Supplementary figures for: "Candidate genes involved in cuticular hydrocarbon differentiation between cryptic, parabiotic ant species"

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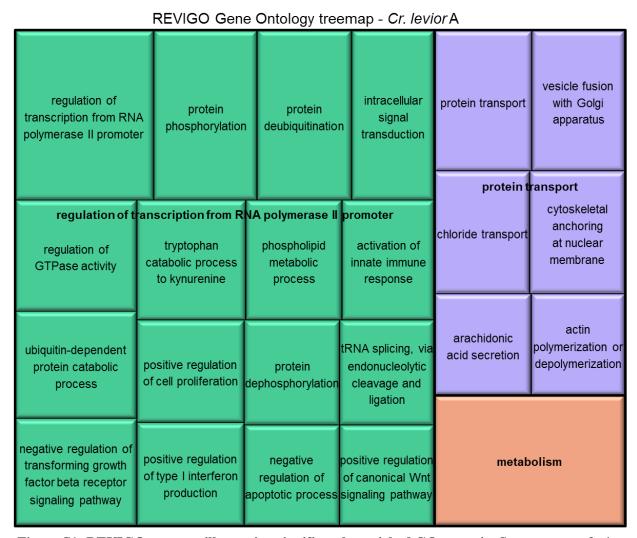


Figure S1: REVIGO treemap illustrating significantly enriched GO terms in *Crematogaster levior* **A.** Significantly enriched GO terms (Fisher-test: p < 0.05) of genes upregulated in *Cr. levior* A compared to B. Relative square sizes are scaled to match the degree of overexpression (Supek *et al.* 2011).

REVIGO Gene Ontology treemap - Cr. levior B proline ubiquitin-dependent catabolic protein deubiquitination protein catabolic metabolism process to oxidation-reduction process glutamate process DNA integration protein maturation ubiquinone peptidoglycan cellular response to biosynthetic by iron-sulfur catabolic process amino acid stimulus process cluster transfer cellular response to amino acid stimulus **DNA** integration innate immune response reciprocal meiotic microtubule-based protein recombination process glycosylation carbohydrate metabolism carbohydrate Golgi organization metabolic process protein ER to Golgi import into regulation of protein Golgi organization vesicle-mediated peroxisome superoxide metabolism endocytosis transport transport matrix, superoxide docking metabolic process

Figure S2: REVIGO treemap illustrating significantly enriched GO terms in *Crematogaster levior* **B.** Significantly enriched GO terms (Fisher-test: p < 0.05) of genes upregulated in *Cr. levior* B compared to A. Relative square sizes are scaled to match the degree of overexpression (Supek *et al.* 2011).

REVIGO Gene Ontology treemap - Ca. femoratus PAT protein glycosylation lipid metabolic process proteolysis lipid metabolism self proteolysis CTP biosynthetic process tetrahydrofolate biosynthetic process self proteolysis peptidyl-diphthamide biosynthetic process from peptidyl-histidine regulation of small GTPase mediated signal transduction actin filament organization regulation of small GTPase interstrand cross-link repair mediated signal transduction

Figure S3: REVIGO treemap illustrating significantly enriched GO terms in *Camponotus* femoratus PAT. Significantly enriched GO terms (Fisher-test: p < 0.05) of genes upregulated in *Ca. femoratus* PAT compared to PS. Relative square sizes are scaled to match the degree of overexpression (Supek et al. 2011).

REVIGO Gene Ontology treemap - Ca. femoratus PS regulation of small GTPase mediated signal transduction sodium ion transport oxidation-reduction process acetylcholine catabolism in synaptic cleft sphingomyelin catabolic process S-adenosylmethionine biosynthesis acetylcholine catabolic process in synaptic cleft nucleotide catabolic process protein phosphorylation peptidyl-diphthamide cell-matrix adhesion protein phosphorylation biosynthetic process phosphorylation from peptidyl-histidine

Figure S4: REVIGO treemap illustrating significantly enriched GO terms in *Camponotus* femoratus PS. Significantly enriched GO terms (Fisher-test: p < 0.05) of genes upregulated in *Ca. femoratus* PS compared to PAT. Relative square sizes are scaled to match the degree of overexpression (Supek et al. 2011).