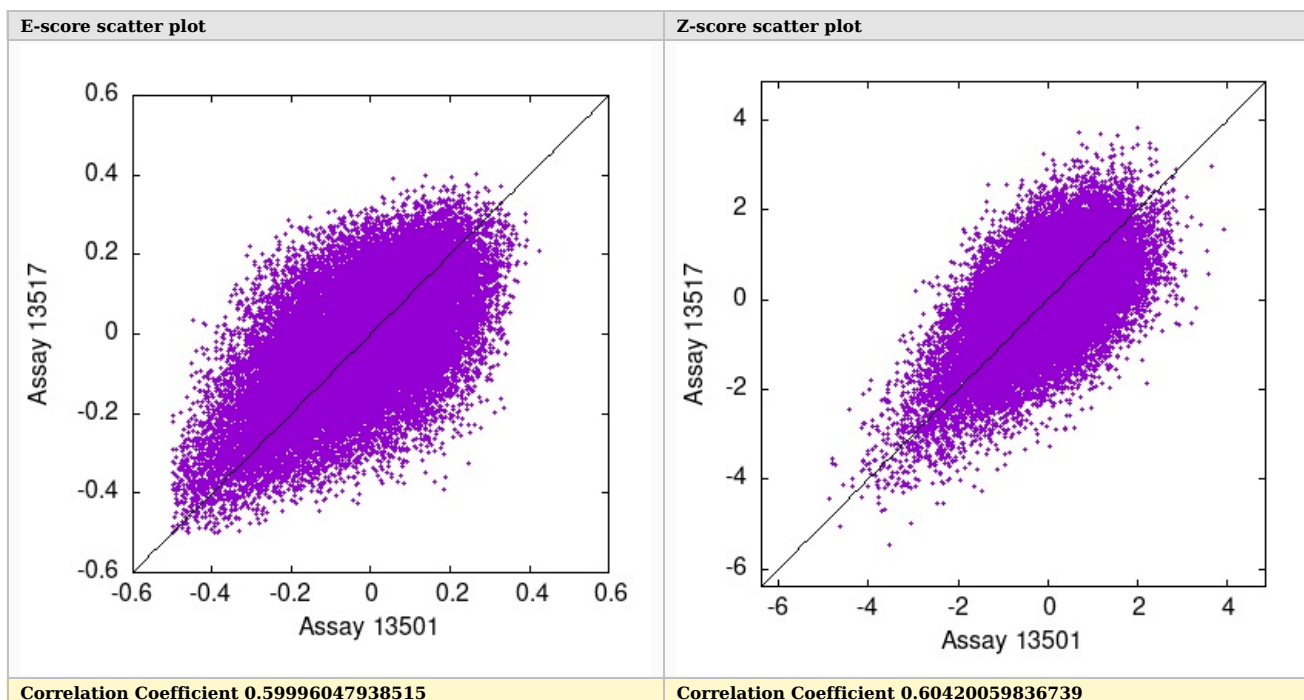


QC report



Top scoring motifs for Assay 13501

Protein ID: pTH13943.1 Gene: BATF2.DBD Domain: bZIP_1 Flag: Reject Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:

Reverse:



Top 10	Scores	Alignment
ACAACAAT	0.42379	-----ATTGTTGT--
TTTCGAAA	0.39567	TTTCGAAA-----
ATTTGTAC	0.39199	-----ATTGTTAC--
CAACAATA	0.39149	-----TATTGTTG--
ATAATATA	0.39128	----TATATTAT----
AATTGTGA	0.39113	-----AATTGTGA--
AAATTTGT	0.37428	-----AAATTTGT--
AAATTGTT	0.37070	-----AAATTGTT--
CGTTAACG	0.36907	-----CGTTAACG--
AATTTGTA	0.36836	-----AATTTGTA--

8 mer Z-scores for probeset 'all'

Forward:

Reverse:



Top 10	Scores	Alignment
TTTCGAAA	3.91971	--TTTCGAAA---
AACGCGTT	3.65111	-AACGCGTT----
AATTGTGA	3.59535	--AATTGTGA---
ACAACAAT	3.54209	---ATTGTTGT--
TAAATTTA	3.41221	--TAAATTTA---
CGTTAACG	3.30314	-----CGTTAACG--
ATTTACTA	3.20429	--ATTTACTA---
ATGATCAT	3.19706	---ATGATCAT--
ACATATGT	3.11320	ACATATGT-----
AGCAATTG	3.09215	-CAATTGCT----

Top scoring motifs for Assay 13517

Protein ID: pTH13943.2 Gene: BATF2.DBD Domain: bZIP_1 Flag: Reject Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:

Reverse:



Top 10	Scores	Alignment
GTTTAAAC	0.40401	---GTTTAAAC---
ACAATACG	0.39733	CGTATTGT-----
TCACGTGA	0.39466	-----TCACGTGA--
AATTAGGT	0.39128	-----AATTAGGT--
ATTATAAT	0.37628	---ATTATAAT----
AAACGTTT	0.37209	--AAACGTTT-----
TGTAGCAA	0.37174	-----TTGCTACA---
ACAATGAT	0.37137	ATCATTGT-----
AGAATTCT	0.37114	AGAATTCT-----
ATTGTTAC	0.36995	---ATTGTTAC----

8 mer Z-scores for probeset 'all'

Forward:

Reverse:



Top 10	Scores	Alignment
ATTATTAC	3.81245	--ATTATTAC--
AATTAGGT	3.71232	---AATTAGGT---
ACAATGAT	3.70055	--ATCATTGT--
AACGTTTG	3.66341	CAAACGTT----
ATTATAAT	3.47608	--ATTATAAT---
CGTTGTAA	3.46108	---TTACAACG--
AATTAATT	3.45047	-AATTAATT---
AGAATTCT	3.44616	--AGAATTCT---
AAACGTTT	3.39894	---AAACGTTT---
ATTGTTGC	3.38980	--ATTGTTGC--