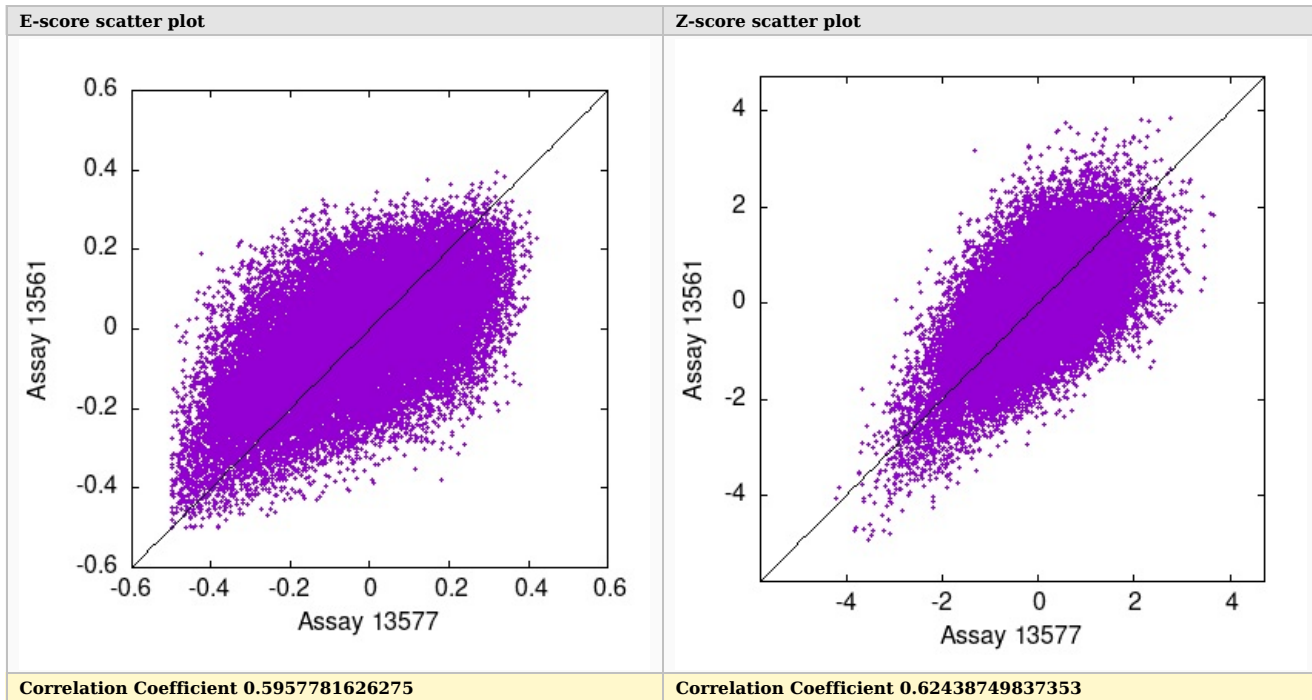


QC report



Top scoring motifs for Assay 13577

Protein ID: pTH13916.2 Gene: DNTTIP1.FL Domain: AT_hook 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 |
| ACTAATTA | 0.42042 | -ACTAATTA- | CTGTATTA | 3.67092 | --TAATACAG- |
| CTGTATTA | 0.40728 | CTGTATTA-- | GAATATTC | 3.58962 | --GAATATTC- |
| GAATATTC | 0.40397 | GAATATTC-- | ACTAACAT | 3.47709 | ---ACTAACAT |
| GATATGTA | 0.40293 | -GATATGTA- | ATATCACA | 3.46030 | ---TGTGATAT |
| TAATAATA | 0.40267 | TAATAATA-- | TTCAACAA | 3.42498 | TTCAACAA--- |
| TTCAACAA | 0.40243 | --TTGTTGAA | TATTTGCA | 3.41715 | --TGCAAAATA- |
| AATATTAA | 0.40011 | -AATATTAA- | TATTAATA | 3.41432 | --TATTAATA- |
| ATAGTAAT | 0.40006 | --ATAGTAAT | AATATTAA | 3.18637 | ---AATATTAA |
| ATATCACA | 0.39712 | --ATATCACA | TAATAATA | 3.16052 | --TAATAATA- |
| AAACGTTT | 0.39501 | AAACGTTT-- | ATTATAAT | 3.14394 | -ATTATAAT-- |

Top scoring motifs for Assay 13561

Protein ID: pTH13916.1 Gene: DNTTIP1.FL Domain: AT_hook 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 |
| AATGCATT | 0.39303 | --AATGCATT- | AAATGCAT | 3.84282 | -AAATGCAT- |
| AAATGCAT | 0.38275 | -AAATGCAT-- | ACAACAAT | 3.81978 | -ACAACAAT- |
| AGCAATTG | 0.37590 | CAATTGCT--- | AATGCATT | 3.77419 | --AATGCATT |
| ACAACAAT | 0.36915 | -ACAACAAT-- | CAATTGCG | 3.76626 | CAATTGCG-- |
| TACAACAA | 0.36847 | TTGTTGTA-- | TGAAGACA | 3.66135 | TGAAGACA-- |
| AACATGCA | 0.36550 | AACATGCA--- | TAACGAAA | 3.62723 | -TAACGAAA- |
| AAGCAATT | 0.36549 | -AATTGCTT-- | TACAACAA | 3.60219 | TTGTTGTA-- |
| TAACGAAA | 0.35580 | --TAACGAAA-- | AACATGCA | 3.58763 | AACATGCA-- |
| ATACAACA | 0.35082 | ---ATACAACA | ACAACGCA | 3.57475 | ACAACGCA-- |
| ATAATGCA | 0.34657 | ATAATGCA--- | AGCAATTG | 3.53843 | CAATTGCT-- |