Figure 1

Candidate tumor suppressor gene (n = 65) screening

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Confirmation with DNA methylation datasets from TCGA/GEO
Criteria 1: Mean Methylation percent (β value) > 0.25 in ESCC samples
Criteria 2: Mean Methylation percent (β value) < 0.25 in adjacent control samples
Criteira 3: Mean Methylation percent (β value) < 0.25 in PBMC and PBL of normals
Criteria 4: At least 2 CpG sites on candidate gene fulfills criteria 1,2 and 3

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Candidate tumor suppressor genes (n = 6) for further validation

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Four candidate biomarkers for multiplex PCR design:
ADHFE1, EOMES, SALL1, TFPI2

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94 pairs of ESCC tumors and adjacent control tissues for validation with targeted bisulfite sequencing

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Model Evaluation: Accuracy, Sensitivity, Specificity, AUC