Supplementary Table 2. Mystery Yeast and La Cuadrilla Case Study Learning Objectives and Workflow.

| Case Study | La Cuadrilla Outbreak | Mystery Yeast Investigation |
|---------------------|--|--|
| Learning Objectives | Compute summary statistics for the provided FASTQ files. Apply CLC tools to trim and filter reads. Apply the CLC Microbial Genomics Module (MGM) Data QC and Taxonomic Profiling tools to process sequence reads. Explain how you can identify different species in a community using next-generation or high- throughput sequencing. Evaluate data from a metagenomics case study (case study scenario and data analyses with CLC). | Compare and contrast Sanger DNA sequencing and next- generation or high-throughput sequencing. Compute summary statistics for the provided FASTQ files. Apply CLC tools to trim and filter reads. Evaluate data from a case study (case study scenario and data analyses with CLC). |
| Format | Group | Individual or Group |
| Concepts | FASTQ files and sequence quality trimming/filtering Metagenomics | Compare and contrast Sanger and NGS Genome assembly Genome sequence scanning Using BLAST to identify sequences |