**Supplementary Table S8**

**Manuscript:**

Houtkamp, I., Van Zijll Langhout, M., Bessem, M., Pirovano, W., & Kort, R. (2023). Multiomics characterization of the of the zoo-housed gorilla gut microbiome reveals bacterial community compositions shifts, fungal cellulose-degrading, and archaeal methanogenic activity. *Gut Microbiome,* 1-25. doi:10.1017/gmb.2023.11

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| --- | --- | --- | --- | --- |
| **UniProt ID** | **Samples** | **Name** | **Organism** | **UniProt Annotation status** |
| **A0A1Y1WF22** | 15\_07\_1\_RNA, 15\_07\_2\_RNA | Homoaconitase, mitochondrial | *Anaeromyces robustus* | Unreviewed- protein inferred from homology |
| **A0A1Y1V9J2** | 15\_07\_2\_RNA | Arg5,6 arginine biosynthetic enzyme | *Piromyces finnis* | Unreviewed- protein inferred from homology |
| **A0A1Y1WWZ0** | 15\_07\_1\_RNA, 15\_07\_2\_RNA,  09\_08\_1\_RNA | Adenylate kinase | *Anaeromyces robustus* | Unreviewed- protein inferred from homology |
| **A0A1Y1XN91** | 15\_07\_2\_RNA | Dihydroorotate dehydrogenase (quinone), mitochondrial | *Anaeromyces robustus* | Unreviewed- protein inferred from homology |
| **A0A1Y2CVY2** | 15\_07\_2\_RNA | Aconitate hydratase, mitochondrial | *Neocallimastix californiae* | Unreviewed- protein inferred from homology |
| **A0A1Y2DRS2** | 15\_07\_2\_RNA | NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial | *Neocallimastix californiae* | Unreviewed- protein inferred from homology |
| **A0A1Y1XPP5** | 15\_07\_1\_RNA, 15\_07\_2\_RNA | Alanine--tRNA ligase | *Anaeromyces robustus* | Unreviewed- protein inferred from homology |
| **A0A1Y2E900** | 15\_07\_1\_RNA, 15\_07\_2\_RNA | Dynamin-type G domain-containing protein | *Neocallimastix californiae* | Unreviewed- protein predicted |
| **A0A1Y2ETS6** | 15\_07\_1\_RNA, 15\_07\_2\_RNA | MSF1-domain-containing protein | *Neocallimastix californiae* | Unreviewed- protein predicted |
| **A0A1Y3NVB7** | 15\_07\_2\_RNA | Aconitate hydratase, mitochondrial | *Piromyces sp. (strain E2)* | Unreviewed- protein inferred from homology |
| **P53587** | 15\_07\_1\_RNA, 15\_07\_2\_RNA | Succinate--CoA ligase [ADP-forming] subunit beta, hydrogenosomal | *Neocallimastix frontalis (Rumen fungus)* | Reviewed - Experimental evidence at transcript level |
| **Q7Z941** | ALL | Succinate--CoA ligase [ADP-forming] subunit alpha, mitochondrial | *Neocallimastix patriciarum (Rumen fungus)* | Unreviewed - Experimental evidence at transcript level |

**Table S8: Hydrogenosomal transcripts detected in ZHG gut metatranscriptome.** Hydrogenosomal or malic enzyme encoding protein sequences belonging to Neocallimastigomycetes detected with ShortBRED amongst RNA reads originating from the ZHG microbiome.