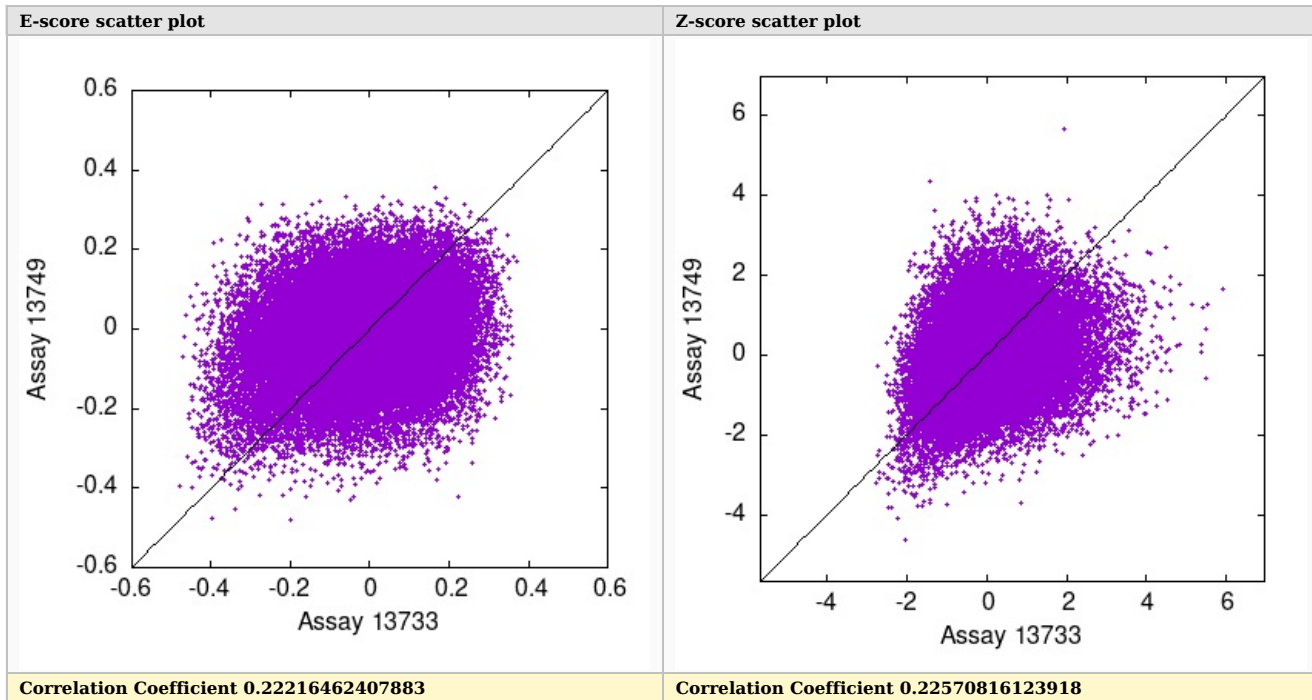


QC report



Top scoring motifs for Assay 13733

Protein ID: pTH14320.1 Gene: PURG.FL Domain: Unknown Flag: Reject Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

TAACGAAA	0.37126	-TTTCGTTA-
GTACTTTA	0.36372	-GTACTTTA-
AGACGAAA	0.35974	--TTTCGTCT
ATATTTTA	0.35903	-ATATTTTA-
AAGAGATA	0.35712	TATCTCTT--
ATAATGCA	0.35451	-ATAATGCA-
AAGATATA	0.35386	TATATCTT--
GTATAATA	0.35329	--TATTATAC
ATAAATAA	0.35181	-ATAAATAA-
AATAATAA	0.35137	-TTATTATT-

8 mer Z-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

TACATACA	5.89974	--TGTATGTA--
TATGTGAA	5.51919	--TATGTGAA--
AGACGAAA	5.48783	---AGACGAAA-
AATGAATC	5.47210	----AATGAATC
AATCAGTA	5.39950	---TACTGATT-
ATATTTTA	5.36470	-ATATTTTA---
GAATAATA	5.36008	----TATTATTC
CATTGATA	5.12459	TATCAATG----
ATATATGA	4.84249	-ATATATGA---
AAGCAGAA	4.81645	---TTCTGCTT-

Top scoring motifs for Assay 13749

Protein ID: pTH14320.2 Gene: PURG.FL Domain: Unknown Flag: Reject Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

GTAACATA	0.35733	---GTAACATA--
ATGCTTAC	0.33331	----ATGCTTAC-
GGTATACA	0.33262	-----TGTATACC
TCAATTGA	0.33066	TCAATTGA-----
CCTCGGCG	0.32218	--CCTCGGCG---
ACCTACGT	0.32024	--ACCTACGT---
ACTTGCAT	0.31571	--ACTTGCAT---
GTTCGAAC	0.31514	--GTTCGAAC---
ATCTGGCG	0.31448	-ATCTGGCG----
CATCGCAC	0.31360	--CATCGCAC---

8 mer Z-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

GTAACATA	5.63013	----TATGTTAC-
CGCGTCCA	4.33044	---TGGACGCG---
GCACGGTA	4.00229	---GCACGGTA---
CACACAGC	3.99891	--CACACAGC---
GTAACGTA	3.93256	----TACGTTAC-
CATCGCAC	3.89799	----CATCGCAC-
AATACAGC	3.89371	-----GCTGTATT
TCAATTGA	3.87761	---TCAATTGA---
ACGACGAT	3.85907	--ACGACGAT---
ACAACCTCG	3.82845	ACAACCTCG-----