

# Package ‘PhenotypeLibrary’

August 15, 2022

**Type** Package

**Title** The OHDSI Phenotype library

**Version** 3.1.6

**Date** 2022-08-15

**Author** Gowtham Rao [aut, cre]

**Maintainer** Gowtham Rao <rao@ohdsi.org>

**Description** A repository to store the content of the OHDSI Phenotype library.

**Imports** checkmate,  
readr,  
dplyr,  
rlang,  
stringr,  
tidyr

**Suggests** DatabaseConnector,  
reactable,  
testthat,  
rmarkdown,  
knitr

**License** Apache License

**RoxygenNote** 7.2.0

**Roxygen** list(markdown = TRUE)

**Encoding** UTF-8

**Language** en-US

**VignetteBuilder** knitr

**URL** <https://ohdsi.github.io/PhenotypeLibrary/>, <https://github.com/OHDSI/PhenotypeLibrary>

**BugReports** <https://github.com/OHDSI/PhenotypeLibrary/issues>

## R topics documented:

getPhenotypeLog . . . . .	2
getPICohortDefinitionSet . . . . .	2
listPhenotypes . . . . .	3
updatePhenotypeLog . . . . .	3

<b>Index</b>	<b>4</b>
--------------	----------

---

getPhenotypeLog	<i>Get phenotype log</i>
-----------------	--------------------------

---

**Description**

Get phenotype log

**Usage**

```
getPhenotypeLog(cohortIds = listPhenotypes())$cohortId)
```

**Arguments**

cohortIds            IDs of cohorts to extraction from the library.

**Value**

Returns a table with one row per cohort definitions with log information such as its release cycle. Example, this function gives us insight on when a cohort definition was added/updated/deprecated by the OHDSI PhenotypeLibrary.

A tibble.

**Examples**

```
getPhenotypeLog(cohortIds = c(1, 2))
```

---

getPlCohortDefinitionSet	<i>Get a cohort definition set</i>
--------------------------	------------------------------------

---

**Description**

Get a cohort definition set

**Usage**

```
getPlCohortDefinitionSet(cohortIds)
```

**Arguments**

cohortIds            IDs of cohorts to extraction from the library.

**Value**

A tibble with the cohort ID, name, sql, and JSON for the provided cohort IDs. Can be used by the CohortGenerator package.

**Examples**

```
cohorts <- listPhenotypes()
subsetIds <- cohorts$cohortId[1:3]
getPlCohortDefinitionSet(subsetIds)
```

---

listPhenotypes	<i>List all phenotypes in the library</i>
----------------	---

---

**Description**

List all phenotypes in the library

**Usage**

```
listPhenotypes()
```

**Value**

A tibble with the cohort ID and name.

**Examples**

```
listPhenotypes()
```

---

updatePhenotypeLog	<i>Update phenotype log</i>
--------------------	-----------------------------

---

**Description**

Update phenotype log

**Usage**

```
updatePhenotypeLog(updates)
```

**Arguments**

updates	Data to update to the log. This is usually the output of <code>ROhdsiWebApi::getCohortDefinitionsMetadata(baseUrl)</code>
---------	---

**Value**

Updates Phenotype Log related to added/updated/deprecated of the OHDSI PhenotypeLibrary.  
A tibble.

# Index

`getPhenotypeLog`, [2](#)  
`getPlCohortDefinitionSet`, [2](#)  
`listPhenotypes`, [3](#)  
`updatePhenotypeLog`, [3](#)