**Table 2 The methylation of ZNF132 gene and control gene in ESCC**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Gene name | Mean（Case） | Mean（Control） | P valuea | P valueb | Sensitivity | Specificity | Area Under Curve（AUC） |
| ZNF132 | 0.36 | 0.11 | 2.2×10-16 | 2.2×10-16 | 70.8% | 80.6% | 0.82 |
| LINE-1 | 0.55 | 0.73 | 2.16×10-8 |  |  |  |  |
| ChrM | 0.03 | 0.02 | 2.59×10-1 |  |  |  |  |

**Figure 1. Hypermethylationof ZNF132 in esophageal squamous cell carcinoma**

**A．**Median % methylation values of 21 CpG site of LINE-1. **B.** Median % methylation of 11 CpG sites of ChrM. **C.** Median % methylation in ESCC and adjacent control tissues of 14 CpG sites of ZNF132 promoter region (without the last one which is hypermethylated in normal). **D.** The methylation of ZNF132 in the 94 cases of ESCC tissues and adjacent tissues (each point represents the absolute ratio of methylation in each tissue) **E.** Represents the overall ROC (Receiver Operating characterstics) curve, which was calculated through a logistic regression model, incorporating the mean methylation percentage of the five genomic regions as the variables, and with the adjustment for gender, age, smoking and alcohol consumption.