

## Packaging signal of SARS-CoV-2

Youngran Park<sup>1,2,\*</sup>, Jongmin Lim<sup>3</sup>, Hyeonggon Cho<sup>3</sup>, Ahyeon Son<sup>1,2</sup>, C. Han Li<sup>1,2</sup>, V. Narry Kim<sup>1,2,\*</sup>,  
Young-suk Lee<sup>3,4,\*</sup>

<sup>1</sup>*Center for RNA Research, Institute for Basic Science, Seoul, Republic of Korea*

<sup>2</sup>*School of Biological Sciences, Seoul National University, Seoul, Republic of Korea*

<sup>3</sup>*Department of Bio and Brain Engineering, KAIST, Daejeon, Republic of Korea*

<sup>4</sup>*Graduate School of Engineering Biology, KAIST, Daejeon, Republic of Korea*

\*Corresponding author: [younggran.park36@gmail.com](mailto:younggran.park36@gmail.com), [narrykim@snu.ac.kr](mailto:narrykim@snu.ac.kr) and [youngsl@kaist.ac.kr](mailto:youngsl@kaist.ac.kr)

Selective genome packaging during viral assembly is a crucial step in the viral life cycle. The nucleocapsid (N) protein is thought to recognize the cis-acting packaging signal within viral genomic RNA, but the packaging signal of SARS-CoV-2 remains elusive. Here, we employed two complementary CLIP-seq techniques and mapped 22 regions interacting with SARS-CoV-2 N proteins. Using the virus-like particle and defective-interfering RNA systems, we discovered putative packaging elements clustered within the nsp12 polymerase-coding region. Synonymous point mutations revealed RNA sequences critical for triggering RNA packaging into virus particles. Furthermore, introducing these mutations to the full-length viral genome in a reverse genetics model impaired viral encapsulation and propagation without impacting viral RNA synthesis. Our study identifies the SARS-CoV-2 packaging signal residing within a highly conserved genome region, which may serve as therapeutic targets for current and future coronavirus outbreaks.