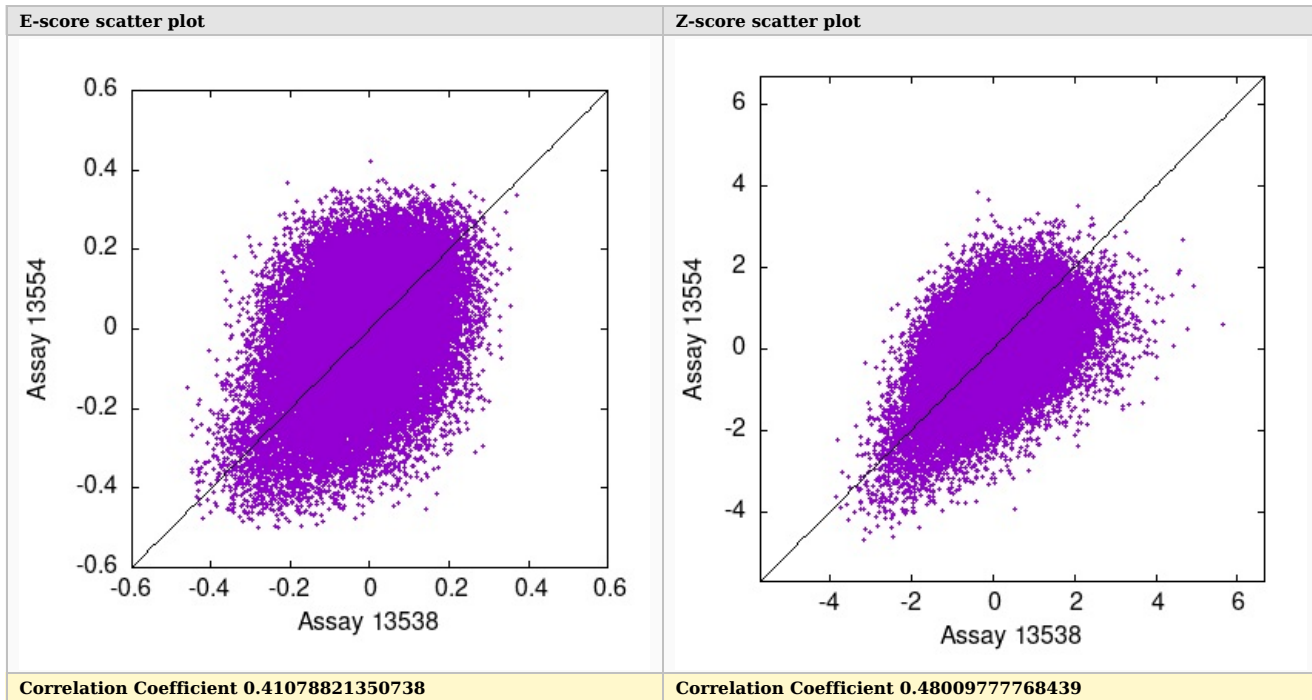


## QC report



### 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'			8 mer Z-scores for probeset 'all'		
Forward:		Reverse:	Forward:		Reverse:
Top 10	Scores	Alignment	Top 10	Scores	Alignment
TATACAAA	0.37200	-TTTGTATA-	ATATACCG	5.63382	ATATACCG----
GAGTGCTA	0.35570	-GAGTGCTA-	CCAACAAA	4.91594	-CCAACAAA---
CCAACAAA	0.35350	--TTTGTGG	AATTGCGT	4.76352	--ACGCAATT--
TACTATAA	0.35267	--TACTATAA	TATACAAA	4.64763	-TATACAAA---
GTTGGTTA	0.34444	-GTTGGTTA-	ATCGCGAT	4.60320	--ATCGCGAT--
CATCTTAA	0.33184	-CATCTTAA-	ATATAGTA	4.55364	ATATAGTA----
AACGAATT	0.33176	AATTGCTT--	ATCACTCA	4.42694	-ATCACTCA---
ACTGCATA	0.32933	-ACTGCATA-	ACAAAACA	4.39723	----ACAAAACA
ACCGGTTA	0.32779	-ACCGGTTA-	ACACCAGA	4.16468	--ACACCAGA--
CACGGTCA	0.32776	-CACGGTCA-	TACTATAA	4.15156	TTATAGTA----

### 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'			8 mer Z-scores for probeset 'all'		
Forward:		Reverse:	Forward:		Reverse:
Top 10	Scores	Alignment	Top 10	Scores	Alignment
GATATGTA	0.42354	GATATGTA---	ATTATAAT	3.84405	-ATTATAAT---
CATTATAG	0.37702	CATTATAG---	GATATGTA	3.63652	GATATGTA----
AACACAAT	0.37151	-ATTGTGTT--	GAATATTC	3.50837	GAATATTC----
CGTAACAA	0.36846	--TTGTTACG-	ACTATTTG	3.31800	-ACTATTTG---
ATATCACA	0.36817	--ATATCACA-	GAATTGTA	3.26066	GAATTGTA----
TCTCGAGA	0.36273	--TCTCGAGA-	ATTATTAC	3.20627	-ATTATTAC---
ATTATTAC	0.36095	-ATTATTAC--	ATTACGGA	3.17087	----ATTACGGA
CATTACAA	0.35958	---CATTACAA	CATAACAC	3.17018	--GTGTTATG--
GAATATTC	0.35811	GAATATTC---	ATATCACA	3.15348	--ATATCACA--
GTAACAAA	0.35469	-TTTGTTCAC--	ATTACAAC	3.14635	-ATTACAAC---