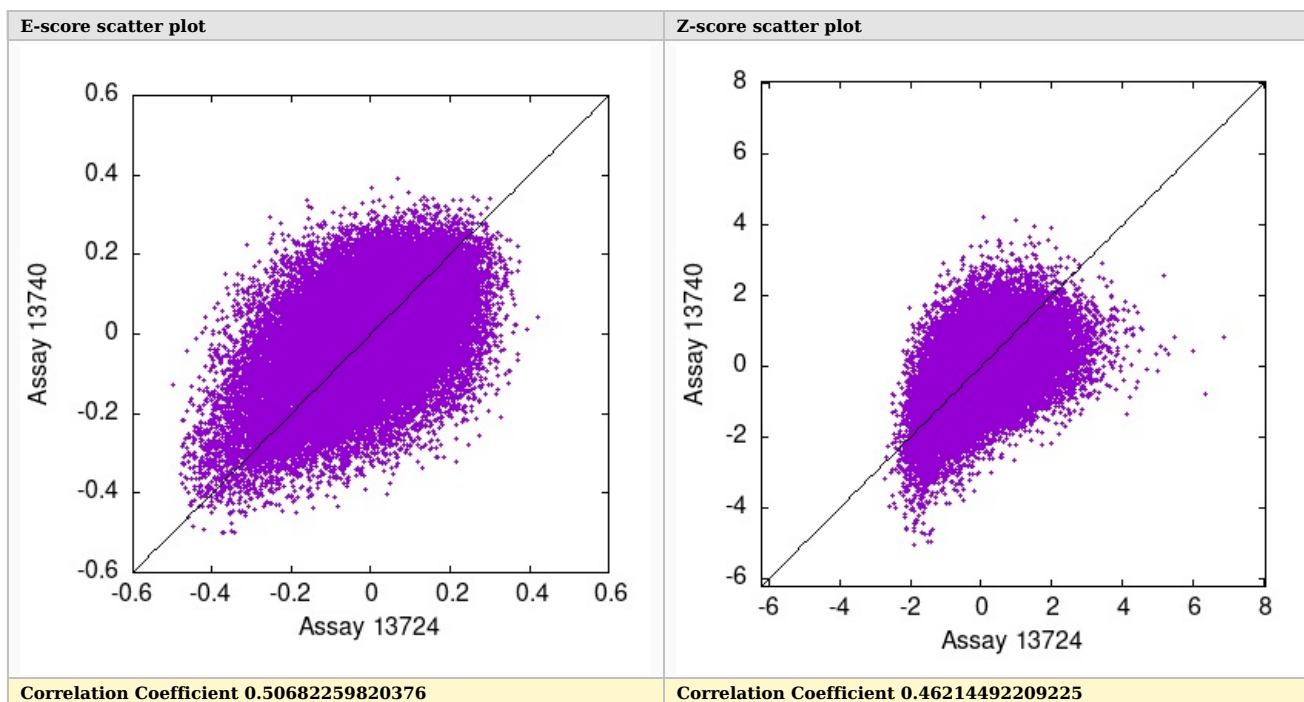


## QC report



## Top scoring motifs for Assay 13724

Protein ID: pTH14306.1 Gene: KCNIP3.FL Domain: Unknown Flag: Reject Array: 1M-ME

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

Forward:

Reverse:



## Top 10

## Scores

## Alignment

AACATGTT	0.42106	-AACATGTT-----
TGTATACA	0.39366	-TGTATACA-----
ACATACAA	0.37437	--ACATACAA-----
ATGTACAT	0.37275	--ATGTACAT-----
TAACGAAA	0.37235	--TAACGAAA-----
AGCAATTG	0.36981	-----CAATTGCT
GTACTTTA	0.36974	TAAAGTAC-----
ATCGATGC	0.36520	--GCATCGAT-----
AGTCATGA	0.36495	--AGTCATGA-----
ACAACCTTA	0.36461	--ACAACCTTA-----

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

Forward:

Reverse:



## Top 10

## Scores

## Alignment

AACATGTT	6.86255	AACATGTT--
ATGTACAT	6.33825	--ATGTACAT--
TGTATACA	6.02036	--TGTATACA--
ACATACAA	5.46788	--ACATACAA--
ACAACCTTA	5.30603	-ACAACCTTA-
TAACAGTA	5.23242	-TAACAGTA-
GTACTTTA	5.15337	--TAAAGTAC--
TATATTAA	5.06944	--TATATTAA--
AGCAATTG	5.01858	-AGCAATTG-
ATATATTA	4.95609	-ATATATTA-

## Top scoring motifs for Assay 13740

Protein ID: pTH14306.2 Gene: KCNIP3.FL Domain: Unknown Flag: Reject Array: 1M-HK

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

Forward:

Reverse:



## Top 10

## Scores

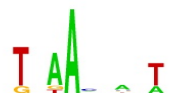
## Alignment

GCTGTGAA	0.39042	-GCTGTGAA-----
CGACTGAA	0.36959	-----CGACTGAA-
AAGCTTTC	0.35785	-----GAAAGCTT
CGCTAAAA	0.34571	--CGCTAAAA-----
ATGTGACA	0.34560	--ATGTGACA-----
TCAATTGA	0.34499	TCAATTGA-----
ATACAAAT	0.34234	--ATTGTGAT-----
CAATGTCA	0.34168	-----TGACATTG-
AATCTGGC	0.33848	-AATCTGGC-----
GTATACGA	0.33839	GTATACGA-----

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

Forward:

Reverse:



## Top 10

## Scores

## Alignment

GCTGTGAA	4.20587	GCTGTGAA-----
AAGCTTTC	4.15935	-----GAAAGCTT-
ACTAAAAT	3.97814	-----ACTAAAAT-
AACCAATC	3.92308	-----AACCAATC-
AAACAGTT	3.67088	-----AACTGTTT
CTGAACGA	3.58133	---CTGAACGA---
GTATACGA	3.56617	--GTATACGA---
ATGAAGTA	3.51980	---ATGAAGTA---
TGTGACAA	3.50740	---TGTGACAA---
CAATGTCA	3.47309	-----CAATGTCA-