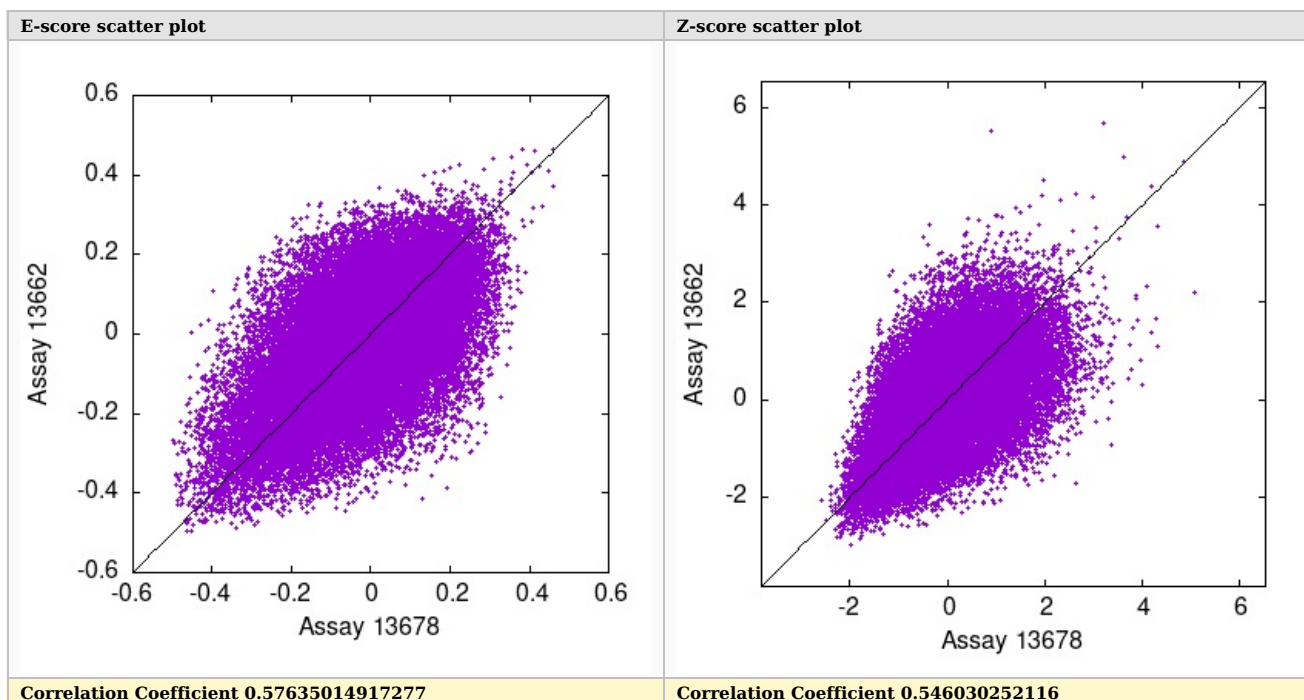




QC report



Top scoring motifs for Assay 13678

Protein ID: pTH14271.2 Gene: DMTF1.DBD Domain: Myb_DNA-binding Flag: Pass_matched_pair Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:		Reverse:	
			
Top 10	Scores	Alignment	
ACATCCGG	0.46048	-CCGGATGT-----	
AAGGATGT	0.46005	-AAGGATGT-----	
CGGATGTA	0.44705	--CGGATGTA-----	
CATCCGGG	0.43111	CCCGGATG-----	
ACATCCGT	0.42517	-ACGGATGT-----	
AGGATGTA	0.41402	--AGGATGTA-----	
TGTTAACA	0.40969	-----TGTTAACA	
AGGATGTG	0.40750	--AGGATGTG-----	
AACATCCG	0.40633	--CGGATGTT-----	
CTACATCC	0.39356	--GGATGTAG----	



8 mer Z-scores for probeset 'all'

Forward:	Reverse:
Top 10	Scores
TGTTAACA	5.05984
AAGGATGT	4.83571
CGGATGTA	4.32388
GTACAACA	4.31636
GATGCATC	4.27578
TACACACA	4.19506
AGGATGTA	4.18975
ACATCCGG	4.08443
GTGTACAC	3.99833
ATTATAAT	3.96923
Alignment	
-----TGTTAACA	
AAGGATGT----	
-CGGATGTA----	
--TGTTGTAC---	
---GATGCATC--	
-TGTGTGTA----	
-AGGATGTA----	
CCGGATGT----	
---GTGTACAC--	
---ATTATAAT--	



Top scoring motifs for Assay 13662

Protein ID: pTH14271.1 Gene: DMTF1.DBD Domain: Myb_DNA-binding Flag: Pass_matched_pair Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:		Reverse:
		
Top 10	Scores	Alignment
AAGGATGT	0.46532	AAGGATGT----
ACATCCCT	0.46321	AGGGATGT----
AGGATGTA	0.45979	-AGGATGTA----
GGATGTAA	0.44364	--GGATGTAA--
GGGATGTA	0.44006	-GGGATGTA---
CTACATCC	0.42773	-GGATGTAG--
ATGTACAT	0.42692	----ATGTACAT
ACATCCGT	0.42315	ACGGATGT----
CAACATCC	0.41786	--GGATGTTG--
ACATCCTC	0.41390	GAGGATGT----

8 mer Z-scores for probeset 'all'

Forward:		Reverse:	
			
Top 10	Scores	Alignment	
ACATCCCT	5.66115	AGGGATGT-----	
ATGTACAT	5.52412	----ATGTACAT-	
GGATGTAA	4.99154	--GGATGTAA---	
AAGGATGT	4.88061	AAGGATGT-----	
GGGATGTA	4.49684	-GGGATGTA----	
AGGATGTA	4.37582	-AGGATGTA----	
TAAATTTA	4.21197	-TAAATTTA----	
ATACACAT	4.17883	--ATGTGTAT---	
ATGTTAAC	4.16678	---ATGTTAAC--	
TGTATACA	4.10172	-----TGTATACA	