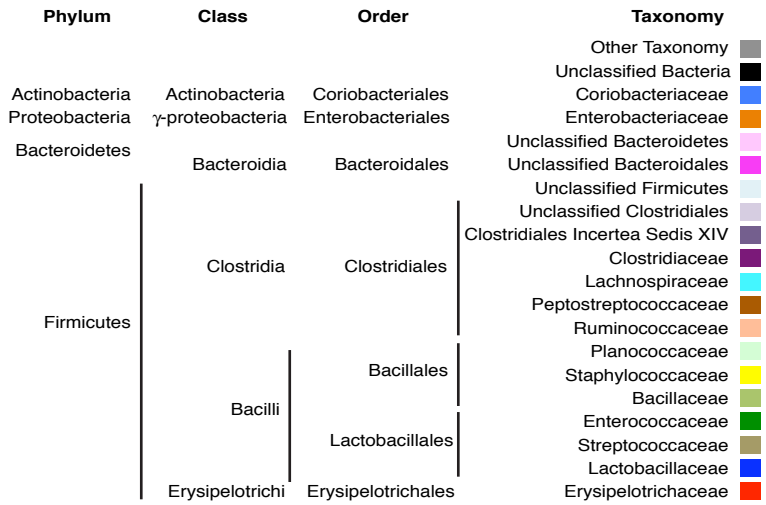
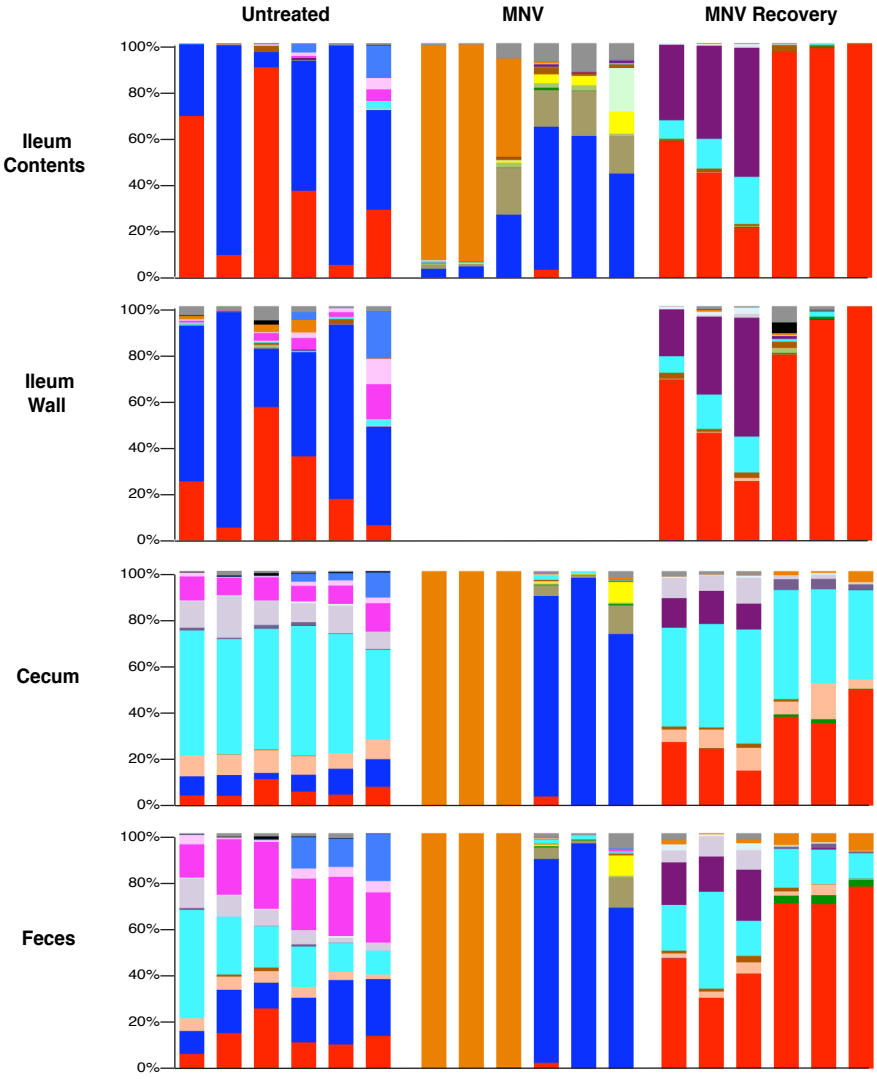
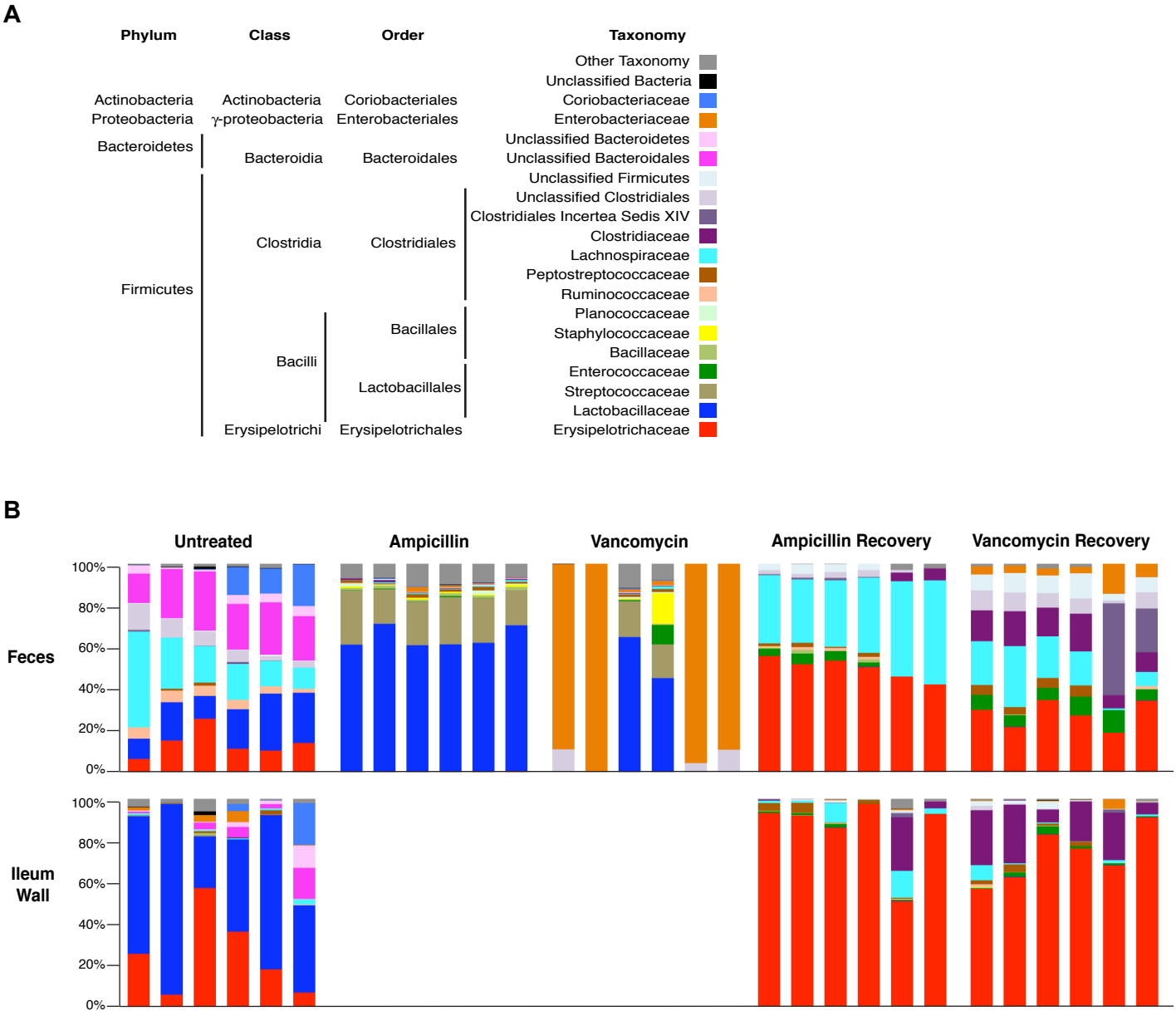
A



B

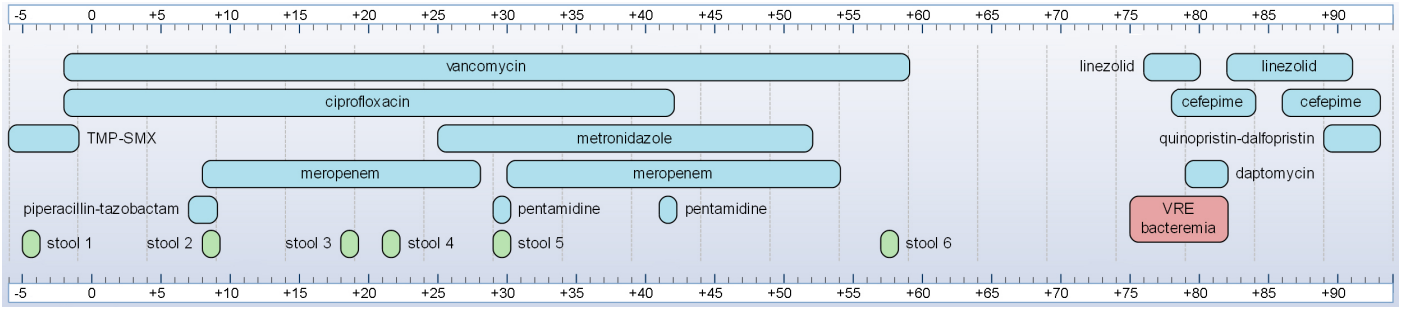


Supplemental Figure 1. MNV treatment alters the composition of the microbiota.
(**A**) Color code for the most predominant bacterial populations found in the murine intestine. (**B**) Phylogenetic classification of 16S rDNA frequencies in the ileum, cecum or feces collected from untreated mice, mice treated with metronidazole+neomycin+vancomycin (MNV), or mice allowed to recover for two weeks from the MNV treatment. Each bar represents the microbiota composition of an individual mouse.

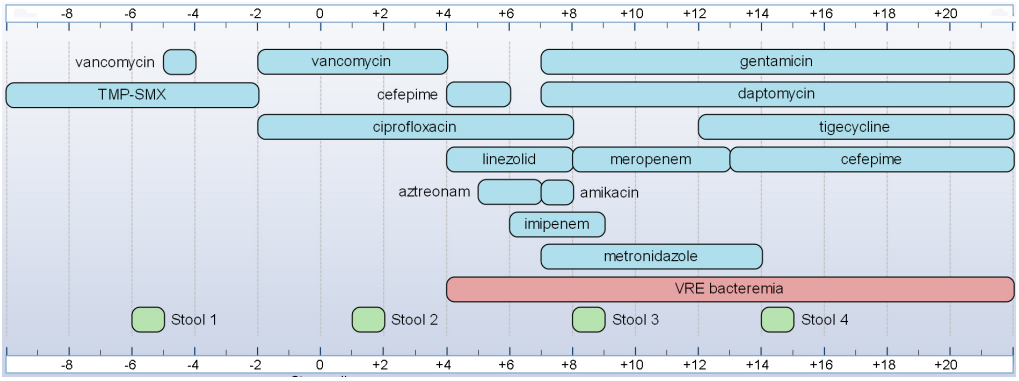


Supplemental Figure 2. Antibiotic treatment alters the composition of the fecal and ileum wall microbiota. (**A**) Color code for the most predominant bacterial populations found in the murine intestine. (**B**) Phylogenetic classification of 16S rDNA frequencies in the ileum wall or feces collected from untreated mice, mice treated with ampicillin or vancomycin, or mice allowed to recover for two weeks from antibiotic treatment. Each bar represents the microbiota composition of an individual mouse.

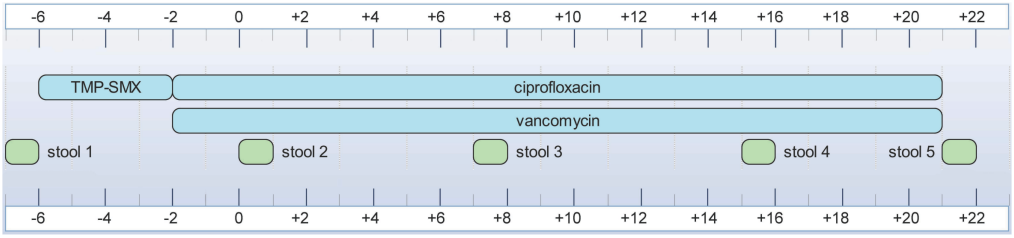
Patient A



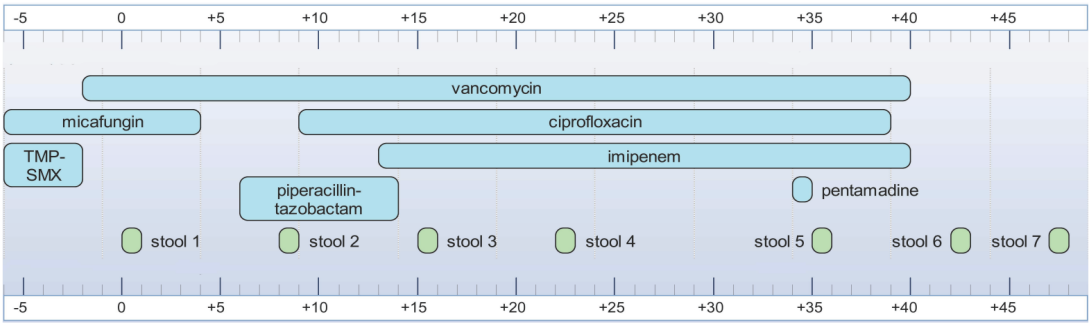
Patient B



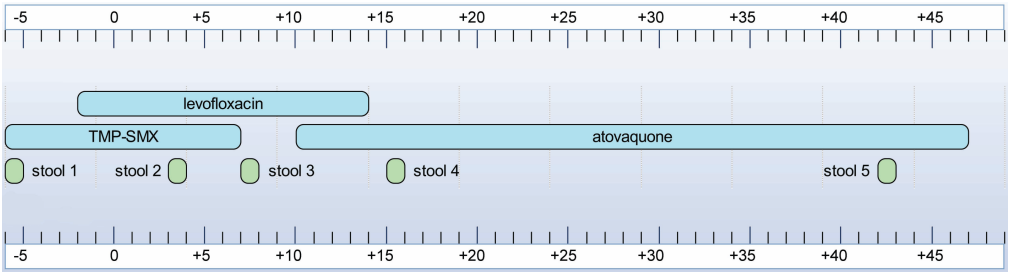
Patient C



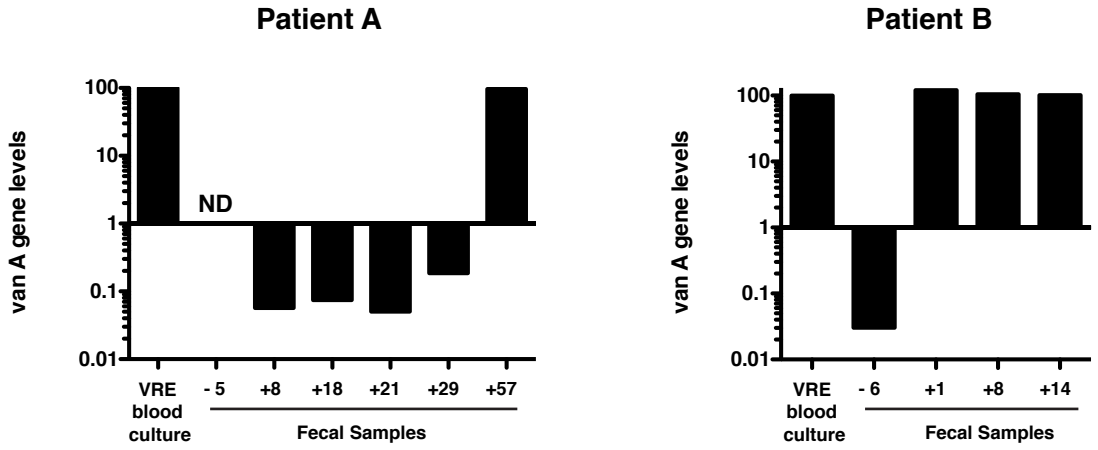
Patient D



Patient E



Supplemental Figure 3. Antibiotic treatment in patients undergoing allo-HSCT.
Antibiotic treatment that each patient received during the transplant course is indicated in blue. The dates of the transplant course are indicated as 0 (day of the transplant), negative value (days before the transplant), positive value (days after the transplant). All antibiotics were administered intravenously except for TMP-SMX and atovaquone, which were administered orally, and pentamidine, which was inhaled. TMP-SMX: Trimethoprim + sulfamethoxazole. The days when the stool samples were collected are indicated in green. The VRE bacteremia period for patients A and B is indicated in red.



Supplemental Figure 4. VRE intestinal expansion in allo-HSCT patients that developed VRE bacteremia. van A gene levels as assessed by qPCR of fecal samples from the two patients that developed VRE bacteremia (see methods). Samples were collected during the transplant course. The timing of the transplant course is indicated as 0 (day of the transplant), negative value (days before the transplant), positive value (days after the transplant). The number of van A gene copies was normalized to the number of 16s rDNA copies in each sample, as assessed by qPCR. Results are expressed relative to the van A gene levels from a pure culture of the VRE strain obtained from the blood culture (assigned as 100%). ND: Non-detectable.

Supplemental Table 1. Patients clinical information.

Patient	Age/sex	Underlying cancer	Transplant type	Time of engraftment (ANC>1000)	Post-HSCT complications	VRE screening rectal swab culture. Before HSCT	VRE screening rectal swab culture. After HSCT	Onset of VRE bacteremia	Duration of VRE bacteremia
A	41/male	T-cell lymphoblastic lymphoma	umbilical cord blood	Day +30	Poor graft function, CMV viremia, suspected GVHD of gut	Negative	Positive (day +52)	Day +75	7 days
B	57/female	T-cell acute lymphoblastic leukemia	umbilical cord blood	Not engrafted	Respiratory failure, encephalopathy	Positive	Positive	Day +4	18 days
C	53/male	diffuse large B-cell lymphoma	umbilical cord blood	Day +11	Clostridium difficile diarrhea	Negative	Positive (day +12)	n/a	n/a
D	46/female	relapsed follicular lymphoma	umbilical cord blood	Day +40	Delayed engraftment, hematuria from BK virus, left lower lobe ground glass opacity	Negative	Negative	n/a	n/a
E	61/female	diffuse large B-cell lymphoma	non-myeloablative	Day +11	biopsy-proven GVHD of the gut	Negative	Negative	n/a	n/a

ANC: Absolute Neutrophil Count.
n/a: non applicable.
GVHD: Graft vs Host Disease