

# INTERLABS - IBIS



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## A Simple and Efficient Genome Library Construction Method in Yeast

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**Jeudi, 1 octobre à 12 h 30**

**Pavillon Charles-Eugène-Marchand, salle Hydro-Québec (1210)**

### Summary:

Yeast strains found in natural and industrial environments exhibit diverse characteristics, but the genetic basis of these strain-specific phenotypes remains largely unclear. Genomic library-based screening provides an effective approach to investigating these relationships. We developed TGN, a simple and efficient method that combines Tagmentation, Gap-repair cloning in yeast, and Oxford Nanopore sequencing to construct and evaluate genomic libraries. Using a genomic library from the lager-brewing yeast *Saccharomyces pastorianus* WH34/70, we identified genes that conferred maltose utilization or low-temperature tolerance on *S. cerevisiae* BY4741. We also applied TGN to the fission yeast *Schizosaccharomyces pombe* and identified *nhe1*<sup>+</sup> and *pac2*<sup>+</sup>, which confer high-salt and high-temperature tolerance, respectively. We are currently investigating the mechanism by which the novel candidate gene *pac2*<sup>+</sup> confers high-temperature tolerance.