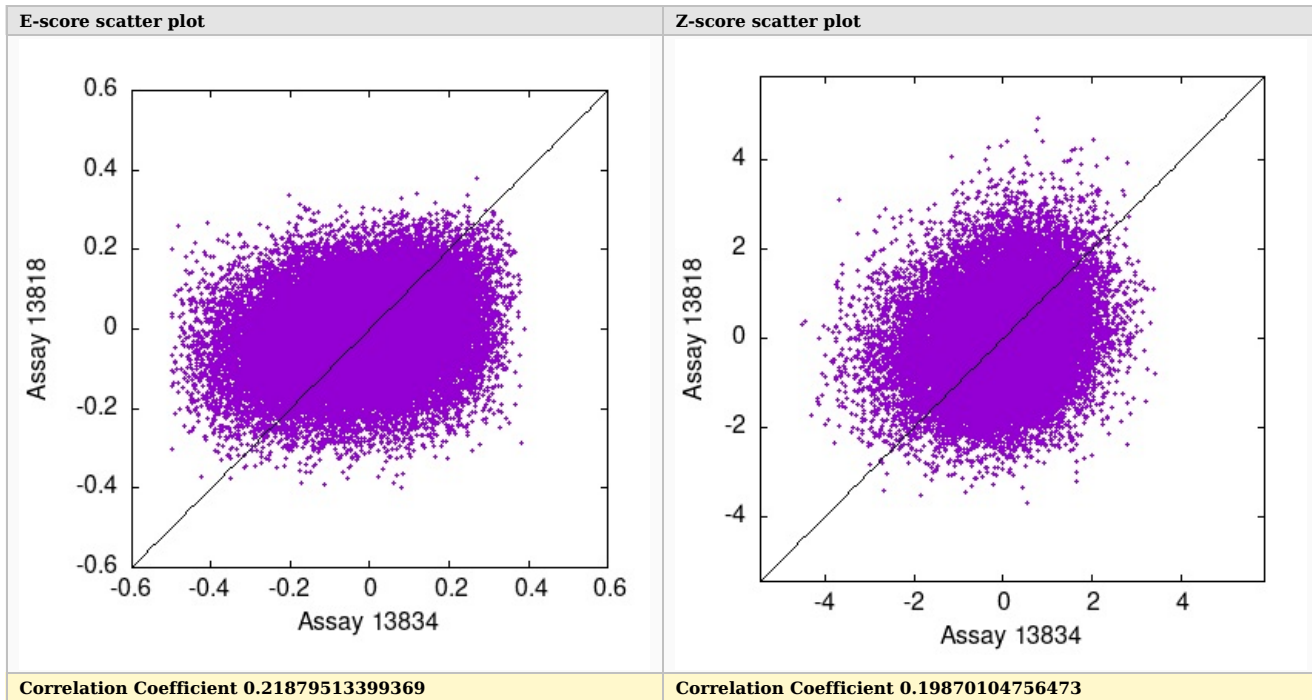


## QC report



## Top scoring motifs for Assay 13834

Protein ID: pTH13912.2 Gene: ARID2 Domain: ARID Flag: Reject Array: 1M-HK

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

Forward:

Reverse:



## Top 10

## Scores

## Alignment

TATTAATA	0.38926	TATTAATA-----
GATCTAGA	0.38146	----GATCTAGA-
ATCTAGAT	0.38034	-----ATCTAGAT
ACTAATTA	0.37815	---TAATTAGT--
GTACATTA	0.37708	---TAATGTAC--
AATATGAA	0.37691	--AATATGAA---
ATAATGTA	0.37642	--ATAATGTA---
ACACAATA	0.37467	---TATTGTGT--
TATAACGA	0.37425	-TATAACGA----
AACATAA	0.37311	--TTATTGTT---

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

Forward:

Reverse:



## Top 10

## Scores

## Alignment

ACTGTCTA	3.40787	ACTGTCTA----
CTAGTAA	3.36730	-CTAGTAA----
AGTATACT	3.30650	----AGTATACT
ATAATGTA	3.23431	--TACATTAT--
ACTAATTA	3.23200	ACTAATTA----
TTCATGAA	3.20394	-TTCATGAA---
ATATTAAG	3.18300	-CTTAATAT---
GTTCAGTA	3.18009	GTTCAGTA----
CTGTAACA	3.14260	--CTGTAACA---
ATCGCGAT	3.12209	-ATCGCGAT---

## Top scoring motifs for Assay 13818

Protein ID: pTH13912.1 Gene: ARID2 Domain: ARID Flag: Reject Array: 1M-ME

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

Forward:

Reverse:



## Top 10

## Scores

## Alignment

AATTGTGA	0.38117	--AATTGTGA-
AAGACTGA	0.34052	AAGACTGA---
ATACAAAA	0.33557	---TTTTGTAT
AACCTCGG	0.33499	CCGAGGTT---
GACTTATA	0.32929	--GACTTATA-
AAACATAG	0.31838	---AAACATAG
GCAAGCGA	0.31221	-TCGCTTGC--
ATAATGCA	0.31002	-TGCATTAT--
ATAAAGC	0.30790	---GCTTTTAT
CTTTCATGC	0.30553	---CTTTCATGC

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

Forward:

Reverse:



## Top 10

## Scores

## Alignment

ATACAAAA	4.93299	---TTTTGTAT-
AAGACTGA	4.67662	----TCAGTCTT
AATTGTGA	4.46812	--AATTGTGA--
AAACATAG	4.43085	---CTATGTTT-
ACGATCGT	4.41897	-ACGATCGT---
CTTTCATGC	4.33704	---CTTTCATGC
AGTGTCGG	4.27600	--AGTGTCGG--
AATTAGTA	4.26733	--AATTAGTA--
GAAATTAA	4.26315	TTAATTTT----
ATAATGCA	4.22846	--ATAATGCA--