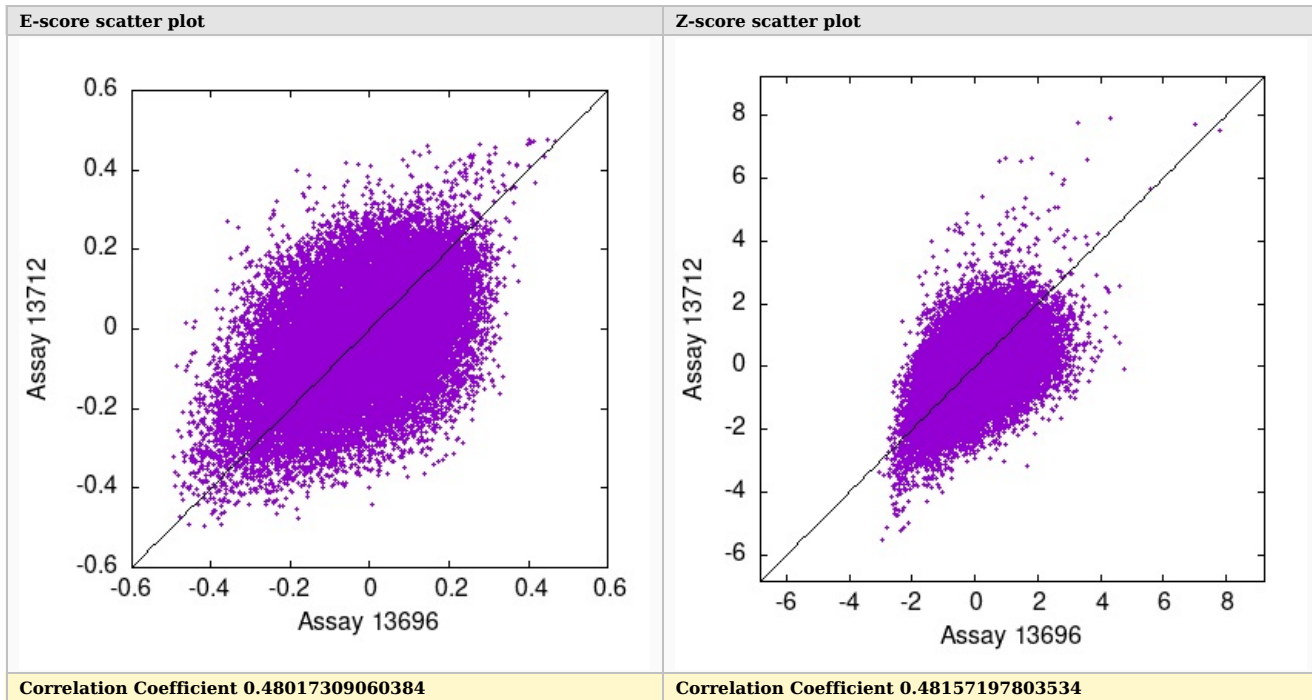


QC report



Top scoring motifs for Assay 13696

Protein ID: pTH13933.1 Gene: ZBED9.DBD Domain: zf-BED Flag: Pass_matched_pair Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:

Reverse:

ACGGCCGA
AACGGCCG
ATCGGCCG
GGCCGAAA
CGGCCGAA
CGGCCGGA
ACGGCCGG
CGGCCGGA
CTACAACA

TCGGCCGT
TCGGCCGT
TCGGCCGT
TCGGCCGT
TCGGCCGT
TCGGCCGT
TCGGCCGT
TCGGCCGT
TCGGCCGT

Top 10

Scores

Alignment

ACGGCCGA 0.46969
AACGGCCG 0.44846
ATCGGCCG 0.43932
GGCCGAAA 0.41789
CGGCCGAA 0.41364
CGGCCGGA 0.40457
ACGGCCGG 0.40215
CGGCCGGA 0.40061
CGGCCGTA 0.39990
CTACAACA 0.37564

--ACGGCCGA--
-AACGGCCG--
---CGGCCGAT--
----GGCCGAAA
---CGGCCGAA--
---CGGCCGGA--
--ACGGCCGG--
--CGGCCGGA--
-TACGGCCG--
CTACAACA----

8 mer Z-scores for probeset 'all'

Forward:

Reverse:

ACGGCCGA
AACGGCCG
ATCGGCCG
AACAACGC
CCGGCCGA
ACTGTATA
ATAATGCA
CGGCCGAA
CATAATAC
ATAACGAA

TCGGCCGT
TCGGCCGT
TCGGCCGT
TCGGCCGT
TCGGCCGT
TCGGCCGT
TCGGCCGT
TCGGCCGT
TCGGCCGT

Top 10

Scores

Alignment

ACGGCCGA 7.79632
AACGGCCG 6.99725
ATCGGCCG 5.58540
AACAACGC 4.77422
CCGGCCGA 4.61157
ACTGTATA 4.58360
ATAATGCA 4.47473
CGGCCGAA 4.29148
CATAATAC 4.27076
ATAACGAA 4.22849

--ACGGCCGA--
-AACGGCCG--
---CGGCCGAT--
--AACAACGC--
--CCGGCCGA--
--ACTGTATA--
ATAATGCA---
---CGGCCGAA--
---GTATTATG
--ATAACGAA--

Top scoring motifs for Assay 13712

Protein ID: pTH13933.2 Gene: ZBED9.DBD Domain: zf-BED Flag: Pass_matched_pair Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:

Reverse:

ACGGCCGA
AACGGCCG
ATCGGCCG
GGCCGAAA
CGGCCGAA
CGGCCGGA
ACGGCCGG
CGGCCGGA
CTACAACA

TCGGCCGT
TCGGCCGT
TCGGCCGT
TCGGCCGT
TCGGCCGT
TCGGCCGT
TCGGCCGT
TCGGCCGT
TCGGCCGT

Top 10

Scores

Alignment

ACGGCCGG 0.47758
AACGGCCG 0.47737
ACGGCCGA 0.47294
CGGCCGAA 0.47136
CGGCCGGA 0.46664
CGGCCGTA 0.46603
GCGGCCCA 0.46562
GGGCCGCA 0.46246
CGGCCCAA 0.45693
ACGGCCCA 0.44436

--ACGGCCGG--
AACGGCCG--
-ACGGCCGA--
--CGGCCGAA--
--CGGCCGGA--
TACGGCCG--
-GCGGCCCA--
--GGGCCGCA--
--CGGCCCAA--
-ACGGCCCA--

8 mer Z-scores for probeset 'all'

Forward:

Reverse:

ACGGCCGA
AACGGCCG
ATCGGCCG
AACAACGC
CCGGCCGA
ACTGTATA
ATAATGCA
CGGCCGAA
CATAATAC
ATAACGAA

TCGGCCGT
TCGGCCGT
TCGGCCGT
TCGGCCGT
TCGGCCGT
TCGGCCGT
TCGGCCGT
TCGGCCGT
TCGGCCGT

Top 10

Scores

Alignment

CGGCCGAA 7.87713
ACGGCCGG 7.76276
AACGGCCG 7.69994
ACGGCCGA 7.49063
GGGCCGCA 6.61453
GCGGCCCA 6.60512
CGGCCGTA 6.56066
ACGGCCCA 6.53691
CGGCCCAA 6.53629
CGGCCGAG 6.11461

--CGGCCGAA--
-ACGGCCGG--
AACGGCCG--
-ACGGCCGA--
--GGGCCGCA--
-GCGGCCCA--
TACGGCCG--
-ACGGCCCA--
--CGGCCCAA--
--CGGCCGAG--