

Figure S1. NEBNext work flow.

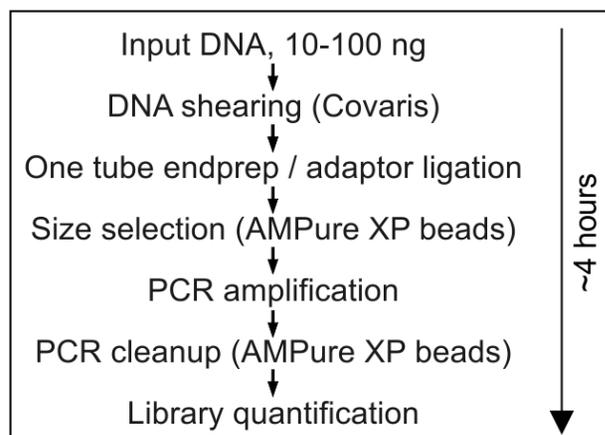


Table S1. Data statistics for all libraries.

Organism	Library prep method	% GC	Starting DNA quantity, ng	PCR cycles	Library concentration, ng/uL	Average fragment size	Library concentration, nM	Total reads	Reads with quality >Q20	Raw read length, bp	Total reads after trimming and normalization	Reads with quality >Q20 after trimming and normalization	Average read length after trimming, bp
<i>B. anthracis</i>	NEBNext	35.4	100	8	14.6	402	55.0	3,240,764	3,046,379	151	2,459,460	2,352,017	148
<i>E. coli</i>	NEBNext	50.5	100	8	11.5	403	43.0	9,079,108	8,848,462	151	2,520,000	2,457,774	151
<i>B. thailandensis A</i>	NEBNext	67.6	10	12	11.0	373	44.5	8,446,330	7,277,554	151	3,234,482	2,813,856	146
<i>B. thailandensis A</i>	NEBNext	67.6	100	10	46.5	404	174.4	9,478,982	7,961,996	151	3,168,918	2,689,132	148
<i>B. thailandensis B</i>	NEBNext	67.6	10	12	12.6	383	49.8	7,722,232	6,594,365	151	3,190,476	2,748,669	147
<i>B. thailandensis B</i>	NEBNext	67.6	100	10	47.6	370	194.9	6,241,068	5,202,194	151	3,142,858	2,665,947	147
<i>B. anthracis</i>	TruSeq	35.4	1000	10	59.1	248	440.7	47,836,056	19,122,933	151	2,459,460	2,362,676	149
<i>E. coli</i>	TruSeq	50.5	1000	10	59.4	299	237.2	18,539,690	17,101,687	151	2,571,428	2,393,342	147
<i>B. thailandensis A</i>	TruSeq	67.6	1000	10	55.4	429	80.3	26,415,536	13,462,977	151	3,147,652	2,104,314	149
<i>B. thailandensis B</i>	TruSeq	67.6	1000	10	39.9	408	40.3	41,077,890	12,813,938	101	4,690,000	2,881,288	101

Table 2a. Statistics for IDBA assemblies of Illumina short-insert data

Sample	Library Prep Kit	Starting DNA, µg	Short-insert coverage	# of contigs >1kb	# of contigs > 50kb	# of contigs > 100kb	N50 for contigs > 1kb (bp)	Largest contig (bp)	Smallest contig (bp)	Assembly Size (bp)
B. anthracis	Tru-Seq	1	69.0x	46	25	16	256,006	889,847	1,130	5,347,313
B. anthracis	NEBNext	0.1	70.0x	48	25	16	256,006	889,847	1,355	5,349,320
E. coli	Tru-Seq	1	61.2x	207	33	16	88,517	300,928	1,003	5,242,710
E. coli	NEBNext	0.1	70.4x	199	35	15	88,517	300,948	1,003	5,216,101
B. thailandensis A	Tru-Seq	1	70.5x	271	39	8	43,887	160,378	1,001	6,582,658
B. thailandensis A	NEBNext	0.1	70.3x	117	50	29	121,177	338,233	1,001	6,575,500
B. thailandensis A	NEBNext	0.01	70.2x	119	48	27	126,565	338,233	1,001	6,575,406
B. thailandensis B	Tru-Seq	1	70.6x	281	35	9	44,682	215,045	1,001	6,587,931
B. thailandensis B	NEBNext	0.1	70.1x	125	46	22	107,215	432,614	1,001	6,579,749
B. thailandensis B	NEBNext	0.01	69.1x	129	40	20	113,254	432,614	1,001	6,579,749

Table 2b. Statistics for Allpaths assemblies of Illumina short-insert data and 454 long-insert data

Sample	Library Prep Kit	Starting DNA, µg	Short-insert coverage	Long-insert coverage	Scaffolds	Number of contigs >1kb	Number of contigs > 50kb	Number of contigs > 100kb	N50 contigs > 1kb (bp)	Largest contig (bp)	Smallest contig (bp)	Assembly Size (bp)
B. anthracis	Tru-Seq	1	69.0x	6.8x	9	23	14	10	831,258	2,508,405	5,048	5,348,296
B. anthracis	NEBNext	0.1	68.7x	6.8x	6	21	13	9	996,207	2,306,221	5,048	5,358,817
E. coli	Tru-Seq	1	61.2x	3.4x	19	96	29	19	148,132	384,555	1,045	5,269,849
E. coli	NEBNext	0.1	70.4x	3.4x	19	82	30	19	180,092	625,412	1,012	5,312,046
B. thailandensis A	Tru-Seq	1	70.5x	7.9x	8	77	44	23	148,050	375,576	1,074	6,603,636
B. thailandensis A	NEBNext	0.1	70.2x	7.9x	6	27	18	15	559,003	1,096,991	1,548	6,650,888
B. thailandensis A	NEBNext	0.01	70.3x	7.9x	4	26	18	14	541,453	1,082,481	1,179	6,652,405
B. thailandensis B	Tru-Seq	1	70.6x	7.7x	3	53	35	24	206,108	575,396	2,863	6,655,446
B. thailandensis B	NEBNext	0.1	69.2x	7.5x	4	27	23	21	343,287	710,311	1,179	6,651,385
B. thailandensis B	NEBNext	0.01	70.1x	7.7x	4	23	17	16	559,910	924,997	1,897	6,660,010