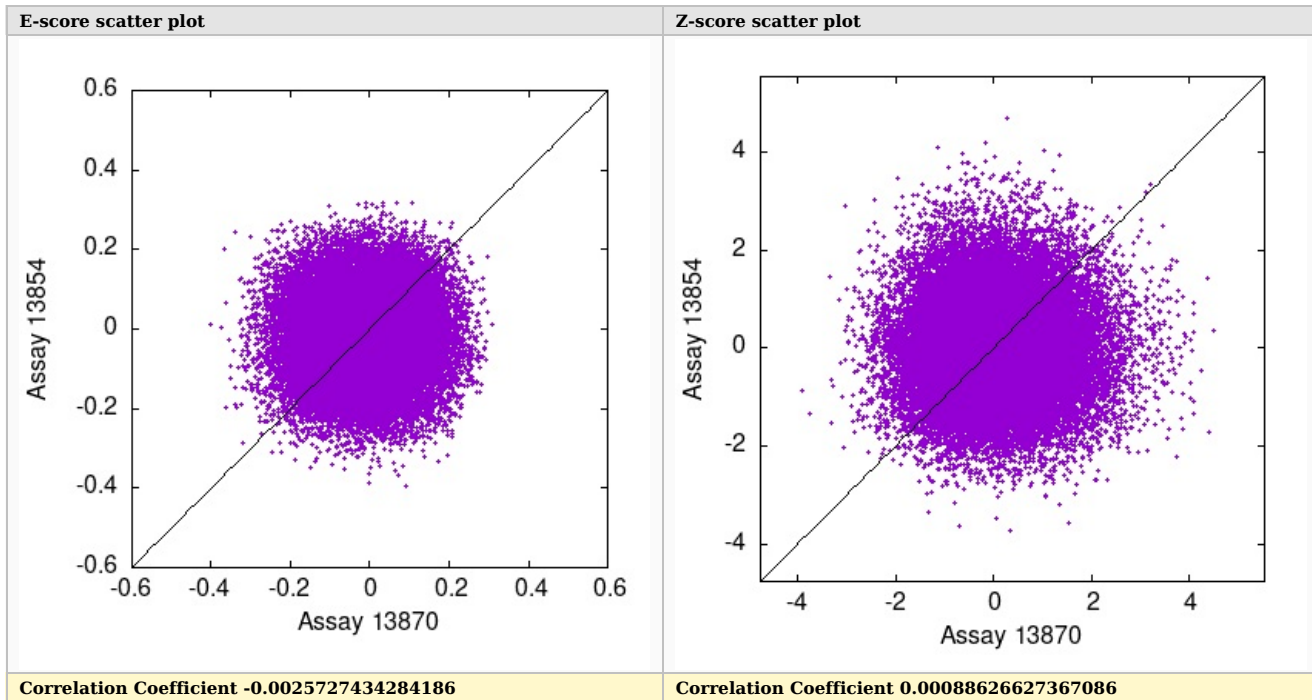


QC report



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'			8 mer Z-scores for probeset 'all'		
Forward:		Reverse:	Forward:		Reverse:
Top 10	Scores	Alignment	Top 10	Scores	Alignment
AGACGTCT	0.30897	AGACGTCT-----	AAATGACA	4.51421	--AAATGACA----
CCGGGCCA	0.29728	--CCGGGCCA----	CTATCGGA	4.39880	CTATCGGA-----
ATCTTGCC	0.29640	-ATCTTGCC-----	CGTAGCTA	4.37911	----CGTAGCTA--
CTATCGGA	0.29423	-----TCCGATAG--	ATCATCTC	4.23273	--GAGATGAT-----
GAGGCAAA	0.29420	---TTTGCCTC----	CCGGGCCA	4.10466	-----TGGCCCGG--
AGGTCATG	0.29011	---CATGACCT----	CCGCGACC	4.09969	-----GGTCGCGG--
AAATGACA	0.28817	-----TGTCATTT--	GAAGTGAA	4.09874	--GAAGTGAA-----
AGATGAGC	0.28755	AGATGAGC-----	CCATGAGG	4.09043	---CCTCATGG----
CCACACGA	0.28620	-----CCACACGA	AATCTCTC	4.08511	--AATCTCTC----
CGTGCCAC	0.28570	---CGTGCCAC----	AACTGATC	4.05633	--AACTGATC----

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'			8 mer Z-scores for probeset 'all'		
Forward:		Reverse:	Forward:		Reverse:
Top 10	Scores	Alignment	Top 10	Scores	Alignment
CATCGAGC	0.31869	GCTCGATG-----	ATCCCAGG	4.68045	-ATCCCAGG--
ATACAAAG	0.31628	-----ATACAAAG	CTCCTGAC	4.17476	--GTCAGGAG--
AGTAATCC	0.31605	---GGATTACT----	TCCTTGAA	4.08684	--TTCAAGGA--
CTGCAGTC	0.31596	----GACTGCAG----	ATACAAAG	4.04022	-ATACAAAG--
CACAGTGA	0.31531	--TCACTGTG----	TATGTGAA	3.98341	--TTACATA--
ATGCTGGG	0.31278	--ATGCTGGG----	ATCTTCTC	3.95295	-ATCTTCTC--
CTATAGGC	0.30988	---CTATAGGC----	ATGGTCTA	3.89158	TAGACCAT---
TATGTGAA	0.30948	----TATGTGAA----	GTCAGAAA	3.80418	--TTTCTGAC--
CGATGAGA	0.30687	---CGATGAGA----	CTGGGGGA	3.79395	TCCCCCAG---
GCTCTGCC	0.30685	---GGCAGAGC----	CATGGCTC	3.78989	-GAGCCATG--