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Cover In this issue, the longitudinal trajectories of thousands of single nucleotide variants within 36 species in a single person's gut microbiome before and after oral antibiotic treatment are tracked using deep, linked-read metagenomic sequencing. Genetic changes were frequently observed in species without obvious changes in species abundance, emphasizing the importance of monitoring diversity below the species level. The illustration depicts the change of various gut microbiome subspecies over time. (Cover artwork by Shirley Chen, https://shirleyjychen.myportfolio.com/ and Xinda Wang, https://www.xinda-wang.com/. [For details, see Roodgar et al., pp. 1433–1446.])