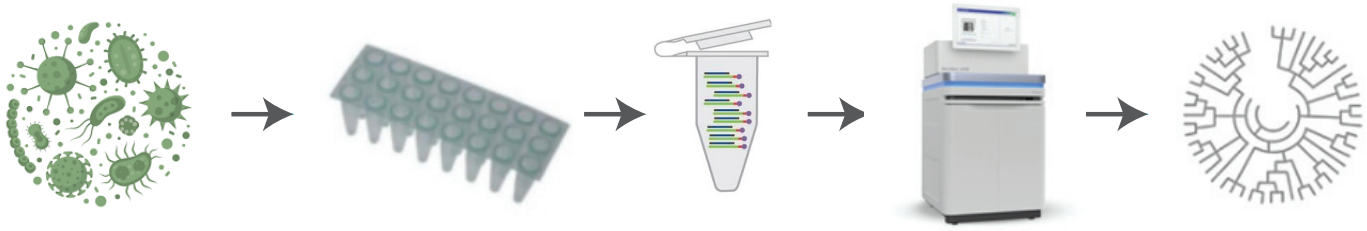
MEDGENOME

MedGenome Inc. Broadens NGS offerings with Loop Genomics Metagenomics Service

MedGenome Inc. has broaden its genomic service offerings with Loop Genomics synthetic long-read sequencing using Illumina short-read sequencers. Loop Genomics uses proprietary LoopSeq™ barcoding technology that attach to unique DNA molecule at 16S site coupled with barcode distribution to enable single-molecule, long-read sequencing on Illumina platform. In addition, the technology offers bioinformatic tools to deliver highly accurate molecular abundance measurements by mapping kilo-base long reads with unique molecular barcodes that have ultra-low error rates and low PCR bias compared to conventional Illumina sequencing. MedGenome utilizes Loop Genomics technology for 16S long-read sequencing that covers the entire V1-V9 regions in a single read that are classified at the species or genus level, with zero false-positive assignments.

Technology	Source & Input Type	Required Amount	Sequencing Method	Analysis Method	Information Obtained
LoopSeq 16S Long Read	Microbiome DNA	>10ng/uL	Illumina NovaSeq or Illumina HiSeq	LoopSeq Analysis	Molecular Abundance

LoopSeq Metagenomics Workflow



Validation Report

At MedGenome, we have successfully intergraded the LoopSeq 16S long read assay into our MedGenome's pipeline; a representative report of microbial DNA standards validated on-site is provided below. The samples include microbial DNA standard from ZymoBIOMICS (catalog no. D6306) and bacterial genomic mixtures from oral, skin, gut and vaginal microbial communities from ATCC (catalog no. MSA-1004, MSA-1005, MSA-1006, and MSA-1007).

Analysis Report

MedGenome's 16S analysis pipeline is able to preprocess reads; perform *de novo* assembly of short reads into contigs; cluster OTUs and annotate with silva_132 database; produce diversity statistics and plots. A summary HTML report is generated with the following deliverable highlights.

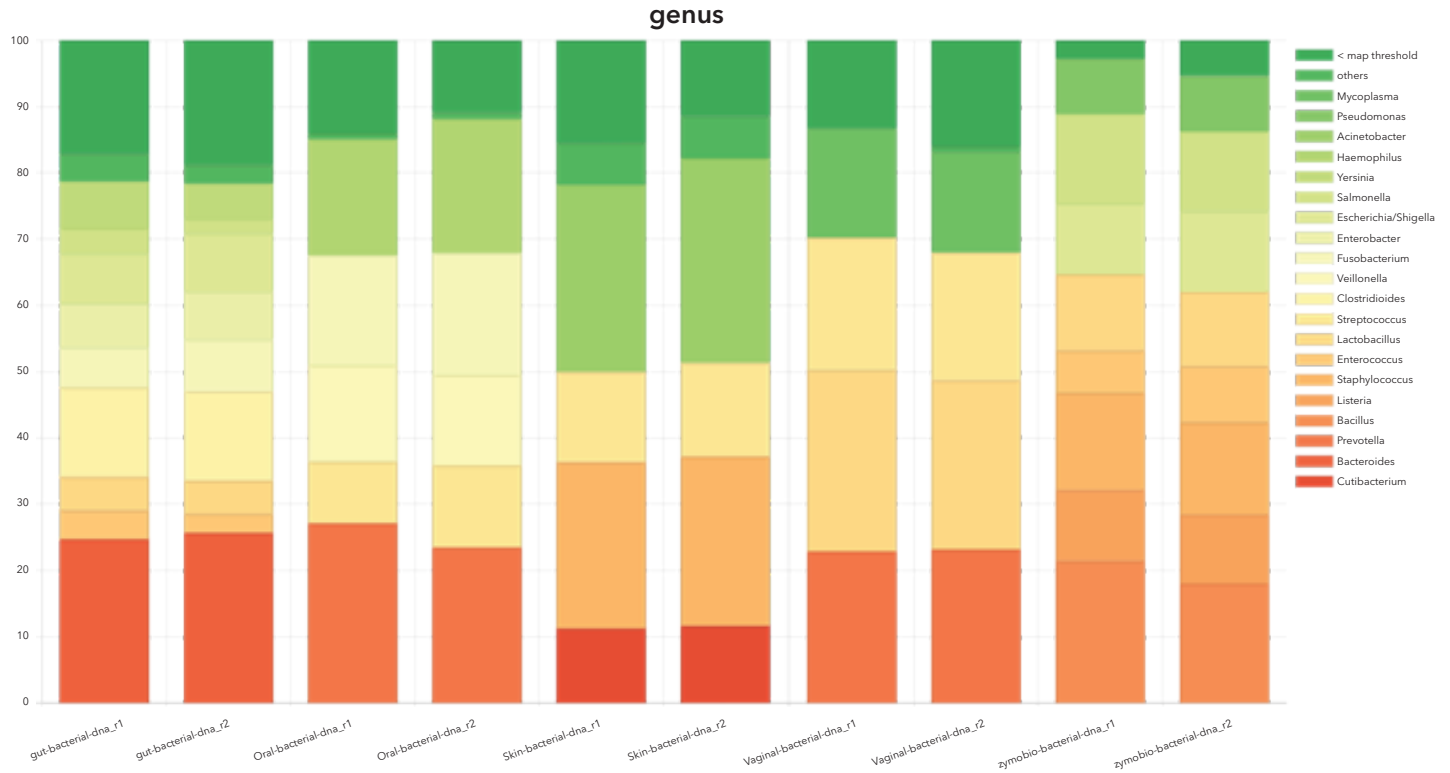


Figure 1. *Taxonomy abundance distribution per sample at genus level.*

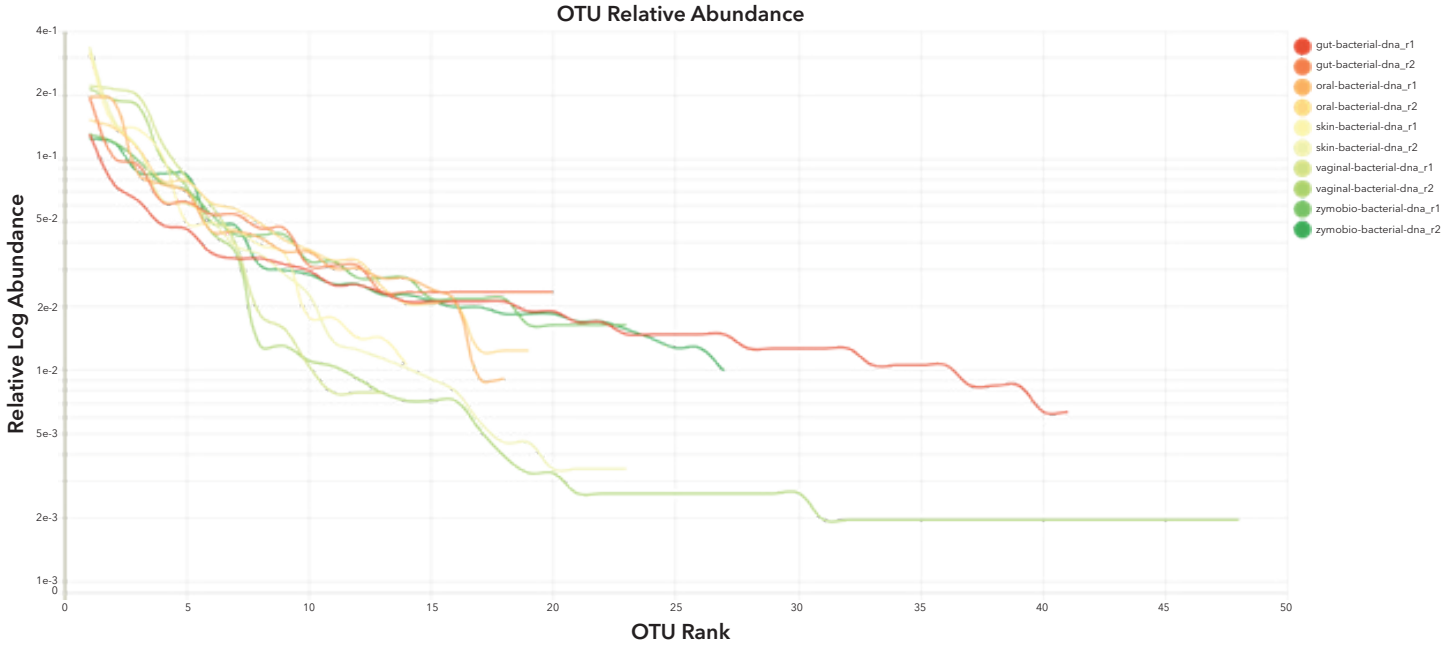


Figure 2. *OTU relative abundance to indicate the percentage of each OTU detected in each sample.*

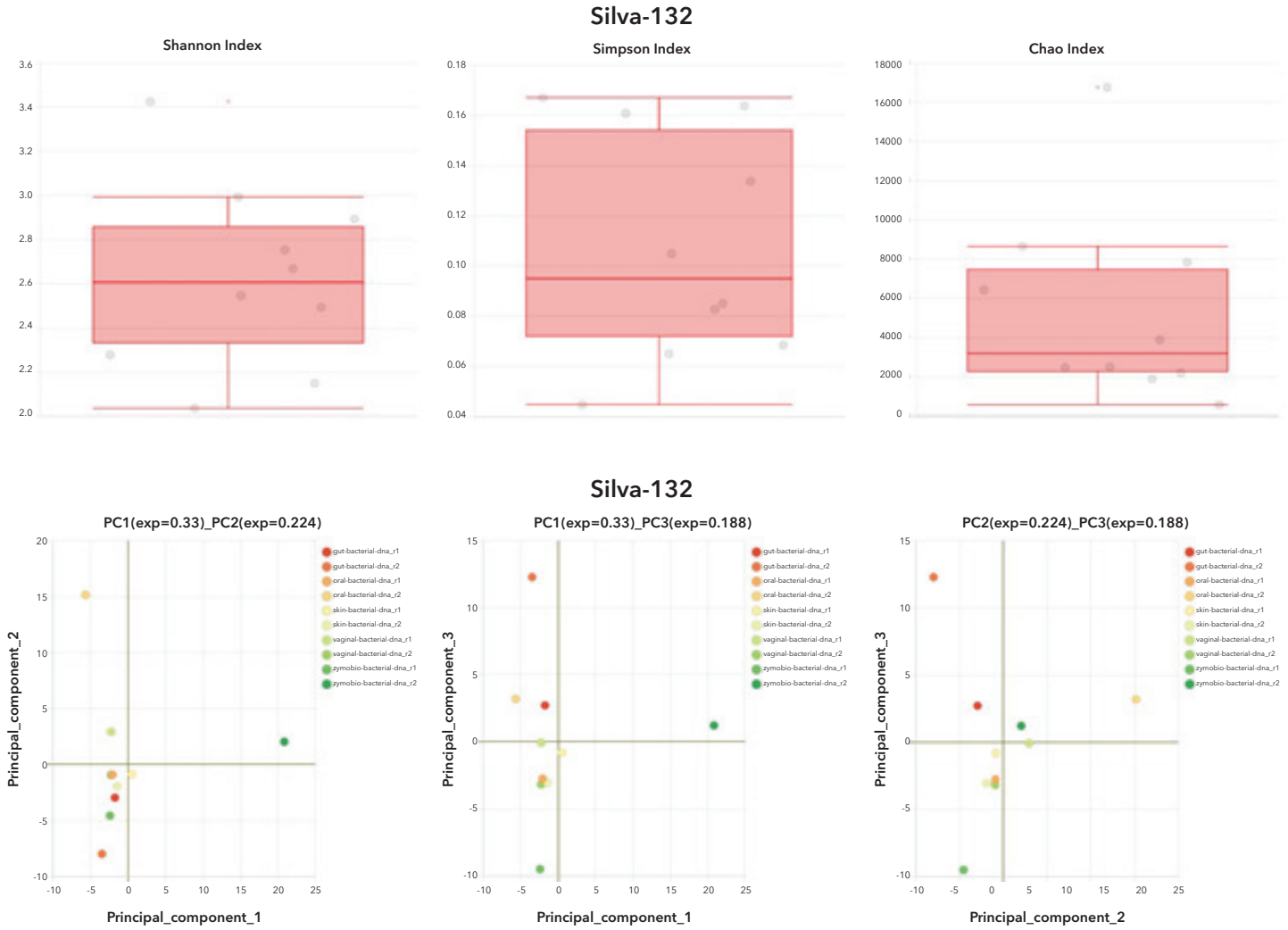


Figure 3. *(A) Alpha diversity calculated by Shannon, Simpson and Chao index to indicate diversity within each sample, (B) Beta diversity presented as (PC1, PC2), (PC1, PC3), (PC2, PC3) to indicate diversity between samples.*