

**Comparative Transcriptomics of Fat Bodies Between Symbiotic and Quasi-Aposymbiotic Adult Females of *Blattella germanica* with Emphasis on the Metabolic Integration with its Endosymbiont *Blattabacterium* and Its Immune System**

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**Table S2.** Endosymbiont load of pooled quasi-aposymbiont and control fat bodies determined by qPCR. *Blattabacterium* load was quantified by the copy number of gene *ureC* (only present in *Blattabacterium*) per ng of fat body DNA of the three fat bodies pooled in each sample. Abbreviation: q-Apo (quasi-aposymbiont).

Pooled Sample	Number of Copies of Gene <i>ureC</i> /ng of Fat Body DNA
q-Apo (pool 1)	5.73
	48.53
	13.33
q-Apo (pool 2)	4.43
	Below the limit of detection
	Below the limit of detection
q-Apo (pool 3)	Below the limit of detection
	Below the limit of detection
	Below the limit of detection
q-Apo (pool 4)	Below the limit of detection
	Below the limit of detection
	Below the limit of detection
Control (pool 1)	$1.03 \times 10^5$
	$1.37 \times 10^5$
	$1.07 \times 10^5$
Control (pool 2)	$1.63 \times 10^5$
	$1.28 \times 10^5$
	$1.21 \times 10^5$
Control (pool 3)	$1.21 \times 10^5$
	$2.20 \times 10^5$
	$2.58 \times 10^5$
Control (pool 4)	$2.24 \times 10^5$
	$1.15 \times 10^5$
	$1.09 \times 10^5$