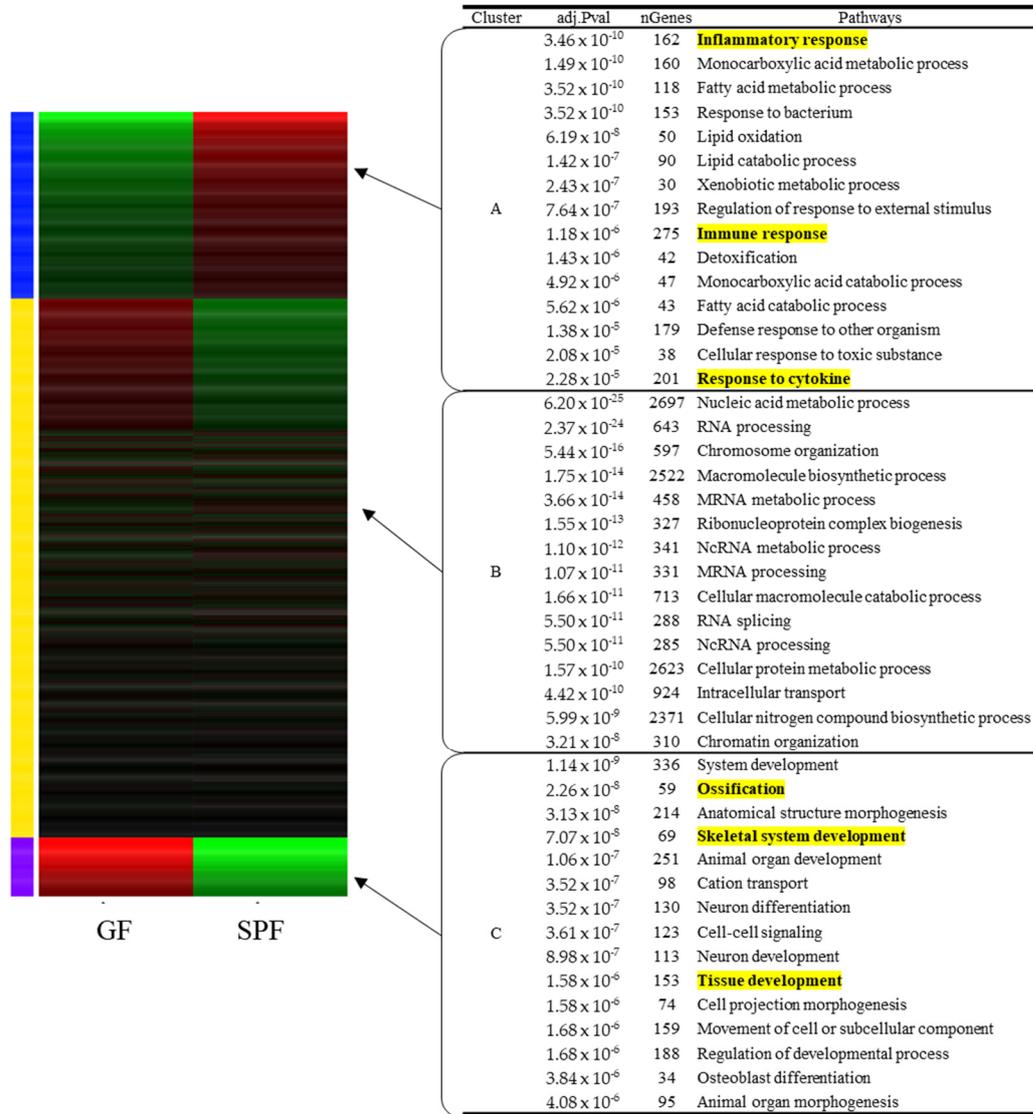


Supplementary figure



Supplementary Figure S1

Effect of the presence or absence of maternal gut microbiome on enriched pathways expressed in fetal-derived chondrocytes.

Enriched pathways in GF-derived and SPF-derived chondrocytes from k-means clusters were annotated by iDEP web application (integrated Differential Expression and Pathway analysis, <http://bioinformatics.sdstate.edu/idep95/>) using gene ontology annotation (GO biological process). Pathways marked in yellow lines were further investigated using quantitative RT-PCR (see text).