

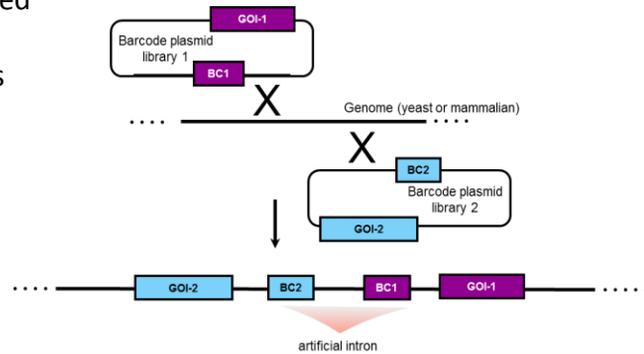
Genomic Combinatorial Screening Platform

Method of creating a double barcode library in order to evaluate genetic or protein interactions simultaneously on a large scale in cell pools

Background

The recent innovation of molecular barcodes has increased High-Throughput Combinatorial Screening (HTCS) efficiency by measuring the relative barcode abundances in pools of barcoded cells. However, large-scale Bar-Seq approaches are not widely used because of several limitations:

- Interaction cannot be evaluated *en masse*
- Libraries must be generated for each DNA element, genotype or combination
- Plasmid Copy number variation results in high rates of false positives and false negatives
- Limited information on the relative strength of interaction between proteins



S. Levy (2015)

Technology

Dr. Sasha Levy has developed a method that allows one to efficiently construct, in any cell type, >10 million combinations of DNA elements, each combination of which is uniquely identified by a double barcode system that resides at a defined genomic location. The double barcode system allows for plasmid libraries to be introduced *en masse* at a single copy in the genomic location and interactions are subsequently assayed simultaneously by pooled growth using next generation sequencing. Because this technology acts as an interaction sequencing platform, it has broad applications in basic research and industry including high-throughput protein or genetic interaction screens, gene deletion and gene identification screening, drug screening, and combinatoric target screening.

Patent number/Publication: Provisional filed on method and kit

Advantages

- **Quantitative information:** changes in interaction strength can be detected
- **Higher Quality Data:** copy noise number is reduced
- **Efficiently create large plasmid /yeast libraries**
- **Libraries can be used repeatedly to assay multiple conditions**

Applications

- **Research tool**
- **Drug Discovery**

Development stage

- **Yeast strains and plasmid libraries**
- **Yeast data, mammalian cells in progress**

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