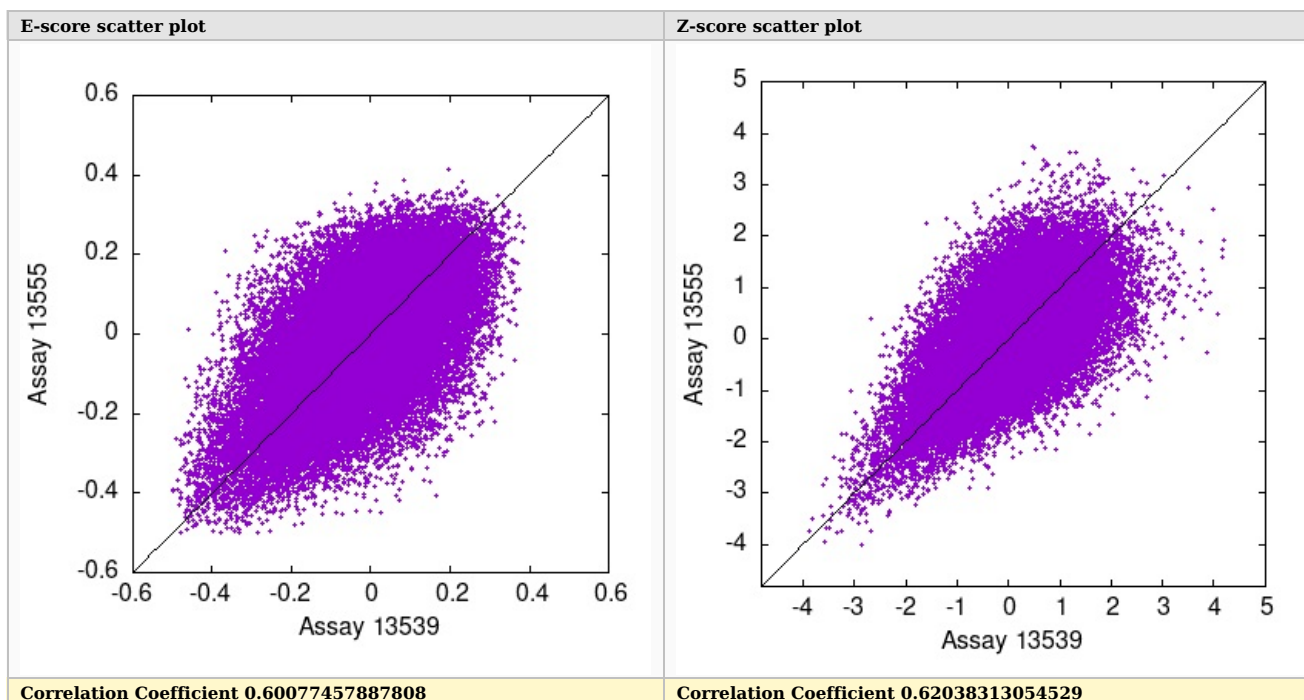




## QC report





### Top scoring motifs for Assay 13539

Protein ID: pTH14219.1 Gene: CAMTA2.DBD Domain: CG-1 Flag: Reject Array: 1M-ME

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

Forward:	Reverse:	
		
Top 10	Scores	Alignment
ATAATATA	0.38635	-ATAATATA-
ATGTATAA	0.38060	--TTATACAT
ATGGTTTA	0.37642	-ATGGTTTA-
AGTGATAG	0.37475	AGTGATAG--
TGGTGTA	0.37400	--TGGTGTA
AAATTATT	0.36911	AATAATTT--
TAAGTACA	0.36594	-TAAGTACA-
CAGAAACA	0.36561	-CAGAAACA-
ATGTTAAT	0.36530	ATTAACAT--
CGTAATAA	0.36298	CGTAATAA--



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

Forward:		Reverse:
		
Top 10	Scores	Alignment
TGGTGTA	4.18931	-TGGTGTA--
ATAATATA	4.17946	ATAATATA---
ATGTATAA	4.16737	--TTATACAT--
ATACAGCA	4.06579	---ATACAGCA
ATGGTTTA	3.99983	ATGGTTTA---
ATTATATA	3.93116	ATTATATA---
ACAATATG	3.86884	ACAATATG---
TACCAAAA	3.82627	TTTTGGTA---
AATATACT	3.80669	AGTATATT---
ATTCGTTA	3.77601	ATTCGTTA---



### Top scoring motifs for Assay 13555

Protein ID: pTH14219.2 Gene: CAMTA2.DBD Domain: CG-1 Flag: Reject Array: 1M-HK

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

Forward:	Reverse:	
		
Top 10	Scores	Alignment
GATATGTA	0.41484	-- -TACATATC
ACCACTAA	0.38708	-ACCACTAA--
ATAGTAAT	0.38435	-ATTACTAT--
CACCACTA	0.37818	CACCACTA---
AACACTTA	0.36598	---AACACTTA-
CAATATAG	0.36101	---CAATATAG
CTGTATTA	0.36101	---CTGTATTA
ATATACAA	0.35935	-ATATACAA--
TACACACA	0.35540	-TACACACA--
GTAAGTGA	0.35524	--TCAGTTAC-

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

Forward:	Reverse:	
		
Top 10	Scores	Alignment
TATTTGCA	3.73745	---TGCAAATA--
TACACACA	3.71197	---TACACACA--
GATATGTA	3.61894	---TACATATC--
GAAATTTT	3.61853	-----GAAATTTT
CACAAATA	3.49324	---CACAAATA--
ATATCACA	3.47078	ATATCACA-----
CAATATAG	3.43381	-----CAATATAG-
CACCACTA	3.41443	---CACCACTA--
GTAAGTGA	3.40303	-----GTAAGTGA-
GTAAGTGA	3.39198	-----TCAGTTAC-