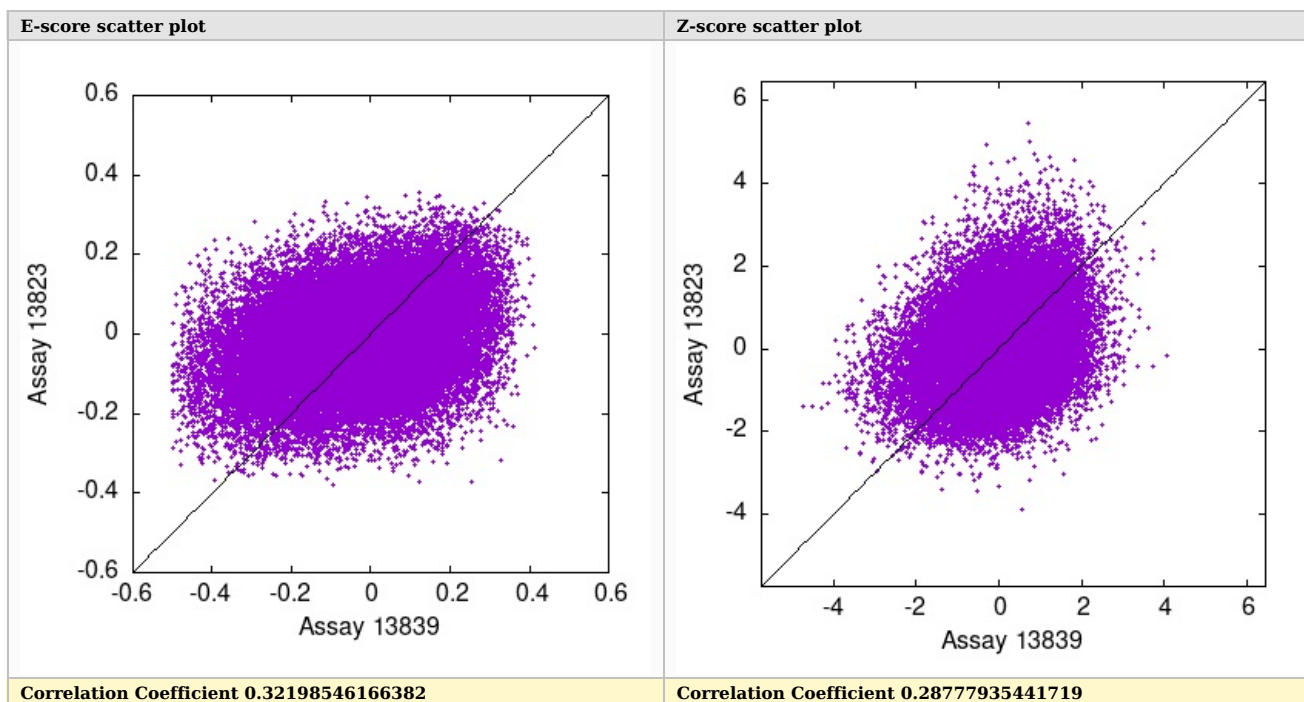


QC report



Top scoring motifs for Assay 13839

Protein ID: pTH13924.2 Gene: SETBP1.DBD.2 Domain: AT_hook Flag: Reject 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
ACTAATTA	0.41449	----TAATTAGT	TATTAACA	4.08022	----TATTAACA
TATTAACA	0.41071	----TATTAACA	ACTAACAT	3.73961	--ATGTTAGT-
ATATTAAG	0.41052	---ATATTAAG-	AATATATT	3.73344	AATATATT----
AAATTGAT	0.40349	---AAATTGAT-	ATATTAAG	3.71761	---ATATTAAG-
AATCAATT	0.39768	----AATCAATT	ACACAATA	3.63655	----TATTGTGT
ACATACTA	0.39626	-ACATACTA---	CTGTATTA	3.50583	-CTGTATTA---
GATATGTA	0.39379	--GATATGTA--	AATTAATT	3.42335	----AATTAATT
AATAATAA	0.39333	--AATAATAA--	ACATTACT	3.41067	---ACATTACT-
AACGTATT	0.39273	AACGTATT----	ACAGCATA	3.40324	----TATGCTGT
ACAGCATA	0.38897	----TATGCTGT	AATATTAA	3.36545	--AATATTAA--

Top scoring motifs for Assay 13823

Protein ID: pTH13924.1 Gene: SETBP1.DBD.2 Domain: AT_hook Flag: Reject 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
AATATAGA	0.35484	----TCTATATT	GTGTTGGA	5.43969	TCCAACAC---
ATATTTAA	0.34808	---TTAAATAT-	CAACAAAG	4.99508	--CAACAAAG-
ACACTAAC	0.34674	--GTTAGTGT--	ACCTAAAA	4.94490	ACCTAAAA---
ATAAACAC	0.34565	---GTGTTTAT-	ATATTTAA	4.69693	ATATTTAA---
CAACAAAG	0.34545	-CTTTGTTG--	TAACACAA	4.64422	TAACACAA---
AACAGAAA	0.33541	--AACAGAAA--	GTATAGCA	4.60571	TGCTATAC---
ACCCAAAA	0.33319	-TTTTGGGT---	AATAATGG	4.56098	---AATAATGG
GTTGGATA	0.33009	--GTTGGATA--	AATCATAA	4.56098	--TTATGATT-
GTGTTGGA	0.32862	GTGTTGGA----	AAGTAAAG	4.50847	--CTTTACTT-
TACGATAA	0.32739	---TACGATAA-	TCCTATAA	4.48571	TCCTATAA---