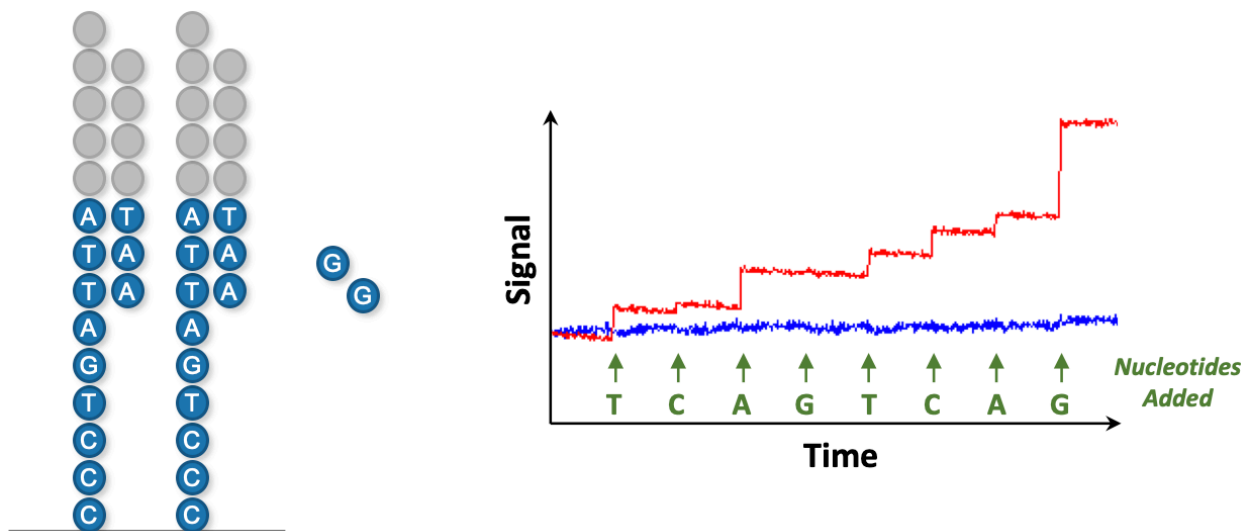**Supplementary Material for Esfandyarpour, et al.**
High accuracy DNA sequencing on a small, scalable platform via electrical detection of single base incorporations
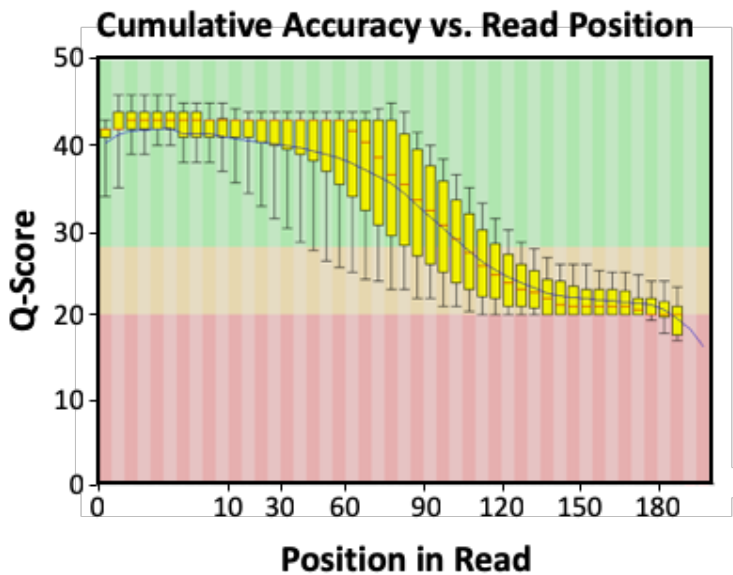

Supplementary Figure 1: Steady-State Signal of Individual Base Incorporations
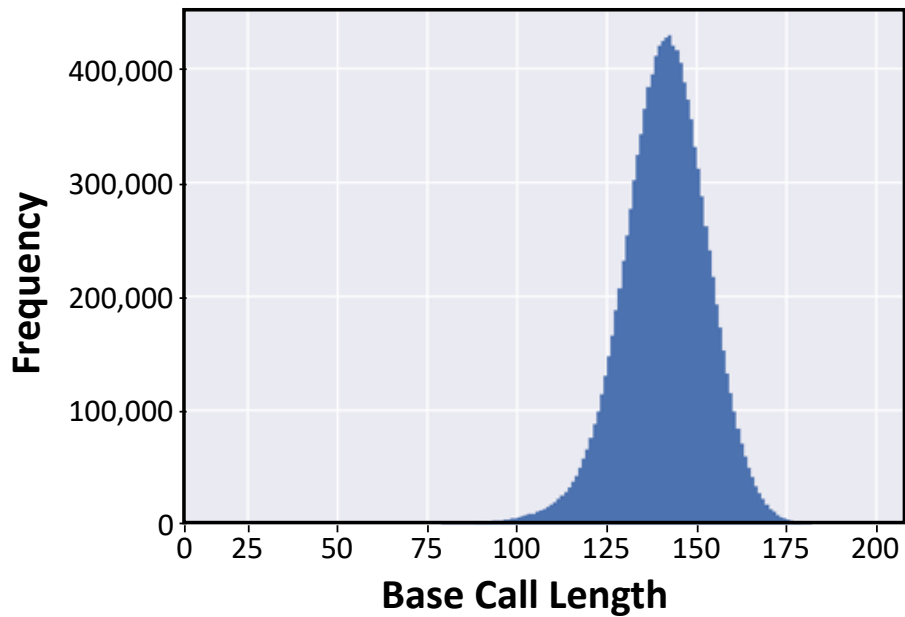
E. coli Read Accuracy* = 99.85%

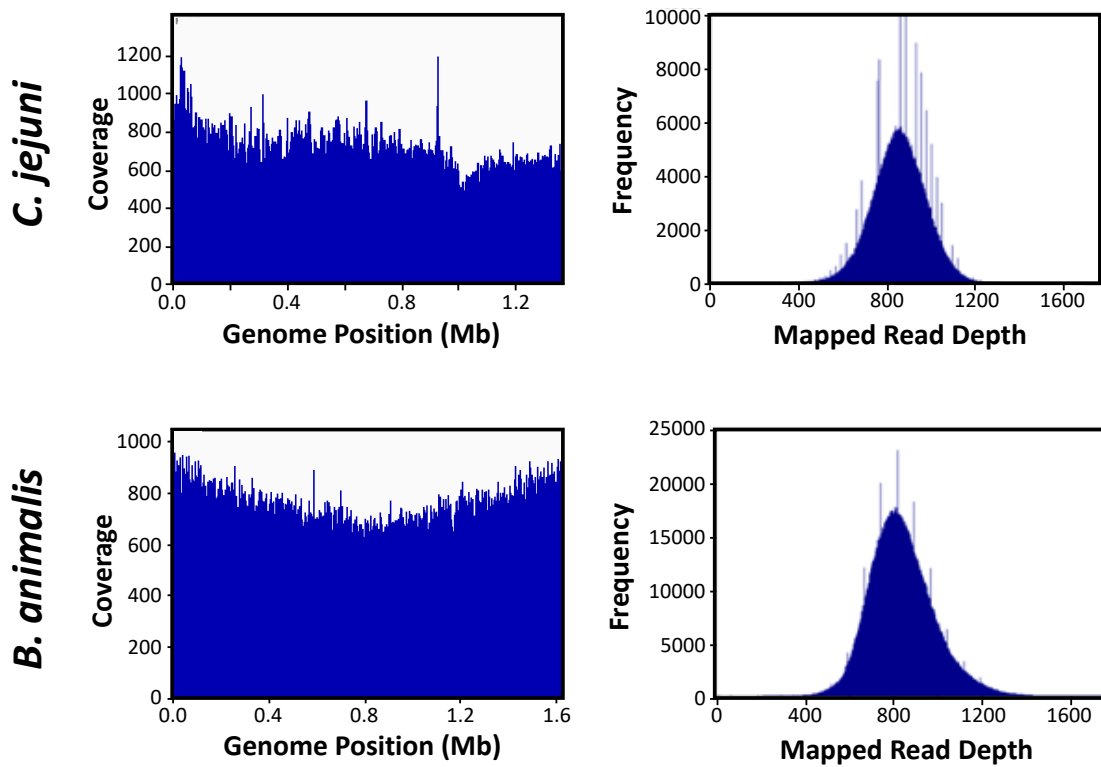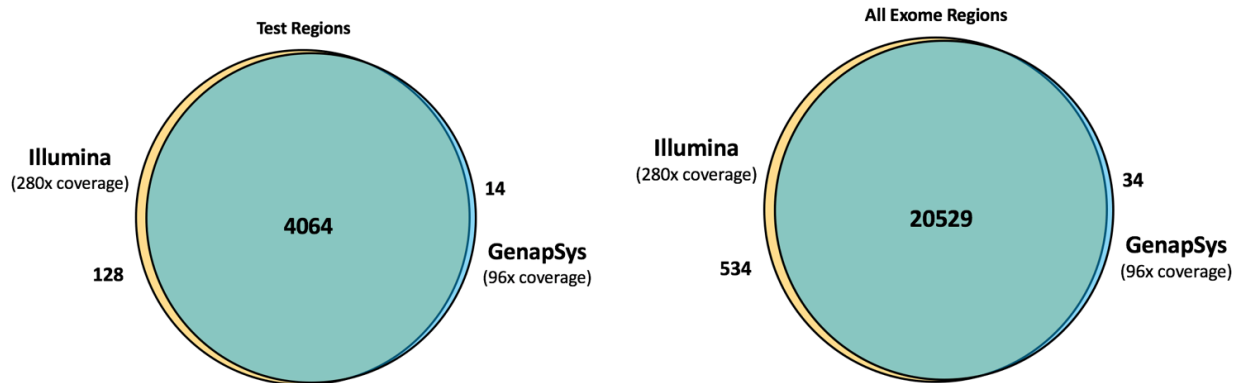| Substitution Errors	Deletion Errors	Insertion Errors
0.016%	0.089%	0.044%

* at base position 75

Supplementary Figure 2: Error Types and Q-Score Distribution

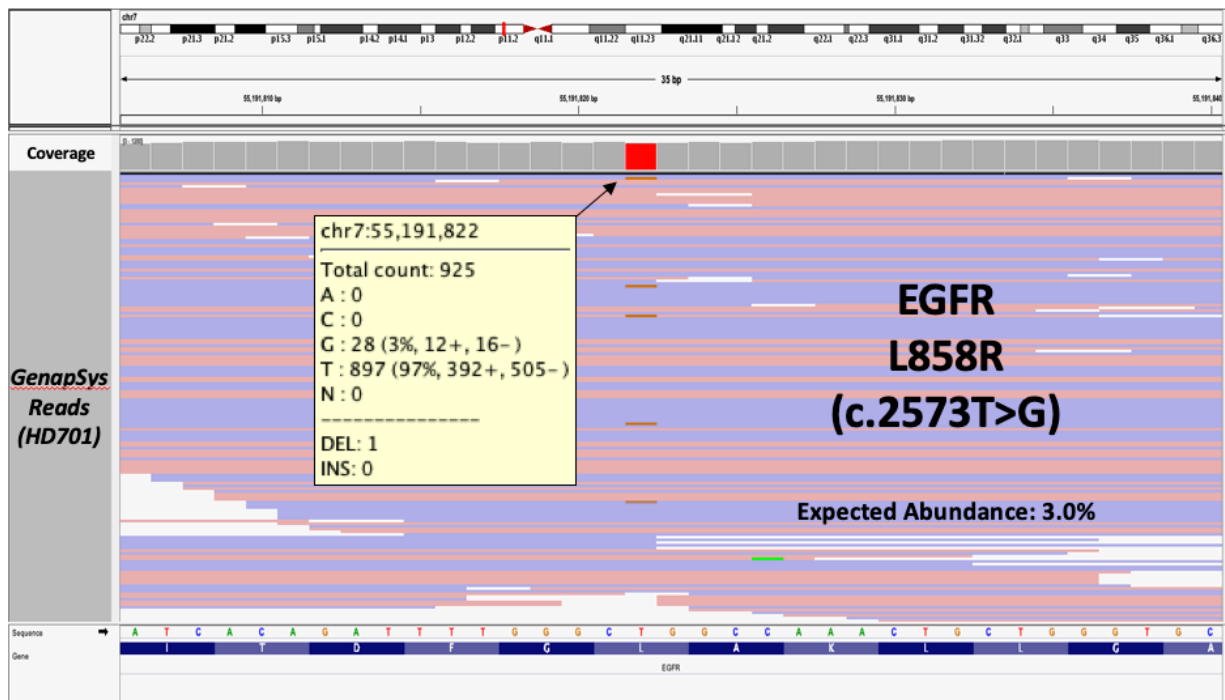**Supplementary Figure 3:** Base Call Length Distribution

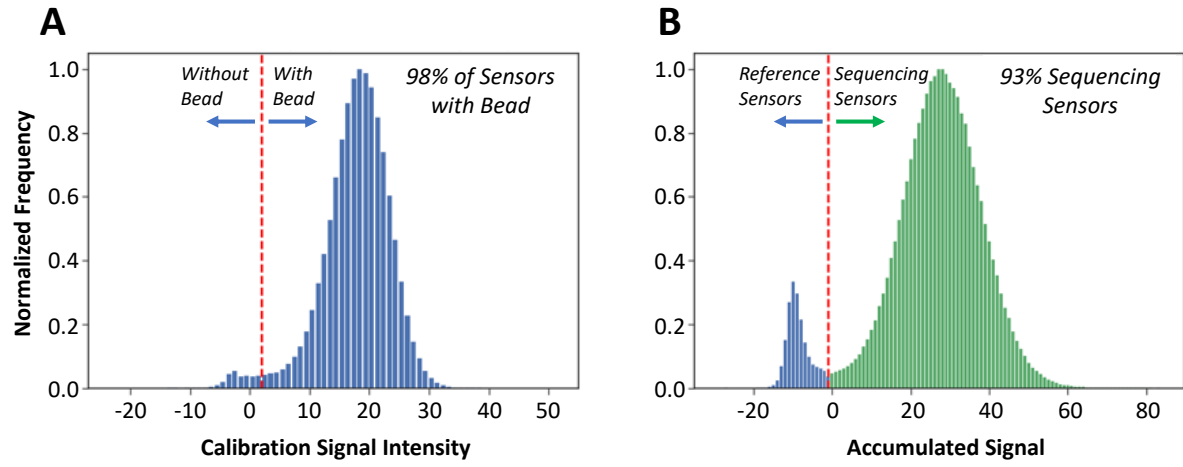**Supplementary Figure 4:** Microbial Genomes

Both analyses use the high confidence regions from GIAB

Supplementary Figure 5: DeepVariant Analysis of SNPs in NA12878 Exome Data

Supplementary Figure 6: Low Frequency Variant Read Visualization

Supplementary Figure 7: Sensor Identification and Active Sensor Determination

Supplementary Table 1: Genomic DNA Samples

DNA Name	Description	Source	Catalog #	Genome Size	GC Content	Reference
E. coli	Escherichia coli K-12	ATCC	10798D-5	4.69 Mb	51.5%	NARG00000000
C. jejuni	Campylobacter jejuni NCTC11168	ATCC	700819D-5	1.64 Mb	30.5%	AL111168
B. animalis	Bifidobacterium animalis subsp. Lactis DSM10140	DSM	10140	1.94 Mb	60.5%	CP001606
NA12878	Human CEPH/UTAH PEDIGREE 1463	Coriell	NA12878	3.2 Gb	40.8%	hg38
HD701	Quantitative Multiplex Reference Standard gDNA	Horizon Discovery	HD701	3.2 Gb	40.8%	hg38

Supplementary Table 2: Targeted Sequencing Statistics

	DNA Sample	
Statistic	**NA12878**	**HD701**
Targeted Panel	xGen Exome Research (v1.0)	xGen Pan-Cancer (v1.5)
Panel Size	39 Mb	0.8 Mb
On Target Rate	78.1%	64.4%
Average Coverage in Target Region	96x	624x
Number of Reads	57,263,646	11,542,744
Number of Mapped Reads	53,656,501	10,528,257
Number of Mapped Reads to Targeted Region	41,922,623	6,776,890