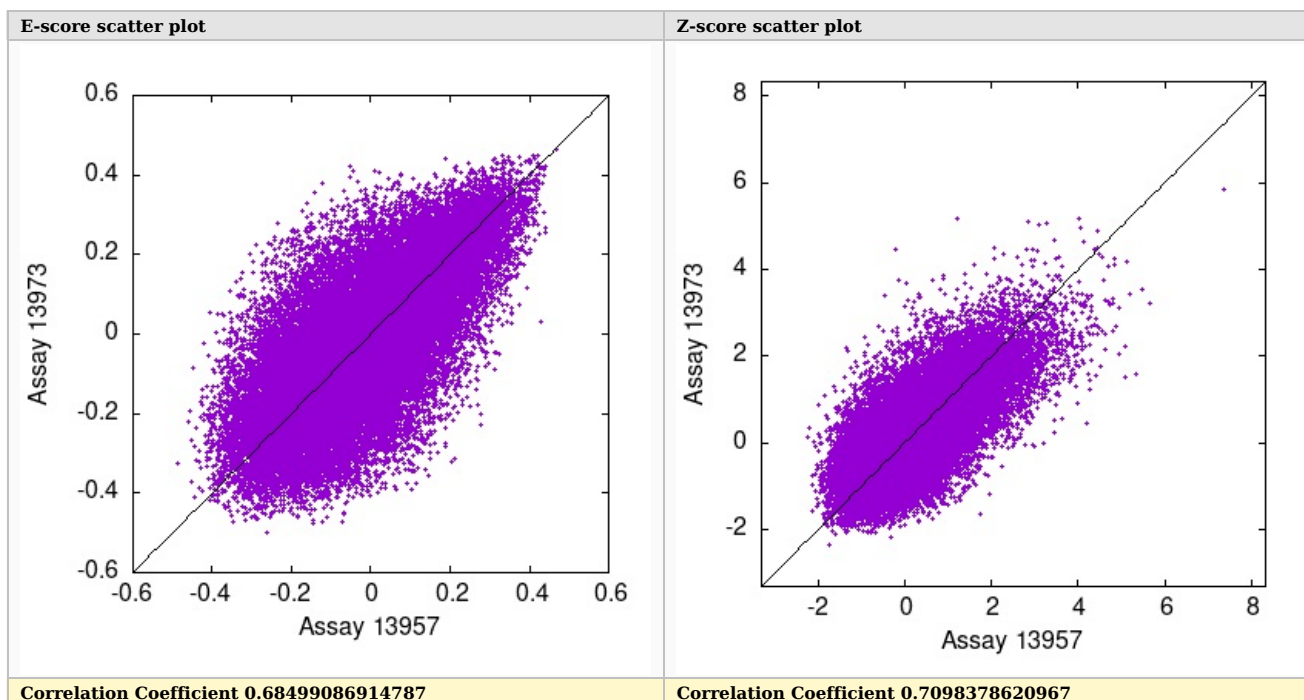


QC report



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'

Forward:	Reverse:

Top 10	Scores	Alignment
CGCGCGCG	0.46901	----CGCGCGCG--
CGTAGCTA	0.44261	----CGTAGCTA--
GCGCGCGC	0.44224	----GCGCGCGC--
GTAACGAC	0.43949	----GTCGTTAC--
ATTACGAC	0.43733	----GTCGTAAT--
TGTCGTAA	0.43701	----TGTCGTAA--
CGACGTCG	0.43629	----CGACGTCG--
CGTCGTTA	0.43474	----CGTCGTTA--
TATTACGA	0.43401	-----TCGTAATA
GACGCGTC	0.42734	GACGCGTC-----

8 mer Z-scores for probeset 'all'

Forward:	Reverse:

Top 10	Scores	Alignment
CGCGCGCG	7.35537	--CGCGCGCG--
ACGACGAC	5.66460	GTCGTCGT---
ATATTCCG	5.47414	--CGGAATAT--
CGTAGCTA	5.31952	--CGTAGCTA--
ATTACGAC	5.20288	--GTCGTAAT--
CGTCGTAA	5.10800	--CGTCGTAA--
GTAACGAC	5.10030	--GTCGTTAC--
CGCGTAAC	5.09424	--CGCGTAAC--
CGACGTCG	4.96092	--CGACGTCG--
GCGCGCGC	4.94465	--GCGCGCGC--

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'

Forward:	Reverse:

Top 10	Scores	Alignment
CGCGCGCG	0.46569	----CGCGCGCG--
TACGACAA	0.44945	---TTGTCGTA--
TATACCGA	0.44917	---TCGGTATA--
CGTCGTAA	0.44877	----CGTCGTAA--
AATTACGG	0.44538	---CCGTAATT--
GTACGACA	0.44381	----GTACGACA--
TACGGAAA	0.44254	TTTCCGTA-----
GTAATTAC	0.44096	----GTAATTAC--
CCGTAATA	0.43984	---CCGTAATA--
TCGTACGA	0.43857	---TCGTACGA--

8 mer Z-scores for probeset 'all'

Forward:	Reverse:

Top 10	Scores	Alignment
CGCGCGCG	5.85886	----CGCGCGCG--
AATTACGG	5.17789	--AATTACGG----
GTAATTAC	5.16165	GTAATTAC-----
TACGGAAA	5.07972	----TACGGAAA--
GTACGACA	5.04962	----GTACGACA--
TACCGGTA	5.03954	----TACCGGTA--
CCGTAATA	4.95661	--TATTACGG----
TACGACAA	4.88057	----TACGACAA--
ACGGCATA	4.68707	-----ACGGCATA
TTACGGAA	4.62670	----TTACGGAA--