`maf_brca`	*Breast cancer maf file*

Description

This maf file was downloaded from the TCGA data portal (v2.5.3). Gene names were converted to approved HGNC symbols and only primary tumour sampels with NCBI build 37 were retained. The file contains mutation information on breast cancer samples as determined by whole exome sequencing.

Usage

```
maf_brca
```

Format

A data frame with 47,114 rows and 55 variables. The main variables used by `SomInaClust` are:

Hugo_Symbol Gene that contains the mutation (e.g. TP53).

Start_Position Lowest numeric position of the mutation on the genomic reference sequence (e.g. 7577094).

Variant_Classification Mutation type (e.g. Missense_Mutation).

Tumor_Sample_Barcode TCGA barcode of the tumor sample (e.g. TCGA-02-0003-01).

c_position_WU CDS nucleotide position of the mutation (e.g. c.844C¿T).

amino_acid_change_WU Amino acid position of the mutation (e.g. p.R282W).

Source

```
https://tcga-data.nci.nih.gov/tcga/tcgaHome2.jsp
```