

**Table S2. Overrepresented ( $P < 0.01$ ) gene ontology classes among genes with expression changes in response to reduced *LCB2* expression.**

Fold change in expression of measured gene	n	GO Process	GO Function	GO Component
>1.5	784	Reproduction Response to oxidative stress Viral reproduction Transposition, RNA-mediated Developmental process Transposition Viral procapsid maturation DNA integration Oxidation-reduction process Monosaccharide catabolic process Response to chemical stimulus DNA recombination	Catalytic activity Aspartic-type endopeptidase activity Structural constituent of cell wall Antioxidant activity RNA-directed DNA polymerase activity Alditol:NADP+ 1-oxidoreductase activity Oxidoreductase activity Ribonuclease H activity Peptidase activity Hydrolase activity, acting on ester bonds Ribonuclease activity Endonuclease activity, active with either ribo- or deoxyribonucleic acids and producing 5'-phosphomonoesters Endonuclease activity	Retrotransposon nucleocapsid Fungal-type cell wall External encapsulating structure
>2	303	Response to oxidative stress Arabinose catabolic process Response to stress	Alditol:NADP+ 1-oxidoreductase activity	Retrotransposon nucleocapsid
>3	81	Response to copper ion	Cadmium ion binding	Fungal-type cell wall
<-1.5	524	-	Structural constituent of ribosome Structural molecule activity	Ribosome Organelle Fungal-type cell wall Non-membrane-bounded organelle Intracellular organelle Ribonucleoprotein complex External encapsulating structure Intracellular non-membrane-bounded organelle
<-2	121	-	-	-
<-3	25	-	-	-

Genome-wide expression data is from microarray analysis in Mnainemeh *et al.* 2004, where *LCB2* expression was reduced in strain *Tet07-LCB2* with 10 µg/ml of doxycycline. GO overrepresentation among responsive genes was calculated using the Generic Gene Ontology Term Finder ([go.princeton.edu](http://go.princeton.edu)), and redundant GO terms were removed ([revigo.irb.hr](http://revigo.irb.hr)).