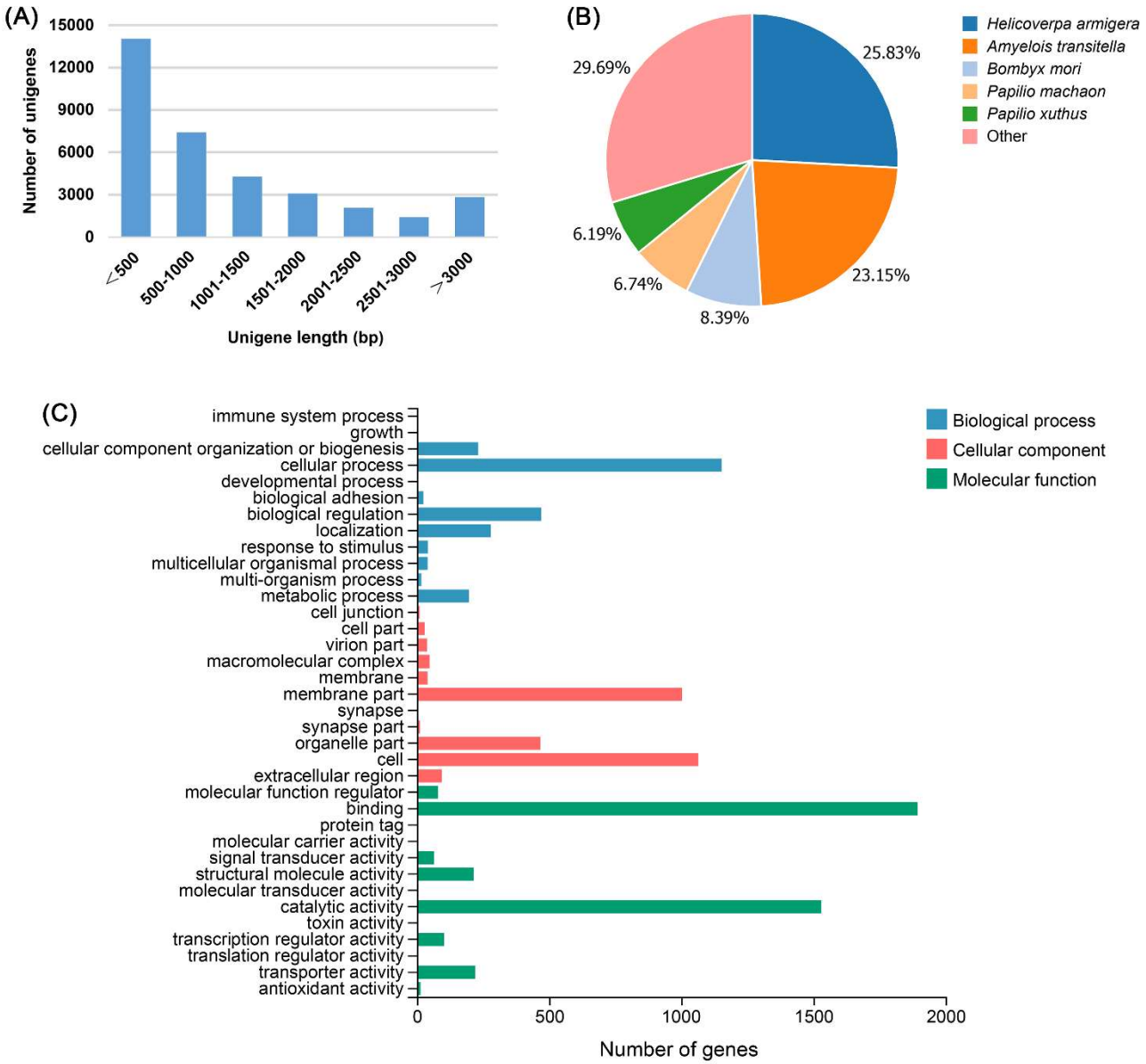


Figure S1. Summary of the *Ostrinia furnacalis* unigene assembly. (A) Unigene size distribution. All of the unigene sizes were calculated. (B) Species distribution of the unigenes based on BLASTX results. (C) GO classification of the unigenes.

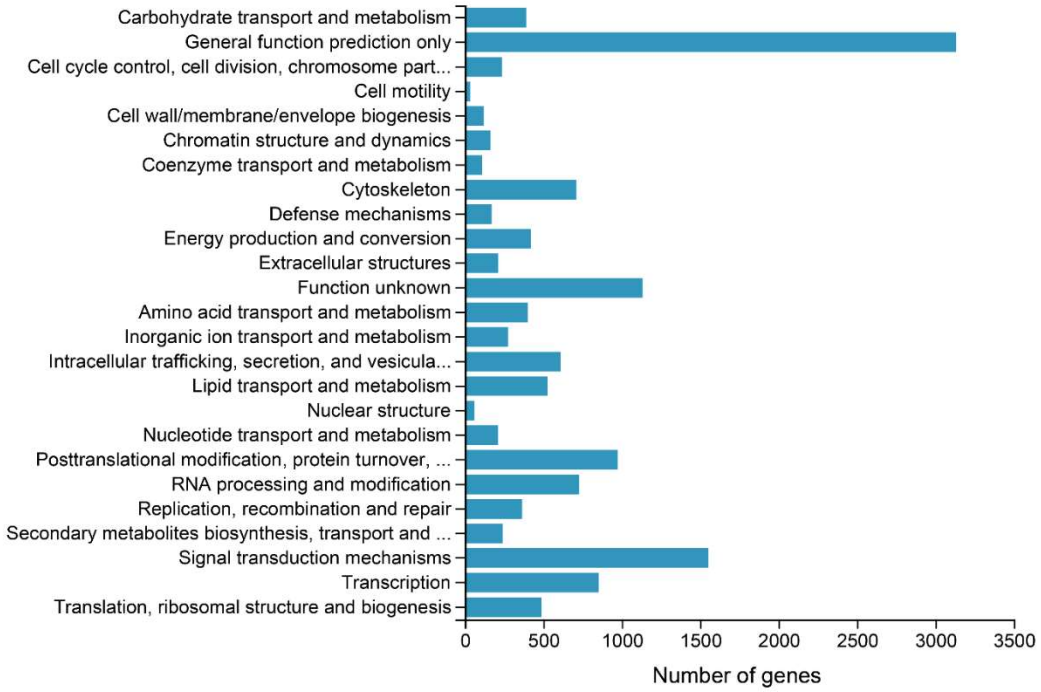


Figure S2. KOG classification of the *O. furnacalis* unigenes.

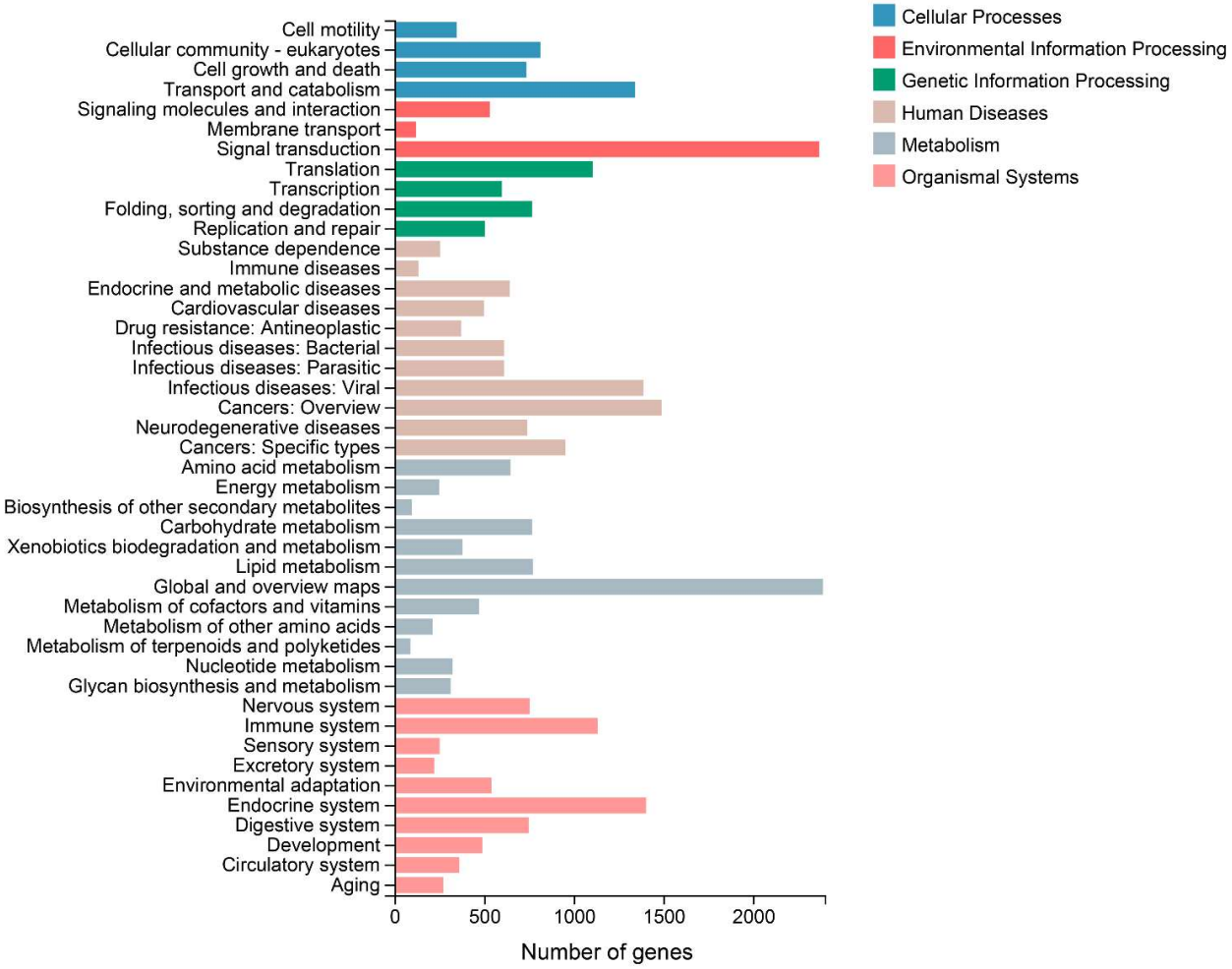
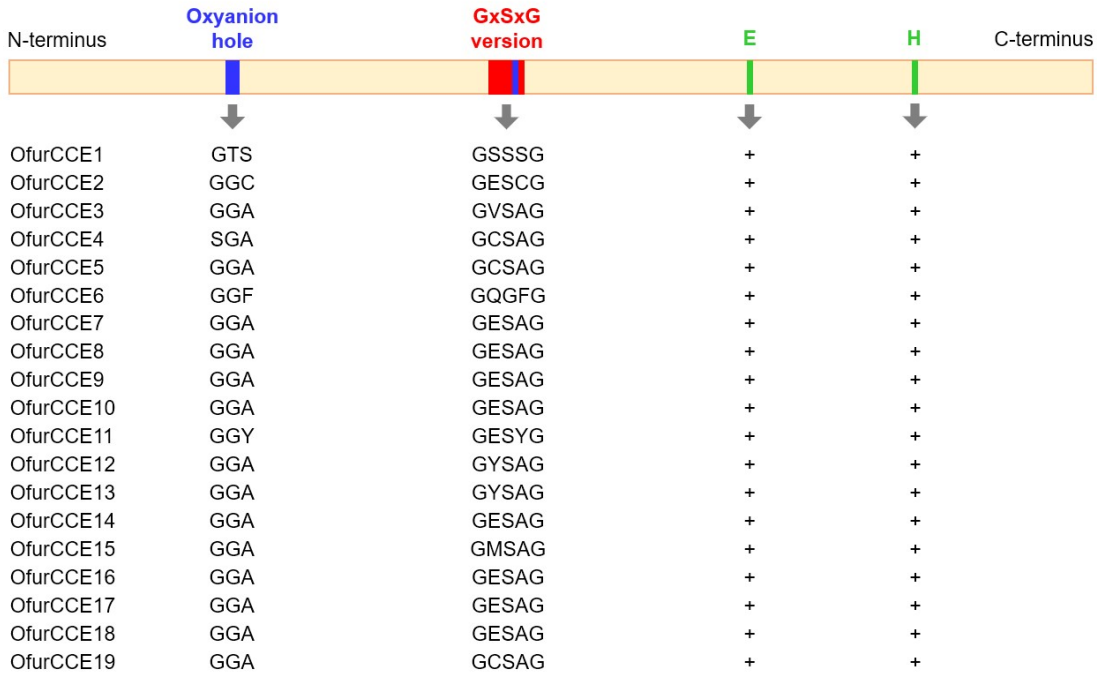


Figure S3. KEGG classification of the *O. furnacalis* unigenes.



OfurCCE1	GTS	GSSSG	+	+
OfurCCE2	GGC	GESCG	+	+
OfurCCE3	GGA	GVSAG	+	+
OfurCCE4	SGA	GCSAG	+	+
OfurCCE5	GGA	GCSAG	+	+
OfurCCE6	GGF	GQGFG	+	+
OfurCCE7	GGA	GESAG	+	+
OfurCCE8	GGA	GESAG	+	+
OfurCCE9	GGA	GESAG	+	+
OfurCCE10	GGA	GESAG	+	+
OfurCCE11	GGY	GESYG	+	+
OfurCCE12	GGA	GYSAG	+	+
OfurCCE13	GGA	GYSAG	+	+
OfurCCE14	GGA	GESAG	+	+
OfurCCE15	GGA	GMSAG	+	+
OfurCCE16	GGA	GESAG	+	+
OfurCCE17	GGA	GESAG	+	+
OfurCCE18	GGA	GESAG	+	+
OfurCCE19	GGA	GCSAG	+	+

Figure S4. Catalytic motifs of the *O. furnacalis* CCEs.

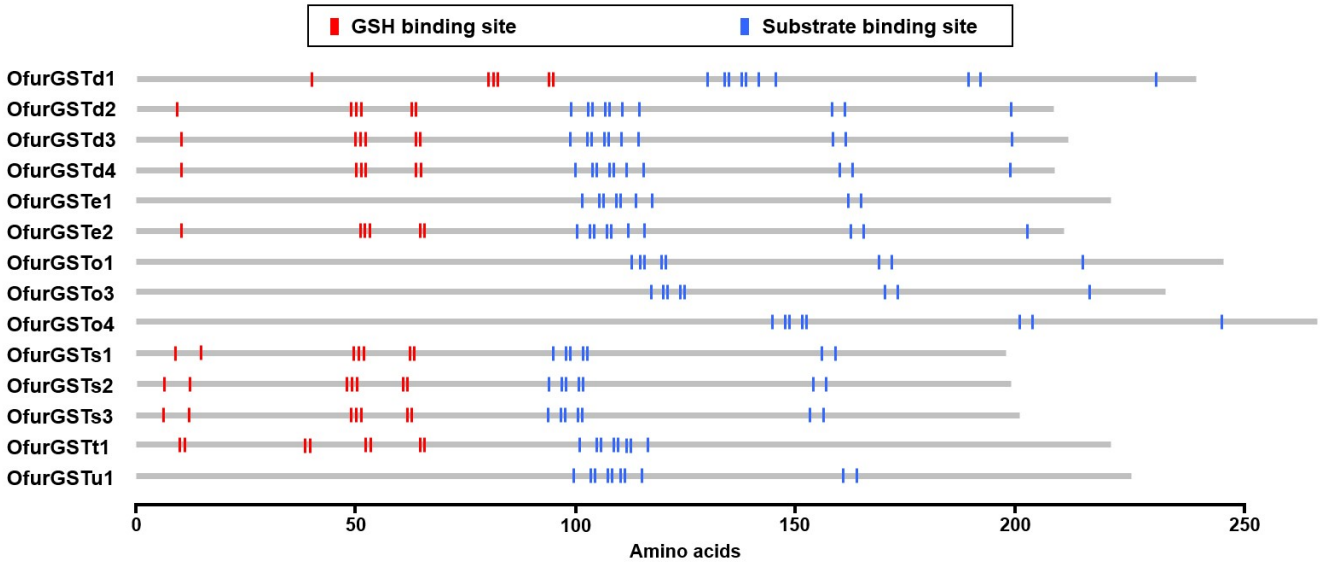


Figure S5. Predicted glutathione binding sites (G-sites) and substrate binding sites (H-sites) of the *O. furnacalis* GSTs. OfurGSTe3, OfurGSTo2 and OfurGSTz1 are not shown in this figure since no G-sites and H-sites are predicted in these proteins.

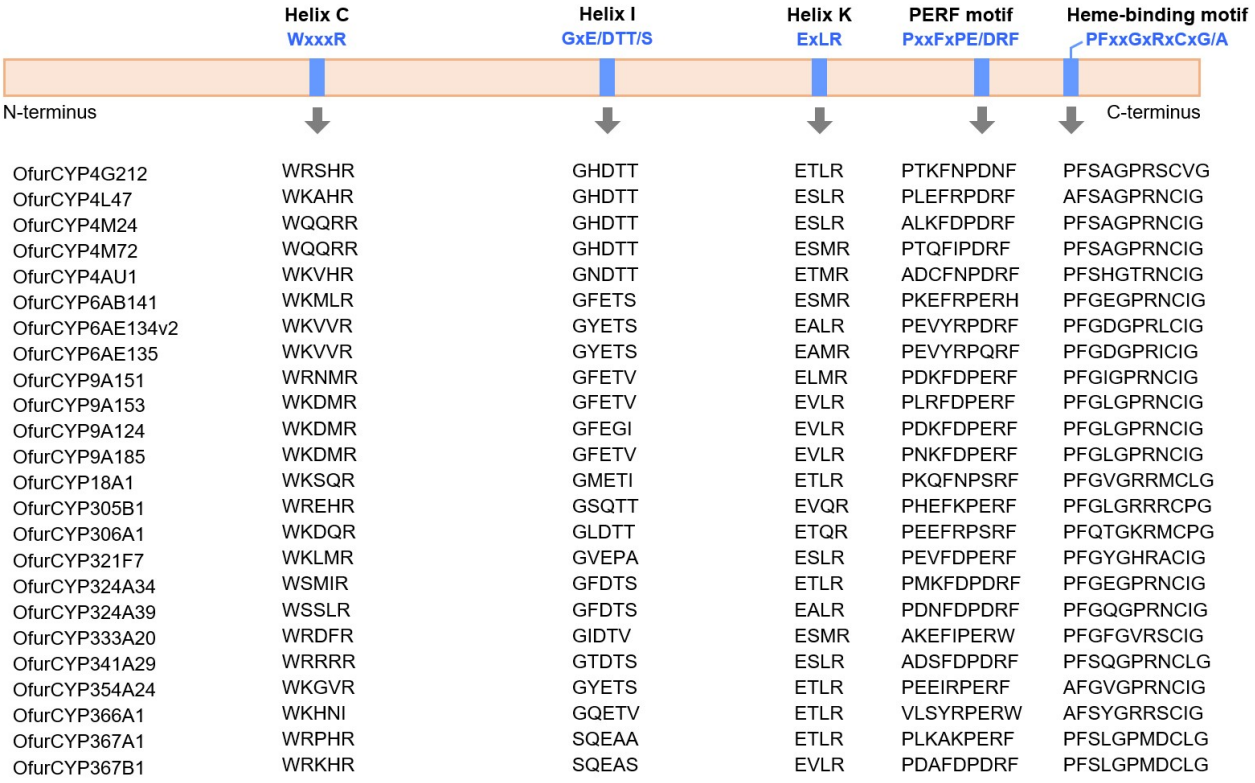


Figure S6. Functional domains of the *O. furnacalis* CYPs.

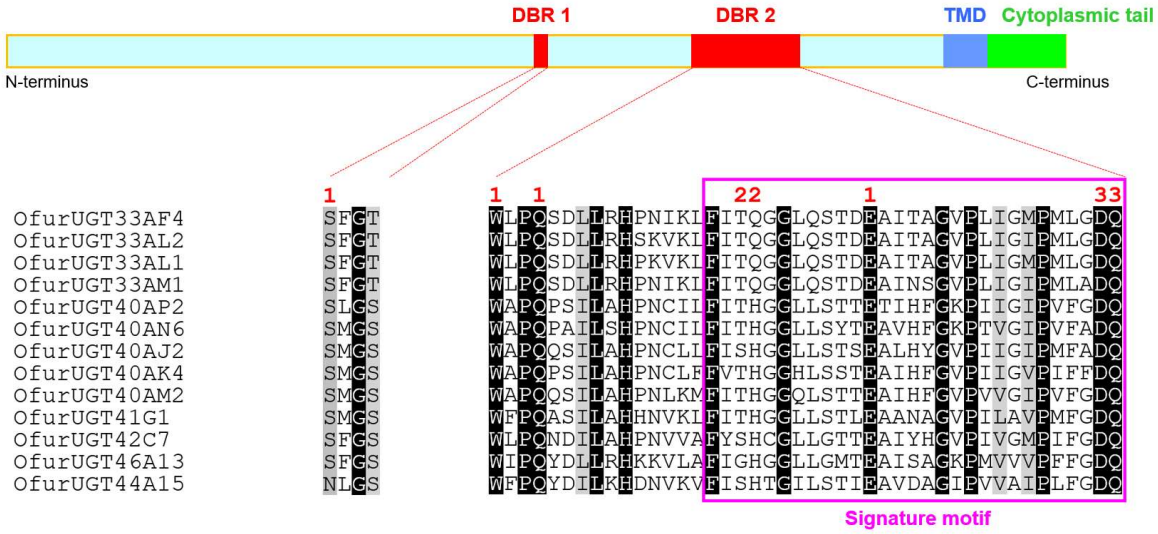


Figure S7. Alignment of the functional domains of *O. furnacalis* UGTs. Upper panel: schematic drawing of *O. furnacalis* UGTs. Two sugar donor-binding regions (DBR1 and DBR2), transmembrane domain (TMD) and cytoplasmic tail are shown. Lower panel: alignment of the DBR1 and DBR2 regions. Key amino acid residues interacting with the sugar donor are numbered 1, 2 and 3 in red (1, nucleotide interacting residues; 2, phosphate interacting residues; 3, glucoside interacting residues).