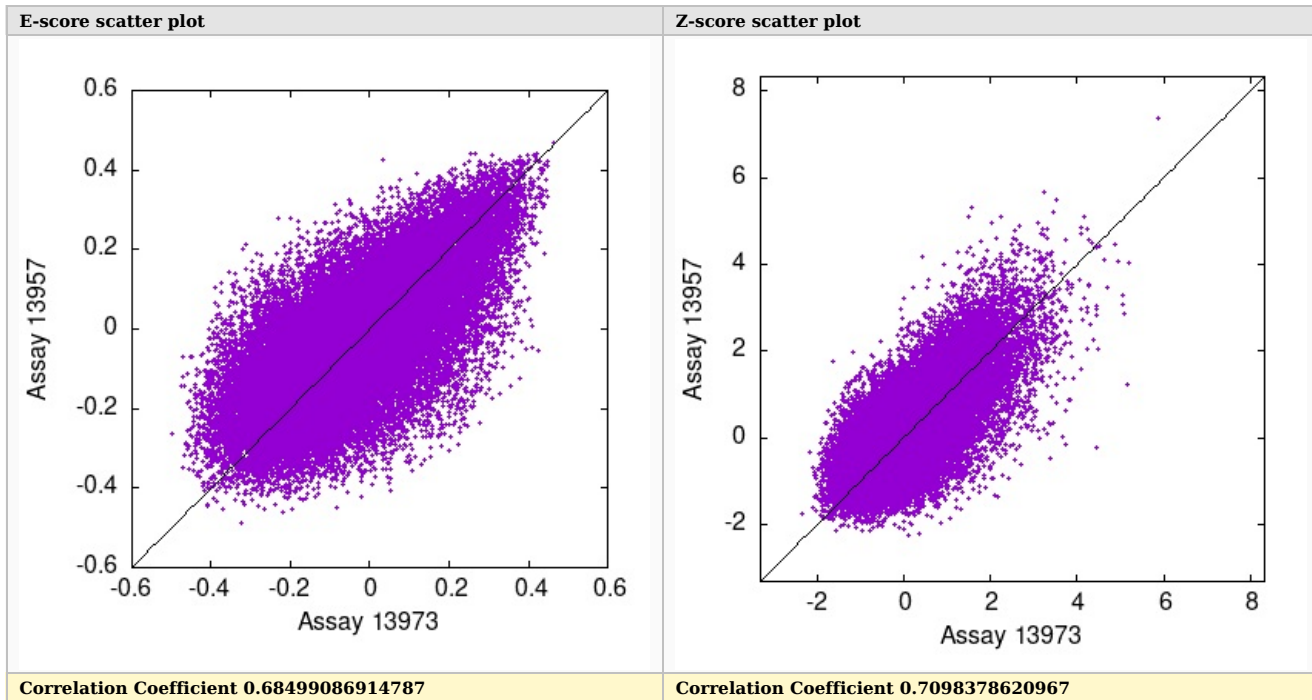


QC report



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' | | | 8 mer Z-scores for probeset 'all' | | |
|-----------------------------------|---------|----------------|-----------------------------------|---------|----------------|
| Forward: | | Reverse: | Forward: | | Reverse: |
| | | | | | |
| Top 10 | Scores | Alignment | Top 10 | Scores | Alignment |
| CGCGCGCG | 0.46569 | ----CGCGCGCG-- | CGCGCGCG | 5.85886 | ----CGCGCGCG-- |
| TACGACAA | 0.44945 | ---TTGTCGTA-- | AATTACGG | 5.17789 | --AATTACGG---- |
| TATACCGA | 0.44917 | ---TCGGTATA-- | GTAATTAC | 5.16165 | GTAATTAC----- |
| CGTCGTAA | 0.44877 | ----CGTCGTAA-- | TACGGAAA | 5.07972 | ----TACGGAAA-- |
| AATTACGG | 0.44538 | ---CCGTAATT-- | GTACGACA | 5.04962 | ----GTACGACA-- |
| GTACGACA | 0.44381 | ----GTACGACA-- | TACCGGTA | 5.03954 | ----TACCGGTA-- |
| TACGGAAA | 0.44254 | TTTCCGTA----- | CCGTAATA | 4.95661 | --TATTACGG---- |
| GTAATTAC | 0.44096 | ----GTAATTAC-- | TACGACAA | 4.88057 | ----TACGACAA-- |
| CCGTAATA | 0.43984 | ---CCGTAATA-- | ACGGCATA | 4.68707 | ----ACGGCATA-- |
| TCGTACGA | 0.43857 | ---TCGTACGA-- | TTACGGAA | 4.62670 | ----TTACGGAA-- |

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' | | | 8 mer Z-scores for probeset 'all' | | |
|-----------------------------------|---------|----------------|-----------------------------------|---------|---------------|
| Forward: | | Reverse: | Forward: | | Reverse: |
| | | | | | |
| Top 10 | Scores | Alignment | Top 10 | Scores | Alignment |
| CGCGCGCG | 0.46901 | ----CGCGCGCG-- | CGCGCGCG | 7.35537 | --CGCGCGCG-- |
| CGTAGCTA | 0.44261 | ----CGTAGCTA-- | ACGACGAC | 5.66460 | GTCGTCGT--- |
| GCAGCGCG | 0.44224 | ----GCAGCGCG-- | ATATTCGG | 5.47414 | --CGGAATAT-- |
| GTAACGAC | 0.43949 | ----GTCGTTAC-- | CGTAGCTA | 5.31952 | --CGTAGCTA-- |
| ATTACGAC | 0.43733 | ----GTCGTAAT-- | ATTACGAC | 5.20288 | ---GTCGTAAT-- |
| TGTCGTAA | 0.43701 | ----TGTCGTAA-- | CGTCGTAA | 5.10800 | ---CGTCGTAA-- |
| CGACGTCG | 0.43629 | ----CGACGTCG-- | GTAACGAC | 5.10030 | ---GTCGTTAC-- |
| CGTCGTTA | 0.43474 | ----CGTCGTTA-- | CGCGTAAC | 5.09424 | ---CGCGTAAC-- |
| TATTACGA | 0.43401 | ----TCGTAATA-- | CGACGTCG | 4.96092 | ---CGACGTCG-- |
| GACGCGTC | 0.42734 | GACGCGTC----- | GCAGCGCG | 4.94465 | --GCAGCGCG-- |