

Supplementary Information File.

KAUST Metagenomic Analysis Platform (KMAP), enabling access to massive analytics of re-annotated metagenomic data.

Authors

Intikhab Alam^{1*}, Allan Anthony Kamau¹, David Kamanda Ngugi², Takashi Gojobori¹, Carlos M. Duarte^{1,3} and Vladimir B. Bajic¹.

Supplementary Materials

Supplementary website: https://www.cbrc.kaust.edu.sa/aamg/KMAP_Data/

Supplementary [Table 1](#), Gene Catalogs, ENA Project Ids, Links to GITs and KMAP Annotations.

Supplementary [Table 2](#), ENA Studies and Samples.

Supplementary [Table 3](#), ~27000 Metagenome Assembly Stats.

Supplementary [Figures](#), Description of SF0. GIT and SF1. Gene Catalog groups.

Supplementary [methods](#), include linux commandlines and database queries.

Supplementary [Binning Document](#).

Supplementary [KMAPtsv2Biome.Example.tgz](#), KMAP GIT format into biom format (requires biom module), see supplementary methods..

Supplementary [KMAP Documentation](#).

KMAP screencast videos.

SV1. Introduction. How to View/Browse data in KMAP:

[KMAP Intro ViewData1.mp4](#)

SV2. How to Compare data in KMAP:

[KMAP Intro CompareData1.mp4](#)

SV3. How to search interesting enzymes (e.g. extremozymes) in KMAP:

[KMAP Extremozymes Query v1.mp4](#)

SV4. How to Search Antibiotic Resistance Genes (ARGs) in different microbial habitats in KMAP

[KMAP Example ARGs in habitats v1.mp4](#)

SV5. How to make/use interactive heatmaps (e.g. pathway modules) in KMAP:

[KMAP Interactive heatmap ARGs in habitats v1.mp4](#)

SV6. How to BLAST a sequence in KMAP Global Proteome:

[KMAP PETase BLAST in GlobalMetaProteome.mp4](#)