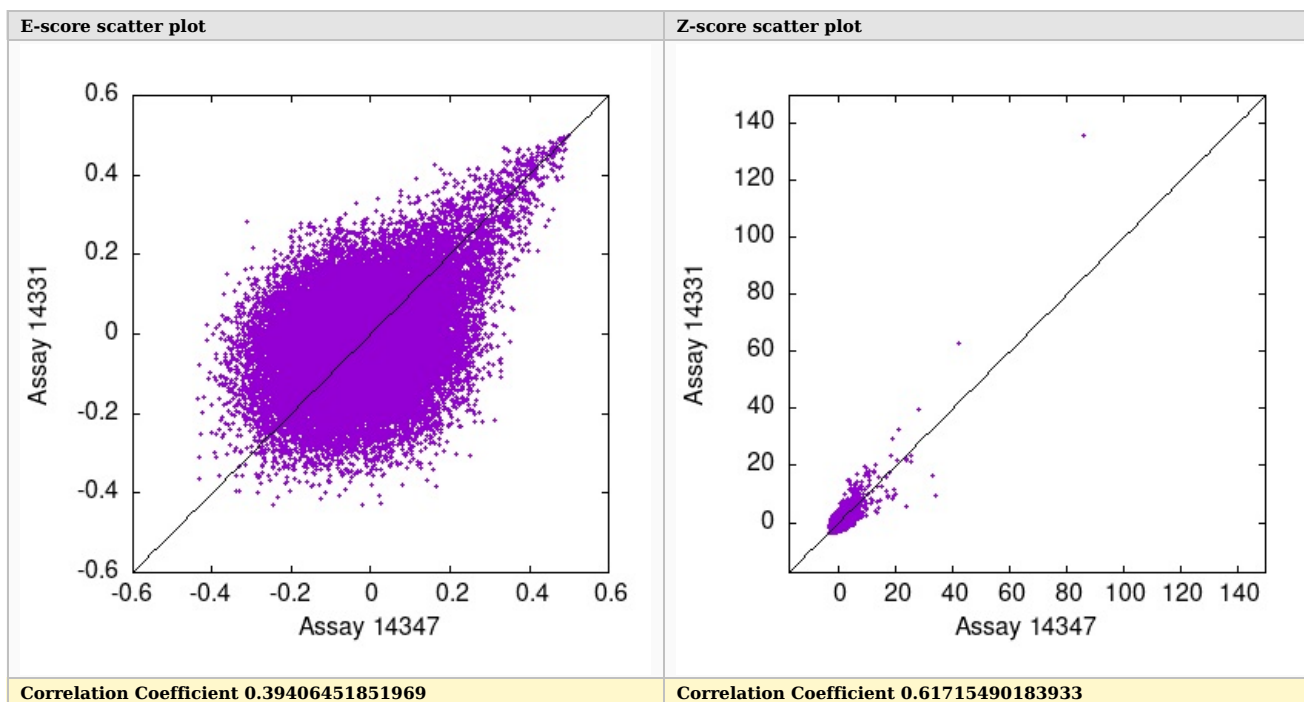


QC report



Top scoring motifs for Assay 14347

Protein ID: pTH15530.2 Gene: FOSL2 Domain: bZIP_1 Flag: Pass_matched_pair Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:		Reverse:	
Top 10	Scores	Alignment	
TGACGTCA	0.49756	----TGACGTCA	
ATGACTCA	0.49447	---ATGACTCA-	
CGATGACG	0.48959	-CGATGACG---	
ATGAGTCA	0.48849	----TGACTCAT	
GATGACGC	0.48817	--GATGACGC--	
AGTCATCA	0.48677	--TGATGACT---	
ACGTCATC	0.48564	--GATGACGT--	
ATGACGCA	0.48554	---ATGACGCA-	
CGTCATAG	0.48470	--CTATGACG---	
ATGATGAC	0.48272	ATGATGAC----	

8 mer Z-scores for probeset 'all'

Forward:		Reverse:	
Top 10	Scores	Alignment	
TGACGTCA	85.68657	----TGACGTCA	
ATGACTCA	41.81745	---ATGACTCA-	
AGTCATCA	33.85547	-TGATGACT---	
CGATGACG	32.87951	-CGATGACG---	
ATGAGTCA	28.11021	----TGACTCAT	
ATGACGCA	25.31750	---ATGACGCA-	
GATGACGC	25.22047	--GATGACGC--	
ACGATGAC	23.69655	ACGATGAC----	
ACGTCATC	23.48304	--GATGACGT--	
ATGATGAC	23.48304	ATGATGAC----	

Top scoring motifs for Assay 14331

Protein ID: pTH15530.1 Gene: FOSL2 Domain: bZIP_1 Flag: Pass_matched_pair Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:		Reverse:	
Top 10	Scores	Alignment	
TGACGTCA	0.49874	----TGACGTCA	
ATGACTCA	0.49563	---ATGACTCA-	
ATGAGTCA	0.49386	----TGACTCAT	
GTGAGTCA	0.49027	----TGACTCAC	
GTGACTCA	0.49004	---GTGACTCA-	
ACGTCATC	0.48904	--GATGACGT--	
CGTCATCA	0.48637	-TGATGACG---	
GTCATCAA	0.48303	TTGATGAC----	
ATGACGTG	0.48294	---ATGACGTG-	
GATGACGC	0.48193	--GATGACGC--	

8 mer Z-scores for probeset 'all'

Forward:		Reverse:	
Top 10	Scores	Alignment	
TGACGTCA	135.63814	----TGACGTCA	
ATGACTCA	62.73703	---ATGACTCA-	
ATGAGTCA	39.88364	----TGACTCAT	
GTGAGTCA	32.57190	----TGACTCAC	
GTGACTCA	29.34414	---GTGACTCA-	
CGTCATCA	23.70289	-TGATGACG---	
GATGACGC	23.70289	--GATGACGC--	
ATGATGAC	22.63697	ATGATGAC----	
ACGTCATC	21.99706	--GATGACGT--	
ATGACGTG	21.99706	---ATGACGTG-	