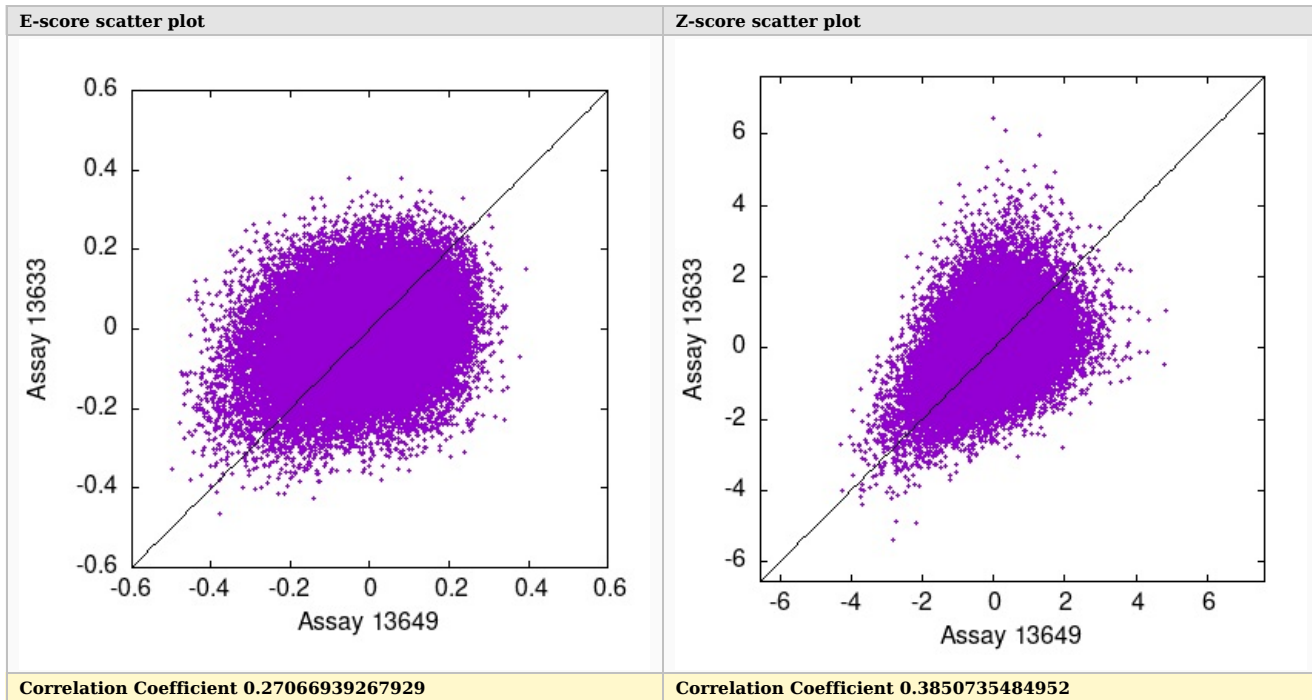


QC report



Top scoring motifs for Assay 13649

Protein ID: pTH14255.2 Gene: HSFX1.DBD 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:		
Top 10	Scores	Alignment	Top 10	Scores	Alignment
AGAATTCT	0.39361	AGAATTCT---	AGAATTCT	4.85693	---AGAATTCT-
GTCATGAC	0.37875	---GTCATGAC	TTATATAA	4.79232	---TTATATAA--
AAATTCGG	0.34911	-AAATTCGG--	TAATATTA	4.35345	---TAATATTA--
ACAATAAG	0.34460	-ACAATAAG--	AAACGTTT	4.31196	---AAACGTTT--
ATATACTC	0.34366	-ATATACTC--	ATATGAGA	4.10851	-----ATATGAGA
TACGCGTA	0.34127	-TACGCGTA-	GGATATAA	4.06859	---GGATATAA--
CAAACGCA	0.34030	CAAACGCA---	GAAATTTC	3.85084	---GAAATTTC--
ATAGTCGA	0.33740	-ATAGTCGA--	CTGTGATA	3.84086	CTGTGATA----
CGGAACAG	0.33590	-CTGTTCG--	TATTAATA	3.83559	---TATTAATA--
ATATTAAG	0.33526	-ATATTAAG--	GCAAACTA	3.81815	---GCAAACTA--

Top scoring motifs for Assay 13633

Protein ID: pTH14255.1 Gene: HSFX1.DBD 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:		
Top 10	Scores	Alignment	Top 10	Scores	Alignment
ATTCGTTA	0.37974	-ATTCGTTA---	GGAATGGA	6.43148	-GGAATGGA----
GGAATGGA	0.37756	---TCCATTCC--	AACAAAGC	6.09640	-GCTTTGTT----
ACACTGAT	0.34816	-ATCAGTGT---	ATTCGTTA	5.95033	---TAACGAAT---
ACTGAGTA	0.34547	TACTCAGT----	CCAACAAC	5.25079	-GTTGTTGG----
AACAAAGC	0.34336	GCTTTGTT----	CACAGTTC	5.11585	-GAACTGTG----
GTGGTGTA	0.33827	---TACACCAC--	TGCCGACA	5.06809	---TGCCGACA---
GGTTATCA	0.33285	-----GGTTATCA	AGTCCAAG	4.99329	CTTGGACT----
GAATGGAC	0.33275	-GTCCATTCC--	GTGGTGTA	4.98279	-GTGGTGTA----
AAGTGATA	0.33069	TATCACTT----	TGGTGTA	4.93709	---TGGTGTA---
GGTTAAGA	0.32792	-----GGTTAAGA	TAAGTACA	4.71537	-----TGACTTAA