WSVL SEQUENCING REQUEST FORM

Requester Name/Laboratory Affiliation: ____

Date: ________________________ ☐ Diagnostic ☐ Research

Accession #: ______________________

Nucleic Acid Type

Genomic DNA Amplicon (note size below) RNA (note type below)

Species and original sample (e.g. skin, colony, etc.):____

____

Total number of samples (fill out attached spreadsheet; add extra pages if needed):__________________

Extraction Method: _______________________________

Is there a large amount (> 10%) of host DNA/RNA included in the sample? Yes No

Read Length Preference (circle both if hybrid analysis needed):

Oxford Nanopore Technologies (400bp - 1,000,000 bp) Illumina Paired (2 x 150 bp)

	Long Reads (ONT)	Short Reads (Illumina)
Nucleic Acid Concentration Required	300 - 1000 ng in 48 ul sample*	100 - 500 ng in 30 ul sample (can go as low as 1 ng)*
Accuracy	98.3%	99.9%

*If measuring nucleic acid concentration on a NanoDrop, know that it WILL overestimate the amount of material you have.

If specific QC parameters (e.g. Q-score, read length) required, please note here: _____________________

____

What is your overall objective (e.g. whole genome assembly)? _____________________________________

____

____

____

____

WSVL SEQUENCING REQUEST FORM

Sample Acc/ID	Organism	Extraction Date	Extraction Kit	Extraction Equipment