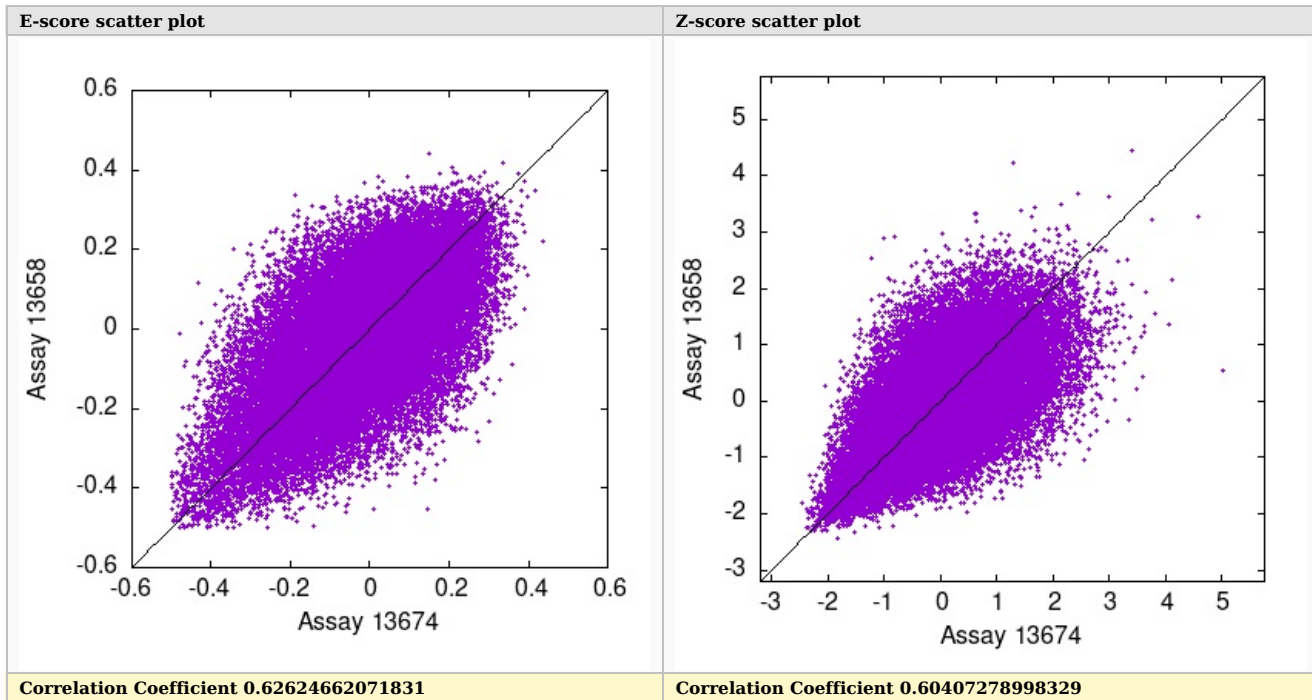


QC report



Top scoring motifs for Assay 13674

Protein ID: pTH14246.2 Gene: NANOGNB.FL Domain: Homeobox Flag: Reject Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

GTGTACAC	0.43616	-GTGTACAC-
TTTGCAAA	0.41605	TTTGCAAA--
ATTATAAT	0.39983	-ATTATAAT-
GTCATGAC	0.39663	-GTCATGAC-
ATGTTAAC	0.39213	-ATGTTAAC-
ATGCATAC	0.39055	-ATGCATAC-
ATGGTCCA	0.38917	-ATGGTCCA-
GATGCATC	0.38865	GATGCATC--
GTGTAACA	0.38681	--TGTTACAC
TGTTAACA	0.38249	--TGTTAACA

8 mer Z-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

GTGTACAC	5.01188	--GTGTACAC-
TTTGCAAA	4.59370	-TTTGCAAA--
GTCATGAC	4.11942	--GTCATGAC-
ACGTACTA	4.06079	---TAGTACGT
TAACGTAA	3.81336	TTACGTTA---
ATGTTAAC	3.76490	--ATGTTAAC-
GTGTAACA	3.65843	---TGTTACAC
TACACACA	3.62363	-TGTGTGTA--
CTGTATTA	3.62275	CTGTATTA---
ATTATAAT	3.58240	--ATTATAAT-

Top scoring motifs for Assay 13658

Protein ID: pTH14246.1 Gene: NANOGNB.FL Domain: Homeobox Flag: Reject Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

ATGTACAT	0.43971	---ATGTACAT--
AATGCATT	0.41810	AATGCATT-----
AACATGTT	0.40690	AACATGTT-----
TAAATTTA	0.39528	TAAATTTA-----
TGTGCACA	0.39489	----TGTGCACA-
CGTTATCA	0.39038	----TGATAACG-
AACGTTGT	0.38977	AACGTTGT-----
GTTTAAAC	0.38974	-----GTTTAAAC
ATATTTAA	0.38475	-ATATTTAA-----
ACATGTTA	0.38327	-ACATGTTA----

8 mer Z-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

AATGCATT	4.45242	--AATGCATT--
ATGTACAT	4.22338	-ATGTACAT---
TAAATTTA	3.68024	---TAAATTTA
GTTTAAAC	3.61846	-GTTTAAAC---
AACATGTT	3.49998	----AACATGTT
TTGCGCAA	3.44384	---TTGCGCAA---
TGTGCACA	3.39401	--TGTGCACA--
ATATTTAA	3.33756	-ATATTTAA---
GTTGCGCA	3.32308	GTTGCGCA----
TTTGCAAA	3.27860	--TTTGCAAA--