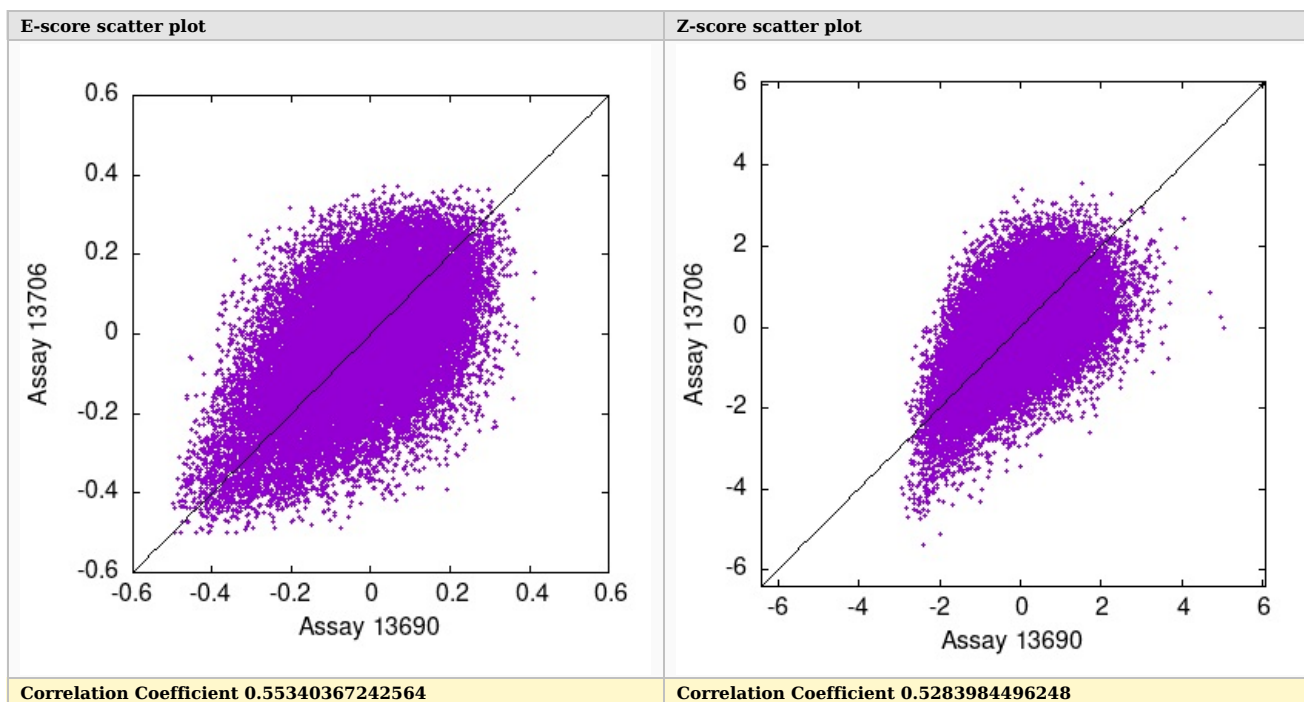


QC report



Top scoring motifs for Assay 13690

Protein ID: pTH13023.1 Gene: RBCK1.sRANBP2 Domain: Unknown Flag: Reject Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

TAAATTTA	0.41399	TAAATTTA----
CTGTATAC	0.41006	---CTGTATAC-
TACATGTA	0.37192	--TACATGTA--
AATTTGTA	0.36994	--AATTTGTA--
AACATGTT	0.36716	--AACATGTT--
TTTGCAAA	0.36713	----TTTGCAAA
ACATATGT	0.36687	-ACATATGT---
GTTGCAAC	0.36228	----GTTGCAAC
CATAAAT	0.36019	GTATTATG----
ATACAAA	0.35917	---TTTTGTAT-

8 mer Z-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

AACATGTT	5.03029	---AACATGTT----
CTGTATAC	4.96164	---CTGTATAC---
TAAATTTA	4.68005	TAAATTTA-----
AATTTGTA	4.03904	--AATTTGTA----
CAAATTTG	3.85655	CAAATTTG-----
GTTGCAAC	3.69908	----GTTGCAAC--
AGAATTCT	3.69478	---AGAATTCT----
TACATGTA	3.65585	--TACATGTA----
AGACGTCT	3.57876	--AGACGTCT---
TAATTACA	3.55541	-----TGTAATTA

Top scoring motifs for Assay 13706

Protein ID: pTH13023.2 Gene: RBCK1.sRANBP2 Domain: Unknown Flag: Reject Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

GTATATGA	0.37280	----GTATATGA--
CGATAACA	0.37262	---CGATAACA----
ACAATTGA	0.37194	---ACAATTGA----
AACAACGT	0.36568	-----AACAACGT
AGTATACA	0.36206	---AGTATACA----
CGTATAAA	0.36124	---CGTATAAA----
AAACTTTA	0.36075	-TAAGTTTT-----
GTATACTA	0.35959	--TAGTATAC----
ATAGTAAT	0.35878	ATTACTAT-----
ATCATACA	0.35829	---ATCATACA----

8 mer Z-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

ACAATTGA	3.57294	----TCAATTGT-
TTCATGAA	3.42536	---TTCATGAA---
GTTCAAGT	3.28052	--GTTCAAGT---
GTAACCTA	3.26304	----TAAGTTAC-
ACGTACTA	3.22490	-----TAGTACGT
GCGCAAAA	3.20771	---GCGCAAAA---
ATCATACA	3.15004	---ATCATACA--
ATGTAACA	3.10636	-TGTTACAT----
ATACCGAA	3.08533	---TTCGGTAT--
CTGAACGA	3.08468	TCGTTACAG-----