

# Package ‘VectraPolarisData’

May 9, 2024

**Title** Vectra Polaris and Vectra 3 multiplex single-cell imaging data

**Version** 1.9.0

**Date** 2022-03-31

**Description** Provides two multiplex imaging datasets collected on Vectra instruments at the University of Colorado Anschutz Medical Campus.  
Data are provided as a Spatial Experiment objects.  
Data is provided in tabular form and has been segmented and phenotyped using Inform software.  
Raw .tiff files are not included.

**URL** <https://github.com/julia-wrobel/VectraPolarisData>

**BugReports** <https://support.bioconductor.org/t/VectraPolarisData>

**biocViews** ExperimentHub, ExperimentData, SpatialData, SingleCellData,  
Homo\_sapiens\_Data, ReproducibleResearch

**Depends** ExperimentHub, SpatialExperiment, utils

**RoxygenNote** 7.1.2

**Suggests** BiocStyle, knitr, rmarkdown, dplyr

**VignetteBuilder** knitr

**Encoding** UTF-8

**License** Artistic-2.0

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

**git\_branch** devel

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### Description

Vectra 3 and Vectra Polaris multiplex imaging datasets, formatted into objects of class `SpatialExperiment`. Datasets may be used for testing of and as examples in packages, for tutorials and workflow demonstrations, or similar purposes.

### Details

The following Vectra multiplex imaging datasets are currently available (see the package vignette for links to details and data dictionaries):

- `HumanLungCancerV3`
- `HumanOvarianCancerVP`

### Value

a `SpatialExperiment` class object with rows corresponding to samples (cells) and columns to features (markers).

### Author(s)

Julia Wrobel

### Examples

```
# retrieve dataset of interest

library(ExperimentHub)
eh <- ExperimentHub()      # initialize hub instance
q <- query(eh, "VectraPolarisData") # retrieve 'VectraPolarisData' records
id <- q$ah_id[1]          # specify dataset ID to load
spe <- eh[[id]]           # load specified dataset
```

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