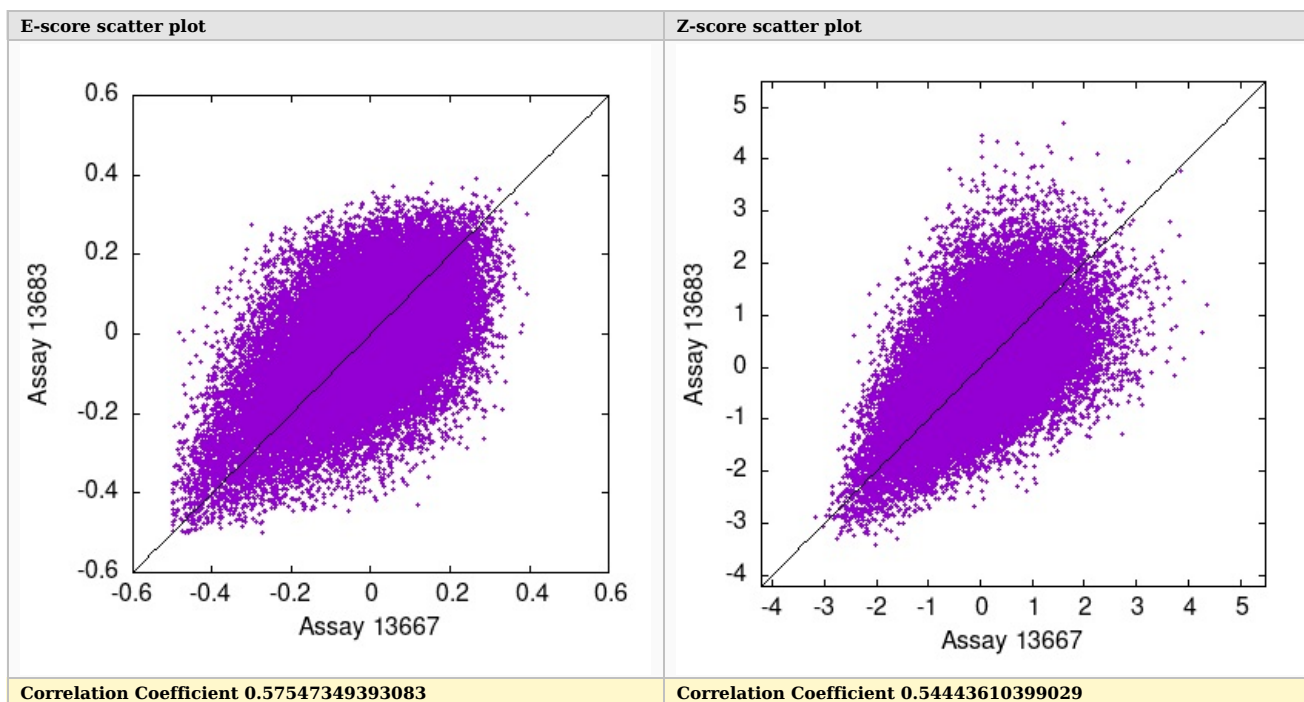


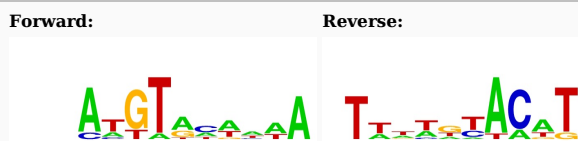
## QC report



### Top scoring motifs for Assay 13667

Protein ID: pTH14279.1 Gene: TTF1.DBD Domain: Myb\_DNA-binding Flag: Reject Array: 1M-ME

#### 8 mer E-scores for probeset 'all'



| Top 10   | Scores  | Alignment    |
|----------|---------|--------------|
| GAAATTAA | 0.39506 | ----GAAATTAA |
| CAATTTCA | 0.39485 | -CAATTTCA--- |
| ATGTACAT | 0.38086 | --ATGTACAT-- |
| TGTGCACA | 0.37869 | ---TGTGCACA- |
| AAACGTAT | 0.37649 | AAACGTAT---- |
| TATGTGAA | 0.36617 | -TATGTGAA--- |
| CTGTAATA | 0.36264 | --CTGTAATA-- |
| ATGTATAA | 0.36123 | --ATGTATAA-- |
| CAATTGCG | 0.35961 | -CAATTGCG--- |
| GTACTATA | 0.35921 | ----GTACTATA |

#### 8 mer Z-scores for probeset 'all'

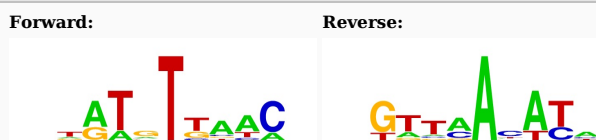


| Top 10   | Scores  | Alignment     |
|----------|---------|---------------|
| GAAATTAA | 4.37505 | --GAAATTAA--  |
| ATGTACAT | 4.26338 | ATGTACAT----  |
| AAACGTAT | 3.91196 | --ATACGTTT--  |
| TACTTTAA | 3.90213 | ---TACTTTAA-- |
| TATGTGAA | 3.86608 | ---TATGTGAA-- |
| GTACTTTA | 3.81949 | --GTACTTTA--  |
| AACAATTG | 3.75668 | --AACAATTG--  |
| TGTGCACA | 3.75222 | -TGTGCACA---  |
| AATTGGCG | 3.69140 | ----AATTGGCG  |
| AGACGTCT | 3.65874 | --AGACGTCT--  |

### Top scoring motifs for Assay 13683

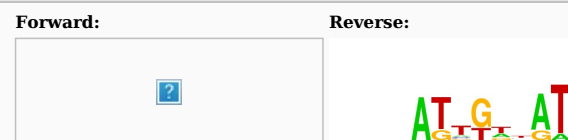
Protein ID: pTH14279.2 Gene: TTF1.DBD Domain: Myb\_DNA-binding Flag: Reject Array: 1M-HK

#### 8 mer E-scores for probeset 'all'



| Top 10   | Scores  | Alignment    |
|----------|---------|--------------|
| TGTTAACA | 0.39165 | ---TGTTAACA  |
| GAAATTGA | 0.37870 | -GAAATTGA--  |
| AATTTCAC | 0.37224 | --AATTTCAC-- |
| TACACACA | 0.36593 | -TGTGTGTA--  |
| ATGTTAAC | 0.36233 | --ATGTTAAC-- |
| GATCACAC | 0.35691 | ---GTGTGATC- |
| ATGTCACA | 0.35568 | --ATGTCACA-  |
| ATAAGATA | 0.35406 | -TATCTTAT--  |
| TAAATATA | 0.34801 | TTATATTA---  |
| AGTGTGAA | 0.34584 | -AGTGTGAA--  |

#### 8 mer Z-scores for probeset 'all'



| Top 10   | Scores  | Alignment       |
|----------|---------|-----------------|
| TGTTAACA | 4.67983 | -TGTTAACA----   |
| AATTTCAC | 4.45543 | --AATTTCAC----  |
| CATTGTGA | 4.33931 | ---TAACAATG--   |
| TATAACAA | 4.33512 | --TATAACAA----  |
| CACATAGA | 4.31645 | --CACATAGA----  |
| TACACACA | 4.26036 | ---TACACACA---- |
| GTAATACA | 4.12399 | TGTATTAC-----   |
| GAAATTGA | 4.10495 | -----TCAATTTT   |
| TATGCATA | 4.10356 | --TATGCATA----  |
| GATCACAC | 4.03116 | --GATCACAC----  |