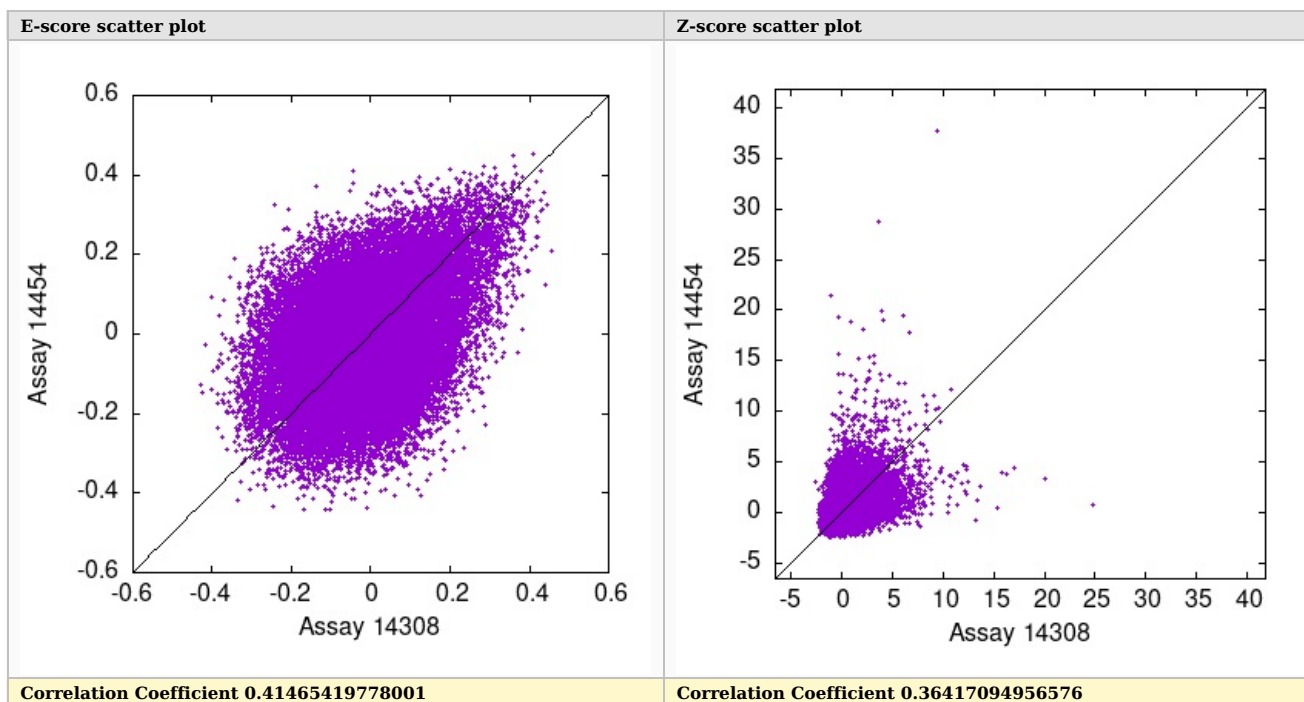


QC report



Top scoring motifs for Assay 14308

Protein ID: pTH14319.3 Gene: PURB.FL Domain: Unknown Flag: Pass_matched_pair Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:

Reverse:

GTGGGTTA

TAACCCAC

Top 10

Scores

Alignment

GTGGGTGA
AGTGGGTG
GTGGGTAA
GGTGGGAA
CACCCACA
ACACCCAC
ACCCACCA
AGGTGGGA
AGCCCAAC
GAGGGTAA

0.45685
0.44434
0.44008
0.43513
0.43287
0.42911
0.42782
0.42775
0.42102
0.42101

--GTGGGTGA-
-AGTGGGTG-
--GTGGGTAA
-GGTGGGAA-
-TGTGGGTG-
--GTGGGTGT
TGGTGGGT--
AGGTGGGA--
-GGTGGGCT-
--GAGGGTAA

8 mer Z-scores for probeset 'all'

Forward:

Reverse:

GTGGGTTA

TAACCCAC

Top 10

Scores

Alignment

GTGGGTGA
AGTGGGTG
GGTGGGAA
AAGTGGGT
CACCCACA
GTGGGTAA
GGTAGGGA
TCCCGCCA
AGGTGGAG
CCAACACA

24.82892
20.11566
17.10084
16.27579
15.81220
15.35330
13.69125
13.35153
13.30178
12.39753

--GTGGGTGA-
-AGTGGGTG-
-GGTGGGAA-
AAGTGGGT--
-TGTGGGTG-
--GTGGGTAA-
-GGTAGGGA-
--TGGCGGGA
-AGGTGGAG-
-TGTGTTGG-

Top scoring motifs for Assay 14454

Protein ID: pTH14319.5 Gene: PURB.FL Domain: Unknown Flag: Pass_matched_pair Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:

Reverse:

AACCCACC

GGTGGTTT

Top 10

Scores

Alignment

AACCCACC
CAACCCAC
AATCCACC
ACCAACCA
GACCAACC
AAACCGAC
ACCAACCT
ACCCACCA
AACCTTCC
AGCCACAC

0.45144
0.44733
0.42350
0.42241
0.41628
0.41404
0.40887
0.40867
0.40813
0.40442

--AACCCACC-
CAACCCAC--
-AATCCACC-
--ACCAACCA
-GACCAACC-
AAACCGAC--
--ACCAACCT
--ACCCACCA
-AACCTTCC-
-AGCCACAC-

8 mer Z-scores for probeset 'all'

Forward:

Reverse:

AACCCACC

GGTGGTTT

Top 10

Scores

Alignment

AACCCACC
CAACCCAC
ACCAACCT
AAACCGAC
AATCCACC
CCAACACG
AAGTGGGT
ACCTACCC
ACGGTCGG
AAACCCAC

37.79456
28.79666
21.39678
19.86329
19.44300
19.25146
18.99940
18.86731
18.15799
17.75728

-AACCCACC--
CAACCCAC--
--ACCAACCT-
AAACCGAC--
-AATCCACC-
---CCAACACG
---ACCACCTT
--ACCTACCC-
---CCGACCGT
AAACCCAC--