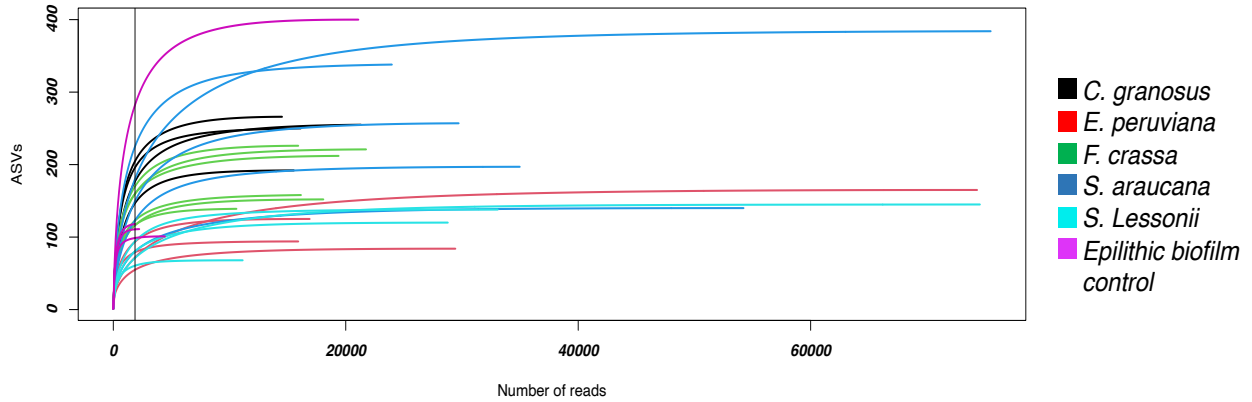


## Supplement 1.

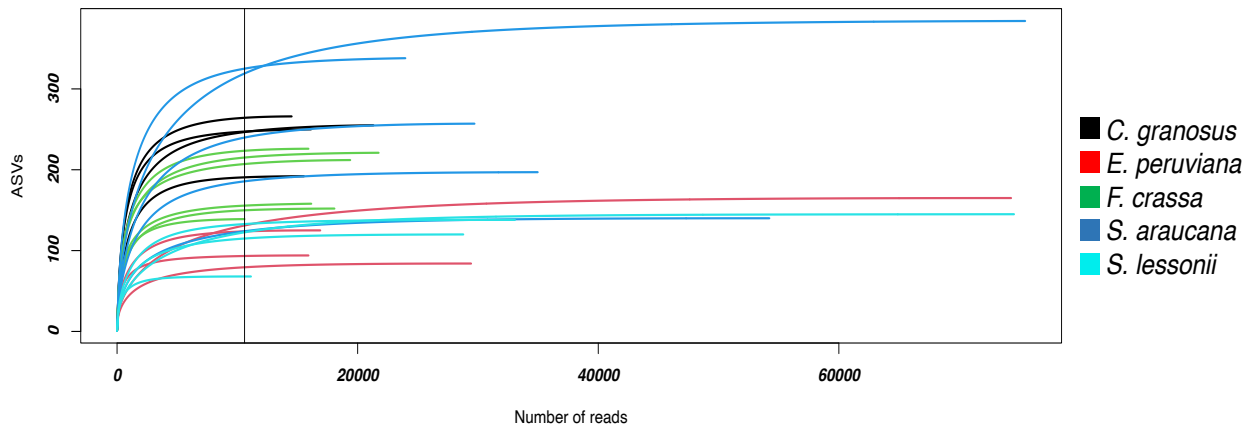
**Table S1:** Description, DNA extraction and 16S rRNA gene sequencing characteristics of the most abundant grazer's microbiota and epilithic biofilm samples.

ID	Treatment/ Microbiota	Foot Area (cm <sup>2</sup> ) or Rock Area (cm <sup>2</sup> )	ng dDNA/uL	Number of QC reads	Number of ASVs	Number of reads after rarefaction with control	Number of ASVs after rarefaction with control	Number of reads after rarefaction without control	Number of ASVs after rarefaction without control
C.granosus_47	<i>C. granosus</i>	8.05	44.6	14521	266	1869	215	10599	265
C.granosus_48	<i>C. granosus</i>	7.16	51	15543	192	1869	135	10599	190
C.granosus_49	<i>C. granosus</i>	5.11	46.8	16135	250	1869	195	10599	246
C.granosus_50	<i>C. granosus</i>	4.08	53.6	21317	255	1869	171	10599	244
E.peruviana_57	<i>E. peruviana</i>	0.09	37.4	29434	84	1869	51	10599	82
E.peruviana_58	<i>E. peruviana</i>	0.24	33.6	16898	125	1869	89	10599	122
E.peruviana_59	<i>E. peruviana</i>	0.22	12.4	74324	165	1869	72	10599	130
E.peruviana_60	<i>E. peruviana</i>	0.32	25.2	15918	94	1869	81	10599	93
F.crassa_38	<i>F. crassa</i>	31.10	45.4	21750	221	1869	169	10599	220
F.crassa_40	<i>F. crassa</i>	26.72	74.4	19390	212	1869	159	10599	204
F.crassa_53	<i>F. crassa</i>	15.37	52.2	10599	139	1869	120	10599	139
F.crassa_54	<i>F. crassa</i>	14.14	36.4	16151	158	1869	127	10599	154
F.crassa_55	<i>F. crassa</i>	27.90	59.6	15917	226	1869	169	10599	226
S.raucana_41	<i>S. Araucana</i>	7.05	59.2	54228	140	1869	86	10599	125
S.raucana_42	<i>S. Araucana</i>	0.43	33	29719	257	1869	141	10599	237
S.raucana_43	<i>S. Araucana</i>	0.06	28.4	34974	197	1869	118	10599	186
S.raucana_44	<i>S. Araucana</i>	0.23	14	75493	384	1869	191	10599	311
S.raucana_45	<i>S. Araucana</i>	0.37	45.2	23971	338	1869	221	10599	328
S.lessonii_62	<i>S. lessonii</i>	0.12	31	74566	145	1869	63	10599	128
S.lessonii_63	<i>S. lessonii</i>	0.11	55.2	28785	120	1869	75	10599	117
S.lessonii_64	<i>S. lessonii</i>	0.20	30	33081	138	1869	98	10599	134
S.lessonii_65	<i>S. lessonii</i>	0.17	65.4	11137	68	1869	61	10599	68
EpilithicBiofilm_1	Epilithic biofilm control	28.25	59	1869	118	1869	118	-	-
EpilithicBiofilm_5	Epilithic biofilm control	23.71	37.2	4449	101	1869	100	-	-
EpilithicBiofilm_27	Epilithic biofilm control	27.39	26.4	21089	400	1869	284	-	-
EpilithicBiofilm_29	Epilithic biofilm control	20.00	30.4	2236	111	1869	111	-	-
<b>TOTAL</b>	-	-	-	<b>683494</b>	<b>1934</b>	<b>48594</b>	<b>958</b>	<b>233178</b>	<b>1205</b>

**Figure S1.** First rarefaction curves with the epilithic biofilm control and the pedal mucus microbiota of *Chiton granosus*, *Echinolittorina peruviana*, *Fissurella crassa*, *Scurria araucana* and *Siphonaria lessonii*. Rarefaction level of 1,869 reads.

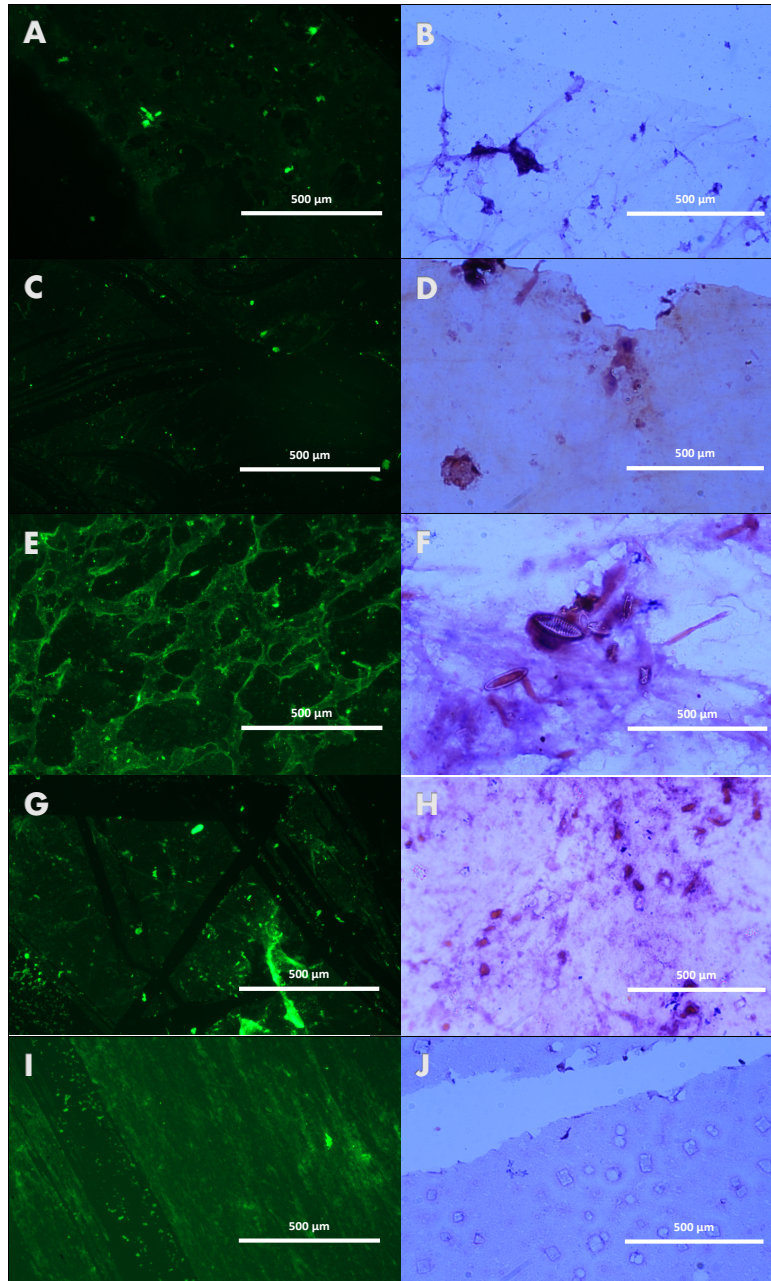


**Figure S2.** Second rarefaction curves with the pedal mucus microbiota of *Chiton granosus*, *Echinolittorina peruviana*, *Fissurella crassa*, *Scurria araucana* and *Siphonaria lessonii*. Rarefaction level of 10,599 reads.



**Supplement 2.**

**Figure S1.** Pedal mucus stained with 0.01% acridine orange (right) and gram (left) of (A, B) *C. granosus*, (C, D) *E. peruviana*, (E, F) *F. crassa*, (G, H) *S. araucana*, and (I, J) *S. lessonii*. Photography by Clara Arboleda-Baena.



### Supplement 3

**Table S1:** Taxa contribution percentage in the microbial community of pedal mucus microbiota of *Chiton granosus*, *Echinolittorina peruviana*, *Fissurella crassa*, *Scurria araucana* and *Siphonaria lessonii* and the Epilithic Biofilm Control. Red color percentage corresponds to the most abundant taxa of mayor microbial phyla, with a relative abundance of reads > 1% (Pedrós-Alió 2012). Rarefaction level <2000 reads.

TAXA	Epilithic Biofilm Control	Microbiota <i>C. granosus</i>	Microbiota <i>E. peruviana</i>	Microbiota <i>F. crassa</i>	Microbiota <i>S. araucana</i>	Microbiota <i>S. lessonii</i>
Acidobacteria	0.16	0.00	0.00	0.02	0.03	0.00
Actinobacteria	0.32	0.08	0.00	0.05	0.04	0.00
Alphaproteobacteria	<b>60.56</b>	<b>20.46</b>	<b>8.57</b>	<b>14.02</b>	<b>23.99</b>	<b>10.71</b>
Bacteroidetes	<b>12.86</b>	<b>66.52</b>	<b>8.09</b>	<b>67.29</b>	<b>49.88</b>	<b>5.09</b>
Cyanobacteria	0.17	0.08	0.03	0.08	0.14	0.00
Dadabacteria	0.24	0.00	0.00	0.00	0.00	0.00
Deinococcus-Thermus	0.00	0.00	0.00	0.00	0.00	0.03
Deltaproteobacteria	0.90	0.04	0.00	0.69	0.12	0.03
Dependentiae	0.59	0.00	0.00	0.00	0.00	0.00
Epsilonbacteraeota	0.04	0.17	<b>14.69</b>	0.96	0.58	<b>6.33</b>
Firmicutes	0.27	0.00	0.00	0.00	0.03	0.13
Fusobacteria	0.00	0.09	0.00	0.00	0.00	0.00
Gammaproteobacteria	<b>1.93</b>	<b>10.95</b>	<b>66.17</b>	<b>12.89</b>	<b>24.87</b>	<b>77.45</b>
Other	0.00	0.00	0.00	0.00	0.00	0.00
Patescibacteria	0.00	0.32	0.00	0.18	0.17	0.01
Planctomycetes	<b>19.74</b>	0.07	0.00	0.12	0.05	0.00
Spirochaetes	0.00	0.00	0.00	0.32	0.00	0.03
Tenericutes	0.00	0.00	0.00	0.03	0.00	0.03
Thaumarchaeota	0.05	0.00	0.00	0.00	0.00	0.00
Unclassified	0.06	0.00	0.00	0.00	0.00	0.00
Verrucomicrobia	<b>2.10</b>	<b>1.20</b>	<b>2.47</b>	<b>3.36</b>	0.08	0.16
<b>TOTAL</b>	<b>100</b>	<b>100</b>	<b>100</b>	<b>100</b>	<b>100</b>	<b>100</b>

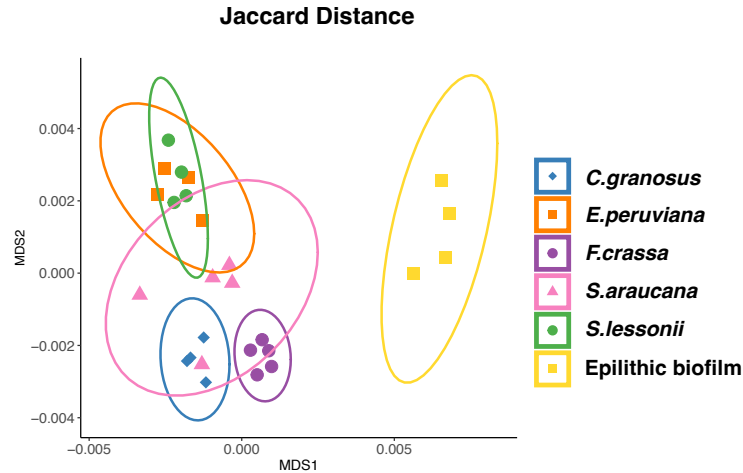


**Table S2:** Total reads of the most abundant ASVs of the pedal mucus microbiota of *Chiton granosus*, *Echinolittorina peruviana*, *Fissurella crassa*, *Scurria araucana*, and *Siphonaria lessonii*. Rarefaction level of 10,599 reads.

Phylum	Class	Order	Family	<i>C.granosus</i>	<i>E.peruviana</i>	<i>F.crassa</i>	<i>S.raucana</i>	<i>S.lessonii</i>	TotalReads	
Bacteroidetes	Bacteroidia	Chitinophagales	Saprosiraceae	149	11	13	31	6	209	
		Cytophagales	Cyclobacteriaceae	46	12	69	15	5	146	
		Flavobacteriales	Crociniomicaceae	3152	0	827	233	0	4213	
			Cryomorpaceae	339	0	60	292	7	699	
			Flavobacteriaceae	3367	821	6291	4669	531	15678	
Epsilonbacteraeota	Campylobacteria	Campylobacterales	Arcobacteraceae	14	1526	124	64	641	2369	
Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	2060	848	1251	2435	1189	7782	
			Alteromonadaceae	307	781	17	240	1095	2439	
	Gammaproteobacteria	Alteromonadales	Colwelliaceae	368	3430	71	551	3900	8320	
			Pseudoalteromonadaceae	29	40	73	416	133	691	
			Shewanellaceae	17	8	47	30	9	112	
			Cellvibrionales	Cellvibrionaceae	18	125	3	25	253	423
		Oceanospirillales	Marinomonadaceae	1	860	17	129	977	1984	
			Nitrocolaceae	83	466	107	480	344	1479	
			Saccharospirillaceae	35	1096	65	54	896	2146	
	Vibrionales	Vibrionaceae	218	244	918	594	475	2447		
	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Rubritaleaceae	130	245	276	11	19	681

Supplement 4.

**Figure S1:** Microbiota compositional similarity of the most abundant grazers of the intertidal rocky shore and the epilithic biofilm. Non-metric multidimensional scaling (NMDS) ordination plots based on Jaccard distances. The shapes denote the microbiota grazer species surrounded by an ellipse showing the 95% confidence interval. Stress = 0.101. Rarefaction level <2000 reads.



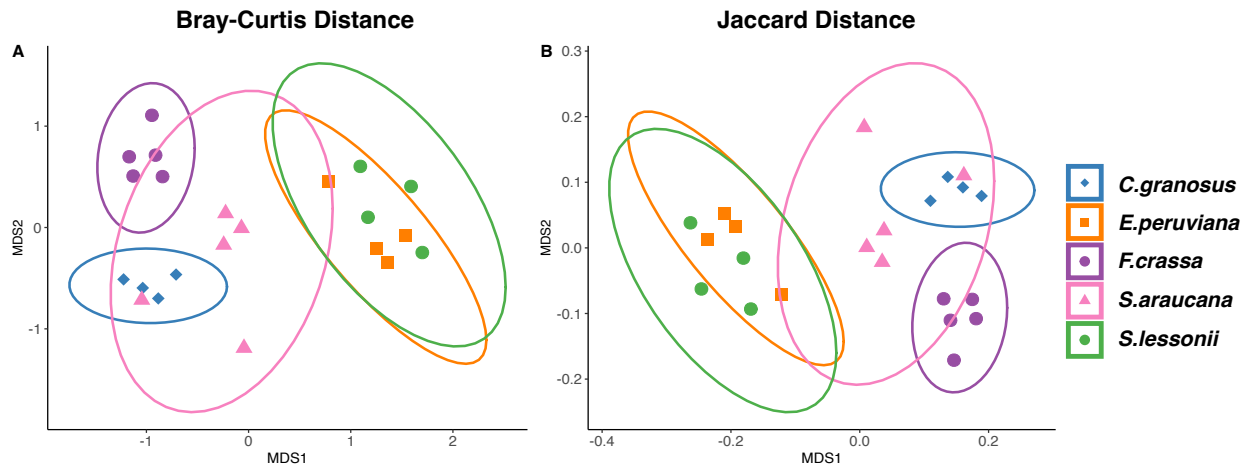
**Table S1: Bray-Curtis distance.** False Discovery Rate (FDR) corrected (Benjamini and Hochberg 1995) pairwise comparisons of the microbial communities of the pedal mucus microbiota of *Chiton granosus*, *Echinolittorina peruviana*, *Fissurella crassa*, *Scurria araucana*, and *Siphonaria lessonii* and the epilithic biofilms. Rarefaction level <2000 reads.

pairs	Df	Sums of Sqs	F. Model	R <sup>2</sup>	p .value	p. adjusted sig
<i>C.granosus</i> vs <i>E.peruviana</i>	1	0.93	5.00	0.45	0.03	0.04
<i>C.granosus</i> vs <i>F.crassa</i>	1	1.04	6.94	0.50	0.01	0.02
<i>C.granosus</i> vs <i>S.araucana</i>	1	0.50	2.14	0.23	0.05	0.05
<i>C.granosus</i> vs <i>S.lessonii</i>	1	0.94	5.62	0.48	0.03	0.04
<i>C.granosus</i> vs Epilithic biofilm	1	1.42	8.04	0.57	0.03	0.04
<i>E.peruviana</i> vs <i>F.crassa</i>	1	1.34	9.67	0.58	0.01	0.02
<i>E.peruviana</i> vs <i>S.araucana</i>	1	0.76	3.45	0.33	0.01	0.02
<i>E.peruviana</i> vs <i>S.lessonii</i>	1	0.05	0.33	0.05	0.91	0.91
<i>E.peruviana</i> vs Epilithic biofilm	1	1.49	9.13	0.60	0.02	0.04
<i>F.crassa</i> vs <i>S.araucana</i>	1	1.00	5.41	0.40	0.01	0.02
<i>F.crassa</i> vs <i>S.lessonii</i>	1	1.37	11.20	0.62	0.01	0.02
<i>F.crassa</i> vs Epilithic biofilm	1	1.70	13.10	0.65	0.01	0.02
<i>S.araucana</i> vs <i>S.lessonii</i>	1	0.78	3.80	0.35	0.01	0.02
<i>S.araucana</i> vs Epilithic biofilm	1	1.44	6.79	0.49	0.01	0.02
<i>S.lessonii</i> vs Epilithic biofilm	1	1.55	10.73	0.64	0.03	0.04

**Table S2: Jaccard distance.** False Discovery Rate (FDR) corrected (Benjamini and Hochberg 1995) pairwise comparisons of the microbial communities of the pedal mucus microbiota of *Chiton granosus*, *Echinolittorina peruviana*, *Fissurella crassa*, *Scurria araucana*, and *Siphonaria lessonii* and the epilithic biofilms. Rarefaction level <2000 reads.

pairs	Df	Sums of Sqs	F. Model	R <sup>2</sup>	p .value	p. adjusted sig
C.granosus vs E.peruviana	1	0.93	5.00	0.45	0.04	0.04
C.granosus vs F.crassa	1	1.04	6.94	0.50	0.01	0.02
C.granosus vs S.araucana	1	0.50	2.14	0.23	0.05	0.05
C.granosus vs S.lessonii	1	0.94	5.62	0.48	0.02	0.03
C.granosus vs Epilithic biofilm	1	1.42	8.04	0.57	0.03	0.04
E.peruviana vs F.crassa	1	1.34	9.67	0.58	0.00	0.02
E.peruviana vs S.araucana	1	0.76	3.45	0.33	0.01	0.02
<b>E.peruviana vs S.lessonii</b>	<b>1</b>	<b>0.05</b>	<b>0.33</b>	<b>0.05</b>	<b>0.91</b>	<b>0.91</b>
E.peruviana vs Epilithic biofilm	1	1.49	9.13	0.60	0.03	0.04
F.crassa vs S.araucana	1	1.00	5.41	0.40	0.01	0.02
F.crassa vs S.lessonii	1	1.37	11.20	0.62	0.02	0.03
F.crassa vs Epilithic biofilm	1	1.70	13.10	0.65	0.01	0.02
S.araucana vs S.lessonii	1	0.78	3.80	0.35	0.01	0.02
S.araucana vs Epilithic biofilm	1	1.44	6.79	0.49	0.01	0.02
S.lessonii vs Epilithic biofilm	1	1.55	10.73	0.64	0.02	0.03

**Figure S2:** Microbiota compositional similarity of the most abundant grazers of the intertidal rocky shore. Non-metric multidimensional scaling (NMDS) ordination plots based on (A) Bray-Curtis and (B) Jaccard distances. The shapes denote the microbiota grazer species surrounded by an ellipse showing the 95% confidence interval. (A) Stress = 0.112, (B) stress = 0.112. Rarefaction level of 10,599 reads.



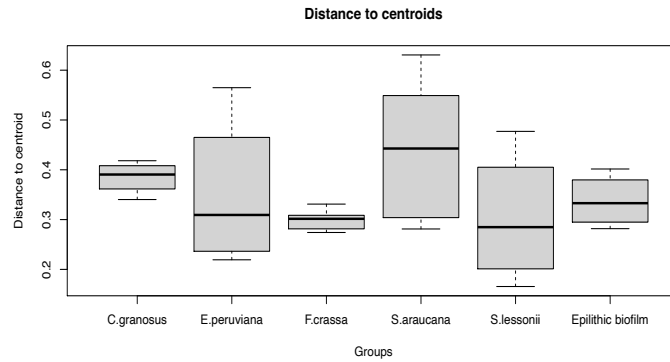
**Table S3: Bray-Curtis distance.** Permanova  $p > 0.001$ . False Discovery Rate (FDR) corrected (Benjamini and Hochberg 1995) pairwise comparisons of the microbial communities of the pedal mucus microbiota of *Chiton granosus*, *Echinolittorina peruviana*, *Fissurella crassa*, *Scurria araucana*, and *Siphonaria lessonii*. Rarefaction level of 10,599 reads.

<b>pairs</b>	<b>Df</b>	<b>SumsOfSqs</b>	<b>F.Model</b>	<b>R2</b>	<b>p.value</b>	<b>p.adjusted</b>	<b>sig</b>
C.granosus vs E.peruviana	1	0.95	5.38	0.47	0.03	0.04	.
C.granosus vs F.crassa	1	1.04	7.41	0.51	0.01	0.02	.
C.granosus vs S.araucana	1	0.51	2.23	0.24	0.04	0.04	.
C.granosus vs S.lessonii	1	0.93	5.88	0.50	0.03	0.04	.
E.peruviana vs F.crassa	1	1.36	10.22	0.59	0.01	0.02	.
E.peruviana vs S.araucana	1	0.78	3.55	0.34	0.01	0.02	.
<b>E.peruviana vs S.lessonii</b>	<b>1</b>	<b>0.05</b>	<b>0.34</b>	<b>0.05</b>	<b>0.93</b>	<b>0.93</b>	.
F.crassa vs S.araucana	1	1.01	5.53	0.41	0.01	0.02	.
F.crassa vs S.lessonii	1	1.38	11.74	0.63	0.01	0.02	.
S.araucana vs S.lessonii	1	0.77	3.76	0.35	0.01	0.02	.

**Table S4: Jaccard distance.** Permanova  $p > 0.001$ . False Discovery Rate (FDR) corrected (Benjamini and Hochberg 1995) pairwise comparisons of the microbial communities of the pedal mucus microbiota of *Chiton granosus*, *Echinolittorina peruviana*, *Fissurella crassa*, *Scurria araucana*, and *Siphonaria lessonii*. Rarefaction level of 10,599 reads.

<b>pairs</b>	<b>Df</b>	<b>SumsOfSqs</b>	<b>F.Model</b>	<b>R2</b>	<b>p.value</b>	<b>p.adjusted</b>	<b>sig</b>
C.granosus vs E.peruviana	1	0.95	5.38	0.47	0.03	0.03	.
C.granosus vs F.crassa	1	1.04	7.41	0.51	0.01	0.02	.
C.granosus vs S.araucana	1	0.51	2.23	0.24	0.02	0.03	.
C.granosus vs S.lessonii	1	0.93	5.88	0.50	0.02	0.03	.
E.peruviana vs F.crassa	1	1.36	10.22	0.59	0.01	0.02	.
E.peruviana vs S.araucana	1	0.78	3.55	0.34	0.01	0.02	.
<b>E.peruviana vs S.lessonii</b>	<b>1</b>	<b>0.05</b>	<b>0.34</b>	<b>0.05</b>	<b>0.91</b>	<b>0.91</b>	.
F.crassa vs S.araucana	1	1.01	5.53	0.41	0.01	0.02	.
F.crassa vs S.lessonii	1	1.38	11.74	0.63	0.01	0.02	.
S.araucana vs S.lessonii	1	0.77	3.76	0.35	0.01	0.02	.

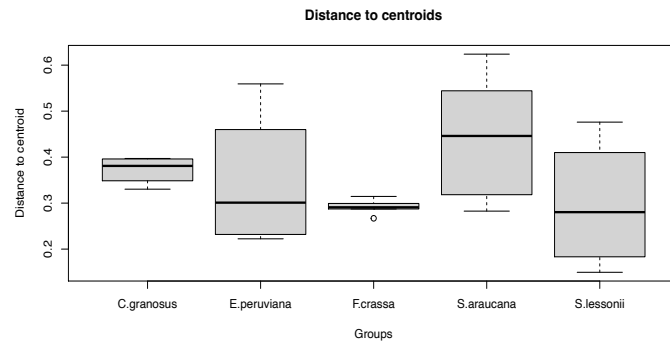
**Figure S3.** PERMDISP analyses for a dataset of rarefaction level <2000 reads. The figure showed the distance to the centroid of *C.granosus*, *E.peruviana*, *F. crassa*, *S.araucana*, and *S. lessonii* and the epilithic biofilms group.



Analysis of Variance Table (Response: Distances)

	Df	Sum Sq.	Mean.Sq	F value	Pr(>F)
Groups	5	0.068535	0.013707	1.176	0.3555
Residuals	20	0.233119	0.011656		

**Figure S4.** PERMDISP analyses for a dataset of rarefaction level 10,599 reads. The figure showed the distance to the centroid of *C.granosus*, *E.peruviana*, *F. crassa*, *S.araucana*, and *S. lessonii* group.

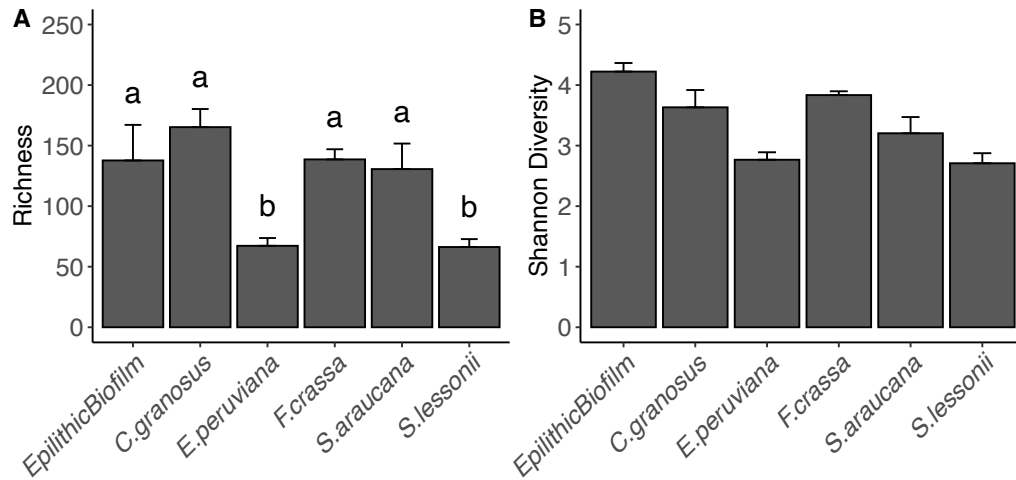


Analysis of Variance Table ( Response: Distances)

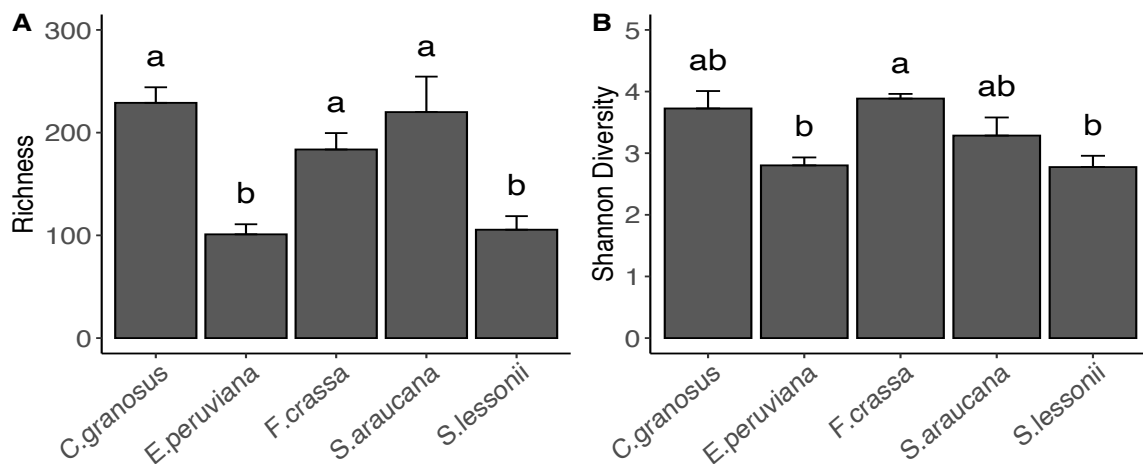
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Groups	4	0.073608	0.018402	1.4046	0.2747
Residuals	17	0.222730	0.013102		

## Supplement 5

**Figure S1.** Mean **A)** richness and **B)** Shannon index diversity of microbial community (Bacteria and Archaea) of the pedal mucus microbiota of *C. granosus*, *F. crassa*, *S. araucana*, *E. peruviana*, *S. lessonii* and the epilithic biofilm (mean + SE). Different letters above bars indicate significant differences (among treatments from Tukey test at the experiment-wise error rate = 0.05). Rarefaction level of 1,869 reads.



**Figure S2.** Mean **A)** richness and **B)** Shannon index diversity of the microbial community (Bacteria and Archaea) of the pedal mucus microbiota of *C. granosus*, *F. crassa*, *S. araucana*, *E. peruviana*, *S. lessonii* (mean + SE). Different letters above bars indicate significant differences (among treatments from Tukey test at the experiment-wise error rate = 0.05). Rarefaction level of 10,599 reads.



**Supplement 6.**

**Table S1:** Tukey post hoc test multiple comparisons of richness of the microbial communities of the pedal mucus microbiota and the epilithic biofilms. 95% family-wise confidence level. Rarefaction level of 1,869 reads.

Comparisons	diff	lwr	upr	p adj
<i>E.peruviana-C.granosus</i>	-0.391	-0.648	-0.134	0.001
<i>F.crassa-C.granosus</i>	-0.074	-0.318	0.170	0.927
<i>S.raucana-C.granosus</i>	-0.120	-0.364	0.123	0.636
<i>S.lessonii-C.granosus</i>	-0.397	-0.654	-0.140	0.001
EpilithicBiofilm- <i>C.granosus</i>	-0.098	-0.355	0.159	0.831
<i>F.crassa-E.peruviana</i>	0.317	0.074	0.561	0.006
<i>S.raucana-E.peruviana</i>	0.271	0.027	0.514	0.024
<i>S.lessonii-E.peruviana</i>	-0.006	-0.263	0.251	1.000
EpilithicBiofilm- <i>E.peruviana</i>	0.293	0.036	0.550	0.020
<i>S.raucana-F.crassa</i>	-0.046	-0.276	0.183	0.987
<i>S.lessonii-F.crassa</i>	-0.323	-0.567	-0.080	0.005
EpilithicBiofilm- <i>F.crassa</i>	-0.024	-0.268	0.219	1.000
<i>S.lessonii-S.raucana</i>	-0.277	-0.521	-0.033	0.020
EpilithicBiofilm- <i>S.raucana</i>	0.022	-0.221	0.266	1.000
EpilithicBiofilm- <i>S.lessonii</i>	0.299	0.042	0.556	0.017

**Table S2:** Tukey post hoc test multiple comparisons of Shannon index of the microbial communities of the pedal mucus microbiota and the epilithic biofilms. 95% family-wise confidence level. Rarefaction level of 1,869 reads.

Comparisons	diff	lwr	upr	p adj
<i>E.peruviana-C.granosus</i>	-0.115	-0.236	0.006	0.069
EpilithicBiofilm- <i>C.granosus</i>	0.069	-0.052	0.190	0.492
<i>F.crassa-C.granosus</i>	0.028	-0.087	0.143	0.971
<i>S.raucana-C.granosus</i>	-0.056	-0.171	0.059	0.649
<i>S.lessonii-C.granosus</i>	-0.126	-0.247	-0.004	0.040
EpilithicBiofilm- <i>E.peruviana</i>	0.184	0.063	0.306	0.001
<i>F.crassa-E.peruviana</i>	0.143	0.028	0.258	0.010
<i>S.raucana-E.peruviana</i>	0.059	-0.056	0.174	0.599
<i>S.lessonii-E.peruviana</i>	-0.010	-0.132	0.111	1.000
<i>F.crassa</i> -EpilithicBiofilm	-0.041	-0.156	0.074	0.863
<i>S.raucana</i> -EpilithicBiofilm	-0.125	-0.240	-0.010	0.028
<i>S.lessonii</i> -EpilithicBiofilm	-0.195	-0.316	-0.073	0.001
<i>S.raucana-F.crassa</i>	-0.084	-0.192	0.025	0.193
<i>S.lessonii-F.crassa</i>	-0.153	-0.268	-0.038	0.005
<i>S.lessonii-S.raucana</i>	-0.070	-0.185	0.045	0.430



**Table S3:** Tukey post hoc test multiple comparisons of richness of the microbial communities of the pedal mucus microbiota. 95% family-wise confidence level. Dataset with a rarefaction level of 10,599 reads.

Comparisons	diff	lwr	upr	p adj
<b>E.peruviana-C.granosus</b>	-0.359	-0.607	-0.111	<b>0.003</b>
<b>F.crassa-C.granosus</b>	-0.100	-0.335	0.136	0.700
<b>S.raucana-C.granosus</b>	-0.039	-0.275	0.197	0.986
<b>S.lessonii-C.granosus</b>	-0.346	-0.594	-0.097	<b>0.004</b>
<b>F.crassa-E.peruviana</b>	0.259	0.023	0.495	<b>0.027</b>
<b>S.raucana-E.peruviana</b>	0.320	0.084	0.556	<b>0.005</b>
<b>S.lessonii-E.peruviana</b>	0.013	-0.235	0.262	1.000
<b>S.raucana-F.crassa</b>	0.061	-0.161	0.283	0.916
<b>S.lessonii-F.crassa</b>	-0.246	-0.481	-0.010	<b>0.039</b>
<b>S.lessonii-S.raucana</b>	-0.307	-0.542	-0.071	<b>0.008</b>

**Table S4:** Tukey post hoc test multiple comparisons of Shannon index of the microbial communities of the pedal mucus microbiota. 95% family-wise confidence level. Dataset with a rarefaction level of 10,599 reads.

Comparisons	diff	lwr	upr	p adj
<b>E.peruviana-C.granosus</b>	-0.121	-0.250	0.008	0.073
<b>F.crassa-C.granosus</b>	0.022	-0.101	0.145	0.981
<b>S.raucana-C.granosus</b>	-0.057	-0.180	0.065	0.622
<b>S.lessonii-C.granosus</b>	-0.127	-0.256	0.002	0.056
<b>F.crassa-E.peruviana</b>	<b>0.143</b>	<b>0.020</b>	<b>0.266</b>	<b>0.018</b>
<b>S.raucana-E.peruviana</b>	0.064	-0.059	0.186	0.530
<b>S.lessonii-E.peruviana</b>	-0.006	-0.135	0.123	1.000
<b>S.raucana-F.crassa</b>	-0.079	-0.195	0.036	0.269
<b>S.lessonii-F.crassa</b>	<b>-0.149</b>	<b>-0.272</b>	<b>-0.026</b>	<b>0.013</b>
<b>S.lessonii-S.raucana</b>	-0.070	-0.192	0.053	0.446

## Supplement 7

**Table S1:** ASVs habitat specialist to a specific pedal mucus microbiota of *Chiton granosus*, *Echinolittorina peruviana*, *Fissurella crassa*, *Scurria araucana* and *Siphonaria lessonii* with the associated probability (p). Number of reads and ASVs Taxa classification is also presented. Dataset with a rarefaction level of 10,599 reads.

ASV	Number of reads	pVal	Microbiota	Phylum	Class	Order	Family	Genus
ASV_12	8759	0.017	<i>E.peruviana</i>	Epsilonbacteraeota	Campylobacteria	Campylobacterales	Arcobacteraceae	Arcobacter
ASV_43	8468	0.009	<i>C.granosus</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Crocinitomicaceae	Crocinitomix
ASV_16	6440	0.038	<i>E.peruviana</i>	Proteobacteria	Gammaproteobacteria	Alteromonadales	Colwelliaceae	Colwellia
ASV_22	6184	0.024	<i>S.araucana</i>	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Pseudophaeobacter
ASV_56	5505	0.001	<i>F.crassa</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Tenacibaculum
ASV_26	4781	0.004	<i>S.araucana</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Polaribacter
ASV_98	3722	0.009	<i>F.crassa</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	NA
ASV_134	3443	0.001	<i>F.crassa</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Polaribacter_4
ASV_51	3269	0.024	<i>S.araucana</i>	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Roseobacter_clade_NAC11-7_lineage
ASV_139	3224	0.001	<i>F.crassa</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Tenacibaculum
ASV_23	2663	0.023	<i>E.peruviana</i>	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Nitrincolaceae	Neptuniibacter
ASV_232	2181	0.001	<i>F.crassa</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	NA
ASV_163	2153	0.003	<i>C.granosus</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Crocinitomicaceae	Crocinitomix
ASV_208	2040	0.006	<i>C.granosus</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Olleya
ASV_166	1942	0.026	<i>C.granosus</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Olleya
ASV_82	1926	0.001	<i>S.araucana</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	NA
ASV_234	1676	0.04	<i>C.granosus</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Crocinitomicaceae	Crocinitomix
ASV_83	1647	0.03	<i>E.peruviana</i>	Proteobacteria	Gammaproteobacteria	Alteromonadales	Colwelliaceae	Colwellia
ASV_138	1484	0.001	<i>F.crassa</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Polaribacter_4
ASV_312	1478	0.002	<i>C.granosus</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Olleya
ASV_274	1464	0.001	<i>F.crassa</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Nonlabens
ASV_150	1435	0.001	<i>S.araucana</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Pseudofulvibacter
ASV_316	1200	0.001	<i>F.crassa</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Lacinutrix
ASV_131	1170	0.001	<i>S.araucana</i>	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Nitrincolaceae	Marinobacterium
ASV_302	959	0.001	<i>F.crassa</i>	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Roseobacter
ASV_264	951	0.012	<i>F.crassa</i>	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Nitrincolaceae	Amphritea
ASV_256	870	0.001	<i>S.lessonii</i>	Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	Paraglaciicola
ASV_586	857	0.001	<i>F.crassa</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Polaribacter_4
ASV_509	829	0.008	<i>C.granosus</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Crocinitomicaceae	Salinirepens
ASV_57	817	0.022	<i>S.lessonii</i>	Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	Alteromonas
ASV_307	807	0.001	<i>S.araucana</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Tenacibaculum
ASV_446	807	0.002	<i>C.granosus</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Cryomorphaceae	NS10_marine_group
ASV_486	802	0.003	<i>F.crassa</i>	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Rubritaleaceae	Rubritalea
ASV_504	796	0.001	<i>F.crassa</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Tenacibaculum
ASV_32	741	0.003	<i>S.lessonii</i>	Proteobacteria	Gammaproteobacteria	Cellvibrionales	Cellvibrionaceae	Aestuariicella
ASV_27	730	0.013	<i>F.crassa</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Polaribacter

ASV_473	729	0.014	<i>F.crassa</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Lacinutrix
ASV_546	729	0.001	<i>F.crassa</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	NA
ASV_240	657	0.011	<i>E.peruviana</i>	Epsilonbacteraeota	Campylobacteria	Campylobacteriales	Arcobacteraceae	Arcobacter
ASV_581	554	0.001	<i>F.crassa</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Tenacibaculum
ASV_640	554	0.001	<i>F.crassa</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	NA
ASV_306	532	0.002	<i>S.raucana</i>	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Nitrincolaceae	Marinobacterium
ASV_734	492	0.001	<i>F.crassa</i>	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Rubritaleaceae	Rubritalea
ASV_728	481	0.005	<i>C.granosus</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Flavirhabdus
ASV_719	444	0.002	<i>F.crassa</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Crocinitomicaceae	NA
ASV_30	442	0.001	<i>F.crassa</i>	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Loktanella
ASV_810	436	0.006	<i>F.crassa</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	NA
ASV_717	417	0.008	<i>C.granosus</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Aurantivirga
ASV_782	414	0.001	<i>F.crassa</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Polaribacter_3
ASV_160	412	0.005	<i>E.peruviana</i>	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Nitrincolaceae	Neptuniibacter
ASV_624	410	0.01	<i>F.crassa</i>	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	NA
ASV_463	400	0.035	<i>F.crassa</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Kordia
ASV_712	400	0.006	<i>C.granosus</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Crocinitomicaceae	Crocinitomix
ASV_803	385	0.001	<i>F.crassa</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	NA
ASV_972	373	0.031	<i>F.crassa</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Tenacibaculum
ASV_986	354	0.002	<i>F.crassa</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	NA
ASV_899	339	0.003	<i>C.granosus</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	NA
ASV_815	318	0.001	<i>F.crassa</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Dokdonia
ASV_558	316	0.011	<i>S.lessonii</i>	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Loktanella
ASV_540	315	0.001	<i>S.raucana</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Tenacibaculum
ASV_537	312	0.006	<i>C.granosus</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Polaribacter_4
ASV_715	300	0.004	<i>S.raucana</i>	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	NA
ASV_753	298	0.001	<i>F.crassa</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Crocinitomicaceae	Crocinitomix
ASV_771	290	0.001	<i>F.crassa</i>	Bacteroidetes	Bacteroidia	Cytophagales	Cyclobacteriaceae	NA
ASV_754	289	0.003	<i>C.granosus</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Tenacibaculum
ASV_992	289	0.002	<i>C.granosus</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	NA
ASV_366	287	0.026	<i>S.raucana</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Tenacibaculum
ASV_668	264	0.001	<i>F.crassa</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Pseudofulvibacter
ASV_354	257	0.001	<i>F.crassa</i>	Proteobacteria	Gammaproteobacteria	Alteromonadales	Pseudoalteromonadaceae	Pseudoalteromonas
ASV_1157	249	0.011	<i>F.crassa</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Tenacibaculum
ASV_854	248	0.041	<i>C.granosus</i>	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Roseobacter
ASV_1062	231	0.001	<i>F.crassa</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	NA
ASV_858	230	0.001	<i>F.crassa</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Algibacter
ASV_1038	230	0.002	<i>F.crassa</i>	Proteobacteria	Deltaproteobacteria	Bdellovibrionales	Bacteriovoracaceae	Peredibacter
ASV_1224	227	0.009	<i>C.granosus</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Tenacibaculum
ASV_1193	223	0.007	<i>C.granosus</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	NA
ASV_1029	221	0.021	<i>C.granosus</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Príca
ASV_1133	217	0.001	<i>C.granosus</i>	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Thalassobius
ASV_1050	214	0.04	<i>C.granosus</i>	Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	Paraglaciocola
ASV_1274	204	0.001	<i>F.crassa</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	NA
ASV_1429	199	0.001	<i>F.crassa</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Tenacibaculum
ASV_1278	195	0.008	<i>F.crassa</i>	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Pseudophaeobacter
ASV_1364	194	0.005	<i>C.granosus</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	NA
ASV_595	180	0.004	<i>C.granosus</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Tenacibaculum
ASV_1174	177	0.005	<i>F.crassa</i>	Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	Vibrio

ASV_1489	172	0.004	<i>C.granosus</i>	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Rubritaleaceae	Rubritalea
ASV_864	169	0.001	<i>F.crassa</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Aquibacter
ASV_1459	167	0.001	<i>F.crassa</i>	Spirochaetes	Spirochaetia	Spirochaetales	Spirochaetaceae	NA
ASV_1639	165	0.001	<i>C.granosus</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Nonlabens
ASV_1551	162	0.001	<i>F.crassa</i>	Proteobacteria	Gammaproteobacteria	Cardiobacteriales	Cardiobacteriaceae	NA
ASV_1523	161	0.001	<i>C.granosus</i>	Bacteroidetes	Bacteroidia	Cytophagales	Cyclobacteriaceae	Persicobacter
ASV_825	152	0.001	<i>E.peruviana</i>	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Rubritaleaceae	Rubritalea
ASV_1536	152	0.001	<i>F.crassa</i>	Proteobacteria	Deltaproteobacteria	Bdellovibrionales	Bacteriovoraceae	NA
ASV_1730	152	0.003	<i>F.crassa</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Pricia
ASV_987	150	0.001	<i>S.saraucana</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Aurantivirga
ASV_1654	149	0.001	<i>C.granosus</i>	Bacteroidetes	Bacteroidia	Chitinophagales	Saprospiraceae	NA
ASV_96	146	0.015	<i>C.granosus</i>	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Sulfitobacter
ASV_145	146	0.001	<i>F.crassa</i>	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Planktotalea
ASV_1335	144	0.043	<i>C.granosus</i>	Patescibacteria	Gracilibacteria	JGI_0000069-P22	NA	NA
ASV_1558	140	0.011	<i>C.granosus</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Olleya
ASV_964	138	0.035	<i>E.peruviana</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	NA
ASV_1377	135	0.002	<i>F.crassa</i>	Proteobacteria	Gammaproteobacteria	Alteromonadales	Shewanellaceae	Shewanella
ASV_700	134	0.002	<i>S.saraucana</i>	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Nitrincolaceae	Neptuniibacter
ASV_1658	134	0.002	<i>C.granosus</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Dokdonia
ASV_481	130	0.003	<i>F.crassa</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Dokdonia
ASV_1848	128	0.003	<i>C.granosus</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Winogradskyella
ASV_1417	127	0.009	<i>E.peruviana</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Polaribacter_4
ASV_879	125	0.033	<i>S.saraucana</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	NA
ASV_1871	124	0.01	<i>C.granosus</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Dokdonia
ASV_1043	122	0.041	<i>S.saraucana</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Nonlabens
ASV_1434	117	0.004	<i>C.granosus</i>	Proteobacteria	Alphaproteobacteria	Rhizobiales	Phyllobacteriaceae	Ahrensia
ASV_1659	117	0.001	<i>C.granosus</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Maribacter
ASV_1118	116	0.005	<i>S.saraucana</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Pseudofulvibacter
ASV_934	115	0.027	<i>S.saraucana</i>	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Nitrincolaceae	Profundimonas
ASV_1918	115	0.002	<i>C.granosus</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Tamlana
ASV_2076	115	0.001	<i>F.crassa</i>	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Rubritaleaceae	Persicirhabdus
ASV_1921	114	0.003	<i>C.granosus</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Winogradskyella
ASV_1640	111	0.028	<i>C.granosus</i>	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Alliioseovarius
ASV_1990	108	0.005	<i>C.granosus</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Dokdonia
ASV_2275	108	0.018	<i>F.crassa</i>	Proteobacteria	Gammaproteobacteria	Cardiobacteriales	Cardiobacteriaceae	NA
ASV_1058	104	0.03	<i>S.saraucana</i>	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Aquimarina
ASV_1119	104	0.012	<i>S.lessonii</i>	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Marinomnadaceae	Marinomonas
ASV_175	101	0.003	<i>C.granosus</i>	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Oceanibulbus

## Supplement 8.

**Table S1:** Tukey post hoc test multiple comparisons of carbohydrates content of the mollusk pedal mucus. 95% family-wise confidence level.

Comparisons	diff	lwr	upr	p adj
E. peruviana-C. granosus	2.221739	-19.699616	24.143094	0.9979968
<b>F. crassa-C. granosus</b>	<b>29.765217</b>	<b>7.843862</b>	<b>51.686573</b>	<b>0.0048901</b>
S. araucana-C. granosus	-9.078261	-30.999616	12.843094	0.7293341
S. lessonii-C. granosus	-1.373913	-23.295268	20.547442	0.9996977
<b>F. crassa-E. peruviana</b>	<b>27.543478</b>	<b>5.622123</b>	<b>49.464834</b>	<b>0.0096315</b>
S. araucana-E. peruviana	-11.300000	-33.221355	10.621355	0.5485567
S. lessonii-E. peruviana	-3.595652	-25.517008	18.325703	0.9873329
<b>S. araucana-F. crassa</b>	<b>-38.843478</b>	<b>-60.764834</b>	<b>-16.922123</b>	<b>0.0002994</b>
<b>S. lessonii-F. crassa</b>	<b>-31.139130</b>	<b>-53.060486</b>	<b>-9.217775</b>	<b>0.0032046</b>
S. lessonii-S. araucana	7.704348	-14.217008	29.625703	0.8283245

**Table S2:** Tukey post hoc test multiple comparisons of protein content of the mollusk pedal mucus. 95% family-wise confidence level.

Comparisons	diff	lwr	upr	p adj
E. peruviana-C. granosus	0.2441584	-0.9536288	1.4419455	0.9718389
<b>F. crassa-C. granosus</b>	<b>1.3365920</b>	<b>0.1388048</b>	<b>2.5343791</b>	<b>0.0241524</b>
S. araucana-C. granosus	-0.2691531	-1.4669403	0.9286340	0.9601363
S. lessonii-C. granosus	0.6728711	-0.5249160	1.8706583	0.4669652
F. crassa-E. peruviana	1.0924336	-0.1053536	2.2902208	0.0845680
S. araucana-E. peruviana	-0.5133115	-1.7110987	0.6844757	0.7045129
S. lessonii-E. peruviana	0.4287128	-0.7690744	1.6265000	0.8189422
<b>S. araucana-F. crassa</b>	<b>-1.6057451</b>	<b>-2.8035323</b>	<b>-0.4079579</b>	<b>0.0054904</b>
S. lessonii-F. crassa	-0.6637208	-1.8615080	0.5340663	0.4801524
S. lessonii-S. araucana	0.9420243	-0.2557629	2.1398114	0.1695123

## Supplement 9.

**Figure S1.** Partition plot of the Linear Discriminant Analyses (LDA) between the Carbohydrates and Proteins content ( $\mu\text{g mL}^{-1}$ ) of the pedal mucus of (A) *Chiton granosus*, (B) *Echinolittorina peruviana*, (C) *Fissurella crassa*, (D) *Scurria araucana*, and (E) *Siphonaria lessonii*. Error rate: 0.5.

