Table S1. Correlation between TJ proteins levels and the abundance, in ASVs, of the phyla detected in RA patients gut microbiota.

Gut microbiota	Occludin (pg/mL)	Claudin-1 (pg/mL)	Zonulin (ng/mL)
Actinobacteria	-0.079	-0.110	0.074
Firmicutes	0.123	0.081	0.131
Synergistetes	-0.035	-0.052	0.057
Coriobacteriaceae	-0.110	-0.125	-0.093
Streptococcaceae	0.074	0.023	0.055
EtOH8	0.024	0.054	-0.052
Unknown family of order *RF32*	**0.222***	0.057	-0.066
Oxalobacteraceae	-0.115	-0.054	0.188
Bifidobacterium	-0.049	-0.081	0.161
Collinsella	-0.144	-0.125	-0.094
Alistipes	-0.093	-0.061	0.067
Weissella	-0.087	-0.096	-0.054
Unknown genus of family *EtOH8*	0.024	0.054	-0.052
Pseudoramibacter_Eubacterium	-0.056	-0.106	0.008
Unknown genus of family *Lachnospiraceae*	0.073	0.140	-0.103
Coprococcus	0.008	-0.118	-0.144
Dorea	-0.040	-0.113	-0.056
rc4_4	**0.241***	0.193	-0.013
Anaerotruncus	-0.082	0.152	-0.052
Veillonella	0.065	**0.272***	-0.088
Mogibacterium	-0.073	-0.095	-0.076
Unknown genus of family *Erysipelotrichaceae*	0.025	-0.128	-0.046
Unknown genus of order *RF32*	**0.222***	0.057	-0.066
Succinatimonas	-0.040	-0.039	-0.041
Synergistes	-0.078	0.073	0.085
Unknown genus of class *TM7-3*	-0.092	-0.185	-0.067

ASVs: amplicon sequence variants. Significance level: * $p<0.05$

Table S2. Correlation between claudin-1 levels and the abundance, in ASVs, of the phyla detected in RA patients according to inflammatory activity.

Gut microbiota	Low inflammatory activity (*n*=53)	High inflammatory activity (*n*=29)
Actinobacteria	-0.175	-0.003
Firmicutes	0.042	0.256
Synergistetes	-0.062	-0.036
Coriobacteriaceae	-0.087	0.010
EtOH8	0.065	0.050
Unknown family of order *RF32*	0.045	0.051
Oxalobacteraceae	-0.082	-0.193
Bifidobacterium	-0.178	-0.001
Collinsella	-0.065	-0.015
Alistipes	-0.265	0.052
Weissella	0.119	-0.208
Pseudoramibacter_Eubacterium	-0.258	-0.211
Unknown genus of family *Lachnospiraceae*	-0.031	**0.615****
Coprococcus	-0.076	-0.152
Dorea	-0.130	0.037
Anaerotruncus	-0.139	-0.033
Veillonella	0.048	**0.858****
Mogibacterium	-0.153	-0.118
Unknown genus of family *Erysipelotrichaceae*	-0.245	0.385
Unknown genus of order *RF32*	0.045	0.051
Synergistes	0.009	0.017
Unknown genus of class *TM7-3*	-0.270	0.235

ASVs: amplicon sequence variants. Significance level: ** $p<0.01$