

Library preparation

- Fragment (50-bp read, F3): 8 slides
- Mate-pair (2 × 25-bp read, F3-R3): 4 slides, insert size: 600–800 bp (A), 800–1,000 (B)



SOLiD sequencing (csfasta, qual)

- 4.9×10^9 reads in total



Mapping using Bioscope 1.3.1

(Indian rhesus macaque reference)

- 3.4×10^9 mapped reads (69.8%)



Selecting high quality reads (analyzed reads)

- 2.8×10^9 mapped reads (58.0%)
- 99.7% coverage and 41.5-fold average depth*

*On the rhesus macaque genome excluding unmapped Ns



Variation analysis

- 9,653,812 SNVs
- 968,792 small indels (1–11 bp)
- 58,507 large indels (44–732 bp)

Total: 12 slides

