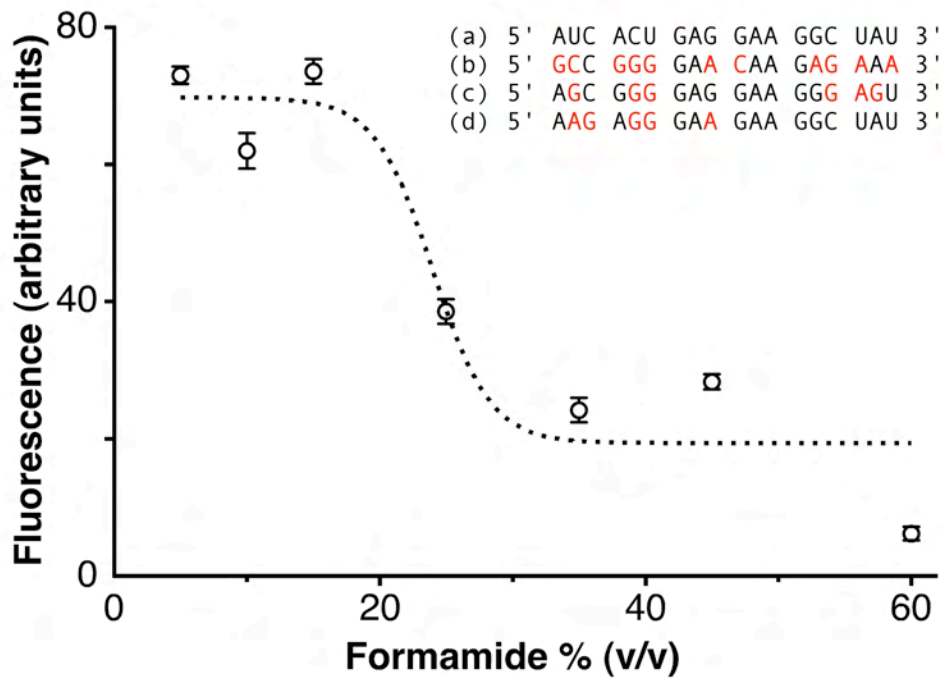


**Supplemental Table S1** Phylogetic identity of different 16S rRNA gene sequence types present among 32 analyzed clones originating from a *Xenoturbella bocki* whole body clone library generated with general bacterial PCR primers.

Clone <sup>a</sup>	Closest relative <sup>b</sup>	Taxonomic affiliation	pairwise identity <sup>b</sup>
Xbod3b (16/32)	Zebrafish digestive tract clone aab54f12 (DQ814869)	<i>Alphaproteobacteria</i> <i>Rhizobiales</i>	99%
Xbod4 (1/32)	South China Sea sponge-associated clone B27 (FJ999599)	<i>Betaproteobacteria</i> <i>Burkholderiales</i>	99%
Xbod8 (2/32)	Drinking water treatment plant clone MF117 (FJ572671)	<i>Betaproteobacteria</i> <i>Burkholderiales</i>	98%
Xbod14 (1/32)	Pepper plant isolate <i>Achromobacter</i> sp. BPZ11 (GQ853553)	<i>Betaproteobacteria</i> <i>Burkholderiales</i>	99%
Xbod17 (7/32)	Drinking water distribution system simulator clone DSSD11 (AY328710)	<i>Alphaproteobacteria</i> <i>Rhodospirillales</i>	93%
Xbod23 (5/32)	Mono Lake isolate <i>Halomonas</i> sp. ML-028 (AF139994)	<i>Gammaproteobacteria</i> <i>Oceanospirillales</i>	99%

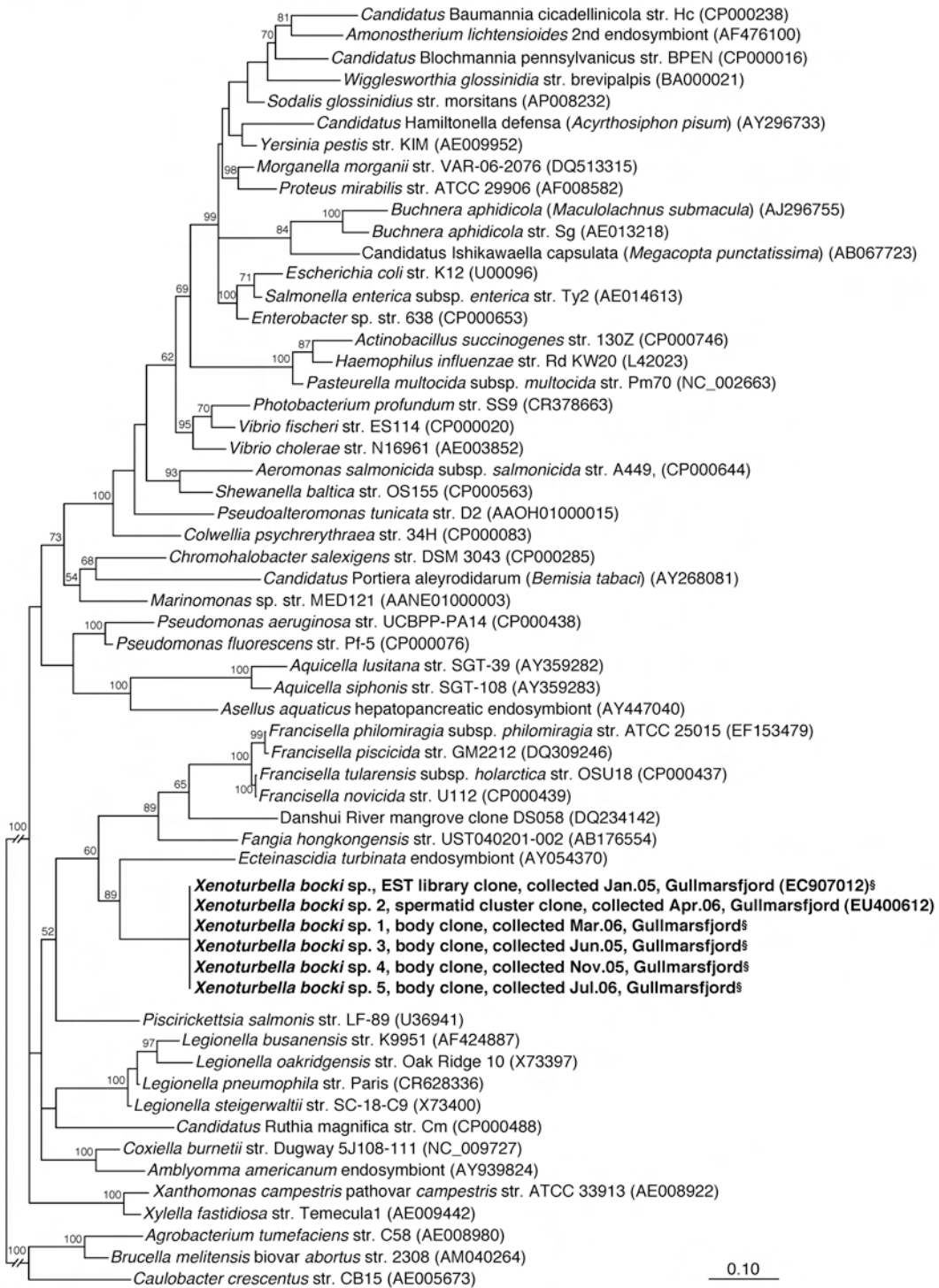
<sup>a</sup> Numbers in parentheses indicate the relative abundance of the respective clones.

<sup>b</sup> As determined by comparison against the NCBI (<http://www.ncbi.nlm.nih.gov>) nr nucleotide sequence database using BLAST.

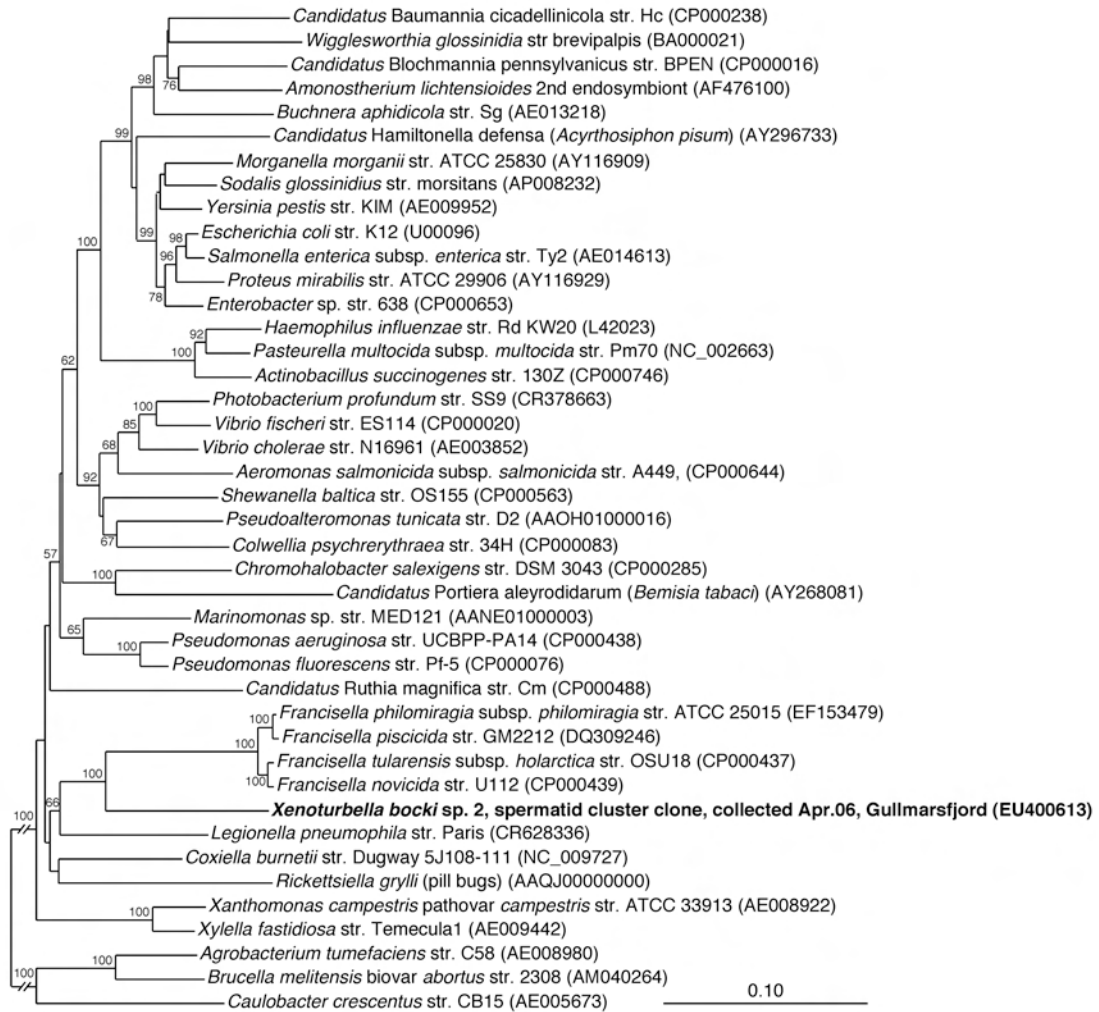


**Supplemental Figure S1** Dissociation curve for probe Xenogam441 determined with transformed *E. coli* JM109(DE3) cells expressing the 16S rRNA gene of the *X. bockii* gammaproteobacterial endosymbiont. The dotted line represents a sigmoidal best fit. Error bars indicate standard errors,  $n = 3$  random microscopic fields of view (630x) images collectively containing at least 200 hybridized cells. The insert shows an alignment of the 16S rRNA probe target region in (a) the *X. bockii* gammaproteobacterial endosymbiont, (b) the *X. bockii* chlamydial endosymbiont, (c) untransformed *E. coli* JM109(DE3) [AB305017] and (d) *Desulfovibrio* strain I8 [FJ655907]; no positive hybridizations were recorded at any formamide concentration tested for the two latter strains. Mismatches against the probe are marked in red.

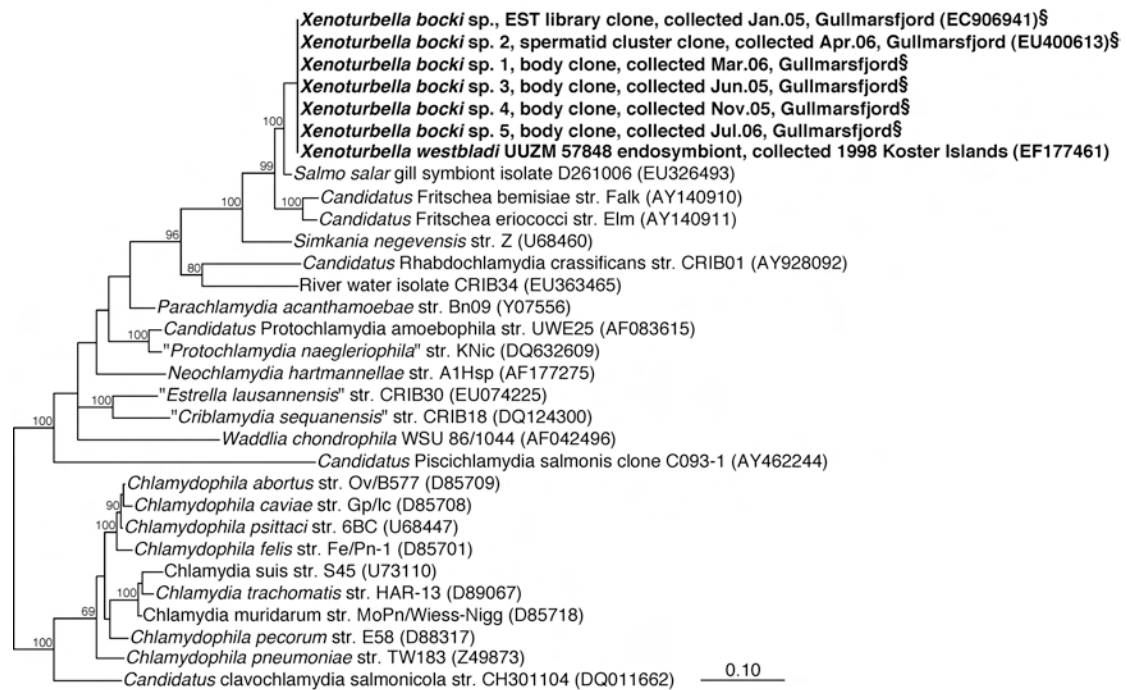
(A) 16S rRNA



(B) 23S rRNA



(C) 16S rRNA



**Supplemental Figure S2** Phylogeny of the *Xenoturbella* endosymbionts (bold) as inferred by Bayesian analysis. (A, B) Position of the gammaproteobacterial endosymbiont among members of the class *Gammaproteobacteria* based on 16S rRNA (A) and 23S rRNA (B) gene sequences; the trees were rooted arbitrarily by three alphaproteobacterial taxa. (C) 16S rRNA gene sequence-based position of the chlamydial endosymbiont among members of the class *Chlamydia*. Bars, 10% estimated sequence divergence. Numbers indicate neighbour-joining-based bootstrap percentage values. §Short sequence added to the tree by the parsimony method.