

Elevated expression of JMJD5 protein due to decreased miR-3656 levels contributes to cancer stem cell-like phenotypes under overexpression of cancer upregulated gene (CUG)2

Natpaphan Yawut^{1#}, Il-Rae Cho^{1#}, Phatcharaphon Budluang¹, Sirichat Kaowinn², Chutima Kaewpiboon³, Byeoleun Jeon⁴, Sang-Woo Kim⁴, Ho Young Kang⁵, Min Kyung Kang⁶, Sang Seok Koh⁶, and Young-Hwa Chung^{1*}

¹BK21 plus, Department of Cogno-Mechatronics Engineering, Optomechatronics Research Center, ⁴Department of Biological Science, ⁵Department of Microbiology, Pusan National University, Busan 46241, Republic of Korea

²Department of General Science and Liberal Arts, King Mongkut's Institute of Technology, Ladkrabang Prince of Chumphon Campus, Chumphon 86160, Thailand

³Department of Biology, Faculty of Science, Thaksin University, Patthalung 93210, Thailand

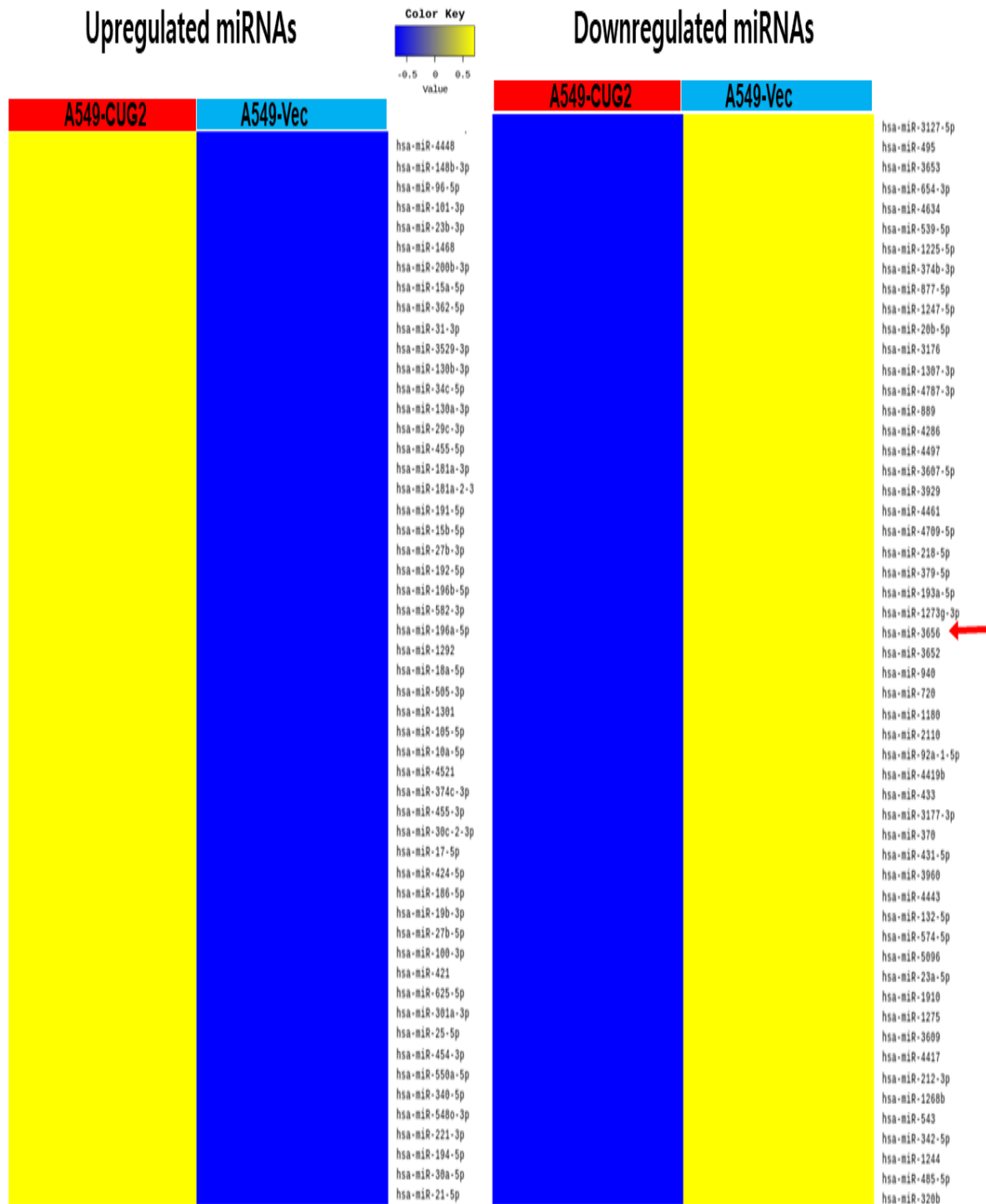
⁶Department of Biomedical Sciences, Dong-A University, Busan 49315, Republic of Korea

Keywords: CUG2, JMJD5, cancer stem cell, KDM8, miR-3656

#; equally contributed

* Corresponding author; Young-Hwa Chung, PhD, Department of Cogno-Mechatronics Engineering, Optomechatronics Research Center, Pusan National University, Busan 46241, Republic of Korea, *Email* ; younghc@pusan.ac.kr

Supplementary Figure S1
(A)

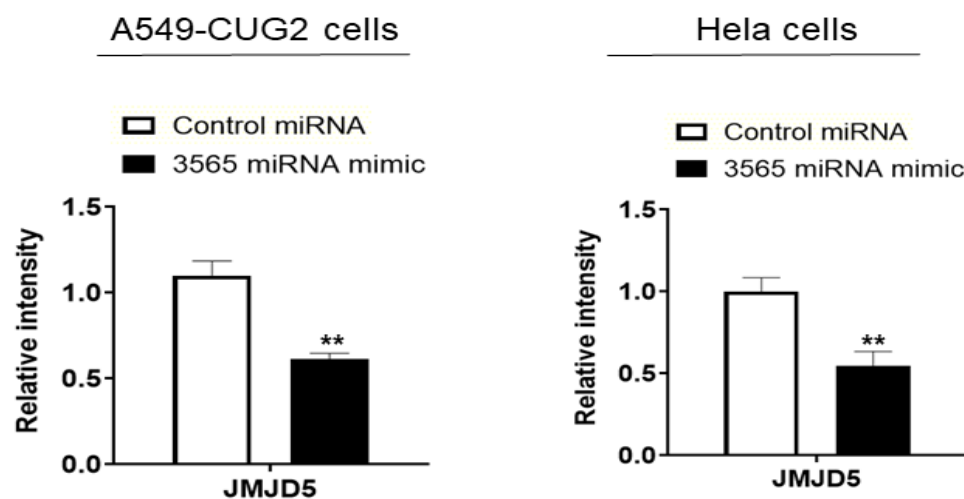


(B)



Relative expression of miRNA isolated from A549- CUG2 and BEAS-CUG2 cells, and their control cells was measured using a human miRNA microarray (AffymetrixGeneChip® miRNA 4.0 Array, Affymetrix, Santa Clara, USA), which was performed by Macrogen (Seoul, Korea). The Affymetrix Gene Chip miRNA array process was performed according to the manufacturer's protocol. Heat maps of the one-way hierarchical clustering were drafted using Z-score for normalized value (log2 based).

Supplementary Figure S2

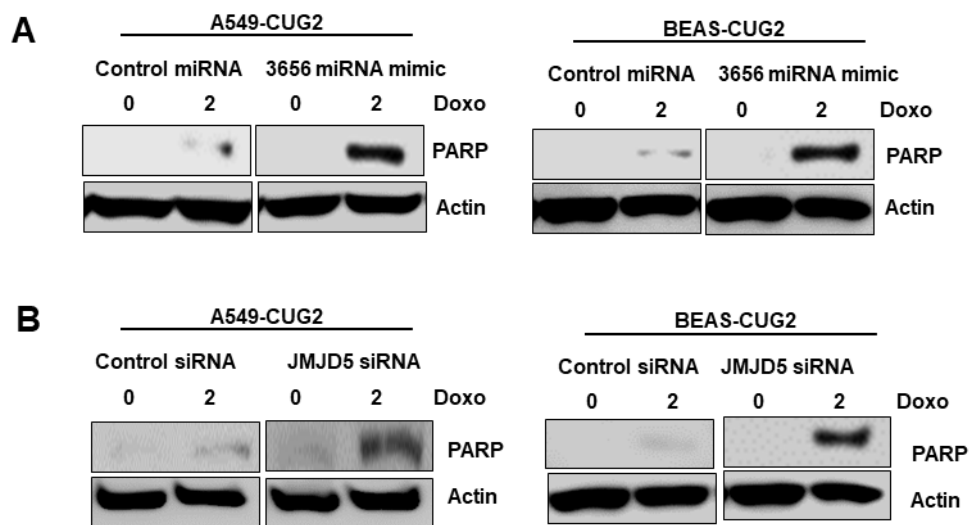


Decreased levels of *JMJD5* transcripts after treatment with the miR-3656 mimic

A real-time RT-PCR was conducted on an AriaMX Real-time system (Agilent Technologies, Santa Clara, USA) using the SYBR Premix EX Taq (Takara, Shiga, Japan) and the following gene-specific primers: *JMJD5*, (forward) 5'-GGAACCATCTCCCCACTACAT-3' and (reverse) 5'-CTGGCTCGTGTTATGGAGAAG-3', *GAPDH* (forward) 5'-CTTTGGTATC GTGGAAGGACTC - 3' and (reverse) 5'-GTAGAGGCAGGGATGATGTTCT -3'. Real-time RT-PCR data were obtained in the form of threshold cycle (Cq) values, and target gene

expression was normalized to GAPDH expression. Relative expression levels of *JMJD5* were calculated using the comparative Cq ($2^{-\Delta\Delta Cq}$) method. The assay was conducted in triplicate. The data designate the mean \pm SD. (** $p < 0.01$, miR-3565 vs miR-control)

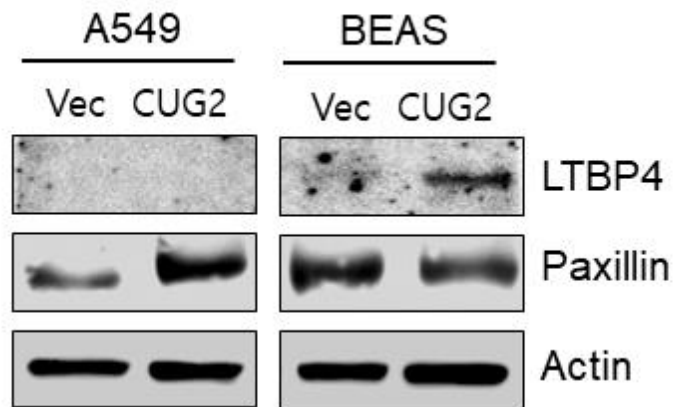
Supplementary Figure S3



Sensitization of apoptosis after treatment with the miR-3656 mimic or JMJD5 siRNA under doxorubicin

Under doxorubicin (2 μ g/ml), A549-CUG2 and BEAS-CUG2 cells were treated with the miR-3656 mimic or JMJD5 siRNA. Cleaved PARP was detected for apoptosis 2 days post-transfection using immunoblotting.

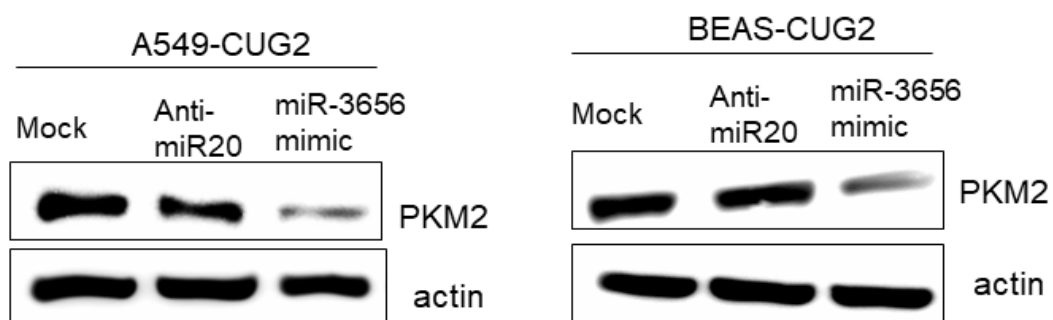
Supplementary Figure S4



Other candidates of target proteins against miR-3656

LTBP4 and paxillin protein levels in A549-CUG2 and BEAS-CUG2 cells were compared with their control cells with immunoblotting.

Supplementary Figure S5



Decreased levels of PKM2 protein after treatment with the miR-3656 mimic

A549-CUG2 and BEAS-CU2 cells were treated with the miR-3656 mimic or anti-miR20.

PKM2 protein was detected 2 days post-transfection using immunoblotting.