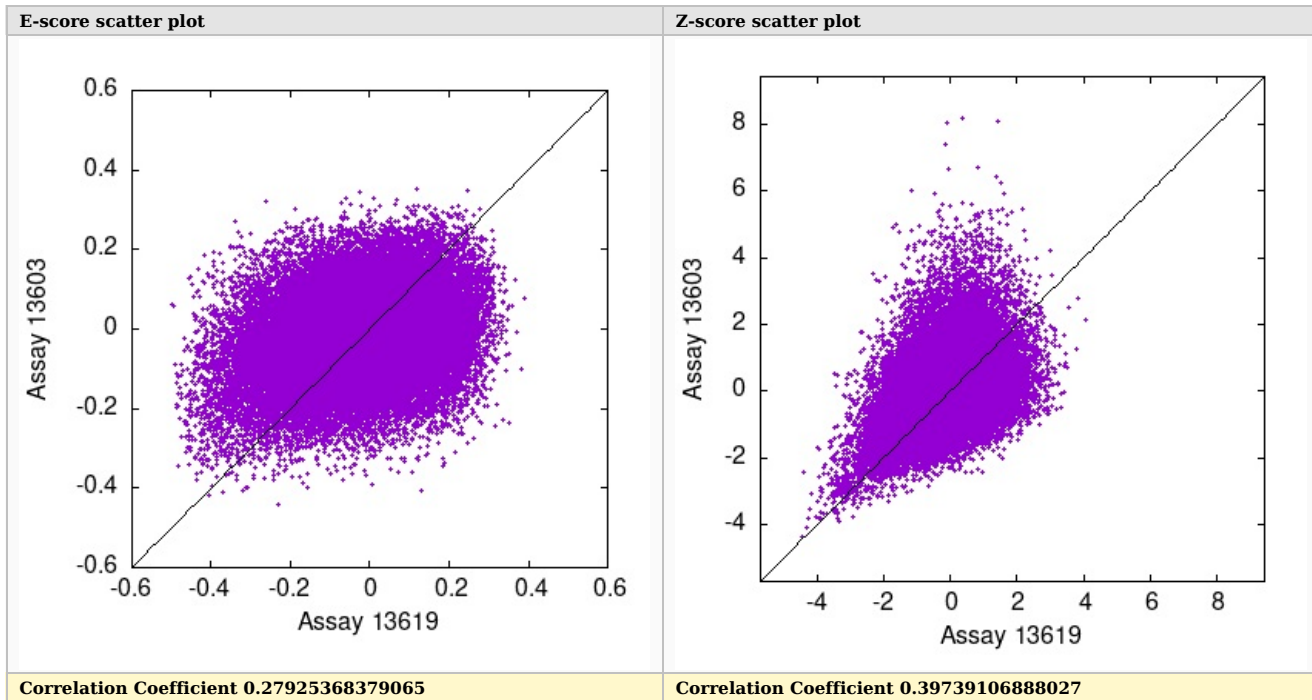


QC report



Top scoring motifs for Assay 13619

Protein ID: pTH14301.2 Gene: DRAP1.FL Domain: Unknown Flag: Reject Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:

Reverse:

ACAAA

ATTTT

Top 10

Scores

Alignment

TACTAGTA	0.39065	TACTAGTA----
GCTGAAAA	0.38072	--GCTGAAAA--
CGCGCGCG	0.37016	--CGCGCGCG--
GATATGTA	0.36811	----TACATATC-
CGAGCAAA	0.35790	--CGAGCAAA--
TATTAATA	0.35335	---TATTAATA--
AATCATGA	0.35214	---AATCATGA--
CTGAACAA	0.35175	-CTGAACAA----
TAATATAA	0.34903	--TAATATAA--
GCATATGC	0.34586	----GCATATGC

8 mer Z-scores for probeset 'all'

Forward:

Reverse:

?

?

Top 10

Scores

Alignment

ATTATAAT	4.04329	----ATTATAAT
TACTAGTA	3.82709	---TACTAGTA-
CGCGCGCG	3.76422	--CGCGCGCG-
AGAATTCT	3.53880	----AGAATTCT
GTACATTA	3.50098	GTACATTA----
TTTGCAAA	3.47404	---TTTGCAAA-
ACAAACAG	3.46391	----ACAAACAG
AATCAATT	3.43372	---AATCAATT-
CGAGCAAA	3.41450	--CGAGCAAA--
TATTAATA	3.40464	---TATTAATA-

Top scoring motifs for Assay 13603

Protein ID: pTH14301.1 Gene: DRAP1.FL Domain: Unknown Flag: Reject Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:

Reverse:

?

GTAAc

Top 10

Scores

Alignment

GGTTATCA	0.35041	--GGTTATCA----
GTTATAAC	0.34687	---GTTATAAC--
GATCGTTA	0.34362	--GATCGTTA----
TGTGCACA	0.33036	--TGTGCACA----
ACAGTTCT	0.32715	ACAGTTCT-----
AACGTGAT	0.32401	-----ATCACGTT
GGGCGAGA	0.32102	-----TCTCGCCC-
CCAACAAC	0.31624	---GTTGTTGG---
GGAATGGA	0.31443	--GGAATGGA----
CTTTAGCA	0.31391	--CTTTAGCA----

8 mer Z-scores for probeset 'all'

Forward:

Reverse:

CAGAA

TTTGG

Top 10

Scores

Alignment

GTTATAAC	8.16776	---GTTATAAC-
TGGTGTA	8.07930	----TTACACCA
GATCGTTA	8.02816	----TAACGATC
CCACGAAG	7.39545	--CCACGAAG-
GGTTATCA	6.70610	----TGATAACC
CCAACAAC	6.67535	---CCAACAAC-
ATTGGTTC	6.42998	--GAACCAAT-
CAAAATTG	6.23487	---CAAAATTG-
GTACGGTA	6.01858	TACCTGAC----
TGCCGACA	5.91224	-TGCCGACA---