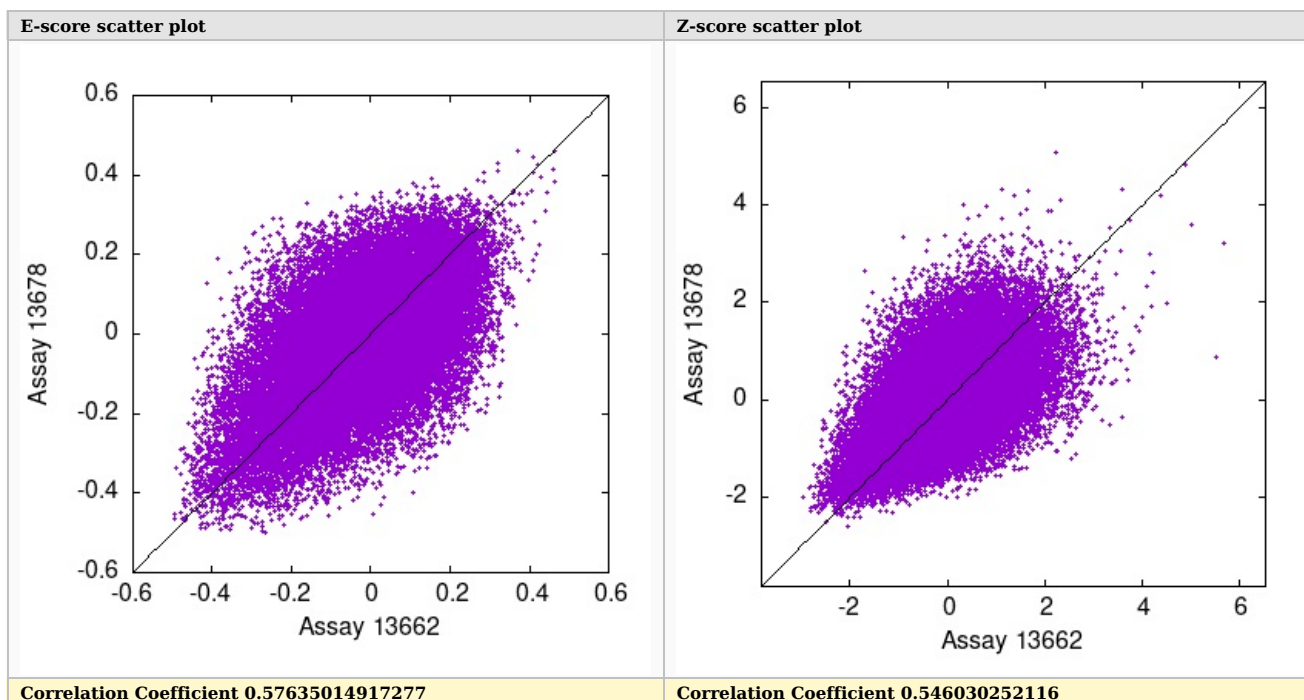




QC report





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	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	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--	