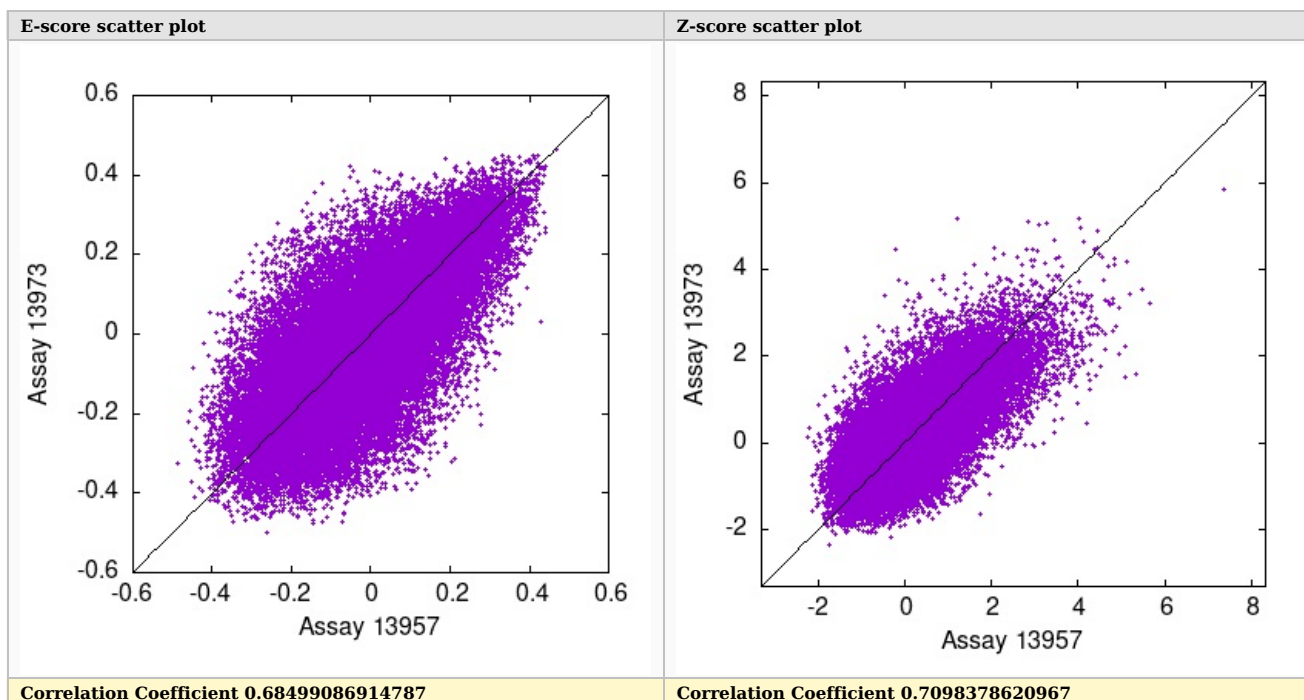


QC report



Top scoring motifs for Assay 13957

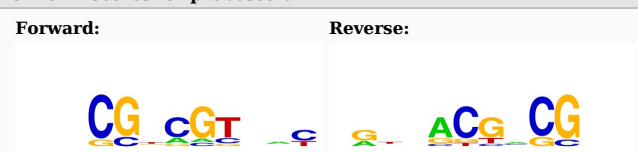
Protein ID: pTH14338.3 Gene: SP140.DBD Domain: SAND Flag: Pass_matched_pair Array: 1M-ME

8 mer E-scores for probeset 'all'



| Top 10 | Scores | Alignment |
|----------|---------|----------------|
| CGCGCGCG | 0.46901 | ----CGCGCGCG-- |
| CGTAGCTA | 0.44261 | ---CGTAGCTA-- |
| GCGCGCGC | 0.44224 | ---GCGCGCGC-- |
| GTAACGAC | 0.43949 | ----GTCGTTAC-- |
| ATTACGAC | 0.43733 | ----GTCGTAAT-- |
| TGTCGTAA | 0.43701 | ----TGTCGTAA-- |
| CGACGTCG | 0.43629 | ----CGACGTCG-- |
| CGTCGTTA | 0.43474 | ----CGTCGTTA-- |
| TATTACGA | 0.43401 | -----TCGTAATA |
| GACGCGTC | 0.42734 | GACGCGTC----- |

8 mer Z-scores for probeset 'all'

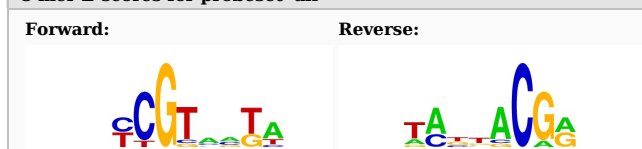


| Top 10 | Scores | Alignment |
|----------|---------|--------------|
| CGCGCGCG | 7.35537 | --CGCGCGCG-- |
| ACGACGAC | 5.66460 | GTCGTCGT--- |
| ATATTCCG | 5.47414 | --CGGAATAT-- |
| CGTAGCTA | 5.31952 | --CGTAGCTA-- |
| ATTACGAC | 5.20288 | --GTCGTAAT-- |
| CGTCGTAA | 5.10800 | --CGTCGTAA-- |
| GTAACGAC | 5.10030 | --GTCGTTAC-- |
| CGCGTAAC | 5.09424 | --CGCGTAAC-- |
| CGACGTCG | 4.96092 | --CGACGTCG-- |
| GCGCGCGC | 4.94465 | --GCGCGCGC-- |

Top scoring motifs for Assay 13973

Protein ID: pTH14338.4 Gene: SP140.DBD Domain: SAND Flag: Pass_matched_pair Array: 1M-HK

8 mer E-scores for probeset 'all'



| Top 10 | Scores | Alignment |
|----------|---------|----------------|
| CGCGCGCG | 0.46569 | ----CGCGCGCG-- |
| TACGACAA | 0.44945 | ---TTGTCGTA-- |
| TATACCGA | 0.44917 | ---TCGGTATA-- |
| CGTCGTAA | 0.44877 | ----CGTCGTAA-- |
| AATTACGG | 0.44538 | ---CCGTAATT-- |
| GTACGACA | 0.44381 | ----GTACGACA-- |
| TACGGAAA | 0.44254 | TTTCCGTA----- |
| GTAATTAC | 0.44096 | ----GTAATTAC-- |
| CGTAATA | 0.43984 | ---CCGTAATA-- |
| TCGTACGA | 0.43857 | ---TCGTACGA-- |

8 mer Z-scores for probeset 'all'



| Top 10 | Scores | Alignment |
|----------|---------|----------------|
| CGCGCGCG | 5.85886 | ----CGCGCGCG-- |
| AATTACGG | 5.17789 | --AATTACGG---- |
| GTAATTAC | 5.16165 | GTAATTAC----- |
| TACGGAAA | 5.07972 | ----TACGGAAA-- |
| GTACGACA | 5.04962 | ----GTACGACA-- |
| TACCGGTA | 5.03954 | ----TACCGGTA-- |
| CCGTAATA | 4.95661 | --TATTACGG---- |
| TACGACAA | 4.88057 | ----TACGACAA-- |
| ACGGCATA | 4.68707 | -----ACGGCATA |
| TTACGGAA | 4.62670 | ----TTACGGAA-- |