


High quality petrel reference genome from the snow petrel, *Padodroma nivea*

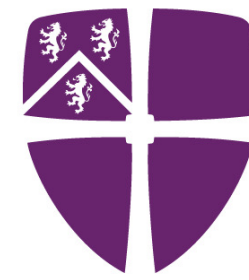


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Acknowledgements



Durham
University



Unlocking evidence for
Antarctic
Sea Ice Evolution *from a*
novel biological archive



British
Antarctic Survey

NATURAL ENVIRONMENT RESEARCH COUNCIL



LEVERHULME
TRUST _____



Snow Petrels

- Antarctic bird
- Ice associated birds
- Nest in rocks
- Long lived
- Monogamous
- Can travel to the South Pole
- Spit in defense



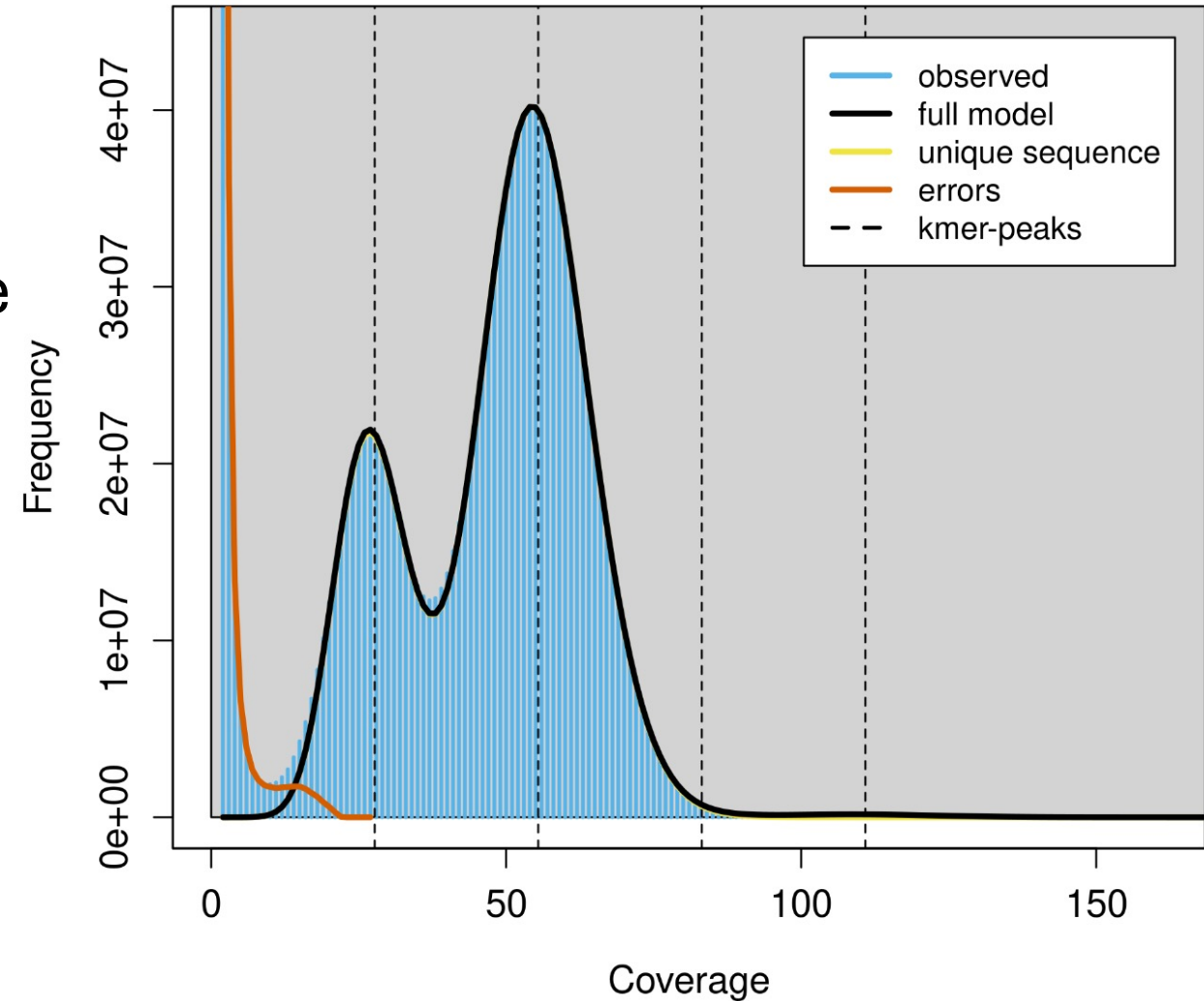
Photo: Thale Damm_Johnsen

Genome Assembly

- Blood from female collected at Utsteinen nunatak
- DNA extracted with EZNA Tissue DNA Kit
- Sequenced by Novogene on PacBio Revio
- 4,331,839 reads
- 55-52,372 bp long
- 16,150.4 average read length



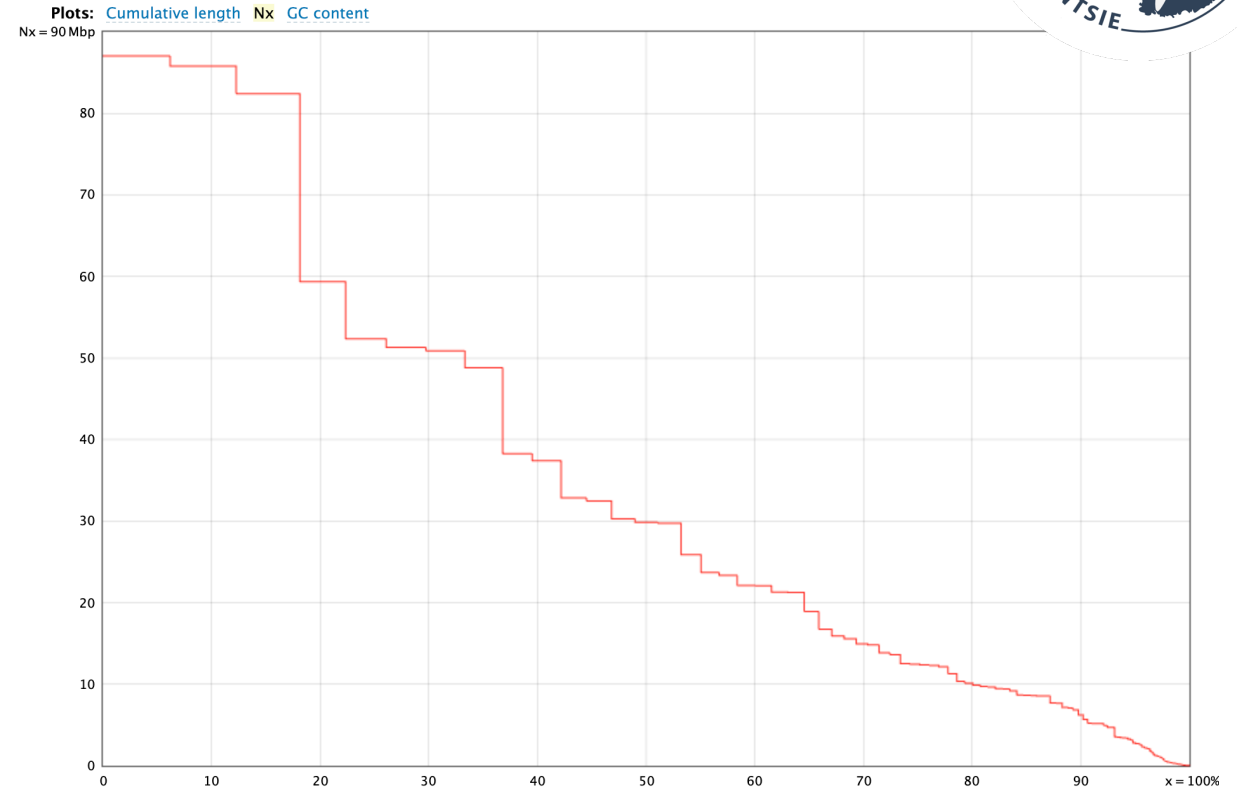
len:1,144,147,974bp uniq:94.5%
aa:99.2% ab:0.826%
kcov:27.7 err:0.0597% dup:0.475 k:21 p:2





Genome Assembly

1. Bam reads to fastq
2. Filtering HiFi reads
97 reads removed
3. HiFi Assembly
4. Check for contamination
NCBI FCS-GX
5. Removed duplicates
purge_dups
6. Check Quality



Number of contigs: 228

Length: 1,335,759,149 bases

Contig N50: 30,282,880

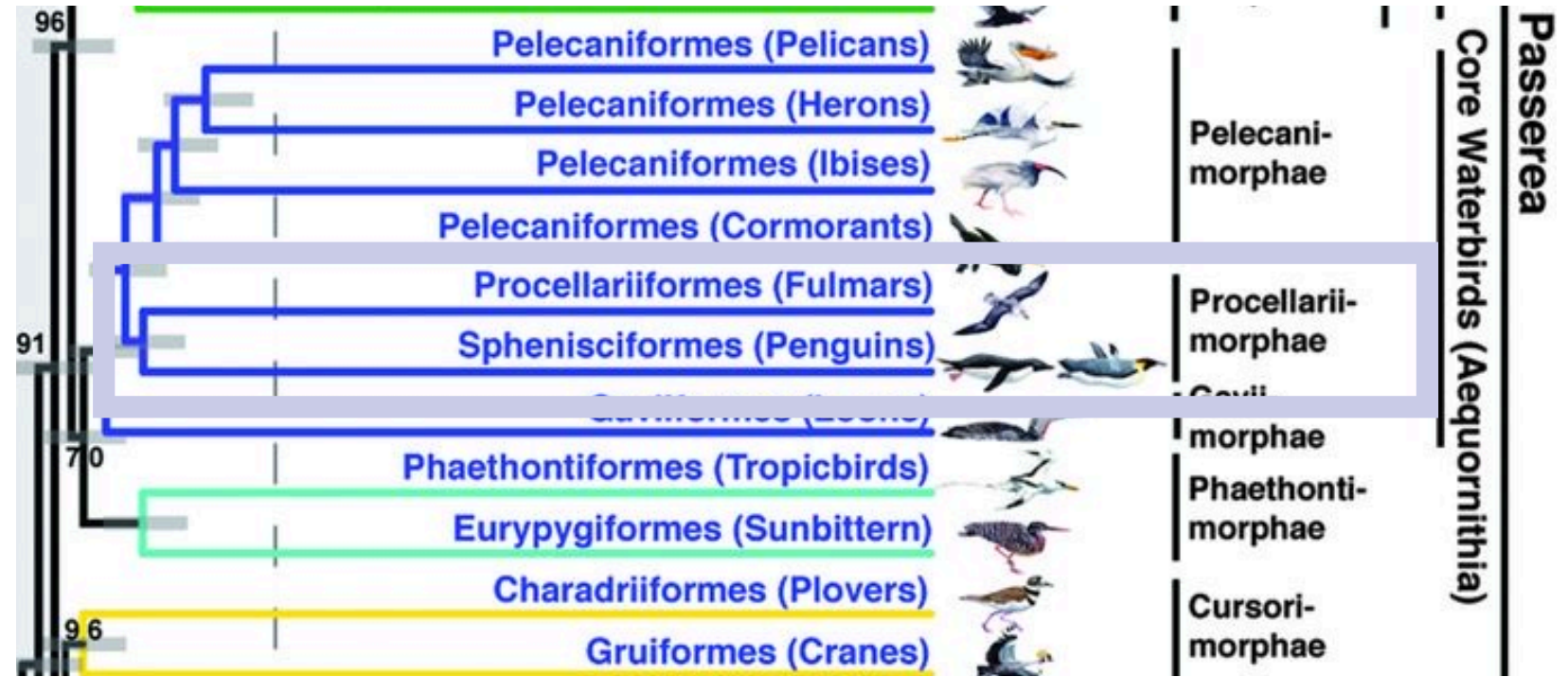
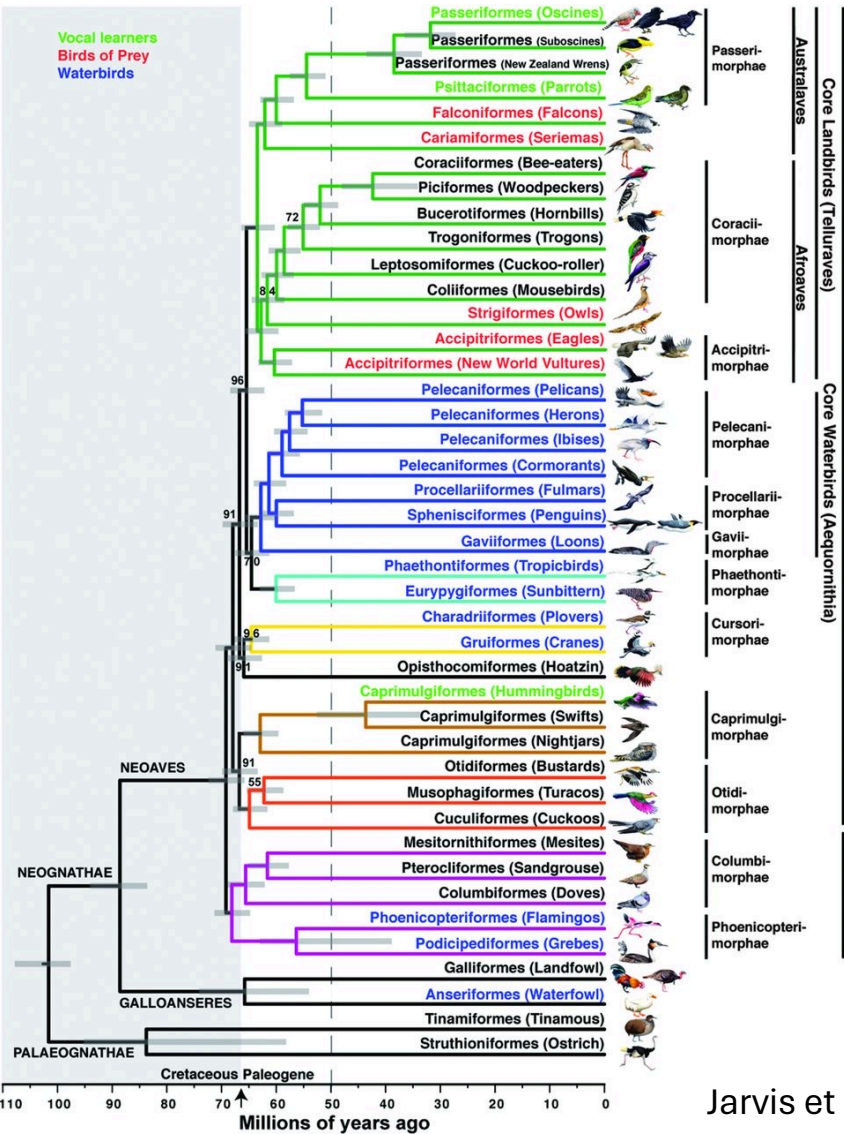


Genome Quality

- What genomes to compare to?
 - Only the species in their genus
- 9 publicly available petrel genomes
 - Average of 69,287 contigs per genome
 - 4,252 is the fewest
- Southern Giant Petrel genome of published in 2021, but only available as raw reads
 - 1,199 contigs

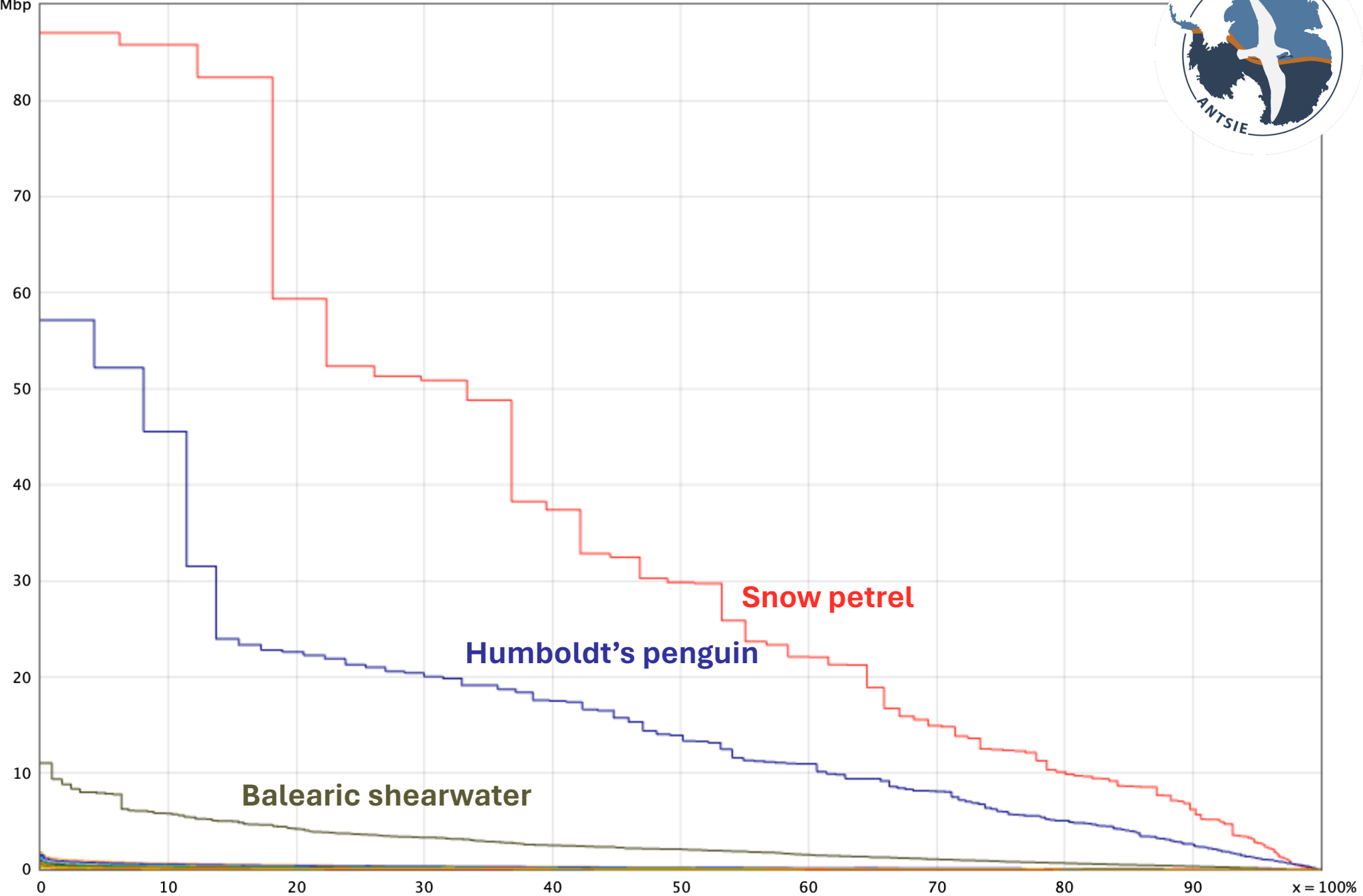


Austrodyptornithes/Procellariimorphae



Contigs

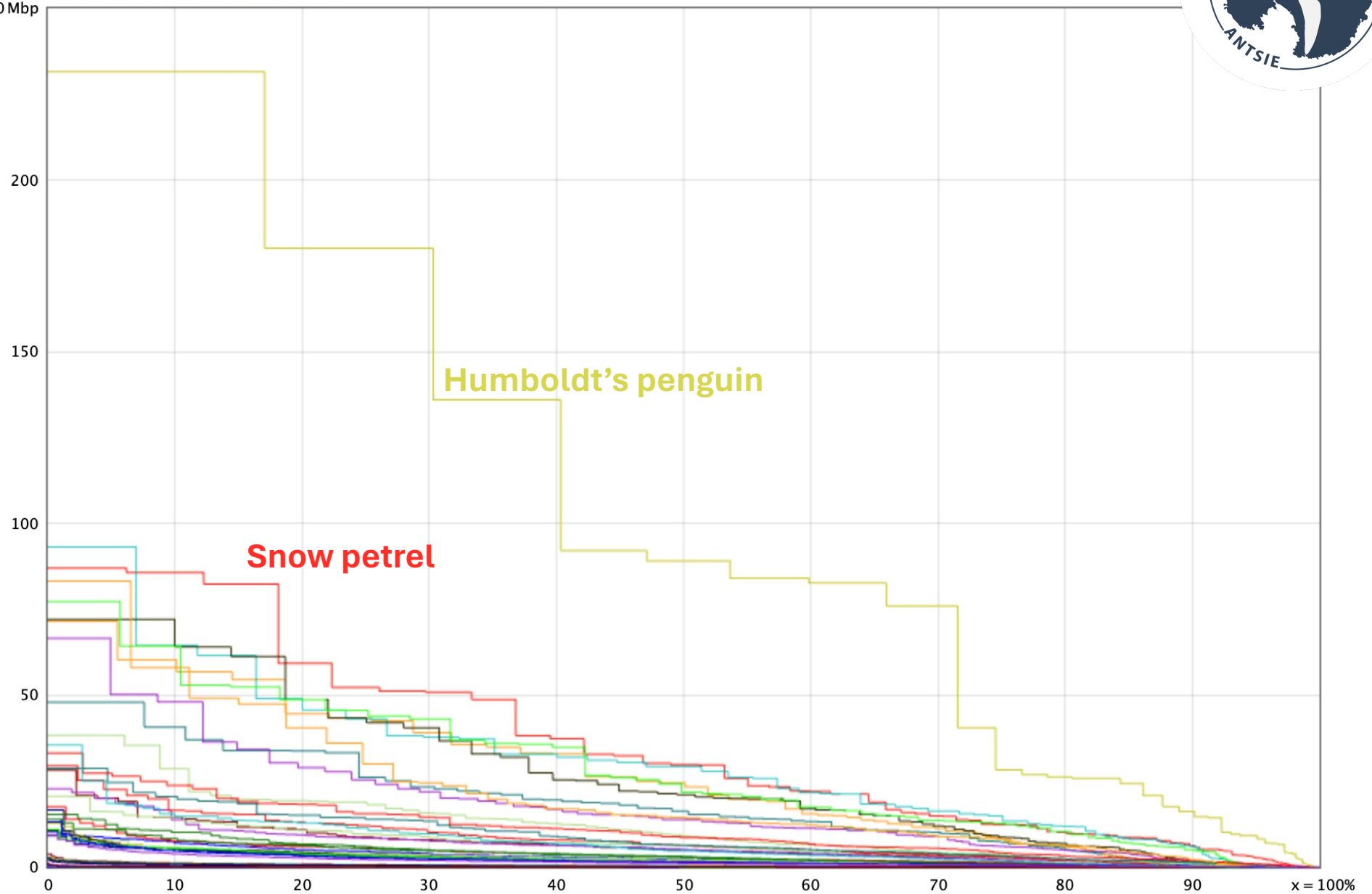
Plots: [Cumulative length](#) [Nx](#) [GC content](#)
Nx = 90 Mbp



Scaffolds



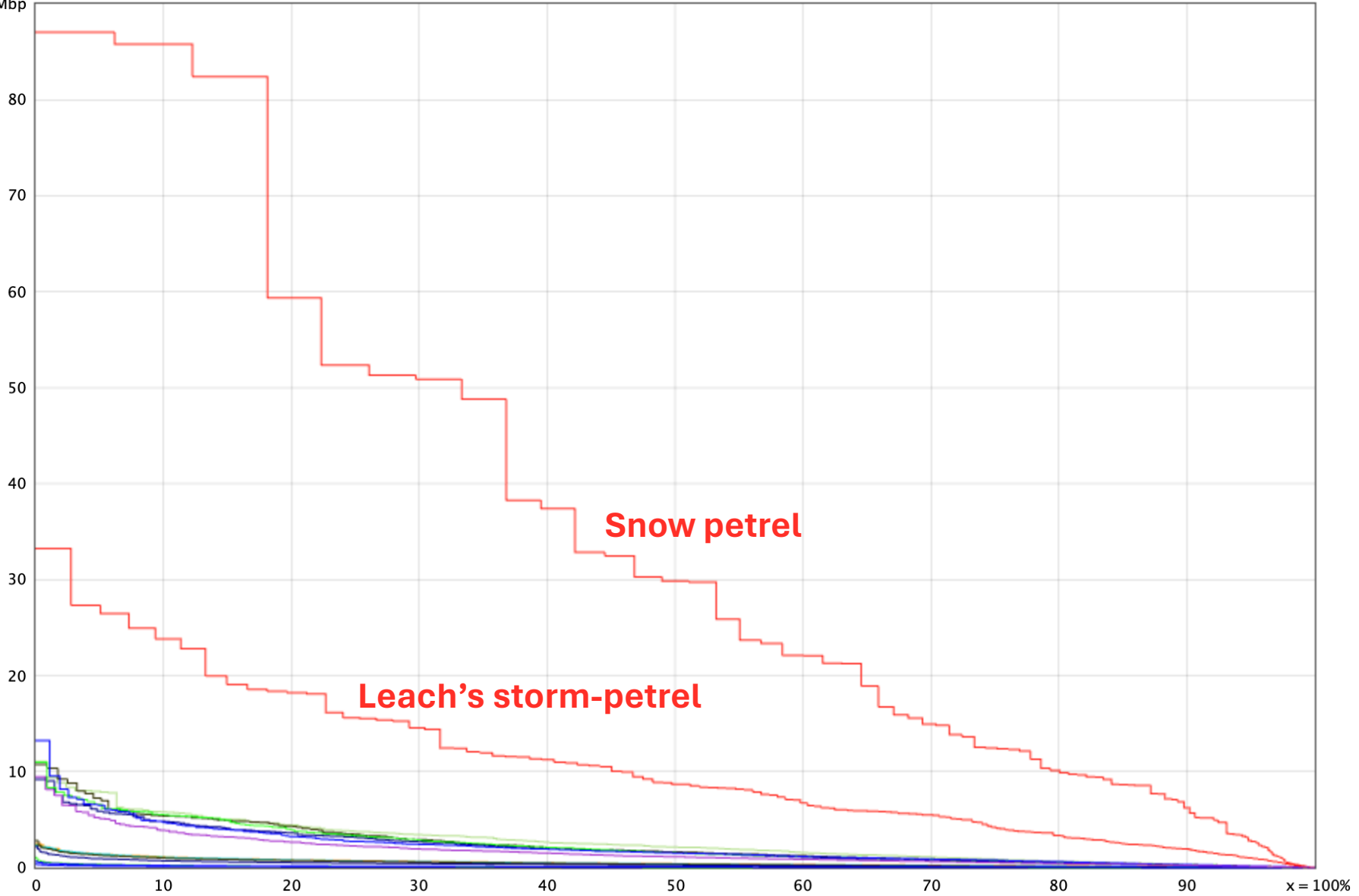
Plots: Cumulative length Nx GC content
Nx = 250 Mbp



Scaffolds for Fulmars only



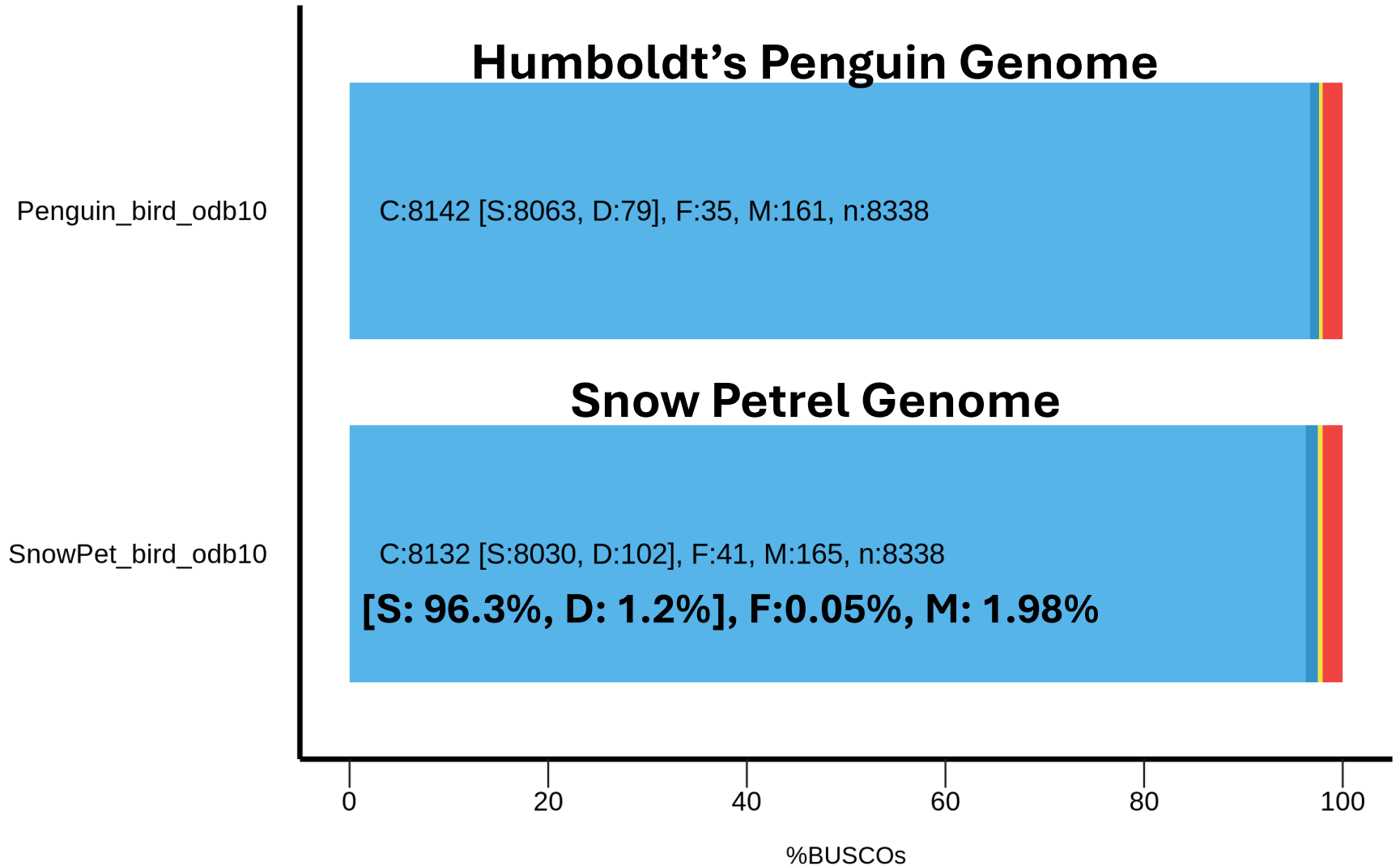
Plots: [Cumulative length](#) [Nx](#) [GC content](#)
Nx = 90 Mbp



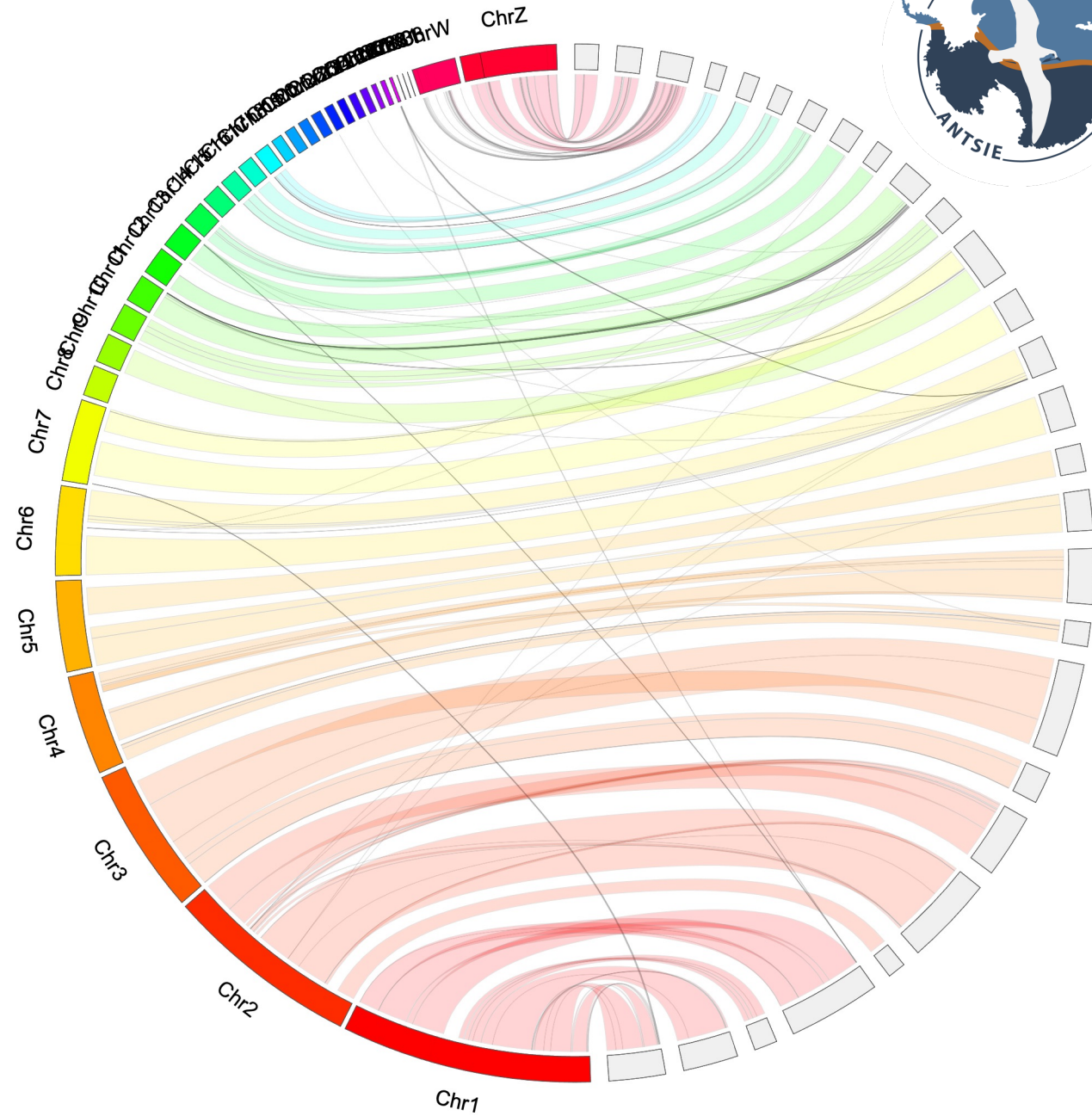
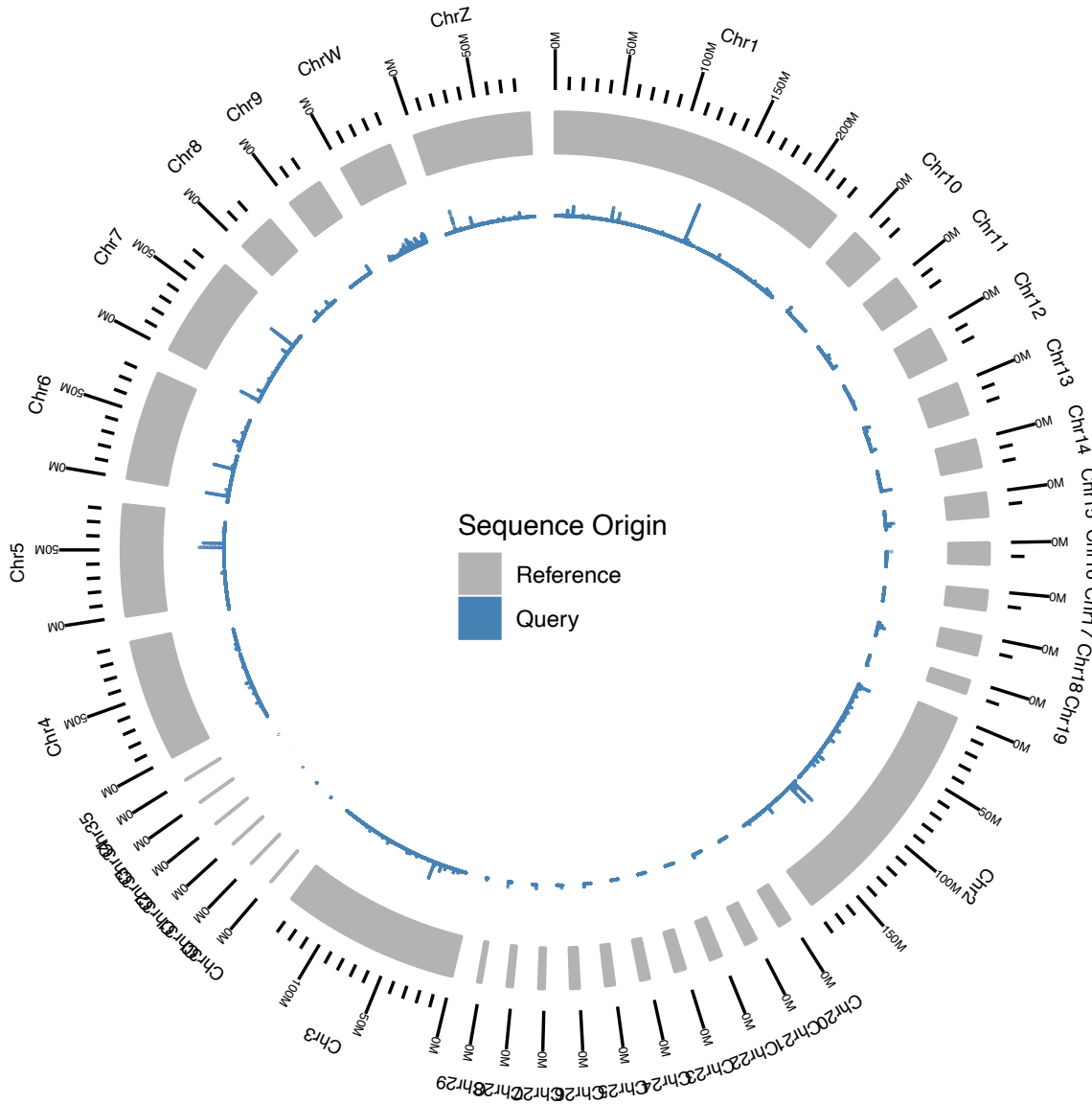
Genome Quality

- Contains complete copies of 97.5% of critical bird genes

BUSCO Assessment Results



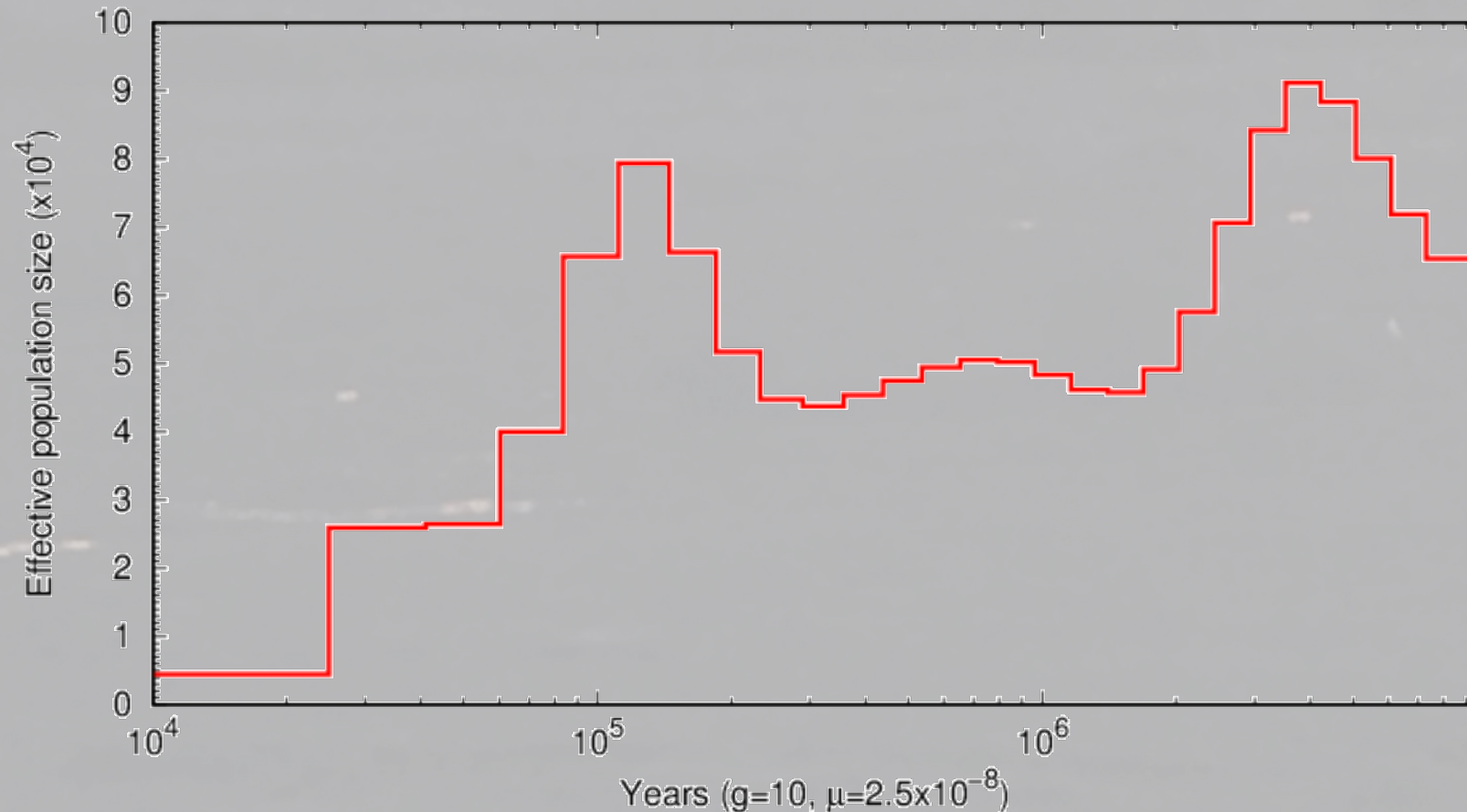
Genome Comparison





Snow Petrel Genetics

- PSMC (pairwise sequential Markovian coalescent)
 - HiFi reads from individual aligned to own reference genome



Future Work

- Short reads from same individual
- Scaffolding
- Remove mtDNA

- Low coverage whole genomes



Questions?

