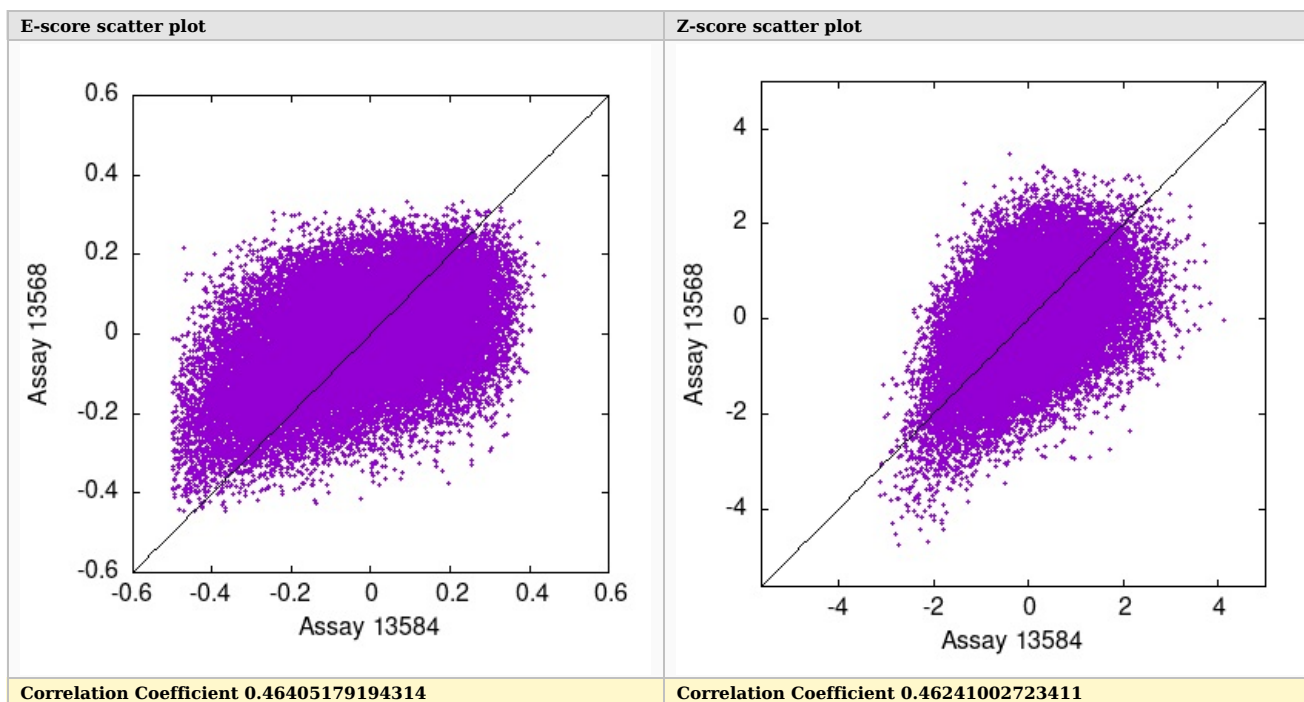


QC report



Top scoring motifs for Assay 13584

Protein ID: pTH13960.2 Gene: DZIP1.DBD Domain: zf-C2H2 Flag: Reject Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:

Reverse:

ATATT AT AT AAATAT

Top 10

Scores

Alignment

| | | |
|-----------|---------|-------------|
| CTGTATTA | 0.43754 | CTGTATTA-- |
| ATAGTAAT | 0.42068 | --ATAGTAAT |
| ATATTAAT | 0.41142 | --ATATTAAT |
| TATTTGCA | 0.40929 | -TATTTGCA- |
| TATATGAA | 0.40583 | -TATATGAA- |
| AAAACCTTA | 0.40281 | -AAAACCTTA- |
| TACACACA | 0.40278 | -TGTGTGTA- |
| GATATGTA | 0.40184 | -GATATGTA- |
| GAAATTTT | 0.39711 | -GAAATTTT- |
| ACAAATA | 0.39597 | -TATTTTGT- |

8 mer Z-scores for probeset 'all'

Forward:

Reverse:

ATTATATA TATAAT

Top 10

Scores

Alignment

| | | |
|----------|---------|-------------|
| CTGTATTA | 4.10800 | --TAATACAG- |
| GCATATAA | 3.81530 | --GCATATAA- |
| TAATATAA | 3.72981 | --TAATATAA- |
| ATAGTAAT | 3.69828 | ATTACTAT--- |
| TAATAATA | 3.63271 | --TAATAATA- |
| ATATCTTA | 3.61135 | --TAAGATAT- |
| GATATGTA | 3.59688 | ---GATATGTA |
| ATATTAAT | 3.49932 | ATTAATAT--- |
| TACACACA | 3.48835 | -TGTGTGTA- |
| CATATAAC | 3.48615 | ---CATATAAC |

Top scoring motifs for Assay 13568

Protein ID: pTH13960.1 Gene: DZIP1.DBD Domain: zf-C2H2 Flag: Reject Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:

Reverse:

TACATTA TAATGTA

Top 10

Scores

Alignment

| | | |
|----------|---------|----------------|
| ACAATGTA | 0.33318 | ---ACAATGTA-- |
| CTGGTAGA | 0.33170 | TCTACCAG----- |
| TACCAATA | 0.32532 | ---TACCAATA--- |
| ACAAATAT | 0.31669 | ---ACAAATAT--- |
| ACTTTAAT | 0.31649 | ---ACTTTAAT--- |
| ACAAAACA | 0.31631 | ---ACAAAACA--- |
| AATCATTA | 0.31544 | --AATCATTA---- |
| ACCGGTTA | 0.31326 | ---ACCGGTTA--- |
| AATGTAGT | 0.31139 | -----AATGTAGT |
| AGTAGTAT | 0.31119 | -ATACTACT----- |

8 mer Z-scores for probeset 'all'

Forward:

Reverse:

TACACTA TACACTA

Top 10

Scores

Alignment

| | | |
|----------|---------|-----------------|
| AAGCGCGA | 3.48286 | ---AAGCGCGA--- |
| CAACATTG | 3.22502 | ---CAACATTG--- |
| AATAGTGT | 3.19100 | -----ACACTATT- |
| GTTACTAA | 3.12008 | TTAGTAAC----- |
| ATGACAAC | 3.11093 | -----ATGACAAC-- |
| ATGTAGAC | 3.09874 | -----GTCTACAT |
| ACCAAAAA | 3.09682 | -----ACCAAAAA- |
| ACTGCGAA | 3.08951 | ---TTCGCAGT---- |
| TAACACTA | 3.08930 | ---TAACACTA--- |
| AATTTTAC | 3.03811 | ---GTAAATT---- |