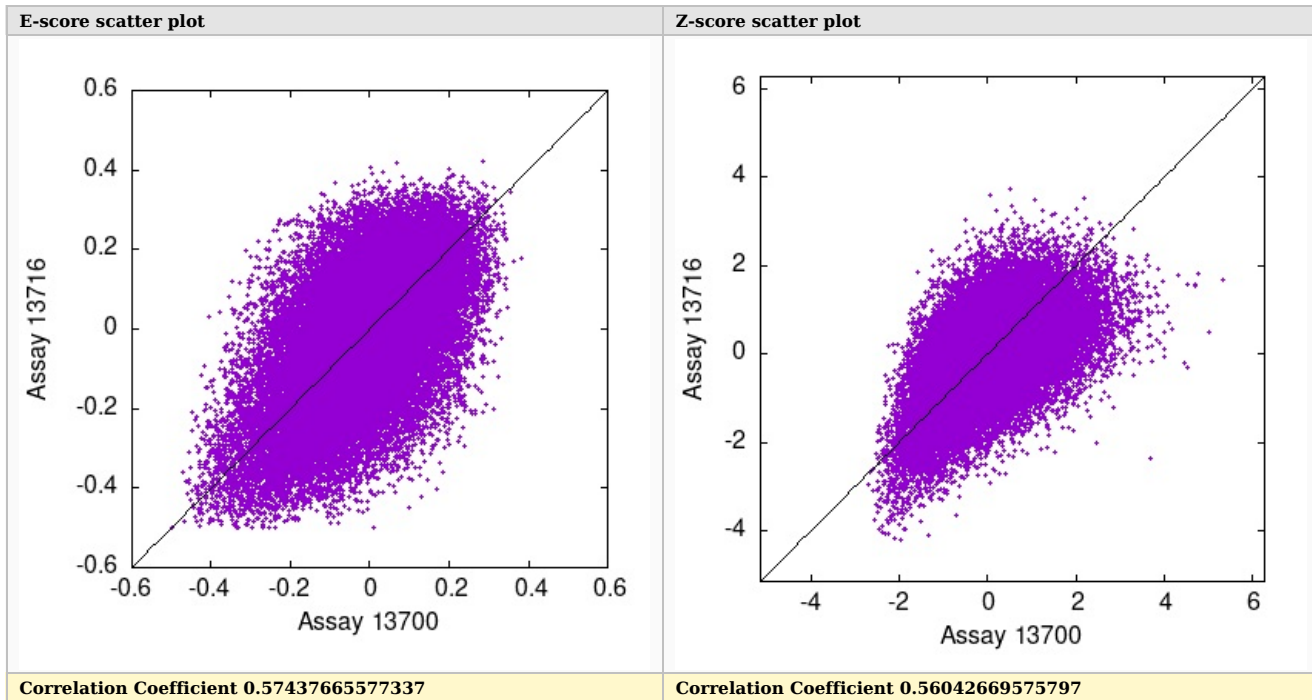


QC report



Top scoring motifs for Assay 13700

Protein ID: pTH14214.1 Gene: TIGD4.DBD Domain: CENP-B_N Flag: Reject Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:

Reverse:

Top 10

Scores

Alignment

GTATAATA	0.38300	--GTATAATA---
CAATTTCA	0.36232	-----CAATTTCA
AATATCAC	0.35430	---AATATCAC--
ATAAATAA	0.34748	---ATAAATAA--
AAACAATA	0.34293	--AAACAATA---
CTGTATAC	0.34278	GTATACAG----
CTCTAATC	0.34249	---GATTAGAG--
ACACACAC	0.34195	--ACACACAC---
ACTGTATA	0.33937	-TATACAGT----
TAACGAAA	0.33825	--TAACGAAA---

8 mer Z-scores for probeset 'all'

Forward:

Reverse:

Top 10

Scores

Alignment

CATAATAC	5.32287	-CATAATAC-
GTATAATA	5.01666	GTATAATA--
AATATCAC	4.77952	-AATATCAC-
ACAAAGAC	4.70126	-ACAAAGAC-
CAATTTCA	4.68611	-CAATTTCA-
CAAGAAAC	4.53761	-CAAGAAAC-
AGTAATAT	4.51692	--ATATTACT
ACGACAAC	4.46782	-ACGACAAC-
GTACTATA	4.31487	-TATAGTAC-
CGTTAATA	4.16604	CGTTAATA--

Top scoring motifs for Assay 13716

Protein ID: pTH14214.2 Gene: TIGD4.DBD Domain: CENP-B_N Flag: Reject Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:

Reverse:

Top 10

Scores

Alignment

CTATTATC	0.42016	-CTATTATC----
ATATCACA	0.41708	-----ATATCACA
GATATGTA	0.40733	-TACATATC----
TATTAATA	0.40234	---TATTAATA---
CACTGATA	0.39423	-----TATCAGTG
CATATCAC	0.39047	---CATATCAC---
TATTATCA	0.38820	--TATTATCA---
ATAGTAAT	0.38755	---ATTACTAT--
CATTACTA	0.38351	--CATTACTA---
ACATTACT	0.38309	AGTAATGT-----

8 mer Z-scores for probeset 'all'

Forward:

Reverse:

Top 10

Scores

Alignment

ATATCACA	3.73177	TGTGATAT-----
GATATGTA	3.60288	--GATATGTA----
ACATTACT	3.52855	---AGTAATGT----
TATTAATA	3.47902	---TATTAATA---
TATTTGCA	3.34073	---TATTTGCA---
CTGTATTA	3.28242	-----CTGTATTA
AGAGATAT	3.24400	--AGAGATAT----
AATAAATT	3.23439	---AATAAATT----
ATACTTTC	3.22002	----ATACTTTC---
ACGTAATA	3.17343	-----ACGTAATA