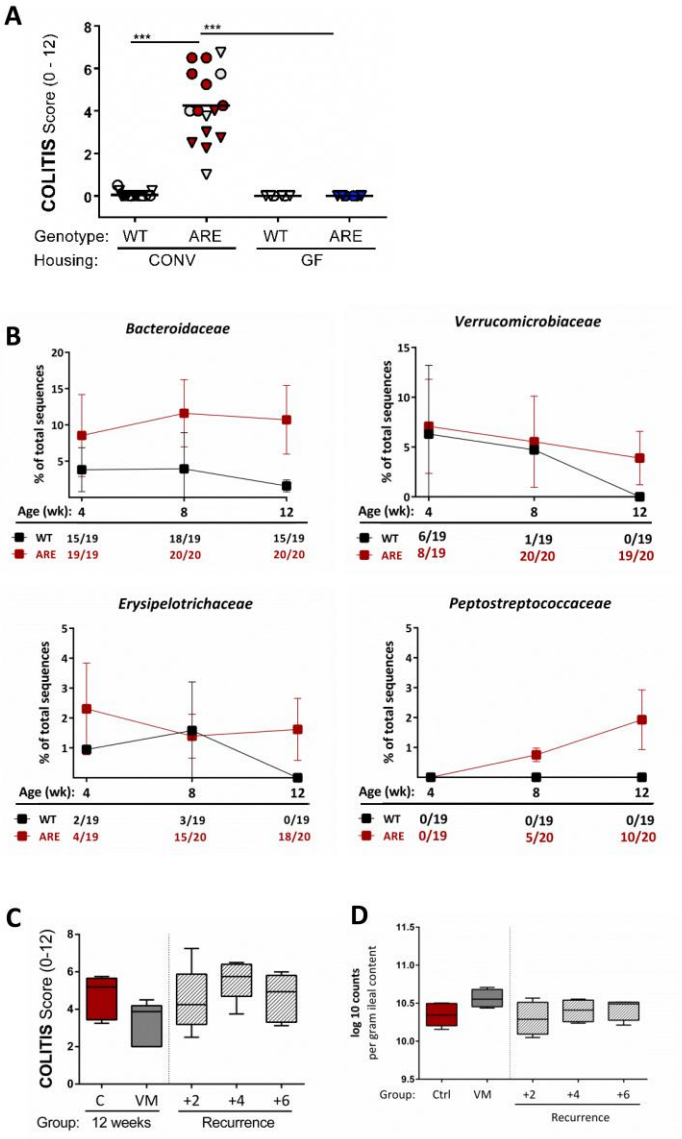
Supplemental Figures:

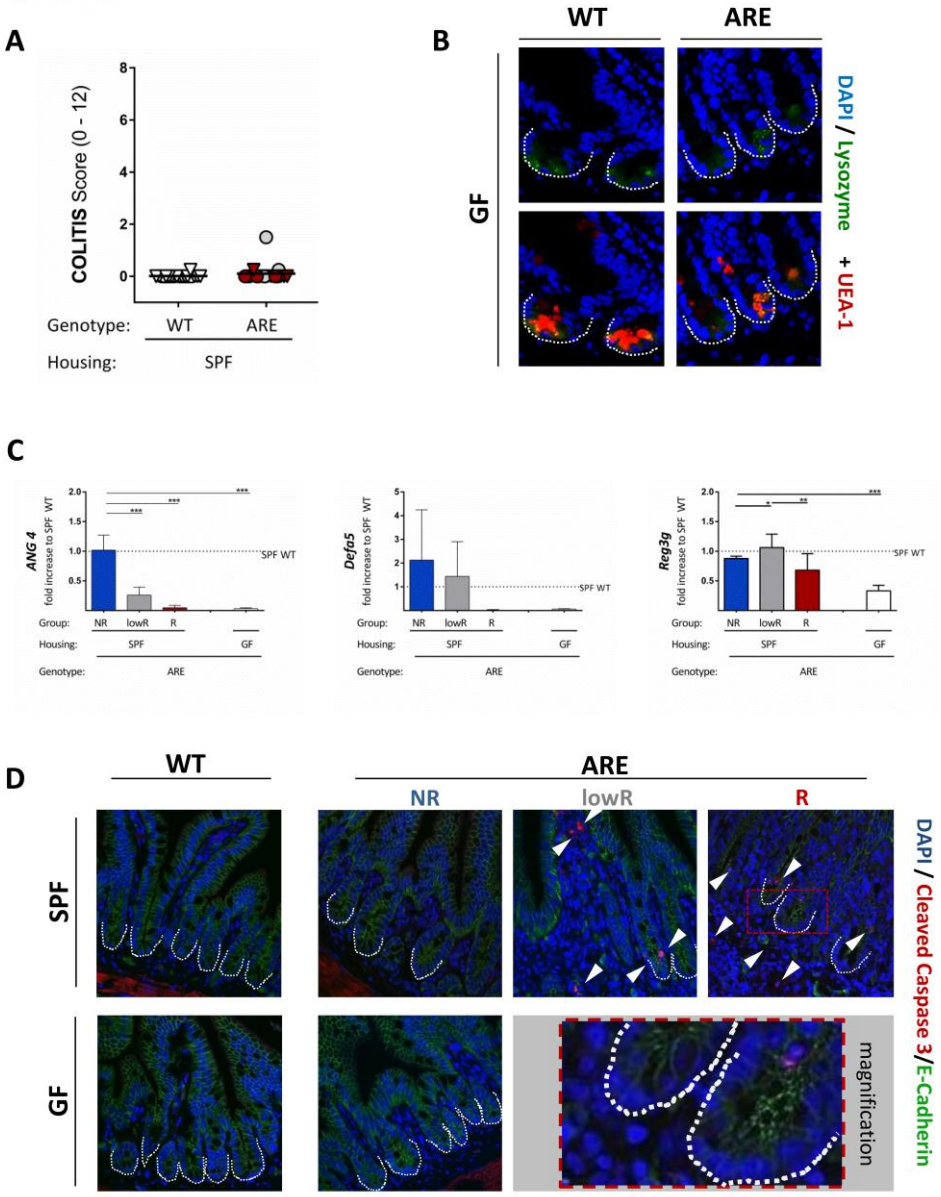
S1: (A) Colitis scores in 18-week-old TNF^{deltaARE} (ARE) and WT littermates in CONV or GF housing. Individuals are color-coded according to ileitis severity: score = 0 (blue); score <4 (grey); score >4 (red). Male mice are displayed as triangles, females as circles. **(B)** Bacterial taxa correlated to TNF^{deltaARE} mice (ARE) or wildtypes (WT) displayed over time. Taxa with a relative sequence abundance <0.5% were excluded from statistical analysis. Prevalence (number of mice positive for a given taxon) is given in the x-axis. **(C)** Colitis scores in TNF^{deltaARE} mice treated for 4 weeks with vancomycin and metronidazole (VM), starting at 8 weeks of age. Recurrence of disease after V/M therapy was followed for 6 weeks (n = 5-6/group). **(D)** Total cell counts (as determined using a THOMA counting chamber).

Supplemental Figures:
Figure S1:



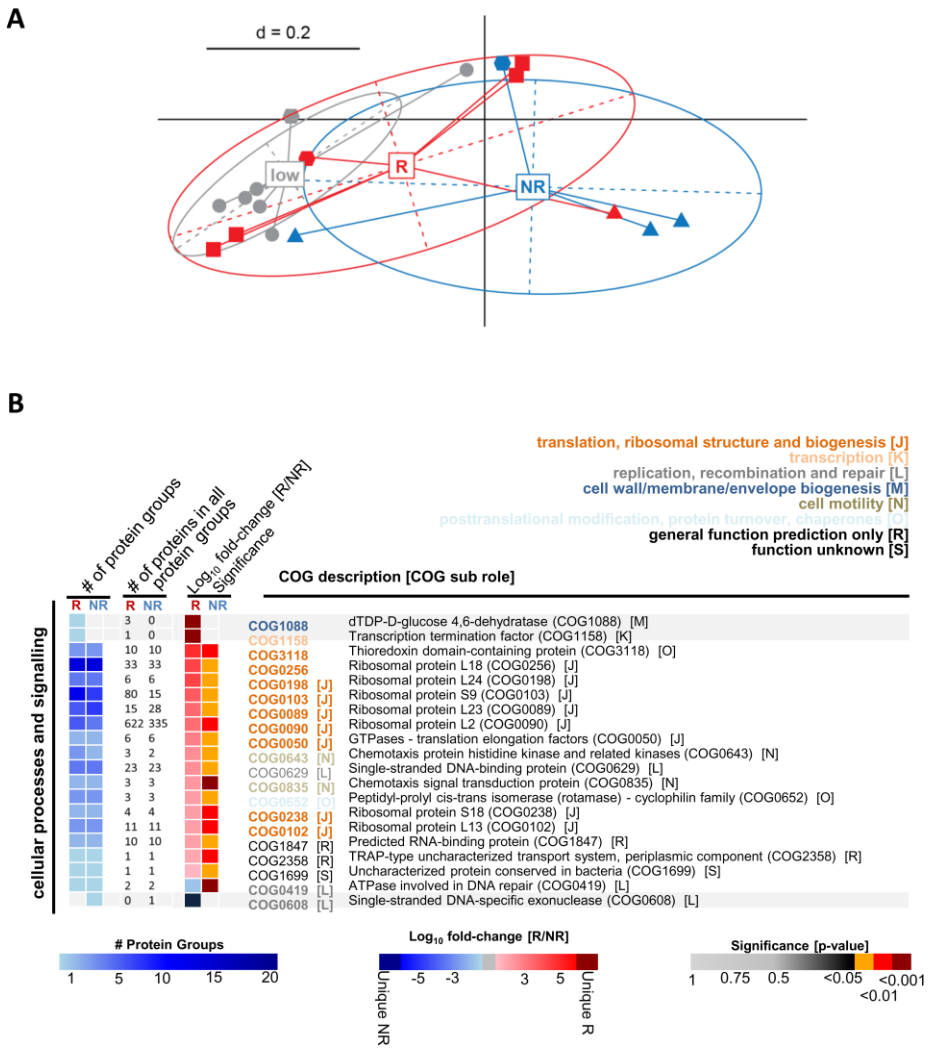
S2: (A) Colitis scores in 18-week-old TNF^{deltaARE} (ARE) and WT littermates in the SPF housing. Individuals are color-coded according to ileitis severity: score = 0 (blue); score <4 (grey); score >4 (red). Male mice are displayed as triangles, females as circles. **(B)** Paneth cell staining of lysozyme, UEA-1 and cryptdin 2 in GF-ARE and -WT mice. **(C)** Ileal expression of a*ngiogenin 4 (ANG4)* and *defensin-α-5* and *reg 3g* as fold-increase to SPF-WT mice (dotted line) normalized to *Gapdh* (n=4-6). **p<0.01; ***p<0.001; One-way ANOVA followed by Tukey´s. **(D)** Staining of cleaved caspase 3 positive cells in the ileal crypts of mice in SPF and GF housing.

Figure S2:



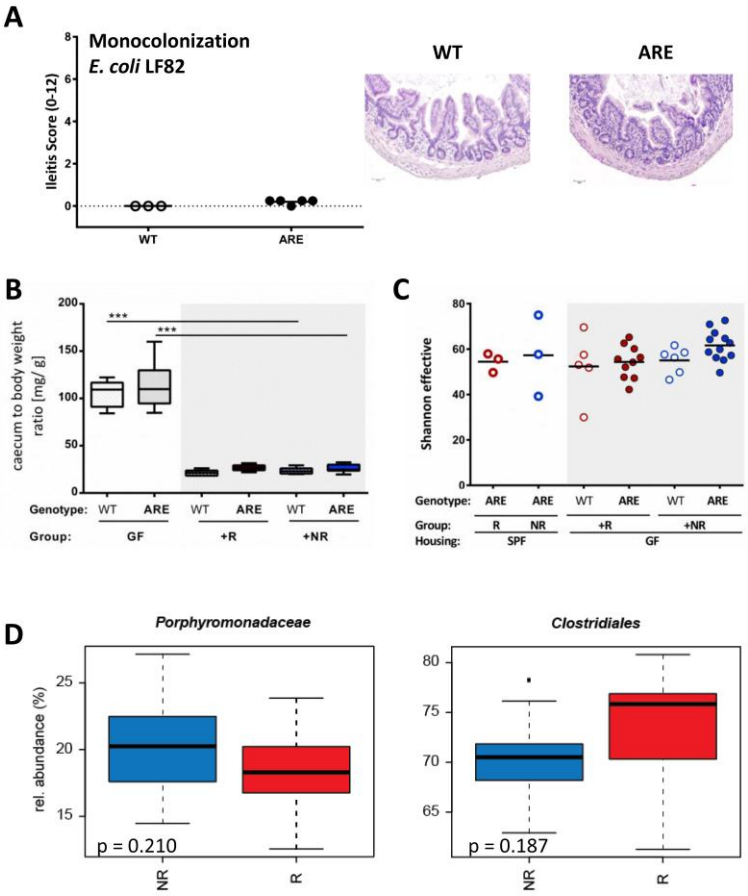
S3: (A) MDS analysis displaying phylogenetic distances between caecal bacterial communities of four-week-old TNF^{deltaARE} mice according to ileitis severity. Responders (R; red) were not yet separated from TNF^{deltaARE} with low ileitis scores (lowR; grey) and from non-responders (NR; blue). Littermates are depicted with identical symbols, suggesting no inheritance of a dominant bacterial profile responsible for later ileitis severity (TNF^{deltaARE} mice from the same litter were found in the three groups of ileitis-severity). **(B)** Significant changes in abundance of protein functions belonging to the COG main role *cellular processes and signalling* between samples from responder (R) and non-responder (NR) mice. Protein group data were log_{10} transformed and normalized by median of bacteria protein data. Protein functions that are unique to either R or NR are shown in grey squares.

Figure S3:



S4: (A) Ileitis Score and representative H&E stained terminal ileal tissue sections of TNF^{deltaARE} and WT mice colonized with *E. coli* LF82 for four weeks. **(B)** Caecum to body weight ratios of WT and TNF^{deltaARE} mice in the GF housing and after four weeks of colonization with responder (+R) or non-responder (+NR) microbiota. **(C)** Shannon effective species counts were not different between any groups of recipient and donor mice. **(D)** Differences of bacterial taxa in responder (R) and non-responder (NR) recipients.

Figure S4:



S5: (A) MLN to body weight ratios of mice colonized with responder-microbiota for 1, 2 or 4 weeks. Groups that were significantly increased when compared to GF TNF^{deltaARE} mice are displayed as red boxes. The dotted line represents mean of respective data in GF TNF^{deltaARE} mice. **(B)** Caecum to body weight ratios**.** ***p<0.001; Two-way ANOVA followed by Holm-sidak.

Figure S5: