SUPPLEMENTAL INFORMATION

Ecotoxicogenomic assessment of soil toxicity associated with the production chain of 2, 5-furandicarboxylic acid (FDCA), a candidate bio-based green chemical building block

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Tables (Supplied as Excel files)

Table S1: All significantly differentially expressed genes in *Folsomia candida* after two days exposure to soil spiked with EC50 concentration of HMF. List of significant genes, description, fold change and adjusted p value encountered in the Limma package for microarray data analysis. Descriptions were derived from BLAST analysis.

Table S2: Significant GO terms found in *Folsomia candida* for EC50 HMF soil treatment compared to control after Gene Ontology Enrichment Analysis. Significantly up- and down-regulated genes were subjected to GO enrichment analysis separately. List of the total number of genes present in this GO term, the number of genes found for this GO term in the significant gene list and p value calculated by the weighted Fisher's Exact Test.

Table S3: Representative GO terms found in *Folsomia candida* for EC50 HMF soil treatment compared to control after summarizing by REVIGO Analysis. Significantly up- and down-regulated genes were subjected to REVIGO analysis separately.

Figure

Figure S1: Effect of FDCA (A), HMF(B) and TPA (C) on the survival of *Folosmia candida* after 28d exposure in sterilized LUFA2.2 soil spiked with different concentration of test chemicals. Lines show the fit of the logistic dose response model to the reproduction data and four biological replicates were employed.

Figure S2: The scatter plot showed of the relationship of normalized gene expression value between the biological replicates of HMF exposure treatment. The treatment contains three biological treatments. The Pearson correlation coefficients are also shown in the plots. All the reported correlation values are highly significant, $p < 0.01$.

Figure S3: Gene ontology (GO) tree resulting from the enrichment analysis. This tree shows part of the biological processes that were significantly affected in *Folsomia candida* after 2-d exposure to HMF in soil. Each sphere contains a GO identifier, a biological process description, significance values of Fisher's exact test (red color represents the significance level, $p < 0.05$). The ratio under the p value represents the number of significant genes divided by the total number of genes belonging to the GO term and present on the array. Cell developmental processes and oxidative response processes were significantly affected in the down-regulated gene set.

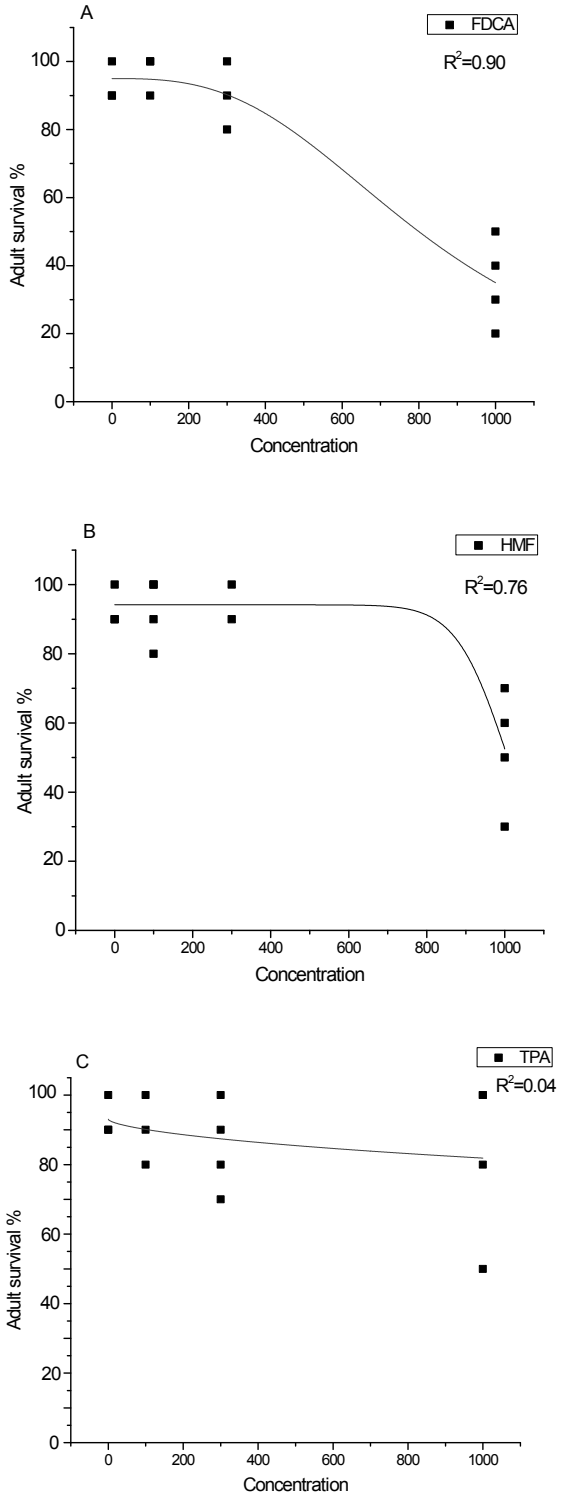
A
FDCA
R^2=0.90
Adult survival %
Concentration
B
HMF
R^2=0.76
Adult survival %
Concentration
C
TPA
R^2=0.04
Adult survival %
Concentration

Figure S1

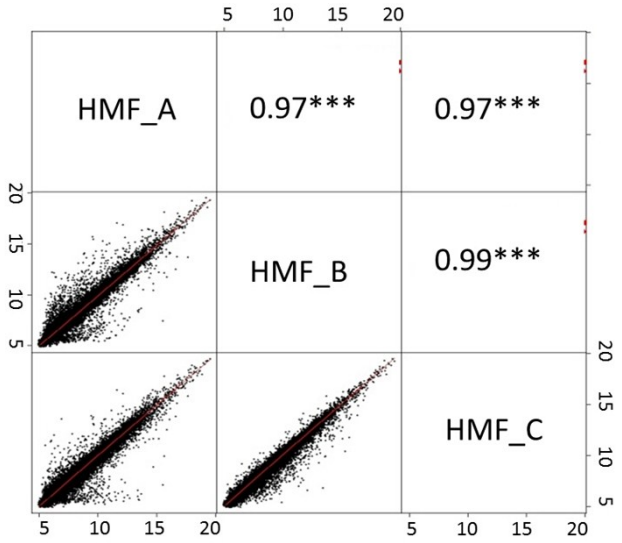

Figure S2

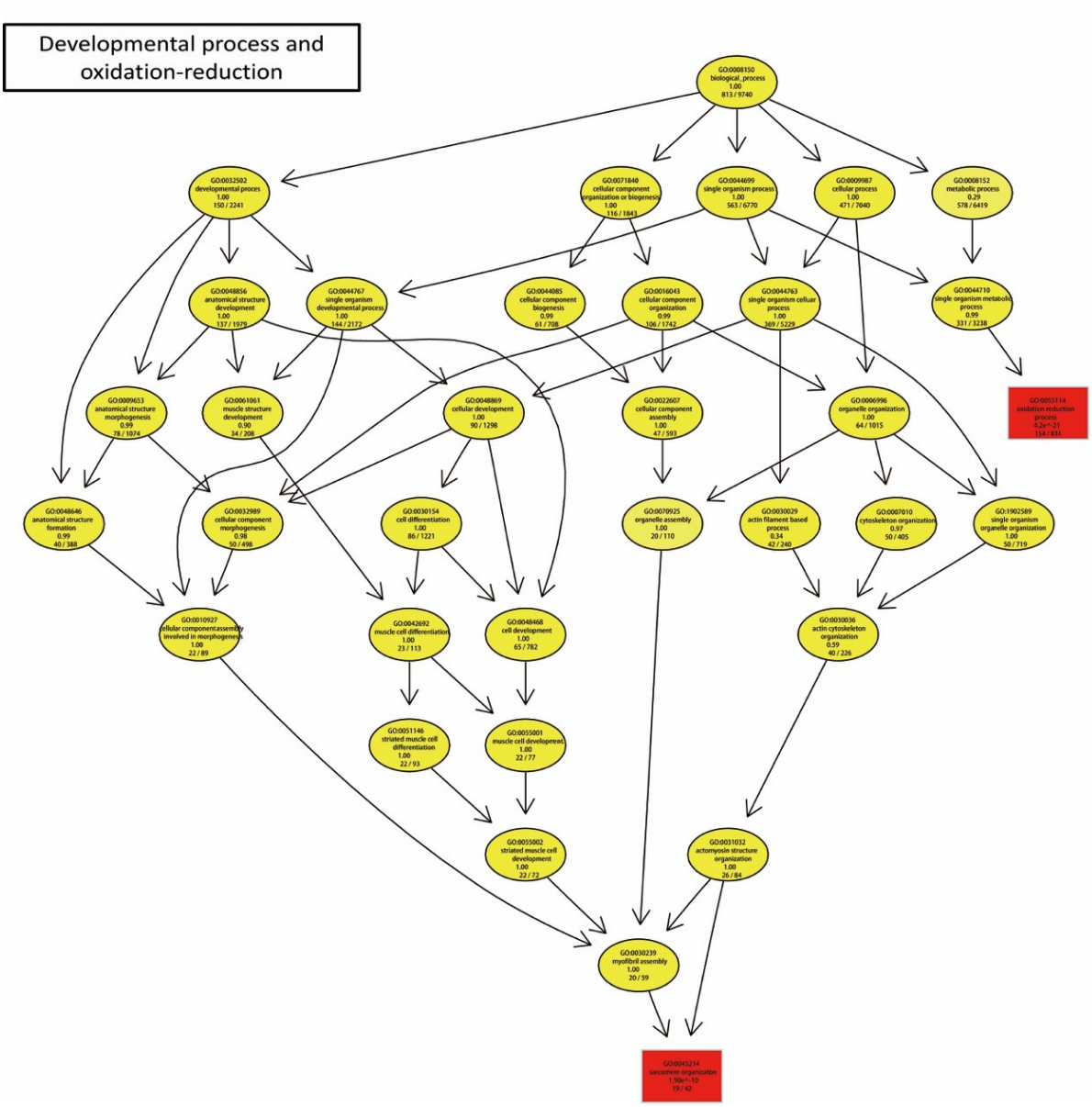
Developmental process and oxidation-reduction
GO:0008150 biological_process 1.00 813 / 9740
GO:0032502 developmental proces 1.00 150 / 2241
GO:0071840 cellular component organization or biogenesis 1.00 116 / 1843
GO:0044699 single organism process 1.00 563 / 6770
GO:0009987 cellular process 1.00 471 / 7040
GO:0008152 metabolic process 0.29 578 / 6419
GO:0048856 anatomical structure development 1.00 137 / 1979
GO:0044767 single organism developmental process 1.00 144 / 2172
GO:0044085 cellular component biogenesis 0.99 61 / 708
GO:0016043 cellular component organization 0.99 106 / 1742
GO:0044763 single organism cellular process 1.00 369 / 5229
GO:0044710 single organism metabolic process 0.99 331 / 3238
GO:0055114 oxidation reduction process 4.2e^-21 154 / 831
GO:0009653 anatomical structure morphogenesis 0.99 78 / 1074
GO:0061061 muscle structure development 0.90 34 / 208
GO:0048869 cellular development 1.00 90 / 1298
GO:0022607 cellular component assembly 1.00 47 / 593
GO:0006996 organelle organization 1.00 64 / 1015
GO:0048646 anatomical structure formation 0.99 40 / 388
GO:0032989 cellular component morphogenesis 0.98 50 / 498
GO:0030154 cell differentiation 1.00 86 / 1221
GO:0070925 organelle assembly 1.00 20 / 110
GO:0030029 actin filament based process 0.34 42 / 240
GO:0007010 cytoskeleton organization 0.97 50 / 405
GO:1902589 single organism organelle organization 1.00 50 / 719
GO:0010927 cellular component assembly involved in morphogenesis 1.00 22 / 89
GO:0042692 muscle cell differentiation 1.00 23 / 113
GO:0048468 cell development 1.00 65 / 782
GO:0030036 actin cytoskeleton organization 0.59 40 / 226
GO:0051146 striated muscle cell differentiation 1.00 22 / 93
GO:0055001 muscle cell development 1.00 22 / 77
GO:0055002 striated muscle cell development 1.00 22 / 72
GO:0031032 actomyosin structure organization 1.00 26 / 84
GO:0030239 myofibril assembly 1.00 20 / 59
GO:0045214 sarcomere organization 1.00e^-10 19 / 42

Figure S3