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Reply to commentary by Dr. J. Zhang and associates on the article "Complete sequence analysis of mitochondrial DNA of aplastic anemia patients", published in *Genet. Mol. Res.* 11 (3): 2130-2137

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We collected bone marrow mtDNA from 15 patients with aplastic anemia; we also collected epithelial cell mtDNA from these patients as a control. Nucleotide changes that were found in both the bone marrow and oral epithelial cells in the same patient were counted as polymorphisms or homoplasmic mutations, and those that had not already been included in the databases (MITOMAP, mtDB, or Genbank) were considered to be new polymorphisms. Changes that were only present in bone marrow were counted as mutations or heteroplasmic mutations.

We provided information concerning the consequences of the listed point mutations (silent mutation/frame shift mutation/stop codon) in Table 1.

