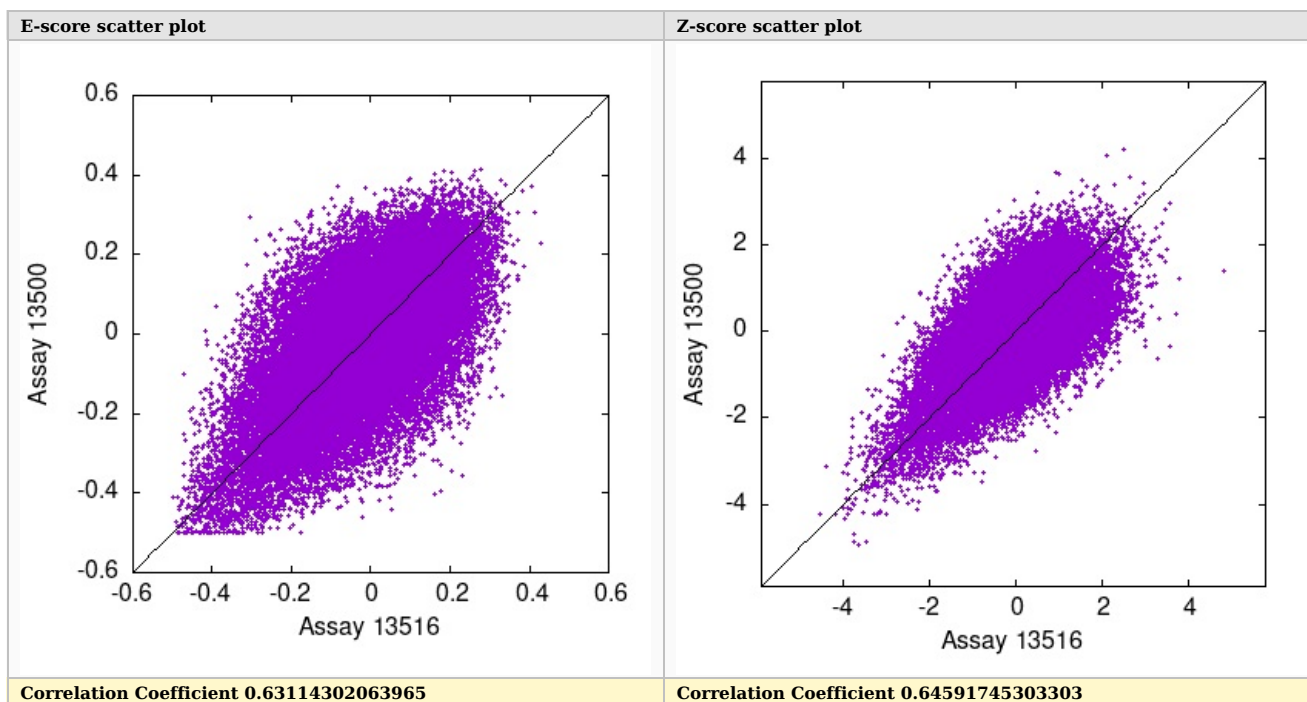


QC report



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:



Top 10

Scores

Alignment

CTTGCAAG	0.42782	---CTTGCAAG--
GTCATGAC	0.41354	----GTCATGAC
GTTTAAAC	0.40455	---GTTTAAAC--
CGTGCACG	0.38646	---CGTGCACG--
AGAATTCT	0.38290	----AGAATTCT
ATTGTTGC	0.37247	ATTGTTGC----
CATCGATG	0.37231	---CATCGATG--
AGTTGGTA	0.37185	--AGTTGGTA---
ATTGCAAT	0.37136	---ATTGCAAT--
ACAGCATA	0.36901	---ACAGCATA--

8 mer Z-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

CTTGCAAG	4.81316	-CTTGCAAG----
GTCATGAC	3.78712	-GTCATGAC----
GCGAAAAA	3.71829	GCGAAAAA----
CGTATAAA	3.55587	-CGTATAAA----
AGAATTCT	3.55440	-AGAATTCT----
ATTATAAT	3.50147	-ATTATAAT----
AATTAATT	3.46215	---AATTAATT--
TCCATGGA	3.45137	-TCCATGGA----
TAACGTTA	3.39275	-----TAACGTTA
AGTTGCAA	3.37363	-AGTTGCAA----

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:



Top 10

Scores

Alignment

TAAATTTA	0.41375	-TAAATTTA---
AATGCATT	0.41060	--AATGCATT---
ACAACAAT	0.40902	--ATTGTTGT--
AATTGTTA	0.40795	-AATTGTTA---
AGACGTCT	0.40238	-AGACGTCT---
ATGATCAT	0.39710	--ATGATCAT--
AGCAATTG	0.39024	CAATTGCT----
TGTGCACA	0.39006	----TGTGCACA
AATTTGTA	0.38913	-AATTTGTA---
ATACACAT	0.38872	-ATGTGTAT---

8 mer Z-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

AATGCATT	4.22965	--AATGCATT
TAAATTTA	4.06934	TAAATTTA--
CGTTAACG	3.67721	--CGTTAACG
AACATGTT	3.66557	AACATGTT--
TTTCGAAA	3.58547	--TTTCGAAA
ACAACAAT	3.50943	-ACAACAAT--
GTTTAAAC	3.44716	-GTTTAAAC--
ACATATAT	3.41434	-ACATATAT--
ATACACAT	3.37586	-ATACACAT--
CATATATG	3.36448	--CATATATG