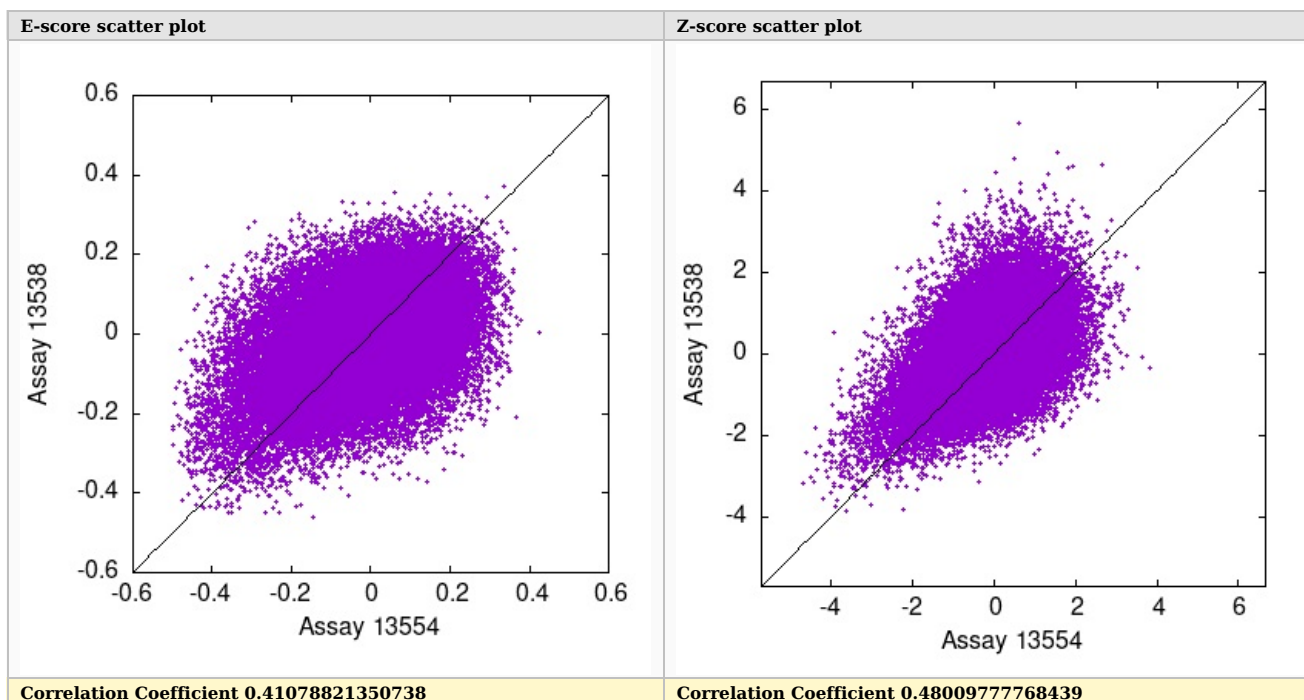




QC report





Top scoring motifs for Assay 13554

Protein ID: pTH14218.2 Gene: CAMTA1.DBD Domain: CG-1 Flag: Reject Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:		Reverse:	
			
Top 10	Scores	Alignment	
GATATGTA	0.42354	GATATGTA- --	
CATTATAG	0.37702	CATTATAG- --	
AACACAAT	0.37151	- ATTGTGTT- -	
CGTAACAA	0.36846	- - TTGTTACG-	
ATATCACA	0.36817	- - ATATCACA-	
TCTCGAGA	0.36273	- - TCTCGAGA-	
ATTATTAC	0.36095	- ATTATTAC- -	
CATTACAA	0.35958	- - - CATTACAA	
GAATATTC	0.35811	GAATATTC- - -	
GTAACAAA	0.35469	- TTTGTTCAC- -	



8 mer Z-scores for probeset 'all'

Forward:		Reverse:
		
Top 10	Scores	Alignment
ATTATAAT	3.84405	-ATTATAAT---
GATATGTA	3.63652	GATATGTA----
GAATATTC	3.50837	GAATATTC----
ACTATTTC	3.31800	-ACTATTTC---
GAATTGTA	3.26066	GAATTGTA----
ATTATTAC	3.20627	-ATTATTAC---
ATTACGGA	3.17087	----ATTACGGA
CATAACAC	3.17018	--GTGTTATG--
ATATCACA	3.15348	--ATATCACA---
ATTACAAC	3.14635	-ATTACAAC---

Top scoring motifs for Assay 13538

Protein ID: pTH14218.1 Gene: CAMTA1.DBD Domain: CG-1 Flag: Reject Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:		Reverse:
		
Top 10	Scores	Alignment
TATACAAA	0.37200	-TTTGTATA-
GAGTGCTA	0.35570	-GAGTGCTA-
CCAACAAA	0.35350	-TTTGTGG-
TACTATAA	0.35267	--TACTATAA
GTTGGTTA	0.34444	-GTTGGTTA-
CATCTTAA	0.33184	-CATCTTAA-
AACGAATT	0.33176	AATTCGTT--
ACTGCATA	0.32933	-ACTGCATA-
ACCGGTTA	0.32779	-ACCGGTTA-
CACGGTCA	0.32776	-CACGGTCA-

8 mer Z-scores for probeset 'all'

Forward:		Reverse:
Top 10	Scores	Alignment
ATATACCG	5.63382	ATATACCG----
CCAACAAA	4.91594	--CCAACAAA---
AATTGCGT	4.76352	--ACGCAATT--
TATACAAA	4.64763	-TATACAAA----
ATCGCGAT	4.60320	--ATCGCGAT--
ATATAGTA	4.55364	ATATAGTA----
ATCACTCA	4.42694	-ATCACTCA---
ACAAAACA	4.39723	----ACAAAACA
ACACCAGA	4.16468	--ACACCAGA--
TACTATAA	4.15156	TTATAGTA----