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Data article

Dataset of mitochondrial genome variants in oncocytic tumors

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ABSTRACT

This dataset presents the mitochondrial genome variants associated with oncocytic tumors. These data were obtained by Sanger sequencing of the whole mitochondrial genomes of oncocytic tumors and the adjacent normal tissues from 32 patients. The mtDNA variants are identified after compared with the revised Cambridge sequence, excluding those defining haplogroups of our patients. The pathogenic prediction for the novel missense variants found in this study was performed with the Mitimpact 2 program. © 2018 Published by Elsevier Inc. This is an open access article

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Subject area	Genetics
More specific subject area	Oncocytic tumors
Type of data	Table, text file
How data was acquired	Sanger sequencing of whole mitochondrial genomes
Data format	Analyzed
Experimental factors	Samples are parafin-bedded tissues
Experimental features	The whole mitochondrial genomes from the tumor tissues were sequenced, the variations were identified by comparing sequences with the revised Cambridge sequence (rCRS) (Gen- Bank number NC_012920); the predictions for pathogenicity of mtDNA variants were established according to the Mitimpact 2 program.
Data source location	Wenzhou, China
Data accessibility	The data are available with this article

Specifications table

Value of the data

- The data identified inherited mtDNA variants associated with patients with oncocytic tumors.
- The data showed some identified mtDNA variants could have functional consequences.
- The data might help to detect new genetic predisposition markers for oncocytomas.

1. Data

The data were presented as tables, where positions, detail changes (Table 1), and the implications were provided (Table 2).

2. Experimental design, materials and methods

We collected 32 cases of the parafin-bedded tissues with oncocytic tumor and matched adjacent normal tissues, mtDNA were amplified by PCR using 24 previously reported pairs of mtDNA primers to cover the whole mtDNA genome as our previous work [1]. MtDNA variants were yielded by comparing sequencing results of the complete mitochondrial genome with the revised Cambridge sequence (rCRS) (GenBank number NC_012920). The heteroplasmy were defined if a double peaks of two residues were verified at the same position in the electro-chromatograms. Pathogenic prediction were analyzed using PolyPhen2 (http://genetics.bwh.harvard.edu/pph2/) [2] and MitImpact 2 [3].

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