

616 bacteria by class, order and family in *H. pylori*-infected children and infected adults.  
617 Analysis was performed as described in **Figure 2b. (e)** Gastric microbiota by genera in  
618 *H. pylori*-infected children and infected adults. Analysis was performed as described in  
619 **Figure 2c.** \* $P < 0.05$ , Student's *t*-test (b) or the Kruskal Wallis test (c).

620 **Figure 5.** Expression of **(a)** *FOXP3*, **(b)** *Il10*, and **(c)** *TGF $\beta$*  mRNA in the gastric  
621 tissue of *H. pylori*-infected children ( $n=11$ ), non-infected children ( $n=10$ ) and *H. pylori*-  
622 infected adults ( $n=13$ ). Expression is normalized to GAPDH mRNA. \* $P < 0.05$  \*\* $P < 0.01$ ,  
623 one-way analysis of variance (ANOVA) with Tukey's post-hoc test.

624 **Figure S1.** The gastric microbiota of non-infected children is similar to that of  
625 non-infected adults. **(a)** Frequencies of gastric bacteria by class, order and family in  
626 non-infected children and non-infected adults. The indicated class, order or family of  
627 bacteria was included when its 16S rDNA sequences were at least 1% of the total  
628 bacterial DNA content in at least one of the four groups of subjects (children and adults  
629 with and without *H. pylori* infection) and when the frequency was significantly different  
630 between any two groups. Stacked bar graphs show the average frequency for each  
631 indicated subject group. *P* values were determined using the Kruskal Wallis test with  
632 multiple comparison correction by applying false discovery rate (FDR) analysis. **(b)**  
633 Gastric microbiota by genera in non-infected children and non-infected adults. The top  
634 25 most abundant genera in the cohort of 86 *H. pylori*-infected and non-infected children  
635 and adults are listed from most to least abundant. The ranking of genera was based on  
636 the average abundance of a given genus for the four groups of subjects. Numbers  
637 correspond to *P* values, and the direction of the arrow indicates an increase or decrease  
638 in the frequency of a given genus in the non-infected children relative to the non-

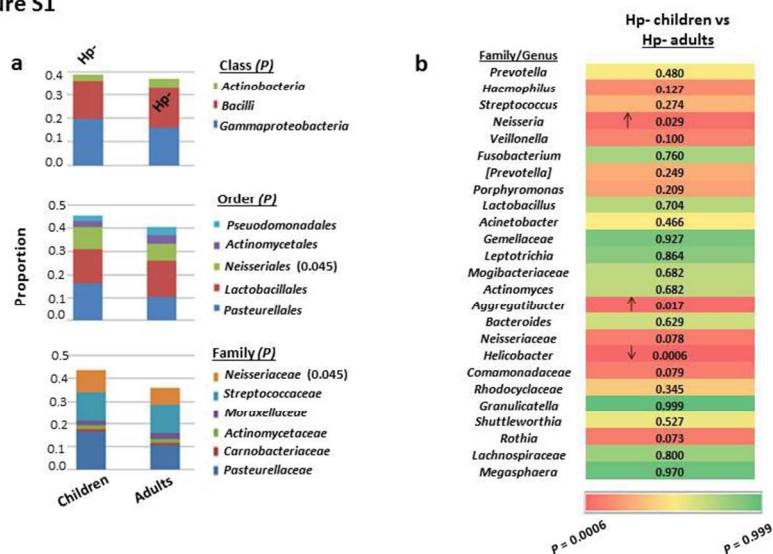
639 infected adults. When a genus could not be assigned, the family is listed. Color  
640 scheme shows red on the left representing the lowest  $P$  value and green on the right  
641 representing the highest  $P$  value.  $P$  values were determined using the Kruskal Wallis  
642 test with multiple comparison correction by applying false discovery rate (FDR) analysis.

643 **Figure S2.** *H. pylori*-negative children harbor a higher frequency of phylum  
644 *Actinobacteria* than *H. pylori*-positive children. Box-and-whisker plot displays the  
645 median, maximum and minimum values for the indicated group.  $*P<0.05$ , Kruskal  
646 Wallis test.

647 **Figure S3.** Richness and abundance distribution of the gastric microbiota in  
648 children and adults without *H. pylori* infection. Alpha diversity was determined using the  
649 Simpson index, and horizontal lines indicate mean  $\pm$ SD. ns, not significant;  $*P<0.05$ ,  
650 Student's  $t$ -test.

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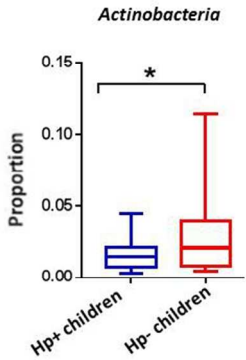
Figure S1



The gastric microbiota of non-infected children is similar to that of non-infected adults. (a) Frequencies of gastric bacteria by class, order and family in non-infected children and non-infected adults. The indicated class, order or family of bacteria was included when its 16S rDNA sequences were at least 1% of the total bacterial DNA content in at least one of the four groups of subjects (children and adults with and without *H. pylori* infection) and when the frequency was significantly different between any two groups. Stacked bar graphs show the average frequency for each indicated subject group. *P* values were determined using the Kruskal Wallis test with multiple comparison correction by applying false discovery rate (FDR) analysis. (b) Gastric microbiota by genera in non-infected children and non-infected adults. The top 25 most abundant genera in the cohort of 86 *H. pylori*-infected and non-infected children and adults are listed from most to least abundant. The ranking of genera was based on the average abundance of a given genus for the four groups of subjects. Numbers correspond to *P* values, and the direction of the arrow indicates an increase or decrease in the frequency of a given genus in the non-infected children relative to the non-infected adults. When a genus could not be assigned, the family is listed. Color scheme shows red on the left representing the lowest *P* value and green on the right representing the highest *P* value. *P* values were determined using the Kruskal Wallis test with multiple comparison correction by applying false discovery rate (FDR) analysis.

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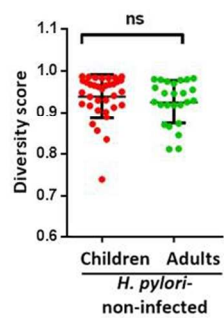
Figure S2.



*H. pylori*-negative children harbor a higher frequency of phylum *Actinobacteria* than *H. pylori*-positive children. Box-and-whisker plot displays the median, maximum and minimum values for the indicated group. \* $P < 0.05$ , Krushal Wallis test.

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Figure S3



Richness and abundance distribution of the gastric microbiota in children and adults without *H. pylori* infection. Alpha diversity was determined using the Simpson index, and horizontal lines indicate mean  $\pm$ SD. ns, not significant; \* $P < 0.05$ , Student's *t*-test.

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**Table S1. Five most abundant phyla in each cohort group**

Cohort Group	Phylum					
	<i>Proteobacteria (non-Helicobacter)</i>	<i>Firmicutes</i>	<i>Bacteroidetes</i>	<i>Fusobacteria</i>	<i>Actinobacteria</i>	Other
Hp+ children	0.43	0.22	0.23	0.08	0.02	0.02
Hp+ adults	0.28	0.38	0.23	0.07	0.03	0.01
Hp- children	0.34	0.29	0.24	0.08	0.03	0.02
Hp- adults	0.32	0.3	0.26	0.07	0.04	0.01

Numbers indicate the mean proportion of a given phylum among all the subjects in the stated cohort group.

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**Table S2. Phyla that comprise the remaining 1.1% in Figure 1a.**

Phylum	Average Frequency
k_Bacteria; p_SR1	0.002309351
k_Bacteria; p_Spirochaetes	0.001823255
k_Bacteria; p_Cyanobacteria	0.00124687
k_Bacteria; p_Verrucomicrobia	0.002209595
No blast hit;Other	0.001324547
k_Bacteria; p_TM7	0.000755521
k_Bacteria; p_Tenericutes	0.000620631
k_Bacteria; p_Acidobacteria	0.000199578
k_Bacteria; p_Synergistetes	0.000136527
k_Bacteria; p_Deferribacteres	9.23913E-05
k_Bacteria; p_[Thermi]	0.00014349
k_Bacteria; p_GN02	4.85554E-05
k_Bacteria; p_Chloroflexi	8.21652E-05
k_Bacteria; p_Gemmatimonadetes	3.01495E-05
k_Bacteria; p_WPS-2	6.64156E-06
k_Bacteria; p_Planctomycetes	8.36299E-06
k_Bacteria; p_SAR406	1.70217E-06
k_Bacteria; p_Armatimonadetes	4.86483E-06
k_Bacteria; p_OD1	6.18398E-07
k_Archaea; p_Euryarchaeota	8.89469E-07
k_Bacteria; p_Nitrospirae	1.88784E-06
k_Archaea; p_Crenarchaeota	1.51988E-06
k_Bacteria; p_TM6	4.37782E-06

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