Dear editors:

First, I would like to express my thanks to all editors and reviewers for your valuable suggestions and advice with respect to the paper I submitted. Based on the suggestions and advice, I have modified and improved the relevant problems one by one.

To be specific, given that all the patients had signed the informed consents and agreements related to the study before blood and tissue sampling and sample SNP detection, the types of pathologies included study were not screened. As a result, the clinically common canalicularadenoma accounted for a majority (42/50) of the cases of colorectal cancer in control group I. The limited nature of our study samples also suggest that in our next study design, we should comprehensively account for all relevant factors. The sample size of the observation group II (normal population) was 40 cases, less than the number of patients in the other two groups. We designed the small sample size for two reasons. First, we wanted to emphasize the sample size of the key research interests(tumorous polyp and colorectal cancer) in view of the limited SNP sequencing scale of samples and second, to avoid statistical correction errors which may be caused by small sample sizes within any given group. The normal tissues around the lesions from patients with tumorous polyps or colorectal cancer were not sampled or studied with the SNP detection because of the small number of samples used. Therefore, the study could have been more complete. However, the relevant suggestions and advice have provided important ideas and pointed out important directions for us in future studies (difference and correlation between genetic imprinting and gene point mutation, carcinogenic mechanisms with regard to single nucleotide polymorphism, etc.).

Also, with regard to patient informed consent and the Ethics Committee, we carefully analyzed and supplemented previously collected clinical data in our paper, and attached a sample of the informed consent form. As for the selection of references, we have reviewed and added recent publications according to the suggestions of the reviewers. However, because part of our study had been carried out as early as 2011 and because of the restricted we have to the latest publications both in terms of domestic and international journals, some of the literature related to preliminary studies may be outdated. We hope that the editors and reviewers will understand the challenge that we face. With respect to data about the general condition of patients, we have provided further detailed information and classifications and presented them in Tab.1. As for the possible lack in clinical data, we hope that the reviewers can kindly point out any specific missing data, so that we may generate them in a timely manner.

Finally, thank you again for your valuable suggestions and advice with respect to the submitted paper. If there are still any shortcomings, I hope that you will point them out.

The studies performed by Kim& Li all suggest that, in the case of sporadic colorectal cancer, although the allele frequency of SNPs is relatively low, these polymorphisms are closely related to the occurrence of colorectal cancer. Further

studies are still required to explore the correlation between colorectal cancer and the location of SNPs.