

**Supplementary Table 2. Analyses of the unique protein coding sequences (CDSs) of *Mycoplasma haemocanis* strain Illinois and *M. haemofelis* strain Ohio2.**

<i>M. haemocanis</i> str. Illinois unique CDSs	Role category (TIGR microbial role categories)	Molecular Function Terms <sup>a</sup>	Biological Process Terms <sup>a</sup>	Cellular Component Terms <sup>a</sup>	Internal Helix <sup>b</sup>	Non-Cytoplasmic (signal peptide) <sup>b</sup>	Subcellular Localization <sup>b</sup>	GenBank Accession Number	
Paralogous family 9	hypothetical protein	ion/voltage-gated chloride channel activity (41%)	ion/chloride transport (41%)	membrane (42%)	1	no	cytoplasmic membrane	AEW45130.1	
	hypothetical protein	catalytic activity (35%)	metabolic process (35%)	cytoplasm (21%)	1	no	unknown	AEW45133.1	
	hypothetical protein	transferase (33%)	transport (30%)	cytoplasm (53%)	1	no	cytoplasmic membrane	AEW45134.1	
	hypothetical protein	nucleotide/ATP binding (39%)	metabolic process (32%)	cytoplasm (37%)	1	no	unknown	AEW45136.1	
	hypothetical protein	catalytic activity (51%)	GTP metabolic process (32%)	cytoplasm (67%)	1	no	unknown	AEW45155.1	
	hypothetical protein	ATP binding (39%)	carbohydrate metabolic process (37%)	cytoplasm (28%)	1	no	unknown	AEW45158.1	
	hypothetical protein	nucleotide binding (37%)	metabolic process (24%)	ribosome (32%)/cytoplasm (24%)	1	no	cytoplasmic membrane	AEW45237.1	
	hypothetical protein	electron carrier activity (38%)/oxidoreductase activity (38%)	fumarate metabolic process (22%)	membrane (46%) cytoplasm (20%)/extracellular (19%)	1	no	unknown	AEW45238.1	
Not in paralogous families	hypothetical protein	ATP binding (39%)	cell adhesion (19%) two-component signal transduction system (46%)/ regulation of transcription, DNA-dependent (46%)/ response to hydrogen peroxide (46%)	membrane (53%)	0	no	cytoplasmic membrane	AEW45062.1	
	hypothetical protein	protein binding (46%)/ two-component response regulator activity (46%)	DNA metabolic process/DNA topological change (100%)	chromosome (100%)	2	no	cytoplasmic membrane	AEW45815.1	
	hypothetical protein	nucleotide/ATP binding (100%)	ATP biosynthetic process (22%)	membrane (70%)	1	no	cytoplasmic membrane	AEW45816.1	
	hypothetical protein	ATP binding (37%)	polysaccharide catabolic process (71%)	membrane (71%)	1	no	unknown	AEW45817.1	
	hypothetical protein	oxidoreductase activity/catalytic activity (42%)	transport (53%)	membrane (53%)	1	no	unknown	AEW45917.1	
	hypothetical protein	methyltransferase (68%)	rRNA modification (37%)	cytoplasm (30%)	0	no	unknown	AEW46011.1	
	hypothetical protein	N.A.*	N.A.*	N.A.*	0	no	unknown	AEW45323.1.1	
	hypothetical protein	N.A.*	N.A.*	N.A.*	0	no	unknown	AEW45878.1	
	CDSs with predicted function (present in other bacteria species, but absent in <i>M. haemofelis</i> str. Ohio2)	50S ribosomal protein L33 phosphotransferase system glucose-specific IIBC component	structural constituent of ribosome (100%)	translation (100%)	ribosome (100%)	0	no	unknown	AEW45065.1
		30S ribosomal protein S14 type Z	sugar:hydrogen symporter activity (100%)	transport (100%)	membrane (100%)	7	no	cytoplasmic membrane	AEW45748.1
		structural constituent of ribosome (100%)	translation (100%)	ribosome (100%)	0	no	cytoplasmic	AEW45925.1	
<i>M. haemofelis</i> str. Ohio2 unique CDSs	Role category (TIGR microbial role categories)	Molecular Function Terms <sup>a</sup>	Biological Process Terms <sup>a</sup>	Cellular Component Terms <sup>a</sup>	Internal Helix <sup>b</sup>	Non-Cytoplasmic (signal peptide) <sup>b</sup>	Subcellular Localization <sup>b</sup>	GenBank Accession Number	
Paralogous family 8	hypothetical protein	metal ion binding/DNA binding (80%)	DNA integration (80%)	N.I.*	1	no	unknown	AEG72490.1	
	hypothetical protein	hydrolase (20%)	lipid metabolism (20%)	membrane (42%)	1	no	cytoplasmic	AEG72498.1	
	hypothetical protein	signal transducer activity/receptor activity (54%)	signal transduction (54%)	membrane (56%)	1	no	unknown	AEG72503.1	
	hypothetical protein	transferase (19%)	transport (18%)	membrane (35%)	1	yes	extracellular	AEG73680.1	
	hypothetical protein	nucleic acid binding (19%)	biological process (13%)	membrane (40%)	1	no	cytoplasmic	AEG72504.1	
	hypothetical protein	N.A.*	transport (91%)	chromosome (91%)	1	no	cytoplasmic	AEG73619.1	
	hypothetical protein	nucleic acid binding (39%)/ hydrolase (39%)	mRNA processing (39%)	chromosome (72%)	1	no	unknown	AEG73558.1	
	hypothetical protein	electron carrier activity (28%)/ heme binding (28%)	transport (28%)	membrane (24%)	1	no	unknown	AEG73559.1	
Paralogous family 11	hypothetical protein	catalytic activity (36%)/ metal ion binding (36%)	cell adhesion (23%)	membrane (27%)	1	no	unknown	AEG72489.1	
	hypothetical protein	nucleic acid binding (41%)/ hydrolase (41%)	DNA repair (37%)	chromosome (52%)	1	no	unknown	AEG72502.1	
	hypothetical protein	heat shock protein binding (49%)	protein transport across membrane (49%)	membrane (41%)	1	yes	unknown	AEG72495.1	
	hypothetical protein	ion/voltage-gated chloride channel activity (35%)	transport (45%)	membrane (53%)	1	yes	unknown	AEG72501.1	
Paralogous family 12	hypothetical protein	protein binding (25%)	protein transport (38%)	cytoplasm (38%)	1	yes	unknown	AEG72499.1	
	hypothetical protein	protein binding (42%)	protein localization (26%)	cytoplasm (56%)	1	yes	unknown	AEG73634.1	
	hypothetical protein	nucleotide/ATP binding (45%)	translation (20%)	cytoplasm (27%) membrane (28%) / cytoplasm	1	yes	extracellular	AEG73653.1	
	hypothetical protein	nucleic acid binding (29%)	DNA catabolic process (15%) regulation of transcription (22%) / DNA recombination/integration (20%)	chromosome (43%)	0	no	unknown	AEG73589.1	
	hypothetical protein	catalytic activity (32%)/ DNA binding (32%)	regulation of transcription (34%)	chromosome (34%)	0	yes	unknown	AEG73145.1	
	hypothetical protein	metal ion binding (55%)	transcription (26%)	cytoplasm (40%)	0	no	unknown	AEG73146.1	
Paralogous family 14.2	hypothetical protein	DNA binding (37%)	regulation of transcription (37%) and replication (35%)	host cell nucleus (35%) / chromosome (34%)	1	no	unknown	AEG73144.1	
	hypothetical protein	RNA binding (74%)	RNA processing (64%)	cytoplasm (25%)	1	no	unknown	AEG73227.1	
Paralogous family 15.2	hypothetical protein	nucleotide/ATP binding (27%)	transport (26%)	membrane (59%)	1	no	unknown	AEG73223.1	
	hypothetical protein	transferase (58%)	spermidine catabolic process (34%)	membrane (29%)	1	no	unknown	AEG72719.1	
	hypothetical protein	metal ion binding (56%)	protein amino acid phosphorylation (28%)	cytoplasm (50%)	1	no	unknown	AEG72717.1	
Not in paralogous families	hypothetical protein	DNA binding (38%)	DNA repair/recombination (37%)	intracellular (44%)	0	no	cytoplasmic membrane	AEG72934.1	
	hypothetical protein	hydrolase (30%)/ protein binding (22%)	regulation of transcription (21%) / pathogenesis (10%)	chromosome (31%) / membrane (22%)	1	yes	unknown	AEG72464.1	
	hypothetical protein	nucleotide binding (43%)	regulation of transcription (34%)	membrane (42%) / chromosome (28%)	0	no	cytoplasmic	AEG73312.1	
	hypothetical protein	catalytic activity (28%) / ATP binding (28%)	viral reproduction (69%)	N.A.*	2	no	cytoplasmic membrane	AEG73767.1	
	hypothetical protein	translation release factor activity (24%)	translational termination (24%)	membrane (42%)	1	yes	unknown	AEG72694.1	
	hypothetical protein	signal transducer activity (59%) / receptor activity (59%)	signal transduction (60%)	membrane (90%)	2	no	cytoplasmic membrane	AEG72554.1	
	hypothetical protein	metalloendopeptidase activity (34%) / metal ion binding (34%)	proteolysis (34%) / pathogenesis (17%)	extracellular region (34%)	0	no	unknown	AEG73596.1	
	hypothetical protein	metal ion binding (28%)	transport (18%)	membrane (50%)	2	no	cytoplasmic membrane	AEG72923.1	
	hypothetical protein	metal ion binding (43%) / DNA binding (35%)	transcription (36%)	cytoplasm (30%)	0	no	cytoplasmic	AEG73063.1	

hypothetical protein	DNA binding (27%)	transcription (27%)	membrane (51%)	0	no	unknown	AEG73391.1
hypothetical protein	structural molecule activity (60%)	transport (17%)/ cell adhesion (15%)	cytoplasm (63%)/ cytoskeleton (63%)	1	no	cytoplasmic membrane	AEG72824.1
hypothetical protein	nucleotide (49%)/ATP binding (31%)	translation (17%)	cytoplasm (36%)	1	no	cytoplasmic	AEG73591.1
hypothetical protein	protein binding (36%)/ receptor activity (42%)	cell adhesion (31%)	membrane (50%)	1	no	cytoplasmic	AEG73116.1
hypothetical protein	metallopeptidase activity (20%)	proteolysis (20%)	membrane (54%)	1	no	cytoplasmic	AEG73115.1
hypothetical protein	protein binding (32%)	phosphate transport (19%)/ cell adhesion (19%)	cytoplasm (35%)	1	no	cytoplasmic	AEG73114.1
hypothetical protein	RNA binding (99%)	evasion by virus of host immune response (99%)	cytoplasm (99%)/ chromosome (99%)	3	no	cytoplasmic membrane	AEG73017.1
hypothetical protein	catalytic activity (56%)/ transferase (44%)	metabolic process (48%)	membrane (100%)	3	no	cytoplasmic membrane	AEG72385.1
hypothetical protein	transaminase/isomerase (100%)	porphyrin biosynthetic process (100%)	cytoplasm (100%)	0	no	cytoplasmic	AEG72616.1
hypothetical protein	nucleotide binding (34%)/ translation initiation factor activity (32%)	translational initiation (32%)/ pathogenesis (20%)	membrane (42%)	1	no	unknown	AEG73324.1
hypothetical protein	N.A.*	N.A.*	N.A.*	2	no	cytoplasmic membrane	AEG73429.1
CDSs with predicted function (present in several bacteria species, but absent in <i>M. haemocanis</i> str. Illinois)	type II site-specific deoxyribonuclease	Type II site-specific deoxyribonuclease activity (83%)	DNA restriction-modification system (83%)	0	no	cytoplasmic	AEG73510.1
	Cytosine-specific methyltransferase	DNA (cytosine-5-) methyltransferase activity (99%)	DNA methylation (99%)/ DNA restriction-modification system (99%)	0	no	unknown	AEG73555.1
	C-5 cytosine-specific DNA methylase	DNA (cytosine-5-) methyltransferase activity (100%)	DNA methylation (100%)/ DNA restriction-modification system (100%)	0	no	cytoplasmic	AEG73509.1

<sup>a</sup> ESG software (sequence similarity-based function prediction) [36].

<sup>b</sup> prediction using PSORTb version 3 software [31].

\* N.A.: no function assigned by ESG software.