

	Sex	Age	DMF	Pocket depth (mm)
A	M	27	0	< 3
B	M	31	1	< 3
C	F	33	12	< 3
D	F	27	1	< 3
E	F	25	0	< 3
F	M	25	0	< 3
G	M	27	0	< 3
H	F	27	1	< 3
I	M	28	5	< 3
K	M	25	6	< 3

Table S1 The information of subjects.

F, female; M, male. DMF is the index that is the number of teeth decayed (D), missing (M) and filled

(F). Pocket depth was measured as an index of periodontal disease. No symptom of caries and

periodontitis were detected. No one has any systemic diseases.

Primer name	sequence	reference
16S rRNA forward	AGRGTTTGATCMTGGCTCAG	Lane, 1991; Weisburg, 1991
16S rRNA reverse	TGCTGCCTCCCGTAGGAGT	Suzuki et al., 1996
LL-37 forward	GAAGACCCAAAGGAATGGCC	Chandra et al., 2011
LL-37 reverse	CAGAGCCCAGAAGCCTGAGC	Chandra et al., 2011
hBD-1 forward	TCATTACAATTGCGTCAGCAG	Wolgin et al., 2012
hBD-1 reverse	TTGCAGCACTTGGCCTTC	Wolgin et al., 2012
hBD-2 forward	TCCTCTTCTCGTTCCTCTTCA	Wolgin et al., 2012
hBD-2 reverse	AGGGCAAAGACTGGATGAC	Wolgin et al., 2012
hBD-3 forward	CCATTATCTTCTGTTTGCTTTGCTC	Bogefors et al., 2012
hBD-3 reverse	CCGCCTCTGACTCTGCAATAATA	Bogefors et al., 2012
ADM forward	GGACATGAAGGGTGCCTCTC	Filho et al., 2015
ADM reverse	TGTTCATGCTCTGGCGGTAG	Filho et al., 2015
IL-6 forward	CGCCCCACACAGACAGCCAC	Pahumunto et al., 2017
IL-6 reverse	AGCTTCGTCAGCAGGCTGGC	Pahumunto et al., 2017
IL-1b forward	CACGCTCCGGGACTCACAGC	Pahumunto et al., 2017
IL-1b reverse	CTGGCCGCCTTTGGTCCCTC	Pahumunto et al., 2017
TNF-a forward	TTCTGCCTGC TGCACCTTTGGA	Pahumunto et al., 2017
TNF-a reverse	TTGATGGCAGAGAGGAGGTTG	Pahumunto et al., 2017
IL-8 forward	TTTCTGATGGAGAGAGCTCTGTCTGG	Pahumunto et al., 2017
IL-8 reverse	AGTGGAACAAGACTTGTGGATCCTGG	Pahumunto et al., 2017
GAPDH forward	GAAGGTCGGAGTCAACGGAT	Zang et al., 2021
GAPDH reverse	CCTGGAAGATGGTGATGGGAT	Zang et al., 2021

Table S2: The sequences of primers used in this study

The sequences of primers used in this study for PCR and the references are shown.

	LL37	hBD1	hBD2	hBD3	ADM	IL6	TNFa	IL1b
hBD1	0.249							
hBD2	-0.16	-0.103						
hBD3	-0.257	0.051	0.005					
ADM	0.715**	0.454*	-0.156	-0.233				
IL6	-0.286	-0.081	0.014	0.394*	-0.513**			
TNFa	-0.325	0.128	0.539**	0.348	-0.332	0.285		
IL1b	0.347	0.194	0.353	-0.236	0.598**	-0.358	0.16	
IL8	-0.405*	-0.16	0.494**	-0.081	-0.382*	0.046	0.493**	0.2

Table S3 Spearman's rank correlation coefficient revealed that the gene expressions.

An asterisk (*) means $P < 0.05$ and two asterisk (**) means $P < 0.001$.

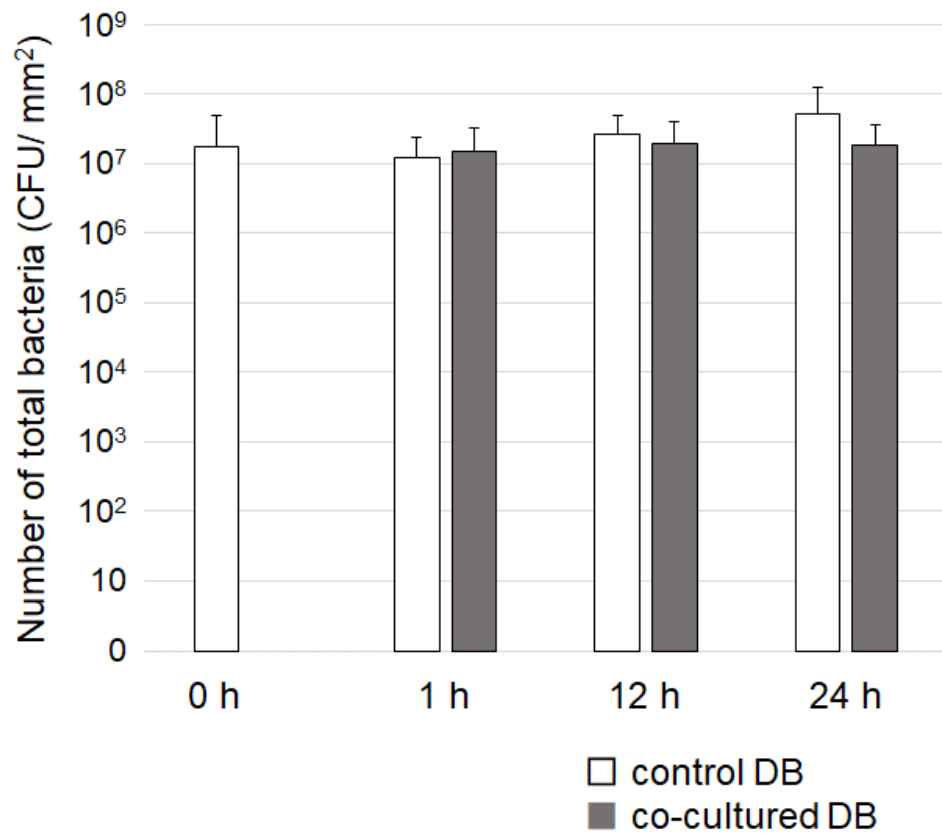


Figure S1: Total bacterial count by quantitative PCR

The number of total bacteria was measured by real-time PCR. Control DB means in situ DB samples

co-cultured with only collagen gel. Co-cultured DB means in situ DB samples co-cultured with RHG.

The significant difference was not observed at any timepoint (Friedman test, $P > 0.05$).

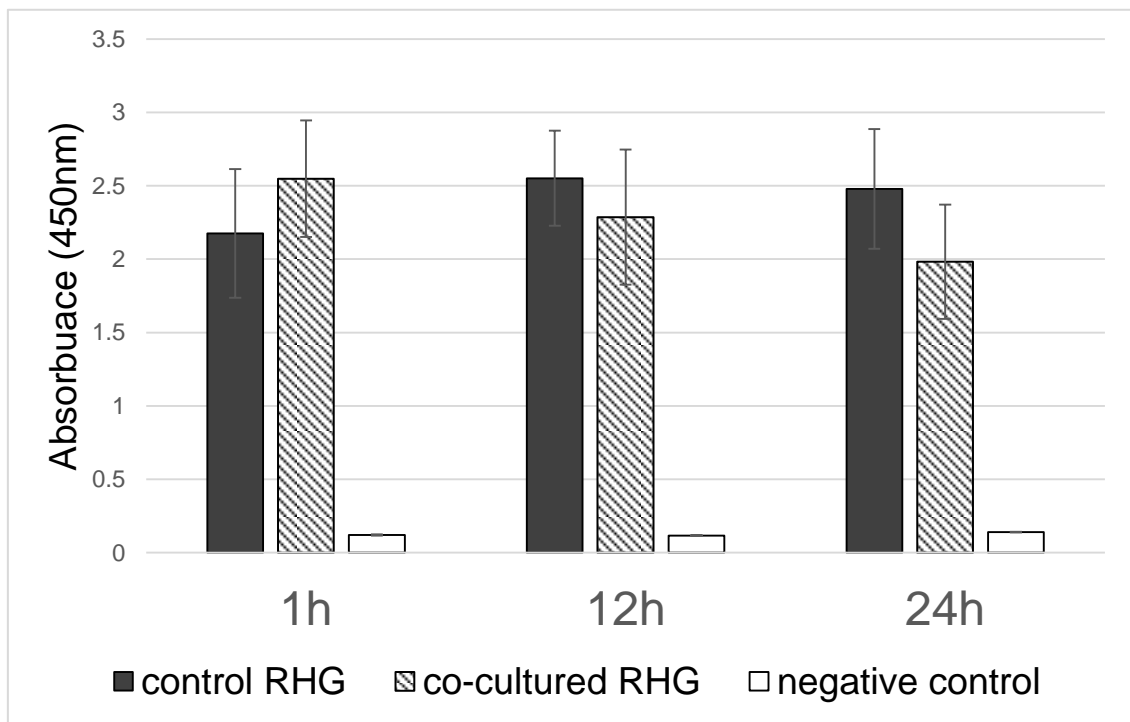


Figure S2: cell viability assay

The viability of co-cultured RHG did not change significantly compared to control RHG. DMEM without cells was used as negative control. There was no significant difference between control and co-cultured RHG in any time point. (One-way analysis of variance and Tukey test).