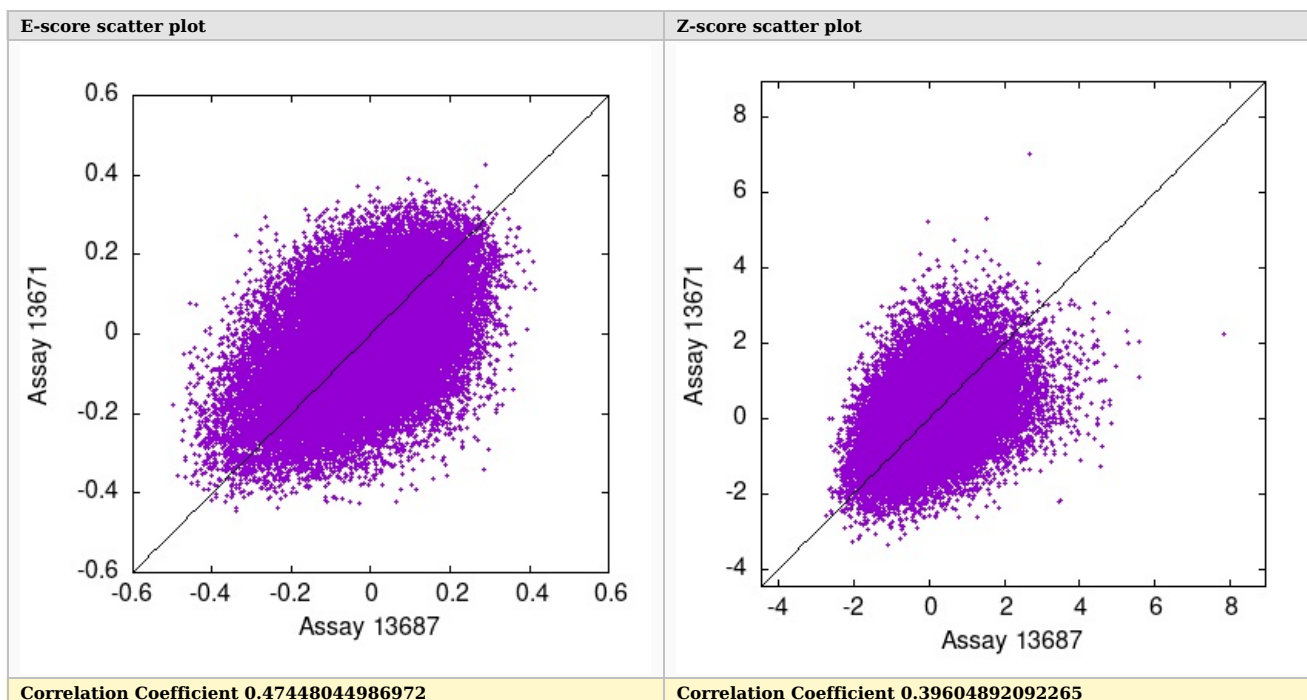




QC report



Top scoring motifs for Assay 13687

Protein ID: pTH14287.2 Gene: CENPS.FL Domain: Unknown Flag: Reject Array: 1M-HK

8 mer E-scores for probeset 'all'

| Forward: | | Reverse: |
|---|---------|---|
|  | |  |
| Top 10 | Scores | Alignment |
| AGATATCT | 0.41488 | --AGATATCT--- |
| TGTTAACA | 0.40809 | --TGTTAACA--- |
| TACCGATA | 0.40074 | -----TACCGATA |
| TCTCGAGA | 0.39819 | --TCTCGAGA-- |
| TATATTGA | 0.39440 | TATATTGA----- |
| GTTATAAC | 0.39189 | -GTTATAAC---- |
| ATATAAAC | 0.38696 | -ATATAAAC---- |
| AACAACAA | 0.37950 | -TTGTTGTT---- |
| TACACACA | 0.37413 | TGTGTGTA----- |
| ATGTTAAC | 0.37229 | -ATGTTAAC---- |

8 mer Z-scores for probeset 'all'

| Forward: | | Reverse: | |
|----------|---------|--------------|--|
| | | | |
| Top 10 | Scores | Alignment | |
| TGTTAACA | 7.82011 | -TGTTAACA-- | |
| ATATAAAC | 5.58579 | -ATATAAAC--- | |
| ATTTAAAT | 5.57230 | -ATTTAAAT--- | |
| GTGTACAC | 5.29108 | -GTGTACAC--- | |
| TAAGTTAA | 5.24216 | ----TTAACTTA | |
| TATTTGCA | 4.98228 | --TATTTGCA-- | |
| ATCTAGAT | 4.86168 | -ATCTAGAT--- | |
| AATATAGA | 4.78978 | AATATAGA---- | |
| CATATAAG | 4.78948 | CATATAAG---- | |
| AGTATACT | 4.77710 | --AGTATACT-- | |



Top scoring motifs for Assay 13671

Protein ID: pTH14287.1 Gene: CENPS.FL Domain: Unknown Flag: Reject Array: 1M-ME

8 mer E-scores for probeset 'all'

| Forward: | Reverse: | |
|----------|----------|------------|
| | | |
| Top 10 | Scores | Alignment |
| TAAATTTA | 0.42398 | --TAAATTTA |
| CAGAAACA | 0.39108 | --CAGAAACA |
| ATTGTACC | 0.38729 | GGTACAAT-- |
| GTATAATA | 0.37862 | -GTATAATA- |
| AATTCGAA | 0.37281 | -TTCGAATT- |
| TAATAAGA | 0.37145 | --TAATAAGA |
| AGTTTTTG | 0.36687 | --CAAAAAC |
| TACAATCA | 0.36077 | --TACAATCA |
| CATAATAC | 0.35955 | -GTATTATG- |
| TAACAGTA | 0.35655 | --TACTGTTA |

8 mer Z-scores for probeset 'all'

| Forward: | | Reverse: | |
|--|---------|---|-------------|
|  | |  | |
| Top 10 | Scores | Alignment | |
| TAAATTTA | 7.01123 | - | -TAAATTTA |
| CAAACTTA | 5.29229 | - | -CAAACTTA |
| AGTTTTTG | 5.20864 | - | -CAAAAAC T- |
| CATAATAC | 4.73742 | - | -CATAATAC |
| ACATGGAT | 4.46173 | - | -ACATGGAT |
| TAACAGTA | 4.45973 | - | -TAACAGTA- |
| CAGAAACA | 4.37108 | - | -CAGAAACA- |
| AAAAATAA | 4.26333 | - | -AAAAATAA |
| ATTGTACC | 4.21875 | GGTACAAT- | - |
| ATAATGCA | 4.18978 | - | -ATAATGCA |