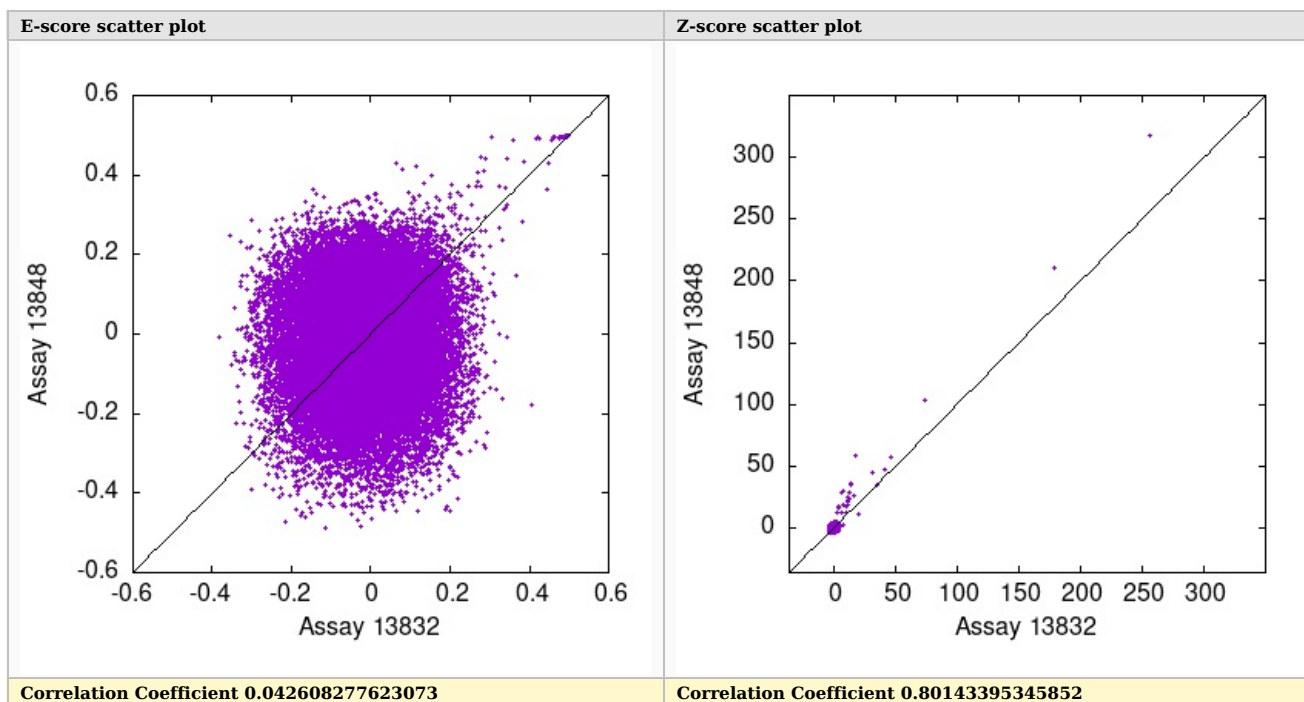


QC report



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'			8 mer Z-scores for probeset 'all'		
Forward:		Reverse:	Forward:		Reverse:
Top 10	Scores	Alignment	Top 10	Scores	Alignment
CCACGTGG	0.49953	-CCACGTGG--	CCACGTGG	255.71584	-CCACGTGG--
CACGTGGG	0.49926	--CACGTGGG-	CACGTGGG	178.43986	--CACGTGGG-
ACCACGTG	0.49907	--CACGTGGT-	ACCACGTG	74.09330	--CACGTGGT-
ACACGTGG	0.49697	--ACACGTGG--	CCACGTGA	46.03343	-TCACGTGG--
CACGTGGC	0.49688	--CACGTGGC-	CACGTGGC	41.17538	--CACGTGGC-
CCACGTGA	0.49662	-TCACGTGG--	CACGTGAC	35.50247	GTCACGTG--
CACGTGAC	0.49612	GTCACGTG---	ACACGTGG	31.09507	-ACACGTGG--
ACGTGGGG	0.49432	---ACGTGGGG	ACGTGGGG	20.00060	---ACGTGGGG
CCACGTGC	0.49086	-GCACGTGG--	CCACGTGC	18.11131	-GCACGTGG--
CACGTGGA	0.48698	--CACGTGGA-	ACACGTGT	17.02041	-ACACGTGT--

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'			8 mer Z-scores for probeset 'all'		
Forward:		Reverse:	Forward:		Reverse:
Top 10	Scores	Alignment	Top 10	Scores	Alignment
CCACGTGG	0.49970	-CCACGTGG--	CCACGTGG	317.19259	-CCACGTGG--
CACGTGGG	0.49964	--CACGTGGG-	CACGTGGG	209.91144	CCCACGTG--
ACCACGTG	0.49893	--CACGTGGT-	ACCACGTG	102.88517	ACCACGTG--
CCACGTGA	0.49801	-TCACGTGG--	CCACGTGC	58.47318	-CCACGTGC-
CCACGTGC	0.49796	-GCACGTGG--	CCACGTGA	57.76483	-CCACGTGA-
CACGTGGC	0.49770	--CACGTGGC-	CACGTGGC	47.27246	GCCACGTG--
ACACGTGG	0.49759	-ACACGTGG--	ACACGTGG	45.21308	-CCACGTGT-
CACGTGAC	0.49674	GTCACGTG---	GCACGTGC	36.48304	-GCACGTGC-
CACGTGGA	0.49652	--CACGTGGA-	CACGTGAC	35.72557	--CACGTGAC
CACGTGCG	0.49571	--CACGTGCG-	CACGTGGA	34.94215	TCCACGTG--