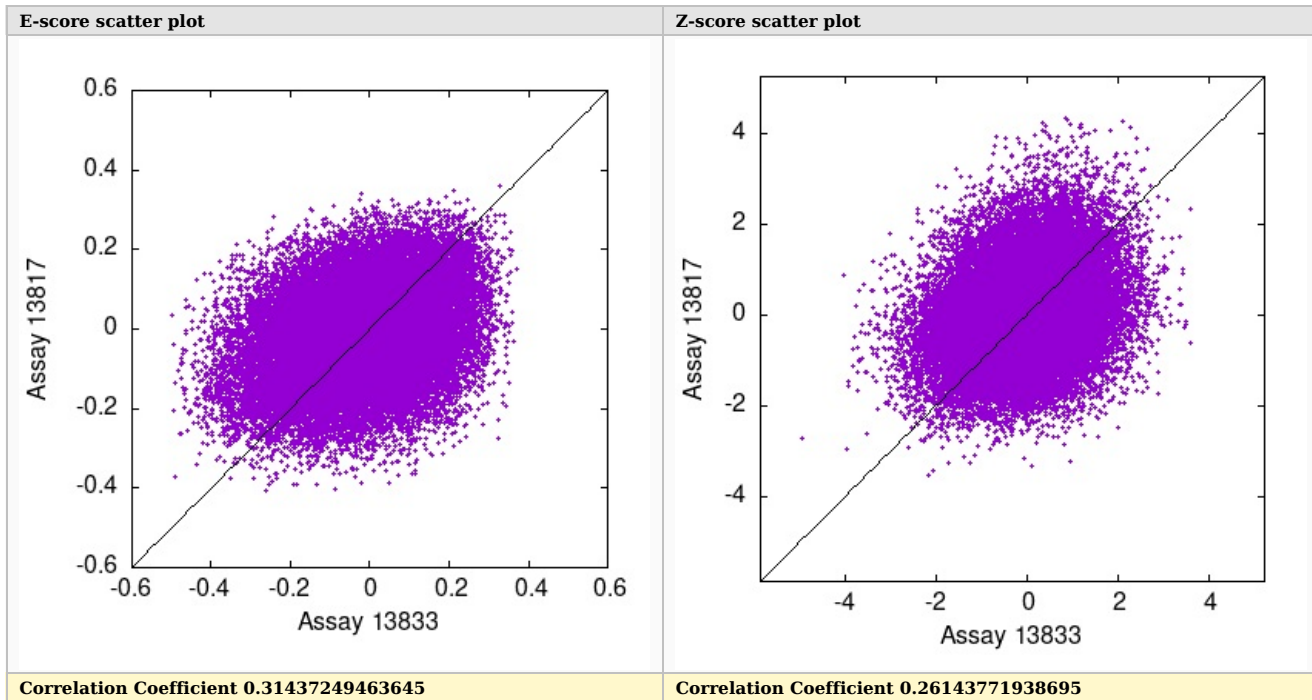


## QC report



### 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'			8 mer Z-scores for probeset 'all'		
Forward:		Reverse:	Forward:		Reverse:
Top 10	Scores	Alignment	Top 10	Scores	Alignment
AGATATCT	0.37174	--AGATATCT--	ATAAGATA	3.61234	---ATAAGATA--
CACATATA	0.36489	-CACATATA----	ACTATAAT	3.60608	---ATTATAGT--
ATAGTTTA	0.35868	----ATAGTTTA--	AAATAAAT	3.48988	--AAATAAAT--
AAATCGAT	0.35868	--AAATCGAT---	AATAAAAT	3.48988	---AATAAAAT--
ACAAAATA	0.35819	-----TATTTTGT	ACATAGAC	3.47886	--ACATAGAC--
TAAGATAA	0.35716	----TTATCTTA--	ATAGTTTA	3.45387	----ATAGTTTA--
ACAAATTA	0.35492	--ACAAATTA---	TAAGATAA	3.44840	TAAGATAA----
ATACATAT	0.35417	ATACATAT-----	ATAACGAT	3.40689	--ATAACGAT--
ATAAGATA	0.35283	-----TATCTTAT	ATCATGAT	3.37403	--ATCATGAT--
ACATATCT	0.35278	--ACATATCT---	AAATCGAT	3.36970	--AAATCGAT--

### 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'			8 mer Z-scores for probeset 'all'		
Forward:		Reverse:	Forward:		Reverse:
Top 10	Scores	Alignment	Top 10	Scores	Alignment
ATACAAAA	0.35921	-ATACAAAA-	GAATATTC	4.31402	---GAATATTC
CGCGAATA	0.34854	TATTCGCG--	GTCGAATA	4.27925	GTCGAATA---
GACTAATA	0.34176	--GACTAATA	ACTACTAA	4.24660	-ACTACTAA--
ATATATAA	0.33164	-ATATATAA-	CATATTAA	4.23189	--TTAATATG-
AACGTAAA	0.32639	-AACGTAAA-	CGCGAATA	4.18441	CGCGAATA---
GATGTATA	0.32574	TATACATC--	AAATAGTC	4.17357	---AAATAGTC
GTAAGCTA	0.32486	--TAGAGTAC	GTACTCTA	4.14316	-TAGAGTAC--
GTGCGCAC	0.32460	-GTGCGCAC-	TACAAACA	4.12471	TACAAACA---
TACAAACA	0.32429	--TACAAACA	GAAGTGTA	4.10976	GAAGTGTA---
TAAAAAAA	0.32288	--TAAAAAAA	CGTAAAAA	4.10851	--CGTAAAAA-