SUPPLEMENTAL FIGURES

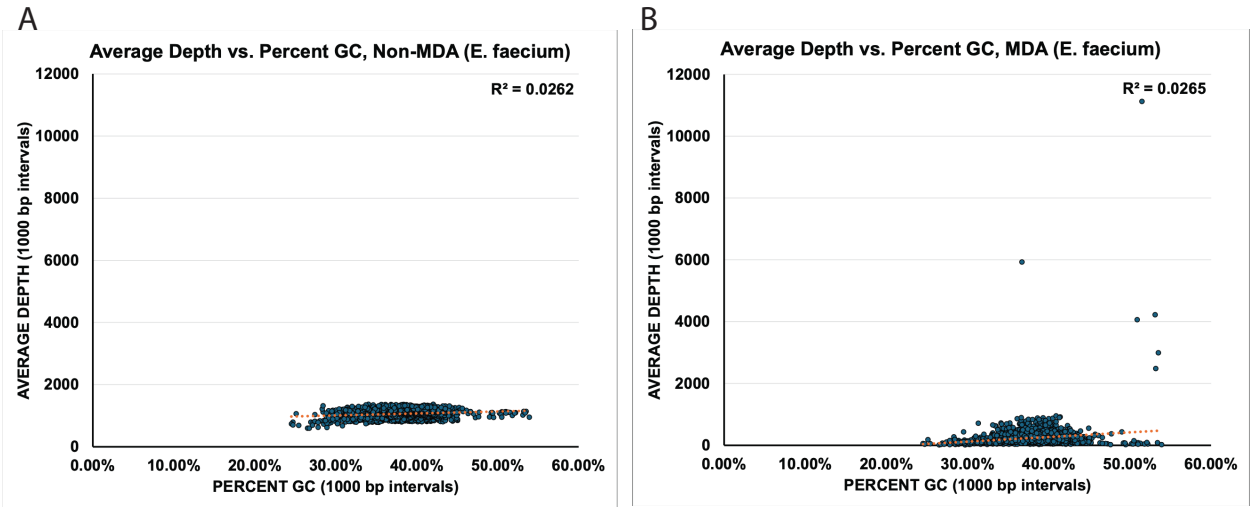

Figure S1. **Square regression correlation coefficient between average depth and average %GC across 1000 base pair sliding window regions of the genomic assembly shows low correlation to %GC.** A correlation analysis of (A) non-amplified and (B) amplified assemblies of *E. faecium.*

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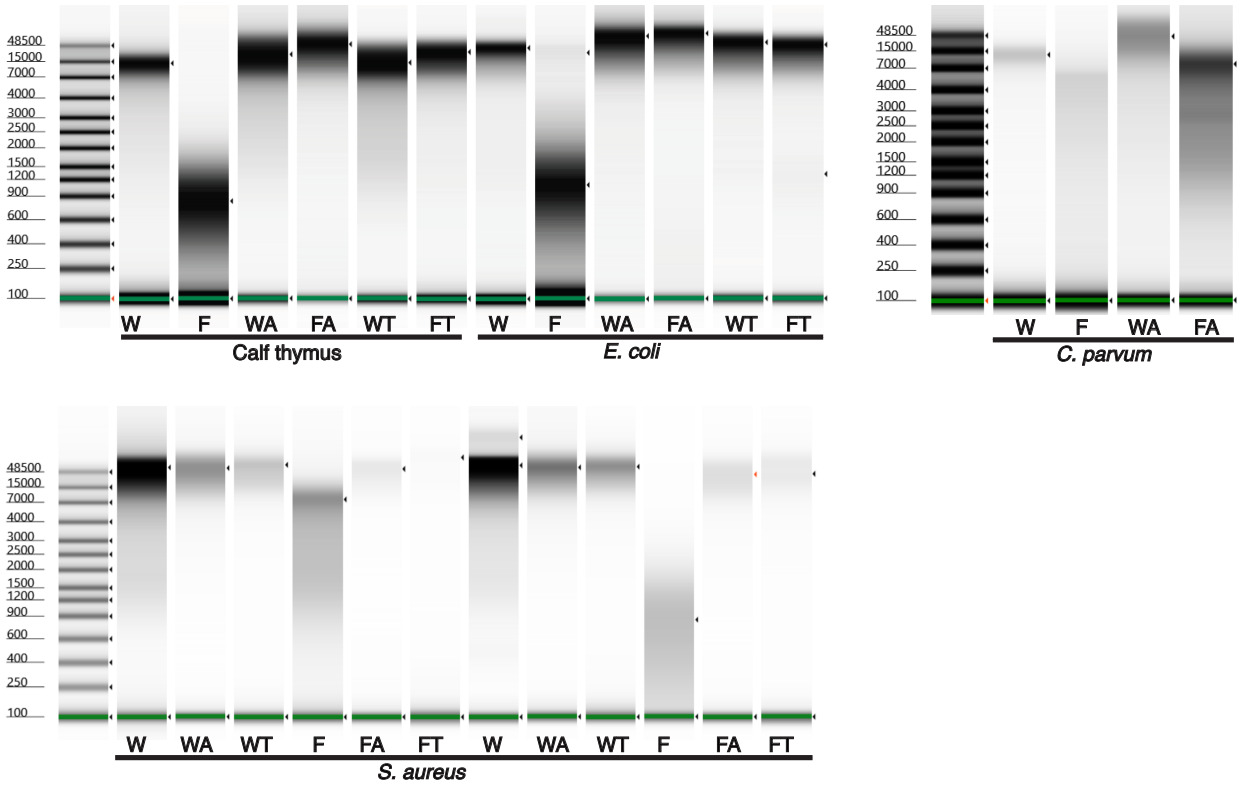

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552 **Figure S2.** Uncropped DNA Fragment and read Size Range pre- and post- Multiple Displacement
553 Amplification using Size-Controlled Fragmented DNA. Uncropped TapeStation results for
554 different organism sets; (W = whole intact DNA; F = Fragmented DNA; WA and FA = after
555 amplification; and WT and FT = after T7 debranching.

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SUPPLEMENTAL TABLES

Table S1 - Whole genome assembly statistics for the data generated using MDA.

Assembly	Condition	Total length (nt)	# of contigs	Largest contig (nt)	GC%	N50	L50	# N's per 100 Kbp
C. meleagridis	WGA (5 ng)	9,171,013	13	1,363,785	30.92	1,103,979	4	0
E. coli	WGA-Intact DNA	6,702,699	252	479,759	50.49	157,769	12	0
	WGA-Fragmented DNA	157,593	12	25,757	49.23	20,338	4	0
E.faecium	400ng (no MDA)	2,775,595	2	2,583,377	38.27	2,583,377	1	0
	1 ng	3,603,364	216	257,348	38.3	64,352	14	0
	1E-1ng	4,287,796	570	83,451	38.66	27,070	49	0
	1E-2 ng	4,146,213	1,066	65,055	38.94	13,948	95	0
	1E-3 ng	1,174	2	670	53.15	670	1	0
	1E-4 ng	78,463	53	15,260	53.83	2,204	7	0
	1E-5 ng	54,253	32	6,962	56.49	3,816	6	0
S. aureus	Intact DNA	2,766,204	3	2,717,982	32.86	2,717,982	1	0
	Fragmented DNA	854,501	198	33,734	33.62	4,926	36	0
	Intact DNA post-WGA	2,763,611	4	2,717,354	32.86	2,717,354	1	0
	Fragmented DNA post-WGA	2,842,696	20	1,890,364	32.84	1,890,364	1	0

563 **Table S2** - Sequencing Statistics for *E. faecium** WGS results at 2.5 ng and 0.2.5 ng starting DNA
564 input.
565

Starting total DNA	**2.5 ng**	**0.25 ng**
Depth	73×	35×
Total length (bp)	2,778,112	2,918,507
Number of contigs	3	35
GC%	38.2	38.28
N50	2,589,111	233,792
L50	1	4
Number of N's per 100 Kbp	0	0

566 *the expected genome size for *E. faecium* species varies between 2.6 and 3.2 Mb
567

568 **Table S3** - Read length distribution among the DNA dilutions for *E. faecium,* based on starting
569 DNA concentration.
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Starting DNA Amount (ng)	Mean Read Length (bp)	Median Read Length (bp)
Control 400	6,134	3,819
2.5	2,533	1,308
2.5E-01	2,305	1,002
2.5E-02	2,390	1,147
2.5E-03	3,121	1,086
2.5E-04	2,555	1,185
2.5E-05	2,641	957

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573 **Table S4.** Comparison between *S. aureus* ATCC-29213 genome sequences assembled before
574 and after CADECT with assembly length, number of contigs, number of reads, and mean read
575 length.
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	Fragmented DNA with MDA before CADECT	**Fragmented DNA with MDA after CADECT**
Assembly length (bp)	2,842,696	2,752,482
Number of contigs	20	3
Number of reads	324,197	292,789
Mean read length (bp)	2,163	1,534
Median read length (bp)	1,352	1,202

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578 **Table S5.** Comparison between *S. aureus* results from CADECT using low DNA input samples.
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DNA input Condition	**Intact DNA**		**Fragmented DNA**	
MDA	No	yes	no	yes
Sequencing coverage input	46.8	92.3	21.7****	77.4
Total number of sequenced base pairs	131,012,134	258,412,289	60,893,145	216,785,548
Number of shorter reads detected*	6,397	49,746	109,830	54,268
Number of non-concatemer reads detected	12,556	44,440	2,548	35,986
Number of putative concatemer reads detected	1,047	5,814	26**	9,746**
Total number of Reads analyzed:	20,000	100,000	112,404	100,000
read loss (%)	37	56	98	64
Total number of non-Concatemer base pairs	103,146,375	153,374,280	5,304,400	96,993,865
Coverage loss (x)	10.0	37.5	19.9	42.8

580 *Shorter reads were reads detected below the default setting of 500 nt window size
581 **Due to size selection putative concatemers were classified as short reads
582 ***Loss if using just the reads characterized as non-concatemeric
583 ****Without the amplification ONT had a bad throughput for the fragmented samples at low
584 input values to generate longer reads, resulting in a low sequencing coverage.