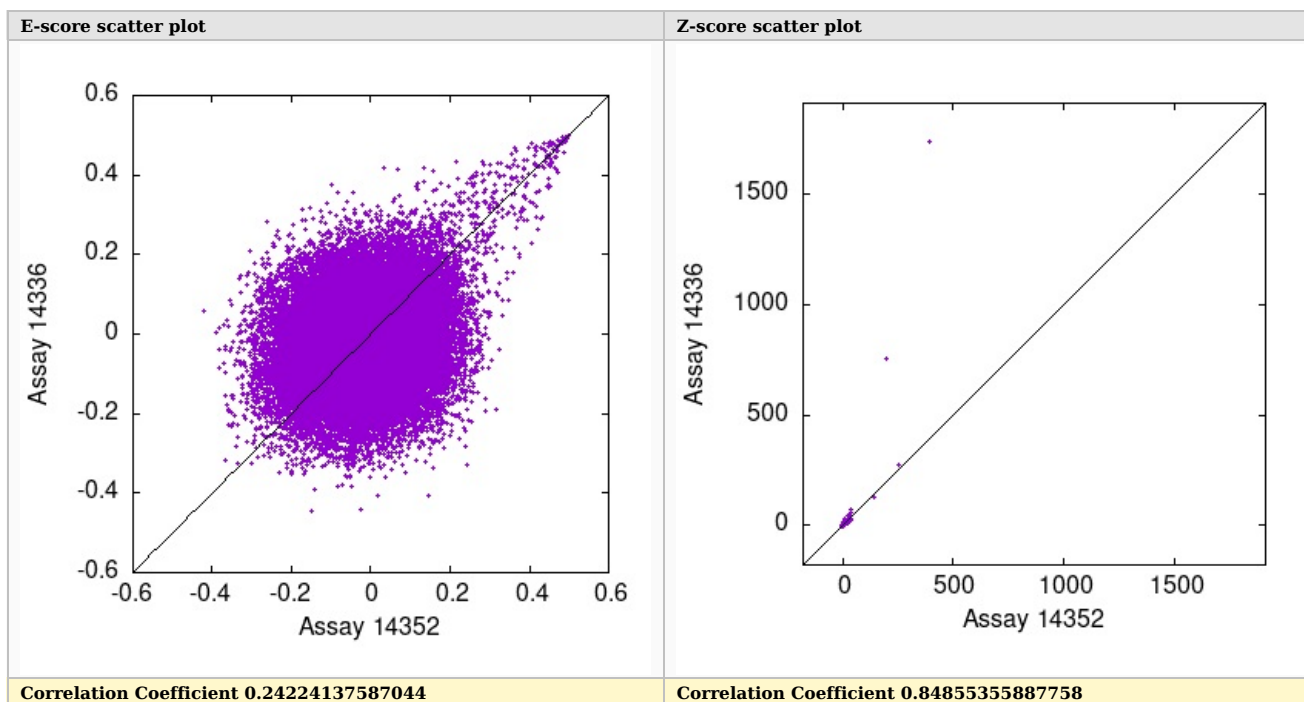


QC report



Top scoring motifs for Assay 14352

Protein ID: pTH15535.2 Gene: GABPA Domain: Ets 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 |
| ACTTCCGG | 0.49934 | -ACTTCCGG- | ACTTCCGG | 390.75416 | -ACTTCCGG- |
| ACCGGAAG | 0.49855 | --CTTCCGGT | ACCGGAAA | 255.52405 | --TTTCCGGT |
| ACCGGAAA | 0.49839 | --TTTCCGGT | ACCGGAAG | 201.17996 | -CTTCCGGT |
| ATTTCCGG | 0.49707 | -ATTTCCGG- | ATTTCCGG | 140.25732 | -ATTTCCGG- |
| CCGGAAAC | 0.49506 | -GTTTCCGG- | CCGGAAAC | 39.49614 | -GTTTCCGG- |
| CGGAAGTC | 0.49429 | GACTTCCG-- | CCGGAAGC | 39.42211 | -GCTTCCGG- |
| AACTTCCG | 0.49382 | AACTTCCG-- | CTTCCGGC | 39.24633 | --CTTCCGGC |
| CCGGAAGC | 0.49365 | -GCTTCCGG- | AACTTCCG | 38.14664 | AACTTCCG-- |
| CACCTCCG | 0.49336 | CACCTCCG-- | CGGAAGTA | 37.92895 | TACTTCCG-- |
| ACTTCCGC | 0.49317 | -ACTTCCGC- | CGGAAGTC | 32.72673 | GACTTCCG-- |

Top scoring motifs for Assay 14336

Protein ID: pTH15535.1 Gene: GABPA Domain: Ets 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 |
| ACTTCCGG | 0.49965 | -ACTTCCGG-- | ACTTCCGG | 1,733.41939 | -ACTTCCGG-- |
| ACCGGAAG | 0.49926 | --CTTCCGGT- | ACCGGAAG | 755.24893 | --CTTCCGGT- |
| ACCGGAAA | 0.49824 | --TTTCCGGT- | ACCGGAAA | 276.32107 | --TTTCCGGT- |
| ATTTCCGG | 0.49673 | -ATTTCCGG-- | ATTTCCGG | 129.02993 | -ATTTCCGG-- |
| AACCGGAA | 0.49591 | ---TTCCGGTT | AACTTCCG | 72.34655 | AACTTCCG--- |
| CGGAAGTC | 0.49555 | GACTTCCG--- | CCGGAAC | 58.98398 | -GTTTCCGG-- |
| AACTTCCG | 0.49511 | AACTTCCG--- | CCGGAAGC | 58.75720 | -GCTTCCGG-- |
| CCGGAAGC | 0.49440 | -GCTTCCGG-- | CGGAAGTC | 49.36761 | GACTTCCG--- |
| CCGGAAC | 0.49426 | -GTTTCCGG-- | ACTTCCGC | 48.22882 | -ACTTCCGC-- |
| ACTTCCGC | 0.49405 | -ACTTCCGC-- | AACCGGAA | 44.86769 | ---TTCCGGTT |