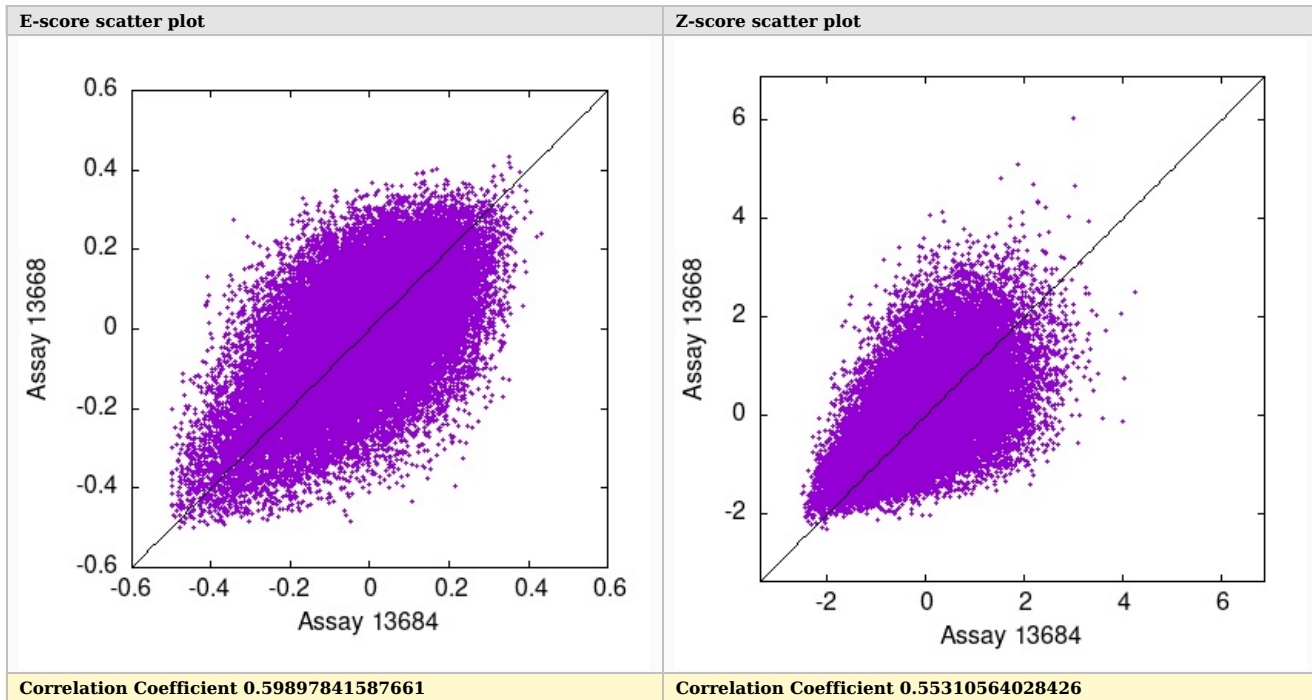


## QC report



### Top scoring motifs for Assay 13684

Protein ID: pTH14283.2 Gene: AEBP1.DBD Domain: Unknown Flag: Reject Array: 1M-HK

8 mer E-scores for probeset 'all'			8 mer Z-scores for probeset 'all'		
Forward:		Reverse:	Forward:		Reverse:
Top 10	Scores	Alignment	Top 10	Scores	Alignment
GATGCATC	0.43152	---GATGCATC---	GATGCATC	4.25727	--GATGCATC----
TACTAGTA	0.42071	---TACTAGTA---	ATCTAGAT	4.02998	ATCTAGAT-----
GTCATGAC	0.40525	---GTCATGAC--	GTGTACAC	4.00901	--GTGTACAC---
TGTTAACA	0.39393	---TGTTAACA---	TGTTAACA	3.97301	-----TGTTAACA
AGTCGACA	0.39376	---AGTCGACA---	GTCATGAC	3.65987	--GTCATGAC---
TCTCGAGA	0.39360	---TCTCGAGA---	AATCGATT	3.59514	--AATCGATT----
GTAATACA	0.39101	-----GTAATACA	CTGTATTA	3.50474	--CTGTATTA---
CTGTATTA	0.39094	CTGTATTA-----	GAACGTTC	3.46689	--GAACGTTC---
GTGTACAC	0.38474	----GTGTACAC--	ATCATACA	3.40832	--TGTATGAT---
AAACGTTT	0.38021	-----AAACGTTT	TACTAGTA	3.36487	--TACTAGTA---

### Top scoring motifs for Assay 13668

Protein ID: pTH14283.1 Gene: AEBP1.DBD Domain: Unknown Flag: Reject Array: 1M-ME

8 mer E-scores for probeset 'all'			8 mer Z-scores for probeset 'all'		
Forward:		Reverse:	Forward:		Reverse:
Top 10	Scores	Alignment	Top 10	Scores	Alignment
AACATGTT	0.43528	-----AACATGTT	AACATGTT	6.02627	-----AACATGTT
TAAATTTA	0.41826	-----TAAATTTA	ATGTACAT	5.08516	---ATGTACAT---
TGTGCACA	0.40887	-----TGTGCACA--	AGACGTCT	4.81583	-----AGACGTCT-
GTTGCAAC	0.40522	----GTTGCAAC--	TAAATTTA	4.70869	-----TAAATTTA
ATGTACAT	0.40388	---ATGTACAT---	AACGCGTT	4.65937	---AACGCGTT---
AGACGTCT	0.39820	----AGACGTCT-	TGTATACA	4.34447	-----TGTATACA-
CTGTATAC	0.39401	---CTGTATAC---	TTGTACAA	4.32097	---TTGTACAA---
GTTTAAAC	0.39363	---GTTTAAAC---	TGTGCACA	4.21311	-----TGTGCACA-
ATCAGTTA	0.39155	ATCAGTTA-----	ATCAGTTA	4.14565	ATCAGTTA-----
ACATACAA	0.38924	---ACATACAA---	AATGCATT	4.12151	-----AATGCATT--