

Supplementary Figure s1

Oral treatment of mice with vancomycin is associated with overgrowth of bacteria within the ileum with vancomycin resistant gram-negative bacteria. Treatment was applied to mice at 3-weeks after colonization with (vancomycin resistant) *P. aeruginosa*. *Cd1d*^{-/-} mice exhibited a significantly increased rate of small intestinal overgrowth with *P. aeruginosa*. (data are mean \pm s.e.m.; probabilities were calculated by Student's t-tests; n=5 for each group, * P < 0.05)

Supplementary Figure s2

(A): Analysis of fixed intestinal tissues from germ-free (n=5; 80 crypts/mouse) and SPF mice (n=5; 80 crypts/mouse) stained with haematoxylin and eosin did not reveal any significant differences in either the number of Pc or the quantity of granules per Pc when WT mice and *Cd1d*^{-/-} animals were compared. (B): Equal expression of lysozyme-p relative to tubulin in crypt fraction obtained from WT and *Cd1d*^{-/-} mice as determined by qPCR. (C): Equal expression and distribution of CDX2 as determined by immunohistochemistry on intestinal tissue derived from WT and *Cd1d*^{-/-} mice in SPF conditions.

Supplementary Figure s3

SPF *Cd1d*^{-/-} display equal expression and distribution of lysozyme immunoreactivity along the crypt axis 24 hours after intraperitoneal injection with 2 μ g of α GalCer (KRN7000) or PBS.

Supplementary Figure s4

Pc of *Cd1d*^{-/-} mice exhibit predominantly smaller granules, whereas granules of larger size are nearly completely absent in comparison to WT mice at t=3 (A) and t=96 (B) hours upon colonization with *E. coli* under germ free conditions and in SPF (C) conditions (diameter in μ m; *P<0.05; **P<0.005; ***P<0.0005).

Figure s1

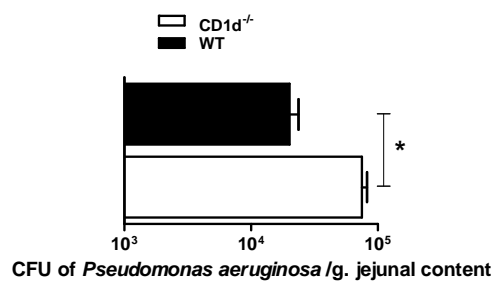


Figure s2

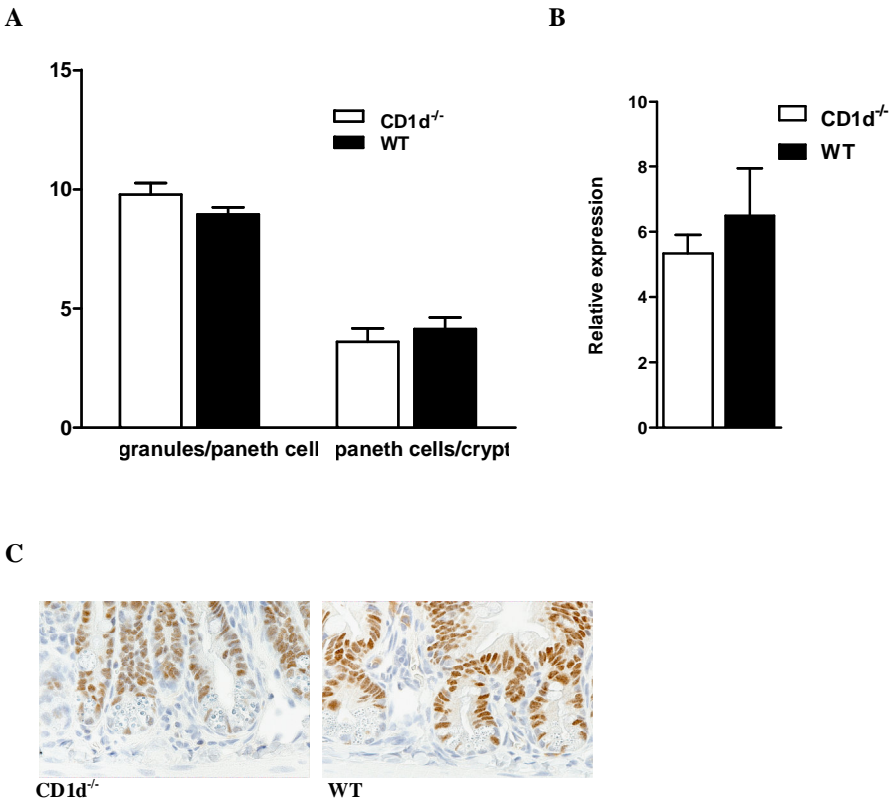


Figure s3

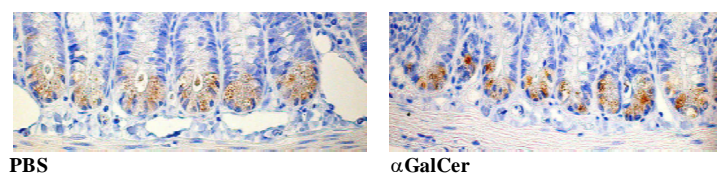
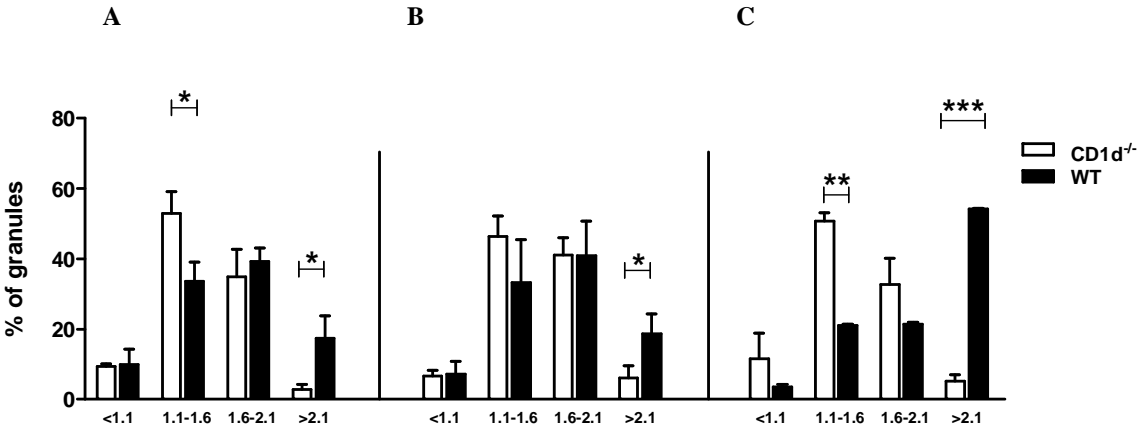


Figure s4



Supplementary Table s1

–	KO1	KO2	KO3	KO4	KO5	WT1	WT2	WT3	WT4	WT5
Clones	77	67	90	93	90	75	63	82	84	90
99% OTUs	29	24	38	45	46	31	24	33	43	28
Bacteroidetes (%)	4	22	6	3	2	0	0	0	0	0
Deferribacteres (%)	0	0	0	0	0	3	3	1	5	0
Firmicutes (Bacilli) (%)	12	49	22	18	12	43	52	40	26	53
Firmicutes (Clostridia) (%)	82	27	72	79	86	55	44	59	69	47
unclassified bacteria (%)	3	2	0	0	0	0	0	0	0	0

Supplementary Table s1:

Microbial diversity in fecal samples of 5 *Cdld*^{-/-} (KO) and 5 WT mice. A total of 811 bacterial near-full-length 16S rDNA sequences were subjected to phylogenetic analysis. In comparison to WT mice, *Cdld*^{-/-} mice display clear shifts in the distribution of phyla that colonize the murine intestine.