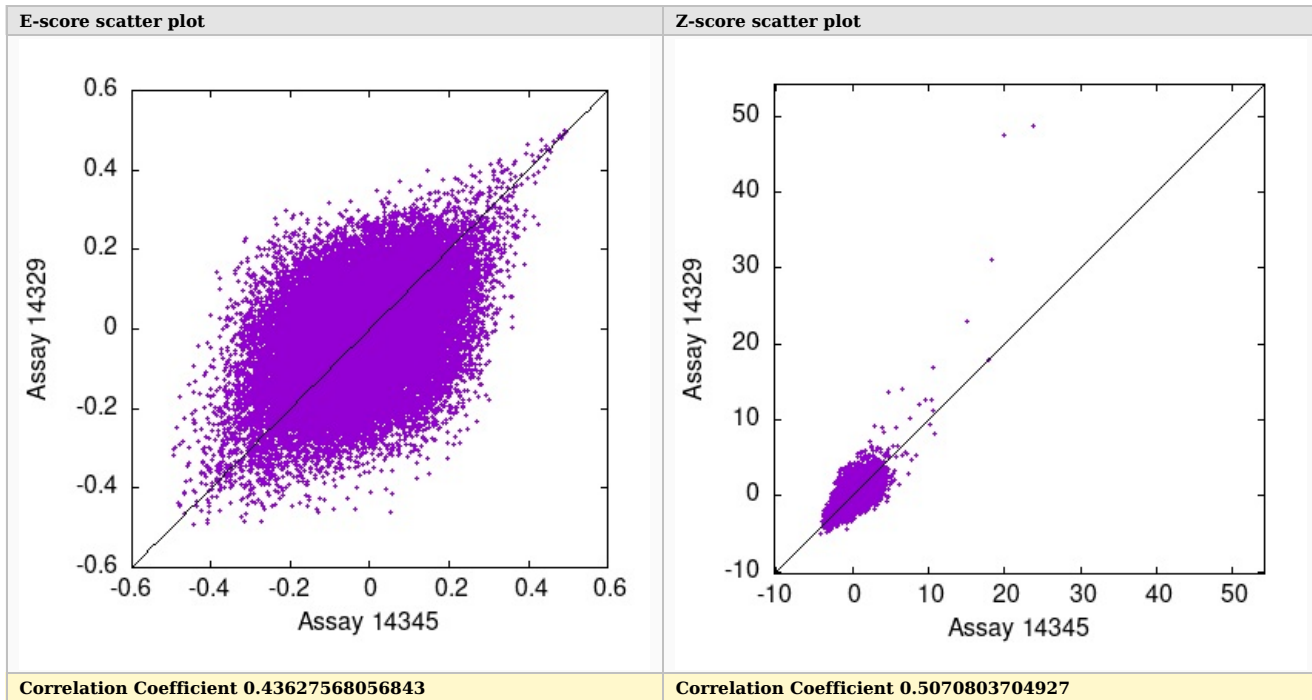


QC report



Top scoring motifs for Assay 14345

Protein ID: pTH15523.2 Gene: JUNB Domain: bZIP_1 Flag: Pass_matched_pair Array: 1M-HK

| 8 mer E-scores for probeset 'all' | | | 8 mer Z-scores for probeset 'all' | | |
|-----------------------------------|---------|-----------|-----------------------------------|----------|-----------|
| Forward: | | Reverse: | Forward: | | Reverse: |
| | | | | | |
| Top 10 | Scores | Alignment | Top 10 | Scores | Alignment |
| ATGACTCA | 0.49500 | ATGACTCA- | ATGACTCA | 23.73626 | ATGACTCA- |
| ATGAGTCA | 0.49049 | -TGACTCAT | ATGAGTCA | 19.84882 | -TGACTCAT |
| GTGAGTCA | 0.48682 | -TGACTCAC | GTGAGTCA | 18.22112 | -TGACTCAC |
| GTGACTCA | 0.48170 | GTGACTCA- | GTGACTCA | 17.88284 | GTGACTCA- |
| ATGACTAA | 0.47923 | ATGACTAA- | ATGACTAA | 15.05573 | ATGACTAA- |
| ATTAGTCA | 0.47385 | -TGACTAAT | ATTAGTCA | 10.83359 | ATTAGTCA- |
| ATGACGCA | 0.46438 | ATGACGCA- | ATGACGCA | 10.60495 | -TGACTAAT |
| TGACGTCA | 0.46361 | -TGACGTCA | TGACGTCA | 10.56336 | -TGACGTCA |
| ATTACTCA | 0.45495 | ATTACTCA- | ATGACGCA | 10.31939 | ATGACGCA- |
| ATGCGTCA | 0.45049 | -TGACGCAT | ATGCGTCA | 10.14866 | -TGACGCAT |

Top scoring motifs for Assay 14329

Protein ID: pTH15523.1 Gene: JUNB Domain: bZIP_1 Flag: Pass_matched_pair Array: 1M-ME

| 8 mer E-scores for probeset 'all' | | | 8 mer Z-scores for probeset 'all' | | |
|-----------------------------------|---------|-----------|-----------------------------------|----------|-----------|
| Forward: | | Reverse: | Forward: | | Reverse: |
| | | | | | |
| Top 10 | Scores | Alignment | Top 10 | Scores | Alignment |
| ATGAGTCA | 0.49748 | -TGACTCAT | ATGACTCA | 48.79270 | ATGACTCA- |
| ATGACTCA | 0.49678 | ATGACTCA- | ATGAGTCA | 47.38880 | -TGACTCAT |
| GTGAGTCA | 0.48759 | -TGACTCAC | GTGAGTCA | 31.11947 | -TGACTCAC |
| ATGACTAA | 0.48658 | ATGACTAA- | ATGACTAA | 22.90196 | ATGACTAA- |
| GTGACTCA | 0.48136 | GTGACTCA- | GTGACTCA | 17.87174 | GTGACTCA- |
| ATTAGTCA | 0.47817 | -TGACTAAT | ATTAGTCA | 16.76451 | -TGACTAAT |
| CTGACTCA | 0.47533 | CTGACTCA- | CTGACTCA | 14.11243 | CTGACTCA- |
| TGACGTCA | 0.47360 | -TGACGTCA | CTGAGTCA | 13.54571 | -TGACTCAG |
| ATGACGCA | 0.47119 | ATGACGCA- | GTGACTAA | 12.70878 | GTGACTAA- |
| CTGAGTCA | 0.46459 | -TGACTCAG | ATGACGCA | 12.62905 | ATGACGCA- |