**Integrative analyses reveal expression and regulation of long noncoding RNA in colorectal cancer**

**Introduction**

**Results**

**Figure 1. Genomic characterization of lncRNAs in colorectal cancer**

a. circos plot showing the lncRNA in normal, primary and recurrence CRC patients

b. coding potential comparison among novel lncRNA, known lncRNAs and protein-coding genes

c. transcript length

d. expression abundance

e. conservation

**Figure 2. Differential expression analysis identify tumorigenesis and metastasis related lncRNAs**

a. vennplot showing tumorigenesis DE lncRNAs from DESeq and EdgeR analysis

b. vennplot showing metastasis DE lncRNAs from DESeq and EdgeR analysis

c. hist graph showing the proportion of DE lncRNAs in novel lncRNA and known lncRNAs

d. heatmap showing tumorigenesis DE lncRNAs

e. heatmap showing metastasis DE lncRNAs

f. DAVID analysis showing pathway enrichment of the identified DE lncRNAs

**Figure 3. TCGA copy number analysis**

a. circos plot showing somatic copy number alterations (SCNAs) frequency in novel and known lncRNA loci in CRC

b. percentages of lncRNAs with significant copy-number alteration (>25% of specimens) in CRC for novel lncRNAs and known lncRNAs respectively

c. heatmap showing pancancer lncRNA gain and loss

**Figure 4. Identification of potential CRC oncogenic lncRNAs**

a,b. venn plot showing the overlap between tumorigenesis/metastasis related lncRNAs and significantly CNAs

c,d. heatmap showing the overlapped lncRNAs

e. chromatin signature around the TSS region of the overlapped lncRNAs (chipseq data of HCT116 cell line)

f. barplot showing the enriched pathways

**Figure 5. Further selection of potential CRC oncogenic lncRNAs**

a. clonogenicity siRNA(shRNA) screeing for potential CRC oncogenic lncRNAs

b. chromatin signature for selected lncRNAs(IGV)

c. qPCR to validate CNA

d. correlation between expression and copy number

e. survival analysis (expression up vs down and gain vs loss)

**Figure 6. Functional assays to validate the function of selected lncRNA**

a. in vitro evaluate the effect of selected lncRNA on growth rate

b. in vitro evaluate migration

c. in vivo evaluate tumor volumes

**Figure 7. downstream genes of selected lncRNA (RNA-Sequencing)**

a. heatmap showing the DE lncRNAs between control and sh-lncRNA

b. pathway enrichment

c. qPCR validation

d. western blot validation

e. FACS

f.

**Discussion**

**Methods**