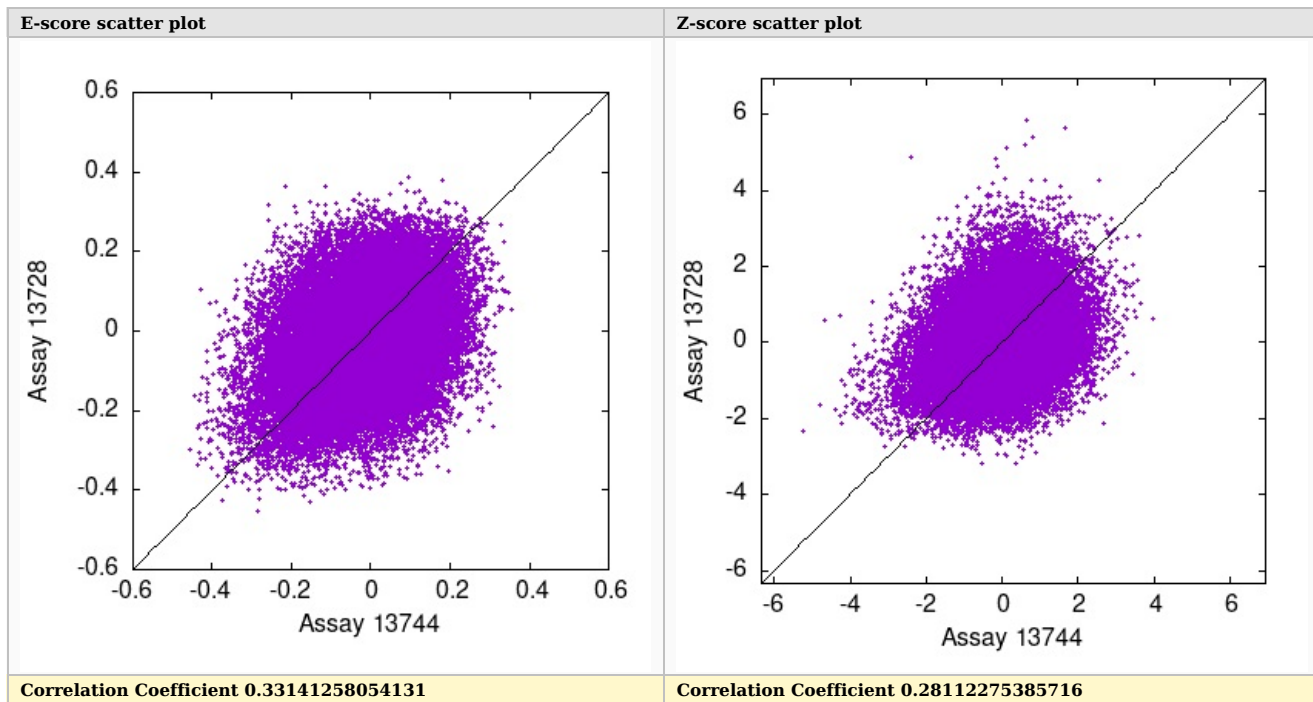


QC report



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'

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-----

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-

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