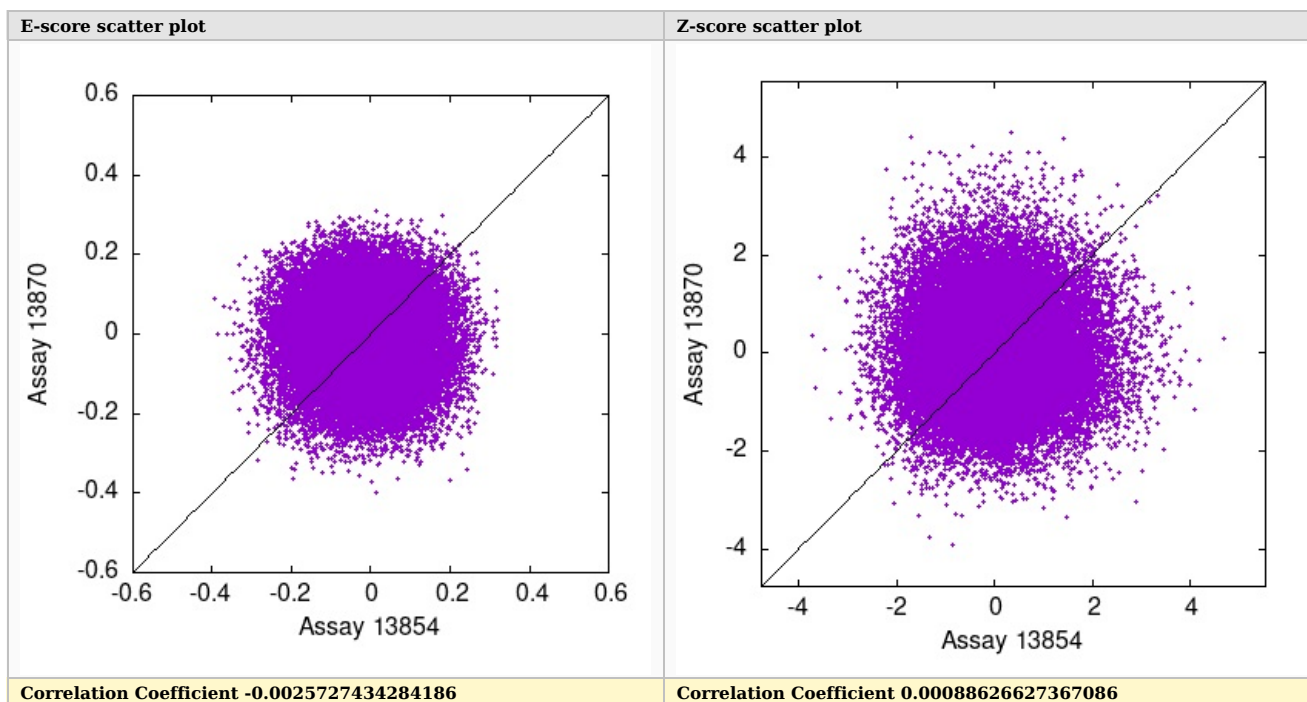


QC report



Top scoring motifs for Assay 13854

Protein ID: pTH14254.1 Gene: HSFX1 Domain: HSF_DNA-bind Flag: Reject Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:	Reverse:

Top 10	Scores	Alignment
CATCGAGC	0.31869	GCTCGATG-----
ATACAAAG	0.31628	-----ATACAAAG
AGTAATCC	0.31605	---GGATTACT--
CTGCAGTC	0.31596	----GACTGCAG-
CACAGTGA	0.31531	--TCACTGTG---
ATGCTGGG	0.31278	--ATGCTGGG---
CTATAGGC	0.30988	---CTATAGGC--
TATGTGAA	0.30948	----TATGTGAA-
CGATGAGA	0.30687	---CGATGAGA--
GCTCTGCC	0.30685	---GGCAGAGC--

8 mer Z-scores for probeset 'all'

Forward:	Reverse:

Top 10	Scores	Alignment
ATCCCAGG	4.68045	--ATCCCAGG--
CTCCTGAC	4.17476	--GTCAGGAG
TCCTTGAA	4.08684	--TTCAAGGA-
ATACAAAG	4.04022	--ATACAAAG--
TATGTGAA	3.98341	--TTCACATA--
ATCTTCTC	3.95295	--ATCTTCTC--
ATGGTCTA	3.89158	TAGACCAT---
GTCAGAAA	3.80418	--TTTCTGAC-
CTGGGGGA	3.79395	TCCCCCAG---
CATGGCTC	3.78989	-GAGCCATG--

Top scoring motifs for Assay 13870

Protein ID: pTH14254.2 Gene: HSFX1 Domain: HSF_DNA-bind Flag: Reject Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:	Reverse:

Top 10	Scores	Alignment
AGACGTCT	0.30897	AGACGTCT-----
CCGGGCCA	0.29728	--CCGGGCCA----
ATCTTGCC	0.29640	-ATCTTGCC-----
CTATCGGA	0.29423	-----TCCGATAG--
GAGGCAAA	0.29420	---TTTGCTCT----
AGGTCATG	0.29011	---CATGACCT----
AAATGACA	0.28817	-----TGTCATTT--
AGATGAGC	0.28755	AGATGAGC-----
CCACACGA	0.28620	-----CCACACGA
CGTGCCAC	0.28570	---CGTGCCAC----

8 mer Z-scores for probeset 'all'

Forward:	Reverse:

Top 10	Scores	Alignment
AAATGACA	4.51421	--AAATGACA----
CTATCGGA	4.39880	CTATCGGA-----
CGTAGCTA	4.37911	----CGTAGCTA--
ATCATCTC	4.23273	-GAGATGAT-----
CCGGGCCA	4.10466	-----TGGCCCGG
CCGCGACC	4.09969	-----GGTCGCGG
GAAGTGAA	4.09874	-GAAGTGAA-----
CCATGAGG	4.09043	--CCTCATGG----
AATCTCTC	4.08511	--AATCTCTC----
AACTGATC	4.05633	--AACTGATC----