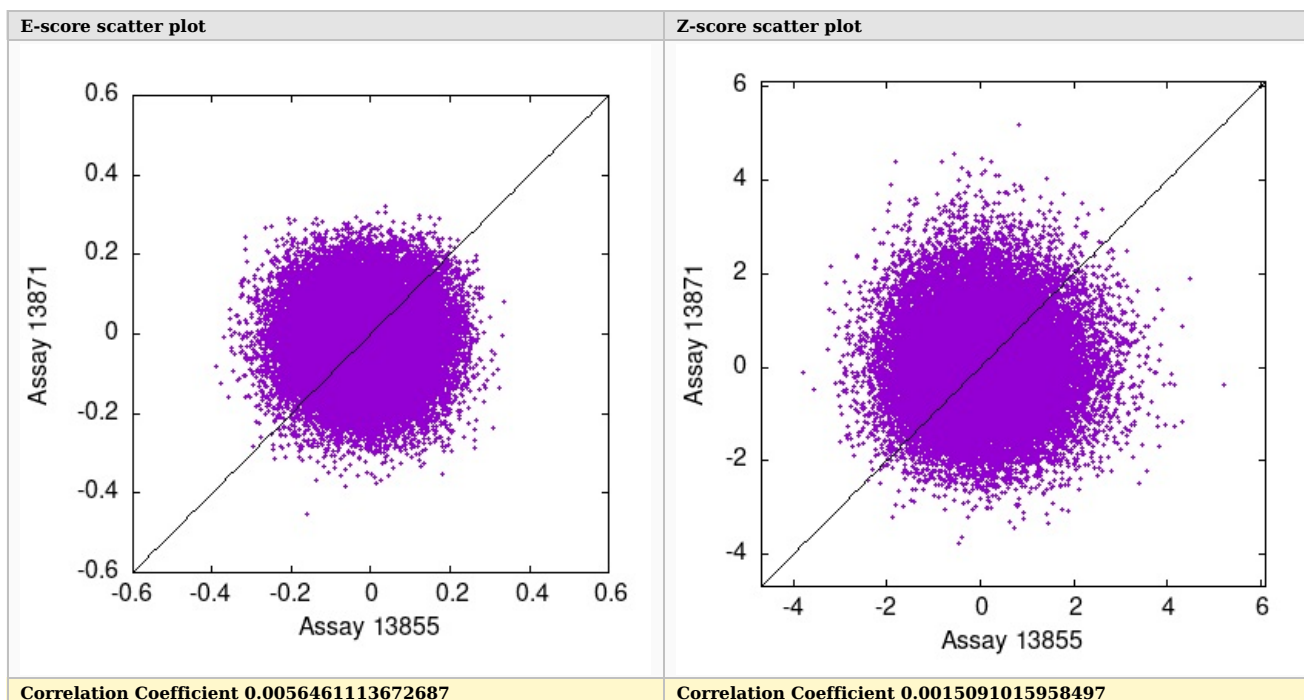


## QC report



### 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'			8 mer Z-scores for probeset 'all'		
Forward:	Reverse:		Forward:	Reverse:	
Top 10	Scores	Alignment	Top 10	Scores	Alignment
ACTCACTC	0.33591	---GAGTGAGT---	TAACGTTA	5.20605	----TAACGTTA--
CACTGTAG	0.33052	CTACAGTG-----	AGCAAATG	4.47924	-AGCAAATG-----
GCCGAAGC	0.32242	-----GCCGAAGC	AGTCGCAC	4.33962	----AGTCGCAC--
TAACGTTA	0.31983	---TAACGTTA---	CACTGTAG	4.33779	-----CACTGTAG--
TAGTGCCA	0.31238	---TAGTGCCA---	ACGTTACC	4.14639	-----ACGTTACC
CACCGGTG	0.30894	CACCGGTG-----	ACTAGGTG	4.14349	--ACTAGGTG----
GAGCCTGA	0.30735	-----GAGCCTGA--	GAGCCTGA	4.07933	----GAGCCTGA--
AGTCGCAC	0.30599	-----GTGCGACT--	TCCGATCA	4.06543	----TCCGATCA--
GGGACAAA	0.30583	--TTTGTCCC-----	GCACTAAC	3.95331	GCACCTAAC-----
ACCCACAC	0.30060	----ACCCACAC---	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'			8 mer Z-scores for probeset 'all'		
Forward:	Reverse:		Forward:	Reverse:	
Top 10	Scores	Alignment	Top 10	Scores	Alignment
CCAAGAAC	0.32148	-----GTTCTTGG-	TTTTAAAA	5.19027	-TTTTAAAA---
GCGTTGAC	0.30552	---GCGTTGAC---	ATGAGTGC	4.56811	--ATGAGTGC--
CATCATGG	0.30498	-----CATCATGG-	CGCCGGTA	4.47119	---TACCGGCG-
CTAATGCA	0.29686	--TGCATTAG----	GAGGGGCC	4.39753	----GAGGGGCC
TCCGTTCA	0.29502	--TCCGTTCA----	CTCCAGC	4.39642	-GCTGGGAG---
AACATGAG	0.29319	-----CTCATGTT	GGTAATCA	4.37870	---TGATTACC-
AGTGGATA	0.29101	TATCCACT-----	CTACGTAG	4.26867	--CTACGTAG--
GACGCCCA	0.29029	--GACGCCCA----	CACGCAAG	4.20941	-CTTGCGTG---
CCCATTC	0.28943	--CCCATTC-----	ACCTTACT	4.17045	ACCTTACT----
ATCTTTTA	0.28941	--ATCTTTTA----	CCCAATCC	4.13242	--GGATTGGG-