



APPENDIX

ลิขสิทธิ์มหาวิทยาลัยเชียงใหม่

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APPENDIX A

Growth curve determination of *S. suis* and Number of Intracellular bacteria recovered from mouse or human macrophage cell lines

Growth curve determination of *S. suis* serotype 2 and serotype 14

Table 27 Optical density (OD₆₀₀) measurement of *S. suis* serotypes 2 and 14 (5 strains)

<i>S. suis</i> strains	Serotype		Hours						
			0	2	4	6	8	10	12
P 1/7	2	1	0.05	0.20	0.50	0.70	0.77	0.81	0.75
		2	0.05	0.30	0.69	0.91	0.93	0.95	0.97
		3	0.05	0.16	0.43	0.67	0.72	0.71	0.74
		Av	0.05	0.22	0.54	0.76	0.81	0.82	0.82
		SD	0.00	0.07	0.13	0.13	0.11	0.12	0.13
TSK 10.4	2	1	0.05	0.11	0.88	0.95	0.98	1.00	1.02
		2	0.05	0.33	1.10	1.13	1.14	1.17	1.21
		3	0.05	0.19	1.00	1.08	1.11	1.11	1.12
		Av	0.05	0.21	0.99	1.05	1.08	1.09	1.12
		SD	0.00	0.11	0.11	0.09	0.09	0.09	0.10
LPH 210/53	2	1	0.05	0.11	0.37	0.68	0.84	0.84	0.83
		2	0.05	0.16	0.54	0.81	0.87	0.87	0.86
		3	0.05	0.14	0.52	0.71	0.70	0.71	0.73
		Av	0.05	0.14	0.48	0.73	0.80	0.81	0.81
		SD	0.00	0.03	0.09	0.07	0.09	0.09	0.07
MNCM 07	14	1	0.05	0.12	0.63	0.76	0.79	0.82	0.80
		2	0.05	0.34	0.84	0.89	0.89	0.89	0.87
		3	0.05	0.22	0.65	0.72	0.73	0.71	0.70
		Av	0.05	0.23	0.71	0.79	0.80	0.81	0.79
		SD	0.00	0.11	0.12	0.09	0.08	0.09	0.09
TD 2.2	14	1	0.05	0.05	0.16	0.72	0.89	0.88	0.89
		2	0.05	0.23	0.68	1.00	1.00	1.01	1.02
		3	0.05	0.14	0.46	0.78	0.83	0.81	0.81
		Av	0.05	0.14	0.43	0.83	0.91	0.90	0.91
		SD	0.00	0.09	0.26	0.15	0.09	0.10	0.11

Table 28 Viable bacterial cell count (cfu/ml) of *S. suis* serotype 2

Strains	P 1/7				
Hour	1	2	3	Average	SD
0	4.29×10^7	3.25×10^7	1.90×10^7	3.15×10^7	1.20×10^7
2	3.22×10^8	5.80×10^8	1.24×10^8	3.42×10^8	2.29×10^8
4	1.23×10^9	2.37×10^9	1.26×10^9	1.62×10^9	6.51×10^8
6	5.00×10^9	8.25×10^9	7.80×10^9	7.02×10^9	1.76×10^9
8	1.50×10^9	2.04×10^{10}	2.05×10^9	7.98×10^9	1.08×10^{10}
10	3.30×10^{10}	2.85×10^9	2.30×10^9	1.27×10^{10}	1.76×10^{10}
12	2.90×10^{10}	5.00×10^9	4.60×10^9	1.29×10^{10}	1.40×10^{10}
Strains	TSK 10.4				
Hour	1	2	3	Average	SD
0	1.78×10^7	3.16×10^7	2.75×10^7	2.56×10^7	7.09×10^6
2	1.02×10^8	2.87×10^8	1.33×10^8	1.74×10^8	9.93×10^7
4	3.85×10^8	2.20×10^9	1.47×10^9	1.35×10^9	9.11×10^8
6	3.50×10^9	1.69×10^{10}	1.01×10^{10}	1.02×10^{10}	6.68×10^9
8	3.00×10^9	2.95×10^9	6.95×10^9	4.30×10^9	2.30×10^9
10	1.00×10^9	1.90×10^9	7.00×10^8	1.20×10^9	6.25×10^8
12	3.50×10^9	2.45×10^9	1.55×10^9	2.50×10^9	9.76×10^8
Strains	LPH 210/53				
Hour	1	2	3	Average	SD
0	6.30×10^7	1.29×10^7	8.00×10^6	2.80×10^7	3.04×10^7
2	1.20×10^8	4.60×10^7	2.19×10^8	1.28×10^8	8.68×10^7
4	2.28×10^9	3.15×10^8	1.37×10^9	1.32×10^9	9.81×10^8
6	4.15×10^9	4.15×10^9	1.15×10^9	3.15×10^9	1.73×10^9
8	2.95×10^9	1.35×10^9	2.55×10^9	2.28×10^9	8.33×10^8
10	1.75×10^9	1.00×10^9	1.90×10^9	1.55×10^9	4.82×10^8
12	2.35×10^9	1.19×10^{10}	2.15×10^9	5.47×10^9	5.57×10^9

Table 29 Viable bacterial cell count (cfu/ml) of *S. suis* serotype 14

Strains	MNCM 07				
Hour	1	2	3	Average	SD
0	2.77×10^7	4.62×10^7	4.10×10^7	3.83×10^7	9.55×10^6
2	1.43×10^8	6.41×10^8	3.19×10^8	3.68×10^8	2.52×10^8
4	2.22×10^9	4.19×10^9	4.07×10^9	3.49×10^9	1.10×10^9
6	5.00×10^9	5.45×10^9	1.96×10^{10}	1.00×10^{10}	8.27×10^9
8	1.25×10^{10}	9.45×10^9	2.95×10^9	8.30×10^9	4.88×10^9
10	9.00×10^9	2.90×10^9	4.50×10^9	5.47×10^9	3.16×10^9
12	5.00×10^9	6.95×10^9	5.40×10^9	5.78×10^9	1.03×10^9
Strains	TD 2.2				
Hour	1	2	3	Average	SD
0	8.40×10^6	8.58×10^7	8.10×10^7	5.84×10^7	4.34×10^7
2	2.77×10^7	6.17×10^8	5.57×10^8	4.00×10^8	3.24×10^8
4	3.16×10^8	3.64×10^9	3.68×10^9	2.54×10^9	1.93×10^9
6	4.00×10^9	8.20×10^9	4.10×10^{10}	1.77×10^{10}	2.03×10^{10}
8	1.15×10^{10}	1.92×10^{10}	5.95×10^9	1.22×10^{10}	6.63×10^9
10	1.05×10^{10}	4.08×10^{10}	5.30×10^9	1.89×10^{10}	1.91×10^{10}

Number of Intracellular bacteria recovered from mouse or human macrophage cell lines

Table 30 Number of intracellular bacteria recovered from mouse macrophage cells (RAW 264.7)

Serotype	Strains		Multiplicity of infection (MOI)				
			1	10	50	100	200
2	P1/7	1	0	0	1.00	2.00	4.50
		2	0	0	0.50	1.00	4.00
		3	0	0	1.00	1.50	5.00
		Sum	0	0	2.50	4.50	13.50
		Av	0	0	0.83	1.50	4.50
		SD	0	0	0.29	0.50	0.50
		% Viability	100.00	100.00	100.00	100.00	85.19
2	TSK 10.4	1	0	3.50	4.50	11.00	14.50
		2	0	4.00	6.50	15.00	17.50
		3	0	3.00	6.00	13.50	16.50
		Sum	0	10.50	17.00	39.50	48.50
		Av	0	3.50	5.67	13.17	16.17
		SD	0	0.50	1.04	2.02	1.53
		% Viability	90.90	100.00	85.71	75.00	73.91
2	LPH 210/53	1	0	0	1.00	1.50	2.50
		2	0	0	1.50	2.00	5.00
		3	0	0	2.00	2.00	4.00
		Sum	0	0	4.50	5.50	11.50
		Av	0	0	1.50	1.83	3.83
		SD	0	0	0.50	0.29	1.26
		% Viability	100.00	100.00	93.33	92.86	88.00
14	MNCM 07	1	0	0.50	1.00	3.50	15.50
		2	0	1.00	1.00	1.50	16.00
		3	0	1.00	1.50	2.00	14.50
		Sum	0	2.50	3.50	7.00	46.00
		Av	0	0.83	1.17	2.33	15.33
		SD	0	0.29	0.29	1.04	0.76
		% Viability	100.00	94.44	94.74	100.00	93.33
14	TD 2.2	1	0	0	0	1.50	8.00
		2	0	0	0	0.50	7.50
		3	0	0	0.50	2.00	4.00
		Sum	0	0	0.50	4.00	19.50
		Av	0	0	0.17	1.33	6.50
		SD	0	0	0.29	0.76	2.18
		% Viability	100.00	100.00	81.25	91.67	70.00

LPH: Lamphun Hospital, MNCM: Maharaj Nakorn Chiang Mai Hospital

Table 31 Number of intracellular bacteria recovered from human macrophage cells

(U 937)

Serotype	Strains		Multiplicity of infection (MOI)				
			1	10	50	100	200
2	P1/7	1	48.00	270.50	293.50	318.50	235.50
		2	35.50	292.50	307.00	280.00	223.50
		3	52.00	285.00	312.00	297.00	232.50
		Sum	135.50	848.00	912.50	895.50	691.50
		Av	45.17	282.67	304.17	298.50	230.50
		SD	8.61	11.18	9.57	19.29	6.25
		% Viability	100.00	100.00	92.86	90.42	76.39
2	TSK 10.4	1	51.50	121.50	322.00	225.50	138.00
		2	56.00	159.50	359.00	348.00	328.50
		3	54.00	146.50	344.00	337.00	322.00
		Sum	161.50	427.50	1025.00	910.50	788.50
		Av	53.83	142.50	341.67	303.50	262.83
		SD	2.26	19.31	18.61	67.77	108.16
		% Viability	100.00	100.00	98.61	96.06	89.34
2	LPH 210/53	1	113.50	171.00	413.50	361.50	286.50
		2	155.00	349.50	382.50	350.50	422.00
		3	132.00	328.00	404.00	359.50	374.00
		Sum	400.50	848.50	1200.00	1071.50	1082.50
		Av	133.50	282.83	400.00	357.17	360.83
		SD	20.79	97.45	15.88	5.86	68.70
		% Viability	100.00	100.00	94.44	93.52	79.37
14	MNCM 07	1	45.50	318.00	330.50	307.50	274.50
		2	44.50	346.00	325.50	315.00	286.50
		3	50.00	332.00	346.50	334.00	292.50
		Sum	140.00	996.00	1002.50	956.50	853.50
		Av	46.67	332.00	334.17	318.83	284.50
		SD	2.93	14.00	10.97	13.66	9.17
		% Viability	100.00	96.16	93.75	87.50	63.33
14	TD 2.2	1	117.00	138.50	267.00	155.00	231.50
		2	141.50	197.50	311.00	141.50	259.00
		3	126.00	167.00	296.50	224.00	241.00
		Sum	384.50	503.00	874.50	520.50	731.50
		Av	128.17	167.67	291.50	173.50	243.83
		SD	12.39	29.51	22.42	44.25	13.97
		% Viability	100.00	100.00	96.67	94.44	92.86

LPH: Lamphun Hospital, MNCM: Maharaj Nakorn Chiang Mai Hospital,

Table 32 Number of intracellular bacteria recovered from mouse and human macrophage cell lines at optimal MOI

Strains	Number of colony post-invasion (CFU/ml)	
	RAW 264.7 (MOI = 200)	U 937 (MOI = 50)
P 1/7	45 ± 0.50	3040 ± 9.57
TSK 10.4	162 ± 1.53	3420 ± 18.61
LPH 210/53	38.3 ± 1.26	4000 ± 15.88
MNCM 07	153 ± 0.76	3340 ± 10.96
TD2.2	65 ± 2.18	2920 ± 22.42

APPENDIX B

Proteomics analyses of *S. suis* by LC-MS/MS

1. Protein expression of *S. suis* after exposure to mouse macrophage cell line RAW 264.7

Table 33 The total proteins of all strains of *S. suis* up-regulated in mouse macrophage cell line RAW 264.7 (261 proteins)

No.	Protein Name	Accession number	ID Score	Function	Peptide sequence
1	Glycosyl transferase family protein	gi 107021846	22.06	Carbohydrate metabolism	EIGGFR
2	UDP-N-acetylglucosamine pyrophosphorylase protein	gi 56476675	15.39	Carbohydrate metabolism	HVEDTTT
3	UDP-3-0-acyl N-acetylglucosamine deacetylase	gi 83942733	27.23	Carbohydrate metabolism	GAVRMVECDAQMA SRLPG
4	glycosyl transferase group 1	gi 158318284	19.77	Carbohydrate metabolism	THGEQGLLHEA
5	glycoside hydrolase family 5	gi 110638545	8.08	Carbohydrate metabolism	ANTGAG
6	alpha-L-arabinofuranosidase	gi 330817052	25.18	Carbohydrate metabolism	GDKAPATLR
7	chorismate mutase	gi 21220254	15.32	Carbohydrate metabolism	GAMPRV
8	phosphoglucomutase/phosphomanno mutase alpha/beta/subunit	gi 94984460	4.14	Carbohydrate metabolism	HDAMGGA
9	mannosyltransferase/glycosyltransferase	gi 116250428	17.88	Carbohydrate metabolism	IIPRGLTV
10	glycosyltransferase	gi 183221392	48.19	Carbohydrate metabolism	LQIPFQSDSEIKQ
11	glycogen debranching enzyme GlgX	gi 209515637	19.76	Carbohydrate metabolism	AAGMYQVGAFPGM AW

Table 33 (Continued)

No.	Protein Name	Accession number	ID Score	Function	Peptide sequence
12	glycoside hydrolase family 3 domain protein	gi 313906653	16.48	Carbohydrate metabolism	NGERVLPDSP
13	diaminopimelate epimerase	gi 154244368	18.38	Carbohydrate metabolism	LGPTSLVSMGN
14	Precorin-8X methylmutase CobH	gi 87301626	19.85	Cell development	LGPTDLDPV
15	lateral flagellar hook basal body protein, LfiE	gi 315126012	21.84	Cell movement	EDVVGAMI
16	ROK family protein	gi 256394472	20.31	cytoskeleton	SAEGMAGIIGD
17	ribonucleoside reductase	gi 86141198	9.95	DNA metabolism	SYGGIM
18	Cytidine/deoxycytidylate deaminase, zinc-binding region	gi 144900009	25.75	DNA metabolism	ISAADSQALITAYEQ C
19	PPE56 gene product	gi 57117096	10.93	Immune response	GISMS
20	cell wall hydrolase/autolysin	gi 150019509	5.1	inflammatory	SPNPATP
21	Aldehyde Dehydrogenase	gi 317053040	25.45	Lipid metabolism	PQIIMPD
22	short-chain dehydrogenase/reductase SDR	gi 146301489	19.74	Lipid metabolism	GYSDAEGNI
23	lipoprotein	gi 225872392	20.3	Lipid metabolism	ASHAPSNY
24	pyrH gene product	gi 15799853	5.3	Nucleotide metabolism	PTATM
25	adenylosuccinate lyase	gi 311748150	25.6	Nucleotide metabolism	AMNYFKQKIKAGEI
26	AMP-dependent synthetase and ligase	gi 148553310	19.62	Nucleotide metabolism	TVGAAIEGT
27	N-acetyl-gamma-glutamyl-phosphate reductase	gi 67921281	5.63	Protein metabolism	GKGSAG
28	acetylornithine and succinylornithine aminotransferase	gi 150391118	15.43	Protein metabolism	EIIAMT

Table 33 (Continued)

No.	Protein Name	Accession number	ID Score	Function	Peptide sequence
29	peptidase S10, serine carboxypeptidase	gi 134292247	16.91	Protein metabolism	
30	uroporphyrin-III C-methyltransferase	gi 154245026	10.13	Protein metabolism	IRPLTVLPV
31	pts system eiibc component	gi 65318956	14.79	Protein metabolism	DVGGI
32	subtilisin-like serine protease	gi 184158969	32.91	Protein metabolism	KTASLSETSVD
33	alkaline serine protease, subtilase family	gi 329896031	13.55	Protein metabolism	RDMLGDDPAQD
34	Integrase catalytic region	gi 288923734	19.69	Protein metabolism	AAILTHQA
35	phenylalanyl-tRNA synthetase subunit beta	gi 42519500	3.28	Protein metabolism	GGYSAK
36	prophage Lp2 protein 51	gi 28378971	29.93	Protein metabolism	DGAAWKPT
37	uroporphyrinogen decarboxylase	gi 260426787	17.62	Protein metabolism	YETVKILRSELPSE
38	peptidase U62 modulator of DNA gyrase	gi 322419812	14.68	Protein metabolism	AAKMQSP
39	anthranilate synthase component I	gi 91790290	16.24	Protein metabolism	ANAPSGG
40	FKBP-type peptidylprolyl isomerase	gi 167648892	16.56	Protein metabolism	QESLAAAQAFMA
41	rhodanese	gi 297529767	29.94	Protein metabolism	GVKITHIVD
42	5-methyltetrahydrofolate-homocysteine methyltransferase	gi 152993401	17.73	Protein metabolism	IPISVHANAG
43	orotidine 5'-phosphate decarboxylase, subfamily 1	gi 256827209	23.51	Protein metabolism	TLGGEEMMRAAVQ GANK
44	chaperone protein DnaJ	gi 325262025	27.91	Response to stress	IKAGSKA
45	antibiotic-resistance protein	gi 15609440	9.98	Response to stress	APEPR

Table 33 (Continued)

No.	Protein Name	Accession number	ID Score	Function	Peptide sequence
46	nitric oxide reductase, cytochrome c-containing subunit	gi 183222303	11.06	Response to stress	HAVGGKGG
47	Copper resistance C protein	gi 94314588	10.68	Response to stress	DKSEGP
48	Short-chain alcohol dehydrogenase	gi 116617968	2.62	Response to stress	SPTPDD
49	heat shock protein dnaJ domain-containing protein	gi 313682988	23.58	Response to stress	GGGFGGFGGGGFGG MNLID
50	aldehyde-alcohol dehydrogenase	gi 315650859	6.68	Response to stress	YENGSGDP
51	hydrolase, alpha/beta fold family protein	gi 119961915	16.44	Response to stress	QGHGRTN
52	DnaJ domain protein	gi 254454322	17.41	Response to stress	TPEAEGKP
53	thiol:disulfide interchange protein DsbA precursor	gi 21672682	13.97	Response to stress	EKIMMP
54	paraquat-inducible protein A	gi 260428559	12.58	Response to stress	MACPSCDA
55	dihydroorotase	gi 219670029	4.27	Response to stress	AHISAK
56	hippurate hydrolase	gi 15890539	14.15	Response to stress	GDTAGLHNAA
57	phosphoesterase PA-phosphatase-like protein	gi 332667713	29.08	Response to stress	ADTISSK
58	spermidine synthase family protein	gi 289705718	20.82	Response to stress	DPTDLTGA
59	superoxide dismutase	gi 335423770	39.33	Response to stress	MDVVSESGKPV MGL
60	nucleotidyl transferase	gi 125973594	11.12	Response to stress	SSVVDK
61	multidrug resistance protein vceB	gi 49475971	16.08	Response to stress	AFGMFM
62	8-OXO-dGTPase domain (mutT domain)	gi 149195428	30.02	Response to stress	CNAYELPQAG
63	methionine sulfoxide reductase B	gi 115523519	9.07	Response to stress	KPATTG

Table 33 (Continued)

No.	Protein Name	Accession number	ID Score	Function	Peptide sequence
64	benzaldehyde lyase	gi 39935827	53.91	Response to stress	GDGALGFHLQ
65	alcohol dehydrogenase	gi 312196743	12.66	Response to stress	AMSFIPS
66	cupin 2 domain-containing protein	gi 116625959	8.8	Response to stress	ADVPNS
67	LysR substrate binding domain protein	gi 313897875	20.75	Response to stress	WSDMESMSIGSS
68	penicillin-binding protein 1	gi 242373467	11.07	Response to stress	ESDDTGSD
69	rhodanese domain protein	gi 311740130	13.42	Response to stress	CHAGGRSM
70	Flagellar biosynthesis pathway component FliR	gi 254255043	11.41	Signal	IGLSMAQMNDP
71	carbamate kinase	gi 257791694	11.56	Signal	AADEFGADM
72	tyrosyl-tRNA synthetase	gi 116750003	21.02	Signal	AACEAAS
73	serine/threonine protein kinase	gi 116624167	6.31	Signal	HSAMEA
74	histidine kinase	gi 257058393	24.53	Signal	ELADNSIEPSPELYL
75	toxin-antitoxin system, antitoxin component, Xre family	gi 288871502	18.5	Signal	IRSITSGRTLPSMSEF
76	phosphoglycerate kinase	gi 283783368	17.46	Signal	KMGLDIGSD
77	signal transduction histidine kinase regulating citrate/malate metabolism	gi 116669865	53.06	Signal	IVVGDSGDGLA
78	diguanylate phosphodiesterase	gi 284045237	18.83	Signal	DPHGAVPP
79	3-phosphoshikimate 1-carboxyvinyltransferase	gi 298527802	42.6	Signal	MGAKISETKNG
80	conjugal transfer mating pair stabilization protein TraG	gi 152973589	36.98	Signal	YSEMASRTESLTGQ M
81	phosphomethylpyrimidine kinase	gi 283783603	32.69	Signal	AAGGYGMCIP

Table 33 (Continued)

No.	Protein Name	Accession number	ID Score	Function	Peptide sequence
82	Signal Transduction Histidine Kinase (STHK) with CheB and CheR activity	gi 88812847	13.68	Signal	APAHEAH
83	flagellar biosynthesis protein FlhA	gi 220913713	1.73	Signal	MAVSTGMI
84	Retron-type reverse transcriptase	gi 238790538	11.06	Transcription	SVGAPS
85	prophage protein	gi 283786267	35.88	Translation	SSAAAISVMKSS
86	polyprenyl synthetase	gi 238024940	12.74	Translation	AVMGGGKR
87	30S ribosomal protein S2	gi 325292737	24.69	Translation	AAIDGILR
88	cysteinyI-tRNA synthetase	gi 258543649	10.01	Translation	AGPVPET
89	lysine--tRNA ligase	gi 282859169	21.45	Translation	ITLLSKSLKPLPVVK QKDGET
90	TrbF	gi 242308857	16.08	Translation	RVKIKSIVP
91	Glycyl-tRNA synthetase, alpha subunit	gi 85711016	13.89	Translation	ACAEVY
92	30S ribosomal protein S10	gi 94987674	27.56	Translation	TGAKVAGPVPLPTE R
93	50S ribosomal protein L22	gi 42518434	10.77	Translation	AKGMAS
94	50S ribosomal protein L5	gi 99080107	19.51	Translation	FRVREGMPMGAKV T
95	EmrB [Pantoea ananatis LMG 20103]	gi 291618290	17.2	Translation	SGQASGRY
96	flagellar hook-basal body complex protein	gi 167835059	24.63	Transport	QAAGGAAGPAT
97	histidine ammonia-lyase	gi 71733361	18.02	Transport	VSQPGVNSG

Table 33 (Continued)

No.	Protein Name	Accession number	ID Score	Function	Peptide sequence
98	radical SAM protein	gi 117925454	11.76	transport	SSNGIP
99	asparagine synthase	gi 22127131	10.85	Protein metabolism	VFAKS
100	M48 peptidase family protein	gi 22127655	5.93	Protein metabolism	PDGTM
101	peptidase M48, Ste24p	gi 186683873	3.48	Protein metabolism	AASHM
102	peptidoglycan linked protein (LPxTG)	gi 168334776	26.72	immune	ADFTGGID
103	exported phospholipase	gi 167563235	11.1	Lipid metabolism	DISARPEGSTT
104	fibronectin-binding protein	gi 86149287	2.38	Cell adhesion	FGADN
105	cadherin	gi 113474267	3.82	Cell adhesion	DINDGSV
106	fibronectin type III domain protein	gi 270292150	10.81	Cell adhesion	KVNGKPVKAT
107	tail protein (tape measure)	gi 334122139	10.07	Cytoskeleton	SGTGGASSEFSR
108	lipoprotein lppf	gi 115377461	7.78	Lipid metabolism	ESRGAGTME
109	purple acid phosphatase/fibronectin domain-containing protein	gi 30260956	14.39	Protein metabolism	AHIGG
110	protein-glutamate methylesterase CheB	gi 254414508	22.07	Protein metabolism	KTTAILLTGMGRDG A
111	S4 domain protein	gi 168187044	22.16	Protein metabolism	THHVAKADAKTMY E
112	FAD dependent oxidoreductase	gi 145221327	14.81	Respiration	DDPKSAV
113	metal dependent phosphohydrolase with GAF sensor	gi 327399278	27.02	Response to stress	GVSILLNR
114	Virulence-associated protein	gi 255020342	11	Response to stress	SGKAADAAG
115	membrane-bound nitrate reductase	gi 199594027	17.24	Response to stress	EGHPDAHTM
116	flagellin domain-containing protein	gi 218886717	25.17	Response to stress	IRIGSVS

Table 33 (Continued)

No.	Protein Name	Accession number	ID Score	Function	Peptide sequence
117	FKBP-type peptidyl-prolyl cis-trans isomerase 2-like protein	gi 134296272	33.03	Response to stress	QLEPQDAFGDYDP
118	metal dependent phosphohydrolase	gi 95930384	9.11	Response to stress	HTPDHI
119	beta-lactamase domain-containing protein	gi 119946225	57.2	Signal	NIESGCIII
120	adenylate cyclase	gi 115380598	26.28	Signal	ASAIQMFE
121	TonB-dependent outer membrane receptor	gi 163857670	23.73	Signal	FFQLKKKNAYVMD YA
122	diguanylate cyclase	gi 114563636	8.17	Signal	APDMSS
123	TonB-dependent receptor	gi 228474120	31.91	Signal	MDVPTGS
124	hydrogenase accessory protein HypB	gi 134291353	11.85	Signal	AHGVRA
125	TonB-dependent receptor for iron transport	gi 124268908	11.58	Signal	GASSGYVNM
126	TonB family protein	gi 157376464	8.91	Signal	GSPIAAE
127	Fimh-like protein	gi 12382239	17.91	Signal	ATNSTCT
128	endo-1,4-beta-xylanase precursor	gi 238836759	28.29	Signal	GDALVDFARSHG
129	ABC superfamily ATP binding cassette transporter ABC protein	gi 311740006	29.83	Transport	DEDFCSRIKLTRQ
130	Mn ²⁺ /Fe ²⁺ transporter	gi 22538160	41.19	Transport	AHIII
131	heavy metal efflux pump CzcA	gi 91978647	15.24	Transport	SAMKDMPDG
132	peptide ABC transporter ATP-binding protein	gi 71733401	15.34	Transport	VDMAQGSGISL
133	chromate transporter permease	gi 110638551	10.38	Transport	IPATVS
134	amino acid efflux protein	gi 111018048	24.64	Transport	PLLPQYLVIATMV

Table 33 (Continued)

No.	Protein Name	Accession number	ID Score	Function	Peptide sequence
135	major facilitator superfamily protein	gi 192292051	19.01	Transport	IAAITAALMIPAALL
136	Na ⁺ /H ⁺ antiporter NhaC	gi 317128784	22.4	Transport	AEWMTLIQNGYNSG A
137	integral membrane protein	gi 291454034	15.06	Transport	GTVEPRGEISDELM
138	ABC transporter integral membrane subunit	gi 319950755	14.71	Transport	SVPAWPVAQ
139	polysaccharide export protein	gi 254477926	20.26	Transport	VLPDAPST
140	major facilitator family transporter	gi 28868676	18.27	Transport	MVMVGLYVRLKLE ETPVF
141	YjgP/YjgQ family permease	gi 116747639	21	Transport	LVALAMPKLMLFAL PMASLLGVL
142	large membrane protein	gi 116630159	6.47	Transport	DTYPV
143	bacteriochlorophyll synthase 44.5 kDa chain	gi 304393720	27.27	Transport	AAASMVWI
144	Sodium dependent transporter	gi 88809093	20.51	Transport	LRGALVMLILTWIGL GL
145	lytic transglycosylase	gi 304316563	31.3	Transport	AAYNGGSGNVS
146	hydrophobe/amphiphile efflux-1 (HAE1) family protein	gi 116692839	10.22	Transport	CMCAA
147	secretion protein HlyD family protein	gi 209517699	24.14	Transport	DNKAAPPA
148	ABC Fe ³⁺ -siderophores transporter, periplasmic binding protein	gi 83950977	13.13	Transport	AMSPTVR
149	major facilitator superfamily permease	gi 182437179	30.5	Transport	GGRRVIAV

Table 33 (Continued)

No.	Protein Name	Accession number	ID Score	Function	Peptide sequence
150	NCS1 nucleoside transporter family protein	gi 114762421	54.61	Transport	IATVWVPA
151	UvrD/REP helicase	gi 317497577	36.93	transport	CLCETKDKMEK
152	citrate/sodium family symporter	gi 15609830	13.33	Transport	ARIGM
153	ABC transporter-like protein	gi 116669397	15.8	Transport	DVTMAV
154	secretion system-associated protein type VI	gi 292489485	15.72	Transport	ASGHATLW
155	oligogalacturonide transporter	gi 241896549	40.61	Transport	ISATQGASI
156	binding--dependent transport system inner membrane component family protein	gi 330447870	19.3	Transport	AAIAYVAS
157	polar amino acid ABC transporter ATPase	gi 300716302	33.72	transport	ILKGVDLTIEK
158	ABC transporter	gi 219670766	18.51	Transport	EATAFT
159	inner-membrane translocator	gi 253999649	19.72	Transport	SAAFMAVGAFAY NFHL
160	translocation protein in type III secretion	gi 163802011	22.34	Transport	SGGGFIAFM
161	alanine racemase	gi 50955527	37.81	Transport	VDIGVSS
162	preprotein translocase, SecA subunit	gi 225010685	32.86	Transport	TLKYKQAESLLKEG SW
163	outer membrane autotransporter barrel domain protein	gi 332185647	20.22	Transport	AAAESAACTAINN
164	gluconate transporter	gi 254037326	23.27	Transport	DSGAANM

Table 33 (Continued)

No.	Protein Name	Accession number	ID Score	Function	Peptide sequence
165	conjugal transfer protein TrbG/VirB9/CagX	gi 209886708	12.71	Transport	ELRLGSGKH
166	propanediol utilization protein PduX	gi 88596640	11.97	Carbohydrate metabolism	MGSEK
167	enoyl-CoA hydratase	gi 297191943	14.95	Lipid metabolism	MQAMDHAA
168	3-oxoacyl-(acyl-carrier-protein) synthase 2	gi 193211802	35.4	Lipid metabolism	AAITPMSVA
169	aconitate hydratase	gi 46579477	31.71	Lipid metabolism	CMISPGSKQV
170	acetyl/propionyl-CoA carboxylase subunit beta	gi 333990288	9.68	Lipid metabolism	GGPDTHHK
171	dephospho-CoA kinase	gi 326386169	12.74	Lipid metabolism	SAVALMMR
172	salicylyl-CoA 5-hydroxylase	gi 17546545	9.83	Lipid metabolism	GIVASGR
173	glycine hydroxymethyltransferase	gi 269792998	6.34	Protein metabolism	SGTTANM
174	2-isopropylmalate synthase/homocitrate synthase family protein	gi 254475905	13.68	Protein metabolism	MNAGTAA
175	fumarate hydratase, class I	gi 39996097	27.5	Protein metabolism	LFMAKGGGSANKT MLFQETKAL
176	NADH:flavin oxidoreductase	gi 154246902	8.56	Respiration	SGGISGR
177	4Fe-4S binding domain protein	gi 289523902	23.98	Respiration	YGPGTKR
178	citrate synthase type II	gi 121605928	19.13	Respiration	VGALSAFYHDSTDI NNP
179	cytochrome-c oxidase chain I	gi 159184458	14.35	Respiration	GMPGPAVDL
180	cytochrome b/b6 domain-containing protein	gi 262197076	28.31	Respiration	EHCGPCH

Table 33 (Continued)

No.	Protein Name	Accession number	ID Score	Function	Peptide sequence
181	oxidoreductase	gi 56965469	29.99	Respiration	FLAENEFVTG
182	Multicopper oxidase family protein	gi 258592099	39.25	Respiration	PMMGMGGGM
183	pyridine nucleotide-disulphide oxidoreductase dimerisation region	gi 194467564	22.5	Respiration	GVDIKTIGEQ
184	NADH-ubiquinone oxidoreductase	gi 149912035	10.28	Respiration	EVFHADT
185	indolepyruvate oxidoreductase subunit B	gi 91790560	13.23	Respiration	LVDLAEQNGY
186	2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylic-acid synthase	gi 329964379	20.15	Respiration	APKPMILEV
187	succinate dehydrogenase iron-sulfur subunit	gi 22126944	12.96	Respiration	AIGHIK
188	phage D3 terminase-like protein	gi 72384751	34.82	Response to stress	YGD LafEMTAEQK
189	(S)-2-hydroxy-acid oxidase subunit D	gi 301052934	48.37	Response to stress	GGIILIFR
190	sulfur oxidation V protein	gi 114767009	45.36	Response to stress	IATDSVN VIA
191	ferrochelatase	gi 26246490	36.4	Response to stress	SCSTVGAVW
192	nitrite reductase (NAD(P)H) large subunit	gi 109898849	8.38	Response to stress	KPAVGS
193	aerobic-type carbon monoxide dehydrogenase large subunit	gi 113866728	29.1	Response to stress	TKPGFAIEIENGAVK NSN
194	imidazole glycerol phosphate synthase subunit hisH	gi 338730811	23.73	Response to stress	VVAAVCNYG
195	beta-carbonic anhydrase	gi 77361680	12.87	Response to stress	EADTYKTA
196	glucose-inhibited division protein A	gi 90421002	22.57	Carbohydrate metabolism	EAIDGMTP

Table 33 (Continued)

No.	Protein Name	Accession number	ID Score	Function	Peptide sequence
197	tyrosine recombinase XerC	gi 119961787	19.53	Cell development	NTAAADGGPM
198	S-layer protein	gi 226357093	10.22	Cell development	GGFTINP
199	cell division protein FtsH	gi 22536201	13.45	Cell division	AMARAM
200	Endonuclease/exonuclease/phosphatase	gi 167587986	39.54	DNA metabolism	CGAGLIRV
201	Endonuclease	gi 313624735	25.03	DNA metabolism	KVQVLNNLVELYG
202	uracil-DNA glycosylase	gi 113460626	24.81	DNA repair	DIMGFQTPSHG
203	Mycobacteriophage excisionase	gi 10956670	17.64	DNA repair	AISTIPPIS
204	DNA gyrase, B subunit	gi 88597733	4.15	DNA replication	AFGCG
205	DNA polymerase I	gi 302039429	12.55	DNA replication	AAAVTAKV
206	Holliday junction DNA helicase RuvA	gi 114798884	15.81	DNA replication	DVPGVAGKSA
207	DNA polymerase III subunit alpha	gi 15607303	8.31	DNA replication	DNTGY
208	DNA protecting protein DprA	gi 222054654	13.44	DNA replication	VVQLPGKH
209	DNA polymerase iii alpha chain protein	gi 84686147	10.29	DNA replication	PGTANGVVF
210	DNA polymerase III subunit beta	gi 323487686	29.97	DNA replication	SRLLEGNYPDTSRLI PA
211	DNA primase, catalytic core	gi 336451151	19.57	DNA replication	TAATTDH
212	A/G-specific adenine glycosylase	gi 47097401	8.36	Nucleotide metabolism	KKNPAA
213	minor capsid protein	gi 332686881	9.52	Response to stress	ARMSSHA
214	Nitrogen assimilation regulatory protein ntrX	gi 330993262	18.32	Response to stress	MMPGNST
215	acetoin expression regulatory protein	gi 117956079	15	Signal	TLSGETTRA

Table 33 (Continued)

No.	Protein Name	Accession number	ID Score	Function	Peptide sequence
216	DUF224 cysteine-rich region domain protein	gi 298530414	9.62	Signal	AISEU
217	ribokinase-like domain-containing protein	gi 146276254	12.62	Signal	TIAGIAH
218	tetraacyldisaccharide 4'-kinase	gi 152996174	12.61	Signal	SRGHGAKM
219	internalin	gi 270284525	35.73	Transcription	ADTISKS
220	colanic acid biosynthesis acetyltransferase WcaF	gi 110637321	34.07	Transcription	KPIIIDD
221	ScrT	gi 15610071	2.79	Transcription	AGHIA
222	SyrB family protein	gi 23499904	4.34	Transcription	GNGPAS
223	single-stranded-DNA-specific exonuclease RecJ	gi 186684853	16.72	Transcription	GKGHIK
224	YadA domain-containing protein	gi 330822225	14.92	Transcription	VNTIAGNTLS
225	transposase IS3518	gi 68536803	21.44	Transcription	EQGMGYTAAANA
226	acetyltransferase	gi 239908682	14.27	transcription	EIAILIGRD
227	DNA-directed RNA polymerase subunit alpha	gi 256826600	22.31	Transcription	DAIEATAH
228	hydrogenase 3 and formate hydrogenase complex, HycG subunit	gi 16130626	7.81	transcription	ASMKAS
229	PAS/PAC sensor-containing diguanylate cyclase	gi 167032619	4.81	Transcription	CPGSDAE
230	integrase catalytic subunit	gi 186685723	10.65	transcription	SSGVVA

Table 33 (Continued)

No.	Protein Name	Accession number	ID Score	Function	Peptide sequence
231	PAS/PAC and Chase sensor-containing diguanylate cyclase/phosphodiesterase	gi 333981851	33.04	transcription	AKAGFAELETIQ
232	yecA family protein	gi 117926141	5.09	transcription	GGHEP
233	transcriptional modulator of MazE/toxin MazF	gi 107021868	13.44	Transcription	LLLMSSSMVD
234	RpiR family phosphosugar-binding transcriptional regulator	gi 300362956	13.97	Transcription	KATNTGDAT
235	transcriptional regulator, GntR family/aminotransferase, classes I and II	gi 229070604	24.02	Transcription	LIYAITGNGTFVAPN A
236	ECF-type sigma factor negative effector	gi 47565484	9.5	Transcription	GHVKES
237	Sigma 54 interacting domain-containing protein	gi 310779409	24.82	Transcription	DMQLSDTARIFGIV
238	ATP-dependent RNA helicase HrpB	gi 197284112	23.99	Transcription	GAMMDN
239	CrcB family protein	gi 90962445	7.77	Transcription	GMVGAFT
240	carboxyltransferase	gi 226362383	16.21	Transcription	TIMSSPKA
241	transcriptional regulatory protein OmpR	gi 329120744	36.13	Transcription	QATVGDAPL
242	sensory box protein	gi 336312809	12.74	Transcription	DKSVNGP
243	ATP-dependent RNA helicase RhlE	gi 183222181	20.92	Transcription	PKLHGSGGGGNRG
244	gatC gene product	gi 15802567	8.17	Transcription	DVKGV
245	periplasmic binding protein/LacI transcriptional regulator	gi 134292548	10.88	Transcription	EQNAAAA

Table 33 (Continued)

No.	Protein Name	Accession number	ID Score	Function	Peptide sequence
246	modulator of DNA gyrase	gi 190890550	10.84	Transcription	AGSYMGS
247	PaaX family transcriptional regulator	gi 290956804	35.22	Transcription	GAAGYGLSDDA
248	N-acetyltransferase GCN5	gi 171060913	20.13	Transcription	AELAHARAD
249	FIST C domain-containing protein	gi 338210181	20	transcription	GHGTMGGW
250	single-stranded DNA-binding protein	gi 336120933	39.56	Transcription	SSGGGGGNFG
251	transposase	gi 158313261	8.7	Transcription	SRNSAK
252	transcriptional regulator	gi 329939824	10.21	Transcription	ADEAIPASA
253	DNA-directed RNA polymerase, beta subunit	gi 320527676	29.68	Transcription	HLVGDKIARIK
254	PAS/PAC sensor hybrid histidine kinase	gi 168700450	14.06	Transcription	EQVAAGFAG
255	WD-40 repeat-containing protein	gi 294817096	10.65	transcription	RPTGGPFGP
256	pirin-like protein	gi 169629532	8.72	Transcription	GEPRGTS
257	DNA modification methyltransferase Spn5252IP type II	gi 332361316	14.36	transcription	GLESQGHE
258	fatty-acid--CoA ligase	gi 260904306	27.23	Lipid metabolism	DKPDTYD
259	fatty oxidation complex, alpha subunit Fad	gi 315180761	18.91	Lipid metabolism	HIAAKAAR
260	cyclopropane-fatty-acyl-phospholipid synthase	gi 71065302	2.83	Lipid metabolism	AGPASKP
261	adenine deaminase	gi 333373438	38.14	Nucleotide metabolism	PLLEGESR

2. Protein expression of *S. suis* after exposure human macrophage cell line U 937

Table 34 The total proteins of all strains of *S. suis* up-regulated in human macrophage cell line U 937 (118 proteins)

No.	Protein Name	Accession number	ID Score	Function	Peptide sequence
1	Galactokinase	gi 166216976	9.38	Carbohydrate metabolism	RAECEK
2	Triosephosphate isomerase	gi 160196655	3.24	Carbohydrate metabolism	KPIIAGNWK
3	Phosphoglycerate kinase	gi 166219343	31.73	Carbohydrate metabolism	LGQDVAFIAGATR
4	Phosphopentomutase	gi 166198546	12.05	Carbohydrate metabolism	IGLGNIPR
5	Phosphoribosylaminoimidazolecarboxamide formyltransferase	gi 166232409	9.29	Carbohydrate metabolism	QRLAAK
6	Undecaprenyl-diphosphatase	gi 158514138	1.58	Carbohydrate metabolism	LNPFQPGK
7	Adenine phosphoribosyltransferase	gi 166215932	7.66	DNA metabolism	VLMHY
8	DNA polymerase III PolC-type	gi 166217456	15.59	DNA replication	LAAGAAGVKR
9	DNA polymerase IV	gi 189044615	2.7	DNA replication	YGDFSTLTK
10	DNA replication and repair protein RecF	gi 166221876	11.03	DNA replication	KLEEFGNR
11	DNA-directed RNA polymerase subunit beta	gi 160177567	16.16	DNA replication	EIAALKEELK
12	DNA-directed RNA polymerase subunit omega	gi 166991544	2.06	DNA replication	MMLKPSIDTLLDK
13	Holliday junction ATP-dependent DNA helicase RuvA	gi 166231449	4.02	DNA replication	GILTKITAK
14	Holliday junction ATP-dependent DNA helicase RuvB	gi 172045570	11.01	DNA replication	IFIEAAK
15	ATP-dependent helicase/deoxyribonuclease subunit B	gi 251764629	10.69	DNA replication	QDWMERMKGGQD

Table 34 (Continued)

No.	Protein Name	Accession number	ID Score	Function	Peptide sequence
16	ATP-dependent helicase/nuclease subunit A	gi 251764570	11.16	DNA replication	ILDKLKR
17	Uracil-DNA glycosylase	gi 166225568	2.74	DNA replication	KKKALITNPK
18	3-oxoacyl-[acyl-carrier-protein] synthase 3	gi 166233403	1.44	Lipid metabolism	TGIGQRHIVTGETTS DLASQVAR
19	Chaperone protein DnaK	gi 166918271	11.64	Stress response	AQALAVK
20	competence-damage inducible protein	gi 189082530	7.95	Stress response	VRTPNNER
21	GTP cyclohydrolase 1	gi 166220295	8.68	Stress response	LARAVEVASR
22	Ribonuclease HII	gi 166226665	1.08	Transcription	KIPKSK
23	Ribonuclease Y	gi 205831666	9.2	Transcription	KDDNLTNKEK
24	Transcriptional regulatory protein SSU05_0402	gi 166227217	4.07	Transcription	SAFGKNGGNMGAS GSVSFMFDKK
25	Transcriptional repressor NrdR	gi 189030868	14.1	Transcription	GSKVKPGKK
26	Polyribonucleotide nucleotidyltransferase	gi 187611303	6.9	Transcription	QANGAVVVR
27	tRNA threonylcarbamoyladenosine biosynthesis protein Gcp	gi 158514128	5.56	Translation	VGRVMGLPYPAGR
28	30S ribosomal protein S12	gi 158514127	4.2	Translation	SPALNVGYNSRKK
29	30S ribosomal protein S15	gi 166234372	7.2	Translation	NLLAYLRR
30	30S ribosomal protein S2	gi 209573686	1.81	Translation	MEEDGTFEVLPK
31	30S ribosomal protein S3	gi 152060911	2.14	Translation	VHPIGMR
32	30S ribosomal protein S4	gi 172045584	5.53	Translation	LGLSLTGTGK
33	30S ribosomal protein S5	gi 172045577	6.93	Translation	AEEVAALR

Table 34 (Continued)

No.	Protein Name	Accession number	ID Score	Function	Peptide sequence
34	30S ribosomal protein S7	gi 166228486	8.31	Translation	EIMDAANNTGAAVK K
35	30S ribosomal protein S8	gi 158706326	3.7	Translation	RVSKPGLR
36	50S ribosomal protein L1	gi 160174492	6.3	Translation	SKNLLAALEK
37	50S ribosomal protein L16	gi 166216116	5.15	Translation	QIEAARIAMTR
38	50S ribosomal protein L17	gi 166218471	9.04	Translation	ILKTEPR
39	50S ribosomal protein L18	gi 166199476	23.31	Translation	LNIFR
40	50S ribosomal protein L19	gi 166219558	6.53	Translation	KISGGVGVER
41	50S ribosomal protein L2	gi 160358625	1.27	Translation	NKDGVEAIVK
42	50S ribosomal protein L20	gi 215274803	1.3	Translation	MLEGGVVS
43	50S ribosomal protein L22	gi 166222005	7.34	Translation	AKGSASPINK
44	50S ribosomal protein L24	gi 166223646	4.36	Translation	GVEAVVVTALPK
45	50S ribosomal protein L27	gi 166225062	2.22	Translation	KGGGSTSNGRDSQA KR
46	50S ribosomal protein L29	gi 166229136	2.39	Translation	ENELKKELFELR
47	50S ribosomal protein L3	gi 166234601	3.67	Translation	MTKGILGKK
48	50S ribosomal protein L30	gi 166230197	3.88	Translation	KTVVALGLGK
49	50S ribosomal protein L33	gi 218547436	9.35	Translation	RNTPDRLQLK
50	50S ribosomal protein L35	gi 166233043	12.74	Translation	RTGSGGLKR
51	50S ribosomal protein L5	gi 166218292	11.39	Translation	LVTVSLPR
52	50S ribosomal protein L7/L12	gi 166222219	4.12	Translation	EGVATAEAEI KAK
53	tRNA dimethylallyltransferase	gi 166216997	9.53	Translation	QVLYDR

Table 34 (Continued)

No.	Protein Name	Accession number	ID Score	Function	Peptide sequence
54	tRNA uridine 5-carboxymethyl amino methyl modification enzyme MnmG	gi 166200626	7.54	Translation	GLENAQMMR
55	Alanine--tRNA ligase	gi 205830232	12.36	Translation	EQQDRAR
56	Aspartate--tRNA ligase	gi 166225436	4.38	Translation	AIVVKGAAADSYSRK
57	Glutamate--tRNA ligase	gi 229470642	4.44	Translation	SIQHIDNMLKSL
58	Glycine--tRNA ligase beta subunit	gi 229558584	10.56	Translation	VGAVLALADK
59	Peptidyl-tRNA hydrolase	gi 166229461	5.66	Translation	LIIGLGNPGR
60	Proline--tRNA ligase	gi 166980163	11.37	Translation	AADGIVEVK
61	Ribosome maturation factor RimP	gi 259645119	2.05	Translation	KEVTIPYQTVAK
62	Ribosome-recycling factor	gi 166231521	8.35	Translation	MTADKEKELLEV
63	Threonine--tRNA ligase	gi 166225509	7.98	Translation	IKITFPDGAVR
64	Translation initiation factor IF-2	gi 166198938	10.16	Translation	AAGEERAKR
65	Peptide deformylase	gi 158514139	1.38	Translation	AAHLIDMDDIIR
66	Queuine tRNA-ribosyltransferase	gi 166227998	2.3	Translation	LTSYHNLYFLINLMK
67	D-alanine--poly(phosphoribitol) ligase subunit 2	gi 166201855	1.53	Translation	IISGVVELMHA
68	Elongation factor 4	gi 166224531	0.6	Translation	AGKKR
69	Elongation factor G	gi 166220179	7.39	Translation	QSGGK
70	Elongation factor Tu	gi 189037416	76.87	Translation	QLDEGLAGDNVGVLLR
71	GTP-binding protein obg	gi 261277713	9.23	Translation	GAKDGDIVR
72	Serine hydroxymethyltransferase	gi 166233758	5.16	Translation	AVMAAQGSILTNR

Table 34 (Continued)

No.	Protein Name	Accession number	ID Score	Function	Peptide sequence
73	UPF0042 nucleotide-binding protein SSU05_0620	gi 166228795	2.87	Translation	NWNVNRSHR
74	UPF0298 protein SSU05_1549	gi 166979778	3.03	Translation	ATILKLKK
75	UPF0348 protein SSU98_0368	gi 158514148	5.84	Translation	GADQLDLVR
76	UPF0374 protein SSU05_0445	gi 167012950	1.29	Translation	TWRDTMVLK
77	Protein translocase subunit SecA	gi 166918865	5.73	Transport	DEAIDGIK
78	UDP-N-acetylmuramate--L-alanine ligase	gi 166224743	3.92	Transport	TSTTGLLAHVMR
79	UDP-N-acetylmuramoylalanine--D-glutamate ligase	gi 158514131	12.43	Transport	TVLLLGLAK
80	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--L-lysine ligase	gi 166224791	2.16	Transport	LLAFTGTKGK
81	4-hydroxy-tetrahydrodipico+ A74:A83linatase synthase	gi 166222603	4.36	Lipid metabolism	MSIQDLRDVK
82	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	gi 166233734	0.19	Translation	NGQGEVALTANK
83	6-phosphofructokinase	gi 166980282	16.01	Carbohydrate metabolism	TFVVEVMGR
84	Acetate kinase	gi 166198161	7.63	Stress response	EVERLK
85	Argininosuccinate lyase	gi 172045582	11.86	Translation	KNPDMAELIR
86	Argininosuccinate synthase	gi 172045627	5.19	Translation	GSAKVVARK
87	Aspartate carbamoyltransferase	gi 158514133	4.27	Protein metabolism	QMQNGVFVR
88	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B	gi 166198828	2.15	Translation	VDANISLRPYGQEK

Table 34 (Continued)

No.	Protein Name	Accession number	ID Score	Function	Peptide sequence
89	ATP synthase epsilon chain	gi 166222502	11.2	Transport	NIDMEMR
90	Chorismate synthase	gi 166218129	4.85	Protein metabolism	VAVGAVAKR
91	Dihydroxy-acid dehydratase	gi 166215418	12.94	Protein metabolism	KADIEEAGR
92	Dtdp-D-Glucose 4,6-Dehydratase	gi 18655655	0.71	Carbohydrate metabolism	QITNILAGIKPK
93	Enloase	gi 409973825	57.28	Unknown	GLVTAVGDEGGFAP K
94	Gamma-glutamyl phosphate reductase	gi 166224851	5.76	Protein metabolism	IDLLVPR
95	Glucosamine-6-phosphate deaminase	gi 167012445	6.33	DNA metabolism	EKLNGGTK
96	GTPase Era	gi 189037680	12.87	Signal	GIIIGK
97	GTP-binding protein EngA	gi 166225868	2.24	DNA metabolism	AMRAIER
98	Hp0197-G5	gi 427930909	0.5	Signal	VMATNLLSETVVEG QNR
99	Ketol-acid reductoisomerase	gi 166233626	3.01	Carbohydrate metabolism	VGAELRKAMPFVGR NDDDAFK
100	Lysine--tRNA ligase	gi 166230595	8.15	Translation	MTALAEQGIDPFGK
101	Mannonate dehydratase	gi 166227203	5.38	Protein metabolism	MKMSFRWYGKK
102	Methenyltetrahydrofolate cyclohydrolase	gi 158705776	4.45	Signal	QADIVVVAIGR
103	Methylenetetrahydrofolate--tRNA-(uracil-5-)-methyltransferase TrmFO	gi 166989572	7.47	Translation	RLDSIIMR
104	MutS2 protein	gi 229486386	21.77	Translation	ARLDLR
105	N-acetylmannosamine-6-phosphate 2-epimerase	gi 158514135	4.77	Carbohydrate metabolism	EEGGIMPLLVK

Table 34 (Continued)

No.	Protein Name	Accession number	ID Score	Function	Peptide sequence
106	NH(3)-dependent NAD(+) synthetase	gi 189030736	6.61	Protein metabolism	ELGVKPSIDPK
107	Phosphate acyltransferase	gi 166221776	0.81	Lipid metabolism	KKEASMVLATK
108	Phosphoenolpyruvate carboxylase	gi 166225901	8.04	Carbohydrate metabolism	RFIDK
109	Phosphoglucosamine mutase	gi 158705922	4.57	Carbohydrate metabolism	MEAEMAGNGR
110	Prolipoprotein diacylglycerol transferase	gi 166990822	3.46	Stress response	MNTIEKRLNMDPIAI K
111	Purine nucleoside phosphorylase DeoD-type	gi 254772578	3.13	DNA metabolism	ILLPGDPLR
112	Pyrrolidone-carboxylate peptidase	gi 166219022	3.23	Transport	AMVEAIHR
113	Segregation and condensation protein A	gi 167016581	1.38	DNA replication	QASLRQSHATIR
114	Shikimate dehydrogenase	gi 166219227	0	Protein metabolism	MNIDGYTRLAAVVA KPIK
115	Tro A	gi 328877178	2.74	Lipid metabolism	MVEALEKTGVAVSK
116	Tyrosine recombinase XerD-like	gi 215277029	1.17	DNA replication	GGAKR
117	UDP-N-acetylenolpyruvoylglucosamine reductase	gi 187609742	1.19	Transport	MKDKIR
118	UDP-N-acetylglucosamine pyrophosphorylase	gi 189041392	1	Transport	MSNNYAILAAGK

3. Protein expression pattern of *S. suis* after exposure to mouse macrophage cell

line RAW 264.7

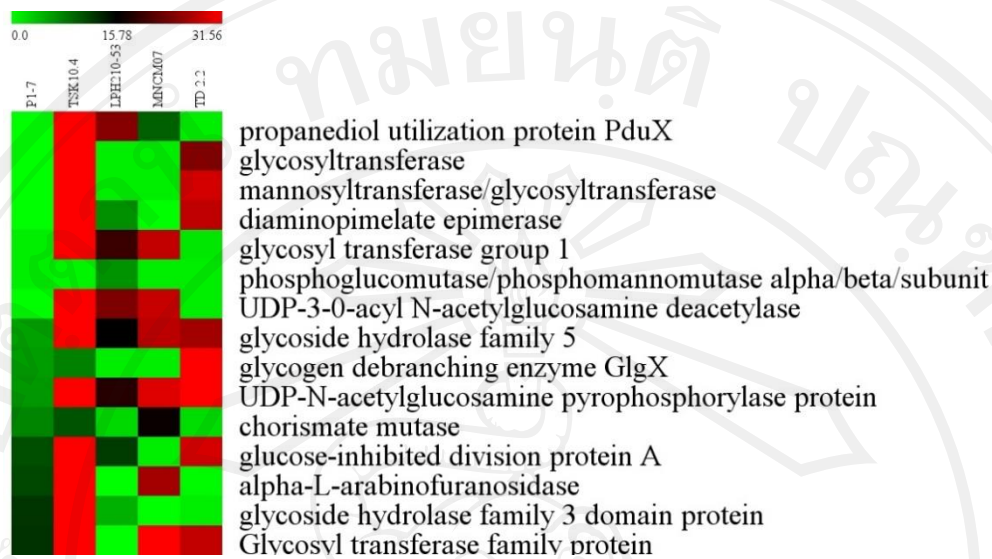


Figure 22 Heat map representation of the carbohydrate metabolism-related proteins of *S. suis* 5 strains; P 1/7, TSK 10.4, LPH 210/53, MNM 07 and TD 2.2. Level of protein expression is marked using a color scale ranging from green (no change), dark (a little) and red (the highest) up-regulation ratio.

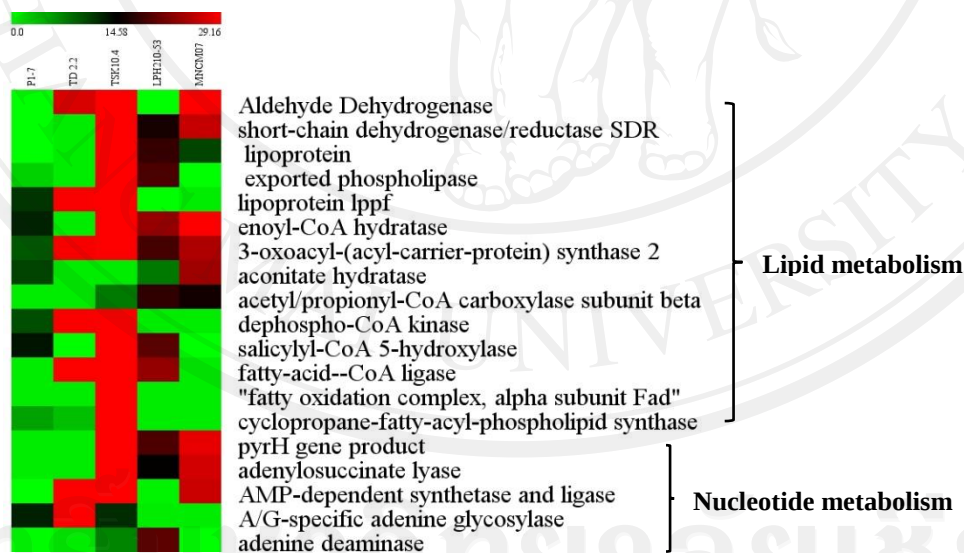


Figure 23 Heat map representation of the lipid metabolism and nucleotide metabolism-related proteins of *S. suis* 5 strains; P 1/7, TSK 10.4, LPH 210/53, MNM 07 and TD 2.2. Level of protein expression is marked using a color scale ranging from green (no change), dark (a little) and red (the highest) up-regulation ratio.

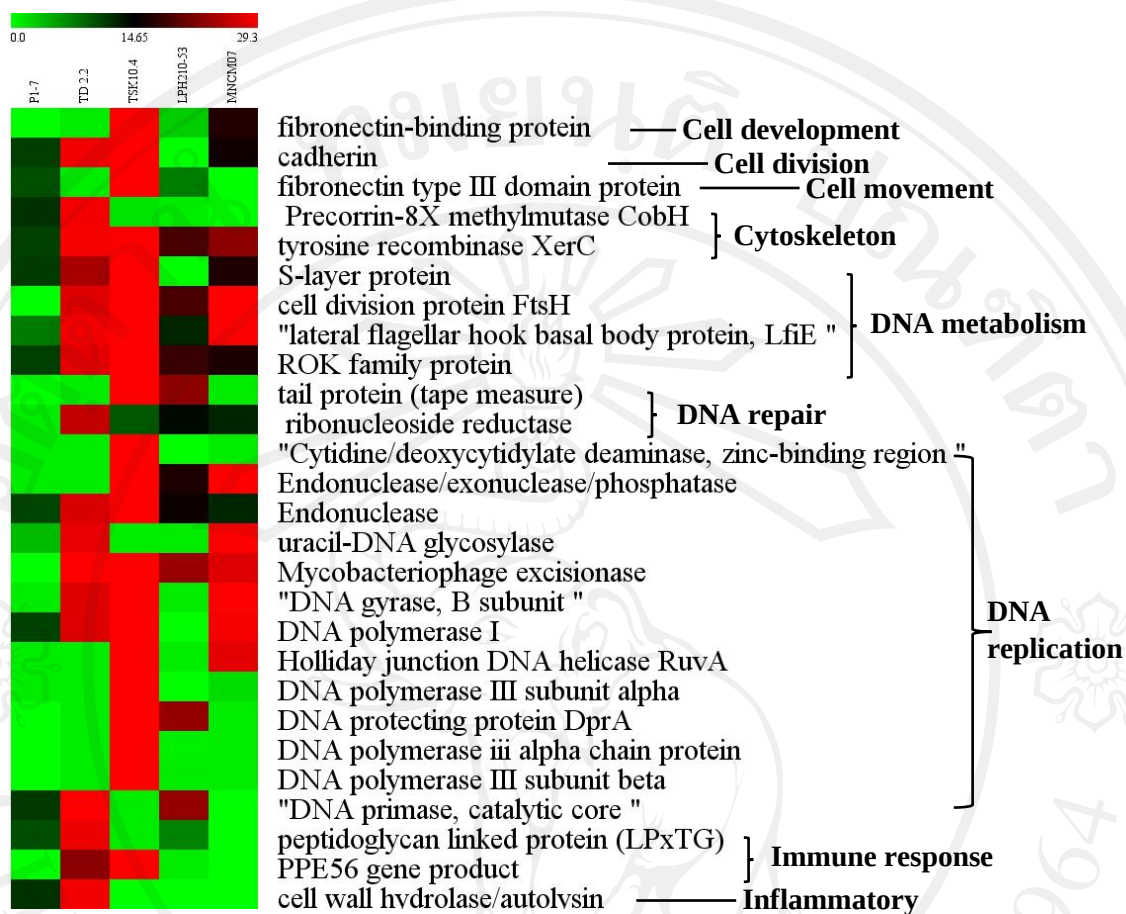


Figure 24 Heat map representation of the cell development, cell division, cell movement, cytoskeleton, DNA metabolism, DNA repair, DNA replication, immune response and inflammatory-related proteins of *S. suis* 5 strains; P 1/7, TSK 10.4, LPH 210/53, MNCM 07 and TD 2.2. Level of protein expression is marked using a color scale ranging from green (no change), dark (a little) and red (the highest) up-regulation ratio.

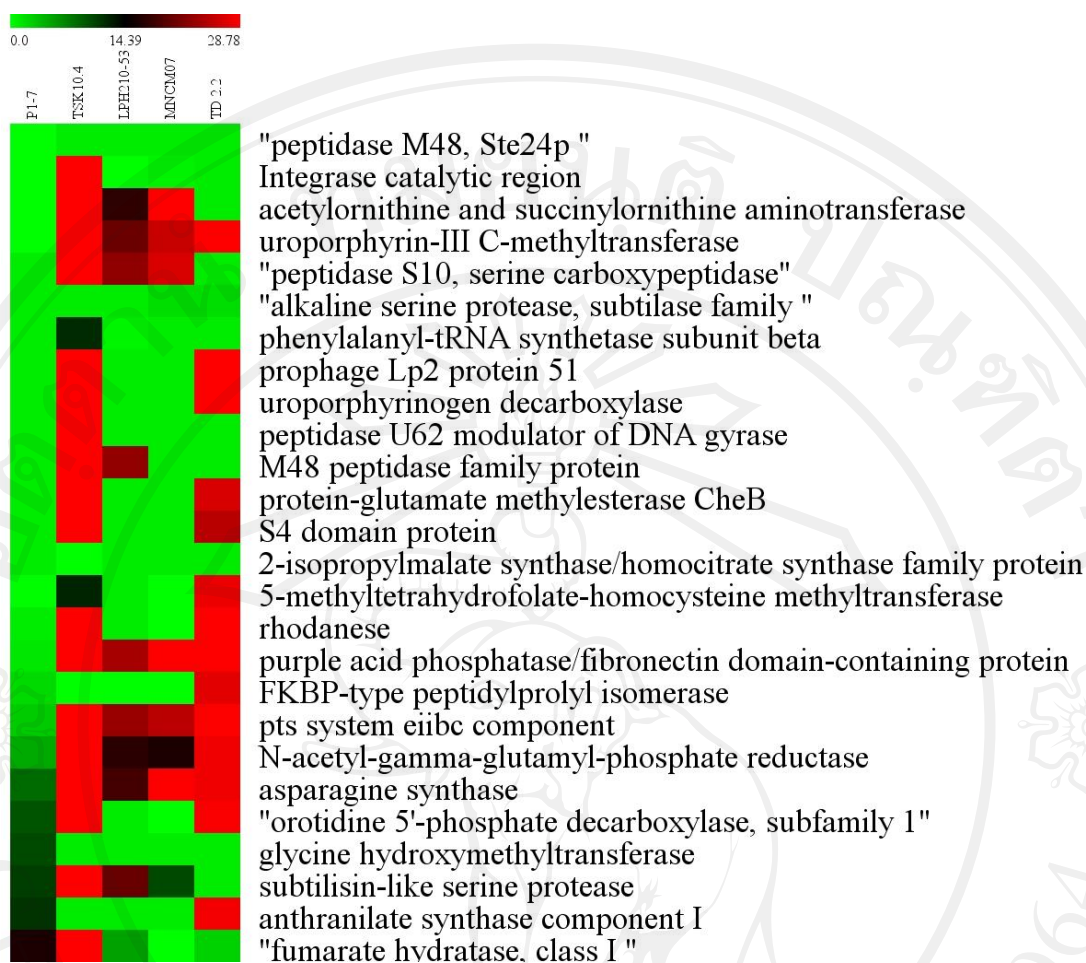


Figure 25 Heat map representation of the protein metabolism-related proteins of *S. suis* 5 strains; P 1/7, TSK 10.4, LPH 210/53, MNCM 07 and TD 2.2. Level of protein expression is marked using a color scale ranging from green (no change), dark (a little) and red (the highest) up-regulation ratio.

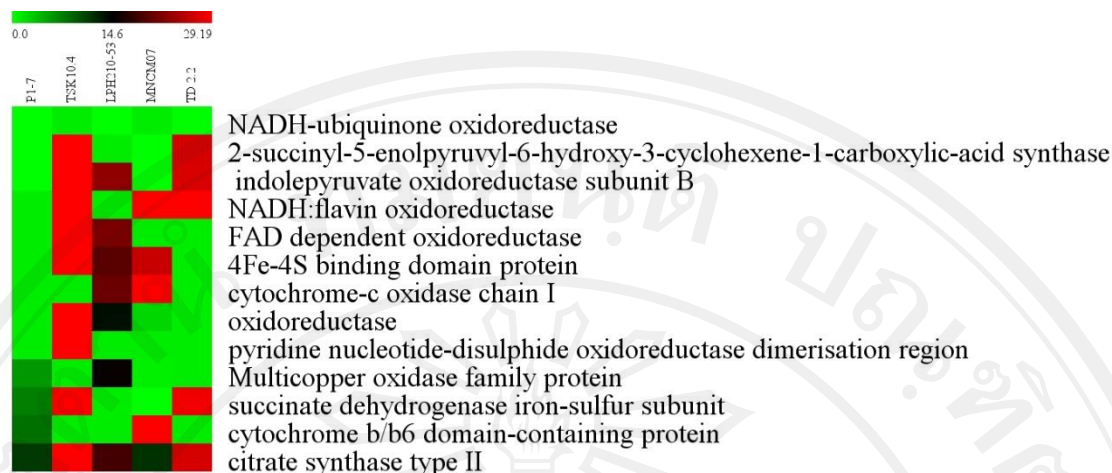


Figure 26 Heat map representation of the respiration-related proteins of *S. suis* 5 strains; P 1/7, TSK 10.4, LPH 210/53, MNCM 07 and TD 2.2. Level of protein expression is marked using a color scale ranging from green (no change), dark (a little) and red (the highest) up-regulation ratio.

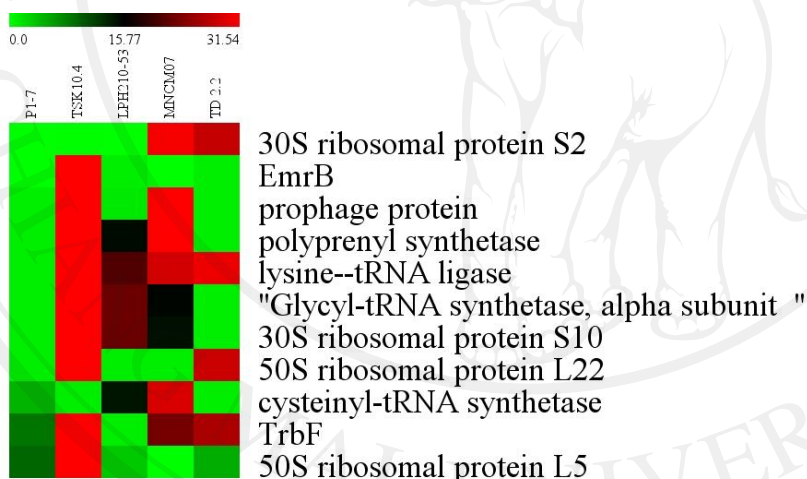


Figure 27 Heat map representation of the translation-related proteins of *S. suis* 5 strains; P 1/7, TSK 10.4, LPH 210/53, MNCM 07 and TD 2.2. Level of protein expression is marked using a color scale ranging from green (no change), dark (a little) and red (the highest) up-regulation ratio.

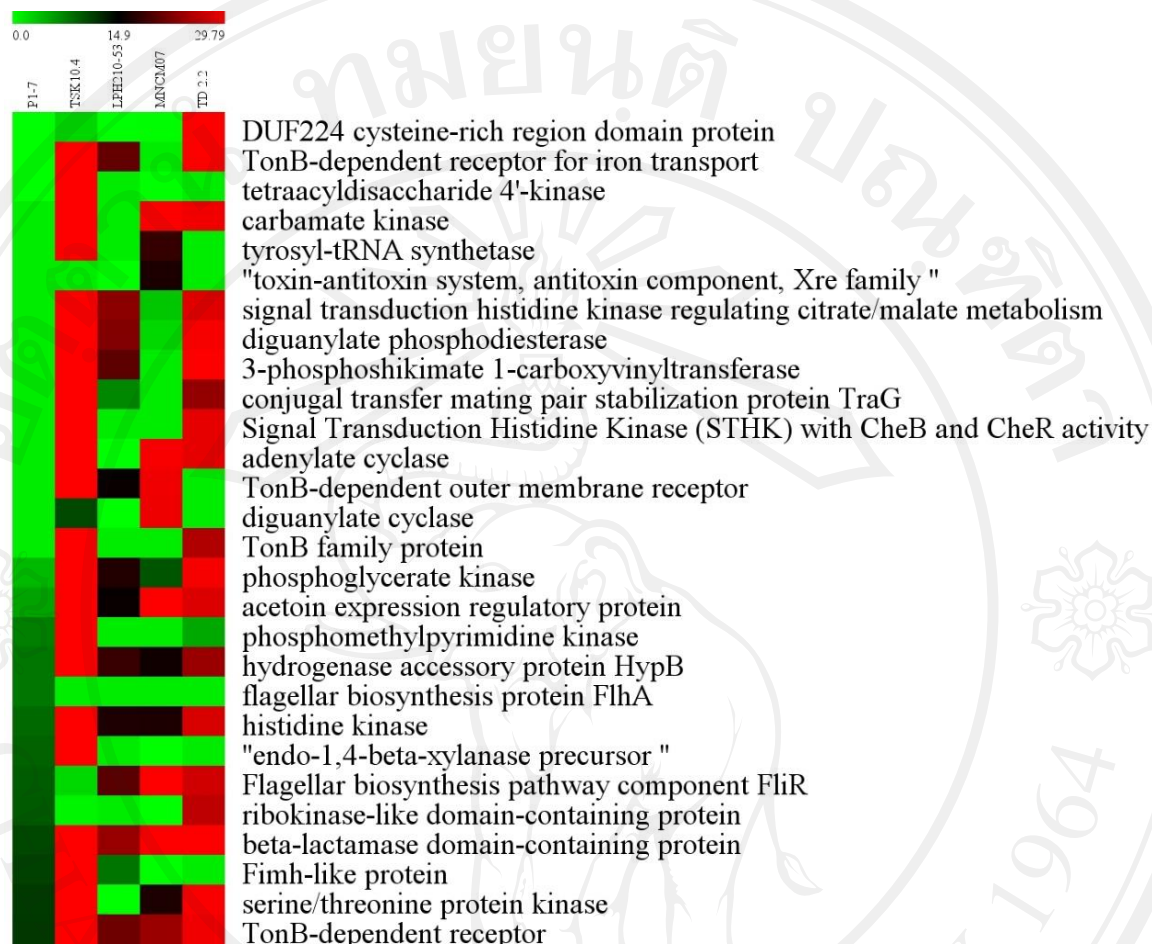


Figure 28 Heat map representation of the signal transduction-related proteins of *S. suis* 5 strains; P 1/7, TSK 10.4, LPH 210/53, MNM07 and TD 2.2. Level of protein expression is marked using a color scale ranging from green (no change), dark (a little) and red (the highest) up-regulation ratio.

4. Protein expression pattern of *S. suis* after exposure to human macrophage cell

line U 937

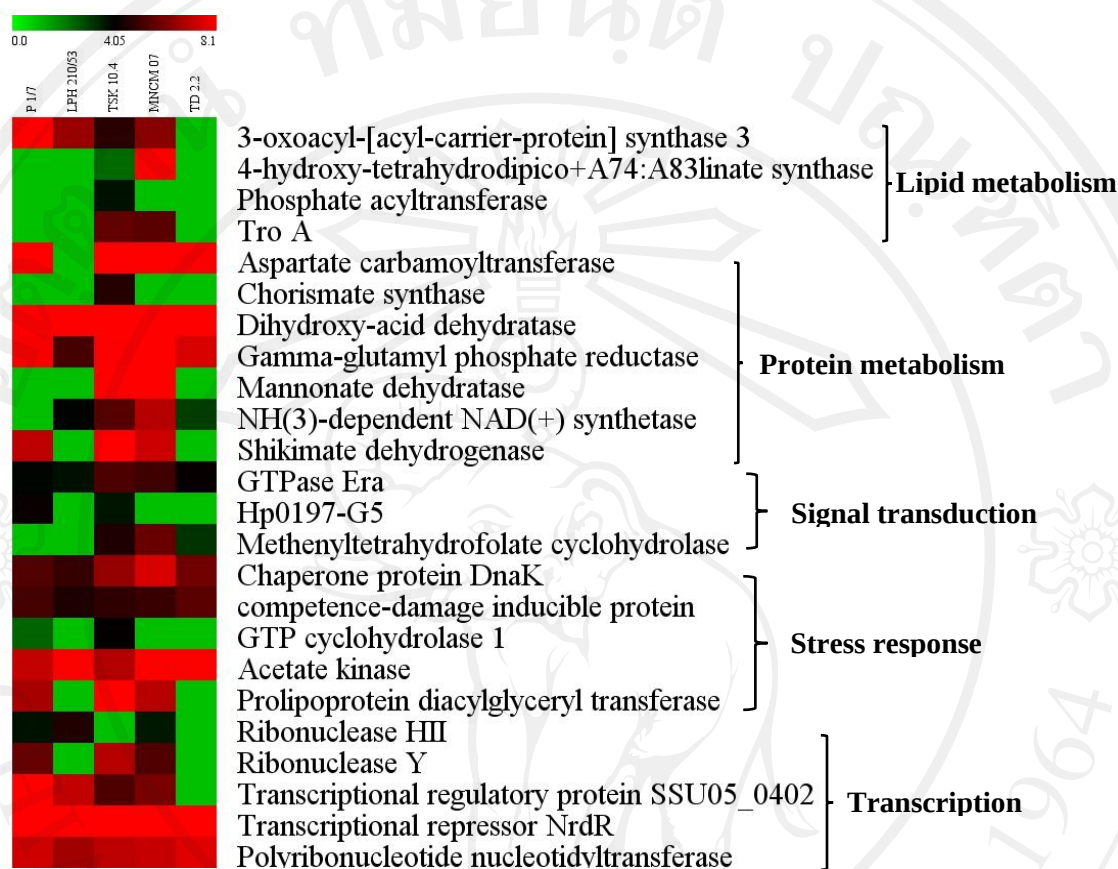


Figure 29 Heat map representation of the lipid metabolism, protein metabolism, signal transduction, stress response and transcription-related proteins of *S. suis* 5 strains; P 1/7, TSK 10.4, LPH 210/53, MNCM 07 and TD 2.2. Level of protein expression is marked using a color scale ranging from green (no change), dark (a little) and red (the highest) up-regulation ratio.

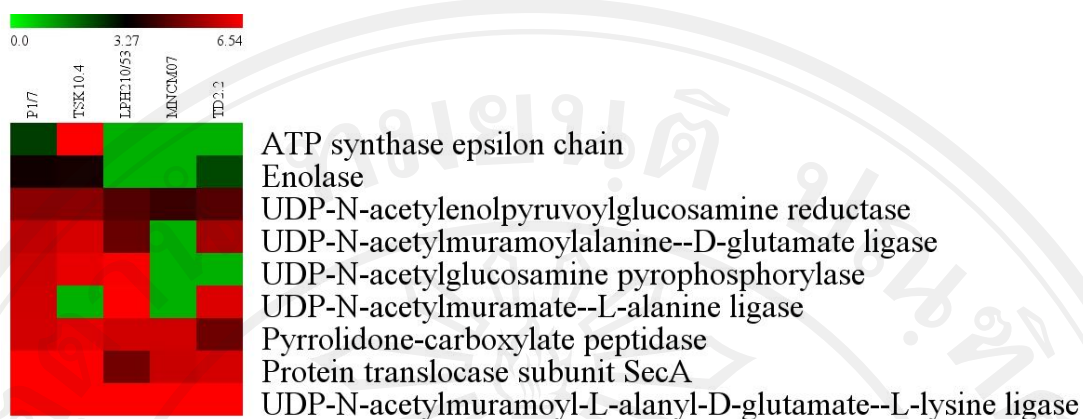


Figure 30 Heat map representation of the transport-related proteins of *S. suis* 5 strains; P 1/7, TSK 10.4, LPH 210/53, MNCM 07 and TD 2.2. Level of protein expression is marked using a color scale ranging from green (no change), dark (a little) and red (the highest) up-regulation ratio.

APPENDIX C

Detection of virulence associated genes of *S. suis*

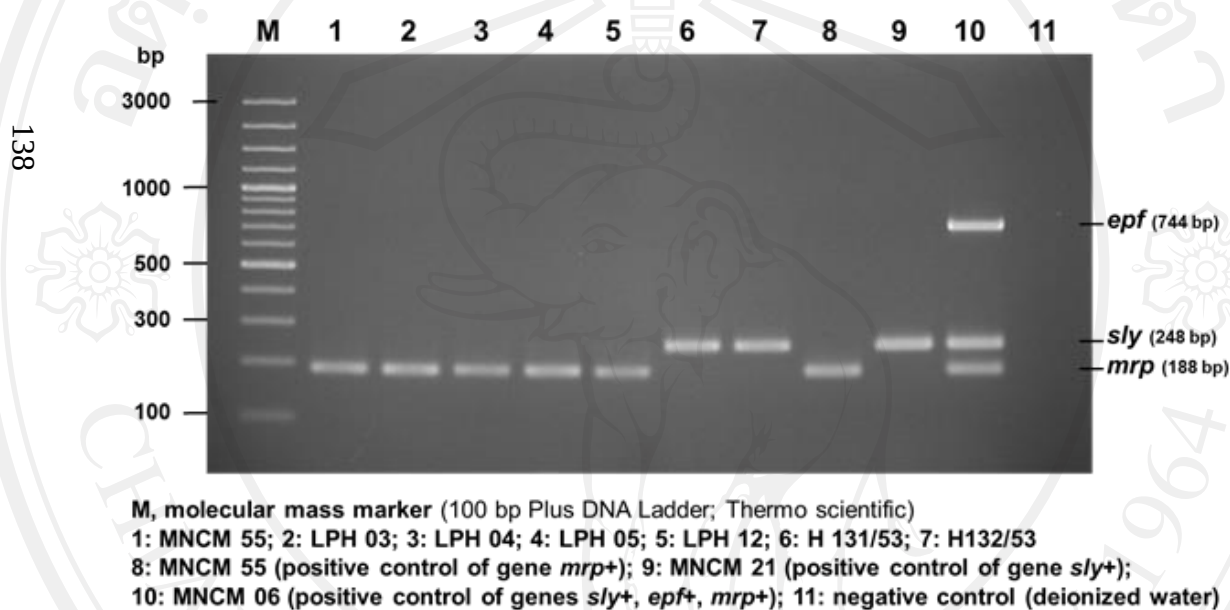
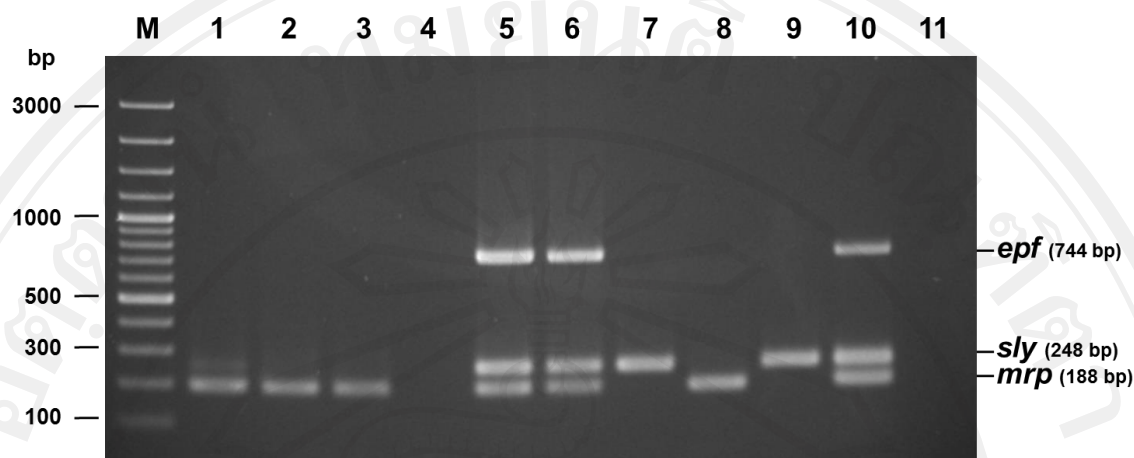


Figure 31 Detection of virulence-associated genes of *S. suis* (patient isolates): suilysin (*sly*), extracellular factor protein (*epf*) and muramidase released protein (*mrp*) by Multiplex-PCR. The amplicon size of those genes were 248 bp, 744 bp and 188 bp, respectively.



M, molecular mass marker (100 bp Plus DNA Ladder; Thermo scientific)

1: T 13.1S; **2:** T13.2S; **3:** T 13.3S; **4:** TCP 40.2S; **5:** TD 2.3; **6:** TDK 5.4; **7:** THD 10.2

8: MNM 55 (positive control of gene *mrp*+); **9:** MNM 21 (positive control of gene *sly*+);

10: MNM 06 (positive control of genes *sly*+, *epf*+, *mrp*+); **11:** negative control (deionized water)

Figure 32 Detection of virulence-associated genes of *S. suis* (healthy pig isolates): suilysin (*sly*), extracellular factor protein (*epf*) and muramidase released protein (*mrp*) by Multiplex-PCR. The amplicon size of those genes were 248 bp, 744 bp and 188 bp, respectively.

APPENDIX D

Media and reagents

1. Culture media

Todd Hewitt Broth (Bacto™) approximate formula* Per Liter

Todd-Hewitt broth powder	30.0 g
Distilled water	1,000 ml

Dissolve 30 g of the powder in 1 L of distilled water. Autoclave at 121°C 15 lbs for 15 minutes.

Brain Heart Infusion (BHI) Agar (BD™) approximate formula* Per Liter

Brain Heart Infusion powder	52.0 g
Distilled water	1,000 ml

Dissolve 52 g of the powder in 1 L of distilled water. Autoclave at 121°C 15 lbs for 15 minutes.

Tryptic soy agar with human blood

Tryptic soy agar powder	40.0 g
Distilled water	1,000 ml

Dissolve 40 g of the powder in 1 L of distilled water. Autoclave at 121°C 15 lbs for 15 minutes. Then, TSA media were taken in water bath at 50-55 °C for cool before adding sterilized human blood (50 ml/L).

Bacterial Storage Medium

Todd Hewitt Broth (Bacto™) powder	6.0 g
Glycerol	20.0 ml

Dissolve 6 g of the THB powder in 180 ml of distilled water and add glycerol 20 ml in THB broth. Autoclave at 121°C 15 lbs for 15 minutes. Then, the solution was dispensed in 1 ml amounts into cryotubes.

2. Reagents and buffers

Phosphate buffer saline (PBS) (pH 7.2 to 7.4)

Phosphate buffer saline powder	10.2 g
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Dissolve PBS powder 10.2 g with 1000 ml of distilled water. Keep PBS in a dry and cool place.

Lysozyme (10 mg/ml)

Lysozyme powder	10 mg
10 mM Tris-HCl (pH 8.0)	1 ml

Lysozyme buffer

10 mM Tris-HCl (pH 8.0), 1 mM EDTA (pH 8.0), 0.1 M NaCl, 5% Triton X-100

Mix to dissolve completely and store at room temperature.

0.5% (w/v) Sodium Dodecyl Sulfate (SDS) ($C_{12}H_{25}NaO_4S$: MW 288.38)

SDS	0.5 g
Distilled water	100.0 ml

Dissolve 0.5 g of SDS in 100 ml of sterile distilled water. Store at room temperature.

Tris-acetate EDTA (TAE) buffer

50X stock solution in 1 liter:

Tris-base (FW = 121)	242.0 g
Glacial acetic acid	57.1 ml
0.5 M EDTA (pH 8.0)	100.0 ml

Dissolve following components in 600 ml of deionized water and adjust the final volume to 1 liter with deionized water.

Agarose gel electrophoresis (1.0%)

Agarose gel powder	1.0 g
TAE buffer (1X)	80.0 ml

Dissolve agarose gel powder 1.0 g in 80 ml of TAE buffer and dissolve by boiling.

Working 0.5 µg/ml Ethidium bromide

Stock 10 mg/ml Ethidium bromide	5.0 µl
Distilled water	100.0 ml

2.1 Reagents for In-gel digestion

20 mM Ammonium bicarbonate (FW 79.06) (50 ml)

Suspend 79.6 mg of Ammonium bicarbonate in 50 ml of sterilized milli Q water

10 mM Ammonium bicarbonate (50 ml)

Add 25 ml of 20 mM Ammonium bicarbonate in 25 ml sterilized milli Q water

10 mM Dithiothreitol/10 mM ammonium bicarbonate (5 ml) (fresh prepare, for sample 96 well)

Suspend 7.7125 mg of Dithiothreitol (FW 154.25) in 5 ml of 10 mM Ammonium bicarbonate

100 mM Iodoacetamide/10 mM ammonium bicarbonate (5 ml) (fresh prepare, for sample 96 well)

Suspend 92.0 mg of Iodoacetamide (FW 184) in 5 ml of 10 mM ammonium bicarbonate

50% acetonitrile/10 mM ammonium bicarbonate

Add 100% Acetonitrile in 20 mM ammonium bicarbonate (ratio 1:1)

10 ng Trypsin in 50% acetonitrile/10 mM ammonium bicarbonate

Add 2 ml of 50% acetonitrile / 10 mM ammonium bicarbonate in 20 µg of Trypsin

30% acetonitrile (5 ml) (used 1.92 ml for sample 96 well)

Add 1.5 ml of 100% Acetonitrile in 3.5 ml of steriled milli Q water ml

0.1% FA (50 ml)

Add 50 µl of FA conc. (trifluoroacetic acid) in 49.95 ml of steriled milli Q water

50% acetonitrile /0.1% FA 10 ml (used 8.64 ml for sample 96 well)

Add 5 ml of 100% Acetonitrile in 5 ml of 0.1% FA

CURRICULUM VITAE

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