

# Data Dictionary

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## Loading the Glioblastoma Data

A resampled version of the Glioblastoma dataset used in the main paper is included in the `CAPPMx` package which can be accessed using the following:

```
library(CAPPMx)
data("MDACC_reproduced")
head(MDACC_reproduced)
```

```
##   Surgery Reason Histologic Grade EOR Gender ATRX MGMT CT SOC RT Dose KPS Age
## 1              1              1   1      1   NA    0  0   1    NA   0   0
## 2              1              1   0      0    1    0  0   1     1   0   1
## 3              1              1   0      1   NA    0  0   1     0   0   1
## 4              1              1   1      1    1    0  1   1     1   0   0
## 5              1              1   1      1    1    0  1   1     1   0   0
## 6              1              1   0      1   NA    0  1   1     1   0   1
##   endpts surv_inds
## 1 30.71429    FALSE
## 2 78.00000    FALSE
## 3 10.56548     TRUE
## 4 64.70833    FALSE
## 5 44.85119    FALSE
## 6 47.42857    FALSE
```

The above scripts load a `data.table` named `MDACC_reproduced` in the environment. Details on the variables included in `MDACC_reproduced` can be found using

```
?CAPPMx::MDACC_reproduced
```