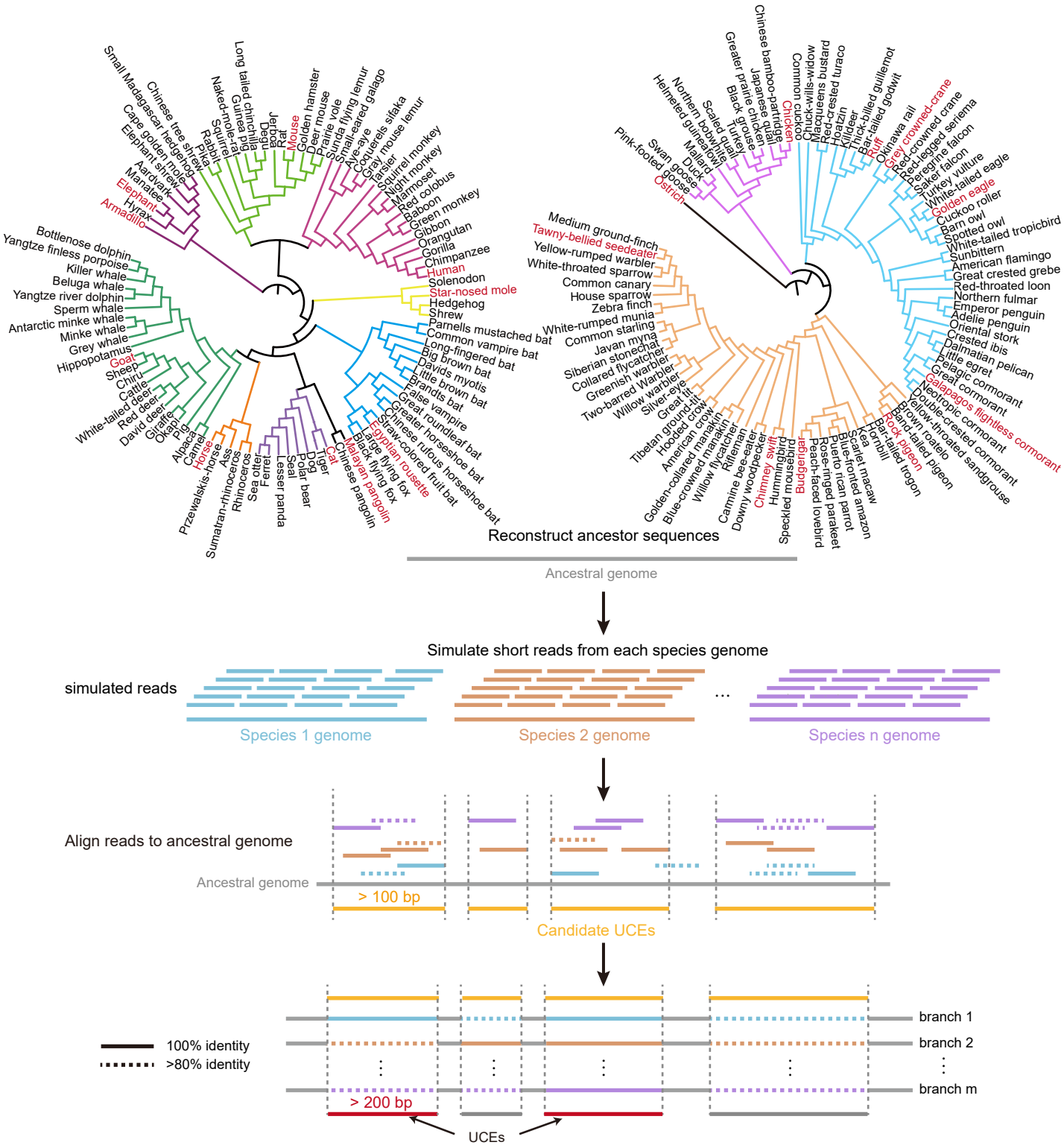
Reconstruct ancestor sequences
Ancestral genome
Simulate short reads from each species genome
simulated reads
Species 1 genome
Species 2 genome
Species n genome
Align reads to ancestral genome
Ancestral genome
> 100 bp
Candidate UCEs
branch 1
branch 2
branch m
100% identity
>80% identity
> 200 bp
UCEs