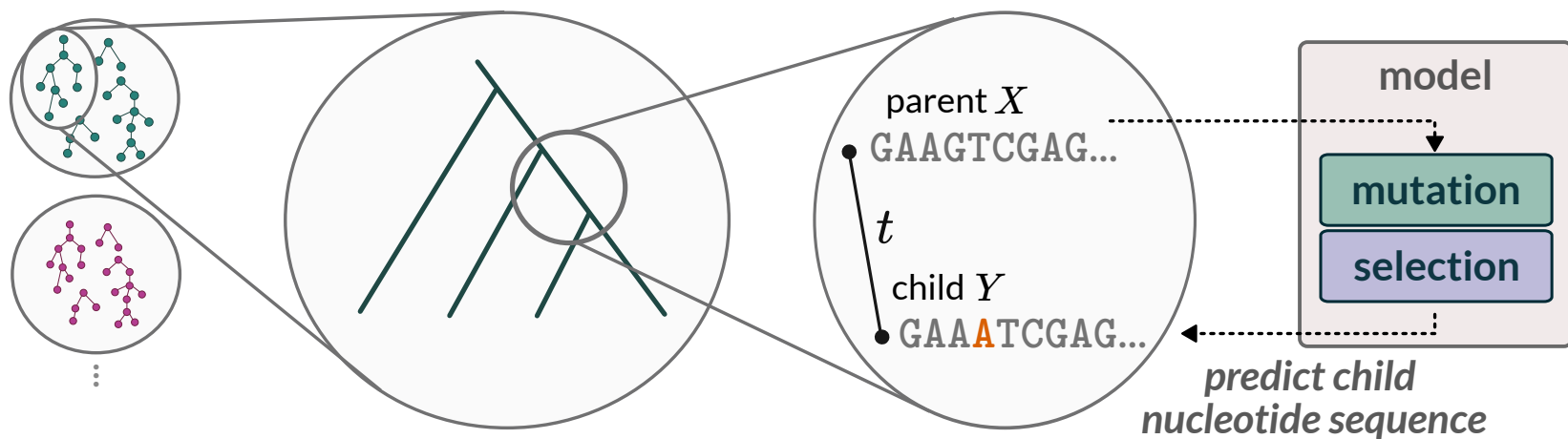


(a) sequences clustered into clonal families

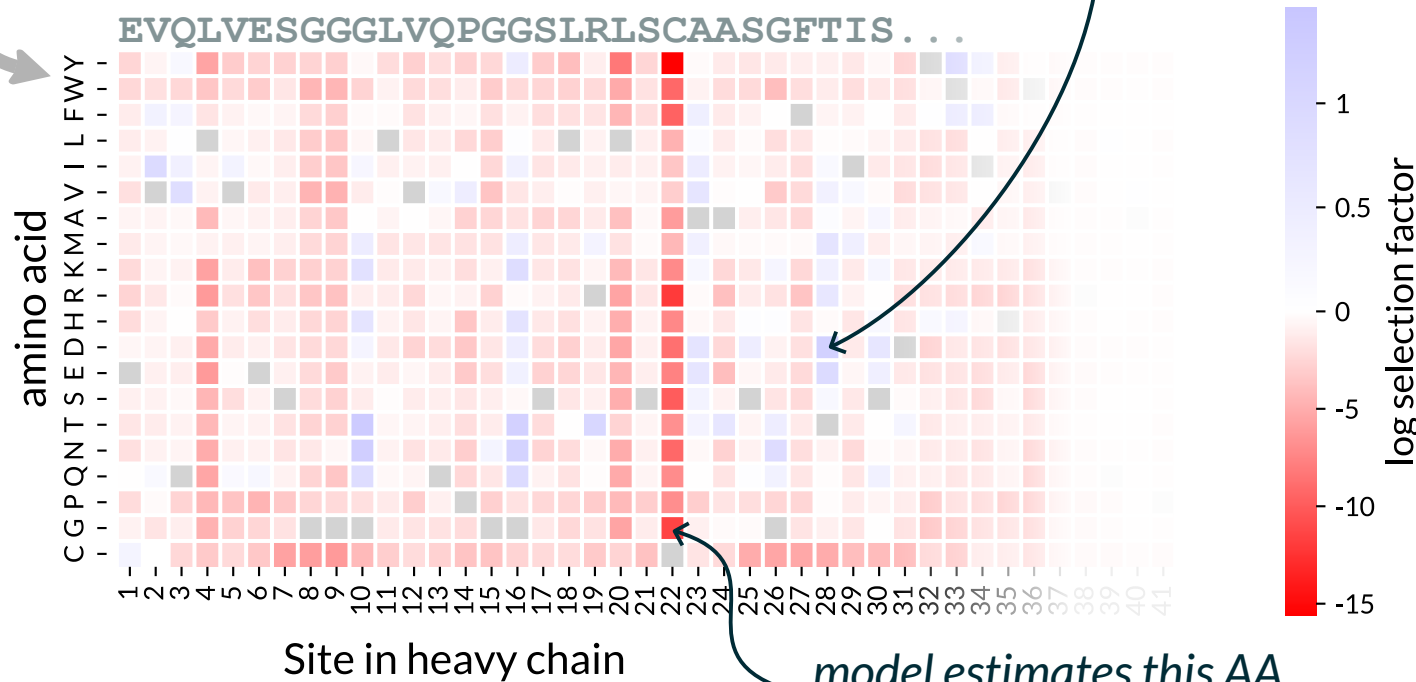


(b) EVQLVESGGGLVQPGGSLRLSCAASGFTIS...

↓ input amino acid sequence

selection: Deep Amino acid Selection Model (DASM)

predict  
selection  
factors



model estimates this AA  
mutation to be **deleterious**