

# Convergence report for Myeloid MPN signatures 20000ROO RData

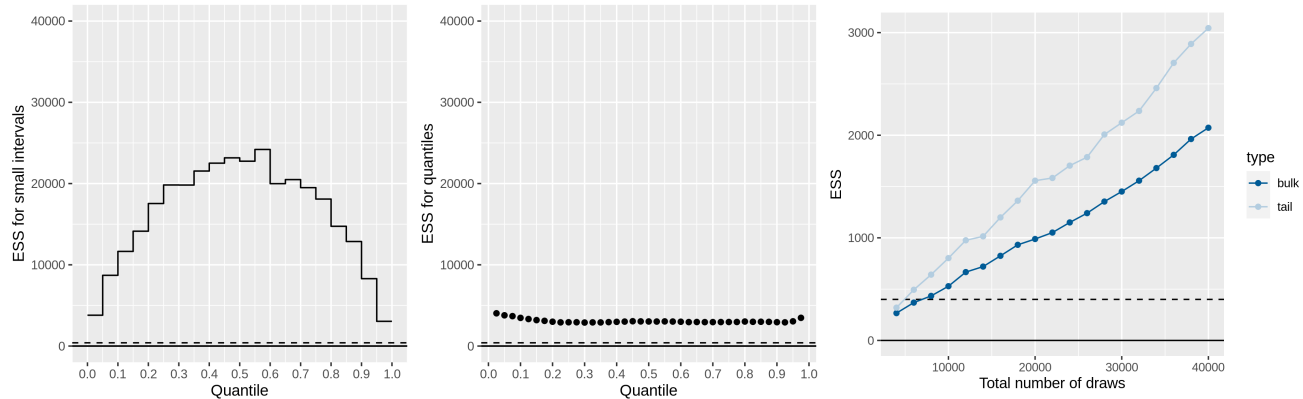
Date of inference: 2020-06-13

**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: 1.00075525975952
- ess bulk: 460.862853668357
- ess tail: 499.034062201511



In the plots below ESS should have high values



## Local ESS for $\beta$

