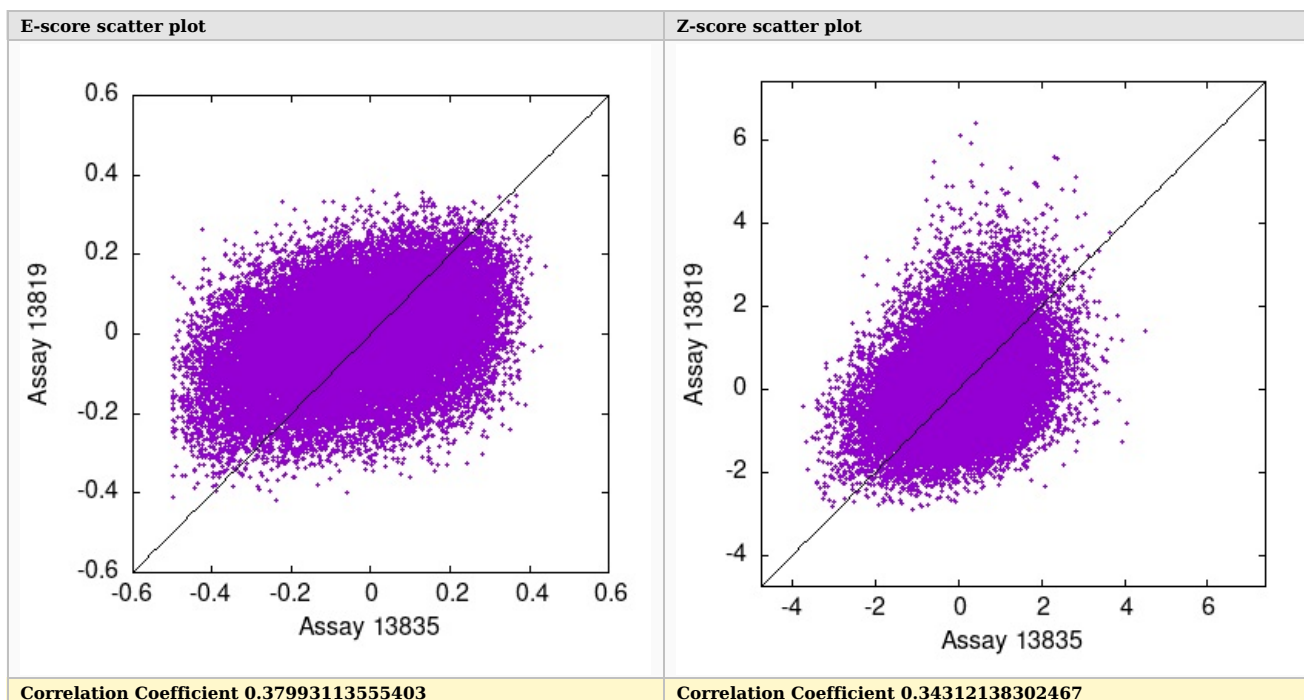


QC report



Top scoring motifs for Assay 13835

Protein ID: pTH13915.2 Gene: AKNA Domain: AT_hook Flag: Reject Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:

Reverse:

AGAAATATA

TACATTTCT

Top 10

Scores

Alignment

GATTAATA	0.44013	-GATTAATA--
AGAGATAT	0.43009	AGAGATAT--
GATATGTA	0.41035	-GATATGTA--
ATACATTA	0.40616	--TAATGTAT-
GAAATGTA	0.40272	-GAAATGTA--
ATTATAAG	0.40259	---ATTATAAG
ACAATGAT	0.40003	ATCATTGT---
GTAATACA	0.39707	-GTAATACA--
GTACATTA	0.39543	--TAATGTAC-
AATAATAA	0.39510	--AATAATAA-

8 mer Z-scores for probeset 'all'

Forward:

Reverse:

AATATATT

TAAATATC

Top 10

Scores

Alignment

AATATATT	4.50776	-AATATATT-
ACGCATAT	4.04429	--ATATGCGT
AGAGATAT	3.94635	AGAGATAT--
GTACATTA	3.94508	--TAATGTAC-
ATATGGTA	3.86791	--ATATGGTA
GATTAATA	3.81447	-GATTAATA-
GATATGTA	3.66954	-GATATGTA-
GAAATGTA	3.63584	-GAAATGTA-
TAAACTCA	3.61693	-TAAACTCA-
ACAATGAT	3.57043	--ATCATTGT

Top scoring motifs for Assay 13819

Protein ID: pTH13915.1 Gene: AKNA Domain: AT_hook Flag: Reject Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:

Reverse:

AACAACA

TGTTT

Top 10

Scores

Alignment

CACAACAC	0.36022	CACAACAC---
ATAGTCTG	0.35592	---CAGACTAT
AACACACA	0.35230	-AACACACA--
ATAATAAA	0.34990	-ATAATAAA--
ACAACAAA	0.34983	-ACAACAAA--
ACACTAAT	0.34596	--ACACTAAT-
AATTCGAA	0.34241	-AATTCGAA--
GTATAATA	0.34119	TATTATAC---
ACACACAG	0.34092	--ACACACAG-
TATCAGCA	0.33471	-TATCAGCA--

8 mer Z-scores for probeset 'all'

Forward:

Reverse:

TAAACAAC

GTGTTT

Top 10

Scores

Alignment

ACAACAAA	6.38313	--ACAACAAA--
AGATTAAA	6.11750	--AGATTAAA--
CACAACAC	5.91768	-CACAACAC---
ACACTAAT	5.59899	--ACACTAAT--
TATAGTAA	5.54502	TTACTATA----
AAGTTTGT	5.46669	-----ACAACTT
ATAGTCTG	5.38619	--CAGACTAT--
AACCAACA	5.30592	-----AACCAACA-
ACACACAC	5.09574	--ACACACAC---
TATTAACA	5.09210	TATTAACA----