Supplementary Material

**Host-microbiome synergistic control on sphingolipid metabolism by mechanotransduction in model arthritis**

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# SUPPLEMENTARY METHODS

**Microbial Taxa Differential Analysis.** The microbial structure analyses in previous independent data1 confirmed that *Lactobacillus* was more abundant in the CIA than NOCIA arm, while it was significantly reduced by MTX , as it happens now in the MTXMS arm (Table S1, Supplementary Data S6-1). The MS therapy correlates with an increase of *Lactobacillus* compared to either MTX or MTXMS. As it has been reported, some species in the *Lactobacillus* genus*,* such as *L. casei*, *L.* *plantarum* and *L. rhamnosus* are (opportunistic) pathogens2,3. This, however, is not observed in our data. Other species, like *L. delbrueckii*,are probiotics, leading to the dual (eubiotic or pathogenic) functions of *Lactobacillus* (see4). This should be further explored with more details on species classification. *Prevotella,* a recognized player in the onset of rheumatoid arthritis, was expanded in the MTX arm compared to CIA in our previous experiment 1, supporting this same trend in MTXMS versus MS (Table S1).

# SUPPLEMENTARY TABLES

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Genus | Batch\_current | | | | Batch\_previous | | | |
| MS/CIA | MTXMS/CIA | CIA/NOCIA | MS/MTXMS | MS/CIA | MTX/CIA | CIA/NOCIA | MS/MTX |
| *Lactobacillus* | -4.137 | -6.446 | 2.03 | 3.028 | - | -2.021 | 2.708 | 2.504 |
| *Prevotella* | - | 6.887 | - | -3.725 | - | 2.108 | - | - |
| *Allobaculum* | -4.18 | -2.929 | 5.418 | - | 2.757 | 2.429 | - | - |
| *Odoribacter* | - | - | -3.078 | - | - | - | 2.917 | - |
| *Blautia* | - | - | 3.862 | - | 4.695 | 3.369 | -3.453 | - |
| *Phascolarctobacterium* | 5.068 | 5.768 | - | - | - | 3.684 | - | - |
| *Adlercreutzia* | - | - | 2.6 | - | -2.002 | - | - | - |

**Supplementary Table S1.** Differential genera in GI-PBMC integration in our previous experiment (batch1,1) and in the current batch (batch2), highlighted from Supplementary Data S6. Log-converted fold-changes of the differential (34 days versus before therapy) normalized genera abundances.

**REFERENCE**

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