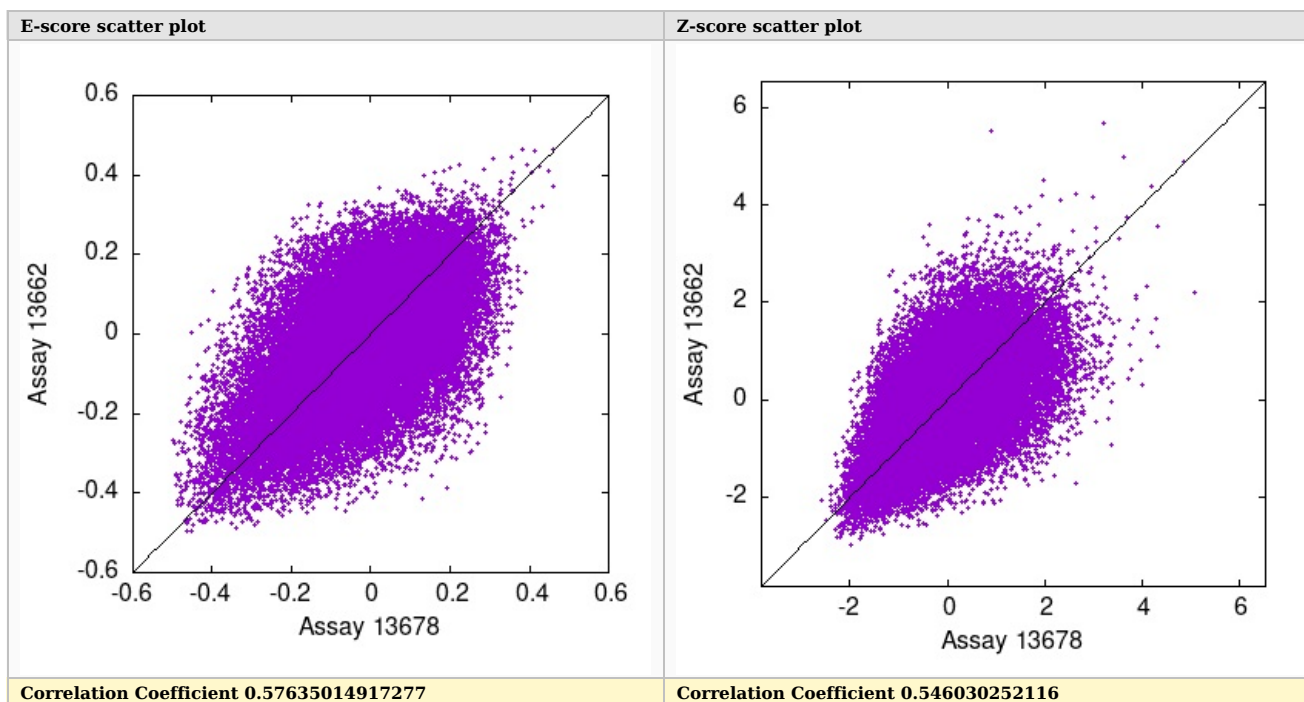


QC report



Top scoring motifs for Assay 13678

Protein ID: pTH14271.2 Gene: DMTF1.DBD Domain: Myb_DNA-binding Flag: Pass_matched_pair Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

ACATCCGG
AAGGATGT
CGGATGTA
CATCCGGG
ACATCCGT
AGGATGTA
TGTTAACA
AGGATGTG
AACATCCG
CTACATCC

0.46048
0.46005
0.44705
0.43111
0.42517
0.41402
0.40969
0.40750
0.40633
0.39356

-CCGGATGT----
-AAGGATGT----
-CGGATGTA----
CCCGGATG-----
-ACGGATGT----
-AGGATGTA----
-----TGTTAACA
--AGGATGTG----
--CGGATGTT---
---GGATGTAG---

8 mer Z-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

TGTTAACA
AAGGATGT
CGGATGTA
GTACAACA
GATGCATC
TACACACA
AGGATGTA
ACATCCGG
GTGTACAC
ATTATAAT

5.05984
4.83571
4.32388
4.31636
4.27578
4.19506
4.18975
4.08443
3.99833
3.96923

----TGTTAACA
AAGGATGT----
-CGGATGTA----
--TGTTGTAC--
---GATGCATC--
-TGTGTGTA----
-AGGATGTA----
CCGGATGT----
---ATTGTACAC-
---ATTATAAT--

Top scoring motifs for Assay 13662

Protein ID: pTH14271.1 Gene: DMTF1.DBD Domain: Myb_DNA-binding Flag: Pass_matched_pair Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

AAGGATGT
ACATCCCT
AGGATGTA
GGATGTAA
GGGATGTA
CTACATCC
ATGTACAT
ACATCCGT
CAACATCC
ACATCCTC

0.46532
0.46321
0.45979
0.44364
0.44006
0.42773
0.42692
0.42315
0.41786
0.41390

AAGGATGT----
AGGGATGT----
-AGGATGTA---
--GGATGTAA--
-GGGATGTA---
--GGATGTAG--
----ATGTACAT
ACGGATGT----
--GGATGTTG--
GAGGATGT----

8 mer Z-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

ACATCCCT
ATGTACAT
GGATGTAA
AAGGATGT
GGGATGTA
AGGATGTA
TAAATTTA
ATACACAT
ATGTTAAC
TGTATACA

5.66115
5.52412
4.99154
4.88061
4.49684
4.37582
4.21197
4.17883
4.16678
4.10172

AGGGATGT----
----ATGTACAT-
--GGATGTAA--
AAGGATGT----
-GGGATGTA----
-AGGATGTA----
-TAAATTTA----
--ATGTGTAT--
---ATGTTAAC-
-----TGTATACA