## **Online Supporting Material**

Gene Symbol	Gene Description	Control Group								WD Group							
GPX1	glutathione peroxidase 1	•															
NOX4	NADPH oxidase 4																
NXN	nucleoredoxin																
PRDX5	peroxiredoxin 5																
ERCC2	excision repair cross-complementing rodent repair deficiency, complementation group 2																
CCS	copper chaperon for superoxid dismutase																
GPX4	glutathione peroxidase 4 (phospolipid hydroperoxidase)																
PRNP	prion protein (p27-30)																
NOXO1	NADPH oxidase organizer 1																
TXNRD3	thioredoxin reductase 3																
GSR	glutathione reductase																
PRDX6	peroxiredoxin 6																
GAB1	GRB-2 associated binding protein 1																
SOD1	superoxide dismutase 1																
PSMB5	proteasome subunit, beta type, 5																
PRDX3	peroxiredoxin 3																
PTGS2	prostaglandin-endoperoxidase synthase 2																
TXNRD1	thioredoxin reductase 1																
NOXA1	NADPH oxidase activator 1																
PTGS1	prostaglandin-endoperoxidase synthase 1																
CAT	catalase																
IDH1	isocitrate dehydrogenase (NADP+), soluble																
PPP1R15B	protein phosphatase 1, regulatory (inhibitory) subunit 15B																
NQO1	NAD(P)H dehydrogenase, quinone 1																

## Supplemental Figure 1

Upregulated oxidative stress related genes in the colon of C57Bl/6J mice after 6 mo feeding of WD (n=8) compared to controls (n=8). Heat map generated by GSEA displays expression levels of oxidative stress genes that were significantly upregulated by the WD at 6 mo. The expression levels of genes significantly modified are color-coded red for high expression and blue for low expression. Significance was determined using a nominal *P*-value < 0.05 and FDR < 0.25.