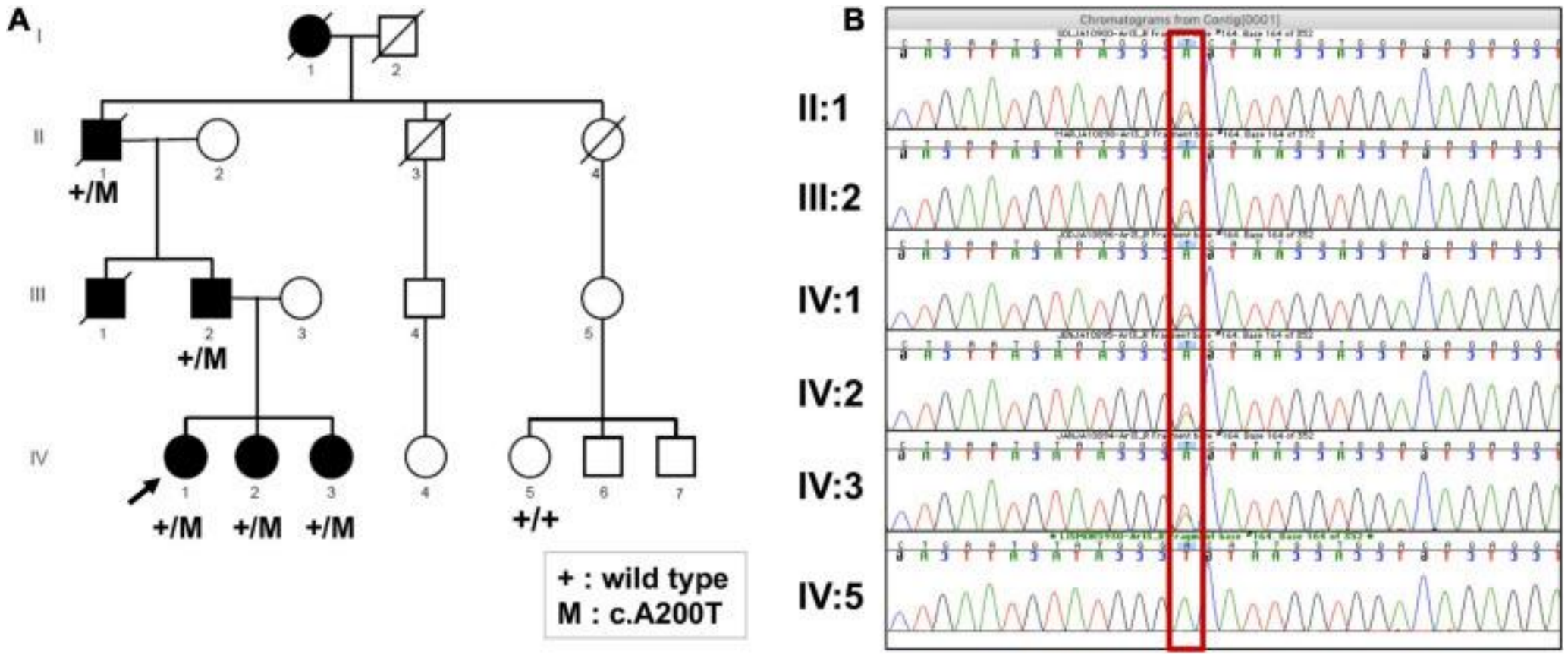

(A) Pedigree of the family, showing members affected and unaffected by the IRD. The segregation of the *ARL3* variant c.A200T is shown where mutation is indicated by "+/M," and its absence is indicated by "+/+." **(B)** Sanger sequencing electropherogram of the available family members confirming the exome sequencing results, as all affected are heterozygous (A/T) and the unaffected is homozygous for the wild-type allele (A/A) (shown in red rectangle).