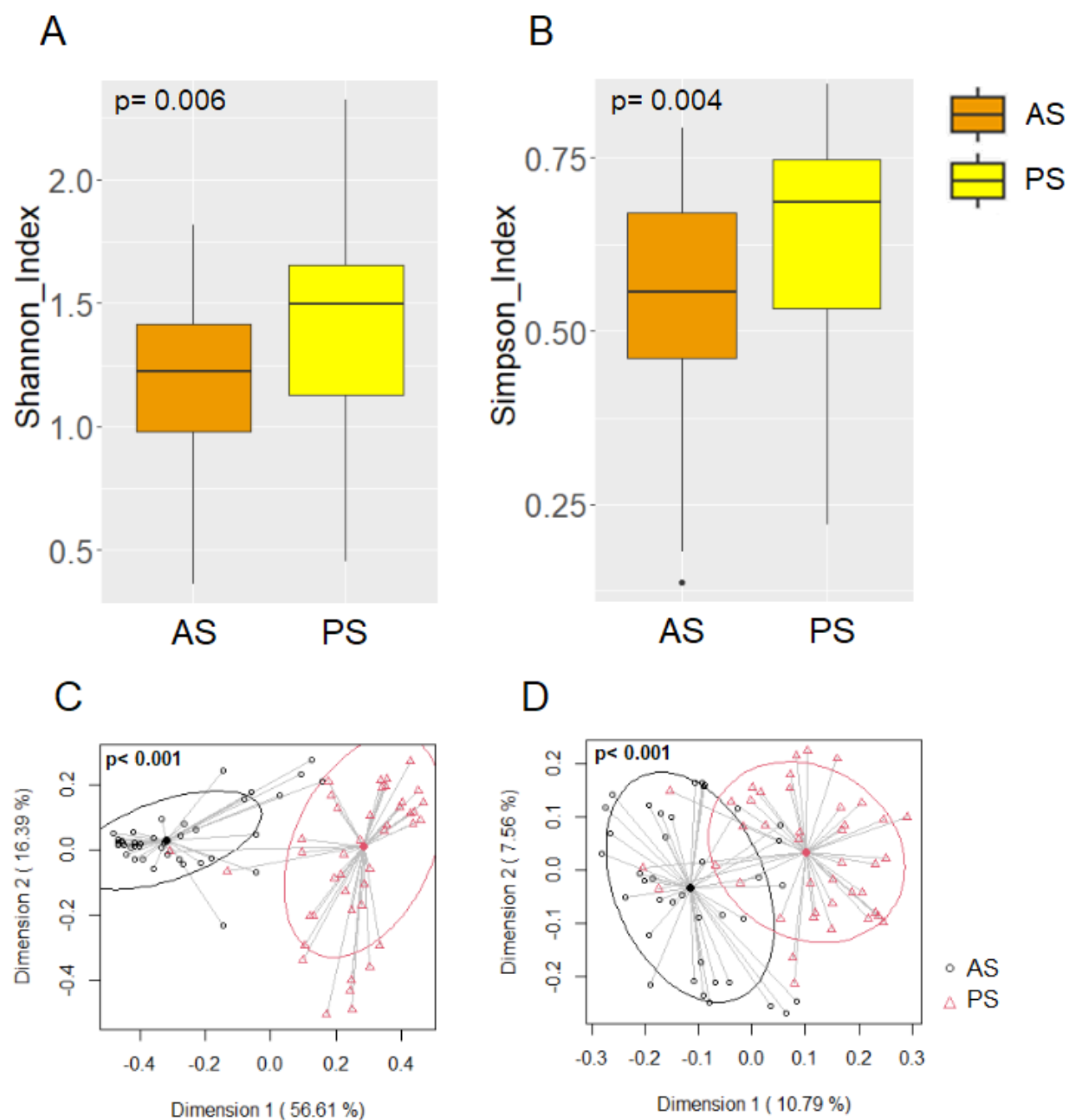
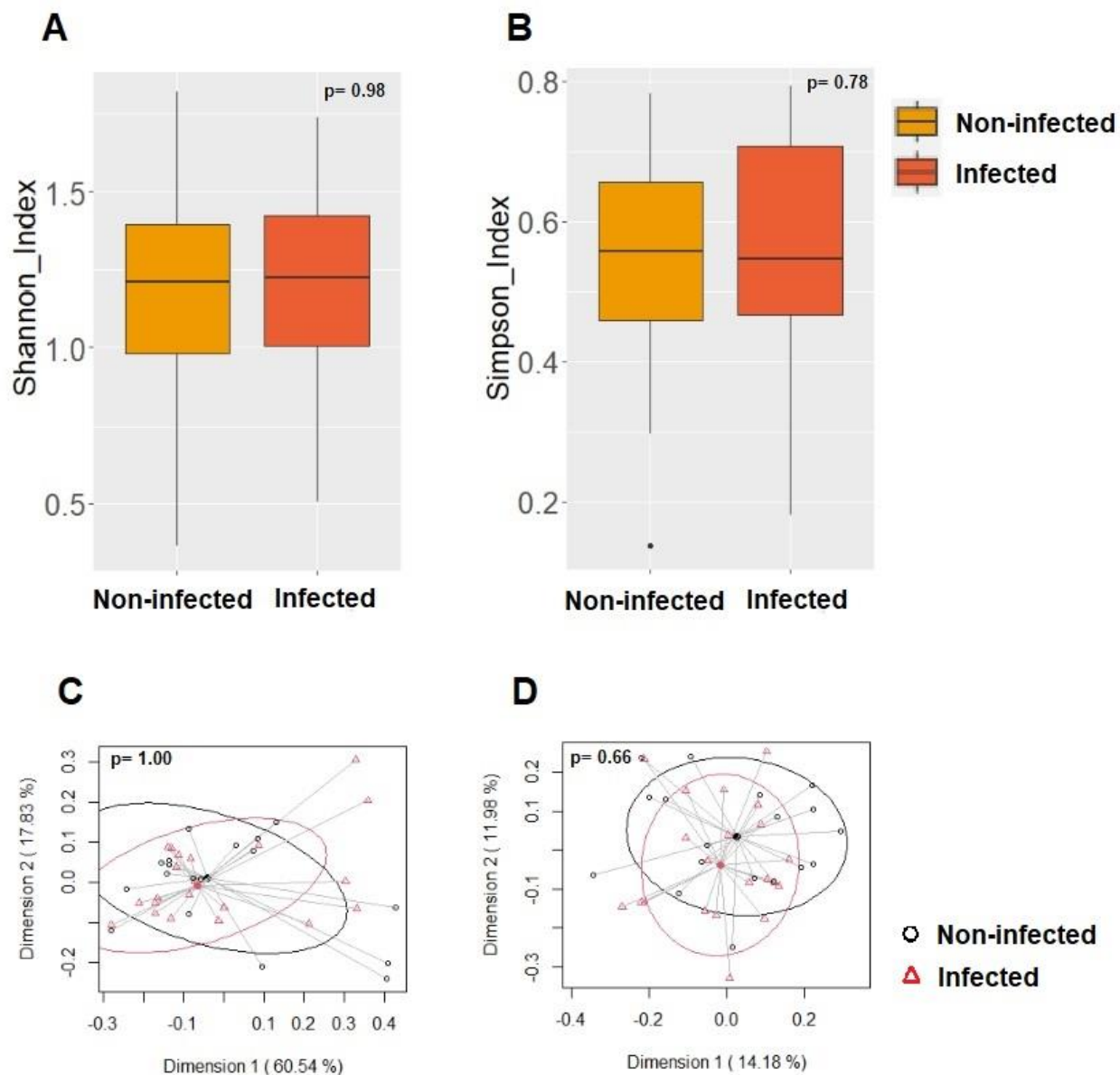


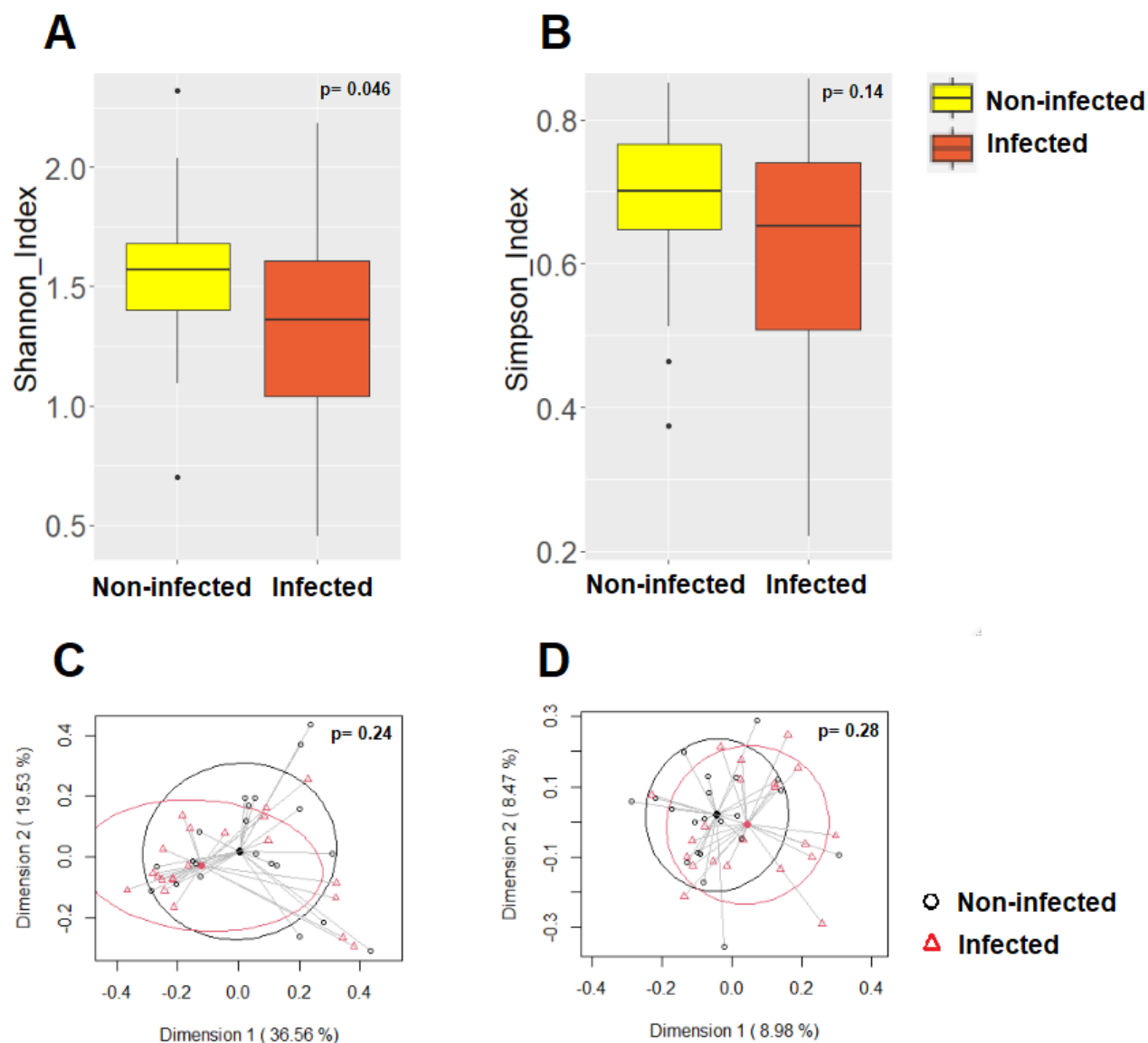
Supplementary Figure 1. Comparison between the values of alpha and beta diversity and statistical analysis (Wilcoxon rank test and PERMANOVA test, respectively), at the ASV level, of the PS and AS samples. (A) Shannon diversity index; (B) Simpson diversity index ; (C) PCoA plots based on the Bray-Curtis dissimilarity index; (D) PCoA plots based on the Jaccard's coefficient for binary data (presence of absence).



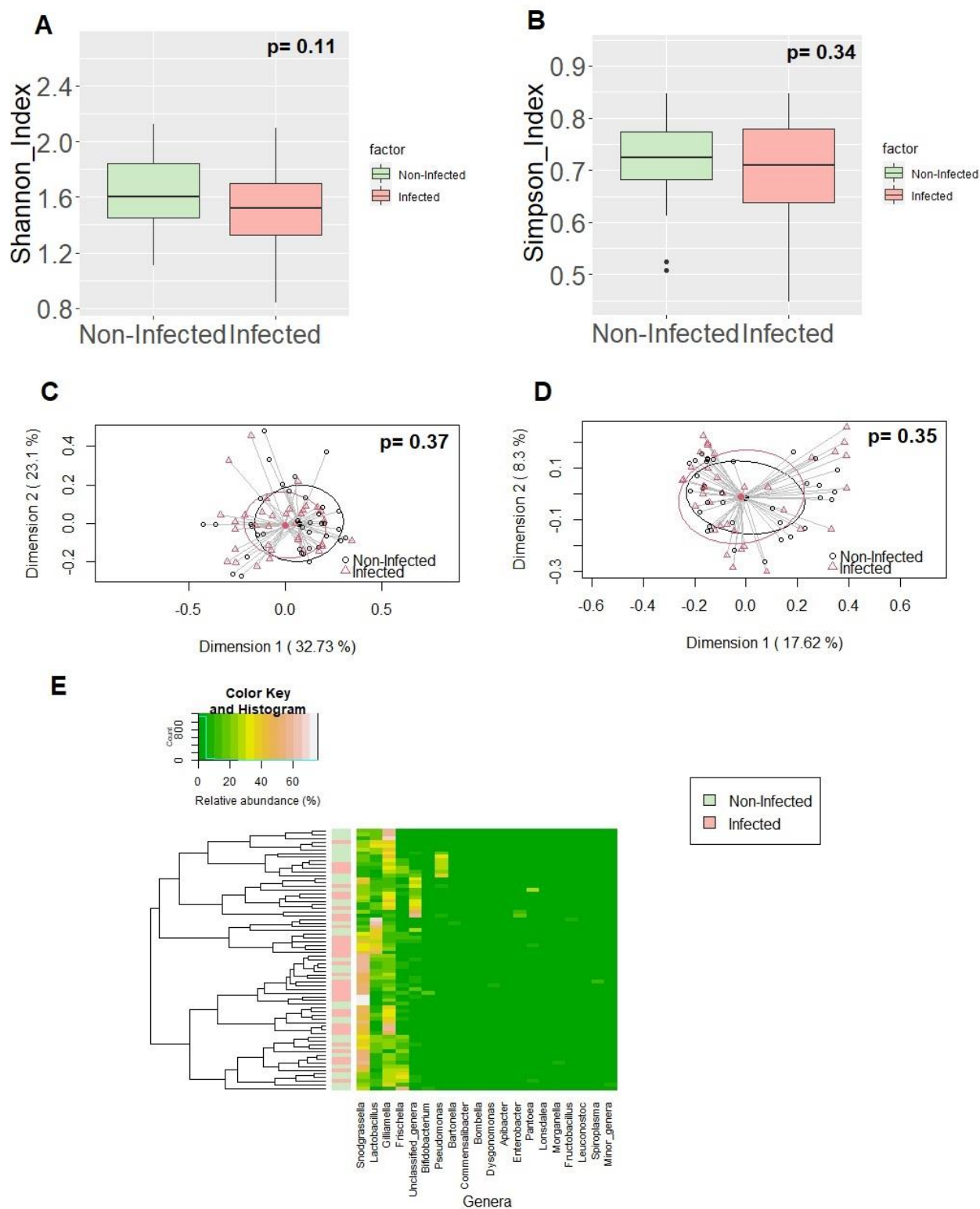
Supplementary Figure 2. Comparison between the values of alpha and beta diversity and statistical analysis (Wilcoxon rank test and PERMANOVA test, respectively), at the ASV level, of the PS samples grouped by *Nosema* spp. infection. (A) Shannon diversity index; (B) Simpson diversity index ; (C) PCoA plots based on the Bray-Curtis dissimilarity index; (D) PCoA plots based on the Jaccard's coefficient for binary data (presence of absence).



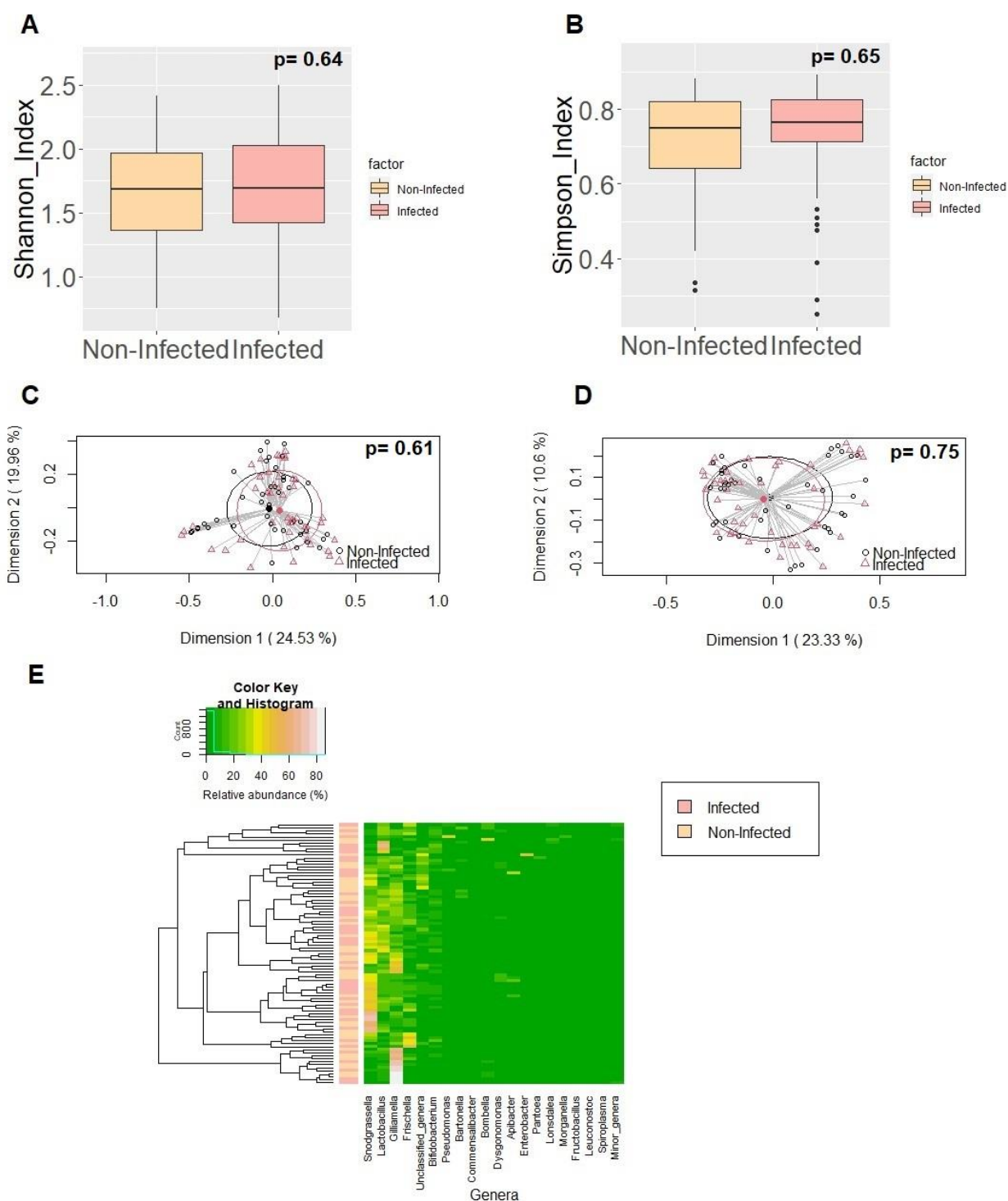
Supplementary Figure 3. Comparison between the values of alpha and beta diversity and statistical analysis (Wilcoxon rank test and PERMANOVA test, respectively), at the ASV level, of the AS samples grouped by *Nosema* spp. infection. (A) Shannon diversity index; (B) Simpson diversity index ; (C) PCoA plots based on the Bray-Curtis dissimilarity index; (D) PCoA plots based on the Jaccard's coefficient for binary data (presence of absence).



Supplementary Figure 4. Comparison between the values of alpha and beta diversity and statistical analysis (Wilcoxon rank test and PERMANOVA test, respectively), at the ASV level, of the 71 AS samples of the spring period grouped by *Nosema* spp. infection. (A) Shannon diversity index; (B) Simpson diversity index ; (C) PCoA plots based on the Bray-Curtis dissimilarity index; (D) PCoA plots based on the Jaccard's coefficient for binary data (presence of absence). (E) Heatmap plot representing the hierarchical clustering (hclust with the complete linkage method for hierarchical clustering), at the genus level, of the AS samples by *Nosema* infection cohorts.



Supplementary Figure 5. Comparison between the values of alpha and beta diversity and statistical analysis (Wilcoxon rank test and PERMANOVA test, respectively), at the ASV level, of the 87 AS samples of the autumn period grouped by *Nosema* spp. infection. (A) Shannon diversity index; (B) Simpson diversity index ; (C) PCoA plots based on the Bray-Curtis dissimilarity index; (D) PCoA plots based on the Jaccard's coefficient for binary data (presence of absence). (E) Heatmap plot representing the hierarchical clustering (hclust with the complete linkage method for hierarchical clustering), at the genus level, of the AS samples by *Nosema* infection cohorts.



Supplementary Table 1. Relative frequencies, medians and interquartile range (IQR) of the most abundant bacterial phyla (bold) and genera (italics) detected in the AS of either non-infected or infected bees collected in spring.

	Non-Infected		Infected		p-value
Phylum/Genera	n (%)	Median (IQR)	n (%)	Median (IQR)	
Proteobacteria	35 (100%)	83.7 (75.46-90.88)	36 (100%)	83.22 (74.61-93.59)	0.82
<i>Snodgrassella</i>	35 (100%)	25.7 (19.91-43.61)	36 (100%)	41.78 (21.65-51.76)	0.17
Gilliamella	35 (100%)	24.35 (15.56-35.97)	36 (100%)	21.4 (14.83-31.93)	0.39
Frischella	33 (94%)	4.29 (0.18-13.24)	29 (81%)	4.27 (0.27-11.95)	0.60
<i>Pseudomonas</i>	12 (34%)	<0.01 (<0.01-0.03)	11 (31%)	<0.01 (<0.01-0.03)	0.82
<i>Bartonella</i>	9 (26%)	<0.01 (<0.01-0.01)	6 (17%)	<0.01 (<0.01-<0.01)	0.34
<i>Commensalibacter</i>	7 (20%)	<0.01 (<0.01-<0.01)	6 (17%)	<0.01 (<0.01-<0.01)	0.60
<i>Bombella</i>	11 (31%)	<0.01 (<0.01-0.01)	16 (44%)	<0.01 (<0.01-0.06)	0.23
<i>Enterobacter</i>	5 (14%)	<0.01 (<0.01-<0.01)	2 (6%)	<0.01 (<0.01-<0.01)	0.25
<i>Pantoea</i>	6 (17%)	<0.01 (<0.01-<0.01)	6 (17%)	<0.01 (<0.01-<0.01)	0.91
<i>Lonsdalea</i>	0 (0%)	<0.01 (<0.01-<0.01)	0 (0%)	<0.01 (<0.01-<0.01)	not detected
<i>Morganella</i>	8 (23%)	<0.01 (<0.01-<0.01)	12 (33%)	<0.01 (<0.01-0.05)	0.42
Firmicutes	35 (100%)	13.4 (7.22-20.95)	36 (100%)	12.27 (5.56-22.8)	0.69
<i>Lactobacillus</i>	35 (100%)	12.24 (6.61-20.9)	36 (100%)	11.92 (5.48-19.95)	0.56
<i>Fructobacillus</i>	12 (34%)	<0.01 (<0.01-0.03)	12 (33%)	<0.01 (<0.01-0.07)	0.81
<i>Leuconostoc</i>	1 (3%)	<0.01 (<0.01-<0.01)	1 (3%)	<0.01 (<0.01-<0.01)	0.98
<i>Spiroplasma</i>	0 (0%)	<0.01 (<0.01-<0.01)	1 (3%)	<0.01 (<0.01-<0.01)	0.34
Actinobacteriota	33 (94%)	1.06 (0.55-2.43)	33 (92%)	0.67 (0.07-1.27)	0.04
<i>Bifidobacterium</i>	33 (94%)	1.06 (0.56-2.38)	31 (86%)	0.63 (0.04-1.25)	0.041
Bacteroidota	23 (66%)	0.02 (<0.01-0.05)	20 (56%)	0.01 (<0.01-0.07)	0.85
<i>Dysgonomonas</i>	4 (11%)	<0.01 (<0.01-<0.01)	1 (3%)	<0.01 (<0.01-<0.01)	0.18
<i>Apibacter</i>	4 (11%)	<0.01 (<0.01-<0.01)	6 (17%)	<0.01 (<0.01-<0.01)	0.64
Acidobacteriota	1 (3%)	<0.01 (<0.01-<0.01)	3 (8%)	<0.01 (<0.01-<0.01)	0.33
Minor_phyla	13 (37%)	<0.01 (<0.01-0.01)	11 (31%)	<0.01 (<0.01-<0.01)	0.63
Minor_genera	35 (100%)	0.14 (0.05-0.24)	34 (94%)	0.13 (0.05-0.3)	0.84
Unclassified_genera	35 (100%)	2.36 (0.96-7.33)	36 (100%)	2.28 (0.18-7.38)	0.73
*: Number of samples in which the phylum/genus was detected (relative frequency of detection).					
† Wilcoxon rank sum test with Bonferroni correction					

Supplementary Table 2. Relative frequencies, medians and interquartile range (IQR) of the most abundant bacterial phyla (bold) and genera (italics) detected in the AS of either non-infected or infected bees collected in autumn.

	Non-Infected		Infected		p-value [†]
Phylum/Genera	n (%) [*]	Median (IQR)	n (%)	Median (IQR)	
Proteobacteria	43 (100%)	75.61 (66.02-86.92)	44 (100%)	76.16 (64.73-81.39)	0.40
<i>Snodgrassella</i>	43 (100%)	22.22 (5.73-39.22)	44 (100%)	26.59 (13.84-41.45)	0.28
<i>Gilliamella</i>	43 (100%)	19.95 (12.41-32.24)	44 (100%)	15.89 (9.58-25.85)	0.31
<i>Frischella</i>	42 (98%)	9.04 (0.49-14.07)	44 (100%)	6.64 (0.95-13.39)	0.66
<i>Pseudomonas</i>	27 (63%)	0.01 (<0.01-0.09)	22 (50%)	<0.01 (<0.01-0.07)	0.22
<i>Bartonella</i>	13 (30%)	<0.01 (<0.01-0.02)	13 (30%)	<0.01 (<0.01-0.04)	0.85
<i>Commensalibacter</i>	20 (47%)	<0.01 (<0.01-0.04)	20 (45%)	<0.01 (<0.01-0.07)	0.90
<i>Bombella</i>	39 (91%)	0.08 (0.02-0.2)	34 (77%)	0.09 (0.01-0.44)	0.97
<i>Enterobacter</i>	10 (23%)	<0.01 (<0.01-<0.01)	11 (25%)	<0.01 (<0.01-<0.01)	0.78
<i>Pantoea</i>	10 (23%)	<0.01 (<0.01-<0.01)	9 (20%)	<0.01 (<0.01-<0.01)	0.71
<i>Lonsdalea</i>	17 (39.53%)	<0.01 (<0.01-0.05)	20 (45%)	<0.01 (<0.01-0.06)	0.82
<i>Morganella</i>	6 (13.95%)	<0.01 (<0.01-<0.01)	1 (2%)	<0.01 (<0.01-<0.01)	0.054
Firmicutes	43 (100%)	16.11 (8.55-24.79)	44 (100%)	19.02 (12.28-25.28)	0.33
<i>Lactobacillus</i>	43 (100%)	15.1 (7.99-24.75)	44 (100%)	17.03 (12.28-24.58)	0.34
<i>Fructobacillus</i>	14 (33%)	<0.01 (<0.01-0.02)	7 (16%)	<0.01 (<0.01-<0.01)	0.12
<i>Leuconostoc</i>	13 (30%)	<0.01 (<0.01-0.01)	15 (34%)	<0.01 (<0.01-0.02)	0.91
<i>Spiroplasma</i>	0 (0%)	<0.01 (<0.01-<0.01)	1 (2%)	<0.01 (<0.01-<0.01)	0.33
Actinobacteriota	43 (100%)	3.76 (2.05-6.88)	43 (98%)	5.76 (1.82-7.74)	0.42
<i>Bifidobacterium</i>	42 (98%)	3.76 (1.88-6.87)	43 (98%)	5.76 (1.81-7.74)	0.35
Bacteroidota	38 (88%)	0.06 (0.01-0.35)	36 (82%)	0.05 (0.01-0.94)	0.88
<i>Dysgonomonas</i>	11 (26%)	<0.01 (<0.01-0.01)	10 (23%)	<0.01 (<0.01-<0.01)	0.67
<i>Apibacter</i>	12 (28%)	<0.01 (<0.01-0.02)	15 (34%)	<0.01 (<0.01-0.05)	0.61
Acidobacteriota	12 (28%)	<0.01 (<0.01-0.01)	10 (23%)	<0.01 (<0.01-<0.01)	0.54
Minor_phyla	16 (37%)	<0.01 (<0.01-<0.01)	15 (34%)	<0.01 (<0.01-<0.01)	0.95
Minor_genera	37 (86%)	0.09 (0.01-0.92)	37 (84%)	0.15 (0.01-0.41)	0.67
Unclassified_genera	43 (100%)	1.85 (0.48-5.9)	44 (100%)	2.91 (0.86-10.47)	0.46
*: Number of samples in which the phylum/genus was detected (relative frequency of detection).					
† Wilcoxon rank sum test with Bonferroni correction					

Supplementary Table 3. Relative frequencies, medians and interquartile range (IQR) of the most abundant bacterial phyla (**bold**) and genera (*italics*) detected in the AS from younger (n= 58) and older (n = 100) bees.

	Younger		Older		p-value[†]
Phylum/Genera	n (%)*	Median (IQR)	n (%)*	Median (IQR)	
Proteobacteria	58 (100%)	78.8 (71.97-87.27)	100 (100%)	80.45 (67.29-89.87)	0.46
<i>Snodgrassella</i>	58 (100%)	38.17 (21.71-51.12)	100 (100%)	22.88 (11.15-41.02)	0.002
<i>Gilliamella</i>	58 (100%)	14.75 (7.09-21.73)	100 (100%)	25.26 (16.57-36.65)	<0.001
<i>Frischella</i>	58 (100%)	4.89 (0.91-13.57)	90 (90%)	6.17 (0.09-13.19)	0.40
<i>Pseudomonas</i>	29 (50%)	<0.01 (<0.01-0.05)	43 (43%)	<0.01 (<0.01-0.06)	0.81
<i>Bombella</i>	47 (81.03%)	0.1 (0.02-0.32)	53 (53%)	0.01 (<0.01-0.06)	<0.001
<i>Bartonella</i>	10 (17.24%)	<0.01 (<0.01-<0.01)	31 (31%)	<0.01 (<0.01-0.06)	0.044
<i>Enterobacter</i>	11 (18.97%)	<0.01 (<0.01-<0.01)	17 (17%)	<0.01 (<0.01-<0.01)	0.98
<i>Pantoea</i>	7 (12.07%)	<0.01 (<0.01-<0.01)	24 (24%)	<0.01 (<0.01-<0.01)	0.055
<i>Lonsdalea</i>	24 (41.38%)	<0.01 (<0.01-0.19)	13 (13%)	<0.01 (<0.01-<0.01)	<0.001
<i>Morganella</i>	3 (5.17%)	<0.01 (<0.01-<0.01)	24 (24%)	<0.01 (<0.01-<0.01)	0.003
<i>Commensalibacter</i>	11 (18.97%)	<0.01 (<0.01-<0.01)	42 (42%)	<0.01 (<0.01-0.03)	0.004
Firmicutes	58 (100%)	18.04 (7.98-25.73)	100 (100%)	13.99 (7.99-21.88)	0.073
<i>Lactobacillus</i>	58 (100%)	17.16 (7.9-23.88)	100 (100%)	13.07 (7.68-21.81)	0.17
<i>Fructobacillus</i>	43 (74.14%)	0.03 (<0.01-0.26)	2 (2%)	<0.01 (<0.01-<0.01)	<0.001
<i>Leuconostoc</i>	20 (34.48%)	<0.01 (<0.01-0.02)	10 (10%)	<0.01 (<0.01-<0.01)	<0.001
<i>Spiroplasma</i>	2 (3.45%)	<0.01 (<0.01-<0.01)	0 (0%)	<0.01 (<0.01-<0.01)	0.064
Actinobacteriota	56 (96.55%)	1.56 (0.09-3.23)	96 (96%)	2.25 (0.89-6.21)	0.033
<i>Bifidobacterium</i>	53 (91.38%)	1.27 (0.06-3.23)	96 (96%)	2.19 (0.83-6.21)	0.017
Bacteroidota	45 (77.59%)	0.02 (<0.01-0.06)	72 (72%)	0.06 (<0.01-0.92)	0.026
<i>Apibacter</i>	4 (6.9%)	<0.01 (<0.01-<0.01)	33 (33%)	<0.01 (<0.01-0.09)	<0.001
<i>Dysgonomonas</i>	3 (5.17%)	<0.01 (<0.01-<0.01)	23 (23%)	<0.01 (<0.01-<0.01)	0.003
Acidobacteriota	12 (20.69%)	<0.01 (<0.01-<0.01)	14 (14%)	<0.01 (<0.01-<0.01)	0.39
Minor_phyla	18 (31.03%)	<0.01 (<0.01-<0.01)	37 (37%)	<0.01 (<0.01-0.01)	0.24
Minor_genera	57 (98.28%)	0.2 (0.08-0.47)	86 (86%)	0.06 (0.01-0.3)	0.001
Unclassified_genera	58 (100%)	1.46 (0.18-7.58)	100 (100%)	2.56 (0.77-9.02)	0.16

*: Number of samples in which the phylum/genus was detected (relative frequency of detection).

† Wilcoxon rank sum test with Bonferroni correction