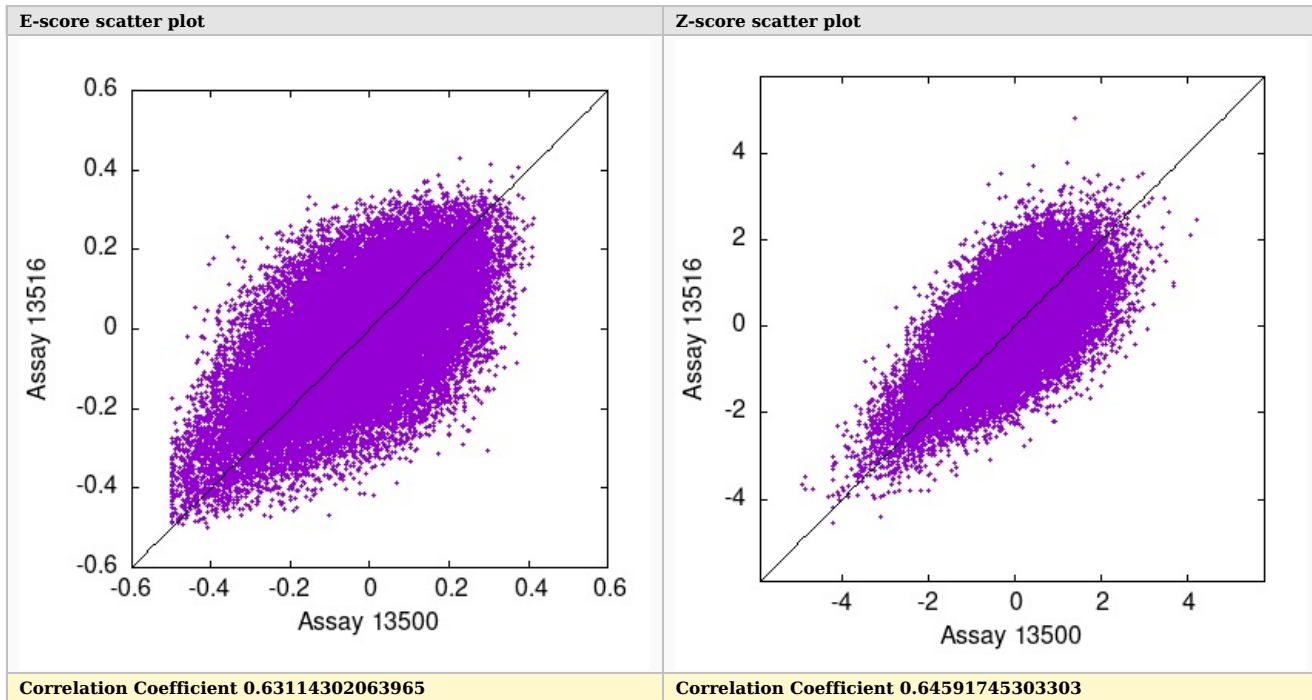


QC report



Top scoring motifs for Assay 13500

Protein ID: pTH13942.1 Gene: BATF2.FL 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
TAAATTTA	0.41375	-TAAATTTA---	AATGCATT	4.22965	--AATGCATT
AATGCATT	0.41060	-AATGCATT---	TAAATTTA	4.06934	TAAATTTA--
ACAACAAT	0.40902	--ATTGTTGT--	CGTTAACG	3.67721	--CGTTAACG
AATTGTTA	0.40795	-AATTGTTA---	AACATGTT	3.66557	AACATGTT--
AGACGTCT	0.40238	-AGACGTCT---	TTTCGAAA	3.58547	--TTTCGAAA
ATGATCAT	0.39710	--ATGATCAT--	ACAACAAT	3.50943	-ACAACAAT-
AGCAATTG	0.39024	CAATTGCT----	GTTTAAAC	3.44716	-GTTTAAAC-
TGTGCACA	0.39006	----TGTGCACA	ACATATAT	3.41434	-ACATATAT-
AATTTGTA	0.38913	-AATTTGTA---	ATACACAT	3.37586	-ATACACAT-
ATACACAT	0.38872	-ATGTGTAT---	CATATATG	3.36448	--CATATATG

Top scoring motifs for Assay 13516

Protein ID: pTH13942.2 Gene: BATF2.FL 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
CTTGCAAG	0.42782	---CTTGCAAG--	CTTGCAAG	4.81316	-CTTGCAAG---
GTCATGAC	0.41354	-----GTCATGAC	GTCATGAC	3.78712	-GTCATGAC----
GTTTAAAC	0.40455	---GTTTAAAC---	GCGAAAAA	3.71829	GCGAAAAA----
CGTGACAG	0.38646	---CGTGACAG--	CGTATAAA	3.55587	-CGTATAAA----
AGAATTCT	0.38290	-----AGAATTCT	AGAATTCT	3.55440	-AGAATTCT----
ATTGTTGC	0.37247	ATTGTTGC-----	ATTATAAT	3.50147	-ATTATAAT----
CATCGATG	0.37231	---CATCGATG--	AATTAATT	3.46215	---AATTAATT--
AGTTGGTA	0.37185	--AGTTGGTA---	TCCATGGA	3.45137	-TCCATGGA----
ATTGCAAT	0.37136	---ATTGCAAT---	TAACGTGA	3.39275	-----TAACGTGA
ACAGCATA	0.36901	---ACAGCATA--	AGTTGCAA	3.37363	-AGTTGCAA----