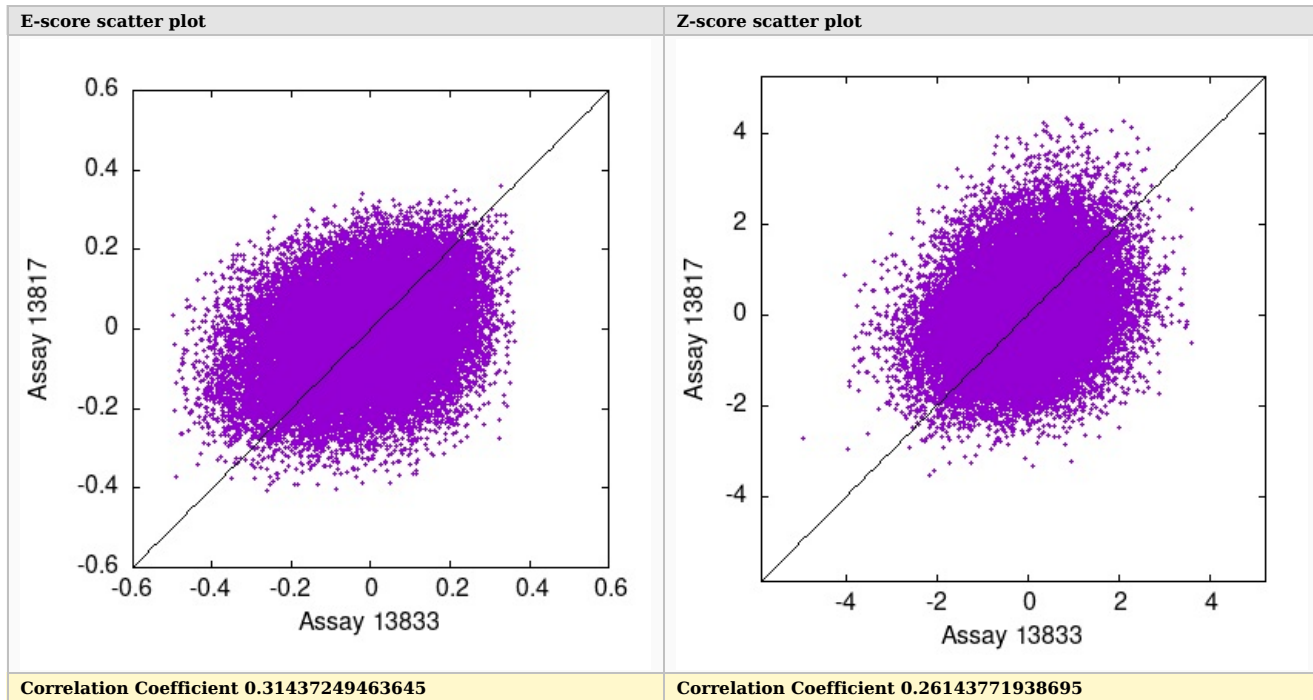


QC report



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'

Forward:

Reverse:



Top 10

Scores

Alignment

AGATATCT	0.37174	--AGATATCT--
CACATATA	0.36489	-CACATATA----
ATAGTTTA	0.35868	----ATAGTTTA--
AAATCGAT	0.35868	---AAATCGAT---
ACAAATA	0.35819	-----TATTTTGT
TAAGATA	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--
TAAGATA	3.44840	TAAGATAA-----
ATAACGAT	3.40689	--ATAACGAT--
ATCATGAT	3.37403	--ATCATGAT--
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'

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-
TACAACAA	0.32429	--TACAACAA
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-