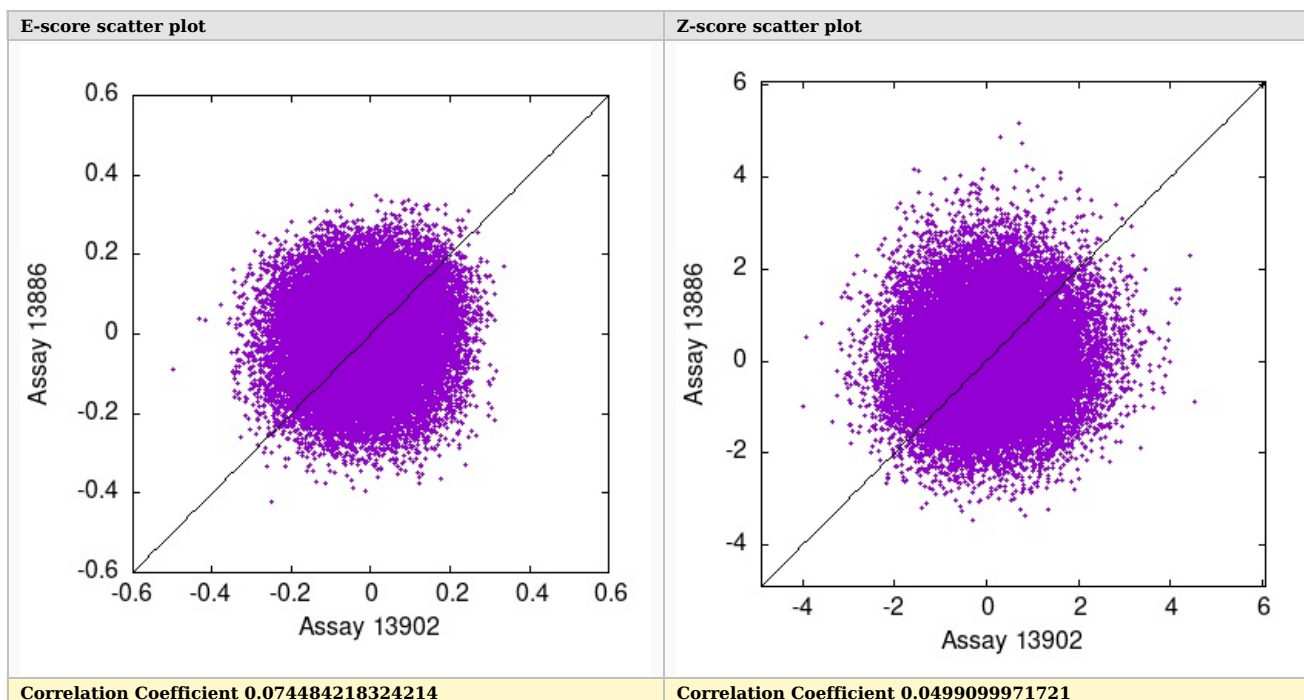


QC report



Top scoring motifs for Assay 13902

Protein ID: pTH14334.2 Gene: RFX8.FL Domain: RFX_DNA_binding

Flag: Reject Array: 1M-HK

8 mer E-scores for probeset 'all'

8 mer Z-scores for probeset 'all'

Forward:			Reverse:		
Top 10	Scores	Alignment	Top 10	Scores	Alignment
TAAATTTA	0.33707	----TAAATTTA	GCTCCAAC	4.53004	---GTTGGAGC--
CACTATTA	0.31645	--TAATAGTG---	TAAATTTA	4.41867	-TAAATTTA----
CGTGATCC	0.31386	CGTGATCC----	CCGTTTGC	4.20521	GCAAAACGG----
GCTCCAAC	0.31352	---GCTCCAAC--	AATACATT	4.19609	---AATGTATT--
AATACATT	0.31161	---AATACATT--	AAAGTCTG	4.13340	-AAAGTCTG----
AAAATGTA	0.31072	-----TACATTTT	AAAATGTA	4.12315	-AAAATGTA----
CACCACTA	0.30852	---CACCACTA--	GGGTTCAC	4.00950	-----TGTAACCC
GGGTTACA	0.30811	-GGGTTACA----	CTGTTCGAC	3.99240	----CTGTTCGAC-
AAAGTCTG	0.30445	---CAGACTTT--	AACTACAA	3.96065	----TTGTAGTT--
CGCGTATC	0.30404	---GATACGCG--	CTACCCAC	3.94290	--GTGGGTAG---

Top scoring motifs for Assay 13886

Protein ID: pTH14334.1 Gene: RFX8.FL Domain: RFX_DNA_binding

Flag: Reject Array: 1M-ME

8 mer E-scores for probeset 'all'

8 mer Z-scores for probeset 'all'

Forward:			Reverse:		
Top 10	Scores	Alignment	Top 10	Scores	Alignment
CCGTAAACA	0.34767	--CCGTAAACA--	ACGATCAT	5.15518	--ACGATCAT--
ATTTATAA	0.33802	---TTATAAAT---	ATTTATAA	4.86443	TTATAAAT----
AATTTGTA	0.33769	--TACAAATT--	CAAATTAC	4.71550	--CAAATTAC--
GGGGCTAA	0.33378	GGGGCTAA----	ACCAATAC	4.23710	--ACCAATAC--
ACGATCAT	0.33138	---ACGATCAT--	GGTCAGTA	4.17709	-GGTCAGTA----
ACCAATAC	0.32819	---ACCAATAC--	GCGCAACA	4.16741	-GCGCAACA----
GCGCAACA	0.32588	--GCGCAACA--	AGGTGATA	4.15735	-----TATCACCT
CCAAACAC	0.32480	---CCAAACAC--	GCAGAATA	4.14496	-GCAGAATA----
AACACACA	0.32412	---AACACACA--	GACGGGGA	4.11437	-GACGGGGA----
AGTAAATA	0.32370	--AGTAAATA--	AGTAAACG	4.08534	---CGTTTACT--