

SUPPLEMENTARY MATERIAL

Effect of Next-Generation Exome Sequencing Depth for Discovery of Diagnostic Variants

**KKyung Kim^{1,2,3†}, Moon-Woo Seong^{4†}, Won-Hyong Chung³, Sung Sup Park⁴,
Sangseob Leem¹, Won Park^{5,6}, Jihyun Kim^{1,2}, KiYoung Lee^{1,2,*†},
Rae Woong Park^{1,2*} and Namshin Kim^{5,6**}**

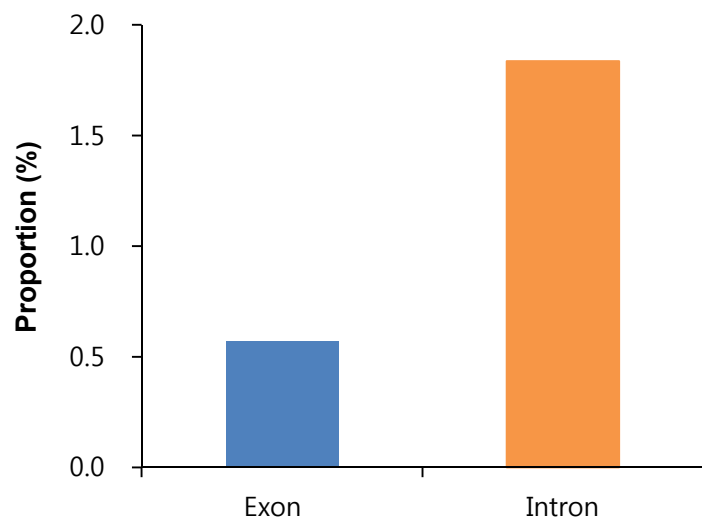
¹Department of Biomedical Informatics, Ajou University School of Medicine, Suwon 443-749, Korea

²Department of Biomedical Science, Graduate School, Ajou University, Suwon 443-749, Korea, ³Korean Bioinformation Center, Korea Research Institute of Bioscience and Biotechnology, Daejeon 305-806, Korea,

⁴Department of Laboratory Medicine, Seoul National University Hospital College of Medicine, Seoul 110-799, Korea, ⁵Department of Functional Genomics, Korea University of Science and Technology, Daejeon 305-806,

Korea, ⁶Epigenomics Research Center, Genome Institute, Korea Research Institute of Bioscience and Biotechnology, Daejeon 305-806, Korea

Figure S2.



Supplementary Fig. 2. Numbers of single nucleotide polymorphisms (SNPs) in the dbSNP database. Coverage of all SNPs in the dbSNP database in intronic (orange) and exonic (blue) regions are depicted.