

# Convergence report for Lung AdenoCA signatures 20000 DMROO RData

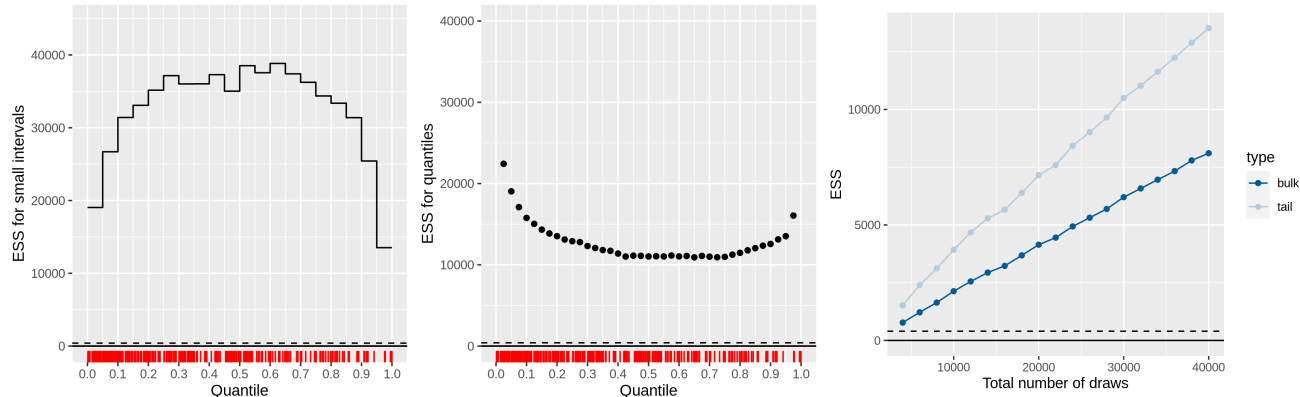
Date of inference: 2020-06-14

**Explanation of parameters** Rhat indicates the ratio of variance within a chain over variance pooling all chains. We recommend running at least four chains by default and only using the sample if R-hat is less than 1.05. ESS bulk/tail indicate the bulk/tail effective sample size estimate, i.e. show the sampling efficiency of mean and median estimates. We recommend running at least four chains by default and only using the sample if R-hat is less than 1.05. Both bulk-ESS and tail-ESS should be at least 100 (approximately) per Markov Chain in order to be reliable and indicate that estimates of respective posterior quantiles are reliable.

- Max Rhat: NA
- ess bulk: 1243.38157564812
- ess tail: 1089.85281521594



In the plots below ESS should have high values



## Local ESS for $\beta$

