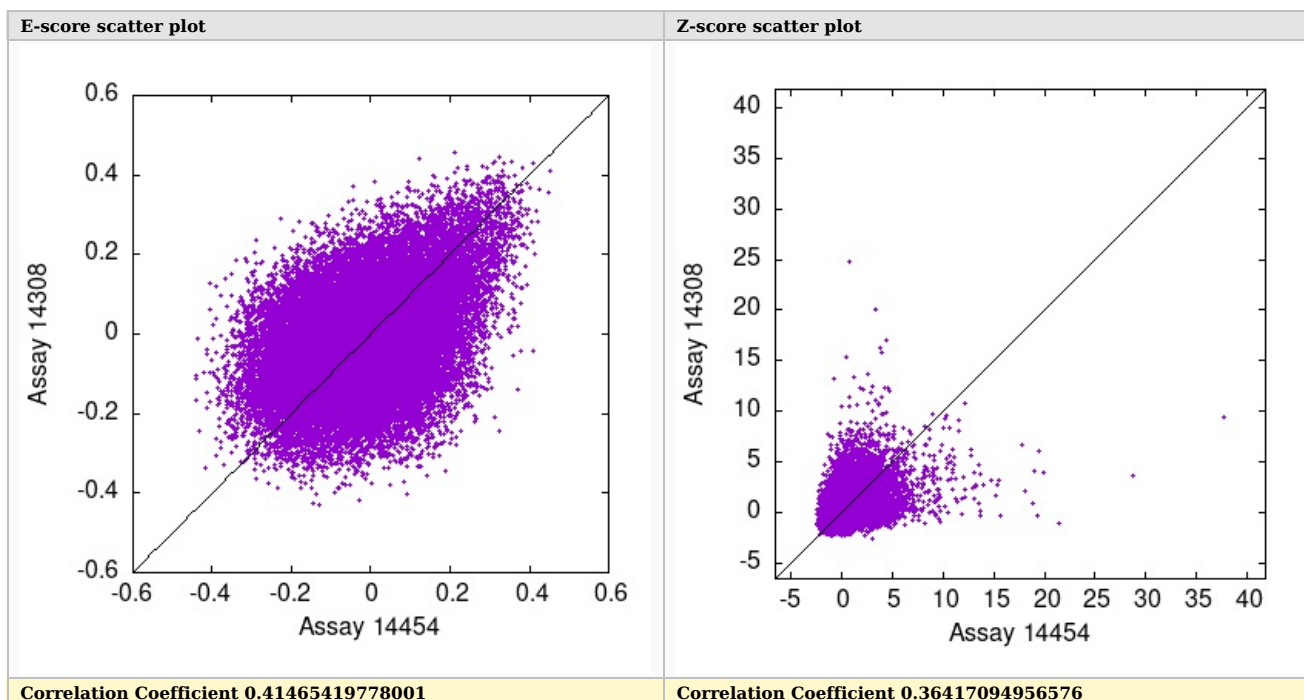


QC report



Top scoring motifs for Assay 14454

Protein ID: pTH14319.5 Gene: PURB.FL Domain: Unknown 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 |
| AACCCACC | 0.45144 | -AACCCACC- | AACCCACC | 37.79456 | -AACCCACC-- |
| CAACCCAC | 0.44733 | CAACCCAC-- | CAACCCAC | 28.79666 | CAACCCAC--- |
| AATCCACC | 0.42350 | -AATCCACC- | ACCAACCT | 21.39678 | --ACCAACCT- |
| ACCAACCA | 0.42241 | --ACCAACCA | AAACCGAC | 19.86329 | AAACCGAC--- |
| GACCAACC | 0.41628 | -GACCAACC- | AATCCACC | 19.44300 | -AATCCACC-- |
| AAACCGAC | 0.41404 | AAACCGAC-- | CCAACACG | 19.25146 | ---CCAACACG |
| ACCAACCT | 0.40887 | --ACCAACCT | AAGGTGGT | 18.99940 | ---ACCACTTT |
| ACCCACCA | 0.40867 | --ACCCACCA | ACCTACCC | 18.86731 | --ACCTACCC- |
| AACCTTCC | 0.40813 | -AACCTTCC- | ACGTCGCG | 18.15799 | ---CCGACCGT |
| AGCCACCA | 0.40442 | -AGCCACCA- | AAACCCAC | 17.75728 | AAACCCAC--- |

Top scoring motifs for Assay 14308

Protein ID: pTH14319.3 Gene: PURB.FL Domain: Unknown 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 |
| GTGGGTGA | 0.45685 | --GTGGGTGA- | GTGGGTGA | 24.82892 | --GTGGGTGA- |
| AGTGGGTG | 0.44434 | -AGTGGGTG- | AGTGGGTG | 20.11566 | -AGTGGGTG-- |
| GTGGGTAA | 0.44008 | --GTGGGTAA | GGTGGGAA | 17.10084 | -GGTGGGAA-- |
| GGTGGGAA | 0.43513 | -GGTGGGAA- | AAGTGGGT | 16.27579 | AAGTGGGT--- |
| CACCCACA | 0.43287 | -TGTGGGTG- | CACCCACA | 15.81220 | -TGTGGGTG-- |
| ACACCCAC | 0.42911 | --GTGGGTGT | GTGGGTAA | 15.35330 | --GTGGGTAA- |
| ACCCACCA | 0.42782 | TGGTGGGT-- | GGTAGGGA | 13.69125 | -GGTAGGGA-- |
| AGGTGGGA | 0.42775 | AGGTGGGA-- | TCCCGCCA | 13.35153 | ---TGGCGGGA |
| AGCCACCA | 0.42102 | -GGTGGGCT- | AGGTGGAG | 13.30178 | -AGGTGGAG-- |
| GAGGGTAA | 0.42101 | --GAGGGTAA | CCAACACA | 12.39753 | -TGTGTTGG-- |