

SUPPLEMENTARY MATERIAL

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

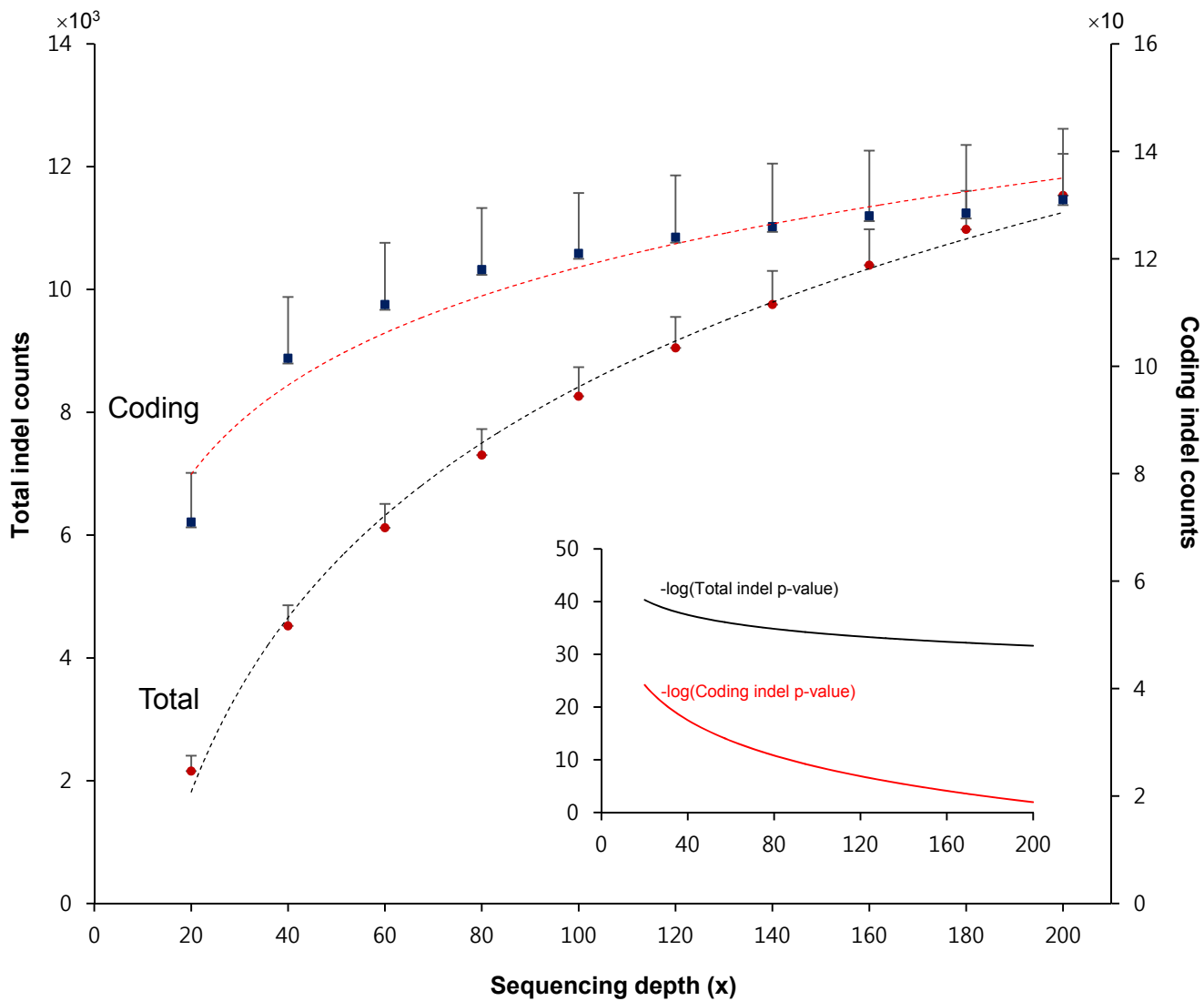
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Figure S1.



Supplementary Fig. 1. Numbers of called functional indels of human genes according to mapped depths. Numbers of indels in coding (blue) and total (red) regions according to average mapped depths per sample (denoted by different shapes) are depicted: dashed lines are trend lines of means, and error ranges are represented. Solid lines in the inner chart represents how numbers of indels are significantly different from each own preceding.