

**Supplemental information**

**Deficiency of miRNA-149-3p shaped gut microbiota  
and enhanced dextran sulfate sodium-induced colitis**

**Qingqing Feng, Yuanqiang Li, Hongli Zhang, Ziwei Wang, Xiaobo Nie, Denglin Yao, Lu Han, Wei-Dong Chen, and Yan-Dong Wang**

**Table S1. The information of antibodies**

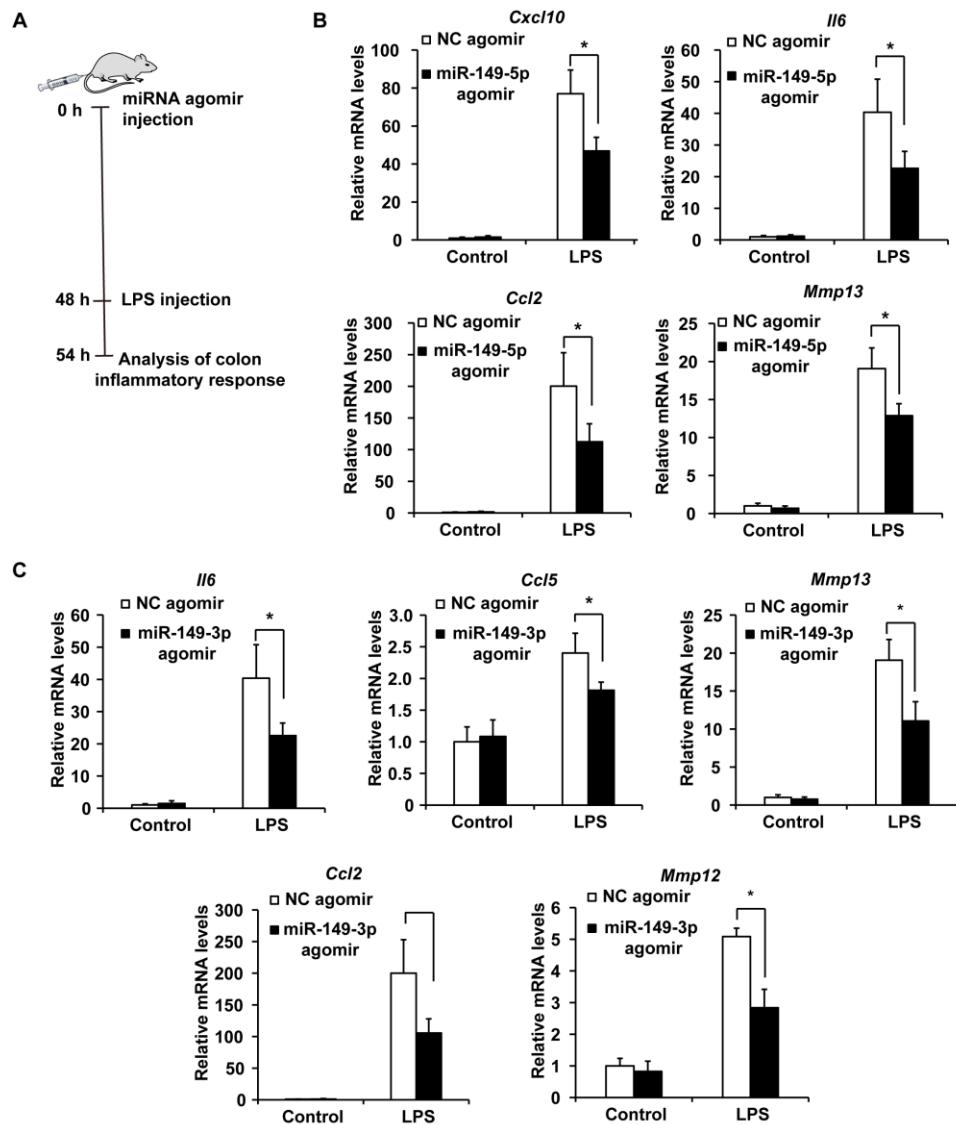
Antibodies	Source	Identifier	Dilution	Origin
p-I $\kappa$ B $\alpha$ (Ser32/36)	Cell Signaling Technology	9246s	1:1000	Danvers, USA.
I $\kappa$ B $\alpha$	Cell Signaling Technology	9242s	1:1000	Danvers, USA.
p-AMPK $\alpha$ (Thr172)	Cell Signaling Technology	2531s	1:1000	Danvers, USA.
AMPK $\alpha$	Cell Signaling Technology	2532s	1:1000	Danvers, USA.
$\beta$ -actin	TransGen Biotech	HC201	1:1000	Beijing, China
Anti-Rabbit IgG	LABLEAD	S0101	1:2000	Beijing, China
Anti-Mouse IgG	LABLEAD	S0100	1:2000	Beijing, China

**Table S2. Primers for qRT-PCR**

Species	Gene	Forward primer	Reverse primer
Human	<i>ACTB</i>	ACTGGGACGACATGGAGAAA	CTGGATAGCAACGTACATGG
	<i>CCL22</i>	GCGTGGTGGTGTGCTAACCTTC	GAGGTGACCAAGGGTGACAG
	<i>CCL5</i>	CCAGCAGTCGTCTTGTAC	CTCTGGGTTGGCACACACTT
	<i>COX2</i>	CAATCATTCCTCCTGTGCCTGATGATTG	GTGCTGGCAAAGAATGCAA
	<i>CXCL17</i>	GATTGGTCCCTGAGAGCCCC	GGTGCCTTGGTGTCTGTTT
	<i>ICAM1</i>	GAGCTGTTGAGAACACCTC	ATAGGTGACTGTGGGTTCA
	<i>IL17A</i>	ATCTCCACCGCAATGAGGAC	CTTGCTGGATGGGGACAGAG
	<i>IL1A</i>	GGAGCTTGTCACCCCAACT	TCCGAAGTCAAGGGCTAGA
	<i>IL1B</i>	AACCTCTCGAGGCACAAGG	CATTGCCACTGTAATAAGCCATCA
	<i>IL6</i>	GATGAGTACAAAAGTCCTGA	GCCCATGCTACATTGCCGA
	<i>CXCL8</i>	CTTCAGAGACAGCAGAGCAC	GTTCTTAGCACTCCTGGC
	<i>NOS2</i>	GATAAGTGACATAAGTGACC	CTGAGGTTGTGATACTGAAG
	<i>CXCL10</i>	TCCACGTGTTGAGATCATTGCT	TGCATCGATTTGCTCCCCT
	<i>CCL2</i>	TAGCAGCCACCTTCATTCCC	TGCTTGGGTCAGCACAGAT
	<i>MMP1</i>	TTCAACCAGGCCAGGTATT	TGTCATCCTGAGCTAGCTGA
	<i>MMP12</i>	TGGCAAAGGTGGAATCCTAG	CATTACGGCCTTGGATCAC
	<i>MMP2</i>	AATACCATCGAGACCATGCG	GATCAGGTGTAGCCAATG
	<i>MMP7</i>	AGGCATGAGTGAGCTACAGT	CACATCTGGCTTCTGCATT
	<i>TNFA</i>	GCGCTC CCCAAGAAGA CAGG	GCTGATTAGAGAGAGGTCCC
Mouse	<i>36b4</i>	GCCCTGCACTCTCGCTTCT	CAACTGGGCACCGAGGCAACAGTTG
	<i>Ptgs2</i>	TGGTGCCTGGTCTGATGATG	GCAATGCGGTTCTGATACTG
	<i>Icam1</i>	TGTGACCAGCCAAGTTGTT	TGGAGTCCAGTACACGGTGA

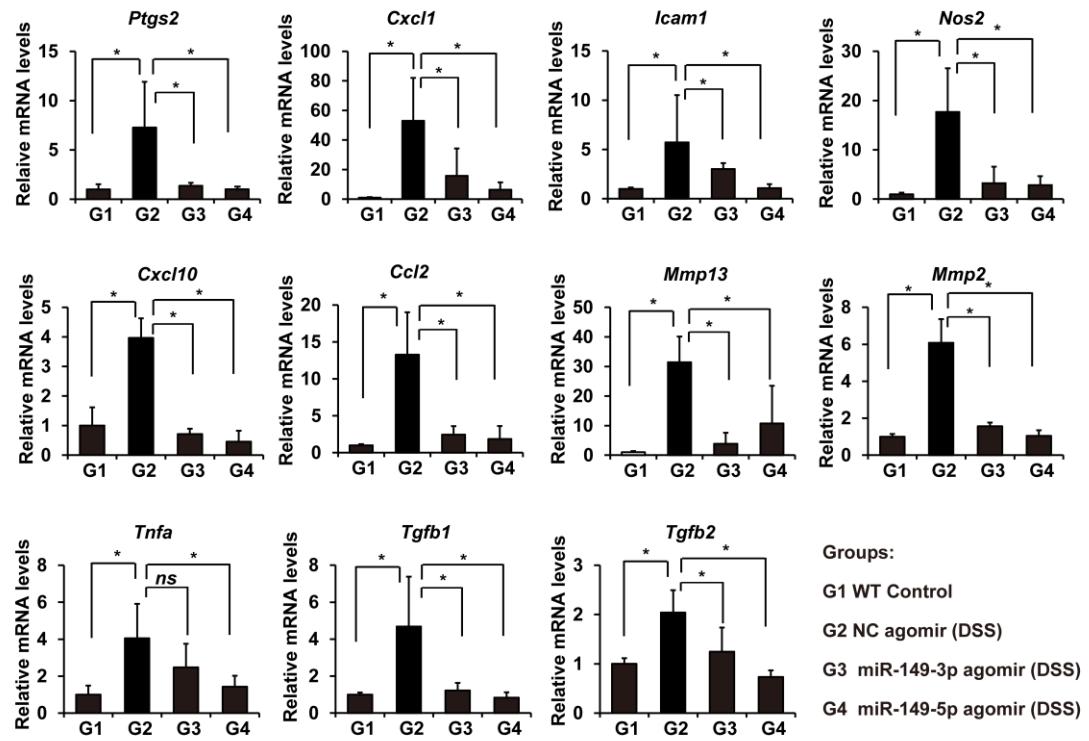
<i>Cxcl1</i>	ACTCAAGAATGGTCGCGAGG	GTGCCATCAGAGCAGTCTGT
<i>Tgfb1</i>	GTCACTGGAGTTGTACGGCA	GGGGCTGATCCCGTTGATT
<i>Il6</i>	AAAACAATCTGAAACTTCCA	CAGAAGACCAGAGGAAATT
<i>Il2</i>	GGAACCTGAAACTCCCCAGG	AATCCAGAACATGCCGCAGA
<i>Ccl2</i>	ATGCTTCTGGCCTGCTGTT	CAGCTTCTTGGAACACCTG
<i>Tgfb2</i>	CCCCGGAGGTGATTCCATC	ATGGCATTTCGGAGGGGAG
<i>Cxcl10</i>	ATGACGGGCCAGTGAGAATG	GAGGCTCTCTGCTGTCCATC
<i>Mmp12</i>	TGATGGCAAAGGTGGTACAC	CCAAGGAATGGCCAAGTTCA
<i>Mmp13</i>	GGCTCCGAGAAATGCAATCT	CCACTTCAGAATGGGACATA
<i>Ccl5</i>	GCTGCTTGCCCTACCTCTCC	TCGAGTGACAAACACGACTGC
<i>Il1a</i>	TTCCCTCAACCAAACCTATAT	ACGGGCTGGTCTTCTCCTTG
<i>Tnfa</i>	CATCAGTTCTATGGCCCAGAC	GGAGTAGACAAGGTACAACCC
<i>Mmp2</i>	CATCGCCCATCATCAAGTTC	ATGGTCTCGATGGTGTCTG

**Figure S1**



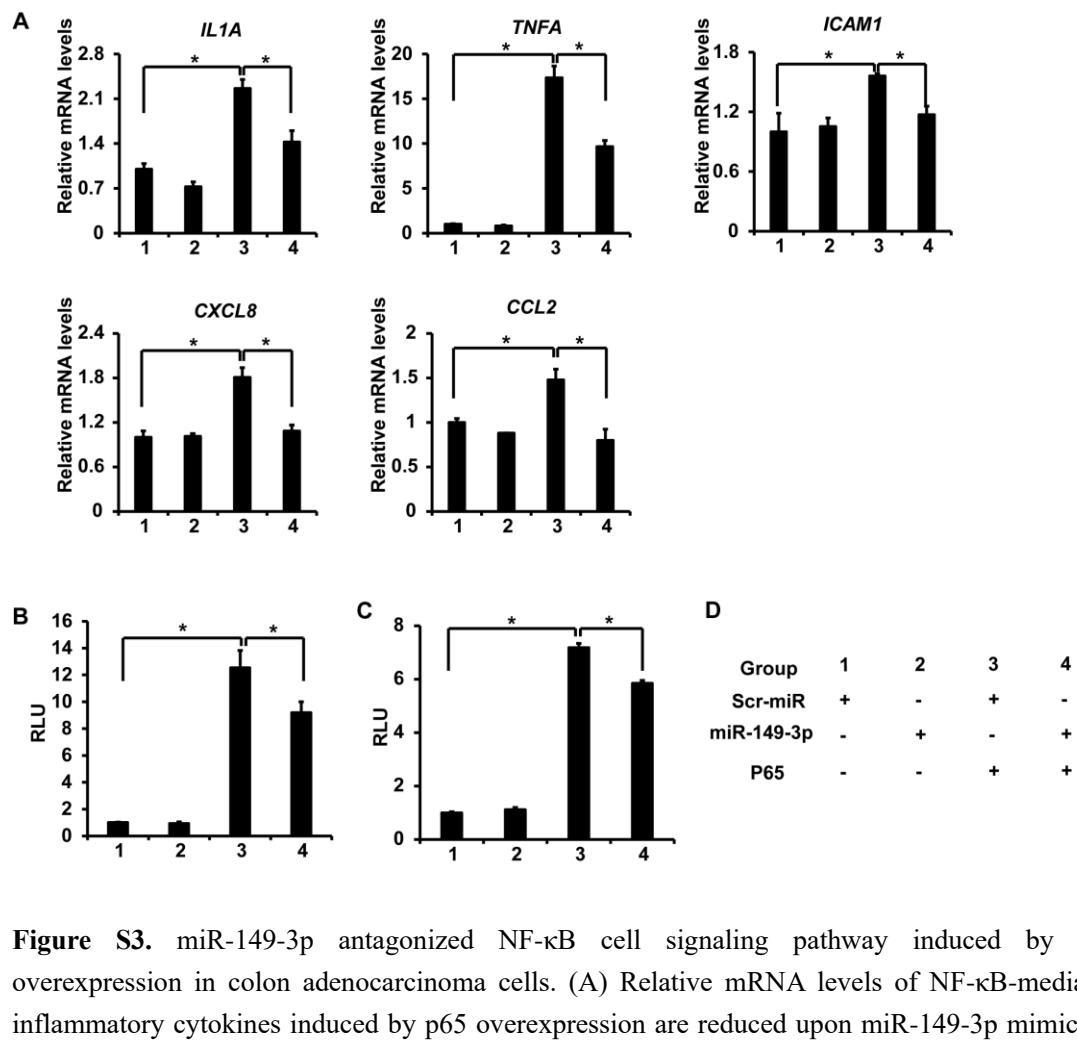
**Figure S1.** miR-149-5p and miR-149-3p regulate LPS-induced colon inflammatory response *in vivo*. (A) Schematic diagram of the experimental process. (B) After LPS administration for 6h, relative mRNA levels of pro-inflammatory genes from pretreated mouse colon with miRNA negative control and miR-149-5p agomirs ( $n=6$ ). (C) miR-149-3p agomirs repressed LPS-induced inflammatory gene levels in mouse colon tissues ( $n = 6$ ). \* $P < 0.05$ .

**Figure S2**



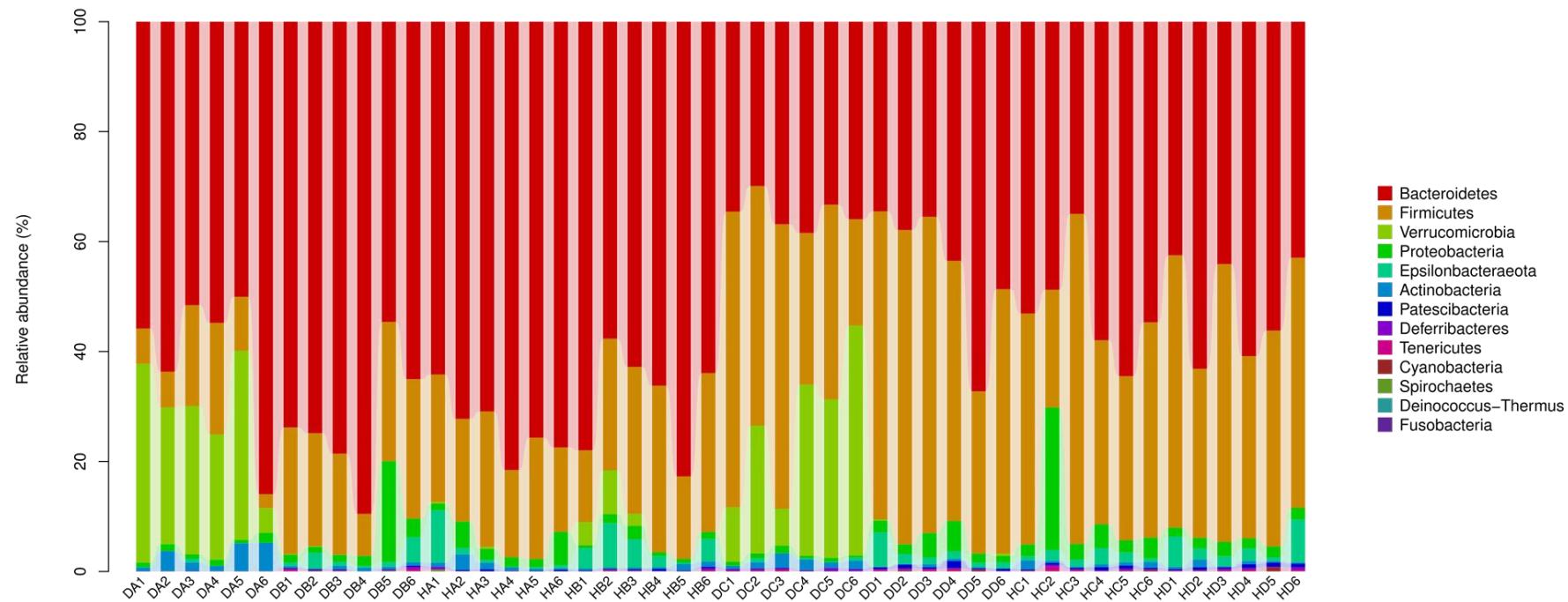
**Figure S2.** miR-149-5p and miR-149-3p agomirs regulate DSS-induced proinflammatory genes in mouse colons (n = 5), \* $P < 0.05$ ; ns, no significant difference.

**Figure S3.**



**Figure S3.** miR-149-3p antagonized NF- $\kappa$ B cell signaling pathway induced by p65 overexpression in colon adenocarcinoma cells. (A) Relative mRNA levels of NF- $\kappa$ B-mediated inflammatory cytokines induced by p65 overexpression are reduced upon miR-149-3p mimics in Caco2 cells (n=3). (B-C) miR-149-3p mimics lessened the luciferase signal of NF- $\kappa$ B activity induced by p65 overexpression in Caco2 (B) and SW480 cells (C) (n=3). RLU, relative luciferase units. (D) Group information. \*P < 0.05.

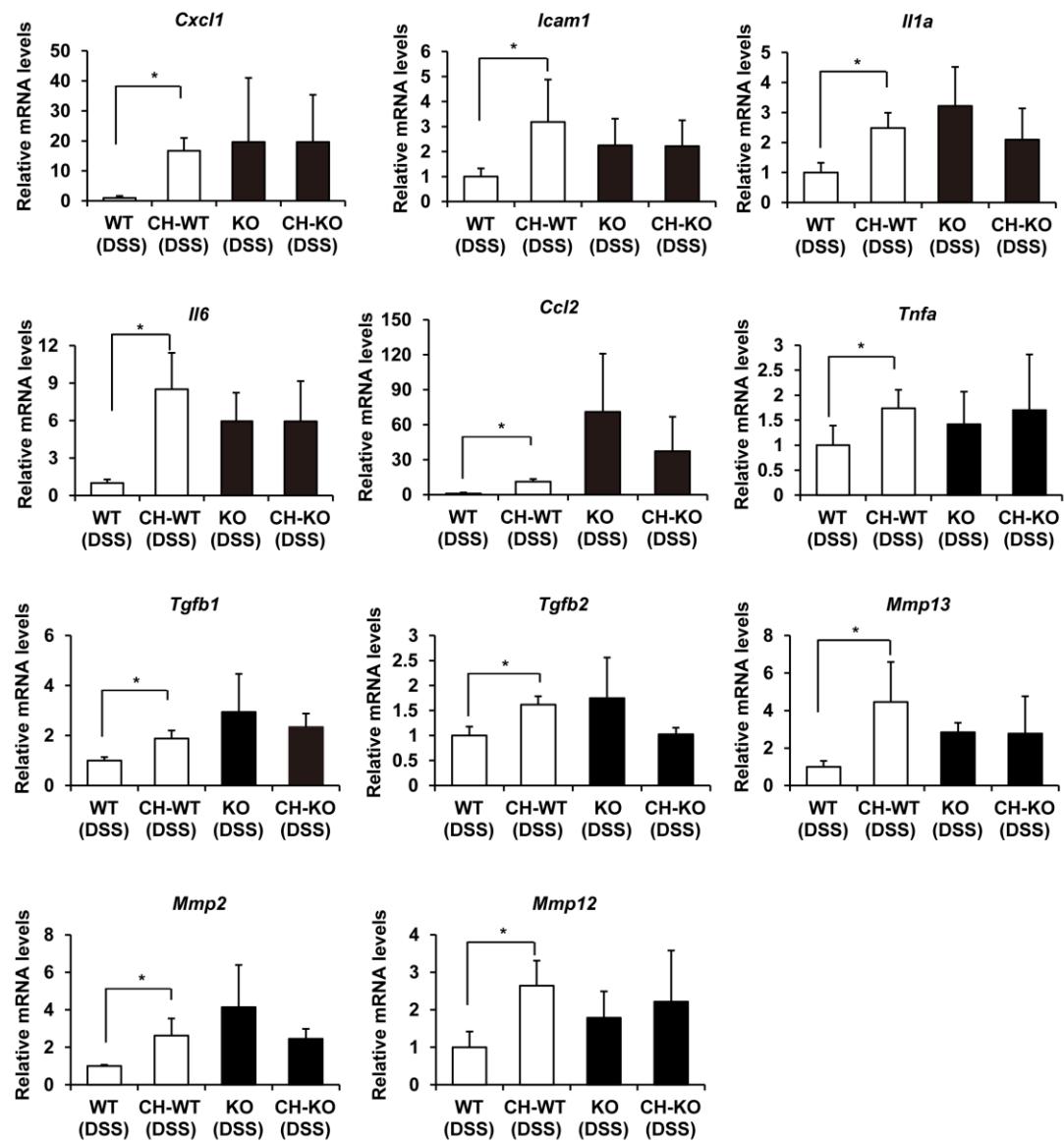
**Figure S4.**



**Figure S4.** Fecal microbiota taxa analysis from WT and miR-149\*<sup>-/-</sup> mice at phylum. To allow natural transfer of the microbiota, WT and miR-149\*<sup>-/-</sup> males at 4-weeks were co-housed. As a control, single type control group was fed at the same conditions when the mice reached 8 weeks, then 2% of DSS was given for 7 days, fecal microbiota were analyzed based on 16S RNA sequencing (n=6). DA1-DA6, WT control group (WT), DB1-DB6, miR-149\*<sup>-/-</sup> control group (KO), HA1-HA6, WT mice co-housed with miR-149\*<sup>-/-</sup> mice (CH-WT), HB1-HB6, miR-149\*<sup>-/-</sup> mice co-housed with WT mice (CH-KO), DC1-DC6, DSS treated WT

control group (WT (DSS)), DD1-DD6, DSS-treated miR-149<sup>\*/-</sup> control group (WT (DSS)), HC1-HC6, DSS-treated CH-WT group (CH-WT (DSS)), HD1-HD6, DSS-treated CH-KO group (CH-KO (DSS)).

**Figure S5.**



**Figure S5.** Relative mRNA levels of inflammatory cytokines induced by DSS administration are increased in CH-WT mice (n= 5). \* $P < 0.05$ .