Which information needs to be provided when submitting metagenome assemblies?

Short Answer

It depends on the level of your metagenome assembly.

Detailed Answer

Have a look at the ENA documentation to get to know the metagenome assembly levels.

When submitting Metagenome-Assembled Genome (MAGs), you would need:

1. a LOCUS TAG of your choice
2. an EMBL file
3. the values that are usually asked for primary assemblies (raw version of the final assembly), which are:

   - COVERAGE: The estimated depth of sequencing coverage
   - PROGRAM: The assembly program
   - PLATFORM: The sequencing platform
   - MINGAPLENGTH: Minimum length of consecutive Ns to be considered a gap (optional)
   - MOLECULETYPE: 'genomic DNA', 'genomic RNA' or 'viral cRNA' (optional)
   - DESCRIPTION: Free text description of the genome assembly (optional)
   - RUN_REF: Comma separated list of run accession(s) (optional)

If you have doubts about the name to give to your MAGs, have a look here.