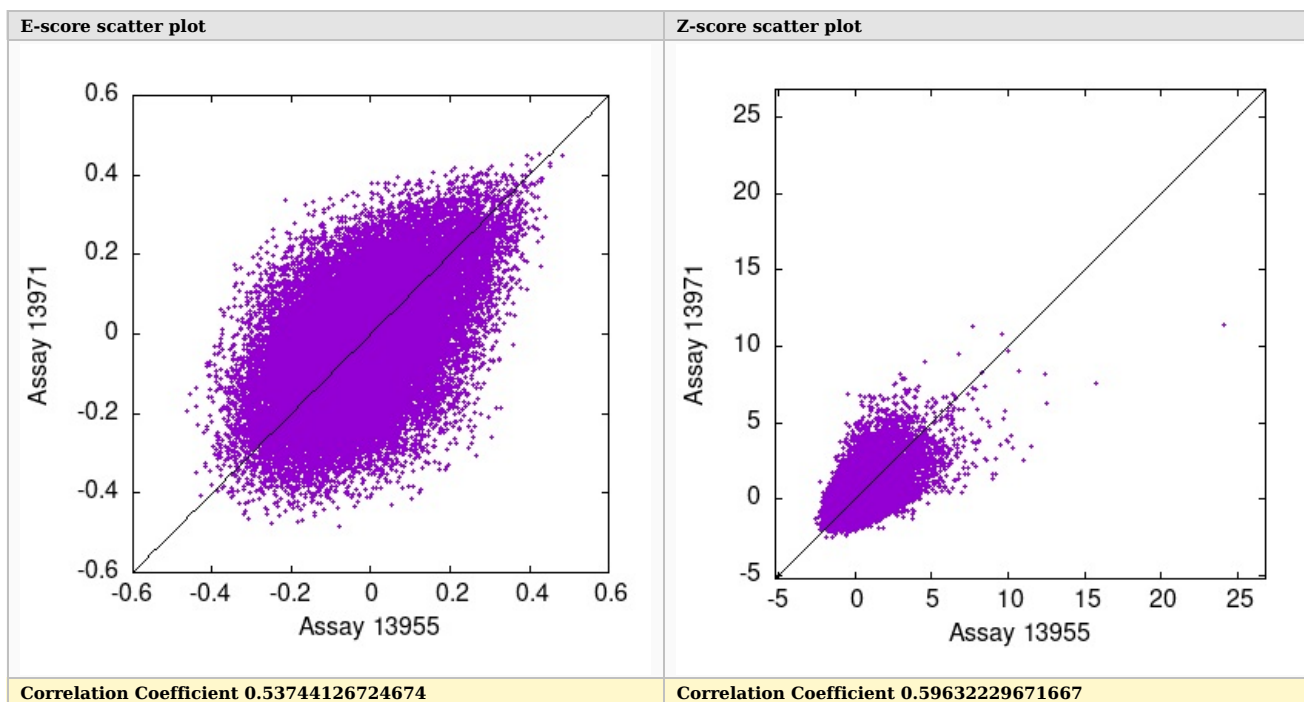


QC report



Top scoring motifs for Assay 13955

Protein ID: pTH14266.3 Gene: MBD1.DBD Domain: MBD Flag: Pass_matched_pair Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:		Reverse:
Top 10	Scores	Alignment
CGCGCGCG	0.48170	CGCGCGCG-----
GCGC GCGC	0.45374	-GCGC GCGC-----
GCGC GCGA	0.45197	-GCGC GCGA-----
CCGC GCGC	0.44211	-GCGCGCGC-----
ATCGCGCG	0.43359	--CGCGCGAT----
ACGATCGT	0.43230	-ACGATCGT-----
GC GCGCAA	0.43106	-GCGCGCAA-----
CGAATTCG	0.42804	-----CGAATTCG
ACGCGTTA	0.42784	-ACGCGTTA-----
CGCGCGAA	0.42494	--CGCGCGAA----

8 mer Z-scores for probeset 'all'

Forward:		Reverse:
Top 10	Scores	Alignment
CGCGCGCG	24.13599	CGCGCGCG--
GCGC GCGC	15.71448	-GCGC GCGC-
ATCGCGCG	12.48915	--CGCGCGAT
GCGC GCGA	12.35399	-GCGCGCGA-
CGCGTAAC	11.49191	--CGCGTAAC
ACGATCGT	11.01298	-ACGATCGT-
GCGATCGC	10.68969	-GCGATCGC-
CGCGTTAA	10.31718	--CGCGTTAA
AGCGCGCG	10.23744	AGCGCGCG--
TACGCGTA	10.01048	--TACGCGTA

Top scoring motifs for Assay 13971

Protein ID: pTH14266.4 Gene: MBD1.DBD Domain: MBD Flag: Pass_matched_pair Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:		Reverse:
Top 10	Scores	Alignment
CGCGCGAA	0.45221	-CGCGCGAA--
TCGC GCGA	0.45055	-TCGC GCGA---
CGCGCGCG	0.44837	-CGCGCGCG--
CGCGAAAA	0.44008	-CGCGAAAA--
GC GCGCGC	0.43105	GCGCGCGC---
CGCAATA	0.42479	---CGCAATA
TACGCGTA	0.42420	-TACGCGTA--
GCGCGCGA	0.42237	GCGCGCGA---
TATCGATA	0.42030	--TATCGATA-
AACGTAAA	0.41854	-AACGTAAA--

8 mer Z-scores for probeset 'all'

Forward:		Reverse:
Top 10	Scores	Alignment
CGCGCGCG	11.43779	-CGCGCGCG---
TCGC GCGA	11.33250	-TCGC GCGA---
CGCGCGAA	10.80646	-CGCGCGAA---
TACGCGTA	9.68331	-TACGCGTA---
CGCGAAAA	9.51677	-CGCGAAAA---
TATCGATA	8.96542	--TATCGATA--
GCGATCGC	8.34905	----GCGATCGC
GCGCGAAA	8.23278	--GCGCGAAA---
GCGCGCGA	8.18592	GCGCGCGA----
CGTAAAA	8.18083	-CGTAAAA---