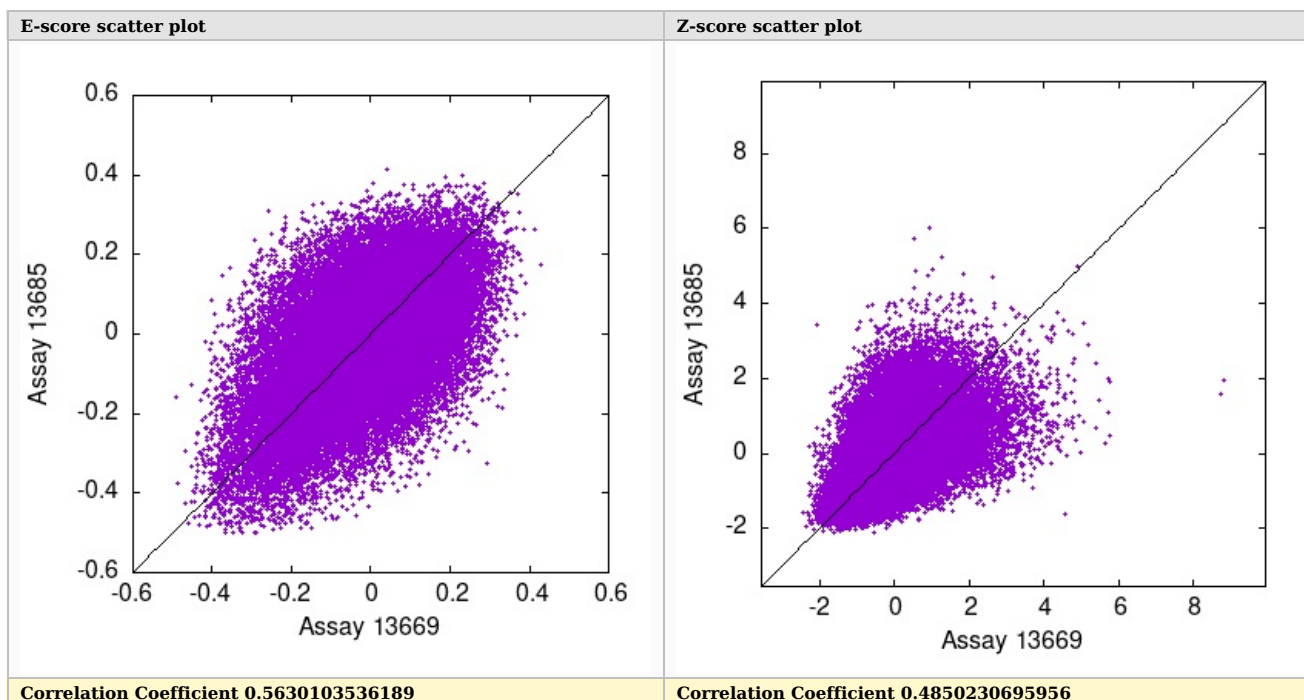


QC report



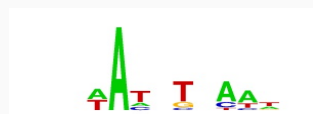
Top scoring motifs for Assay 13669

Protein ID: pTH14284.1 Gene: ARHGAP35.DBD Domain: Unknown Flag: Reject Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

ATGTACAT	0.42727	--ATGTACAT-
AATGCATT	0.41172	--AATGCATT-
TAACGAAA	0.39094	-TAACGAAA--
ATTTAAAT	0.38818	--ATTTAAAT-
TCTGCAGA	0.38687	---TCTGCAGA
CAATTTCA	0.37917	CAATTTCA--
AATTTGTA	0.37779	--AATTTGTA--
GTAATTTA	0.37464	GTAAATTTA--
ATACAACA	0.37445	--ATACAACA-
ACGTAATA	0.37209	--ACGTAATA-

8 mer Z-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

AATGCATT	8.79750	---AATGCATT-
ATGTACAT	8.73919	----ATGTACAT
TACATGTA	5.77943	-TACATGTA---
AGTAATAT	5.75512	AGTAATAT----
CAATTTCA	5.73575	--CAATTTCA--
GTAATATA	5.71656	-GTAATATA---
AAATTTGT	5.65032	--AAATTTGT--
ACTAGTCA	5.45993	---ACTAGTCA--
GTATAATA	5.38781	--TATTATAC--
AACATGTT	5.38251	---AACATGTT-

Top scoring motifs for Assay 13685

Protein ID: pTH14284.2 Gene: ARHGAP35.DBD Domain: Unknown Flag: Reject Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

TCTCGAGA	0.41284	--TCTCGAGA-
TCTTAAGA	0.39836	--TCTTAAGA-
GTCATGAC	0.39631	-GTCATGAC--
GTAACGTA	0.38027	-TACGTTAC--
AAGTACTT	0.37963	---AAGTACTT
ATATCACA	0.37662	--TGTGATAT-
GACAAACA	0.37629	TGTTTGTC---
GATGCATC	0.37430	--GATGCATC-
ATTCACAG	0.37414	-CTGTGAAT--
ATCTGTAC	0.37409	-ATCTGTAC--

8 mer Z-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

TGTAGCAA	6.02837	---TGTAGCAA-
TCTCGAGA	5.72559	---TCTCGAGA-
GTCATGAC	5.22295	---GTCATGAC-
TGTATACA	4.99616	---TGTATACA-
ATCGCGAT	4.90711	---ATCGCGAT-
TCGCGCGA	4.88882	---TCGCGCGA-
GTATACAC	4.77243	---GTATACAC-
ATTATAAT	4.76568	---ATTATAAT-
ATCTGTAC	4.69524	ATCTGTAC----
ATGTTGAA	4.42790	--ATGTTGAA--