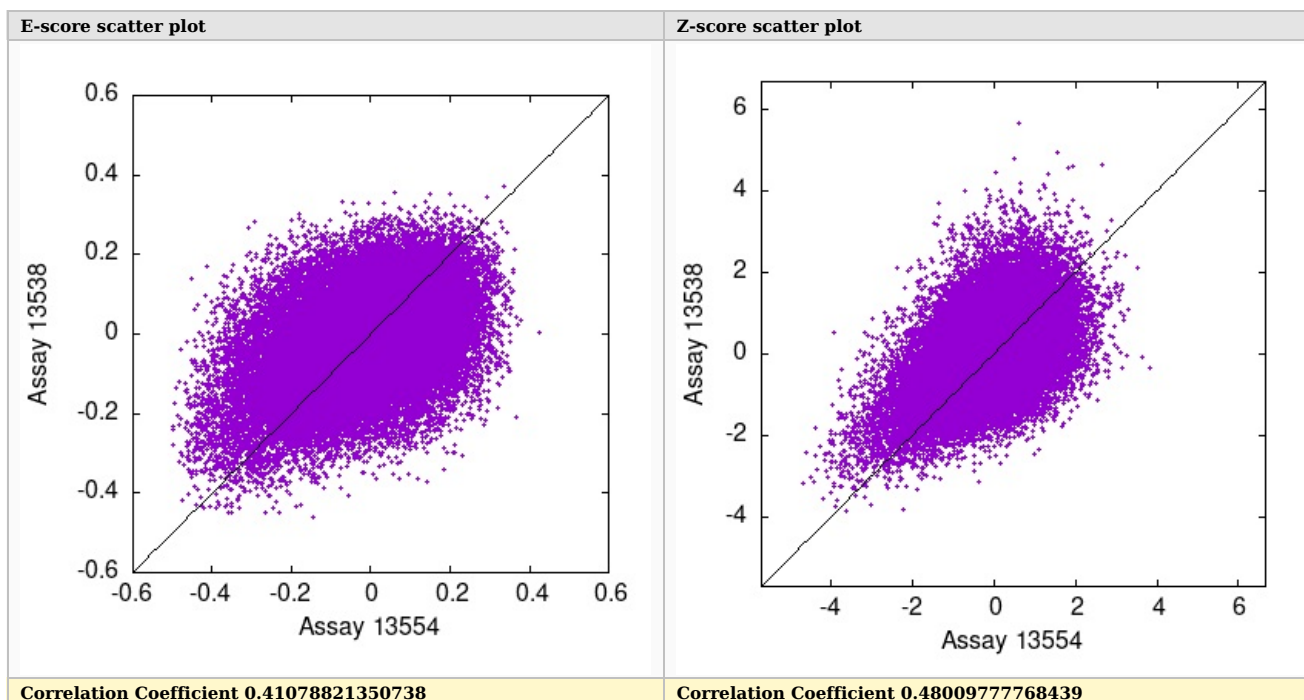


QC report



Top scoring motifs for Assay 13554

Protein ID: pTH14218.2 Gene: CAMTA1.DBD Domain: CG-1 Flag: Reject Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:

Reverse:

ATTTACA

TGTAAT

Top 10

Scores

Alignment

GATATGTA 0.42354
CATTATAG 0.37702
AACACAAT 0.37151
CGTAACAA 0.36846
ATATCACA 0.36817
TCTCGAGA 0.36273
ATTATTAC 0.36095
CATTACAA 0.35958
GAATATTC 0.35811
GTAACAAA 0.35469

GATATGTA---
CATTATAG---
-ATTGTGTT--
--TTGTTACG-
--ATATCACA-
--TCTCGAGA-
-ATTATTAC--
---CATTACAA
GAATATTC---
-TTTGTTCAC--

8 mer Z-scores for probeset 'all'

Forward:

Reverse:

GA TATTA

TAATA TC

Top 10

Scores

Alignment

ATTATAAT 3.84405
GATATGTA 3.63652
GAATATTC 3.50837
ACTATTTC 3.31800
GAATTGTA 3.26066
ATTATTAC 3.20627
ATTACGGA 3.17087
CATAACAC 3.17018
ATATCACA 3.15348
ATTACAAC 3.14635

-ATTATAAT---
GATATGTA----
GAATATTC----
-ACTATTTC---
GAATTGTA----
-ATTATTAC---
---ATTACGGA
--GTGTTATG--
--ATATCACA--
-ATTACAAC---

Top scoring motifs for Assay 13538

Protein ID: pTH14218.1 Gene: CAMTA1.DBD Domain: CG-1 Flag: Reject Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:

Reverse:

TTGTTA

TAAACA

Top 10

Scores

Alignment

TATACAAA 0.37200
GAGTGCTA 0.35570
CCAACAAA 0.35350
TACTATAA 0.35267
GTTGGTTA 0.34444
CATCTTAA 0.33184
AACGAATT 0.33176
ACTGCATA 0.32933
ACCGGTTA 0.32779
CACGGTCA 0.32776

-TTTGTATA-
-GAGTGCTA-
--TTTGTGG-
--TACTATAA
-GTTGGTTA-
-CATCTTAA-
AATTCGTT--
-ACTGCATA-
-ACCGGTTA-
-CACGGTCA-

8 mer Z-scores for probeset 'all'

Forward:

Reverse:

ATACGAAA

TTTGTAT

Top 10

Scores

Alignment

ATATACCG 5.63382
CCAACAAA 4.91594
AATTGCGT 4.76352
TATACAAA 4.64763
ATCGCGAT 4.60320
ATATAGTA 4.55364
ATCACTCA 4.42694
ACAAAACA 4.39723
ACACCAGA 4.16468
TACTATAA 4.15156

ATATACCG----
-CCAACAAA---
--ACGCAATT--
-TATACAAA---
--ATCGCGAT--
ATATAGTA----
-ATCACTCA---
---ACAAAACA
--ACACCAGA--
TTATAGTA----