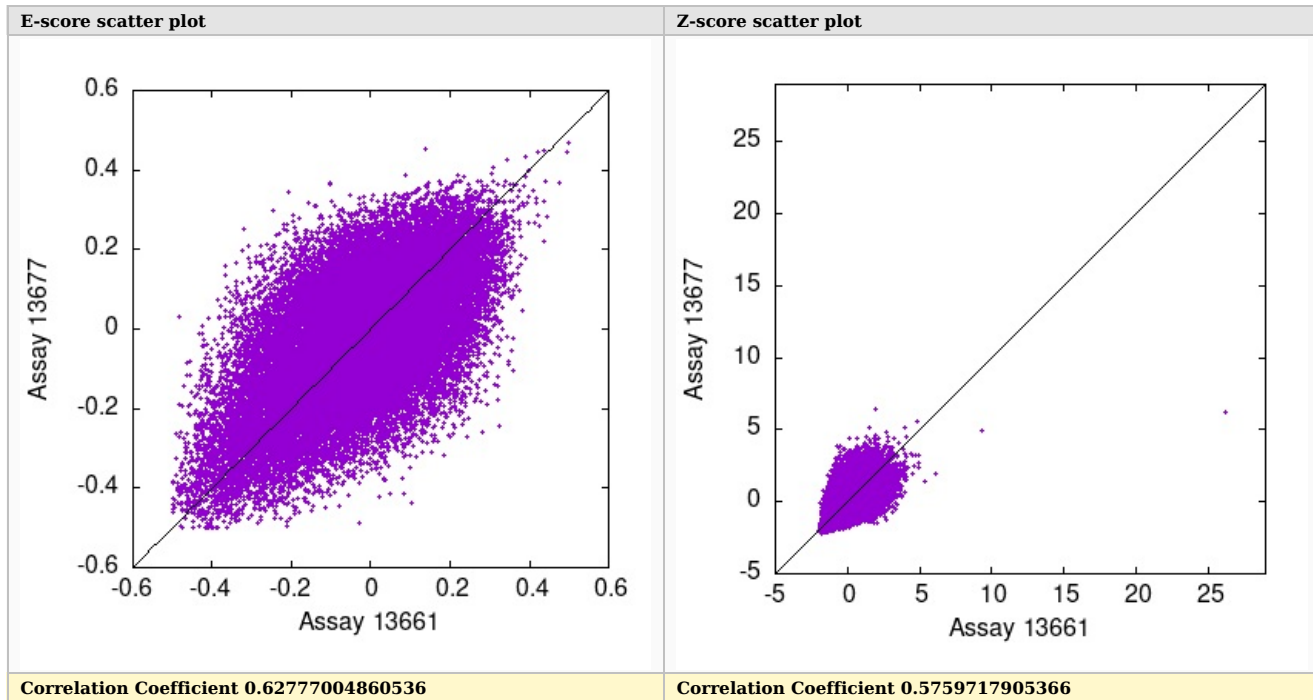


QC report



Top scoring motifs for Assay 13661

Protein ID: pTH14259.1 Gene: MSANTD1.DBD Domain: MADF_DNA_bdg 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 |
| ACTTAAGT | 0.49988 | --ACTTAAGT | ACTTAAGT | 26.12302 | --ACTTAAGT-- |
| CACTTAAG | 0.49444 | --CACTTAAG-- | CACTTAAG | 9.29489 | --CACTTAAG-- |
| AACTTAAG | 0.47579 | --AACTTAAG-- | AACTTAAG | 6.13794 | --AACTTAAG-- |
| GCACTTAA | 0.44618 | GCACTTAA-- | ATGTACAT | 5.33846 | --ATGTACAT-- |
| CTTAAGTA | 0.44170 | -TACTTAAG- | ATGTTAAC | 4.94068 | --ATGTTAAC-- |
| CCACTTAA | 0.43728 | CCACTTAA-- | TGTATACA | 4.93963 | --TGTATACA-- |
| ACTTAAGC | 0.43647 | --ACTTAAGC | GCACTTAA | 4.92702 | GCACTTAA-- |
| TCTTAAGA | 0.43647 | --TCTTAAGA | TCTTAAGA | 4.80196 | --TCTTAAGA-- |
| ATGTACAT | 0.42512 | --ATGTACAT | TAAATTTA | 4.70474 | ---TAAATTTA |
| ACTTAAGA | 0.42087 | --ACTTAAGA | AATGCATT | 4.65082 | --AATGCATT-- |

Top scoring motifs for Assay 13677

Protein ID: pTH14259.2 Gene: MSANTD1.DBD Domain: MADF_DNA_bdg 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 |
| ACTTAAGT | 0.46669 | --ACTTAAGT-- | GATGCATC | 6.44176 | -GATGCATC-- |
| GATGCATC | 0.45206 | --GATGCATC-- | ACTTAAGT | 6.24752 | --ACTTAAGT-- |
| TCTTAAGA | 0.44927 | --TCTTAAGA-- | TCTTAAGA | 5.56741 | -TCTTAAGA-- |
| ACTTAAGA | 0.44583 | --ACTTAAGA-- | CGCTTAAG | 5.14748 | CGCTTAAG-- |
| CACTTAAG | 0.44432 | -CACTTAAG-- | ACTTAAGA | 5.13291 | --ACTTAAGA-- |
| CTCTTAAG | 0.43489 | ---CTTAAGAG- | CACTTAAG | 4.91856 | CACTTAAG-- |
| ATCTTAAG | 0.42645 | ---CTTAAGAT- | CTCTTAAG | 4.83284 | --CTTAAGAG- |
| TATCTTAA | 0.40686 | ---TTAAGATA | TATCTTAA | 4.61817 | ---TTAAGATA |
| ACACTTAA | 0.39812 | ACACTTAA--- | AACGTTTG | 4.56545 | AACGTTTG--- |
| CGCTTAAG | 0.39093 | -CGCTTAAG-- | CTTAAGAC | 4.55179 | --CTTAAGAC- |