

Direct links to access Cogent™ NGS software example datasets

We appreciate your interest in example data for use with Cogent NGS Analysis Pipeline (CogentAP) and Cogent NGS Discovery Software (CogentDS).
Please use the links below to access your dataset of choice:

Shasta™ total RNA-seq data (raw)
~100,000 PBMCs | single-cell total RNA-seq | raw FASTQ files | 1.2TB
<https://takarabio.files.com/f/7ad763f3ef925470>

Shasta total RNA-seq data (demultiplexed)
100,000 PBMCs | single-cell total RNA-seq | demultiplexed data files | 2 TB
<https://takarabio.files.com/f/8f8c432d0c246226>

Shasta total RNA-seq data (subset)
10,000 PBMC subset at original depths | single-cell total RNA-seq | demultiplexed FASTQ files | 126 GB
<https://takarabio.files.com/f/acdde3138fe9666c>

Shasta whole-genome amplification (WGA) data
1,500 immortalized cancer cells | single-cell DNA-seq | demultiplexed FASTQ files | 418 GB
<https://takarabio.files.com/f/7aa783611a62a3e6>

SMART-Seq® Pro (Shasta mRNA-seq) data
714 PBMCs | single-cell mRNA-seq | demultiplexed FASTQ files | 27 GB
<https://takarabio.files.com/f/d83fb62217044814>

Please contact Technical Support at technical_support@takarabio.com for additional support with installation or usage, or to provide feedback about the product.

Alternatively, you can follow the instructions [here](#) to download datasets via command line.