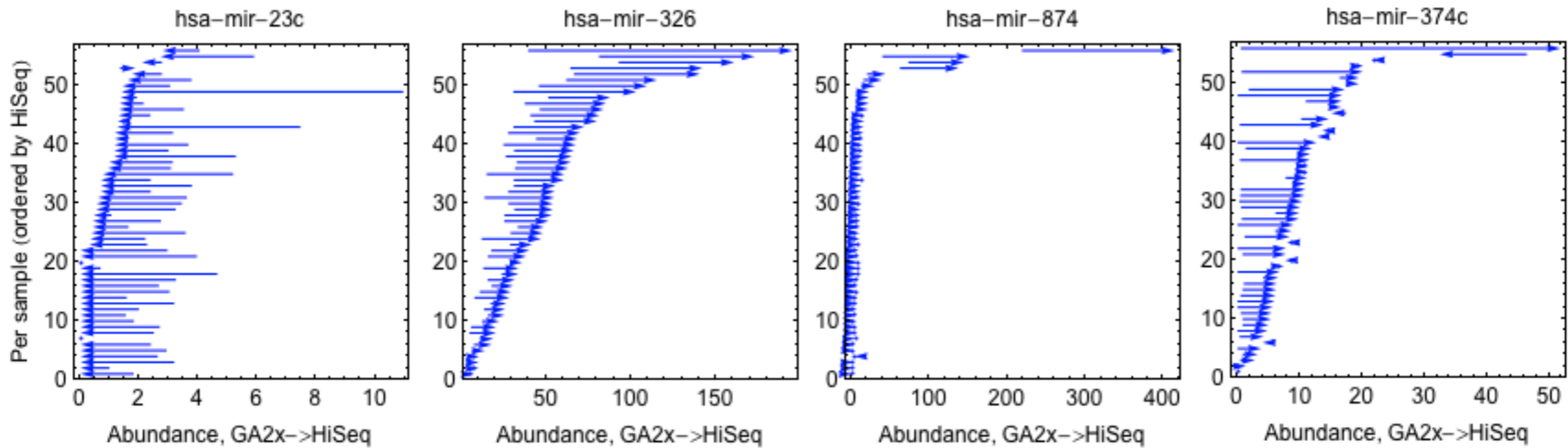
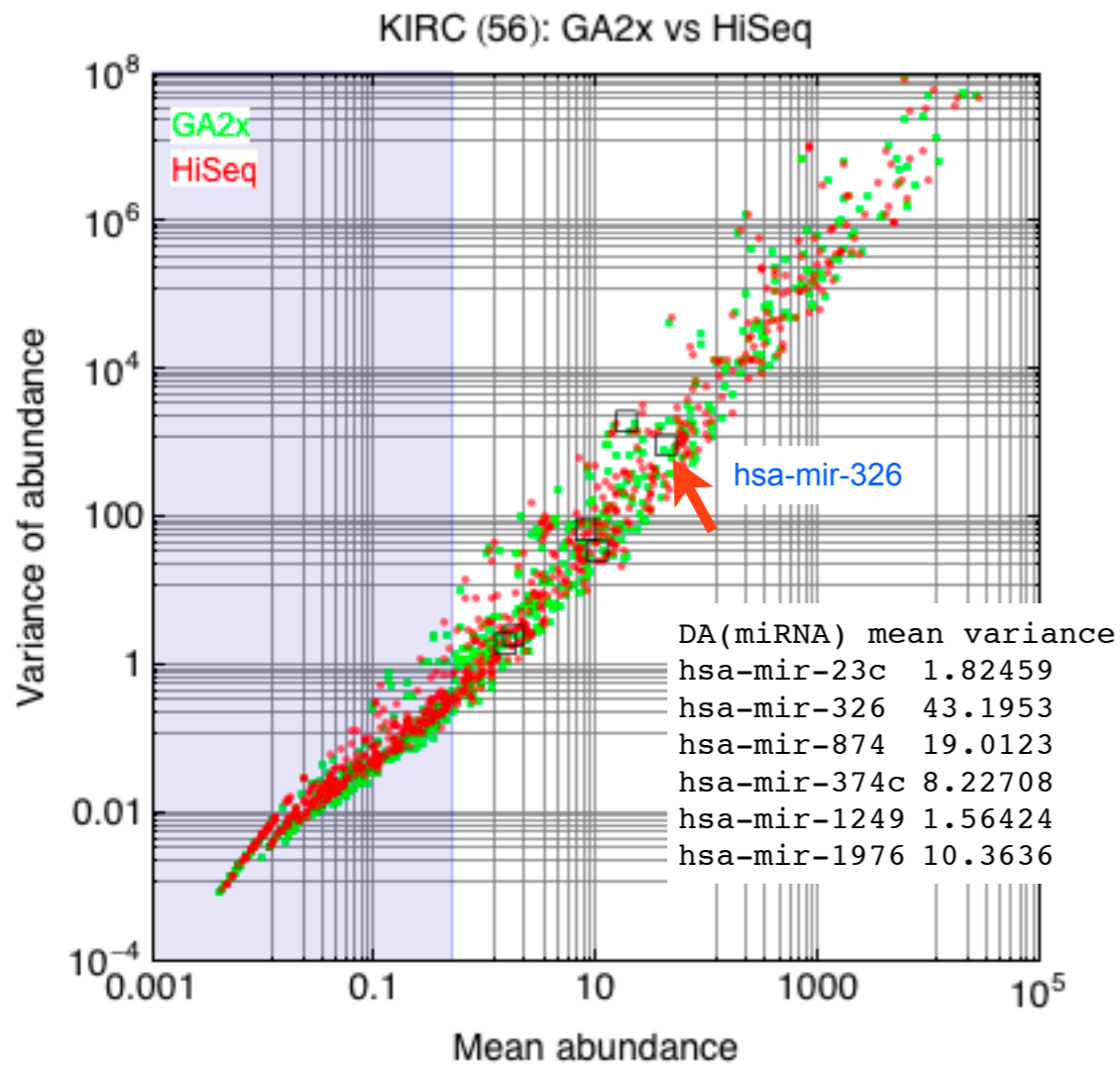
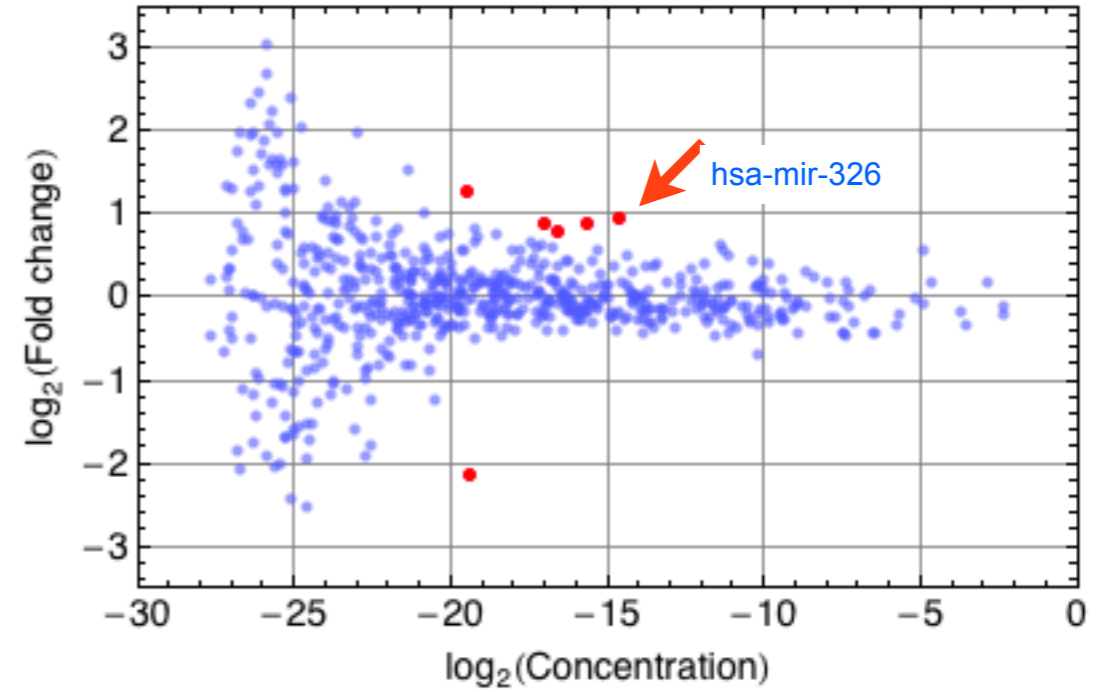
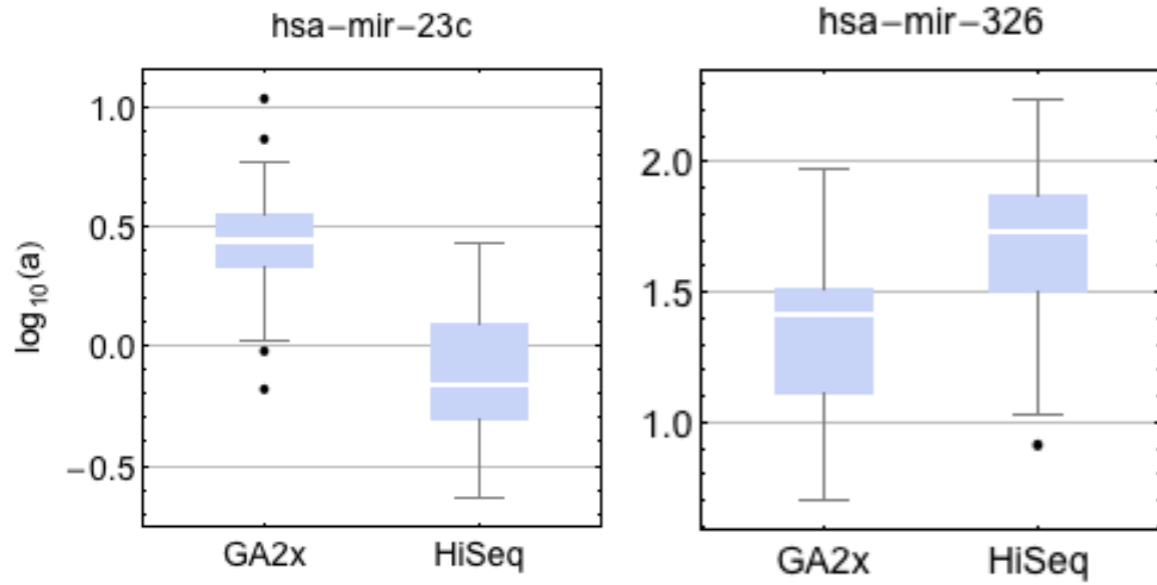


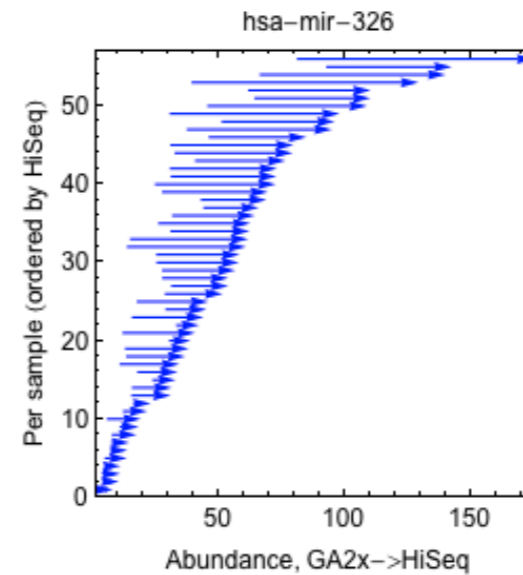
| logConc      | logFC  | P.Value | adj.P.Val         |
|--------------|--------|---------|-------------------|
| hsa-mir-23c  | -19.43 | -2.20   | 8.01e-12 5.91e-09 |
| hsa-mir-326  | -14.64 | 0.991   | 2.39e-06 0.00088  |
| hsa-mir-874  | -15.61 | 0.961   | 9.25e-06 0.0023   |
| hsa-mir-374c | -17.01 | 0.963   | 2.23e-05 0.00411  |
| hsa-mir-1249 | -19.48 | 1.30    | 4.74e-05 0.0070   |
| hsa-mir-1976 | -16.60 | 0.854   | 0.00014 0.017     |
| ...          |        |         |                   |



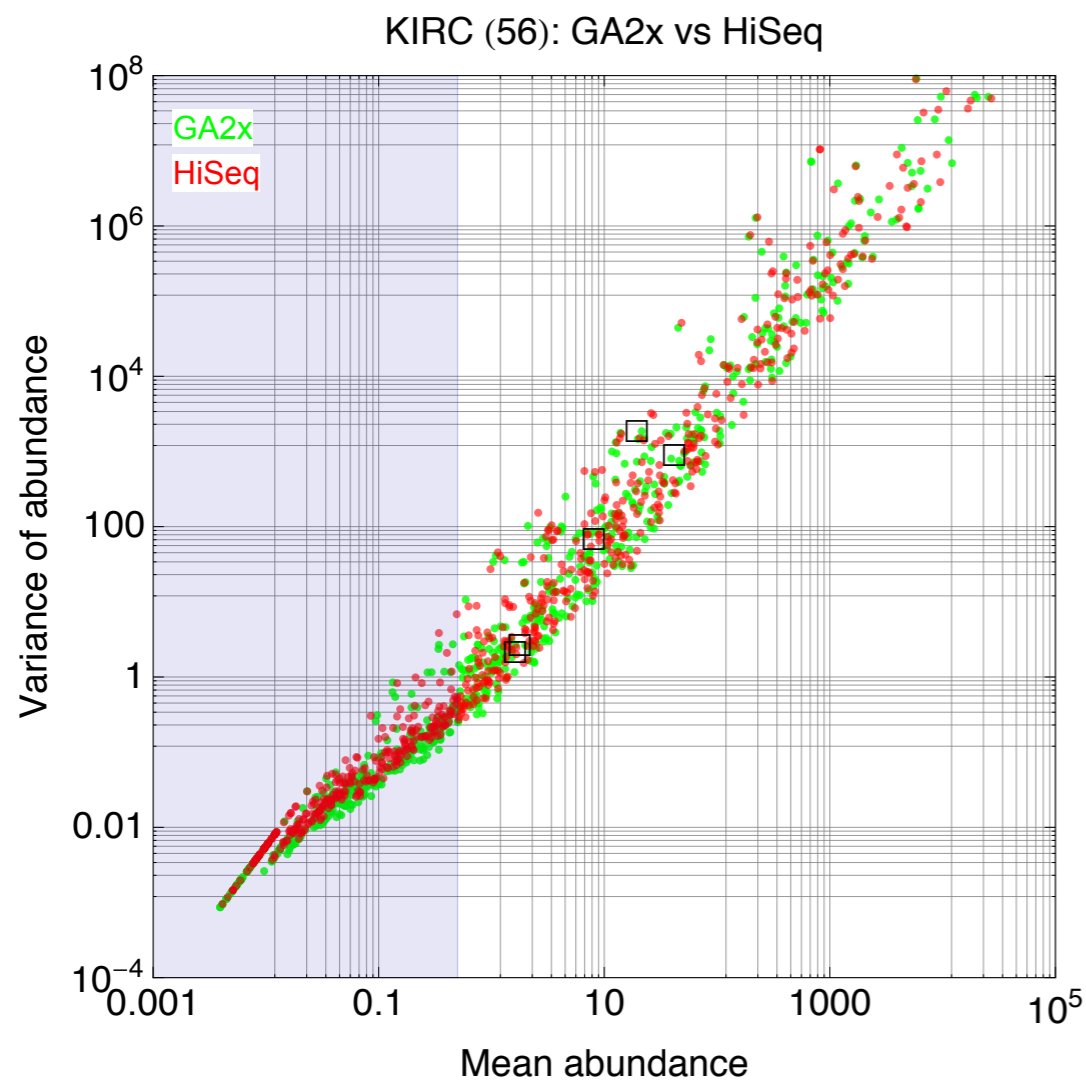
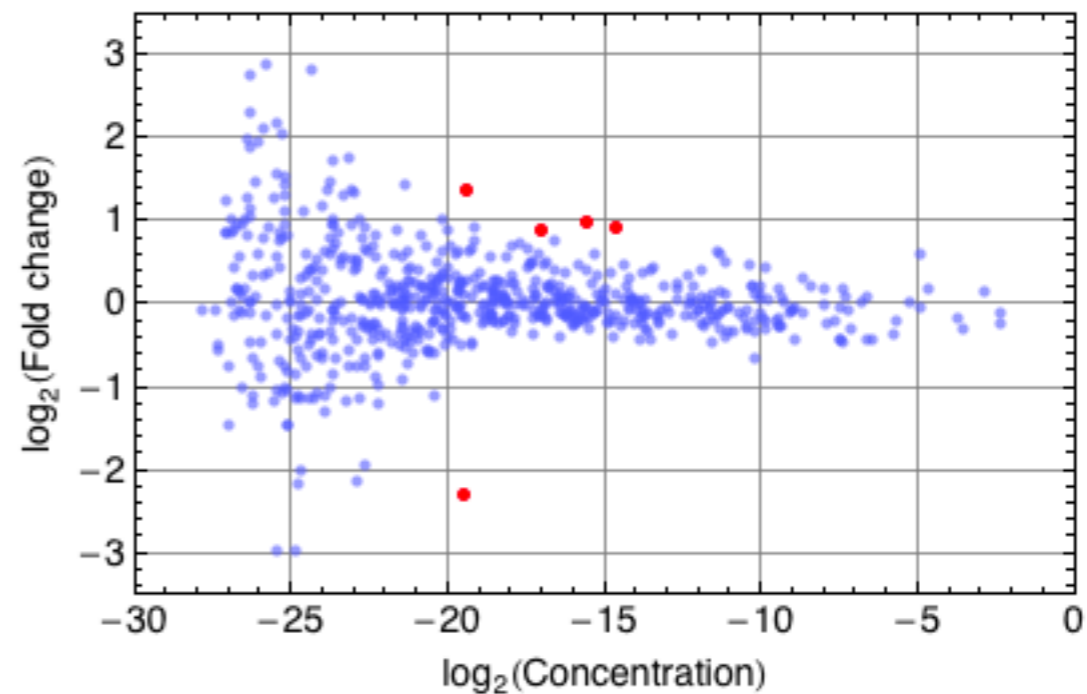
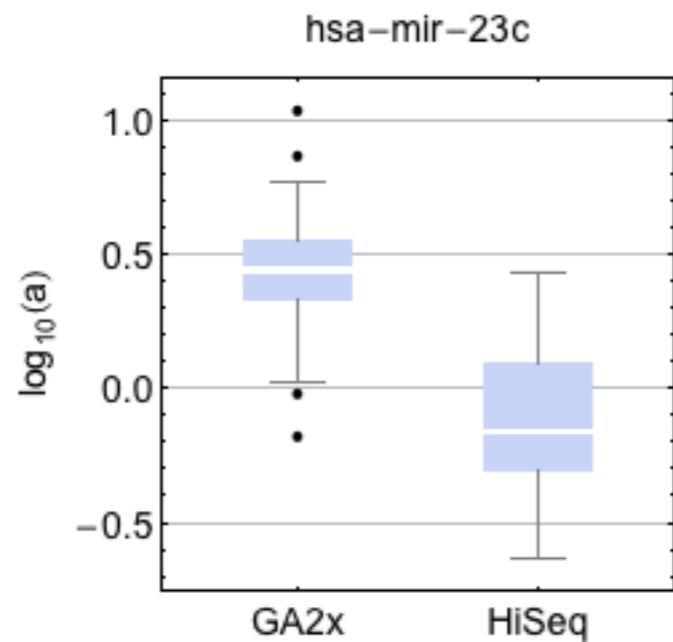
# KIRC/P GA2x vs HiSeq, subsample 2, 735 miRNAs



| gene               | logConc | logFC  | P.Value  | adj.P.Val |
|--------------------|---------|--------|----------|-----------|
| hsa-mir-23c        | -19.40  | -2.133 | 1.69e-11 | 1.24e-08  |
| <b>hsa-mir-326</b> | -14.65  | 0.975  | 3.10e-06 | 0.00114   |
| hsa-mir-874        | -15.701 | 0.906  | 2.55e-05 | 0.00625   |
| hsa-mir-374c       | -17.033 | 0.911  | 5.31e-05 | 0.00813   |
| hsa-mir-1249       | -19.485 | 1.280  | 5.53e-05 | 0.00813   |
| hsa-mir-1976       | -16.611 | 0.797  | 0.00037  | 0.0450    |
| ...                |         |        |          |           |

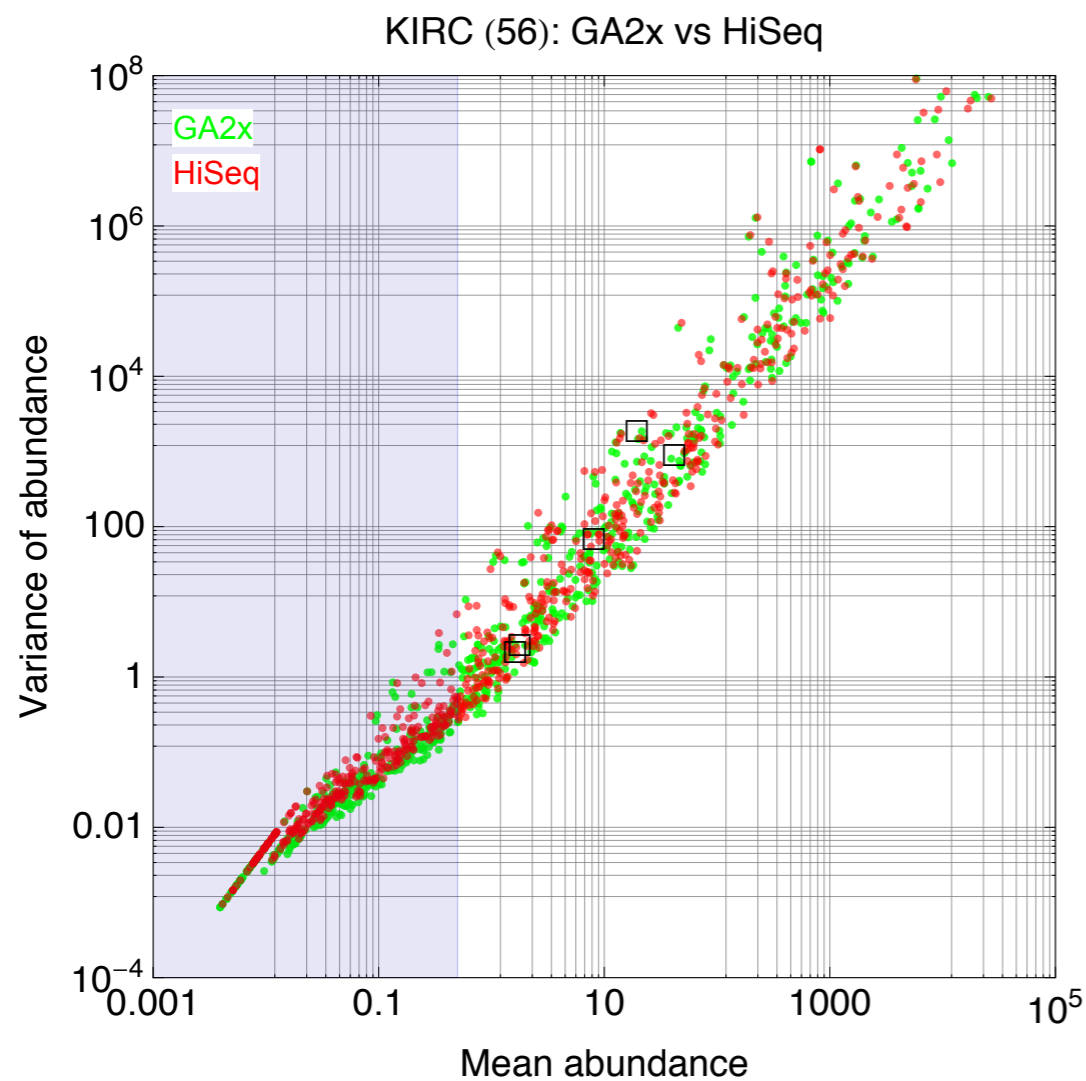
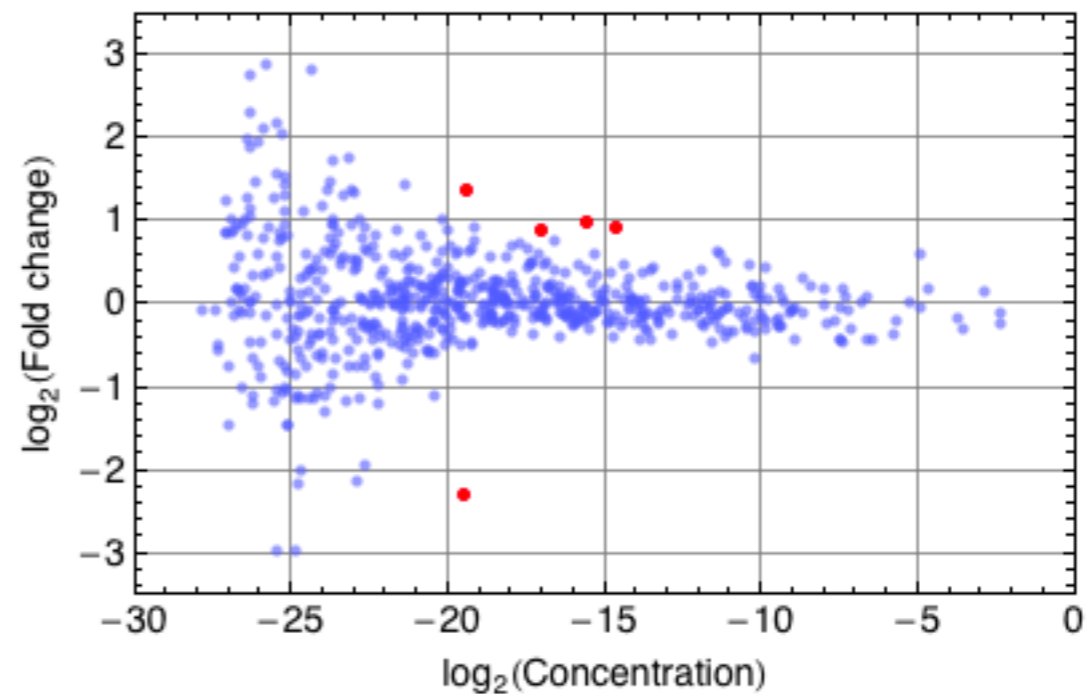
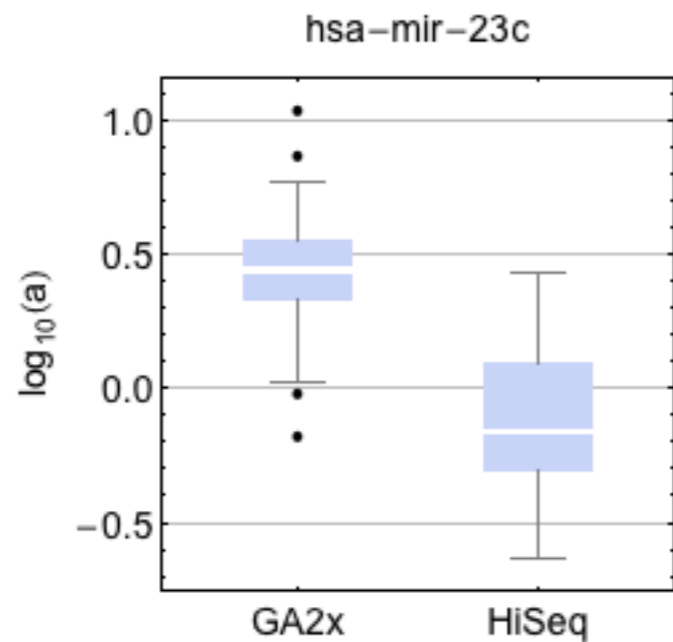


# KIRC/P GA2x vs HiSeq, subsample 1, 735 miRNAs



| gene         | logConc | logFC | P.Value  | adj.P.Val |
|--------------|---------|-------|----------|-----------|
| hsa-mir-23c  | -19.477 | -2.29 | 2.88e-12 | 2.12e-09  |
| hsa-mir-874  | -15.620 | 0.984 | 5.62e-06 | 0.0021    |
| hsa-mir-326  | -14.679 | 0.923 | 1.13e-05 | 0.0024    |
| hsa-mir-1249 | -19.440 | 1.376 | 1.32e-05 | 0.0024    |
| hsa-mir-374c | -17.047 | 0.884 | 0.000101 | 0.0148    |

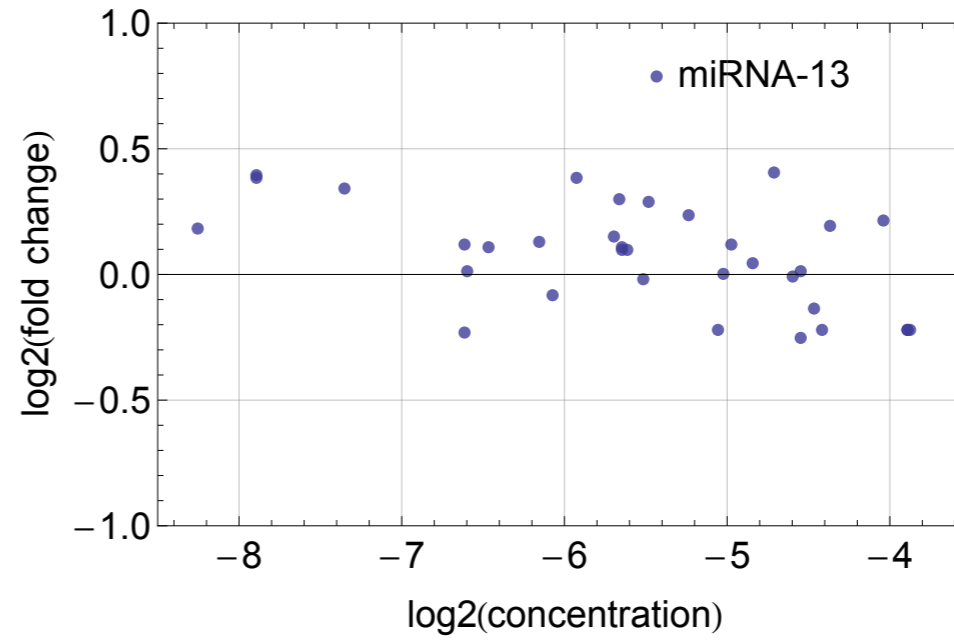
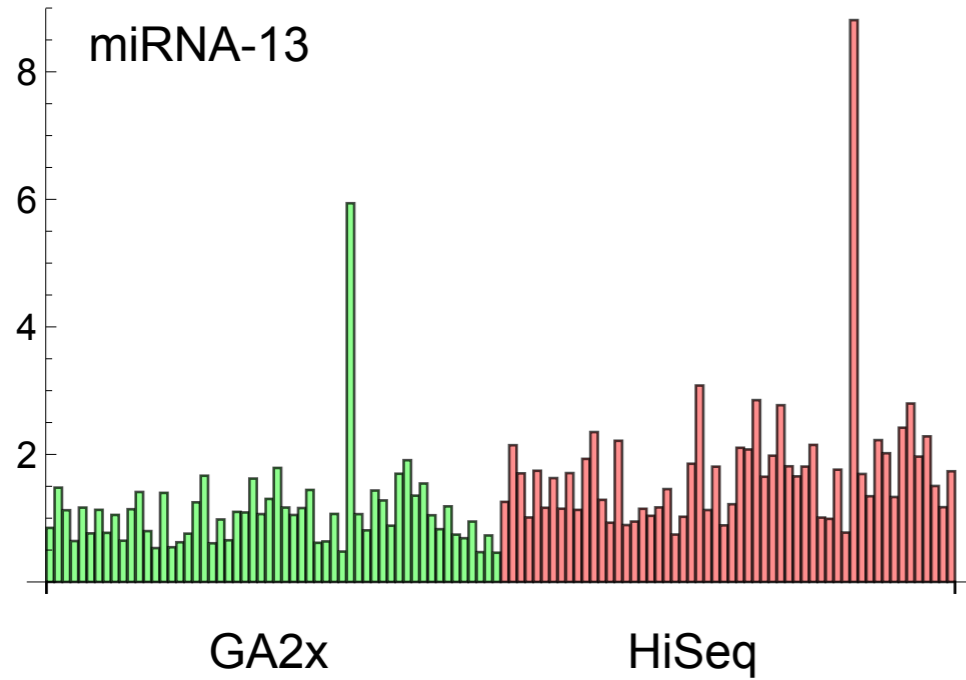
# KIRC/P GA2x vs HiSeq, subsample 1, 735 miRNAs



| gene         | logConc | logFC | P.Value  | adj.P.Val |
|--------------|---------|-------|----------|-----------|
| hsa-mir-23c  | -19.477 | -2.29 | 2.88e-12 | 2.12e-09  |
| hsa-mir-874  | -15.620 | 0.984 | 5.62e-06 | 0.0021    |
| hsa-mir-326  | -14.679 | 0.923 | 1.13e-05 | 0.0024    |
| hsa-mir-1249 | -19.440 | 1.376 | 1.32e-05 | 0.0024    |
| hsa-mir-374c | -17.047 | 0.884 | 0.000101 | 0.0148    |

# KIRC/P GA2x vs HiSeq, subsample 5, 35 miRNAs

Differential abundance analysis, edgeR v1.5.1



| gene  | logConc  | logFC     | P.Value     | adj.P.Val |
|-------|----------|-----------|-------------|-----------|
| mi-13 | -5.4255  | 0.783499  | 0.000945101 | 0.0330785 |
| mi-23 | -4.70622 | 0.406441  | 0.0291534   | 0.510185  |
| mi-1  | -3.89152 | -0.221841 | 0.120596    | 0.751885  |
| mi-2  | -3.89345 | -0.220216 | 0.120596    | 0.751885  |
| mi-3  | -3.87952 | -0.220564 | 0.122239    | 0.751885  |
| mi-34 | -4.04362 | 0.211961  | 0.152072    | 0.751885  |
| ...   |          |           |             |           |