Project ID	MEF-26-01	Date Form was Generated	3/17/2026
Client	Memelio Fermentuotas	Reported Generated by	Michelle Scriver

Sample Information

Received Samples	Extracted DNA	*Assays Performed*	Illumina DNA Prep, Bioinformatics
Number of Samples	17	☑	Library passed QC

Sequencing Run Details

Sequencing Run ID S26006

Sequencing Date	3/13/2026	*Illumina Chemistry*	P1, 300 XLEAP
Instrument	NextSeq2000	*Read Type*	Paired End
Instrument ID	VL00805	*Read Lengths*	2 x 151 bp

Loading Details

PhiX Spike Concentration (%)	25
Library Loading Concentration (pM)	750

Sequencing Run Metrics

Yield (Gb)	37.21	*Error Rate (%)*	0.37
%>Q30	91.92	*Aligned to PhiX (%)*	13.76

☑ Run passed Illumina specifications

Comments

NA

Library quality control acceptance criteria

Library pools must meet these QC criteria before sequencing: concentration ≥ 2 nM after pooling and clean-up, verified in triplicate with a Qubit fluorometer (Thermo Fisher Scientific, USA); fragment size assessed with a Bioanalyzer (Agilent Technologies, USA), showing the expected library profile and absence of indexing primers or adapter dimers. The Sequench negative control must show no detectable targeted fragments.

Run quality metrics and specifications

Yield (Gb): Total bases after filtering, reflecting sequencing capacity.
%>Q30: Phred score ≥30, base call accuracy ≥99.9%, primary quality indicator.
Error rate (%): Average per-base mismatch versus PhiX reference.
% aligned to PhiX: Percentage of reads aligning to PhiX.

Run acceptance for Yield (Gb) and % bases ≥ Q30 is based on Illumina performance specifications generated using a PhiX control library at supported cluster densities (Tables 1 and 2). This is updated per Illumina specifications.The operational targets applied locally are: PhiX error rate < 6%; % aligned to PhiX > 1%.

Table 1. Sequencing output per flow cell (Gb)

MiSeq

Read length	Nano Kit v2	Micro Kit v2	Kit v2	Kit v3
1×36 bp	N/A	N/A	0.54–0.61	N/A
2×25 bp	N/A	N/A	0.75–0.85	N/A
2×75 bp	N/A	N/A	N/A	3.3–3.8
2×150 bp	0.30	1.2	4.5–5.1	N/A
2×250 bp	0.50	N/A	7.5–8.5	N/A
2×300 bp	N/A	N/A	N/A	13.2–15

NextSeq 2000 with XLEAP-SBS chemistry

Read length	P1	P2	P3	P4
1×50 bp	N/A	N/A	N/A	90
2×50 bp	10	40	120	180
2×100 bp	N/A	80	240	360
2×150 bp	30	120	360	540
2×300 bp	60	240	N/A	N/A

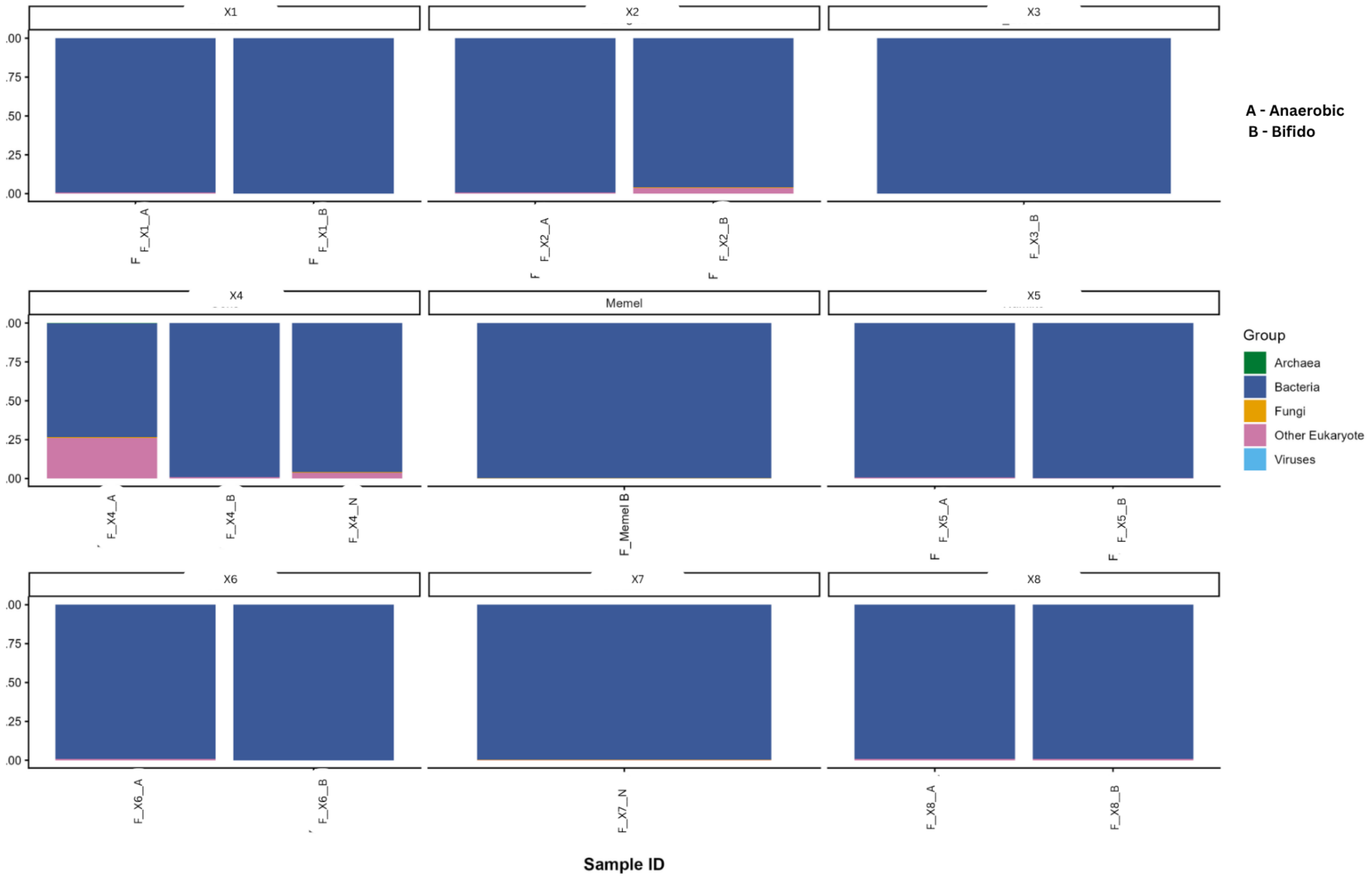
Table 2. Quality score specifications (% > Q30)

MiSeq

Read length	Kit v2	Kit v3
2×25, 2×75, 2×150, 2×250 bp	≥ 75–90%	≥ 70–85%
2×300 bp	N/A	≥ 70%

NextSeq 2000 with XLEAP-SBS chemistry

Read length	All P1-P4
1×50 - 2×150 bp	≥ 90%
2×300 bp	≥ 85%



Genus-Level Relative Abundance For Samples by Organsim Type

s://www.sequench.co.nz/

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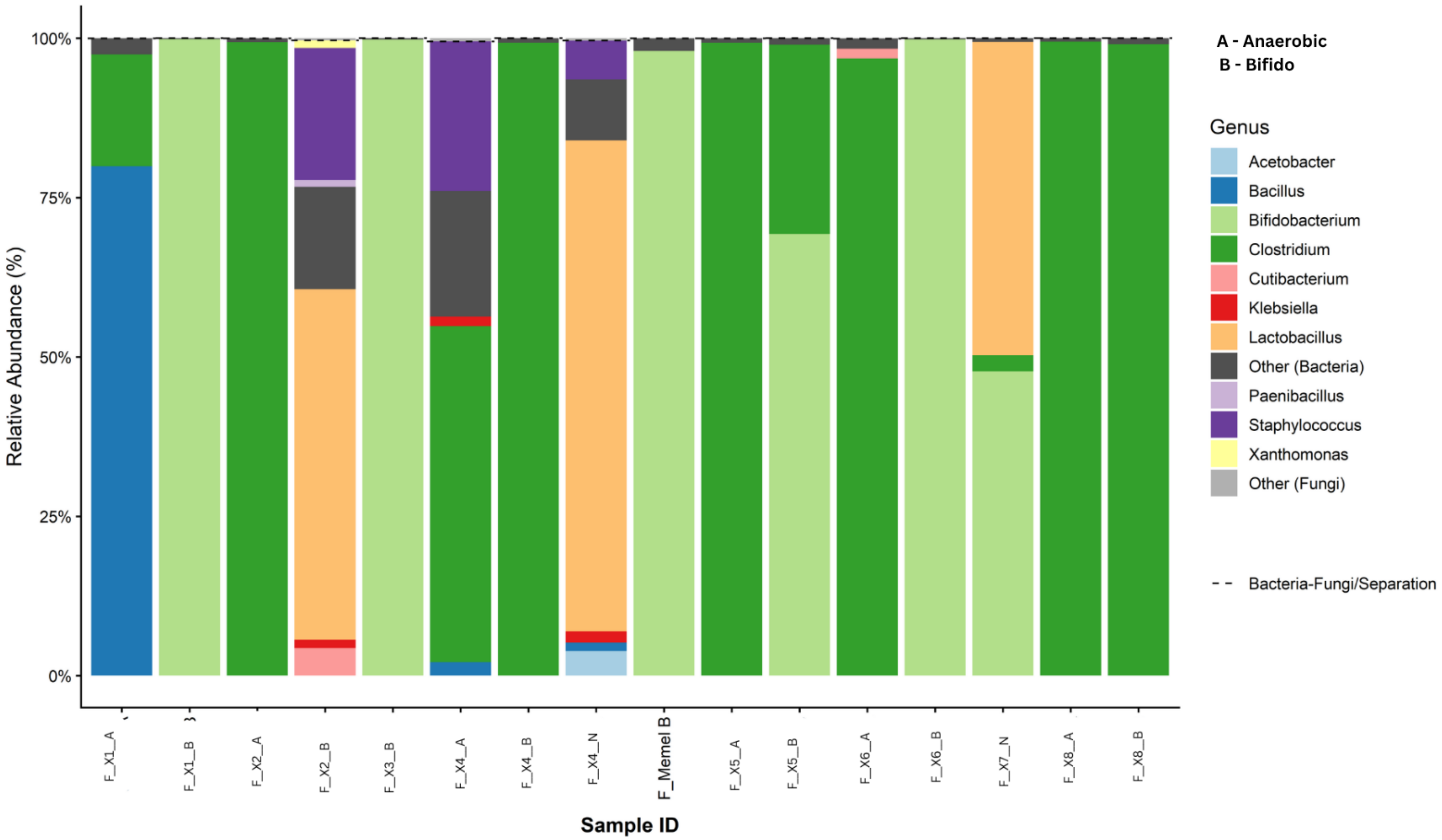
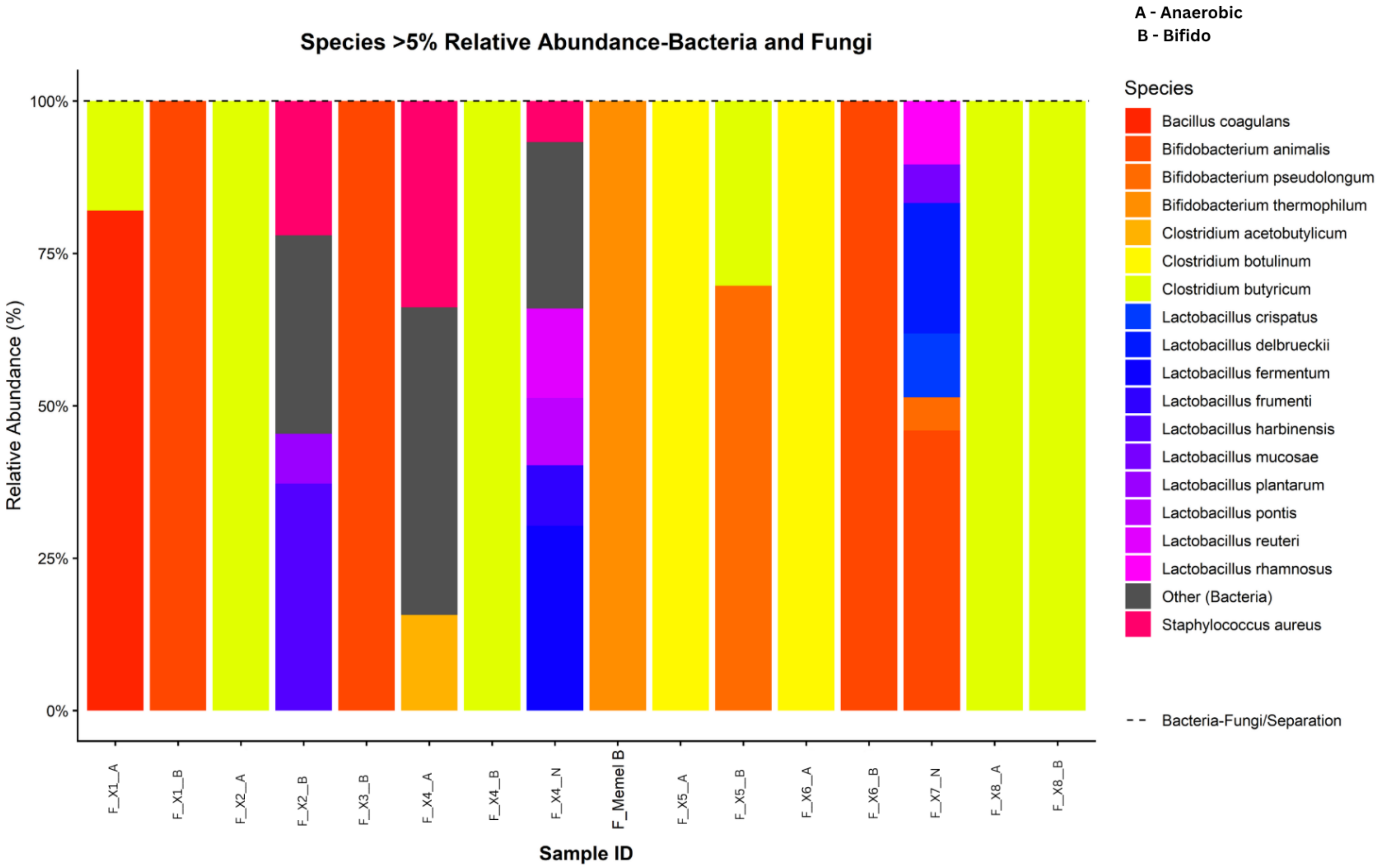
Genus >1% Relative Abundance-Bacteria and Fungi



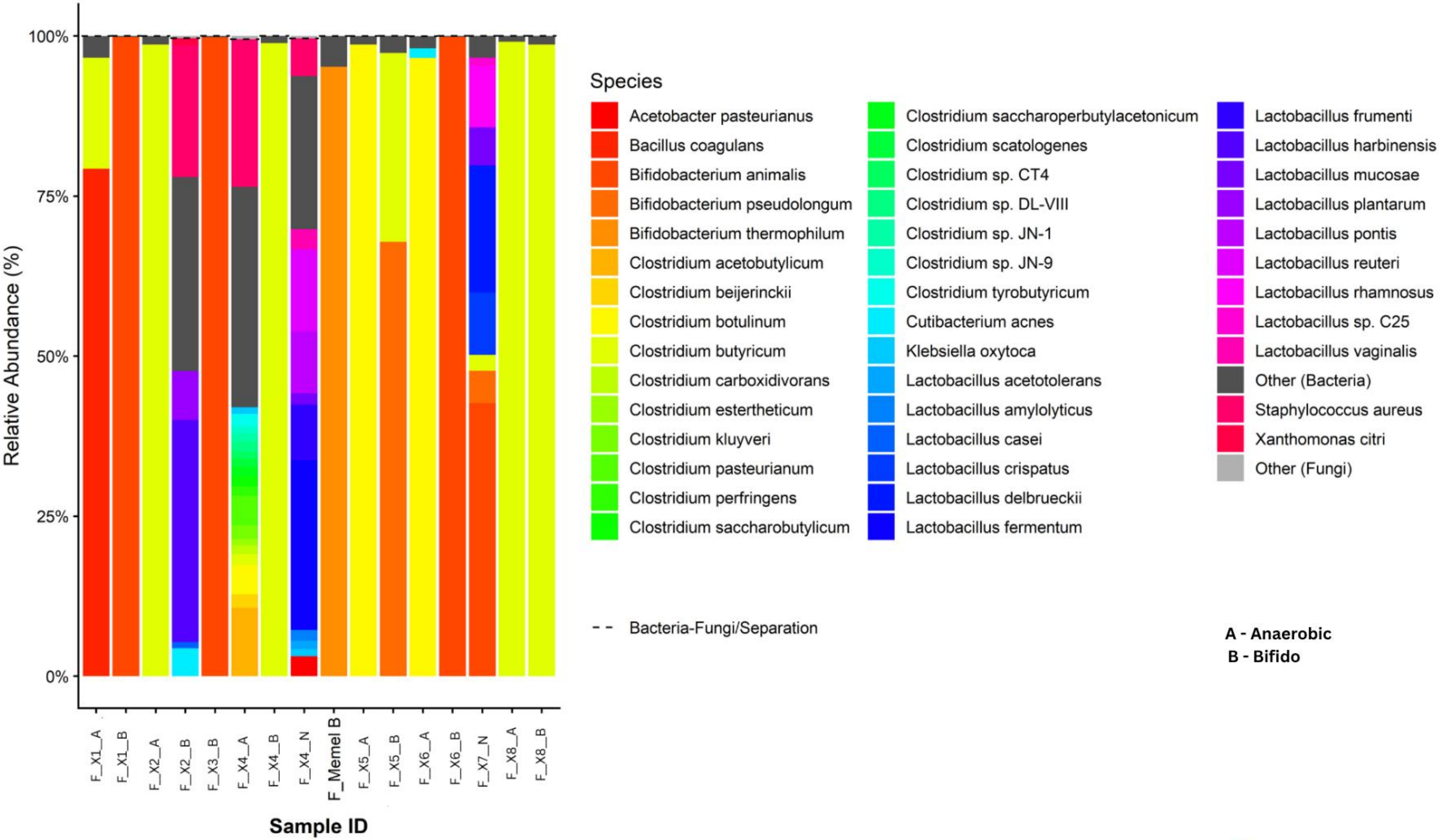
https://www.sequench.co.nz/



SEQUENCH

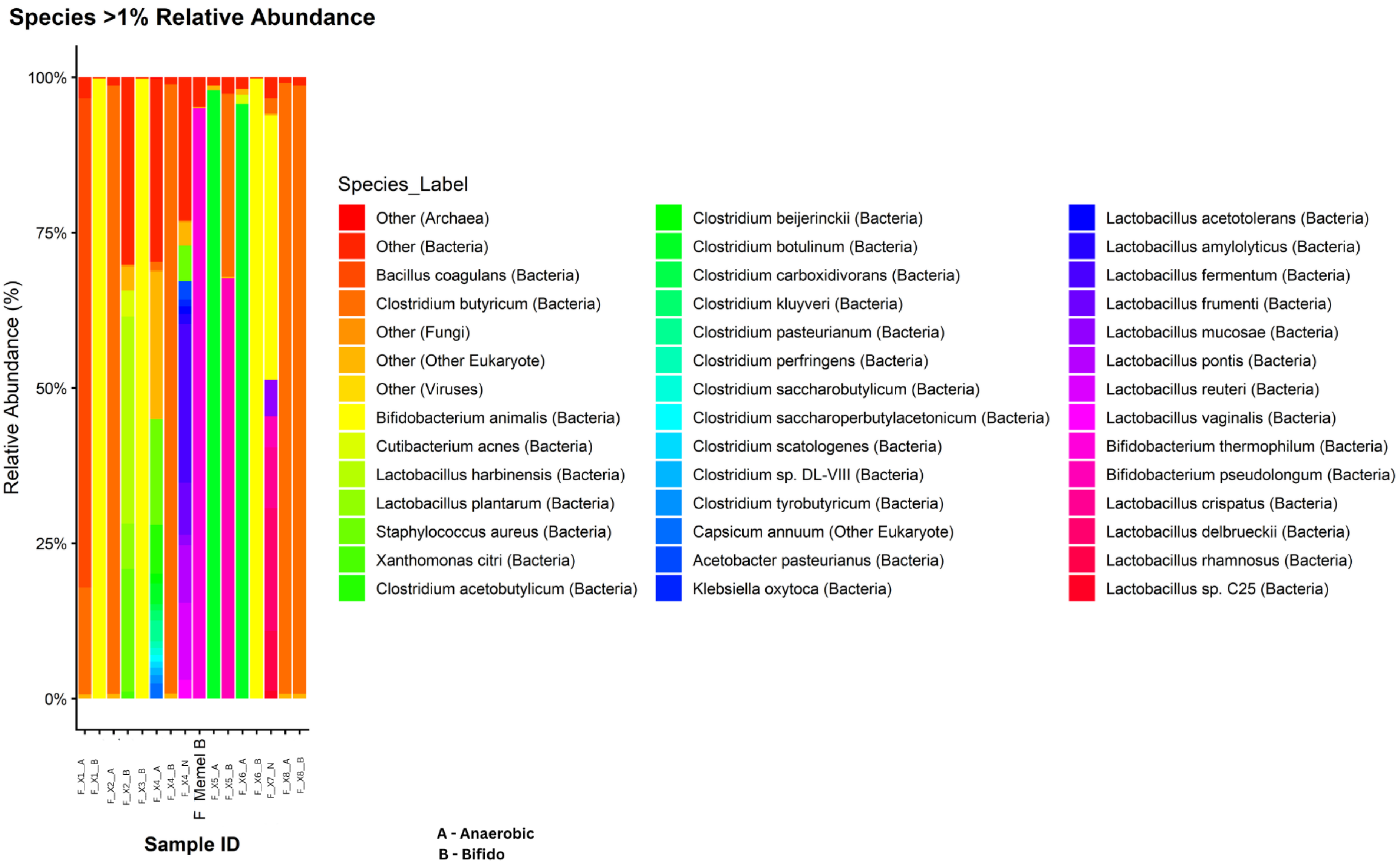
https://www.sequench.co.nz/

Species >1% Relative Abundance-Bacteria and Fungi



A - Anaerobic
B - Bifido

https://www.sequench.co.nz/



A - Anaerobic
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