## MITOCHONDRIAL DNA SEQUENCING WITH PRECISION ID MTDNA WHOLE GENOME PANEL ON ION S5XL

<u>Yong Sheng LEE<sup>1</sup></u>, Annabel Suan TAY<sup>1</sup>, Bing Hong SHUE<sup>1</sup>, Si Zhen TAN<sup>1</sup>, See Ying HOE<sup>1</sup>, Sim Hwee POOK<sup>1</sup>, Christopher Kiu Choong SYN<sup>1,2</sup>

<sup>1</sup>DNA Profiling Laboratory, Applied Sciences Group, Health Sciences Authority

<sup>2</sup>Department of Biological Sciences, National University of Singapore

The value of mitochondrial DNA (mtDNA) control region sequencing towards missing person identification using traditional Sanger sequencing has been well reported. Recent development in massively parallel sequencing with semi-automation platforms has allowed for the sequencing of the entire mtDNA genome with relative ease, as compared to Sanger sequencing, giving a much higher power of discrimination. The present study is a preliminary evaluation of the performance of the Precision ID mtDNA Whole Genome Panel on Ion S5xL, in particular the possibility of obtaining mtDNA data from samples where autosomal STR testing was unsuccessful. The first part of this study involved a sensitivity study using serially diluted DNA extracted from blood samples, as well as sequencing of hair shafts of different lengths. The second part of this study involved a comparison of the results from standard autosomal STR testing and mtDNA whole genome sequencing of degraded blood samples. In addition, a case study on dried bone samples was provided to illustrate the possible use of mtDNA whole genome sequencing in casework situations.