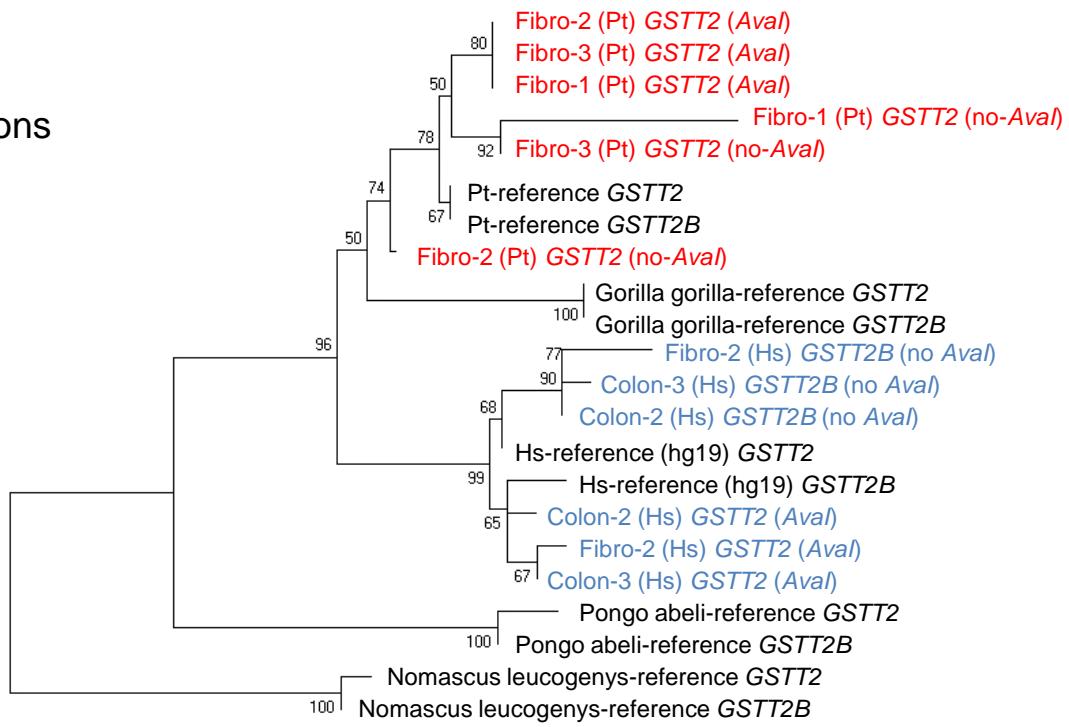
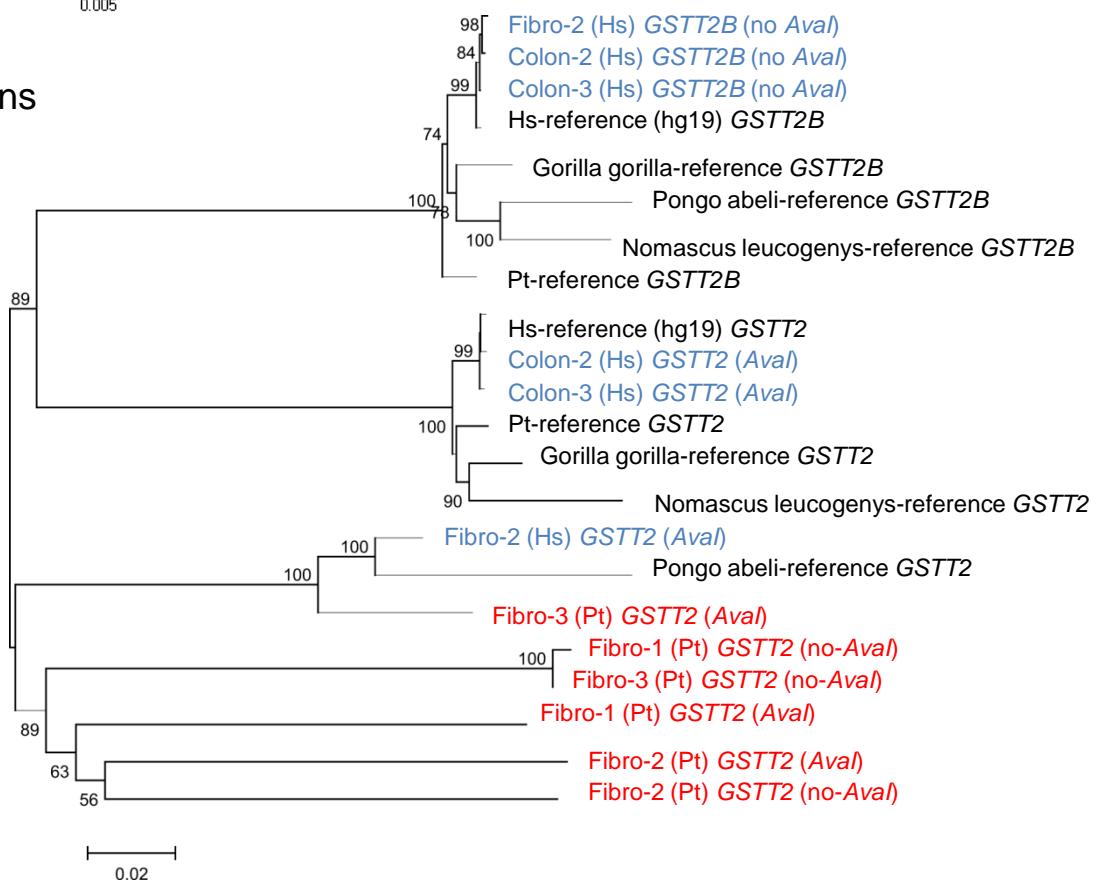


## Exons



## Introns



**Figure S6.** Neighbor joining tree of *GSTT2* exons (top) and introns (bottom) based on maximum composite likelihood. Numbers on branches represent confidence levels of the standard error test of branch length; only values >50% are shown. Note that exons are less diverged than introns. The sequences obtained from this study are shown in red (chimpanzees) and in blue (humans).