

# Package ‘AneuFinderData’

December 26, 2024

**Type** Package

**Title** WGSCS Data for Demonstration Purposes

**Version** 1.34.0

**Date** 2016-12

**Author** Aaron Taudt

**Maintainer** Aaron Taudt <aaron.taudt@gmail.com>

**Description** Whole-genome single cell sequencing data for demonstration purposes in the AneuFinder package.

**Depends** R (>= 3.3)

**License** file LICENSE

**biocViews** CopyNumberVariationData, LungCancerData, Homo\_sapiens\_Data, SequencingData

**NeedsCompilation** no

**RoxygenNote** 5.0.1

**git\_url** <https://git.bioconductor.org/packages/AneuFinderData>

**git\_branch** RELEASE\_3\_20

**git\_last\_commit** 4c07ed4

**git\_last\_commit\_date** 2024-10-29

**Repository** Bioconductor 3.20

**Date/Publication** 2024-12-26

## Contents

|                            |          |
|----------------------------|----------|
| BB150803_IV_074 . . . . .  | 2        |
| hg19_diploid . . . . .     | 2        |
| KK150311_VI_07 . . . . .   | 2        |
| metastasis_liver . . . . . | 3        |
| primary_lung . . . . .     | 3        |
| <b>Index</b>               | <b>4</b> |

---

BB150803\_IV\_074

*Example BAM-file*

---

**Description**

A BAM-file for demonstration purposes of the functions in package **AneuFinder**.

**Format**

A BAM file with aligned reads.

**Source**

A single cell from T-cell Acute Lymphoblastic Leukemia in mouse. The file has been downsampled to 20% of the coverage to reduce the file size. For further details see TODO: insert publication (tumor ID T386).

---

hg19\_diploid

*Diploid BAM-file*

---

**Description**

A BAM-file with reads from a diploid human brain cell for demonstration purposes of the functions in package **AneuFinder**.

**Format**

A BED file with aligned reads.

**Source**

A single cell with WGSCS reads of a human brain cell. Unpublished data.

---

KK150311\_VI\_07

*Example BED-file*

---

**Description**

A BED-file for demonstration purposes of the functions in package **AneuFinder**.

**Format**

A BED file with aligned reads.

**Source**

A single cell with Strand-seq reads. Unpublished data.

---

|                  |                                 |
|------------------|---------------------------------|
| metastasis_liver | <i>Liver metastasis results</i> |
|------------------|---------------------------------|

---

**Description**

Liver metastasis results in the form of Hidden Markov Models saved as RData, generated by the **AneuFinder** package.

**Format**

Files with aneuHMM objects.

**Source**

Patient material from a liver metastasis of a 79 year old women. For details see TODO:insert publication.

---

|              |                                    |
|--------------|------------------------------------|
| primary_lung | <i>Primary lung cancer results</i> |
|--------------|------------------------------------|

---

**Description**

Primary lung cancer results in the form of Hidden Markov Models saved as RData, generated by the **AneuFinder** package.

**Format**

Files with aneuHMM objects.

**Source**

Patient material from a primary small cell lung cancer of a 79 year old women. For details see TODO:insert publication.

# Index

bam (BB150803\_IV\_074), [2](#)

BB150803\_IV\_074, [2](#)

bed (KK150311\_VI\_07), [2](#)

diploid (hg19\_diploid), [2](#)

hg19\_diploid, [2](#)

KK150311\_VI\_07, [2](#)

liver (metastasis\_liver), [3](#)

lung (primary\_lung), [3](#)

metastasis (metastasis\_liver), [3](#)

metastasis\_liver, [3](#)

primary (primary\_lung), [3](#)

primary\_lung, [3](#)