

Supplementary Table S1. Validated miRs from the identified miR signature.

| miRNAs | Fold Change (log2) |
|----------------|--------------------|
| <i>miR-127</i> | -0.251 |
| <i>miR-133</i> | -0.174 |
| <i>miR-143</i> | -0.728 |
| <i>miR-145</i> | -0.817 |
| <i>miR-1a</i> | -0.701 |
| <i>miR-205</i> | 1.339 |
| <i>miR-30c</i> | -1.550 |
| <i>miR-31</i> | 3.457 |
| <i>miR-375</i> | -2.328 |

miRs were validated by RT-qPCR using an independent set of murine samples (inflamed n=8; flat n=6; and polypoid n=8). Data are expressed as log2 fold-change. Positive and negative values indicate upregulation and downregulation of the indicated miR, respectively.