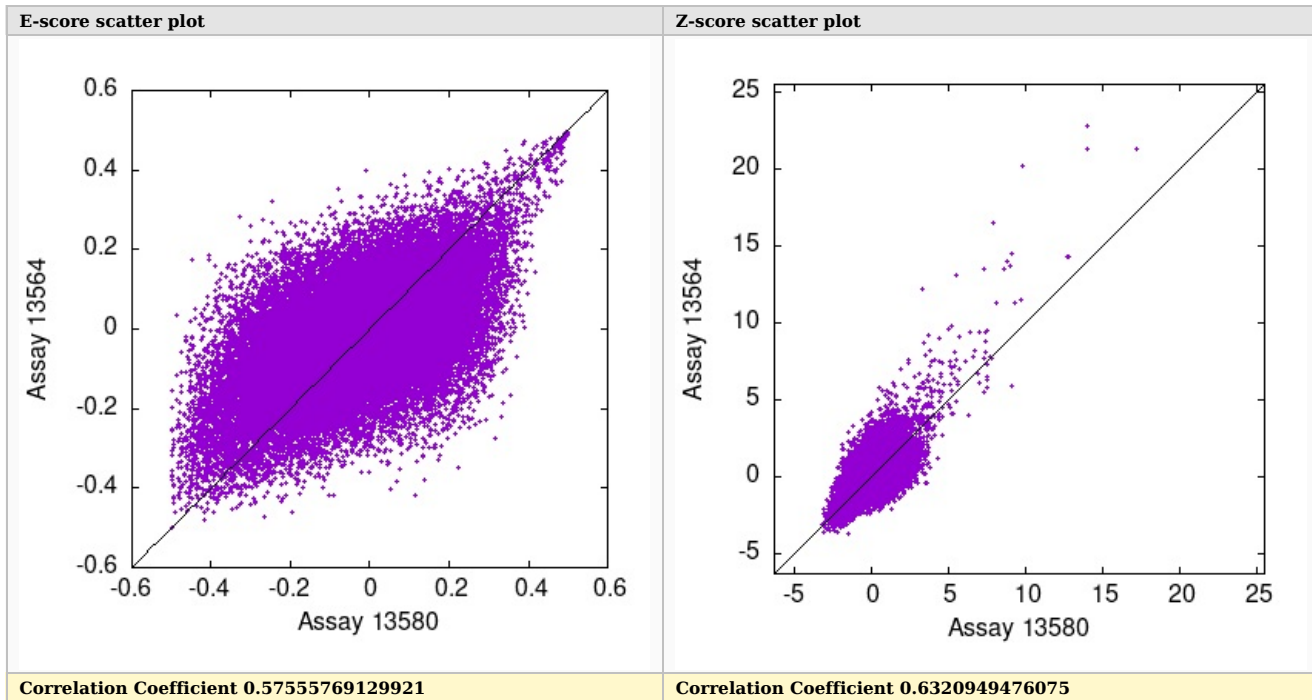


QC report



Top scoring motifs for Assay 13580

Protein ID: pTH13945.2 Gene: CREB3L3.DBD Domain: bZIP_1 Flag: Pass_matched_pair Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

CACGTGGC	0.49859	-CACGTGGC-
CCACGTGG	0.49796	CCACGTGG--
ACGTGGCA	0.49747	--ACGTGGCA
ACACGTGG	0.49742	ACACGTGG--
CCACGTCA	0.49742	TGACGTGG--
ACACGTGT	0.49434	ACACGTGT--
CACGTGGA	0.49303	-CACGTGGA-
ACACGTCA	0.49195	ACACGTCA--
GCCACGTA	0.49181	-TACGTGGC-
ACGTGGAA	0.49161	--ACGTGGAA

8 mer Z-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

CACGTGGC	17.16189	--CACGTGGC-
ACGTGGCA	13.95145	---ACGTGGCA
CCACGTGG	13.94711	-CCACGTGG--
ACACGTGG	12.82390	--ACACGTGG--
CCACGTCA	12.71450	-TGACGTGG--
ACACGTGT	9.79122	-ACACGTGT--
ACACGTCA	9.63662	-ACACGTCA--
CACGTGGA	9.27870	--CACGTGGA-
CACGTGTC	9.06563	GACACGTG---
TACGTGGA	9.03202	--TACGTGGA-

Top scoring motifs for Assay 13564

Protein ID: pTH13945.1 Gene: CREB3L3.DBD Domain: bZIP_1 Flag: Pass_matched_pair Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

ACGTGGCA	0.49666	---ACGTGGCA
CACGTGGC	0.49612	--CACGTGGC-
ACACGTGT	0.49552	-ACACGTGT--
CCACGTGG	0.49527	-CCACGTGG--
ATGACGTG	0.49213	ATGACGTG---
CCACGTCA	0.49001	-TGACGTGG--
ACACGTGG	0.48927	-ACACGTGG--
CACGTGTC	0.48826	GACACGTG---
CACGTGTA	0.48821	TACACGTG---
ACACGTCA	0.48762	-ACACGTCA--

Forward:

Reverse:



Top 10

Scores

Alignment

CCACGTGG	22.81855	--CCACGTGG--
ACGTGGCA	21.25263	---ACGTGGCA
CACGTGGC	21.24526	---CACGTGGC-
ACACGTGT	20.17508	--ACACGTGT--
ATGACGTG	16.43306	-ATGACGTG---
CACGTGTC	14.46116	-GACACGTG---
ACACGTGG	14.24348	--ACACGTGG--
CCACGTCA	14.22991	--TGACGTGG--
ACGTGTCA	13.94907	TGACACGT----
CACGTGTA	13.65206	-TACACGTG---