



**Supplementary Fig. 1.** Overview of analysis. Paired tumor and normal tissues were collected from 44 CRC patients by the University of Minnesota BioNet as a part of a previous study. The 16s rRNA gene sequencing was performed prior, as a part of the previous study. The small RNAs were sequenced on an Illumina HiSeq 2000 platform. A detailed description of the analysis was described in methods section.