

About Mudi

To facilitate the use of whole-genome sequencing in forward-genetic analysis by experimental researchers, we developed a browser-accessible tool, Mutation discovery (Mudi). This tool is optimized for mutation identification by pooled-linkage analysis, which specifically enriches causative mutations in a pool of mutant segregants obtained by backcrossing (Birkeland et al., 2010). The Mudi system includes all the processes required for mutation identification. In addition, one-click operation of the system also provides annotation and prioritization by allele frequency and map quality.

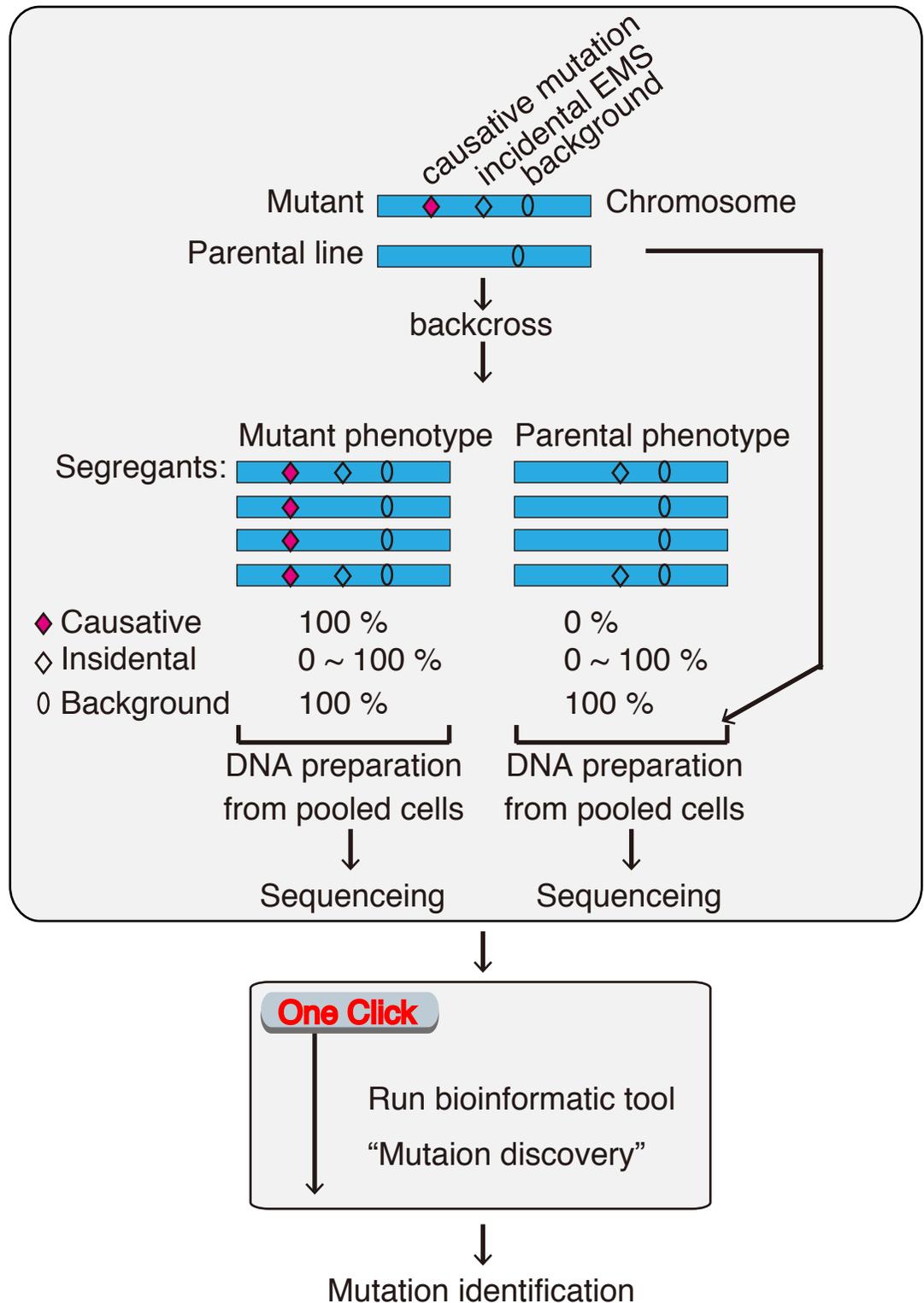
Pooled-linkage analysis

The scheme represents the segregation of a causative mutation (black diamond), incidental EMS-induced mutations (white diamonds), and background mutations (ovals) following a backcross of a mutant to the parental strain.

For pooled-linkage analysis, mutant segregants (We recommend 20~) obtained after the backcross are pooled. The genomes of the pooled mutants and the parental strain are sequenced. Optionally, pooled libraries from segregants exhibiting the parental phenotype can be used as the parental sample.

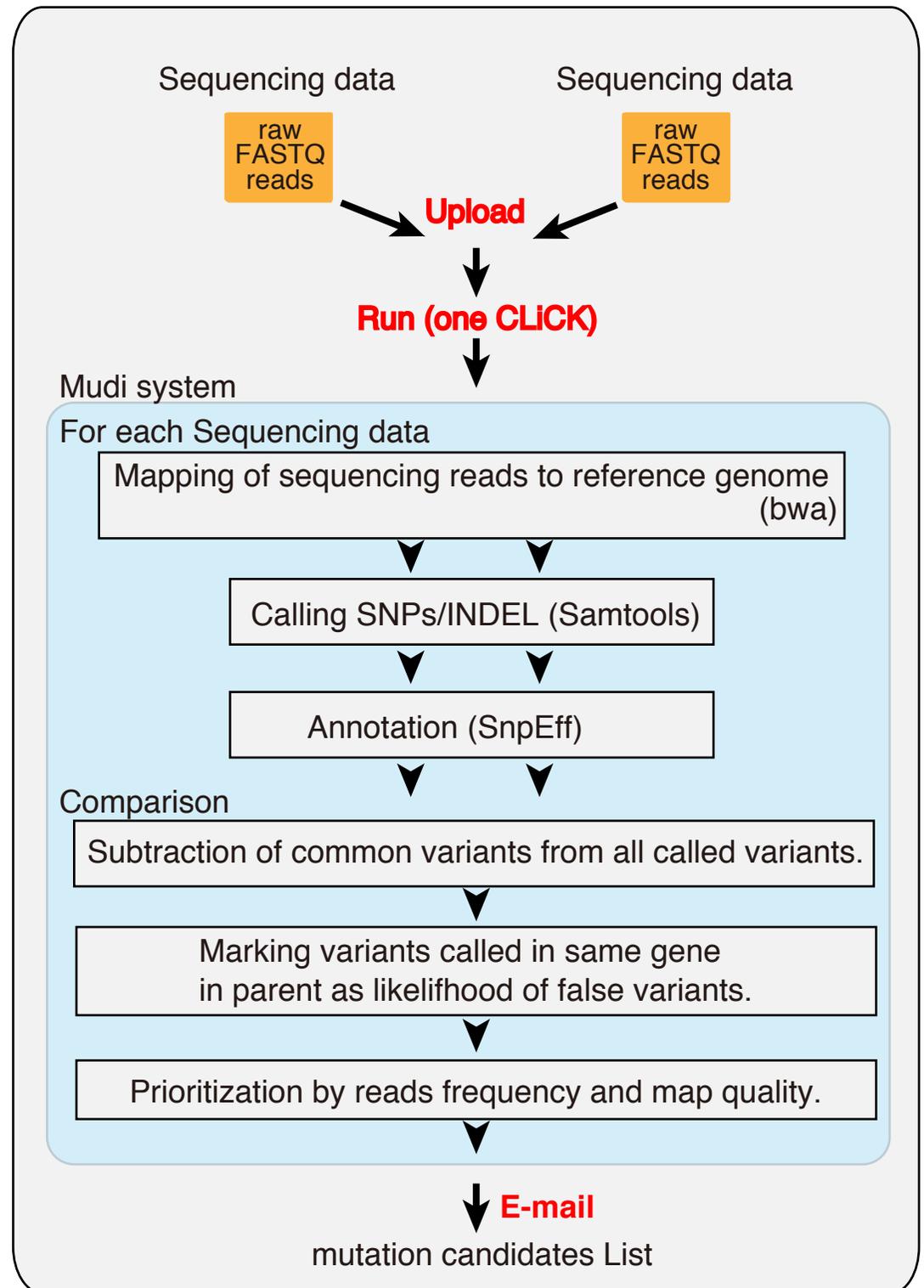
reference:

Birkeland, S.R., Jin, N., Ozdemir, A.C., Lyons, R.H., Weisman, L.S., & Wilson, T.E. (2010). Discovery of Mutations in *Saccharomyces cerevisiae* by Pooled Linkage Analysis and Whole-Genome Sequencing. *Genetics* 186, 1127–1137.



Workflow of the Mudi system

Flowchart illustrating all processes used in Mudi. Mudi accepts two sets of sequencing data, runs all steps sequentially, and outputs a list of candidate mutations within few hours.



bwa <http://bio-bwa.sourceforge.net/>
samtools <http://samtools.sourceforge.net/>
Snpeff <http://snpeff.sourceforge.net/>