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A *lacZ* reporter gene expression atlas for 313 adult KOMP mutant mouse lines

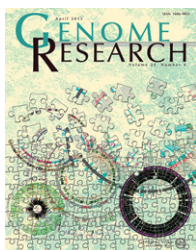
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Errata

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^{OA}Open Access paper



Cover Metagenomics data typically consist of a huge number of DNA sequence fragments from the genomes of microbial community members collected directly from an environment. Partial and sometimes complete genomes can be reconstructed and the metabolic capabilities of specific organisms revealed. In this issue, a study demonstrates how combining short- and long-read DNA sequencing technologies can improve genome recovery and microbial community analysis. The figure is a symbolic representation of the metagenomics analysis process in which the diverse genomes are recovered using short, and now also long, DNA sequencing read data, a process that conceptually resembles one of solving jigsaw puzzles. (Cover illustration is by Zosia Rostomian, Berkeley Lab Public Affairs, and is based on a concept by Jillian Banfield and Itai Sharon. [For details, see Sharon et al., pp. 534–543.]