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Subtypes of Barrett's Esophagus and Esophageal Adenocarcinoma Based on Genome-wide Methylation Analysis

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Abstract

Objective: To determine if DNA methylation subtypes exist in esophageal adenocarcinoma (EAC) and its precursor Barrett's esophagus (BE).

Design: We performed genome-wide DNA methylation profiling on samples of non-dysplastic BE from cancer-free patients (N=59), EAC (N=23), normal squamous esophagus (N=33) and normal fundus (n=9), and identified methylation subtypes using a recursively partitioned mixture

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Competing interests: All authors have no competing interests.

Accession codes: HumanMethylation450 array data for 89 samples (N = 23 EAC; N = 59 BE from cancer-free patients; N = 7 BE from EAC patients) have been deposited at the Gene Expression Omnibus under accession numbers GSE81334.