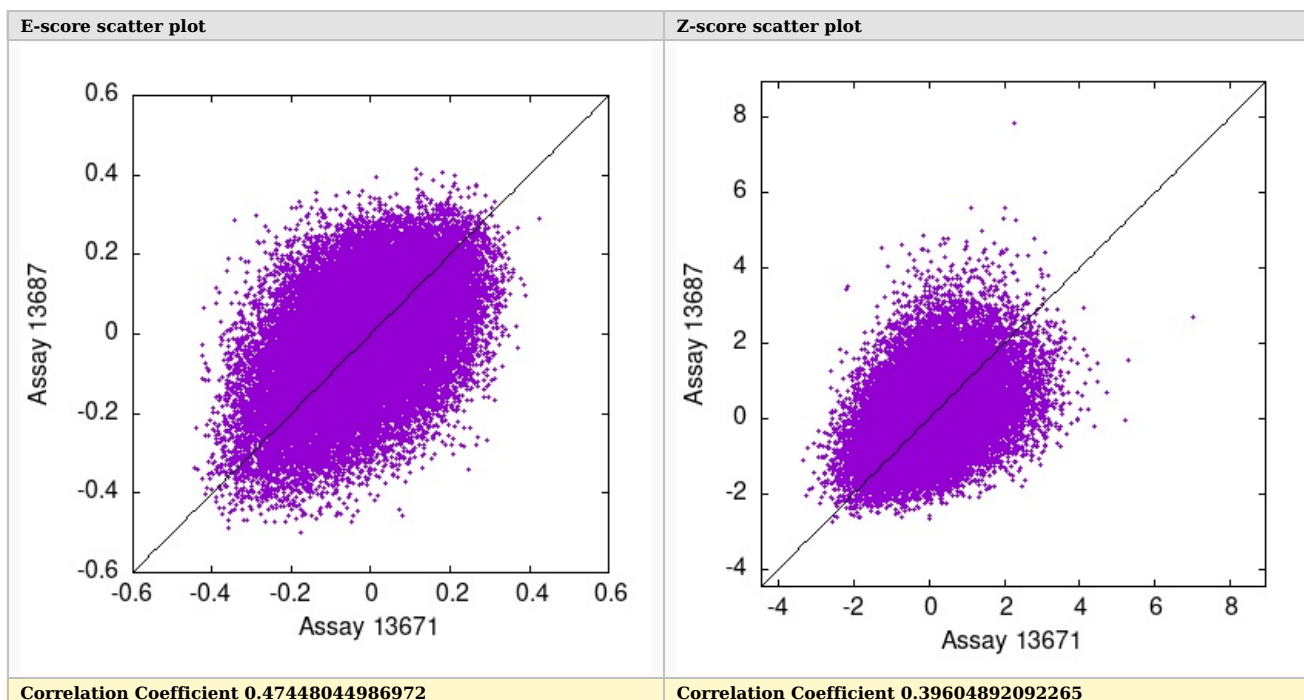


QC report



Correlation Coefficient 0.47448044986972

Correlation Coefficient 0.39604892092265

Top scoring motifs for Assay 13671

Protein ID: pTH14287.1 Gene: CENPS.FL Domain: Unknown Flag: Reject Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

TAAATTTA	0.42398	--TAAATTTA
CAGAAACA	0.39108	--CAGAAACA
ATTGTACC	0.38729	GGTACAAT--
GTATAATA	0.37862	-GTATAATA-
AATTCGAA	0.37281	-TTCGAATT-
TAATAAGA	0.37145	--TAATAAGA
AGTTTTTG	0.36687	--CAAAAAC
TACAATCA	0.36077	--TACAATCA
CATAATAC	0.35955	-GTATTATG-
TAACAGTA	0.35655	--TACTGTTA

8 mer Z-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

TAAATTTA	7.01123	--TAAATTTA
CAAACTTA	5.29229	--CAAACTTA
AGTTTTTG	5.20864	--CAAAAAC
CATAATAC	4.73742	--CATAATAC
ACATGGAT	4.46173	--ACATGGAT
TAACAGTA	4.45973	-TAACAGTA-
CAGAAACA	4.37108	-CAGAAACA-
AAAAATAA	4.26333	--AAAAATAA
ATTGTACC	4.21875	GGTACAAT--
ATAATGCA	4.18978	--ATAATGCA

Top scoring motifs for Assay 13687

Protein ID: pTH14287.2 Gene: CENPS.FL Domain: Unknown Flag: Reject Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

AGATATCT	0.41488	--AGATATCT--
TGTTAACA	0.40809	--TGTTAACA--
TACCGATA	0.40074	-----TACCGATA
TCTCGAGA	0.39819	--TCTCGAGA--
TATATTGA	0.39440	TATATTGA----
GTTATAAC	0.39189	-GTTATAAC----
ATATAAAC	0.38696	-ATATAAAC----
AACACAA	0.37950	-TTGTTGTT----
TACACACA	0.37413	TGTGTGTA----
ATGTTAAC	0.37229	-ATGTTAAC----

8 mer Z-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

TGTTAACA	7.82011	--TGTTAACA--
ATATAAAC	5.58579	-ATATAAAC---
ATTTAAAT	5.57230	-ATTTAAAT---
GTGTACAC	5.29108	-GTGTACAC---
TAAGTTAA	5.24216	-----TTAACTTA
TATTTGCA	4.98228	--TATTTGCA--
ATCTAGAT	4.86168	-ATCTAGAT---
AATATAGA	4.78978	AATATAGA----
CATATAAG	4.78948	CATATAAG----
AGTATACT	4.77710	--AGTATACT--