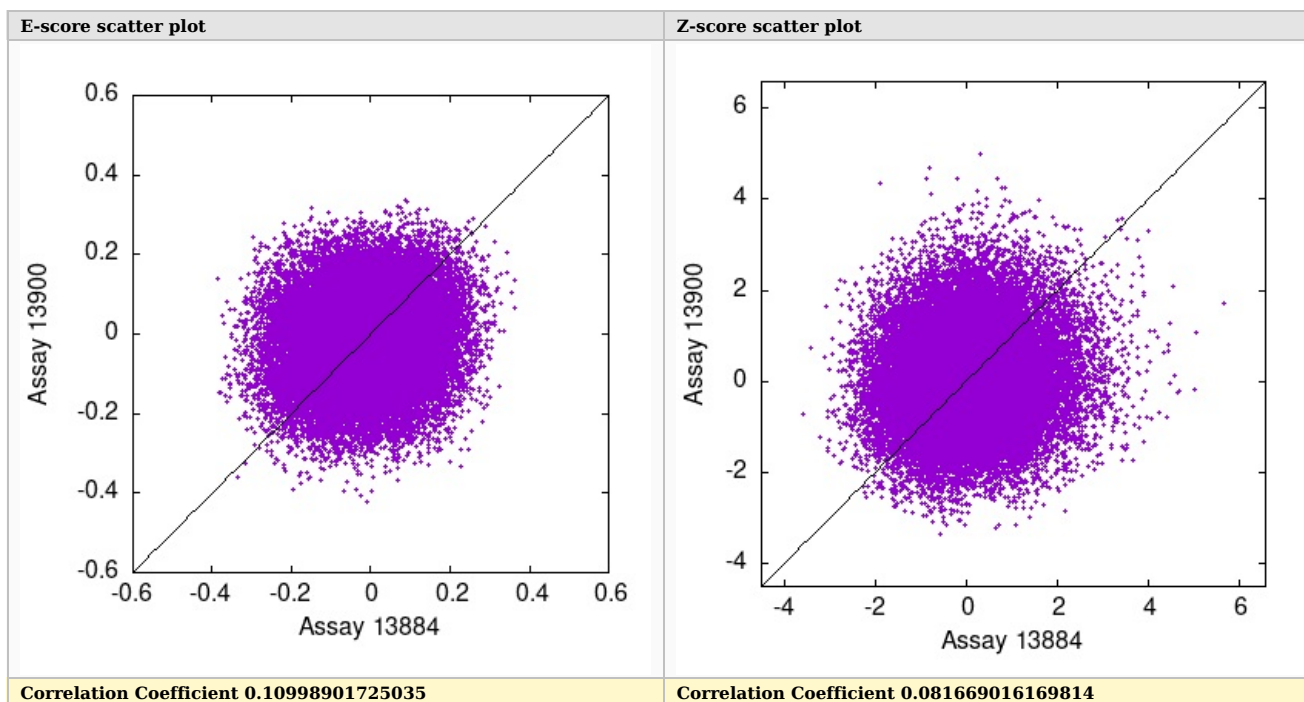


QC report



Top scoring motifs for Assay 13884

Protein ID: pTH14281.1 Gene: NFX1.DBD Domain: zf-NF-X1 Flag: Reject Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:

Reverse:



8 mer Z-scores for probeset 'all'

Forward:

Reverse:



Top 10	Scores	Alignment	Top 10	Scores	Alignment
GTATAATA	0.36495	GTATAATA-----	AAGCAGAA	5.65334	-AAGCAGAA---
AAGCAGAA	0.36195	-----AAGCAGAA	ACCAATAC	5.05933	-ACCAATAC---
ACCAATAC	0.35716	--ACCAATAC----	ATAGTCTG	5.03017	--CAGACTAT--
AAACACAC	0.34352	--AAACACAC----	ACAAATAA	4.69217	-ACAAATAA---
AAAGCAGA	0.34213	----AAAGCAGA-	TATAACCA	4.66031	----TATAACCA
ACAAACC	0.33549	--ACAAACC----	GTTCTGA	4.57957	-TCAGAAAC---
ATAATAAA	0.33005	--ATAATAAA----	AATAAAAT	4.54761	---AATAAAAT
GTACTTTA	0.32680	---TAAAGTAC---	GGAGATA	4.49053	GGAGATA----
CAAGAAC	0.32383	--CAAGAAC----	GATATAA	4.48701	--GATATAA---
ATAAAGC	0.32329	--ATAAAGC----	CCAACAC	4.45079	--CCAACAC---

Top scoring motifs for Assay 13900

Protein ID: pTH14281.2 Gene: NFX1.DBD Domain: zf-NF-X1 Flag: Reject Array: 1M-HK

8 mer E-scores for probeset 'all'

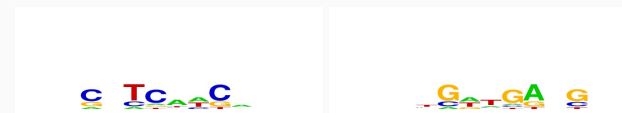
Forward:

Reverse:



Forward:

Reverse:



Top 10	Scores	Alignment	Top 10	Scores	Alignment
ACCCACCC	0.33653	-GGGTGGGT-	ACCCACCC	4.99902	--ACCCACCC--
ATACAAAT	0.33250	-ATACAAAT-	ACATGTGG	4.67832	--CCCATGT---
ACAACAG	0.32056	--ACAACAG	GTGTACAC	4.46555	---GTGTACAC--
GGGCAATA	0.31861	-GGGCAATA-	CCCTGTTA	4.46527	-----TAACAGGG
ACCACCAC	0.31559	--ACCACCAC	ATGAAGTA	4.44288	TACTTCAT----
AGTGCGAT	0.31472	AGTGCGAT--	CACCACTA	4.36347	--CACCACATA--
GGACGATA	0.31223	-GGACGATA-	CGTCATCA	4.25917	--CGTCATCA--
GGGGACAC	0.30812	-GGGGACAC-	GGTATACA	4.25903	--GGTATACA--
GAAATAA	0.30757	--GAAATAA	CCAGGACC	4.18129	--GGTCTGG---
ATATTGAA	0.30721	--TTCAATAT	CATCGACG	4.10327	--CATCGACG---