

From sample to fastq

# Outline

- Brief overview of library preparation procedure
- Sequencing costs
- Estimate cost for your own experiment

# Requirements for library preparation protocol

- To prepare libraries for hundreds of samples, we need a protocol that is
  - Cheap
  - Efficient
  - Reliable
- Sometimes robustness to sample degradation is also important

# One example of a library preparation technique



## RESEARCH ARTICLE

### Inexpensive Multiplexed Library Preparation for Megabase-Sized Genomes

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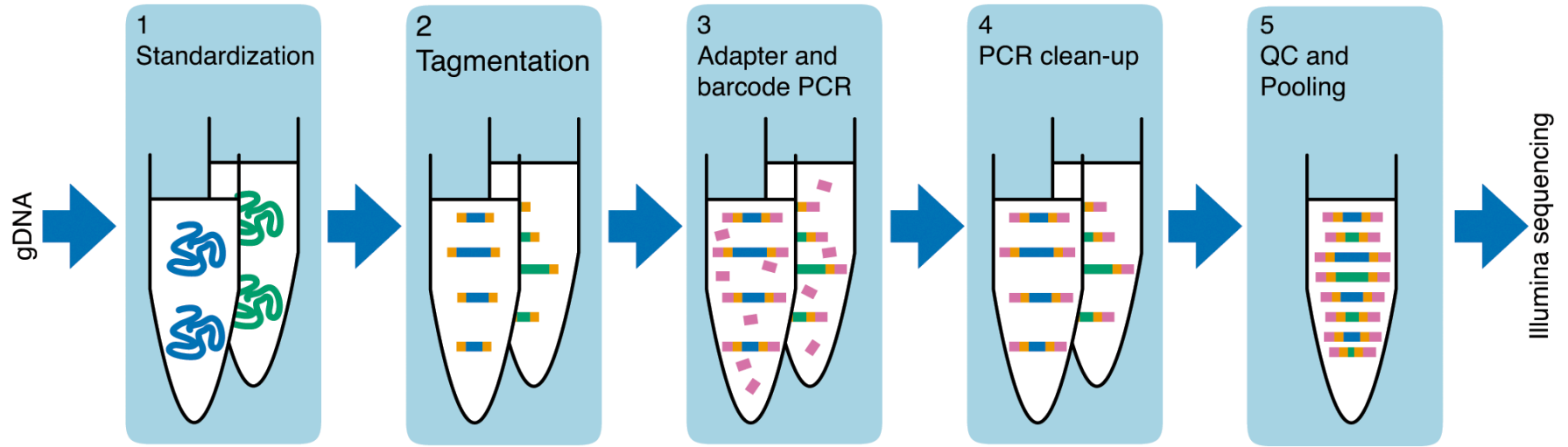
## OPEN ACCESS

**Citation:** Baym M, Kryazhimskiy S, Lieberman TD, Chung H, Desai MM, Kishony R (2015) Inexpensive Multiplexed Library Preparation for Megabase-Sized Genomes. PLoS ONE 10(5): e0128036. doi:10.1371/journal.pone.0128036

## Abstract

Whole-genome sequencing has become an indispensable tool of modern biology. However, the cost of sample preparation relative to the cost of sequencing remains high, especially for small genomes where the former is dominant. Here we present a protocol for rapid and inexpensive preparation of hundreds of multiplexed genomic libraries for Illumina sequencing. By carrying out the Nextera tagmentation reaction in small volumes, replacing costly re-

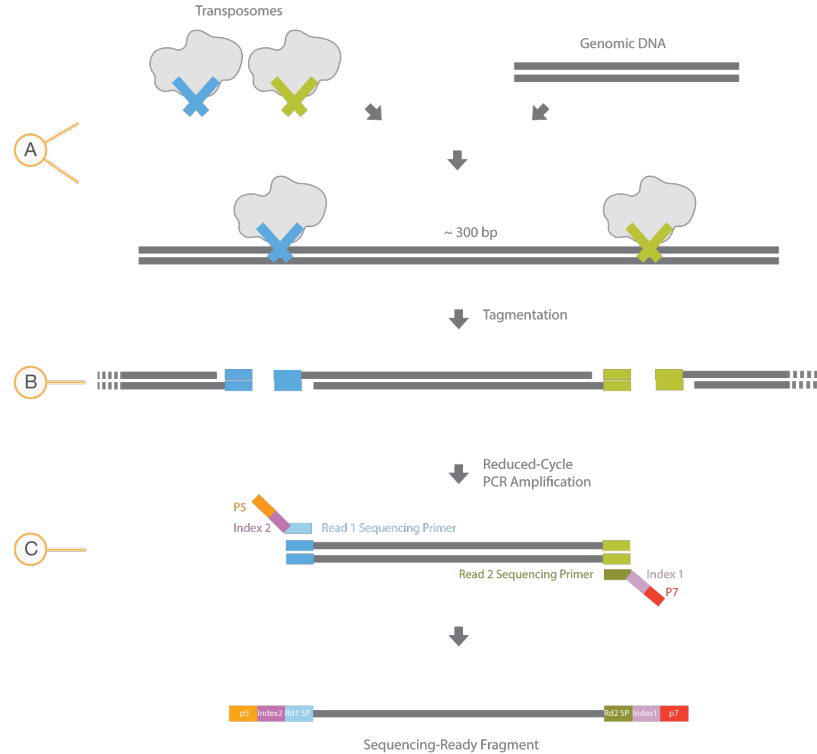
# Library preparation protocol



Transposome with adapters  
combined with template DNA

Tagmentation to fragment  
and add adapters

Limited-cycle PCR to add  
index adapter sequences








## Sequencing-Ready Fragment




### Index 2 Primer



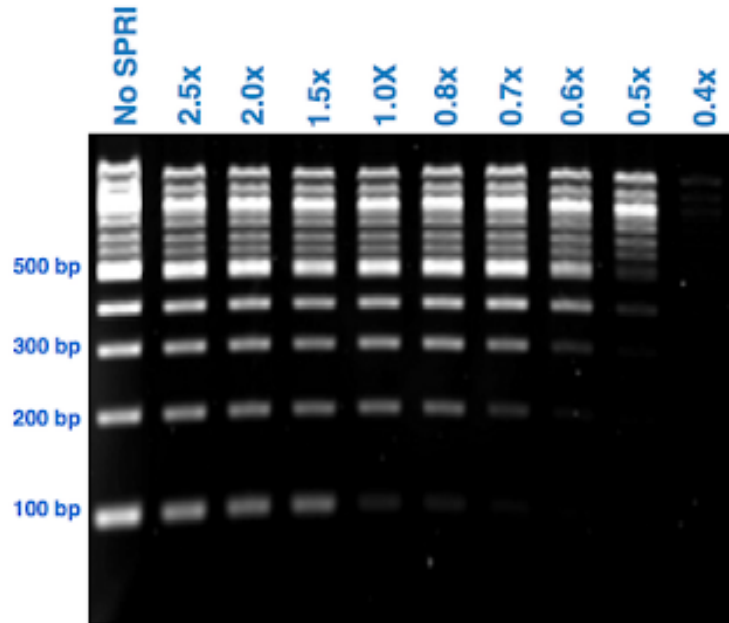
-  P5 – complementary to Illumina flow cell oligo
-  Indexing sequence 2
-  Read 1 Sequencing Primer

### Index 1 Primer



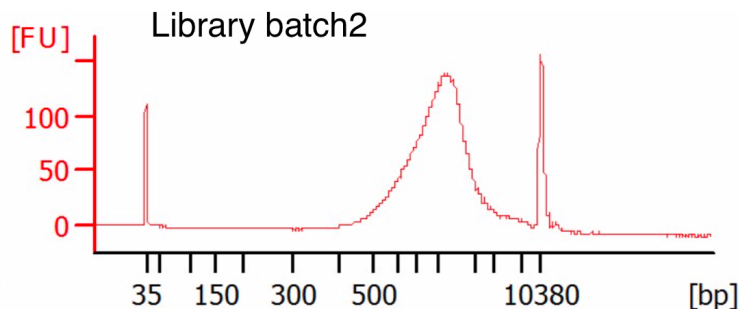
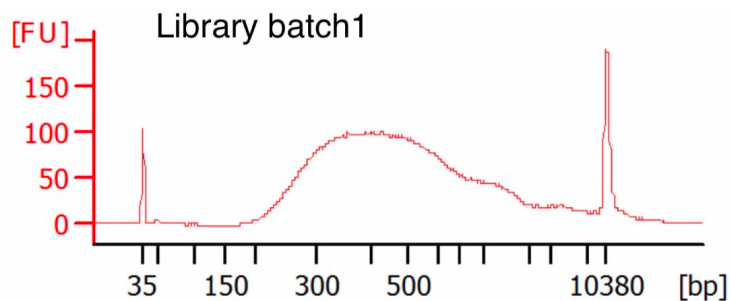
-  Read 2 Sequencing Primer
-  Indexing sequence 1
-  P7 – complementary to Illumina flow cell oligo

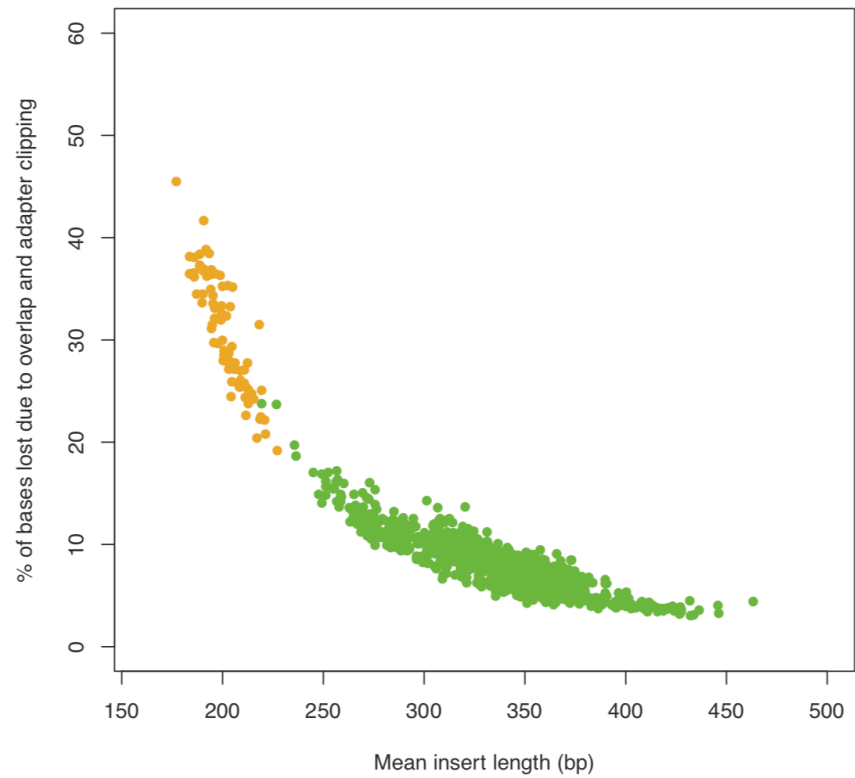
# Size selection with Ampure beads



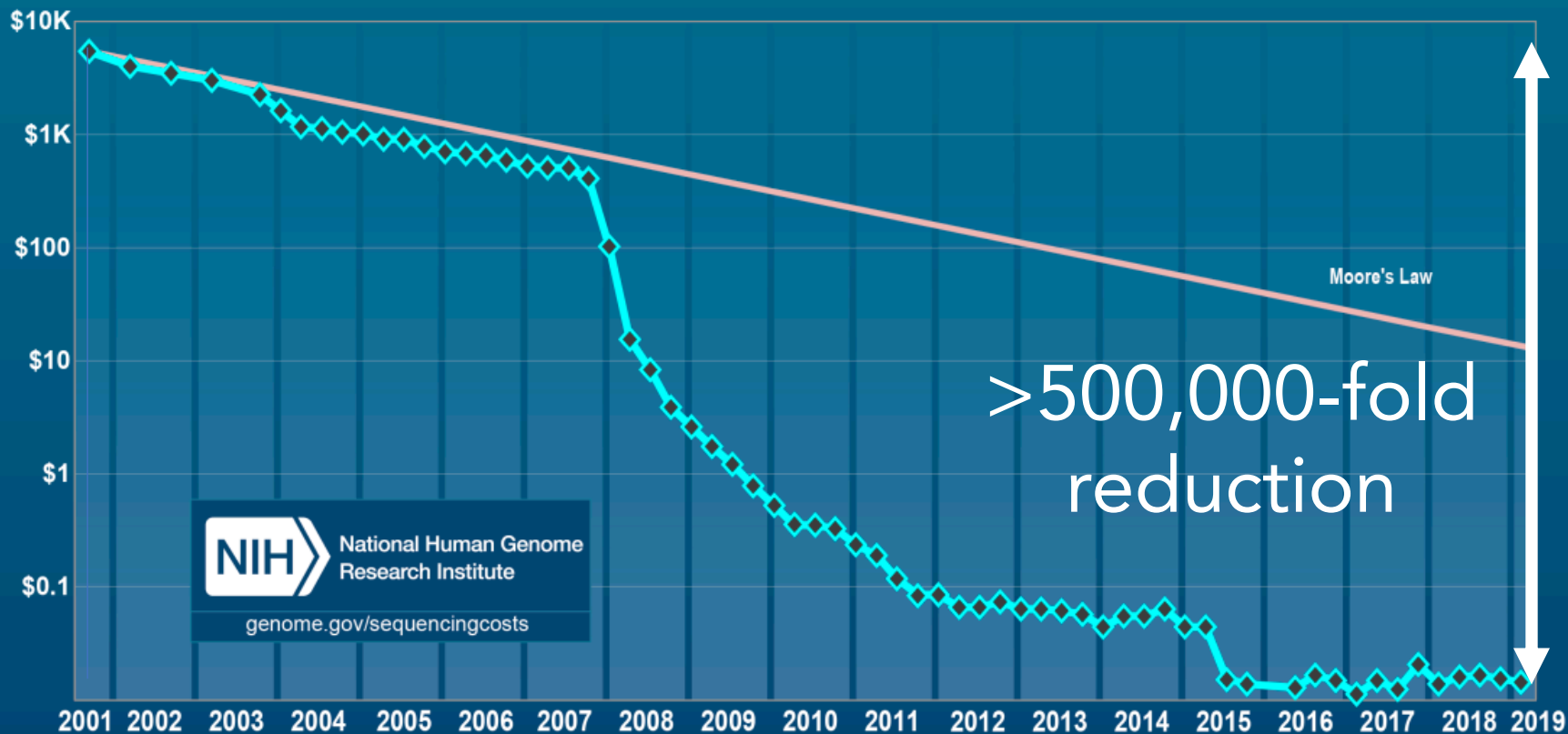


# Two examples of our library pools



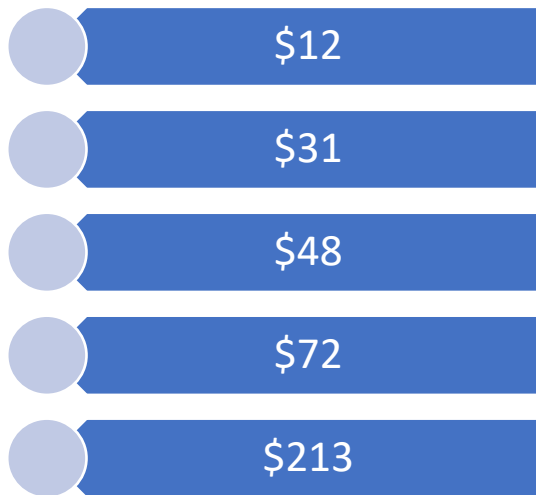


## Cost per Raw Megabase of DNA Sequence



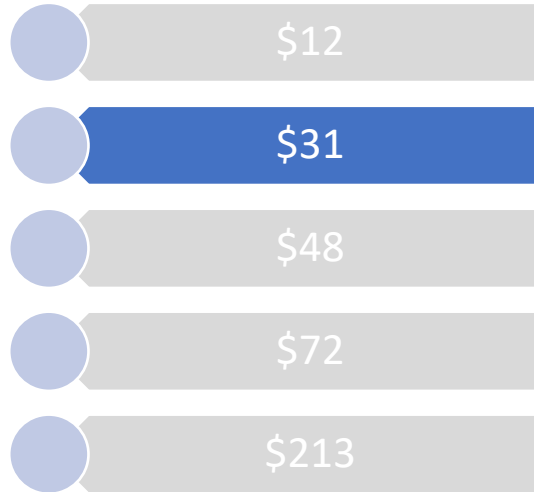
# What is the current price for 2x sequencing of an Atlantic silverside?

Genome size ~650 Mb



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# Example costs for other genome sizes

Library preparation and sequencing to 2x genome coverage\*

Genome size (Mb)	Cost (USD)
500	28
750	34
1,000	40
3,000	87

\*Cost estimates do not include labor and assume that samples are sequenced efficiently on 110 Gb HiSeq X Ten lanes (assumed costs: USD 1,300 per lane and USD 8 per library)

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Library preparation and sequencing to 2x coverage\*

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Compare to:

\$30 per sample for RADseq  
\$15 per sample for RADcapture

Meek and Larson. 2019. Mol Ecol Res

\*Cost estimates do not include labor and assume that samples are sequenced efficiently on 110 Gb HiSeq X Ten lanes (assumed costs: USD 1,300 per lane and USD 8 per library)

# Exercise – how much will your experiment cost?

- Assumed costs:
  - Library preparation: \$8 per sample
  - Sequencing: \$1,300 for 110 Gb
  - Target coverage per sample: Expect to lose at least 30-50% of your data in filtering



# Exercise – how much will your experiment cost?

- Assumed costs:
  - Library preparation: \$8 per sample
  - Sequencing: \$1,300 for 110 Gb
  - Target coverage per sample: Expect to lose at least 30-50% of your data in filtering
- **Example:** I would like to have 1x coverage for downstream analysis for 40 individuals from each of 5 populations (200 individuals total) of my favorite animal with a genome size of ~800 Mb
- **Calculation:** I will target 2x coverage raw sequencing. This means
$$2 * 800 \text{ Mb/individual} * 200 \text{ individuals} = 320,000 \text{ Mb (320 Gb)} \quad [\text{I can fit this in three 110 Gb lanes}]$$
My total cost is thus (3 lanes \* \$1,300 per lane) + 200 libraries \* \$8 per library) = **\$5,500**