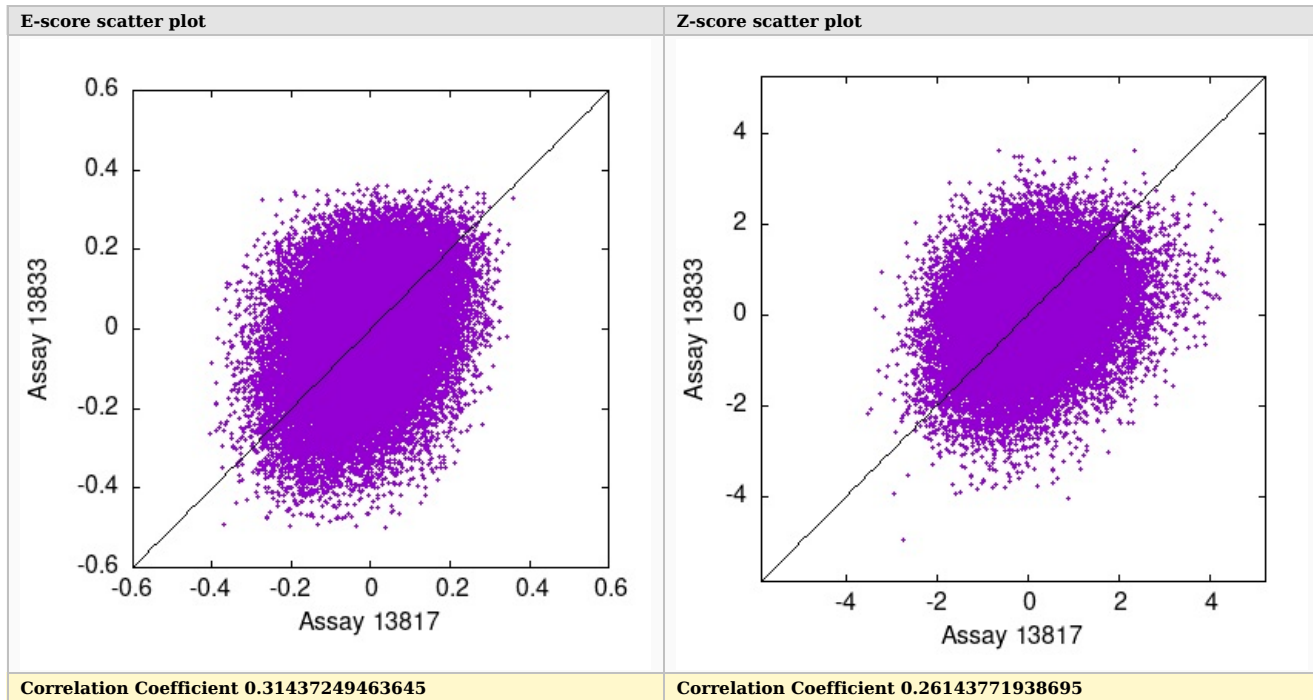




## QC report





### Top scoring motifs for Assay 13817

Protein ID: pTH13911.1 Gene: KDM5B.DBD Domain: ARID Flag: Reject Array: 1M-ME

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

Forward:		Reverse:	
			
Top 10	Scores	Alignment	
ATACAAAA	0.35921	-ATACAAAA-	
CGCGAATA	0.34854	TATTCGCG--	
GACTAATA	0.34176	--GACTAATA	
ATATATAA	0.33164	-ATATATAA-	
AACGTAAA	0.32639	-AACGTAAA-	
GATGTATA	0.32574	TATACATC--	
GTACTCTA	0.32486	--TAGAGTAC	
GTGCGCAC	0.32460	-GTGCGCAC-	
TACAAACA	0.32429	--TACAAACA	
TAAAAAAA	0.32288	--TAAAAAAA	



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

Forward:		Reverse:	
			
Top 10	Scores	Alignment	
GAATATTC	4.31402	---GAATATTC	
GTCGAATA	4.27925	GTCGAATA--	
ACTACTAA	4.24660	--ACTACTAA--	
CATATTAA	4.23189	--TTAATATG-	
CGCGAATA	4.18441	CGCGAATA--	
AAATAGTC	4.17357	---AAATAGTC	
GTACTCTA	4.14316	-TAGAGTAC--	
TACAAACA	4.12471	TACAAACA--	
GAAGTGTA	4.10976	GAAGTGTA--	
CGTAAAAA	4.10851	--CGTAAAAA-	



### Top scoring motifs for Assay 13833

Protein ID: pTH13911.2 Gene: KDM5B.DBD Domain: ARID Flag: Reject Array: 1M-HK

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

Forward:	Reverse:	
		
Top 10	Scores	Alignment
AGATATCT	0.37174	--AGATATCT---
CACATATA	0.36489	---CACATATA---
ATAGTTTA	0.35868	----ATAGTTTA--
AAATCGAT	0.35868	--AAATCGAT---
ACAAAATA	0.35819	-----TATTTTGT
TAAGATAA	0.35716	----TTATCTTA--
ACAAATTA	0.35492	--ACAAATTA---
ATACATAT	0.35417	ATACATAT-----
ATAAGATA	0.35283	-----TATCTTAT
ACATATCT	0.35278	--ACATATCT---

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

Forward:	Reverse:	
		
Top 10	Scores	Alignment
ATAAGATA	3.61234	--ATAAGATA-
ACTATAAT	3.60608	--ATTATAGT-
AAATAAAT	3.48988	--AAATAAAT--
AATAAATT	3.48988	--AATAAATT--
ACATAGAC	3.47886	--ACATAGAC--
ATAGTTTA	3.45387	----ATAGTTTA
TAAGATAA	3.44840	TAAGATAA----
ATAACGAT	3.40689	--ATAACGAT--
ATCATGAT	3.37403	--ATCATGAT--
AAATCGAT	3.36970	--AAATCGAT--