**Supplementary Material: to section Materials and Methods**

**Animals**

All C57BL6 mice were bred and maintained under standard conditions and conform to the guidelines for the Care and Use of Laboratory Animals of the National Academy of Karlsruhe, Germany after approval by the institutional Animal Care Committee.

Tamoxifen-inducible villin-Cre dependent kindlin 2 intestine-specific C57BL6 knockout mice were a gift from R. Faessler and propagated for the purpose of this study in the animal facilities of the University of Heidelberg. All mice types were cohoused in the sense that wild-type and kindlin 2(-/-) mice generated in-house by embryonic transfer were kept under identical breeding conditions in the same environment. They received Las Vendi Rod18 complete diet (Soest, Germany) ad libitum. They were kept in conventional caging with ABBEDD LPE-E-001 (Vienna, Austria) bedding at 22° C with a 12h/12h light/dark cycle.

**Description of the colitis cores**

Quantitative evaluation of the UC phenotype included the macroscopic colitis score with determination of total colon weight (including stool content), length, and stool appearance, as well as the histopathological colitis score after hematoxylin and eosin (HE) staining with determination of the extent of inflammation, crypt architecture, hyperemia/edema, and immunocyte infiltration. Histology assessment was performed by three independent investigators in a blinded manner.

**Bacterial 16S rDNA sequencing**

In detail, after purification, extraction and amplification of the bacterial DNA by quantitative real-time PCR, the DNA-concentration was estimated with Nanodrop 2000c Spectrophotometer (NanoDrop Technoligies, Wilmington, DE, USA). Afterwards 454/pyrosequencing (454-GS Junior DNA sequencing platform; Roche Applied Science, Basel, Switzerland) with 16S rDNA specific primers (314f/1061r) was employed. According to the manufacturer-applied initial quality filter, 113405 of 220355 sequences passed for further analysis. The median length of sequences was 667bp. The specific primers included probe-specific sequence-barcodes (MIDs). Afterwards the bioinformatical analysis was performed. Additional quality filter controls were performed: deletion of sequences with following characteristics: > 6 homopolymeres, > 1 “N”-bases, reads < 400bp and > 800bp, reads with average p-value < 25, deletion and trimming of sequences with low q-value. A total amount of 71% of sequences passed all quality filters (80513 raw sequences). Afterwards artificial PCR products consisiting of chimieric 16S rDNA sequences were removed. After all filter processes 78483 reads were found. Reads with identical sequences > 97% were clustered in operational taxonomic unit (OUT). Each OUT was matched with SILVA rRNA reference database (release 119). A total amount of 1333 OTUs was identified.