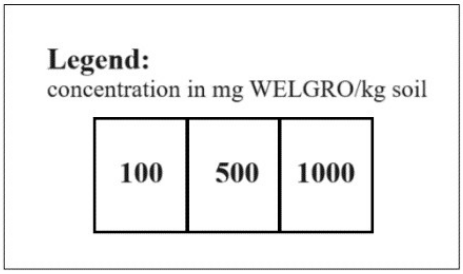
Supporting Information

Figures S1 to S14: KEGG graphs – rendered by Pathview.

Each rectangle (corresponding to a gene) is divided in 3, corresponding to the different WELGRO® concentrations, as depicted:



2 days:

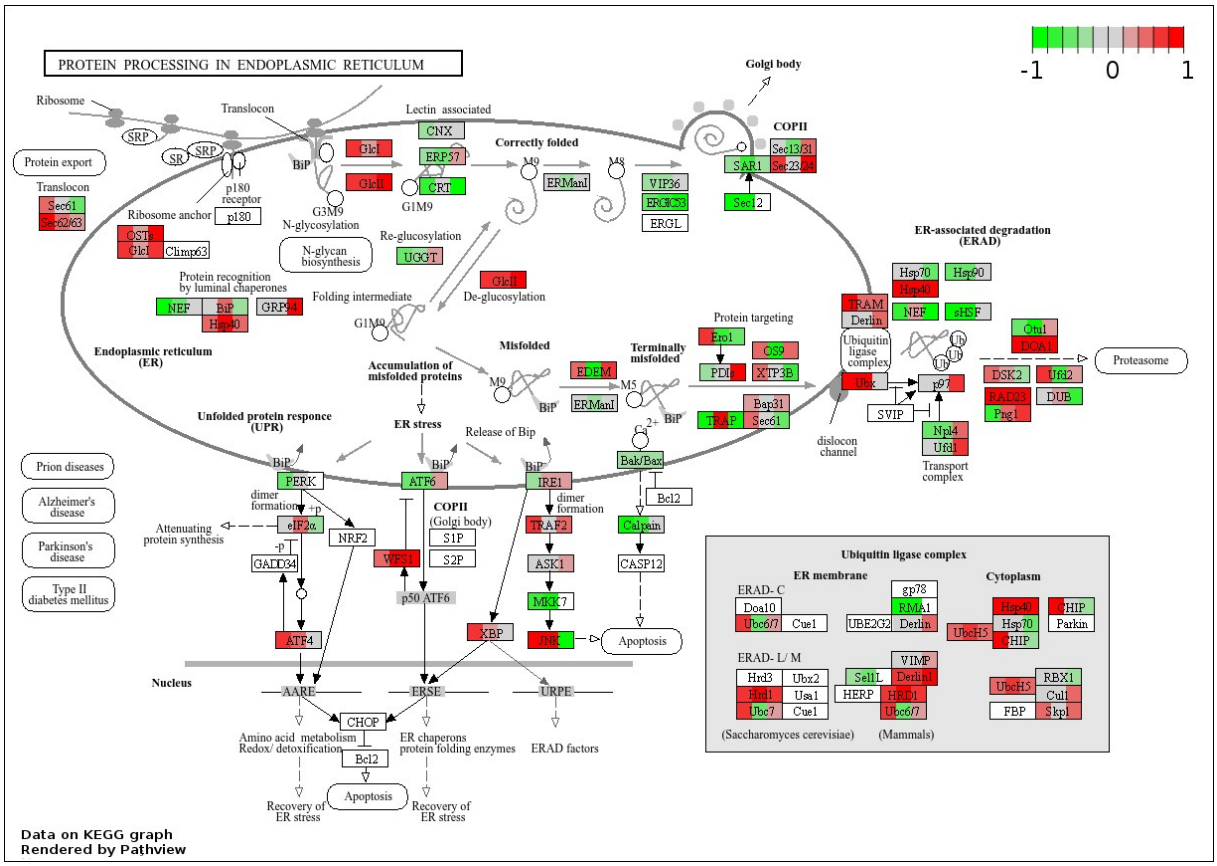


Figure S1: Fold-change (treatments versus control) of genes representing components of the "Protein processing in endoplasmic reticulum" KEGG pathway ko04141, as an example of pathways that are significantly affected in *Enchytraeus crypticus* exposed to WELGRO® for 2 days. Green and red indicate down- and up-regulation, respectively. Details in this pathway can be retrieved from the following website: https://www.genome.jp/pathway/ko04141 (for interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article).

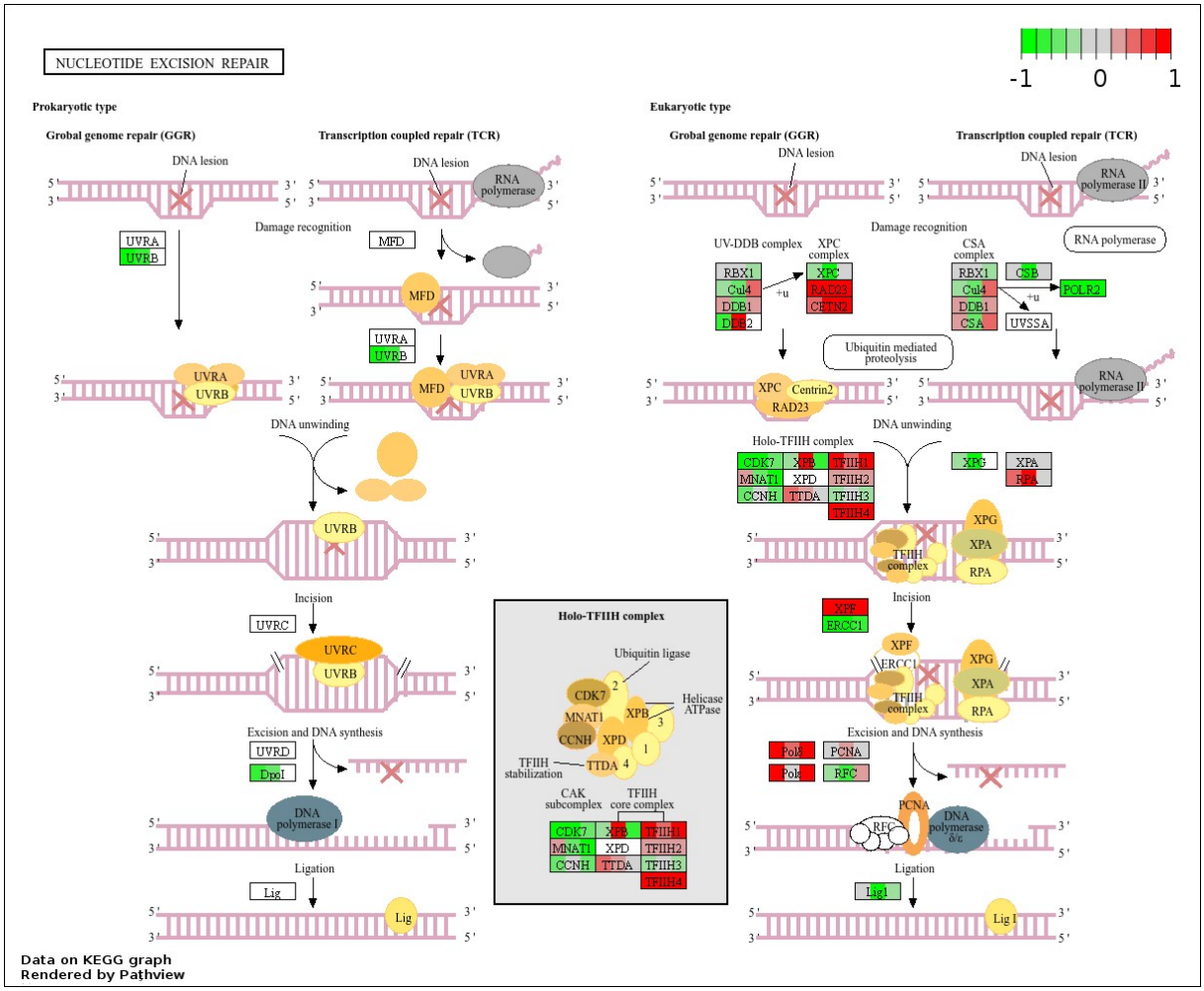


Figure S2: Fold-change (treatments versus control) of genes representing components of the "Nucleotide excision repair" KEGG pathway ko03420, as an example of pathways that are significantly affected in *Enchytraeus crypticus* exposed to WELGRO® for 2 days. Green and red indicate down- and up-regulation, respectively. Details in this pathway can be retrieved from the following website: https://www.genome.jp/pathway/ko03420 (for interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article).

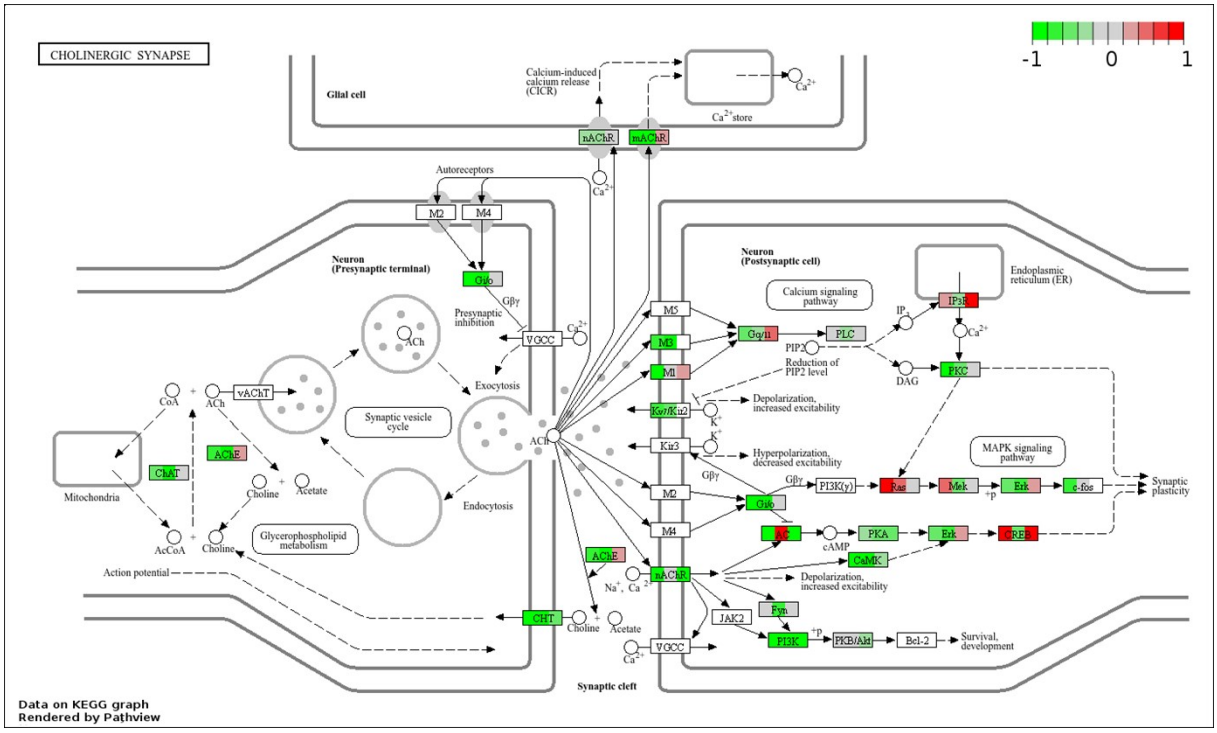


Figure S3: Fold-change (treatments versus control) of genes representing components of the "Cholinergic synapse" KEGG pathway ko04725, as an example of pathways that are significantly affected in *Enchytraeus crypticus* exposed to WELGRO® for 2 days. Green and red indicate down- and up-regulation, respectively. Details in this pathway can be retrieved from the following website: https://www.genome.jp/pathway/ko04725 (for interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article).

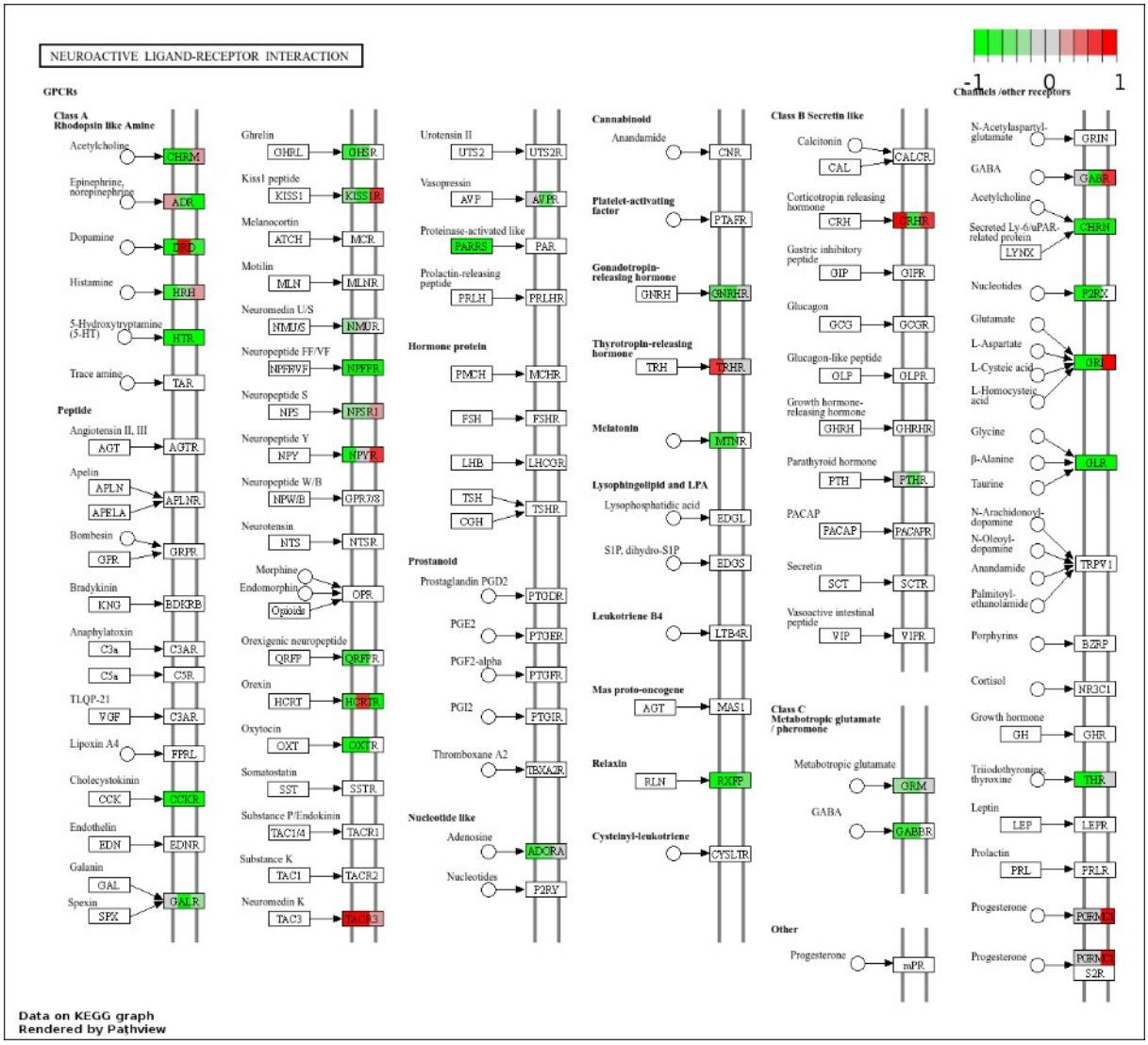


Figure S4: Fold-change (treatments versus control) of genes representing components of the "Neuroactive ligand-receptor interaction" KEGG pathway ko04080, as an example of pathways that are significantly affected in *Enchytraeus crypticus* exposed to WELGRO® for 2 days. Green and red indicate down- and up-regulation, respectively. Details in this pathway can be retrieved from the following website: https://www.genome.jp/pathway/ko04080 (for interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article).

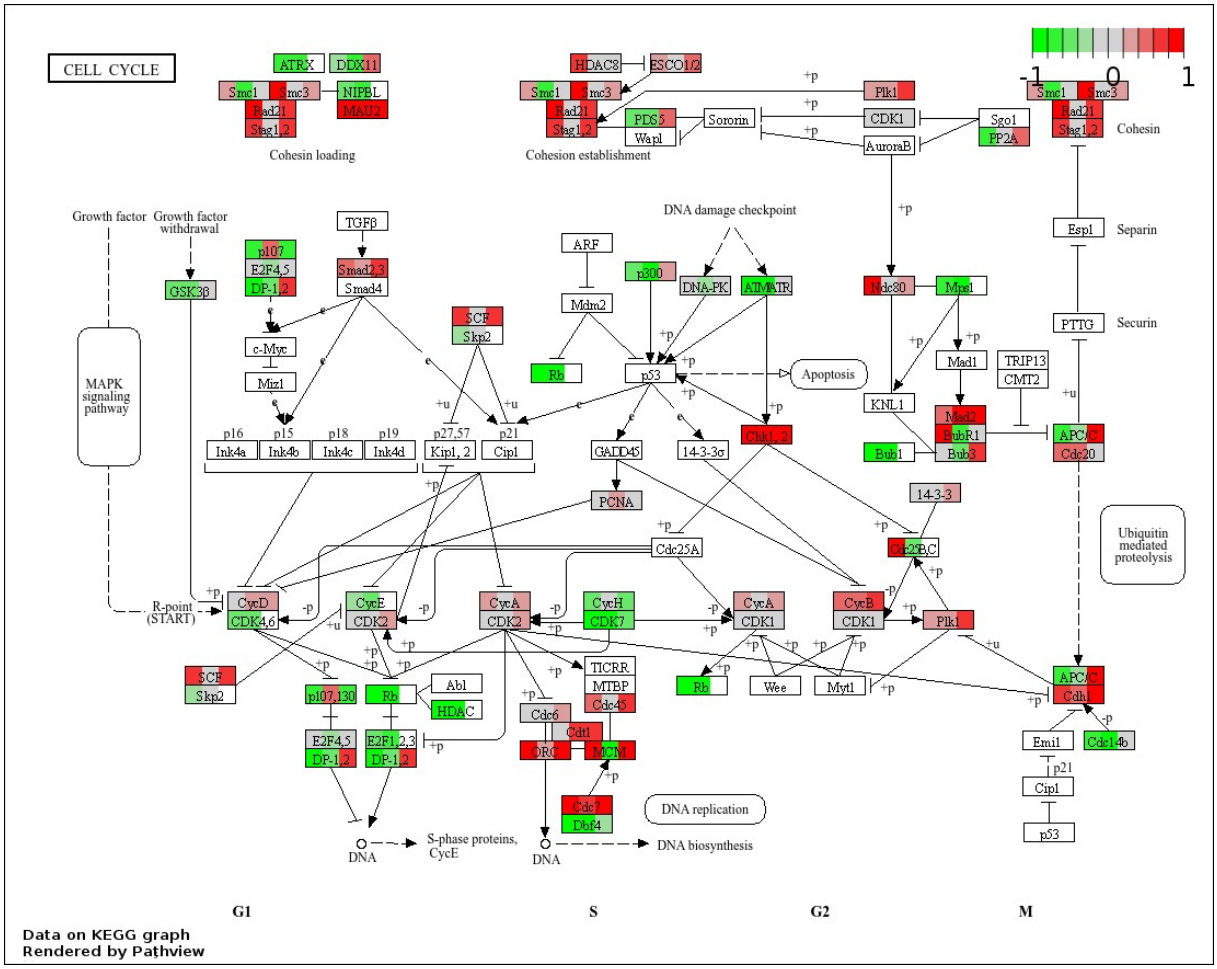


Figure S5: Fold-change (treatments versus control) of genes representing components of the "Cell cycle" KEGG pathway ko04110, as an example of pathways that are significantly affected in *Enchytraeus crypticus* exposed to WELGRO® for 2 days. Green and red indicate down- and up-regulation, respectively. Details in this pathway can be retrieved from the following website: https://www.genome.jp/pathway/ko04110 (for interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article).

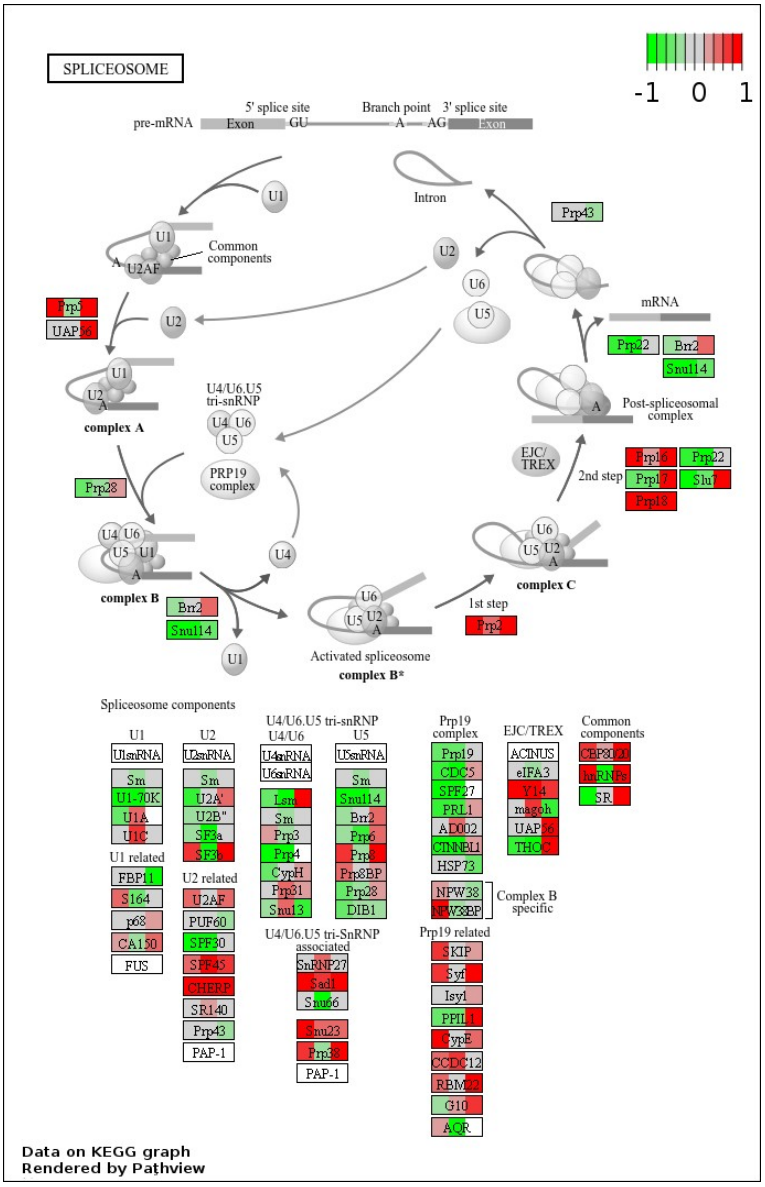


Figure S6: Fold-change (treatments versus control) of genes representing components of the "Spliceosome" KEGG pathway ko03040, as an example of pathways that are significantly affected in *Enchytraeus crypticus* exposed to WELGRO® for 2 days. Green and red indicate down- and up-regulation, respectively. Details in this pathway can be retrieved from the following website: https://www.genome.jp/pathway/ko03040 (for interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article).

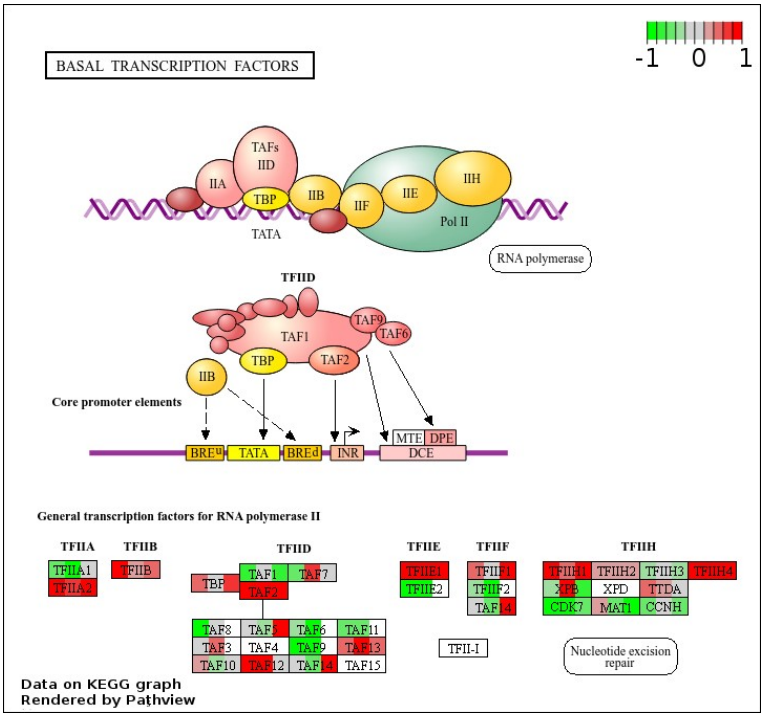


Figure S7: Fold-change (treatments versus control) of genes representing components of the "Basal transcription factors" KEGG pathway ko03022, as an example of pathways that are significantly affected in *Enchytraeus crypticus* exposed to WELGRO® for 2 days. Green and red indicate down- and up-regulation, respectively. Details in this pathway can be retrieved from the following website: https://www.genome.jp/pathway/ko03022 (for interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article).

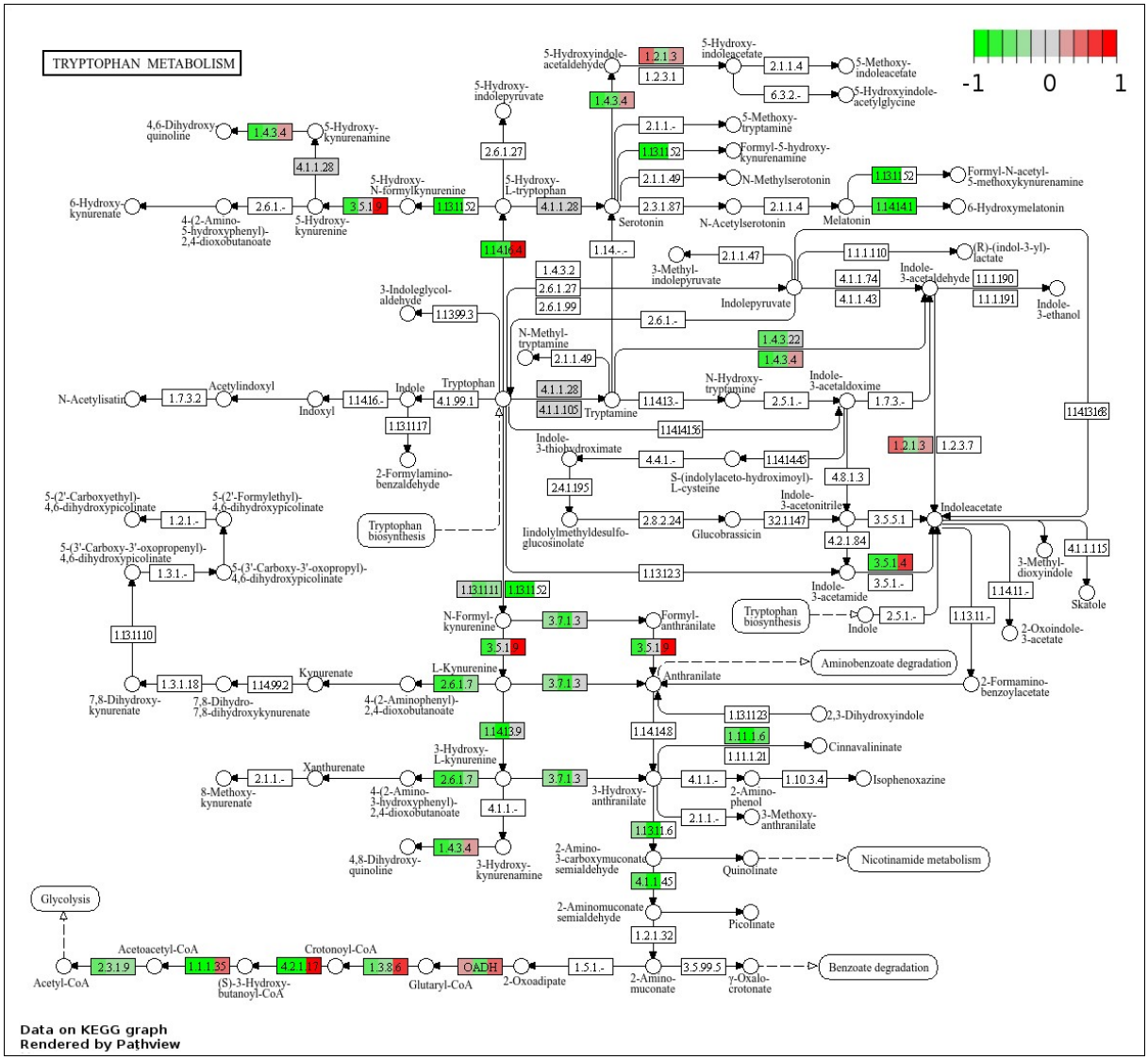


Figure S8: Fold-change (treatments versus control) of genes representing components of the "Tryptophan metabolism" KEGG pathway ko00380, as an example of pathways that are significantly affected in *Enchytraeus crypticus* exposed to WELGRO® for 2 days. Green and red indicate down- and up-regulation, respectively. Details in this pathway can be retrieved from the following website: https://www.genome.jp/pathway/ko00380 (for interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article).

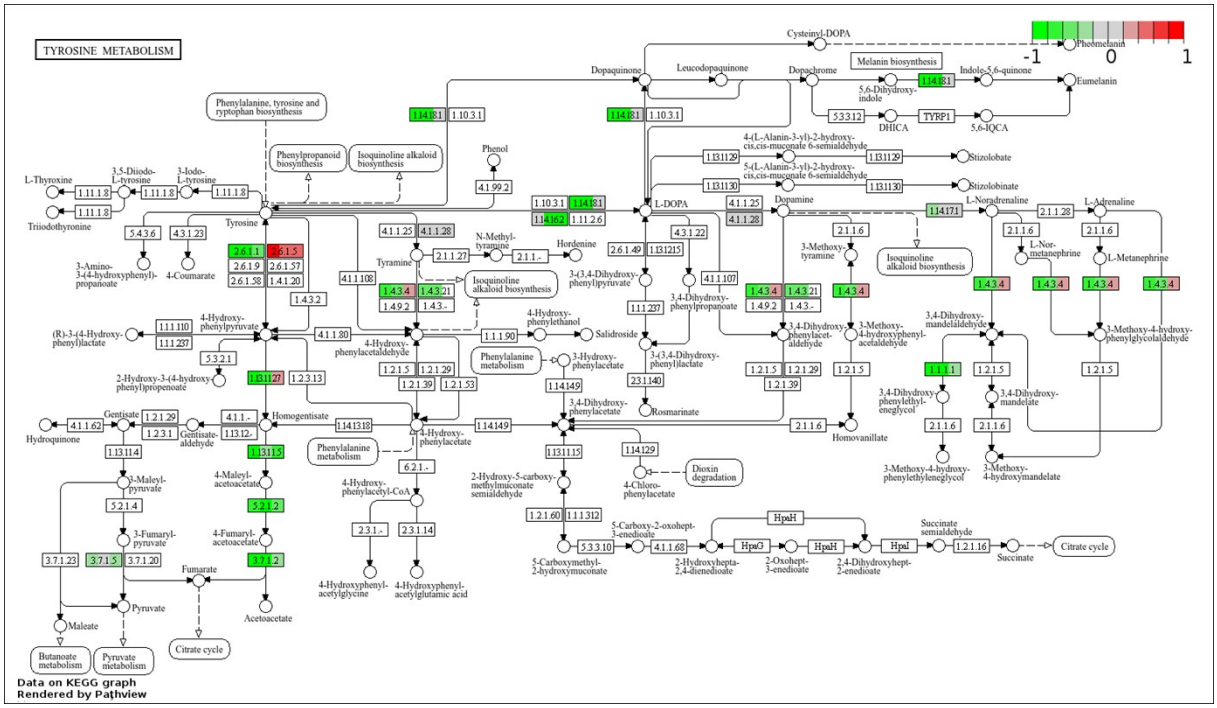


Figure S9: Fold-change (treatments versus control) of genes representing components of the "Tyrosine metabolism" KEGG pathway ko00350, as an example of pathways that are significantly affected in *Enchytraeus crypticus* exposed to WELGRO® for 2 days. Green and red indicate down- and up-regulation, respectively. Details in this pathway can be retrieved from the following website: https://www.genome.jp/pathway/ko00350 (for interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article).

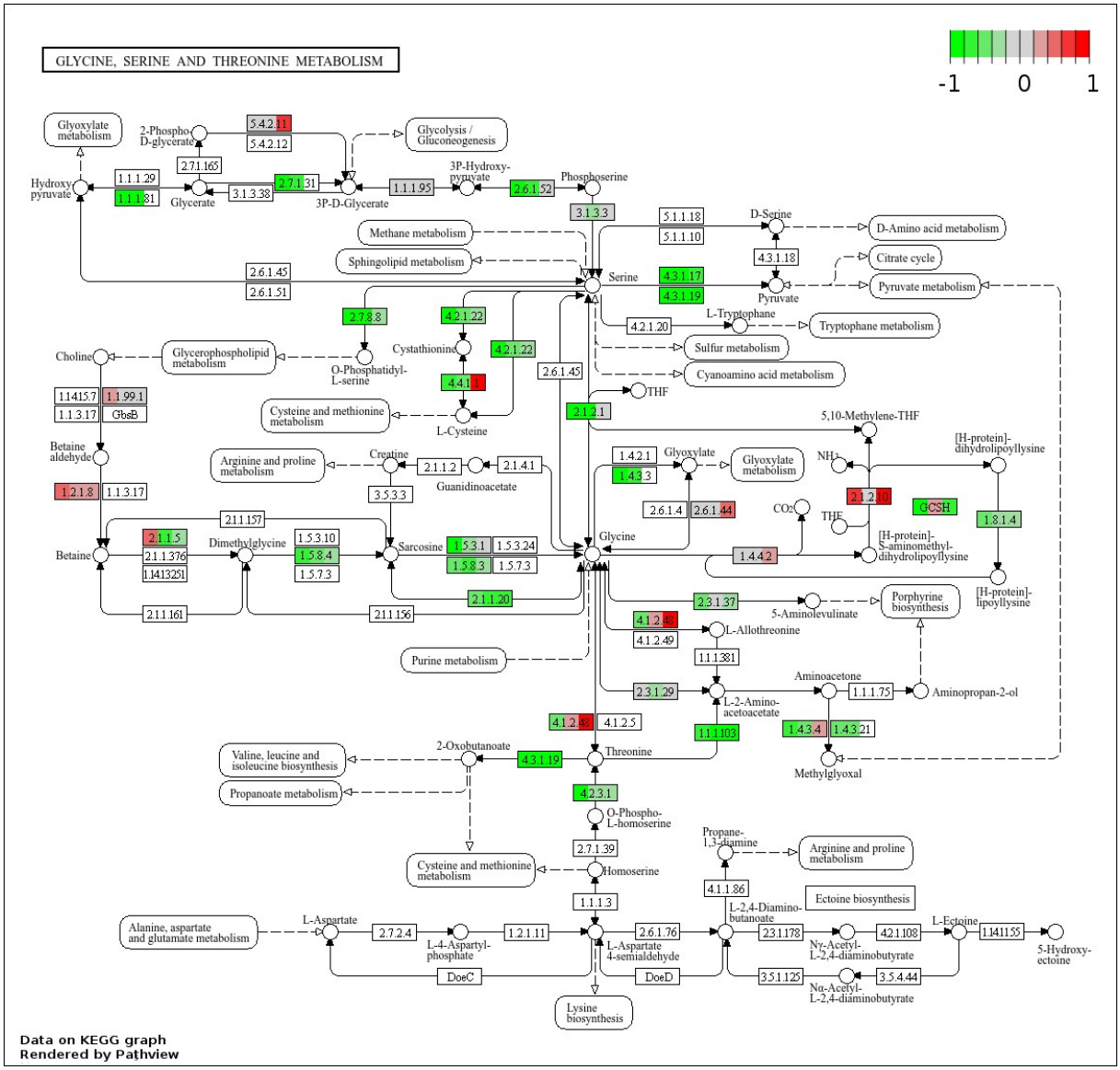


Figure S10: Fold-change (treatments versus control) of genes representing components of the "Glycine, serine and threonine metabolism" KEGG pathway ko00260, as an example of pathways that are significantly affected in *Enchytraeus crypticus* exposed to WELGRO® for 2 days. Green and red indicate down- and up-regulation, respectively. Details in this pathway can be retrieved from the following website: https://www.genome.jp/pathway/ko00260 (for interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article).

21 days:

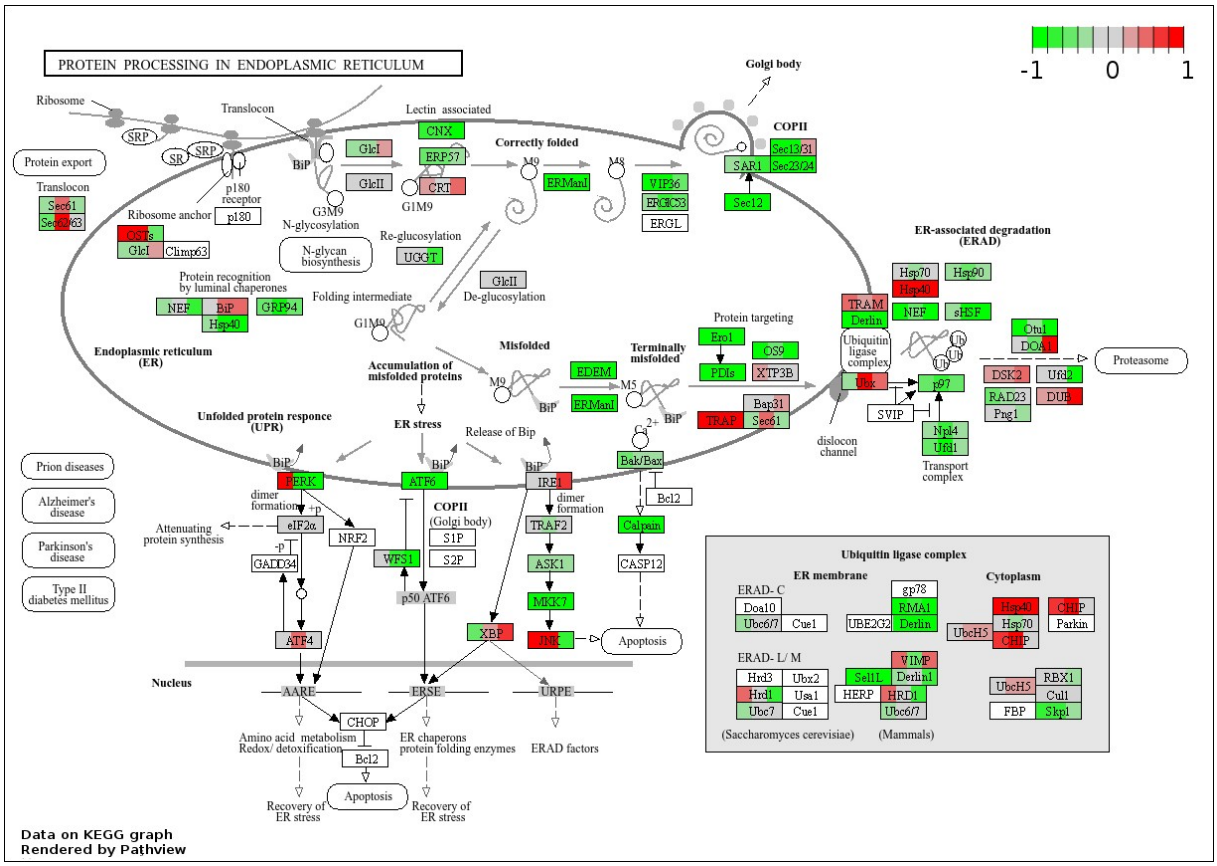


Figure S11: Fold-change (treatments versus control) of genes representing components of the "Protein processing in endoplasmic reticulum" KEGG pathway ko04141, as an example of pathways that are significantly affected in *Enchytraeus crypticus* exposed to WELGRO® for 21 days. Green and red indicate down- and up-regulation, respectively. Details in this pathway can be retrieved from the following website: https://www.genome.jp/pathway/ko04141 (for interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article).

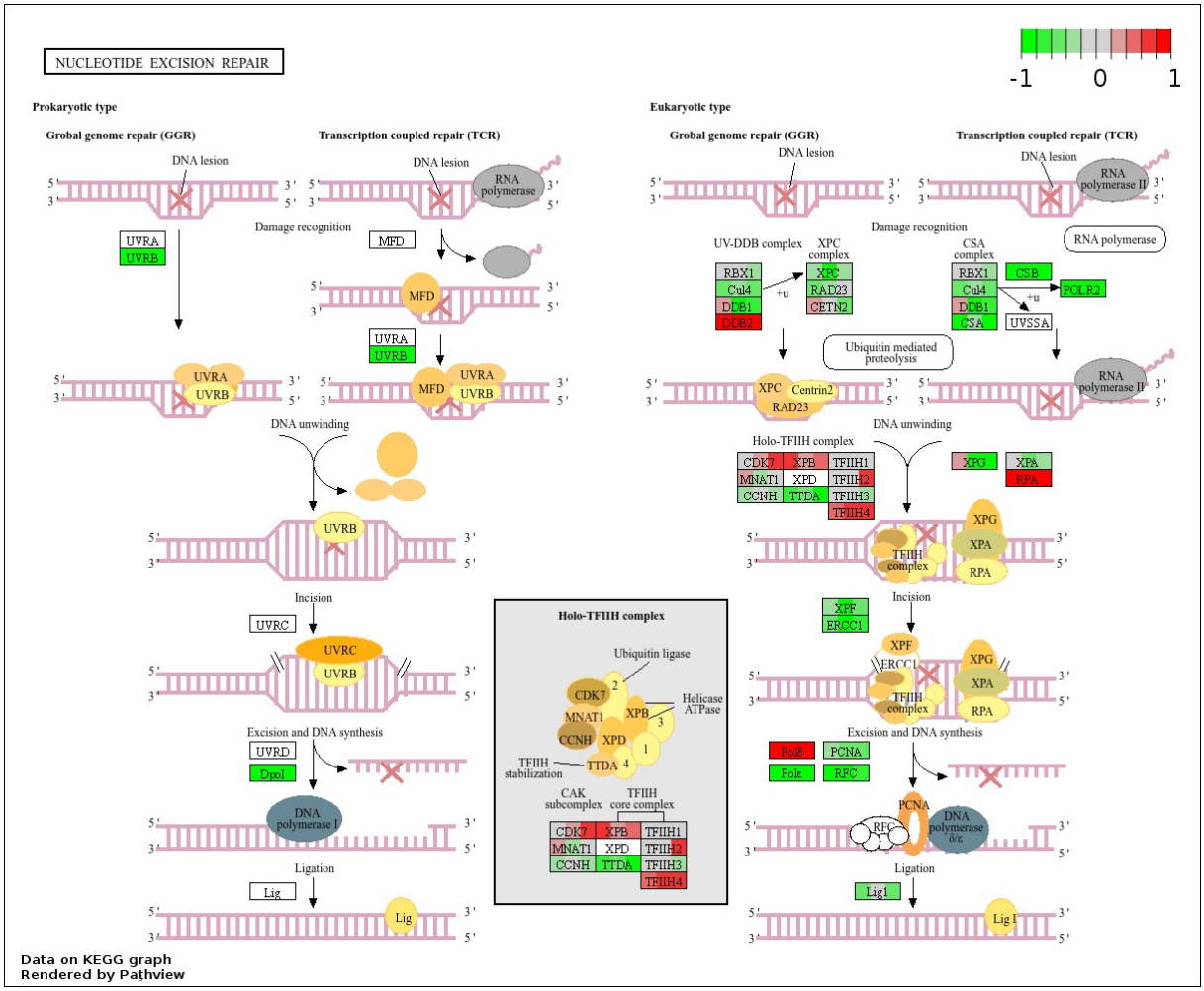


Figure S12: Fold-change (treatments versus control) of genes representing components of the "Nucleotide excision repair" KEGG pathway ko03420, as an example of pathways that are significantly affected in *Enchytraeus crypticus* exposed to WELGRO® for 21 days. Green and red indicate down- and up-regulation, respectively. Details in this pathway can be retrieved from the following website: https://www.genome.jp/pathway/ko03420 (for interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article).

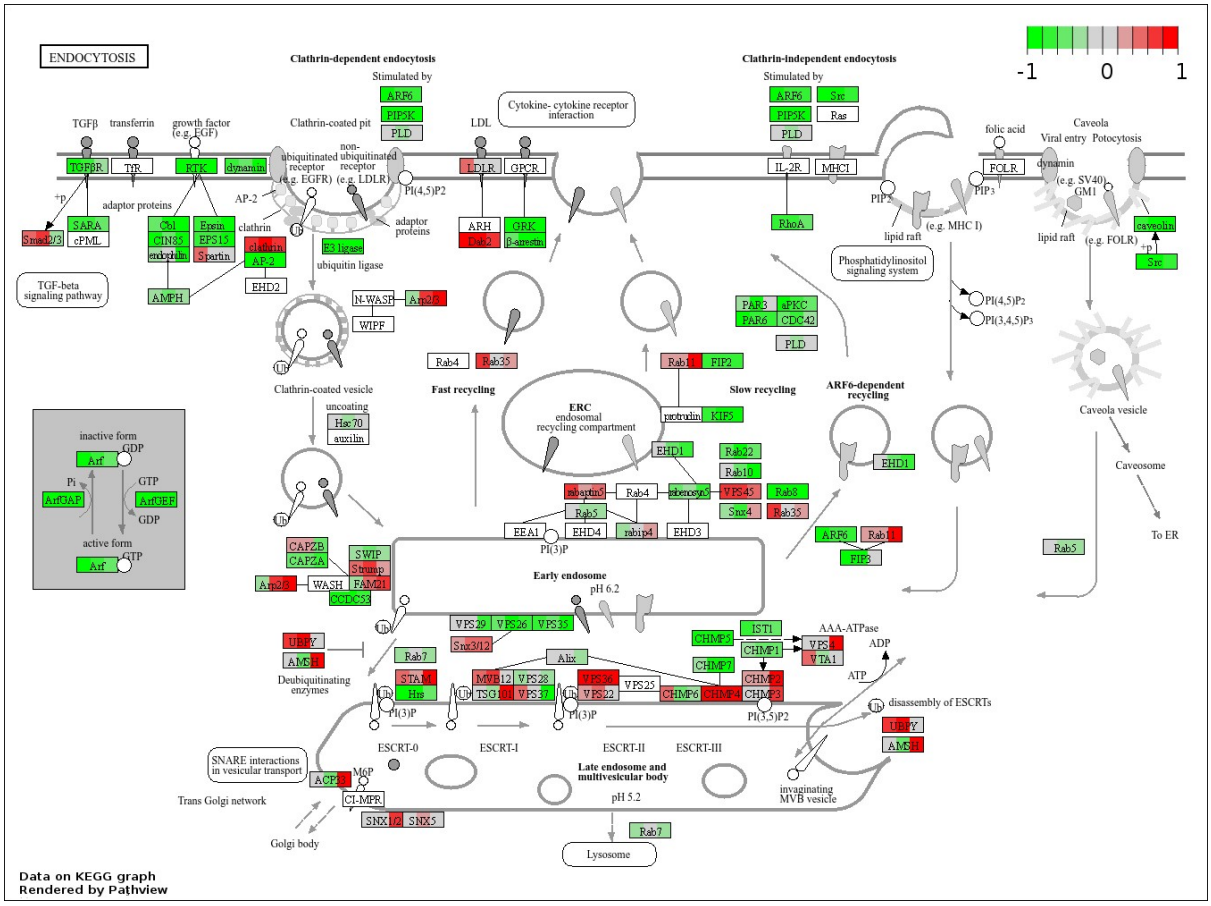


Figure S13: Fold-change (treatments versus control) of genes representing components of the "Endocytosis" KEGG pathway ko04144, as an example of pathways that are significantly affected in *Enchytraeus crypticus* exposed to WELGRO® for 21 days. Green and red indicate down- and up-regulation, respectively. Details in this pathway can be retrieved from the following website: https://www.genome.jp/pathway/ko04144 (for interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article).

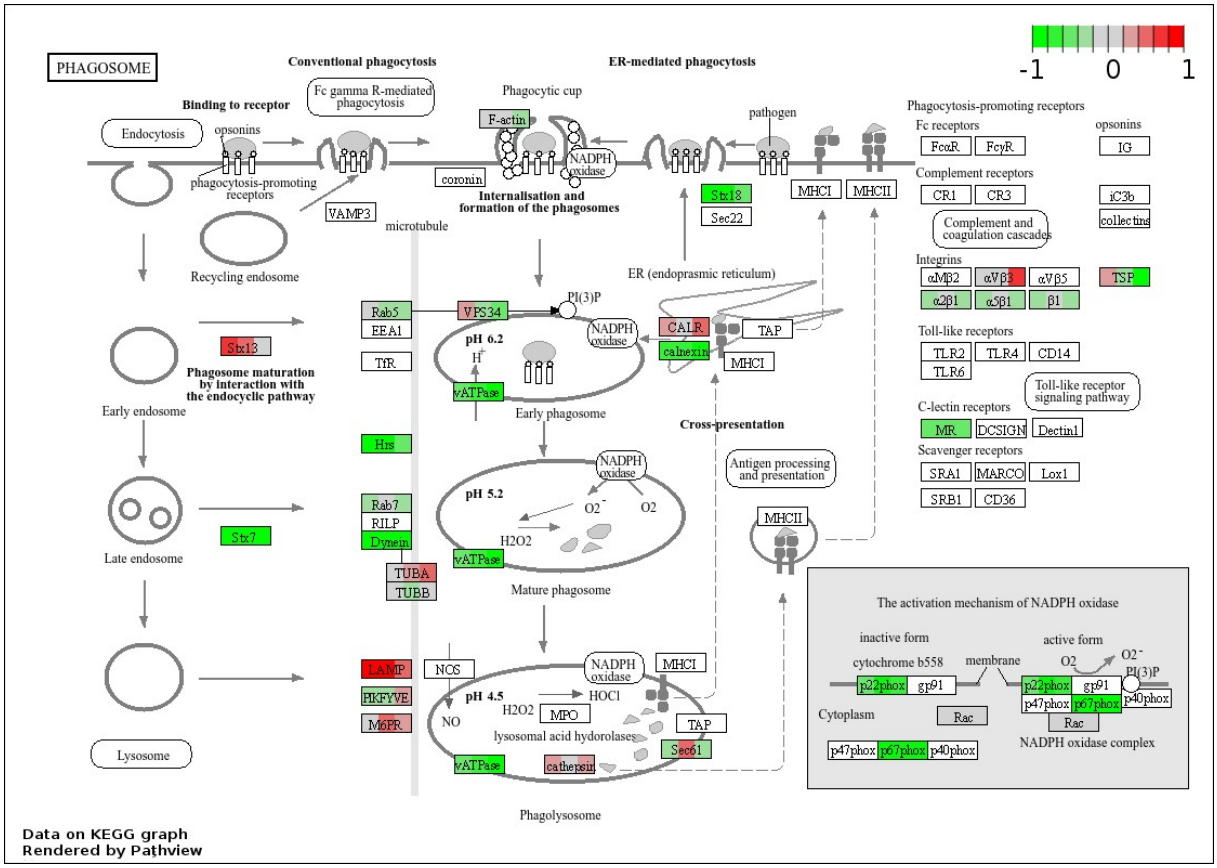


Figure S14: Fold-change (treatments versus control) of genes representing components of the "Phagosome" KEGG pathway ko04145, as an example of pathways that are significantly affected in *Enchytraeus crypticus* exposed to WELGRO® for 21 days. Green and red indicate down- and up-regulation, respectively. Details in this pathway can be retrieved from the following website: https://www.genome.jp/pathway/ko04145 (for interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article).