Supplementary Table S2. Mapping of reads to reconstructed pL6-like plasmids.

Plasmid[a]	Size (bp)	Reads[b]	Reads mapped[c] (threshold %)	Coverage (Fold)	Total Reads	Similarity (%)[d]
pCOLO-c1	5,857	ERR7916263	1,744 (0%)	42	72,140,396	100
pHILL-c1	6,187	SRR26978067 + SRR26968577	4,213 (1%)	147	56,053,528 + 17,295,462	99.7
pHILL-c2	7,625	SRR26978067	580 (1%)	18	17,295,462	99.8
pTYRR-r1	5,844	SRR5637210	391 (1%)	28	1,052,913	99.3
pCABO-c1	5,007	SRR8816317	1,504 (0%) ---------- 2,876 (1%)	74 ---------- 142	28,870,606 ---------- 28,870,606	100 -------- 99.7
pCABO-c2	5,889	SRR8816317	1122 (1%)	47	28,870,606	99.7
pCABO-c6	5,864	SRR8816317	1177 (1%)	50	28,870,606	99.7
pCABO-c9	6,930	SRR8816317	556 (1%)	20	28,870,606	99.7
pCABO-c10	5,219	SRR8816317	772 (1%)	37	28,870,606	99.7
pCABO-s1	6,206	SRR8816317	998 (1%)	40	28,870,606	99.7
pCABO-s5	5,017	SRR8816317 + SRR8816318	1,053 (1%)	35	28,870,606 25,000,000	99.9
pISLA-c6	5,881	SRR21894959 SRR23092357	1,327 (1%)	33	145,294,990 + 99,692,172	99.7
pISLA-s1	5,606	SRR23092357	1,809 (1%)	47	99,692,172	99.8
pMALL-c2	5,504	ERR5979340	1510 (1%)	48	81,576,380	99.8
pPOLA-c1	6,075	SRR13926770	1,415 (0%)	59	8,866,062	100

[a] Plasmid names with suffix -c were assembled by contig extension; a sequence from an assembled contig was extended by rounds of repeated read mapping (see Methods). The suffix -s refers to plasmids assembled using metaplasmidspades (see Methods). The suffix -r in pTYRR-r1 indicates the initial contig was assembled from RNA-seq reads, and then extended by repeated rounds of read mapping to metagenomic reads.

[b] NCBI SRA read accessions are given. These were downloaded via the ENA (www.ebi.ac.uk/ena), trimmed and size filtered (see Methods), producing the number of reads shown in the Total Reads column.

[c] Number of reads mapped to the reference sequence at a maximum level of base differences shown in parentheses. In most cases a base difference tolerance of up to 1% was applied, while in some cases it could be set to zero % mismatches and the coverage still remained high. For pCABO-c1, values are given for both of the applied stringencies. The Geneious mapper (Geneious Prime version 2023.2.1) was set to custom sensitivity, fine tuning = none, minimum mapping quality = 40, only map paired reads which = both map, maximum mismatches per read = 1%, maximum ambiguity = 1.

[d] Average percentage identity of mapped reads to the reference sequence, as calculated by the Geneious mapper.