EPIGENETIC PROFILING H3K27Ac USING DATA ChIP-Seq LUNG CANCER CELLS CAUSED BY SMOKE CIGARETTE IN R PROGRAM

By: Tri Atmaja Huda

Statistics Department Faculty of Mathematics and Natural Sciences

Universitas Islam Indonesia

E-mail: 14611213@students.uii.ac.id

ABSTRACT

Lung cancer is the most common type of cancer and is the first cause of death in cancer, this is due to the poor prognosis of this cancer throughout the world. Environmental factors such as tobacco smoke can modulate the formation and maintenance of DNA methylation, and thus can affect lung cancer through complex mechanisms. Therefore, in this study epigenetic profiling was conducted to look at genes that influence lung cancer, so that it is expected to provide specific treatment for profiling results to improve the quality of prognosis, accelerate the healing process of lung cancer patients, and reduce levels deaths caused by lung cancer. The method used in this study was data analysis of ChIP-Seq against histone modification of H3K27Ac, epigenomic markers related to the expression of active genes in lung cancer cells caused by cigarette smoke, based on packages in Bioconductor using the R program. Based on this study a group was obtained genes that have the mechanism, function, and the same role of genes undergoing changes due to exposure to cigarette smoke, namely signaling by receptor tyrosine kinases are the most dominant with 441 genes and the adjusted P-value value is 0.015 and the gene ratio is 0.044. Then the most dominant disease association was non-small cell lung carcinoma with 415 genes and the adjusted P-value value was 0.00206 and the gene ratio was 0.057. The genes that affect non-small cell lung carcinoma or lung cancer are CYP2E1, NAPSA, CYP1A1, EGFR, and 411 other genes.

Keywords: Lung Cancer, ChIP-Seq, Epigenetic Profiling, Genes