Supplementary material:

Table 1: Results of the processing of fragment and mate-pair libraries

	Fragments		**Mate-paired**	
Feature	Raw data	Simplifier	Raw data	Simplifier
Number of Contigs	24,344	18,523	17,149	14,153
N50	552	642	697	717
Blastx vs NR(time)	109h36m	91h59m	103h4m	87h32m
Blast hits	4,171,658	3,178,597	3,309,206	2,734,811

NR - NCBI non-redundant databank. Comparative analysis of the number of contigs, value of N50, time for execution of Blast and quantity of hits generated, among the contigs originated from the mate-pair and fragment libraries of *Escherichia coli* DH10B before and after the application of Simplifier.

Table 2: Number of *Escherichia coli* DH10B contigs eliminated using Simplifier

	Size range (bp)				
Library	Up to 100	101-499	501-999	1,000-1,999	2,000-2,999
Mate-paired	12	2,056	723	198	7
Fragments	117	5,134	517	53	0

Number of contigs removed by applying Simplifier to mate-paired and fragment library data, classified by contig length.