VERSION 1

FEB 05, 2021

Protocols for " Efficient and stable metabarcoding sequencing data using DNBSEQ-G400 sequencer validated by comprehensive community analyses" V.1

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GigaScience Press

BGI

Xiaohuan Sun

OPEN ACCESS

DOI:

dx.doi.org/10.17504/protocols.io.brtpm6mn

External link:

<https://doi.org/https://doi.org/10.1101/2020.07.02.185710>

Collection Citation: Xiaohuan Sun, Yuehua Hu, Zewei Song 2021. Protocols for " Efficient and stable metabarcoding sequencing data using DNBSEQ-G400 sequencer validated by comprehensive community analyses".

protocols.io

<https://dx.doi.org/10.17504/protocols.io.brtpm6mn>

MANUSCRIPT CITATION:

Sun X, Hu Y, Wang J, Fang C, Li J, Han M, Wei X, Zheng H, Luo X, Jia Y, Gong M, Xiao L, Song Z, Efficient and stable metabarcoding sequencing data using a DNBSEQ-G400 sequencer validated by comprehensive community analyses.

GigaByte doi:

<https://doi.org/10.1101/2020.07.02.185710>

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Protocol status: Working
We use this protocol and it's working

Created: Jan 26, 2021

Last Modified: Feb 05, 2021

COLLECTION integer ID:
46671

ABSTRACT

Sequencing in DNBSEQ-G400 of this study was carried out in BGI-Shenzhen. Amplicons from 1276 soil samples were randomly and equally distributed into 3 DNBSEQ runs for both 2×200 paired-end (PE200) and 400 bases single-end sequencing (SE400). The left libraries of total 1276 samples were repetitively sequenced two more times by SE400 using different DNBSEQ-G400 machines. Three randomly chosen soil samples from each forest plot (ALS268, LJ105 and NBH217) were all amplified 3 times separately as PCR replicates. The corresponding 9 sequencing libraries were sequenced repetitively by 3 DNBSEQ runs. Sequencing was carried out using the entire lane of the Illumina MiSeq platform in the University of Minnesota Genomic Center. Amplicons of the 1276 forest soil were normalized and pooled randomly in equal molar ratios into 8 parallel sequencing runs on MiSeq platform. Again, three randomly chosen soil samples from each forest plot (ALS268, LJ105 and NBH217) were all amplified 3 times separately as PCR replicates. The corresponding 9 sequencing libraries were sequenced repetitively by 8 MiSeq runs.

Schematic representation of sequencing strategy at DNBSEQ-G400 and Illumina MiSeq platforms.

Protocol

NAME

High-throughput microbial metabarcoding amplification Protocol sequenced by DNBSEQ-G400

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Library construction of metabarcoding at DNBSEQ-G400 with MGIEasy universal DNA library prep Kit

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Sequencing at DNBSEQ-G400 platform with PE200 and SE400 modes

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Sample preparation for Illumina MiSeq Dual Index metabarcoding

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