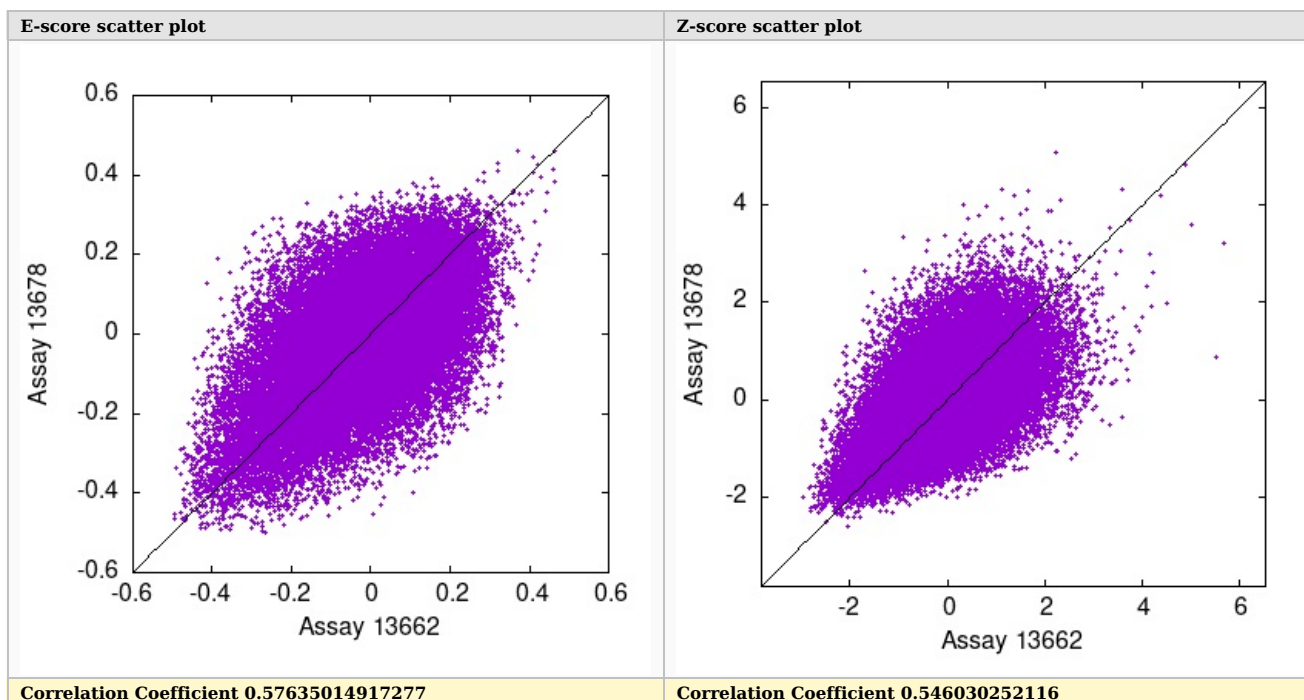




QC report



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	



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

8 mer Z-scores for probeset 'all'

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