

# Package ‘MetaGxPancreas’

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**Type** Package

**Title** Transcriptomic Pancreatic Cancer Datasets

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**Description** A collection of pancreatic Cancer transcriptomic datasets that are part of the MetaGx-Data package compendium.

**License** Artistic-2.0

**Depends** Biobase, stats, lattice, impute, AnnotationHub, ExperimentHub,  
R (>= 3.6.0)

**Imports** SummarizedExperiment

**Suggests** testthat, xtable

**NeedsCompilation** no

**biocViews** ExpressionData, ExperimentHub, CancerData,  
Homo\_sapiens\_Data, ArrayExpress, GEO, NCI, MicroarrayData,  
ExperimentData

**LazyData** yes

**RoxygenNote** 6.1.1

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BADEA

*BADEA Study Pancreatic Cancer Dataset***Description**

An expression set object containing pancreatic cancer data

**Format**

eSet object

**Details**

more details can be found in the experimentData section of the object

**Source**

<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=gse15471>

**References**

Badea et al, Hepatogastroenterology 2008

**Examples**

```
BADEAEset = loadPancreasEsets()$esets$BADEA
experimentData(BADEAEset)
```

---

BALAGURANATH

*BALAGURUNATHAN Study Pancreatic Cancer Dataset*

---

**Description**

An expression set object containing pancreatic cancer data

**Format**

eSet object

**Details**

more details can be found in the experimentData section of the object

**Source**

<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE11838>

**References**

Balagurunathan et al, Mol Cancer Ther 2008

**Examples**

```
BALAGURANATHset = loadPancreasEsets()$esets$BALAGURANATH
experimentData(BALAGURANATHset)
```

---

BAUER

*BAUER Study Pancreatic Cancer Dataset*

---

**Description**

An expression set object containing pancreatic cancer data

**Format**

eSet object

**Details**

more details can be found in the experimentData section of the object

**Source**

<https://www.ebi.ac.uk/arrayexpress/experiments/E-MTAB-1791/>

**References**

Bauer et al, 2016, Gastroenterology

**Examples**

```
BAUERESet = loadPancreasEsets()$esets$BAUER  
experimentData(BAUERESet)
```

---

CHEN

*CHEN Study Pancreatic Cancer Dataset*

---

**Description**

An expression set object containing pancreatic cancer data

**Format**

eSet object

**Details**

more details can be found in the experimentData section of the object

**Source**

<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE57495>

**References**

Chen et al, PLoS One 2015

**Examples**

```
CHENESet = loadPancreasEsets()$esets$CHEN  
experimentData(CHENESet)
```

---

COLLISON

*COLLISON Study Pancreatic Cancer Dataset*

---

**Description**

An expression set object containing pancreatic cancer data

**Format**

eSet object

**Details**

more details can be found in the experimentData section of the object

**Source**

<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE17891>

**References**

Collisson et al., Nat Med 2011

**Examples**

```
COLLISONset = loadPancreasEsets()$esets$COLLISON
experimentData(COLLISONset)
```

---

duplicates	<i>a list containing the names of patients that are believed to be duplicates across datasets</i>
------------	---

---

**Description**

The object is a list where each element is a patient ID that is believed to be a duplicate of a patient in another dataset. Patients are designated as duplicated if they have Spearman correlations greater than or equal to 0.98 with other patient expression profiles

**Format**

A list with 130 elements, each of which is a patient ID.

---

GRUTZMANN	<i>GRUTZMANN Study Pancreatic Cancer Dataset</i>
-----------	--

---

**Description**

An expression set object containing pancreatic cancer data

**Format**

eSet object

**Details**

more details can be found in the experimentData section of the object

**Source**

[https://www.ebi.ac.uk/arrayexpress/experiments/E-MEXP-950/?query=pilarsky&s\\_page=1&s\\_pagesize=50](https://www.ebi.ac.uk/arrayexpress/experiments/E-MEXP-950/?query=pilarsky&s_page=1&s_pagesize=50)

**References**

Grutzmann et al, Neoplasia, 2004

**Examples**

```
GRUTZMANNEset = loadPancreasEsets()$esets$GRUTZMANN
experimentData(GRUTZMANNEset)
```

---

HAIDER

*HAIDER Study Pancreatic Cancer Dataset*

---

**Description**

An expression set object containing pancreatic cancer data

**Format**

eSet object

**Details**

more details can be found in the experimentData section of the object

**Source**

<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE56560>

**References**

haider et al, Genome medicine, 2014

**Examples**

```
HAIDEReset = loadPancreasEsets()$esets$HAIDER  
experimentData(HAIDEReset)
```

---

HAMIDI

*HAMIDI Study Pancreatic Cancer Dataset*

---

**Description**

An expression set object containing pancreatic cancer data

**Format**

eSet object

**Details**

more details can be found in the experimentData section of the object

**Source**

<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE77858>

**References**

NA

**Examples**

```
HAMIDIEset = loadPancreasEsets()$esets$HAMIDI  
experimentData(HAMIDIEset)
```

---

ICGCMICRO

*ICGCMICRO Study Pancreatic Cancer Dataset*

---

**Description**

An expression set object containing pancreatic cancer data

**Format**

eSet object

**Details**

more details can be found in the experimentData section of the object

**Source**

<http://icgc.org/icgc/cgp/68/304/798>

**References**

Nones et al, Int. J. Cancer, 2014

**Examples**

```
ICGCMICROEset = loadPancreasEsets()$esets$ICGCMICRO  
experimentData(ICGCMICROEset)
```

---

ICGCSEQ

*ICGCSEQ Study Pancreatic Cancer Dataset*

---

**Description**

An expression set object containing pancreatic cancer data

**Format**

eSet object

**Details**

more details can be found in the experimentData section of the object

**Source**

<http://icgc.org/icgc/cgp/68/304/798>

**References**

Bailey et al, Nature, 2016

**Examples**

```
ICGCSEQEset = loadPancreasEsets(removeSeqSubset = FALSE)$esets$ICGCSEQ  
experimentData(ICGCSEQEset)
```

---

JANKY

*JANKY Study Pancreatic Cancer Dataset*

---

**Description**

An expression set object containing pancreatic cancer data

**Format**

eSet object

**Details**

more details can be found in the experimentData section of the object

**Source**

<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE62165>

**References**

Janky et al, BMC Cancer 2016

**Examples**

```
JANKYEset = loadPancreasEsets()$esets$JANKY  
experimentData(JANKYEset)
```

---

KIRBY

*KIRBY Study Pancreatic Cancer Dataset*

---

**Description**

An expression set object containing pancreatic cancer data

**Format**

eSet object

**Details**

more details can be found in the experimentData section of the object



**Source**

<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE79670>

**References**

Kirby et al., Mol Oncol 2016

**Examples**

```
KIRBYEset = loadPancreasEsets()$esets$KIRBY
experimentData(KIRBYEset)
```

---

loadPancreasDatasets    *Function to load Pancreatic cancer SummarizedExperiment objects from the Experiment Hub*

---

**Description**

This function returns pancreatic cancer datasets from the hub and a vector of patients from the datasets that are duplicates based on a spearman correlation > 0.98

**Usage**

```
loadPancreasDatasets(removeSeqSubset = TRUE, rescale = FALSE,
  minNumberGenes = 0, minNumberEvents = 0, minSampleSize = 0,
  keepCommonOnly = FALSE, imputeMissing = FALSE,
  removeDuplicates = FALSE)
```

**Arguments**

removeSeqSubset	currently only removes the ICGSSEQ dataset as it contains the same patients as the ICGS microarray dataset (default TRUE, currently just ICGSSEQ)
rescale	apply centering and scaling to the expression sets (default FALSE)
minNumberGenes	an integer specifying to remove expression sets with less genes than this number (default 0)
minNumberEvents	an integer specifying how man survival events must be in the dataset to keep the dataset (default 0)
minSampleSize	an integer specifying the minimum number of patients required in a summarizedExperiment (default 0)
keepCommonOnly	remove entrezIDs not common to all datasets (default FALSE)
imputeMissing	remove patients from datasets with missing expression values
removeDuplicates	remove patients with a Spearman correlation greater than or equal to 0.98 with other patient expression profiles (default TRUE)

**Value**

a list with 2 elements. The First element named summarizedExperiments contains the datasets. The second element named duplicates contains a vector with patient IDs for the duplicate patients (those with Spearman correlation greater than or equal to 0.98 with other patient expression profiles).

**Examples**

```
experimentsAndDups = loadPancreasDatasets()
```

---

loadPancreasEsets	<i>Function to load pancreas cancer expression sets from the Experiment Hub</i>
-------------------	---

---

**Description**

This function returns pancreas cancer datasets from the hub and a vector of patients from the datasets that are most likely duplicates

**Usage**

```
loadPancreasEsets(removeDuplicates = TRUE, quantileCutoff = 0,
  rescale = FALSE, minNumberGenes = 0, minNumberEvents = 0,
  minSampleSize = 0, removeSeqSubset = TRUE, keepCommonOnly = FALSE,
  imputeMissing = FALSE)
```

**Arguments**

removeDuplicates	remove patients with a Spearman correlation greater than or equal to 0.98 with other patient expression profiles (default TRUE)
quantileCutoff	A numeric between 0 and 1 specifying to remove genes with standard deviation below the required quantile (default 0)
rescale	apply centering and scaling to the expression sets (default FALSE)
minNumberGenes	an integer specifying to remove expression sets with less genes than this number (default 0)
minNumberEvents	an integer specifying how man survival events must be in the dataset to keep the dataset (default 0)
minSampleSize	an integer specifying the minimum number of patients required in an eset (default 0)
removeSeqSubset	currently only removes the ICGSSEQ dataset as it contains the same patients as the ICGS microarray dataset (default TRUE, currently just ICGSSEQ)
keepCommonOnly	remove probes not common to all datasets (default FALSE)
imputeMissing	remove patients from datasets with missing expression values

**Value**

a list with 2 elements. The First element named `esets` contains the datasets. The second element named `duplicates` contains a vector with patient IDs for the duplicate patients (those with Spearman correlation greater than or equal to 0.98 with other patient expression profiles).

**Examples**

```
esetsAndDups = loadPancreasEsets()
```

---

LUNARDI

*LUNARDI Study Pancreatic Cancer Dataset*

---

**Description**

An expression set object containing pancreatic cancer data

**Format**

eSet object

**Details**

more details can be found in the `experimentData` section of the object

**Source**

<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE55643>

**References**

Lunardi S et al, 2014, Oncotarget

**Examples**

```
LUNARDIEset = loadPancreasEsets()$esets$LUNARDI  
experimentData(LUNARDIEset)
```

---

OUH

*OUH Study Pancreatic Cancer Dataset*

---

**Description**

An expression set object containing pancreatic cancer data

**Format**

eSet object

**Details**

more details can be found in the experimentData section of the object

**Source**

<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE60980>

**References**

Sandhu et al, Mol Onc, 2015

**Examples**

```
OUHeset = loadPancreasEsets()$esets$OUH
experimentData(OUHeset)
```

---

PCSI

*PCSI Study Pancreatic Cancer Dataset*

---

**Description**

An expression set object containing pancreatic cancer data

**Format**

eSet object

**Details**

more details can be found in the experimentData section of the object

**Source**

URL unavailable (private dataset)

**References**

Notta et al, Nature 2016

**Examples**

```
PCSIeSet = loadPancreasEsets()$esets$PCSI  
experimentData(PCSIeSet)
```

---

PEI

*PEI Study Pancreatic Cancer Dataset*

---

**Description**

An expression set object containing pancreatic cancer data

**Format**

eSet object

**Details**

more details can be found in the experimentData section of the object

**Source**

<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=gse16515>

**References**

Pei et al, Cancer Cell 2009

**Examples**

```
PEIEset = loadPancreasEsets()$esets$PEI  
experimentData(PEIEset)
```

---

TCGA

*TCGA Study Pancreatic Cancer Dataset*

---

**Description**

An expression set object containing pancreatic cancer data

**Format**

eSet object

**Details**

more details can be found in the experimentData section of the object

**Source**

<https://portal.gdc.cancer.gov/projects/TCGA-PAAD>

**References**

TCGA Research Network, Cancer Cell 2017

**Examples**

```
TCGAEset = loadPancreasEsets()$esets$TCGA  
experimentData(TCGAEset)
```

---

UNC

*UNC Study Pancreatic Cancer Dataset*

---

**Description**

An expression set object containing pancreatic cancer data

**Format**

eSet object

**Details**

more details can be found in the experimentData section of the object

**Source**

<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE71729>

**References**

Moffitt et al, Nat Genet 2015

**Examples**

```
UNCset = loadPancreasEsets()$esets$UNC  
experimentData(UNCset)
```

---

WINTER

*WINTER Study Pancreatic Cancer Dataset*

---

**Description**

An expression set object containing pancreatic cancer data

**Format**

eSet object

**Details**

more details can be found in the experimentData section of the object

**Source**

<http://www.ebi.ac.uk/arrayexpress/experiments/E-MEXP-2780/>

**References**

Winter et al, PLoS Comput Biol, 2012

**Examples**

```
WINTEREset = loadPancreasEsets()$esets$WINTER
experimentData(WINTEREset)
```

---

YANG

*YANG Study Pancreatic Cancer Dataset*

---

**Description**

An expression set object containing pancreatic cancer data

**Format**

eSet object

**Details**

more details can be found in the experimentData section of the object

**Source**

<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE62452>

**References**

Yang et al, 2016, Cancer Research

**Examples**

```
YANGset = loadPancreasEsets()$esets$YANG  
experimentData(YANGset)
```

---

ZHANG

*ZHANG Study Pancreatic Cancer Dataset*

---

**Description**

An expression set object containing pancreatic cancer data

**Format**

eSet object

**Details**

more details can be found in the experimentData section of the object

**Source**

<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE28735>

**References**

Zhang et al, PLoS One 2012

**Examples**

```
ZHANGset = loadPancreasEsets()$esets$ZHANG  
experimentData(ZHANGset)
```



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