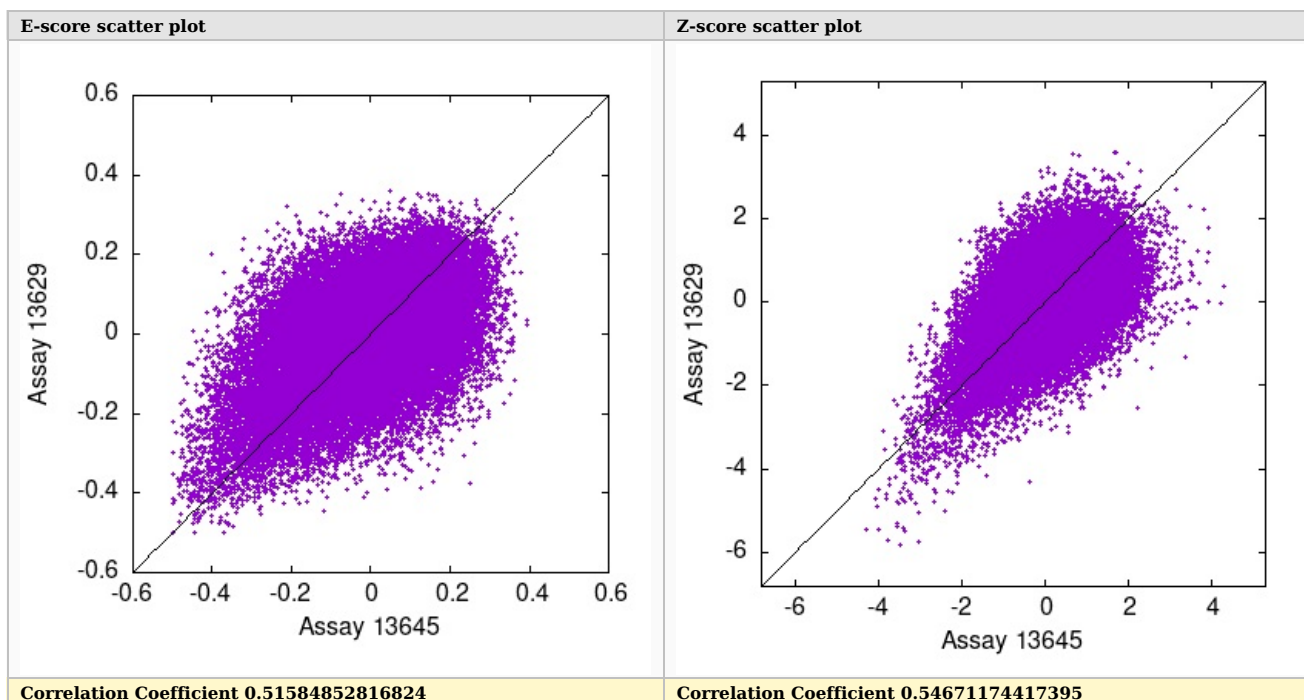




## QC report





### Top scoring motifs for Assay 13645

Protein ID: pTH14230.2 Gene: GATAD2B.DBD Domain: GATA Flag: Reject Array: 1M-HK

#### 8 mer E-scores for probeset 'all'

Forward:		Reverse:	
			
Top 10	Scores	Alignment	
ATATCACA	0.39543	--ATATCACA--	
GATATGTA	0.39351	-GATATGTA--	
ATATTAAG	0.37865	--ATATTAAG--	
CTGTATTA	0.36660	CTGTATTA---	
ATCAGTAC	0.36363	--GTACTGAT--	
GCACTATA	0.36204	---TATAGTGC	
ACCACTAA	0.36161	-ACCACTAA--	
AGTTTTTC	0.36144	---GAAAAACT	
AATTCGGC	0.36129	---AATTCGGC	
CATATATG	0.36114	-CATATATG--	



#### 8 mer Z-scores for probeset 'all'

Forward:		Reverse:	
			
Top 10	Scores	Alignment	
AATTTAAA	4.29443	- TTTAAATT	
ATATCACA	4.21259	ATATCACA-	
TATTTGCA	3.93794	- TATTTGCA	
GTCATGAC	3.92227	GTCATGAC-	
ATATTAAG	3.91785	ATATTAAG-	
ATTATAAT	3.87726	ATTATAAT-	
CATATATG	3.82713	- CATATATG	
TATTAATA	3.72685	- TATTAATA	
ATATTAAT	3.71627	ATATTAAT-	
ATCAGTAC	3.66757	GTACTGAT-	



### Top scoring motifs for Assay 13629

Protein ID: pTH14230.1 Gene: GATAD2B.DBD Domain: GATA Flag: Reject Array: 1M-ME

#### 8 mer E-scores for probeset 'all'

Forward:		Reverse:	
			
Top 10	Scores	Alignment	
CGAACAGA	0.35976	- - -CGAACAGA	
ACATACCG	0.35227	--ACATACCG--	
TACATACA	0.35076	--TACATACA--	
AGTTGTCA	0.35035	--TGACAACT--	
ACTGATTG	0.34935	--CAATCAGT--	
ACAAAACA	0.34841	--ACAAAACA--	
CGCAAAAC	0.34483	-CGCAAAAC---	
TAATAACA	0.34014	--TAATAACA--	
TCGAGTAA	0.33786	TCGAGTAA----	
ATACCAAT	0.33699	----ATACCAAT	

#### 8 mer Z-scores for probeset 'all'

Forward:		Reverse:
		
Top 10	Scores	Alignment
ACTGATTG	3.61947	CAATCAGT--
GAACAACA	3.61863	--TGTTGTTC
ACACTCAA	3.56207	--TTGAGTGT
TAATAACA	3.54007	-TGTTATTA-
ACATTAGT	3.33254	ACATTAGT--
TACCGACA	3.22968	-TGTCGGTA-
GTGTGTAA	3.18945	--GTGTGTAA
AATGTGAA	3.18338	-AATGTGAA-
ATTTGTAC	3.17723	--ATTTGTAC
CATTTGTA	3.17111	-CATTTGTA-