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Epigenomic dysregulation in youth vapers: implications for disease risk assessment

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Despite the ongoing epidemic of youth vaping, the long-term health consequences of electronic cigarette use are largely unknown. We investigated the epigenomic effects of vaping versus smoking by analyzing the oral cell methylome in healthy young vapers and smokers, relative to non-users. Whereas vapers and smokers differed in the number of differentially methylated regions (DMRs) (831 vs 2,863), they shared striking similarities in the distribution and patterns of DNA methylation, chromatin states, binding motifs, and molecular pathways. There was substantial overlap in DMR-associated genes between vapers and smokers, with the shared subset of genes enriched for transcriptional regulation, signaling, tobacco use disorders and cancer-related pathways. A remarkable finding was the identification of a common hypermethylated DMR at the promoter of Hypermethylated In Cancer 1 (*HIC1*), a gene frequently silenced in smoking-related cancers. Our data support a potential link between epigenomic dysregulation in youth vapers and disease risk. These novel findings have significant implications for public health and tobacco product regulation.