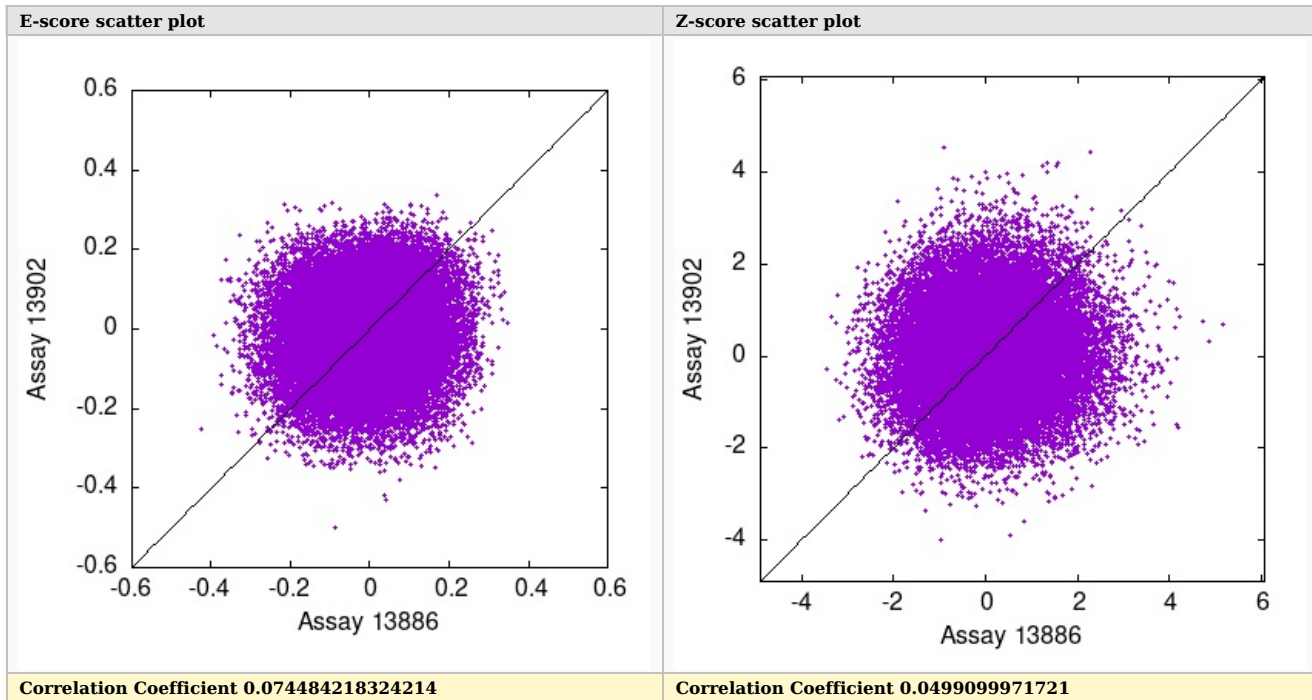


QC report



Top scoring motifs for Assay 13886

Protein ID: pTH14334.1 Gene: RFX8.FL Domain: RFX_DNA_binding

Flag: Reject Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

CCGTAACA	0.34767	--CCGTAACA--
ATTTATAA	0.33802	---TTATAAAT---
AATTTGTA	0.33769	--TACAAATT--
GGGGCTAA	0.33378	GGGGCTAA----
ACGATCAT	0.33138	---ACGATCAT---
ACCAATAC	0.32819	---ACCAATAC---
GCGCAACA	0.32588	--GCGCAACA--
CCAACAC	0.32480	---CCAACAC---
AACACACA	0.32412	---AACACACA---
AGTAAATA	0.32370	--AGTAAATA--

8 mer Z-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

ACGATCAT	5.15518	--ACGATCAT--
ATTTATAA	4.86443	TTATAAAT----
CAAATTAC	4.71550	--CAAATTAC--
ACCAATAC	4.23710	---ACCAATAC---
GGTCAAGTA	4.17709	-GGTCAAGTA---
GCGCAACA	4.16741	-GCGCAACA---
AGGTGATA	4.15735	---TATCACCT---
GCAGAATA	4.14496	-GCAGAATA---
GACGGGGA	4.11437	-GACGGGGA---
AGTAAACG	4.08534	---CGTTTACT---

Top scoring motifs for Assay 13902

Protein ID: pTH14334.2 Gene: RFX8.FL Domain: RFX_DNA_binding

Flag: Reject Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

TAAATTTA	0.33707	-----TAAATTTA
CACTATTA	0.31645	--TAATAGTG---
CGTGATCC	0.31386	CGTGATCC-----
GCTCCAAC	0.31352	---GCTCCAAC---
AATACATT	0.31161	---AATACATT---
AAAATGTA	0.31072	-----TACATTTT
CACCACTA	0.30852	-----CACCACTA-
GGGTTACA	0.30811	-GGGTTACA-----
AAAGTCTG	0.30445	---CAGACTTT---
CGCGTATC	0.30404	---GATACGCG---

8 mer Z-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

GCTCCAAC	4.53004	---GTGGGAGC---
TAAATTTA	4.41867	-TAAATTTA----
CCGTTTGC	4.20521	GCAAACGG-----
AATACATT	4.19609	---AATGTATT---
AAAGTCTG	4.13340	-AAAGTCTG-----
AAAATGTA	4.12315	-AAAATGTA-----
GGGTTACA	4.00950	-----TGTAACCC
CTGTCGAC	3.99240	----CTGTCGAC---
AACTACAA	3.96065	----TTGTAGTT---
CTACCCAC	3.94290	--GTGGGTAG---