

Figure S2. A neighbour-joining (NJ) rooted tree of annotated OBPs for *R. ferrugineus* (Rfer), *Bombyx mori* (Bmori), *Anomala osakana* (Aosa), *A. octiescosrara* (Aoct), *A. cuprea* (Acup), *P. japonica* (Pjap), *Drosophila* and *Tribolium castaneum* (Tcas) OBPs. The tree was constructed by the neighbour-joining method using MEGA6 [statistical method: NJ; phylogeny test: bootstrap method; model: JTT model and gaps/missing data treatment: pairwise deletion] and generated with a bootstrap procedure using 1000 replications. The branches are coloured, and bootstrap values above 50% are indicated. *Bombyx mori* OBPs (Gong et al. 2009) were used as a reference to classify *R. ferrugineus* OBPs. Different colour codes indicate OBP subfamilies. Red: Minus-C, green: CRLBP, black: ABPI, pink: Plus-C, magenta: PBP/GOBP and blue: ABPII. The *RferOBP1768* and *RferOBP23* clades are highlighted in yellow and green, respectively. Sequence logos of the aligned *R. ferrugineus* *RferOBP1768* and *RferOBP23* orthologues are given in Figure S3. The protein sequences were aligned using MUSCLE. The branch containing *Drosophila* OBP LUSH (PDB: 2GTE) was used as an outgroup to root the tree. Phylogenetic tree was visualized with the software FigTree (<http://tree.bio.ed.ac.uk/software/figtree/>). Scale: 0.4 amino acid substitutions per site.

