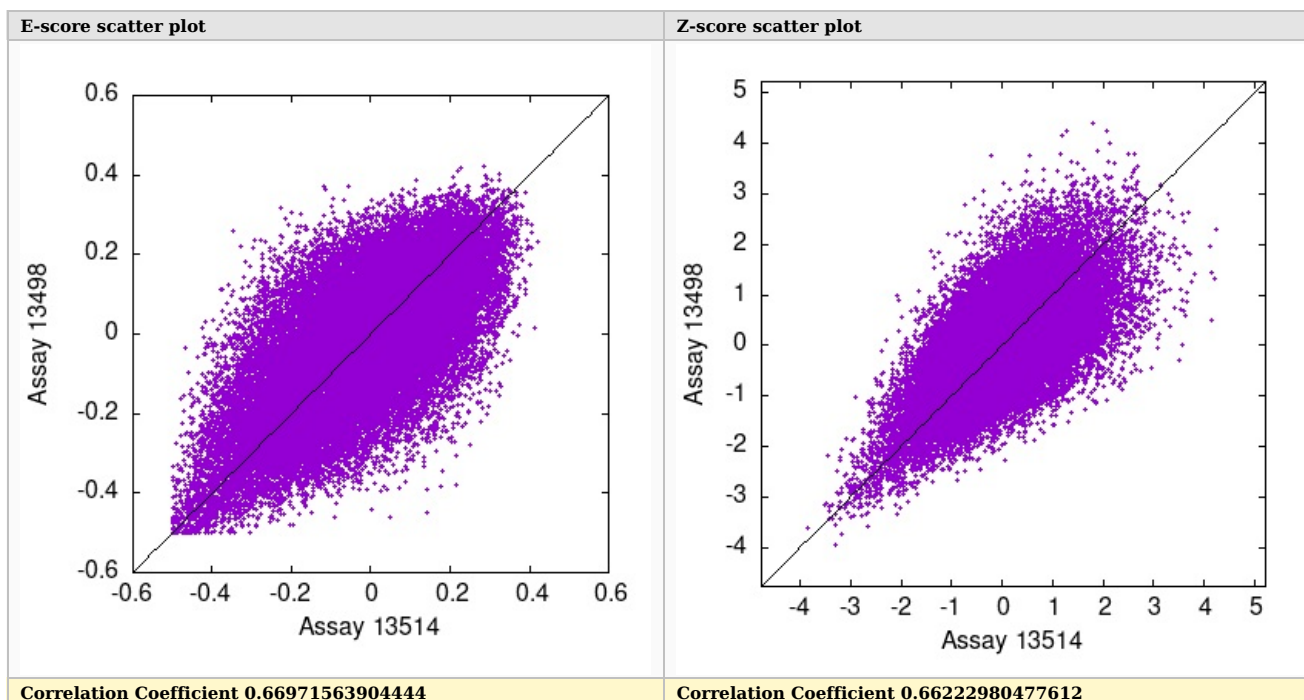


QC report



Top scoring motifs for Assay 13514

Protein ID: pTH13914.2 Gene: AKNA.DBD.1 Domain: AT_hook Flag: Reject Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

GATATGTA	0.41972	---TACATATC
TACACACA	0.41441	---TACACACA
CTGTATTA	0.40618	TAATACAG---
ATAGTAAT	0.40606	--ATAGTAAT--
ATATTAAT	0.40397	--ATTAATAT--
CACATATA	0.40374	---CACATATA
ATACATAA	0.39632	--ATACATAA--
ATATCTTA	0.39371	--ATATCTTA--
AACACTTA	0.39292	-AACACTTA--
CACAAATA	0.39291	-CACAAATA--

8 mer Z-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

ACAAAATA	4.25834	-ACAAAATA-
TATTTGCA	4.21344	-TGCAAATA-
AATTTAAA	4.16610	-AATTTAAA-
CACATATA	4.15070	-CACATATA-
ATATCTTA	4.12499	TAAGATAT--
GATATGTA	3.81935	-TACATATC-
GTAATGTA	3.75833	-GTAATGTA-
CACAAATA	3.73501	-CACAAATA-
AATATATT	3.68514	-AATATATT-
CTGTATTA	3.66898	--TAATACAG

Top scoring motifs for Assay 13498

Protein ID: pTH13914.1 Gene: AKNA.DBD.1 Domain: AT_hook Flag: Reject Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:

Reverse:



Top 10

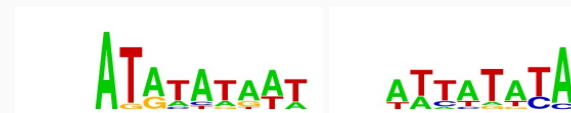
Scores

Alignment

ATGTATAA	0.42295	-ATGTATAA--
TAACGAAA	0.41882	--TAACGAAA--
ATAATGCA	0.41023	--TGCAATAT--
ATATAAAT	0.40294	-ATATAAAT--
ATATATAA	0.39907	-ATATATAA--
ATTATATA	0.39308	--TATATAAT--
ATACAATA	0.39229	-ATACAATA--
ACAAATAA	0.38801	-ACAAATAA--
CATAATAC	0.38783	---GTATTATG
TAAATTTA	0.38537	TAAATTTA---

Forward:

Reverse:



Top 10

Scores

Alignment

ATGTATAA	4.39247	-ATGTATAA--
ATATATAA	4.26458	-ATATATAA--
ATTATATA	4.24762	--TATATAAT--
TAACGAAA	4.14867	--TAACGAAA--
ATGTTAAT	3.99572	-ATGTTAAT--
AATATATG	3.84875	AATATATG--
AGATATAT	3.80127	-AGATATAT--
ATATAAAT	3.80046	-ATATAAAT--
ATAATGCA	3.78109	--TGCATTAT--
ATCATTTA	3.77515	--TAAATGAT--