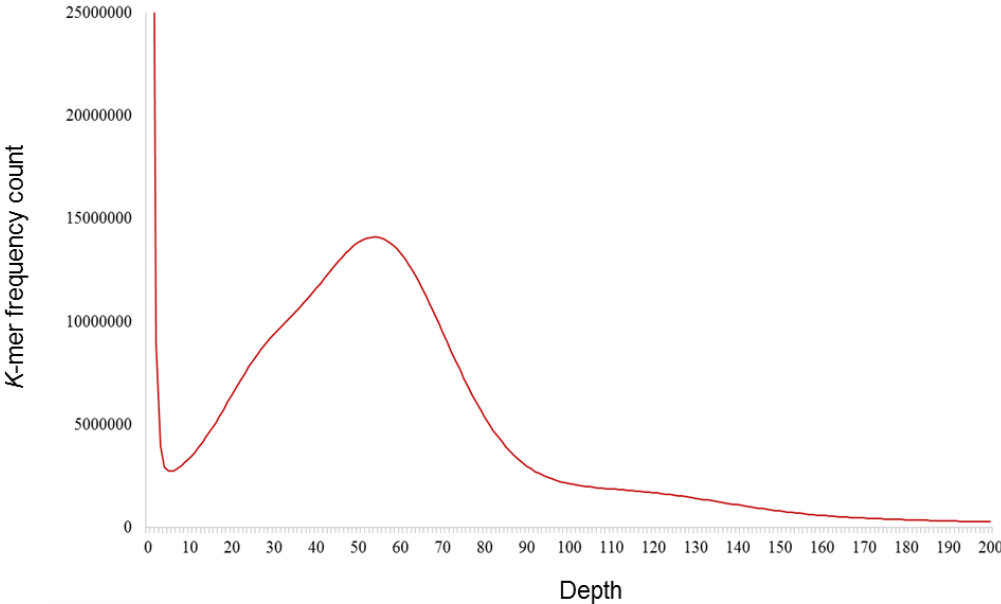
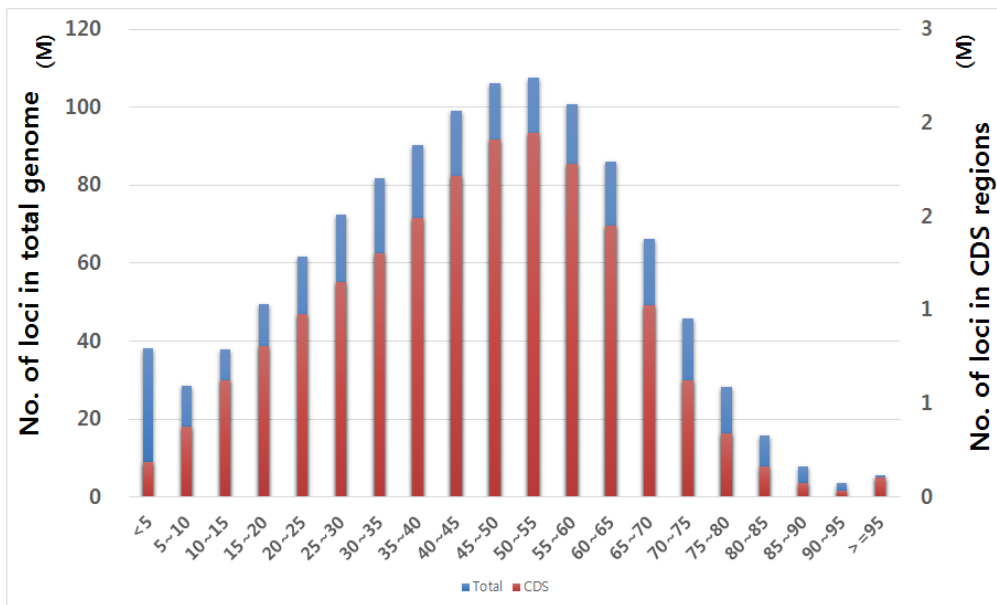


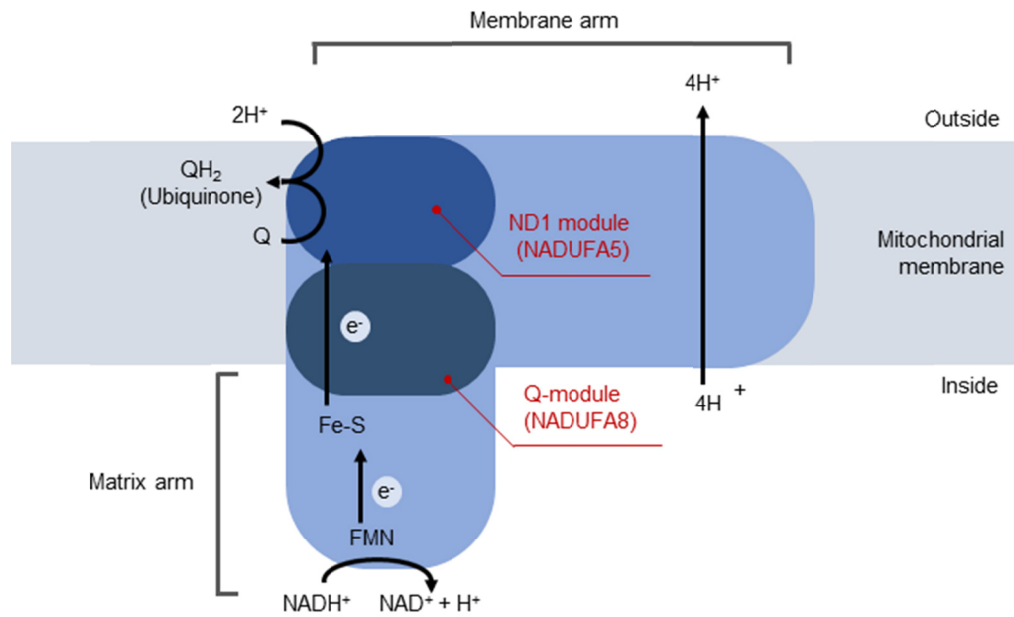
Supplementary Fig. S1. Quality scores obtained for all base positions by FastQC.



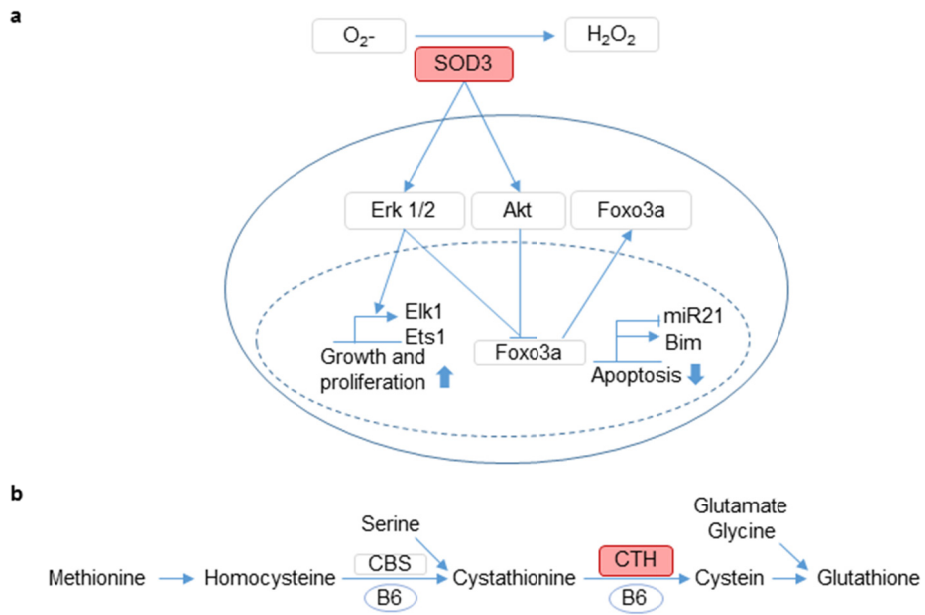
Supplementary Fig. S2. Estimation of genome size using 17-mers.



Supplementary Fig. S3. Distribution of read depths mapped to the gray-crowned crane reference genome (blue) and CDS (red) regions.



Supplementary Fig. S4. Schematic overview of the protein structure and electron transfer in NADH-ubiquinone oxidoreductase. The red line indicates the location of the ND1 module and Q-module. Red-crowned crane PSGs are represented with red text.



Supplementary Fig. S5. Schematic overview of signal transduction pathways. (a)

Depiction of cellular responses to *SOD3*. (b) Depiction of a homocysteine metabolic pathway

involving *CTH*.