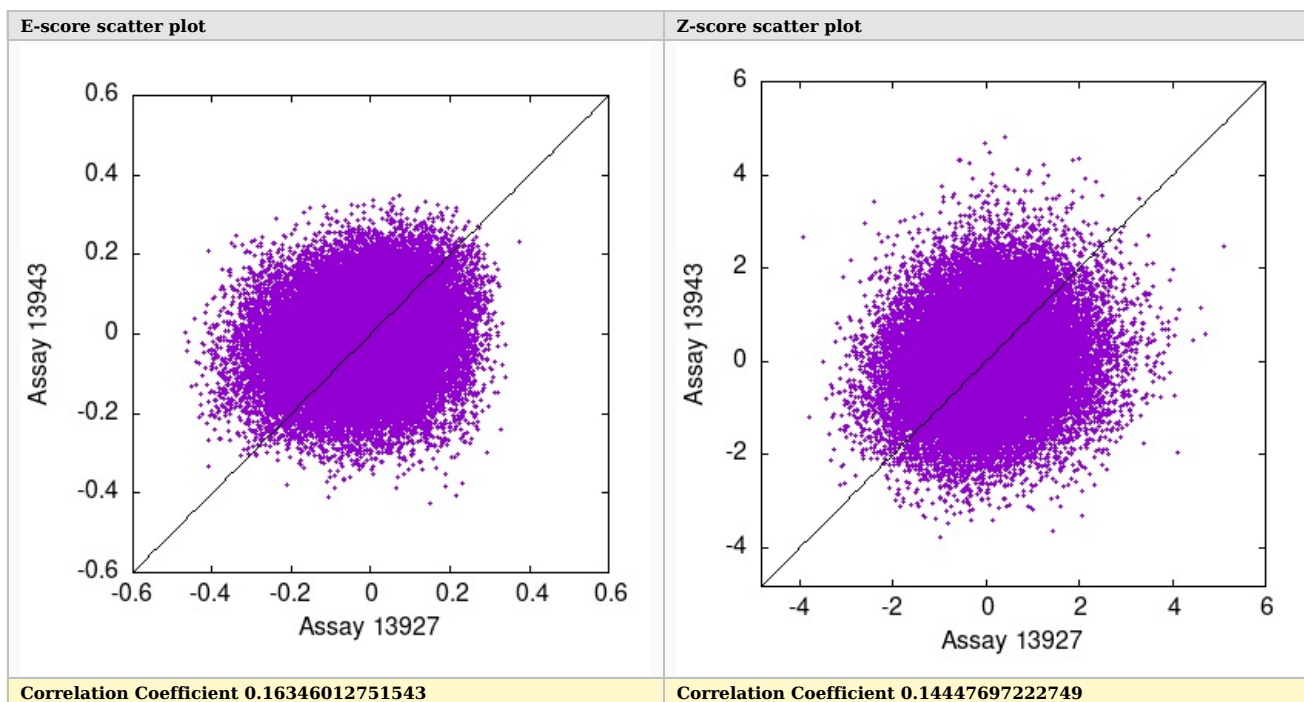


## QC report



## Top scoring motifs for Assay 13927

Protein ID: pTH14244.1 Gene: MKX.FL Domain: Homeobox Flag: Reject Array: 1M-ME

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

Forward:

Reverse:



## Top 10

## Scores

## Alignment

AACAAAGC	0.37407	--AACAAAGC--
AACTAGTG	0.33884	--CACTAGTT--
AACGTTGT	0.33866	-ACAACGTT---
ACACTAAT	0.33356	-ACACTAAT---
TGGTTAAA	0.33201	---TTTAACCA-
GCAATTGC	0.32665	-GCAATTGC---
TTGACAAA	0.32483	TTGACAAA----
ATTATTAC	0.32162	-GTAATAAT---
CAACTTCG	0.32081	----CGAAGTTG
AACACTAA	0.32057	AACACTAA----

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

Forward:

Reverse:



## Top 10

## Scores

## Alignment

AACAAAGC	5.09609	--GCTTTGTT---
GCAACAA	4.69167	-----TTGTTTGC
CAGCAACG	4.59416	---CGTTGCTG--
AACGTTGT	4.44998	-AACGTTGT----
AACGTCAA	4.13141	--TTGCAGTT---
GCAATTGC	4.10810	-GCAATTGC----
ATGTACAA	4.09185	-----TTGTACAT
GGATAAAA	4.05932	---TTTTATCC--
CACAACAC	4.05330	--GTGTTGTG---
CAACGTTG	4.00079	CAACGTTG----

## Top scoring motifs for Assay 13943

Protein ID: pTH14244.2 Gene: MKX.FL Domain: Homeobox Flag: Reject Array: 1M-HK

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

Forward:

Reverse:



## Top 10

## Scores

## Alignment

ATATACAA	0.34991	-TTGTATAT--
CTTATAAG	0.34012	--CTTATAAG--
AAAGAAAG	0.33565	-CTTCTTTT--
GTAATGTA	0.33166	--TACATTAC--
TATACCGA	0.32905	TCGGTATA---
CATGATCC	0.32679	---GGATCATG
CTGTATTA	0.32665	-CTGTATTA--
GAGATATA	0.32335	--TATATCTC-
CGTTCGAC	0.32230	---GTCGAACG
ATTACTAC	0.32160	---GTAGTAAT

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

Forward:

Reverse:



## Top 10

## Scores

## Alignment

CATAATAC	4.80063	---GTATTATG--
ATTACTAC	4.68572	GTAGTAAT-----
AGCATGGG	4.48470	---AGCATGGG--
GACGTAA	4.34646	---TTAACGTC--
CATGATCC	4.32918	-GGATCATG----
GTAATGTA	4.32918	---GTAATGTA--
AATCGATT	4.30729	-----AATCGATT
AGTGTGTG	4.26438	-----AGTGTGTG
TACATGTA	4.22464	---TACATGTA--
ACACACAC	4.12125	----GTGTGTGT-