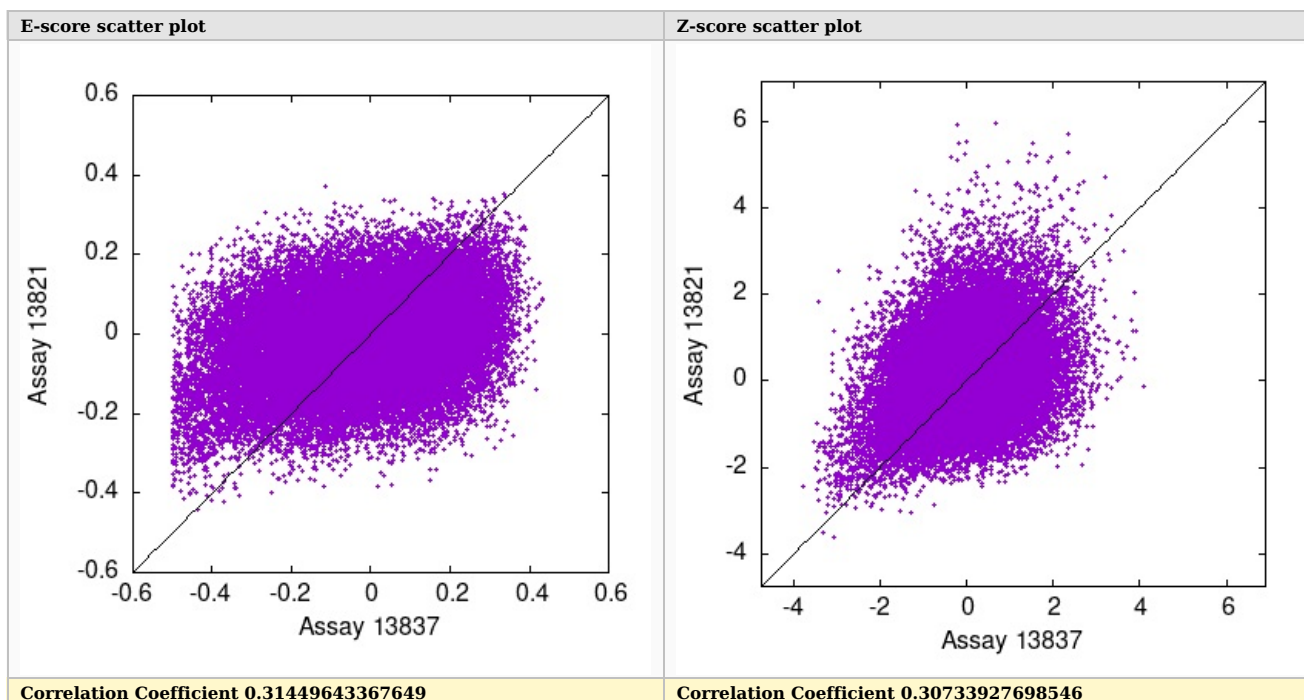


QC report



Top scoring motifs for Assay 13837

Protein ID: pTH13922.2 Gene: SCML4.DBD 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
ATAGTAAT	0.43463	--ATAGTAAT--	GATATGTA	4.07819	--GATATGTA--
ACAAAATA	0.43437	ACAAAATA---	AATATATT	3.92110	--AATATATT--
CTGTATTA	0.42534	---CTGTATTA	CACATATA	3.88521	--CACATATA--
AATAAATT	0.42515	--AATAAATT--	AATAAATT	3.86519	--AATAAATT--
AATATATT	0.41881	--AATATATT--	ACAAAATA	3.85148	ACAAAATA---
ATCTAGAT	0.41765	---ATCTAGAT	ATAATGTA	3.79979	ATAATGTA---
AGAAATAT	0.41617	--AGAAATAT--	ATAGTAAT	3.68101	--ATAGTAAT--
ATAATGTA	0.41515	ATAATGTA---	TATTAATA	3.63313	--TATTAATA--
GATATGTA	0.41445	--GATATGTA--	AGATATCT	3.62515	---AGATATCT
AGATATCT	0.41155	---AGATATCT	AATTTAAA	3.58852	--AATTTAAA--

Top scoring motifs for Assay 13821

Protein ID: pTH13922.1 Gene: SCML4.DBD 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
ACACACAC	0.37235	--GTGTGTGT--	CCAACACA	5.93516	--TGTGTTGG--
AATTTGTA	0.35407	-AATTTGTA--	CAGCAACC	5.92351	-GGTTGCTG--
AATTAATT	0.34265	-AATTAATT--	CTATATTA	5.68917	-CTATATTA--
ATTAATTA	0.34249	TAATTAAT---	ACACACAC	5.53141	-GTGTGTGT--
CATATAAC	0.33948	---GTTATATG	AATATCAC	5.48571	---GTGATATT
AATATCAC	0.33820	--AATATCAC--	ATCCACAC	5.47055	-GTGTGGAT--
GTGTGGTA	0.33676	-GTGTGGTA--	AATTTGTA	5.27062	-AATTTGTA--
CCAACACA	0.33665	---TGTGTTGG	TATAAATA	5.23456	-TATTTATA--
GTATAATA	0.33634	--TATTATAC--	GTGTGGTA	5.22243	-GTGTGGTA--
ATATTATA	0.33444	-ATATTATA--	ACAACACC	5.19517	GGTGTGTT--