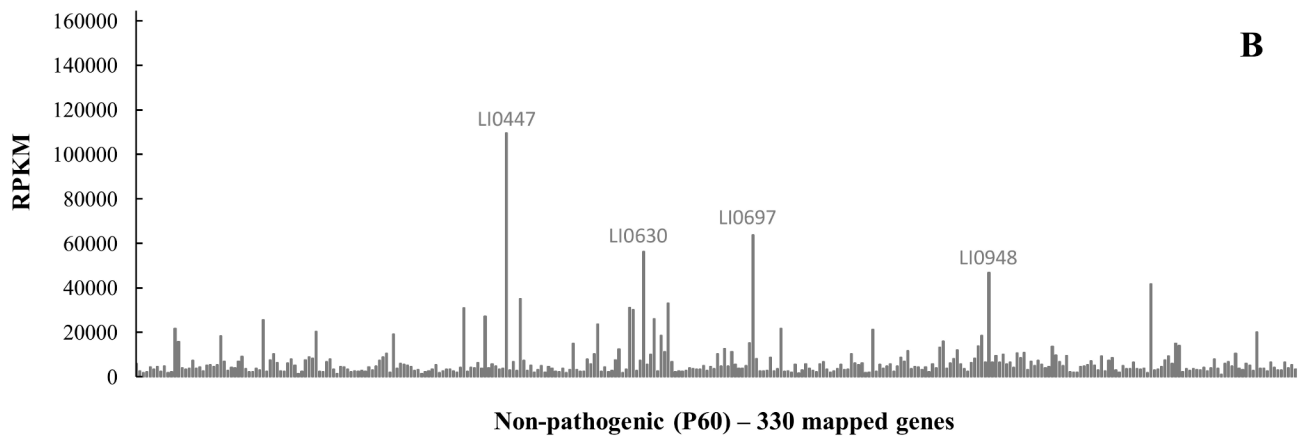
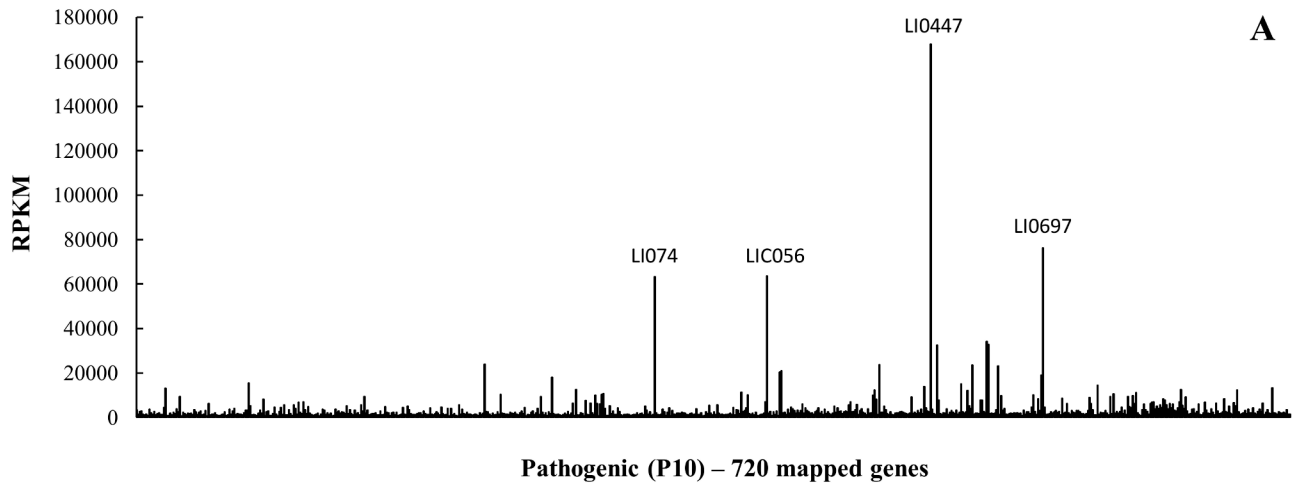


**Supplementary Figure 4.1.** Reproducibility of biological replicates. RPKM of replicate 1 plotted on the y-axis and replicate 2 on the x-axis. Each spot represents a single gene. Black circles represent genes expressed by the pathogenic isolate (PHE/MN1-00 at passage 10) and the linear regression (solid trendline -  $r^2 = 0.862$ ). Gray squares represent genes expressed by the non-pathogenic isolate (PHE/MN1-00 at passage 60) and the linear regression (dashed trend line -  $r^2 = 0.813$ ).



**Supplementary Figure 4.2.** RPKM representing the transcription levels (y-axis) and the number of mapped genes (x-axis) onto the *L. intracellularis* reference genome. (A) Pathogenic variant showing 720 expressed genes. (B) Non-pathogenic variant showing 330 expressed genes. The locus tags of the four highest expressed genes are described.

## Chapter 5

**Supplementary Table 5.1.** Primers used for one-step RT-PCR and for validation of RNA-seq expression data by quantitative reverse transcriptase PCR assay.

	<b>Gene symbol</b>	<b>Gene product</b>	<b>Primers</b>
<i>Sus scrofa</i>	APEX1	APEX nuclease 1	GGCAGAAGATGGGGATGA GCTCCCGCCTTACTCTTCTT
	CTR1	High-affinity copper uptake protein	CGGCACAGGGTACTTTCTCT ATGCTCTGTGATGTCCACGA
	DAD1	Defender against cell death 1	GATTTCCCTGGACAAGAGC CTGAAGAAAATCCATGTGTCCA
	LOC100154612	Cytosolic IMP-GMP	ATTAGCGTGGGCTGCATAGT GATAGAGAAGGCTGGAATGAGG
	LOC100522924	Vit K epoxide reductase subunit 1	TCAGTTGTTCCCGCGTCT CACCTGCTCCACCAGTCC
	LOC100523440	Cationic amino acid transporter 3	GGATATGGGATCCGACACAG GGTGGAGGCTGGTAGCTG
	LOC100737281	Tumor necrosis factor ligand 10	ATGGCGGTGATGCAGACT GATCAGGATCAACACACAGGTC
	LOC100737320	Olfactomedin-4-like	TGTTGGCTGGCAAGACATAG GCGTAAATCACCCACAATCC
	LOC100739719	Tetraspanin-6-like	TCCAGCTGATCGGAATCTTT GAGGAATAGGCCCATGTTACAC
	SLC10A2	Sodium/bile acid cotransporter 2	TGGCTCTGGGAATGATGC TCCAGAGTTGACCCACAGTTT
	SLC5A1	Sodium/glucose cotransporter 5	TGCGTCATGTGTGGGTACTION CATCCCTGGCATCACTATGAC
	SPP1	Secreted phosphoprotein 1	AAGTTCCGCAGATCCGAAG CCACATGTGACGTGAGGTCT
	SST	Somatostatin	TGGAGCCTGAAGATTTGTCC CCGGGTTTGAGTTAGCTGAT
	LOC100621117	Gastric inhibitory polypeptide-like	AGCTGGCCCATCAGTCTAAC ATCATCATCACCGGGGTTCC
	LOC100623884	Sucrase-isomaltase, intestinal-like	GGAATTGTTATTTCTCGGTCCA TGTCTCCAAGCCAGTGTCC
	LOC100738195	Facilitated glucose transporter	AGCAGCCCAAGGATCTCTC TGCTGAGATCTGTGAGTTGAGT

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LI0005	Superoxide dismutase	TCATATCCATGAAGGAGGATCA GGAGTCCAGCTGTTAGATGTCC
LI0447	Hypothetical protein	CCCAGCGTTTTACCTATGA TCGCTGCATATCCTTTTATGG
LI0457	$\sigma$ 54-like protein	CAGCTTGTAAATGACTCCCCAGT TCAGCTAATTCAACCCGTGA
LI0625	Chaperonin GroEL	AGCTGCGGTTGAAGAAGGTA TTAATGGAGCGGACAAAAGC
LI0691	Peptidoglycan-associated protein	GTAGAACAATCTTTAGCAACGGAGT AATAATCCCATCAGTTATAGTTTCTGC
LI0825	Lipid A core-O-antigen ligase	CATCTGAGTGGTTAGCTGCAA CACAAAAGCTAAAACAATCCCTCT
LI0902	Outer membrane protein	TGCATGAAACAGTCATTAATCAAA CCCTAAATTATTATGACCATCAGTGAG
LI0959	30S ribosomal protein S10	CAGCAAGAAATACAGGTGCAAG TTGCTCACGGGACTTTTTATC
LIC056	Hypothetical protein	GGGAAATCCTTGCCCTTATC AAAACACCTGCGACAGTACCTAA
LIC091	Hypothetical protein	AGGATCTTCAGGAAGTTCGTCTT CATTGCCTGGAGTACCAACA
LI0590*	GMP synthase	TTCTTCCATCCCCATAACA TTGGAGACATCCCTTTCCCTG
LI0159*	Serine hydroxymethyltransferase	TTTGCTGCAATAACGTGCAT GCACATATTGCTGGGCTTGT
LI0913*	Aspartate ammonia-lyase	CCATAAGCTCAAGAGCACGA CTGCAGCACTTGCAAACAAT

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\* *L. intracellularis* housekeeping genes used in the one-step RT-PCR to evaluate the quality of the bacterial RNA from microdissected enterocytes to be submitted for RNA-seq analysis.

**Supplementary Table 5.2.** Sequencing and mapping of each biological replicate.

Replicate	Total of reads	Host mapping		Bacterial mapping	
		Total	%	Total	%
C1	22,095,120	18,262,951	82.7	-	-
C2	20,763,571	17,968,464	86.5	-	-
C3	21,959,750	18,851,746	85.8	-	-
C4	21,791,650	16,996,110	78.0	-	-
C5	22,919,618	19,244,285	84.0	-	-
L1	22,951,725	18,670,807	81.3	992,740	4.3
L2	21,827,033	16,902,098	77.4	1,198,431	5.5
L3	22,656,091	17,902,168	79.0	878,530	3.9
L4	22,030,140	19,259,072	87.4	782,892	3.6
L5	22,365,938	18,743,681	83.8	1,149,608	5.1