

Dear IMG users,

This is to notify you of our intention to **replace some older public metagenomes sequenced, assembled and/or annotated by the JGI with new improved versions.**

The differences between new and original versions may include:

1. Reassembly with [SPAdes](#) resulting in larger assemblies with improved contiguity
2. Consistent reannotation with the standard [JGI Metagenome Annotation Pipeline](#)
3. Contig and scaffold coverage information enabling function abundance comparisons

New versions will receive **new genome ids, new contig ids and new gene ids**. The mapping between the latest genome id and genome ids of old version(s) will be preserved in IMG and GOLD, but mapping at the contig or gene level will not be provided, as it exceeds our computational capacity. Old genome ids will be searchable through IMG UI and users will be redirected to newer versions.

Older versions of the JGI datasets will remain available for real-time analysis in IMG for another three to six months, after which **they will be removed** and only the latest version will be available for analysis via IM UI.

**We will start deleting older versions from IMG on Sept 1, 2018.**

If an older version was available for download through the JGI portals, it will remain available in the portals after this version is deleted from IMG. In the case of the Human Microbiome Project Phase I Datasets, the original versions will not be available for download through the JGI portals and are instead available through the Human Microbiome Project Data Analysis and Coordination Center ([DACC](#)).

We apologize for any inconvenience this may cause. We are committed to supporting scientists worldwide with their genome and metagenome data analysis needs, but limited funding for IMG forces us to restrict the number of datasets available for real-time analysis via IMG UI.

If you have questions, please do not hesitate to [contact us](#).

Sincerely,  
IMG Support Team