

TCGA LGG [IDHwt/MGMGunmeth] Survival data

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TCGA LGG Survival data for G2/G3 patients with IDHwt and unmethylated MGMT promoter

Survival data for LGG IDHwt and unmethylated MGMT promoter (1 = dead)

```
# select IDs of patients fitting criteria
s1 <- rownames(lgg_annotatons[which(lgg_annotatons$MGMT.promoter.status ==
  "Unmethylated" & lgg_annotatons$IDH.status == "WT"), ])
table(lgg_annotatons[s1, ]$Vital.status..1.dead., useNA = "always")
```

```
##
##      0      1 <NA>
##    35     20      6
```

Prepare data for survival curve:

```
tab1 <- data.frame(vital_status = lgg_annotatons[s1, "Vital.status..1.dead."],
  survival_months = lgg_annotatons[s1, "Survival..months."])
rownames(tab1) <- s1
print(tab1)
```

```
##          vital_status survival_months
## TCGA-CS-5395          1      20.9942811
## TCGA-DH-5140          1      19.9429243
## TCGA-HT-8015          0       0.0985647
## TCGA-HT-A5RA          0      14.6861403
## TCGA-HT-A5RC          1       5.3224938
## TCGA-P5-A5F6          0       1.2813411
## TCGA-DB-A640          0      18.8258577
## TCGA-HT-A617          0      16.1317559
## TCGA-HT-A61C          0       3.3840547
## TCGA-QH-A6CS          0       4.1725723
## TCGA-QH-A6CV          0       2.9569410
## TCGA-DB-A75P          0       3.8111684
## TCGA-HT-A74H          0       2.4312626
## TCGA-QH-A6CX          0      -0.0328549
## TCGA-DU-A76K          1      11.4006503
## TCGA-DU-A7TB          0      42.2842563
## TCGA-S9-A6WM          0       9.2979367
## TCGA-DU-A7TD          1       7.4909172
## TCGA-E1-A7YD         NA           NA
## TCGA-E1-A7YJ         NA           NA
## TCGA-E1-A7YL         NA           NA
## TCGA-E1-A7YM         NA           NA
## TCGA-E1-A7YQ         NA           NA
## TCGA-E1-A7Z2         NA           NA
```

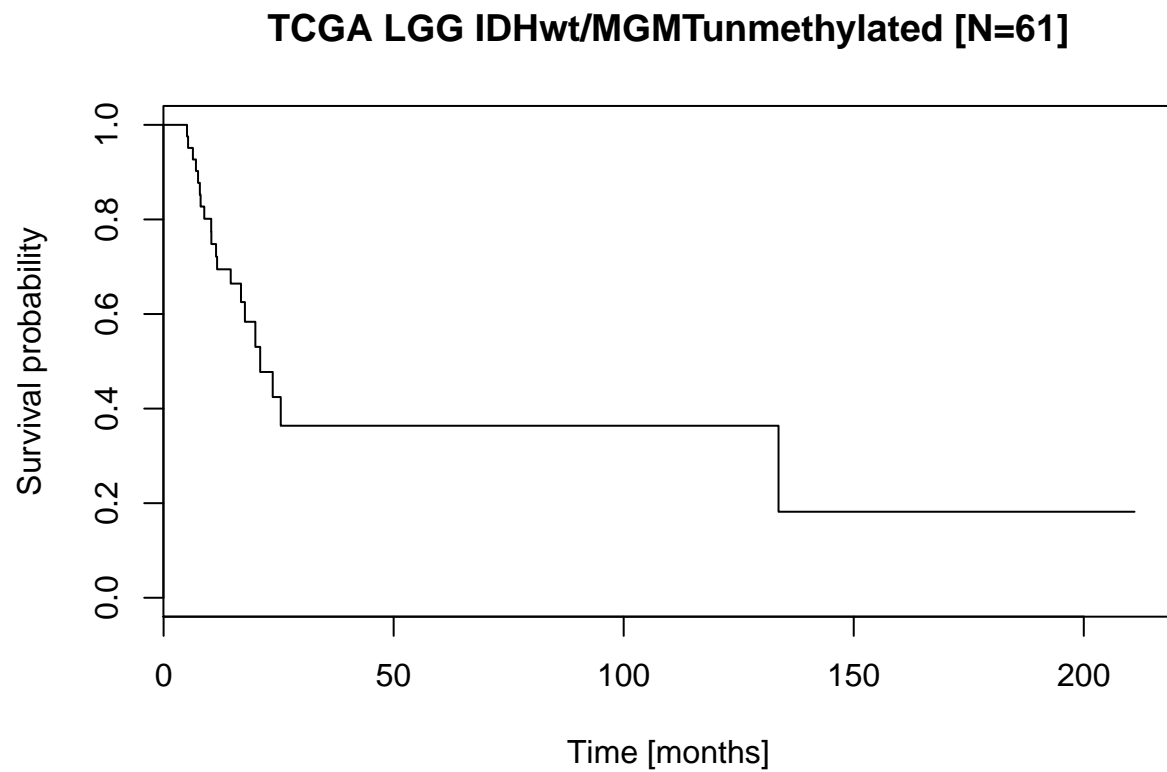
## TCGA-S9-A7IX	0	19.6143753
## TCGA-S9-A7R2	1	10.3821484
## TCGA-TM-A84B	0	11.9920385
## TCGA-TM-A84C	0	15.0803991
## TCGA-TM-A84J	0	17.4788068
## TCGA-VM-A8C9	0	30.0622335
## TCGA-VM-A8CD	1	7.8851760
## TCGA-VW-A8FI	1	8.0494505
## TCGA-DU-5854	0	8.4437093
## TCGA-DU-6392	0	211.0270227
## TCGA-DU-6402	1	7.0309486
## TCGA-DU-6403	1	11.6306346
## TCGA-DU-6404	1	133.6537332
## TCGA-DU-6406	1	16.8217088
## TCGA-FG-5963	1	25.4625475
## TCGA-CS-5397	1	6.3738506
## TCGA-CS-6188	0	23.8198025
## TCGA-CS-6669	0	7.3923525
## TCGA-CS-6186	1	17.6759362
## TCGA-DU-7013	1	8.8379681
## TCGA-DU-7290	1	10.3492935
## TCGA-DU-8158	1	5.0925095
## TCGA-DU-8161	1	23.7212378
## TCGA-DU-8162	1	14.5875756
## TCGA-DU-8165	0	19.1215518
## TCGA-FG-8181	0	12.9448306
## TCGA-HT-7680	0	0.7556627
## TCGA-HT-7691	0	0.0985647
## TCGA-HT-7854	0	39.4587349
## TCGA-HT-7857	0	0.2299843
## TCGA-HT-8011	0	16.2303206
## TCGA-HT-8019	0	32.9863196
## TCGA-HT-8104	0	12.2220228
## TCGA-HT-8558	0	1.7084548
## TCGA-HT-8564	0	15.7046422
## TCGA-HT-A4DS	0	0.2299843
## TCGA-P5-A5EY	0	2.3655528

```
SurvObj <- with(tab1, Surv(survival_months, vital_status))
surv <- survfit(SurvObj ~ 1, conf.type = "none")
summary(surv)
```

```
## Call: survfit(formula = SurvObj ~ 1, conf.type = "none")
##
## 6 observations deleted due to missingness
##      time n.risk n.event survival std.err
##      5.09   41     1    0.976  0.0241
##      5.32   40     1    0.951  0.0336
##      6.37   39     1    0.927  0.0407
##      7.03   38     1    0.902  0.0463
##      7.49   36     1    0.877  0.0514
##      7.89   35     1    0.852  0.0557
##      8.05   34     1    0.827  0.0594
##      8.84   32     1    0.801  0.0629
```

##	10.35	30	1	0.775	0.0663
##	10.38	29	1	0.748	0.0692
##	11.40	28	1	0.721	0.0717
##	11.63	27	1	0.695	0.0738
##	14.59	23	1	0.664	0.0765
##	16.82	17	1	0.625	0.0814
##	17.68	15	1	0.584	0.0860
##	19.94	11	1	0.531	0.0931
##	20.99	10	1	0.477	0.0978
##	23.72	9	1	0.424	0.1003
##	25.46	7	1	0.364	0.1026
##	133.65	2	1	0.182	0.1385

Kaplan-Meier plot



Note that the `echo = FALSE` parameter was added to the code chunk to prevent printing of the R code that generated the plot.