**How to Prepare a Custom Primer for Drop-off at the HTSF**

**ALL STEPS MUST BE COMPLETED IN ORDER TO HAVE YOUR SAMPLE(S) PROCESSED.**

**INCOMPLETE DELIVERY WILL DELAY SAMPLE(S) PROCESSING UNTIL ISSUES ARE FIXED**

**Responsibilities of the Study:**

**Completed in the Study’s lab:**

1. Submit samples to TracSeq website (see additional instructions).
2. Custom primer(s) needs to be indicated on submission.
   1. List the sample name.
   2. List the nucleotide sequence of the primer(s).
   3. TracSeq will list custom primer preparation details for you to review.
3. Print the confirmed manifest for drop off at the HTSF and note the BATCH number.
4. Prepare the aliquot for delivery to the HTSF.
   1. Primer(s) needs to be place in a 1.5ul tube **ONLY. Smaller 0.5 µl tube are not permitted and will be returned to project.**
   2. Concentration must be 100 uM.
   3. The volume needs to be **25 µl per lane** to be sequenced on submission. Make sure there is enough primer delivered. It is problematic to start preparing a run and not have enough primer. We need the extra volume in case a run needs to be repeated.
5. Label Custom Primer Tube clearly with the following information.
   1. STUDY NAME
   2. BATCH number
   3. Primer Name(s)
6. Prepare samples AND custom primer(s) for drop-off at the HTSF.
   1. Provide both samples and custom primer(s) when delivering materials to the HTSF.
   2. Custom primer(s) will be delivered to the sequencing group when samples are ready for sequencing.
   3. **Excess primer(s) WILL NOT be saved**. Custom primer aliquots MUST be delivered with each batch. We will not take primers from other projects in order to prevent possible cross contamination.
   4. If there is not enough volume in the custom primer tube, the sample will be bumped from sequencing until a new tube can be provided. This will most likely delay sequencing for 24 or more hours.