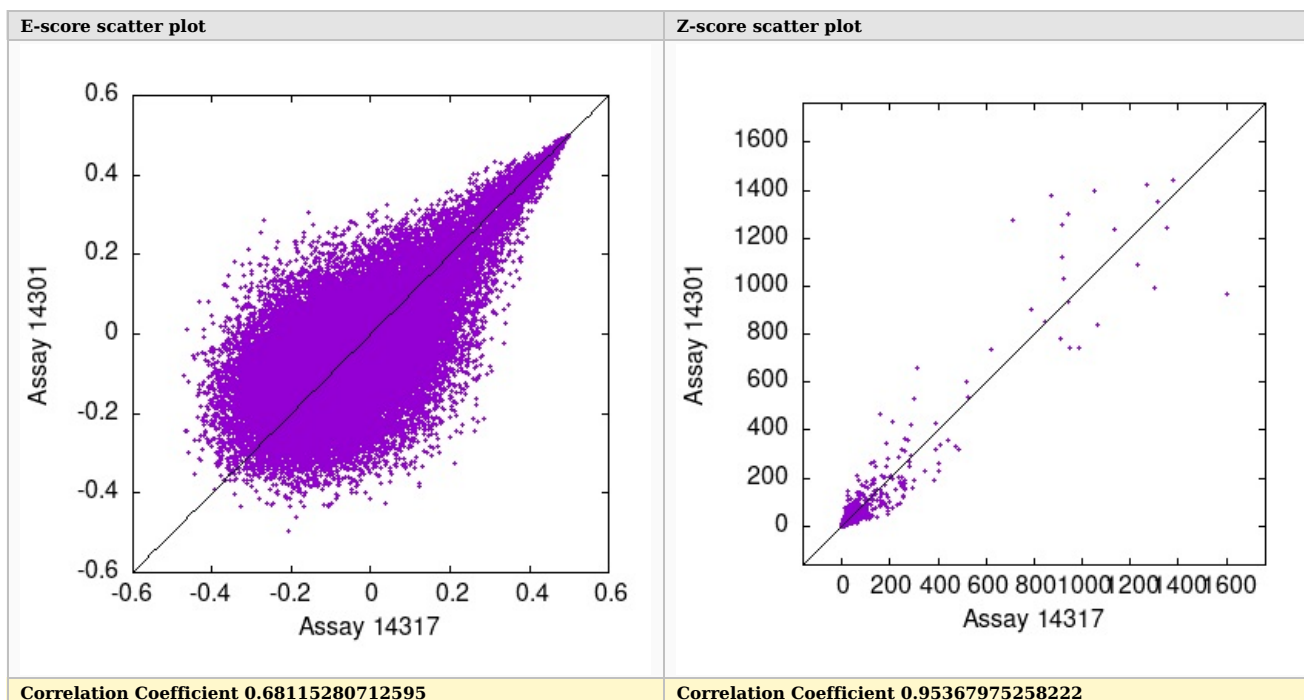


QC report



Top scoring motifs for Assay 14317

Protein ID: pTH15518.2 Gene: MAX 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	0.49940	-CCACGTGG-	CCACGTGG	1,602.26022	-CCACGTGG-
ACCACGTG	0.49898	ACCACGTG--	ACCACGTG	1,379.58511	ACCACGTG--
CACGTGCG	0.49828	--CACGTGCG	GCACGTGC	1,349.30495	-GCACGTGC-
CCACGTGC	0.49797	-CCACGTGC-	CACGTGCG	1,315.59066	--CACGTGCG
AGCACGTG	0.49785	--CACGTGCT	CCACGTGC	1,302.72612	-CCACGTGC-
CACGTGGC	0.49732	GCCACGTG--	CACGTGGC	1,266.79247	GCCACGTG--
GCACGTGC	0.49715	-GCACGTGC-	AGCACGTG	1,230.41947	--CACGTGCT
CACGTGGG	0.49681	CCCACGTG--	ACACGTGT	1,136.18882	-ACACGTGT-
ACACGTGC	0.49667	-ACACGTGC-	CACGTGTA	1,060.64731	--CACGTGTA
ATCACGTG	0.49654	ATCACGTG--	CACGTGTC	1,047.38629	--CACGTGTC

Top scoring motifs for Assay 14301

Protein ID: pTH15518.1 Gene: MAX 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
ACCACGTG	0.49880	--CACGTGGT	ACCACGTG	1,439.76366	--CACGTGGT
ACACGTGT	0.49841	-ACACGTGT-	CACGTGGC	1,421.73233	--CACGTGGC
CACGTGGC	0.49834	--CACGTGGC	CACGTGTC	1,398.90262	GACACGTG--
AACACGTG	0.49796	AACACGTG--	ACACGTGG	1,378.70233	-ACACGTGG-
CCACGTGG	0.49779	-CCACGTGG-	CACGTGCG	1,349.22796	--CACGTGCG
ACACGTGG	0.49773	-ACACGTGG-	ACACGTGC	1,300.86293	-ACACGTGC-
CACGTGCG	0.49744	--CACGTGCG	AACACGTG	1,277.04390	AACACGTG--
GCACGTGC	0.49721	-GCACGTGC-	CCACGTGA	1,255.94120	-TCACGTGG-
AGCACGTG	0.49711	AGCACGTG--	GCACGTGC	1,245.61358	-GCACGTGC-
CACGTGTC	0.49691	GACACGTG--	ACACGTGT	1,239.04553	-ACACGTGT-