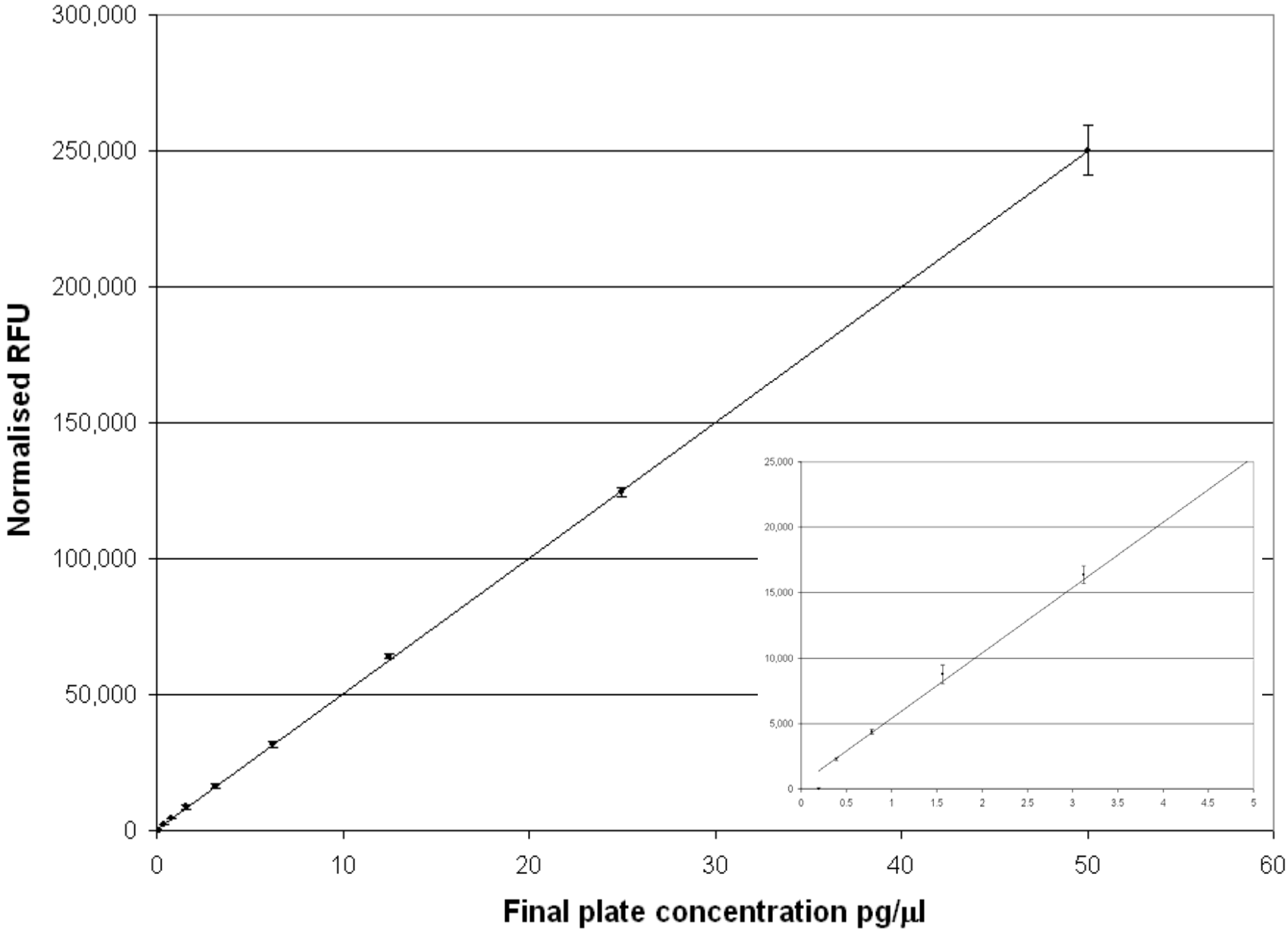
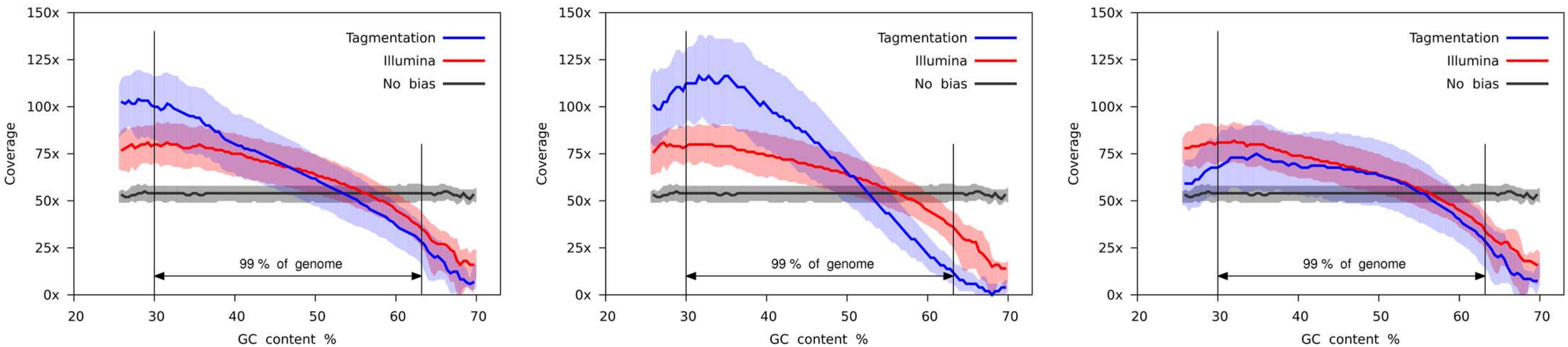
Supplementary Figure-1 Nicholas Parkinson.



Supplemental Figure-2 Nicholas Parkinson.



Supplemental Table-1 Nicholas Parkinson.

Method	Illumina non-barcoded (n=4)	Illumina barcoded (n=7)	Tagmentation (n=6)
Gross flowcell lane yield	54,578,916 +/- 5,250,157	60,126,589 +/- 4,289,408	63,889,183 +/- 2,265,128
Flowcell lane reads >phred 20	33,977,386 +/- 1,627,427 (62.2%)	39,890,981 +/- 9,989,032 (66.3%)	42,881,429 +/- 10,065,397 (67.2%)
>phred 20 reads with correct barcodes	N/A	37,625,293 +/- 9,908,756 (62.6%)	41,909,177 +/- 9,839,476 (65.6%)

Supplemental Table-2 Nicholas Parkinson.

Barcode	PE Adapter	Sequence
CAG	1	/5Phos/AGATCGGAAGAGCGGTTCAGCAGGAATGCCGAG
	2	ACACTCTTTCCCTACACGACGCTCTTCCGATCT**C***A
TCAG	1	/5Phos/**A**AGATCGGAAGAGCGGTTCAGCAGGAATGCCGAG
	2	ACACTCTTTCCCTACACGACGCTCTTCCGATCT**TC***A
GTCAG	1	/5Phos/**AC**AGATCGGAAGAGCGGTTCAGCAGGAATGCCGAG
	2	ACACTCTTTCCCTACACGACGCTCTTCCGATCT**GTC***A
AGTCAG	1	/5Phos/**ACT**AGATCGGAAGAGCGGTTCAGCAGGAATGCCGAG
	2	ACACTCTTTCCCTACACGACGCTCTTCCGATCT**AGTC***A
TAGTCAG	1	/5Phos/**ACTA**AGATCGGAAGAGCGGTTCAGCAGGAATGCCGAG
	2	ACACTCTTTCCCTACACGACGCTCTTCCGATCT**TAGTC***A

Supplemental Table-3 Nicholas Parkinson.

Target DNA	*E. coli* gDNA						
Method	Illumina	Tagmentation					
DNA input	1µg	*AcuI*	*BsgI*/*BpmI**	Blended from all 4	*AcuI*	*BsgI*/*BpmI*	Blended from all 4
		1ng	2x 1ng	4x 1ng	100pg	2x 100pg	4x 100pg
Demultiplexed Reads >Phred 20	3,932,654 (100%)	2,007,577 (100%)	3,187,700 (100%)	5,190,980 (100%)	2,598,467 (100%)	2,594,089 (100%)	2,679,960 (100%)
Uniquely Mapped read pairs	3,831,507 (97.4%)	1,947,625 (97.0%)	3,083,131 (96.7%)	5,025,947 (96.8%)	2,532,052 (97.4%)	2,521,795 (97.2%)	2,523,912 (94.2%)
Genome Alignment Phred Q >150-150	3,814,547 (97.0%)	1,939,653 (96.6%)	3,068,900 (96.3%)	5,002,152 (96.4%)	2,517,717 (96.9%)	2,507,854 (96.7%)	2,509,754 (93.6%)
Read pairs with 98th percentile of library fragment length	3,813,816 (97.0%)	1,933,513 (96.3%)	3,054,574 (95.8%)	4,989,823 (96.1%)	2,494,242 (96.0%)	2,484,887 (95.8%)	2,485,272 (92.7%)
Non-Redundant read pairs	3,770,853 (95.9%)	1,707,743 (85.1%)	2,608,202 (81.8%)	4,064,141 (78.3%)	1,911,917 (73.6%)	2,077,998 (80.1%)	2,087,567 (77.9%)
Library Diversity (% unique fragments)	98.9%	88.3%	85.4%	81.4%	76.7%	83.6%	84.0%

Supplemental Table-4 Nicholas Parkinson.

Target DNA	*E. coli* gDNA						
Method	Illumina	Tagmentation					
DNA Input	1μg	*AcuI*	*BsgI*/*BpmI**	Blended from all 4	*AcuI*	*BsgI*/*BpmI*	Blended from all 4
		1ng	2x 1ng	4x 1ng	100pg	2x 100pg	4x 100pg
% Genome sequenced at coverage ≥1x	98%	96%	96%	98%	96%	97%	97%
% Genome sequenced at coverage ≥5x	97%	89%	90%	93%	89%	93%	93%
% Genome sequenced at coverage ≥10x	91%	79%	79%	80%	74%	79%	79%
Median genome coverage	19x	18x	18x	18x	16x	17x	17x
Coverage dispersion (IQR 25^{th} -75^{th})	14x - 24x	11x - 26x	11x - 26x	12x - 25x	9x-26x	11x-26x	11x-26x