Steyaert et al.[1] used HiFi long-read genome sequencing on 293 individuals from 114 previously undiagnosed rare disease families. It identified definitive genetic causes in 11.8% of cases and potential candidates in another 5.4%, showing that long-read sequencing can uncover disease-causing variants missed by traditional methods—especially structural variants and repeat expansions.

These are promising results, but the diagnostic yield remains relatively low, highlighting how limited our understanding of the human genome still is.

1. https://genome.cshlp.org/content/early/2025/03/26/gr.279414.124