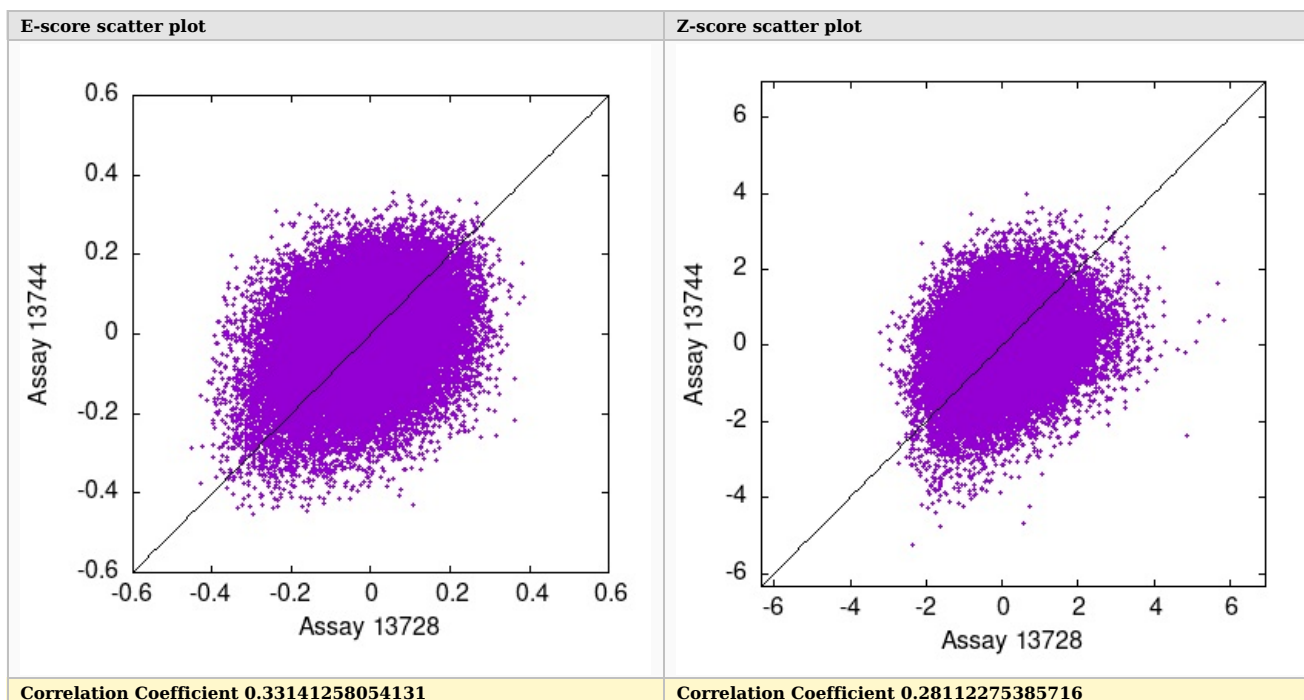


QC report



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---
ATATTAA	4.32117	--ATATTAA--
GTACTATA	4.27729	---TATAGTAC

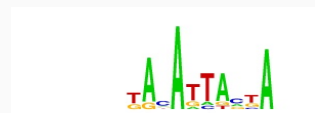
Top scoring motifs for Assay 13744

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-----