

## SUPPLEMENTARY MATERIAL

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

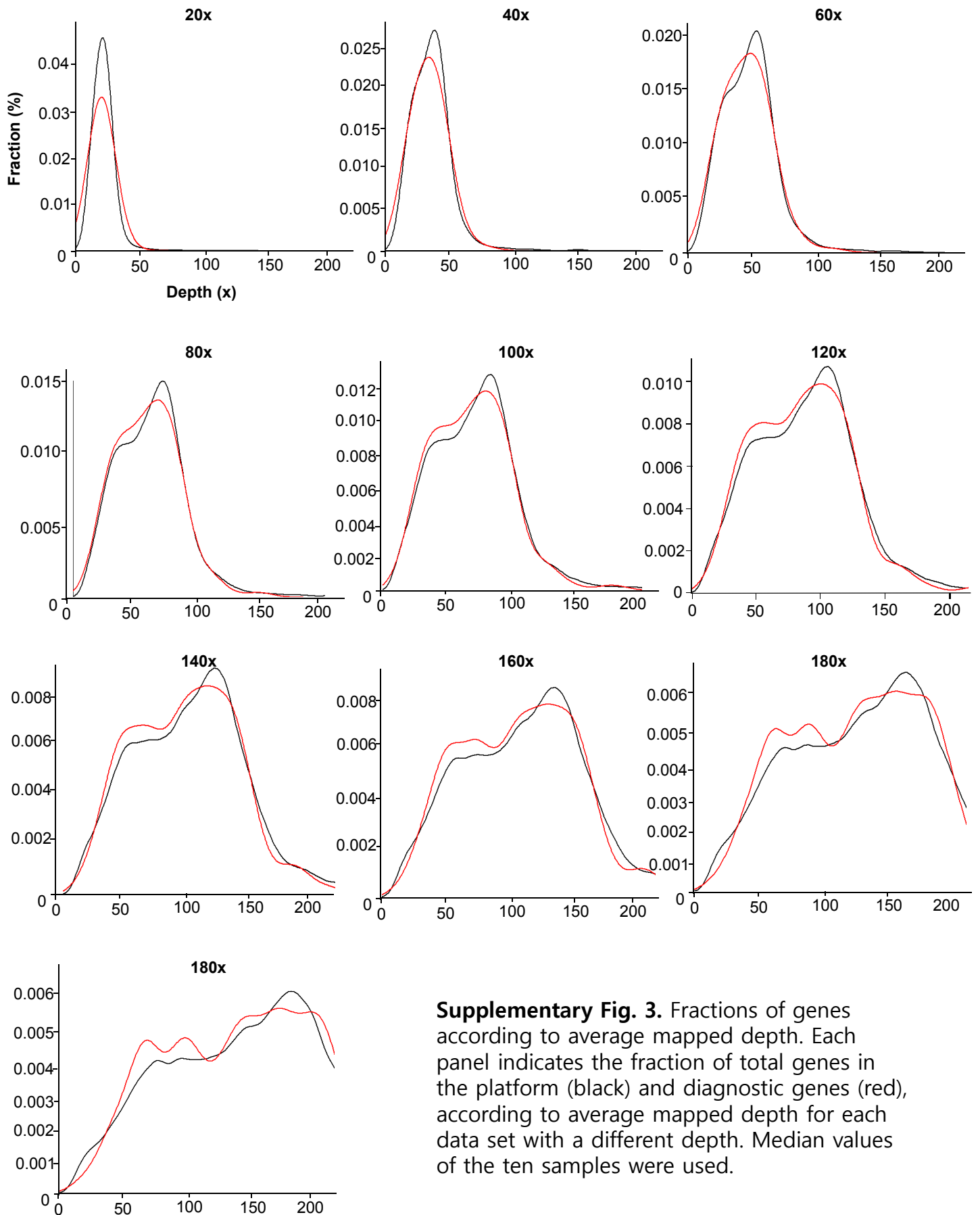
**KKyung Kim<sup>1,2,3†</sup>, Moon-Woo Seong<sup>4†</sup>, Won-Hyong Chung<sup>3</sup>, Sung Sup Park<sup>4</sup>,  
Sangseob Leem<sup>1</sup>, Won Park<sup>5,6</sup>, Jihyun Kim<sup>1,2</sup>, KiYoung Lee<sup>1,2,\*†</sup>,  
Rae Woong Park<sup>1,2\*</sup> and Namshin Kim<sup>5,6\*\*</sup>**

<sup>1</sup>Department of Biomedical Informatics, Ajou University School of Medicine, Suwon 443-749, Korea

<sup>2</sup>Department of Biomedical Science, Graduate School, Ajou University, Suwon 443-749, Korea, <sup>3</sup>Korean Bioinformation Center, Korea Research Institute of Bioscience and Biotechnology, Daejeon 305-806, Korea, <sup>4</sup>Department of Laboratory Medicine, Seoul National University Hospital College of Medicine, Seoul 110-799, Korea, <sup>5</sup>Department of Functional Genomics, Korea University of Science and Technology, Daejeon 305-806, Korea, <sup>6</sup>Epigenomics Research Center, Genome Institute, Korea Research Institute of Bioscience and

Biotechnology, Daejeon 305-806, Korea

**Figure S3.**



**Supplementary Fig. 3.** Fractions of genes according to average mapped depth. Each panel indicates the fraction of total genes in the platform (black) and diagnostic genes (red), according to average mapped depth for each data set with a different depth. Median values of the ten samples were used.