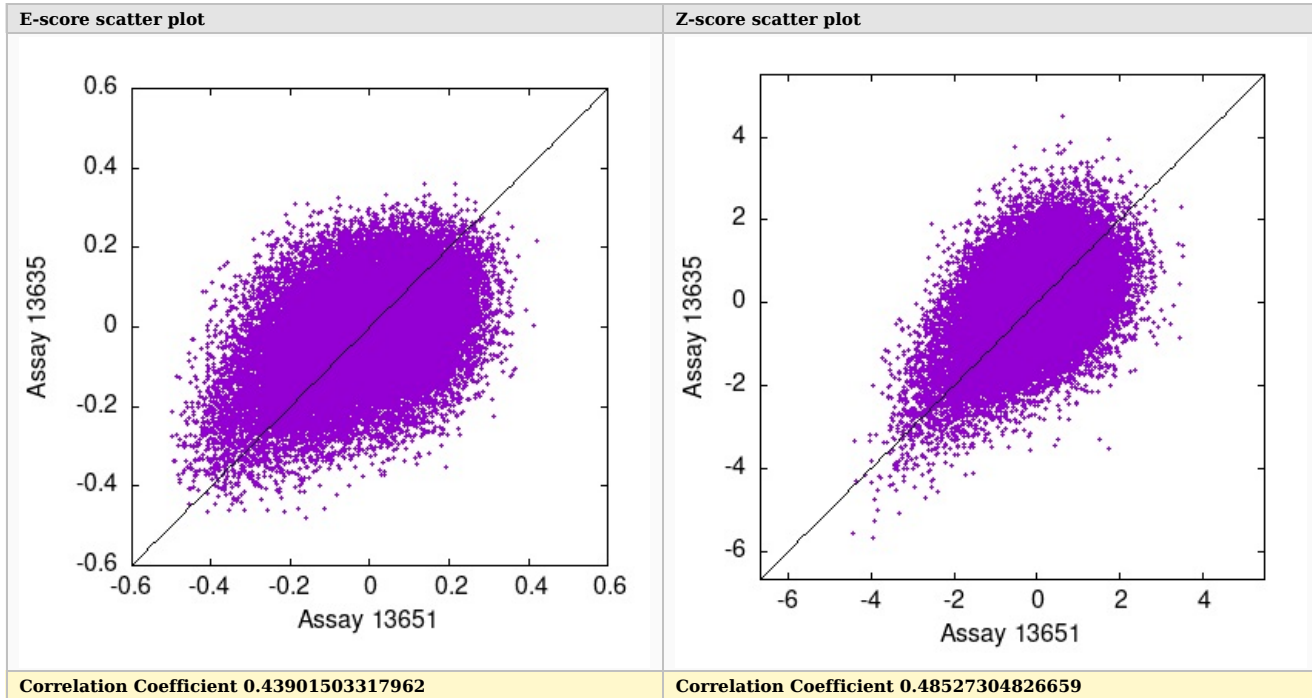


QC report



Top scoring motifs for Assay 13651

Protein ID: pTH14302.2 Gene: GLMP.FL Domain: Unknown Flag: Reject Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:

Reverse:



| Top 10 | Scores | Alignment |
|----------|---------|----------------|
| GTCATGAC | 0.42261 | ----GTCATGAC-- |
| AAACGTTT | 0.41249 | AAACGTTT----- |
| GCATATGC | 0.39340 | --GCATATGC--- |
| ATTGCAA | 0.37551 | ----ATTGCAA--- |
| AATGTTTG | 0.36670 | -AATGTTTG---- |
| ATCCGGAT | 0.36589 | ----ATCCGGAT-- |
| ATCAGCTG | 0.36274 | ----ATCAGCTG-- |
| TCGCGCGA | 0.36088 | ----TCGCGCGA-- |
| TTTGCAA | 0.36082 | ----TTTGCAA--- |
| ATGCGCAT | 0.36029 | ----ATGCGCAT-- |

8 mer Z-scores for probeset 'all'

Forward:

Reverse:



| Top 10 | Scores | Alignment |
|----------|---------|-----------------|
| AAACGTTT | 3.52642 | -----AAACGTTT- |
| GTTTAAAC | 3.51516 | --GTTTAAAC----- |
| GTCATGAC | 3.49629 | --GTCATGAC----- |
| GCATATGC | 3.46646 | --GCATATGC----- |
| CTTGCAAG | 3.46116 | --CTTGCAAG----- |
| ACAACAG | 3.40362 | ----ACAACAG---- |
| ACAATTCA | 3.29458 | ACAATTCA----- |
| CTGTGATA | 3.22475 | --CTGTGATA----- |
| ATCAGCTG | 3.09325 | ----ATCAGCTG--- |
| AACGCGTT | 3.09072 | -----AACGCGTT |

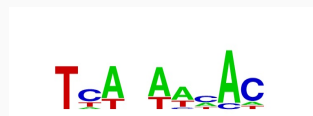
Top scoring motifs for Assay 13635

Protein ID: pTH14302.1 Gene: GLMP.FL Domain: Unknown Flag: Reject Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:

Reverse:



| Top 10 | Scores | Alignment |
|----------|---------|--------------|
| CACAACAC | 0.36119 | --CACAACAC-- |
| CACATTCA | 0.35986 | --CACATTCA-- |
| GTTATAAC | 0.33417 | GTTATAAC---- |
| ATACACAT | 0.33289 | ----ATACACAT |
| ATTATCTG | 0.33178 | --CAGATAAT-- |
| CAGACAAC | 0.32769 | --CAGACAAC-- |
| CAACACCA | 0.32447 | ----CAACACCA |
| ATCTTTAC | 0.32150 | --ATCTTTAC-- |
| TCTTTACA | 0.32142 | --TCTTTACA-- |
| GTTTTGTA | 0.31523 | --TACAAAAC-- |

8 mer Z-scores for probeset 'all'

Forward:

Reverse:



| Top 10 | Scores | Alignment |
|----------|---------|----------------|
| CACATTCA | 4.49182 | -----CACATTCA |
| CGTTATAA | 3.93562 | CGTTATAA----- |
| ACAACGCA | 3.86694 | --ACAACGCA---- |
| GTTTTGTA | 3.81185 | ----TACAAAAC-- |
| ACCAGATA | 3.76989 | ---ACCAGATA--- |
| ATATTGTA | 3.69959 | ---TACAATAT--- |
| AGACACAT | 3.68969 | --AGACACAT--- |
| ATACACAT | 3.62571 | --ATACACAT--- |
| GAATCCAA | 3.59861 | GAATCCAA----- |
| TCTTTACA | 3.50631 | -TCTTTACA---- |