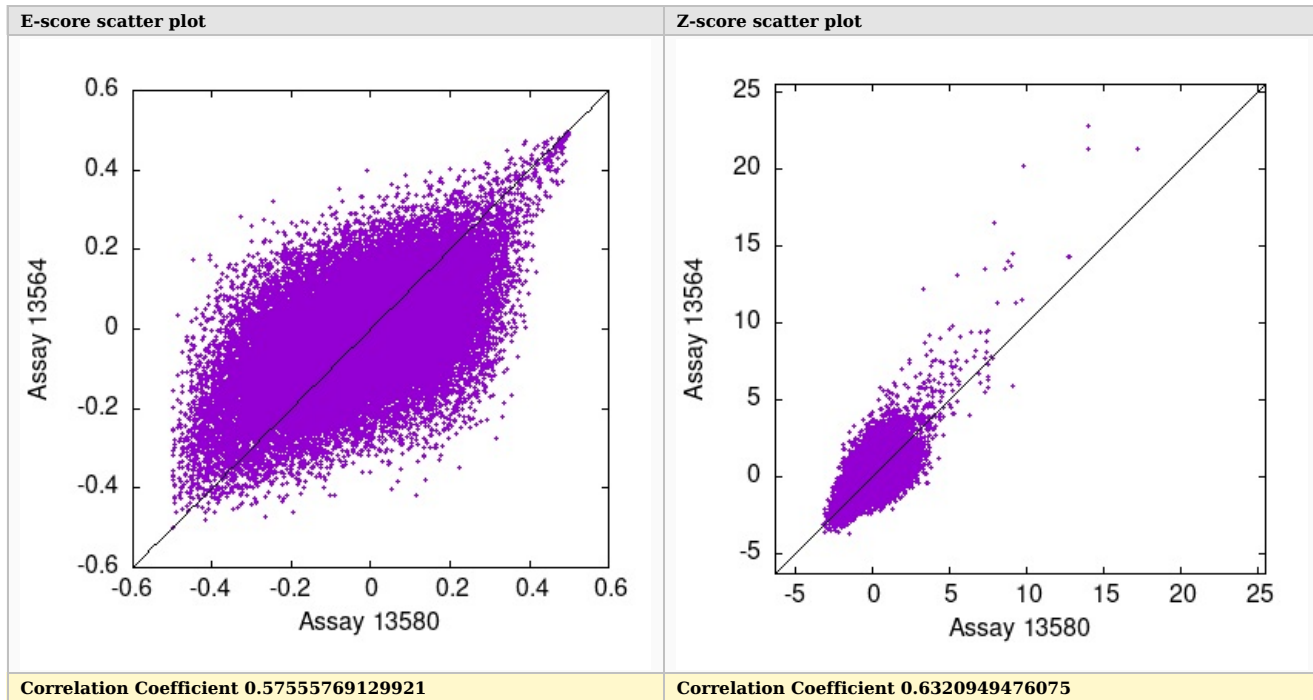


## QC report



## 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'			8 mer Z-scores for probeset 'all'		
Forward:		Reverse:	Forward:		Reverse:
Top 10	Scores	Alignment	Top 10	Scores	Alignment
CACGTGGC	0.49859	-CACGTGGC-	CACGTGGC	17.16189	--CACGTGGC-
CCACGTGG	0.49796	CCACGTGG--	ACGTGGCA	13.95145	---ACGTGGCA
ACGTGGCA	0.49747	--ACGTGGCA	CCACGTGG	13.94711	-CCACGTGG--
ACACGTGG	0.49742	ACACGTGG--	ACACGTGG	12.82390	---ACACGTGG--
CCACGTCA	0.49742	TGACGTGG--	CCACGTCA	12.71450	-TGACGTGG--
ACACGTGT	0.49434	ACACGTGT--	ACACGTGT	9.79122	-ACACGTGT--
CACGTGGA	0.49303	-CACGTGGA-	ACACGTCA	9.63662	-ACACGTCA--
ACACGTCA	0.49195	ACACGTCA--	CACGTGGA	9.27870	--CACGTGGA-
GCCACGTA	0.49181	-TACGTGGC-	CACGTGTC	9.06563	GACACGTG---
ACGTGGAA	0.49161	--ACGTGGAA	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'			8 mer Z-scores for probeset 'all'		
Forward:		Reverse:	Forward:		Reverse:
Top 10	Scores	Alignment	Top 10	Scores	Alignment
ACGTGGCA	0.49666	---ACGTGGCA	CCACGTGG	22.81855	--CCACGTGG--
CACGTGGC	0.49612	--CACGTGGC-	ACGTGGCA	21.25263	----ACGTGGCA
ACACGTGT	0.49552	-ACACGTGT--	CACGTGGC	21.24526	---CACGTGGC-
CCACGTGG	0.49527	-CCACGTGG--	ACACGTGT	20.17508	--ACACGTGT--
ATGACGTG	0.49213	ATGACGTG---	ATGACGTG	16.43306	-ATGACGTG---
CCACGTCA	0.49001	-TGACGTGG--	CACGTGTC	14.46116	-GACACGTG---
ACACGTGG	0.48927	-ACACGTGG--	ACACGTGG	14.24348	--ACACGTGG--
CACGTGTC	0.48826	GACACGTG---	CCACGTCA	14.22991	--TGACGTGG--
CACGTGTA	0.48821	TACACGTG---	ACGTGTCA	13.94907	TGACACGT---
ACACGTCA	0.48762	-ACACGTCA--	CACGTGTA	13.65206	-TACACGTG---