Supplementary Table 1. The assembly quality of contig clusters generated by MaxBin for three species in synthetic data set.

Species	Completeness	Contamination	N50	#contigs
Lactobacillus gasseri	98.4%	0	74,718	55
Enterococcus faecalis	99.6%	0.4%	41,628	131
Citrobacter rodentium	100%	14.9%	26,428	1,034

Supplementary Table 2. Comparison of accuracy of inference of relative distance of contigs to the replication origin using DEMIC (correlation between PC1 and true distances) and direct sorting of contigs in single sample (average of correlations between single sample estimated distances and true distances). Also presented in the table are the average variance of coverage across samples (average over contigs after filtering) and across contigs (average over samples) in synthetic data sets.

Species	DEMIC	Single sample	Aver. var samples	Aver. var contigs
Lactobacillus gasseri	0.902	0.846 (*n*=36)	5.51 (*n*=29)	0.10 (*n*=36)
Enterococcus faecalis	0.948	0.915 (*n*=36)	3.7 (*n*=72)	0.09 (*n*=36)
Citrobacter rodentium	0.964	0.756 (*n*=50)	0.73 (*n*=144)	0.15 (*n*=50)

Supplementary Table 3. The assembly quality and marker lineage of seven contig clusters with different growth rates in healthy and Crohn's disease samples of PLEASE data set.

Contig cluster	Completeness	Contamination	Control vs. Crohn's	Marker lineage
metabat2.187	61.7%	0	High	*k__Bacteria*
metabat2.239	58.5%	1.8%	High	*o__Clostridiales*
metabat2.250	66.6%	0.8%	High	*p__Proteobacteria*
metabat2.259	79.3%	2.1%	High	*k__Bacteria*
metabat2.270	72.0%	2.0%	High	*f__Lachnospiraceae*
metabat2.369	68.8%	2.8%	High	*f__Lachnospiraceae*
metabat2.55	55.2%	1.9%	Low	*o__Clostridiales*