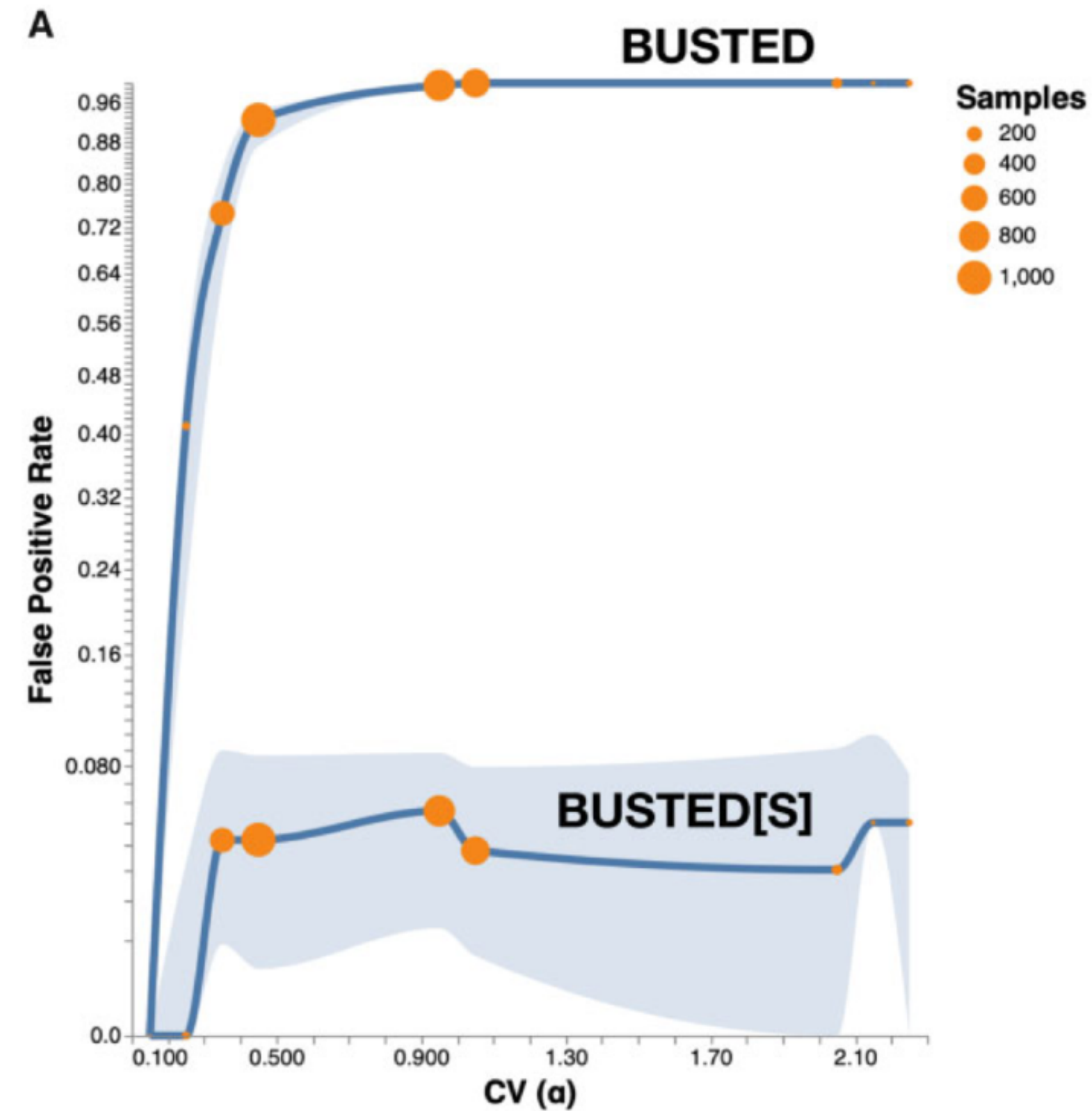


Why do we need to improve codon models?



Incorporating MNMs into the branch-site model eliminates the signature of positive selection in many genes.

