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Determination of the site preference of G to T mutation in di- and trinucleotide sequences. To analyze site preference of G to T mutation caused by *Mth1/Ogg1/Mutyh* deficiency, the 239 data of G to T mutation detected in G2–G8 were subjected (C to A mutations were converted to G to T mutation). The reference exon sequences and the 101 nucleotides those containing each mutation site (shown in Supplementary Data S1 online) were used to determine the site preference of mutation. The ratio shown in Fig. 5b, c were calculated as follows (data were summarized in Supplementary Table S2 online).

(A) The number of each di- or tri-nucleotides sequences in the reference exon sequence were counted by 1 nucleotide sliding.
(B) The number of each di- or tri-nucleotides sequences that include mutated guanine site were counted.
(C) The frequency of each di- or tri-nucleotides sequences was calculated as follows: (A) /number of total nucleotide in reference exon sequence.
(D) Total number of di- or tri-nucleotides sequences that include mutated guanine site were 478 and 717, respectively.
(E) The expected value for a random mutation for each di- or tri-nucleotides sequences were calculated as (C) × (D).
(F) The ratio (observed mutation for the expected value for a random mutation) was calculated as (B)/(E).

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Author contributions

M.O. and K.S. designed the study, analysed data, and wrote the paper. R.F. and Y.G. designed and performed exome and sequencing analyses. Y.I. and T.I. performed bioinformatic analysis. T.T. gave conceptual advice. M.F. quantitated 8-oxodG. M.H. analysed hydrocephalus mice. Y.N. was involved in the study design and preparation of the paper. All authors discussed the results and commented on the manuscript.

Additional information

Supplementary information accompanies this paper at http://www.nature.com/scientificreports

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