**Table S2: Evaluation of the small positive values added in read counts for Med-pgQ2 and UQ-pgQ2 given the nominal FDR0.05.** The number of true positive (TP) and false positive (FP) genes, positive predictive value (PPV), the actual false discovery rate (FDR), sensitivity and specificity for Med-pgQ2 and UQ-pgQ2 methods are computed from the MAQC2 data. The results for the choice of the small positive values added the read counts (0.05, 0.10, 0.15, 0.20, 0.30, 0.40 and 0.50).

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  | Small Positive # added | # of TP genes | # of FP genes | PPV | Actual FDR | Sensitivity | Specificity |
| Med-pgQ2 | 0.05 | 347 | 17 | 0.953 | 0.047 | 0.890 | 0.887 |
| 0.10 | 362 | 22 | 0.943 | 0.057 | 0.928 | 0.850 |
| 0.15 | 366 | 26 | 0.934 | 0.066 | 0.938 | 0.828 |
| 0.20 | 369 | 30 | 0.925 | 0.075 | 0.946 | 0.801 |
| 0.30 | 374 | 39 | 0.906 | 0.094 | 0.946 | 0.795 |
| 0.40 | 377 | 45 | 0.893 | 0.101 | 0.962 | 0.722 |
| 0.50 | 377 | 48 | 0.887 | 0.112 | 0.967 | 0.682 |
| UQ-pgQ2 | 0.05 | 344 | 18 | 0.950 | 0.050 | 0.882 | 0.881 |
| 0.10 | 364 | 21 | 0.946 | 0.055 | 0.933 | 0.861 |
| 0.15 | 367 | 31 | 0.922 | 0.078 | 0.941 | 0.795 |
| 0.20 | 372 | 35 | 0.914 | 0.086 | 0.954 | 0.768 |
| 0.30 | 375 | 42 | 0.899 | 0.107 | 0.962 | 0.721 |
| 0.40 | 376 | 50 | 0.882 | 0.117 | 0.964 | 0.669 |
| 0.50 | 376 | 53 | 0.877 | 0.123 | 0.964 | 0.649 |
| DESeq | - | 363 | 59 | 0.860 | 0.140 | 0.931 | 0.609 |
| TMM-edgeR | - | 377 | 97 | 0.796 | 0.205 | 0.964 | 0.358 |