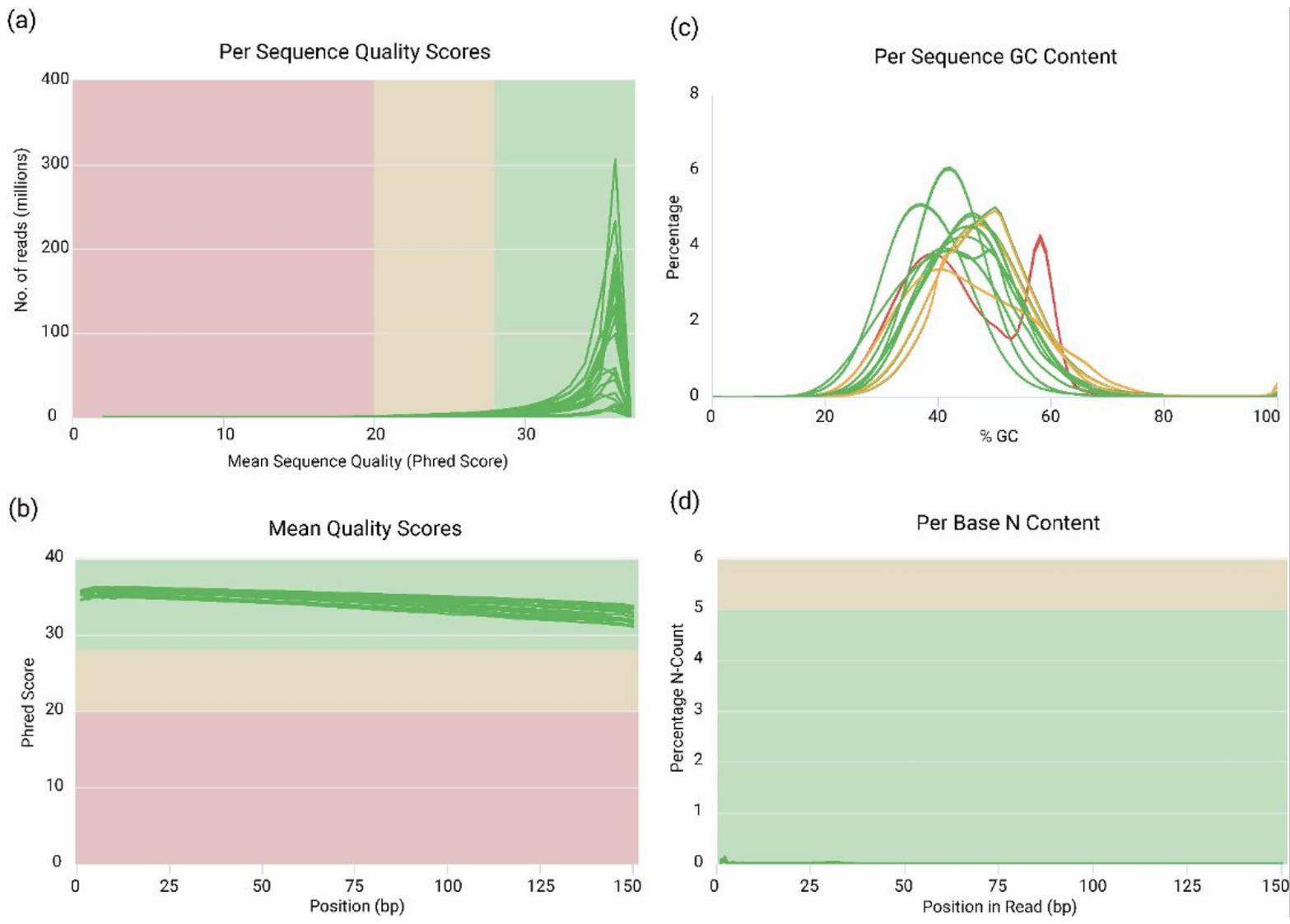
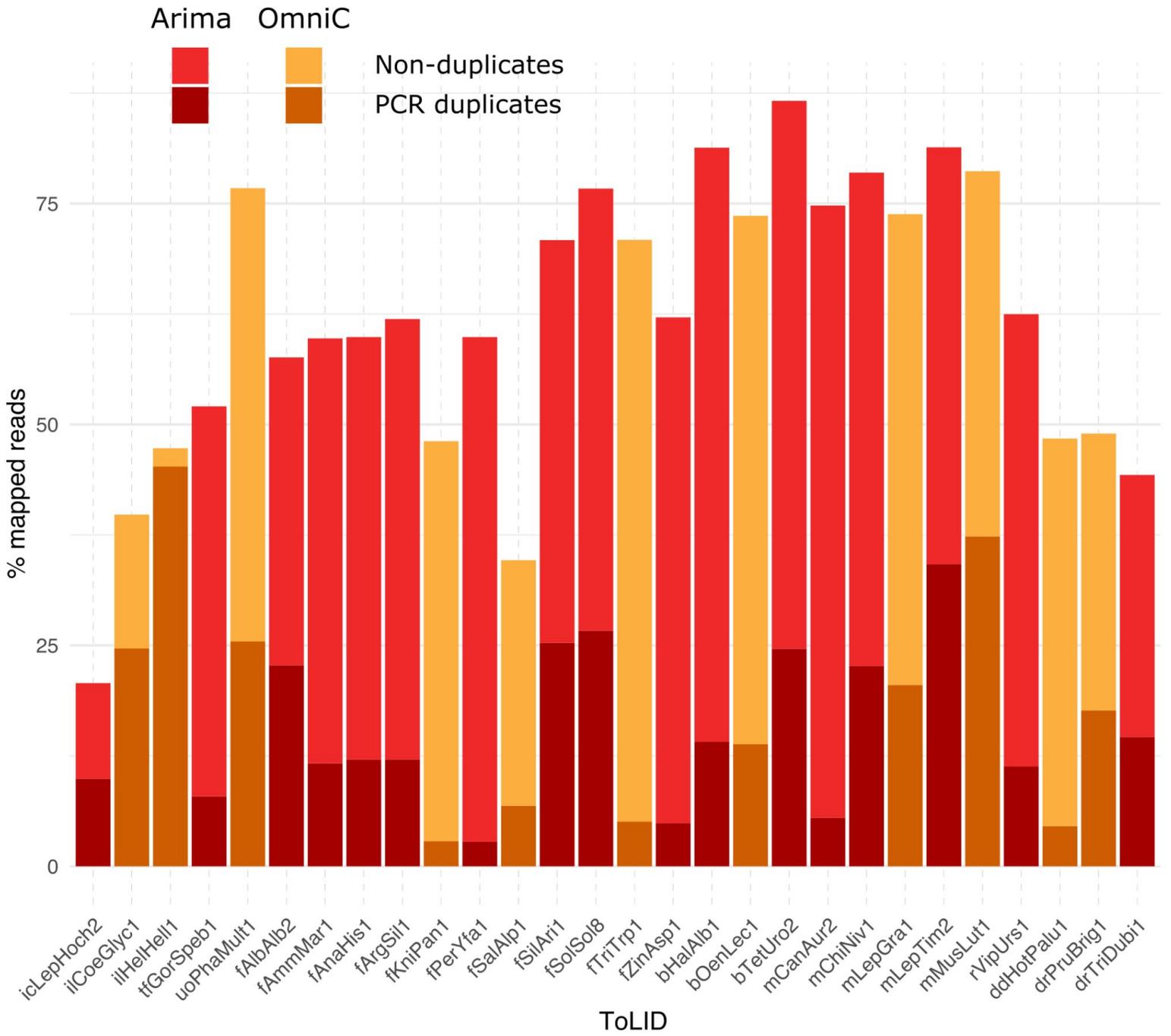


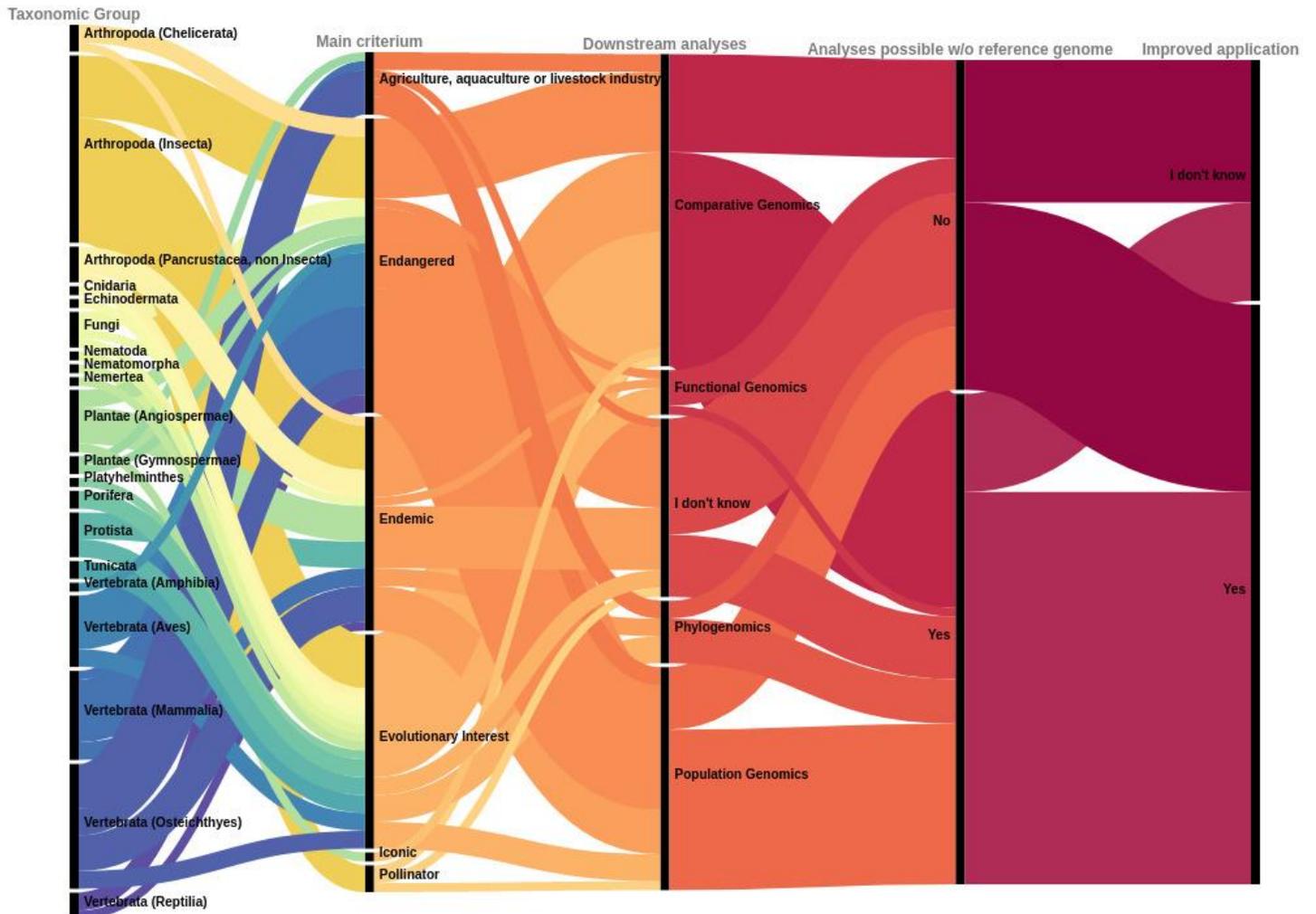
Extended Data Figure 1: Quality Assessment of RNA-seq Data . (a) Per Sequence Quality Scores: Distribution of quality scores across all sequences, with the y-axis representing the number of reads in millions. (b) Mean Quality Scores: The average quality score at each position in a read. (c) Per Sequence GC Content: The GC content distribution across all sequences. (d) Per Base N Content: The proportion of N content at each base position in the reads, reflecting ambiguous base calls.



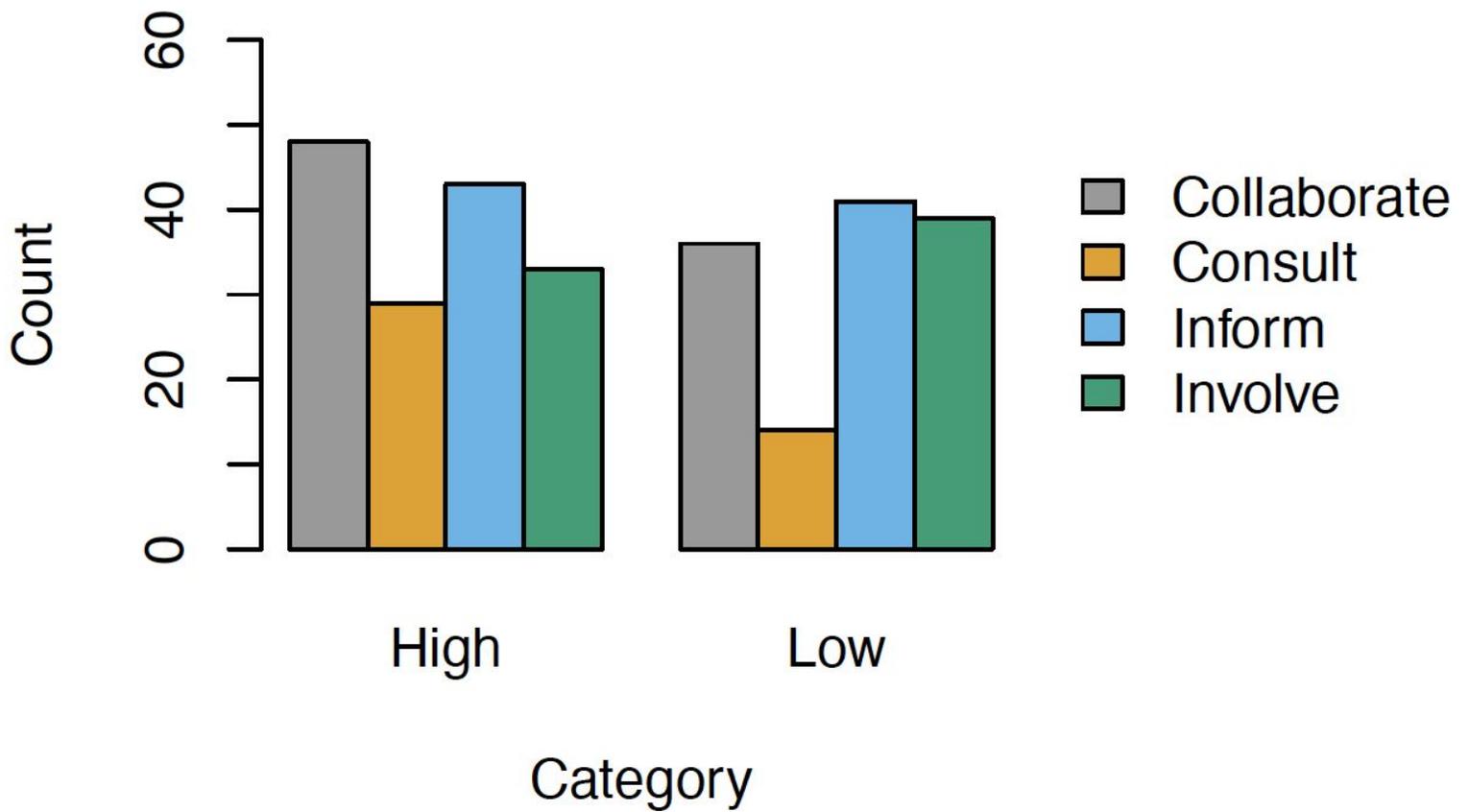
Extended Data Figure 2: Quality Assessment of Hi-C Sequencing Data. (a) Per Sequence Quality Scores: Distribution of quality scores across all sequences, with the y-axis representing the number of reads in millions. (b) Mean Quality Scores: The average quality score at each position in a read. (c) Per Sequence GC Content[HL2] : The GC content distribution across all sequences. (d) Per Base N Content: The proportion of N content at each base position in the reads, reflecting ambiguous base calls.



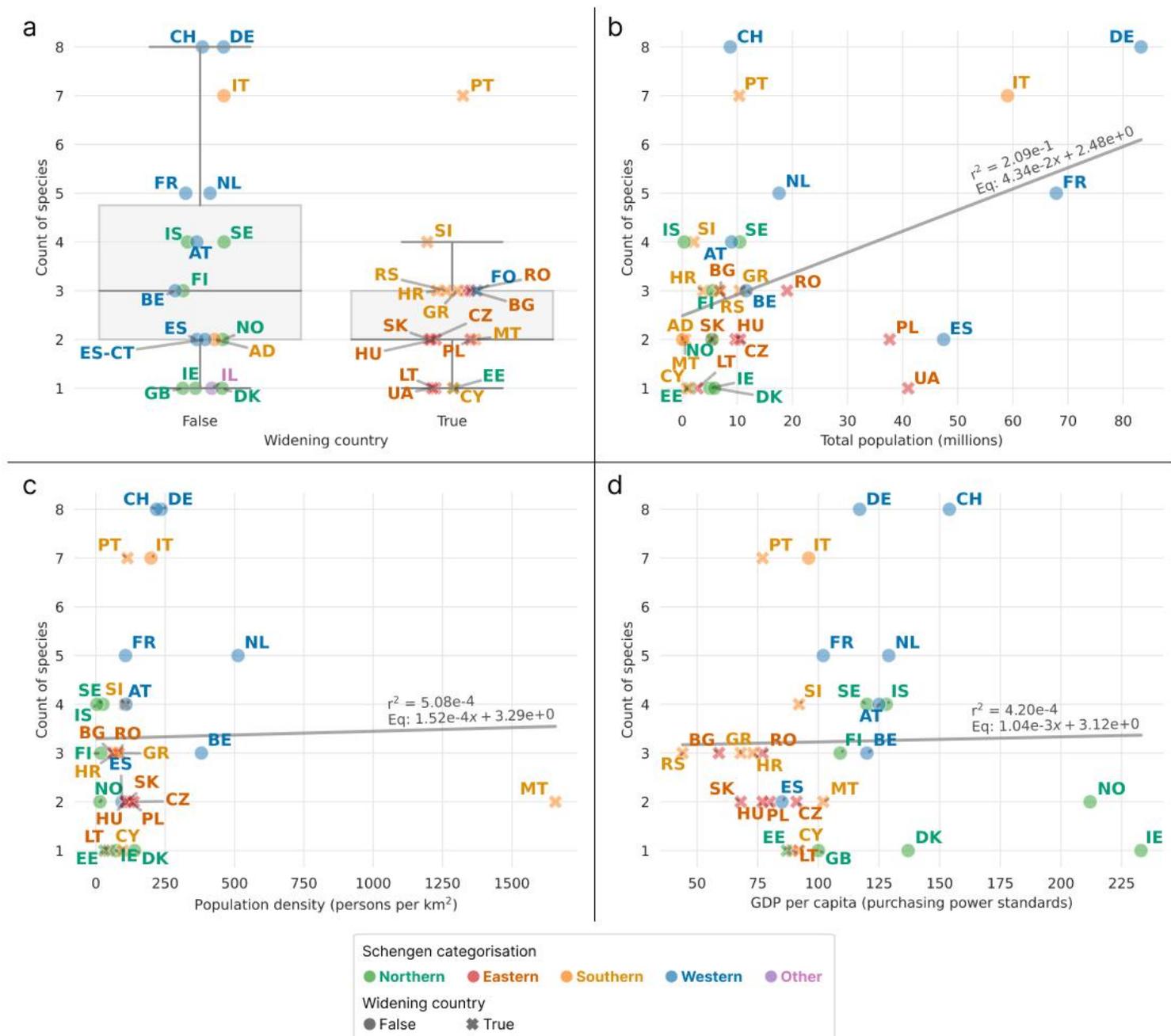
Extended Data Figure 4: Hi-C reads mapping metrics for completed (pre-curation and curated) assemblies according to kits used (Arima or OmniC).



Extended Data Figure 5: Summary of genome team data analysis survey responses.

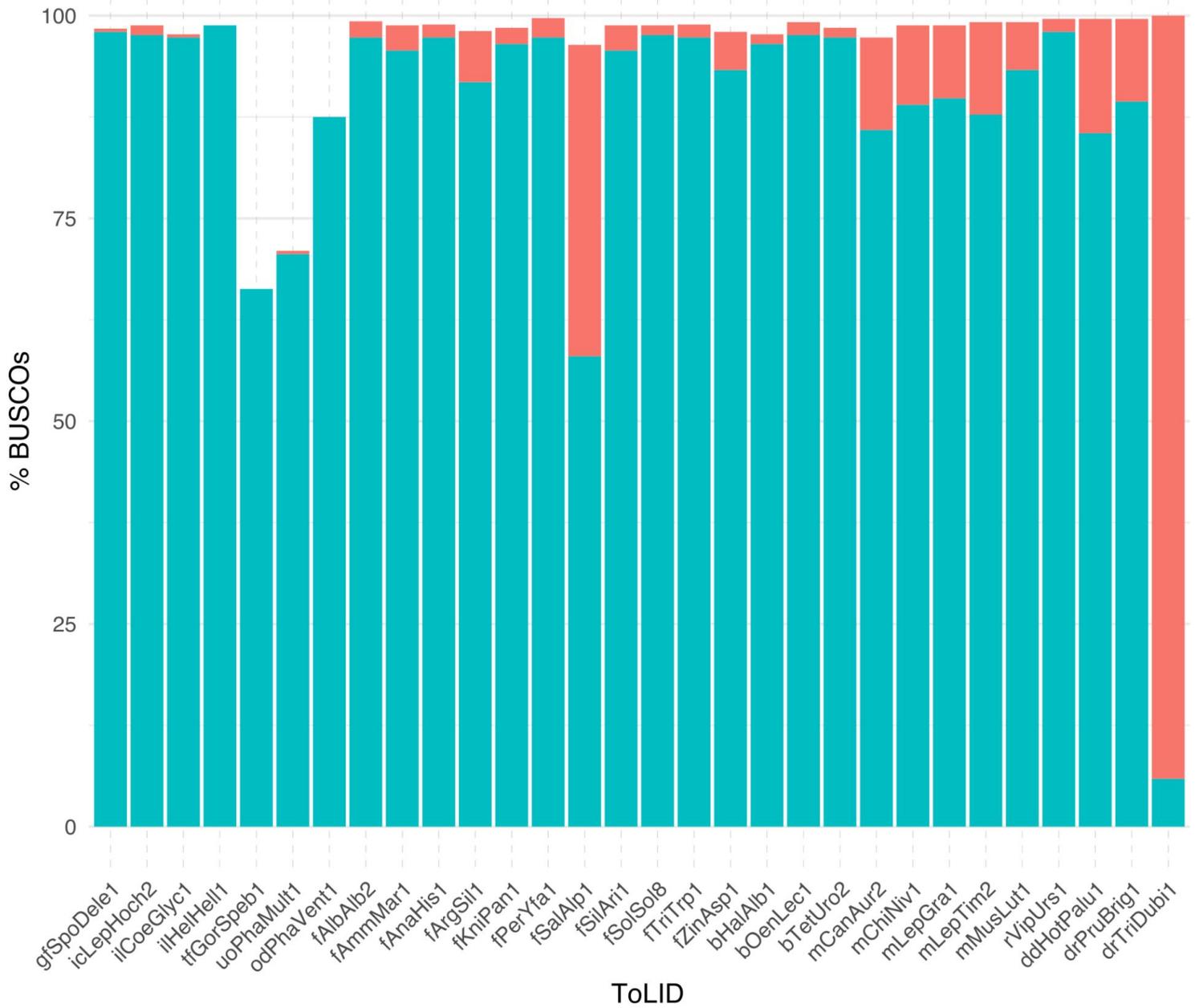
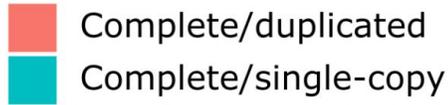


Extended Data Figure 6: The differences in how participants from countries with a GBARD higher than 1000 MM (High) and those with a GBARD lower than 1000 MM (Low) divided interested parties into the four categories of engagement.



Extended Data Figure 7. Relationship between number of species attributed per country and country characteristics. Distribution of the number of species attributed per country: (a) Categorized as non-Widening or Widening; (b) Total population; (c) Population density; (d) Gross Domestic Product (GDP) per capita in purchasing power standards. Data points labelled with ISO country codes. Country-level data for population, population density and GDP per capita in PPS, as sourced from Eurostat (2022).

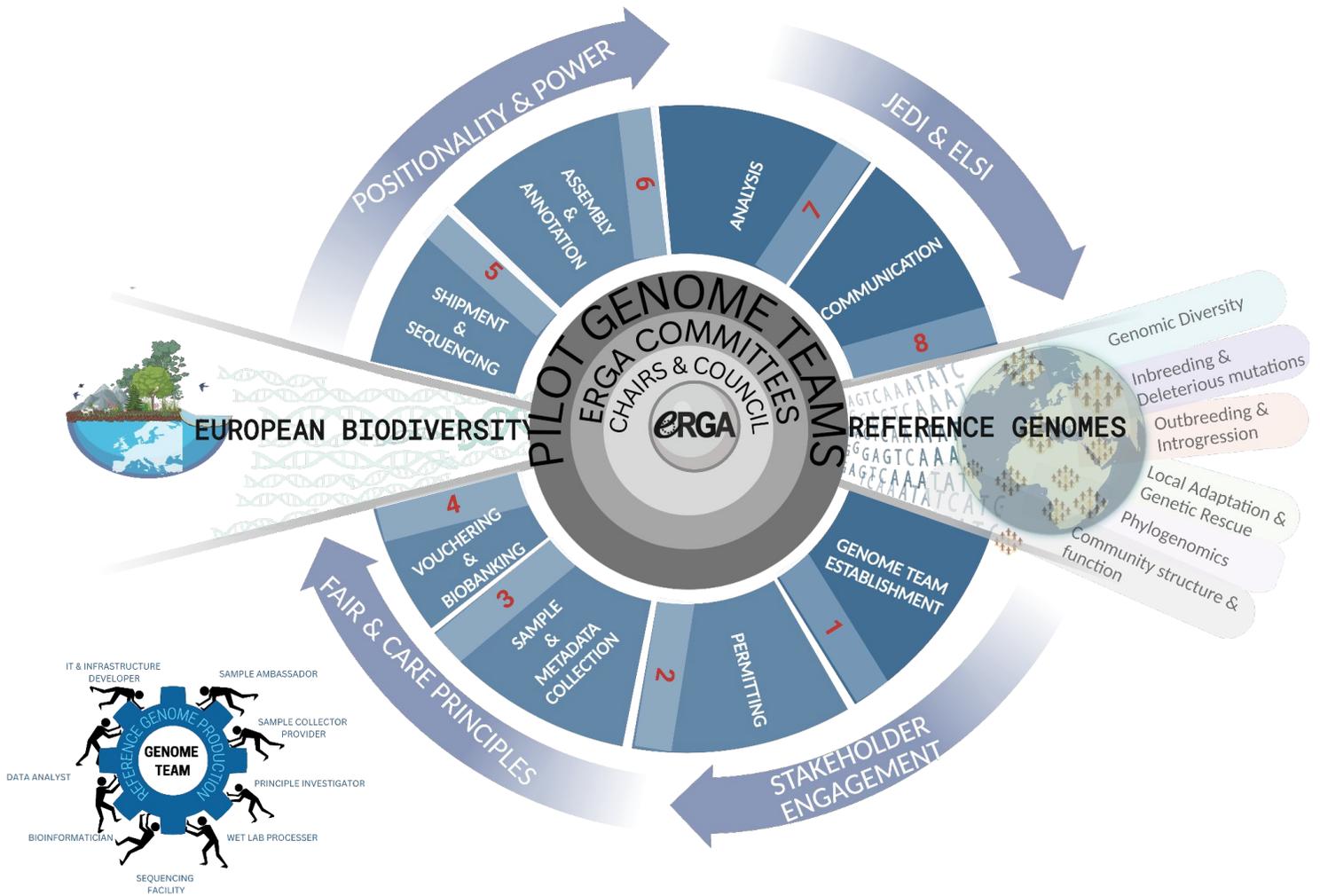
Eukaryota (n:255)



Extended Data Figure X: BUSCO completeness scores (single and duplicated) for completed (pre-curation and curated) assemblies using "Eukaryota" orthologs database.

Extended Data Figure X: Sequencing QC metaanalysis of data produced in Florence.
<Await contribution from Henrique>

OTHER - MAY NOT BE USED



Extended Data Figure X: Establishing an inclusive, accessible, distributed and pan-European genomic infrastructure that could support the streamlined and scalable production of genomics resources for all European species.