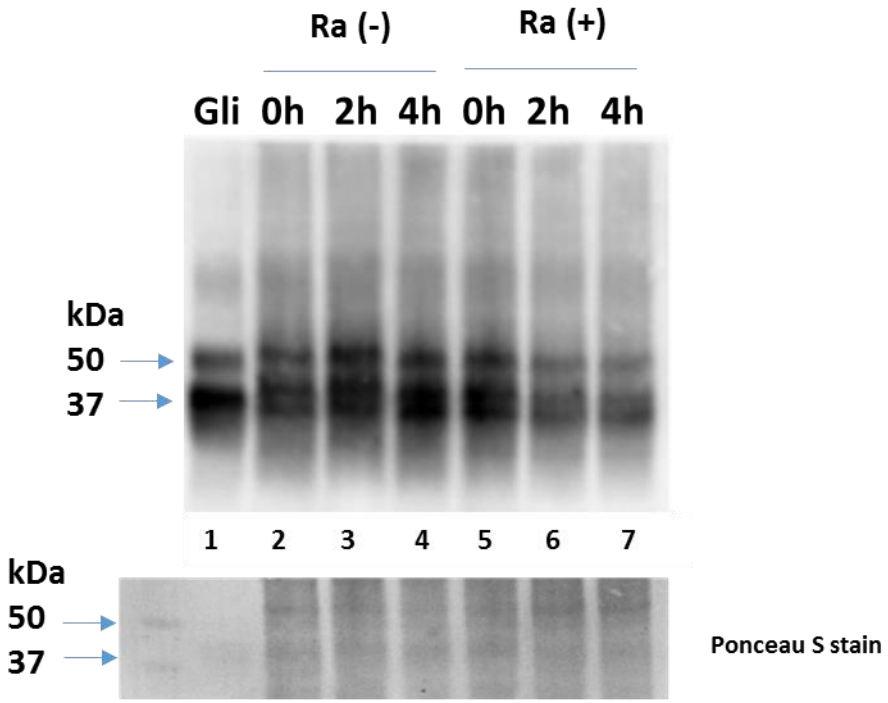

Supplemental Figure 1 Enzymatic degradation of gliadins in mouse chow *in vitro* detected by immunoblotting. Mouse chow was supplemented with *R. aeria* (Ra+) and without (Ra-) and incubated at 37°C for 0, 2 and 4 hr. Aliquots (10 μl) of 60% ethanol-extracted sample supernatants were loaded. Lane1: Gliadin control (Gli, 15 μg); Lane 2: Ra (-) at 0 hour; Lane 3: Ra (-) at 2 hr; Lane 4: Ra (-) at 4 hr; Lane 5: Ra (+) at 0 hr; Lane 6: Ra (+) at 2 hr; Lane 7: Ra (+) at 4 hr, blue (arrow) points to the gliadin bands at 37 and 50 kDa.

MIC Susceptibility of Two Rothia Species to Antimicrobics

Category	Antimicrobics	MIC (μg/ml)	
		Rm	Ra
Aminoglyosides	Amikacin	<4	<4
	Gentamicin	<1	<1
	Streptomycin	<1000	<1000
	Tobramycin	4	8
Beta-lactams			
Cephalosporins	Cefepime	<2	<2
	Cefotaxime	<1	<1
	Ceftazidime	4	8
	Ceftaroline	<0.12	<0.12
	Ceftriaxone	<8	<8
Carbapenems	Doripenem	<0.12	0.25
	Ertapenem	<0.25	0.5
	Imipenem	<1	<1
	Meropenem	<1	<1
Monobactams	Aztreonam	>16	>16
Penicillins	Ampicillin	<0.12	<0.12
	Oxacillin+2%NaCl	<0.25	<0.25
	Penicillin	<0.06	<0.06
Glycopeptides	Vancomycin	<1~1	2
	Telavancin	<0.06	0.12
Glycylcyclines	Tigecycline	<0.06	0.12
Lincosamides	Clindamycin	<0.5~0.5	>2
Lipopeptides	Daptomycin	0.5~1	4
Macrolides	Erythromycin	<0.25	4
Nitrpfurans	Nitrofurantoin	<32	<32
Oxazolidinones	Linezolid	<1~1	1
Polymyxins	Colistin	>4	>4
	Polymixin B	>4	>4
Quinolones	Ciprofloxacin	2~4	2~4
	Gatifloxacin	<1	<1
	Levofloxacin	<1~2	1
	Moxifloxacin	<0.25	0.5
Rifamycins	Rifampin	<0.5	<0.5
Tetracyclins	Doxycycline	<2	<2
	Minocycline	<2	<2
	Tetracycline	<2	<2
Others	Chloramphenicol	<2	<2
Combinations	Piperacillin / tazobactam constant 4	<8/4	<8/4
	Quinupristin / dalfopristin	0.25	0.12
	Ticarcillin / clavulanic acid constant 2	<16/2	<16/2
	Trimethoprim / sulfamethoxazole	<0.5/9.5	<0.5/9.5

Supplemental Figure 2, MIC (minimal inhibitory concentration) susceptibility of two *Rothia* species to antibiotics The experiment was performed by using MIC susceptibility plates (Sensititre, Thermofisher Scientific/ Trek diagnostic systems). MIC was recorded as the lowest concentration of antibiotic that inhibits visible growth . Rm: *Rothia musinoginosa*; Ra: *Rothia aeria*

There are some concerns that *Rothia* bacteria may cause side effects in patients if they colonize non-naturally areas of the human body. Here data shows that Rm and Ra are susceptible to antibiotics and to 70% ethanol (Figure 2 A). Notably, the dead Rm/Ra still exhibit gluten degrading activity (Figure 2 B-D), indicating that these inactivated Rm and Ra maintain gluten proteolytic activity to benefit CD patients.

>BAV86562.1 glycerol-3-phosphate ABC transporter [*Rothia aeria*]

MAITAGLPATAAPAGDPDTPVAQDIARNSREHAVLSDSMKKAEGNIPVFVQFKGKGAYEQTQSPAVLANKQAPTNKQ
AEVQAIKTQVQSQAQAAAQSTGAKTLYTTHNIMRGVALQGDAAQIRALANNPEVERITPIVPKKKQNAGSVVDTGAA
ENWARENSGYT**GKDVKIAVVDSGIDYTHADFGGPGTVEAFNKATKLTEMPAADSGLYDAKKYIGGYDLVGDSYDGTN**
QTAPDNNPIDCSAGGHGTHVAGTAAGYGVNQDGTTFRGDYSKLTAEQLNQMKIGPGAAPEAQLYSFRVFGCTGTTGV
VVQALDRTLDPNGDGDFSDRANIVNLSIGGEFSPPDDADAYAVESLNRQGVLAVVSAGNATDYYGRGDTYSDSGQPA
NAVSALTVANSIGSSYAVDSMEIQAPANVAGKVPGDYTVSYTYTGAKPEALTGTVVTPSESNKFGCEAFSAEDAAKI
KDKWVFLEWANADGSLPCGSKVRFDNVEKAGGKGVVLSSEEEKPALPIGGNESIPGFRVAKSASAKVREAAANGELK
VRLGTDLKESLRVPSNKKDQLTASSARGYHGTYGYTKPDVAAPGNNISSARVGTGTDGISYTGTSMSAPFAAGVAAQ
VLQANQSYGPTQLKAAIMNSANHDVRTADGNVYAVDRVGSGRIDAKAAAETKVLLYNADRPAQVSQTFGVLEYAVNE
GKQTLTREMTVENFDSHTHTYNISYAGSTDMPGVEFSLPSNITVNPGEKKNFTVTITIDPAAMEKTMDPAMEKTHNS
VDPYGDGTELVPEQYRQFIASESGRILLTEGAATLRAPIHAAPKPASAMKVEGSSVEIPAGEHQANLKLTGTELNQR
GYKSLLGAFEHGASIERTSPVKLDVSSNAKANMQHVGAASTAPALKASGGNPNDGLLAFGISTWANWDVVSTENTFT
VNIDTDGNNRADYMLVTDRAKGIDFPIVRLYGYKNGNLEQIAYYPLNNAWGDTDTNMMDSNALVMAVPLKDLGLSAE
KTKDIKYSVSATTQYAWTNVSETGWINYRPFDPKLWFSGTAATVPGFFADAPSSELVAHRAEGATDVKALFLHMHNT
TGDLSGLNGAAGNRAQVLEVTEQQQLDPAPSRFTDVPAENQFYAEINWLAQRRITTGYPDGTFRPGENVERGAMAAY
FYRLAGTPQFTAPDNPTFSDVPKSHPFYKEIEWMAARGITTGYGDGTFRPSASVNRDAMAAFFYRYANSPQFAAPAA
SPFKDVPANSQFYKEIAWLAEQGITKGWDDGTYRPGEPIHRDAMAAFLYRYSDKVLK

Supplemental Figure 3. Amino acid sequence of *R. aeria* BAV86562.1. In bold: domain cd07474 representing the peptidase S8 family domain in Vpr-like proteins. BAV86562.1 is not an ABC transporter protein as its name suggests, since it lacks the LSGGQ domains characteristic of the ABC transporter family. The highlighted D, S and H residues comprise the catalytic triad of the subtilisin enzyme.