

substitutions/site on human lineage

A

B

Annotation Model

■ Phastcons Priority

■ Feature Priority

PhyloFit
estimates

phastcons
with
CDS

CDS
without
phastcons

CDS
with
phastcons

introns+UTRs

other

12Mya

6Mya

phastcons

CDS

3' UTR

5' UTR

intron

neutral

feature

