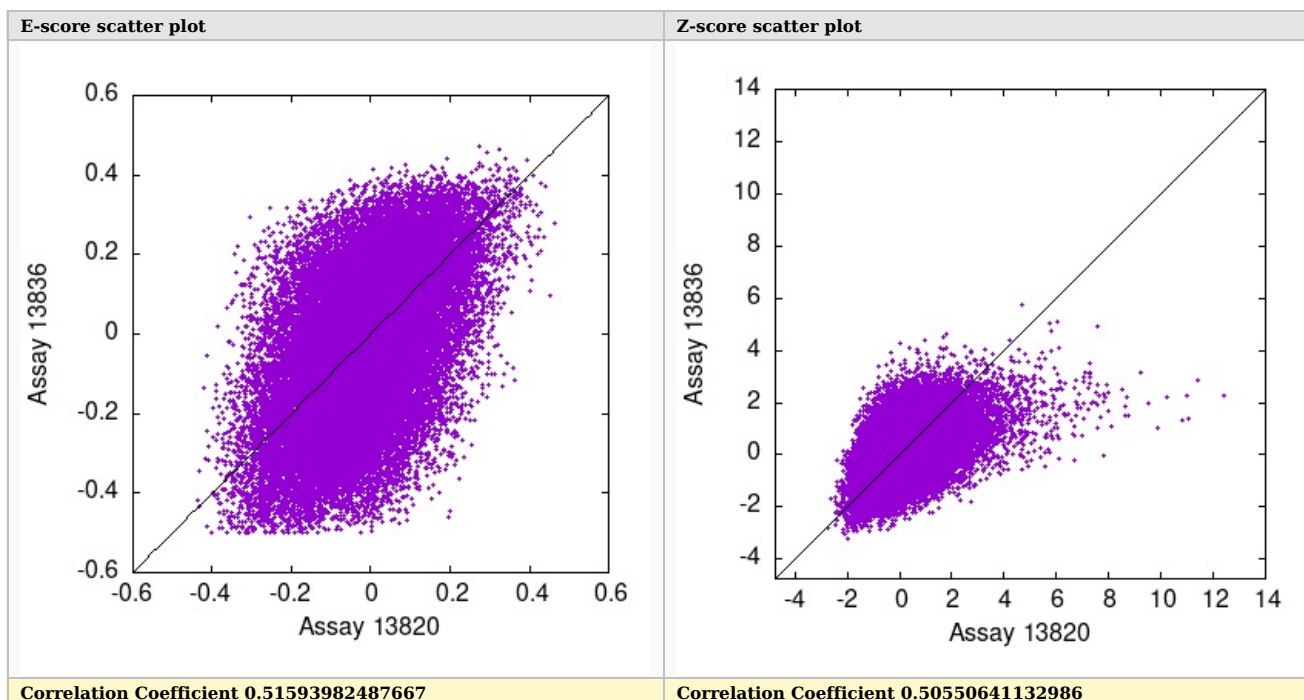


QC report



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'			8 mer Z-scores for probeset 'all'		
Forward:		Reverse:	Forward:		Reverse:
Top 10	Scores	Alignment	Top 10	Scores	Alignment
ATATATAT	0.46494	--ATATATAT	ATATATAT	12.45736	-ATATATAT-
TATATATA	0.45108	-TATATATA-	ATAATATA	11.39868	--TATATTAT
ATAATATA	0.44157	-ATAATATA-	ATAAATAA	11.09748	-ATAAATAA-
ATAAATAA	0.43619	--TTATTTAT	ATATTATA	10.98871	-ATATTATA-
ATAATAAA	0.43009	-ATAATAAA-	ATTAATTA	10.82018	--TAATTAAT
ATATTATA	0.42925	TATAATAT--	ATAATAAA	10.23424	-ATAATAAA-
ATTATTTA	0.42847	-ATTATTTA-	TATATATA	9.86533	TATATATA--
ATTAATTA	0.42433	--TAATTAAT	AAATATTA	9.56100	-AAATATTA-
TTAATTAA	0.42255	-TTAATTAA-	AATAATAA	9.22059	-AATAATAA-
TAATAAAA	0.42082	--TAATAAAA	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'			8 mer Z-scores for probeset 'all'		
Forward:		Reverse:	Forward:		Reverse:
Top 10	Scores	Alignment	Top 10	Scores	Alignment
AATAAATT	0.47097	--AATAAATT-	AATAAATT	5.76353	----AATAAATT
ACAAAATA	0.46285	--ACAAAATA-	AATATATT	5.12227	AATATATT----
AAATAAAT	0.45816	-AAATAAAT--	ACAAAATA	5.07066	-ACAAAATA--
AATATATT	0.44023	--AATATATT-	ATATTAAT	4.89913	---ATATTAAT-
ATAGTAAT	0.43967	-ATAGTAAT--	TATTAATA	4.75962	----TATTAATA
ATATTAAT	0.43826	-ATATTAAT--	ATAGTAAT	4.60989	---ATAGTAAT-
CTGTATTA	0.42786	-TAATACAG--	GATATGTA	4.49622	--GATATGTA--
ATACATTA	0.42690	---ATACATTA	AAATAAAT	4.38385	---AAATAAAT-
GATATGTA	0.42616	--GATATGTA-	TATTTGCA	4.37924	---TATTTGCA
CACATATA	0.42162	CACATATA--	ATCTAGAT	4.26922	---ATCTAGAT-