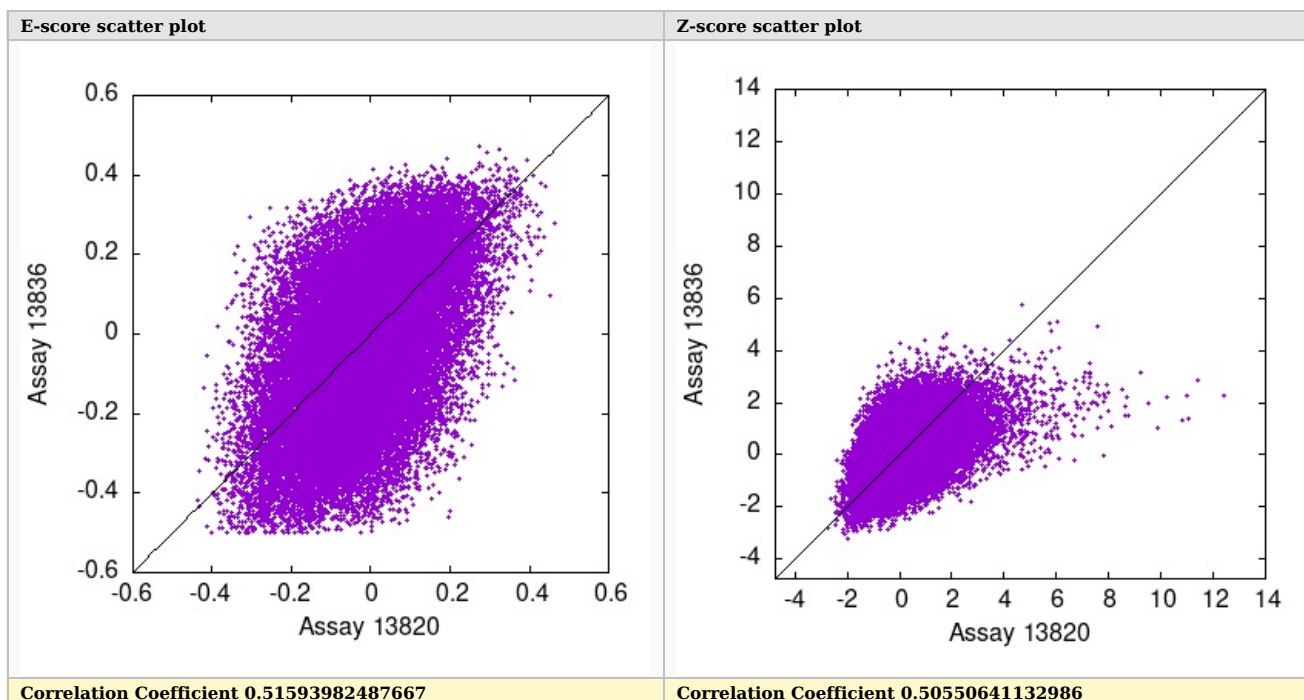




QC report





Top scoring motifs for Assay 13820

Protein ID: pTH13920.1 Gene: PHF21A.DBD Domain: AT_hook Flag: Pass_matched_pair Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:		Reverse:	
			
Top 10	Scores	Alignment	
ATATATAT	0.46494	--ATATATAT	
TATATATA	0.45108	-TATATATA-	
ATAATATA	0.44157	-ATAATATA-	
ATAAATAA	0.43619	--TTATTTAT	
ATAATAAA	0.43009	-ATAATAAAA-	
ATATTATA	0.42925	TATAATAT--	
ATTATTTA	0.42847	-ATTATTTA-	
ATTAATTA	0.42433	--TAATTAAT	
TTAATTAA	0.42255	-TTAATTAA-	
TAATAAAA	0.42082	--TAATAAAA	



8 mer Z-scores for probeset 'all'

Forward:		Reverse:	
			
Top 10	Scores	Alignment	
ATATATAT	12.45736	-ATATATAT-	
ATAATATA	11.39868	--TATATTAT	
ATAAATAA	11.09748	-ATAAATAA-	
ATATTATA	10.98871	-ATATTATA-	
ATTAATTA	10.82018	--TAATTAAT	
ATAATAAA	10.23424	-ATAATAAA-	
TATATATA	9.86533	TATATATA--	
AAATATTA	9.56100	-AAATATTA-	
AATAATAA	9.22059	-AATAATAA-	
TATAAATA	8.74300	TATAAATA--	



Top scoring motifs for Assay 13836

Protein ID: pTH13920.2 Gene: PHF21A.DBD Domain: AT_hook Flag: Pass_matched_pair Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:		Reverse:	
			
Top 10	Scores	Alignment	
AATAAATT	0.47097	--AATAAATT--	
ACAAAATA	0.46285	--ACAAAATA--	
AAATAAAT	0.45816	-AAATAAAT--	
AATATATT	0.44023	--AATATATT--	
ATAGTAAT	0.43967	-ATAGTAAT--	
ATATTAAT	0.43826	-ATATTAAT--	
CTGTATTA	0.42786	-TAATACAG--	
ATACATTA	0.42690	---ATACATTA	
GATATGTA	0.42616	--GATATGTA	
CACATATA	0.42162	CACATATA---	

8 mer Z-scores for probeset 'all'

Forward:		Reverse:	
			
Top 10	Scores	Alignment	
AATAAATT	5.76353	----AATAAATT	
AATATATT	5.12227	AATATATT----	
ACAAAATA	5.07066	-ACAAAATA---	
ATATTAAT	4.89913	---ATATTAAT-	
TATTAATA	4.75962	----TATTAATA	
ATAGTAAT	4.60989	---ATAGTAAT-	
GATATGTA	4.49622	--GATATGTA--	
AAATAAAT	4.38385	---AAATAAAT-	
TATTTGCA	4.37924	---TATTTGCA	
ATCTAGAT	4.26922	---ATCTAGAT-	