

SUPPLEMENTARY MATERIALS:

Supplementary table 1: Strains and plasmids used in this study

Strain or plasmid	Genotype and antibiotic resistance phenotype	Reference or source
<i>E. coli</i> strains		
Top10	F- <i>mcrA</i> Δ (<i>mrr-hsdRMS-mcrBC</i>) Φ 80 <i>lacZ</i> Δ M15 <i>ΔlacX74 recA1 ara Δ139 Δ(ara-leu)7697 galU galK</i> <i>rpsL</i> (StrR) <i>endA1 nupG</i>	Invitrogen
BL21 (DE3)	F- <i>ompT gal [dcm] [lon] hsdSB (rB- mB-)</i> DE3	Studier et al., 1990
BL21 gold (DE3)	F- <i>ompT gal [dcm] [lon] hsdSB (rB- mB-)</i> Tetr DE3 <i>endA lacZ Hte.</i>	Stratagene
<i>E. coli</i> plasmids		
pET101/103	CarbR	Invitrogen
pET-vjbR	VjbR fused to a 6x Histidine tag at C-terminus	This Study
pET-gntR4	GntR4 fused to a 6x Histidine tag at C-terminus	This Study
pET-araC8	AraC8 fused to a 6x Histidine tag at C-terminus	This Study
pET-arsR6	ArsR6 fused to a 6x Histidine tag at C-terminus	This Study
pET-deoR1	DeoR1 fused to a 6x Histidine tag at C-terminus	This Study
pSURS1	A fusion between pSU19 and pRS528 plasmids containing <i>lacZYA</i> and P15A ori for promoter expression analysis. CmR	This Study
pSURS2	463 bp fragment upstream of <i>virB1</i> cloned in BamHI/EcoRI sites of pSURS1	This Study
pSURS2b	463 bp fragment upstream of <i>virB1</i> cloned in BamHI/EcoRI sites of pSURS1 containing HindIII site at <i>virB</i> promoter box	This Study
pSURS7	<i>Pvjbr</i> 333 bp upstream of <i>vjbR</i> (BAB2_0118)	This Study
pSURS7b	<i>PtetR-vjbr</i> 473 bp upstream of <i>tetR</i> (BAB2_0117)	This Study
pSURS13r	323 bp fragment upstream of BAB2_0762	This Study
pSURS14	317 bp fragment upstream of BAB2_1069 (BRA1111)	This Study
pSURS17f	183 bp fragment upstream of BAB1_1881	This Study
pSURS18f	147 bp fragment upstream of BAB2_0328	This Study

pSURS18r	147 bp fragment upstream of BAB2_0329	This Study
pSURS19	175 bp fragment upstream of BAB1_1651	This Study
pSURS21	790 bp fragment upstream of BAB1_0108	This Study
pSURS22	320 bp fragment upstream of BR0951 (<i>B. suis</i>)	This Study
pSURS23	449 bp fragment upstream of BAB1_1066	This Study
pSURS25	375 bp fragment upstream of BAB1_1837	This Study
pSURS29	290 bp fragment upstream of BAB1_1994	This Study
pSURS30	637 bp fragment upstream of BAB2_1106	This Study
pSURS31	399 bp fragment upstream of BAB1_1058	This Study
pSURS32	432 bp fragment upstream of BAB1_0604	This Study
pSURS35	704 bp fragment upstream of BAB2_0403	This Study
pWIL1	pCR2.1 containing 123 bp fragment of <i>PvirB</i>	This Study

B. abortus strains

2308	Wild type	Deyoe
ADH3	$\Delta virB2$ (non polar) in 2308	Den Hartigh et al., 2004
ADH17	$\Delta vjBR::kan$ in 2308	This Study
MDJ15	pFT/BAB1_1652 in 2308	This Study
MDJ16	pFT/BAB1_1652 in ADH3	This Study
MDJ11	pFT/BR1038(303-410) in 2308	This Study
MDJ12	pFT/BR1038(303-410) in ADH3	This Study
MDJ42	pFT/BR1038(303-390) in 2308	This Study
MDJ43	pFT/BR1038(303-390) in ADH3	This Study
MDJ24	pFT/BAB1_1058(303-418) in 2308	This Study
MDJ26	pFT/BAB1_1058(303-418) in ADH3	This Study
MDJ40	pFT/BAB1_1058(303-398) in 2308	This Study
MDJ41	pFT/BAB1_1058(303-398) in ADH3	This Study
MDJ44	pFT/BAB1_1058(303-369) in 2308	This Study
MDJ45	pFT/BAB1_1058(303-369) in ADH3	This Study
MDJ50	pFT/BAB2_0403 in 2308	This Study
MDJ51	pFT/BAB2_0403 in ADH3	This Study
ADH58	<i>PvirB1::lacZ</i> in 2308	This Study
ADH60	<i>PvirB1::lacZ</i> in ADH17	This Study
MDJ30	<i>PvceC::lacZ</i> in 2308	This Study
MDJ31	<i>PvceC::lacZ</i> in ADH17	This Study

L. pneumophila strains

Lp01	Wild type	Berger and Isberg, 1993
	DotA mutant	

B. abortus or *L. pneumophila* plasmids

pFLAGTEM1	β -lactamase reporter cloning vector	Raffatellu et al., 2005
pFT/GST	pFLAGTEM1 expressing FT::GST	This Study
pFT/BAB1_1652	pFLAGTEM1 expressing TEM1::BAB1_1652	This Study
pFT/BAB2_0056	pFLAGTEM1 expressing TEM1::BAB2_0056	This Study
pFT/BAB2_0095	pFLAGTEM1 expressing TEM1::BAB2_0095	This Study
pFT/BAB1_0604	pFLAGTEM1 expressing TEM1::BAB1_0604	This Study
pFT/BR1038wt	pFLAGTEM1 expressing TEM1::BR1038(303-410)	This Study
pFT/BR1038-20	pFLAGTEM1 expressing TEM1::BR1038(303-390)	This Study
pFT/BAB1_1058wt	pFLAGTEM1 expressing TEM1::BAB1_1058(303-418)	This Study
pFT/BAB1_1058-20	pFLAGTEM1 expressing TEM1::BAB1_1058(303-398)	This Study
pFT/BAB1_1058-49	pFLAGTEM1 expressing TEM1::BAB1_1058(303-369)	This Study
pFT/BAB2_0403	pFLAGTEM1 expressing TEM1::BAB2_0403	This study
pFT/BAB1_1705	pFLAGTEM1 expressing TEM1::BAB1_1705	This study
pFT/BAB1_0119	pFLAGTEM1 expressing TEM1::BAB1_0119	This study
pFT/BAB1_1674	pFLAGTEM1 expressing TEM1::BAB1_1674	This study
pFT/BAB1_0939	pFLAGTEM1 expressing TEM1::BAB1_0939	This study
pFT/BAB1_0339	pFLAGTEM1 expressing TEM1::BAB1_0339	This study
pFT/BAB1_0651	pFLAGTEM1 expressing TEM1::BAB1_0651	This study
pFT/BAB1_0740	pFLAGTEM1 expressing TEM1::BAB1_0740	This study
pVjbR-F	up- and downstream fragments of <i>vjbR</i> separated by KIXX cassette	This study
pFT/RalF	pFlagTEM1 expressing FT::RalF	This Study
pFT/RalF K368A	pFlagTEM1 expressing FT::RalF(K368A)	This Study
pFT/RalF L372T	pFlagTEM1 expressing FT::RalF(L372T)	This Study
pFT/RalFc	pFlagTEM1 expressing FT::RalF(350-374)	This Study
pTFT/RalFc	In pFT/RalFc expressing FT::RalF(350-374) and DsRed	This Study

Supplementary Table 2. *Brucella* spp. containing predicted consensus sequence in promoter

<i>B. abortus</i> 2308 ORF	<i>B. suis</i> 1330 ORF	<i>B. melitensis</i> 16M ORF	<i>virB</i> promoter box	Gene name/Predicted function	Downstream genes possibly in operon
<u>Amino acid biosynthesis</u>					
BAB1_0926	BR0908	BMEI1061	ATTAGAGGGTTTCGGCTT	aroQ	BAB1_0925-BAB1_0923
BAB1_1031	BR1013	BMEI0971	ATCAGCGCGACCACGCAT	Aminoacyl-tRNA synthetase	BAB1_1030-BAB1_1034
BAB1_0335	BR0305	BMEI1617	AACAGGCATAAAGAAAAC	metZ	BAB1_0334
BAB1_0813	BR0793	BMEI1166	ATCAGTCAATAAGCACTT	O-acetylhomoserine/O-acetylserine sulfhydrylase family protein	-
BAB2_0751	BRA0486	BMEI10781	CTCCCCGAAAGGGAGGAT	homoserine O-succinyltransferase	-
BAB1_2087	BR2086	BMEI2040	ATGCTCTAAAAAGATACC	hisE	BAB1_2088
<u>Biosynthesis of cofactors, prosthetic groups, and carriers</u>					
BAB1_1161	BR1138	BMEI0846	ATGAGCCAGTCAGGGGAT	triosephosphate isomerase, tpiA-1	BAB1_1161-BAB1_1148
BAB1_0972	BR0957	BMEI1020	ATGATCTATCTCGCAACC	mobA	BAB1_0971-BAB1_0968
BAB1_1719	BR1707	BMEI0329	ATGCCCGAATTCGATCAT	thiamine-phosphate pyrophosphorylase (putative)	BAB1_1720-BAB1_1726
<u>Cell envelope: Biosynthesis and degradation of murein sacculus and peptidoglycan</u>					
BAB1_0607	BR0583	BMEI1351	ATGAGGCAAATCTCGCCT	penicillin binding protein	BAB1_0606-BAB1_0604
BAB2_0312	BRA0923	BMEI10374	AAGAGCGCGGGCGCTGAT	alanine racemase	BAB2_0311

BAB2_0781	BRA0455	BMEI0811	AACCTCGATCCAGAAGCT	membrane protein	BAB2_0782
<u>Cellular processes: Adaptations to atypical conditions/Pathogenesis/Detoxification</u>					
BAB1_0672	BR0652	BMEI1296	ATGGCCGATATCTCTGTA	RelA/SpoT protein	BAB1_0673-BAB1_0675
BAB1_2150	BR2149	BMEI1980	GATCGCCATTTGCCGGAT	Dps family protein	-
BAB2_1106	BRA1147	BMEI0150	ATGCTTAAGGTGGAAATT	flagellin family protein	-
BAB1_1030	BR1012	BMEI0972	AACCTCTCGATAACGCTT	glutathione reductase	BAB1_1031-BAB1_1034
BAB1_1441	BR1422	BMEI0587	ATTTCGATGGATGGAGCAT	competence protein ComL, putative	BAB1_1440-BAB1_1438
BAB1_1880	BR1878	BMEI0183	GTCTTCCAGATAAAGGTT	competence protein F	BAB1_1879-BAB1_1876
-	BR0971	BMEI1007	GGCCGCTTTTTTACTGTT	omp	
-	BRA0173	BMEI1069	ATCCGGCATATCTCTCAC	omp	
BAB1_0108	BR0111	BMEI1837	ATCCGTGATCTCGCAGCT	cyclic beta 1-2 glucan synthetase	BAB1_0109
BAB2_0067	BRA0068	BMEI0026	ATGCTCCAGATCGCAGAT	virB2	BAB2_0066-BAB2_0057
BAB2_0068	BRA0069	BMEI0025	ATGACCGATATCGCTGAT	virB1	BAB2_0067-BAB2_0057
BAB1_0402	BR0372	BMEI1553	ATCCTGCATATCTATGCC	bacA	-
BAB1_0801	BR0780	-	AACCTCCATGCCCTGAT	sugE protein	-
BAB2_0205	BRA0211	BMEI1033	TGCAGCCATATCTTGTTT	pmbA	BAB2_0206-BAB2_0210

Central intermediary metabolism

BAB1_1837	BR1829	BMEI0222	ATGCGCCATGCCGAACAT	carbonic anhydrase, putative	-
BAB2_0253	BRA0981	BMEI0316	ATGGTTCAAATGGCAAAT	2-deoxy-d-gluconate 3-dehydrogenase, putative	BAB2_0253-BAB2_0263

DNA metabolism: DNA replication, recombination, and repair

BAB1_1224	BR1202	BMEI0787	ATTTTCGGAATTGCTGAT	recA	BAB1_1223
BAB2_0625	BRA0615	BMEI0656	AGGGCCGCTATAGCCGAT	UMUC-like DNA-repair protein	BAB2_0624

Energy metabolism: Amino acids and amines

BAB2_0513	BRA0727	BMEI0559	ATGCGTTAAAGCGCGCCT	glycine cleavage system protein	BAB2_0514-BAB2_0516
BAB1_1806	BR1798	BMEI0252	GGTATCCATTTTCGGGAT	ATP synthase	BAB1_1807 and BAB1_1804
-	BR0202	BMEI1747	ATGTGCGGGATGACTCTT	aldehyde dehydrogenase family protein	-
BAB2_0835	BRA0386	BMEI0880	ATGCTTCAAATAGAAGAG	acetate kinase	BAB2_0836
BAB2_0459	BRA0779	BMEI0512	ATGCTGCAACTGGCAGAC	6-phosphogluconolactonase	BAB2_0458
BAB2_0460	BRA0778	BMEI0513	ATGTGTGCATTTGCGGTT	glucose-6-phosphate 1-dehydrogenase	BAB2_0459-BAB2_0458
BAB2_0935	BRA0268	BMEI0980	AGGAGTAAAACCGAAGAT	ribitol dehydrogenase	BAB2_0934

Fatty acid and phospholipid metabolism: Biosynthesis/Degradation

BAB1_0484	BR0459	BMEI1475	ATCCTGCATGCCGCTAAC	acpP	BAB1_0485-BAB1_0489
BAB1_1994	BR1994	BMEI0075	AACCGCCGTCTTCCCTGAT	1-acyl-sn-glycerol-3-phosphate acyltransferase, putative	BAB1_1993
BAB1_2173	BR2172	BMEI1957	AACCGCGAAGACGAGGCT	3-oxoacyl-(acyl-carrier-protein) synthase I	BAB1_2172
BAB1_2174	BR2173	BMEI1956	AAGATTGAACGGGCTGTT	3-hydroxyl decanoyl dehydratase fabA	BAB1_2173-BAB1_2172
BAB2_0668	BRA0572	BMEI10695	ATTTCGCTGCCTGACGGTT	phosphatidylcholine synthase	BAB2_0669-BAB2_0673
BAB1_1528	BR1510	BMEI0503	ATGATTAATGAATATCAT	long-chain acyl-CoA thioester hydrolase, putative	-
BAB2_0439	BRA0799	BMEI10492	TTGCGCGATGTAGCTGTT	acyl-CoA dehydrogenase family protein	-

Hypothetical proteins: Conserved and not conserved

BAB1_0119	BR0122	BMEI1826	ACGAGTCATAAAACTGAT	hypothetical protein	BAB1_0120-BAB1_0121
BAB1_0294	BR0263	BMEI1658	AGCTTTCATAATGCTGAT	hypothetical protein	-
BAB1_0608	BR0584	-	AGGCGAGATTTGCCTCAT	conserved hypothetical protein	BAB1_0609
BAB1_0651	BR0628	BMEI1314	ATCTGGTTTAACGTGCAT	conserved hypothetical protein	BAB1_0650
BAB1_0939	BR0922	BMEI1051	ATCAGCCATTTTGCGCTG	conserved hypothetical protein	BAB1_0938
BAB1_1058	BR1038	BMEI0948	ATCATATATTTCCCGCAT	hypothetical protein	-
BAB1_1295	BR1276	BMEI0723	ATTTGCCCATGCGAGCAT	hypothetical protein	BAB1_1294-BAB1_1287

BAB1_1651	BR1633	-	ATTTGATATATGAAGGAT	hypothetical protein	BAB1_1652
BAB1_1678	BR1664	-	AACCCTGATGAAGCAGAT	hypothetical protein	BAB1_1677-BAB1_1674
BAB1_1708	BR1696	-	AGCTTCGGTTTCGCGCCT	hypothetical protein	BAB1_1707-BAB1_1693
BAB2_0038	BRA0039	BMEI10054	AGGTTCGCACTGCCGGAT	hypothetical protein	BAB2_0039-BAB2_0041
BAB2_0801	BRA0441	-	ATGAGCTATCTACCGCTT	conserved hypothetical protein	-
BAB2_0892	BRA0313	-	AAATATGAGATAGCCGAT	conserved hypothetical protein	-
-	BR0023	BMEI1919	AGTTGCGATTTAGCTCTT	acetoacetyl-COA synthase	
BAB1_0087	BR0090	BMEI1857	ATCATTAACACGCACTT	hypothetical protein	-
BAB1_0101	BR0104	BMEI1844	ATCTGCGCATTGGCAGAT	conserved hypothetical protein	-
BAB1_0155	BR0156	BMEI1791	AACTGCGATATGGGGCGT	hypothetical protein	BAB1_0156-BAB1_0157
BAB1_0329	BR0299	BMEI1623	ATCTTCGTTATCCGGAAT	Pollen allergen Poa pIX/Phl pVI, C-terminal	-
BAB1_0336	BR0306	BMEI1616	GTTTTCTTTATGCCTGTT	2'-deoxycytidine 5'-triphosphate deaminase	BAB1_0337-BAB1_0340
BAB1_0339	BR0309	BMEI1613	TTCAGCGATACATCAGAT	conserved hypothetical protein	BAB1_0340
BAB1_0342	BR0312	BMEI1610	ATTTTCCATTTAGAGCAT	conserved hypothetical protein	BAB1_0341
BAB1_0343	BR0313	BMEI1609	ATGCTCTAAATGGAAAAT	conserved hypothetical protein	-
BAB1_0452	BR0426	BMEI1508	ATTTGCCGCATGGTGGTT	conserved hypothetical protein	-
BAB1_0587	BR0562	BMEI1371	ATGCTCTAAAGGTATAAC	conserved hypothetical protein	-

BAB1_0587	BR0562	BMEI1371	ATCTTCTATTTGAAGCAT	conserved hypothetical protein	-
BAB1_0597	BR0572	BMEI1361	GGTTGCGAGCTTCAGGAT	conserved hypothetical protein	BAB1_0598
BAB1_0598	BR0573	BMEI1360	CTGAGCCATATGGCGGTT	Amidase	-
BAB1_0604	BR0580	BMEI1354	ATCCGCTATGCCGACCAT	conserved hypothetical protein (effector cand.)	-
BAB1_0812	BR0792	BMEI1167	AAGTGCTTATTGACTGAT	conserved hypothetical protein	BAB1_0811-BAB1_0808
BAB1_0852	BR0831	BMEI1132	ATCATCGATCTGTCGGTC	hypothetical protein	BAB1_0853
BAB1_1529	BR1511	BMEI0502	ATGATATTCATTAATCAT	conserved hypothetical protein	BAB1_1530-BAB1_1533
BAB1_1881	BR1879	BMEI0182	ATGCTCGAAAGAGAAGAT	hypothetical protein	BAB1_1882
BAB2_0056	BRA0057	BMEII0037	AAGACCTATAGAGCGGTT	hypothetical protein	BAB2_0055
BAB2_0163	BRA0167	BMEII1075	TTTAGCAATATCGAGGAT	conserved hypothetical protein	BAB2_0164-BAB2_0165
BAB2_0328	BRA0907	-	AACCGCAAACCGCTGAT	hypothetical protein	BAB2_0327
BAB2_0403	BRA0833	BMEII0457	ATCGGCCTCATCCAACAT	conserved hypothetical protein	-
BAB2_0616	BRA0627	BMEII0649	GTCAGCGATGTGGCGTAT	conserved hypothetical protein	-
BAB2_0947	BRA0256	BMEII0991	ATCAGCCAAAGCTGTTTT	lipase	BAB2_0946-BAB2_0934
BAB2_1069	BRA1111	BMEII0188	ATCAGCCATATCGATAAC	conserved hypothetical protein	BAB2_1071 (BRA1112)
BAB2_1131	BRA1172	BMEII0123	AGCCGCCTTTTTTCATCAT	conserved hypothetical protein	BAB2_1132-BAB2_1135

Protein fate: Degradation/Secretion/Folding

BAB1_0118	BR0121	BMEI1827	ATCAGTTTTATGACTCGT	hypothetical protein	BAB1_0117-BAB1_0110
BAB1_2151	BR2150	BMEI1979	ATCCGGCAAATGGCGATC	protease	BAB1_2152-BAB1_2171
BAB2_0586	BRA0654	BMEI10626	ATTTGCCTTTTGC GGTT	renal dipeptidase family protein	BAB2_0585-BAB2_0580
BAB1_0901	BR0882	BMEI1084	ATCGGAGATAGCAGGCAT	tatB	BAB1_0902-BAB1_0907
BAB1_1162	BR1139	BMEI0845	ATCCCCTGACTGGCTCAT	rotamase family protein	BAB1_1163-BAB1_1167
BAB2_0782	BRA0454	BMEI10812	TTCTTCTGTTTGAAGCAT	polypeptide deformylase	-

Protein synthesis

BAB1_1728	BR1716	BMEI0322	ATCCGCAGGAAAGCGCAT	ribosomal protein L31	-
BAB2_0269	BRA0966	BMEI10332	ATCCGCCAGTTGGCGGCC	ribosomal protein S21	-
BAB1_1183	BR1161	BMEI0824	ATCCGTCATATCCATGAT	translation elongation factor Ts	BAB1_1182-BAB1_1171
BAB1_1815	BR1807	BMEI0242	GTTTCGCTTATTGCCGCAT	leuS	BAB1_1814
BAB1_1815	BR1807	BMEI0242	GATTTCCCTCCTTCAGCAT	leuS	BAB1_1814

Purines, pyrimidines, nucleosides, and nucleotides

BAB2_0326	BRA0909	BMEI10387	AAAAGCGTTTTGGCTGAT	formyltetrahydrofolate deformylase purU	-
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BAB2_0587	BRA0653	BMEI0627	AACCCGCAAAAGGCAAAT	adenine deaminase	-
<u>Regulatory functions: DNA interactions</u>					
BAB1_1201	BR1179	BMEI0808	ATCAGGAAAATAGCGATT	transcriptional regulator, MerR family	-
BAB1_2175	BR2174	BMEI1955	AACAGCCCGTTCAATCTT	regulator ferric uptake	BAB1_2176
BAB2_0117	BRA0118	BMEI1117	ATCAGCTTTATCAACGGAT	transcriptional regulator, TetR family	BAB2_0118 (vjbR)
BAB2_0250	BRA0984	BMEI0312	GGCTTCCAATTGAATGAT	transcriptional regulator	BAB2_0251
BAB2_0313	BRA0922	BMEI0375	ATCAGCGCCCGCGCTCTT	alanine catabolic operon transcriptional regulator	-
BAB2_0329	BRA0906	BMEI0390	ATCAGCGGTTTTGCGGTT	transcriptional regulator, LysR family	BAB2_0330
BAB2_0762	BRA0474	BMEI0791	ATCAGCCAGTAGGCTGAT	ompR response regulator	BAB2_0763 (envZ)
BAB2_0780	BRA0456	BMEI0810	AGCTTCTGGATCGAGGTT	bacterial regulatory protein, ArsR family	BAB2_0779-BAB2_0778
BAB2_1041	BRA1082	BMEI0219	AACCGTGAAAAAGAGAAT	transcriptional regulator, IclR family	BAB2_1042
BAB2_1099	BRA1140	BMEI0158	ATCATTTAGCCCGCTATT	transcriptional regulator (ftcR)	-
BAB2_1128	BRA1169	BMEI0127	ATGCTTCAAATATAGACT	transcriptional regulator IclR family protein	BAB2_1127-BAB2_1122
BAB1_1059	BR1039	BMEI0947	ATGCGGGAAATATATGAT	sensory box histidine kinase/response regulator	BAB1_1060-BAB1_1061
BAB1_1539	BR1522	BMEI0492	AACCGCAATGTGGTTCAT	osmolarity sensor protein EnvZ, putative	-

Tat (Sec-independent) protein export: has twin-arginine signal sequence

BAB1_0047	BR0050	BMEI1893	AACCATAAGATCGCAAAT	lipoprotein, putative	-
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Transcription: Transcription factors

BAB1_0157	BR0158	BMEI1789	ATCTTTTATTTTAGGCAT	RNA polymerase sigma-54 factor	-
BAB1_1498	BR1479	BMEI0532	AACAGGAAATCGGCTACT	RNA polymerase sigma-70	BAB1_1497-BAB1_1495
BAB1_1498	BR1479	BMEI0532	ATGATGAAGTCCGATGCC	RNA polymerase sigma-70	BAB1_1497-BAB1_1495
BAB1_1665	BR1650	BMEI0378	ATGATGCATATATATGTC	RNA polymerase sigma-70 family protein	-

Transport and binding proteins

?	BR1954	?	ATCATCCAACGATCACAT	ABC transporter	
BAB1_1627	BR1611	BMEI0412	AGGTTCCGGCTAAAGCAT	ABC transporter	BAB1_1626-BAB1_1624
BAB2_0611	BRA0632	-	ATGCCCCAACCGCTGGT	bacterial extracellular solute-binding protein	BAB2_0612-BAB2_0615
BAB2_1040	BRA1081	BMEI0220	ATTCTCTTTTTTACGGTT	peptide ABC transporter, permease protein	BAB2_1040-BAB2_1035
BAB2_1129	BRA1170	BMEI0126	AGTCTATATTTGAAGCAT	Amino acid permease protein	BAB2_1130-BAB2_1135
-	BRA0304	BMEI0945	ATCTGATTTTTTACATGTT	sugar ABC transporter	BRA0305-BRA0312
BAB1_0738	BR0720	BMEI1233	ATTTGCCCGTTGACGCTT	L-lactate permease, lldP	BAB1_0737-BAB1_0735
BAB2_0738	BRA0500	BMEI0770	AACATTGAAACATATGAT	monovalent cation/proton antiporter, MnhA/PhaA subunit	BAB2_0737-BAB2_0726

-	BRA0311	BMEI0935	GATTTTCGCCATCGAGGTT	transporter	BRA0312
BAB1_1727	BR1715	BMEI0323	ATGCGCTTTCCTGCGGAT	ABC transporter, ATP binding/permease protein	-
BAB2_0113	BRA0115	BMEI1120	ATGCGCGTTATCGTTGAA	ABC transporter	BAB2_0112-BAB2_0110
<u>Unknown function: General/Enzymes of unknown specificity</u>					
BAB1_0739	BR0721	BMEI1231	AAGCGTCAACGGGCAAAT	oxidoreductase, putative	BAB1_0740
BAB1_1066	BR1046	BMEI0940	AACCGCCTTTTTGCGGTT	phosphoribosyltransferase family protein	BAB1_1065
BAB1_1664	BR1649	BMEI0379	AACCGCTCTTTTGGGAAT	acetyltransferase, GNAT family	-
BAB2_0097	BRA0099	BMEI1134	GTCCCTCGATCTGGCGGTT	amidase	BAB2_0096-BAB2_0092
BAB2_0098	BRA0100	BMEI1133	AACCGCCAGATCGAGGAC	ornithine/DAP/arginine decarboxylase family	-
BAB2_0252	BRA0982	BMEI0314	ATTTGCCATTTGAACCAT	glutamine amidotransferase, class I	-
BAB2_0461	BRA0777	BMEI0514	AACCGCAAATGCACACAT	oxidoreductase, short-chain dehydrogenase/reductase family	-
BAB2_0555	BRA0685	BMEI0598	ATCCGCGAAAGCCCTCTT	phosphatase, Ppx/GppA family	BAB2_0554
BAB2_0644	BRA0596	BMEI0673	GACGCCGATAAAGTTGAA	aminoacyl-tRNA synthetase	BAB2_0645-BAB2_0648
BAB2_1015	BRA1054	BMEI0246	AACCCCATACAGAAGCC	nitroreductase family protein	BAB2_1016
-	BR0951	BMEI1023	ATGCTCTAAATAGAAAAT	glutathione S-transferase domain protein	-
-	BRA0301	BMEI0947	AAGATCAATATCTCGAAT	cyclic nucleotide-binding protein	-
BAB1_0882	BR0863	BMEI1103	AAGTTCAATTAAGCAGTT	TIM-barrel protein, yjbN family	-

BAB1_1106	BR1083	BMEI0899	ATGACCAAGAGCGCGGAT	BRO family protein: COG3617	BAB1_1105-BAB1_1103
BAB1_1133	BR1110	BMEI0873	ATGCCCGATAGCGATGCG	ATP/GTP-binding site motif A (P-loop)	BAB1_1132-BAB1_1129
BAB1_1147	BR1124	BMEI0859	TTCAGCCCCATCGGGGAT	lipoic acid synthetase, lipA	BAB1_1146
BAB1_1718	BR1706	BMEI0330	ATGCCCGAATTCGATCAT	hypothetical protein	BAB1_1717-BAB1_1709
BAB2_0307	BRA0928	BMEI0369	AAGCGAGAAAACGCTCAT	amidohydrolase	BAB2_0308
BAB2_0361	BRA0875	BMEI0419	AGTTTCGCGCTGCCTCTT	GTP binding protein	BAB2_0362-BAB2_0365
BAB2_0859	BRA0344	BMEI0904	ATGCTTCAAATAGAAGGT	EAL domain protein	-
BAB2_1072	BRA1113	BMEI0186	AGCATCATTATGGAGCAT	pemK family protein (transcriptional regulator, growth inhibitor)	-
BAB2_1072	BRA1113	BMEI0186	AGGAGTCATGCCGCTGAT	pemK family protein (transcriptional regulator, growth inhibitor)	-

Supplementary Table 3. Promoters with a putative *PvirB* box activated by VjbR in *E. coli*.

ORF	<i>PvirB</i> box	Gene name/Predicted function	Downstream genes
BAB2_0068	ATGACCGATATCGCTGAT	<i>virB1</i>	BAB2_0067-BAB2_0057 <i>virB2-virB12</i>
BAB2_0067	ATCTGCGATCTGGAGCAT	<i>virB2</i>	BAB2_0066-BAB2_0057 <i>virB3-virB12</i>
BAB2_0117	ATCAGCTTTATCAACGGAT	Transcriptional regulator (<i>tetR</i>)	BAB2_0118 <i>vjbR</i>
BAB2_0762	ATCAGCCAGTAGGCTGAT	<i>ompR</i> response regulator	BAB2_0763 <i>envZ</i> osmolarity sensor
BAB1_1881	ATGCTCGAAAGAGAAGAT	Hypothetical protein	BAB1_1882 transporter
BAB2_0328	AACCGCAAAACCGCTGAT	Hypothetical protein	BAB2_0327 aldehyde dehydrogenase
BAB2_0329	ATCAGCGGTTTTGCGGTT	Transcriptional regulator (<i>lysR12</i>)	BAB2_0330 oxidoreductase
BAB1_1651	ATTTGATATATGAAGGAT	Hypothetical protein	BAB1_1652 (<i>vceA</i>)
BAB1_1066	AACCGCCTTTTTGCGGTT	Phosphoribosyl transferase family	BAB1_1065 <i>mutT</i>
BAB1_1837	ATGCGCCATGCCGAACAT	Carbonic anhydrase, putative	-
BRA1111	ATCAGCCATATCGATAAC	Conserved hypothetical protein (<i>bopA</i>)	BRA1112 (BAB2_1071) hypothetical
BAB1_0108	ATCCGTGATCTCGCAGCT	Cyclic beta 1-2 glucan synthetase	BAB1_0109 <i>pncB</i>
BR0951	ATGCTCTAAATAGAAAAT	Glutathione S-transferase domain	BR0950 oxidoreductase (putative)
BAB2_1106	ATGCTTAAGGTGGAAATT	Flagellin family protein (<i>fliC</i>)	-
BAB1_0604	ATCCGCTATGCCGACCAT	hypothetical protein	-
BAB1_1058	ATCATATATTTCCCGCAT	hypothetical protein (<i>vceC</i>)	-
BAB1_1994	AACCGCCGTCTTCCTGAT	1-acyl-sn-glycerol-3-phosphate acyltransferase	BAB1_1993 inorganic pyrophosphatase
BAB2_0403	ATCGGCCTCATCCAACAT	hypothetical protein	-
consensus	ATCCGCGATATCGCGGAT		

Supplementary table 4. Similarity (%) between VceC amino acid sequences of *Brucella* spp. and *O. anthropi*. Amino acid sequences of BR1038, BCAN_A1051, BSUIS_A1081, BOV_1003, BAB1_1058, BruAb1_1043, BMEI0948, Oant_2123, and a predicted ORF from *O. intermedium* were aligned pairwise using ClustalW (MacVector 7.2).

VceC Identity (%)	<i>B. suis</i> 1330	<i>B. canis</i>	<i>B. suis</i> 23445	<i>B. ovis</i>	<i>B. abortus</i> 2308	<i>B. abortus</i> 9-941	<i>B. melitensis</i> 16M	<i>O. anthropi</i>
<i>B. suis</i> 1330	100							
<i>B. canis</i> ATCC 23365	99	100						
<i>B. suis</i> ATTC 23445	88	88	100					
<i>B. ovis</i>	87	87	98	100				
<i>B. abortus</i> 2308	88	88	99	98	100			
<i>B. abortus</i> 9-941	88	88	99	98	100	100		
<i>B. melitensis</i> 16M	75	75	85	86	85	85	100	
<i>O. anthropi</i>	56	55	63	61	62	62	50	100
<i>O. intermedium</i>	56	56	62	61	62	62	50	81

Supplementary table 5. Primers used in this study

Purpose ^a	Name	Sequence ^b
pET-vjbR	VjbR-F	AAACATATGAGTCTTGATCTCGTTCATTT
	VjbR-R	TCCGTCGACGAGATGCTGTACCTCGGG
pET-gntR4	GntR4-F	AAACATATGCGGCTGGTCGCGGAAGGTATC
	GntR4-R	TCCGTCGACGGATCTTGCGGCCTTCATGGC
pET-araC8	AraC8-F	AAACATATGTCCGTATTGCTGACAACG
	AraC8-R	TCCGTCGACGCATTCGTAATTTAAGCAATTTG
pET-deoR1	DeoR1-F	AAACATATGATACCGGCTGAACGGCAG
	DeoR1-R	TCCGTCGACGATTTTCCCTTCGACTTTGCC
pET-arsR6	ArsR6-F	AAACATATGACTAACAAGTTACTTTTTATG
	ArsR6Xho-R	TCCCTCGAGTTGGTGCGCCACCGCCATCAT
pSURS1	pACYC184-R	TCCTTCCTGCAGCTGATGTCCGGCGGTGCTTTTG
	pACYC184-F	AATTAAGTCGACGCTAGCGGAGTGATACTGGCT
pSURS2	PVirBBamH1-F	AAAGGATCCATCGCCATGACAGGCATATTTTC
	PVirBEcoR1-R	TCCGAATTCTAGGATCGTCTCCTTCTCAGAG
pSURS7	PvjbRBamH1-F	AAAGGATCCATTCGGGACAATGTGGAGTCC
	PvjbREcoR1-R	TCCGAATTCTGGAAATATCCTTGGTGATGAA
pSURS7b	PvjbR2BamH1-F	AAAGGATCCGGGGATGTTTTCAATATAGCC
	PvjbR2EcoR1-R	TCCGAATTCAAAGCAGGACTCTTAACTTTTTTC
pSURS13R	13REcoR1-F	TCCGAATTCTTTGCTGTTCCATTGCCGT
	13RBamH1-R	AAAGGATCCGCGAAGTCTGCGCTATTGG
pSURS14	14BamH1-F	AAAGGATCCTGCGATGGGGCACCATCG
	14EcoR1-R	TCCGAATTCTGGTTCCTCTGGGGTCGCA

pSURS17F	17FBamH1-F	AAAGGATCCTGCATTGCCCCCGTTC
	17FEcoR1-R	TCCGAATTCGGGATTCTATCTTCTCTTTCGAGC
pSURS18F	18FBamH1-F	AAAGGATCCTCCATTCTCGCATTAAACATAGTT
	18FEcoR1-R	TCCGAATTCGCGAAAATTTCCGTTGAAA
pSURS18R	18REcoR1-F	TCCGAATTCCTCCATTCTCGCATTAAACATAGTT
	18RBamH1-R	AAAGGATCCTGCGAAAATTTCCGTTGAAA
pSURS19	19BamH1-F	AAAGGATCCAGCAGAAATTC CAATGTATCTCC
	19EcoR1-R	TCCGAATTCGGATTAATCGGTGTCGCAG
pSURS21	21BamH1-F	AAAGGATCCTATGCCCGGTGATTGAAGG
	21EcoR1-R	TCCGAATTCCTTCATATTGTTTCGAGCGG
pSURS22	22BamH1-F	AAAGGATCCGAAACACGCCGCGCCTA
	22EcoR1-R	TCCGAATTCGGTTATACCTGTGCAATTGAGGA
pSURS23	23BamH1-F	AAAGGATCCAAGCGGTTTTGCGTCGGA
	23EcoR1-R	TCCGAATTCGAAACGCTCCATGGATC
pSURS25	25BamH1-F	AAAGGATCCTCTGGCGCGCTACCTTTC
	25EcoR1-R	TCCGAATTCAGCGTTTGAATATCCCTATCG
pSURS29	29BamH1-F	AAAGGATCCGCTGCGTGTGCTCTTCACC
	29EcoR1-R	TCCGAATTCGTATTGGCGAGGGCCC
pSURS30	30BamH1-F	AAAGGATCCATCTCAACCCCGCCTCTGTC
	30EcoR1-R	TCCGAATTCAGTTTTTTGCCCTTGGGAA
pSURS31	31BamH1-F	AAAGGATCCGTGCTTCTCCGTTTCAGCCG
	31EcoR1-R	TCCGAATTCACGGATGGGCGGATATTAC
pSURS32	32BamH1-F	AAAGGATCCCCTGAACGACAATGTCTCCAA
	32EcoR1-R	TCCGAATTCCTTACATCCTGGGCGTTACG

pSURS35	35BamH1-F	AAAGGATCCGATGCGGGAGATCAGTGAGTT
	35EcoR1-R	TCCGAATTC CCGGTTCTCCCATGACAGG
pFT/GST	GST-F1	TCCATATGTCTAGATCCCCTATACTAGGTTATTG
	GST-R1	AACTGCAGTCAACGCGGAACCAGATCCGATTTTG ATCCGGACTCTCTAGACATCCAGAAATTGAAAAAGCCCAA GAGAG
pFT/RalF	RalF-BspE1-F	
	RalF-Bcl1-R	ATGATCACTGCAGGCCATTTACCCAGATTTGTG
pFT/RalF(K368A)	RalF-K368A-R	ACTGCAGATTA AAATTTTAATTGTCTACCTGCTTC
pFT/RalF(L372T)	RalF-L372T-R	ACTGCAGATTA AAATTTTGTGTTGTCTACCTTTTTTC
pFT/RalF(350-374)	RalF-F	CGTCTAGACTGGCACTTAAGGAGGGCGTTC
	RalF-R	GCGCTGCAGGCCATTTACCCAGATTTGTGGAG
pFT/BAB1_1652	BR1634-F	TCCTCTAGAAAATCATCATCACGGCAGCA
	BR1634-R	AAACTGCAGCTAGTTCTTGGGCGCGTGGCC
pFT/BAB1_1058	BAB1_1058-F	TCCTCTAGAGAACGTTCCAGAGCGTCCAGAA
	BAB1_1058-R	AAACTGCAGCTAATTGCGGGTTTCTCCCTTG
pFT/BR1038	BR1038-F2	TCCTCTAGAGAACGTTCCAGAGCGTCCAGAA
	BR1038-R	AAACTGCAGTCAACTCGCCAAGCAGCTTTT
pFT/BAB1_1058-20	BAB1058-20-R	AAACTGCAGCTAGGTTTCTTCGGCCTTGGC
pFT/BR1038-20	BR1038-20-R	AAACTGCAGCTACCGGCTGTTTCATCGGTAGG
pFT/BAB1_1058-49	BAB1058-49-R	AAACTGCAGCTACA ACTCCTCCATATTTTCATCTTTAC
pFT/BAB2_0056	BRA0057-F	TCCTCTAGACGTGAAGCTCTGACAAGCGGA
	BRA0057-R	AAACTGCAGCTATTTTCTGGGGGCTTTTCC
pFT/BAB2_0095	BRA0097-F	TCCTCTAGACTGGTTTCGCTCTGGCCCAGG
	BRA0097-R	AAACTGCAGTCAGCCAGTCTTTCTTTTCGC
pFT/BAB1_0604	BAB0604-F	TCCTCTAGAGCGGTGAGTGTATGCCTACC
	BAB0604-R	AAACTGCAGCTATTTGACCGACCTGATGGG

BAB1-0119	BAB1-0119Xba1-F	TCCTCTAGAGCGACCAATGTTTTTCATGC
	BAB1-0119PstI-R	AAACTGCAGCTACAATAAAGGAAACCGGCC
BAB1-0651	BAB1-0651Xba1-F	TCCTCTAGAGAAAATTTTGGATTTGGACGC
	BAB1-0651PstI-R	AAACTGCAGTCATTTCGTTCTCCCAAATG
BAB1-0740	BAB1-0740Xba1-F	TCCTCTAGATCGGTGATCGGTGATGTGTT
	BAB1-0740PstI-R	AAACTGCAGTCAGAATTTGTCTAGCAGGTCCTG
BAB1-1674	BAB1-1674Xba1-F	TCCTCTAGACTCGCCGCGATTTGCT
	BAB1-1674PstI-R	AAACTGCAGTTAGCGGTCTTTTTCTTGTCCG
BAB1-1705	BAB1-1705Xba1-F	TCCTCTAGAGCATCTGTTTCTTCGCAGGAA
	BAB1-1705PstI-R	AAACTGCAGTCAGCACTTGGCGCGACT
BAB2-0403	BAB2-0403Xba1-F	TCCTCTAGAAAGATGCGCCGCTTACCTG
	BAB2-0403PstI-R	AAACTGCAGTCAGTCGAACAGCGGTCCG
ADH17	VjbR-up-F	TATCCGCCTCCTGCCTGCCTG
	VjbR-up-R	<u>CCCGGGAAGTATCGCTTTGAAAGGAAG</u>
	VjbR-dn-F	<u>CCCGGGTCAACATGGTCGCGCGGAAAC</u>
	VjbR-dn-R	<u>CTGCAGGCAGGAATTGCGCATGACCCG</u>
ADH58, ADH60	virB-1F	<u>CTGCAGGTGGGGCTATGAGGTGAT</u>
	virB874R	<u>TCTAGAAGGATCGTCTCCTTCTCA</u>
MDJ30, MDJ31	vceC-Pst1-F	AAACTGCAGCTTTCGGTGATGGATGCCG
	vceCXba1-R	TCCTCTAGAGGCTGCCTGGATATTTGATGTG
EMSA	PvirB100-F	CCCTCACAAGCATATTTGTCC
	PvirB463-R	TAGGATCGTCTCCTTCTCAGAG
EMSA	PvirB1ig2-F	GACGGCGTAGTTGTTTTCTAA
	virB1369R	GCTCAATAAAAGGGAAATGCTCC
EMSA	RTgyrA-F	TGATGCCCTCGTGCGTATG

RTgyrA-R

TTCCGTGACCTTTTCCAGACG

^a plasmid constructs correspond to those listed in Table 1

^b underlined nucleotides indicate restriction sites used for cloning the resulting amplicons

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VceC in:
B. suis 1330      1 MKEWLSGIIGESAANIVGFVLIFAILLGGIFVVLGIIIRRFSGGTFVSSGR 50
B. canis         1 MKEWLSGIIGESAANIVGFVLIFAILLGGIFVVLGIIIRRFSGGTFVSSGR 50
B. suis ATCC 23  1 MKEWLSGIIGESAANIVGFVLIFAILLGGIFVVLGIIIRRFSGGTFVSSGR 50
B. ovis          1 MLSGIIGESATNIVGFVLIFAILLGGIFVVLGIIIRRFSGGTFVSSGR 47
B. melitensis 1  1 0
B. abortus 2308 1 MKEWLSGIIGESAANIVGFVLIFAILLGGIFVVLGIIIRRFSGGTFVSSGR 50
O. anthropi      1 MKEWLSGIIGESAANIVGFILIFAILLGGIFVVLGIIIRRFSGGTFVSNGR 50
O. intermedium   1 MKEWLSGIIGESAANIVGFILIFAILLGGIFVVLGIIIRRFSGGTFVSNGR 50

B. suis 1330      51 MRQPRLSVMDAAAVDSRRKLVLRDDVEHLLLIGGPTDVVVEQNIVLES 100
B. canis         51 MRQPRLSVMDAAAVDSRRKLVLRDDVEHLLLIGGPTDVVVEQNIVLES 100
B. suis ATCC 23  51 MRQPRLSVMDAAAVDSRRKLVLRDDVEHLLLIGGPTDVVVEQNIVLES 100
B. ovis          48 MRQPRLSVMDAAAVDSRRKLVLRDDVEHLLLIGGPTDVVVEQNIVLES 97
B. melitensis 1  1 MMDAAAVDSRRKLVLRDDVEHLLLIGGPTDVVVEQNIVLES 43
B. abortus 2308  51 MRQPRLSVMDAAAVDSRRKLVLRDDVEHLLLIGGPTDVVVEQNIVLES 100
O. anthropi      51 TRQPRLSVMDAAAVDSRRKLVLRDDVEHLLLIGGPTDVVVEQNIVMES 100
O. intermedium   51 TRQPRLSVMDAAAVDSRRKLVLRDDVEHLLLIGGPTDVVVEQNIVMES 100
      *****

B. suis 1330      101 RAGTHAPGTHALGTHAQSSRIEPEHIERFRQHEVLAN-EKTERPALSVQS 149
B. canis         101 RAGTHAPGTHALGTHAQSSRIEPEHIERFRQHEVLAN-EKTERPALSVQS 149
B. suis ATCC 23  101 RAGTHAPGTHALGTHAQSSRIEPEHIERFRQHEVLAN-EKTERPALSVQS 149
B. ovis          98 RAGTHAPGTHALGTHAQSSRIEPEHIERFRQHEVLAN-EKTERPALSVQS 146
B. melitensis 1  44 RAGTHAPGTHALGTHAQSSRIEPEHIERFRQHEVLAN-EKTERPALSVQS 92
B. abortus 2308  101 RAGTHAPGTHALGTHAQSSRIEPEHIERFRQHEVLAN-EKTERPALSVQS 149
O. anthropi      101 RA--HAR-----VQASRIEPEHIERFKQHEATLTNDKAERPALSQT 140
O. intermedium   101 RA--HAR-----VQPSRIEPEHIERFKQHEVLTN---EKTPALSLQT 137
      ** ** * *****.*** . ****.*

B. suis 1330      150 QPGDEREETIQLSSAIAAPVYRKPEPPKAENVRPAPSEPAPMRAP-QPPV 198
B. canis         150 QPGDEREETIQLSSAIAAPVYRKPEPPKAENVRPAPSEPAPMRAP-QPPV 198
B. suis ATCC 23  150 QPGDEREETIQLSSAIAAPVYRKPEPPKAENVRPAPSEPAPMRAP-QPPV 198
B. ovis          147 QPGDEREETIQLSSAIAAPVYRKPEPPKAENVRPAPSEPAPMRAP-QPPV 195
B. melitensis 1  93 QPGDEREETIQLSSAIAAPVYRKPEPPKAENVRPAPSEPAPMRAP-QPPV 141
B. abortus 2308  150 QPGDEREETIQLSSAIAAPVYRKPEPPKAENVRPAPSEPAPMRAP-QPPV 198
O. anthropi      141 PQAEKDEAIQITSAIEAPVYRKPEPAREE---PVQQAAPVVRVPPQAPT 187
O. intermedium   138 PPANEKDEAIQISSAIEETPAYRKPEPAREE---PAPQAATVVRVPPQAPA 184
      *.*.*.*.*.*.* * ***** . * * * . * . * * *

B. suis 1330      199 TPPPA--APRPEAPASQVS-EPHPRPASNYPSQPRTVLPPRPAPSAAPNS 245
B. canis         199 TPPPA--APRPEAPASQVS-EPHPRPASNYPSQPRTVLPPRPAPSAAPNS 245
B. suis ATCC 23  199 TPPPA--APRPEAPASQVS-EPHPRPASNYPSQPRTVLPPRPAPSAAPNS 245
B. ovis          196 TPPPA--APRPEAPASQVS-EPHPRPASNYPSQPRTVLPPRPAPSAAPNS 242
B. melitensis 1  142 TPPPA--APRPEAPASQVS-EPHPRPASNYPSQPRTVLPPRPAPSAAPNS 188
B. abortus 2308  199 TPPPA--APRPEAPASQVS-EPHPRPASNYPSQPRTVLPPRPAPSAAPNS 245
O. anthropi      188 APIPP-RPPVEKSAQPPQPRPAPNYPPQPRTVLPPRPAPSAAPNS 235
O. intermedium   185 VASHSSQSPVEPKAQPMQARQPRPAPNYPPQPRTVLPPRPAPSAAPNS 233
      * * * ***** * * *

B. suis 1330      246 VRAHPAYPLSQVSRGVVSTSNIQ-----AATVATAATANLGSIVPERE 289
B. canis         246 VRAHPAYPLSQVSRGVVSTSNIQ-----AATVATAATANLGSIVPERE 289
B. suis ATCC 23  246 VRAHPAYPLSQVSRGVVSTSNIQ-----AATVATAATANLGSIVPERE 289
B. ovis          243 VRAHPAYPLSQVSRGVVSTSNIQ-----AATVASAATANLGSIVPERE 286
B. melitensis 1  189 VRAHPAYPLSQVSRGVVSTSNIQ-----AATVASAATANLGSIVPERE 232
B. abortus 2308  246 VRAHPAYPLSQVSRGVVSTSNIQ-----AATVASAATANLGSIVPERE 289
O. anthropi      236 TRAHPAYPLSQVSRGVLSTSSGATATAAGVAAAASVASANLGSIVPERE 285
O. intermedium   234 TRAHPAYPLSQVSRGVVSTSSGG-VTATGVAAAATSVASANLGSIVPERE 282
      *****.* ** * . . * .*****

B. suis 1330      290 S-AAPAKP-----AAPAPNQPERSERPERPERPQORIEPVVVF 326
B. canis         290 S-AAPAKP-----AAPAPNQPERSERPERPERPQORIEPVVVF 326
B. suis ATCC 23  290 S-AAPAKP-----AAPAPNQPERSERPERPERPQORIEPVVVF 326
B. ovis          287 S-AAPAKP-----AAPAPNQPERSERPERPERPQORIEPVVVF 323
B. melitensis 1  233 S-AAPAKP-----AAPAPNQPERSERPERPERPQORIEPVVVF 269
B. abortus 2308  290 S-AAPAKP-----AAPAPNQPERSERPERPERPQORIEPVVVF 326
O. anthropi      286 TTVADKSPVDVTGPTVSSSTAAPAFSAS--SE-PER-VEPEIVVAESKPV 331
O. intermedium   283 TTVADKSPVTLDVAGPMVSTTAAPAFSTP--SE-PKR-IEPEIPIAASKPA 328
      . * * * ***** * * * * * .

B. suis 1330      327 VAQEVROPESADDDLDLGGTLHDAIMADLGSN--AGKD-ENMEELARLR 373
B. canis         327 VAQEVROPESADDDLDLGGTLHDAIMADLGSN--AGKD-ENMEELARLR 373
B. suis ATCC 23  327 VAQEVROPESADDDLDLGGTLHDAIMADLGSN--AGKD-ENMEELDTAS 373
B. ovis          324 VAQEVROPESADDDLDLGGTLHDAIMADLGSN--AGKD-ENMEELDTAS 370
B. melitensis 1  270 VAQEVROPESADDDLDLGGTLHDAIMADLGSN--AGKD-ENMEELDTAS 316
B. abortus 2308  327 VAQEVROPESADDDLDLGGTLHDAIMADLGSN--AGKD-ENMEELDTAS 373
O. anthropi      332 ETEAVA-VETPSDNLADLGGALHEAIAADVNSESAASADAKDAISFDTEF 380
O. intermedium   329 VSEPVS-PEPPGDDLADLGNALQDAITADINSQSASASESKEAASFDFTEF 377
      .. * * * * **..*.* * * * .

B. suis 1330      374 WKTNY SARLIFHLPMNSRKMMPRPKPKSKTKWKSCLAS 410
B. canis         374 WKTNY SARLIFHLPMNSRKMMPRPKPKSKTKWKSCLAS 410
B. suis ATCC 23  374 LEDELLSSLDISPTDEQPEDAKAEETIEDEMEKLLGELTKGETRN 418
B. ovis          371 LEDELLSSLDISPTDEQPEDAKAEETIEDEMEKLLGELTKGETRN 415
B. melitensis 1  317 LEDELLSSLDISPTDEQPEDAKAEETIEDEMEKLLGELTKGETRN 361
B. abortus 2308  374 LEDELLSSLDISPTDEQPEDAKAEETIEDEMEKLLGELTKGETRN 418
O. anthropi      381 FENELSSLDISATDDVVED-KAKDDIEDEMEKLLGELTKDEIRRS 425
O. intermedium   378 FENELLRSLDISATDDTLED-KTKDDIEDEMEKLLGELTKDGIRRD* 423
      * * * * *

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Supplementary Figure 1. Multiple alignment of VceC amino acid sequences of *Brucella* species and *Ochrobactrum* species *anthropi* and *intermedium* using ClustalW (MacVector 7.2). Proteins aligned are BR1038, BCAN_A1051, BSUIS_A1081, BOV_1003, BMEI0948, BAB1_1058 and Oant_2123, and a predicted ORF from the *O. intermedium* genome (Brettin, Tsolis et al, unpublished results).