In the page 2:

ESCC accounts for more than 90% esophageal cancers in China nowadays[1](#_ENREF_1). In the past several years, genetic research to esophageal carcinoma have received several important achievements. Genome-wide association study (GWAS) identified serials of ESCC susceptibility genes[2-5](#_ENREF_2), such as *PLCE1*, *C20orf54*. Meanwhile, ESCC associated miRNA-SNPs[6](#_ENREF_6),[7](#_ENREF_7), copy number variations (CNV)[8](#_ENREF_8) and somatic mutations[9](#_ENREF_9) has been widely identified. However, the mortality rate of ESCC was not be effectively controlled even with this achievement. Considering the characteristics of highly invasive, metastatic and poor prognosis, there is an urgent need for identifying diagnostic and prognostic biomarkers for ESCC.

In the page 4:

then followed by next-generation sequencing and the details could be found in our previous study[10](#_ENREF_10),[11](#_ENREF_11)

In the page 5:

Average methylation fraction (AMF) to each loci or whole promoters was calculated to make the differential methylation test which has been applied in our previous studies[10-12](#_ENREF_10),.

In the page 10: What’s cancer lines?

Effects of ZNF132 expression on cancer cell characteristics of esophagus cancer lines in vitro ??

Effects of ZNF132 expression esophagus cancer cell?? lines in vitro

1. Zhang, Y. Epidemiology of esophageal cancer. *World J Gastroenterol* **19**, 5598-606 (2013).

2. Wu, C. *et al.* Genome-wide association study identifies common variants in SLC39A6 associated with length of survival in esophageal squamous-cell carcinoma. *Nat Genet* **45**, 632-8 (2013).

3. Wu, C. *et al.* Genome-wide association study identifies three new susceptibility loci for esophageal squamous-cell carcinoma in Chinese populations. *Nat Genet* **43**, 679-84 (2011).

4. Wang, L.D. *et al.* Genome-wide association study of esophageal squamous cell carcinoma in Chinese subjects identifies susceptibility loci at PLCE1 and C20orf54. *Nat Genet* **42**, 759-63 (2010).

5. Bass, A.J. & Meyerson, M. Genome-wide association study in esophageal squamous cell carcinoma. *Gastroenterology* **137**, 1573-6 (2009).

6. Shen, F. *et al.* Genetic variants in miR-196a2 and miR-499 are associated with susceptibility to esophageal squamous cell carcinoma in Chinese Han population. *Tumour Biol* **37**, 4777-84 (2016).

7. Zhang, P. *et al.* miR-449b rs10061133 and miR-4293 rs12220909 polymorphisms are associated with decreased esophageal squamous cell carcinoma in a Chinese population. *Tumour Biol* **36**, 8789-95 (2015).

8. Song, Y. *et al.* Identification of genomic alterations in oesophageal squamous cell cancer. *Nature* **509**, 91-5 (2014).

9. Integrated genomic characterization of oesophageal carcinoma. *Nature* **541**, 169-175 (2017).

10. Pu, W. *et al.* Targeted bisulfite sequencing identified a panel of DNA methylation-based biomarkers for esophageal squamous cell carcinoma (ESCC). *Clin Epigenetics* **9**, 129 (2017).

11. Wang, C. *et al.* Identification of Hyper-Methylated Tumor Suppressor Genes-Based Diagnostic Panel for Esophageal Squamous Cell Carcinoma (ESCC) in a Chinese Han Population. *Front Genet* **9**, 356 (2018).

12. Guo, S. *et al.* Identification and validation of the methylation biomarkers of non-small cell lung cancer (NSCLC). *Clin Epigenetics* **7**, 3 (2015).