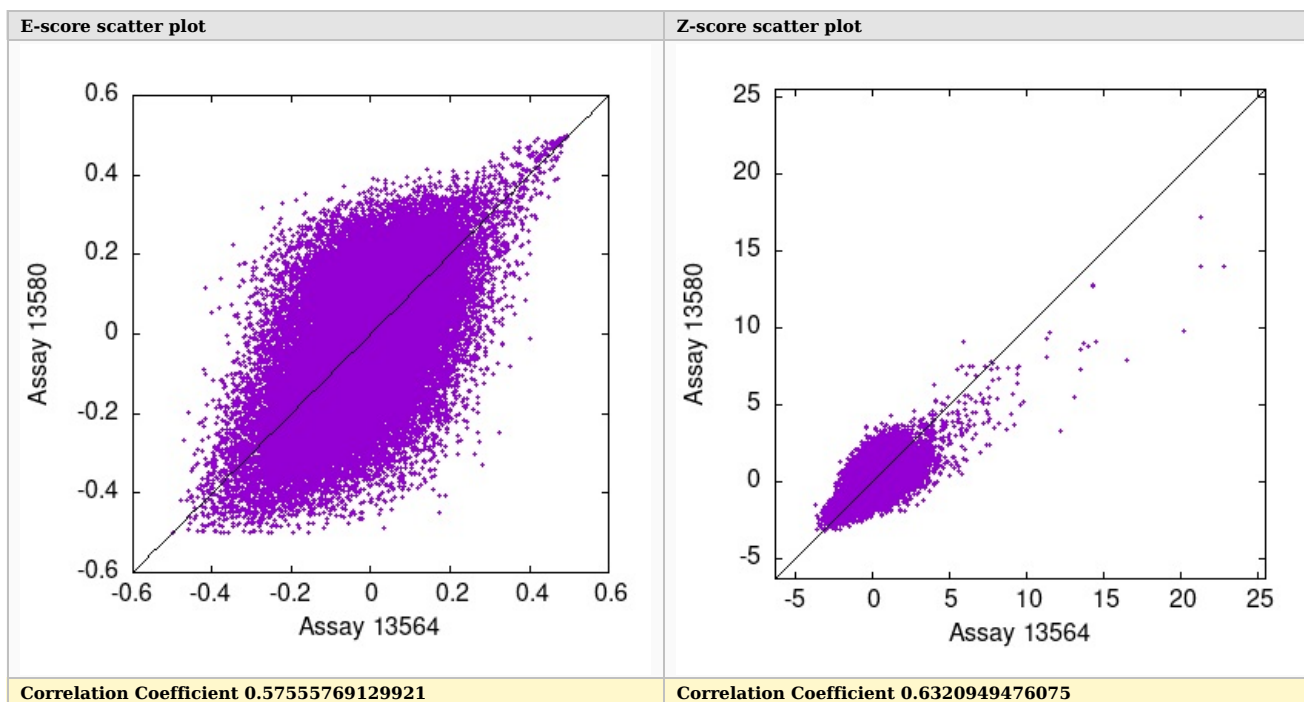


QC report



Top scoring motifs for Assay 13564

Protein ID: pTH13945.1 Gene: CREB3L3.DBD Domain: bZIP_1 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 |
| ACGTGGCA | 0.49666 | ---ACGTGGCA | CCACGTGG | 22.81855 | --CCACGTGG-- |
| CACGTGGC | 0.49612 | --CACGTGGC- | ACGTGGCA | 21.25263 | ---ACGTGGCA |
| ACACGTGT | 0.49552 | -ACACGTGT-- | CACGTGGC | 21.24526 | ---CACGTGGC- |
| CCACGTGG | 0.49527 | --CCACGTGG-- | ACACGTGT | 20.17508 | --ACACGTGT-- |
| ATGACGTG | 0.49213 | ATGACGTG--- | ATGACGTG | 16.43306 | -ATGACGTG--- |
| CCACGTCA | 0.49001 | -TGACGTG-- | CACGTGTC | 14.46116 | -GACACGTG--- |
| ACACGTGG | 0.48927 | -ACACGTGG-- | ACACGTGG | 14.24348 | --ACACGTGG-- |
| CACGTGTC | 0.48826 | GACACGTG--- | CCACGTCA | 14.22991 | --TGACGTG-- |
| CACGTGTA | 0.48821 | TACACGTG--- | ACGTGTCA | 13.94907 | TGACACGT--- |
| ACACGTCA | 0.48762 | -ACACGTCA-- | CACGTGTA | 13.65206 | -TACACGTG--- |

Top scoring motifs for Assay 13580

Protein ID: pTH13945.2 Gene: CREB3L3.DBD Domain: bZIP_1 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 |
| CACGTGGC | 0.49859 | -CACGTGGC- | CACGTGGC | 17.16189 | --CACGTGGC- |
| CCACGTGG | 0.49796 | CCACGTGG-- | ACGTGGCA | 13.95145 | ---ACGTGGCA |
| ACGTGGCA | 0.49747 | --ACGTGGCA | CCACGTGG | 13.94711 | -CCACGTGG-- |
| ACACGTGG | 0.49742 | ACACGTGG-- | ACACGTGG | 12.82390 | -ACACGTGG-- |
| CCACGTCA | 0.49742 | TGACGTGG-- | CCACGTCA | 12.71450 | -TGACGTGG-- |
| ACACGTGT | 0.49434 | ACACGTGT-- | ACACGTGT | 9.79122 | -ACACGTGT-- |
| CACGTGGA | 0.49303 | -CACGTGGA- | ACACGTCA | 9.63662 | -ACACGTCA-- |
| ACACGTCA | 0.49195 | ACACGTCA-- | CACGTGGA | 9.27870 | --CACGTGGA- |
| GCCACGTA | 0.49181 | -TACGTGGC- | CACGTGTC | 9.06563 | GACACGTG--- |
| ACGTGGAA | 0.49161 | --ACGTGGAA | TACGTGGA | 9.03202 | --TACGTGGA- |