

Table 1. Comparison of main genomic characteristics. Louse symbionts highlighted by grey background.

Bacterium	Genome size (Mb)	GC%	No. of protein coding genes	Source
Neisseriaceae - <i>Hoplopleura acanthopus</i>	1.6	33.4	1421	this study
Neisseriaceae - <i>Polyplax serrata</i>	1.8	34	1789	this study
<i>Legionella polyplacis</i> - <i>Polyplax serrata</i>	0.5	23	473	CP021497.1
<i>Riesia</i> spp.	0.5-0.6	25-28.5	476-557	Boyd et al., 2017
<i>Puchtella pedicinophila</i>	0.6	24.2	564	Boyd et al., 2017
<i>Sodalis</i> (<i>Proechinophthirus fluctus</i>)	2.2	50	1287†	Boyd et al., 2016
<i>Snodgrassella alvi</i>	2.5	41.3	2125	CP007446.1
<i>Neisseria meningitidis</i>	2.2	51.7	2118	NC_003112.2

† number of genes annotaed in the shotgun library avaiable in the GenBank under the accession numbers [LECR01000001-92](#)