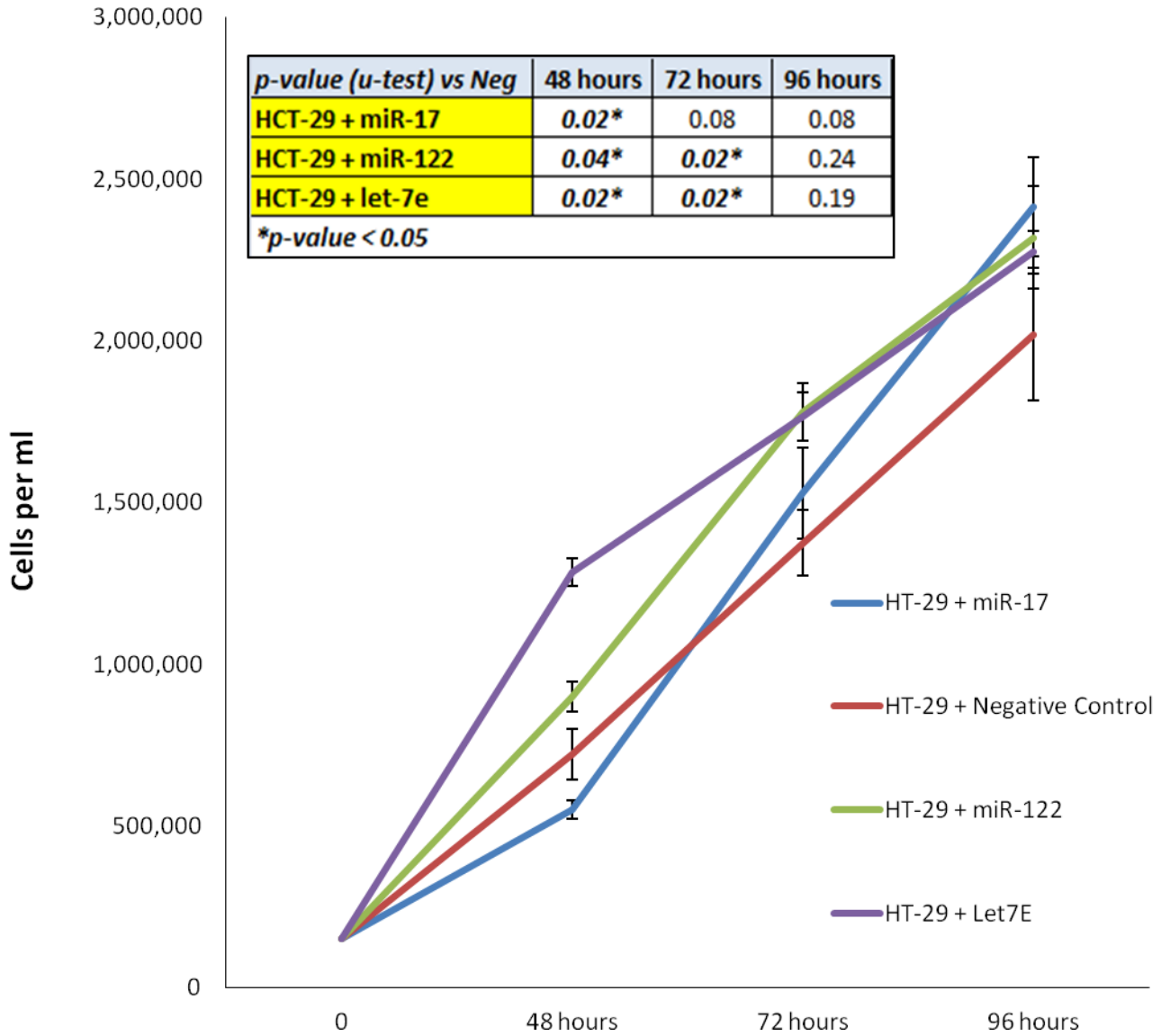
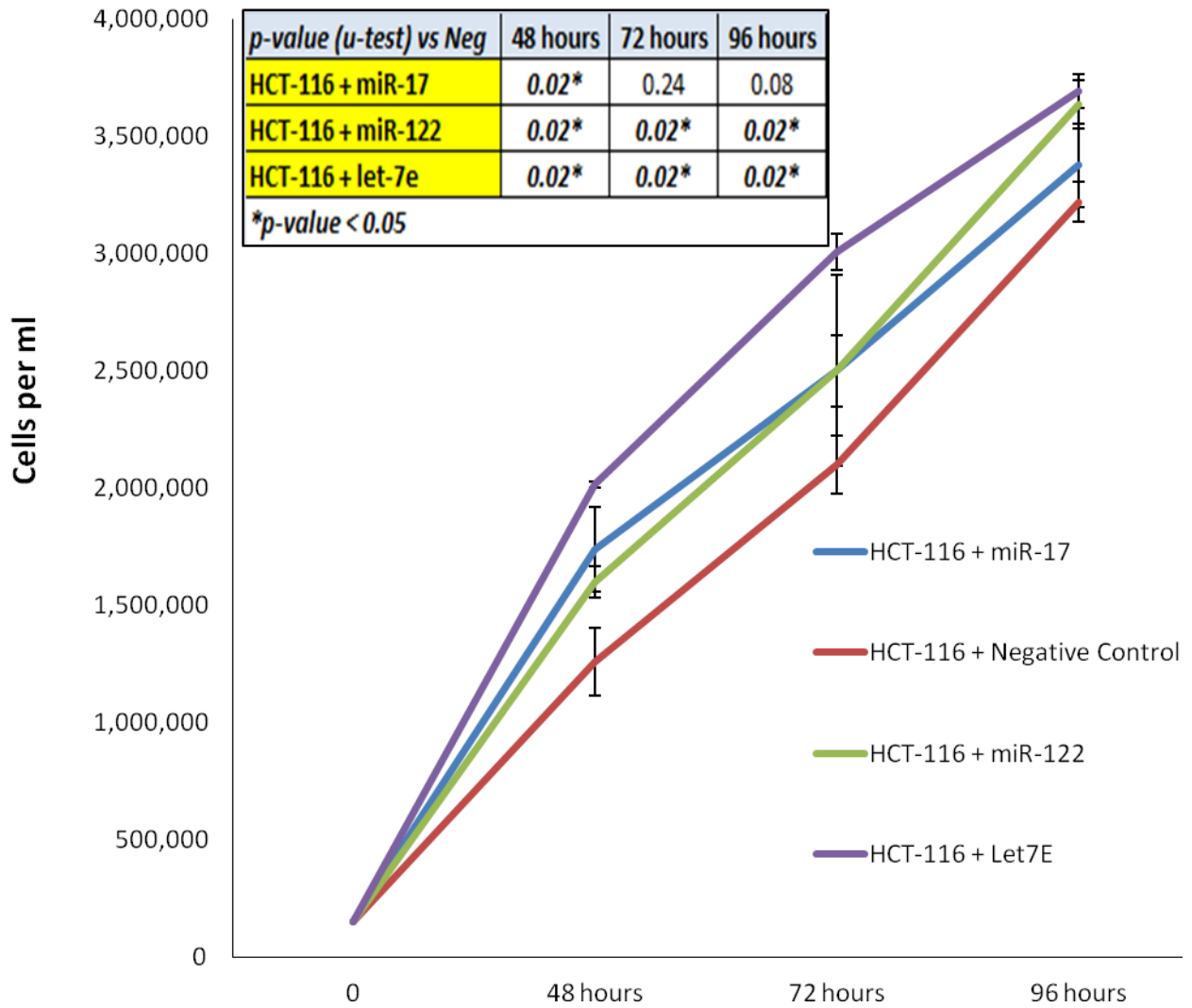
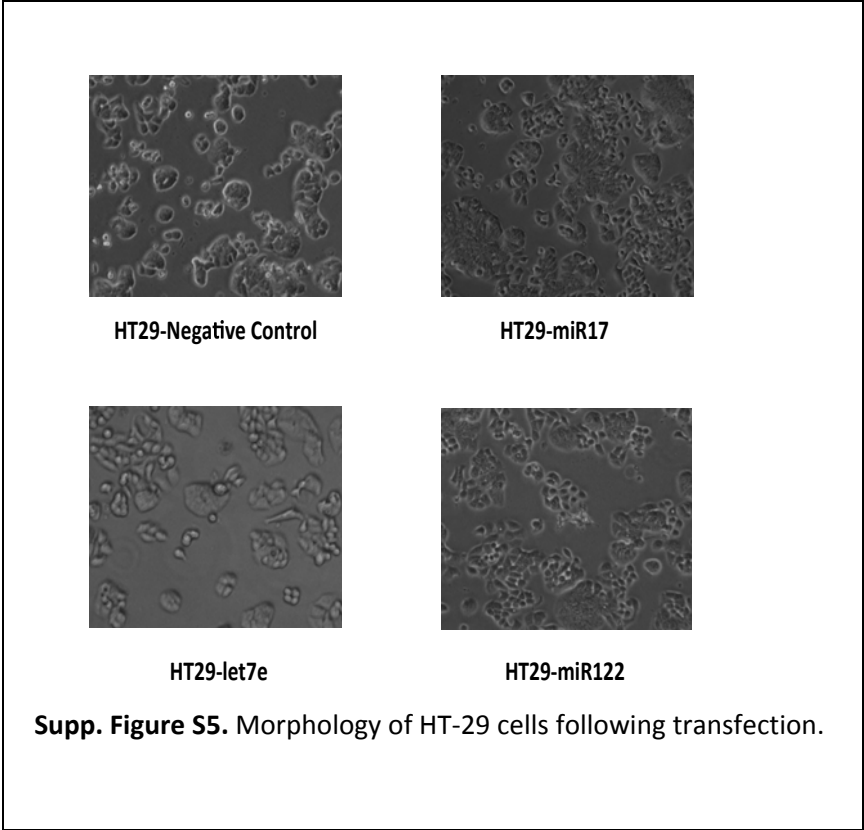
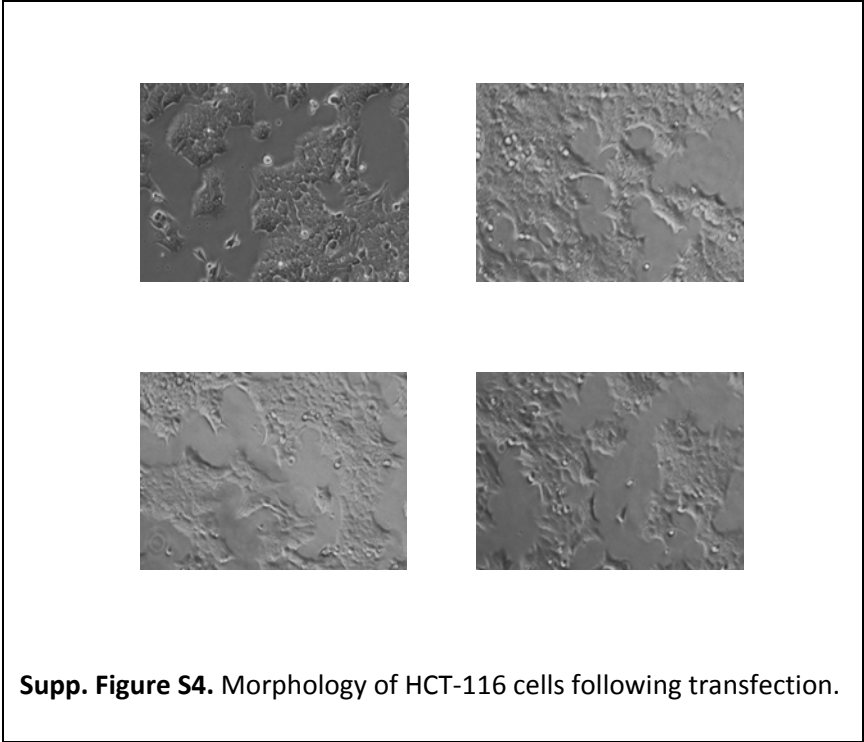


Supp. Figure S1. Plots of differentially expressed microRNAs by disease stage for *all patients*. Box plots showing the minimum, median, maximum and interquartile ranges for all six patients, three replicates for each sample. Dotted line shows the mean trend over stage across all patients and replicates with corresponding fold changes of raw data expression values. A higher C_t value implies a lower miRNA expression; thus, negative fold changes imply down regulation. The fold changes from normal to dysplasia, dysplasia to cancer, and from normal to cancer are shown on top of the box plots, respectively.

Supplementary figure 2: HT-29 Growth Curves After Transfection with miR-17, miR-122, let-7e, and Negative Control

Supplementary figure 3: HCT-116 Growth Curves After Transfection with miR-17, miR-122, let-7e, and Negative Control





Supp. Table S1. miRNA RT-PCR cancer array format

| | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 |
|---|--------------|----------|----------|----------|------------|-------------|-------------|----------|-------------|-------------|------------|
| A | let-7a | miR-133b | miR-122 | miR-20b | miR-335 | miR-196a | miR-125a-5p | miR-96 | miR-96 | miR-222 | miR-148b |
| B | miR-184 | miR-214 | miR-18b | miR-18b | miR-378 | let-7b | miR-205 | miR-181a | miR-130a | miR-199a-3p | miR-140-5p |
| C | miR-146b -5p | miR-132 | miR-183 | miR-183 | miR-34c-5p | miR-30c | miR-148a | miR-134 | let-7g | miR-138 | miR-373 |
| D | let-7e | miR-218 | miR-146a | miR-146a | miR-212 | miR-135b | miR-206 | miR-124 | miR-21 | miR-181d | miR-301a |
| E | miR-100 | miR-10b | miR-155 | miR-1 | miR-363 | miR-150 | let-7i | miR-27b | miR-7 | miR-127-5p | miR-29a |
| F | let-7d | miR-9 | miR-10a | miR-10a | miR-181b | miR-15b | miR-16 | miR-210 | miR-106a/17 | miR-98 | miR-34a |
| G | miR-144 | miR-128a | miR-215 | miR-215 | miR-19a | miR-193a-5p | miR-18a | miR-125b | miR-126 | miR-27a | miR-372 |
| H | miR-23b | miR-203 | miR-181c | SNORD48 | SNORD47 | SNORD44 | U6 | miRTC | miRTC | PPC | PPC |

 Housekeeping Genes (H5-H8)

 miRTC: Reverse Transcription Control

 PPC: Positive PCR Control

Supp. Table S2. Percentage of cells (as detected by flow cytometry) in each cell-cycle phase following transfection of the sporadic colorectal cancer cell line HT-29 with the three different dysregulated microRNAs *let-7e*, *miR-17*, and *miR-122*

| | HT-29 Negative Control Transfection (% cells) | HT-29 <i>let-7e</i> Transfection (% cells) | HT-29 <i>miR-17</i> Transfection (% cells) | HT29 <i>miR-122</i> Transfection (% cells) |
|--------------|---|--|--|--|
| G0/G1 | 22.5 | 18.9 | 23.9 | 16.2 |
| S | 11.2 | 7.03 | 6.5 | 7.9 |
| G2M | 27.3 | 27.7 | 30.2 | 25.5 |

Supp. Table S3. Percentage of cells (as detected by flow cytometry) in each cell-cycle phase following transfection of the sporadic colorectal cancer cell line HCT-116 with the three different dysregulated microRNAs *let-7e*, *miR-17*, and *miR-122*

| | HCT-116 Negative Control Transfection (% cells) | HCT-116 <i>let-7e</i> Transfection (% cells) | HCT-116 <i>miR-17</i> Transfection (% cells) | HCT-116 <i>miR-122</i> Transfection (% cells) |
|--------------|---|--|--|---|
| G0/G1 | 26.8 | 24.9 | 19.1 | 22.5 |
| S | 11.8 | 18.5 | 17.7 | 18.5 |
| G2M | 33.8 | 36.3 | 35.6 | 33.8 |