

Figure S1. Principal Component Analysis of full dataset (48 samples): Munich, Germany (M9 and M12; purple), Nicosia, Cyprus (C2; teal), Kuala Lumpur, Malaysia (KL; green) and Siavonga, Zambia (ZI; orange). Filled (closed) symbols represent stress samples and empty (open) symbols represent control samples. The sample indicated by the dashed outline was identified as outlier and removed from subsequent analyses.

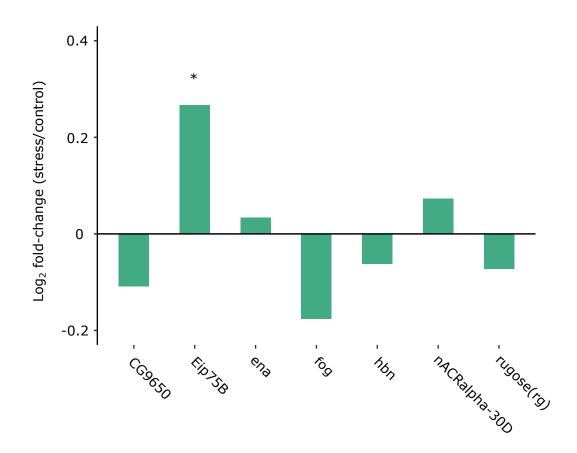


Figure S2. MSB-induced Log_2 fold-change (stress/control) of candidate oxidative stress-susceptible genes identified in a genome-wide association (GWA) study by Weber et al. (2012). Asterisk indicates the adjusted *P*-value from a Wald test as applied in DESeq2: *P < 0.05.

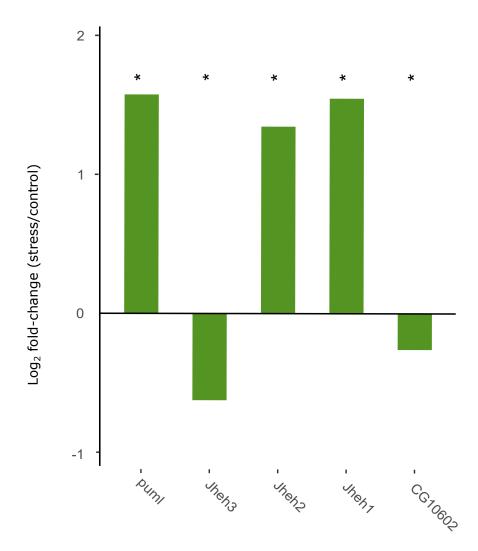


Figure S3. MSB-induced Log_2 fold-change (stress/control) of candidates in the epoxide hydrolase gene family. Asterisk indicates the adjusted *P*-value from a Wald test as applied in DESeq2: *P < 0.05.

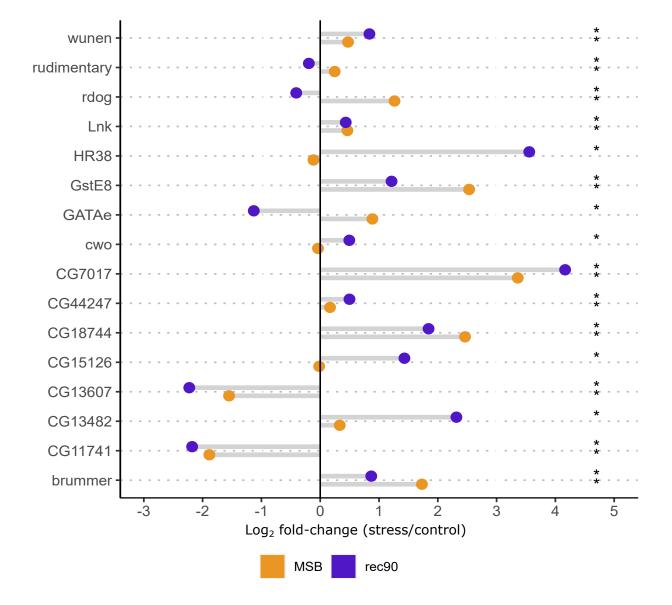


Figure S4. Comparisons of \log_2 fold-change (stress/control) in MSB oxidative stress (orange) and cold shock (von Heckel et al. 2016) (purple) of genes reported to have significant genotype environment interaction according to von Heckel et al. (2016). Asterisk indicates the adjusted *P*-value from a Wald test as applied in DESeq2: *P < 0.05.

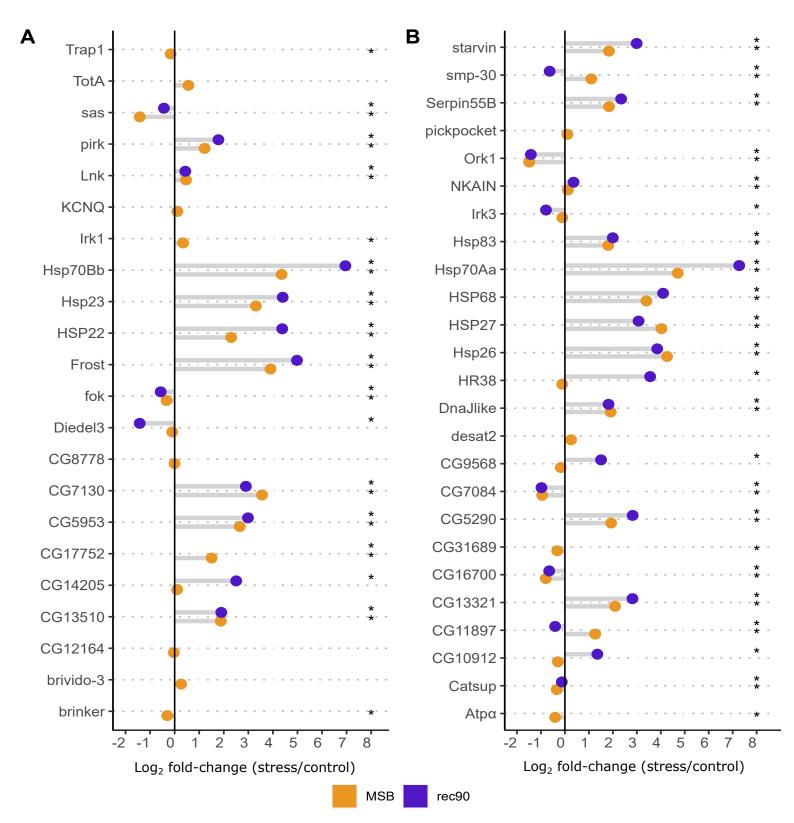


Figure S5. Comparisons of Log_2 fold-change (stress/control) in MSB oxidative stress (orange) and cold shock (von Heckel et al. 2016) (purple) experiments of (A) 22 viable and (B) not viable/malformed candidate genes identified by von Heckel et al. (2016) for RNAi knockdown. Asterisk indicates the adjusted *P*-value from a Wald test as applied in DESeq2: *P < 0.05.

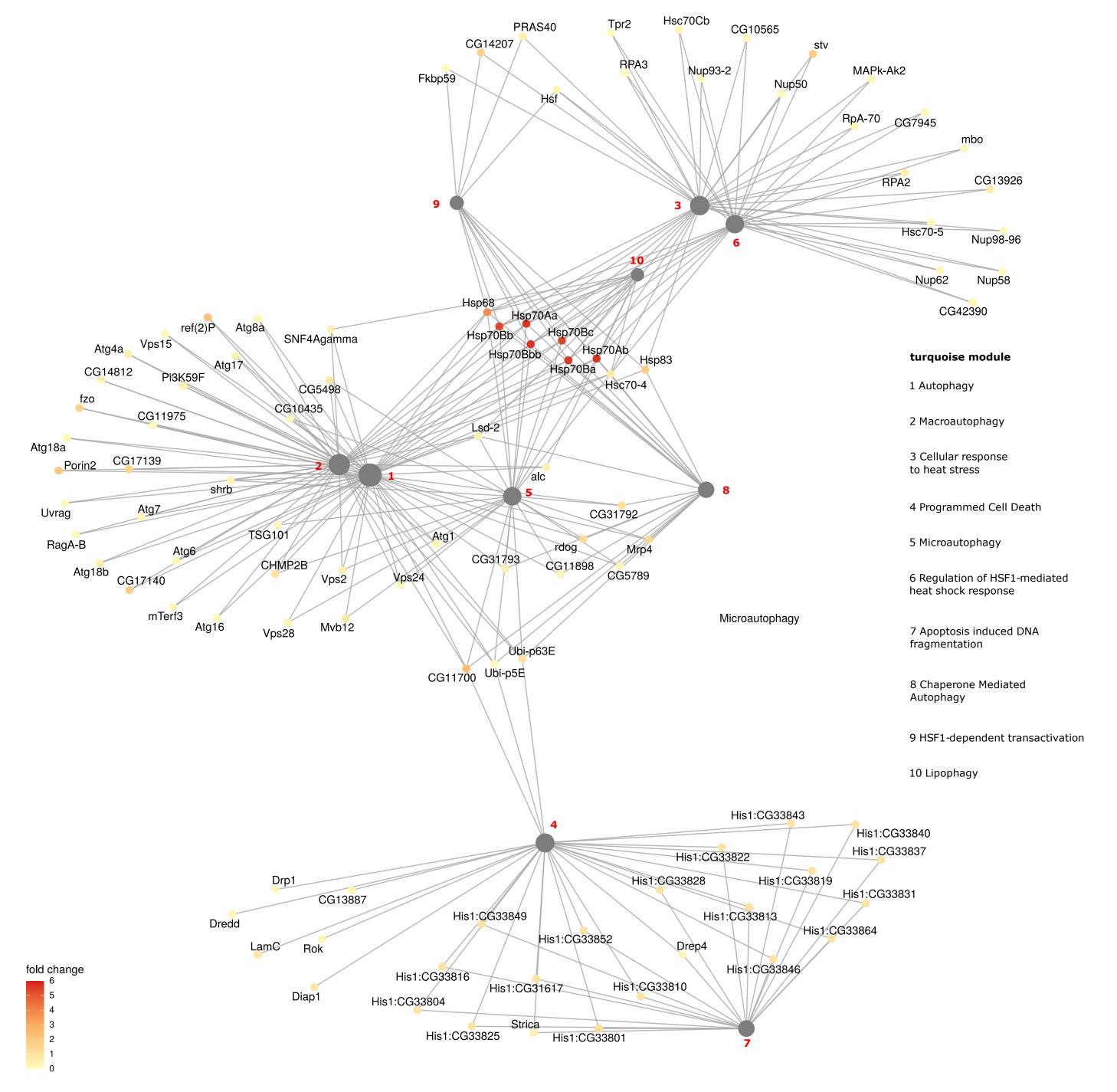
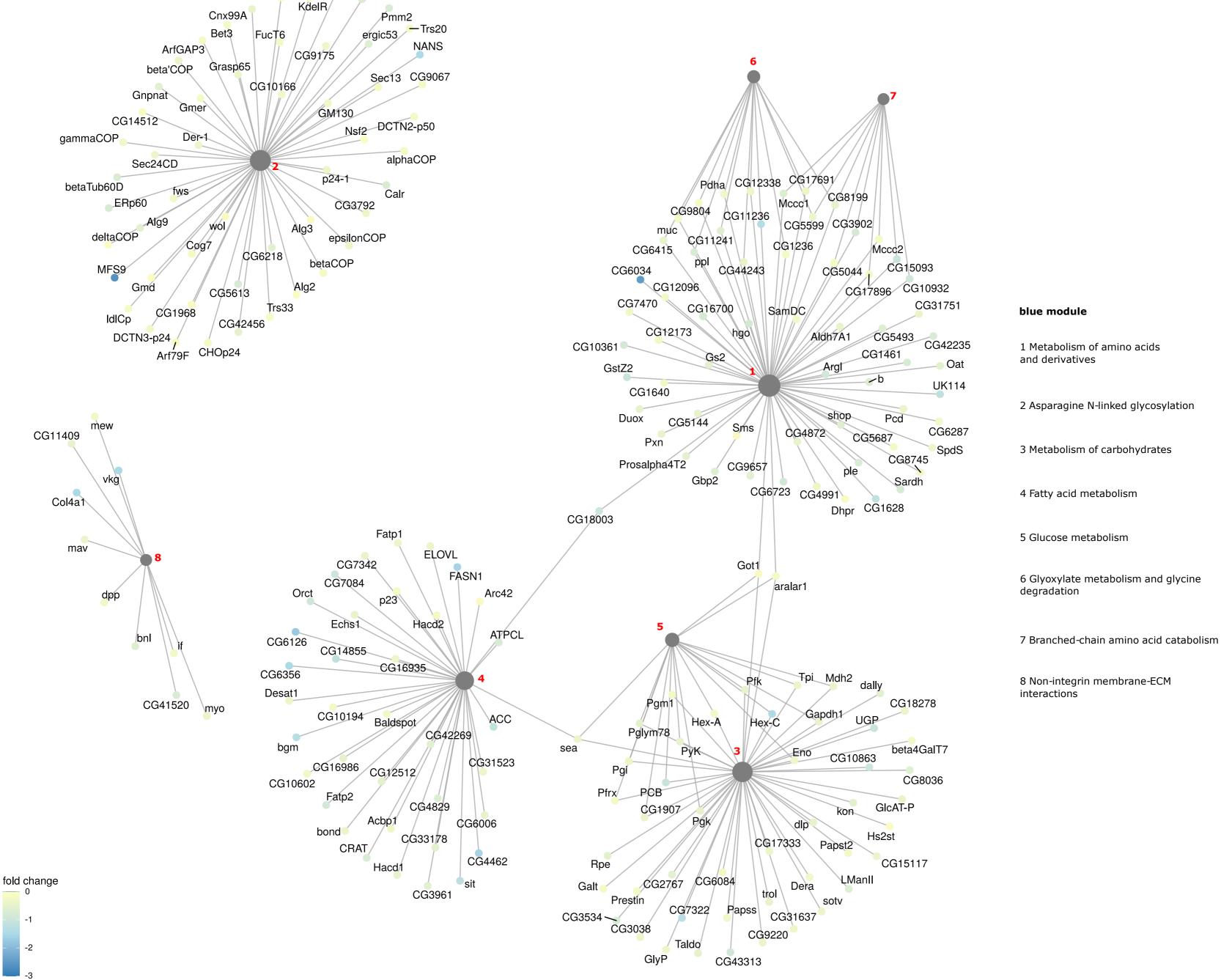


Figure S6A. The 10 reactome pathways that show the highest enrichment for genes under oxidative stress from the WGCNA's turquoise module are shown.



p115 Csas

Gos₂₈

Figure S6B. The 8 reactome pathways that show the highest enrichment for genes under oxidative stress from the WGCNA's blue module are shown.

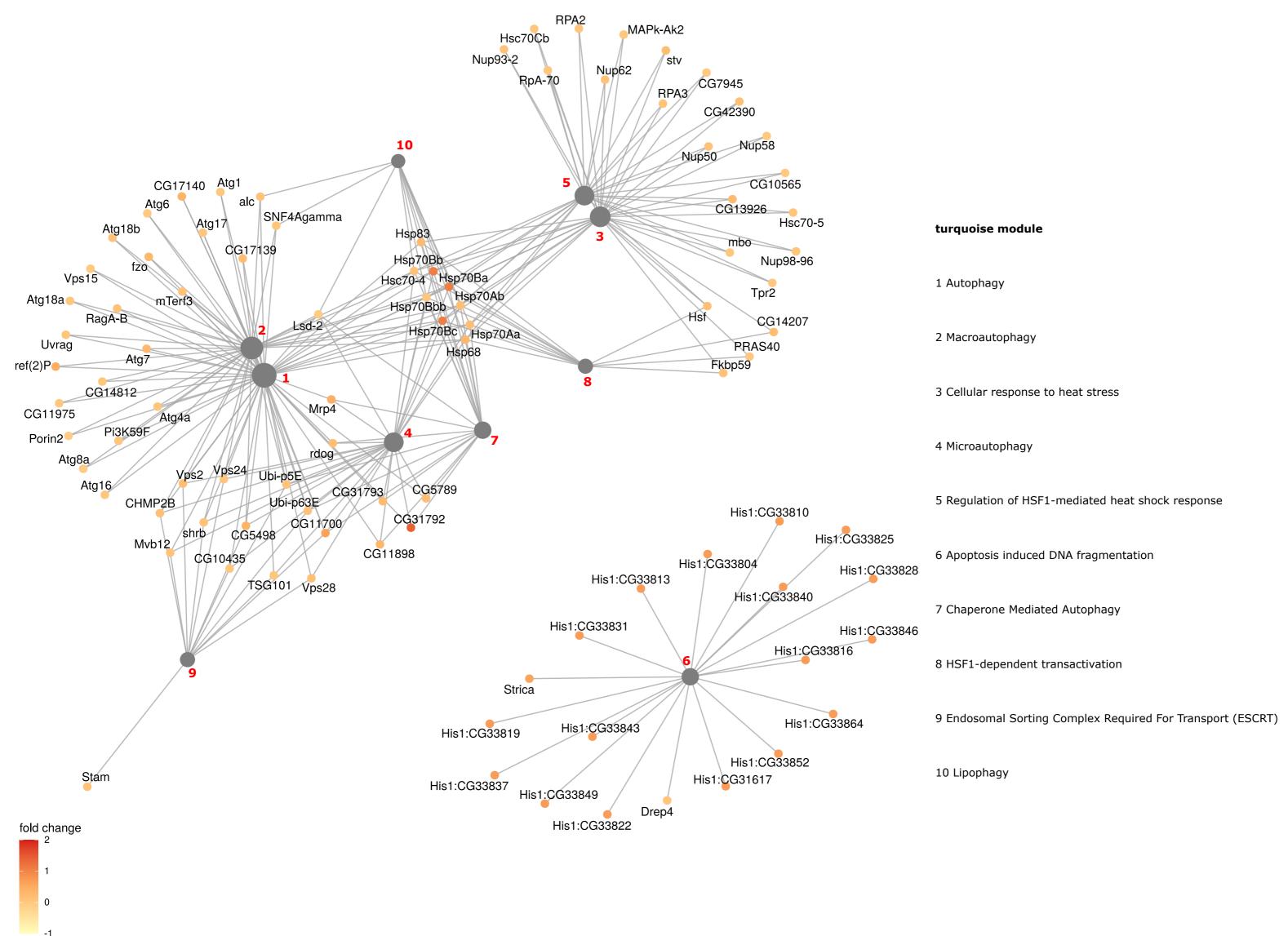
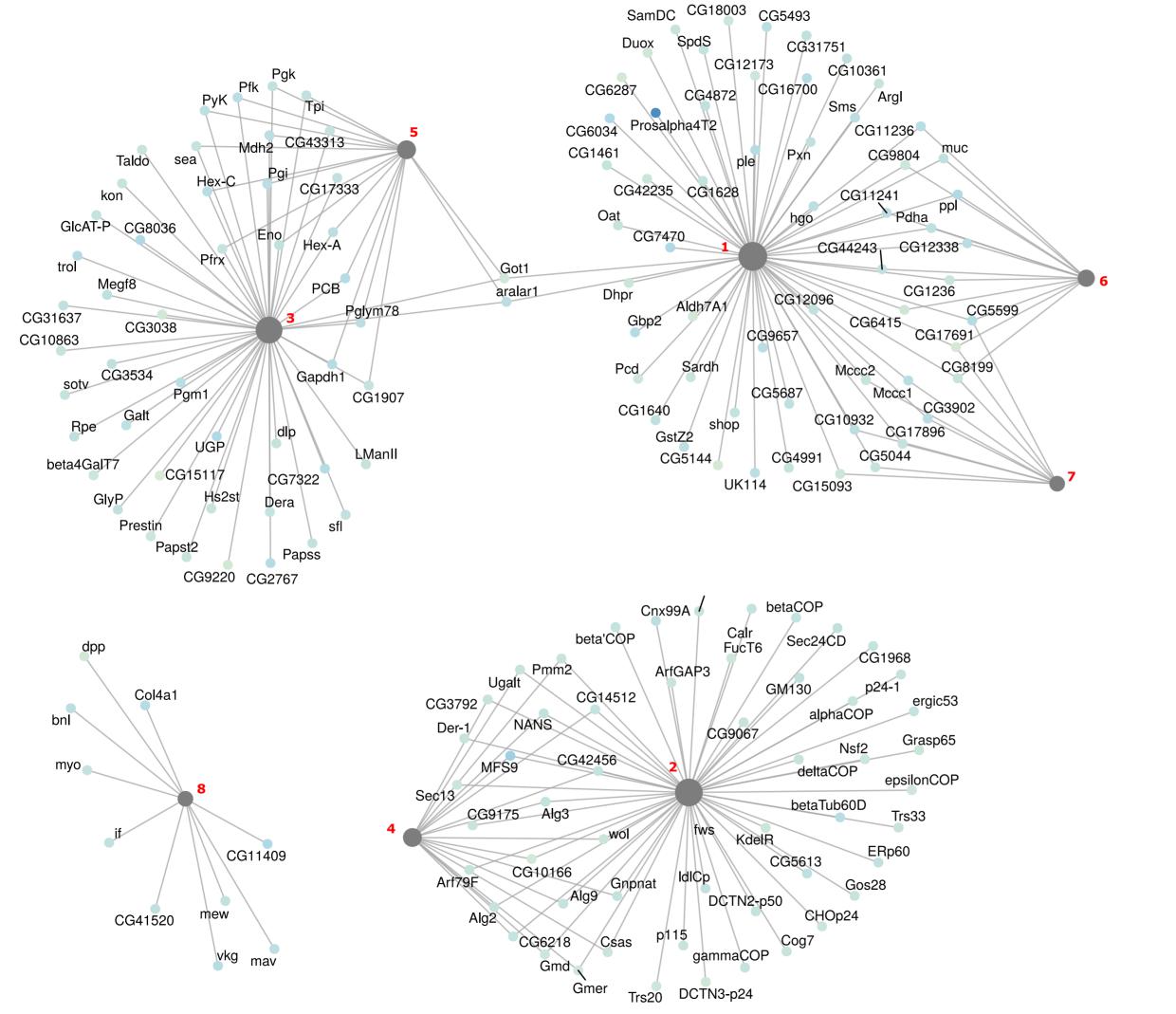


Figure S7A. The 10 reactome pathways that show the highest enrichment for genes under oxidative stress in the deletion background relative to non-deletion from the WGCNA's turquoise module are shown.



fold change

blue module

- 1 Metabolism of amino acids and derivatives
- 2 Asparagine N-linked glycosylation
- 3 Metabolism of carbohydrates
- 4 Biosynthesis of the N-glycan (dolichol lipid-linked oligosaccharide, LLO) and transfer to a nascent protein
- 5 Glucose metabolism
- 6 Glyoxylate metabolism and glycine degradation
- 7 Branched-chain amino acid catabolism
- 8 Non-integrin membrane-ECM interactions

Figure S7B. The 8 reactome pathways that show the highest enrichment for genes under oxidative stress in the deletion background relative to non-deletion from the WGCNA's blue module are shown.