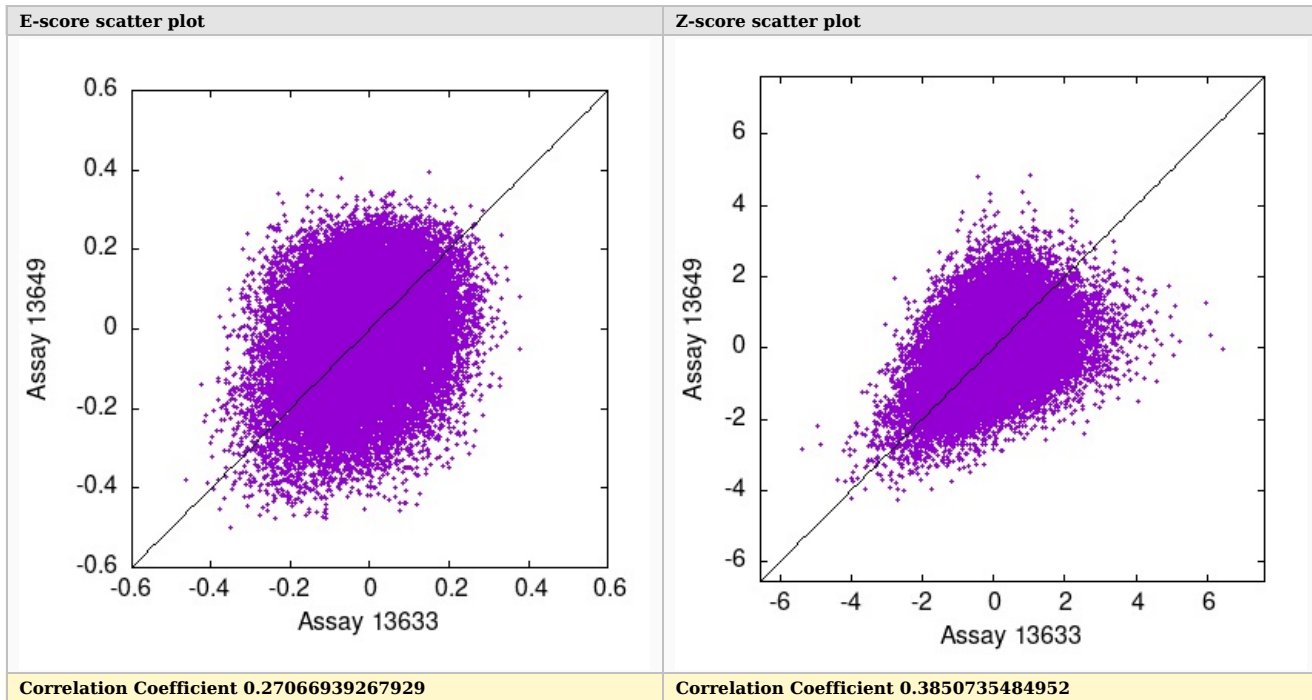


## QC report



## 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:



Forward:

Reverse:



## Top 10

## Scores

## Alignment

ATTCGTTA	0.37974	-ATTCGTTA---
GGAATGGA	0.37756	--TCCATTCC--
AACTGAT	0.34816	-ATCAGTGT---
ACTGAGTA	0.34547	TACTCAGT----
AACAAAGC	0.34336	GCTTTGTT----
GTGGTGTA	0.33827	--TACACCAC--
GGTATATCA	0.33285	----GGTTATCA
GAATGGAC	0.33275	-GTCCATTG---
AAGTGATA	0.33069	TATCACTT----
GGTTAAGA	0.32792	----GGTTAAGA

## Top 10

## Scores

## Alignment

GGAATGGA	6.43148	-GGAATGGA----
AACAAAGC	6.09640	-GCTTTGTT----
ATTCGTTA	5.95033	--TAACGAAT---
CCAACAAC	5.25079	-GTTGTTGG----
CACAGTTC	5.11585	-GAACGTGTG----
TGCCGACA	5.06809	--TGCCGACA---
AGTCCAAG	4.99329	CTTGGACT----
GTGGTGTA	4.98279	-GTGGTGTA----
TGGTGATA	4.93709	--TGGTGATA---
TAAGTACA	4.71537	-----TGTACTTA

## 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:



Forward:

Reverse:



## Top 10

## Scores

## Alignment

AGAATTCT	0.39361	AGAATTCT---
GTCATGAC	0.37875	---GTCATGAC
AAATTCGG	0.34911	-AAATTCGG--
ACAATAAG	0.34460	-ACAATAAG--
ATATACTC	0.34366	-ATATACTC--
TACGCGTA	0.34127	--TACGCGTA-
CAAACGCA	0.34030	CAAACGCA---
ATAGTCGA	0.33740	-ATAGTCGA--
CGGAACAG	0.33590	-CTGTCCG---
ATATTAAG	0.33526	-ATATTAAG--

## Top 10

## Scores

## Alignment

AGAATTCT	4.85693	---AGAATTCT-
TTATATAA	4.79232	---TTATATAA--
TAATATTA	4.35345	---TAATATTA--
AAACGTTT	4.31196	---AAACGTTT--
ATATGAGA	4.10851	-----ATATGAGA
GGATATAA	4.06859	---GGATATAA--
GAAATTTT	3.85084	---GAAATTTT--
CTGTGATA	3.84086	CTGTGATA----
TATTAATA	3.83559	---TATTAATA--
GCAAACCTA	3.81815	---GCAAACCTA--