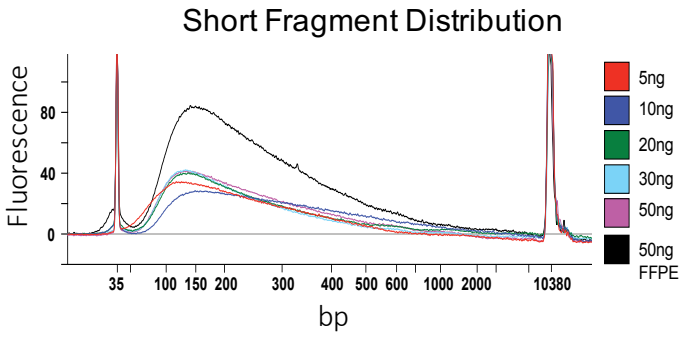
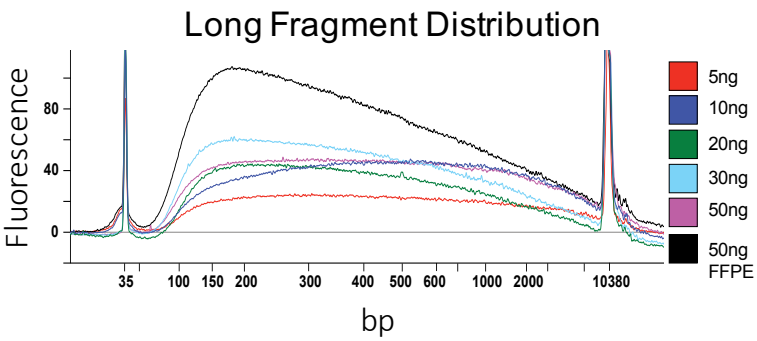
SeqOnce Biosciences

RhinoSeq™
Fastest DNA Library Prep Kit
Data Sheet

High Quality Across Complex Sample Types

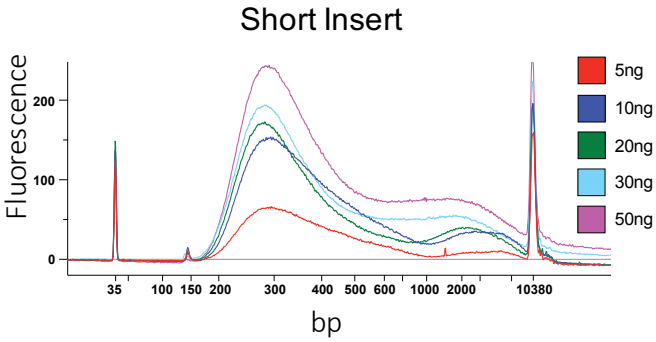
Adjustable Fragment Distribution

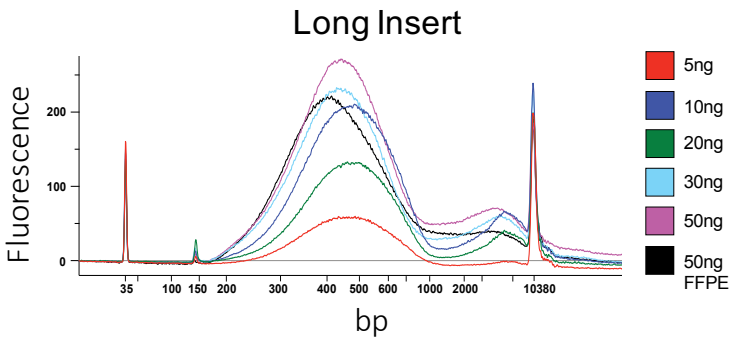




Single fragmentation reagent volume (buffer and enzyme for 10 – 100ng input)
Adjustable for controlled fragment distribution

Library Fragment Length Distribution





Single library construction reagent volume (buffer and enzymes) for 10 – 100ng inputs
Identical conditions for microbial and human gDNA fragment/library construction

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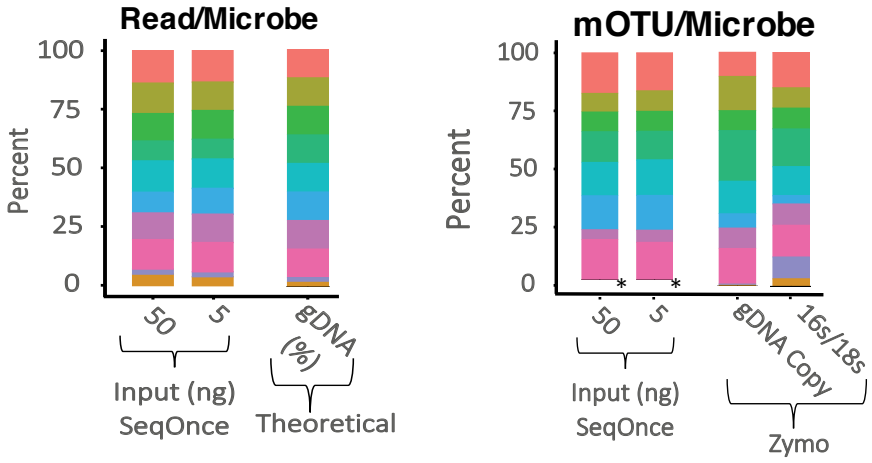
Microbial Characteristics

Species	GC %	Gram Strain	gDNA Abun. (%)
P. aeruginosa	66.2	-	12
E. coli	56.8	-	12
S. enterica	52.2	-	12
L. fermentum	52.8	+	12
E. faecalis	37.5	+	12
S. aureus	32.7	+	12
L. monocytogenes	38.0	+	12
B. subtilis	43.8	+	12
S. cerevisiae	38.4	Yeast	2
C. neoformans	48.2	Yeast	2

Community Sequencing



*Was not included in the mOTU analysis

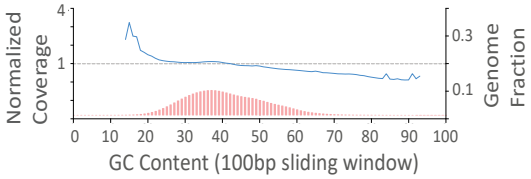
Microbial Community Sequencing:
The Zymo Research Microbial Community DNA Standard was used to assay library construction efficiency using the SeqOnce RhinoSeq kit. Zymo indicates mOTU variance as high as 15%.

Human Shallow Sequencing

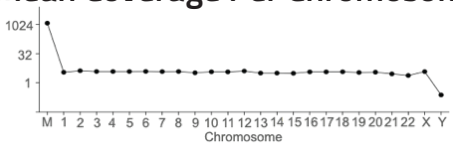
Mapping Characteristics

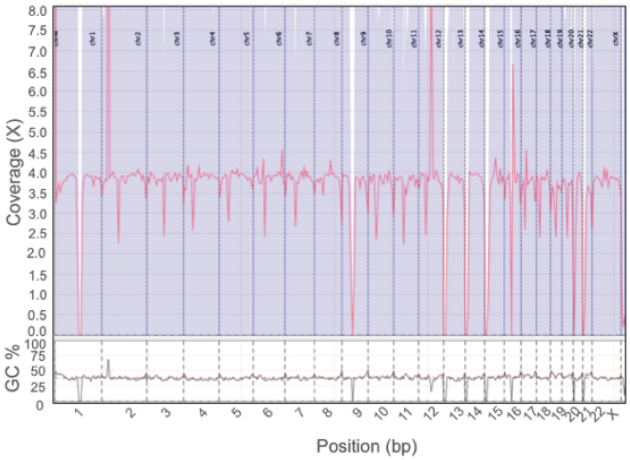
Average Insert Size (bp)	Input (ng)	Depth (bp)	Genome Coverage	Mapped Reads
102	50	1-10 (avg: 3.6)	+80%	91%

GC Bias



Mean Coverage Per Chromosome





Human Shallow Sequencing and GC Bias:
The RhinoSeq kit was used to generate 50ng input Human short insert gDNA libraries and sequenced (2x150bp reads) to 1-10x coverage. As illustrated, the RhinoSeq kit resulted in minimal GC bias as a result of shallow sequencing. Further analysis and re-sequencing to greater depth with Human gDNA and Human FFPE DNA is ongoing.