

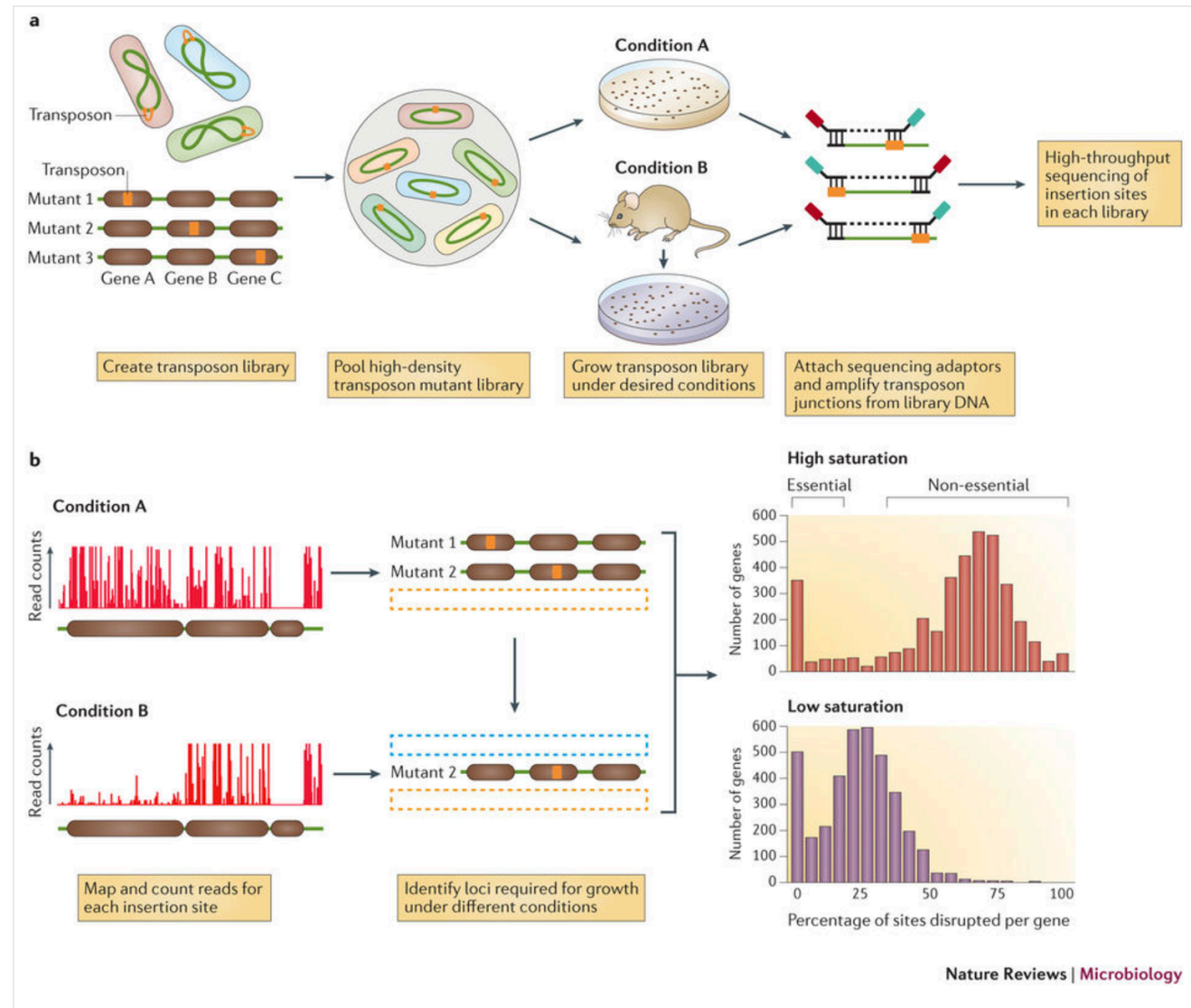
Support for Functional Genomics Data in PATRIC



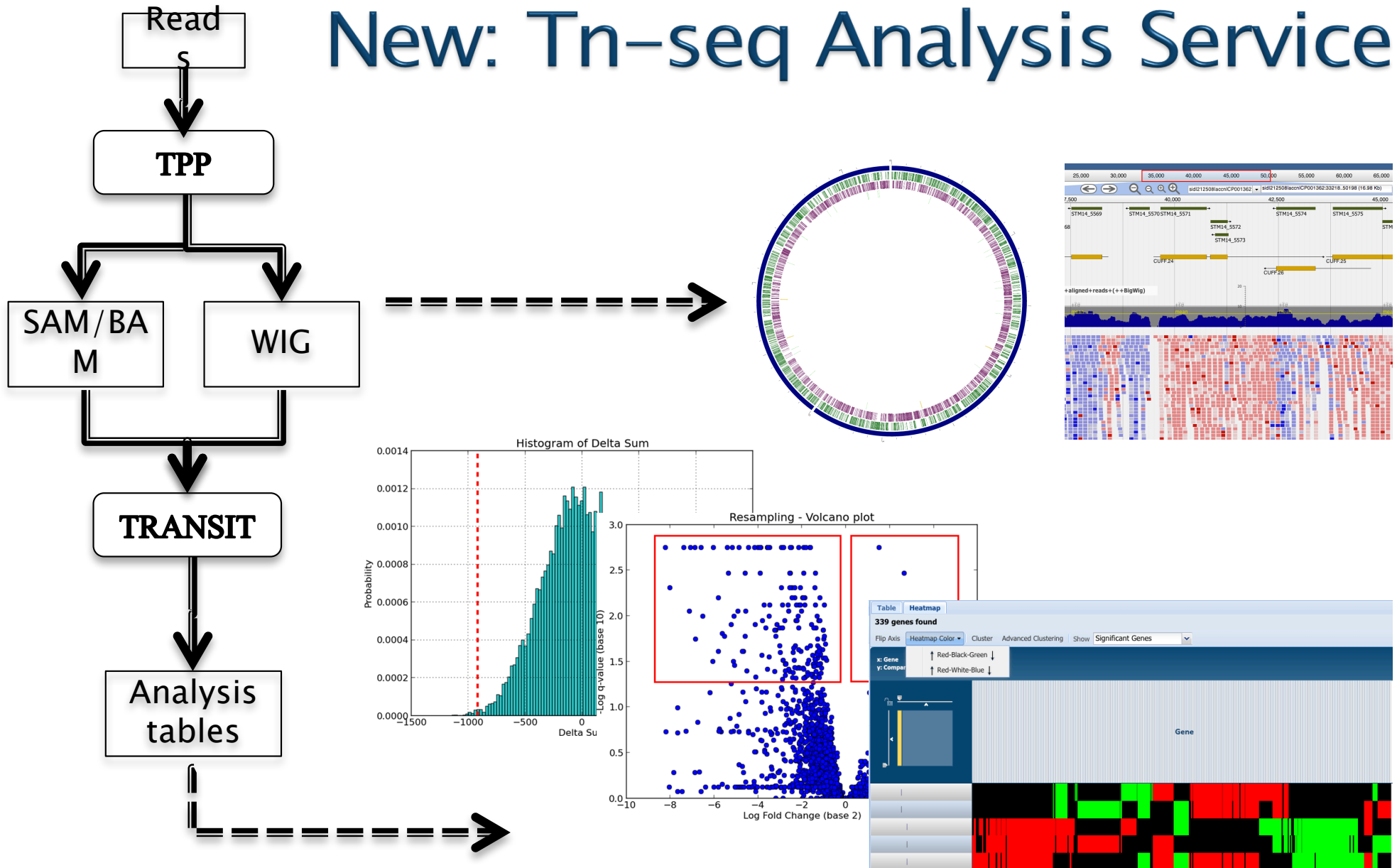
Tn-Seq

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Nature Reviews Microbiology 14, 119–128 (2016) | doi:10.1038/nrmicro.2015.7



New: Tn-seq Analysis Service



M. A. DeJesus, C. Ambadipudi, R. Baker, C. Sasseti, and T. R. Ioerger, "TRANSIT - A Software Tool for Himar1 TnSeq Analysis," *PLOS Comput Biol*, vol. 11, no. 10, p. e1004401, Oct. 2015.

Tn-Seq Analysis Service v1

- ▶ Initial Release, v1: March 2017
- ▶ TRANSIT pipeline (in support of Mariner transposon)
 - Interface support
 - Single growth condition/Gumbel
 - Conditionally essential genes/Resampling
 - Uses PATRIC annotations and genomes
 - Includes call to BWA via TRANSIT TPP module
 - Input: fastq files
 - Output: wig and SAM files, TRANSIT analysis tables

Relative Fitness Analysis

Example: *MTB essential genes identified using Tn-seq [FLUTE]*

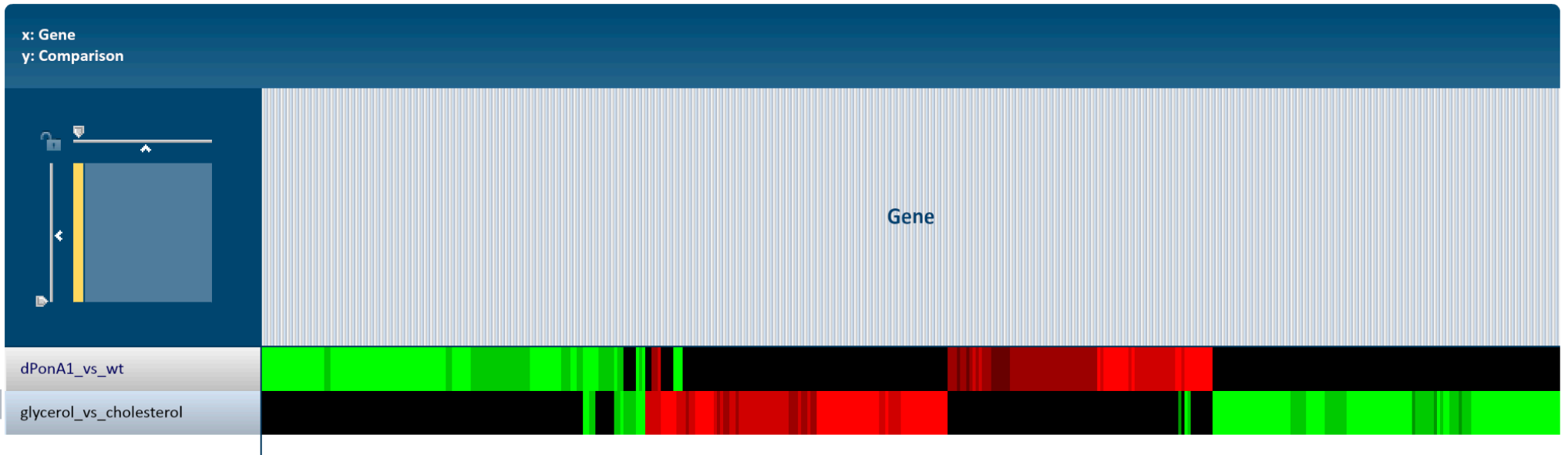
Table Heatmap

Filter By
 ↑ ↓ ↑↓

DOWNLOAD

<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	Title	Strain	<input type="checkbox"/>	Genome	PATRIC ID	Gene Symbol	Product	Comp	Up	Down
<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	dPonA1_vs_wt		<input type="checkbox"/>	Mycobacterium tuberculosis H37Rv	fig 83332.12.peg.97	hycP	Hydrogenase-4 component E	2	1	0
<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	glycerol_vs_cholesterol		<input type="checkbox"/>	Mycobacterium tuberculosis H37Rv	fig 83332.12.peg.772	pqqE	Mycofactocin radical SAM maturase	2	0	2
<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>			<input type="checkbox"/>	Mycobacterium tuberculosis H37Rv	fig 83332.12.peg.773	lldD1	Mycofactocin system heme/flavin dehy	2	0	2
<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>			<input type="checkbox"/>	Mycobacterium tuberculosis H37Rv	fig 83332.12.peg.775		Mycofactocin system glycosyltransfera	2	0	2
<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>			<input type="checkbox"/>	Mycobacterium tuberculosis H37Rv	fig 83332.12.peg.805	rpmD	LSU ribosomal protein L30p (L7e)	2	0	1
<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>			<input type="checkbox"/>	Mycobacterium tuberculosis H37Rv	fig 83332.12.peg.817	mapA	Methionine aminopeptidase (EC 3.4.11.2)	2	1	1

Flip Axis
 Color
 Cluster
 Advanced
 Show



Tn-Seq Analysis v2

- ▶ Expected Release, May 2017
- ▶ Consider BWA to HISAT2 for faster alignment
- ▶ Genome browser and circular browser streaming for alignments
- ▶ Heatmap representation of log fold change Treatment vs Control
- ▶ Control vs. Treatment volcano plots for identification of essentiality and for QC

Functionalizing Lists of Unknown TB Entities (FLUTE)

- ▶ MTB Tn-seq data and conditional essential genes
- ▶ Working on designing Tn-seq data analysis service, storage and visualization solutions
- ▶ Two in vitro H37Rv strains (wildtype and a knockout) two replicates each
- ▶ Wildtype:
 - U19_73_R1.fastq.gz
 - U19_74_R1.fastq.gz
- ▶ Rv1432 Knockout:
 - U19_91_R1.fastq.gz
 - U19_92_R1.fastq.gz

DeJesus, Michael A., Subhalaxmi Nambi, Clare M. Smith, Richard E. Baker, Christopher M. Sasseti, and Thomas R. Ioerger. 2017. "Statistical Analysis of Genetic Interactions in Tn-Seq Data." *Nucleic Acids Research* 45 (11): e93–e93. doi:10.1093/nar/gkx128.