

“NSAIDs modulate clonal evolution in Barrett’s
esophagus”
Using *BEClonalEvolutionNSAID* for reproducing
results

Rumen Kostadinov

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1 Figure 3

```
> library("BEClonalEvolutionNSAID")
```

```
> con = connectDb(dbname = "sbep")
```

```
[1] "Patient 126"  
[1] "Patient 294"  
[1] "Patient 297"  
[1] "Patient 315"  
[1] "Patient 360"  
[1] "Patient 388"  
[1] "Patient 437"  
[1] "Patient 555"  
[1] "Patient 638"  
[1] "Patient 652"  
[1] "Patient 662"  
[1] "Patient 672"  
[1] "Patient 791"  
[1] 0.2787203  
[1] 0.03782836  
[1] 0.002839879  
[1] 0.09362534  
[1] 0.09171611  
[1] 0.01715497  
[1] 0.1899201
```

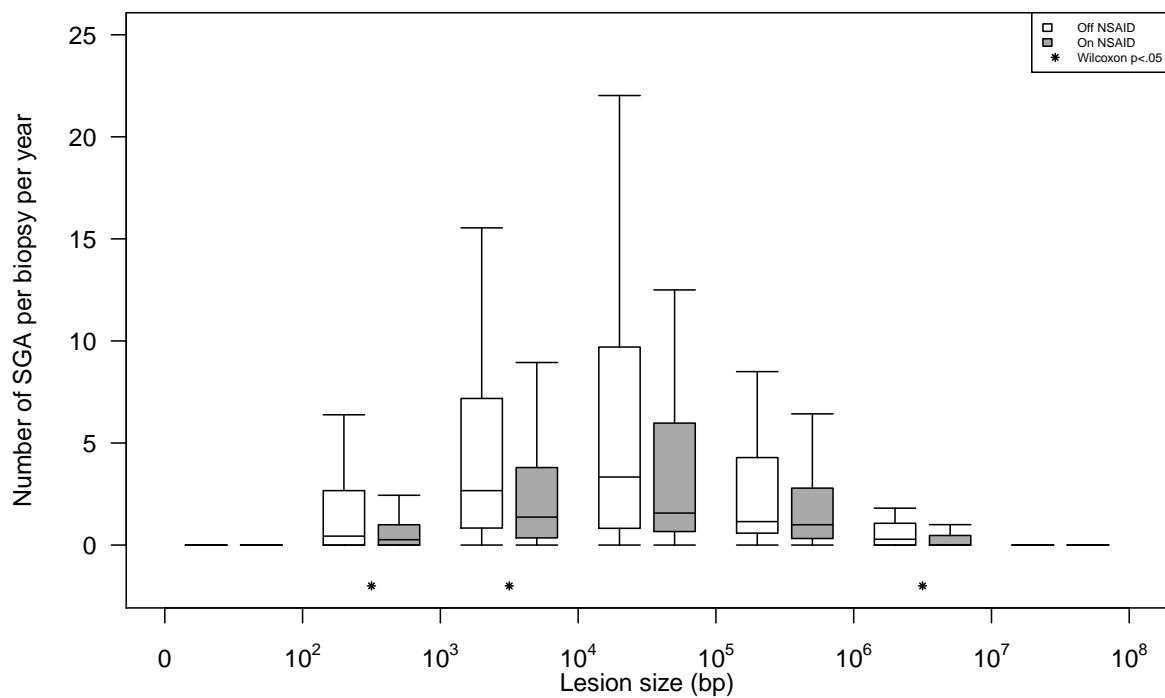


Figure 1: Number of newly acquired SGA events

```
[1] "Patient 126"
[1] "Patient 294"
[1] "Patient 297"
[1] "Patient 315"
[1] "Patient 360"
[1] "Patient 388"
[1] "Patient 437"
[1] "Patient 555"
[1] "Patient 638"
[1] "Patient 652"
[1] "Patient 662"
[1] "Patient 672"
[1] "Patient 791"
[1] 0.0001247999
[1] 0.005664292
[1] 0.000588388
[1] 1.319588e-06
[1] 4.818289e-05
[1] 0.009581463
```

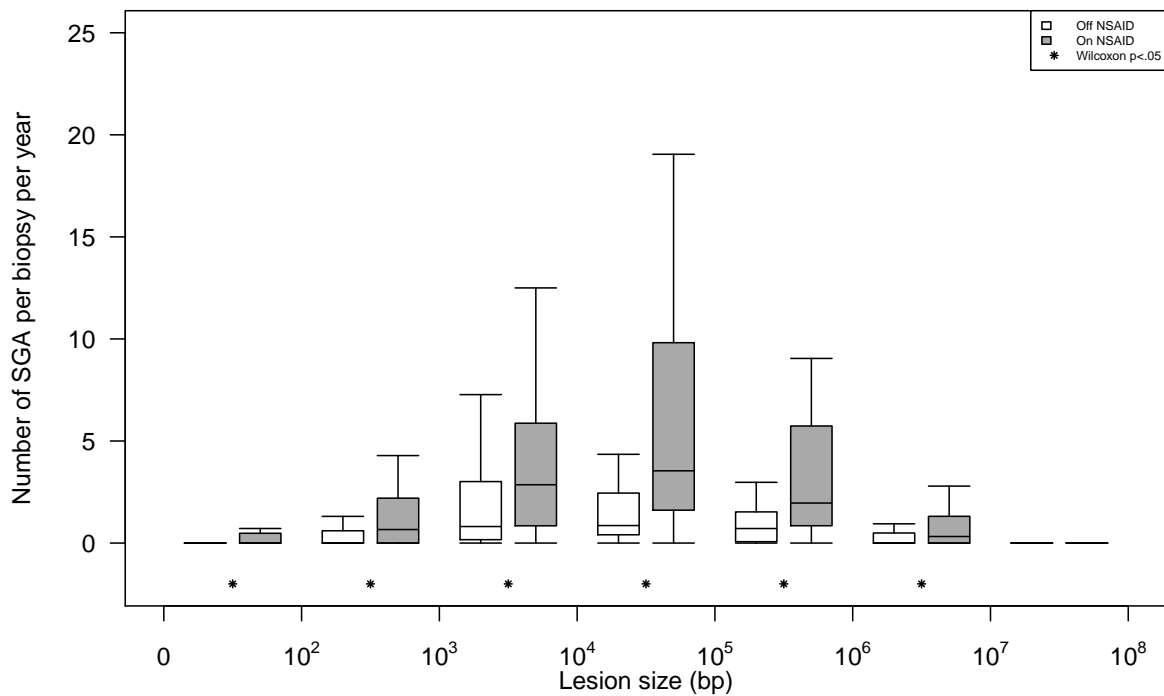


Figure 2: Number of regressing SGA events

[1] 0.3642115

2 System information

This analysis was carried out on a linux machine with 12GB of RAM using the following packages:

```
> sessionInfo()
```

R version 2.12.1 (2010-12-16)

Platform: i686-pc-linux-gnu (32-bit)

locale:

```
[1] LC_CTYPE=en_US.UTF-8      LC_NUMERIC=C
[3] LC_TIME=en_US.UTF-8       LC_COLLATE=en_US.UTF-8
[5] LC_MONETARY=C             LC_MESSAGES=en_US.UTF-8
[7] LC_PAPER=en_US.UTF-8      LC_NAME=C
[9] LC_ADDRESS=C              LC_TELEPHONE=C
[11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C
```

attached base packages:

```
[1] stats      graphics  grDevices  utils      datasets  methods
[7] base
```

other attached packages:

```
[1] Cairo_1.5-0      RMySQL_0.7-5
[3] DBI_0.2-5         BEClonalEvolutionNSAID_1.0.0
```