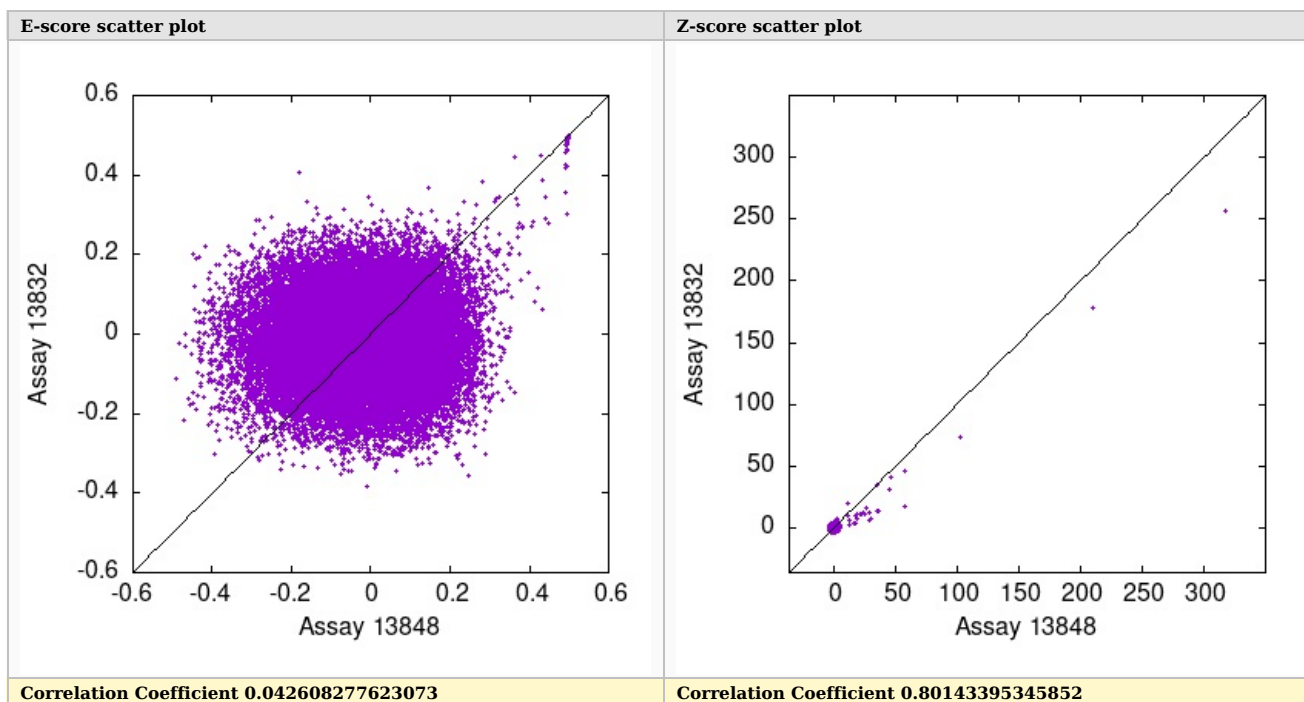


QC report



Top scoring motifs for Assay 13848

Protein ID: pTH13940.2 Gene: USF3.DBD Domain: HLH Flag: Pass matched_pair Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:

Reverse:

CACGTGG

cCACGTG

Top 10

Scores

Alignment

CCACGTGG	0.49970	-CCACGTGG-
CACGTGGG	0.49964	--CACGTGGG
ACCACGTG	0.49893	--CACGTGGT
CCACGTGA	0.49801	-TCACGTGG-
CCACGTGC	0.49796	-GCACGTGG-
CACGTGGC	0.49770	--CACGTGGC
ACACGTGG	0.49759	-ACACGTGG-
CACGTGAC	0.49674	GTCACGTG--
CACGTGGA	0.49652	--CACGTGGA
CACGTGCG	0.49571	--CACGTGCG

8 mer Z-scores for probeset 'all'

Forward:

Reverse:

cCACGTG

CACGTGG

Top 10

Scores

Alignment

CCACGTGG	317.19259	-CCACGTGG-
CACGTGGG	209.91144	CCCACGTG--
ACCACGTG	102.88517	ACCACGTG--
CCACGTGC	58.47318	--CCACGTGC-
CCACGTGA	57.76483	-CCACGTGA-
CACGTGGC	47.27246	GCCACGTG--
ACACGTGG	45.21308	--CCACGTGT-
GCACGTGC	36.48304	-GCACGTGC-
CACGTGAC	35.72557	--CACGTGAC
CACGTGGA	34.94215	TCCACGTG--

Top scoring motifs for Assay 13832

Protein ID: pTH13940.1 Gene: USF3.DBD Domain: HLH Flag: Pass matched_pair Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:

Reverse:

CACGTGG

CCACGTG

Top 10

Scores

Alignment

CCACGTGG	0.49953	-CCACGTGG--
CACGTGGG	0.49926	--CACGTGGG
ACCACGTG	0.49907	--CACGTGGT-
ACACGTGG	0.49697	-ACACGTGG--
CACGTGGC	0.49688	--CACGTGGC-
CCACGTGA	0.49662	-TCACGTGG--
CACGTGAC	0.49612	GTCACGTG---
ACGTGGGG	0.49432	---ACGTGGGG
CCACGTGC	0.49086	-GCACGTGG--
CACGTGGA	0.48698	--CACGTGGA-

8 mer Z-scores for probeset 'all'

Forward:

Reverse:

CACGTGG

cCACGTG

Top 10

Scores

Alignment

CCACGTGG	255.71584	-CCACGTGG--
CACGTGGG	178.43986	--CACGTGGG
ACCACGTG	74.09330	--CACGTGGT-
CCACGTGA	46.03343	-TCACGTGG--
CACGTGGC	41.17538	--CACGTGGC-
CACGTGAC	35.50247	GTCACGTG---
ACACGTGG	31.09507	-ACACGTGG--
ACGTGGGG	20.00060	---ACGTGGGG
CCACGTGC	18.11131	-GCACGTGG--
ACACGTGT	17.02041	-ACACGTGT--