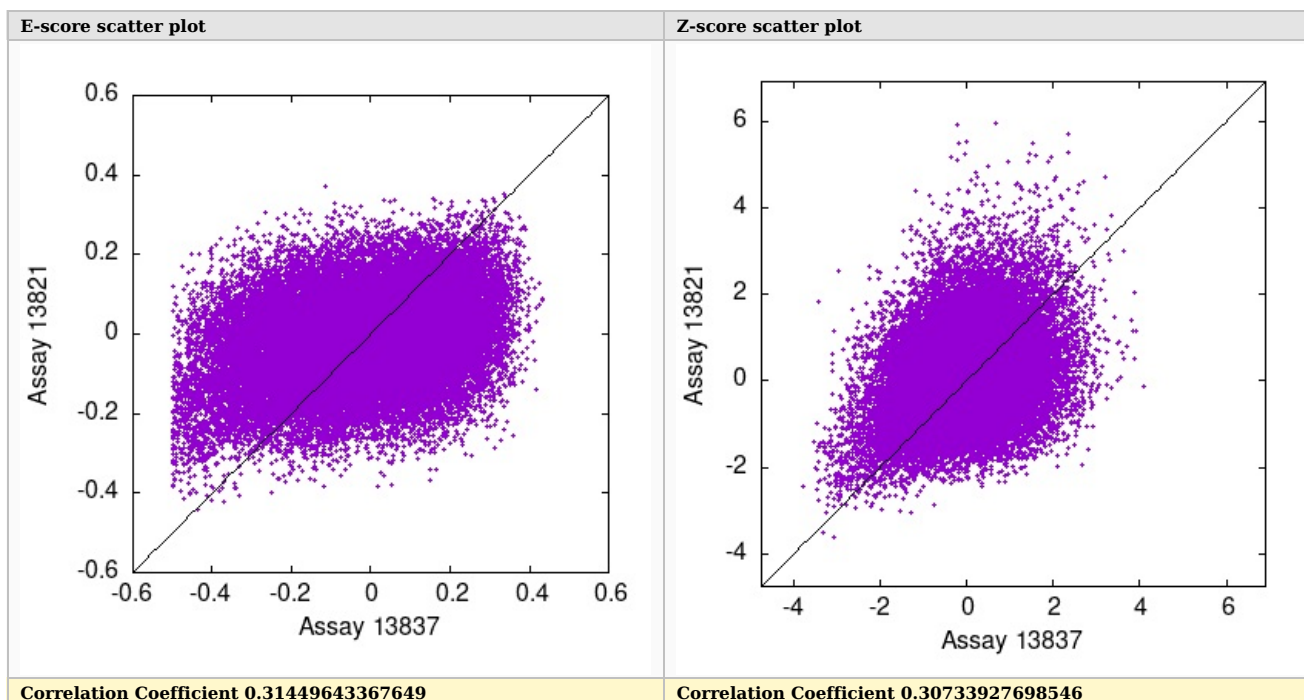


QC report



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'

Forward:	Reverse:	
Top 10	Scores	Alignment
ATAGTAAT	0.43463	--ATAGTAAT--
ACAAAATA	0.43437	ACAAAATA---
CTGTATTA	0.42534	---CTGTATTA
AATAAATT	0.42515	--AATAAATT--
AATATATT	0.41881	--AATATATT--
ATCTAGAT	0.41765	---ATCTAGAT
AGAAATAT	0.41617	--AGAAATAT--
ATAATGTA	0.41515	ATAATGTA---
GATATGTA	0.41445	--GATATGTA--
AGATATCT	0.41155	---AGATATCT

8 mer Z-scores for probeset 'all'

Forward:		Reverse:	
Top 10	Scores	Alignment	
GATATGTA	4.07819	--	GATATGTA-
AATATATT	3.92110	--	AATATATT-
CACATATA	3.88521	--	CACATATA-
AATAAATT	3.86519	--	AATAAATT-
ACAAAATA	3.85148	ACAAAATA	---
ATAATGTA	3.79979	ATAATGTA	---
ATAGTAAT	3.68101	--	ATAGTAAT-
TATTAATA	3.63313	--	TATTAATA-
AGATATCT	3.62515	---	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'

Forward:		Reverse:
Top 10	Scores	Alignment
ACACACAC	0.37235	--GTGTGTGT--
AATTTGTA	0.35407	-AATTTGTA--
AATTAATT	0.34265	-AATTAATT--
ATTAATTA	0.34249	TAATTAAT---
CATATAAC	0.33948	---GTTATATG
AATATCAC	0.33820	--AATATCAC--
GTGTGGTA	0.33676	-GTGTGGTA--
CCAACACA	0.33665	---TGTGTTGG
GTATAATA	0.33634	--TATTATAC--
ATATTATA	0.33444	-ATATTATA--

8 mer Z-scores for probeset 'all'

Forward:		Reverse:
		
Top 10	Scores	Alignment
CCAACACA	5.93516	--TGTGTTGG--
CAGCAACC	5.92351	-GGTTGCTG--
CTATATTA	5.68917	-CTATATTA--
ACACACAC	5.53141	-GTGTGTGT--
AATATCAC	5.48571	---GTGATATT
ATCCACAC	5.47055	-GTGTGGAT--
AATTTGTA	5.27062	-AATTTGTA--
TATAAATA	5.23456	-TATTTATA--
GTGTGGTA	5.22243	-GTGTGGTA--
ACAACACC	5.19517	GGTGTGTG---