

**Supplementary table 1.** Metadata for 12 patients to compare microbiota composition between gastric tissue and gastric fluid.

	Gastric cancer (n = 6)	Dysplasia (n = 6)	<i>P</i> value
Age, years	62.5 ± 16.8	56.7 ± 4.8	0.445
Gender			1.000
male	4 (66.7%)	3 (50.0%)	
female	2 (33.3%)	3 (50.0%)	
CLO test			1.000
negative	3 (50.0%)	2 (33.3%)	
positive	3 (50.0%)	4 (66.7%)	
Hp.IgG			1.000
negative	1 (16.7%)	1 (16.7%)	
positive	5 (83.3%)	5 (83.3%)	
Diagnosis			0.007
AMD	2 (33.3%)	0 (0.0%)	
AWD	4 (66.7%)	0 (0.0%)	
HGD	0 (0.0%)	1 (16.7%)	
LGD	0 (0.0%)	5 (83.3%)	
Pepsinogen I	77.4 ± 34.6	38.6 ± 21.2	0.041
Pepsinogen II	22.5 ± 7.2	17.2 ± 8.5	0.272
Pepsinogen I/II	3.8 ± 2.4	2.4 ± 1.3	0.246
Gastrin	38.9 ± 15.1	20.7 ± 9.6	0.032

CLO, *Campylobacter*-like organism; Hp, *Helicobacter pylori*; IgG, Immunoglobulin G; AMD, moderately differentiated adenocarcinoma; AWD, well-differentiated adenocarcinoma; HGD, high-grade dysplasia; LGD, low-grade dysplasia.

**Supplementary table 2.** Metadata for 15 donors\* for 1-month gastric tissue transplantation.

	CSG (n = 5)	IM (n = 5)	GC (n = 5)	<i>P</i> value
Age, years	59.8 ± 5.9	49.2 ± 9.5	66.8 ± 8.7	0.017
Gender				0.435
male	1 (20.0%)	2 (40.0%)	3 (50.0%)	
female	4 (80.0%)	3 (60.0%)	2 (40.0%)	
CLO test				0.301
negative	4 (80.0%)	2 (40.0%)	4 (80.0%)	
positive	1 (20.0%)	3 (60.0%)	1 (20.0%)	
Hp.IgG				0.153
negative	4 (80.0%)	1 (20.0%)	3 (60.0%)	
positive	1 (20.0%)	4 (80.0%)	2 (40.0%)	
Pepsinogen I	47.5 ± 15.6	52.7 ± 14.9	48.8 ± 25.0	0.906
Pepsinogen II	9.6 ± 2.1	21.0 ± 9.9	11.5 ± 4.7	0.272
Pepsinogen I/II	4.9 ± 0.7	2.9 ± 1.1	4.2 ± 0.7	0.008
Gastrin	24.3 ± 11.5	53.8 ± 21.3	61.2 ± 90.2	0.537
IM_tissue				0.092
no	5 (100.0%)	2 (40.0%)	4 (80.0%)	
yes	0 (20.0%)	3 (60.0%)	1 (20.0%)	

\*Donor cohort independent from Supplementary Tables 3 and 4.

CSG, chronic superficial gastritis; IM, intestinal metaplasia; GC, gastric cancer;

CLO, *Campylobacter*-like organism; Hp, *Helicobacter pylori*; IgG, Immunoglobulin G.

**Supplementary table 3.** Metadata for 12 donors\* for 1-month gastric fluid transplantation

	CSG (n = 4)	IM (n = 4)	GC (n = 4)	<i>P</i> value
Age, years	52.8 ± 10.9	66.2 ± 8.8	61.5 ± 15.3	0.317
Gender				0.368
male	1 (25.0%)	3 (75.0%)	2 (50.0%)	
female	3 (75.0%)	1 (25.0%)	2 (50.0%)	
CLO test				0.264
negative	0 ( 0.0%)	1 (25.0%)	2 (50.0%)	
positive	4 (100.0%)	3 (75.0%)	2 (50.0%)	
Hp.IgG				0.264
negative	1 (25.0%)	0 ( 0.0%)	2 (50.0%)	
positive	3 (75.0%)	4 (100.0%)	2 (50.0%)	
Pepsinogen I	65.9 ± 27.2	96.9 ± 49.4	52.2 ± 27.2	0.253
Pepsinogen II	23.1 ± 14.1	41.9 ± 33.5	15.4 ± 6.4	0.248
Pepsinogen I/II	3.3 ± 1.1	2.9 ± 1.3	3.6 ± 1.5	0.777
IM_tissue				0.012
no	4 (100.0%)	0 ( 0.0%)	1 (25.0%)	
yes	0 ( 0.0%)	4 (100.0%)	3 (75.0%)	

\*Donor cohort independent from Supplementary Tables 2 and 4.

CSG, chronic superficial gastritis; IM, intestinal metaplasia; GC, gastric cancer;

CLO, *Campylobacter*-like organism; Hp, *Helicobacter pylori*; IgG, Immunoglobulin G.

Supplementary table 4. Metadata for 8 donors\* and 16 recipients for long-term (1 year) gastric tissue transplantation

Donor information										Recipient information				
Donor index	Age, years	Gender	CLO test	Hp.IgG	Pepsinogen I	Pepsinogen II	Pepsinogen I/II	Gastrin	IM_tissue	Recipient index	Inoculated donor's gastric tissue location	Metaplasia	Dysplasia	16S rRNA gene sequencing (antrum/corpus)
CSG_1	61	F	Positive	Positive	100.9	35.9	2.8	25.0	No	CSG_1A	Antrum			o/o
CSG_2	49	F	Positive	Negative	42.8	9.1	4.7	12.0	No	CSG_1B	Corpus			o / failed <sup>b</sup>
										CSG_1C	Antrum			o/o
										CSG_1D	Corpus			o/o
										CSG_1E	Antrum			o/o
CSG_3	62	F	Positive	Positive	73.9	34.6	2.1	42.6	No	CSG_1F	Corpus	o	o	o/o
IM_1	60	M	Negative	Positive	57.1	11.9	4.8	21.6	Yes	IM_2A	Antrum	o	o	o/o
IM_2	78	F	Positive	Positive	160.5	88.6	1.8	65.9	Yes	IM_2B	Corpus	o		o/o
										IM_2C	Antrum		o	o/o
										IM_2D <sup>a</sup>	Corpus		-	-
GC_1	69	F	Negative	Negative	37.3	7.7	4.8	33.1	Yes	GC_3A	Antrum			o / failed <sup>b</sup>
GC_2	75	F	Negative	Negative	90.3	18.2	5.0	222.0	No	GC_3B	Corpus		o	o / failed <sup>b</sup>
										GC_3C	Antrum	o		o / failed <sup>b</sup>
										GC_3D	Corpus			o/o
GC_3	40	M	Positive	Positive	29	13.2	2.2	29.1	Yes	GC_3E	Antrum	o	o	o/o
										GC_3F	Corpus	o	o	o/o

\*Donor cohort independent from Supplementary Tables 2 and 3.

<sup>a</sup>This subject died 7 months after GMT.

<sup>b</sup>16S rRNA gene sequencing was not conducted since the sequencing library construction failed.

CSG, chronic superficial gastritis; IM, intestinal metaplasia; GC, gastric cancer;  
CLO, *Campylobacter*-like organism; Hp, *Helicobacter pylori*; IgG, Immunoglobulin G.