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Abstract
LRRK2-PD represents the most common form of autosomal dominant Parkinson's disease. We identified the LRRK2 p.L1795F variant in three families and six additional unrelated cases using genetic data from over 50,000 individuals. Carriers with available genotyping data shared a common haplotype. The clinical presentation resembles other LRRK2-PD forms. Combined with published functional evidence showing strongly enhanced LRRK2 kinase activity, we provide evidence that LRRK2 p.L1795F is pathogenic. © The Author(s) 2025.

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