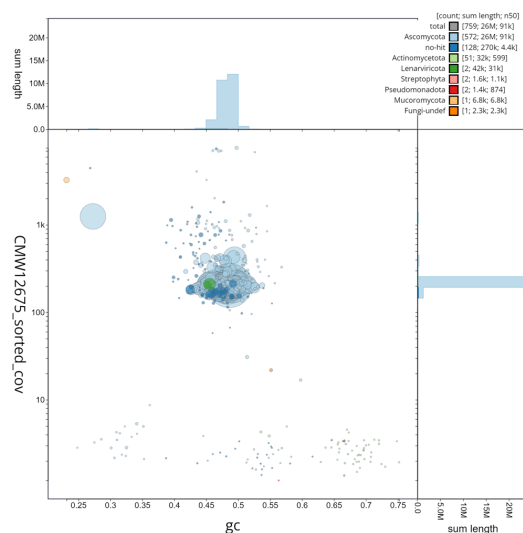
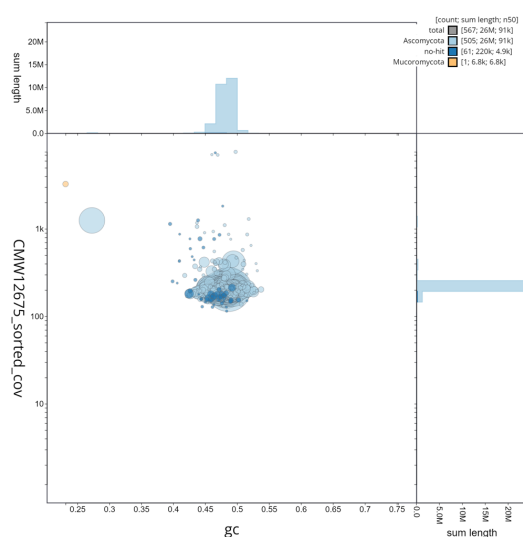


Ceratocystis pirilliformis
CMW-IA:5519

Unfiltered



Filtered



Ceratocystis pirilliformis
CMW-IA:4944

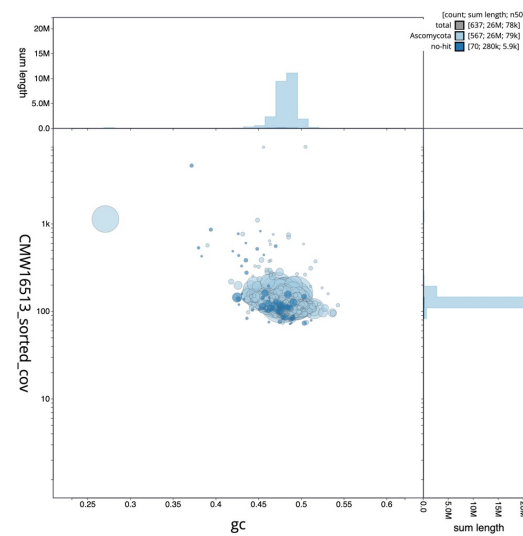
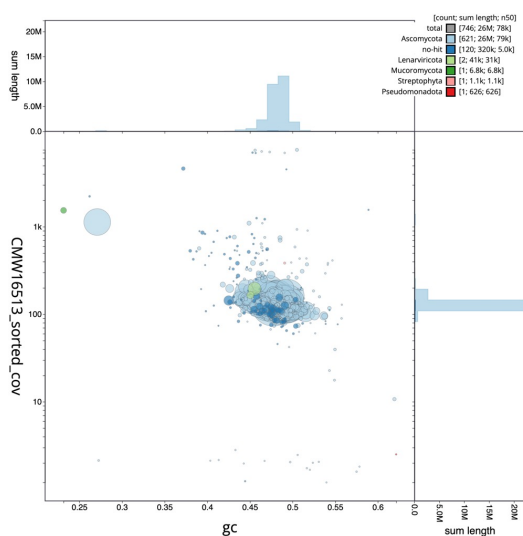


Fig. S1 Taxon-annotated GC-coverage plots (BlobPlots) for the two *Ceratocystis pirilliformis* genomes (CMW-IA:5519 and CMW-IA:4944). Both the unfiltered (left) and filtered (right) genomes are shown. The initial assemblies (v1.1) were filtered to keep contigs $\geq 1\,000$ bp in length and with at least 100X (CMW-IA:5519) or 67X (CMW-IA:4944) coverage depth.

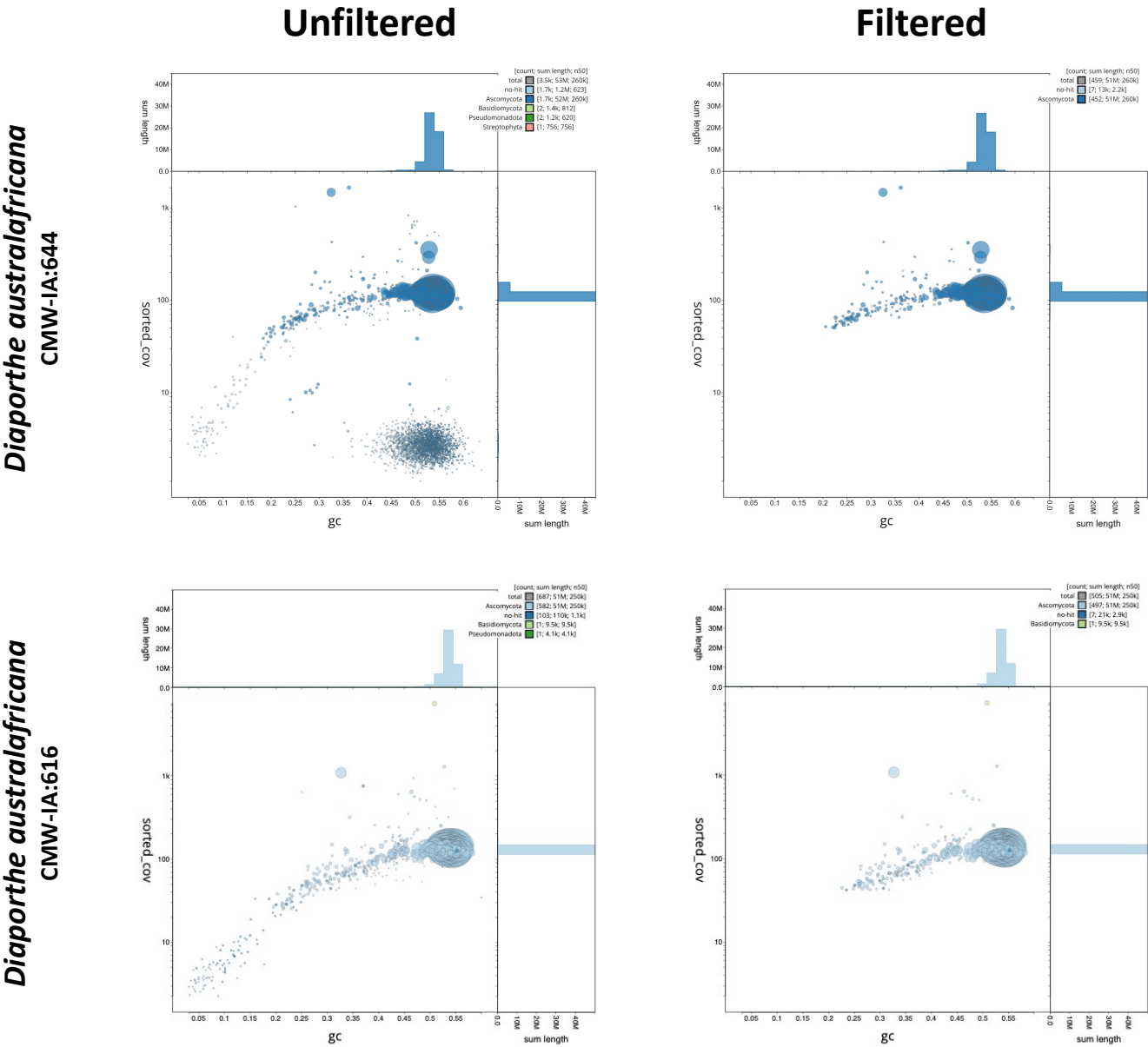


Fig. S2 Taxon-annotated GC-coverage plots (BlobPlots) for the two *Diaporthe australafricana* genomes (CMW-IA:644 and CMW-IA:616). Both the unfiltered (left) and filtered (right) genomes are shown. The initial assemblies (v1.1) were filtered to keep contigs $\geq 1\,000$ bp in length and with at least 15X coverage depth.

Fusarium ophioides
CMW-IA 5007

Fusarium ophioides
CMW-IA:5006

Fusarium ophioides
CMW-IA:4746

Unfiltered

Filtered

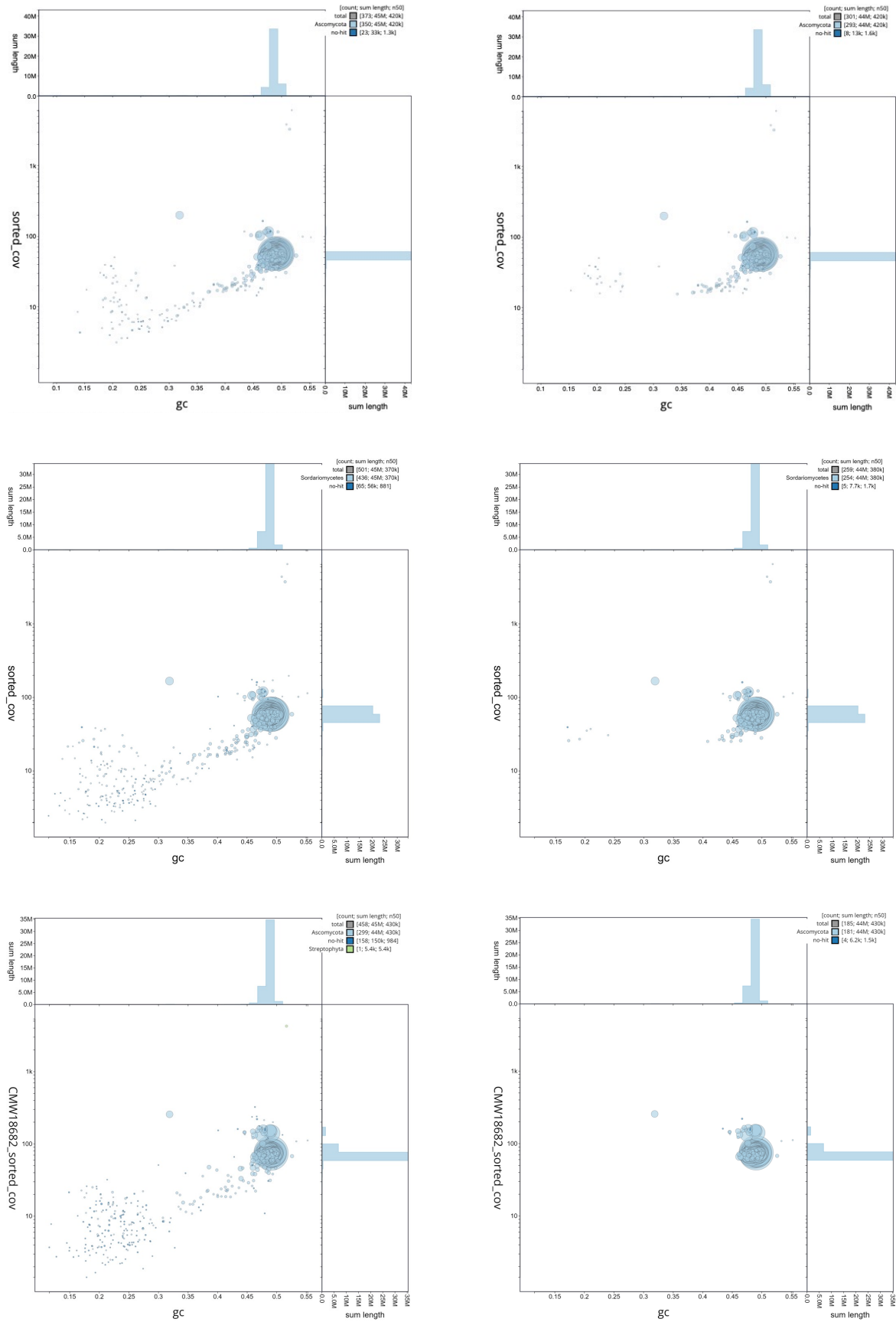


Fig. S3 Taxon-annotated GC-coverage plots (BlobPlots) for the three *Fusarium ophioides* genomes (CMW-IA:5007, CMW-IA:5006, and CMW-IA:4746). Both the unfiltered (left) and filtered (right) genomes are shown. The initial assemblies (v1.1) were filtered to keep contigs ≥ 1 000 bp in length and with at least 25X coverage depth.

Paecilomyces lecythidis
CMW-IA:5739

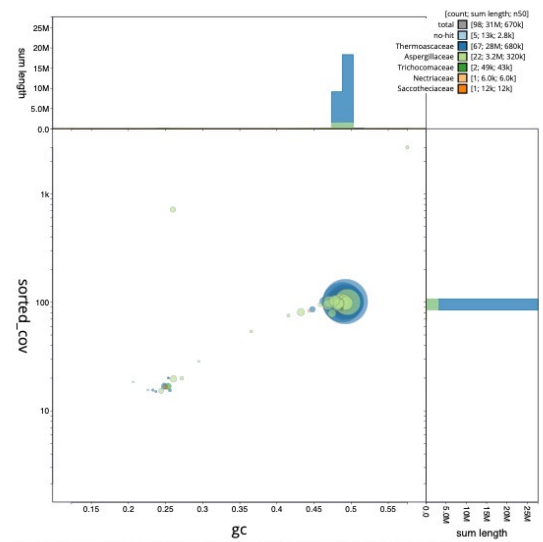
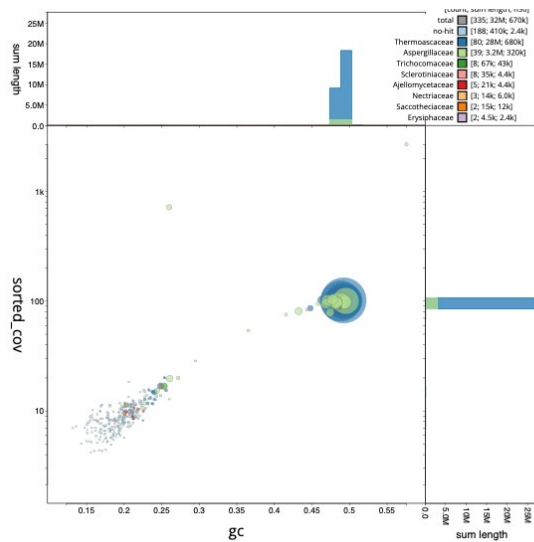


Fig. S4 Taxon-annotated GC-coverage plots (BlobPlots) for the two *Paecilomyces lecythidis* genomes (CMW-IA:5739 and CMW-IA:550). Both the unfiltered (left) and filtered (right) genomes are shown. The initial assemblies (v1.1) were filtered to keep contigs $\geq 1\,000$ bp in length and with at least 15X coverage depth.

Sporothrix stenoceras
CMW-IA:5313

Sporothrix stenoceras
CMW-IA:5347

Sporothrix stenoceras
CMW-IA:5364

Unfiltered

Filtered

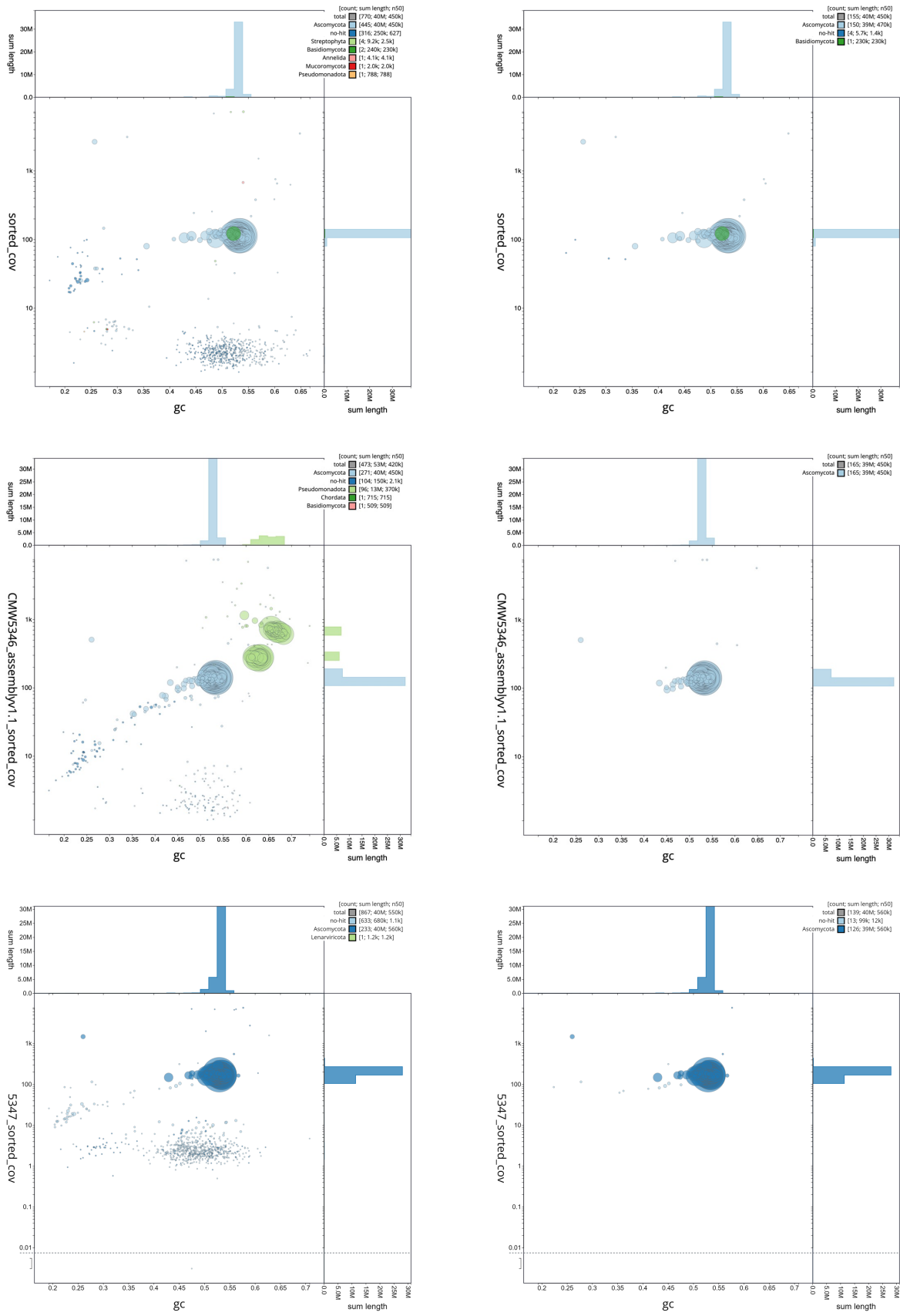


Fig. S5 Taxon-annotated GC-coverage plots (BlobPlots) for the three *Sporothrix stenoceras* genomes (CMW-IA:5313, CMW-IA:5347, and CMW-IA:5364). Both the unfiltered (left) and filtered (right) genomes are shown. The initial assemblies (v1.1) were filtered to keep contigs ≥ 1 000 bp in length and with at least 50X coverage depth. The assembly for CMW-IA:5347 was also filtered based on taxonomy, removing contigs labelled as *Pseudomonadota*, a bacterial phylum.