Figure S2. Targeted PCR assays on termite and roach gut DNA using Cys clade specific *fdhF* primers (Cys499F1b, 1045R), which yield a ca. 600 bp product (ladder left lane: NEB 2-log). Templates are: ZAS-2, *T. primitia* str. ZAS-2 genomic DNA; Zn, *Z. nevadensis*; Rh, *R. hesperus*; Im, *I. minor*; Cp, *C. punctulatus*; JT1, *R. tibialis*; cs9, *Coptotermes* sp. Cost009; cs3, *Nasutitermes* sp. Cost003; cs4, *Rhynchotermes* sp. Cost004; cs6, *Microcerotermes* sp. Cost006; cs7, *Nasutitermes corniger* Cost007; cs8, *Microcerotermes* sp. Cost008; cs10, *Amitermes* sp. Cost010; JT2, *Amitermes* sp. JT2; JT5, *Gnathamitermes* sp. JT5. Numbers in ZAS-2 genomic lanes refer to the number of genome copies per reaction. Copy numbers (10^6 copies/gut) in the lower termite *Z. nevadensis* were estimated from band strength in dilution-to-extinction PCR of *T. primitia* ZAS-2 DNA (assuming a yield of 1 μg total DNA/gut typically observed in QIAGEN DNA extractions, 10% derived from prokaryotes, and 10^4 copies/ng gut DNA in *Z. nevadensis*). As correct sized Cys bands were not present in higher termites, the detection limit (100 copies/ng gut DNA) was used to estimate a maximum abundance of 10^3 copies/gut for lower termite Cys clade FDH genes in higher termites (assuming a yield of 0.25 μg total DNA/gut, 100% derived from prokaryotes).