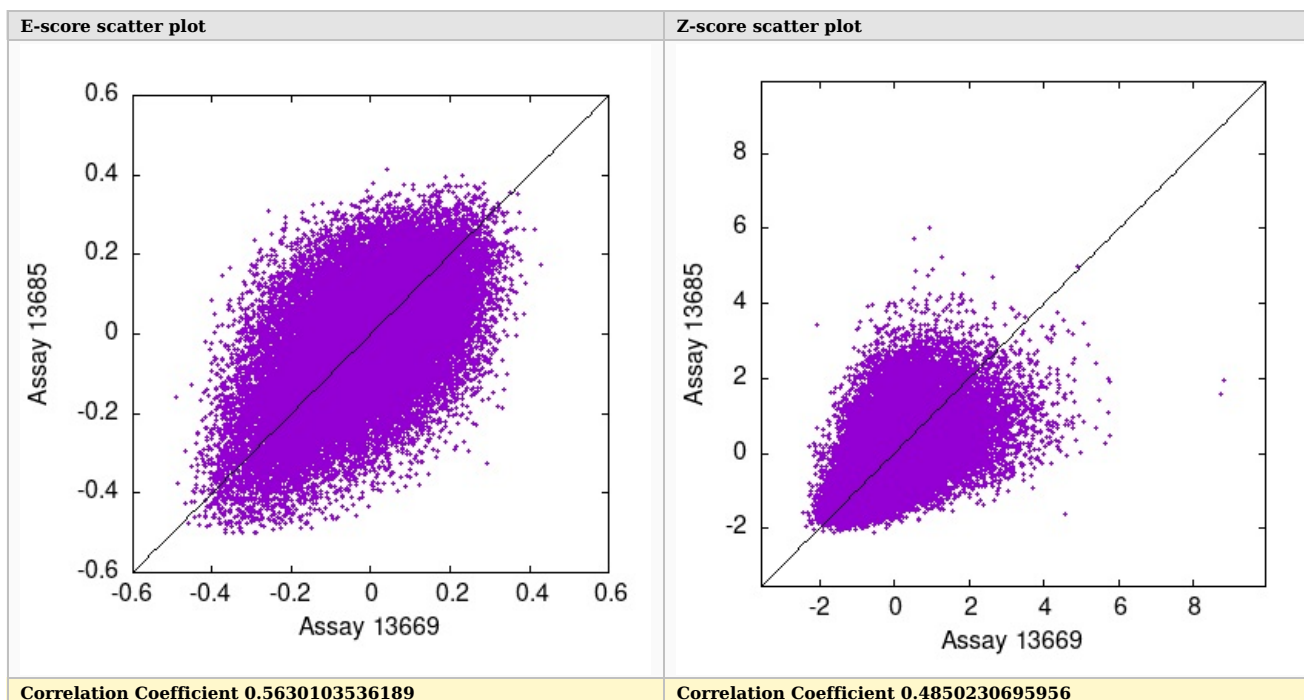


QC report



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--
GTACTTTA	0.37464	GTACTTTA--
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--