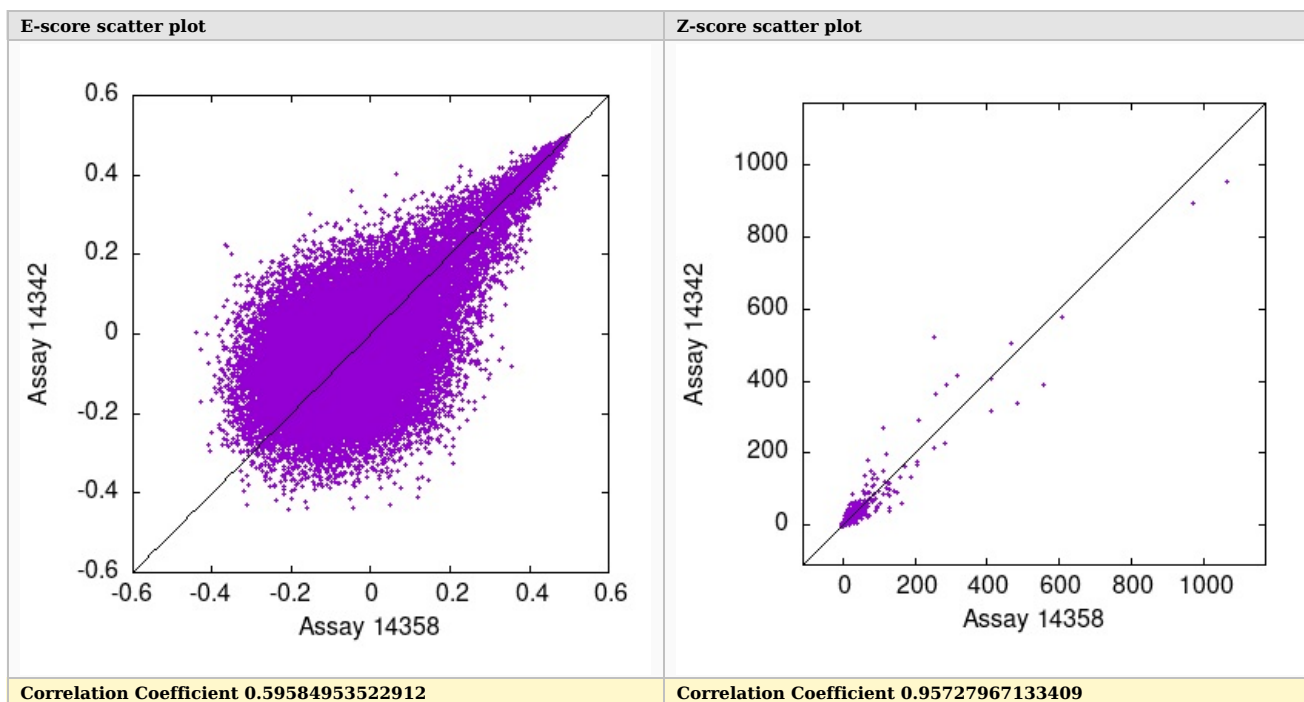


QC report



Correlation Coefficient 0.59584953522912

Correlation Coefficient 0.95727967133409

Top scoring motifs for Assay 14358

Protein ID: pTH15541.2 Gene: YY1 Domain: zf-C2H2 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
AATGGCGG	0.49899	--AATGGCGG--	AATGGCGG	1,064.57402	--AATGGCGG--
CGCCATTA	0.49889	TAATGGCG--	CGCCATTA	968.89604	TAATGGCG--
AAATGGCG	0.49737	AAATGGCG--	ATGGCGGC	608.41217	--ATGGCGGC
ATGGCGGC	0.49688	--ATGGCGGC	AAATGGCG	556.67557	AAATGGCG--
AATGGCGC	0.49666	--AATGGCGC--	AATGGCGT	484.07731	--AATGGCGT--
AATGGCGT	0.49637	--AATGGCGT--	CAATGGCG	465.54422	CAATGGCG--
CAATGGCG	0.49599	CAATGGCG--	AATGGCCG	410.52233	--AATGGCCG--
AATGGCCG	0.49568	--AATGGCCG--	AATGGCGC	409.32435	--AATGGCGC--
ACCGCCAT	0.49554	--ATGGCGGT	CCGCCATA	315.75487	-TATGGCGG-
ATGGCGGA	0.49432	--ATGGCGGA	ACCGCCAT	287.13251	--ATGGCGGT

Top scoring motifs for Assay 14342

Protein ID: pTH15541.1 Gene: YY1 Domain: zf-C2H2 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
AATGGCGG	0.49911	--AATGGCGG--	AATGGCGG	954.60671	--AATGGCGG--
CGCCATTA	0.49831	-TAATGGCG--	CGCCATTA	895.38033	TAATGGCG--
CAATGGCG	0.49700	--CAATGGCG--	ATGGCGGC	578.21040	--ATGGCGGC
AAAATGGC	0.49665	AAAATGGC--	ATGGCGGA	522.28850	--ATGGCGGA
ATGGCGGC	0.49650	---ATGGCGGC	CAATGGCG	507.07371	CAATGGCG--
ATGGCGGA	0.49630	---ATGGCGGA	CCGCCATA	417.40760	-TATGGCGG-
AAATGGCG	0.49565	--AAATGGCG--	AATGGCCG	404.96078	--AATGGCCG--
CCGCCATA	0.49556	--TATGGCGG--	ACCGCCAT	391.36187	--ATGGCGGT
AATGGCGT	0.49551	---AATGGCGT--	AAATGGCG	387.77317	AAATGGCG--
AATGGCCG	0.49514	---AATGGCCG--	CATGGCGG	364.78234	-CATGGCGG-