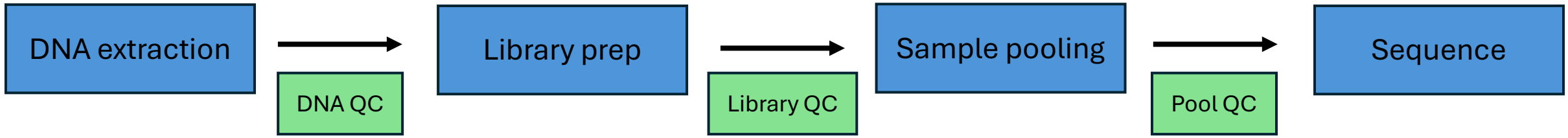
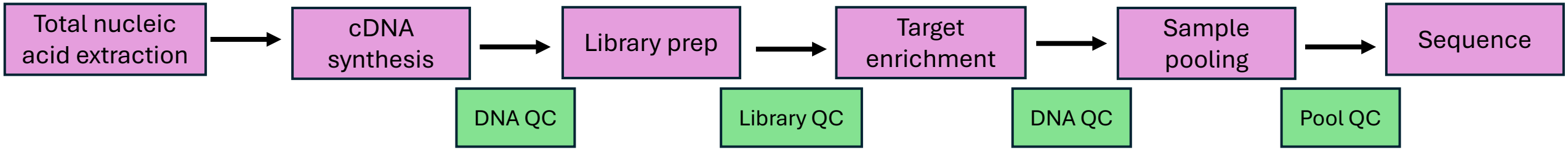
Whole Genome Shotgun Sequencing Workflow



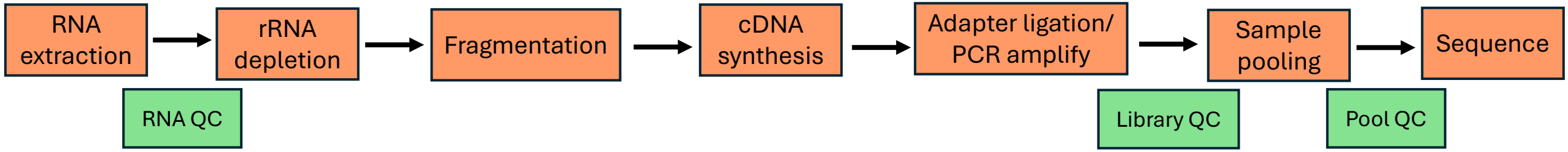
After DNA extraction, samples are quantified to ensure they meet the minimum requirements for library prep. Samples are then normalized so that equal amounts of DNA from each sample within a project go into library preparation. Library controls are always included to confirm that library preparation worked as expected and contamination of reagents didn't occur. Library quality control consists of quantification of each library sample, as well as checking the fragment sizes. Once libraries pass library QC, samples are pooled. The concentration and fragment size of each pool is confirmed one last time prior to sequencing.

Viral Capture Workflow



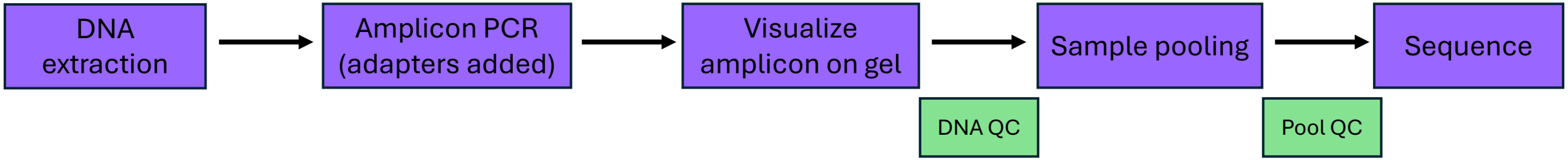
After total nucleic acid extraction, samples go through cDNA synthesis. DNA is quantified using Qubit, a fluorescence-based assay, to ensure that cDNA synthesis was successful and produced enough DNA for library preparation. Samples are then normalized so that equal amounts of DNA from each sample within a project go into library preparation. Library controls are always included to confirm that library preparation worked as expected and contamination of reagents didn't occur. Library quality control consists of quantification of each library sample, as well as checking the fragment sizes. Libraries then go through target enrichment. After target enrichment, another quantification step is done so samples are pooled correctly. The concentration and fragment size of each pool is confirmed one last time prior to sequencing.

Metatranscriptomics/mRNA sequencing workflow



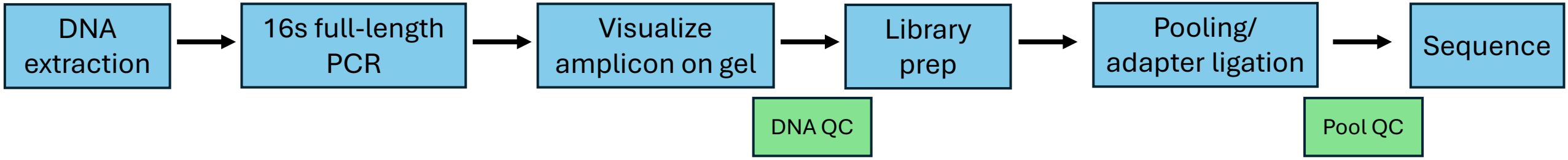
Once RNA has been extracted, samples are quantified, and the RNA integrity numbers (RIN score) are determined to ensure the samples meet the minimum requirements for RNA library prep. Samples are then normalized so that equal amounts of RNA from each sample within a project go through ribosomal RNA (rRNA) depletion. Next, rRNA depleted samples go through fragmentation, cDNA synthesis, and then adapter ligation and PCR amplification. RNA controls are always included to confirm that library preparation worked as expected and contamination of reagents didn't occur. Library quality control consists of quantification of each library sample, as well as checking the fragment sizes. Once libraries pass library QC, samples are pooled. The concentration and fragment size of each pool is confirmed one last time prior to sequencing.

Amplicon Sequencing Workflow



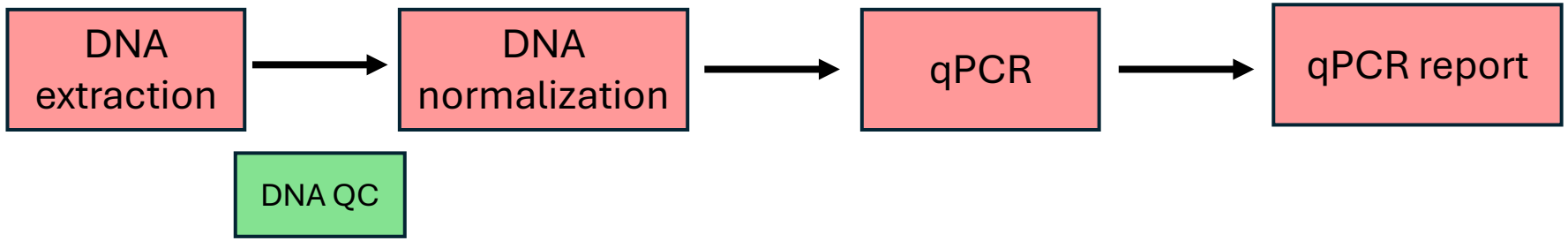
Once DNA has been extracted from the samples, PCR is performed using specific primers that will amplify the region of interest as well as attach sequencer adapters and indices. PCR controls are always included to ensure that amplification works as expected, and that reagents remain free from contamination. Amplicons are visualized on agarose gels and quantified using PicoGreen prior to pooling. The final pool is quantified, and the average fragment size is confirmed before sequencing.

16s Full-Length Long-read Sequencing Workflow



After DNA has been extracted from the samples, PCR is performed using primers that will amplify the full-length 16s gene. PCR controls are always included to ensure that amplification works as expected, and that reagents remain free from contamination. Amplicons are visualized on agarose gels to confirm that the correct PCR product was amplified and quantified using PicoGreen. Samples are then normalized to a specific target input to ensure that equal amounts of DNA from each sample go through library prep. After library prep, samples are pooled together and go through adapter ligation. The final pool is quantified, and the average fragment size is confirmed before sequencing.

qPCR Workflow



After DNA extraction, samples are quantified to determine concentration. Based on their concentrations, samples are normalized to a specific input amount to ensure each sample has equal amounts of DNA going into each reaction. Each qPCR sample is done in triplicate reactions to minimize copy number calculation error due to potential pipetting mistakes. Threshold cycles (ct) values from samples are compared against ct values from a standard curve to determine total copy numbers within each sample. A qPCR report containing ct values and calculated copy numbers is delivered to each collaborator who submits a qPCR request.