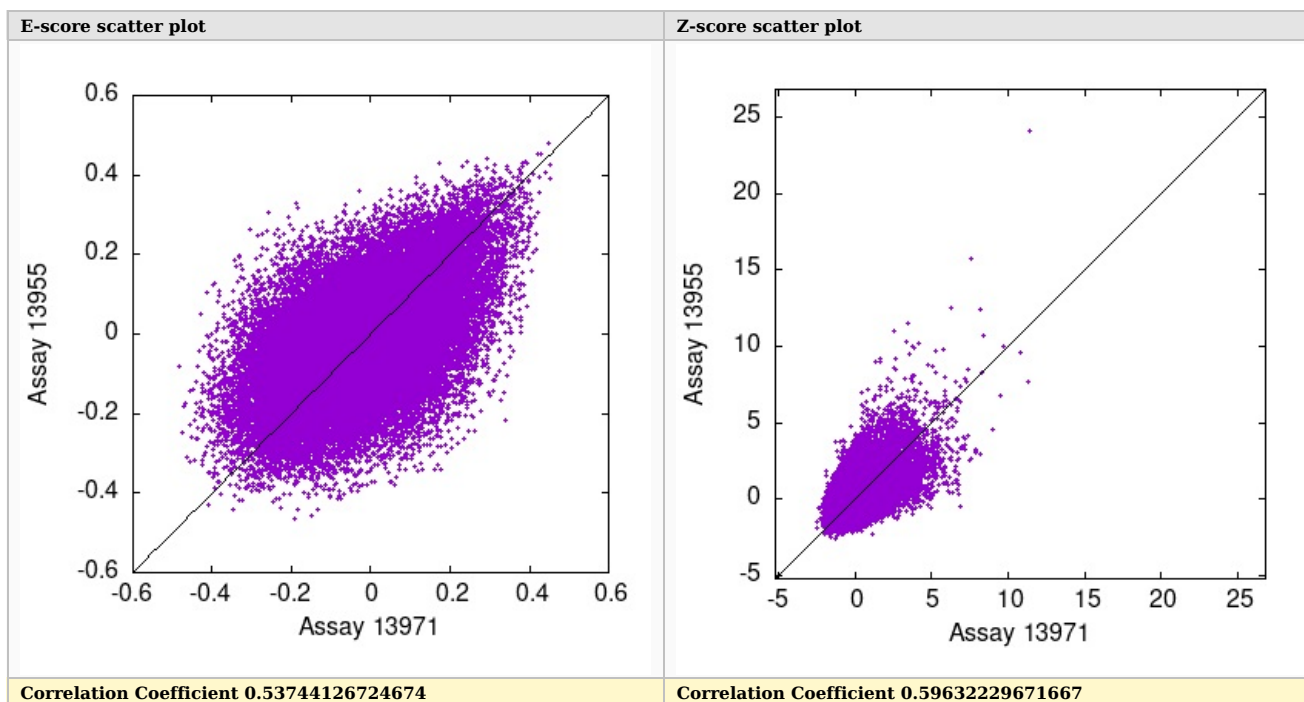


QC report



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--	
TCGCGCGA	0.45055	TCGCGCGA---	
CGCGCGCG	0.44837	-CGCGCGCG--	
CGCGAAAA	0.44008	-CGCGAAAA--	
GC GCGCGC	0.43105	GCGCGCGC---	
CGCGAATA	0.42479	--CGCGAATA	
TACGCGTA	0.42420	-TACGCGTA--	
GC GCGCGA	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---	
TCGCGCGA	11.33250	TCGCGCGA----	
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----	
CGCTAAAA	8.18083	-CGCTAAAA---	

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-----	
GC GCGCGC	0.45374	-GC GCGCGC-----	
CGCGCGCA	0.45197	-GC GCGCGA-----	
CCGCGCGC	0.44211	-GC GCGCGC-----	
ATCGCGCG	0.43359	--CGCGCGAT----	
ACGATCGT	0.43230	-ACGATCGT-----	
GCGCGCAA	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--	
GCGCGCGC	15.71448	-GCGCGCGC--	
ATCGCGCG	12.48915	--CGCGCGAT	
GCGCGCGA	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	