

Table 3. Absence and presence of genes associated with DNA repair in bacteria with small genomes and low GC content

Species	<i>ung</i>	<i>mutM</i>	<i>mutY</i>	Genome size, Mbp	GC content, %
<i>Carsonella ruddii</i>	—	—	—	0.16	17
<i>Wigglesworthia glossinidia brevipalpis</i>	+	—	—	0.69	22
<i>Buchnera aphidicola</i> Sg	—*	—	+	0.64	25
<i>Blochmannia floridanus</i>	+	—	+	0.70	27
<i>Fusobacterium nucleatum</i> ATCC 25586	+	—	—	2.17	27
<i>Borrelia burgdorferi</i> B31	+	—	—	1.52	28
<i>Ehrlichia ruminantium</i> Gardel	—	+	—	1.50	28
<i>Rickettsia prowazekii</i> Madrid E	—	—	—	1.11	29
<i>Mycoplasma genitalium</i> G-37	+	+	—	0.58	32
<i>Baumannia cicadellincola</i>	+	+	—	0.68	33
<i>Wolbachia pipientis</i> wBM	—	+	—	1.08	34

The *ung*, *mutM*, and *mutY* genes are widespread among members of the major bacterial phyla, whereas *mug* and *vsr* genes are present only in a smaller number of species. A gene was considered absent if no annotated gene with the same function was found and no homologues were found in BLAST searches with a cutoff of $P < 10^{-6}$ using the *S. typhimurium* sequence and excluding the *mutY* homologue *nth*.

*Pseudogene.