## Supplemental Material to:

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The gut microbiota and mucosal homeostasis; colonized at birth or at adulthood, does it matter?

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## SUPPLEMENTARY INFORMATION FOR

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**Figure S1.** Comparison of the temporal expression profiles of genes associated with immune response. Screenshots of detailed model profiles windows for the data of STEM. Only profiles that are statistically significant and are involved in immune functions are shown. Along the top of each window are the temporal expression patterns and the statistical analysis for the p-value based on the permutation test that STEM uses. The coloured boxes at the bottom-left of each window correspond to the model expression profile available in STEM.



**Figure S2.** Transcriptome signatures that distinguishe jejnual mucosa immune responses to the colonizing microbiota in conventionalized and conventionally raised mice. (A) The ingenuity protein-protein interaction network derived by plotting STEM output genes involved in the temporal expression profiles involved in immune response in the jejunum. The identified genes share 76% similarity (indicated with red arrows) with the transcriptional signatures proposed to be regulating the transcriptional changes during conventionalization along the gastrointestinal tract.<sup>1</sup> (B) Heat map of the genes that constitute the core regulatory network.

Reference:

1. El Aidy S, van Baarlen P, Derrien M, Lindenbergh-Kortleve DJ, Hooiveld G, Levenez F, et al. Temporal and spatial interplay of microbiota and intestinal mucosa drive establishment of immune homeostasis in conventionalized mice. Mucosal Immunol 2012; 5:567-79.