

# HMM\_Summary

Xiang Ji

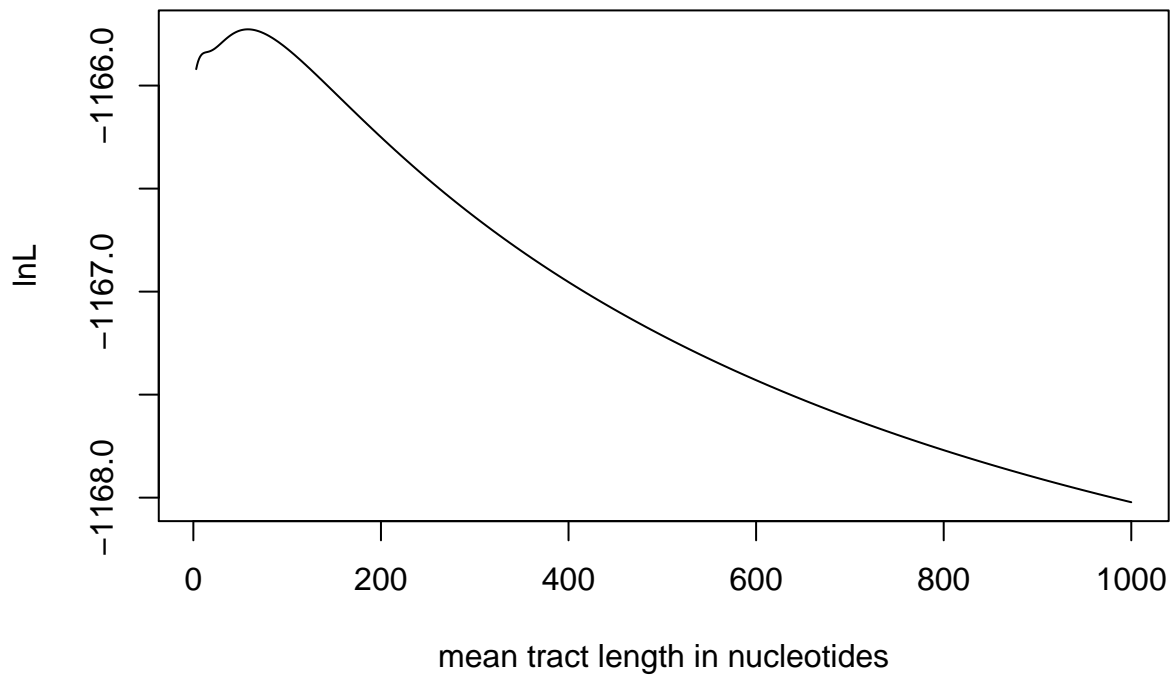
8/29/2017

This R markdown file summarizes the MG94+IS-IGC+HMM analysis results.

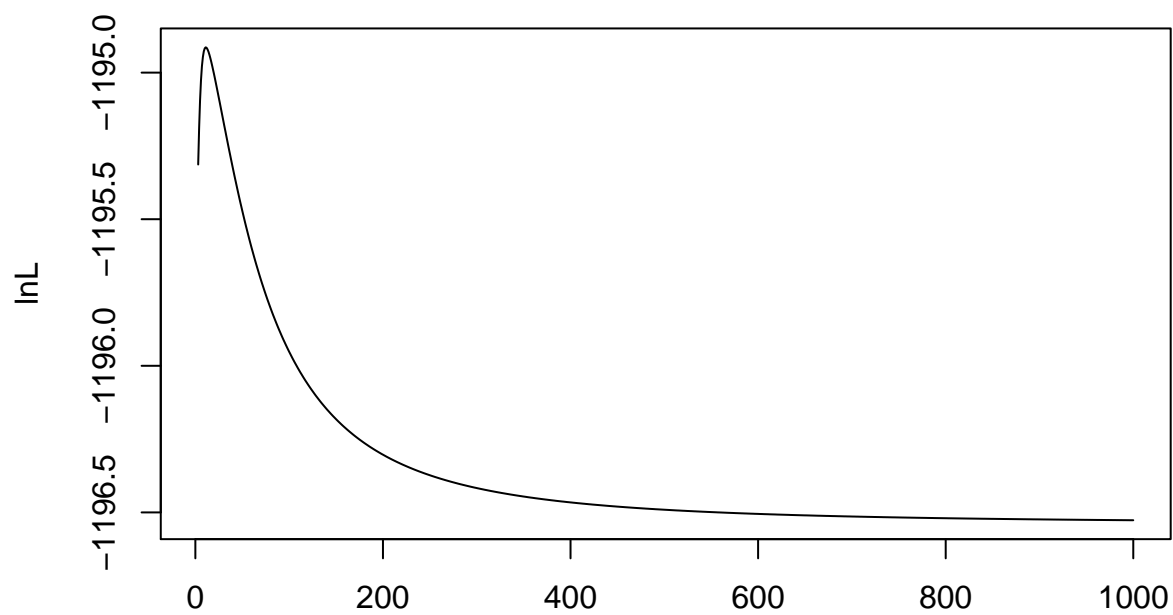
```
rm(list=ls()) # clean up workspace
setwd("/Users/xji3/GitFolders/YeastIGCTract/HMMAnalyses/")
filtered.pairs <- readLines('./Filtered_pairs.txt')

tract.length.list <- 3:1000
# Now plot individual lnL surface along mean tract length of each gene pair
# all other parameters are fixed at MLE
for (pair in filtered.pairs){
  plot.file.name <- paste("HMM", pair, "lnL_1D_surface.txt", sep = "_")
  plot_file <- paste("./plot/", plot.file.name, sep = "")
  summary_mat <- read.table(plot_file)
  assign(paste(pair, "lnL_1D_surface", sep = "_"), summary_mat)
  plot(tract.length.list, summary_mat[, 2], type = "l",
       main = paste(pair, "lnL_surface", sep = "_"),
       xlab = "mean tract length in nucleotides",
       ylab = "lnL")
}
```

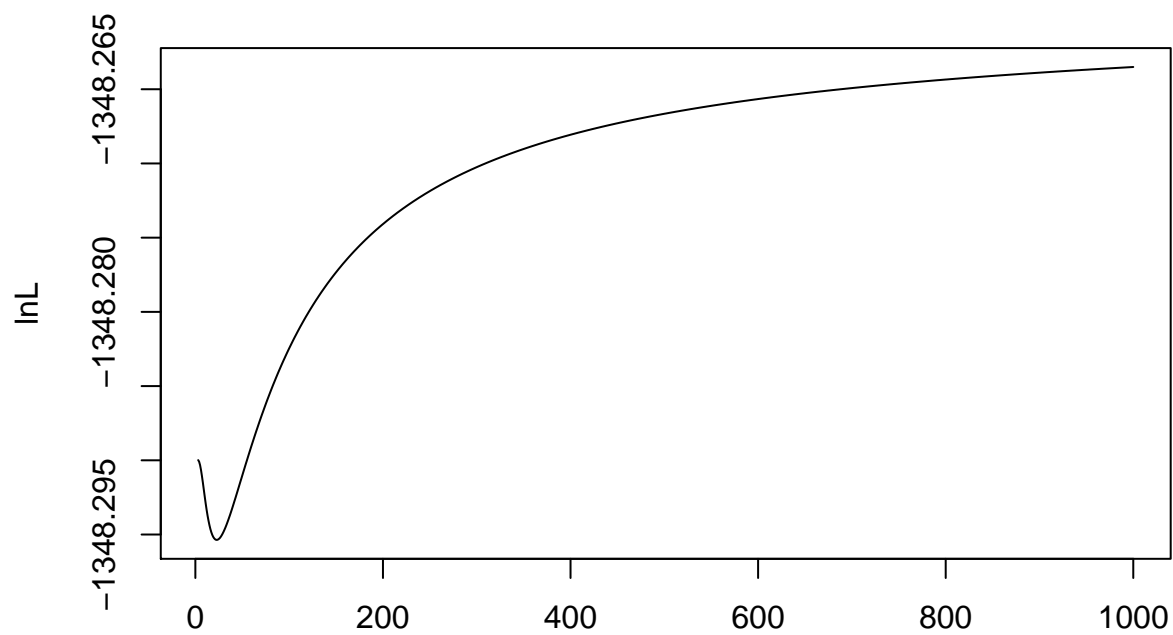
## YLR406C\_YDL075W\_lnL\_surface



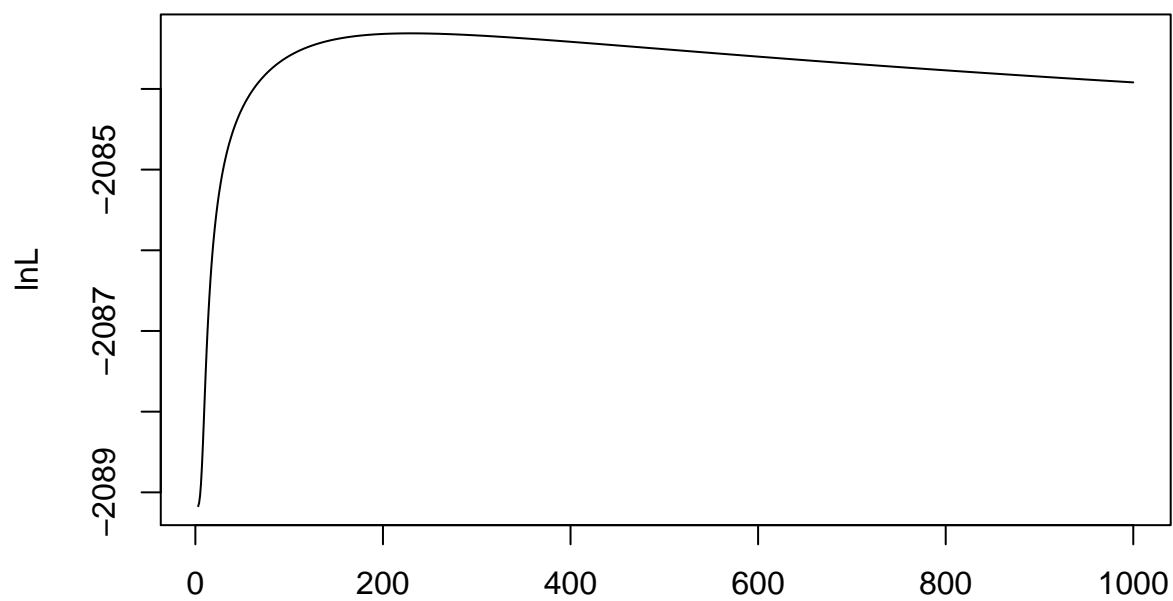
**YER131W\_YGL189C\_InL\_surface**



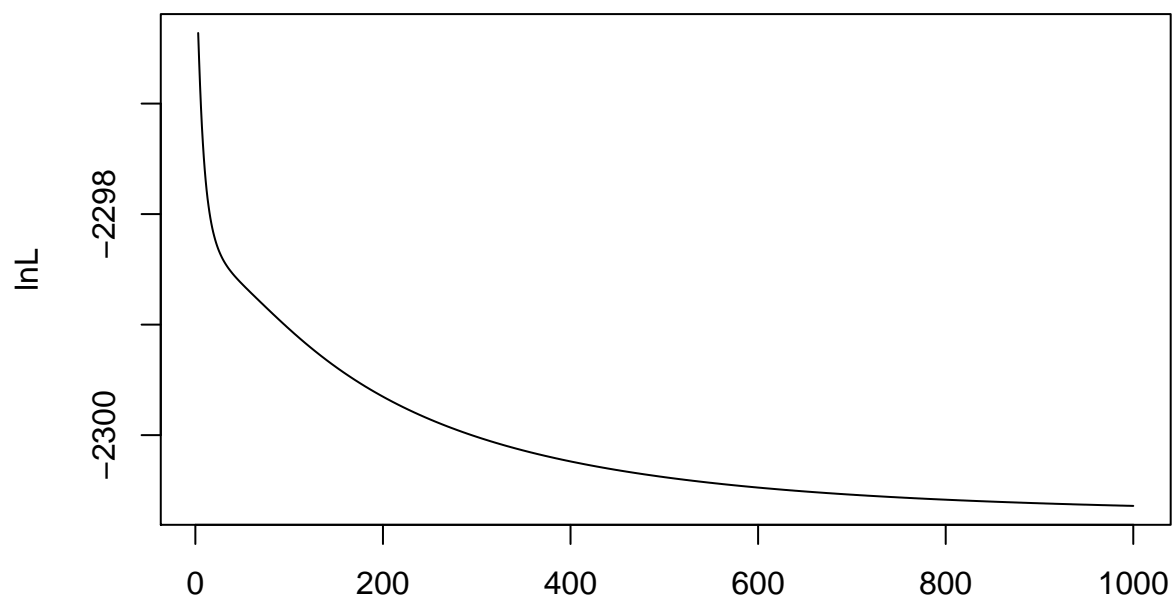
mean tract length in nucleotides  
**YML026C\_YDR450W\_InL\_surface**



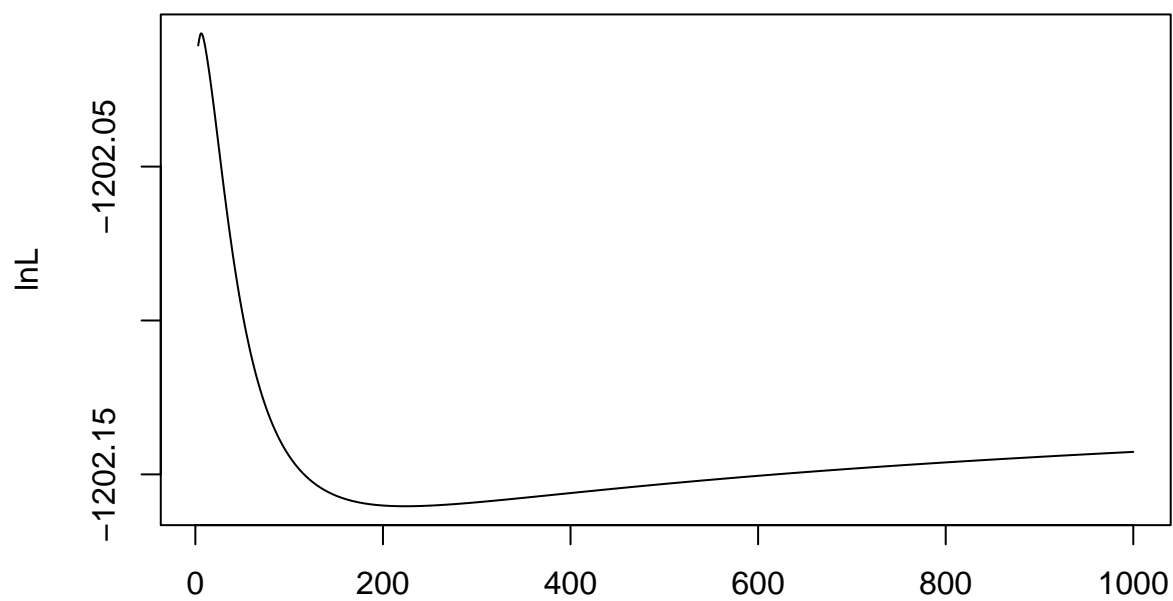
**YNL301C\_YOL120C\_InL\_surface**



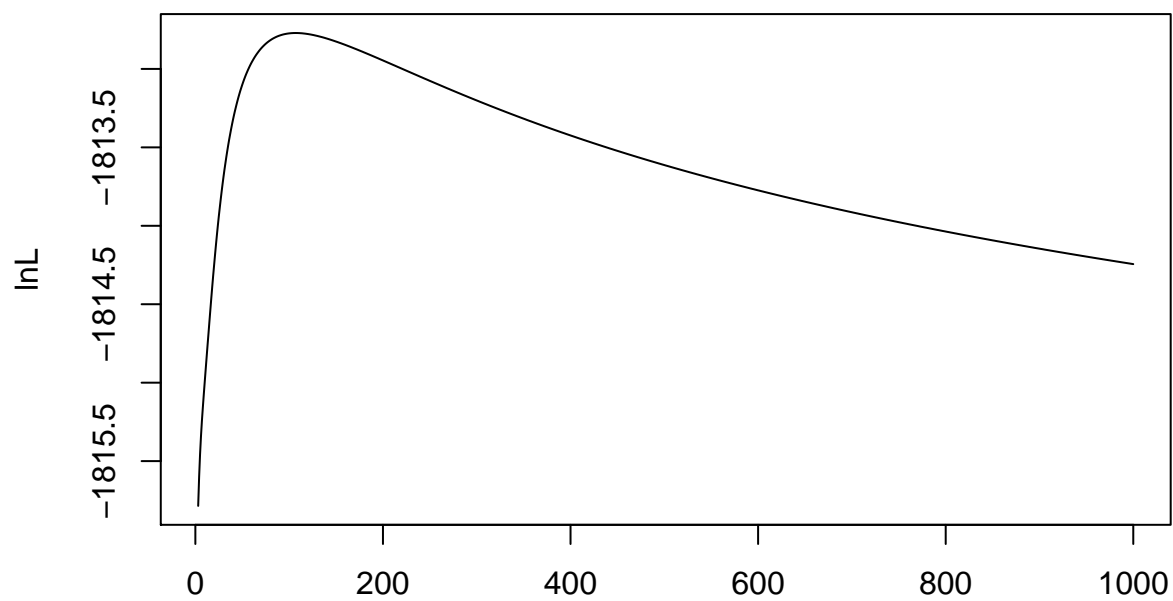
mean tract length in nucleotides  
**YNL069C\_YIL133C\_InL\_surface**



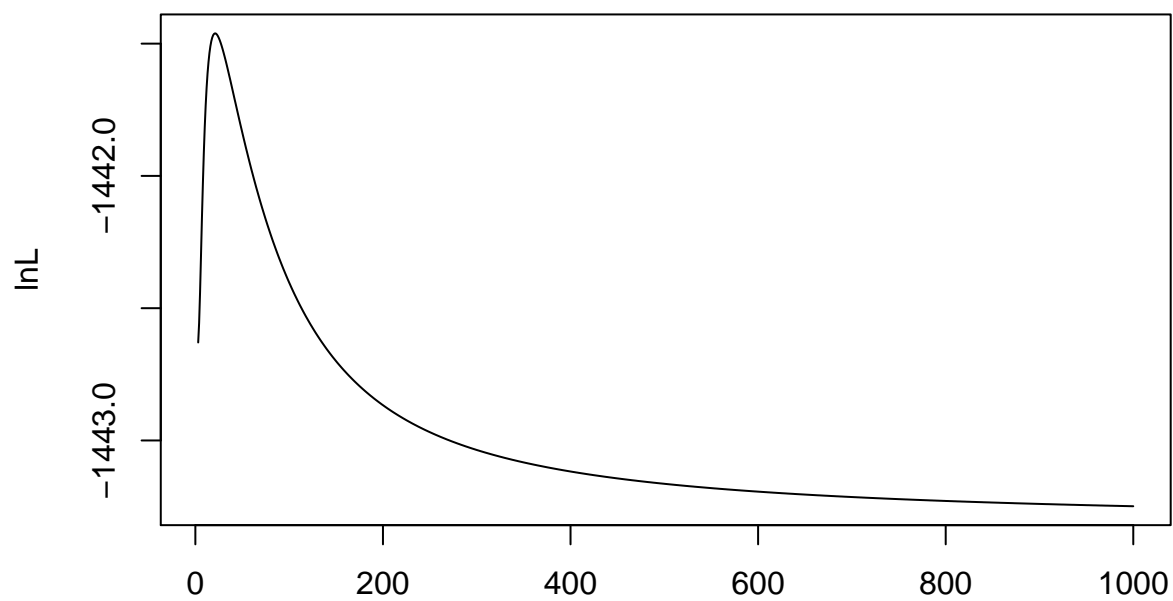
**YMR143W\_YDL083C\_InL\_surface**



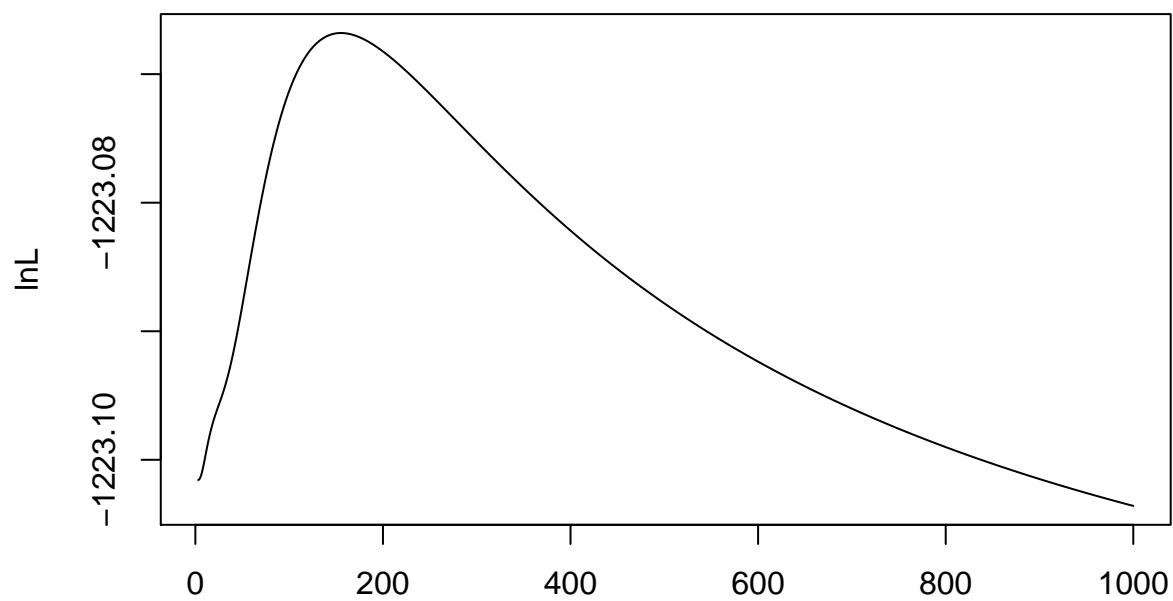
mean tract length in nucleotides  
**YJL177W\_YKL180W\_InL\_surface**



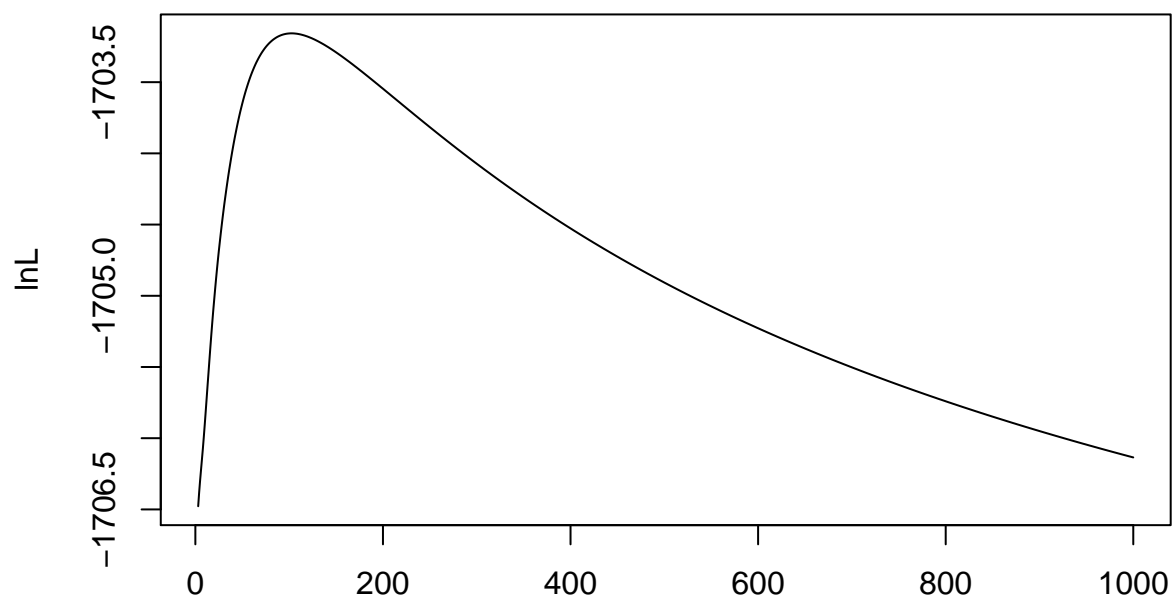
**YBR191W\_YPL079W\_InL\_surface**



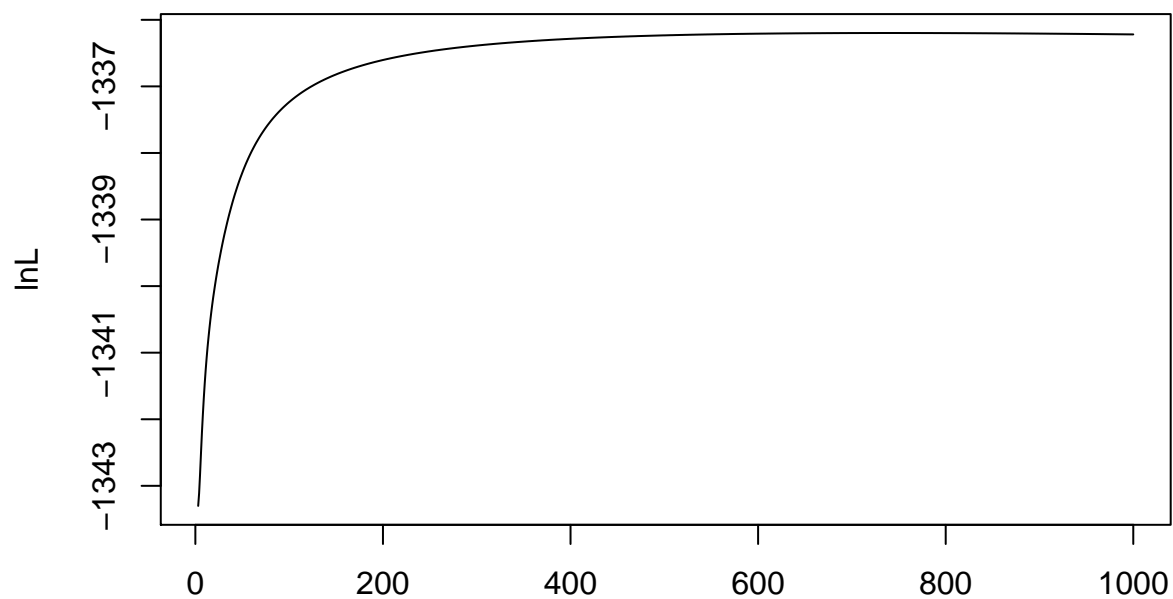
mean tract length in nucleotides  
**YER074W\_YIL069C\_InL\_surface**



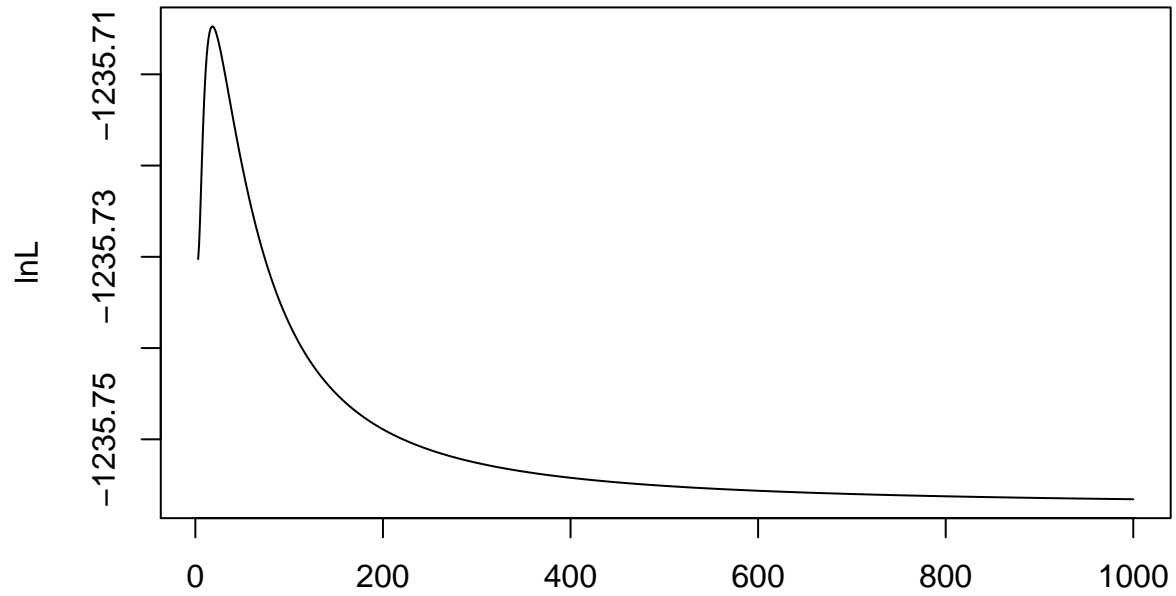
**YDR418W\_YEL054C\_InL\_surface**



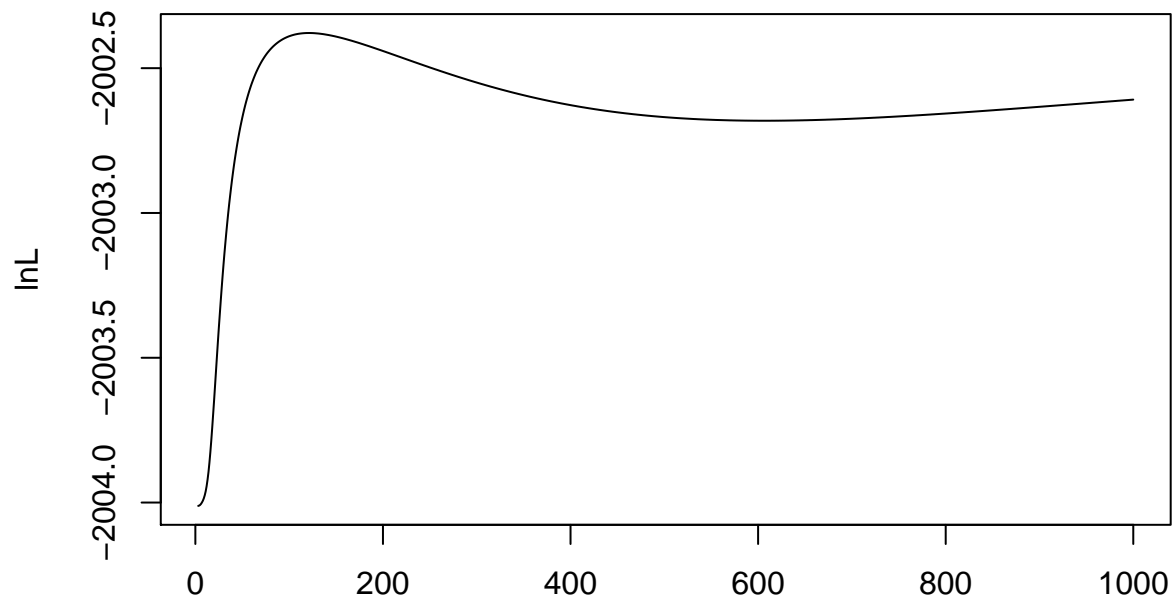
mean tract length in nucleotides  
**YBL087C\_YER117W\_InL\_surface**



**YLR333C\_YGR027C\_InL\_surface**



mean tract length in nucleotides  
**YMR142C\_YDL082W\_InL\_surface**



YER102W\_YBL072C\_InL\_surface

