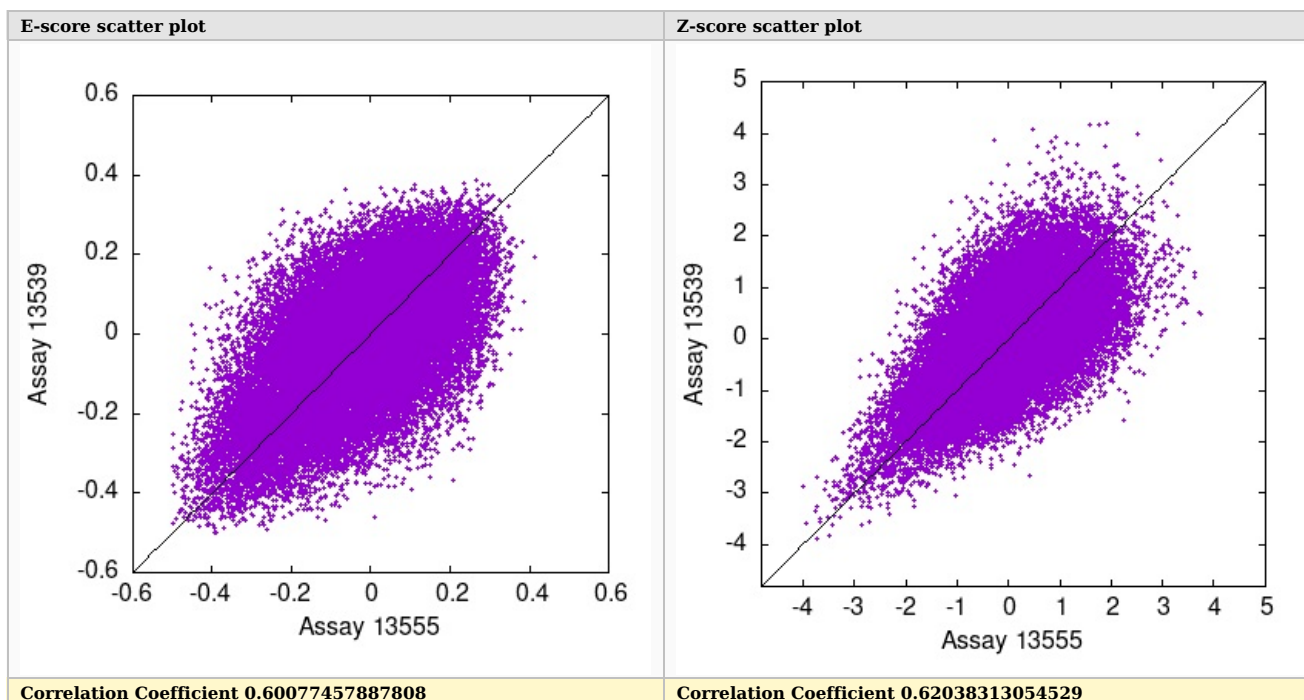


QC report



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'			8 mer Z-scores for probeset 'all'		
Forward:	Reverse:		Forward:	Reverse:	
Top 10	Scores	Alignment	Top 10	Scores	Alignment
GATATGTA	0.41484	---TACATATC	TATTTGCA	3.73745	----TGCAAATA--
ACCACTAA	0.38708	-ACCACTAA--	TACACACA	3.71197	----TACACACA--
ATAGTAAT	0.38435	-ATTACTAT--	GATATGTA	3.61894	----TACATATC--
CACCACTA	0.37818	CACCACTA--	GAAATTTT	3.61853	-----GAAATTTT
AACACTTA	0.36598	-AACACTTA--	CACAAATA	3.49324	----CACAAATA--
CAATATAG	0.36101	---CAATATAG	ATATCACA	3.47078	ATATCACA-----
CTGTATTA	0.36101	---CTGTATTA	CAATATAG	3.43381	-----CAATATAG
ATATACAA	0.35935	-ATATACAA--	CACCACTA	3.41443	----CACCACTA--
TACACACA	0.35540	-TACACACA--	GTAATGTA	3.40303	-----GTAATGTA
GTAAGTGA	0.35524	--TCAGTTAC-	GTAAGTGA	3.39198	-----TCAGTTAC-

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'			8 mer Z-scores for probeset 'all'		
Forward:	Reverse:		Forward:	Reverse:	
Top 10	Scores	Alignment	Top 10	Scores	Alignment
ATAATATA	0.38635	-ATAATATA-	TGGTGTA	4.18931	-TGGTGTA--
ATGTATA	0.38060	--TTATACAT	ATAATATA	4.17946	ATAATATA---
ATGGTTTA	0.37642	-ATGGTTTA-	ATGTATA	4.16737	-TTATACAT--
AGTGATAG	0.37475	AGTGATAG--	ATACAGCA	4.06579	---ATACAGCA
TGGTGTA	0.37400	--TGGTGTA	ATGGTTTA	3.99983	ATGGTTTA---
AAATTATT	0.36911	AATAATTT--	ATTATATA	3.93116	ATTATATA---
TAAGTACA	0.36594	-TAAGTACA-	ACAATATG	3.86884	ACAATATG---
CAGAAACA	0.36561	-CAGAAACA-	TACCAAAA	3.82627	TTTTGGTA---
ATGTTAAT	0.36530	ATTAACAT--	AATATACT	3.80669	AGTATATT---
CGTAATAA	0.36298	CGTAATAA--	ATTCTGTA	3.77601	ATTCTGTA---