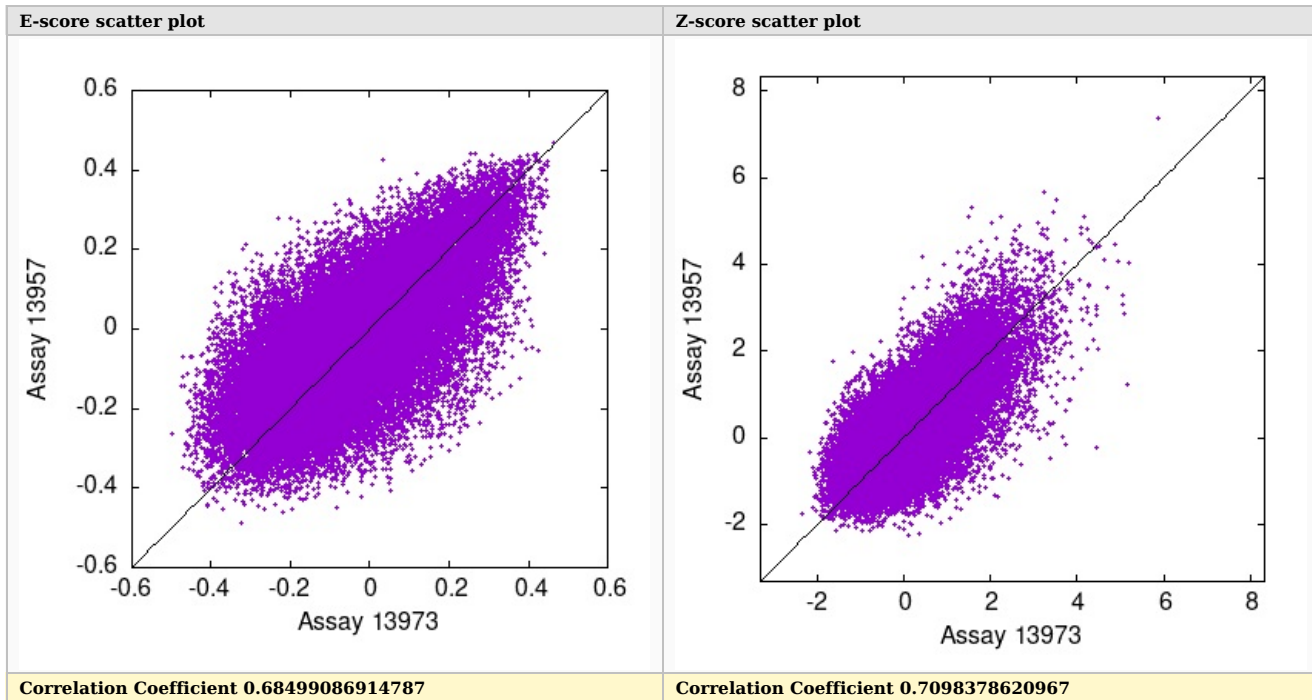


QC report



Top scoring motifs for Assay 13973

Protein ID: pTH14338.4 Gene: SP140.DBD Domain: SAND 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
CGCGCGCG	0.46569	----CGCGCGCG--	CGCGCGCG	5.85886	----CGCGCGCG--
TACGACAA	0.44945	---TTGTCGTA--	AATTACGG	5.17789	--AATTACGG----
TATACCGA	0.44917	---TCGGTATA--	GTAATTAC	5.16165	GTAATTAC-----
CGTCGTAA	0.44877	----CGTCGTAA--	TACGGAAA	5.07972	----TACGGAAA--
AATTACGG	0.44538	---CCGTAATT--	GTACGACA	5.04962	----GTACGACA--
GTACGACA	0.44381	----GTACGACA--	TACCGGTA	5.03954	---TACCGGTA--
TACGGAAA	0.44254	TTTCGGTA----	CCGTAATA	4.95661	--TATTACGG----
GTAATTAC	0.44096	----GTAATTAC--	TACGACAA	4.88057	----TACGACAA--
CCGTAATA	0.43984	---CCGTAATA--	ACGGCATA	4.68707	-----ACGGCATA--
TCGTACGA	0.43857	---TCGTACGA--	TTACGGAA	4.62670	----TTACGGAA--

Top scoring motifs for Assay 13957

Protein ID: pTH14338.3 Gene: SP140.DBD Domain: SAND 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
CGCGCGCG	0.46901	----CGCGCGCG--	CGCGCGCG	7.35537	--CGCGCGCG--
CGTAGCTA	0.44261	----CGTAGCTA--	ACGACGAC	5.66460	GTCGTCGT---
GCAGCGCG	0.44224	----GCAGCGCG--	ATATTCGG	5.47414	--CGGAATAT--
GTAACGAC	0.43949	----GTCGTTAC--	CGTAGCTA	5.31952	--CGTAGCTA--
ATTACGAC	0.43733	----GTCGTAAT--	ATTACGAC	5.20288	---GTCGTAAT--
TGTCGTAA	0.43701	----TGTCGTAA--	CGTCGTAA	5.10800	---CGTCGTAA--
CGACGTCG	0.43629	----CGACGTCG--	GTAACGAC	5.10030	---GTCGTTAC--
CGTCGTTA	0.43474	----CGTCGTTA--	CGCGTAAC	5.09424	---CGCGTAAC--
TATTACGA	0.43401	-----TCGTAATA	CGACGTCG	4.96092	---CGACGTCG--
GACGCGTC	0.42734	GACGCGTC-----	GCAGCGCG	4.94465	--GCAGCGCG--