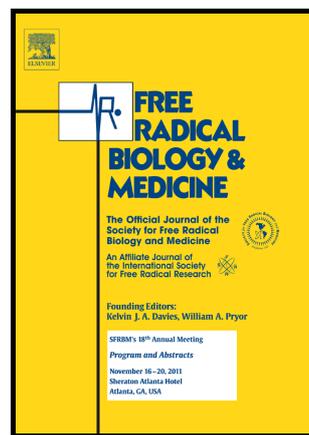


Author's Accepted Manuscript

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www.elsevier.com

PII: S0891-5849(18)31326-1
DOI: <https://doi.org/10.1016/j.freeradbiomed.2018.08.004>
Reference: FRB13868

To appear in: *Free Radical Biology and Medicine*

Received date: 11 February 2018
Revised date: 20 July 2018
Accepted date: 1 August 2018

Cite this article as: Seungyeon Lee, Sungbin Park, Hyunkyung Lee, Dawoon Jeong, Juyeon Ham, Eun Ha Choi and Sun Jung Kim, ChIP-seq analysis reveals alteration of H3K4 trimethylation occupancy in cancer-related genes by cold atmospheric plasma, *Free Radical Biology and Medicine*, <https://doi.org/10.1016/j.freeradbiomed.2018.08.004>

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ChIP-seq analysis reveals alteration of H3K4 trimethylation occupancy in cancer-related genes by cold atmospheric plasma

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Abstract

Cold atmospheric plasma (CAP) has gained attention for use in cancer treatment owing to its ability to preferentially induce cancer cell death; however, the involved molecular mechanism remains to be elucidated. Herein, an epigenetic effect of CAP on cancer cells was examined by performing a genome-wide ChIP-seq for H3K4me3 in MCF-7 breast cancer cell line. Consequently, 899 genes showed significantly changed methylation level at H3K4 with constructing “Cellular Compromise, DNA Replication, Recombination, Repair, and Cell Cycle” as the top network. Comparisons with expression array data revealed a coincidence between histone modification and gene expression for 18 genes, and the association was confirmed by ChIP-PCR and qRT-PCR for selected genes. The expression of the affected

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