

Supplementary Materials:

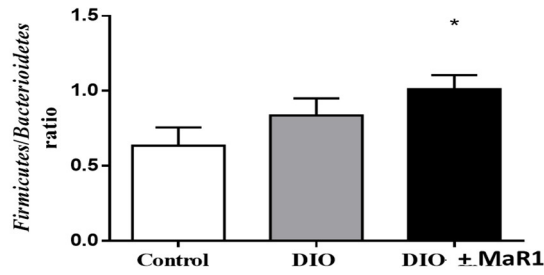


Figure S1. *Firmicutes/Bacteroidetes* ratio in Control and DIO mice treated by oral gavage with Maresin 1 (MaR1; 50 µg/kg/day) or treated with vehicle for 10 days. Data are expressed as mean ± SE (n=7-8). (□) Control; (■) DIO; (■) DIO+ MaR1. * $p < 0.05$ vs. Control.

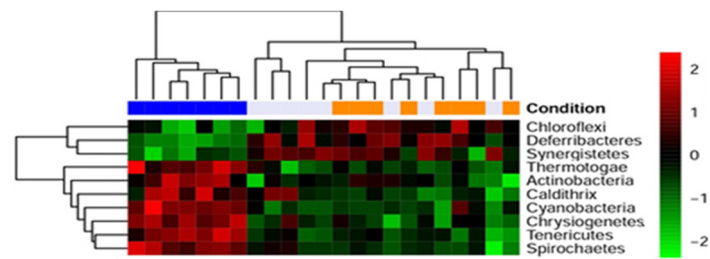


Figure S2. Heat map illustrating the relative abundance of the most different *Phyla* according to treatment group. (■) Control; (■) DIO; (■) DIO+MaR1. In the heatmap, red and green indicate high and low abundance respectively relative to the mean abundance of all samples for each *Phyla*. DIO mice were treated by oral gavage with Maresin 1 (MaR1; 50 µg/kg/day) for 10 days.

Table S1. Taqman assays used for the gene expression analyses.

Name	Gen	TaqMan probe
Interleukin 6	<i>Il-6</i>	Mm00446190_m1
Interleukin 1 beta	<i>Il-1β</i>	Mm00434228_m1
Monocyte chemoattractant protein 1	<i>Mcp-1</i>	Mm00441242_m1
Tumor Necrosis Factor alpha	<i>Tnf-α</i>	Mm00443258_m1
18S ribosomal RNA	<i>18S</i>	Mm03928990_g1

Table S2. Differential bacterial taxonomic profile at the *Phylum* level in DIO *vs.* Control and DIO+MaR1 *vs.* Control mice.

Down-regulated DIO <i>vs.</i> Control				Down-regulated DIO+MaR1 <i>vs.</i> Control		
<i>Phylum</i>	LogFC	<i>p</i>	adj. <i>p</i> Value	LogFC	<i>p</i>	adj. <i>p</i> Value
<i>Tenericutes</i>	-3.316	<0.001	<0.001	-3.542	<0.001	<0.001
<i>Caldithrix</i>	-2.358	0.001	0.003	-1.894	0.005	0.011
<i>Spirochaetes</i>	-2.217	<0.001	<0.001	-2.160	<0.001	<0.001
<i>Verrucomicrobia</i>	-1.862	0.050	0.087	-2.468	0.011	0.022
<i>Chrysiogenetes</i>	-1.470	<0.001	<0.001	-1.539	<0.001	<0.001
<i>Thermotogae</i>	-1.328	<0.001	<0.001	-1.610	<0.001	<0.001
<i>Cyanobacteria</i>	-1.039	<0.001	<0.001	-1.186	<0.001	<0.001
<i>Actinobacteria</i>	-0.770	0.002	0.005	-0.743	0.003	0.007

Up-regulated DIO <i>vs.</i> Control				Up-regulated DIO+ MaR1 <i>vs.</i> Control		
<i>Phylum</i>	LogFC	<i>p</i>	adj. <i>p</i> Value	LogFC	<i>p</i>	adj. <i>p</i> Value
<i>Proteobacteria</i>	0.225	0.334	0.467	0.480	0.046	0.065
<i>Firmicutes</i>	0.385	0.106	0.171	0.556	0.023	0.037
<i>Chloroflexi</i>	0.605	0.003	0.007	0.442	0.025	0.037
<i>Nitrospirae</i>	0.671	0.040	0.077	0.745	0.024	0.037
<i>Synergistetes</i>	0.935	0.005	0.011	1.667	<0.001	<0.001
<i>Deferribacteres</i>	3.508	<0.001	<0.001	3.809	<0.001	<0.001

Negative Log Fold Change (LogFC) was related to lower representation in DIO or DIO+MaR1 compared to Control group, whereas positive LogFC corresponds to those *Phyla* that were increased in DIO or DIO+MaR1 compared with Control mice. *Phyla* were organized by their LogFC. DIO mice were treated by oral gavage with Maresin 1 (MaR1; 50 µg/kg/day) for 10 days.

Table S3. Differential bacterial taxonomic profile at the *Genus* level in DIO vs. Control mice.

Down-regulated in DIO vs. Control			Up-regulated in DIO vs. Control		
<i>Genus</i>	LogFC	<i>p</i>	<i>Genus</i>	LogFC	<i>p</i>
<i>Anaeroplasma</i>	-7.855	6.99 ×10 ⁻¹¹	<i>Caldilinea</i>	0.484	0.043
<i>Sutterella</i>	-7.764	2.98 ×10 ⁻⁰⁹	<i>Moraxella</i>	0.641	0.033
<i>Johnsonella</i>	-7.137	3.74 ×10 ⁻¹⁷	<i>Deferribacter</i>	0.724	0.023
<i>Coprococcus</i>	-6.327	7.67 ×10 ⁻⁰⁶	<i>Methylobacterium</i>	0.802	0.029
<i>Allobaculum</i>	-6.151	2.27 ×10 ⁻⁰⁶	<i>Ehrlichia</i>	0.819	0.032
<i>Anaerostipes</i>	-6.067	6.59 ×10 ⁻¹¹	<i>Deinococcus</i>	0.836	0.026
<i>Limnobacter</i>	-5.800	3.63 ×10 ⁻⁰⁸	<i>Microcoleus</i>	0.854	0.010
<i>Desulfosarcina</i>	-5.609	2.62 ×10 ⁻⁰⁸	<i>Amoebophilus</i>	0.889	0.005
<i>Brachyspira</i>	-5.035	2.03 ×10 ⁻¹¹	<i>Paenibacillus</i>	0.900	0.002
<i>Bifidobacterium</i>	-4.636	2.78 ×10 ⁻⁰⁹	<i>Streptomyces</i>	0.904	0.006
<i>Turicibacter</i>	-4.396	6.05 ×10 ⁻⁰⁴	<i>Adlercreutzia</i>	0.955	0.017
<i>Geobacter</i>	-4.185	1.26 ×10 ⁻⁰⁵	<i>Dehalobacterium</i>	0.969	0.029
<i>Roseburia</i>	-3.873	5.55 ×10 ⁻⁰⁴	<i>Streptococcus</i>	1.085	0.001
<i>Novispirillum</i>	-3.805	3.41 ×10 ⁻⁰³	<i>Oscillospira</i>	1.162	0.005
<i>Sarcina</i>	-3.800	1.15 ×10 ⁻⁰²	<i>Pseudomonas</i>	1.183	0.013
<i>Pseudobutyriovibrio</i>	-3.653	1.31 ×10 ⁻⁰³	<i>Gluconobacter</i>	1.260	0.038
<i>Anaerovibrio</i>	-3.620	2.35 ×10 ⁻⁰⁸	<i>Enterobacter</i>	1.429	0.035
<i>Lachnobacterium</i>	-3.512	1.59 ×10 ⁻⁰⁵	<i>Flavobacterium</i>	1.436	0.003
<i>Dysgonomonas</i>	-3.418	3.94 ×10 ⁻¹¹	<i>Helicobacter</i>	1.460	<0.001
<i>Prostheco bacter</i>	-3.377	2.45 ×10 ⁻⁰²	<i>Desulfovibrio</i>	1.476	0.001
<i>Acholeplasma</i>	-3.171	1.25 ×10 ⁻⁰⁴	<i>Slackia</i>	1.487	0.031
<i>Mesoplasma</i>	-3.134	2.69 ×10 ⁻⁰⁴	<i>Kitasatospora</i>	1.496	0.016
<i>Luteolibacter</i>	-3.076	4.24 ×10 ⁻⁰²	<i>Pedobacter</i>	1.502	<0.001
<i>Legionella</i>	-3.049	2.62 ×10 ⁻⁰⁹	<i>Chromatium</i>	1.520	0.002
<i>Uliginosibacterium</i>	-2.716	9.35 ×10 ⁻⁰⁶	<i>Alkaliphilus</i>	1.717	0.000
<i>Eggerthella</i>	-2.661	7.98 ×10 ⁻⁰⁵	<i>Thermobaculum</i>	1.770	0.003
<i>Eubacterium</i>	-2.638	6.29 ×10 ⁻⁰⁵	<i>Holdemania</i>	1.787	0.005

Table S3 continuation

Down-regulated in DIO vs. Control			Up-regulated in DIO vs. Control		
<i>Genus</i>	LogFC	<i>p</i>	<i>Genus</i>	LogFC	<i>p</i>
<i>Lysobacter</i>	-2.603	2.01 ×10 ⁰²	<i>Ruminococcus</i>	1.807	<0.001
<i>Caldithrix</i>	-2.444	6.28 ×10 ⁰⁴	<i>Capnocytophaga</i>	1.860	<0.001
<i>Pectinatus</i>	-2.435	3.28 ×10 ⁰⁵	<i>Segetibacter</i>	2.018	<0.001
<i>Marinitoga</i>	-2.371	4.30 ×10 ⁰⁷	<i>Rhodothermus</i>	2.051	<0.001
<i>Desulfotomaculum</i>	-2.334	2.83 ×10 ⁰⁴	<i>Escherichia</i>	2.068	0.029
<i>Prevotella</i>	-2.331	1.17 ×10 ⁰²	<i>Caldanaerobacter</i>	2.069	<0.001
<i>Faecalibacterium</i>	-2.210	1.79 ×10 ⁰⁴	<i>Smithella</i>	2.196	<0.001
<i>Parapedobacter</i>	-2.135	2.13 ×10 ⁰⁵	<i>Sphaerisporangium</i>	2.218	<0.001
<i>Mannheimia</i>	-2.119	5.64 ×10 ⁰⁴	<i>Corynebacterium</i>	2.274	<0.001
<i>Petrotoga</i>	-2.039	1.24 ×10 ⁰³	<i>Gluconacetobacter</i>	2.283	<0.001
<i>Rhodospirillum</i>	-2.023	2.48 ×10 ⁰²	<i>Lachnospira</i>	2.303	0.001
<i>Sedimentibacter</i>	-1.932	7.17 ×10 ⁰⁶	<i>Rikenella</i>	2.325	<0.001
<i>Heliorestis</i>	-1.803	2.49 ×10 ⁰⁵	<i>Odoribacter</i>	2.380	<0.001
<i>Muricauda</i>	-1.792	1.64 ×10 ⁰⁶	<i>Gillisia</i>	2.478	<0.001
<i>Selenomonas</i>	-1.762	5.57 ×10 ⁰⁴	<i>Caloramator</i>	2.616	<0.001
<i>Acinetobacter</i>	-1.565	1.92 ×10 ⁰³	<i>Vagococcus</i>	3.060	<0.001
<i>Desulfurispirillum</i>	-1.556	1.63 ×10 ⁰⁵	<i>Acidaminobacter</i>	3.127	<0.001
<i>Coralimargarita</i>	-1.516	2.01 ×10 ⁰²	<i>Peptococcus</i>	3.289	<0.001
<i>Microbacterium</i>	-1.400	1.94 ×10 ⁰³	<i>Enterococcus</i>	3.727	<0.001
<i>Butyrivibrio</i>	-1.357	4.22 ×10 ⁰²	<i>Bilophila</i>	3.758	<0.001
<i>Stenotrophomonas</i>	-1.282	1.77 ×10 ⁰²	<i>Mucispirillum</i>	3.793	<0.001
<i>Candidatus Phytoplasma</i>	-1.249	8.32 ×10 ⁰⁴	<i>Aquimarina</i>	4.552	<0.001
<i>Butyricimonas</i>	-1.229	5.14 ×10 ⁰³	<i>Anaerotruncus</i>	4.761	<0.001
<i>Emticicia</i>	-1.182	5.08 ×10 ⁰³	<i>Lactococcus</i>	8.302	<0.001
<i>Caldicellulosiruptor</i>	-1.169	3.32 ×10 ⁰³			
<i>Luteibacter</i>	-1.165	2.26 ×10 ⁰²			
<i>Kribbella</i>	-1.159	2.39 ×10 ⁰²			
<i>Bradyrhizobium</i>	-1.151	1.09 ×10 ⁰³			
<i>Parabacteroides</i>	-1.125	3.97 ×10 ⁰³			
<i>Paraprevotella</i>	-0.982	3.58 ×10 ⁰²			
<i>Dolichospermum</i>	-0.978	2.33 ×10 ⁰²			
<i>Olivibacter</i>	-0.975	6.84 ×10 ⁰⁴			
<i>Marinobacter</i>	-0.917	2.95 ×10 ⁰³			
<i>Dyadobacter</i>	-0.877	8.02 ×10 ⁰³			
<i>Ferroidobacterium</i>	-0.796	2.15 ×10 ⁰²			
<i>Rhodobacter</i>	-0.786	3.47 ×10 ⁰²			
<i>Thermus</i>	-0.742	7.25 ×10 ⁰³			

Negative Log Fold Change (LogFC) was related to lower representation in DIO compared to Control whereas Positive LogFC corresponds to those *Genera* that were increased in DIO compared with Control. *Genera* were organized by their LogFC.