Genetic defects of *CHM* and visual acuity outcome in 24 choroideremia patients from 16 Japanese families

Running title: *CHM* variants in Japanese choroideremia patients

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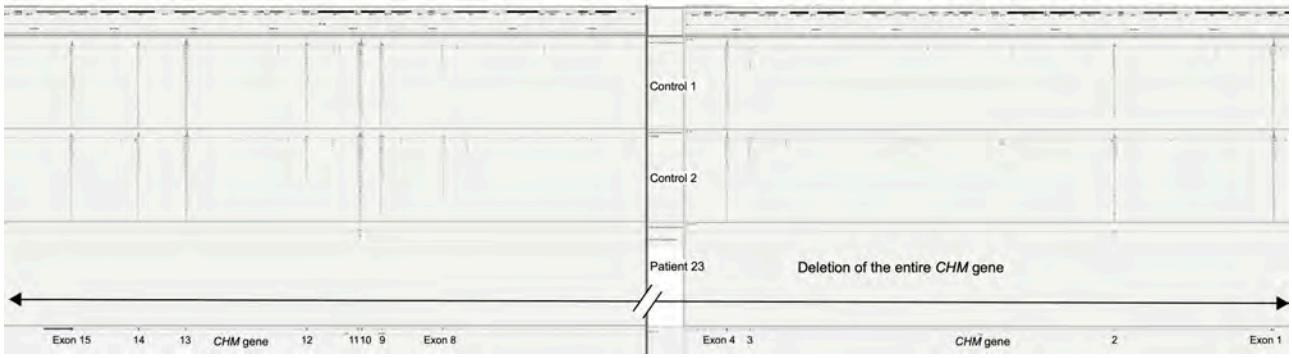
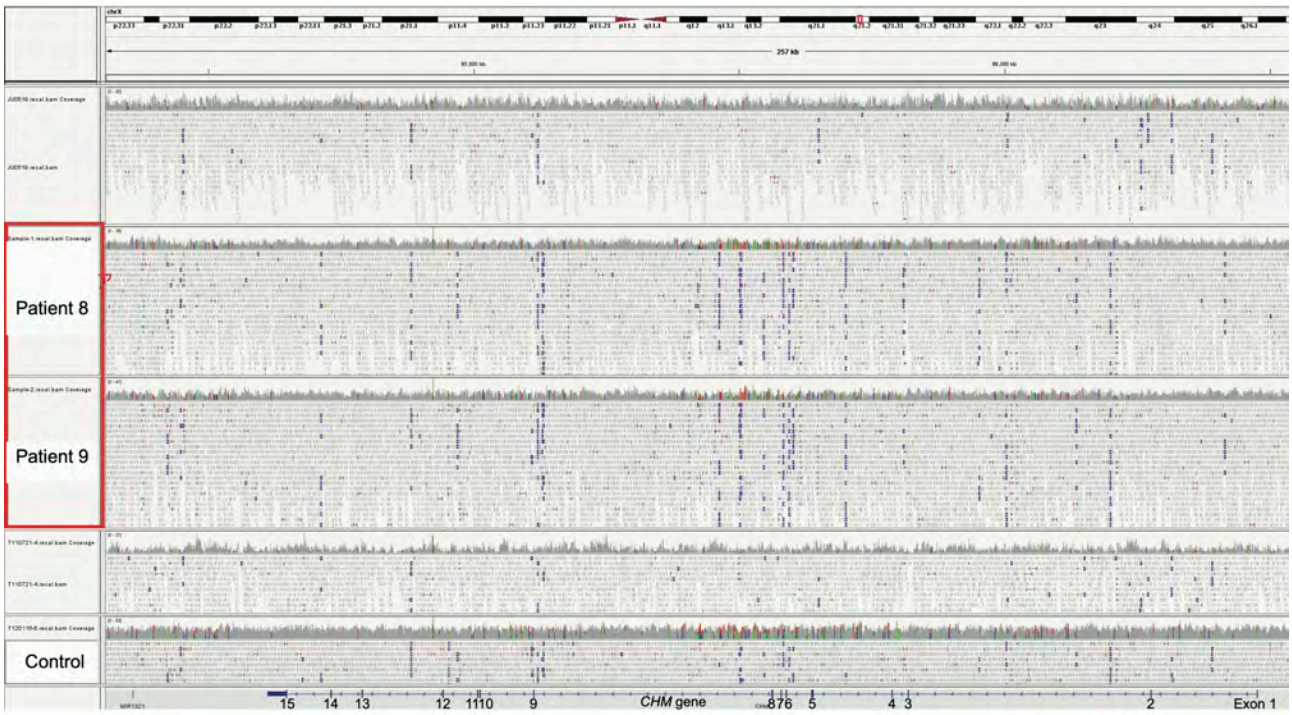


Supplementary Figure 1 Whole-exome sequencing data of patient 23 and two controls Whole-exome sequencing revealed an extremely large deletion of probably 5.0 mb encompassing the entire *CHM* gene and other genes (*TGIF2LX, CPXCR1, KLHL4, DACH2, MIR1321, POF1B, SATL1, UBE2DNL*) in the vicinity of *CHM*. The Integrative Genomics Viewer visualization of the *CHM* gene region demonstrated a deletion of the entire *CHM* gene (exons 1–15).



Supplementary Figure 2 Whole-genome sequencing (WGS) data of the *CHM* gene region for patients 8 and 9 and one control

The Integrative Genomics Viewer visualization revealed no decrease in read depth of any exons or introns in either patient, indicating no obvious deletion region in the *CHM* gene.