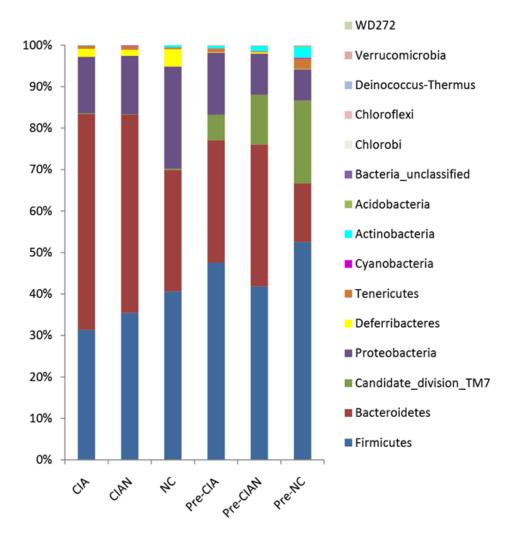
## **Supplementary information**

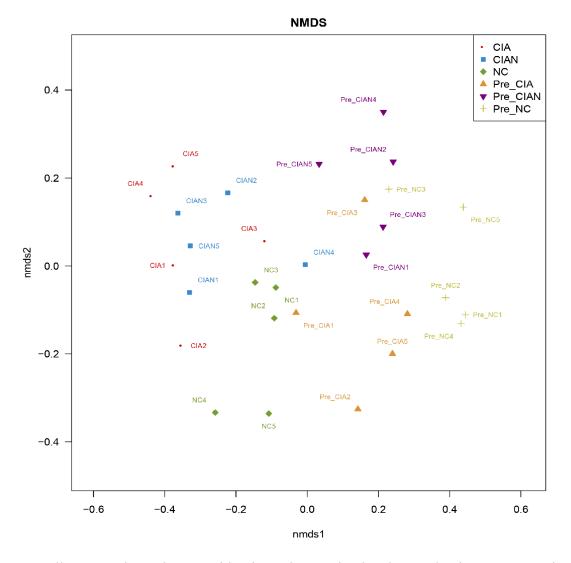
Role of the Gut Microbiome in Modulating Arthritis Progression in Mice

Xiaofei Liu, Benhua Zeng, Juan Zhang, Wenxia Li, Fangxiang Mou, Heng Wang,Qinghua Zou, Bing Zhong, Like Wu, Hong Wei, &Yongfei Fang

Supplementary Figure 1. Bacterial species compositions of microbiota communities at the phylum level.



Phyla are plotted according to their relative abundance within each microbiota community, as determined by the number of reads assigned to each phylum. Bars represent the relative abundances of phyla in individual groups.



Supplementary Figure 2. Non-metric multidimensional scaling of OTUs.

Overall, OTUs showed  $\geq$  97% identity atthe species level scored using Bray–Curtis similarity analysis. Samples clustered according to CIA-susceptibility and collagen induction. Analysis of similarity (ANOSIM) showed that microbiota composition differed significantly among groups classified according to CIA-susceptibility and collagen induction.

Supplementary Table 1. Analysis of differentially abundant taxa prior to arthritis onset.<sup>a</sup>

Differentially abundant features analysis prior to arthritis onset								
Genus	pre-CIA		pre-CIAN		Between-group comparisons p Values			
	Mean (%)	s.d	Mean (%)	s.d	Pre-CIA vs Pre-CIAN			
Enterorhabdus	0.0036	0.0009	0.0107	0.0031	0.0202*			
Alistipes	0.0919	0.0223	0.1819	0.0364	0.0249*			
Candidatus_Saccharimo	0.0809	0.0269	0.1770	0.0288	0.0125*			
Anaerotruncus	0.0023	0.0006	0.0148	0.0040	0.0030**			
Incertae_Sedis	0.0007	0.0004	0.0044	0.0015	0.0126*			
Intestinimonas	0.0017	0.0004	0.0057	0.0014	0.0065**			
Lactobacillus	0.4382	0.0710	0.1907	0.0645	0.0079**			
Desulfovibrio	0.0309	0.0215	0.1077	0.0266	0.0192*			

<sup>a</sup>Symbols indicate significantly different abundances. Abundances with matching symbols were not significantly different from each other. Pre-, prior to arthritis onset; CIA, mice with collagen-induced arthritis; CIAN, mice without arthritis after collagen induction.

Supplementary	Table 2.Analysis	of differentially	abundant taxa	after arthritis
onset. <sup>a</sup>				

Genus	CIA		CIAN		NC		Between-group comparisons p Values	
	Mean (%)	s.d	Mean (%)	s.d	Mean (%)	s.d	CIA vs NC	CIA vs CIAN
Enterorhabdus	0.0011	0.0003	0.0003	0.0002	0.0014	0.0008	0.0008**	0.0267 *
Alistipes	0.0938	0.0090	0.1554	0.0115	0.1170	0.0271	0.5591	0.0008 **
Desulfovibrio	0.0257	0.0050	0.0407	0.0212	0.0054	0.0017	0.0017 **	0.5803
prevotella	0.0252	0.0056	0.0367	0.0278	0.0012	0.0011	0.0011 **	0.7743
Myroides	0.0000	0.0000	0.0001	0.0001	0.0001	0.0000	0.0000 **	0.4240
Odoribacter	0.1085	0.0164	0.1130	0.0217	0.0476	0.0106	0.0052 **	0.9150
Parabacteroides	0.0077	0.0027	0.0084	0.0040	0.0015	0.0003	0.0238 *	0.9282
Rikenella	0.0006	0.0004	0.0003	0.0001	0.0035	0.0014	0.0407 *	0.6695
Acetatifactor	0.0008	0.0003	0.0008	0.0005	0.0001	0.0001	0.0259 *	0.9669
Blautia	0.0841	0.0227	0.0890	0.0255	0.0288	0.0077	0.0206 *	0.9256
Brochothrix	0.0000	0.0000	0.0000	0.0000	0.0002	0.0001	0.0227 *	1.0000
Coprococcus	0.0146	0.0063	0.0050	0.0009	0.0017	0.0007	0.0374 *	0.1401
ncertae_Sedis	0.0047	0.0016	0.0051	0.0017	0.0011	0.0003	0.0003**	0.6297
Lactococcus	0.0009	0.0004	0.0020	0.0009	0.0043	0.0017	0.0415 *	0.2788
Ruminococcus	0.0074	0.0032	0.0123	0.0082	0.0008	0.0004	0.0355 *	0.6814
Streptococcus	0.0006	0.0001	0.0030	0.0018	0.0053	0.0015	0.0057 **	0.2327
Pseudomonas	0.0002	0.0001	0.0013	0.0005	0.0028	0.0014	0.0623	0.0417*

indicate significantly different abundances (\*p < 0.05;\*\*p < 0.01). <sup>a</sup>Symbols Abundances with matching symbols were not significantly different from each other. CIA, mice with collagen-induced arthritis; CIAN, mice without arthritis after collagen induction; NC, untreated control.