

# Available Expression data of TCGA OV

**This is for survival analysis of OV data from TCGA.**

Date: 04/14/2015

587 patients in total.

## 1. Berkeley Lab Affy Human Exon 1.0 v2:

```
file = "lbl.gov_OV.HuEx-1_0-st-v2.sdrf.txt"
tbl = GetTCGATable(file)
sample = unique(substr(tbl$Comment..TCGA.Barcode., 1, 15))
patient = unique(substr(sample[substr(sample, 14, 15)=="01"], 1, 12))
length(patient)
```

```
## [1] 571
```

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## 2. Broad Affy HG-U133A:

```
file = "broad.mit.edu_OV.HT_HG-U133A.sdrf.txt"
tbl = GetTCGATable(file)
sample = unique(substr(tbl$Comment..TCGA.Barcode., 1, 15))
patient = unique(substr(sample[substr(sample, 14, 15)=="01"], 1, 12))
length(patient)
```

```
## [1] 570
```

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## 3. UNC Aiglent G4502A\_07.2:

```
file = "unc.edu_OV.AgilentG4502A_07_2.sdrf.txt"
tbl = GetTCGATable(file)
sample = unique(substr(tbl$Comment..TCGA.Barcode., 1, 15))
patient = unique(substr(sample[substr(sample, 14, 15)=="01"], 1, 12))
length(patient)
```

```
## [1] 31
```

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#### 4. UNC Aiglent G4502A\_07.3:

```
file = "unc.edu_OV.AgilentG4502A_07_3.sdrf.txt"
tbl = GetTCGATable(file)
sample = unique(substr(tbl$Comment..TCGA.Barcode., 1, 15))
patient = unique(substr(sample[substr(sample, 14, 15)=="01"], 1, 12))
length(patient)
```

```
## [1] 543
```

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#### 5. Harvard RNA-Seq DGE:

```
file = "hms.harvard.edu_OV.IlluminaGA_mRNA_DGE.sdrf.txt"
tbl = GetTCGATable(file)
sample = unique(substr(tbl$Comment..TCGA.Barcode., 1, 15))
patient = unique(substr(sample[substr(sample, 14, 15)=="01"], 1, 12))
length(patient)
```

```
## [1] 31
```

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#### 6. UNC RNA-SeqV2:

```
file = "unc.edu_OV.IlluminaHiSeq_RNASeqV2.1.1.0.sdrf.txt"
tbl = GetTCGATable(file)
sample = unique(substr(tbl$Comment..TCGA.Barcode., 1, 15))
patient = unique(substr(sample[substr(sample, 14, 15)=="01"], 1, 12))
length(patient)
```

```
## [1] 262
```

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#### 7. BC RNA-Seq:

```
file = "bcgsc.ca_OV.IlluminaHiSeq_RNASeq.sdrf.txt"
tbl = GetTCGATable(file)
sample = unique(substr(tbl$Comment..TCGA.Barcode., 1, 15))
patient = unique(substr(sample[substr(sample, 14, 15)=="01"], 1, 12))
length(patient)
```

```
## [1] 422
```