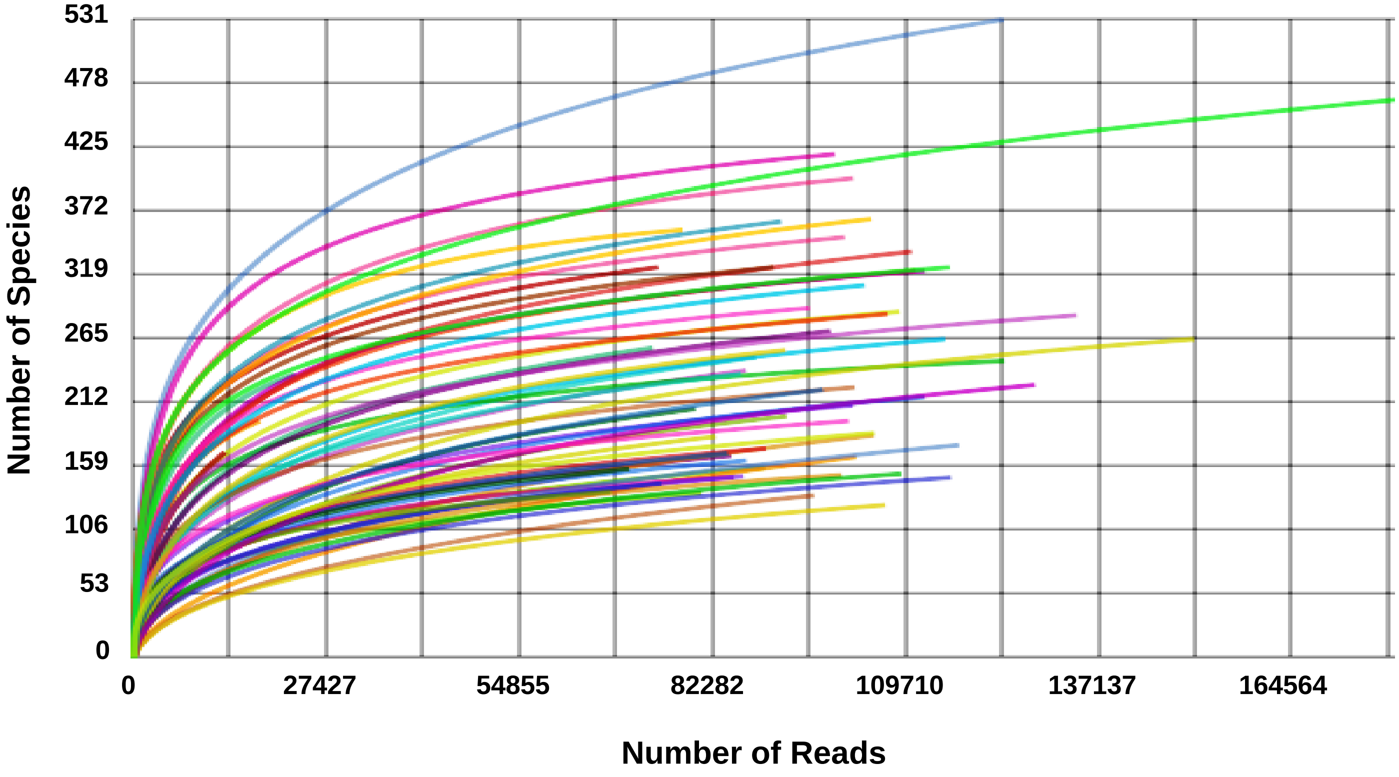

Figure S1. Rarefaction curves of the species number for 60 uterine swabs.

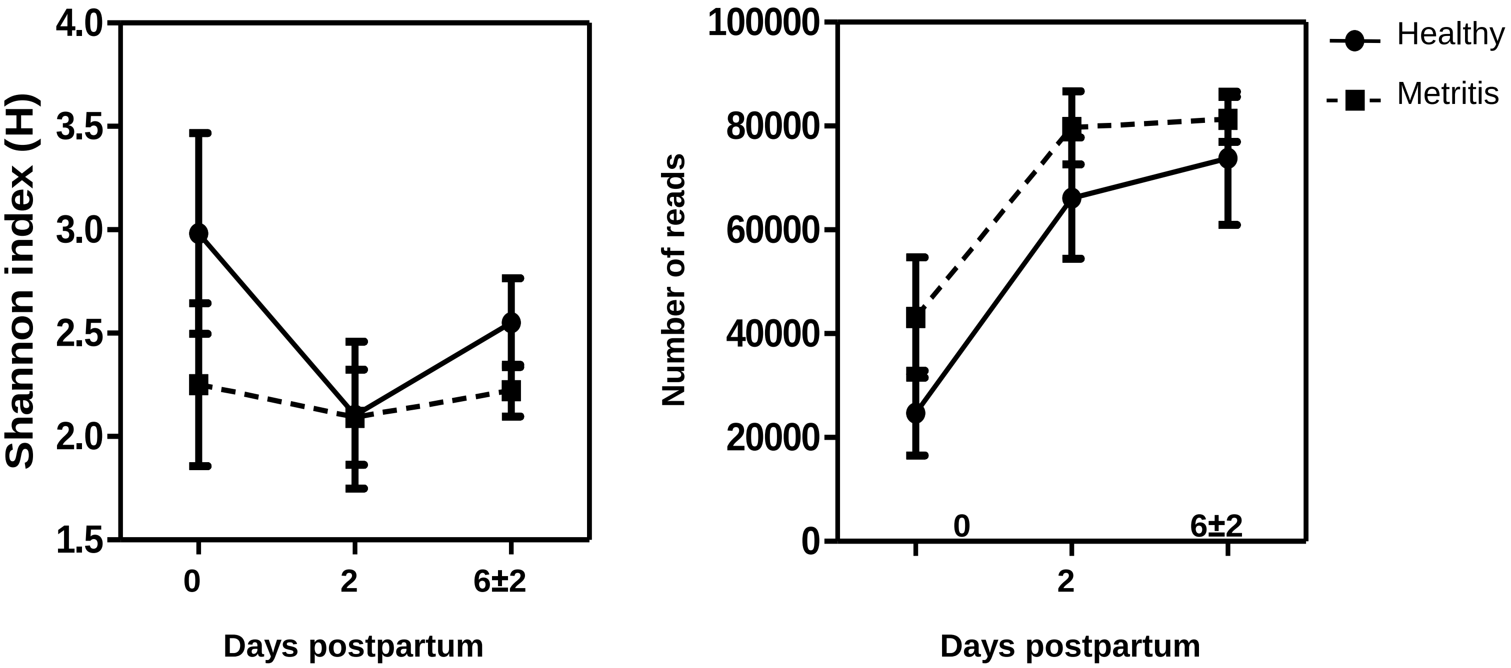

Figure S2. Diversity and abundance. The Shannon index (left) and number of reads (right) are plotted in the healthy (solid line) and metritic (dotted line) cows across the time. Data are presented by mean ± SEM. There is no significant difference between the healthy and metritic cows.

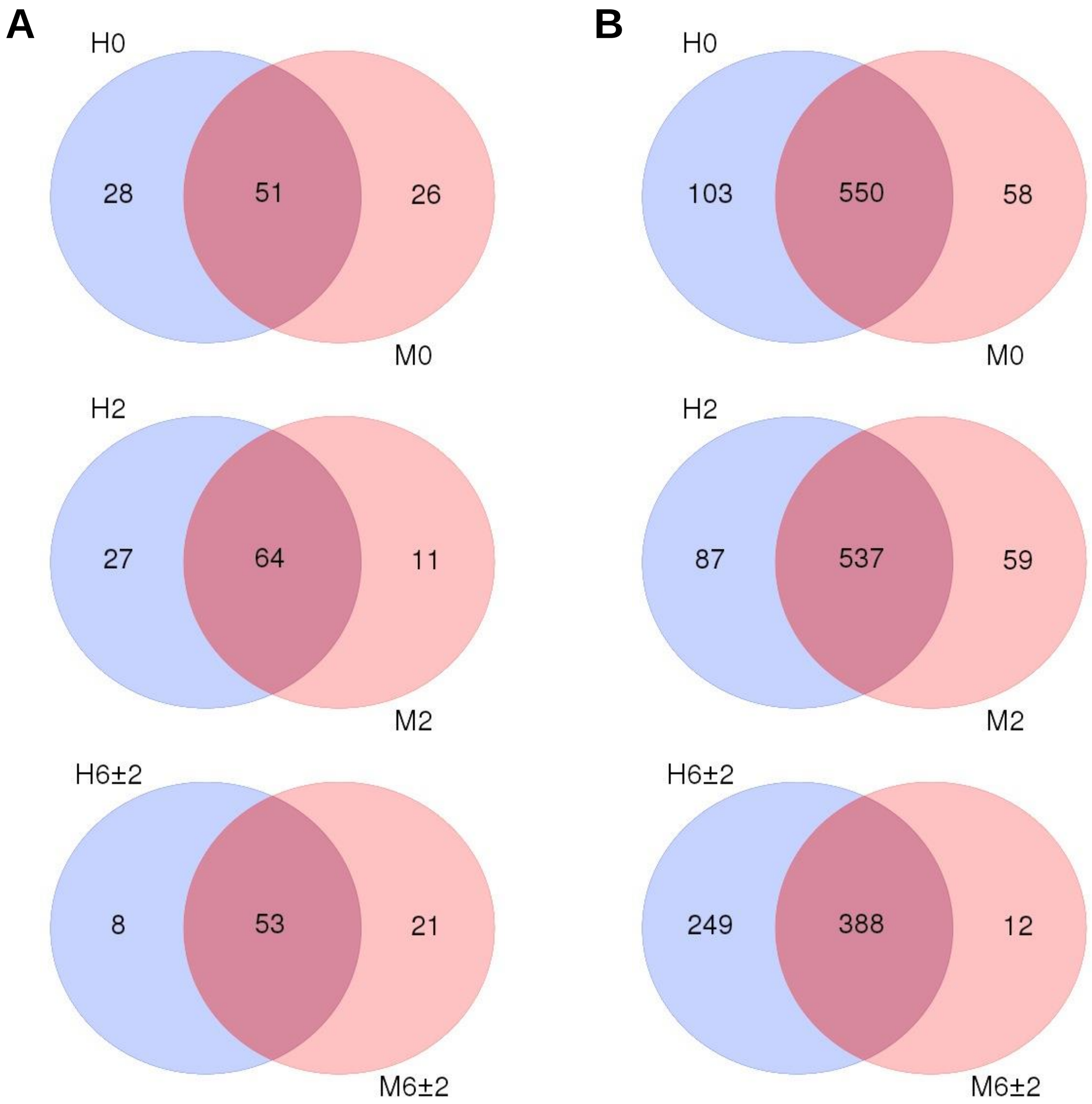

Figure S3. Venn diagrams. Venn diagrams show core genera shared by all of the dairy cows within each health status group (A), and genera that were found in any of the dairy cows within each group (B). Shared and unique genera between healthy (H) and metritic (M) cows are shown at calving (0), 2, and 6±2 days postpartum.

Table S1. MG-RAST IDs.

Healthy

Days postpartum	ID
0	4566115
0	4566138
0	4566163
0	4566147
0	4566112
0	4566141
0	4566137
0	4566122
2	4566171
2	4566113
2	4566149
2	4566144
2	4566142
2	4566139
2	4566116
2	4566133
2	4566145
4	4566154
4	4566136
6	4566172
6	4566148
6	4566140
6	4566117
8	4566150
8	4566146
8	4566143
8	4566135
8	4566114
Total	N = 28

Metritis

Days postpartum	ID
0	4566118
0	4566121
0	4566125
0	4566128
0	4566131
0	4566151
0	4566158
0	4566155
0	4566168
2	4566152
2	4566123
2	4566126
2	4566129
2	4566132
2	4566119
2	4566156
2	4566159
2	4566161
2	4566164
2	4566166
2	4566169
4	4566153
4	4566124
6	4566170
6	4566160
6	4566134
6	4566127
8	4566167
8	4566165
8	4566162
8	4566130
8	4566120
Total	N = 32

Table S2. Distribution of the 30 most abundant genera isolated from the uteri of healthy and metritic dairy cows at 0, 2, and 6 ± 2 days post parturition (DPP).

		Healthy (%)			Metritis (%)		
Genus	All	0 DPP	2 DPP	6±2 DPP	0 DPP	2 DPP	6±2 DPP
Fusobacterium	15.7	5.2	16.1	15.7	8.6	20.4	23.4
Bacteroides	13.9	8.6	5.0	12.5	14.3	12.1	28.3
Coxiella	12.7	39.6	1.0	0.1	43.2	3.6	0.1
Porphyromonas	9.9	11.4	5.5	9.6	9.2	4.1	19.7
Ureaplasma	5.2	0.1	19.0	6.2	0.03	5.8	0.1
Sneathia	4.7	0.3	8.8	8.7	0.5	7.3	1.4
Mycoplasma	4.6	0.9	5.7	2.9	0.5	13.3	1.8
Gallibacterium	3.2	0.2	12.5	1.4	0.2	4.3	0.8
Helcococcus	3.0	0.7	1.1	4.2	1.5	1.1	8.2
Prevotella	2.9	1.8	1.5	3.2	2.2	3.2	4.8
Streptococcus	2.5	1.0	3.3	2.0	1.8	5.8	0.5
Escherichia	2.1	0.6	0.1	6.4	0.03	3.9	0.03
Ruminococcus	1.9	2.9	2.0	2.5	2.5	1.7	0.1
Blautia	1.1	1.2	1.5	1.6	1.0	1.4	0.1
Acholeplasma	1.0	1.0	2.4	1.7	0.6	0.6	0.2
Clostridium	1.0	1.3	1.0	1.2	1.2	0.8	0.5
Filifactor	0.9	0.9	0.6	0.9	0.7	0.7	1.7
Peptoniphilus	0.9	1.1	0.6	1.3	0.6	0.5	1.1
Pedobacter	0.8	1.7	0.6	0.8	1.3	0.6	0.1
Serratia	0.7	0.2	0.1	2.0	0.02	1.3	0.01
Campylobacter	0.6	0.2	0.1	2.1	0.1	0.1	0.9
Candidatus Blochmannia	0.6	0.9	0.8	0.6	0.4	0.5	0.4
Treponema	0.5	0.3	0.4	1.4	0.2	0.4	0.4
Oscillospira	0.4	0.8	0.4	0.4	0.8	0.3	0.02
Caloramator	0.4	0.7	0.2	0.6	0.5	0.3	0.1
Pasteurella	0.4	0.05	0.6	1.3	0.03	0.03	0.1
Arcanobacterium/Trueperella	0.3	0.02	0.03	0.2	0.3	0.2	1.0
Peptostreptococcus	0.3	0.4	0.3	0.3	0.3	0.2	0.5
Mannheimia	0.3	0.004	1.1	0.1	0.005	0.5	0.002
Bifidobacterium	0.2	0.3	0.7	0.3	0.03	0.1	0.03

Table S3. Correlations among the 30 most abundant genera and uterine discharge score at 6 ± 2 days post parturition (DPP).

Genera[1]	UDS	*Fusobacterium*	Bacteroides	Coxiella	Porphyromonas	Ureaplasma	Sneathia	Mycoplasma	Gallibacterium	Helcococcus	Prevotella	Streptococcus	Escherichia	Ruminococcus	Blautia	Acholeplasma	Clostridium	Filifactor	Peptoniphilus	Pedobacter	Serratia	Campylobacter	Candidatus Blochmannia	Treponema	Oscillospira	Caloramator	Pasteurella	Arcanobacterium/Trueperella	Peptostreptococcus	Mannheimia	Bifidobacterium
UDS	1																														
Fusobacterium	0.49	1																													
Bacteroides	0.51	0.51	1																												
Coxiella	.	.	.	1																											
Porphyromonas	.	.	.	.	1																										
Ureaplasma	.	.	.	0.51	-0.53	1																									
Sneathia	-0.43	.	.	.	.	.	1																								
Mycoplasma	-0.43	.	.	.	-0.62	0.47	.	1																							
Gallibacterium	.	.	.	.	.	.	0.44	.	1																						
Helcococcus	0.42	0.51	.	.	.	.	.	.	.	1																					
Prevotella	.	.	.	.	0.63	.	.	.	.	.	1																				
Streptococcus	.	.	.	0.42	.	.	.	.	.	.	.	1																			
Escherichia	-0.54	.	-0.52	.	.	.	.	.	.	.	.	0.49	1																		
Ruminococcus	.	-0.56	-0.62	.	.	0.60	.	.	.	.	.	.	0.50	1																	
Blautia	.	-0.55	.	.	.	.	.	.	.	.	.	.	.	0.51	1																
Acholeplasma	.	.	.	.	.	.	0.47	.	0.45	.	.	.	.	.	.	1															
Clostridium	.	-0.63	-0.48	.	.	.	.	.	.	.	.	.	.	0.51	0.63	.	1														
Filifactor	.	.	0.46	.	0.66	.	.	-0.59	.	.	.	.	.	.	-0.47	.	.	1													
Peptoniphilus	.	.	.	.	0.53	.	.	.	.	.	0.53	.	.	.	.	.	.	0.54	1												
Pedobacter	-0.47	-0.49	.	.	.	0.47	.	.	.	-0.56	.	.	.	0.69	0.57	0.46	.	.	.	1											
Serratia	-0.48	.	-0.52	.	.	.	.	.	.	.	.	0.42	.	0.53	.	.	.	.	.	.	1										
Campylobacter	.	.	.	.	.	.	.	.	.	.	.	0.47	.	.	.	.	.	0.49	.	.	.	1									
Candidatus Blochmannia	-0.44	.	.	.	.	0.51	0.56	.	.	.	0.46	.	.	.	.	0.49	0.47	.	.	0.61	.	.	1								
Treponema	-0.49	.	-0.59	.	.	.	.	0.42	.	.	.	0.52	0.55	.	0.54	.	.	.	.	0.54	0.52	.		1							
Oscillospira	-0.48	-0.50	.	.	-0.50	0.45	.	.	.	.	.	.	0.42	0.73	.	.	0.53	-0.45	.	0.51	0.43	.	.	.	1						
Caloramator	.	-0.55	-0.59	.	.	.	.	.	.	.	.	.	.	0.59	0.54	.	0.47	.	.	.	.	.	.	0.65	0.69	1					
Pasteurella	-0.43	.	-0.43	0.43	-0.44	0.48	.	.	.	.	-0.52	.	.	0.66	.	.	.	.	.	0.45	.	.	.	0.67	0.54	.	1				
Arcanobacterium/Trueperella	.	.	.	.	.	.	.	.	-0.47	.	.	.	.	.	-0.70	.	.	.	.	.	.	.	.	.	-0.53	-0.45	.	1			
Peptostreptococcus	.	.	.	.	0.57	.	.	.	.	.	0.43	.	.	.	.	.	.	0.46	.	.	.	.	.	.	.	.	.	.	1		
Mannheimia	-0.63	.	.	.	.	.	0.58	.	.	.	.	.	.	.	.	.	.	.	.	0.58	.	.	0.65	0.61	.	.	0.56	.	.	1	
Bifidobacterium	.	.	.	0.45	-0.52	0.52	.	.	.	.	.	.	.	.	.	.	.	.	.	0.51	.	.	0.44	.	.	.	.	.	.	.	1

[1] except UDS*;* UDS = uterine discharge score (1 = not fetid normal lochia, viscous, clear, red, or brown; 2 = cloudy mucoid discharge with flecks of pus; 3 = not fetid mucopurulent discharge with ≤ 50% pus; 4 = not fetid mucopurulent discharge with ≥ 50% pus; 5 = fetid red-brownish, watery discharge). Only significant ($P \leq 0.05$) Spearman r_s coefficients of correlation are presented.

Table S4. Results for discriminant analysis performed using the 25 most abundant genera in the uteri at 0, 2, and 6 ± 2 DPP.

Item	Eigenvalue[a]	Canonical correlation[b]	$R^{2,c}$	Number misclassified[d]	Wilks' Lambda	*P*
0 DPP[e]	21.7	0.98	0.96	0	0.04	< 0.001
2 DPP	23.8	0.98	0.96	0	0.04	< 0.001
6 ± 2 DPP	21.3	0.98	0.96	0	0.04	< 0.001

[a] First canonical (canonical 1) discriminant functions were used in the analysis.

[b] Multiple correlation between the predictors (microbial genera) and the discriminant function.

[c] Canonical correlation squared. Proportion of variation in group assignment explained by the model.

[d] Number of cows incorrectly classified into a healthy or metritic group.

[e] DPP = days postpartum. 0 DPP = calving.

Table S5. Distribution of the 30 most abundant species plus *Trueperella pyogenes* (the 52nd most prevalent) isolated from the uteri of healthy and metritic dairy cows at 0, 2, and 6 ± 2 days post parturition (DPP).

		Healthy (%)			Metritis (%)		
Species	All	0 DPP	2 DPP	6±2 DPP	0 DPP	2 DPP	6±2 DPP
Fusobacterium necrophorum	14.7	6.1	14.8	15.8	9.5	18.1	20.2
Coxiella burnetii	8.8	28.3	0.1	0.01	32.2	0.8	0.01
Porphyromonas levii	8.4	12.7	5.9	9.4	8.5	3.5	11.4
Bacteroides heparinolyticus	7.6	4.0	1.8	7.0	5.4	7.9	16.8
Ureaplasma diversum	6.0	0.4	20.9	7.2	0.1	7.0	0.1
Sneathia sanguinegens	5.4	0.5	9.4	10.6	0.7	8.3	1.5
Bacteroides pyogenes	4.9	3.6	2.0	4.0	7.4	2.3	10.0
Mycoplasma californicum	4.1	0.6	5.4	1.3	0.2	13.7	1.5
Gallibacterium melopsittaci	3.9	0.5	14.6	1.7	0.3	5.4	0.9
Helcococcus ovis	3.3	0.9	1.2	4.6	2.0	1.3	8.6
Fusobacterium gonidiaformans	2.5	0.8	2.1	1.7	1.2	4.2	4.4
Bacteroides denticanum	1.6	1.9	0.9	1.4	2.8	0.8	2.1
Serratia entomophila	1.3	0.5	0.07	3.3	0.04	3.2	0.02
Streptococcus suis	1.0	0.1	2.7	0.1	0.04	2.9	0.05
Escherichia albertii	1.0	0.3	0.04	2.7	0.02	2.4	0.01
Filifactor villosus	1.0	1.0	0.5	0.9	0.8	0.9	1.7
Streptococcus uberis	0.9	0.4	0.7	1.7	0.3	1.7	0.4
Candidatus Blochmannia rufipes	0.9	1.8	1.0	0.8	1.0	0.6	0.4
Streptococcus pluranimalium	0.9	0.05	0.5	0.1	4.9	0.2	0.001
Porphyromonas cansulci	0.8	0.06	0.02	0.02	0.2	0.05	4.0
Porphyromonas asaccharolytica	0.7	0.08	0.03	0.5	0.4	0.5	2.6
Porphyromonas canis	0.7	1.1	0.4	0.5	1.1	0.5	1.1
Escherichia coli	0.7	0.2	0.03	2.0	0.01	1.6	0.01
Clostridium alkalicellulosi	0.6	1.2	0.6	0.5	1.0	0.3	0.06
Prevotella albensis	0.6	0.6	0.3	0.6	0.7	0.6	0.5
Peptoniphilus coxii	0.5	0.8	0.4	0.4	0.4	0.5	0.9
Caloramator mitchellensis	0.5	1.0	0.3	0.8	0.8	0.3	0.1
Peptoniphilus indolicus	0.5	0.8	0.3	1.0	0.4	0.1	0.3
Mycoplasma canadense	0.5	0.01	0.04	1.7	0.4	0.2	0.2
Oscillospira spp.	0.4	1.0	0.4	0.3	0.8	0.2	0.01
Trueperella pyogenes	0.2	0.02	0.01	0.1	0.1	0.1	0.6