

# Package ‘PCAWG7’

October 20, 2020

**Title** Repository of data from 'Repertoire of Mutational Signatures in Human Cancer'  
**Version** 0.0.3  
**Description** Contains data from Alexandrov, Kim, Haradhdhala, Huang et al.,  
                  'Repertoire of Mutational Signatures in Human Cancer'. Please see ?PCAWG7.  
**License** GPL-3  
**Language** en-US  
**Encoding** UTF-8  
**LazyData** true  
**Depends** R (>= 3.5),  
**RoxygenNote** 7.1.1

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exposure	<i>PCAWG7 SigProfiler assignments (exposures).</i>
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### Description

PCAWG7 SigProfiler assignments (exposures).

### Usage

exposure

**Format**

A list with the elements:

**PCAWG** A list with the elements:

**SBS96** Strand-agnostic single-base substitutions in trinucleotide context.

**DBS78** Strand-agnostic doublet-base substitutions.

**ID** Strand-agnostic indels. These are signature assignments for the PCAWG platinum genomes.

**TCGA** A list with the elements:

**SBS96** As above.

**ID** As above. These are signature assignments for the TCGA exomes.

**other.genome** A list with the element:

**SBS96** As above. This contains signature assignments for non-TCGA genomes.

**other.exome** A list with the element:

**SBS96** As above. This contains signature assignments for non-TCGA exomes.

**Source**

Files of <https://www.synapse.org/#!/Synapse:syn12009743>, 2019 Oct 09, populated by data-raw/sig.profiler.

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PCAWG.sample.id	<i>Vectors of the PCAWG tumor_wgs_icgc_specimin_ids.</i>
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**Description**

Note that the PCAWG7 spectra catalogs have 2 sample ids that were blacklisted after the mutational signature analysis was underway. The blacklisted samples are SP116419 and SP116883, which are in `PCAWG.sample.id$black`.

**Usage**

`PCAWG.sample.id`

**Format**

A list with the elements:

**white** Whitelisted IDs

**grey** Greylisted IDs

**black** Blacklisted IDs

**Source**

[https://dcc.icgc.org/api/v1/download?fn=/PCAWG/data\\_releases/latest/release\\_may2016.v1.4.with\\_consensus\\_calls.tsv](https://dcc.icgc.org/api/v1/download?fn=/PCAWG/data_releases/latest/release_may2016.v1.4.with_consensus_calls.tsv), 2019 Oct 09

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PCAWG.WGS.DBS	<i>Doublet Base Substitution (SBS) spectra (deprecated).</i>	<i>Use <a href="#">spectra\$PCAWG\$DBS78</a> instead.</i>
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**Description**

Doublet Base Substitution (SBS) spectra (deprecated). Use [spectra\\$PCAWG\\$DBS78](#) instead.

**Usage**

PCAWG.WGS.DBS

**Format**

An object of class `matrix` (inherits from `array`) with 78 rows and 2780 columns.

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PCAWG.WGS.SBS.96	<i>Single Base Substitution (SBS) spectra in trinucleotide context (deprecated).</i>	<i>Use <a href="#">spectra\$PCAWG\$SBS96</a> instead.</i>
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**Description**

Single Base Substitution (SBS) spectra in trinucleotide context (deprecated). Use [spectra\\$PCAWG\\$SBS96](#) instead.

**Usage**

PCAWG.WGS.SBS.96

**Format**

An object of class `matrix` (inherits from `array`) with 96 rows and 2780 columns.

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PCAWG7	<i>PCAWG7: A package of data from 'Repertoire of Mutational Signatures in Human Cancer'</i>
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**Description**

This is a data package with 3 main package variables: [exposure](#), [signature](#), and [spectra](#).

**Details**

There are also PDF plots of the signatures in `data-raw/plots/`.

The reference for the data is

Alexandrov, L.B., Kim, J., Haradhvala, N.J. et al. The repertoire of mutational signatures in human cancer. *Nature* 578, 94-101 (2020). <https://doi.org/10.1038/s41586-020-1943-3>.

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signature	<i>PCAWG7 SigProfiler reference signatures.</i>
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### Description

PCAWG7 SigProfiler reference signatures.

### Usage

signature

### Format

A list with the elements:

**genome** A list with the elements:

**SBS96** Strand-agnostic single-base substitutions in trinucleotide context.

**SBS192** Transcriptionally stranded single-base substitutions in trinucleotide context.

**DBS78** Strand-agnostic doublet-base substitutions.

**ID** Strand-agnostic indels.

**exome** A list with the elements:

**SBS96** As above, for exome count signatures, which look different than genome count signatures, because of differences in trinucleotide frequencies in exomes versus whole genomes.

### Source

Subdirectories of <https://www.synapse.org/#!Synapse:syn12009743>, 2019 Oct 09, populated by data-raw/populate.variable.signature.R.

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spectra	<i>PCAWG7 mutational spectra (catalogs).</i>
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### Description

PCAWG7 mutational spectra (catalogs).

### Usage

spectra

**Format**

A list with the elements:

**SBS96** Deprecated.

**DBS78** Deprecated.

**PCAWG** A list with the elements:

**SBS96** Strand-agnostic single-base substitutions in trinucleotide context.

**SBS192** Single-base substitutions in transcripts based on the sense strand.

**SBS1536** Strand-agnostic single-base substitutions in pentanucleotide context.

**DBS78** Strand-agnostic doublet-base substitutions.

**ID** Strand-agnostic indels.

**TCGA** A list with the same elements as the PCAWG element.

**other.genome** A list with the same elements as the PCAWG element but with ID omitted.

**other.exome** A list with the same elements as the PCAWG element but with ID omitted.

**Source**

Files below <https://www.synapse.org/#!Synapse:syn11801889>, 2019 Oct 09. Populated by data-raw/spectra/load.package.variable.specra.R.

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