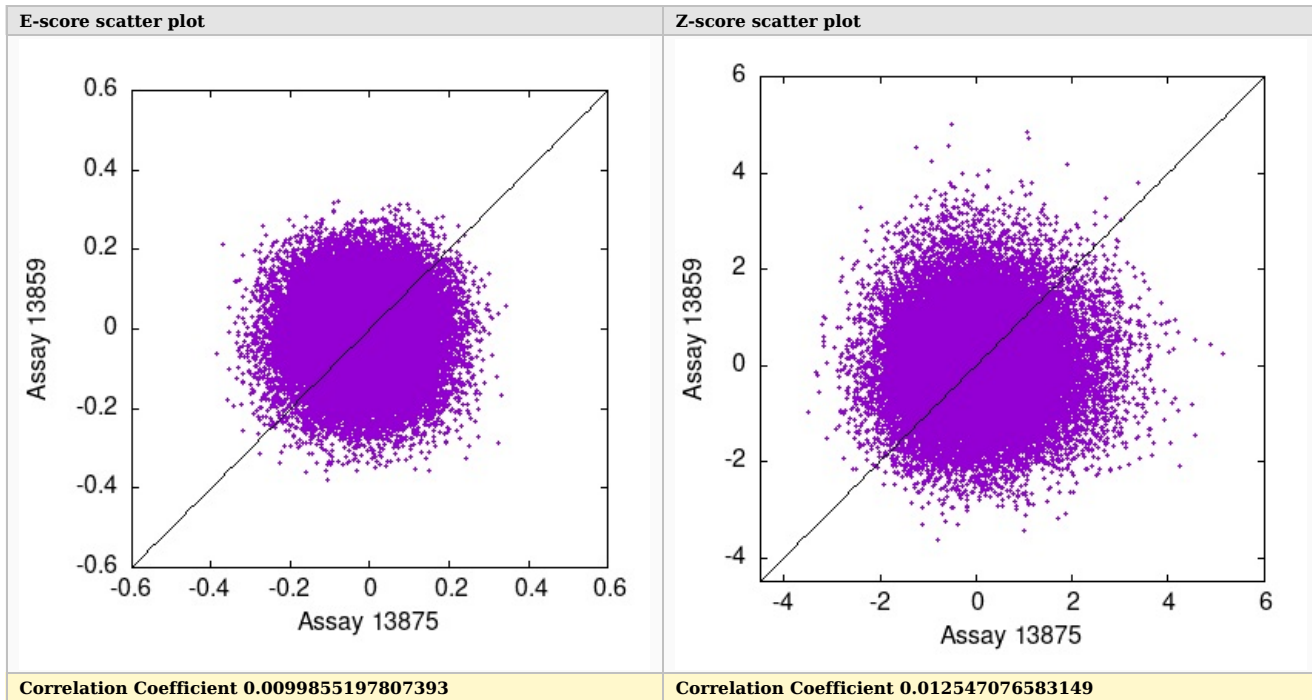


## QC report



### Top scoring motifs for Assay 13875

Protein ID: pTH14264.2 Gene: PIN1.FL Domain: MBD Flag: Reject

Array: 1M-HK

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

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

Forward:			Reverse:		
Top 10	Scores	Alignment	Top 10	Scores	Alignment
AACGTTAT	0.34250	ATAACGTT----	ATCATAAT	5.13370	--ATCATAAT----
AGACGTCT	0.33077	-AGACGTCT----	CATGGTGC	4.88160	GCACCATG-----
CATCCGCG	0.32609	----CGCGGATG-	AAAAATGC	4.57009	--AAAAATGC----
AGCTCAAT	0.32283	----AGCTCAAT-	AGACGCAA	4.55332	AGACGCAA-----
GACGCTCC	0.31962	--GACGCTCC--	CATCCGCG	4.49333	----CATCCGCG--
CATGGTGC	0.30858	----GCACCATG	AGACGTCT	4.25178	AGACGTCT-----
GCCGCATA	0.30839	--GCCGCATA--	TACCAGTA	4.22272	-TACCAGTA-----
ACGCAACA	0.30314	---ACGCAACA--	AACAGCGG	4.21636	--AACAGCGG----
CGGACCGA	0.30049	---TCGGTCCG--	ATAGTTTC	4.16143	-----ATAGTTTC
AACTGATC	0.29996	-----GATCAGTT	ACCAATAG	4.14669	--ACCAATAG----

### Top scoring motifs for Assay 13859

Protein ID: pTH14264.1 Gene: PIN1.FL Domain: MBD Flag: Reject

Array: 1M-ME

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

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

Forward:			Reverse:		
Top 10	Scores	Alignment	Top 10	Scores	Alignment
TTAGCTAA	0.32249	----TTAGCTAA----	GTTATAAC	5.00503	--GTTATAAC----
GGAGGGAA	0.31824	TTCCCTCC-----	AATCTCAT	4.84359	--AATCTCAT----
CTCCGAAA	0.31405	----CTCCGAAA----	AAACCCAG	4.71279	--AAACCCAG----
TAACGTTA	0.31246	----TAACGTTA----	GAGTTAAC	4.56034	GTTAACCT-----
ATGCTTTC	0.30822	-----GAAAGCAT	GATGCGTA	4.54070	---TACGCATC----
ACTAGCCG	0.30305	-ACTAGCCG-----	CAATTCCA	4.25426	--CAATTCCA----
GTTATAAC	0.30292	-----GTTATAAC----	CAATACCG	4.19815	-CAATACCG-----
ACGACCTG	0.30046	-----ACGACCTG----	ACGCACGA	4.05754	-----TCGTGCGT
ACTCAAAA	0.29966	---ACTCAAAA----	GAGCCTGA	3.97658	TCAGGCTC-----
GTGCGCAA	0.29824	-----GTGCGCAA----	ATGTAATC	3.96036	---ATGTAATC----