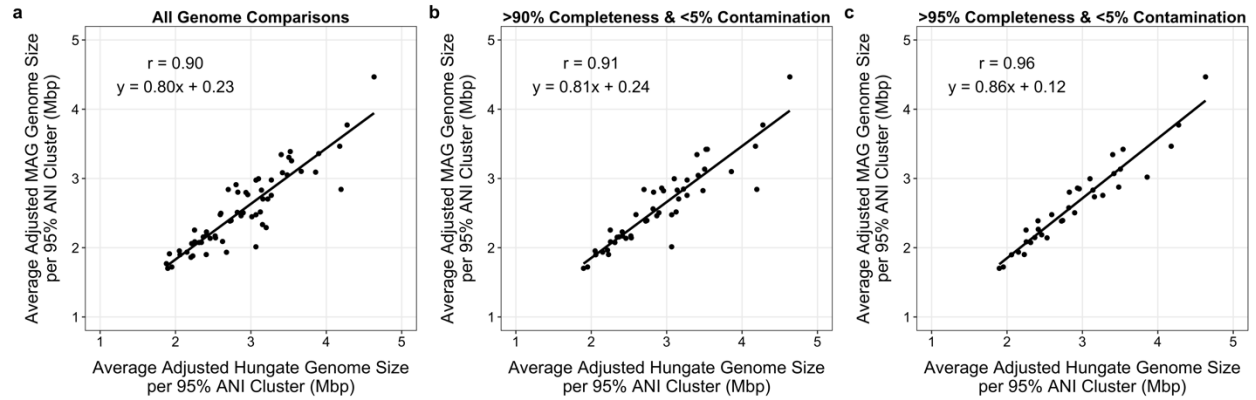# SUPPLEMENTARY INFORMATION

**Insights into rumen microbial biosynthetic gene cluster diversity through genome-resolved metagenomics**

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**Supplementary Figure 1: The genome sizes of MAGs are largely congruent with genome sizes of isolates from the Hungate1000 Collection in the same 95% ANI cluster.** Pearson correlation and linear regression analysis were calculated to compare the average adjusted genome size for all MAGs and Hungate1000 genomes[1] of the same 95% ANI cluster **(a)**, those genomes with ≥90% completeness and ≤5% contamination from the same 95% ANI cluster **(b)**, and those genomes with ≥95% completeness and ≤5% contamination from the same 95% ANI cluster **(c)**.
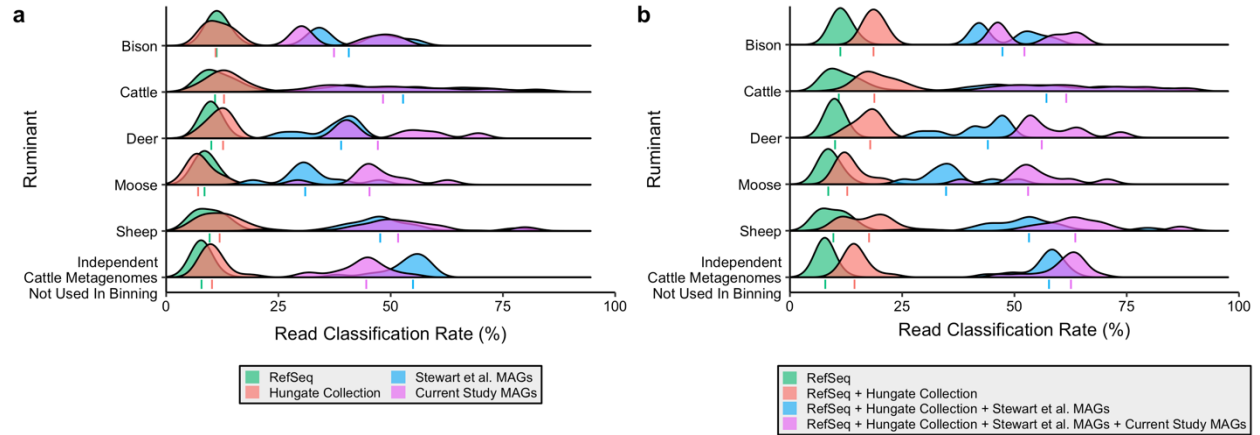
**Supplementary Figure 2: Rumen MAGs improve metagenomic classification.** Classification rates of reads from the 412 metagenomes used to bin MAGs and 16 cattle metagenomes not applied in genome binning using a combination of genomes from RefSeq, the Hungate1000 Collection[1], Stewart *et al.* studies[2,3], and the current study as databases. The four genomic databases were utilized to classify reads independently **(a)** or used to incrementally build larger databases for classification **(b)**. A database including rumen MAGs from the Stewart *et al.* studies and the current study improved classifications rates for bison, cattle, deer, moose, sheep, and independent cattle metagenomes a median 33.3%, 42.1%, 40.9%, 40.1%, 45.0%, and 46.8% compared to a database of mainly isolate genomes from RefSeq and the Hungate1000 collection. The lines denote the median proportions of sample reads classified by the dataset or combinations of datasets.

**Supplementary Table 1: Characteristics and sources of rumen metagenomic datasets used for the reconstruction of MAGs.**

| Ruminant | QC Bases (Gbp) | Samples | Database | Accession | Publication |
|---|---|---|---|---|---|
| Bison | 52.3 | 8 | NCBI BioProject | PRJNA214227 | NA |
| Cattle | 22.8 | 16 | NCBI BioProject | PRJNA627251 | Current Study |
| Cattle | 43.5 | 27 | NCBI BioProject | PRJNA627299 | Current Study |
| Cattle | 33.3 | 23 | NCBI BioProject | PRJNA627299 | Current Study |
| Cattle | 166.0 | 1 | NCBI BioProject | PRJNA60251 | [4] |
| Cattle | 85.1 | 8 | NCBI BioProject | PRJEB10338 | [5] |
| Cattle | 52.7 | 64 | MG-RAST | mgp4126 | [6] |
| Cattle | 12.5 | 14 | NCBI BioProject | PRJEB8939 | [7] |
| Cattle | 60.6 | 9 | NCBI BioProject | PRJNA322715 | [8] |
| Cattle | 4.8 | 1 | NCBI BioProject | PRJNA270714 | [9] |
| Cattle | 20.9 | 2 | NCBI BioProject | PRJNA291523 | [10] |
| Cattle | 125.0 | 16 | NCBI BioProject | PRJNA214227 | NA |
| Cattle | 666.0 | 42 | NCBI BioProject | PRJEB21624 | [2] |
| Cattle | 73.0 | 7 | NCBI BioProject | PRJNA319009 | [11] |
| Cattle | 762.7 | 82 | NCBI BioProject | PRJEB23561 | [12] |
| Deer (White-tailed) | 34.2 | 4 | NCBI BioProject | PRJNA214227 | NA |
| Deer (Red) | 28.6 | 4 | NCBI BioProject | PRJNA214227 | NA |
| Moose | 40.9 | 3 | NCBI BioProject | PRJNA301235 | [13] |
| Moose | 67.9 | 6 | NCBI BioProject | PRJEB12797 | [14] |
| Sheep | 113.5 | 16 | NCBI BioProject | PRJNA214227 | [15] |
| Sheep | 118.3 | 39 | MG-RAST | mgp7948, mgp7949, mgp7950, mgp7957, mgp7958, mgp7959, mgp7960, mgp7961, mgp7962, mgp7963, mgp7964, mgp7965, mgp7966, mgp7967, mgp7968, mgp7969, mgp7970, mgp7974, mgp7975, mgp8090, mgp8091, mgp8092, mgp8093, mgp8094, mgp8095, mgp8096, mgp8097, mgp8098, mgp8099, mgp8108, mgp8109, mgp8110, mgp8111, mgp8112, mgp8113, mgp8114, mgp8115, mgp8116, mgp8117 | [16] |
| Sheep | 656.5 | 20 | NCBI BioProject | PRJNA202380 | [17] |

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