An example of a sequence analysis pipeline in QIIME

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This is just an example of a good way to get started with a 16S rRNA gene pyrosequencing survey. The two things you start out with, after sequencing is completed, are the SFF file (sequencing data) and your mapping file (your experimental data about the samples you submitted for sequencing). Hopefully the sequencing center will also send you the fasta, qual, and sff.txt files. One thing you may want to insert in there would be chimera checking with identify_chimeric_seqs.py - input files would be the "Rep set aligned (FASTA)" file (not the pfiltered one) and the reference alignment. Once you've identified chimeric seqs, all you have to do is delete them from the OTU table.