

Table S1. Automatically set parameters

Parameter	Stage	Default setting
SGA Quality Trim (-q)	1	fixed to 10, not optimized
SGA Quality Filter (-f)	1	fixed to 20, not optimized
SGA Min Read Length (-m)	1	fixed to 30, this should be larger than IDBA's min k -mer
IDBA min k -mer	2	29, most k -mers of this size are unique in a microbial genome but larger values may be better
IDBA max k -mer	2	maximum read length of trimmed reads
SSPACE Overhang MinOverlap (-m)	3,5	Max of 15 and floor of binary logarithm of genome size, plus 3.99
SSPACE ExtendCall MinBases (-o)	3,5	fixed to 1
SSPACE Minimum Links (-k)	3,5	base 1.4 logarithm of E_links , minus 11.5, where $E_links = \frac{2c\mu}{l_r}$ and c is coverage
SSPACE Min Link Ratio (-a)	3,5	fixed to 0.6,0.3. These values give higher accuracy than SSPACE defaults
SSPACE Merge MinOverlap (-n)	3,5	floor of (binary logarithm of mean insert size, scaled by 1.24, plus 0.99)
SSPACE Insert Mean	3,5	Calculated using EM-clustering
SSPACE Insert StDev	3,5	Calculated using EM-clustering
DBSCAN ϵ	4	Derived from coverage as described in main text
DBSCAN $MinPts$	4	Derived from coverage as described in main text