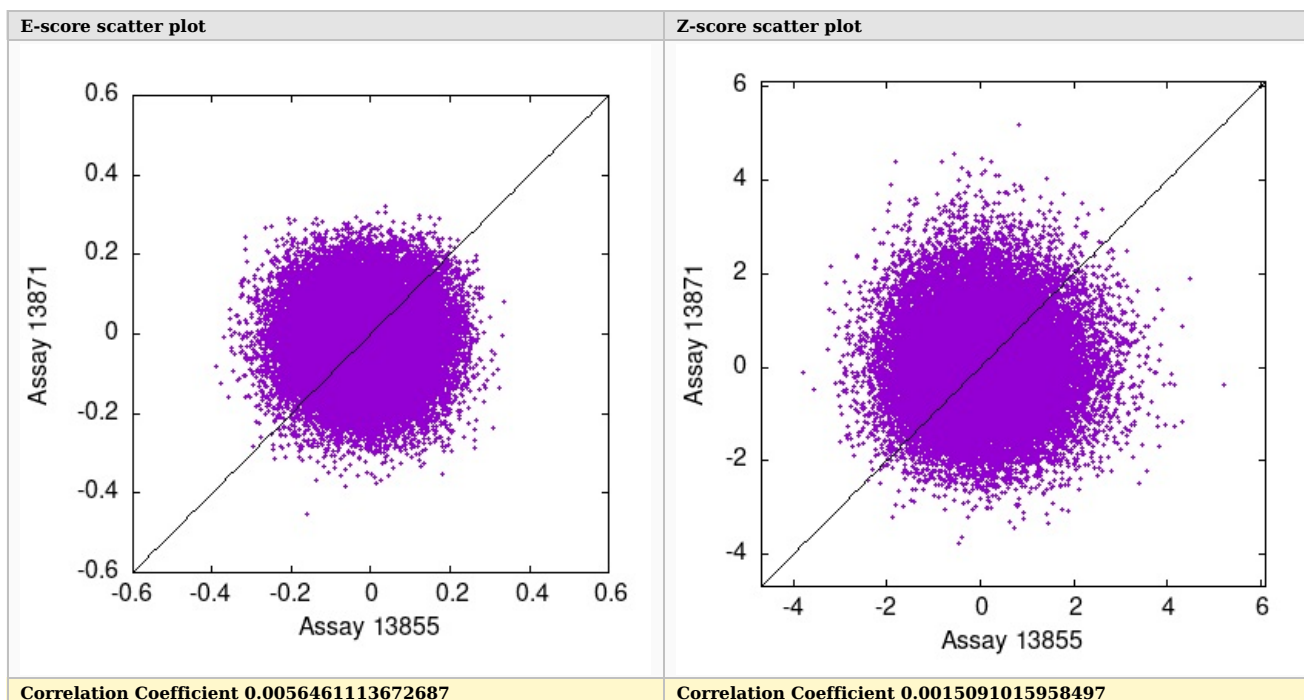


## QC report





Correlation Coefficient 0.0056461113672687

Correlation Coefficient 0.0015091015958497



### Top scoring motifs for Assay 13855

Protein ID: pTH14258.1 Gene: MSANTD1.FL Domain: MADF\_DNA\_bdg Flag: Reject Array: 1M-ME

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

Forward:		Reverse:	
			
Top 10	Scores	Alignment	
ACTCACTC	0.33591	---GAGTGAGT---	
CACTGTAG	0.33052	CTACAGTG-----	
GCCGAAGC	0.32242	-----GCCGAAGC	
TAACGTTA	0.31983	---TAACGTTA---	
TAGTGCCA	0.31238	---TAGTGCCA---	
CACCGGTG	0.30894	CACCGGTG-----	
GAGCCTGA	0.30735	-----GAGCCTGA--	
AGTCGCAC	0.30599	-----GTGCGACT--	
GGGACAAA	0.30583	--TTTGTCCC-----	
ACCCCCAC	0.30060	----ACCCCCAC---	



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

Forward:		Reverse:	
			
Top 10	Scores	Alignment	
TAACGTTA	5.20605	----TAACGTTA--	
AGCAAATG	4.47924	-AGCAAATG-----	
AGTCGCAC	4.33962	----AGTCGCAC--	
CACTGTAG	4.33779	-----CACTGTAG--	
ACGTTACC	4.14639	-----ACGTTACC	
ACTAGGTG	4.14349	--ACTAGGTG----	
GAGCCTGA	4.07933	----GAGCCTGA--	
TCCGATCA	4.06543	----TCCGATCA--	
GCACTAAC	3.95331	GCACCTAAC-----	
ATCGGCAT	3.92000	----ATCGGCAT--	



### Top scoring motifs for Assay 13871

Protein ID: pTH14258.2 Gene: MSANTD1.FL Domain: MADF\_DNA\_bdg Flag: Reject Array: 1M-HK

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

Forward:	Reverse:	
		
Top 10	Scores	Alignment
CCAAGAAC	0.32148	----GTTCTTGG-
GCGTTGAC	0.30552	---GCGTTGAC---
CATCATGG	0.30498	----CATCATGG-
CTAATGCA	0.29686	--TGCATTAG----
TCCGTTCA	0.29502	--TCCGTTCA----
AACATGAG	0.29319	-----CTCATGTT
AGTGGATA	0.29101	TATCCACT-----
GACGCCCA	0.29029	--GACGCCCA----
CCCATTC	0.28943	--CCCATTC-----
ATCTTTTA	0.28941	--ATCTTTTA----

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

Forward:		Reverse:
		
Top 10	Scores	Alignment
TTTTAAAA	5.19027	-TTTTAAAA--
ATGAGTGC	4.56811	--ATGAGTGC--
CGCCGGTA	4.47119	---TACCGGCG-
GAGGGGCC	4.39753	----GAGGGGCC
CTCCAGC	4.39642	-GCTGGGAG---
GGTAATCA	4.37870	---TGATTACC-
CTACGTAG	4.26867	--CTACGTAG--
CACGCAAG	4.20941	-CTTGCGTG---
ACCTTACT	4.17045	ACCTTACT----
CCCAATCC	4.13242	--GGATTGGG-