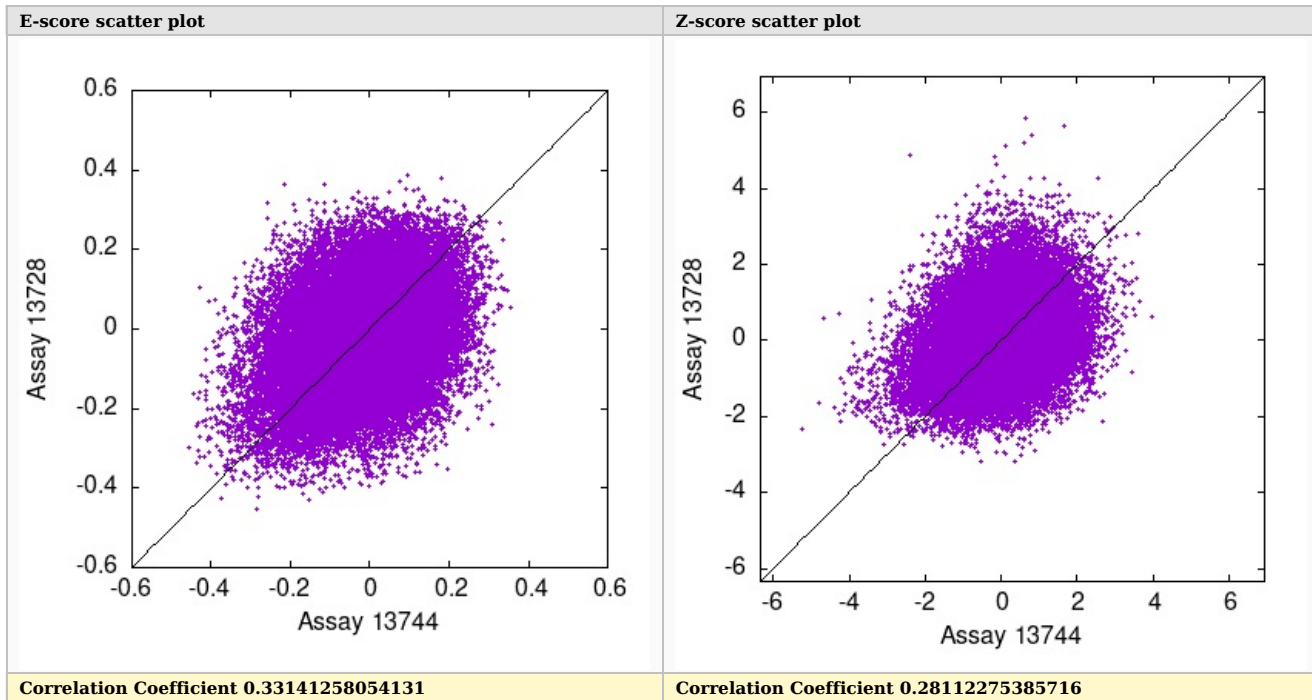


## QC report



### Top scoring motifs for Assay 13744

Protein ID: pTH14312.2 Gene: PCGF2.FL Domain: Unknown 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
GTACAGCA	0.35726	---GTACAGCA----	TATTACGA	3.97584	---TATTACGA----
ACAGTGAT	0.34927	----ACAGTGAT---	ATAATTAT	3.64127	-ATAATTAT-----
GTTATGCA	0.33841	----TGCATAAC----	AAAAAATA	3.61882	AAAAAATA-----
AGTACTAA	0.33783	-----TTAGTACT	GTTATGCA	3.55793	----GTTATGCA---
ACATTAGT	0.33516	----ACATTAGT---	AGTACTAA	3.51377	----AGTACTAA---
ATTAACAA	0.33279	-----ATTAACAA-	GCTATAGC	3.50417	-GCTATAGC-----
AAATTACG	0.33163	----AAATTACG---	AAATTACG	3.45415	---AAATTACG----
TATTACGA	0.33109	-----TATTACGA--	ACGCGTTG	3.45338	-----ACGCGTTG
AGAATTCT	0.32906	----AGAATTCT---	ACGACACT	3.44738	---AGTGTGCT----
TATCGACA	0.32619	TATCGACA-----	ACATTAGT	3.43470	--ACATTAGT-----

### Top scoring motifs for Assay 13728

Protein ID: pTH14312.1 Gene: PCGF2.FL Domain: Unknown 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
AAGACTAG	0.38526	---AAGACTAG	ATGTGAAG	5.83827	--ATGTGAAG-
CATAAAAC	0.38063	-CATAAAAC--	CATAAAAC	5.66696	---CATAAAAC
ACACATAC	0.37331	ACACATAC---	ACACATAC	5.42345	--ACACATAC-
TGTATACA	0.36503	-TGTATACA--	AAGACTAG	5.21524	--AAGACTAG-
CTTATACA	0.36211	-CTTATACA--	TATACAGA	5.11233	---TATACAGA
AACATGCA	0.35384	-AACATGCA--	TACATGTA	4.87779	-TACATGTA--
CAATAGTG	0.35294	--CAATAGTG-	TTACGTAA	4.83432	--TTACGTAA-
TTACGTAA	0.35102	--TTACGTAA-	CAATAGTG	4.64027	CAATAGTG---
GTACTATA	0.34742	---TATAGTAC	ATATTAA	4.32117	--ATATTAA--
ATGTGAAG	0.34366	--CTTCACAT-	GTACTATA	4.27729	---TATAGTAC