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SomInaClust\_results\_brca

*SomInaClust breast cancer results*

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## Description

SomInaClust output example obtained after running `SomInaClust_det` on the `maf_brca` file.

## Usage

`SomInaClust_results_brca`

## Format

A data frame with 15,764 rows and 18 variables, sorted on increasing values of `DG_q`:

**row.names** Gene name

**CDS** Gene CDS length. Given by given by the reference file `ref_v71_CDSlength`

**n\_mut** Total number of mutations

**n\_clust** Number of mutation clusters (i.e. hot spots), as given by the reference file `ref_v71_clusters`

**n\_OG** Number of OG mutations, i.e. missense mutations or in-frame indels

**n\_mut\_in\_clust** Number of OG mutations located on hot spot locations

**min\_clustersize** Minimum number of mutations in a cluster. NA when `define_clustersize` is FALSE

**corr\_factor\_OG** Background mutation rate correction factor that was used for the calculation of OG parameters. Given by given by the reference file `ref_v71_corr`

**n\_TSG\_total** Number of TSG mutations, i.e. nonsense mutations or frameshift indels

**n\_TSG\_nonsense** Number of nonsense mutations

**corr\_factor\_TSG** Background mutation rate correction factor that was used for the calculation of TSG parameters. Given by given by the reference file `ref_v71_corr`

**n\_sil** Number of silent mutations

**OG\_score** OG score

**TSG\_score** TSG score

**OG\_p** OG p-value

**log\_OG\_p** logarithm of OG p-value. To be used to sort data when `OG_p`  $1e-300$

**TSG\_p** TSG p-value

**log\_TSG\_p** logarithm of TSG p-value. To be used to sort data when `TSG_p`  $1e-300$

**DG\_p** Driver gene p-value

**log\_DG\_p** logarithm of driver gene p-value. To be used to sort data when `DG_p`  $1e-300$

**OG\_q** OG q value, after FDR correction of `OG_p`

**TSG\_q** TSG q value, after FDR correction of `TSG_p`

**DG\_q** Driver gene q value, after FDR correction of `DG_p`