

Differential Methylation Regions (MDR) within genome  
of colorectal cancer derived from TCGA  
HumanMethylation450k dataset

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# Chapter 1

## Summary

This is a *sample* book written in **Markdown**. You can use anything that Pandoc's Markdown supports, e.g., a math equation  $a^2 + b^2 = c^2$ .

The **bookdown** package can be installed from CRAN or Github:

```
install.packages("bookdown")  
# or the development version  
# devtools::install_github("rstudio/bookdown")
```

Remember each Rmd file contains one and only one chapter, and a chapter is defined by the first-level heading #.

To compile this example to PDF, you need XeLaTeX. You are recommended to install TinyTeX (which includes XeLaTeX): <https://yihui.name/tinytex/>.

## Chapter 2

# Sample Information

Table 2.1: sample distribution

	site	sampleNumber
1	Cecum	71
2	Sigmoid colon	68
3	Ascending colon	58
4	Rectum, NOS	52
5	Colon, NOS	47
6	Rectosigmoid junction	47
7	Descending colon	14
8	Transverse colon	14
9	Hepatic flexure of colon	13
10	Splenic flexure of colon	5
11	—	3
12	Connective, subcutaneous and other soft tissues of abdomen	2

## Chapter 3

# Literature

Here is a review of existing methods.

## Chapter 4

# Methods

We describe our methods in this chapter.

## Chapter 5

# Applications

Some *significant* applications are demonstrated in this chapter.

### 5.1 Example one

### 5.2 Example two

## Chapter 6

# Final Words

We have finished a nice book.