Summary:

This protocol is for the submission of DNA for the generation of paired-end libraries for sequencing on the Illumina MiSeq platform. If you quantify your DNA, then please use a fluorometric-based method (picogreen or Qubit) and send us the concentrations on the second tab of the plate map. Libraries are prepared using the Illumina DNA prep kit (formerly Nextera DNA Flex). The process uses bead-linked transposomes during tagmentation to fragment and normalize the DNA simultaneously. After libraries are cleaned they are quantified and pooled before being loaded onto the MiSeq. Libraries are prepared for sequencing following standard Illumina guidelines, normalized to 4nM, and loaded at 12-20pM with 1% PhiX spike-in. Clients choose a 300-cycle, 500-cycle, or 600-cycle kit for sequencing and FASTQ files are distributed upon completion.

Reagents and Materials:

<table>
<thead>
<tr>
<th>Reagent/Material</th>
<th>Vendor</th>
<th>Stock Number</th>
</tr>
</thead>
<tbody>
<tr>
<td>Aluminum foil, sterile</td>
<td>VWR</td>
<td>89049-034</td>
</tr>
<tr>
<td>Full-skirted PCR plate (twin.tec)</td>
<td>Eppendorf</td>
<td>951020401</td>
</tr>
</tbody>
</table>

Protocol:

1. In a clean hood, add at least 20 µL of DNA to each well of the twin.tec plates. Seal with sterile foil seal. Clearly label plates with PI, Reference ID, Plate number and date.

*IMPORTANT: Seal plates very well to reduce evaporation and cross contamination between wells.*
2. Fill out submission form on MiCORES. Our facility name is **UMich Microbiome Core**.

3. Send [electronic plate map](#) and shipment tracking information to microbiomecore@umich.edu.

4. Deliver on dry ice to:

   **University of Michigan Microbiome Core**  
   University of Michigan Medical School  
   Internal Medicine/Infectious Diseases  
   1500 MSRB1  
   1150 W. Medical Center Drive  
   Ann Arbor, MI 48109-5666

   Please include reference ID on package documentation.