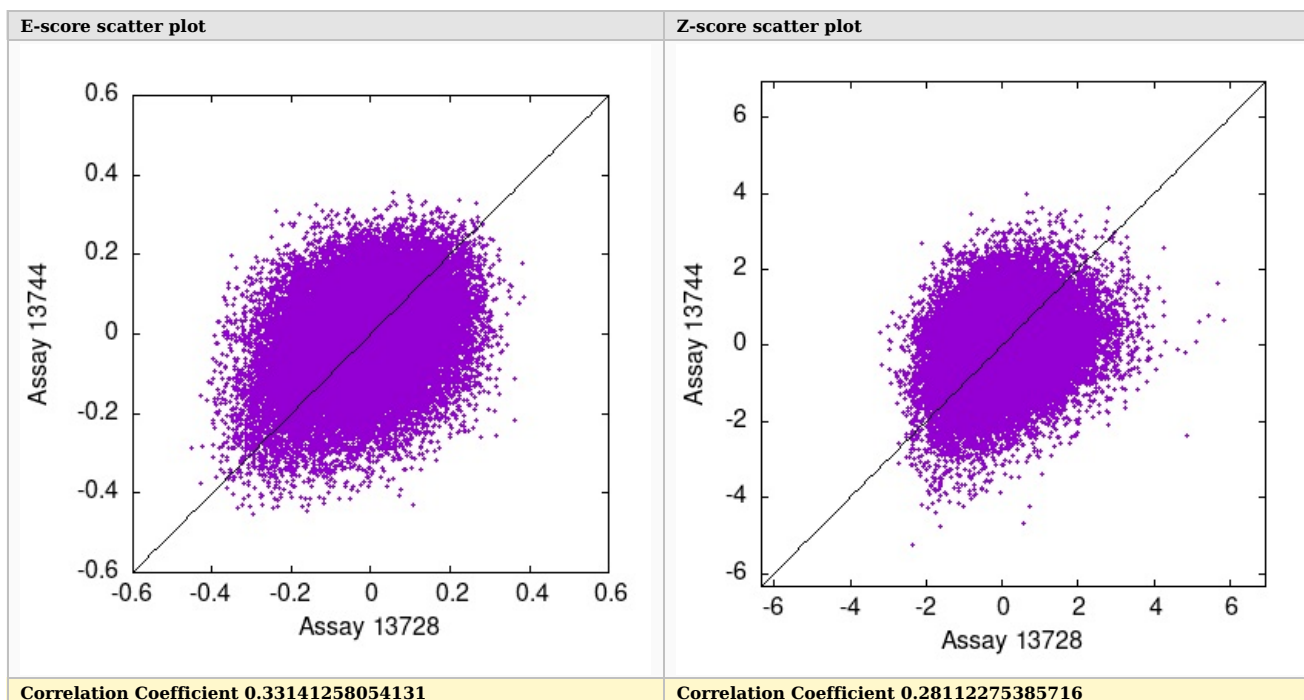




## QC report



### 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'

Forward:		Reverse:	
			
Top 10	Scores	Alignment	
AAGACTAG	0.38526	--	-AAGACTAG
CATAAAAC	0.38063	-	-CATAAAAC--
ACACATAC	0.37331		ACACATAC--
TGTATACA	0.36503	-	-TGTATACA--
CTTATACA	0.36211	-	-CTTATACA--
AACATGCA	0.35384		-AACATGCA--
CAATAGTG	0.35294	--	-CAATAGTG-
TTACGTAA	0.35102	--	-TTACGTAA-
GTACTATA	0.34742	---	-TATAGTAC
ATGTGAAG	0.34366	--	-CTTCACAT-

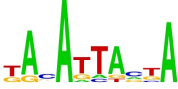

#### 8 mer Z-scores for probeset 'all'

Forward:		Reverse:	
Top 10	Scores	Alignment	
ATGTGAAG	5.83827	--	ATGTGAAG--
CATAAAAC	5.66696	---	CATAAAAC
ACACATAC	5.42345	--	ACACATAC--
AAGACTAG	5.21524	--	AAGACTAG--
TATACAGA	5.11233	---	TATACAGA
TACATGTA	4.87779	-	TACATGTA--
TTACGTAA	4.83432	--	TTACGTAA--
CAATAGTG	4.64027	CAATAGTG	---
ATATTTAA	4.32117	--	ATATTTAA--
GTACTATA	4.27729	---	TATAGTAC



### 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'

Forward:	Reverse:	
		
Top 10	Scores	Alignment
GTACAGCA	0.35726	--GTACAGCA----
ACAGTGAT	0.34927	-----ACAGTGAT---
GTTATGCA	0.33841	-----TGCATAAC----
AGTACTAA	0.33783	-----TTAGTACT----
ACATTAGT	0.33516	-----ACATTAGT----
ATTAACAA	0.33279	-----ATTAACAA----
AAATTACG	0.33163	-----AAATTACG----
TATTACGA	0.33109	-----TATTACGA----
AGAATTCT	0.32906	-----AGAATTCT----
TATCGACA	0.32619	TATCGACA-----

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

Forward:		Reverse:
		
Top 10	Scores	Alignment
TATTACGA	3.97584	---TATTACGA---
ATAATTAT	3.64127	-ATAATTAT-----
AAAAAATA	3.61882	AAAAAATA-----
GTTATGCA	3.55793	---GTTATGCA---
AGTACTAA	3.51377	---AGTACTAA---
GCTATAGC	3.50417	-GCTATAGC-----
AAATTACG	3.45415	--AAATTACG-----
ACGCGTTG	3.45338	-----ACGCGTTG---
ACGACACT	3.44738	---AGTGTCTG-----
ACATTAGT	3.43470	--ACATTAGT-----