

**Supplementary Table S3.** Cloning and sequencing of bacterial 16S rRNA gene sequences from maternal symbiotic M4 region, and offspring eggs and newborn nymphs of *M. gracilicorne*.

Mother-offspring set <sup>a</sup>	Accession number of 16S rRNA gene of bacterial clone	Sequence similarity to mother-derived 16S rRNA gene <sup>b</sup>	BLAST top hit <sup>c</sup>
<b>CKSI20-12</b>			
Mother	<a href="#">LC594159</a>	100% (515/515)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg1-1	<a href="#">LC594143</a>	100% (515/515)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg1-2	<a href="#">LC594144</a>	76.9% (384/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg1-3	<a href="#">LC594145</a>	76.9% (384/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg1-4	<a href="#">LC594146</a>	76.7% (383/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg1-5	<a href="#">LC594147</a>	76.7% (383/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg1-6	<a href="#">LC594148</a>	92.2% (475/515)	NR_041697; <i>Citrobacter gillenii</i> strain CDC 4693-86 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg1-7	<a href="#">LC594149</a>	76.7% (383/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg1-8	<a href="#">LC594150</a>	76.7% (383/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph1-1	<a href="#">LC594160</a>	76.7% (383/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph1-2	<a href="#">LC594161</a>	100% (515/515)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph1-3	<a href="#">LC594162</a>	76.7% (383/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph1-4	<a href="#">LC594163</a>	77.7% (388/499)	NR_074155; <i>Ehrlichia ruminantium</i> strain Welgevonden ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph1-5	<a href="#">LC594164</a>	76.9% (384/499)	NR_044747; 4.11E-177; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph1-6	<a href="#">LC594165</a>	55.2% (278/503)	Host 18S rRNA sequence
Nymph1-7	<a href="#">LC594166</a>	88.5% (456/515)	NR_025335; <i>Pragia fontium</i> strain DSM 5563 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph1-8	<a href="#">LC594167</a>	76.4% (386/505)	NR_135210; <i>Methylobacterium indicum</i> strain SE2.11 ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg2-1	<a href="#">LC594151</a>	79.8% (405/507)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg2-2	<a href="#">LC594152</a>	87.0% (445/511)	NR_152004; <i>Acinetobacter lactucae</i> strain NRRL B-41902 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg2-3	<a href="#">LC594153</a>	76.7% (383/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg2-4	<a href="#">LC594154</a>	83.3% (426/511)	NR_112030; <i>Stenotrophomonas maltophilia</i> strain ATCC 13637 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg2-5	<a href="#">LC594155</a>	76.7% (383/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg2-6	<a href="#">LC594156</a>	55.0% (277/503)	Host 18S rRNA sequence
Egg2-7	<a href="#">LC594157</a>	76.9% (384/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg2-8	<a href="#">LC594158</a>	80.0% (402/502)	NR_113608; <i>Agrobacterium rubi</i> strain NBRC 13261 ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph2-1	<a href="#">LC594168</a>	76.9% (384/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph2-2	<a href="#">LC594169</a>	78.6% (390/496)	NR_118559; <i>Rhizobium skieniewicense</i> Ch11 ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph2-3	<a href="#">LC594170</a>	76.9% (384/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph2-4	<a href="#">LC594171</a>	76.9% (384/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph2-5	<a href="#">LC594172</a>	76.9% (384/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S

			ribosomal RNA, partial sequence
Nymph2-6	<a href="#">LC594173</a>	76.9% (384/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph2-7	<a href="#">LC594174</a>	55.2% (278/503)	Host 18S rRNA sequence
Nymph2-8	<a href="#">LC594175</a>	99.8% (514/515)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
<b>CKSI20-13</b>			
Mother	<a href="#">LC594192</a>	100% (515/515)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg1-1	<a href="#">LC594176</a>	76.7% (383/499)	NR_044747; 4.11E-177; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg1-2	<a href="#">LC594177</a>	76.7% (383/499)	NR_044747; 4.11E-177; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg1-3	<a href="#">LC594178</a>	84.0% (426/507)	NR_113867; <i>Sphingomonas aquatilis</i> strain NBRC 16722 ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg1-4	<a href="#">LC594179</a>	76.7% (383/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg1-5	<a href="#">LC594180</a>	94.4% (478/506)	NR_118335; <i>Klebsiella michiganensis</i> strain W14 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg1-6	<a href="#">LC594181</a>	78.3% (391/499)	NR_149816; <i>Microbacterium zae</i> strain 1204 (Actinobacteria) 16S ribosomal RNA, partial sequence
Egg1-7	<a href="#">LC594182</a>	76.7% (383/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg1-8	<a href="#">LC594183</a>	76.5% (382/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 1-1	<a href="#">LC594193</a>	76.7% (383/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 1-2	<a href="#">LC594194</a>	78.0% (392/502)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 1-3	<a href="#">LC594195</a>	76.7% (383/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 1-4	<a href="#">LC594196</a>	80.7% (382/473)	NR_026519; <i>Agrobacterium larrymoorei</i> strain AF3.10 ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 1-5	<a href="#">LC594197</a>	77.5% (386/498)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 1-6	<a href="#">LC594198</a>	76.7% (383/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 1-7	<a href="#">LC594199</a>	99.6% (513/515)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 1-8	<a href="#">LC594200</a>	79.1% (399/504)	NR_108571; <i>Paracoccus caeni</i> strain MJ17 ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg2-1	<a href="#">LC594184</a>	78.5% (396/504)	NR_036805; <i>Legionella fallonii</i> strain LLAP10 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA gene, partial sequence
Egg2-2	<a href="#">LC594185</a>	87.3% (447/512)	NR_113855; <i>Pseudomonas cremoricolorata</i> DSM 17059 = NBRC 16634 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg2-3	<a href="#">LC594186</a>	76.7% (383/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg2-4	<a href="#">LC594187</a>	76.5% (382/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg2-5	<a href="#">LC594188</a>	72.8% (365/501)	NR_113706; <i>Sphingobacterium multivorum</i> strain NBRC 14947 (Bacteroidetes) 16S ribosomal RNA, partial sequence
Egg2-6	<a href="#">LC594189</a>	79.2% (406/512)	NR_042568; <i>Stenotrophomonas humi</i> strain R-32729 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg2-7	<a href="#">LC594190</a>	78.7% (403/512)	NR_029319; <i>Pseudomonas anguilliseptica</i> strain S 1 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg2-8	<a href="#">LC594191</a>	79.2% (404/510)	NR_042578; <i>Sphingomonas pseudosanguinis</i> strain G1-2 ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 2-1	<a href="#">LC594201</a>	76.7% (383/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 2-2	<a href="#">LC594202</a>	78% (390/500)	NR_026519; <i>Agrobacterium larrymoorei</i> strain AF3.10 ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 2-3	<a href="#">LC594203</a>	79.2% (400/505)	NR_158122; <i>Consotaela salsifontis</i> strain USBA 369 ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 2-4	<a href="#">LC594204</a>	78.8% (402/510)	NR_116711; <i>Sphingomonas humanensis</i> strain JSM 083058 ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence

Nymph 2-5	<a href="#">LC594205</a>	76.8% (385/501)	NR_028838; <i>Devosia neptuniae</i> strain J1 ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 2-6	<a href="#">LC594206</a>	81.7% (233/285)	NR_026519; <i>Agrobacterium larrymoorei</i> strain AF3.10 ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 2-7	<a href="#">LC594207</a>	79.4% (399/502)	NR_044213; <i>Devosia crocina</i> strain IPL20 ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 2-8	<a href="#">LC594208</a>	77.9% (396/508)	NR_113807; <i>Ahrensia kielensis</i> strain NBRC 15762 ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
<b>CKSI20-14</b>			
Mother	<a href="#">LC594225</a>	100% (515/515)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg1-1	<a href="#">LC594209</a>	78.6% (398/506)	NR_026519; <i>Agrobacterium larrymoorei</i> strain AF3.10 ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg1-2	<a href="#">LC594210</a>	83.4% (425/509)	NR_112030; <i>Stenotrophomonas maltophilia</i> strain ATCC 13637 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg1-3	<a href="#">LC594211</a>	76.5% (382/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg1-4	<a href="#">LC594212</a>	76.7% (383/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg1-5	<a href="#">LC594213</a>	88.9% (444/499)	NR_118335; <i>Klebsiella michiganensis</i> strain W14 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg1-6	<a href="#">LC594214</a>	99.6% (513/515)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg1-7	<a href="#">LC594215</a>	98.4% (507/515)	NR_114159; <i>Yokenella regensburgei</i> strain NBRC 102600 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg1-8	<a href="#">LC594216</a>	76.5% (382/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 1-1	<a href="#">LC594226</a>	55.2% (278/503)	Host 18S rRNA sequence
Nymph 1-2	<a href="#">LC594227</a>	55.2% (278/503)	Host 18S rRNA sequence
Nymph 1-3	<a href="#">LC594228</a>	99.6% (513/515)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 1-4	<a href="#">LC594229</a>	99.8% (514/515)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 1-5	<a href="#">LC594230</a>	76.1% (380/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 1-6	<a href="#">LC594231</a>	77.5% (384/495)	NR_117429; <i>Pseudonocardia alni</i> strain DSM 44104 (Actinobacteria) 16S ribosomal RNA, partial sequence
Nymph 1-7	<a href="#">LC594232</a>	76.5% (382/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 1-8	<a href="#">LC594233</a>	76.9% (384/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg2-1	<a href="#">LC594217</a>	79.6% (404/507)	NR_112030; <i>Stenotrophomonas maltophilia</i> strain ATCC 13637 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg2-2	<a href="#">LC594218</a>	74.3% (290/390)	NR_148840; <i>Taibaiella coffeisolii</i> strain TZCO2 (Bacteroidetes) 16S ribosomal RNA, partial sequence
Egg2-3	<a href="#">LC594219</a>	83.3% (424/509)	NR_112030; <i>Stenotrophomonas maltophilia</i> strain ATCC 13637 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg2-4	<a href="#">LC594220</a>	87.5% (448/512)	NR_102854; <i>Pseudomonas entomophila</i> L48 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg2-5	<a href="#">LC594221</a>	81.7% (417/510)	NR_148635; <i>Comamonas piscis</i> strain CN1 ( $\beta$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg2-6	<a href="#">LC594222</a>	81.4% (416/511)	NR_148635; <i>Comamonas piscis</i> strain CN1 ( $\beta$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg2-7	<a href="#">LC594223</a>	84.2% (428/508)	NR_041370; <i>Dyella ginsengisoli</i> strain Gsoil 3046 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg2-8	<a href="#">LC594224</a>	72.9% (369/506)	NR_113311; <i>Sphingobacterium pakistanense</i> strain NCCP-246 (Bacteroidetes) 16S ribosomal RNA, partial sequence
Nymph 2-1	<a href="#">LC594234</a>	99.6% (513/515)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 2-2	<a href="#">LC594235</a>	76.5% (382/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 2-3	<a href="#">LC594236</a>	76.3% (381/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 2-4	<a href="#">LC594237</a>	99.6% (513/515)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 ( $\gamma$ -Proteobacteria) 16S

			ribosomal RNA, partial sequence
Nymph 2-5	<a href="#">LC594238</a>	76.5% (382/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 2-6	<a href="#">LC594239</a>	99.8% (514/515)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 16S ribosomal RNA, partial sequence
Nymph 2-7	<a href="#">LC594240</a>	76.7% (383/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 2-8	<a href="#">LC594241</a>	76.5% (382/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
<b>CKSI20-15</b>			
Mother	<a href="#">LC594258</a>	100% (515/515)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg1-1	<a href="#">LC594242</a>	77.4% (391/505)	NR_044391; <i>Sphingobacterium siyangense</i> strain SY1 (Bacteroidetes) 16S ribosomal RNA, partial sequence
Egg1-2	<a href="#">LC594243</a>	73.5% (361/491)	NR_044391; <i>Sphingobacterium siyangense</i> strain SY1 (Bacteroidetes) 16S ribosomal RNA, partial sequence
Egg1-3	<a href="#">LC594244</a>	98.4% (506/514)	NR_116748; <i>Pantoea breneri</i> strain LMG 5343 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg1-4	<a href="#">LC594245</a>	97.6% (503/515)	NR_025331; <i>Buttiauxella izardii</i> strain S3/2-161 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg1-5	<a href="#">LC594246</a>	79.9% (403/504)	NR_024863; <i>Neorhizobium huautlense</i> strain SO2 ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg1-6	<a href="#">LC594247</a>	83.1% (425/511)	NR_029319; <i>Pseudomonas anguilliseptica</i> strain S 1 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg1-7	<a href="#">LC594248</a>	73.8% (359/486)	NR_108531; <i>Chryseobacterium tractae</i> strain 1084-08 (Bacteroidetes) 16S ribosomal RNA, partial sequence
Egg1-8	<a href="#">LC594249</a>	76.9% (384/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 1-1	<a href="#">LC594259</a>	76.7% (383/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 1-2	<a href="#">LC594260</a>	76.9% (384/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 1-3	<a href="#">LC594261</a>	76.8% (382/497)	NR_114151; <i>Ochrobactrum oryzae</i> strain NBRC 102588 ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 1-4	<a href="#">LC594262</a>	80.7% (411/509)	NR_029202; <i>Amaricoccus macauensis</i> strain Ben104 ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 1-5	<a href="#">LC594263</a>	76.9% (384/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 1-6	<a href="#">LC594264</a>	79.9% (403/504)	NR_117103; <i>Rhodococcus cerastii</i> strain C5 (Actinobacteria) 16S ribosomal RNA, partial sequence
Nymph 1-7	<a href="#">LC594265</a>	79.9% (402/503)	NR_117103; <i>Rhodococcus cerastii</i> strain C5 (Actinobacteria) 16S ribosomal RNA, partial sequence
Nymph 1-8	<a href="#">LC594266</a>	79.8% (405/507)	NR_108571; <i>Paracoccus caeni</i> strain MJ17 ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg2-1	<a href="#">LC594250</a>	76.9% (384/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg2-2	<a href="#">LC594251</a>	72.6% (367/505)	NR_113706; <i>Sphingobacterium multivorum</i> strain NBRC 14947 (Bacteroidetes) 16S ribosomal RNA, partial sequence
Egg2-3	<a href="#">LC594252</a>	76.9% (384/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg2-4	<a href="#">LC594253</a>	72.6% (367/505)	NR_044391; <i>Sphingobacterium siyangense</i> strain SY1 (Bacteroidetes) 16S ribosomal RNA, partial sequence
Egg2-5	<a href="#">LC594254</a>	82.3% (421/511)	NR_029319; <i>Pseudomonas anguilliseptica</i> strain S 1 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg2-6	<a href="#">LC594255</a>	90.6% (466/514)	NR_126317; <i>Cedecea lapagei</i> strain DSM 4587 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg2-7	<a href="#">LC594256</a>	99.4% (512/515)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg2-8	<a href="#">LC594257</a>	72.0% (356/494)	NR_044391; <i>Sphingobacterium siyangense</i> strain SY1 (Bacteroidetes) 16S ribosomal RNA, partial sequence
Nymph 2-1	<a href="#">LC594267</a>	99.6% (513/515)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 2-2	<a href="#">LC594268</a>	76.9% (384/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 2-3	<a href="#">LC594269</a>	99.8% (514/515)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence

Nymph 2-4	<a href="#">LC594270</a>	99.2% (511/515)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 2-5	<a href="#">LC594271</a>	99.4% (512/515)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 2-6	<a href="#">LC594272</a>	76.9% (384/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 2-7	<a href="#">LC594273</a>	98.6% (508/515)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 2-8	<a href="#">LC594274</a>	99.4% (512/515)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
<b>CKSI20-16</b>			
Mother	<a href="#">LC594291</a>	100% (515/515)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg1-1	<a href="#">LC594275</a>	76.7% (383/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg1-2	<a href="#">LC594276</a>	75.9% (383/504)	NR_125697; <i>Trichocoleus desertorum</i> strain ATA4-8-CV2 (Cyanobacteria) 16S ribosomal RNA, partial sequence
Egg1-3	<a href="#">LC594277</a>	76.4% (386/505)	NR_135210; <i>Methylobacterium indicum</i> strain SE2.11 ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg1-4	<a href="#">LC594278</a>	76.7% (383/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg1-5	<a href="#">LC594279</a>	79.1% (402/508)	NR_028944; <i>Microbacterium aerolatum</i> strain V-73 (Actinobacteria) 16S ribosomal RNA, partial sequence
Egg1-6	<a href="#">LC594280</a>	79.1% (398/503)	NR_028944; <i>Microbacterium aerolatum</i> strain V-73 (Actinobacteria) 16S ribosomal RNA, partial sequence
Egg1-7	<a href="#">LC594281</a>	78.5% (395/503)	NR_135210; <i>Methylobacterium indicum</i> strain SE2.11 ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg1-8	<a href="#">LC594282</a>	84.0% (431/513)	NR_148578; <i>Pantoea beijingensis</i> strain JZB2120001 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 1-1	<a href="#">LC594292</a>	73.6% (372/505)	NR_169321; <i>Pedobacter indicus</i> strain SM1810 (Bacteroidetes) 16S ribosomal RNA, partial sequence
Nymph 1-2	<a href="#">LC594293</a>	99.8% (514/515)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 1-3	<a href="#">LC594294</a>	99.8% (514/515)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 1-4	<a href="#">LC594295</a>	76.5% (382/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 1-5	<a href="#">LC594296</a>	99.4% (512/515)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 1-6	<a href="#">LC594297</a>	88.9% (444/499)	NR_116752; <i>Pantoea septica</i> strain LMG 5345 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 1-7	<a href="#">LC594298</a>	76.7% (383/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 1-8	<a href="#">LC594299</a>	71.5% (352/492)	NR_042540; <i>Flavobacterium ceti</i> strain 454-2 (Bacteroidetes) 16S ribosomal RNA, partial sequence
Egg2-1	<a href="#">LC594283</a>	76.7% (383/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg2-2	<a href="#">LC594284</a>	76.7% (383/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg2-3	<a href="#">LC594285</a>	99.8% (514/515)	NR_114154; <i>Leclercia adecarboxylata</i> strain NBRC 102595 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg2-4	<a href="#">LC594286</a>	99.6% (513/515)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg2-5	<a href="#">LC594287</a>	99.6% (513/515)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg2-6	<a href="#">LC594288</a>	76.5% (382/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg2-7	<a href="#">LC594289</a>	93.2% (480/515)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg2-8	<a href="#">LC594290</a>	99.8% (514/515)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 2-1	<a href="#">LC594300</a>	76.7% (383/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 2-2	<a href="#">LC594301</a>	94.6% (475/502)	NR_041797; <i>Alkalimonas amylolytica</i> strain N10 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 2-3	<a href="#">LC594302</a>	76.7% (383/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S

			ribosomal RNA, partial sequence
Nymph 2-4	<a href="#">LC594303</a>	99.6% (513/515)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 2-5	<a href="#">LC594304</a>	76.7% (383/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 2-6	<a href="#">LC594305</a>	76.7% (383/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 2-7	<a href="#">LC594306</a>	55.2% (278/503)	Host 18S rRNA sequence
Nymph 2-8	<a href="#">LC594307</a>	99.6% (513/515)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
<b>CKSI20-17</b>			
Mother	<a href="#">LC594324</a>	100% (515/515)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg1-1	<a href="#">LC594308</a>	75.9% (383/504)	NR_125697; <i>Trichocoleus desertorum</i> strain ATA4-8-CV2 (Cyanobacteria) 16S ribosomal RNA, partial sequence
Egg1-2	<a href="#">LC594309</a>	76.2% (385/505)	NR_125697; <i>Trichocoleus desertorum</i> strain ATA4-8-CV2 (Cyanobacteria) 16S ribosomal RNA, partial sequence
Egg1-3	<a href="#">LC594310</a>	75.9% (383/504)	NR_125697; <i>Trichocoleus desertorum</i> strain ATA4-8-CV2 (Cyanobacteria) 16S ribosomal RNA, partial sequence
Egg1-4	<a href="#">LC594311</a>	75.5% (381/504)	NR_125697; <i>Trichocoleus desertorum</i> strain ATA4-8-CV2 (Cyanobacteria) 16S ribosomal RNA, partial sequence
Egg1-5	<a href="#">LC594312</a>	73.9% (367/496)	NR_117881; <i>Loriellopsis cavernicola</i> strain LF-B5 (Cyanobacteria) 16S ribosomal RNA, partial sequence
Egg1-6	<a href="#">LC594313</a>	75.9% (383/504)	NR_125697; <i>Trichocoleus desertorum</i> strain ATA4-8-CV2 (Cyanobacteria) 16S ribosomal RNA, partial sequence
Egg1-7	<a href="#">LC594314</a>	75.9% (383/504)	NR_125697; <i>Trichocoleus desertorum</i> strain ATA4-8-CV2 (Cyanobacteria) 16S ribosomal RNA, partial sequence
Egg1-8	<a href="#">LC594315</a>	75.9% (383/504)	NR_125697; <i>Trichocoleus desertorum</i> strain ATA4-8-CV2 (Cyanobacteria) 16S ribosomal RNA, partial sequence
Nymph 1-1	<a href="#">LC594325</a>	73.7% (376/510)	NR_040847; <i>Cutibacterium acnes</i> strain ATCC 6919 (Actinobacteria) 16S ribosomal RNA, partial sequence
Nymph 1-2	<a href="#">LC594326</a>	86.4% (442/511)	NR_117677; <i>Acinetobacter baumannii</i> strain DSM 30007 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 1-3	<a href="#">LC594327</a>	76.9% (384/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 1-4	<a href="#">LC594328</a>	76.9% (384/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 1-5	<a href="#">LC594329</a>	55.4% (279/503)	Host 18S rRNA sequence
Nymph 1-6	<a href="#">LC594330</a>	76.9% (384/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 1-7	<a href="#">LC594331</a>	82.2% (418/508)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 1-8	<a href="#">LC594332</a>	76.5% (382/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg2-1	<a href="#">LC594316</a>	76.5% (382/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg2-2	<a href="#">LC594317</a>	76.7% (383/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg2-3	<a href="#">LC594318</a>	77.3% (386/499)	NR_115996; <i>Rhizobium soli</i> DS-42 ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg2-4	<a href="#">LC594319</a>	76.9% (384/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg2-5	<a href="#">LC594320</a>	76.7% (383/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg2-6	<a href="#">LC594321</a>	79.7% (398/499)	NR_026519; <i>Agrobacterium larrymoorei</i> strain AF3.10 ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg2-7	<a href="#">LC594322</a>	76.9% (384/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg2-8	<a href="#">LC594323</a>	78.5% (392/499)	NR_113713; <i>Neorhizobium galegae</i> strain NBRC 14965 ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 2-1	<a href="#">LC594333</a>	77.1% (385/499)	NR_115996; <i>Rhizobium soli</i> DS-42 ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 2-2	<a href="#">LC594334</a>	86.8% (444/511)	NR_152004; <i>Acinetobacter lactucae</i> strain NRRL B-41902 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 2-3	<a href="#">LC594335</a>	77.1% (385/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S

			ribosomal RNA, partial sequence
Nymph 2-4	<a href="#">LC594336</a>	85.9% (439/511)	NR_044454; <i>Acinetobacter soli</i> strain B1 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 2-5	<a href="#">LC594337</a>	76.7% (383/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 2-6	<a href="#">LC594338</a>	100% (515/515)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 2-7	<a href="#">LC594339</a>	86.6% (443/511)	NR_152004; <i>Acinetobacter lactucaae</i> strain NRRL B-41902 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 2-8	<a href="#">LC594340</a>	86.8% (444/511)	NR_152004; <i>Acinetobacter lactucaae</i> strain NRRL B-41902 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
<b>CKSI20-18</b>			
Mother	<a href="#">LC594357</a>	100% (515/515)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg1-1	<a href="#">LC594341</a>	75.6% (380/502)	NR_125697; <i>Trichocoleus desertorum</i> (Cyanobacteria) strain ATA4-8-CV2 16S ribosomal RNA, partial sequence
Egg1-2	<a href="#">LC594342</a>	76.7% (383/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg1-3	<a href="#">LC594343</a>	67.7% (334/493)	NR_109614; <i>Caldicoprobacter guelmensis</i> strain D2C22 (Firmicutes) 16S ribosomal RNA, partial sequence
Egg1-4	<a href="#">LC594344</a>	76.7% (383/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg1-5	<a href="#">LC594345</a>	55.0% (277/503)	Host 18S rRNA sequence
Egg1-6	<a href="#">LC594346</a>	76.7% (383/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg1-7	<a href="#">LC594347</a>	100% (515/515)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg1-8	<a href="#">LC594348</a>	100% (515/515)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph1-1	<a href="#">LC594358</a>	77.8% (390/501)	NR_113149; <i>Brevifollis gellamyliticus</i> strain DC2c-G4 (Verrucomicrobia) 16S ribosomal RNA, partial sequence
Nymph1-2	<a href="#">LC594359</a>	100% (515/515)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph1-3	<a href="#">LC594360</a>	76.9% (384/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph1-4	<a href="#">LC594361</a>	98.6% (508/515)	NR_041697; <i>Citrobacter gillenii</i> strain CDC 4693-86 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph1-5	<a href="#">LC594362</a>	76.9% (384/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph1-6	<a href="#">LC594363</a>	97.6% (501/513)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph1-7	<a href="#">LC594364</a>	76.7% (383/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph1-8	<a href="#">LC594365</a>	99.6% (513/515)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg2-1	<a href="#">LC594349</a>	78.6% (398/506)	NR_026519; <i>Agrobacterium larrymoorei</i> strain AF3.10 ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg2-2	<a href="#">LC594350</a>	76.9% (384/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg2-3	<a href="#">LC594351</a>	79.0% (280/354)	NR_044762; <i>Anaplasma phagocytophilum</i> strain Webster ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg2-4	<a href="#">LC594352</a>	94.8% (480/506)	NR_118335; <i>Klebsiella michiganensis</i> strain W14 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg2-5	<a href="#">LC594353</a>	76.9% (384/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg2-6	<a href="#">LC594354</a>	94.5% (484/512)	NR_118335; <i>Klebsiella michiganensis</i> strain W14 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg2-7	<a href="#">LC594355</a>	76.7% (383/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Egg2-8	<a href="#">LC594356</a>	76.9% (384/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 2-1	<a href="#">LC594366</a>	77.3% (393/508)	NR_134768; <i>Microbacterium panaciterrae</i> strain DCY56 (Actinobacteria) 16S ribosomal RNA, partial sequence
Nymph 2-2	<a href="#">LC594367</a>	99.8% (514/515)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence

Nymph 2-3	<a href="#">LC594368</a>	99.8% (514/515)	NR_118120; <i>Pantoea rodasii</i> strain LMG 26273 ( $\gamma$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 2-4	<a href="#">LC594369</a>	83.4% (424/508)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 2-5	<a href="#">LC594370</a>	76.9% (384/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 2-6	<a href="#">LC594371</a>	80.1% (403/503)	NR_117103; <i>Rhodococcus cerastii</i> strain C5 (Actinobacteria) 16S ribosomal RNA, partial sequence
Nymph 2-7	<a href="#">LC594372</a>	76.9% (384/499)	NR_044747; <i>Ehrlichia ewingii</i> strain Stillwater ( $\alpha$ -Proteobacteria) 16S ribosomal RNA, partial sequence
Nymph 2-8	<a href="#">LC594373</a>	72.2% (365/505)	NR_041407; <i>Sphingobacterium daejeonense</i> strain TR6-04 (Bacteroidetes) 16S ribosomal RNA, partial sequence

<sup>a</sup>Each field-collected mother was individually reared, and first-laid eggs and second-laid eggs were harvested. Two eggs from the first clutch were defined as “Egg1”, and subjected to DNA extraction, PCR and cloning of bacterial 16S rRNA gene. For each egg sample, up to eight 16S rRNA gene clones were picked and sequenced, which were designated as “Egg1-1”–“Egg1-8”. The remaining eggs were maintained, and a newborn nymph was picked as “Nymph1”, and bacterial 16S rRNA clones “Nymph1-1”–“Nymph1-8” were sequenced in the same way. Similarly, two eggs and a nymph from the second clutch were defined as “Egg2” and “Nymph2”, and 16S rRNA gene clones “Egg2-1”–“Egg2-8” and “Nymph2-1”–“Nymph2-8” were determined.

<sup>b</sup>Percentage in terms of (number of matched nucleotide sites/number of aligned nucleotide sites), where gap-containing sites were omitted.

<sup>c</sup>Among the BLAST top hit entries, a representative one with species identification is shown with sequence accession number and biological description.