Supplementary Material

Supplementary Table S1. Individual metadata and clinical condition description of infected group guinea pigs (*Cavia porcellus*). Code (IP : Infected Peru; II : Infected Inti)

N°	**Code**	**Breed**	**Sex**	**Weight (g)**	**Euthanasia method**			**Clinical findings**	
					Xylazine (mL)	**Ketamine (mL)**	**T61 (ml)**	**No. of nodules**	**Diameter (cm)**
1	IP 1	Peru	Female	1 404	0.14	1.12	2	1	3.5
2	IP 2	Peru	Female	612	0.06	0.49	0.8	2	3 - 3.5
3	IP 3	Peru	Male	1 586	0.16	1.27	2	4	3.3 - 3.8 - 2.5 - 2.7
4	IP 4	Peru	Female	1 293	0.13	01.03	2	2	2 - 4.1
5	IP 5	Peru	Female	661	0.07	0.53	0.8	2	2 - 5
6	IP 6	Peru	Female	946	0.1	0.76	1.5	1	2.1
7	IP 7	Peru	Male	442	0.04	0.35	0.8	7	7.7 and 5.8
8	IP 8	Peru	Male	615	0.06	0.49	0.8	1	2.3
9	IP 9	Peru	Male	1 551	0.16	1.24	2	2	2.7 and 3.4
10	IP 10	Peru	Female	1 165	0.12	0.93	1.5	4	2.6, 3.2, 2.9 and 1.8
11	IP 11	Peru	Female	1 150	0.12	0.92	1.5	3	2.5, 1.8 and 4.5
12	IP 12	Peru	Female	1 095	0.11	0.88	1.5	5	2.7, 2.4, 1.3, 1.9, 2.1, and 1.3
13	IP 13	Peru	Male	664	0.07	0.53	0.8	1	4.7
14	II 1	Inti	Female	957	0.1	0.77	1.5	2	2.7
15	II 2	Inti	Male	610	0.06	0.5	0.8	1	2.0
16	II 3	Inti	Male	720	0.07	0.58	1	1	1,7
17	II 4	Inti	Female	1 406	0.14	1.12	2	1	3.2
18	II 5	Inti	Male	650	0.06	0.52	0.8	4	1.6 - 1.4 - 1.6
19	II 6	Inti	Female	1 350	0.14	01.08	2	1	2
20	II 7	Inti	Female	1 645	0.16	1.32	2	1	3,1
21	II 8	Inti	Female	1 547	0.15	1.24	2	3	2.6 - 3.4 - 3.9
22	II 9	Inti	Male	1 030	0.1	0.82	1.5	1	3.2 x 3.4
23	II 10	Inti	Female	1 885	0.2	1.51	2	1	4 x 3.5

Supplementary Table S2. Individual metadata and baseline parameters of healthy group guinea pigs (*Cavia porcellus*). Code (SP : Healthy Peru; II : Healthy Inti)

ID	**Code**	**Breed**	**Sex**	**Weight (g)**	**Euthanasia method**	**Clinical findings**	
						No. of nodules	**Diameter (cm)**
1	SP 1	Peru	Female	862	Cervical dislocation	3	1.1 x 0.7
2	SP 2	Peru	Male	740	Cervical dislocation	5	0.7
3	SP 3	Peru	Male	584	Cervical dislocation	4	0.6 - 0.55
4	SP 4	Peru	Male	675	Cervical dislocation	4	0.65 - 0.4
5	SP 5	Peru	Male	836	Cervical dislocation	4	0.65 - 0.6
6	SP 6	Peru	Male	760	Cervical dislocation	5	0.3 - 0.8
7	SP 7	Peru	Female	709	Cervical dislocation	4	0.65
8	SP 8	Peru	Male	798	Cervical dislocation	5	0.5
9	SP 9	Peru	Male	735	Cervical dislocation	3	0.65
10	SP 10	Peru	Male	715	Cervical dislocation	6	0.5
11	SP 11	Peru	Male	728	Cervical dislocation	4	0.65
12	SI 1	Inti	Female	1051	Cervical dislocation	6	1 x 0.6
13	SI 2	Inti	Male	756	Cervical dislocation	4	0.35 - 0.75
14	SI 3	Inti	Male	746	Cervical dislocation	7	0.35 - 0.55 - 0.7
15	SI 4	Inti	Male	727	Cervical dislocation	4	1.05 - 0.6
16	SI 5	Inti	Male	782	Cervical dislocation	4	0.8
17	SI 6	Inti	Male	832	Cervical dislocation	3	0.5 - 0.55
18	SI 7	Inti	Male	728	Cervical dislocation	7	0.3 - 0.4 - 0.5 - 0.45
19	SI 8	Inti	Female	639	Cervical dislocation	4	0.85
20	SI 9	Inti	Male	840	Cervical dislocation	4	0.65
21	SI 10	Inti	Male	594	Cervical dislocation	6	0.75
22	SI 11	Inti	Male	776	Cervical dislocation	3	0.7
23	SI 12	Inti	Male	693	Cervical dislocation	4	0.3 - 1.0

Supplementary Table S3. Quality control parameters of genomic DNA extracted by fluorometry and spectrophotometry. Code (IP : Infected Peru; II : Infected Inti; SP : Healthy Peru; II : Healthy Inti). Samples marked with an asterisk (*) were excluded from downstream analyses because they did not yield sequencing data due to low bacterial DNA concentration in the libraries at the time of sequencing.

ID	Code	QUBIT (ng/µl)	Nanodrop (ng/µl)	A260/A280	A260/A230
1	IP 2	24.0	51.7	1.84	1.67
2	IP 3	31.6	30.8	1.88	1.67
3	IP 4	50.5	35	1.89	1.95
4	IP 6	48.1	136	1.87	2.07
5	IP 7*	33.5	31.9	2.04	1.86
6	IP 8	139	582.5	1.93	2.36
7	IP 9	189	426.9	1.76	1.27
8	IP 10	125	198.3	1.89	2.25
9	IP 11	239	673.0	1.94	2.34
10	IP 12	314	517.6	1.93	2.36
11	IP 13	59.7	165.6	1.92	2.19
12	II 1	350	489.2	1.92	2.27
13	II 2	150	455.3	1.97	2.36
14	II 3	1000	2182.6	1.96	2.43
15	II 4	26.4	64.7	1.91	2.14
16	II 5	77.5	170.0	1.92	2.34
17	II 6	267	482.1	1.94	2.34
18	II 7	67.3	268.8	1.94	2.30
19	II 8	55.6	124.7	1.93	2.28
20	II 9	31.0	61.9	1.88	2.00
21	II 10	62.4	122.1	1.90	2.29
22	SI 1	36.1	193.0	1.83	1.97
23	SI 2	477	743.2	1.89	2.36
24	SI 4*	980	1296.0	1.90	2.40
25	SI 5	383	1150.1	1.90	2.38
26	SI 6*	451	1375.6	1.91	2.40
27	SI 7	474	1760.8	1.94	2.42

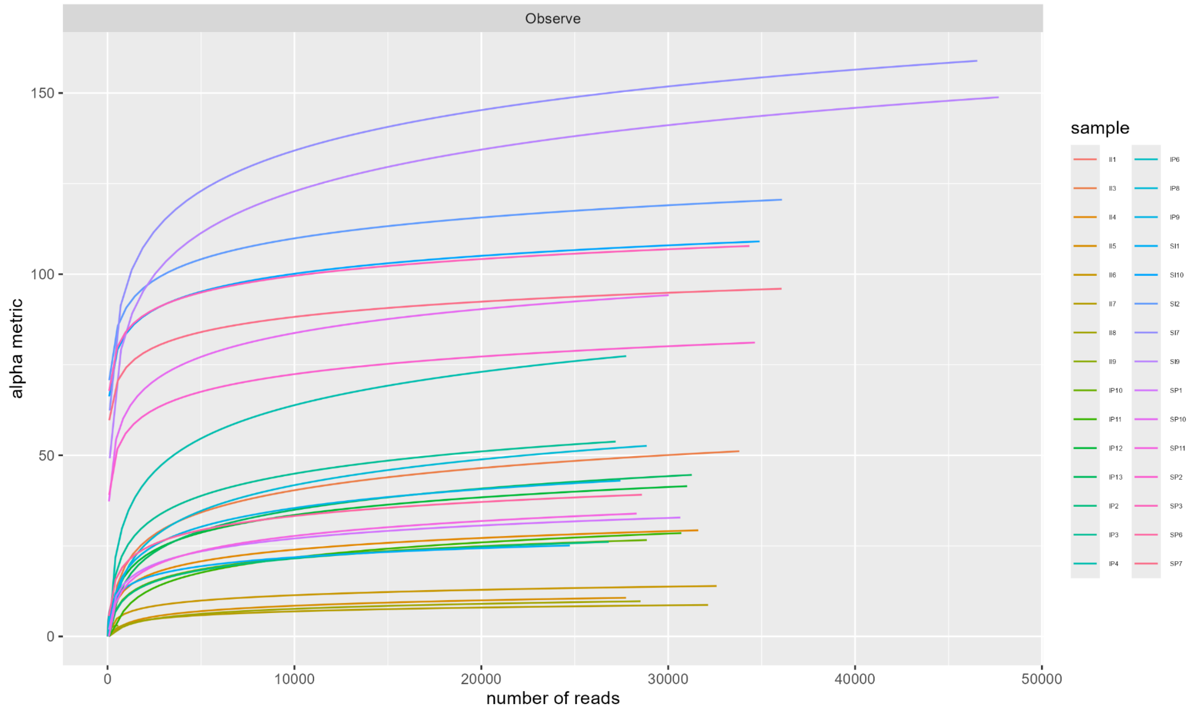
28	SI 8*	270	770.7	1.91	2.39
29	SI 9	600	935.1	1.89	2.39
30	SI 10	498	837.4	1.91	2.39
31	SI 11*	330	591.7	1.92	2.37
32	SI 12*	242	633.0	1.93	2.37
33	SP 1	48.9	223.2	1.93	2.09
34	SP 2	540.0	1107.2	1.95	2.34
35	SP 3	610.0	1192.8	1.97	2.35
36	SP 4*	128.0	450.9	2.01	2.29
37	SP 5	318.0	777.9	1.97	2.33
38	SP 6	236.0	632.6	2.00	2.31
39	SP 7	266.0	472.4	1.96	2.28
40	SP 8	1000	1220	1.89	2.41
41	SP 9*	770.0	1058.9	1.92	2.38
42	SP 10	264	989.0	1.93	2.42
43	SP 11	365	763.2	1.90	2.20

Supplementary Table S4. Metadata and analytical classification of all samples. Code (IP : Infected Peru; II : Infected Inti; SP : Healthy Peru; II : Healthy Inti), (+) : positive for the genetic marker, (–) : negative for the genetic marker.

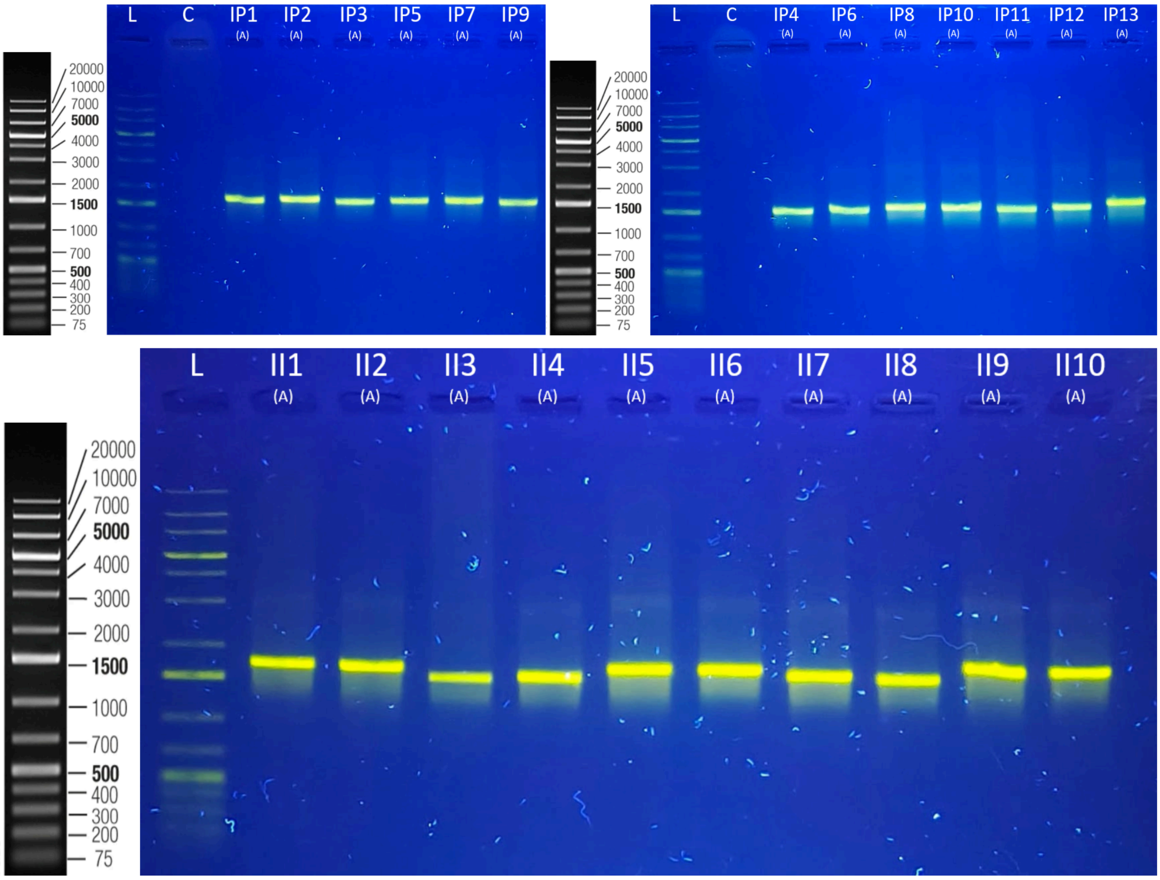
Sample ID	**Group Code**	**Health Status**	**Breed**	**16S ARN**	**sodA (Streptococcus spp.)**	**comB (*S. equi* subsp. *zooepidemicus*)**	**seeI (*S. equi* subsp. *equi*)**
IP 2	IP	Infected	Peru	+	+	+	–
IP 3	IP	Infected	Peru	+	+	+	–
IP 4	IP	Infected	Peru	+	+	+	–
IP 6	IP	Infected	Peru	+	+	+	–
IP 7	IP	Infected	Peru	+	+	+	–
IP 8	IP	Infected	Peru	+	–	–	–
IP 9	IP	Infected	Peru	+	+	+	–
IP 10	IP	Infected	Peru	+	+	+	–
IP 11	IP	Infected	Peru	+	+	+	–
IP 12	IP	Infected	Peru	+	+	+	–
IP 13	IP	Infected	Peru	+	+	+	–
II 1	II	Infected	Inti	+	–	–	–
II 2	II	Infected	Inti	+	+	+	–

II 3	II	Infected	Inti	+	–	–	–
II 4	II	Infected	Inti	+	+	+	–
II 5	II	Infected	Inti	+	+	+	–
II 6	II	Infected	Inti	+	+	+	–
II 7	II	Infected	Inti	+	+	+	–
II 8	II	Infected	Inti	+	+	+	–
II 9	II	Infected	Inti	+	+	+	–
II 10	II	Infected	Inti	+	+	+	–
SI 1	SI	Healthy	Inti	+	–	–	–
SI 2	SI	Healthy	Inti	+	–	–	–
SI 5	SI	Healthy	Inti	+	–	–	–
SI 7	SI	Healthy	Inti	+	–	–	–
SI 9	SI	Healthy	Inti	+	–	–	–
SI 10	SI	Healthy	Inti	+	–	–	–
SP 1	SP	Healthy	Peru	+	–	–	–
SP 2	SP	Healthy	Peru	+	–	–	–
SP 3	SP	Healthy	Peru	+	–	–	–
SP 5	SP	Healthy	Peru	+	–	–	–
SP 6	SP	Healthy	Peru	+	–	–	–
SP 7	SP	Healthy	Peru	+	–	–	–
SP 8	SP	Healthy	Peru	+	–	–	–
SP 10	SP	Healthy	Peru	+	–	–	–
SP 11	SP	Healthy	Peru	+	–	–	–

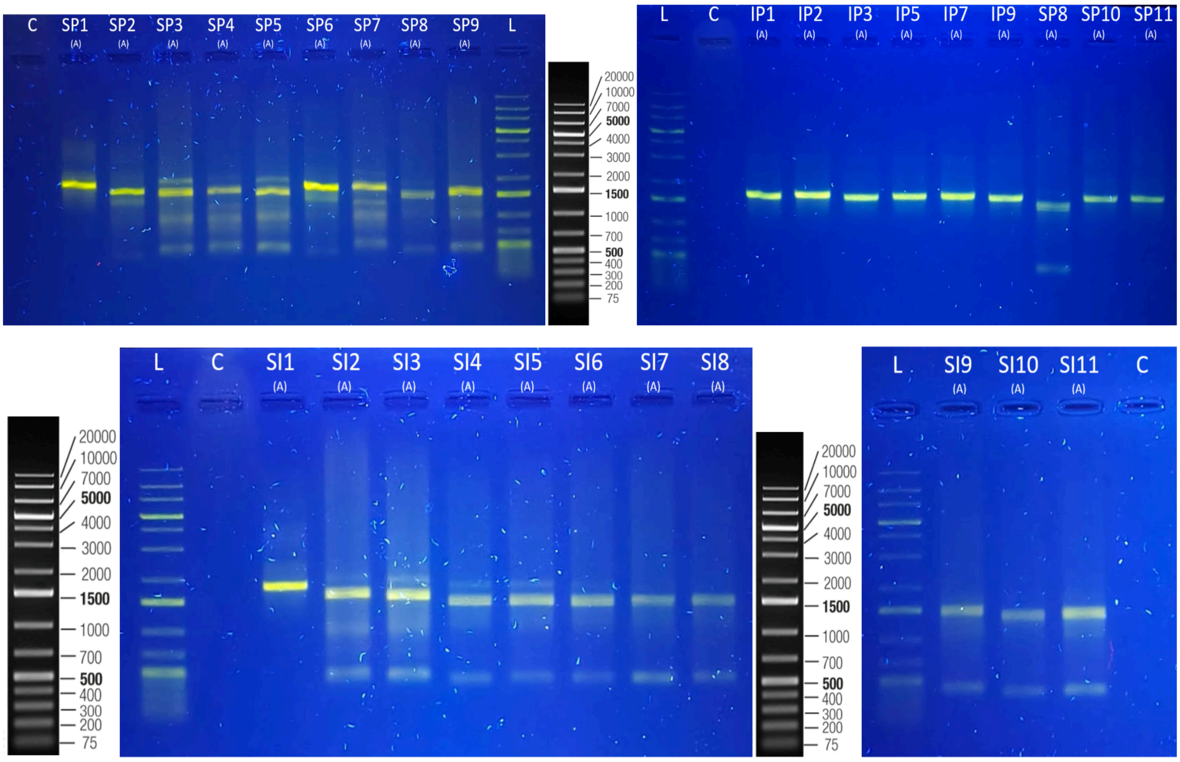
Supplementary Figure S1. Rarefaction curves of all samples included in the 16S rRNA dataset. Each curve represents an individual sample, showing the relationship between sequencing depth (number of reads) and alpha diversity (observed features). Samples that did not meet the minimum sequencing depth threshold (<10,000 reads) were excluded prior to downstream analyses, before alpha and beta diversity calculations.



Supplementary Figure S2. Agarose gel electrophoresis of 16S rRNA gene amplification (internal control) using universal primers 27F/1492R in infected guinea pigs. Samples are grouped according to breed and health status, where IP corresponds to infected Peru breed and II corresponds to infected Inti breed. Each lane represents an individual sample identified by its corresponding code. The expected amplicon size is approximately 1,500 bp, confirming the presence of bacterial DNA in all analyzed samples. L indicates the molecular weight marker (100 bp DNA ladder), and C corresponds to the negative control. The absence of amplification in the negative control confirms the specificity of the reaction.



Supplementary Figure S3. Agarose gel electrophoresis of 16S rRNA gene amplification (internal control) using universal primers 27F/1492R in healthy guinea pigs. Samples are grouped according to breed and health status, where SP corresponds to healthy Peru breed and SI corresponds to healthy Inti breed. Each lane represents an individual sample identified by its corresponding code. The expected amplicon size is approximately 1,500 bp, confirming the presence of bacterial DNA in all analyzed samples. L indicates the molecular weight marker (100 bp DNA ladder), and C corresponds to the negative control. The absence of amplification in the negative control confirms the specificity of the reaction.



Supplementary Figure S4. Representative anatomical images of cervical lymph nodes in healthy guinea pigs (*Cavia porcellus*) from the Peru breed. Arrows indicate the mandibular cervical lymph nodes, which appear as small, well-defined, non-enlarged structures without signs of abscess or inflammation. These images serve as a reference for normal anatomy to distinguish healthy from diseased lymph nodes.

Supplementary Figure S5. Representative gross lesions of cervical lymphadenitis in guinea pigs (*Cavia porcellus*). The image shows enlarged cervical lymph nodes with multiple encapsulated abscesses and irregular morphology, in contrast to the normal anatomy. These macroscopic features support the clinical classification of infected cases.

Supplementary Figure S6. Representative isolated cervical lymph nodes from healthy guinea pigs (*Cavia porcellus*). The image shows small, well-defined, pale structures of varying sizes, consistent with normal lymph node morphology.