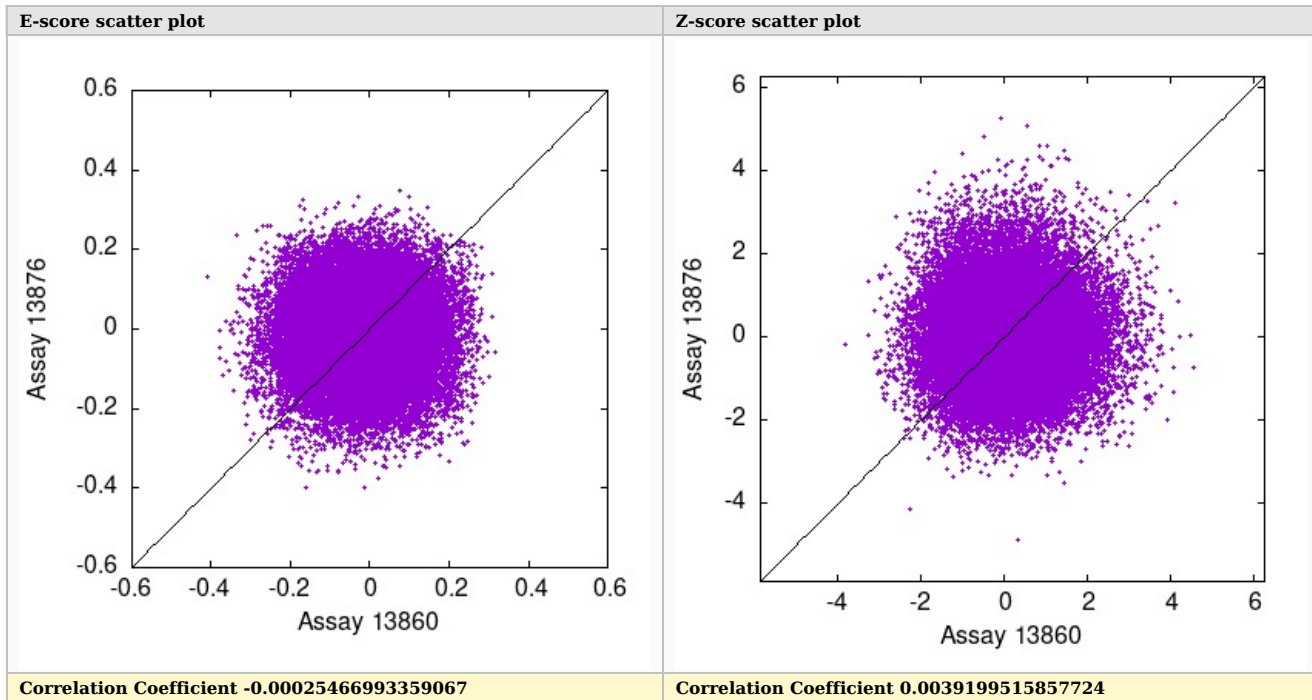


QC report



Top scoring motifs for Assay 13860

Protein ID: pTH14265.1 Gene: SETDB2.DBD Domain: MBD Flag: Reject 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 |
| CTGCTAGC | 0.31586 | ----GCTAGCAG-- | AACTAGTA | 4.54383 | ---AACTAGTA-- |
| AAGTATCA | 0.30972 | ---AAGTATCA--- | AAGTATCA | 4.46800 | --AAGTATCA--- |
| AGACTATG | 0.30829 | -CATAGTCT----- | GGTACTTA | 4.21375 | --TAAGTACC--- |
| GAGAAAAA | 0.30068 | ---GAGAAAAA--- | AGCCGGGA | 4.17264 | --AGCCGGGA--- |
| GGGACAAC | 0.29793 | ----GGGACAAC-- | CTCTGTGC | 4.09519 | ----GCACAGAG |
| AGTCCAAT | 0.29548 | ----AGTCCAAT-- | ATTGTGCA | 4.06398 | ----TGCACAAT-- |
| CGTAATTA | 0.29193 | CGTAATTA----- | CCGGCCGA | 4.05389 | ----CCGGCCGA-- |
| AGCCGGGA | 0.28922 | -----TCCCGGCT | AAACGACA | 4.02506 | --AAACGACA--- |
| AACTTCAG | 0.28713 | CTGAAGTT----- | TCAGGCGA | 3.99994 | TCAGGCGA----- |
| ATGATCGG | 0.28709 | ----ATGATCGG-- | CGACGTCG | 3.90850 | --CGACGTCG--- |

Top scoring motifs for Assay 13876

Protein ID: pTH14265.2 Gene: SETDB2.DBD Domain: MBD Flag: Reject 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 |
| AACTGATC | 0.34822 | -GATCAGTT-- | CGGGGGAG | 5.23852 | ---CTCCCCCG--- |
| CTCGGTAA | 0.33458 | ---CTCGGTAA--- | GAATTCCA | 5.06781 | --GAATTCCA----- |
| GCGGTGAC | 0.33158 | GTACACGC--- | CACCCCAA | 4.81740 | ---CACCCCAA--- |
| ATAGTTAG | 0.32364 | ---ATAGTTAG--- | TCCATTAA | 4.58757 | --TCCATTAA----- |
| TGAGATCA | 0.31660 | ---TGAGATCA--- | AACTGATC | 4.58217 | -AACTGATC----- |
| CGGGGGAG | 0.31121 | ---CGGGGGAG--- | AATATGTC | 4.46958 | AATATGTC----- |
| GACTATAC | 0.31099 | ---GACTATAC--- | TCTCACCA | 4.39627 | --TCTCACCA----- |
| CACCCCAA | 0.30867 | ---CACCCCAA--- | CGCGAGCG | 4.31418 | -CGCTCGCG----- |
| ACAAGATA | 0.30771 | --ACAAGATA--- | CCATTTAA | 4.29259 | -----CCATTTAA |
| GGACAGGA | 0.30477 | GGACAGGA--- | CTCGGTAA | 4.29058 | ----TTACCGAG--- |