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# Preparing multiplexed WGS/MetaG libraries with the Illumina DNA Prep kit for the Illumina NextSeq or MiSeq

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## **ABSTRACT**

The preparation of (meta)genomic libraries using the Illumina Nextera Flex (now "DNA Prep") kit with CD/UDI indices at the IMR.

Based upon Illumina protocol 10000000254 16 v10 (Aug. 2021).

#### **MATERIALS**

The following materials list contains those consumables+quantities used specifically at the IMR to complete the present protocol for 192 metagenomes (2 plates) on the NextSeq2000.

### **Pre-Library Sample Quantification**

Quant-iT 1X HS dsDNA Kit (1000 samples)

Optical plate

PCR microplates 96-well Bio-Rad

PCR microplates sealing film Bio-Rad

Tips ClipTip 20

Tips ClipTip 200

Tips ClipTip 300

Reservoir

UltraPure water

## **Illumina Library Preparation**

Nextera Flex DNA Sample Prep Kit (96 samples)

IDT for Illumina DNA/RNA UD Indexes Set A, Tagmentation (96 Indexes, 96 Samples)

IDT for Illumina DNA/RNA UD Indexes Set B, Tagmentation (96 Indexes, 96 Samples)

PCR microplates 96-well Bio-Rad

PCR microplates sealing film Bio-Rad

Manual p1000 tips Tips ClipTip 20

Tips ClipTip 200

PCR tube strips (Axygen, 8 x 0.2 mL)

15 mL Falcon tubes

50 mL Falcon tubes

Ethanol

Reservoir

UltraPure water

## **Post-Library Quantification and Pooling**

Quant-iT 1X HS dsDNA Kit (1000 samples)

Optical plate

PCR microplates sealing film Bio-Rad

Tips ClipTip 20

Tips ClipTip 300

PCR tube strips (Axygen, 8 x 0.2 mL)

1.5 mL Eppendorf tubes

Reservoir

## **Loading and Sequencing**

PhiX Control Kit v3 (at least for 5 stocks)

NextSeq 2000 P3 Kit 300 cycle

Quant-iT 1X HS dsDNA Kit (1000 samples)

**Qubit Tubes** 

1.5 mL Eppendorf tubes

Various manual pipette tips

# **Prepare and Quantify gDNA**

- Using two 96-well PCR plates, prepare  $230 \, \mu L$  of 1:10 dilution using nuclease-free water (NFW) for up to 192 gDNA samples.
- Quantify  $\underline{\mathbb{Z}}$  5  $\mu \underline{\mathbb{L}}$  of the **1:10 diluted gDNA** using the Invitrogen Quant-iT dsDNA HS assay kit on the fluorescent 96-well plate reader.

#### Note

Sample concentrations are required for calculating equal molar DNA ratios for library preparation input. Our standard practice is to add the appropriate volume of each sample so that  $\frac{\pi}{2}$  5 ng of gDNA are added to each sample well.

# **Perform Illumina DNA Prep Kit Library Preparation**

Follow the library preparation instructions as described for the **Illumina DNA Prep** kit (<a href="https://support.illumina.com/content/dam/illumina-support/documents/documentation/chemistry\_documentation/illumina\_prep/illumina-dna-prep-reference-guide-1000000025416-10.pdf">https://support.illumina.com/content/dam/illumina-support/documentation/chemistry\_documentation/illumina\_prep/illumina-dna-prep-reference-guide-1000000025416-10.pdf</a>) with the below modifications.

### Note

We were originally doing up to 96 samples (1 plate) on the NextSeq550 and so using the **Nextera DNA CD Indexes (96 Indexes)** for indexing. However, we have now increased to up to 192 samples (2 plates) on the NextSeq2000 and so are now using the **IDT for Illumina DNA/RNA UD Indexes Set A and B, Tagmentation (96+96 Indexes)** for indexing.

- **3.1** Amplify Tagmented DNA: use 12 PCR cycles (based on 5 ng of input DNA).
- 3.2 Final library clean-up: wash beads with 80% ethanol as described, remove excess ethanol and allow beads to dry on the magnet for 00:05:00. Remove the plates from the magnet and add Δ 60 μL of Resuspension Buffer (RSB) to the beads. Pipette mix until thoroughly resuspended and incubate at room temperature for 00:02:00. Place the plates back on the magnet until clear and transfer Δ 55 μL of the supernatant into new 96-well plates.

# **Quantify and Pool Final Library**

- 4 Quantify Δ 5 μL of each **tagmented**, **amplified and purified** sample using the Invitrogen Quant-iT dsDNA HS assay kit on the fluorescent 96-well plate reader.
- 5 Pool equal molar amounts of up to 192 samples in a 1.5 mL microcentrifuge tube.

6 **Dilute** pooled library with RSB to the recommended loading concentration specific to the intended sequencer per Illumina's guidelines.