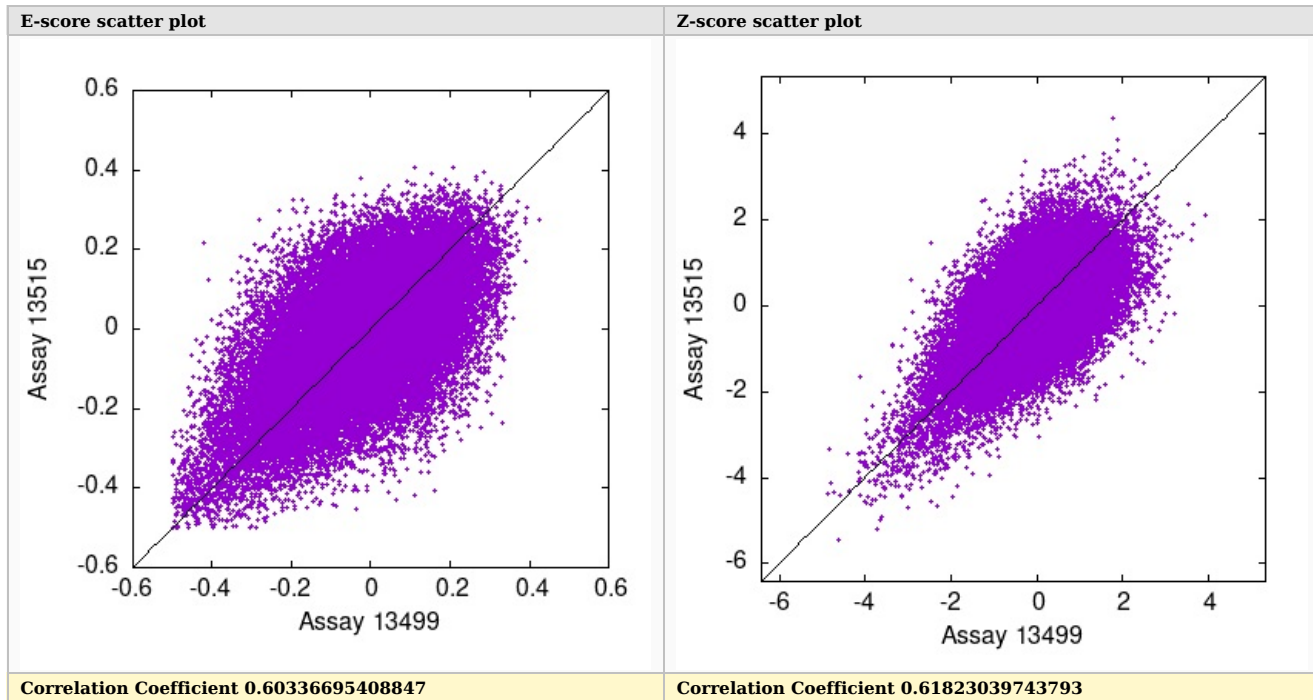


## QC report



### Top scoring motifs for Assay 13499

Protein ID: pTH13934.1 Gene: HLHA9.FL Domain: HLH Flag: Reject Array: 1M-ME

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

Forward:

Reverse:



Forward:

Reverse:



| Top 10   | Scores  | Alignment        | Top 10   | Scores  | Alignment      |
|----------|---------|------------------|----------|---------|----------------|
| ACAACAAT | 0.42379 | -----ATTGTTGT--  | TTTCGAAA | 3.91971 | --TTTCGAAA---  |
| TTTCGAAA | 0.39567 | TTTCGAAA-----    | AACGCGTT | 3.65111 | -AACGCGTT----  |
| ATTTGTAC | 0.39199 | -----ATTTGTAC--  | AATTGTTA | 3.59535 | --AATTGTTA---  |
| CAACAATA | 0.39149 | -----TATTGTTG--  | ACAACAAT | 3.54209 | ---ATTGTTGT--- |
| ATAATATA | 0.39128 | ----TATATTAT---- | TAAATTTA | 3.41221 | --TAAATTTA---  |
| AATTGTTA | 0.39113 | -----AATTGTTA--  | CGTTAACG | 3.30314 | -----CGTTAACG  |
| AAATTTGT | 0.37428 | -----AAATTTGT--  | ATTTACTA | 3.20429 | ---ATTTACTA--- |
| AAATTGTT | 0.37070 | -----AAATTGTT--  | ATGATCAT | 3.19706 | ---ATGATCAT--- |
| CGTTAACG | 0.36907 | -----CGTTAACG    | ACATATGT | 3.11320 | ACATATGT-----  |
| AATTTGTA | 0.36836 | -----AATTTGTA--  | AGCAATTG | 3.09215 | -CAATTGCT----  |

### Top scoring motifs for Assay 13515

Protein ID: pTH13934.2 Gene: HLHA9.FL Domain: HLH Flag: Reject Array: 1M-HK

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

Forward:

Reverse:



Forward:

Reverse:



| Top 10   | Scores  | Alignment    | Top 10   | Scores  | Alignment       |
|----------|---------|--------------|----------|---------|-----------------|
| ATGCGCAT | 0.40751 | ----ATGCGCAT | TGTTAACA | 4.35698 | --TGTTAACA----  |
| CGATAACA | 0.40549 | ---CGATAACA- | ATTGTTGC | 3.87656 | ATTGTTGC-----   |
| TGTTAACA | 0.39493 | ---TGTTAACA- | CAACGTTG | 3.61733 | -----CAACGTTG-  |
| TATTAATA | 0.38933 | ---TATTAATA- | AGTTAACT | 3.55370 | --AGTTAACT----  |
| ATTGTTGC | 0.38217 | -ATTGTTGC--- | CGATAACA | 3.46063 | --CGATAACA----  |
| CGCGCGCG | 0.38125 | ---CGCGCGCG- | TGTGTTAA | 3.45116 | TGTGTTAA-----   |
| GTTTAAAC | 0.37560 | ----GTTTAAAC | AAACGTTT | 3.40775 | -----AAACGTTT-  |
| GCGCAAAA | 0.37418 | ---GCGCAAAA- | ACAAACAG | 3.39530 | ---ACAAACAG---- |
| CAATGTCA | 0.37105 | CAATGTCA---- | CAGTACTG | 3.38004 | ---CAGTACTG---- |
| GTTATAAC | 0.36778 | ----GTTATAAC | AACGTTTG | 3.37657 | -----AACGTTTG   |