

Table 1. Essential genes identified by different methods

Organism	Number of protein-coding essential genes	Method of identification	Ref.
<i>Saccharomyces cerevisiae</i>	878	Single-gene-specific mutagenesis	[14]
<i>Haemophilus influenzae</i>	642	Saturation transposon mutagenesis	[8]
<i>Acinetobacter baylyi</i>	499	Single-gene-specific mutagenesis	[15]
<i>Mycoplasma pulmonis</i>	461	Saturation transposon mutagenesis	[12]
<i>Mycoplasma genitalium</i>	381	Saturation transposon mutagenesis	[10]
<i>Salmonella enterica</i> Typhi	356	Saturation transposon mutagenesis	[13]
<i>Pseudomonas aeruginosa</i>	335	Saturation transposon mutagenesis	[11]
<i>Helicobacter pylori</i>	323	Saturation transposon mutagenesis	[9]
<i>Escherichia coli</i>	303	Single-gene-specific mutagenesis	[16]
<i>Staphylococcus aureus</i>	302	Antisense RNA inhibition	[17]
<i>Bacillus subtilis</i>	271	Single-gene-specific mutagenesis	[18]
Numbers of genomes compared			
2	256	Comparative genomics	[3]
5	180	Comparative genomics	[4]
7	156	Comparative genomics	[5]
100	63	Comparative genomics	[6]
147	35	Comparative genomics	[7]

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