**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 |  |  |  |  |

*P*-valuea is calculated through the Wilcoxon rank-sum test followed by FDR (false discovery rate) adjustment for multiple correction

*P*-valueb determined by logistic regression.