Proteomics of anatomical sections of the gut of *Nosema*-infected Western honey bee (*Apis mellifera*) reveals different early responses to *Nosema* spp. isolates

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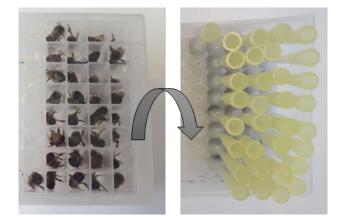


Figure S1: Experimental procedure to infect individual bees with a *Nosema* inoculum To infect a large number of bees individually with a *Nosema* inoculum, we have developed the following method. After 15 hours of fasting each bee was place individually in a homemade "inoculated-96-well deep bottom plate". It consists of a 96-well deep bottom plate with holes at the bottom. After placing the bees in the holes, the box is covered with a plastic film. The box is turned over, then 10-200 μ L pipette tips containing the syrup are placed in front of each bee. Bees were either fed with 10 μ L of 50% syrup containing 100,000 spores for the experimental bees, or fed with syrup alone for the control bees. The bees were kept in this device the time to consume all of the syrup. They were then removed from the device and then placed by experimental group in boxes with syrup *ad libitum* until tissues collection.

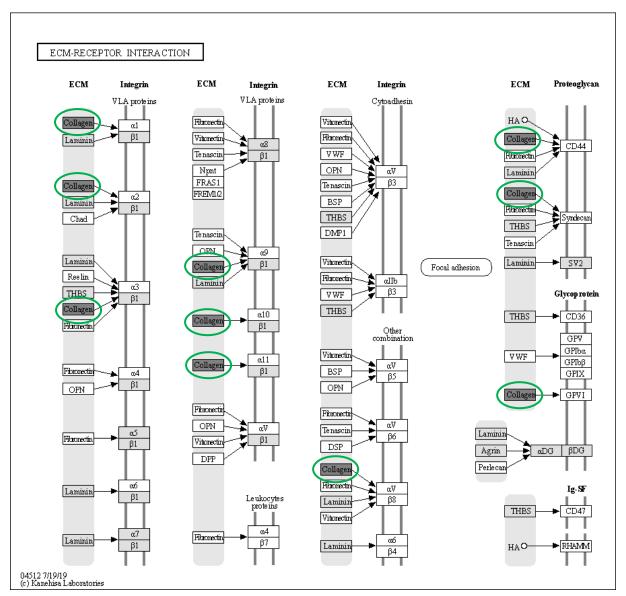
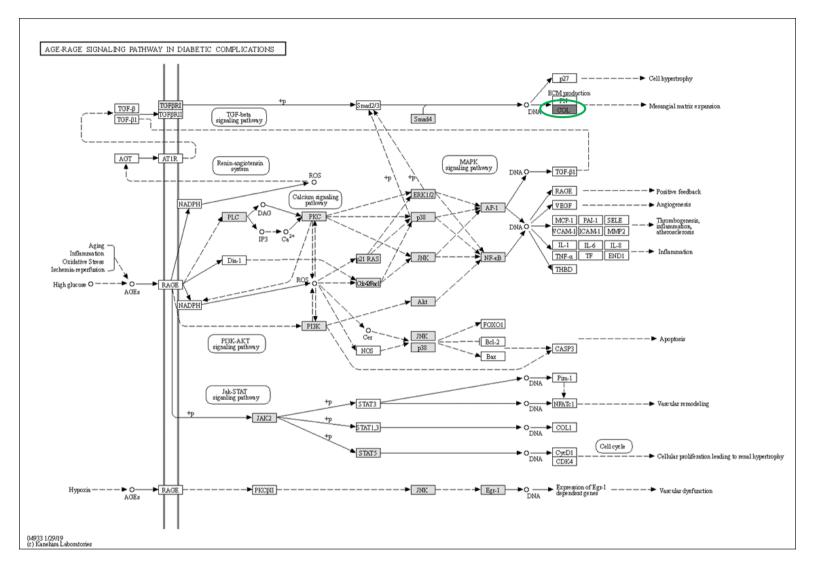
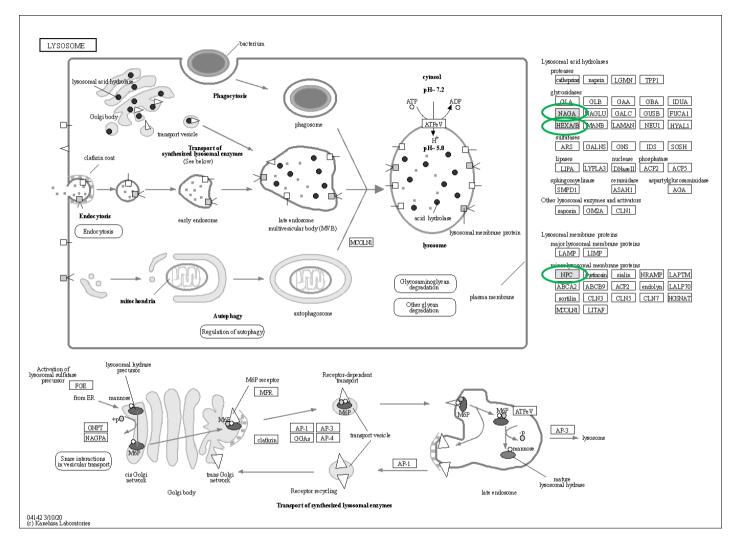


Figure S2: Mapping of the up-regulated proteins of *A. mellifera* in a context of infection by *Nosema spp.* isolates.

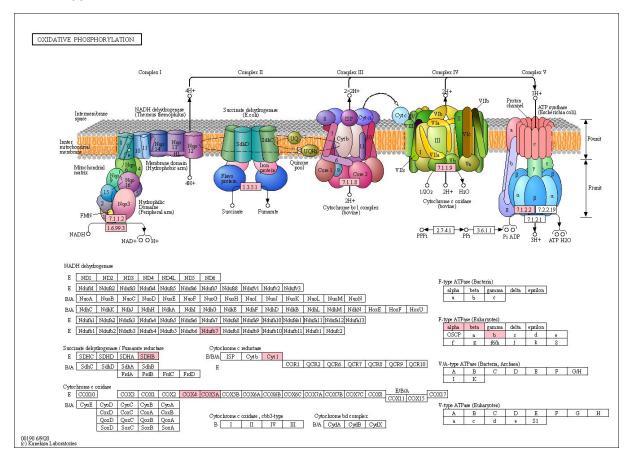
S2A: Mapping of the pathway ECM-receptor interaction (KEGG Pathways number ame04512). In a presence of *Nosema* spores the two Collagen IV NC1 domain-containing proteins of *A. mellifera* upregulated are involved in the protein processing in endoplasmic reticulum pathway (in green circles).



S2B: Mapping of the pathway AGE-RAGE signaling pathway in diabetic complications (KEGG Pathways number ame04933). In a presence of *Nosema* spores the two Collagen IV NC1 domain-containing proteins of *A. mellifera* up-regulated are involved in the protein processing in endoplasmic reticulum pathway (in green circle).

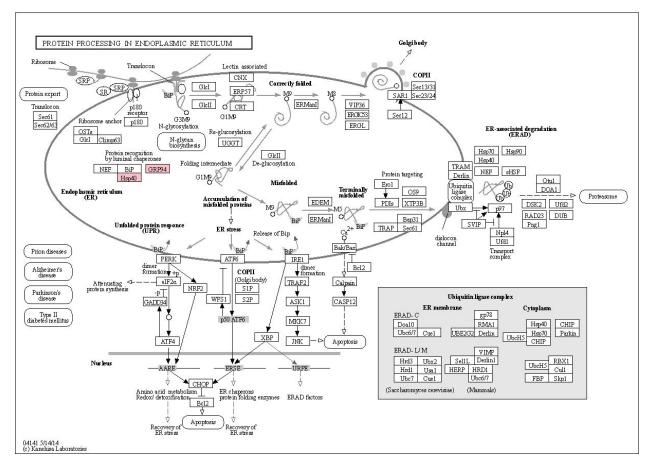


S2C: Mapping of the lysosome pathway (KEGG Pathways number ame04933). In a presence of *Nosema* spores the three proteins (Alpha-galactosidase, Betahexosaminidase and ML domain-containing protein) of *A. mellifera* up-regulated are involved in the protein processing in endoplasmic reticulum pathway (in green circles).

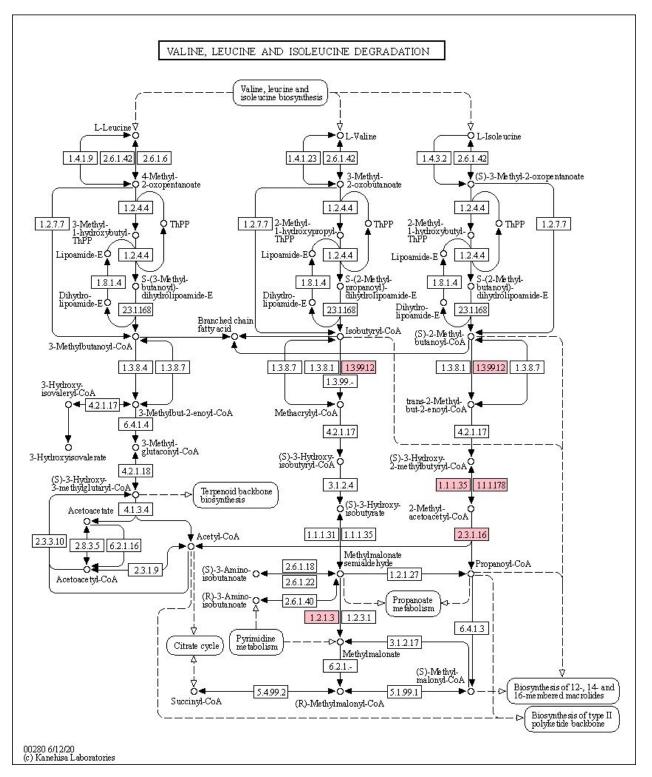


Figures S3: Mapping of the down-regulated proteins of *A. mellifera* in a context of infection by *Nosema spp.* isolates.

S3A: Mapping of the pathway oxidative phosphorylation (KEGG Pathways number ame00190). In a presence of *Nosema* spores the eight proteins (ATP synthase subunit b, cytochrome c oxidase subunit 5A, ATP synthase subunit alpha, cytochrome c oxidase subunit 4 isoform 1, cytochrome c1, succinate dehydrogenase iron-sulfur subunit, ATP synthase subunit beta, NADH dehydrogenase 1 beta subcomplex subunit 7) of *A. mellifera* down-regulated are involved in the oxidative phosphorylation pathway (in red).



S3B: Mapping of the pathway protein processing in endoplasmic reticulum (KEGG Pathways number ame04141). In a presence of *Nosema* spores the two proteins (HATPase_c domain-containing protein and Uncharacterized protein with the accession number A0A088ABL3) of *A. mellifera* down-regulated are involved in the protein processing in endoplasmic reticulum pathway (in red).



S3C: Mapping of the pathway valine, leucine and isoleucine degradation (KEGG Pathways number ame00280). In a presence of *Nosema* spores the four proteins (short/branched chain specific acyl-CoA dehydrogenase, aldehyde dehydrogenase, trifunctional enzyme subunit beta,3-hydroxyacyl-CoA dehydrogenase type-2) of *A. mellifera* down-regulated are involved in the oxidative phosphorylation pathway (in red).

Table S1: PCR results of the four Nosema isolates.

Nosema species were confirmed by PCR analysis. The presence of *Nosema* was scored as 1 and 0 for its absence.

Apis mellij	fera		
Condition of Nosema infection		PCR confirmation	
	Apiary	N. ceranae	N. apis
<i>N. ceranae</i> from <i>A. cerana</i> from Thailand	1	1	0
(NC1)	2	1	0
	3	1	0
<i>N. ceranae</i> from <i>A. mellifera</i> from Thailand	1	1	0
(NC2)	2	1	0
	3	1	0
<i>N. ceranae</i> from <i>A. mellifera</i> from France (NF)	1	1	0
	2	1	0
	3	1	0
N. apis (NA)	1	0	1
	2	0	1
	3	0	1

Table S2: Nosema spores counted for each experimental modality.

Apis mellifera									
Nosema spp.	Apiary								
		Result	MEAN	SD	SE				
<i>N.ceranae</i> from <i>A. cerana</i> from Thailand (NC1)		27,600,000	25,366,666.67	4,488,132.50	2,591,224.50				
	1	28,300,000							
		20,200,000							
		22,900,000	24,433,333.33	1,418,919.77	819,213.71				
	2	25,700,000							
		24,700,000							
		22,700,000	23,266,666.67	1,530,795.00	883,804.90				
	3	22,100,000							
		25,000,000							
<i>N.ceranae</i> from <i>A. mellifera</i> from Thailand		51,700,000	43,733,333.33	8,103,291.51	4,678,437.53				
	1	44,000,000							
		35,500,000							
(NC2)		41,100,000	44,700,000.00	4,467,661.58	2,579,405.61				
	2	43,300,000							
		49,700,000							
		46,900,000	49,000,000.00	2,206,807.64	1,274,100.99				
	3	48,800,000							
		51,300,000							
<i>N. ceranae</i> from <i>A. mellifera</i> from France (NF)		26,000,000	25,066,666.67	901,849.950	520,683.311				
	1	24,200,000							
		25,000,000							
	2	26,300,000	25,766,666.67	1,955,334.58	1,128,912.94				
		27,400,000							
		23,600,000							
		26,700,000	25,166,666.67	2,318,045.15	1,338,323.99				
	3	26,300,000							
		22,500,000							
N. apis (NA)		26,000,000	20,366,666.7	4,880,915.21	2,817,997.71				
	1	17,700,000							
		17,400,000							
		16,100,000	17,466,666.7	1,266,227.99	731,057.073				
	2	17,700,000							
		18,600,000							
		13,400,000	15,500,000.00	1,835,755.97	1,059,874.20				
	3	16,800,000							
		16,300,000							