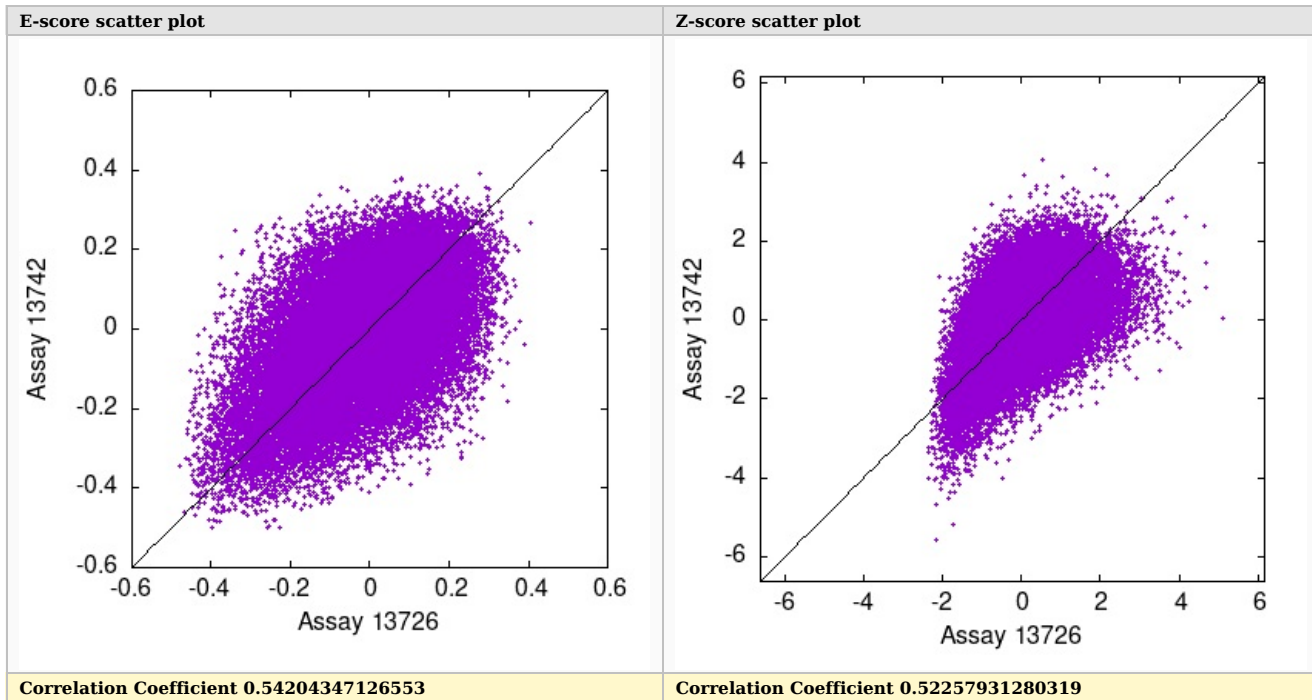


QC report



Top scoring motifs for Assay 13726

Protein ID: pTH14309.1 Gene: NKRF.DBD Domain: Unknown Flag: Reject Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:

Reverse:



Top 10	Scores	Alignment
TAACGAAA	0.40582	-TAACGAAA-
ATGTACAT	0.39108	ATGTACAT--
ATAAACAT	0.37685	--ATAAACAT
GTAATA	0.37637	-TATAGTAC-
ATATACAG	0.36815	ATATACAG--
CTACAACA	0.36772	--CTACAACA
ATTGGAAT	0.36697	--ATTGGAAT
ATAACAC	0.36344	--ATAACAC
TATACAAA	0.35629	-TATACAAA-
AACGAAAT	0.34983	--AACGAAAT

8 mer Z-scores for probeset 'all'

Forward:

Reverse:



Top 10	Scores	Alignment
ATGTACAT	5.10341	-ATGTACAT--
TATACAAA	4.67532	--TATACAAA-
GTAATA	4.66453	--TATAGTAC-
TAACGAAA	4.66062	--TAACGAAA-
AATGTTCA	4.25678	AATGTTCA---
AATAATAA	4.18596	--AATAATAA-
CTACAACA	4.14201	---CTACAACA
TATATGCA	4.12802	--TATATGCA-
ATAACAT	4.11442	---ATAACAT
ACATACAA	4.03627	-ACATACAA--

Top scoring motifs for Assay 13742

Protein ID: pTH14309.2 Gene: NKRF.DBD Domain: Unknown Flag: Reject Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:

Reverse:



Top 10	Scores	Alignment
CACATATA	0.39109	--CACATATA----
TAACGTAA	0.38005	-TAACGTAA-----
ACCATACT	0.37489	--ACCATACT----
CACTGATA	0.37326	--CACTGATA----
ACTCTACT	0.36115	----ACTCTACT--
ATGTATGC	0.36091	---GCATACAT---
ACATTATA	0.35935	-----TATAATGT
AGTTTTTC	0.35701	---AGTTTTTC---
TACGTCAA	0.35700	TTGACGTA-----
TATAAGCA	0.35357	--TGCTTATA----

8 mer Z-scores for probeset 'all'

Forward:

Reverse:



Top 10	Scores	Alignment
TAACGTAA	4.05640	--TAACGTAA--
CACATATA	3.84130	-TATATGTG--
GATTTGTA	3.68761	-GATTTGTA--
AGAATTCT	3.68577	AGAATTCT---
ACCATACT	3.65246	AGTATGGT---
ATTTACAG	3.41585	--ATTTACAG-
ATTTGTAG	3.38508	--ATTTGTAG-
ACAAACAG	3.32198	CTGTTTGT---
CACTGATA	3.30977	-CACTGATA--
ACTCTACT	3.23233	---ACTCTACT