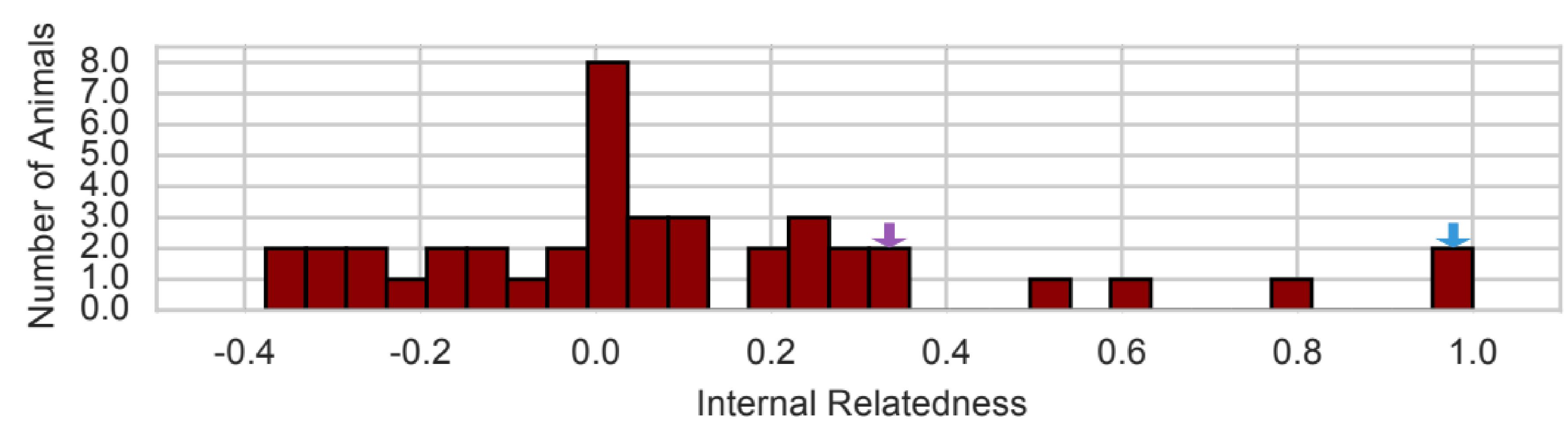
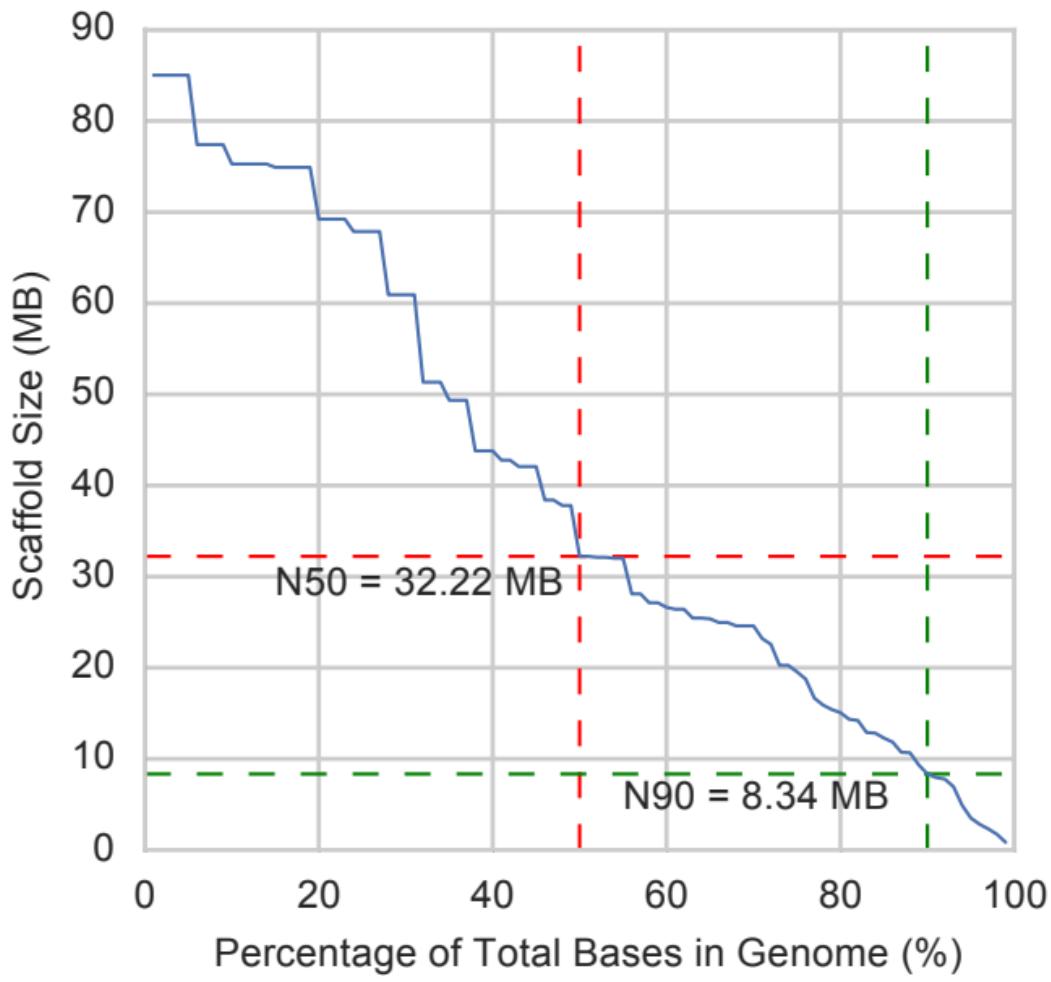
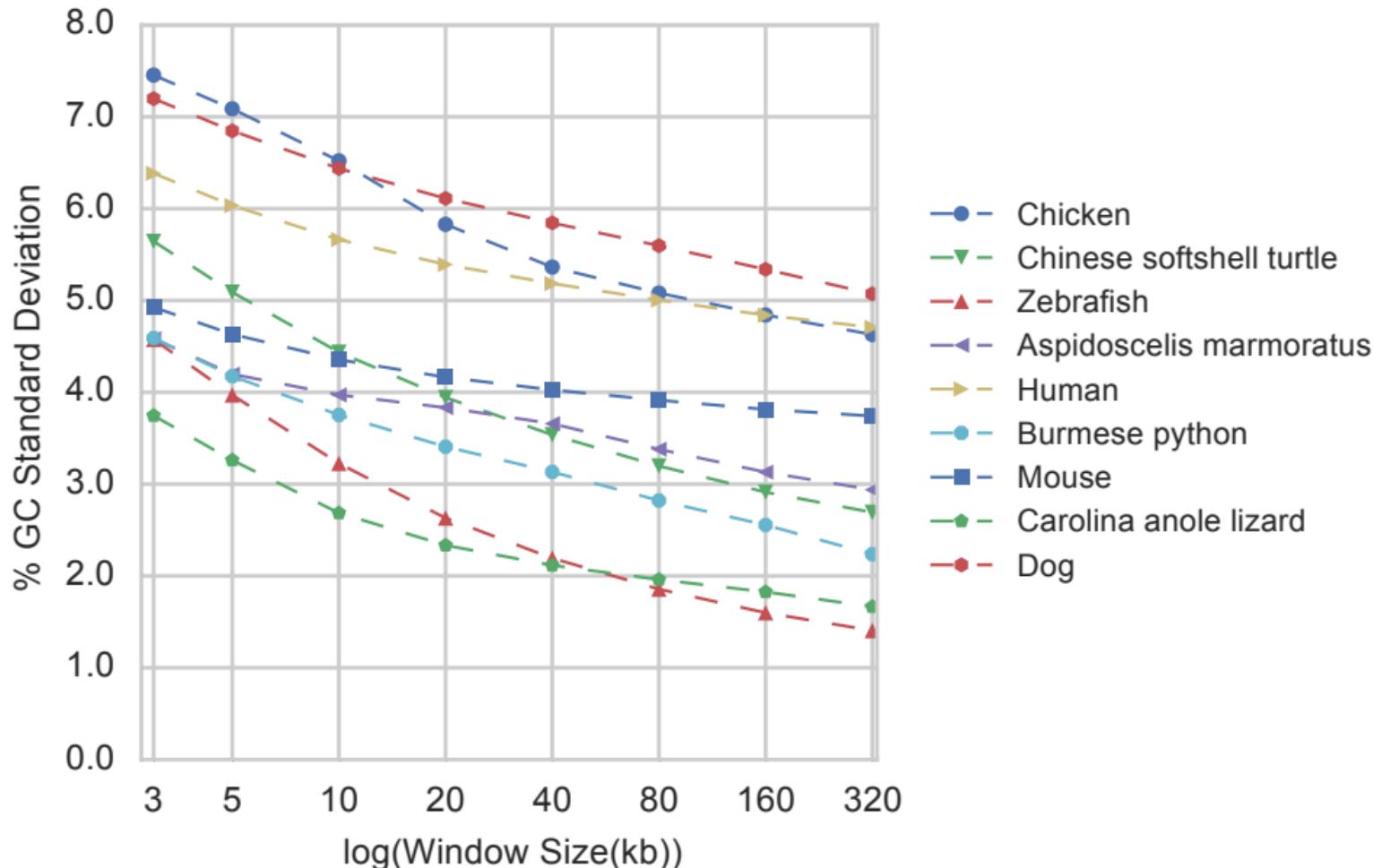


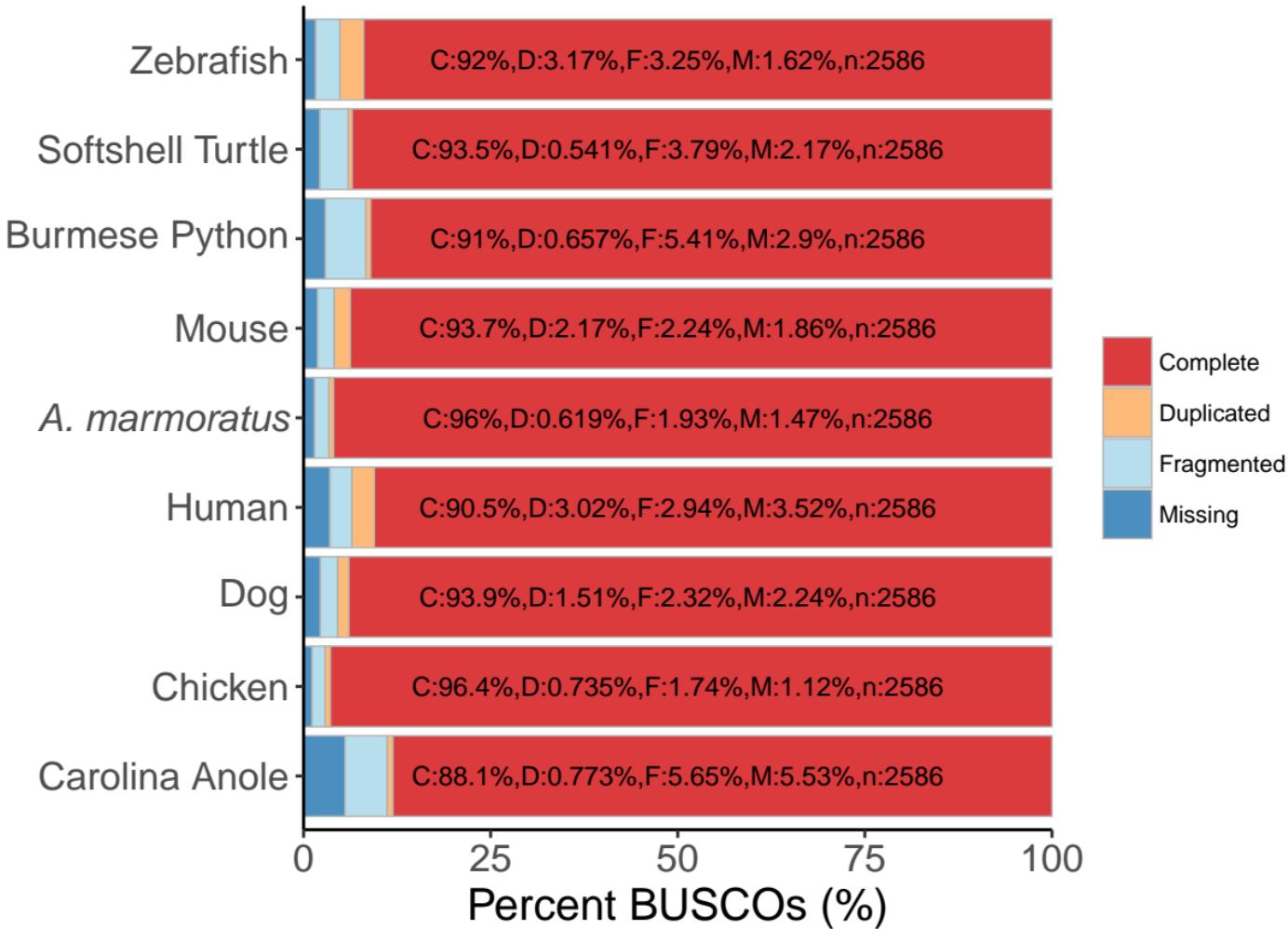
ID#	animal	Ai5013	Cvanu7	Cvanu24	D106
4272	male ino	299	333	303	202
302	male gul	205	248	323	214
122	female mar	214	257	328	200
8449	offspring 1		257	352	295
8450	offspring 2		257	328	299

ID#	animal	D111	MS1	MS7	MS8
4272	male ino	292	336	293	265
302	male gul	246	281	231	116
122	female mar	150		217	116
8449	offspring 1	150		217	119
8450	offspring 2	150		217	113

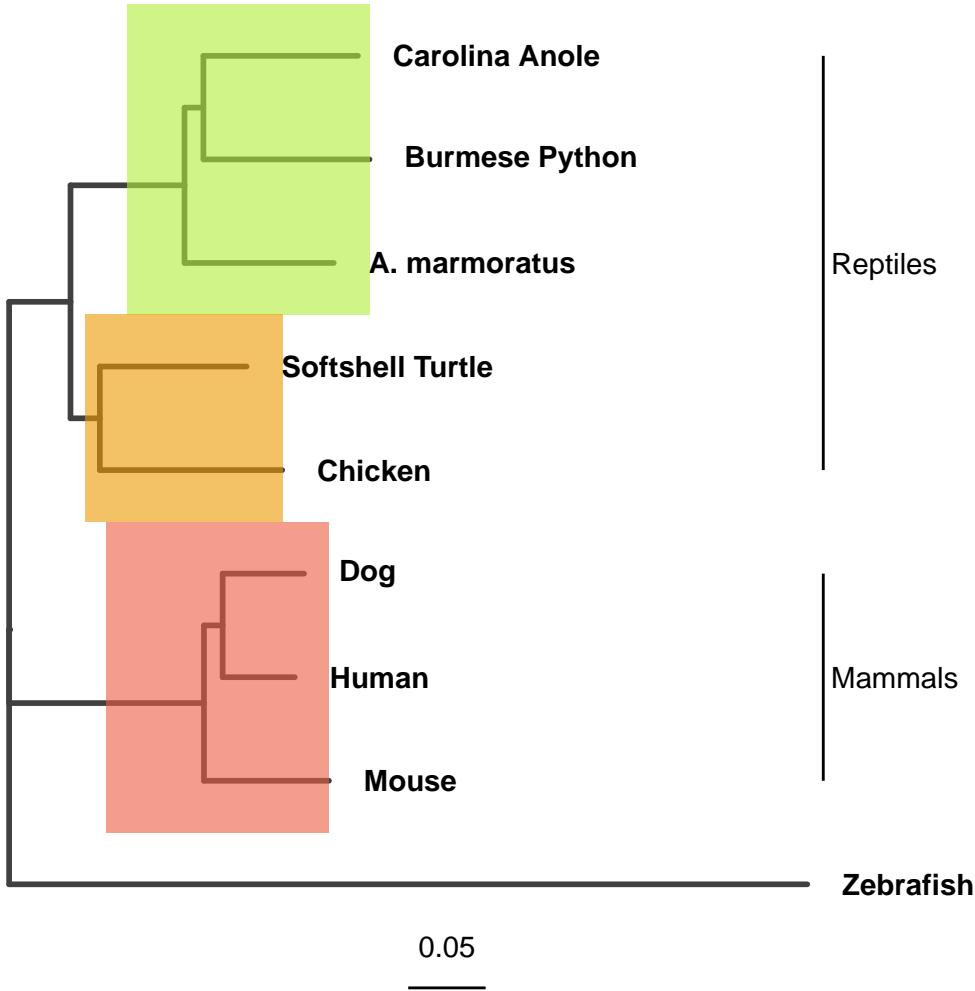


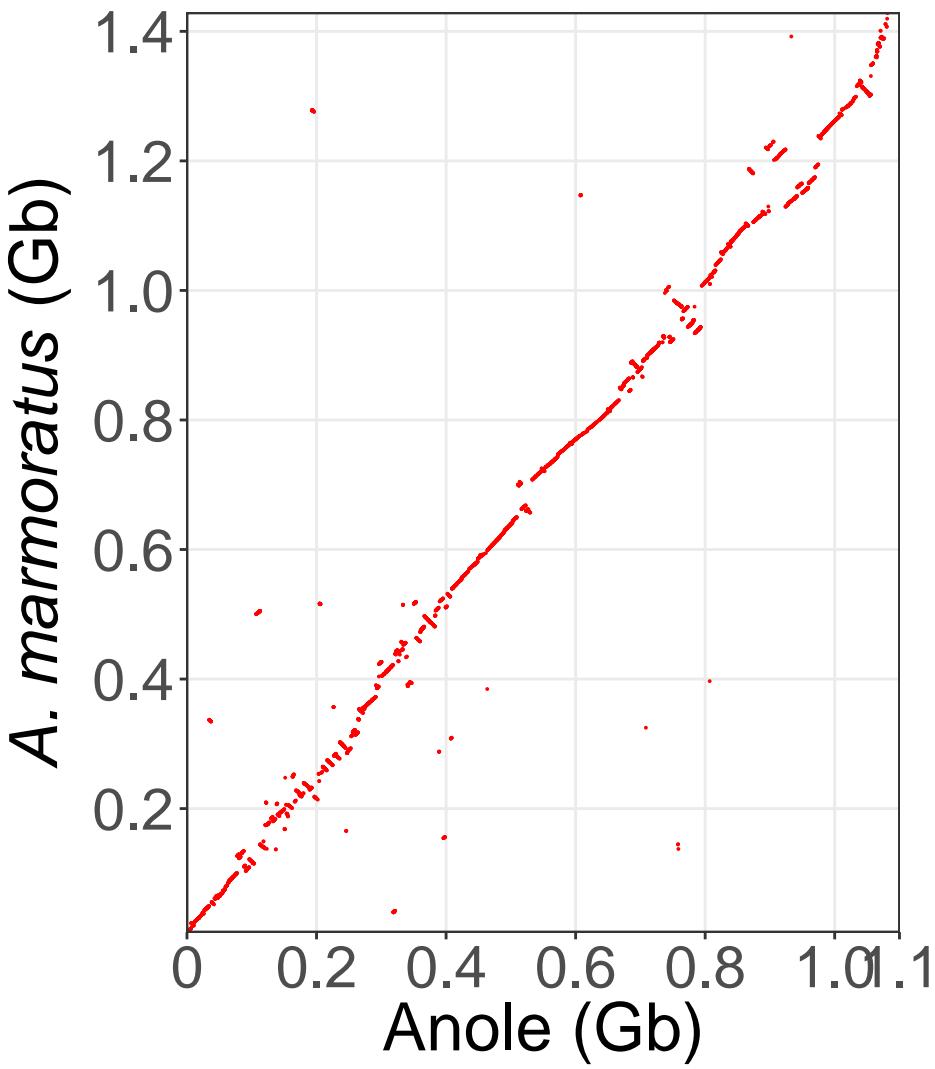


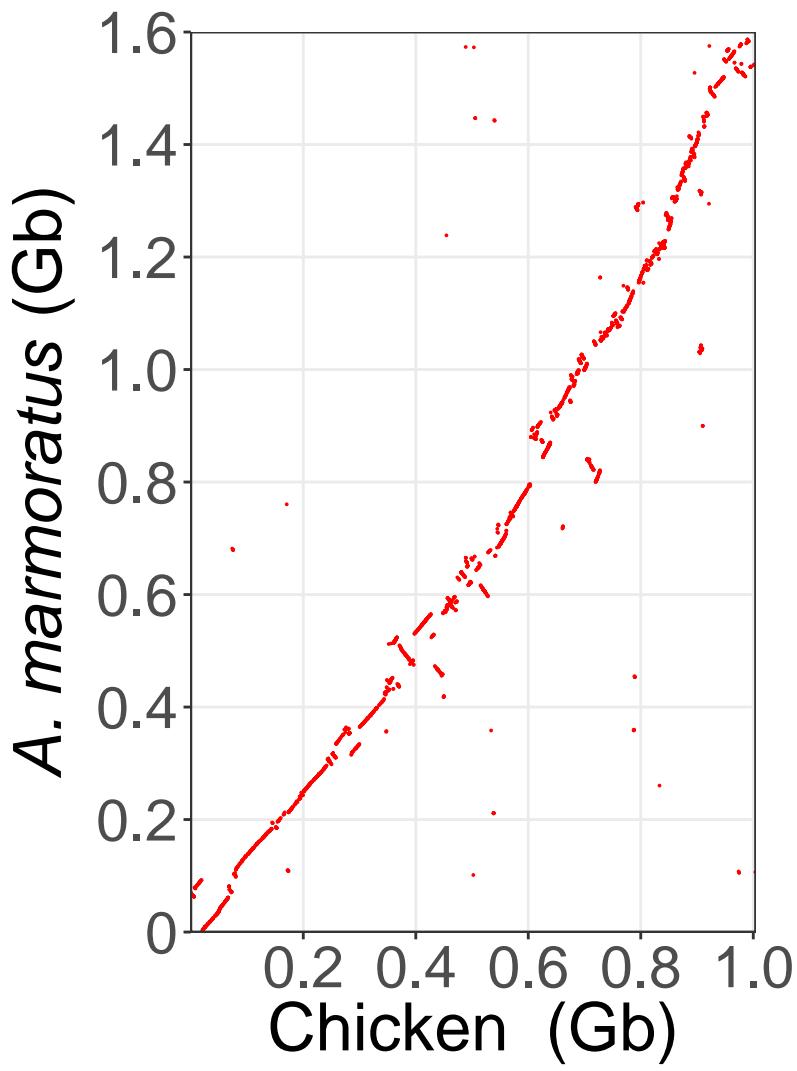




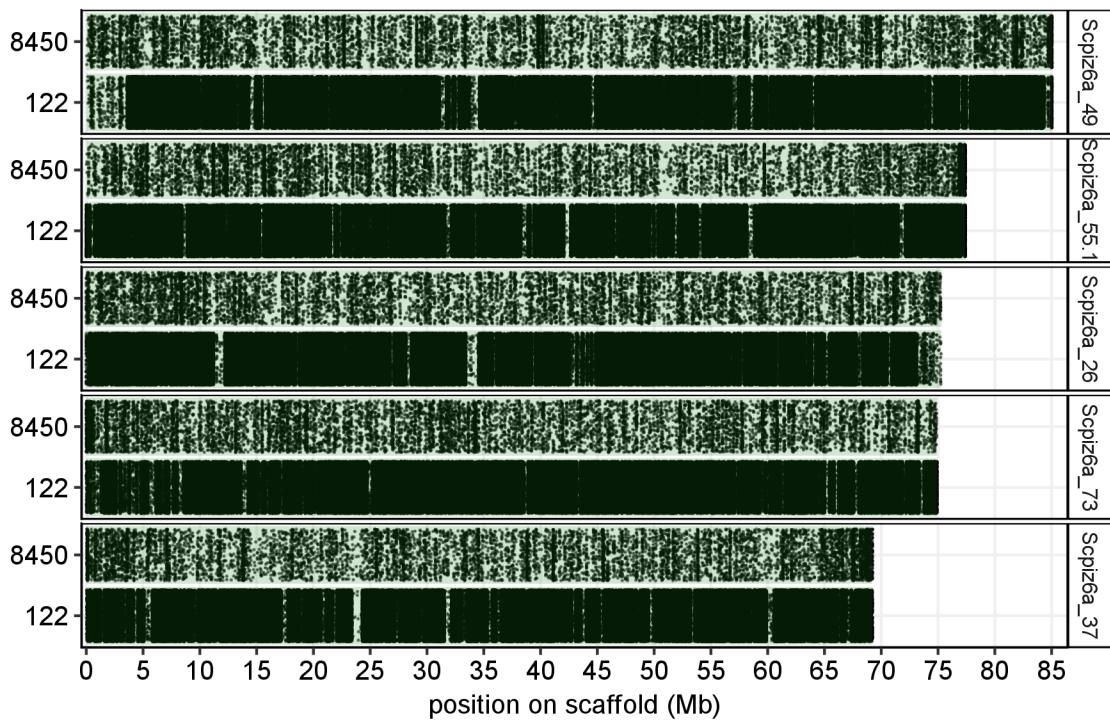
1,536 BUSCOs  
Gblocks and Bootstrap 100 times

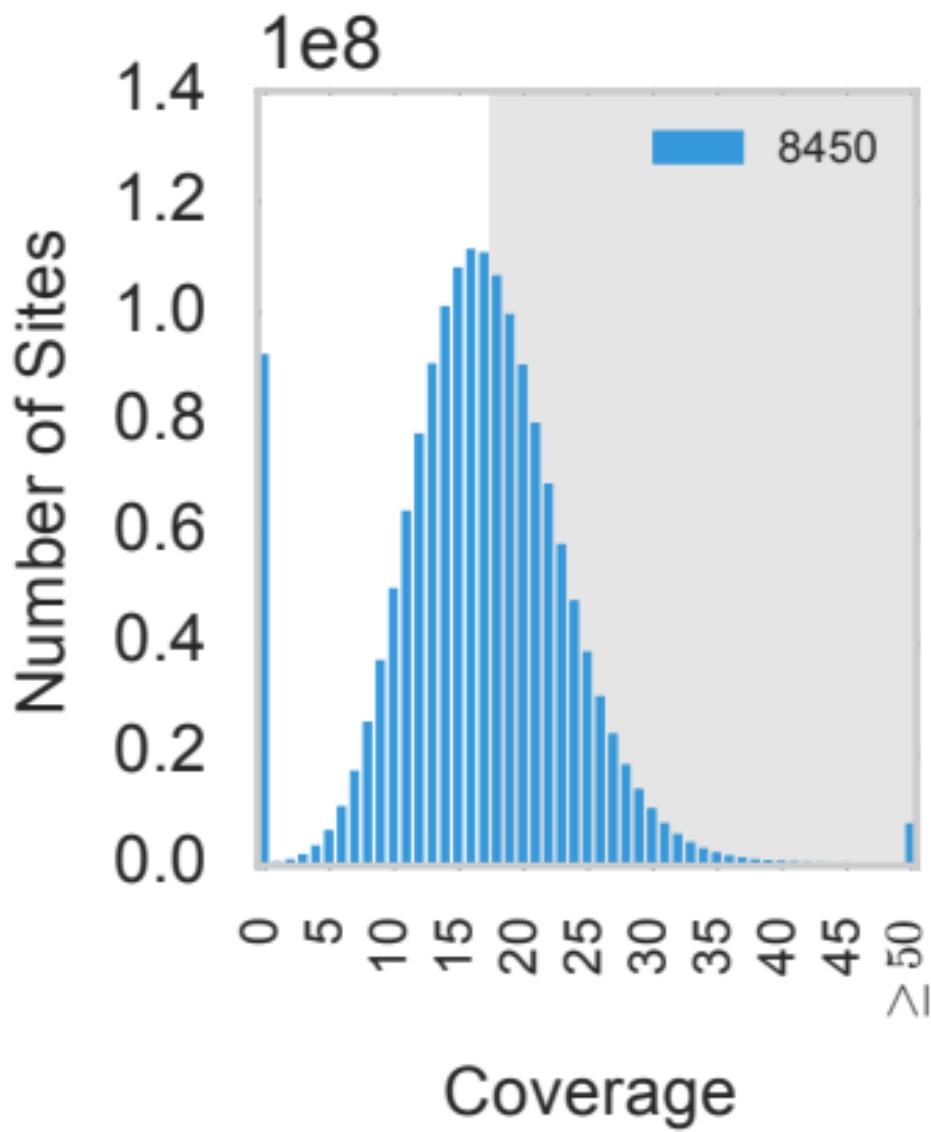


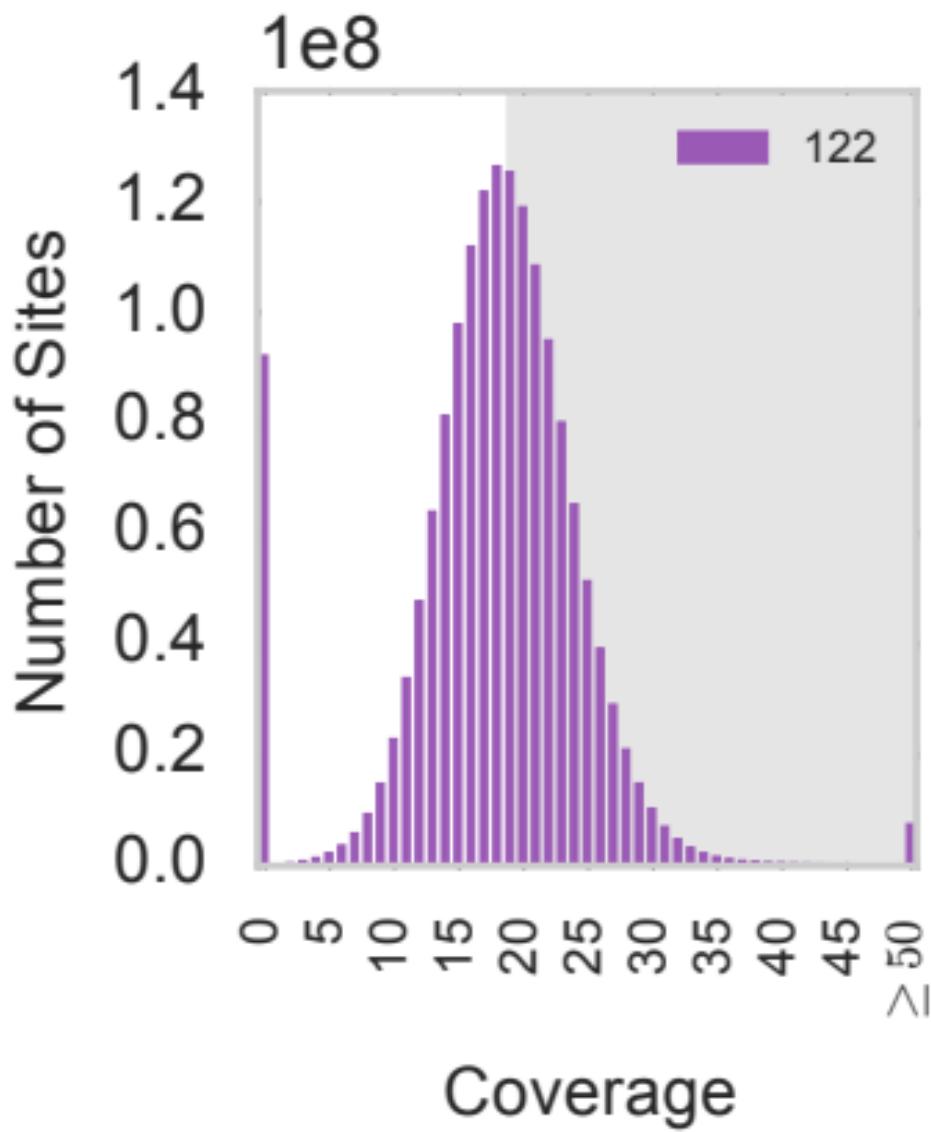


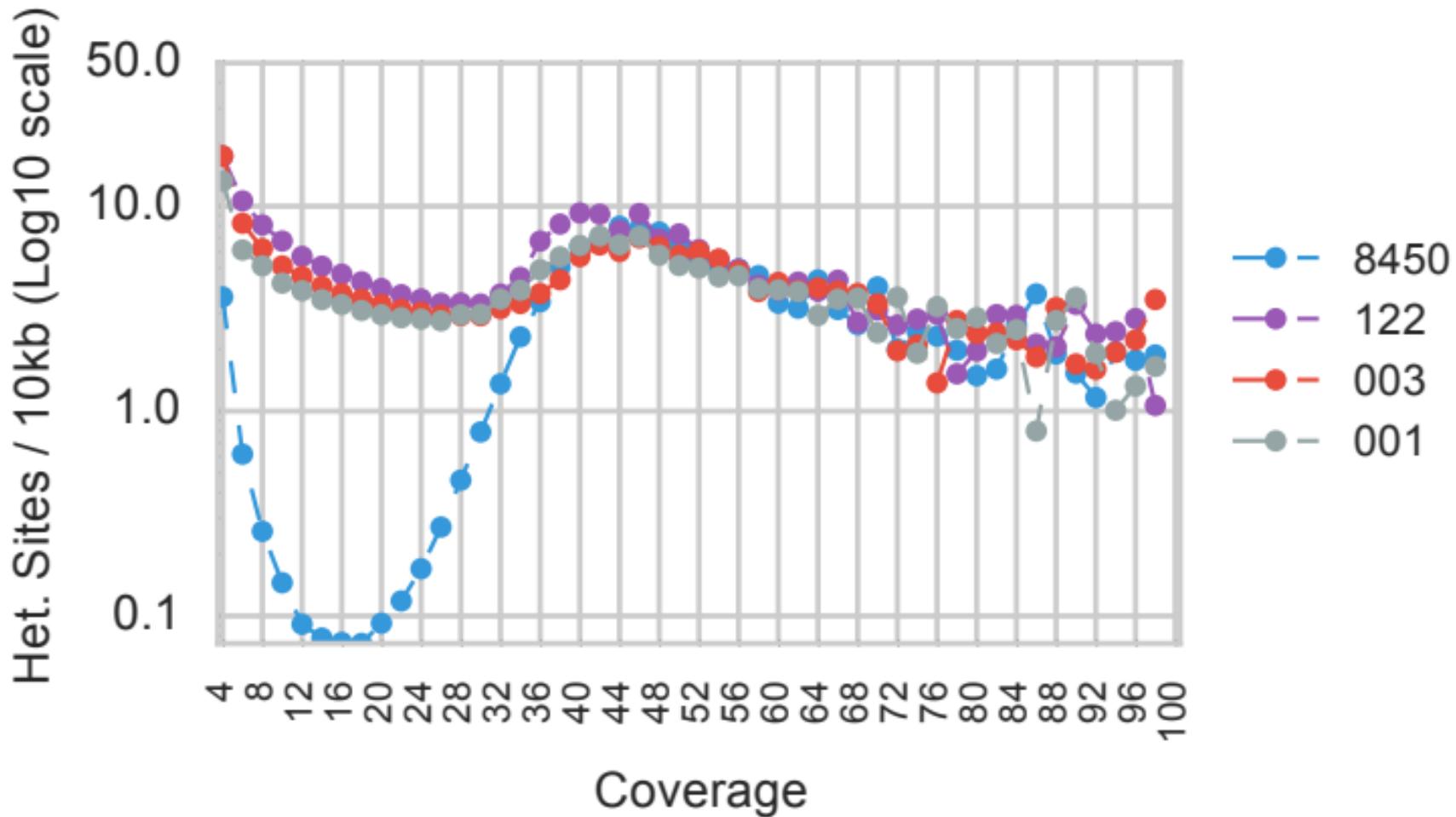


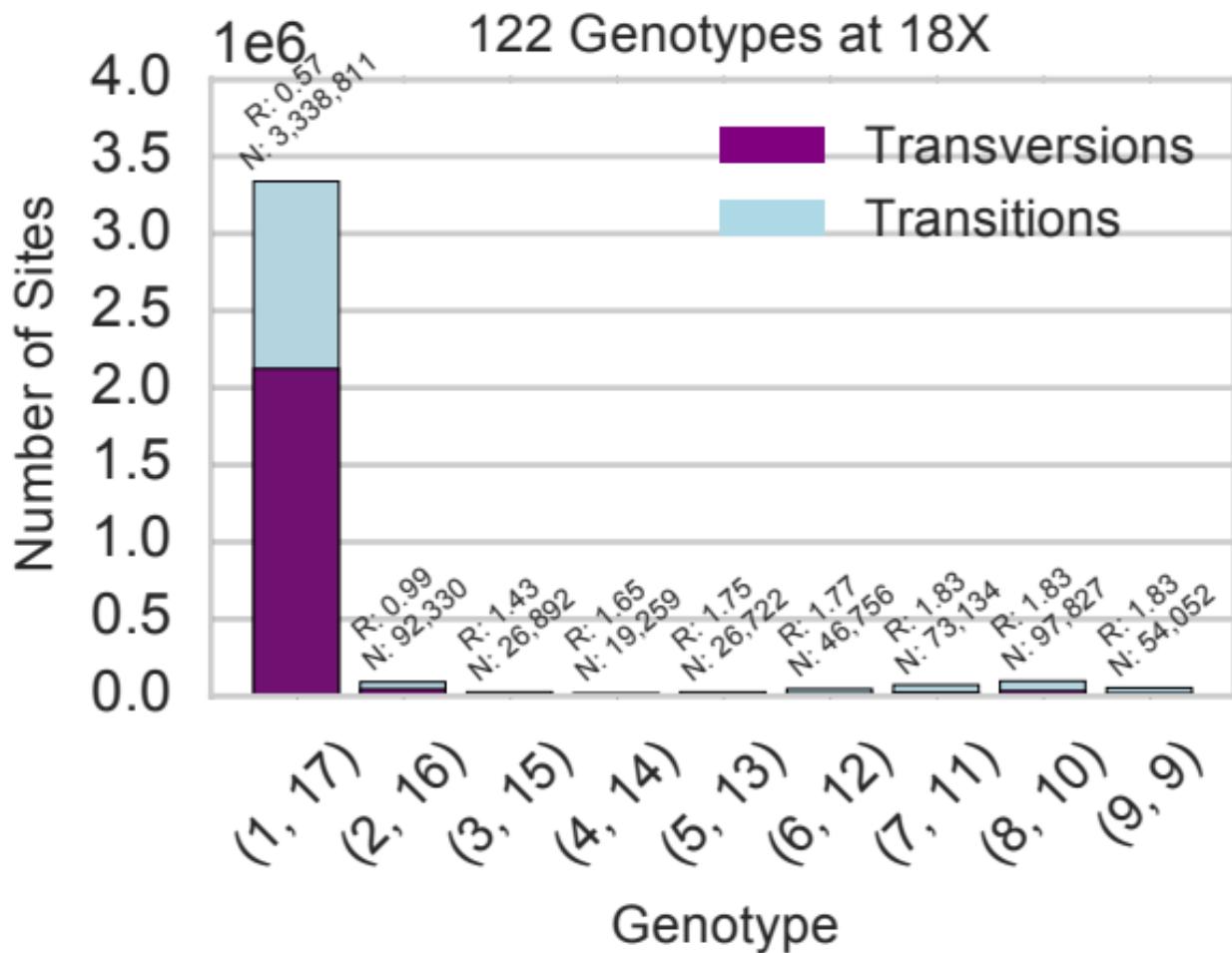
Het sites 8-36x in 8450 & 122

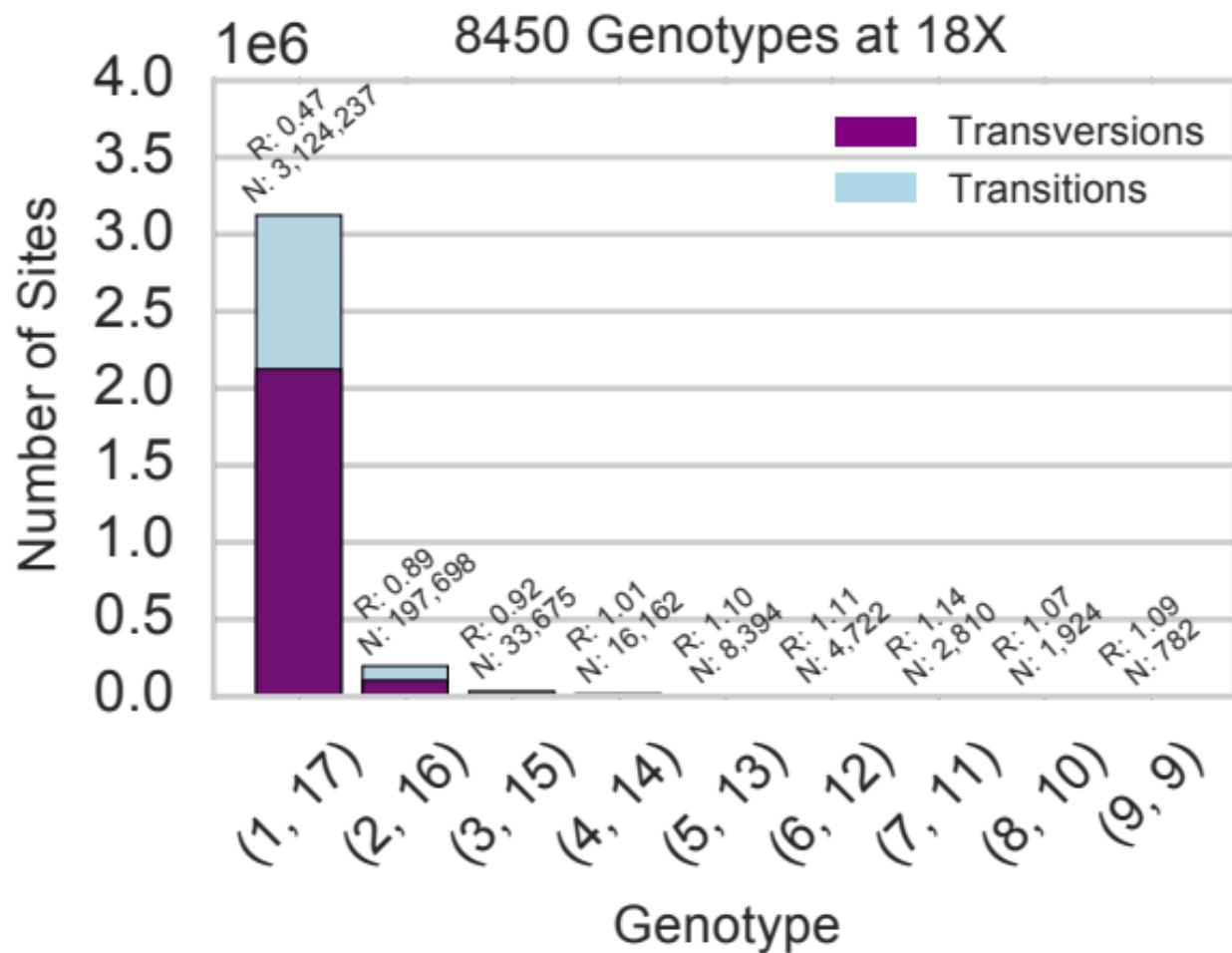


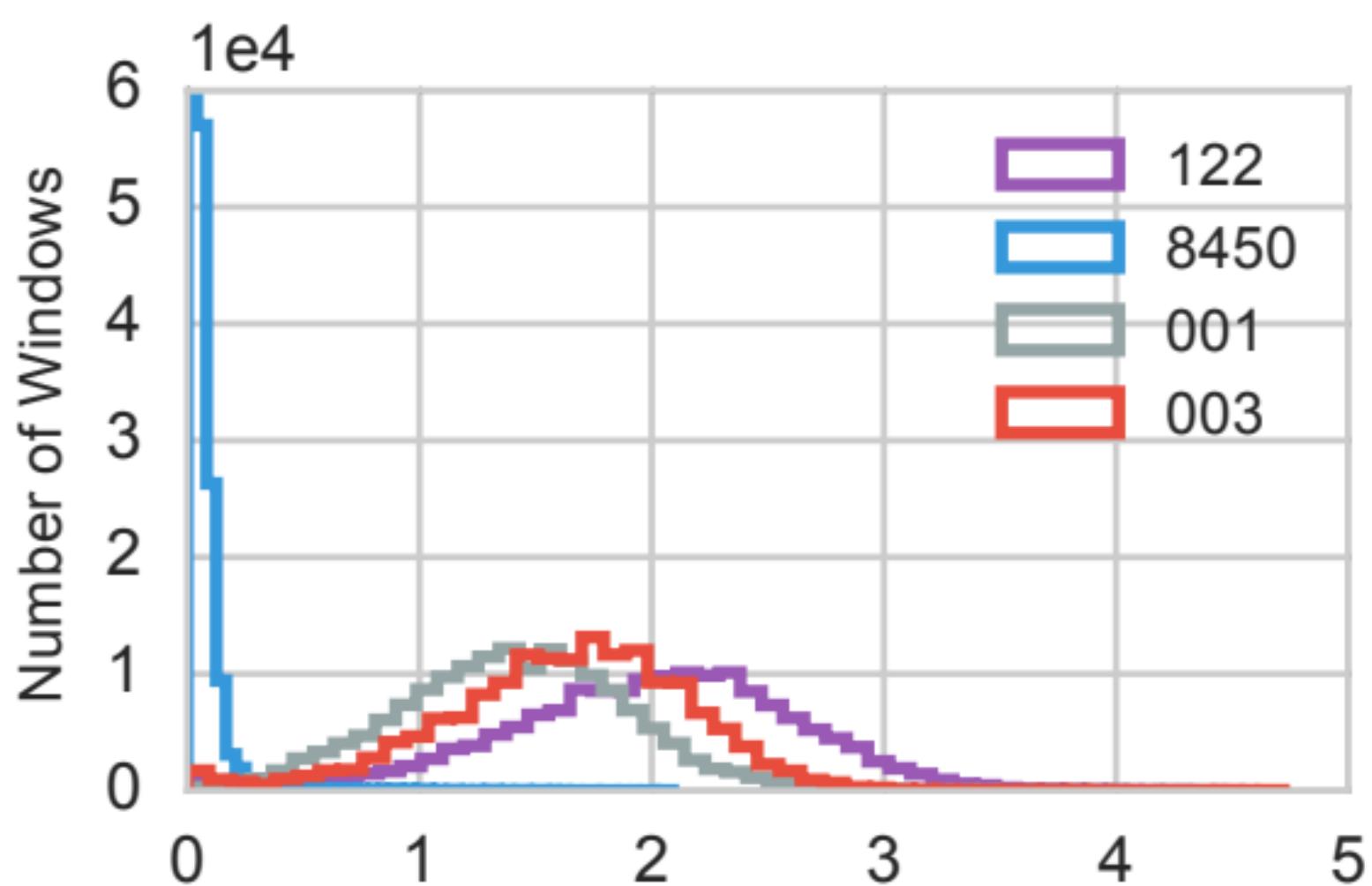






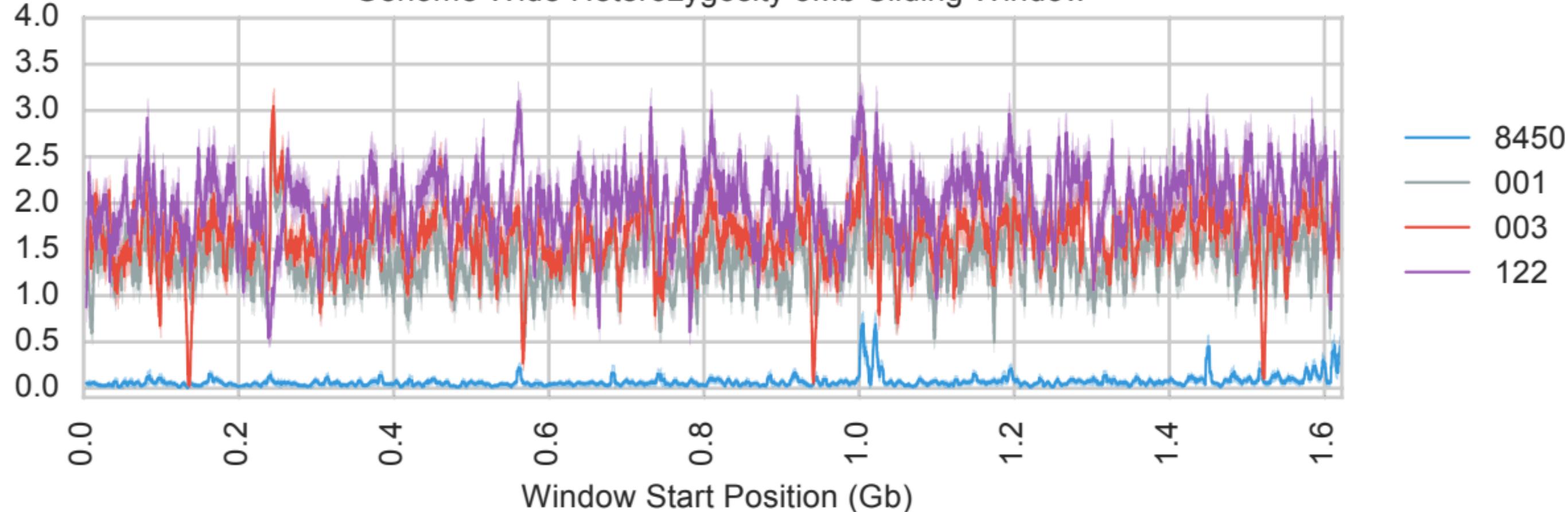




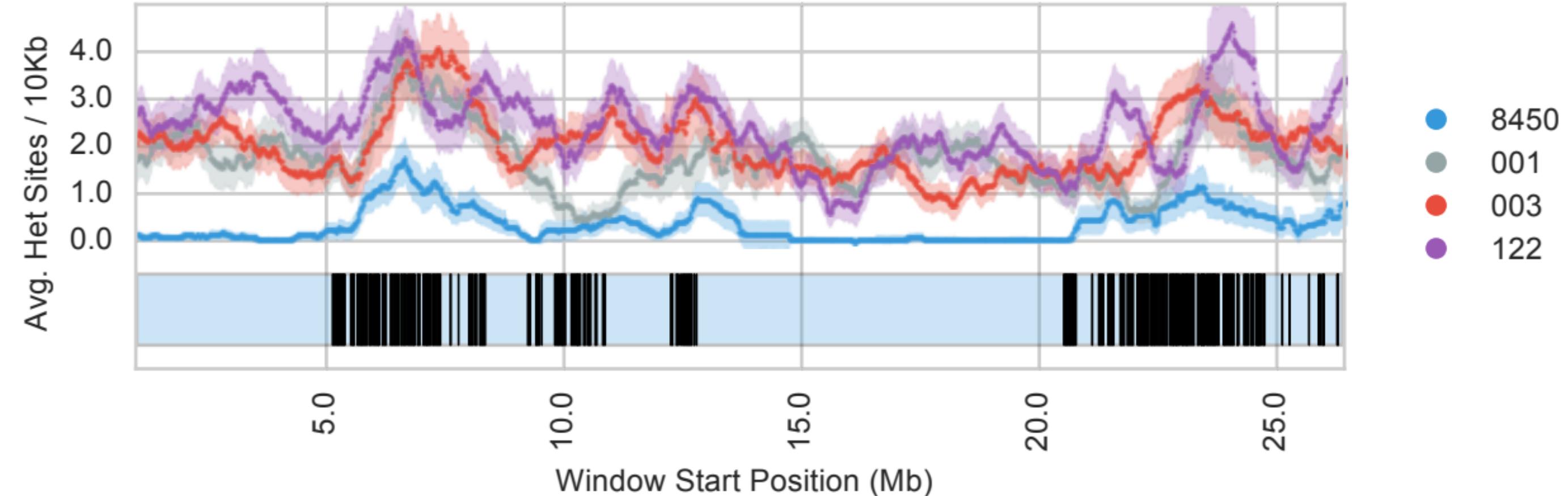


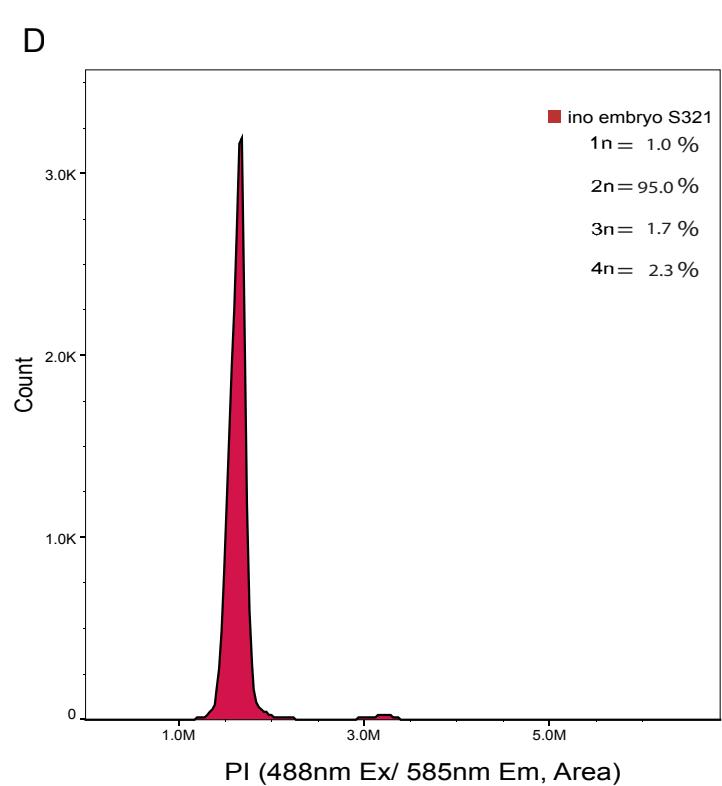
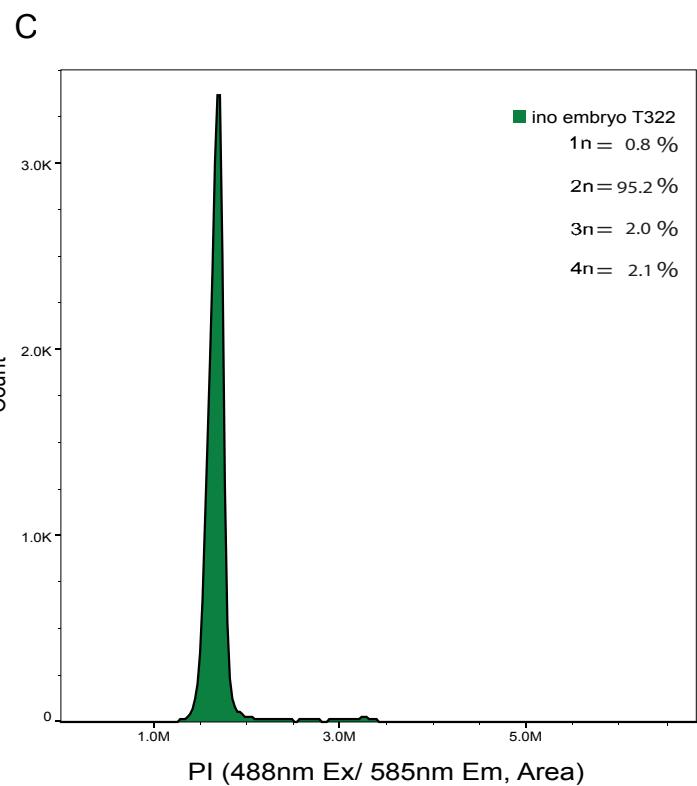
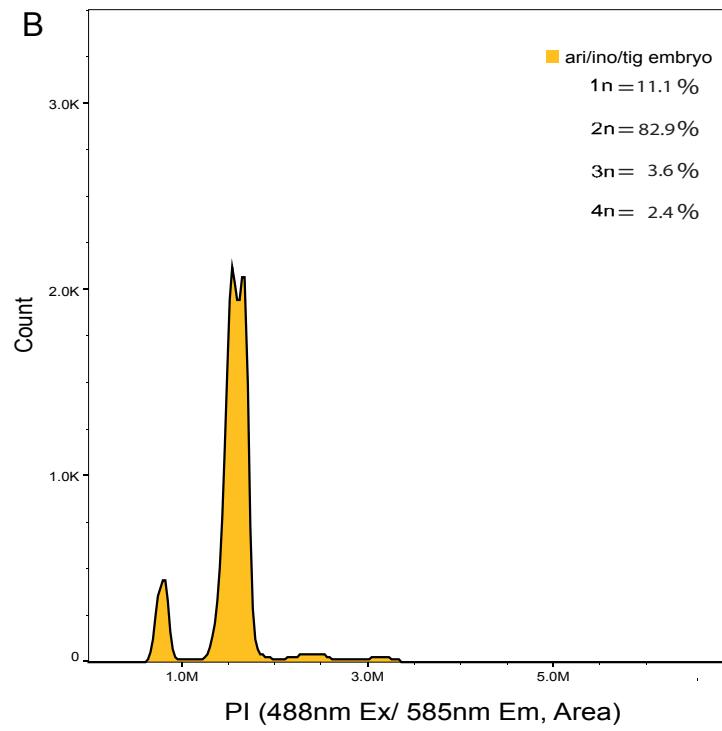
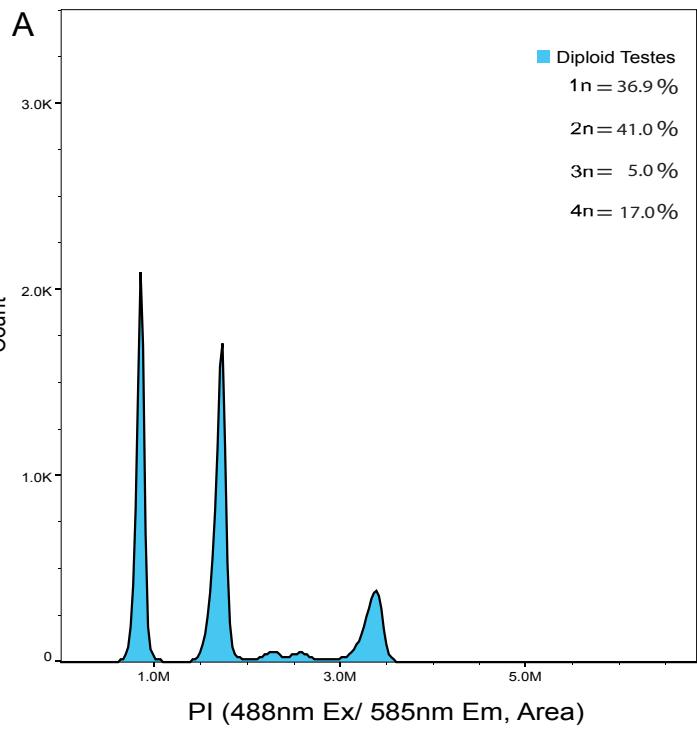
# Genome Wide Heterozygosity 5Mb Sliding Window

Avg. Het. Sites / 10kb

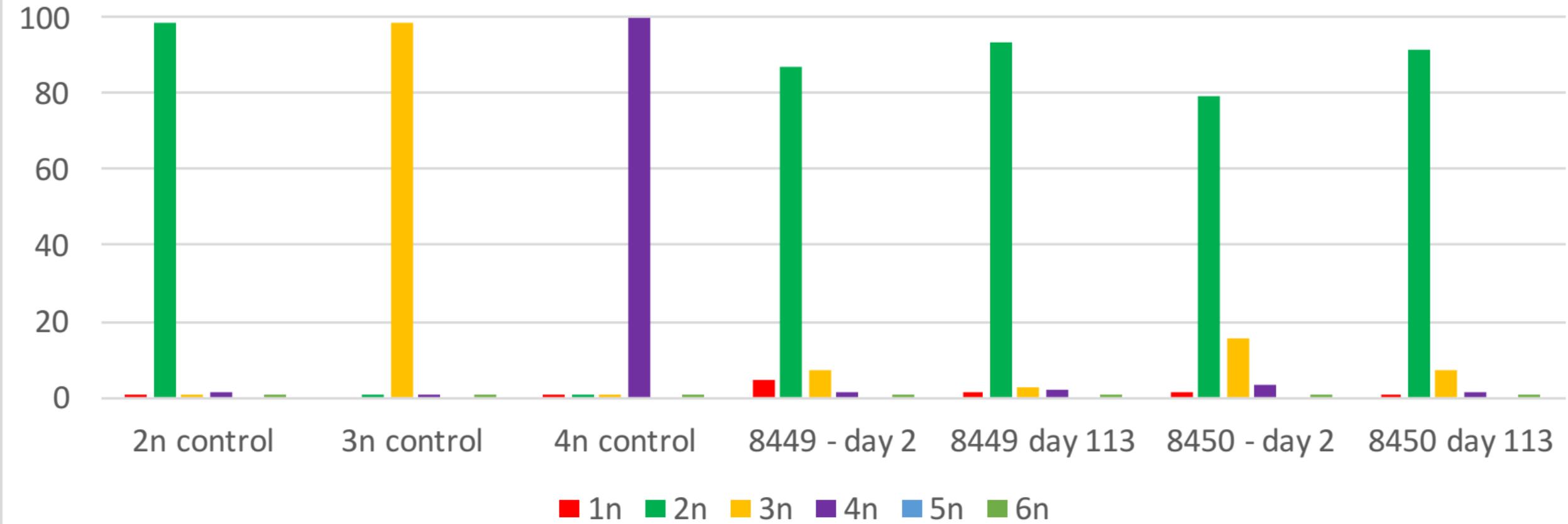


# 1Mb Sliding Window Scaffold: Scpiz6a\_45

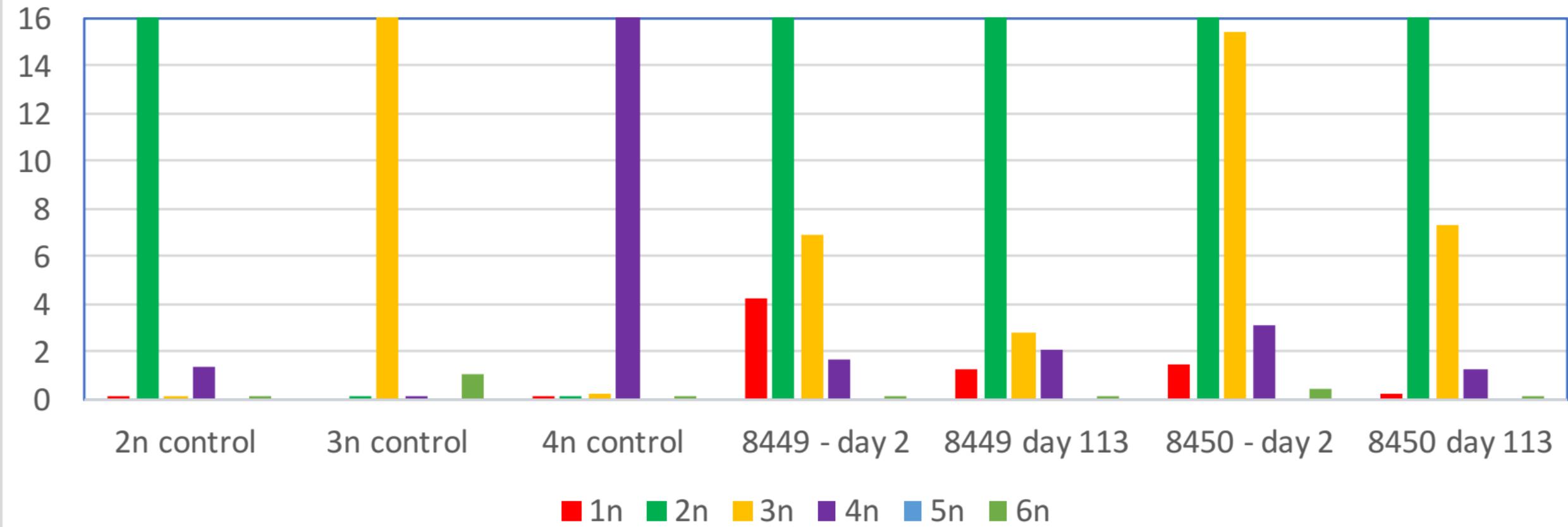




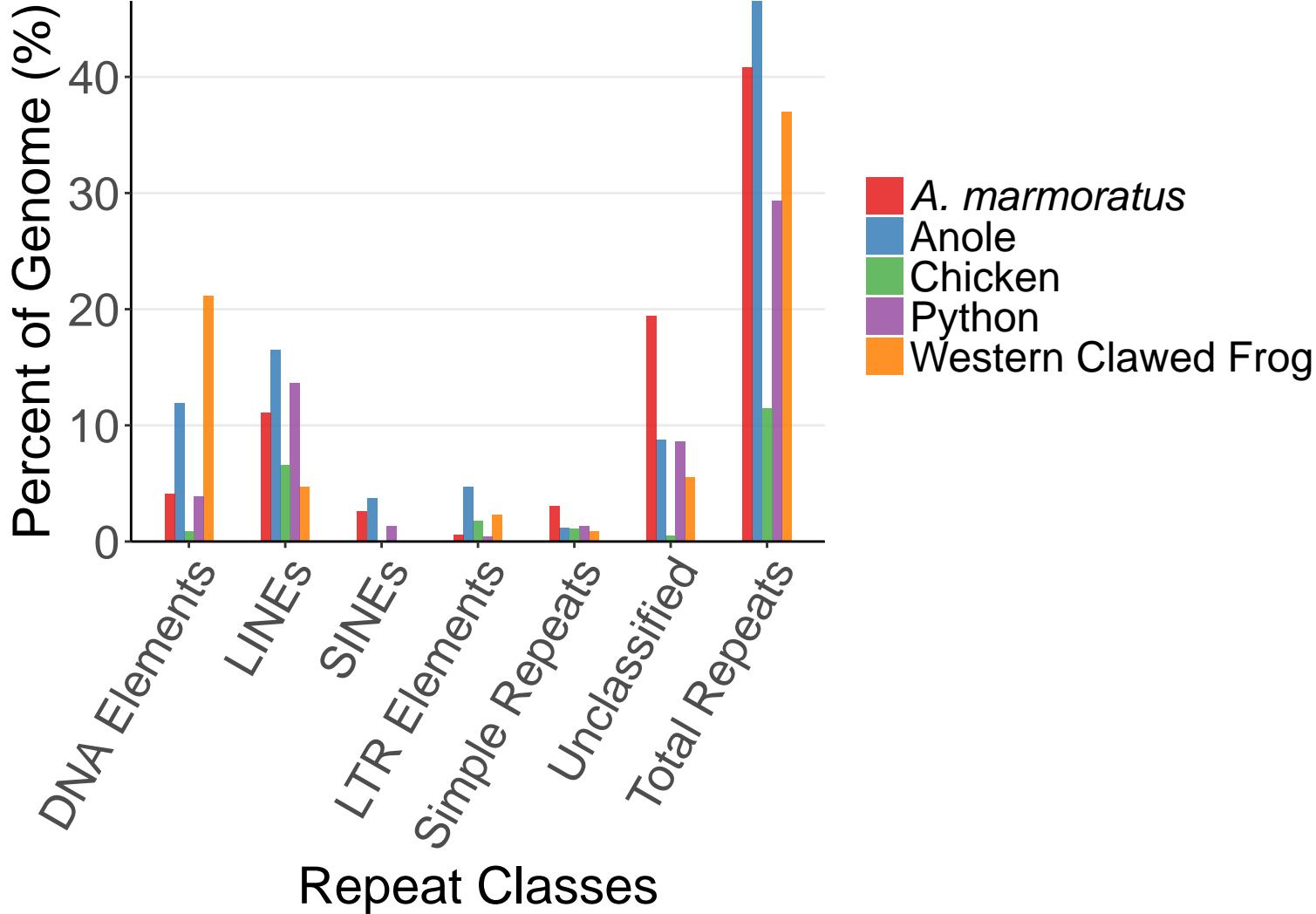
## Ploidy Distribution

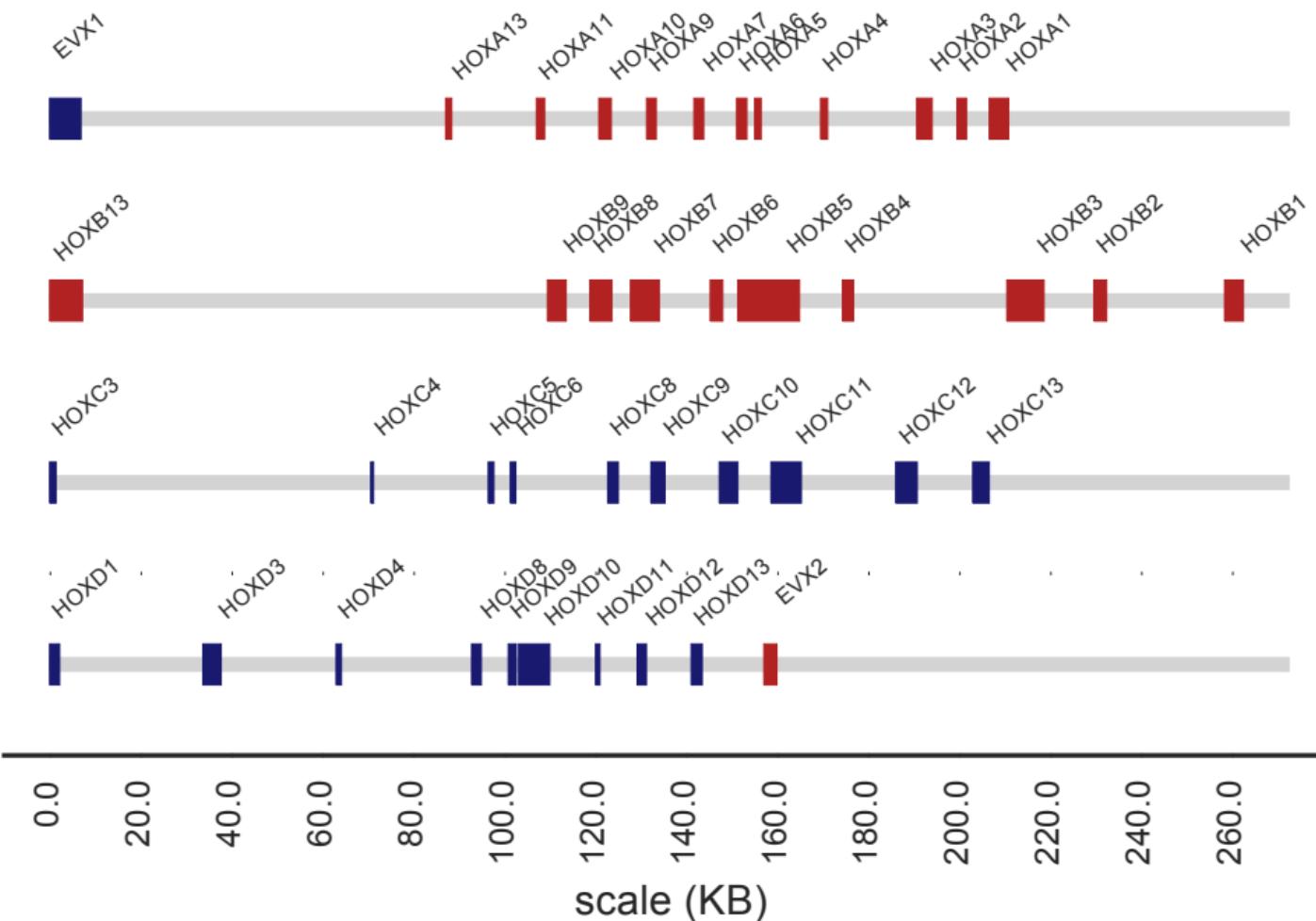


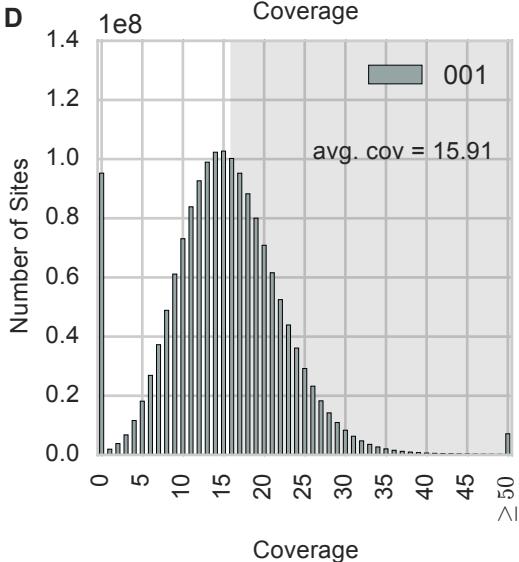
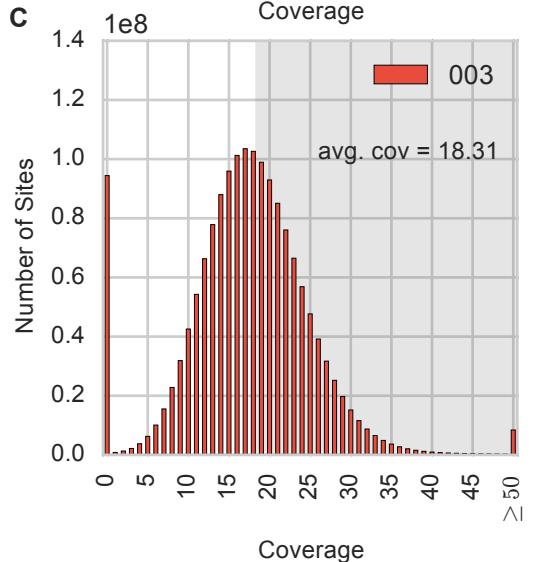
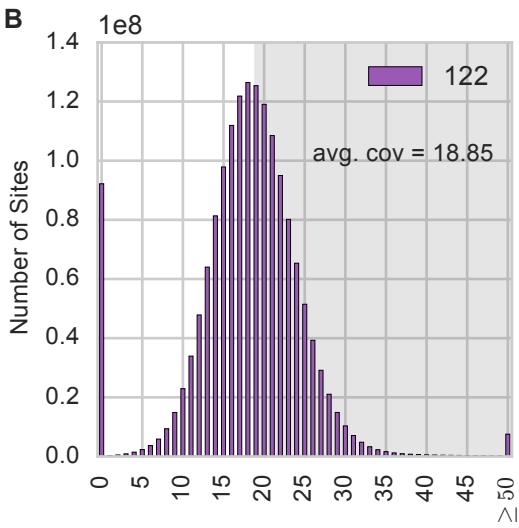
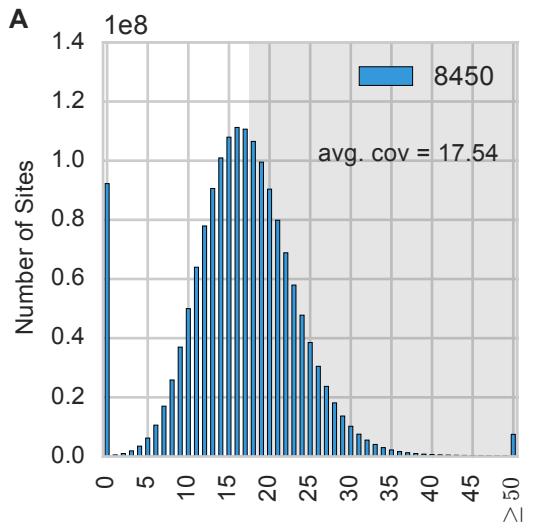
## Ploidy Distribution

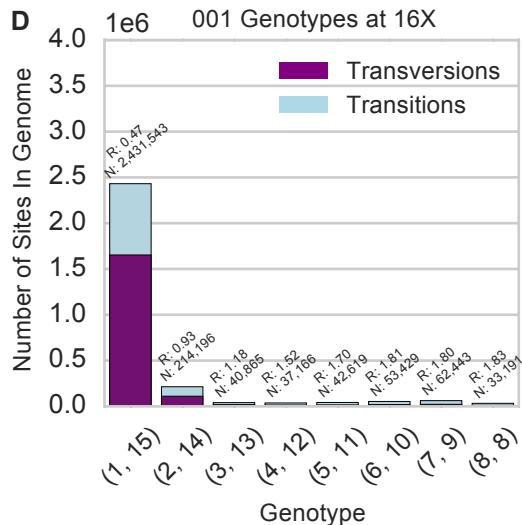
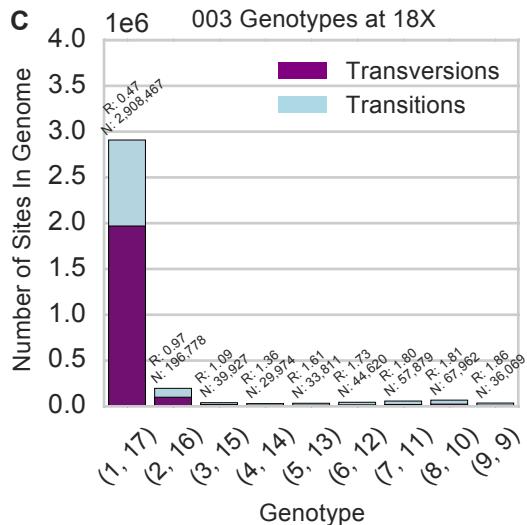
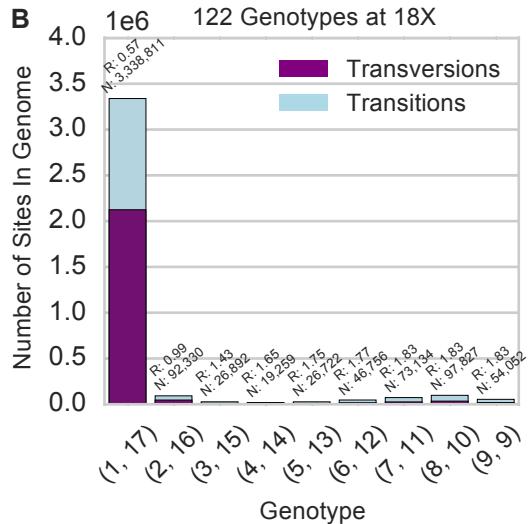
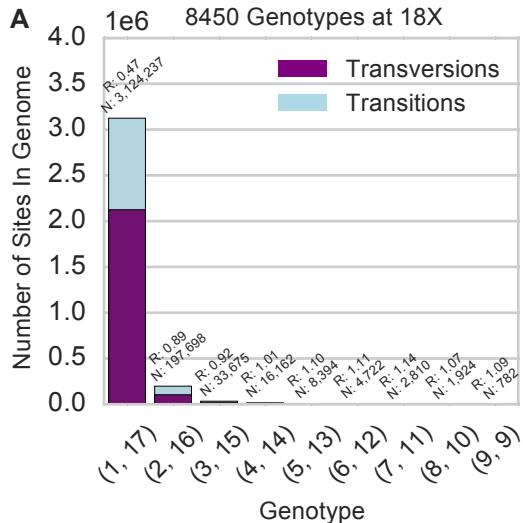


# Repeat Classes in Genomes









### Ratio of 122:8450 Average Het sites to per 10kb 5.0Mb Sliding Window

