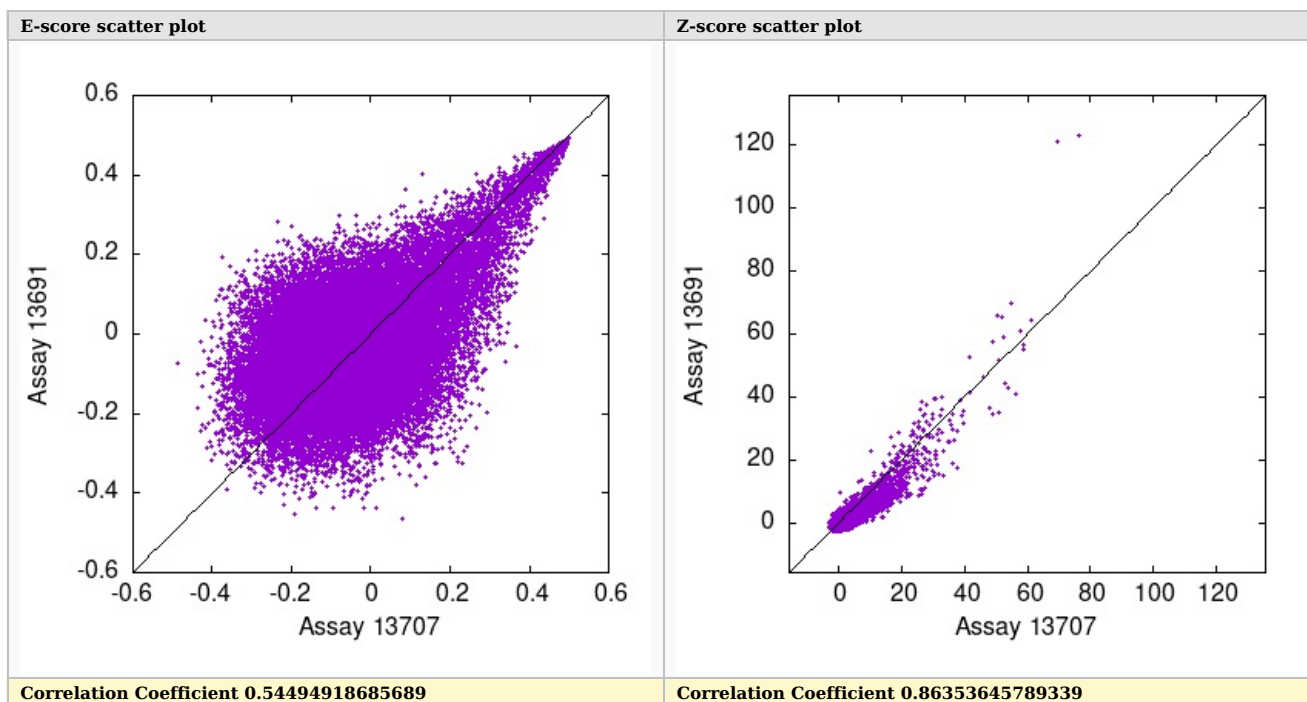


QC report



Top scoring motifs for Assay 13707

Protein ID: pTH13927.2 Gene: FAM200B.DBD Domain: zf-BED 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 |
| GCGACCCA | 0.49891 | -GCGACCCA- | GCGACCCA | 76.38583 | -GCGACCCA- |
| CGCGACCC | 0.49767 | CGCGACCC-- | CGCGACCC | 69.39329 | CGCGACCC-- |
| ACGACCCA | 0.49752 | -ACGACCCA- | ACGACCCA | 60.99655 | -ACGACCCA- |
| ATGGGTCG | 0.49718 | --CGACCCAT | ATGGGTCG | 58.94006 | --CGACCCAT |
| GGGTCGCA | 0.49688 | TGCGACCC-- | GGGTCGCA | 58.62658 | TGCGACCC-- |
| CGACCCAC | 0.49640 | --CGACCCAC | CGACCCAC | 57.72511 | --CGACCCAC |
| GCGACCCC | 0.49508 | -GCGACCCC- | GCGACCCC | 56.24566 | -GCGACCCC- |
| CGACCCAA | 0.49493 | --CGACCCAA | CACGACCC | 54.69189 | CACGACCC-- |
| GGGTCGTA | 0.49461 | TACGACCC-- | GGGTCGTA | 54.04737 | TACGACCC-- |
| GCGACCC | 0.49436 | GCGACCC-- | CGGTCGCG | 52.65244 | -GCGACCCG- |

Top scoring motifs for Assay 13691

Protein ID: pTH13927.1 Gene: FAM200B.DBD Domain: zf-BED 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 |
| GCGACCCA | 0.49636 | -GCGACCCA- | GCGACCCA | 123.03463 | -GCGACCCA- |
| CGCGACCC | 0.49509 | CGCGACCC-- | CGCGACCC | 121.24000 | CGCGACCC-- |
| ACGACCCC | 0.49177 | -ACGACCCC- | CACGACCC | 69.65754 | CACGACCC-- |
| CGACCCAC | 0.49163 | --CGACCCAC | CGACCCAA | 66.01732 | --CGACCCAA |
| GCGACCCC | 0.49102 | GCGACCCC-- | ACGACCCC | 65.26430 | -ACGACCCC- |
| ACGACCCA | 0.49075 | -ACGACCCA- | ACGACCCA | 64.17999 | -ACGACCCA- |
| GGGTCGCA | 0.49006 | TGCGACCC-- | CGACCCAC | 60.97356 | --CGACCCAC |
| ATGGGTCG | 0.48974 | --CGACCCAT | GCGACCCC | 59.06954 | GCGACCCC-- |
| CACGACCC | 0.48913 | CACGACCC-- | AGGGTCGC | 57.63452 | -GCGACCCCT- |
| AGGGTCGC | 0.48880 | -GCGACCCCT- | GGGTCGCA | 56.50584 | TGCGACCC-- |