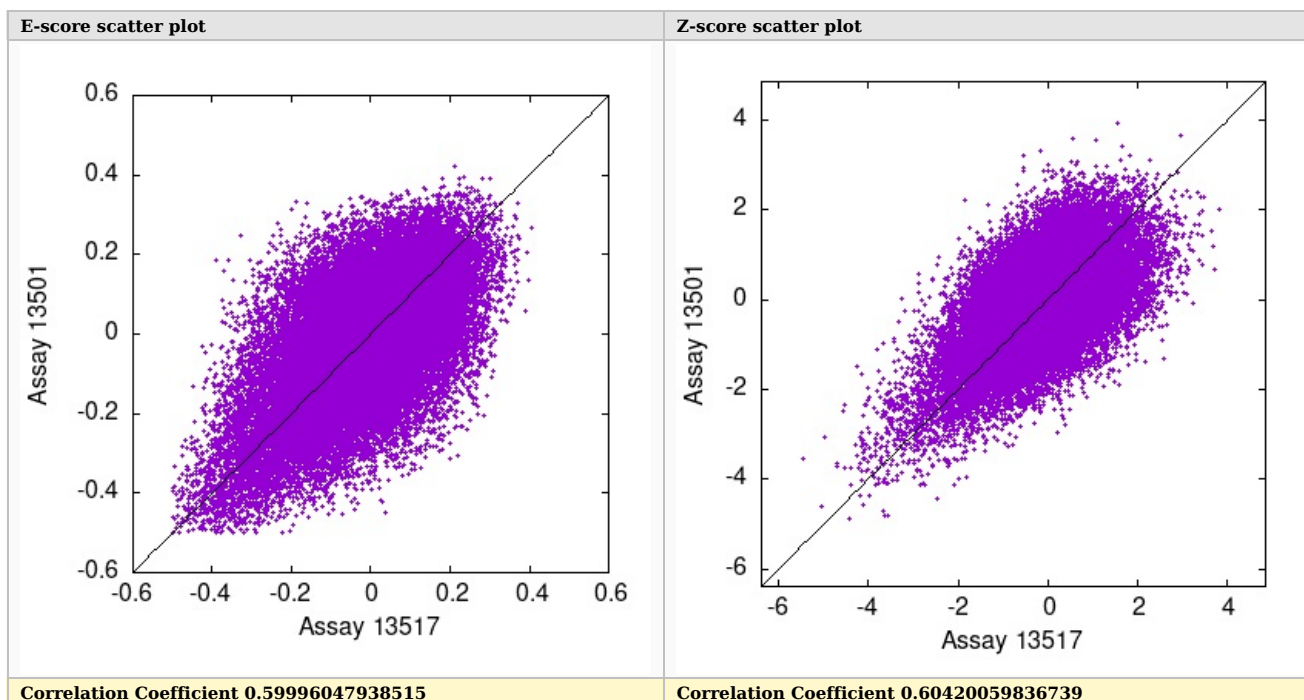


QC report



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:



8 mer Z-scores for probeset 'all'

Forward:

Reverse:



Top 10	Scores	Alignment	Top 10	Scores	Alignment
GTTTAAAC	0.40401	---GTTTAAAC---	ATTATTAC	3.81245	--ATTATTAC--
ACAATACG	0.39733	CGTATTGT-----	AATTAGGT	3.71232	----AATTAGGT
TCACGTGA	0.39466	-----TCACGTGA	ACAATGAT	3.70055	--ATCATTGT--
AATTAGGT	0.39128	-----AATTAGGT--	AACGTTTG	3.66341	CAACCGTT----
ATTATAAT	0.37628	---ATTATAAT----	ATTATAAT	3.47608	--ATTATAAT--
AAACGTTT	0.37209	--AAACGTTT-----	CGTTGTAA	3.46108	---TTACAACG--
TGTAGCAA	0.37174	----TTGCTACA---	AATTAATT	3.45047	-AATTAATT---
ACAATGAT	0.37137	ATCATTGT-----	AGAATTCT	3.44616	--AGAATTCT--
AGAATTCT	0.37114	AGAATTCT-----	AAACGTTT	3.39894	-AAACGTTT---
ATTGTTAC	0.36995	---ATTGTTAC---	ATTGTTGC	3.38980	--ATTGTTGC--

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:



8 mer Z-scores for probeset 'all'

Forward:

Reverse:



Top 10	Scores	Alignment	Top 10	Scores	Alignment
ACAACAAT	0.42379	-----ATTGTTGT--	TTTCGAAA	3.91971	--TTTCGAAA--
TTTCGAAA	0.39567	TTTCGAAA-----	AACGCGTT	3.65111	-AACGCGTT----
ATTGTGAC	0.39199	-----ATTGTGAC---	AATTGTGA	3.59535	--AATTGTGA--
CAACAATA	0.39149	-----TATTGTTG---	ACAACAAT	3.54209	---ATTGTTGT--
ATAATATA	0.39128	----TATATTAT----	TAAATTTA	3.41221	--TAAATTTA--
AATTGTGA	0.39113	-----AATTGTGA---	CGTTAACG	3.30314	-----CGTTAACG
AAATTTGT	0.37428	-----AAATTTGT----	ATTACTA	3.20429	--ATTACTA----
AAATTGTT	0.37070	-----AAATTGTT----	ATGATCAT	3.19706	---ATGATCAT--
CGTTAACG	0.36907	-----CGTTAACG----	ACATATGT	3.11320	ACATATGT-----
AATTTGTA	0.36836	-----AATTTGTA----	AGCAATTG	3.09215	-CAATTGCT----