

Table S1: Dataset classification

ID	Name	Number of Genes	Taxonomic class	Type of Association	Obligatoriness for the bacterium	Obligatoriness for the host	Location	Transmission
HODCD	<i>Candidatus Hodgkinia cicadicola</i> Dsem	203	ALP	M	O	P	I	V
CARRP	<i>Candidatus Carsonella ruddii</i> PV	214	GAM	M	O	P	I	V
SULMW	<i>Candidatus Sulcia muelleri</i> GWSS	266	FLA	M	O	P	I	V
BUCCC	<i>Buchnera aphidicola</i> Cc	396	GAM	M	O	P	I	V
MYCGE	<i>Mycoplasma genitalium</i> G37	553	MOL	P	O	S	CA	H
BUCAI	<i>Buchnera aphidicola</i> APS	619	GAM	M	O	P	I	V
BLASB	<i>Blattabacterium</i> sp. Bge	638	FLA	M	O	P	I	V
BAUCH	<i>Baumannia cicadellinicola</i>	657	GAM	M	O	P	I	V
BLOFL	<i>Candidatus Blochmannia floridanus</i>	668	GAM	M	O	P	I	V
WIGBR	<i>Wigglesworthia glossinidia</i>	671	GAM	M	O	P	I	V
BLOPB	<i>Candidatus Blochmannia pennsylvanicus</i>	718	GAM	M	O	P	I	V
MYCHJ	<i>Mycoplasma hyopneumoniae</i> J	754	MOL	P	O	S	CA	H
RICTY	<i>Rickettsia typhi</i> Wilmington	976	ALP	P	O	S	I	V
CHLTR	<i>Chlamydia trachomatis</i> D/UW-3/CX	987	CHL	P	O	S	I	H
WOLTR	<i>Wolbachia pipientis</i> wBm	1188	ALP	M	O	P	I	V
WOLPM	<i>Wolbachia pipientis</i> wMel	1416	ALP	P	O	S	I	V
BARQU	<i>Bartonella quintana</i> Toulouse	1433	ALP	P	O	S	CA	H
LAWIP	<i>Lawsonia intracellularis</i> PHE/MN1-00	1530	DEL	P	O	S	I	H
ORITB	<i>Orientia tsutsugamushi</i> Boryong	1580	ALP	P	O	S	I	V
HELPI	<i>Helicobacter pylori</i> 26695	1718	EPS	P	O	S	CA	H
STRTD	<i>Streptococcus thermophilus</i> LMD-9	1836	BAC	C	FA	S	E	H
NEIG2	<i>Neisseria gonorrhoeae</i> NCCP11945	1947	BET	P	O	S	CA	H
WOLSU	<i>Wolinella succinogenes</i> DSM 1740	2138	EPS	C	FA	S	E	H
STRA5	<i>Streptococcus agalactiae</i> 2603V/R	2160	BAC	P	FA	S	E	H
THICR	<i>Thiomicrospira crumigena</i> XCL-2	2353	EPS	FL	FL	FL	FL	FL
HAMD5	<i>Candidatus Hamiltonella defensa</i> T5A	2387	GAM	M	O	S	CA	V
LACG3	<i>Lactobacillus casei</i> ATCC 334	2949	BAC	C	FA	S	E	H
LISMO	<i>Listeria monocytogenes</i> EGD-e	3084	BAC	P	FA	S	CA	H
XYLFA	<i>Xylella fastidiosa</i> 9a5c	3261	GAM	P	FA	S	E	H
BRUME	<i>Brucella melitensis</i> bv 1 16M	3492	ALP	P	O	S	CA	H
DESPS	<i>Desulfotalea psychrophila</i> Lsv54	3600	DEL	FL	FL	FL	FL	FL
PSEHT	<i>Pseudoalteromonas haloplanktis</i> TAC125	3612	GAM	FL	FL	FL	FL	FL
VIBCH	<i>Vibrio cholerae</i> O1 biovar El Tor str. N16961	4025	GAM	P	FA	S	E	H
BACA2	<i>Bacillus amyloliquefaciens</i> FZB42	4033	BAC	C	FA	S	E	H
YERPE	<i>Yersinia pestis</i> CO92	4344	GAM	P	O	S	CA	H
BACSU	<i>Bacillus subtilis</i> 168	4353	BAC	FL	FL	FL	FL	FL
ECOLI	<i>Escherichia coli</i> K-12	4390	GAM	C	FA	S	E	H
YERPY	<i>Yersinia pseudotuberculosis</i> YPIII	4618	GAM	P	FA	S	CA	H
SODGM	<i>Sodalis glossinidius</i> morsitans	4649	GAM	M	O	S	CA	V
RHOS4	<i>Rhodobacter sphaeroides</i> 2.4.1	4672	ALP	FL	FL	FL	FL	FL
MYCTU	<i>Mycobacterium tuberculosis</i> H37Rv	4679	ACT	P	O	S	CA	H
SALTI	<i>Salmonella enterica</i> serovar Typhi	4712	GAM	P	FA	S	CA	H
SHIFL	<i>Shigella flexneri</i> 2a str. 301	4728	GAM	P	FA	S	CA	H
ERWCT	<i>Erwinia carotovora</i> subsp. atroseptica SCRI1043	4765	GAM	P	FA	S	E	H

continue on the next page

Table S1 – continue on the next page

ID	Name	Number of Genes	Taxonomic class	Type of Association	Obligatoriness of the bacterium for the bacterium	Obligatoriness of the association for the host	Location	Transmission
PHOLL	Photorhabdus luminescens TTO1	4801	GAM	P	O	S	CA	H
BURMA	Burkholderia mallei ATCC 23344	5129	BET	P	O	S	CA	H
PSEE4	Pseudomonas entomophila L48	5241	GAM	P	FA	S	E	H
ECO57	Escherichia coli O157:H7	5549	GAM	P	FA	S	E	H
BACHK	Bacillus thuringiensis serovar konkukian str. 97-27	5599	BAC	P	FA	S	E	H
AGRT5	Agrobacterium tumefaciens C58	5700	ALP	P	FA	S	E	H
BACAN	Bacillus anthracis Ames Ancestor	5886	BAC	P	O	S	CA	H
CUPTR	Cupriavidus taiwanensis LMG19424	5940	BET	M	FA	S	E	H
PSEAB	Pseudomonas aeruginosa UCBPP-PA14	6254	GAM	P	FA	S	E	H
FRAAA	Frankia alni ACN14a	6763	ACT	M	FA	S	E	H
RHIME	Sinorhizobium meliloti 1021	6933	ALP	M	FA	S	E	H
PSEFS	Pseudomonas fluorescens SBW25	6960	GAM	C	FA	S	E	H
MYCS2	Mycobacterium smegmatis MC2 155	7223	ACT	C	FA	S	E	H
RALEH	Ralstonia eutropha H16	7279	BET	FL	FL	FL	FL	FL

Association: C, commensal; M, mutualist; P, parasite; FL, free-living. **Obligatoriness of the association for the bacterium:** FA, facultative; O, obligatory. **Obligatoriness of the association for the host:** P, primary symbiont; S, secondary symbiont. **Location:** I, obligatory intracellular; CA, cell associated; E, extracellular. **Transmission:** H, horizontal; V, vertical.