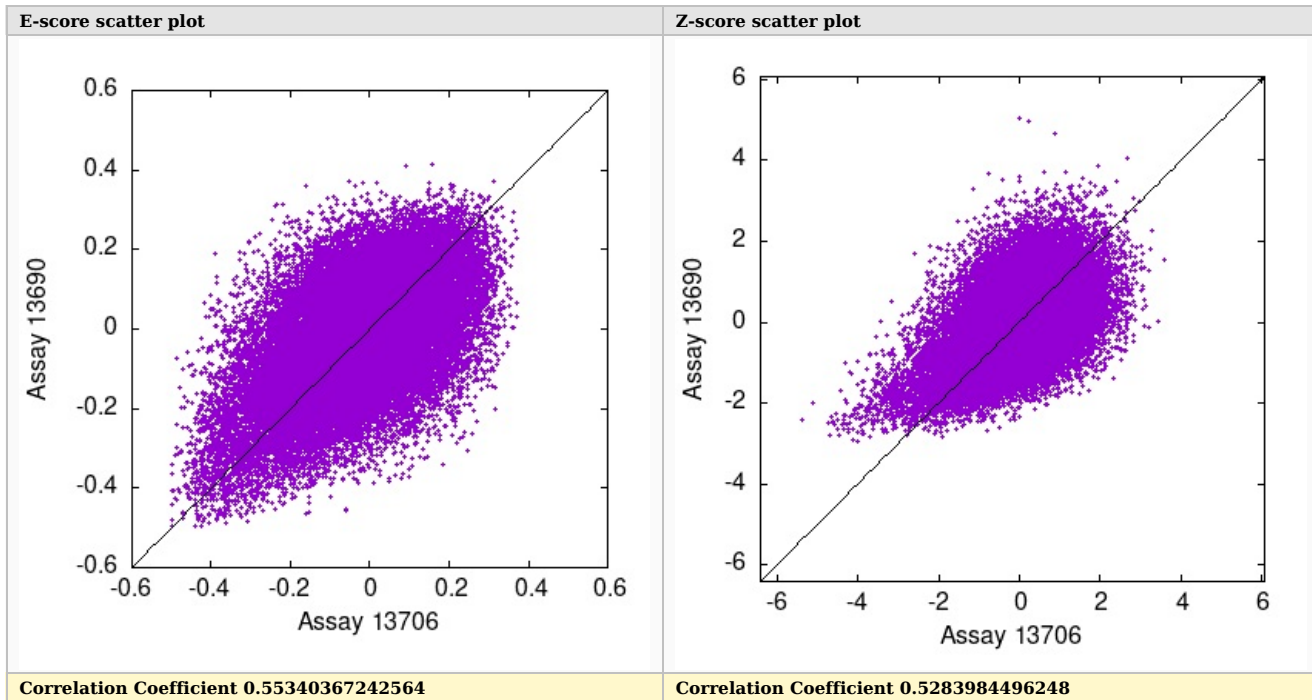


QC report



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---
AAAACCTTA	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--
GTTCAGTA	3.28052	--GTTCAGTA---
GTAACCTTA	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	TCGTTCAG----

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
CATAATAC	0.36019	GTATTATG----
ATACAAAA	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---
CAAAATTTG	3.85655	CAAAATTTG-----
GTTGCAAC	3.69908	----GTTGCAAC--
AGAATTCT	3.69478	-AGAATTCT-----
TACATGTA	3.65585	--TACATGTA----
AGACGTCT	3.57876	---AGACGTCT---
TAATTACA	3.55541	-----TGTAATTA