

## PROFIL TRANSKRIPTOM DARI DATA *NEXT GENERATION SEQUENCING* TERKAIT INFLAMASI PADA KASUS KANKER NASOFARING DI INDONESIA

### INTISARI

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**Latar Belakang :** Di Indonesia kanker nasofaring menduduki peringkat 5 sebagai penyakit tumor ganas berbahaya. Inflamasi merupakan *hallmark of cancer* yang berperan sebagai pintu utama proses karsinogenesis. *Next Generation Sequencing* (NGS) merupakan alat yang dapat melihat ekspresi suatu gen dari seluruh sekuens genom. NGS dapat mempelajari dinamika transkriptomik untuk melihat mekanisme suatu penyakit, salah satunya kanker.

**Tujuan :** NGS digunakan untuk membuat profil transkriptom terkait proses inflamasi pada kasus kanker nasofaring di Indonesia. Gen – gen serta peranannya dalam *pathway* dari profil transkriptom yang terdeteksi untuk dipelajari dan dipahami mekanisme kanker nasofaring terkait inflamasi.

**Metode :** Penelitian ini menggunakan metode brushing untuk pengambilan sampel kontrol dan metode biopsi jaringan untuk sampel kanker. Isolasi RNA total menggunakan *Rneasy® RNA Extraction Mini Kit*. Pengukuran konsentrasi dan kemurnian RNA total menggunakan *Qubit assay* dan *nanodrop*. Sintesis *library cDNA* menggunakan *TruSeq® RNA Library Preparation Kit V2*. *Sequencing* sampel menggunakan mesin NGS *Illumina NextSeq 550 platform*. Analisis bioinformatik menggunakan *software* FASTQC, HISAT2, edgeR, DAVID dan PANTHER.

**Hasil :** Dari 31 sampel yang diambil terdapat 7 sampel kanker dan 2 sampel kontrol yang dilakukan sekuensing. Dari 9 sampel yang terdapat 25.943 gen yang mengalami perubahan ekspresi gen secara signifikan berdasarkan nilai FDR dan p – value dengan nilai standar < 0,05. Berdasarkan analisis *pathway* terkait inflamasi didapatkan 13 gen yang terdeteksi dan terlibat dalam 3 *pathway*.

**Kesimpulan :** Profil transkriptom kanker nasofaring terkait inflamasi menggunakan NGS dapat dilakukan, dengan didapatkan 13 gen yaitu HTR2A, NGF, TRPA1, PRKCG, ADCY8, CXCL9, CXCL 10, CXCL 11, MYLK2, COL20A1, MYH2, ACTC1 yang mengalami *upregulated*, kecuali ALOX15 yang mengalami *downregulated*. Terdapat 3 *pathway* yang ditemukan terkait inflamasi pada kanker nasofaring yaitu jalur *Inflammatory Mediator Regulation of TRP Channels*, jalur *Toll-Like Receptor Signalling*, dan jalur *Inflammation Mediated by Chemokine and Cytokine Signaling*.

**Kata kunci:** Kanker nasofaring, transkriptom, inflamasi, NGS

## TRANSCRIPTOME PROFILE OF DATA NEXT GENERATION SEQUENCING INFLAMMATION ON NASOPHARYNGEAL CARCINOMA IN INDONESIA

### ABSTRACT

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**Background:** In Indonesia nasopharyngeal carcinoma is ranked as a dangerous malignant tumor. Inflammation is a hallmark of cancer that acts as the main door to the process of carcinogenesis. Next-Generation Sequencing (NGS) is a tool that can see the expression of a gene from all genome sequences. NGS can study transcriptomic dynamics to see the mechanism of a disease, one of which is cancer.

**Purpose:** NGS is used to create a transcriptome profile related to the inflammatory process in cases of nasopharyngeal carcinoma in Indonesia. Genes and their role in the pathway of the transcriptome profile that is detected to be studied and understood the mechanism of inflammation-related nasopharyngeal carcinoma.

**Methods:** This study used the brushing method for control sampling and tissue biopsy methods for cancer samples. Isolate total RNA using the Rneasy® RNA Extraction Mini Kit. Measurement of total RNA concentration and purity using Qubit assay and nanodrop. Synthesis of cDNA library using TruSeq® RNA Library Preparation Kit V2. Sequencing samples using the NGS Illumina NextSeq 550 platform engine. Bioinformatic analysis using FASTQC, HISAT2, edgeR, DAVID and PANTHER software.

**Results:** From 31 samples taken there were 7 cancer samples and 2 control samples that were sequenced. From 9 samples, there were 25,943 genes that had significant changes in gene expression based on FDR and p-values with a standard value  $<0.05$ . Based on the analysis of inflammation-related pathways, 13 genes were detected and involved in 3 pathways.

**Conclusion:** Inflammatory nasopharyngeal carcinoma profile related to inflammation using NGS can be done, with 13 genes obtained, namely HTR2A, NGF, TRPA1, PRKCG, ADCY8, CXCL9, CXCL 10, CXCL 11, MYLK2, COL20A1, MYH2, ACTC1 that have upregulated, except ALOX15 which downregulated. There are 3 pathways that are found to be associated with inflammation in nasopharyngeal carcinoma, namely the Inflammatory Mediator Regulation of TRP Channels, the Toll-Like Receptor Signaling Pathway, and the Inflammation Mediated by Chemokine and Cytokine Signaling pathways.

**Keywords:** Nasopharyngeal carcinoma, transcriptome, inflammation, NGS