

Part 3: Kraken2 Statistics

Kraken2 classification results have been compiled and saved as CSV files.

The Kraken2 results data includes:

- Sample names
- Species classifications
- Unaligned clade reads
- Non-human clade reads
- Dataset information (unaligned/nonhuman)
- Merged input read counts from RRstats
- Additional optional columns (confidence, minimum hit groups, etc.)

Data source: Combined from unaligned_kreports/ and nonhuman_kreports/

Processing: output_processing.R with species filtering and merging

Merging: Combined with runtime and read statistics by sample name

Output location: Check outputs/ directory for:

- sample_report_data_with_metadata*op.csv (combined data)
- sample_report_data_[dataset]_*op.csv (dataset-specific files)

Key findings:

- Average number of species found per sample before secondary filtering: 611.55
- Average number of species found per sample after secondary filtering: 80.075
- Number of unique species across all unaligned samples: 579

Homo sapiens: 66784243.6

Severe acute respiratory syndrome-related coronavirus: 3677261.7

Fusobacterium pseudoperiodonticum: 541689.5

Solobacterium moorei: 460470.5

Cupriavidus pauculus: 378178.25

Veillonella atypica: 293441.4

Sphingomonas paucimobilis: 263914.894736842

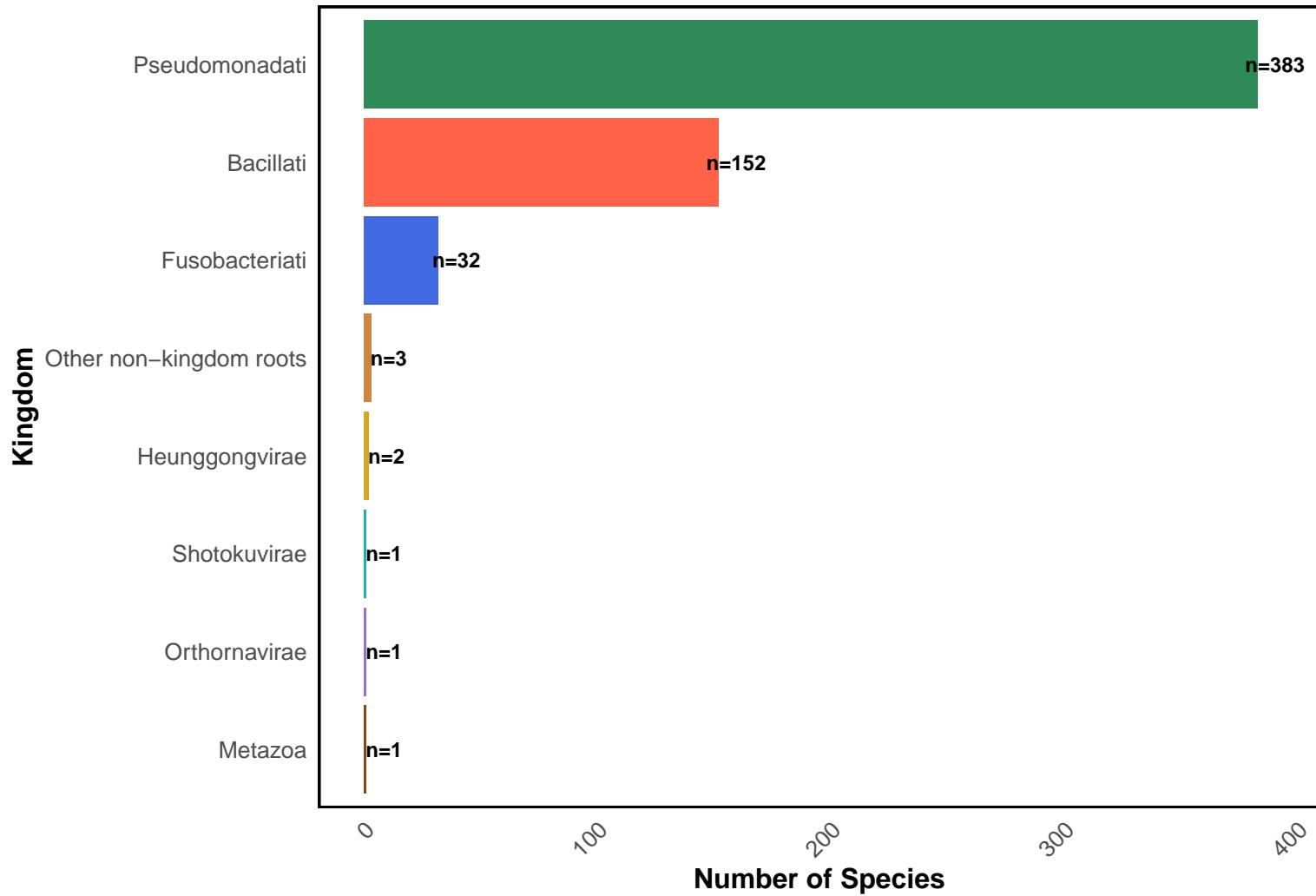
Staphylococcus aureus: 223765.111111111

Selenomonas sputigena: 167271

Haemophilus parahaemolyticus: 162031

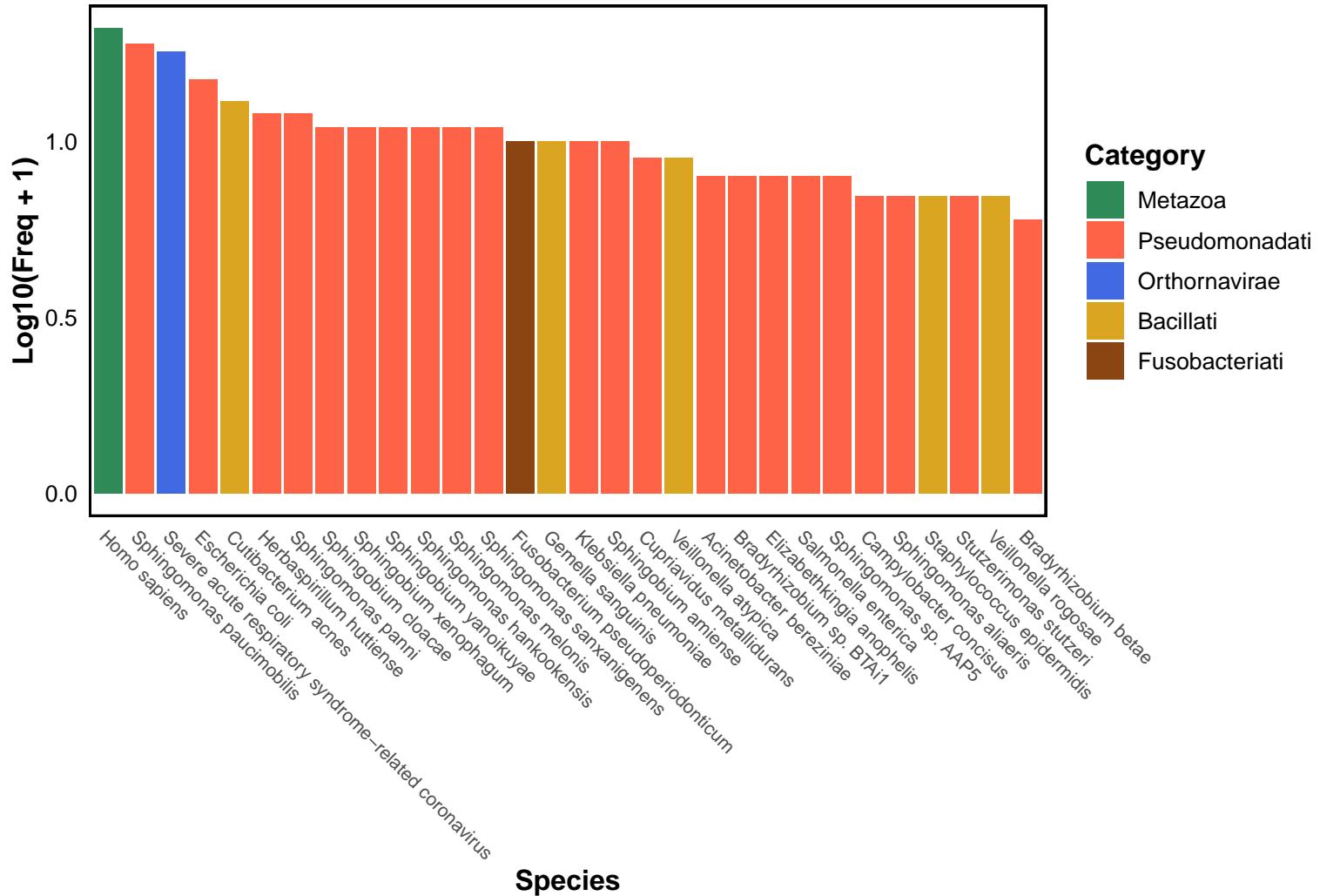
Species per Kingdom – All Samples

Total species: 575



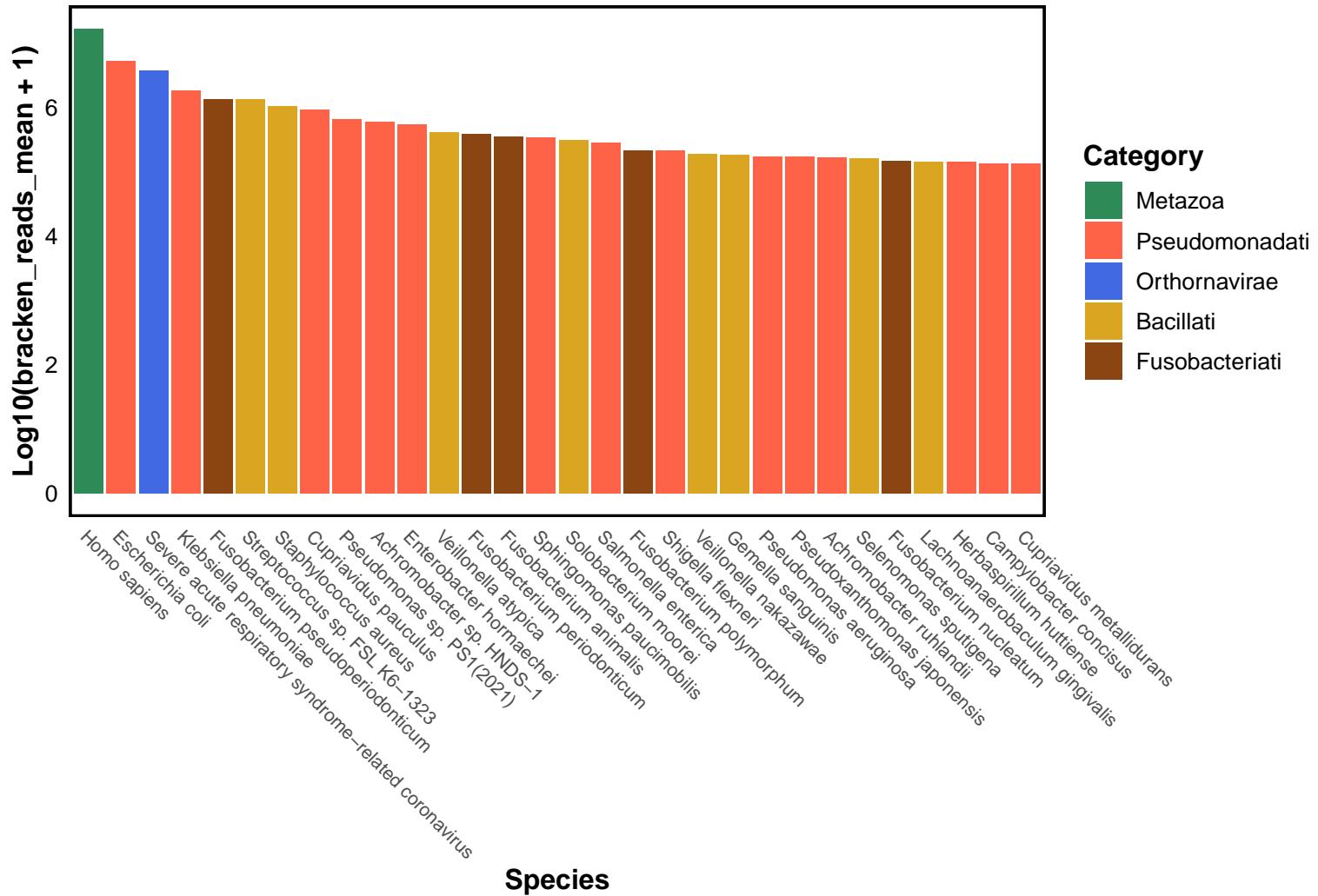
Species by Kingdom – All Samples

Top 30 species by Log10(Freq + 1)



Species by Kingdom – All Samples

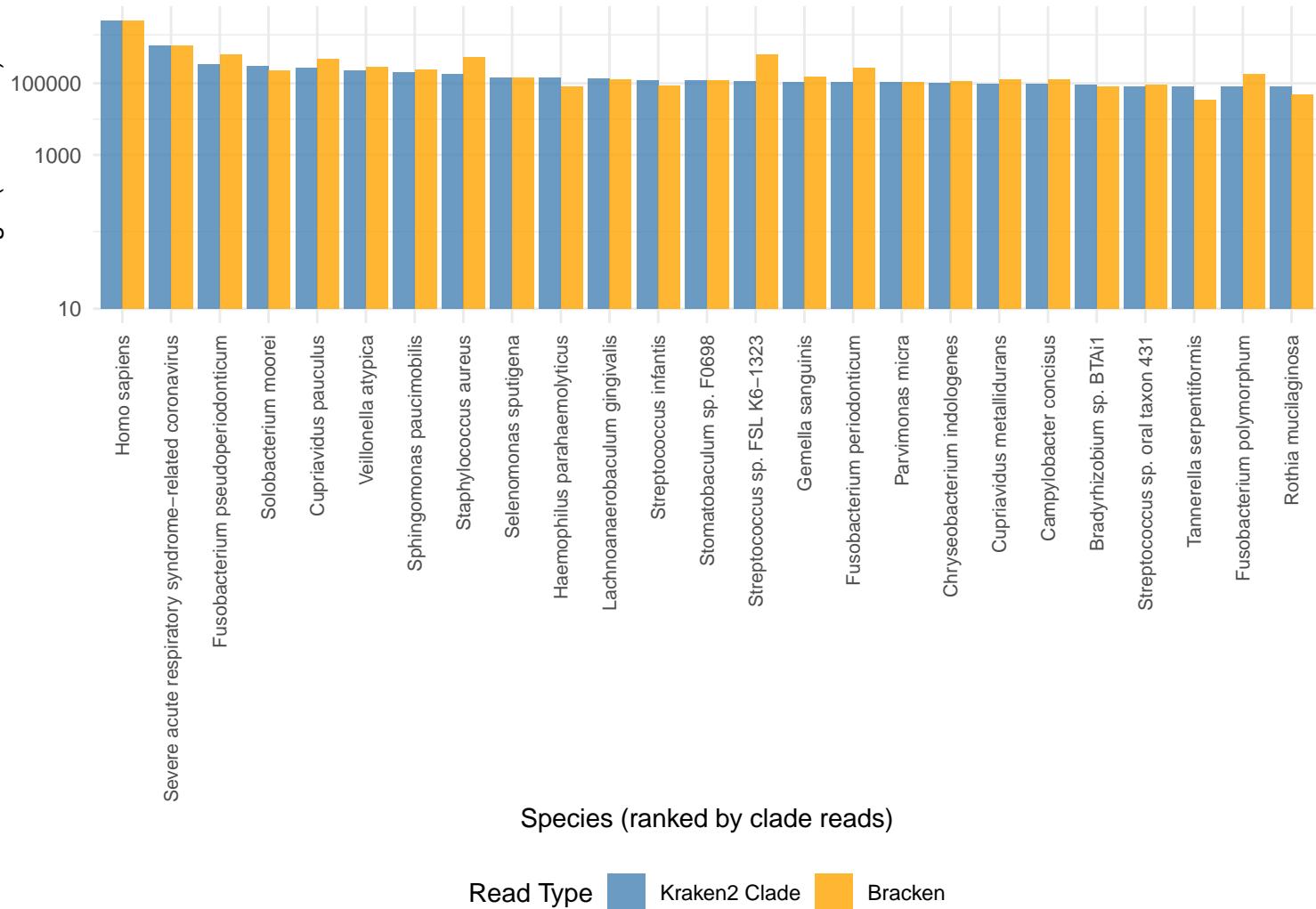
Top 30 species by Log10(bracken_reads_mean + 1)



Kraken2 Clade Reads vs Bracken Reads (Top 25 Species)

Ranked by Kraken2 clade reads (log10 scale)

Log10(Reads + 1)



Species by Kingdom – All Samples

Top 30 species by avg_percentage

