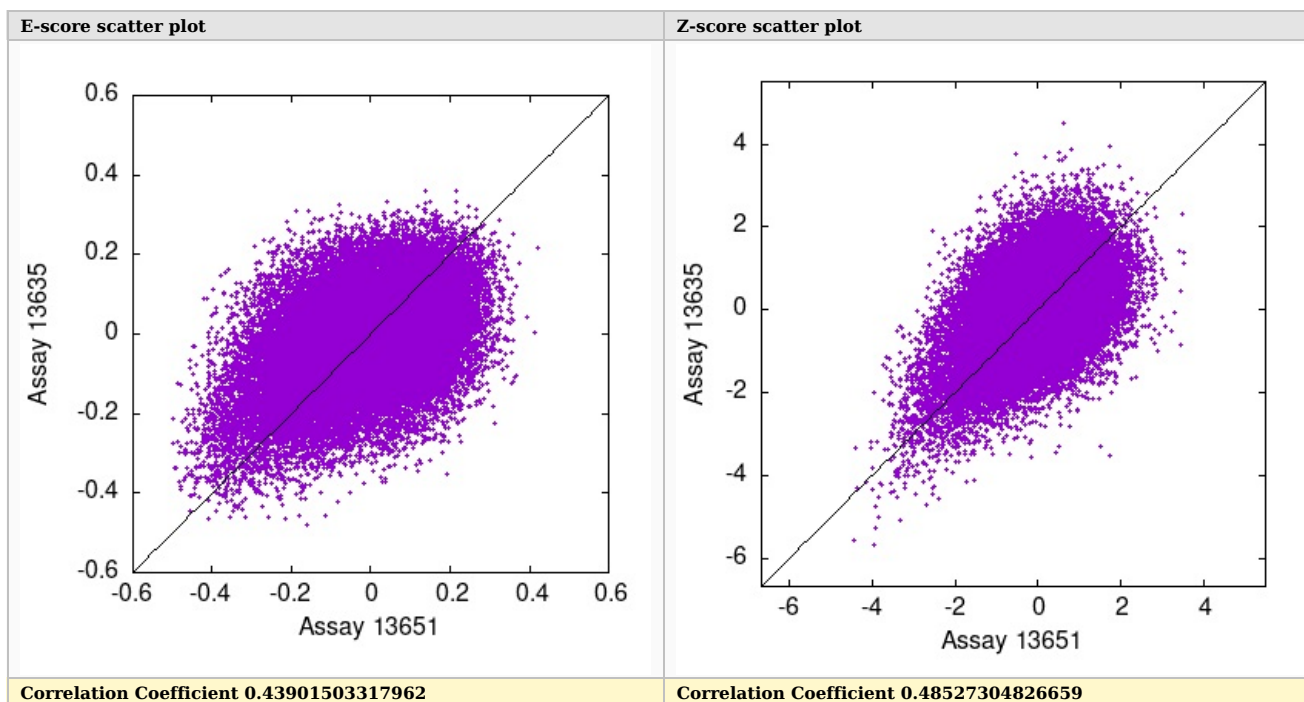


QC report



Top scoring motifs for Assay 13651

Protein ID: pTH14302.2 Gene: GLMP.FL Domain: Unknown Flag: Reject Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

GTCATGAC	0.42261	---GTCATGAC---
AAACGTTT	0.41249	AAACGTTT----
GCATATGC	0.39340	--GCATATGC--
ATTGCAA	0.37551	----ATTGCAA--
AATGTTTG	0.36670	-AATGTTTG----
ATCCGGAT	0.36589	----ATCCGGAT--
ATCAGCTG	0.36274	----ATCAGCTG--
TCGCGCGA	0.36088	----TCGCGCGA--
TTTGCAA	0.36082	----TTTGCAA--
ATGCGCAT	0.36029	----ATGCGCAT--

8 mer Z-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

AAACGTTT	3.52642	-----AAACGTTT-
GTTTAAAC	3.51516	--GTTTAAAC-----
GTCATGAC	3.49629	-GTCATGAC-----
GCATATGC	3.46646	-GCATATGC-----
CTTGCAAG	3.46116	--CTTGCAAG-----
ACAACAG	3.40362	----ACAACAG----
ACAATTCA	3.29458	ACAATTCA-----
CTGTGATA	3.22475	--CTGTGATA-----
ATCAGCTG	3.09325	----ATCAGCTG----
AACGCGTT	3.09072	-----AACGCGTT

Top scoring motifs for Assay 13635

Protein ID: pTH14302.1 Gene: GLMP.FL Domain: Unknown Flag: Reject Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

CACAACAC	0.36119	--CACAACAC--
CACATTCA	0.35986	--CACATTCA--
GTTATAAC	0.33417	GTTATAAC----
ATACACAT	0.33289	----ATACACAT--
ATTATCTG	0.33178	--CAGATAAT--
CAGACAAC	0.32769	--CAGACAAC--
CAACACCA	0.32447	----CAACACCA--
ATCTTTAC	0.32150	--ATCTTTAC--
TCTTTACA	0.32142	-TCTTTACA----
GTTTTGTA	0.31523	--TACAAAAC--

8 mer Z-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

CACATTCA	4.49182	-----CACATTCA
CGTTATAA	3.93562	CGTTATAA-----
ACAACGCA	3.86694	-ACAACGCA-----
GTTTTGTA	3.81185	---TACAAAAC---
ACCAGATA	3.76989	---ACCAGATA---
ATATTGTA	3.69959	---TACAATAT---
AGACACAT	3.68969	--AGACACAT---
ATACACAT	3.62571	--ATACACAT---
GAATCCAA	3.59861	GAATCCAA-----
TCTTTACA	3.50631	-TCTTTACA-----