**Table S1.** Relative abundance of 2181 OTUs in all samples. OTUs, operational taxonomic units.

**Table S2.** Oral microbial diversity index in all samples.

**Table S3.** Different bacterial phyla among the CRA cohort, CRC cohort, and healthy controls cohort. CRA, colorectal adenoma; CRC, colorectal cancer.

**Table S4.** Abundance of the different bacterial phyla (log2FC, *p* value and q value) between the CRA cohort and CRC cohort. CRA, colorectal adenoma; CRC, colorectal cancer; FC, fold change.

**Table S5.** Abundance of the different bacterial genera (log2FC, *p* value and q value) between the CRA cohort and CRC cohort. CRA, colorectal adenoma; CRC, colorectal cancer; FC, fold change.

**Table S6.** Abundance of the different bacterial phyla (log2FC, *p* value and q value) between CRA cohort and healthy controls cohort. CRA, colorectal adenoma; FC, fold change.

**Table S7.** Abundance of the different bacterial genera (log2FC, *p* value and q value) between the CRA cohort and healthy controls cohort. CRA, colorectal adenoma; FC, fold change.

**Table S8.** Abundance of the different bacterial phyla (log2FC, *p* value and q value) between the CRC cohort and healthy controls cohort. CRC, colorectal cancer; FC, fold change.

**Table S9.** Abundance of the different bacterial genera (log2FC, *p* value and q value) between the CRC cohort and healthy controls cohort. CRC, colorectal cancer; FC, fold change.

**Table S10.** Five optimal OTU markers selected in the discovery phase between the CRA cohort and healthy controls cohort. CRA, colorectal adenoma; OTU, operational taxonomic unit.

**Table S11.** Five optimal OTU markers selected in the discovery phase between the CRC cohort and healthy controls cohort. CRC, colorectal cancer; OTU, operational taxonomic unit.