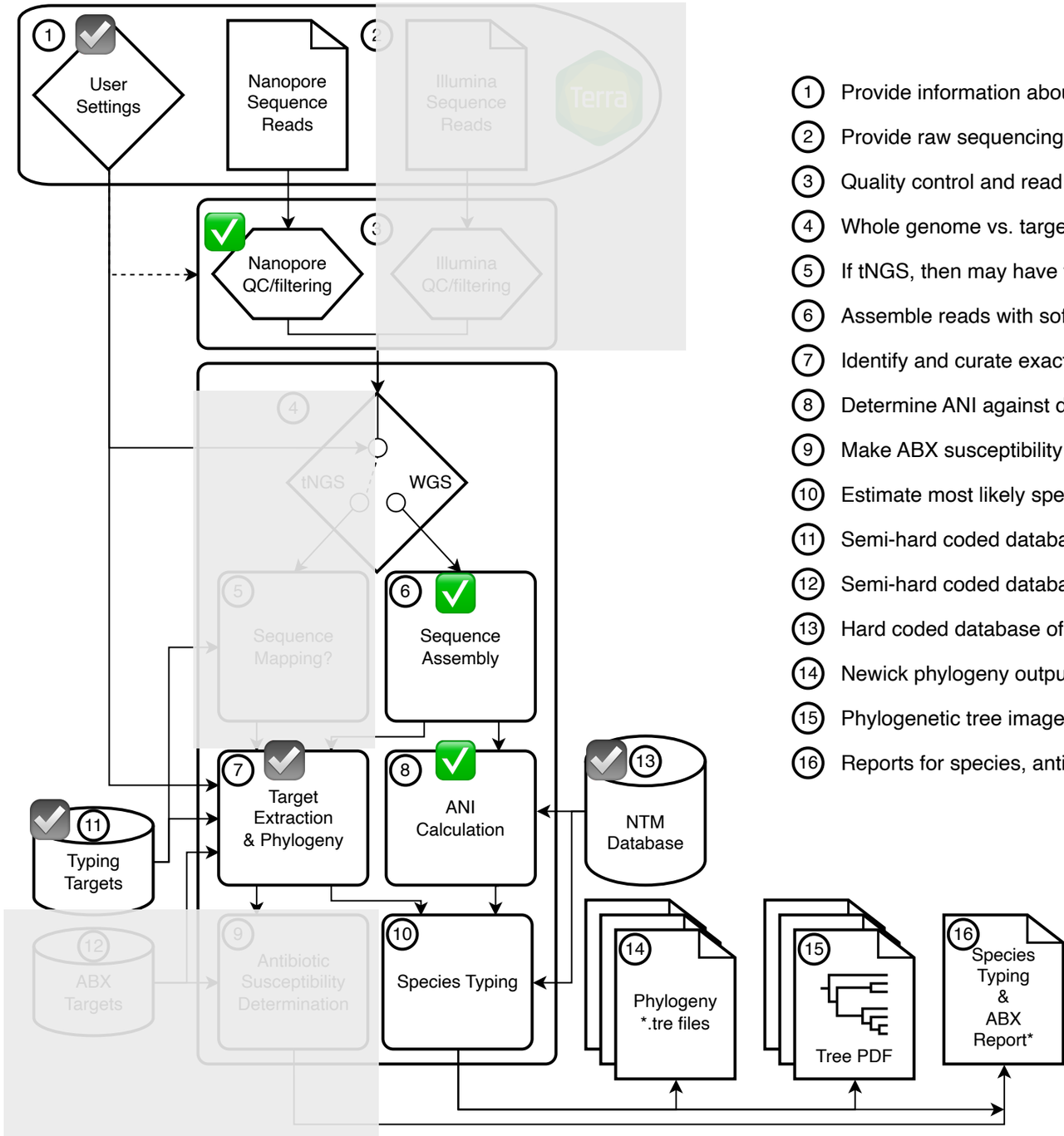

1. Provide information about sequencing types and desired outputs, etc.
2. Provide raw sequencing filenames/locations.
3. Quality control and read filtering (optional)?
4. Whole genome vs. targeted sequencing branch point. (Will tNGS be used?)
5. If tNGS, then may have to map reads instead of assemble, but maybe not.
6. Assemble reads with software appropriate for sequence type (unicycler).
7. Identify and curate exact target sequences. Build phylogenies for each and concatenated.
8. Determine ANI against database known NTM assemblies.
9. Make ABX susceptibility determinations based on appropriate existing methodology.
10. Estimate most likely species based on target/genomic phylogenies and/or ANI.
11. Semi-hard coded database of sequence targets (hsp65, rpoB, tlyC, etc.). Could be updatable.
12. Semi-hard coded database of antibiotic targets and rules. Could be updatable.
13. Hard coded database of NTM assemblies and pre-computed ANI comparisons.
14. Newick phylogeny outputs for use in any tree visualization program.
15. Phylogenetic tree images.
16. Reports for species, antibiotics, logs, intermediate files, etc.