

**PROFIL TRANSKRIPTOMIK DATA NGS (*Next-Generational Sequence*)  
ANALISIS BIOINFORMATIKA TERKAIT *SENESCENCE CELL* PADA  
SAMPEL NPC (*Nasopharyngeal Carcinoma*) INDONESIA**

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**INTISARI**

**Latar belakang:** NPC (*Nasopharyngeal Carcinoma*) adalah kanker peringkat kelima berdasarkan Global Cancer Observatory dalam peringkat kasus kejadian dan kematian. NPC sering didiagnosa terlambat, sehingga penting ditemukan kandidat biomarker untuk diagnosis. Penelitian ini ingin memprediksi biomarker untuk NPC yang dikaitkan dengan penanda kanker “Penuaan Sel”.  
**Metode:** Penelitian ini menggunakan data RNA sekuensing dari 9 sampel yang terdiri atas 2 sampel jaringan normal hasil *swab brushing* dan 7 sampel kanker nasofaring hasil biopsi segar untuk disekuensing dengan total RNA-nya dengan NGS. RNA sekuensing telah dilakukan sebelumnya menggunakan teknologi NGS (*Next-Generational Sequencing*) digunakan untuk mendapatkan profil transkriptomik sebagai data genomik untuk mendapatkan DEGs (*Differentially Expressed Genes/Gen-gen* terekspresi signifikan). DEGs diperoleh dari hasil analisis alat bioinformatik menggunakan: FastaQC, Geneious, Hisat2, Htseq, edgeR. Hasil DEGs kemudian diprediksi pathway terkait “Penuaan Sel” dengan Diana MiR-Path, TargetScan, PantherDB, DAVID, MirDB, dan MirTarBase.  
**Hasil:** Berdasarkan DEGs yang diperoleh, didapatkan total 17 miRNA yang signifikan lebih tinggi pada jaringan NPC dibandingkan jaringan normal. Salah satu miRNA yang ditemukan adalah MIR4300 dengan nilai *log folding change* dengan nilai paling signifikan sebesar 9 kali lipat. MIR4300 ditemukan memiliki heatmap pada interaksi dengan matriks ekstraseluler, dan target mRNAnya MAP3K2.  
**Kesimpulan:** Penelitian menunjukkan bahwa data miRNA dapat dikaitkan dengan pertanda kanker yaitu Penuaan Sel, dan miRNA 4300 dapat dijadikan kandidat biomarker untuk diagnosa penyakit NPC.

**Kata kunci:** Kanker Nasofaring, *Next-Generational Sequencing*, Profil Transkriptom

**TRANSCRIPTOMIC PROFILING OF NGS (Next-Generational Sequence)  
DATA ANALYSIS OF BIOINFORMATICS RELATED TO SENESCENCE  
CELLS IN INDONESIAN NPC (Nasopharyngeal Carcinoma) SAMPLES**

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**ABSTRACT**

**Background:** NPC (Nasopharyngeal Carcinoma) is the fifth most common cancer based on the Global Cancer Observatory in terms of incidence and mortality. NPC is often diagnosed late, so it is important to find candidate biomarkers for diagnosis. This study wanted to predict biomarkers for NPC associated with the cancer marker "Senescent Cell". **Methods:** This study used RNA sequencing data from 9 samples consisting of 2 normal tissue samples from swab brushing and 7 nasopharyngeal cancer samples from fresh biopsies. Previously, RNA sequencing was carried out using next generation sequencing (NGS) technology. to be sequenced with its total RNA with NGS. NGS technology is used to obtain transcriptomic profiles as genomic data to obtain DEGs (Differentially Expressed Genes/significantly expressed genes). DEGs were obtained from the analysis of bioinformatic tools using: FastaQC, Geneious, Hisat2, Htseq, edgeR. The results of DEGs were then predicted for pathways related to "Cell Aging" with Diana MiR-Path, TargetScan, PantherDB, DAVID, MirDB, and MirTarBase. **Results:** Based on the DEGs obtained, a total of 17 miRNAs were found which were significantly higher in NPC tissue than in normal tissue. One of the MiRNAs found was MIR4300 with a log folding change value of 9 times the most significant value. MIR4300 was found to have a heatmap on interactions with the extracellular matrix, and its mRNA target MAP3K2. **Conclusion:** Research shows that miRNA data can be associated with a hallmark of the cancer called Senescent Cell, and miRNAs can be used as candidate biomarkers for diagnosis of NPC disease.

**Keywords:** Nasopharyngeal Carcinoma, Next-Generational Sequencing, Transcriptome Profile.