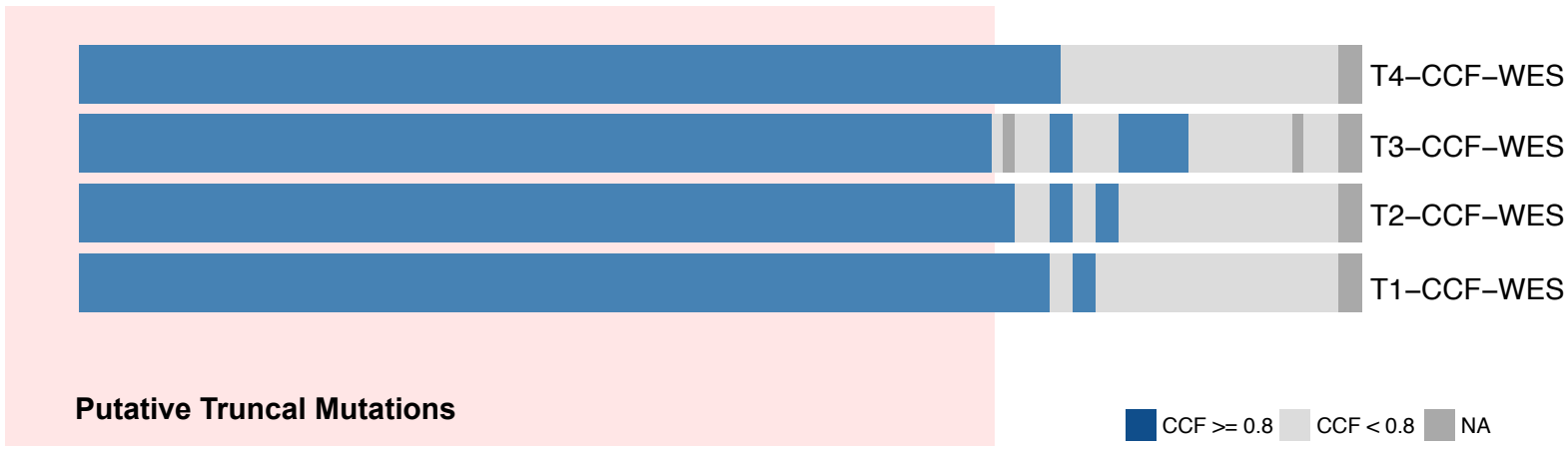
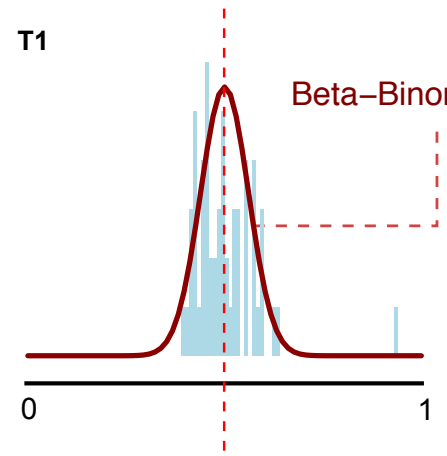
A PATIENT 52

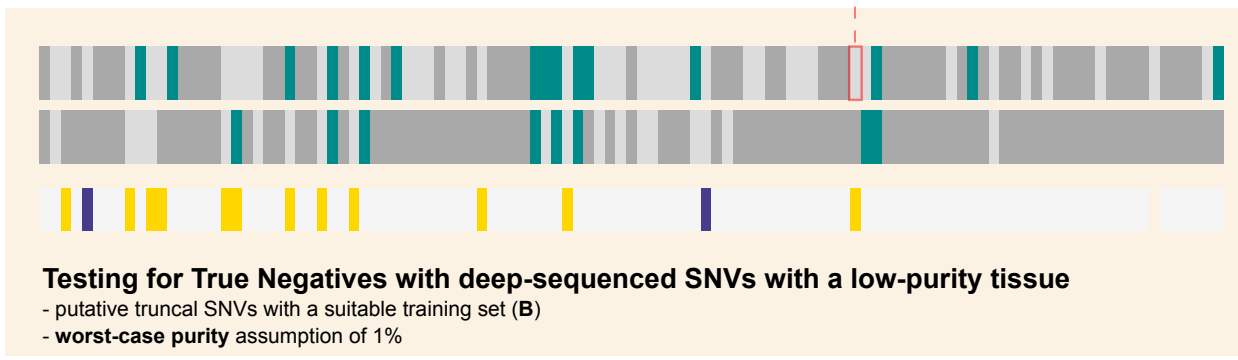


B Training model



VAF *Number of reads (NV)s with mutant alllele from a primary region with CN = **c**.*

C Test data



Idea *Assume they are putative truncal, their VAF should follow the same distribution of all the other clonal SNVs* (**B**)

Test *Use the fit distribution fit to write a null hypothesis* (H_0) *for the model in which these SNVs are truncal, but undetected in the targeted panels.*

Rejecting the null means having evidence that those SNVs are unlikely truncal.

D Statistical testing

Null hypothesis

$$H_0: \sum_{w=1}^{k} \text{BetaBin}(v = w | \hat{r}; \mu, \rho).$$

purity π=0.01

Test power