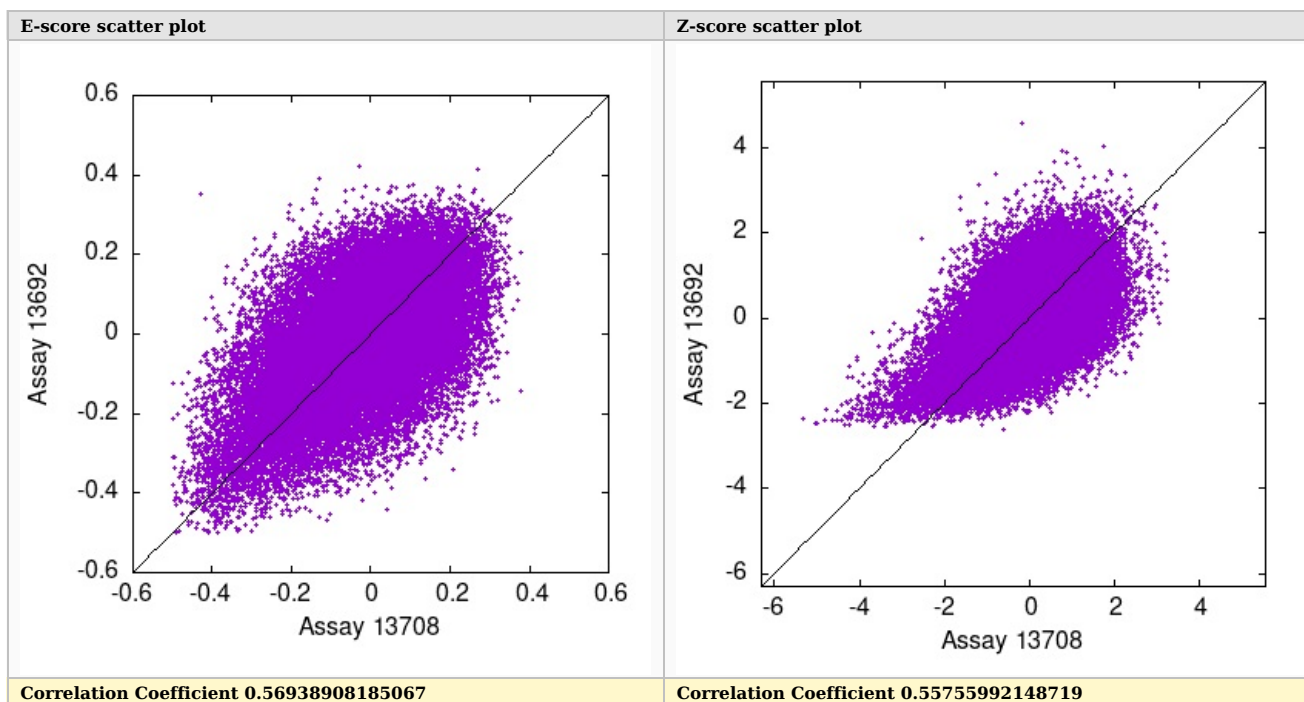


## QC report



## Top scoring motifs for Assay 13708

Protein ID: pTH13928.2 Gene: SGSM2.DBD Domain: zf-BED Flag: Reject Array: 1M-HK

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

Forward:

Reverse:



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

Forward:

Reverse:



## Top 10

## Scores

## Alignment

AGTTTTTC	0.38012	---AGTTTTTC--
TATTTGCA	0.37927	----TGCAAATA
TTCATGAA	0.37212	-TTCATGAA----
CGTAACAA	0.37207	-----CGTAACAA
ACTTTCTA	0.36948	TAGAAAGT-----
AAAGCTTA	0.36273	--AAAGCTTA--
AATGTAAC	0.36079	---AATGTAAC--
ATATGTGC	0.35052	--ATATGTGC--
ACGTAACA	0.35002	----ACGTAACA-
ATATCACA	0.34874	----ATATCACA-

## Top 10

## Scores

## Alignment

TATTTGCA	3.23367	----TGCAAATA--
TATAAGCA	3.23262	----TGCTTATA--
ACAATTTG	3.19088	-----CAAATTGT
ATATGTGC	3.16268	--GCACATAT---
ATACATAT	3.08935	---ATACATAT---
ATCATACA	3.08371	ATCATACA-----
TTCATGAA	3.06014	----TTCATGAA--
ACCATACT	3.05205	----ACCATACT--
ACAGTGAT	3.03816	---ACAGTGAT---
ACAATACG	3.02855	ACAATACG-----

## Top scoring motifs for Assay 13692

Protein ID: pTH13928.1 Gene: SGSM2.DBD Domain: zf-BED Flag: Reject Array: 1M-ME

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

Forward:

Reverse:



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

Forward:

Reverse:



## Top 10

## Scores

## Alignment

AACATGTT	0.42263	AACATGTT-----
TAAATTTA	0.41608	----TAAATTTA----
AATTCGAA	0.39118	-----TTCGAATT--
GCAATTGC	0.37699	-----GCAATTGC
ATGTACAT	0.37311	----ATGTACAT----
TTGTACAA	0.37152	----TTGTACAA----
ATTCGAAT	0.37151	-----ATTCGAAT--
GTTGCAAC	0.37037	-----GTTGCAAC--
TGTTGCAA	0.36932	----TGTTGCAA----
GTATAATA	0.36670	----TATTATAC----

## Top 10

## Scores

## Alignment

AACATGTT	4.56457	AACATGTT---
GTTGCAAC	4.03121	--GTTGCAAC-
TGTGCACA	3.94177	TGTGCACA---
TAAATTTA	3.87385	TAAATTTA---
ACTATAGT	3.73834	--ACTATAGT-
GCAATTGC	3.66229	GCAATTGC---
TTGTACAA	3.64974	---TTGTACAA
ATTTATTG	3.55070	---ATTTATTG
TAACAGTA	3.44958	TAACAGTA---
ATTCGAAT	3.41695	--ATTCGAAT-