

SUPPLEMENTAL TABLES & FIGURES

Supplemental Table S1. Sample metadata and sequence processing statistics for each stage of the *dada2* denoising pipeline implemented in *QIIME2* v2019.4.

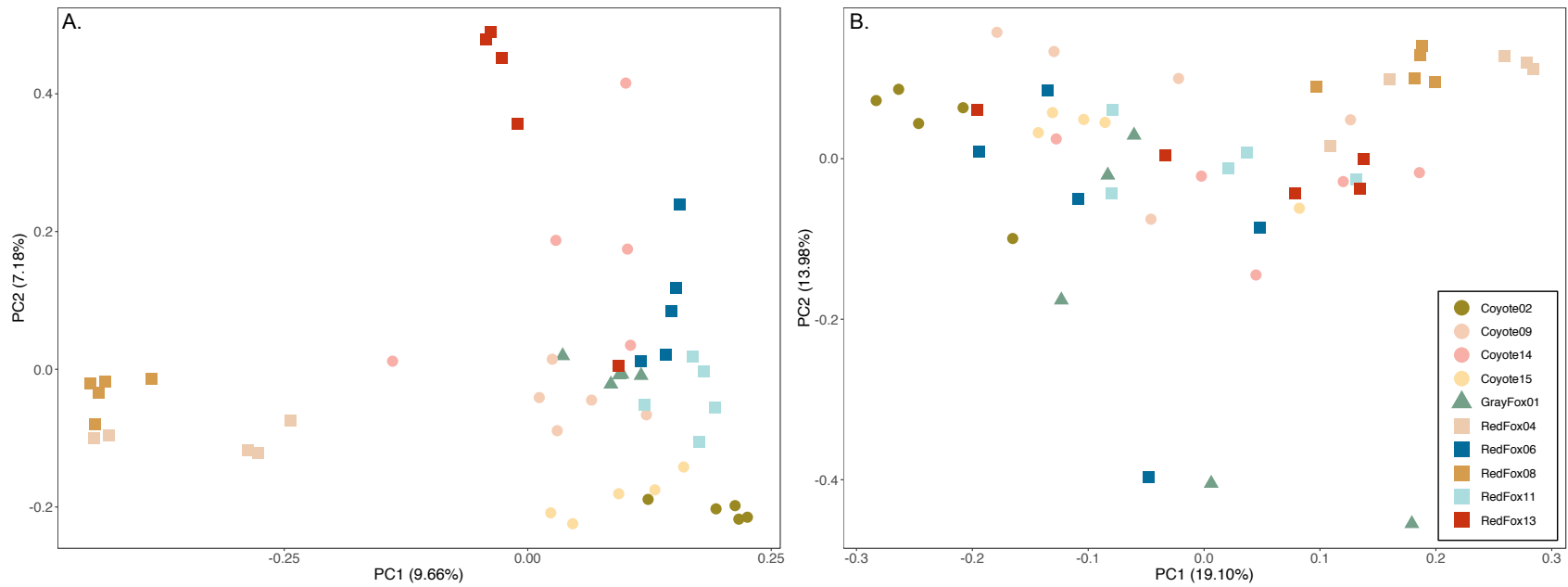
Sample	Individual	Body Site	Mange	Raw	Filtered	Denoised	Merged	Non-chimeric
Sample001	Coyote01	Axilla	N	21880	21460	21211	20323	20318
Sample002	Coyote01	Flank	N	19921	19224	18726	17056	17053
Sample003	Coyote01	Ext. Ear	N	23282	22705	22189	20714	20702
Sample004	Coyote01	Groin	N	22307	21460	20996	18645	18597
Sample005	Coyote01	Leg	N	14010	13740	13284	12113	12110
Sample006	Coyote01	Feces	N	42790	41668	41450	40176	39773
Sample007	Coyote02	Axilla	N	34661	33742	32714	28442	28374
Sample008	Coyote02	Flank	N	32241	31450	30596	25559	25474
Sample009	Coyote02	Ext. Ear	N	26067	25433	24612	20560	20421
Sample010	Coyote02	Groin	N	35941	34529	33286	27620	27589
Sample011	Coyote02	Leg	N	24420	23845	23372	20910	20910
Sample012	Coyote03	Axilla	Y	28306	27017	25999	21460	21384
Sample013	Coyote03	Flank	Y	31527	30782	29924	26527	26508
Sample014	Coyote03	Ext. Ear	Y	27237	26792	25758	22549	22542
Sample015	Coyote03	Groin	Y	33222	32677	31576	27342	27269
Sample016	Coyote03	Leg	Y	27294	26883	26071	23309	23284
Sample017	Coyote04	Axilla	Y	23290	22464	21870	19271	19224
Sample018	Coyote04	Flank	Y	24863	24429	23722	21659	21584
Sample019	Coyote04	Ext. Ear	Y	22292	21937	21339	19382	19306
Sample020	Coyote04	Groin	Y	26914	26394	25780	24032	23980
Sample021	Coyote04	Leg	Y	35549	35049	34300	31853	31753
Sample022	Coyote05	Axilla	Unk	33548	32422	31613	28500	28491
Sample023	Coyote05	Flank	Unk	38426	37151	36068	32869	32798
Sample024	Coyote05	Ext. Ear	Unk	28579	27554	26875	24312	24258
Sample025	Coyote05	Groin	Unk	46654	45061	43252	36312	36189
Sample026	Coyote05	Leg	Unk	26783	25892	25109	22394	22219
Sample027	Coyote06	Axilla	Y	30134	29327	29144	28481	28119

Sample028	Coyote06	Flank	Y	29076	28468	28300	27678	27559
Sample029	Coyote06	Ext. Ear	Y	48530	47202	46647	43752	43505
Sample030	Coyote06	Groin	Y	21978	21428	21220	20313	19973
Sample031	Coyote06	Leg	Y	33429	32852	32661	31772	31703
Sample032	Coyote07	Axilla	Y	37741	37029	36899	35555	34737
Sample033	Coyote07	Flank	Y	40204	39358	38854	36406	35824
Sample034	Coyote07	Ext. Ear	Y	27471	26564	25704	22593	22509
Sample035	Coyote07	Groin	Y	29636	28091	27972	25960	24267
Sample036	Coyote07	Leg	Y	14629	14270	13999	13233	13233
Sample037	Coyote08	Axilla	Y	43555	42887	42708	41674	40514
Sample038	Coyote08	Flank	Y	23519	23140	23053	22648	22328
Sample039	Coyote08	Ext. Ear	Y	62047	60594	60202	58765	58646
Sample040	Coyote08	Groin	Y	27548	26938	26803	26050	25592
Sample041	Coyote08	Leg	Y	40075	38521	37911	35059	34588
Sample042	Coyote09	Axilla	N	38705	38124	37924	37177	37040
Sample043	Coyote09	Flank	N	29913	29290	28450	25421	25414
Sample044	Coyote09	Ext. Ear	N	32290	31807	31315	30053	29800
Sample045	Coyote09	Groin	N	38723	37498	36734	33413	33402
Sample046	Coyote09	Leg	N	31017	30329	29494	25584	25584
Sample047	Coyote10	Axilla	Y	24923	24459	24276	23821	23665
Sample048	Coyote10	Flank	Y	34535	33325	33010	32030	31969
Sample049	Coyote10	Ext. Ear	Y	25538	25053	24828	24091	24036
Sample050	Coyote10	Groin	Y	26185	25455	25295	24581	24542
Sample051	Coyote10	Leg	Y	23103	22689	22610	22289	22289
Sample052	Coyote11	Axilla	Y	26320	25733	25586	24429	24208
Sample053	Coyote11	Flank	Y	26473	25880	25638	24280	23976
Sample054	Coyote11	Ext. Ear	Y	24999	24379	24093	22787	22536
Sample055	Coyote11	Groin	Y	47912	46327	46058	44134	42606
Sample056	Coyote11	Leg	Y	27332	26843	26535	25767	25247
Sample057	Coyote12	Axilla	Y	22901	22411	22067	20689	20689
Sample058	Coyote12	Flank	Y	9160	8849	8676	8146	8112
Sample059	Coyote12	Ext. Ear	Y	37803	36633	35937	34136	34032
Sample060	Coyote12	Groin	Y	17988	17586	17046	16172	16135

Sample061	Coyote12	Leg	Y	21884	21394	20977	19999	19997
Sample062	Coyote13	Axilla	Y	318	276	216	152	152
Sample063	Coyote13	Flank	Y	24762	24139	23825	22783	22187
Sample064	Coyote13	Ext. Ear	Y	24572	23710	23344	20675	20580
Sample065	Coyote13	Groin	Y	44941	43545	43390	42686	41686
Sample066	Coyote13	Leg	Y	27261	26172	25972	25207	25038
Sample067	Coyote14	Axilla	N	24867	24344	24165	23564	23365
Sample068	Coyote14	Flank	N	34128	33267	32865	31360	31233
Sample069	Coyote14	Ext. Ear	N	23589	22874	22206	19363	19348
Sample070	Coyote14	Groin	N	20079	19648	19171	17101	17087
Sample071	Coyote14	Leg	N	27085	25835	25475	24560	24541
Sample072	Coyote15	Axilla	N	24297	23952	22981	19613	19541
Sample073	Coyote15	Flank	N	36185	35588	34415	30440	30248
Sample074	Coyote15	Ext. Ear	N	27551	27153	26573	24617	24431
Sample075	Coyote15	Groin	N	21389	20999	19923	16392	16313
Sample076	Coyote15	Leg	N	34751	33306	31768	24774	24475
Sample077	GrayFox01	Axilla	N	26003	25431	25015	22566	22542
Sample078	GrayFox01	Flank	N	36943	36220	36026	35639	35448
Sample079	GrayFox01	Ext. Ear	N	10981	10579	10370	9937	9937
Sample080	GrayFox01	Groin	N	6211	6048	5863	5289	5289
Sample081	GrayFox01	Leg	N	37515	37011	36839	36508	36249
Sample082	GrayFox02	Axilla	Y	24511	23550	23393	21973	21537
Sample083	GrayFox02	Flank	Y	18440	18094	17959	17572	17391
Sample084	GrayFox02	Ext. Ear	Y	22054	21469	21267	20437	20335
Sample085	GrayFox02	Groin	Y	36630	35789	35618	34348	33341
Sample086	GrayFox02	Leg	Y	30891	29825	29616	28345	28075
Sample087	RedFox01	Center Back	Y	10707	10351	10068	9525	9522
Sample088	RedFox01	Ear	Y	8401	8176	7961	7363	7360
Sample089	RedFox01	Perianal	Y	11617	11276	11170	10844	10844
Sample090	RedFox01	Lip	Y	16955	16613	16482	16155	16116
Sample091	RedFox01	Nose	Y	7390	7097	6952	6451	6440
Sample092	RedFox02	Axilla	Y	25280	24807	24575	23967	23843
Sample093	RedFox02	Flank	Y	24765	24172	23644	21972	21939

Sample094	RedFox02	Ext. Ear	Y	16522	16042	15746	14815	14717
Sample095	RedFox02	Groin	Y	33869	31156	30881	28114	28064
Sample096	RedFox02	Leg	Y	25940	25339	25099	24173	24028
Sample097	RedFox03	Axilla	Y	22710	22373	22201	21812	21564
Sample098	RedFox03	Flank	Y	30133	29493	29324	27747	27414
Sample099	RedFox03	Ext. Ear	Y	21128	20669	20517	19110	19036
Sample100	RedFox03	Groin	Y	11925	11653	11480	11116	11050
Sample101	RedFox03	Leg	Y	26193	25011	24770	23553	23354
Sample102	RedFox04	Axilla	N	22057	21046	20877	20402	20399
Sample103	RedFox04	Flank	N	35549	34340	33876	31278	31180
Sample104	RedFox04	Ext. Ear	N	51241	49443	48641	45517	45256
Sample105	RedFox04	Groin	N	25295	24731	24493	23899	23705
Sample106	RedFox04	Leg	N	27010	26151	25980	25364	25223
Sample107	RedFox05	Axilla	Y	20807	20382	20306	20196	20160
Sample108	RedFox05	Flank	Y	10386	10161	9974	9587	9571
Sample109	RedFox05	Ext. Ear	Y	23427	23105	22946	22465	22411
Sample110	RedFox05	Groin	Y	9529	9245	9164	9005	9000
Sample111	RedFox05	Leg	Y	29618	29147	28964	27786	26951
Sample112	RedFox05	Feces	Y	37572	36118	35830	33293	32962
Sample113	RedFox06	Axilla	N	26804	26057	25638	24404	24247
Sample114	RedFox06	Flank	N	49845	48866	47369	42186	42049
Sample115	RedFox06	Ext. Ear	N	10965	10718	10393	9773	9755
Sample116	RedFox06	Groin	N	18970	18255	17677	13888	13772
Sample117	RedFox06	Leg	N	42852	41922	40979	36185	35033
Sample118	RedFox06	Feces	N	40038	38921	38633	36785	36575
Sample119	RedFox07	Axilla	Y	1810	1690	1569	1353	1353
Sample120	RedFox07	Flank	Y	1470	1383	1290	1137	1137
Sample121	RedFox07	Ext. Ear	Y	40520	39431	39242	38752	38483
Sample122	RedFox07	Groin	Y	65229	63691	63397	60378	58376
Sample123	RedFox07	Leg	Y	41419	40743	40597	40012	39611
Sample124	RedFox08	Axilla	N	26546	25817	25487	23929	23899
Sample125	RedFox08	Flank	N	57950	56300	55466	52325	51867
Sample126	RedFox08	Ext. Ear	N	30058	29223	28659	26911	26885

Sample127	RedFox08	Groin	N	27783	26889	26303	24667	24562
Sample128	RedFox08	Leg	N	27233	26468	25858	23793	23582
Sample129	RedFox09	Axilla	Y	34948	34016	33849	33218	33141
Sample130	RedFox09	Flank	Y	30389	29933	29637	28443	28320
Sample131	RedFox09	Ext. Ear	Y	27316	26800	26601	26217	25778
Sample132	RedFox09	Groin	Y	37234	36322	36023	35606	35606
Sample133	RedFox09	Leg	Y	39676	38413	37968	35973	35574
Sample134	RedFox10	Axilla	Y	28930	28364	28022	27036	26925
Sample135	RedFox10	Flank	Y	33170	32197	31730	30387	30114
Sample136	RedFox10	Ext. Ear	Y	24691	23936	23781	23171	23171
Sample137	RedFox10	Groin	Y	29538	28969	28624	27860	27639
Sample138	RedFox10	Leg	Y	44650	43886	43524	42535	41992
Sample139	RedFox11	Axilla	N	6218	5989	5796	5215	5153
Sample140	RedFox11	Flank	N	34023	33074	32220	28765	28742
Sample141	RedFox11	Ext. Ear	N	13049	12657	12195	10853	10833
Sample142	RedFox11	Groin	N	23474	22555	22316	21190	21186
Sample143	RedFox11	Leg	N	42699	41395	41000	37965	37376
Sample144	RedFox12	Axilla	Y	31266	30772	30595	29882	29032
Sample145	RedFox12	Flank	Y	46195	44887	44448	40845	39906
Sample146	RedFox12	Ext. Ear	Y	48650	47339	46912	42652	42136
Sample147	RedFox12	Groin	Y	22500	21918	21737	21172	20700
Sample148	RedFox12	Leg	Y	46691	45758	45467	42561	42208
Sample149	RedFox13	Axilla	N	27153	26820	26294	24599	24217
Sample150	RedFox13	Flank	N	23406	23010	22466	20417	20206
Sample151	RedFox13	Ext. Ear	N	35123	34150	33217	29877	29660
Sample152	RedFox13	Groin	N	43264	42534	42132	40797	40047
Sample153	RedFox13	Leg	N	52624	51323	50902	48869	47900



Supplemental Figure S1. Principal coordinate analysis (PCoA) of uninfected individuals showed significant clustering by individual (PERMANOVA; Bray-Curtis, $pseudo-F=2.984$, $p=0.001$; Weighted UniFrac, $pseudo-F=3.470$, $p=0.001$) rather than body site (Bray-Curtis, $pseudo-F=0.781$, $p=0.997$; Weighted UniFrac, $pseudo-F=0.950$, $p=0.574$) using both (A) Bray-Curtis and (B) phylogeny-based Weighted UniFrac distances.

Supplemental Table S2. Results from alpha (Kruskal-Wallis test) and beta (PERMANOVA) diversity significance tests. Given that mange infection status exerted the strongest influence on alpha and beta diversity, we analyzed the full composite dataset in downstream analyses, with mange infection as our variable of interest.

A.

	Variable	Kruskal-Wallis <i>H</i>	<i>p</i> -value
Chao1	State	4.879	0.300
	Species	2.468	0.291
	Age	2.771	0.428
	Sex	6.871	0.032
	Year Sampled	6.526	0.089
	Mange	10.711	0.001

	Variable	Kruskal-Wallis <i>H</i>	<i>p</i> -value
Evenness	State	6.343	0.175
	Species	1.448	0.485
	Age	3.436	0.329
	Sex	6.546	0.038
	Year Sampled	4.659	0.199
	Mange	8.643	0.003

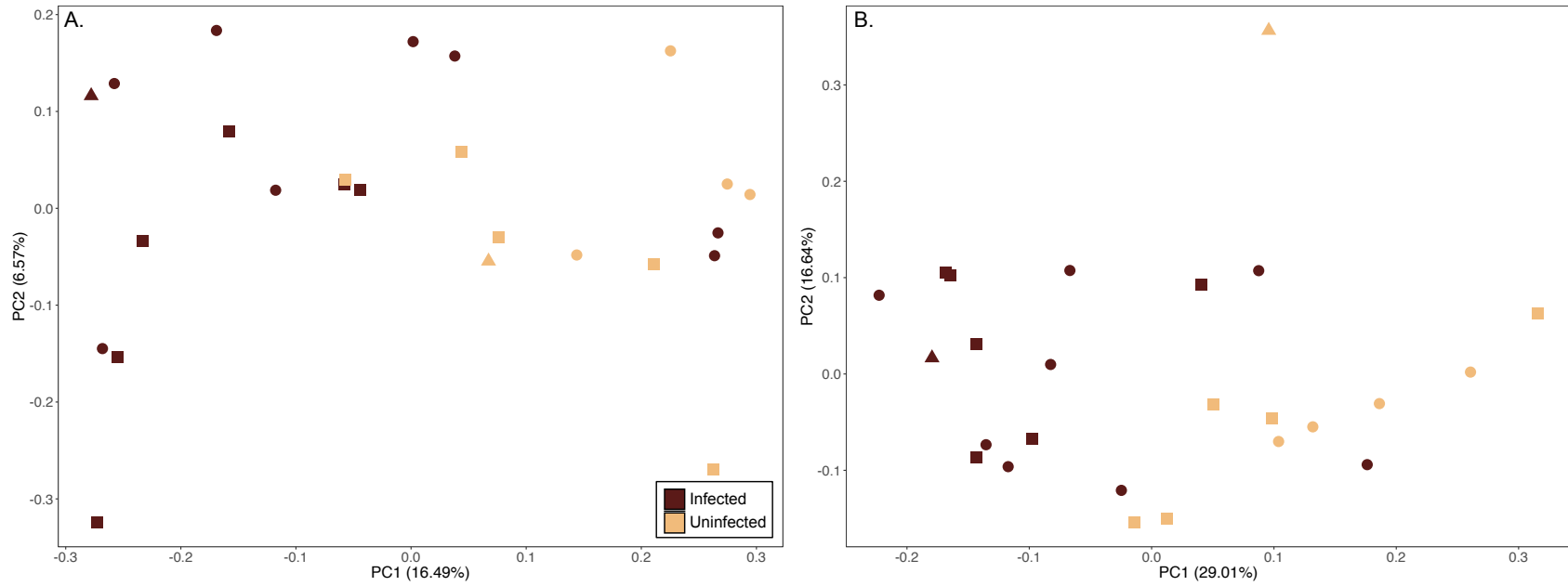
B.

	Variable	<i>Pseudo-F</i>	<i>p</i> -value
Bray-Curtis	State	1.341	0.015†
	Species	1.025	0.358
	Age	1.075	0.271
	Sex	2.120	0.001
	Year Sampled	1.220	0.085
	Mange	3.885	0.001

	Variable	<i>Pseudo-F</i>	<i>p</i> -value
Weighted UniFrac	State	1.324	0.135
	Species	1.244	0.22
	Age	0.880	0.627
	Sex	2.395	0.008
	Year Sampled	1.846	0.011†
	Mange	4.398	0.001

	Variable	<i>Pseudo-F</i>	<i>p</i> -value
Unweighted UniFrac	State	1.267	0.021†
	Species	1.103	0.215
	Age	0.982	0.525
	Sex	1.554	0.007
	Year Sampled	1.230	0.047†
	Mange	2.211	0.006

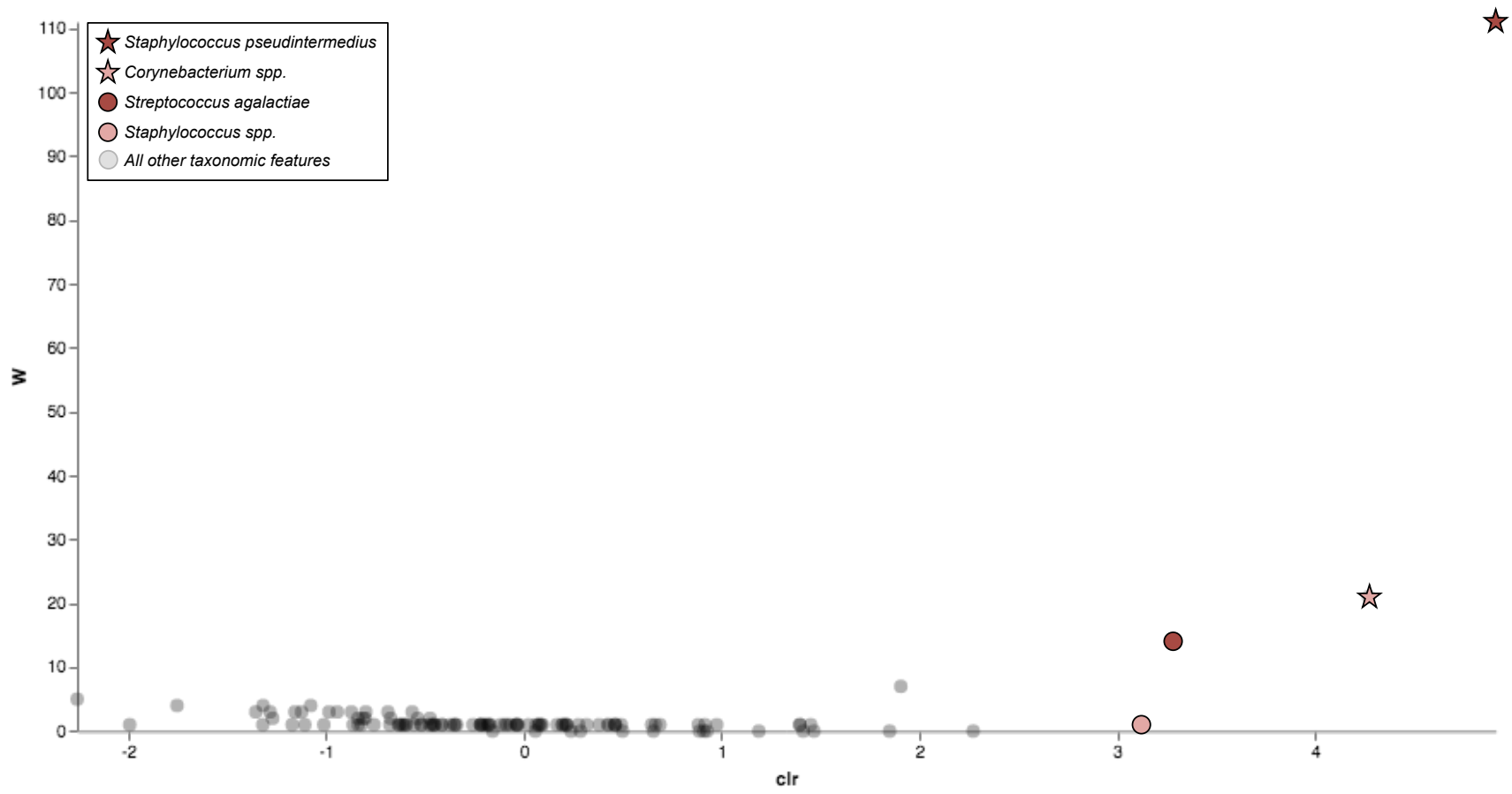
† *q*-values from pairwise tests were not significant



Supplemental Figure S2. Principal coordinate analysis (PCoA) showed significant differences between infection groups using both (A) Unweighted (PERMANOVA; $pseudo-F=2.211$, $p=0.006$) and (B) Weighted ($pseudo-F=4.398$, $p=0.001$) UniFrac distances.

Supplemental Table S3. Relative abundance of taxonomic groups by species and infection status. Across all three species, mange-infected individuals exhibited increased Bacilli and Actinobacteria, and decreased Other when compared to uninfected individuals.

Taxonomic Class	Coyote		Gray Fox		Red Fox	
	Infected	Uninfected	Infected	Uninfected	Infected	Uninfected
Actinobacteria	22.460%	12.927%	40.401%	31.758%	28.219%	7.875%
Alphaproteobacteria	3.642%	9.956%	0.673%	5.291%	0.831%	3.530%
Bacilli	32.249%	5.523%	26.874%	0.747%	42.096%	14.602%
Bacteroidia	4.147%	2.974%	2.621%	0.145%	1.367%	2.649%
Betaproteobacteria	1.196%	2.608%	0.380%	0.403%	1.277%	2.972%
Clostridia	6.806%	4.487%	12.417%	0.240%	2.291%	17.902%
Flavobacteriia	3.922%	2.465%	0.532%	37.814%	5.023%	4.135%
Fusobacteriia	4.111%	4.340%	5.303%	4.291%	0.717%	3.969%
Gammaproteobacteria	12.557%	16.224%	6.656%	11.002%	12.030%	23.138%
Other	8.911%	38.496%	4.143%	8.310%	6.148%	19.229%



Supplemental Figure S3. Analysis of the composition of microbes (ANCOM) returned one taxonomic feature as consistently and significantly associated with mite infection status: *Staphylococcus pseudintermedius* (indicated with a red star). Three additional taxa that commonly co-occurred with *S. pseudintermedius* included *Corynebacterium spp.* (pink star), *Streptococcus agalactiae* (red circle), and *Staphylococcus spp.* (pink circle).

Supplemental Table S4. NCBI BLASTn results for the two features exhibiting increased relative abundance in mange-infected individuals: (A) 3f0449c545626dd14b585e9c7b2d16f4 (class: Bacilli) and (B) e3e89166daa575e51d7a14bc65f11153 (class: Actinobacteria).

	Species	Max Score	E value	% Identity	Accession No.
A.	<i>Staphylococcus pseudintermedius</i>	410	1.00E-110	100%	LC437049.1
	<i>Staphylococcus pseudintermedius</i>	410	1.00E-110	100%	LC437042.1
	<i>Staphylococcus pseudintermedius</i>	410	1.00E-110	100%	LC437038.1
	<i>Staphylococcus pseudintermedius</i>	410	1.00E-110	100%	LC437037.1
	<i>Staphylococcus pseudintermedius</i>	410	1.00E-110	100%	LC437027.1
	<i>Staphylococcus spp.</i>	410	1.00E-110	100%	MK954146.1
	<i>Staphylococcus spp.</i>	410	1.00E-110	100%	MK954144.1
	<i>Staphylococcus pseudintermedius</i>	410	1.00E-110	100%	MK681220.1
	<i>Staphylococcus pseudintermedius</i>	410	1.00E-110	100%	MK681219.1
	<i>Staphylococcus pseudintermedius</i>	410	1.00E-110	100%	CP035740.1
	<i>Staphylococcus pseudintermedius</i>	410	1.00E-110	100%	CP035741.1
	<i>Staphylococcus pseudintermedius</i>	410	1.00E-110	100%	CP035742.1
	<i>Staphylococcus pseudintermedius</i>	410	1.00E-110	100%	CP035743.1
	<i>Staphylococcus pseudintermedius</i>	410	1.00E-110	100%	CP032682.1
	Uncultured <i>Staphylococcus spp.</i>	410	1.00E-110	100%	MH728109.1
	B.	<i>Corynebacterium resistens</i>	412	3.00E-111	100%
Uncultured bacterium		412	3.00E-111	100%	KX998044.1
Uncultured bacterium		412	3.00E-111	100%	KF084913.1
Uncultured bacterium		412	3.00E-111	100%	KF084799.1
Uncultured bacterium		412	3.00E-111	100%	KF084787.1
Uncultured bacterium		412	3.00E-111	100%	KF073670.1
Uncultured bacterium		412	3.00E-111	100%	KF063189.1
<i>Corynebacterium resistens</i>		412	3.00E-111	100%	NR_074826.1
Uncultured <i>Corynebacterium spp.</i>		412	3.00E-111	100%	AB587824.1
Uncultured <i>Corynebacterium spp.</i>		412	3.00E-111	100%	AB587823.1
Uncultured bacterium		412	3.00E-111	100%	JX052081.1
Uncultured bacterium		412	3.00E-111	100%	JX051886.1
<i>Corynebacterium auriscanis</i>		412	3.00E-111	100%	EU911931.2
<i>Corynebacterium resistens</i>		412	3.00E-111	100%	CP002857.1
Uncultured bacterium		412	3.00E-111	100%	JF238803.1