Supplementary Table S7. Up-regulated putative virulence factors of the 'red-complex' in disease. These virulence factors were identified bibliographically or by BLAST alignment to the VFDB as described in the methods section. In red are proteins with potential protease or peptidase activities. In green are proteins probably involved in iron metabolism.

Organism	ORF ID	Annotation in PATRIC	Homolog in VFDB database
P. gingivalis	VBIPorGin134034_0009	ATP-dependent Clp protease ATP-binding subunit ClpA	chaperone [Pseudomonas fluorescens str. SBW25]
P. gingivalis	VBIPorGin134034_0042	Phosphatidate cytidylyltransferase EC 2.7.7.41	phosphatidate cytidylyltransferase [Enterococcus faecalis str. V583]
P. gingivalis	VBIPorGin134034_0063	Acyl-acyl-carrier-protein--UDP-N-acetylglucosamine O-acyltransferase EC 2.3.1.129	UDP-N-acetylglucosamine acyltransferase [Haemophilus ducreyi str. 35000HP]
P. gingivalis	VBIPorGin134034_0065	UDP-3-O-3-hydroxymyristoyl glucosamine N-acyltransferase EC 2.3.1.-	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase [Haemophilus influenzae str. PittGG (nontypeable)]
P. gingivalis	VBIPorGin134034_0078	Arabinose 5-phosphate isomerase EC 5.3.1.13	arabinose-5-phosphate isomerase [Campylobacter jejuni str. 269.97 (subsp. doylei)]
P. gingivalis	VBIPorGin134034_0107	Probable UDP-N-acetyl-D-mannosaminuronic acid transferase EC 2.4.1.-	UDP-N-acetyl-D-mannosamine transferase [Streptococcus pneumoniae str. Hungary19A-6 (serotype 19A)]
P. gingivalis	VBIPorGin134034_0108	UDP-N-acetylglucosamine 2-epimerase EC 5.1.3.14	UDP-N-acetylglucosamine 2-epimerase [Vibrio vulnificus str. YJ016 chromosome I]
P. gingivalis	VBIPorGin134034_0178	Undecaprenyl pyrophosphate synthetase EC 2.5.1.31	undecaprenyl diphosphate synthase [Enterococcus faecalis str. V583]
P. gingivalis	VBIPorGin134034_0250	Hemolysins and related proteins containing CBS domains	CBStransporter associated domain protein [Clostridium perfringens str. ATCC 13124]
P. gingivalis	VBIPorGin134034_0287	Glycosyl transferase	putative bactoprenol glucosyl transferase [Shigella flexneri str. 301 (serotype 2a)]
P. gingivalis	VBIPorGin134034_0320	UDP-glucose 4-epimerase EC 5.1.3.2	UDP-glucose-4-epimerase [Haemophilus ducreyi str. 35000HP]
P. gingivalis	VBIPorGin134034_0323	FIG00936311 hypothetical protein	hypothetical protein [Listeria monocytogenes str. EGD-e (serovar 12a)]
P. gingivalis	VBIPorGin134034_0323	FIG00936311 hypothetical protein	hypothetical protein [Listeria monocytogenes str. EGD-e (serovar 12a)]
P. gingivalis	VBIPorGin134034_0323	FIG00936311 hypothetical protein	hypothetical protein [Listeria monocytogenes str. EGD-e (serovar 12a)]
P. gingivalis	VBIPorGin134034_0398	Tyrosine-protein kinase Wzc EC 2.7.10.2	chain length regulator (capsular polysaccharide biosynthesis) [Vibrio fischeri str. ES114 chromosome I]
P. gingivalis	VBIPorGin134034_0411	Hemolysins and related proteins containing CBS domains	CBStransporter associated domain protein [Clostridium perfringens str. ATCC 13124]
P. gingivalis	VBIPorGin134034_0471	Protein export cytoplasm protein SecA ATPase RNA helicase TC 3.A.5.1.1	ATPase SecA2 [Mycobacterium avium str. 104]
P. gingivalis	VBIPorGin134034_0471	Protein export cytoplasm protein SecA ATPase RNA helicase TC 3.A.5.1.1	ATPase SecA2 [Mycobacterium avium str. 104]
P. gingivalis	VBIPorGin134034_0542	HtrA protease chaperone protein	serine protease MucD precursor [Pseudomonas aeruginosa str. PAO1]
P. gingivalis	VBIPorGin134034_0543	RNA polymerase sigma factor RpoD	RNA polymerase sigma factor RpoS [Legionella pneumophila str. Paris]
P. gingivalis	VBIPorGin134034_0562	Alkyl hydroperoxide reductase protein C EC 1.6.4.-	alkylhydroperoxide reductase [Mycobacterium intracellulare str. MOTT36Y]
P. gingivalis	VBIPorGin134034_0589	iron compound ABC transporter 2C ATP-binding protein	ABC transporter [Pseudomonas syringae str. B728a (pv. syringae)]
P. gingivalis	VBIPorGin134034_0616	Vitamin B12 ABC transporter 2C permease component BtuC	cobalaminFe3+-siderophores transport systems permease component [Corynebacterium glutamicum str. ATCC 13032 (Bielefeld)]
P. gingivalis	VBIPorGin134034_0632	Succinate-semialdehyde dehydrogenase 2C CoA-dependent	hypothetical protein [Listeria innocua str. Clip11262 (serovar 6a)]
P. gingivalis	VBIPorGin134034_0649	FKBP-type peptidyl-prolyl cis-trans isomerase FkpA precursor EC 5.2.1.8	macrophage infectivity potentiator [Legionella pneumophila str. Paris]
P. gingivalis	VBIPorGin134034_0651	FKBP-type peptidyl-prolyl cis-trans isomerase FklB EC 5.2.1.8	macrophage infectivity potentiator [Legionella pneumophila str. Lens]
P. gingivalis	VBIPorGin134034_0685	Two-component system response regulator	putative two-component system response regulator [Pseudomonas fluorescens str. SBW25]
P. gingivalis	VBIPorGin134034_0687	Glycosyl transferase 2C group 2 family protein	glycosyl transferase family 2 [Yersinia pseudotuberculosis str. YPIII (serotype O:3)]
P. gingivalis	VBIPorGin134034_0904	Phosphoribosylaminoimidazole-succinocarboxamide synthase EC 6.3.2.6	phosphoribosylaminoimidazole-succinocarboxamide synthase [Mycobacterium smegmatis str. MC2 155]
P. gingivalis	VBIPorGin134034_0954	ABC transporter 2C ATP-binding protein	Fe(3+) ions import ATP-binding protein fbpC [Neisseria gonorrhoeae str. NCCP11945]
P. gingivalis	VBIPorGin134034_1006	Transcriptional regulatory protein rprY	putative two-component response regulator [Mycobacterium leprae str. TN]

Supplementary Table S7. Up-regulated putative virulence factors of the 'red-complex' in disease. These virulence factors were identified bibliographically or by BLAST alignment to the VFDB as described in the methods section. In red are proteins with potential protease or peptidase activities. In green are proteins probably involved in iron metabolism.

P. gingivalis	VBIPorGin134034_1037	ClpB protein	putative ClpAB-type chaperone [Pseudomonas aeruginosa str. UCBPP-PA14]
P. gingivalis	VBIPorGin134034_1053	bacterial sugar transferase	putative capsular polysaccharide biosynthesis glycosyltransferase [Vibrio cholerae str. O395 chromosome II]
P. gingivalis	VBIPorGin134034_1056	pigmentation and extracellular proteinase regulator	probable aminotransferase WbpE [Pseudomonas aeruginosa str. PAO1]
P. gingivalis	VBIPorGin134034_1061	UDP-glucose dehydrogenase EC 1.1.1.22	UDP-glucose 6-dehydrogenase [Bacillus thuringiensis str. Al Hakam]
P. gingivalis	VBIPorGin134034_1066	Glycosyl transferase 2C family 2	WbcM protein [Yersinia enterocolitica str. 105.5R(r) (subsp. palearctica)]
P. gingivalis	VBIPorGin134034_1091	ABC transporter 2C ATP-binding protein 2C putative	ABC transporter ATP-bindingpermease protein [Pseudomonas syringae str. 1448A (pv. phaseolicola)]
P. gingivalis	VBIPorGin134034_1092	ABC transporter ATP-binding protein	lipoprotein inner membrane ABC-transporter [Yersinia pestis str. Pestoides F]
P. gingivalis	VBIPorGin134034_1099	Probable polybeta-D-mannuronate O-acetylase EC 2.3.1.-	membrane bound O-acyl transferase MBOAT family protein [Pseudomonas putida str. W619]
P. gingivalis	VBIPorGin134034_1107	8-amino-7-oxononanoate synthase EC 2.3.1.47	hypothetical protein [Vibrio cholerae str. N16961 (O1 biovar eltor) chromosome II]
P. gingivalis	VBIPorGin134034_1151	3-oxoacyl-acyl-carrier protein reductase EC 1.1.1.100	hypothetical protein [Streptococcus agalactiae str. NEM316 (serotype III)]
P. gingivalis	VBIPorGin134034_1178	Ornithine aminotransferase EC 2.6.1.13	2 4-diaminobutyrate 4-transaminase [Pseudomonas putida str. W619]
P. gingivalis	VBIPorGin134034_1182	UDP-glucose dehydrogenase EC 1.1.1.22	UDP-glucoseGDP-mannose dehydrogenase-like protein [Pseudomonas aeruginosa str. LESB58]
P. gingivalis	VBIPorGin134034_1192	GDP-mannose 4 2C6 dehydratase EC 4.2.1.47	GDP-mannose 4 6-dehydratase [Brucella suis str. 1330 chromosome I]
P. gingivalis	VBIPorGin134034_1196	Ferrous iron transport protein B	ferrous iron transporter B [Legionella pneumophila str. Corby]
P. gingivalis	VBIPorGin134034_1278	surface antigen 2C putative	hypothetical protein [Listeria monocytogenes str. EGD-e (serovar 12a)]
P. gingivalis	VBIPorGin134034_1278	surface antigen 2C putative	hypothetical protein [Listeria monocytogenes str. EGD-e (serovar 12a)]
P. gingivalis	VBIPorGin134034_1435	Manganese superoxide dismutase EC 1.15.1.1	[Mn] superoxide dismutase [Mycobacterium smegmatis str. MC2 155]
P. gingivalis	VBIPorGin134034_1437	FIG00935712 hypothetical protein	streptococcal pyrogenic exotoxin B [Streptococcus pyogenes str. MGAS6180 (serotype M28)]
P. gingivalis	VBIPorGin134034_1446	dTDP-glucose 4 2C6-dehydratase EC 4.2.1.46	dTDP-glucose 4 6-dehydratase [Vibrio fischeri str. ES114 chromosome I]
P. gingivalis	VBIPorGin134034_1448	dTDP-4-dehydrorhamnose 3 2C5-epimerase EC 5.1.3.13	dTDP-6-deoxy-D-xylo-4-hexulose-3 5-epimerase [Vibrio vulnificus str. YJ016 chromosome I]
P. gingivalis	VBIPorGin134034_1449	Glucose-1-phosphate thymidylyltransferase EC 2.7.7.24	D-glucose-1-phosphate thymidylyltransferase [Vibrio vulnificus str. YJ016 chromosome I]
P. gingivalis	VBIPorGin134034_1527	GTP pyrophosphokinase EC 2.7.6.5 2C pppGpp synthetase I	GTP pyrophosphokinase RelA [Mycobacterium sp. str. JDM601]
P. gingivalis	VBIPorGin134034_1539	ABC transporter ATP-binding protein YvcR	ABC transporter related [Haemophilus somnus str. 2336]
P. gingivalis	VBIPorGin134034_1569	Lipoprotein releasing system ATP-binding protein LolD	Fe(3+) ions import ATP-binding protein fbpC [Neisseria gonorrhoeae str. NCCP11945]
P. gingivalis	VBIPorGin134034_1591	ABC transporter 2C ATP-binding protein 2C MsbA family	fused lipid transporter subunits of ABC superfamily: membrane componentATP-binding component [Haemophilus influenzae str. PittEE (nontypeable)]
P. gingivalis	VBIPorGin134034_1631	3-oxoacyl-acyl-carrier-protein synthase 2C KASII EC 2.3.1.41	3-oxoacyl-[acyl-carrier-protein] synthase 2 [Mycobacterium smegmatis str. MC2 155]
P. gingivalis	VBIPorGin134034_1647	8-amino-7-oxononanoate synthase EC 2.3.1.47	hypothetical protein [Vibrio parahaemolyticus str. RIMD 2210633 chromosome II]
P. gingivalis	VBIPorGin134034_1667	V-type ATP synthase subunit A EC 3.6.3.14	type III secretion system ATPase [Vibrio parahaemolyticus str. RIMD 2210633 chromosome I]
P. gingivalis	VBIPorGin134034_1668	V-type ATP synthase subunit B EC 3.6.3.14	type III secretion system ATP synthase [Yersinia pestis str. Pestoides F]
P. gingivalis	VBIPorGin134034_1680	3-deoxy-manno-octulosonate cytidylyltransferase EC 2.7.7.38	3-deoxy-D-manno-octulosonate cytidylyltransferase [Haemophilus somnus str. 2336]
P. gingivalis	VBIPorGin134034_1688	Enolase EC 4.2.1.11	enolase [Streptococcus gordonii str. Challis (substr. CH1)]
P. gingivalis	VBIPorGin134034_1822	bacterial sugar transferase	Sugar transferase involved in lipopolysaccharide synthesis [Vibrio vulnificus str. CMCP6 chromosome II]
P. gingivalis	VBIPorGin134034_1863	Phosphoglucomutase EC 5.4.2.2	probable phosphomannomutase [Haemophilus ducreyi str. 35000HP]

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P. gingivalis	VBIPorGin134034_1974	oxidoreductase 2C Gfo Idh MocA family	probable oxidoreductase WpbB [Pseudomonas aeruginosa str. PAO1]
P. gingivalis	VBIPorGin134034_1978	NAD-dependent glyceraldehyde-3-phosphate dehydrogenase EC 1.2.1.12	glyceraldehyde-3-phosphate dehydrogenase [Streptococcus pneumoniae str. TIGR4 (serotype 4)]
P. gingivalis	VBIPorGin134034_2041	Diaminopimelate decarboxylase EC 4.1.1.20	diaminopimelate decarboxylase LysA [Mycobacterium sp. str. JDM601]
P. gingivalis	VBIPorGin134034_2043	Cell division transporter 2C ATP-binding protein FtsE TC 3.A.5.1.1	iron(III) ABC transporter ATP-binding protein [Haemophilus somnus str. 129PT]
P. gingivalis	VBIPorGin134034_2066	Mannose-1-phosphate guanylyltransferase GDP EC 2.7.7.22	Mannose-1-phosphate guanylyltransferase ManC protein [Yersinia enterocolitica str. 105.5R(r) (subsp. palearctica)]
P. gingivalis	VBIPorGin195531_0002	2 2C3 2C4 2C5-tetrahydropyridine-2 2C6-dicarboxylate N-acetyltransferase EC 2.3.1.89	probable acetyltransferase [Bordetella avium str. 197N]
P. gingivalis	VBIPorGin195531_0013	Two-component system response regulator	putative two-component system response regulator [Pseudomonas fluorescens str. SBW25]
P. gingivalis	VBIPorGin195531_0037	Phosphatidate cytidylyltransferase EC 2.7.7.41	phosphatidate cytidylyltransferase [Enterococcus faecalis str. V583]
P. gingivalis	VBIPorGin195531_0041	Cell division transporter 2C ATP-binding protein FtsE TC 3.A.5.1.1	ABC transporter related [Haemophilus somnus str. 2336]
P. gingivalis	VBIPorGin195531_0043	Diaminopimelate decarboxylase EC 4.1.1.20	diaminopimelate decarboxylase LysA [Mycobacterium sp. str. JDM601]
P. gingivalis	VBIPorGin195531_0061	Enolase EC 4.2.1.11	enolase [Streptococcus gordonii str. Challis (substr. CH1)]
P. gingivalis	VBIPorGin195531_0077	GTP pyrophosphokinase EC 2.7.6.5 2C pppGpp synthetase II Guanosine-3' 2C5'-bisdiphosphate 3'-pyrophosphohydrolase EC 3.1.7.2	GTP pyrophosphokinase RelA [Mycobacterium marinum str. M]
P. gingivalis	VBIPorGin195531_0081	V-type ATP synthase subunit B EC 3.6.3.14	type III secretion system ATP synthase [Yersinia pestis str. Pestoides F]
P. gingivalis	VBIPorGin195531_0082	V-type ATP synthase subunit A EC 3.6.3.14	type III secretion system ATPase [Vibrio parahaemolyticus str. RIMD 2210633 chromosome I]
P. gingivalis	VBIPorGin195531_0222	bacterial sugar transferase	Sugar transferase involved in lipopolysaccharide synthesis [Vibrio vulnificus str. CMCP6 chromosome II]
P. gingivalis	VBIPorGin195531_0260	Phosphoglucomutase EC 5.4.2.2	probable phosphomannomutase [Haemophilus ducreyi str. 35000HP]
P. gingivalis	VBIPorGin195531_0327	Acyl-acyl-carrier-protein--UDP-N-acetylglucosamine O-acyltransferase EC 2.3.1.129	UDP-N-acetylglucosamine acyltransferase [Haemophilus ducreyi str. 35000HP]
P. gingivalis	VBIPorGin195531_0329	UDP-3-O-3-hydroxymyristoyl glucosamine N-acyltransferase EC 2.3.1.-	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase [Haemophilus influenzae str. PittGG (nontypeable)]
P. gingivalis	VBIPorGin195531_0343	Arabinose 5-phosphate isomerase EC 5.3.1.13	arabinose-5-phosphate isomerase [Campylobacter jejuni str. 269.97 (subsp. doylei)]
P. gingivalis	VBIPorGin195531_0367	UDP-N-acetyl-D-mannosamine dehydrogenase EC 1.1.1.-	UDP-N-acetyl-D-mannosaminuronate dehydrogenase [Vibrio vulnificus str. CMCP6 chromosome I]
P. gingivalis	VBIPorGin195531_0369	probable glycosyltransferase	Glycosyltransferase [Bacillus cereus str. ATCC 14579]
P. gingivalis	VBIPorGin195531_0377	Dolichol-phosphate mannosyltransferase EC 2.4.1.83 in lipid-linked oligosaccharide synthesis cluster	Glycosyltransferase involved in cell wall biogenesis [Streptococcus thermophilus str. LMD-9 (nonpathogenic)]
P. gingivalis	VBIPorGin195531_0379	UDP-N-acetylglucosamine 2-epimerase EC 5.1.3.14	UDP-N-acetylglucosamine 2-epimerase [Vibrio vulnificus str. YJ016 chromosome I]
P. gingivalis	VBIPorGin195531_0386	Ferrochelatase 2C protoheme ferro-lyase EC 4.99.1.1	ferrochelatase [Haemophilus influenzae str. Rd KW20 (serotype d)]
P. gingivalis	VBIPorGin195531_0397	Malonyl CoA-acyl carrier protein transacylase EC 2.3.1.39	Type I modular polyketide synthase [Mycobacterium ulcerans str. Agy99 plasmid pMUM001]
P. gingivalis	VBIPorGin195531_0397	Malonyl CoA-acyl carrier protein transacylase EC 2.3.1.39	Type I modular polyketide synthase [Mycobacterium ulcerans str. Agy99 plasmid pMUM001]
P. gingivalis	VBIPorGin195531_0397	Malonyl CoA-acyl carrier protein transacylase EC 2.3.1.39	Type I modular polyketide synthase [Mycobacterium ulcerans str. Agy99 plasmid pMUM001]
P. gingivalis	VBIPorGin195531_0397	Malonyl CoA-acyl carrier protein transacylase EC 2.3.1.39	Type I modular polyketide synthase [Mycobacterium ulcerans str. Agy99 plasmid pMUM001]
P. gingivalis	VBIPorGin195531_0445	Undecaprenyl pyrophosphate synthetase EC 2.5.1.31	undecaprenyl diphosphate synthase [Enterococcus faecalis str. V583]
P. gingivalis	VBIPorGin195531_0524	Hemolysins and related proteins containing CBS domains	CBStransporter associated domain protein [Clostridium perfringens str. ATCC 13124]
P. gingivalis	VBIPorGin195531_0530	2-Keto-3-deoxy-D-manno-octulosonate-8-phosphate synthase EC 2.5.1.55	2-dehydro-3-deoxyphosphooctonate aldolase [Haemophilus ducreyi str. 35000HP]

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P. gingivalis	VBIPorGin195531_0580	Lipoprotein releasing system ATP-binding protein LolD	Fe(3+) ions import ATP-binding protein fbpC [Neisseria gonorrhoeae str. NCCP11945]
P. gingivalis	VBIPorGin195531_0627	GTP pyrophosphokinase EC 2.7.6.5 2C pppGpp synthetase I	GTP pyrophosphokinase RelA [Mycobacterium sp. str. JDM601]
P. gingivalis	VBIPorGin195531_0708	3-deoxy-D-manno-octulosonic-acid transferase EC 2.-.-.-	Three-deoxy-D-manno-octulosonic-acid transferase domain protein [Haemophilus somnus str. 2336]
P. gingivalis	VBIPorGin195531_0710	Glucose-1-phosphate thymidylyltransferase EC 2.7.7.24	D-glucose-1-phosphate thymidylyltransferase [Vibrio vulnificus str. YJ016 chromosome I]
P. gingivalis	VBIPorGin195531_0711	dTDP-4-dehydrorhamnose 3 2C5-epimerase EC 5.1.3.13	dTDP-6-deoxy-D-xylo-4-hexulose-3 5-epimerase [Vibrio vulnificus str. YJ016 chromosome I]
P. gingivalis	VBIPorGin195531_0724	FIG00935712 hypothetical protein	Streptopain precursor [Streptococcus pyogenes str. MGAS10750 (serotype M4)]
P. gingivalis	VBIPorGin195531_0728	Manganese superoxide dismutase EC 1.15.1.1	[Mn] superoxide dismutase [Mycobacterium smegmatis str. MC2 155]
P. gingivalis	VBIPorGin195531_0864	Phosphoribosylaminoimidazole-succinocarboxamide synthase EC 6.3.2.6	phosphoribosylaminoimidazole-succinocarboxamide synthase [Mycobacterium smegmatis str. MC2 155]
P. gingivalis	VBIPorGin195531_0919	ABC transporter 2C ATP-binding protein	Fe(3+) ions import ATP-binding protein fbpC [Neisseria gonorrhoeae str. NCCP11945]
P. gingivalis	VBIPorGin195531_0929	Ferrous iron transport protein B	ferrous iron transporter B [Legionella pneumophila str. Corby]
P. gingivalis	VBIPorGin195531_1015	Glycosyl transferase 2C family 2	WbcM protein [Yersinia enterocolitica str. 105.5R(r) (subsp. palearctica)]
P. gingivalis	VBIPorGin195531_1027	UDP-glucose dehydrogenase EC 1.1.1.22	UDP-glucose 6-dehydrogenase [Bacillus thuringiensis str. Al Hakam]
P. gingivalis	VBIPorGin195531_1071	Phosphomannomutase EC 5.4.2.8 Phosphoglucosamine mutase EC 5.4.2.10	phosphomannomutase [Pseudomonas putida str. KT2440]
P. gingivalis	VBIPorGin195531_1076	Transcriptional regulatory protein rprY	putative two-component response regulator [Mycobacterium leprae str. TN]
P. gingivalis	VBIPorGin195531_1111	ABC transporter 2C ATP-binding protein 2C putative	ABC transporter ATP-bindingpermease protein [Pseudomonas syringae str. 1448A (pv. phaseolicola)]
P. gingivalis	VBIPorGin195531_1112	ABC transporter ATP-binding protein	lipoprotein inner membrane ABC-transporter [Yersinia pestis str. CO92 (biovar Orientalis)]
P. gingivalis	VBIPorGin195531_1118	Probable polybeta-D-mannuronate O-acetylase EC 2.3.1.-	membrane bound O-acyl transferase MBOAT family protein [Pseudomonas putida str. W619]
P. gingivalis	VBIPorGin195531_1124	8-amino-7-oxononanoate synthase EC 2.3.1.47	hypothetical protein [Vibrio cholerae str. N16961 (O1 biovar eltor) chromosome II]
P. gingivalis	VBIPorGin195531_1162	3-oxoacyl-acyl-carrier protein reductase EC 1.1.1.100	hypothetical protein [Streptococcus agalactiae str. NEM316 (serotype III)]
P. gingivalis	VBIPorGin195531_1214	Lipid-A-disaccharide synthase EC 2.4.1.182	lipid-A-disaccharide synthase [Haemophilus somnus str. 129PT]
P. gingivalis	VBIPorGin195531_1253	oxidoreductase 2C Gfo Idh MocA family	probable oxidoreductase WpbB [Pseudomonas aeruginosa str. PAO1]
P. gingivalis	VBIPorGin195531_1309	8-amino-7-oxononanoate synthase EC 2.3.1.47	hypothetical protein [Vibrio parahaemolyticus str. RIMD 2210633 chromosome II]
P. gingivalis	VBIPorGin195531_1325	3-oxoacyl-acyl-carrier-protein synthase 2C KASII EC 2.3.1.41	3-oxoacyl-[acyl-carrier-protein] synthase 2 [Mycobacterium smegmatis str. MC2 155]
P. gingivalis	VBIPorGin195531_1421	FIG00936311 hypothetical protein	hypothetical protein [Listeria monocytogenes str. EGD-e (serovar 12a)]
P. gingivalis	VBIPorGin195531_1421	FIG00936311 hypothetical protein	hypothetical protein [Listeria monocytogenes str. EGD-e (serovar 12a)]
P. gingivalis	VBIPorGin195531_1421	FIG00936311 hypothetical protein	hypothetical protein [Listeria monocytogenes str. EGD-e (serovar 12a)]
P. gingivalis	VBIPorGin195531_1457	Translation elongation factor Tu	elongation factor Tu [Mycoplasma gallisepticum str. R]
P. gingivalis	VBIPorGin195531_1503	Carbonic anhydrase EC 4.2.1.1	putative carbonic anhydrase [Salmonella typhimurium str. LT2 plasmid pSLT]
P. gingivalis	VBIPorGin195531_1528	Hemolysins and related proteins containing CBS domains	CBStransporter associated domain protein [Clostridium perfringens str. ATCC 13124]
P. gingivalis	VBIPorGin195531_1541	Mannose-6-phosphate isomerase EC 5.3.1.8	mannose-6-phosphate isomerase [Bacillus thuringiensis str. Al Hakam]
P. gingivalis	VBIPorGin195531_1587	Protein export cytoplasm protein SecA ATPase RNA helicase TC 3.A.5.1.1	ATPase SecA2 [Mycobacterium avium str. 104]
P. gingivalis	VBIPorGin195531_1587	Protein export cytoplasm protein SecA ATPase RNA helicase TC 3.A.5.1.1	ATPase SecA2 [Mycobacterium avium str. 104]
P. gingivalis	VBIPorGin195531_1656	HtrA protease chaperone protein	serine protease MucD precursor [Pseudomonas aeruginosa str. PAO1]

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P. gingivalis	VBIPorGin195531_1657	RNA polymerase sigma factor RpoD	RNA polymerase sigma factor RpoS [Legionella pneumophila str. Paris]
P. gingivalis	VBIPorGin195531_1679	Alkyl hydroperoxide reductase protein C EC 1.6.4.-	alkylhydroperoxide reductase [Mycobacterium intracellulare str. MOTT36Y]
P. gingivalis	VBIPorGin195531_1700	Tetraacyldisaccharide 4'-kinase EC 2.7.1.130	tetraacyldisaccharide 4-kinase [Haemophilus influenzae str. Rd KW20 (serotype d)]
P. gingivalis	VBIPorGin195531_1707	iron compound ABC transporter 2C ATP-binding protein	ABC transporter [Pseudomonas syringae str. B728a (pv. syringae)]
P. gingivalis	VBIPorGin195531_1708	Vitamin B12 ABC transporter 2C permease component BtuC	iron ABC transporter permease [Corynebacterium pseudotuberculosis str. FRC41]
P. gingivalis	VBIPorGin195531_1733	Vitamin B12 ABC transporter 2C permease component BtuC	cobalaminFe3+-siderophores transport systems permease component [Corynebacterium glutamicum str. ATCC 13032 (Bielefeld)]
P. gingivalis	VBIPorGin195531_1749	Succinate-semialdehyde dehydrogenase 2C CoA-dependent	hypothetical protein [Listeria innocua str. Clip11262 (serovar 6a)]
P. gingivalis	VBIPorGin195531_1769	FKBP-type peptidyl-prolyl cis-trans isomerase FkpA precursor EC 5.2.1.8	macrophage infectivity potentiator [Legionella pneumophila str. Paris]
P. gingivalis	VBIPorGin195531_1771	FKBP-type peptidyl-prolyl cis-trans isomerase FklB EC 5.2.1.8	macrophage infectivity potentiator [Legionella pneumophila str. Lens]
P. gingivalis	VBIPorGin195531_1782	DNA-binding response regulator	two component transcriptional regulator winged helix family [Mycobacterium vanbaalenii str. PYR-1]
P. gingivalis	VBIPorGin195531_1805	Two-component system response regulator	putative two-component system response regulator [Pseudomonas fluorescens str. SBW25]
P. gingivalis	VBIPorGin195531_1960	FIG00935743 hypothetical protein	streptococcal pyrogenic exotoxin B [Streptococcus pyogenes str. MGAS6180 (serotype M28)]
P. gingivalis	VBIPorGin195531_2015	surface antigen 2C putative	hypothetical protein [Listeria monocytogenes str. EGD-e (serovar 12a)]
P. gingivalis	VBIPorGin195531_2015	surface antigen 2C putative	hypothetical protein [Listeria monocytogenes str. EGD-e (serovar 12a)]
P. gingivalis	VBIPorGin195531_2098	Ferrous iron transport protein B	ferrous iron transporter B [Legionella pneumophila str. Corby]
P. gingivalis	VBIPorGin195531_2104	GDP-mannose 4 2C6 dehydratase EC 4.2.1.47	GDP-mannose 4 6-dehydratase [Brucella suis str. 1330 chromosome I]
P. gingivalis	VBIPorGin195531_2114	UDP-glucose dehydrogenase EC 1.1.1.22	UDP-glucoseGDP-mannose dehydrogenase-like protein [Pseudomonas aeruginosa str. LESB58]
P. gingivalis	VBIPorGin195531_2118	Ornithine aminotransferase EC 2.6.1.13	diaminobutyrate--2-oxoglutarate aminotransferase [Pseudomonas fluorescens str. Pf-5]
P. gingivalis	VBIPorGin195531_2154	Mannose-1-phosphate guanylyltransferase GDP EC 2.7.7.22	Mannose-1-phosphate guanylytransferase ManC protein [Yersinia enterocolitica str. 105.5R(r) (subsp. palearctica)]
P. gingivalis	VBIPorGin239392_0023	Hemolysins and related proteins containing CBS domains	CBStransporter associated domain protein [Clostridium perfringens str. ATCC 13124]
P. gingivalis	VBIPorGin239392_0081	Ferrous iron transport protein B	ferrous iron transporter B [Legionella pneumophila str. Corby]
P. gingivalis	VBIPorGin239392_0091	ABC transporter 2C ATP-binding protein	Fe(3+) ions import ATP-binding protein fbpC [Neisseria gonorrhoeae str. NCCP11945]
P. gingivalis	VBIPorGin239392_0121	Lipoprotein releasing system ATP-binding protein LolD	Fe(3+) ions import ATP-binding protein fbpC [Neisseria gonorrhoeae str. NCCP11945]
P. gingivalis	VBIPorGin239392_0155	ABC transporter 2C ATP-binding protein 2C putative	ABC transporter ATP-bindingpermease protein [Pseudomonas syringae str. 1448A (pv. phaseolicola)]
P. gingivalis	VBIPorGin239392_0156	ABC transporter ATP-binding protein	lipoprotein inner membrane ABC-transporter [Yersinia pestis str. Pestoides F]
P. gingivalis	VBIPorGin239392_0183	Phosphatidate cytidylyltransferase EC 2.7.7.41	phosphatidate cytidylyltransferase [Enterococcus faecalis str. V583]
P. gingivalis	VBIPorGin239392_0191	Glycosyl transferase 2C group 2 family protein	glycosyl transferase family 2 [Yersinia pseudotuberculosis str. YPIII (serotype O:3)]
P. gingivalis	VBIPorGin239392_0231	FKBP-type peptidyl-prolyl cis-trans isomerase FklB EC 5.2.1.8	macrophage infectivity potentiator [Legionella pneumophila str. Lens]
P. gingivalis	VBIPorGin239392_0234	FKBP-type peptidyl-prolyl cis-trans isomerase FkpA precursor EC 5.2.1.8	macrophage infectivity potentiator [Legionella pneumophila str. Paris]
P. gingivalis	VBIPorGin239392_0254	Succinate-semialdehyde dehydrogenase 2C CoA-dependent	hypothetical protein [Listeria innocua str. Clip11262 (serovar 6a)]
P. gingivalis	VBIPorGin239392_0270	Vitamin B12 ABC transporter 2C permease component BtuC	cobalaminFe3+-siderophores transport systems permease component [Corynebacterium glutamicum str. ATCC 13032 (Bielefeld)]
P. gingivalis	VBIPorGin239392_0295	Vitamin B12 ABC transporter 2C permease component BtuC	iron ABC transporter permease [Corynebacterium pseudotuberculosis str. FRC41]

Supplementary Table S7. Up-regulated putative virulence factors of the 'red-complex' in disease. These virulence factors were identified bibliographically or by BLAST alignment to the VFDB as described in the methods section. In red are proteins with potential protease or peptidase activities. In green are proteins probably involved in iron metabolism.

P. gingivalis	VBIPorGin239392_0319	UDP-glucose dehydrogenase EC 1.1.1.22	UDP-glucose 6-dehydrogenase [Bacillus thuringiensis str. Al Hakam]
P. gingivalis	VBIPorGin239392_0327	bacterial sugar transferase	putative capsular polysaccharide biosynthesis glycosyltransferase [Vibrio cholerae str. O395 chromosome II]
P. gingivalis	VBIPorGin239392_0343	ClpB protein	putative ClpAB-type chaperone [Pseudomonas aeruginosa str. UCBPP-PA14]
P. gingivalis	VBIPorGin239392_0375	Transcriptional regulatory protein rprY	putative two-component response regulator [Mycobacterium leprae str. TN]
P. gingivalis	VBIPorGin239392_0409	oxidoreductase 2C Gfo Idh MocA family	probable oxidoreductase WpbB [Pseudomonas aeruginosa str. PAO1]
P. gingivalis	VBIPorGin239392_0414	NAD-dependent glyceraldehyde-3-phosphate dehydrogenase EC 1.2.1.12	glyceraldehyde-3-phosphate dehydrogenase [Streptococcus pneumoniae str. TIGR4 (serotype 4)]
P. gingivalis	VBIPorGin239392_0427	8-amino-7-oxononanoate synthase EC 2.3.1.47	hypothetical protein [Vibrio parahaemolyticus str. RIMD 2210633 chromosome II]
P. gingivalis	VBIPorGin239392_0577	FIG00936311 hypothetical protein	hypothetical protein [Listeria monocytogenes str. EGD-e (serovar 12a)]
P. gingivalis	VBIPorGin239392_0577	FIG00936311 hypothetical protein	hypothetical protein [Listeria monocytogenes str. EGD-e (serovar 12a)]
P. gingivalis	VBIPorGin239392_0577	FIG00936311 hypothetical protein	hypothetical protein [Listeria monocytogenes str. EGD-e (serovar 12a)]
P. gingivalis	VBIPorGin239392_0580	UDP-glucose 4-epimerase EC 5.1.3.2	UDP-glucose-4-epimerase [Haemophilus ducreyi str. 35000HP]
P. gingivalis	VBIPorGin239392_0764	UDP-3-O-3-hydroxymyristoyl glucosamine N-acyltransferase EC 2.3.1.-	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase [Haemophilus influenzae str. PittGG (nontypeable)]
P. gingivalis	VBIPorGin239392_0765	N-acetylglucosamine deacetylase EC 3.5.1.- 3R-hydroxymyristoyl-acyl carrier protein dehydratase EC 4.2.1.-	UDP-3-O-acyl-GlcNAc deacetylase [Haemophilus ducreyi str. 35000HP]
P. gingivalis	VBIPorGin239392_0766	Acyl-acyl-carrier-protein--UDP-N-acetylglucosamine O-acyltransferase EC 2.3.1.129	UDP-N-acetylglucosamine acyltransferase [Haemophilus ducreyi str. 35000HP]
P. gingivalis	VBIPorGin239392_0815	UDP-glucose dehydrogenase EC 1.1.1.22	UDP-glucoseGDP-mannose dehydrogenase-like protein [Pseudomonas aeruginosa str. LESB58]
P. gingivalis	VBIPorGin239392_0826	GDP-L-fucose synthetase EC 1.1.1.271	GDP-fucose synthetase [Campylobacter jejuni str. 269.97 (subsp. doylei)]
P. gingivalis	VBIPorGin239392_0875	Probable polybeta-D-mannuronate O-acetylase EC 2.3.1.-	membrane bound O-acyl transferase MBOAT family protein [Pseudomonas putida str. W619]
P. gingivalis	VBIPorGin239392_0939	Enolase EC 4.2.1.11	enolase [Streptococcus gordonii str. Challis (substr. CH1)]
P. gingivalis	VBIPorGin239392_0956	GTP pyrophosphokinase EC 2.7.6.5 2C pppGpp synthetase II Guanosine-3' 2C5'-bisdiphosphate 3'-pyrophosphohydrolase EC 3.1.7.2	GTP pyrophosphokinase RelA [Mycobacterium marinum str. M]
P. gingivalis	VBIPorGin239392_0960	V-type ATP synthase subunit B EC 3.6.3.14	type III secretion system ATP synthase [Yersinia pestis str. Pestoides F]
P. gingivalis	VBIPorGin239392_0961	V-type ATP synthase subunit A EC 3.6.3.14	type III secretion system ATPase [Vibrio parahaemolyticus str. RIMD 2210633 chromosome I]
P. gingivalis	VBIPorGin239392_1056	Glycosyl transferase	putative bactoprenol glucosyl transferase [Shigella flexneri str. 301 (serotype 2a)]
P. gingivalis	VBIPorGin239392_1078	Glycosyltransferase	putative bactoprenol glucosyl transferase [Shigella flexneri str. 301 (serotype 2a)]
P. gingivalis	VBIPorGin239392_1141	surface antigen 2C putative	hypothetical protein [Listeria monocytogenes str. EGD-e (serovar 12a)]
P. gingivalis	VBIPorGin239392_1141	surface antigen 2C putative	hypothetical protein [Listeria monocytogenes str. EGD-e (serovar 12a)]
P. gingivalis	VBIPorGin239392_1219	ABC transporter 2C ATP-binding protein	daunorubicin resistance ABC transporter ATPase subunit [Mycobacterium gilvum str. PYR-GCK]
P. gingivalis	VBIPorGin239392_1229	3-oxoacyl-acyl-carrier protein reductase EC 1.1.1.100	hypothetical protein [Streptococcus agalactiae str. NEM316 (serotype III)]
P. gingivalis	VBIPorGin239392_1298	ABC transporter 2C ATP-binding protein 2C MsbA family	fused lipid transporter subunits of ABC superfamily: membrane componentATP-binding component [Haemophilus influenzae str. PittEE (nontypeable)]
P. gingivalis	VBIPorGin239392_1319	2-Keto-3-deoxy-D-manno-octulosonate-8-phosphate synthase EC 2.5.1.55	2-dehydro-3-deoxyphosphooctonate aldolase [Haemophilus ducreyi str. 35000HP]
P. gingivalis	VBIPorGin239392_1326	Hemolysins and related proteins containing CBS domains	CBStransporter associated domain protein [Clostridium perfringens str. ATCC 13124]
P. gingivalis	VBIPorGin239392_1345	Lipopolysaccharide ABC transporter 2C ATP-binding protein LptB	ABC transporter related [Haemophilus somnus str. 2336]

Supplementary Table S7. Up-regulated putative virulence factors of the 'red-complex' in disease. These virulence factors were identified bibliographically or by BLAST alignment to the VFDB as described in the methods section. In red are proteins with potential protease or peptidase activities. In green are proteins probably involved in iron metabolism.

P. gingivalis	VBIPorGin239392_1357	Alkyl hydroperoxide reductase protein C EC 1.6.4.-	alkylhydroperoxide reductase [Mycobacterium intracellulare str. MOTT36Y]
P. gingivalis	VBIPorGin239392_1372	Lipid-A-disaccharide synthase EC 2.4.1.182	lipid-A-disaccharide synthase [Haemophilus ducreyi str. 35000HP]
P. gingivalis	VBIPorGin239392_1438	3-deoxy-D-manno-octulosonic-acid transferase EC 2.-.-.-	Three-deoxy-D-manno-octulosonic-acid transferase domain protein [Haemophilus somnus str. 2336]
P. gingivalis	VBIPorGin239392_1440	Glucose-1-phosphate thymidylyltransferase EC 2.7.7.24	D-glucose-1-phosphate thymidylyltransferase [Vibrio vulnificus str. YJ016 chromosome I]
P. gingivalis	VBIPorGin239392_1443	dTDP-glucose 4 2C6-dehydratase EC 4.2.1.46	dTDP-glucose 4 6-dehydratase [Vibrio fischeri str. ES114 chromosome I]
P. gingivalis	VBIPorGin239392_1454	FIG00935712 hypothetical protein	streptococcal pyrogenic exotoxin B [Streptococcus pyogenes str. MGAS6180 (serotype M28)]
P. gingivalis	VBIPorGin239392_1573	Undecaprenyl pyrophosphate synthetase EC 2.5.1.31	undecaprenyl diphosphate synthase [Enterococcus faecalis str. V583]
P. gingivalis	VBIPorGin239392_1603	2 2C3 2C4 2C5-tetrahydropyridine-2 2C6-dicarboxylate N-acetyltransferase EC 2.3.1.89	probable acetyltransferase [Bordetella avium str. 197N]
P. gingivalis	VBIPorGin239392_1644	bacterial sugar transferase	Sugar transferase involved in lipopolysaccharide synthesis [Vibrio vulnificus str. CMCP6 chromosome II]
P. gingivalis	VBIPorGin239392_1690	HtrA protease chaperone protein	serine protease MucD precursor [Pseudomonas aeruginosa str. PAO1]
P. gingivalis	VBIPorGin239392_1698	Phosphoglucomutase EC 5.4.2.2	probable phosphomannomutase [Haemophilus ducreyi str. 35000HP]
P. gingivalis	VBIPorGin239392_1734	Cell division transporter 2C ATP-binding protein FtsE TC 3.A.5.1.1	iron(III) ABC transporter ATP-binding protein [Haemophilus somnus str. 129PT]
P. gingivalis	VBIPorGin239392_1736	Diaminopimelate decarboxylase EC 4.1.1.20	diaminopimelate decarboxylase LysA [Mycobacterium sp. str. JDM601]
P. gingivalis	VBIPorGin239392_1816	8-amino-7-oxononanoate synthase EC 2.3.1.47	hypothetical protein [Vibrio cholerae str. N16961 (O1 biovar eltor) chromosome II]
P. gingivalis	VBIPorGin239392_1832	Heat shock protein 60 family chaperone GroEL	60 kDa chaperonin (Protein Cpn60)(groEL protein)(Heat shock protein B). [Legionella pneumophila str. Lens]
P. gingivalis	VBIPorGin239392_1848	Ornithine aminotransferase EC 2.6.1.13	2 4-diaminobutyrate 4-transaminase [Pseudomonas mendocina str. ymp]
P. gingivalis	VBIPorGin239392_1936	Probable UDP-N-acetyl-D-mannosaminuronic acid transferase EC 2.4.1.-	UDP-N-acetyl-D-mannosamine transferase [Streptococcus pneumoniae str. Hungary19A-6 (serotype 19A)]
P. gingivalis	VBIPorGin239392_1937	UDP-N-acetylglucosamine 2-epimerase EC 5.1.3.14	UDP-N-acetylglucosamine 2-epimerase [Vibrio vulnificus str. YJ016 chromosome I]
P. gingivalis	VBIPorGin239392_1944	Ferrochelatase 2C protoheme ferro-lyase EC 4.99.1.1	ferrochelatase [Haemophilus influenzae str. PittEE (nontypeable)]
P. gingivalis	VBIPorGin239392_1955	Malonyl CoA-acyl carrier protein transacylase EC 2.3.1.39	Type I modular polyketide synthase [Mycobacterium ulcerans str. Agy99 plasmid pMUM001]
P. gingivalis	VBIPorGin239392_1955	Malonyl CoA-acyl carrier protein transacylase EC 2.3.1.39	Type I modular polyketide synthase [Mycobacterium ulcerans str. Agy99 plasmid pMUM001]
P. gingivalis	VBIPorGin239392_1955	Malonyl CoA-acyl carrier protein transacylase EC 2.3.1.39	Type I modular polyketide synthase [Mycobacterium ulcerans str. Agy99 plasmid pMUM001]
P. gingivalis	VBIPorGin239392_1955	Malonyl CoA-acyl carrier protein transacylase EC 2.3.1.39	Type I modular polyketide synthase [Mycobacterium ulcerans str. Agy99 plasmid pMUM001]
P. gingivalis	VBIPorGin239392_1965	Transcriptional regulator	FlrA; sigma-54-dependent transcriptional activator [Vibrio fischeri str. ES114 chromosome I]
P. gingivalis	VBIPorGin239392_2009	Phosphoribosylaminoimidazole-succinocarboxamide synthase EC 6.3.2.6	phosphoribosylaminoimidazole-succinocarboxamide synthase [Mycobacterium smegmatis str. MC2 155]
P. gingivalis	VBIPorGin239392_2041	GTP pyrophosphokinase EC 2.7.6.5 2C pppGpp synthetase I	GTP pyrophosphokinase RelA [Mycobacterium sp. str. JDM601]
P. gingivalis	VBIPorGin26334_0007	ATP-dependent Clp protease ATP-binding subunit ClpA	chaperone [Pseudomonas fluorescens str. SBW25]
P. gingivalis	VBIPorGin26334_0012	Two-component system response regulator	putative two-component system response regulator [Pseudomonas fluorescens str. SBW25]
P. gingivalis	VBIPorGin26334_0037	Phosphatidate cytidylyltransferase EC 2.7.7.41	phosphatidate cytidylyltransferase [Enterococcus faecalis str. V583]
P. gingivalis	VBIPorGin26334_0090	Cell division transporter 2C ATP-binding protein FtsE TC 3.A.5.1.1	ABC transporter related [Haemophilus somnus str. 2336]
P. gingivalis	VBIPorGin26334_0168	NAD-dependent glyceraldehyde-3-phosphate dehydrogenase EC 1.2.1.12	glyceraldehyde-3-phosphate dehydrogenase [Streptococcus pneumoniae str. TIGR4 (serotype 4)]
P. gingivalis	VBIPorGin26334_0201	Lipid-A-disaccharide synthase EC 2.4.1.182	lipid-A-disaccharide synthase [Haemophilus ducreyi str. 35000HP]
P. gingivalis	VBIPorGin26334_0222	UDP-N-acetyl-D-mannosamine dehydrogenase EC 1.1.1.-	UDP-N-acetyl-D-mannosaminuronate dehydrogenase [Vibrio vulnificus str. CMCP6 chromosome I]

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P. gingivalis	VBIPorGin26334_0223	probable glycosyltransferase	Glycosyltransferase [Bacillus cereus str. ATCC 14579]
P. gingivalis	VBIPorGin26334_0229	Dolichol-phosphate mannosyltransferase EC 2.4.1.83 in lipid-linked oligosaccharide synthesis cluster	Glycosyltransferase involved in cell wall biogenesis [Streptococcus thermophilus str. LMD-9 (nonpathogenic)]
P. gingivalis	VBIPorGin26334_0230	Probable UDP-N-acetyl-D-mannosaminuronic acid transferase EC 2.4.1.-	UDP-N-acetyl-D-mannosamine transferase [Streptococcus pneumoniae str. Hungary19A-6 (serotype 19A)]
P. gingivalis	VBIPorGin26334_0231	UDP-N-acetylglucosamine 2-epimerase EC 5.1.3.14	UDP-N-acetylglucosamine 2-epimerase [Vibrio vulnificus str. YJ016 chromosome I]
P. gingivalis	VBIPorGin26334_0249	Malonyl CoA-acyl carrier protein transacylase EC 2.3.1.39	Type I modular polyketide synthase [Mycobacterium ulcerans str. Agy99 plasmid pMUM001]
P. gingivalis	VBIPorGin26334_0249	Malonyl CoA-acyl carrier protein transacylase EC 2.3.1.39	Type I modular polyketide synthase [Mycobacterium ulcerans str. Agy99 plasmid pMUM001]
P. gingivalis	VBIPorGin26334_0249	Malonyl CoA-acyl carrier protein transacylase EC 2.3.1.39	Type I modular polyketide synthase [Mycobacterium ulcerans str. Agy99 plasmid pMUM001]
P. gingivalis	VBIPorGin26334_0249	Malonyl CoA-acyl carrier protein transacylase EC 2.3.1.39	Type I modular polyketide synthase [Mycobacterium ulcerans str. Agy99 plasmid pMUM001]
P. gingivalis	VBIPorGin26334_0260	Transcriptional regulator	transcriptional regulator FleQ [Pseudomonas entomophila str. L48]
P. gingivalis	VBIPorGin26334_0296	Undecaprenyl diphosphate synthase EC 2.5.1.31	undecaprenyl diphosphate synthase [Enterococcus faecalis str. V583]
P. gingivalis	VBIPorGin26334_0369	Hemolysins and related proteins containing CBS domains	CBStransporter associated domain protein [Clostridium perfringens str. ATCC 13124]
P. gingivalis	VBIPorGin26334_0449	ABC transporter ATP-binding protein YvcR	ABC transporter related [Haemophilus somnus str. 2336]
P. gingivalis	VBIPorGin26334_0465	GTP pyrophosphokinase EC 2.7.6.5 2C pppGpp synthetase I	GTP pyrophosphokinase RelA [Mycobacterium sp. str. JDM601]
P. gingivalis	VBIPorGin26334_0540	3-deoxy-D-manno-octulosonic-acid transferase EC 2.-.-.-	Three-deoxy-D-manno-octulosonic-acid transferase domain protein [Haemophilus somnus str. 2336]
P. gingivalis	VBIPorGin26334_0543	dTDP-4-dehydrorhamnose 3 2C5-epimerase EC 5.1.3.13	dTDP-6-deoxy-D-xylo-4-hexulose-3 5-epimerase [Vibrio vulnificus str. YJ016 chromosome I]
P. gingivalis	VBIPorGin26334_0544	dTDP-4-dehydrorhamnose reductase EC 1.1.1.133	dTDP-4-dehydrorhamnose reductase [Vibrio vulnificus str. YJ016 chromosome I]
P. gingivalis	VBIPorGin26334_0545	dTDP-glucose 4 2C6-dehydratase EC 4.2.1.46	dTDP-glucose 4 6-dehydratase [Vibrio fischeri str. ES114 chromosome I]
P. gingivalis	VBIPorGin26334_0554	FIG00935712 hypothetical protein	streptococcal pyrogenic exotoxin B [Streptococcus pyogenes str. MGAS6180 (serotype M28)]
P. gingivalis	VBIPorGin26334_0631	HtrA protease chaperone protein	serine protease MucD precursor [Pseudomonas aeruginosa str. PAO1]
P. gingivalis	VBIPorGin26334_0632	RNA polymerase sigma factor RpoD	RNA polymerase sigma factor RpoS [Legionella pneumophila str. Paris]
P. gingivalis	VBIPorGin26334_0651	Alkyl hydroperoxide reductase protein C EC 1.6.4.-	alkylhydroperoxide reductase [Mycobacterium intracellulare str. MOTT36Y]
P. gingivalis	VBIPorGin26334_0660	Lipopolysaccharide ABC transporter 2C ATP-binding protein LptB	ABC transporter related [Haemophilus somnus str. 2336]
P. gingivalis	VBIPorGin26334_0670	Tetraacyldisaccharide 4'-kinase EC 2.7.1.130	tetraacyldisaccharide 4-kinase [Haemophilus influenzae str. Rd KW20 (serotype d)]
P. gingivalis	VBIPorGin26334_0675	iron compound ABC transporter 2C ATP-binding protein	ABC transporter [Pseudomonas syringae str. B728a (pv. syringae)]
P. gingivalis	VBIPorGin26334_0697	Vitamin B12 ABC transporter 2C permease component BtuC	cobalaminFe3+-siderophores transport systems permease component [Corynebacterium glutamicum str. ATCC 13032 (Bielefeld)]
P. gingivalis	VBIPorGin26334_0698	FIG00936204 hypothetical protein	ATP-binding component of ferric enterobactin transport [Shigella flexneri str. 301 (serotype 2a)]
P. gingivalis	VBIPorGin26334_0711	Succinate-semialdehyde dehydrogenase 2C CoA-dependent	hypothetical protein [Listeria innocua str. Clip11262 (serovar 6a)]
P. gingivalis	VBIPorGin26334_0729	FKBP-type peptidyl-prolyl cis-trans isomerase FkpA precursor EC 5.2.1.8	macrophage infectivity potentiator (Mip) [Legionella pneumophila str. Philadelphia 1]
P. gingivalis	VBIPorGin26334_0731	FKBP-type peptidyl-prolyl cis-trans isomerase FklB EC 5.2.1.8	macrophage infectivity potentiator [Legionella pneumophila str. Paris]
P. gingivalis	VBIPorGin26334_0742	DNA-binding response regulator	two component transcriptional regulator winged helix family [Mycobacterium vanbaalenii str. PYR-1]
P. gingivalis	VBIPorGin26334_0765	Two-component system response regulator	putative two-component system response regulator [Pseudomonas fluorescens str. SBW25]
P. gingivalis	VBIPorGin26334_0767	Glycosyl transferase 2C group 2 family protein	glycosyl transferase family 2 [Yersinia pseudotuberculosis str. YPIII (serotype O:3)]

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P. gingivalis	VBIPorGin26334_0844	surface antigen 2C putative	hypothetical protein [Listeria monocytogenes str. EGD-e (serovar 12a)]
P. gingivalis	VBIPorGin26334_0844	surface antigen 2C putative	hypothetical protein [Listeria monocytogenes str. EGD-e (serovar 12a)]
P. gingivalis	VBIPorGin26334_0927	8-amino-7-oxononanoate synthase EC 2.3.1.47	hypothetical protein [Vibrio cholerae str. N16961 (O1 biovar eltor) chromosome II]
P. gingivalis	VBIPorGin26334_0933	Probable polybeta-D-mannuronate O-acetylase EC 2.3.1.-	membrane bound O-acyl transferase MBOAT family protein [Pseudomonas putida str. W619]
P. gingivalis	VBIPorGin26334_0939	ABC transporter ATP-binding protein	lipoprotein inner membrane ABC-transporter [Yersinia pestis str. CO92 (biovar Orientalis)]
P. gingivalis	VBIPorGin26334_0940	ABC transporter 2C ATP-binding protein 2C putative	ABC transporter ATP-bindingpermease protein [Pseudomonas syringae str. 1448A (pv. phaseolicola)]
P. gingivalis	VBIPorGin26334_0967	Phosphoribosylaminoimidazole-succinocarboxamide synthase EC 6.3.2.6	phosphoribosylaminoimidazole-succinocarboxamide synthase [Mycobacterium smegmatis str. MC2 155]
P. gingivalis	VBIPorGin26334_0993	ABC transporter 2C ATP-binding protein	daunorubicin resistance ABC transporter ATPase subunit [Mycobacterium gilvum str. PYR-GCK]
P. gingivalis	VBIPorGin26334_0999	Calcium-transporting ATPase	hypothetical protein [Salmonella enterica str. RSK2980 (subsp. arizonae serovar 62:z4 z23:--)]
P. gingivalis	VBIPorGin26334_1069	GDP-mannose 4 2C6 dehydratase EC 4.2.1.47	GDP-mannose 4 6-dehydratase [Brucella suis str. 1330 chromosome I]
P. gingivalis	VBIPorGin26334_1070	GDP-L-fucose synthetase EC 1.1.1.271	GDP-fucose synthetase [Campylobacter jejuni str. 269.97 (subsp. doylei)]
P. gingivalis	VBIPorGin26334_1073	Ferrous iron transport protein B	ferrous iron transporter B [Legionella pneumophila str. Corby]
P. gingivalis	VBIPorGin26334_1179	Transcriptional regulatory protein rprY	putative two-component response regulator [Mycobacterium leprae str. TN]
P. gingivalis	VBIPorGin26334_1182	Phosphomannomutase EC 5.4.2.8 Phosphoglucosamine mutase EC 5.4.2.10	phosphomannomutase [Pseudomonas putida str. KT2440]
P. gingivalis	VBIPorGin26334_1202	ClpB protein	probable ClpAB-type chaperone [Pseudomonas aeruginosa str. PAO1]
P. gingivalis	VBIPorGin26334_1226	bacterial sugar transferase	putative capsular polysaccharide biosynthesis glycosyltransferase [Vibrio cholerae str. O395 chromosome II]
P. gingivalis	VBIPorGin26334_1229	pigmentation and extracellular proteinase regulator	probable aminotransferase WbpE [Pseudomonas aeruginosa str. PAO1]
P. gingivalis	VBIPorGin26334_1234	UDP-glucose dehydrogenase EC 1.1.1.22	UDP-glucose 6-dehydrogenase [Bacillus thuringiensis str. Al Hakam]
P. gingivalis	VBIPorGin26334_1241	Glycosyl transferase 2C family 2	WbcM protein [Yersinia enterocolitica str. 105.5R(r) (subsp. palearctica)]
P. gingivalis	VBIPorGin26334_1263	Diaminopimelate decarboxylase EC 4.1.1.20	diaminopimelate decarboxylase LysA [Mycobacterium sp. str. JDM601]
P. gingivalis	VBIPorGin26334_1297	Ferrous iron transport protein B	ferrous iron transporter B [Legionella pneumophila str. Corby]
P. gingivalis	VBIPorGin26334_1306	ABC transporter 2C ATP-binding protein	Fe(3+) ions import ATP-binding protein fbpC [Neisseria gonorrhoeae str. NCCP11945]
P. gingivalis	VBIPorGin26334_1316	branched chain amino acid transport ATP-binding protein	iron(III) ABC transporter ATP-binding protein [Haemophilus influenzae str. Rd KW20 (serotype d)]
P. gingivalis	VBIPorGin26334_1317	branched-chain amino acid ABC transporter 2C ATP-binding protein	iron-utilization ATP-binding protein hFbpC [Haemophilus influenzae str. 86-028NP (nontypeable)]
P. gingivalis	VBIPorGin26334_1363	3-oxoacyl-acyl-carrier protein reductase EC 1.1.1.100	hypothetical protein [Streptococcus agalactiae str. NEM316 (serotype III)]
P. gingivalis	VBIPorGin26334_1392	Ornithine aminotransferase EC 2.6.1.13	2 4-diaminobutyrate 4-transaminase [Pseudomonas mendocina str. ymp]
P. gingivalis	VBIPorGin26334_1434	Heat shock protein 60 family chaperone GroEL	Hsp60 60K heat shock protein HtpB [Legionella pneumophila str. Philadelphia 1]
P. gingivalis	VBIPorGin26334_1474	Pantoate--beta-alanine ligase EC 6.3.2.1	pantoate--beta-alanine ligase [Mycobacterium gilvum str. PYR-GCK]
P. gingivalis	VBIPorGin26334_1485	Mannose-6-phosphate isomerase EC 5.3.1.8	mannose-6-phosphate isomerase [Bacillus thuringiensis str. Al Hakam]
P. gingivalis	VBIPorGin26334_1494	Hemolysins and related proteins containing CBS domains	CBStransporter associated domain protein [Clostridium perfringens str. ATCC 13124]
P. gingivalis	VBIPorGin26334_1508	Tyrosine-protein kinase Wzc EC 2.7.10.2	chain length regulator (capsular polysaccharide biosynthesis) [Vibrio fischeri str. ES114 chromosome I]
P. gingivalis	VBIPorGin26334_1517	Carbonic anhydrase EC 4.2.1.1	putative carbonic anhydrase [Salmonella typhimurium str. LT2 plasmid pSLT]
P. gingivalis	VBIPorGin26334_1563	Membrane-associated zinc metalloprotease	membrane-associated zinc metalloprotease putative [Pseudomonas fluorescens str. Pf-5]

Supplementary Table S7. Up-regulated putative virulence factors of the 'red-complex' in disease. These virulence factors were identified bibliographically or by BLAST alignment to the VFDB as described in the methods section. In red are proteins with potential protease or peptidase activities. In green are proteins probably involved in iron metabolism.

P. gingivalis	VBIPorGin26334_1589	FIG00936311 hypothetical protein	hypothetical protein [Listeria monocytogenes str. EGD-e (serovar 12a)]
P. gingivalis	VBIPorGin26334_1589	FIG00936311 hypothetical protein	hypothetical protein [Listeria monocytogenes str. EGD-e (serovar 12a)]
P. gingivalis	VBIPorGin26334_1589	FIG00936311 hypothetical protein	hypothetical protein [Listeria monocytogenes str. EGD-e (serovar 12a)]
P. gingivalis	VBIPorGin26334_1592	UDP-glucose 4-epimerase EC 5.1.3.2	UDP-glucose 4-epimerase [Bacillus cereus str. ATCC 10987]
P. gingivalis	VBIPorGin26334_1605	Glycosyltransferase	putative bactoprenol glucosyl transferase [Shigella flexneri str. 301 (serotype 2a)]
P. gingivalis	VBIPorGin26334_1628	Glycosyl transferase	putative bactoprenol glucosyl transferase [Shigella flexneri str. 301 (serotype 2a)]
P. gingivalis	VBIPorGin26334_1678	3-oxoacyl-acyl-carrier-protein synthase 2C KASII EC 2.3.1.41	3-oxoacyl-[acyl-carrier-protein] synthase 2 [Mycobacterium smegmatis str. MC2 155]
P. gingivalis	VBIPorGin26334_1696	8-amino-7-oxononanoate synthase EC 2.3.1.47	hypothetical protein [Vibrio parahaemolyticus str. RIMD 2210633 chromosome II]
P. gingivalis	VBIPorGin26334_1726	3-deoxy-manno-octulosonate cytidylyltransferase EC 2.7.7.38	3-deoxy-D-manno-octulosonate cytidylyltransferase [Haemophilus somnus str. 2336]
P. gingivalis	VBIPorGin26334_1734	GTP pyrophosphokinase EC 2.7.6.5 2C pppGpp synthetase II Guanosine-3' 2C5'-bisdiphosphate 3'-pyrophosphohydrolase EC 3.1.7.2	GTP pyrophosphokinase RelA [Mycobacterium marinum str. M]
P. gingivalis	VBIPorGin26334_1738	V-type ATP synthase subunit B EC 3.6.3.14	type III secretion system ATP synthase [Yersinia pestis str. Pestoides F]
P. gingivalis	VBIPorGin26334_1739	V-type ATP synthase subunit A EC 3.6.3.14	type III secretion system ATPase [Vibrio parahaemolyticus str. RIMD 2210633 chromosome I]
P. gingivalis	VBIPorGin26334_1887	ABC transporter 2C ATP-binding protein 2C putative	ABC transporter ATP-bindingpermease protein [Pseudomonas syringae str. 1448A (pv. phaseolicola)]
P. gingivalis	VBIPorGin26334_1888	ABC transporter ATP-binding protein	lipoprotein inner membrane ABC-transporter [Yersinia pestis str. CO92 (biovar Orientalis)]
P. gingivalis	VBIPorGin26334_1922	Phosphoglucomutase EC 5.4.2.2	probable phosphomannomutase [Haemophilus ducreyi str. 35000HP]
P. gingivalis	VBIPorGin26334_1982	Acyl-acyl-carrier-protein--UDP-N-acetylglucosamine O-acyltransferase EC 2.3.1.129	UDP-N-acetylglucosamine acyltransferase [Haemophilus ducreyi str. 35000HP]
P. gingivalis	VBIPorGin26334_1984	UDP-3-O-3-hydroxymyristoyl glucosamine N-acyltransferase EC 2.3.1.-	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase [Haemophilus influenzae str. 86-028NP (nontypeable)]
P. gingivalis	VBIPorGin26334_1998	Arabinose 5-phosphate isomerase EC 5.3.1.13	arabinose-5-phosphate isomerase [Campylobacter jejuni str. 269.97 (subsp. doylei)]
P. gingivalis	VBIPorGin26334_2018	oxidoreductase 2C short chain dehydrogenase reductase family	cylG protein [Streptococcus agalactiae str. A909 (serotype Ia)]
P. gingivalis	VBIPorGin26334_2043	Mannose-1-phosphate guanylyltransferase GDP EC 2.7.7.22	Mannose-1-phosphate guanylytransferase ManC protein [Yersinia enterocolitica str. 105.5R(r) (subsp. palearctica)]
T. forsythia	VBITanFor42681_0010	3-oxoacyl-acyl-carrier-protein synthase 2C KASI EC 2.3.1.41	beta-ketoacyl synthase [Mycobacterium sp. str. MCS]
T. forsythia	VBITanFor42681_0016	iron chelate uptake ABC transporter 2C FeCT family 2C permease protein	Iron-related transport system membrane protein [Corynebacterium diphtheriae str. NCTC 13129 (biotype gravis)]
T. forsythia	VBITanFor42681_0095	ABC transporter ATP-binding protein	alpha-hemolysin translocation ATP-binding protein HlyB [Escherichia coli str. 536 (UPEC)]
T. forsythia	VBITanFor42681_0108	Lipid A export ATP-binding permease protein MsbA	ABC transporter ATP-bindingpermease protein [Pseudomonas syringae str. DC3000 (pv. tomato)]
T. forsythia	VBITanFor42681_0109	Lipid A export ATP-binding permease protein MsbA	ABC transporter ATP-bindingpermease protein [Pseudomonas syringae str. 1448A (pv. phaseolicola)]
T. forsythia	VBITanFor42681_0157	Acyl-coenzyme A synthetases AMP-fatty acid ligases	vibriobactin-specific 2 3-dihydroxybenzoate-AMP ligase [Vibrio cholerae str. N16961 (O1 biovar eltor) chromosome I]
T. forsythia	VBITanFor42681_0239	NAD-dependent glyceraldehyde-3-phosphate dehydrogenase EC 1.2.1.12	glyceraldehyde-3-phosphate dehydrogenase [Streptococcus agalactiae str. NEM316 (serotype III)]
T. forsythia	VBITanFor42681_0261	UDP-glucose 4-epimerase EC 5.1.3.2	UDP-glucose 4-epimerase [Bacillus cereus str. ATCC 10987]
T. forsythia	VBITanFor42681_0280	Glucose-1-phosphate thymidylyltransferase EC 2.7.7.24	D-glucose-1-phosphate thymidylyltransferase [Vibrio vulnificus str. YJ016 chromosome I]
T. forsythia	VBITanFor42681_0289	Pantoate--beta-alanine ligase EC 6.3.2.1	pantoate--beta-alanine ligase [Mycobacterium abscessus str. ATCC 19977]
T. forsythia	VBITanFor42681_0384	HtrA protease chaperone protein	serine protease MucD precursor [Pseudomonas aeruginosa str. UCBPP-PA14]
T. forsythia	VBITanFor42681_0415	ABC transporter ATP-binding protein YvcR	ABC transporter related [Haemophilus somnus str. 2336]

Supplementary Table S7. Up-regulated putative virulence factors of the 'red-complex' in disease. These virulence factors were identified bibliographically or by BLAST alignment to the VFDB as described in the methods section. In red are proteins with potential protease or peptidase activities. In green are proteins probably involved in iron metabolism.

T. forsythia	VBITanFor42681_0425	glycosyltransferase 2C group 1 family protein	Mannosyltransferase [Brucella suis str. ATCC 23445 chromosome I]
T. forsythia	VBITanFor42681_0484	UDP-glucose dehydrogenase EC 1.1.1.22	UDP-glucose 6-dehydrogenase [Bacillus cereus str. ATCC 10987]
T. forsythia	VBITanFor42681_0493	polysaccharide biosynthesis protein	exopolysaccharide biosynthesis protein [Streptococcus thermophilus str. CNRZ1066 (nonpathogenic)]
T. forsythia	VBITanFor42681_0501	V-type ATP synthase subunit A EC 3.6.3.14	Secretion system apparatus ATP synthase ssaN [Yersinia enterocolitica str. 105.5R(r) (subsp. palearctica)]
T. forsythia	VBITanFor42681_0581	ATP synthase alpha chain EC 3.6.3.14	flagellar protein export ATPase FliI [Campylobacter fetus str. 82-40 (subsp. fetus)]
T. forsythia	VBITanFor42681_0588	ATP synthase beta chain EC 3.6.3.14	type III secretion system ATPase [Pseudomonas aeruginosa str. LESB58]
T. forsythia	VBITanFor42681_0597	Probable polybeta-D-mannuronate O-acetylase EC 2.3.1.-	membrane bound O-acyl transferase MBOAT family protein [Pseudomonas putida str. F1]
T. forsythia	VBITanFor42681_0624	thermolysin metallopeptidase 2C catalytic domain protein	Zinc metalloproteinase precursor [Listeria monocytogenes str. Clip81459 (serotype 4b)]
T. forsythia	VBITanFor42681_0635	Cell division transporter 2C ATP-binding protein FtsE TC 3.A.5.1.1	Fe(3+) ions import ATP-binding protein fbpC [Neisseria gonorrhoeae str. NCCP11945]
T. forsythia	VBITanFor42681_0637	Diaminopimelate decarboxylase EC 4.1.1.20	diaminopimelate decarboxylase [Mycobacterium vanbaalenii str. PYR-1]
T. forsythia	VBITanFor42681_0665	GTP pyrophosphokinase EC 2.7.6.5 Guanosine-3' 2C5'-bisdiphosphate 3'-pyrophosphohydrolase EC 3.1.7.2	GTP pyrophosphokinase RelA [Mycobacterium sp. str. JDM601]
T. forsythia	VBITanFor42681_0714	arylsulfatase	predicted PE--lipooligosaccharide phosphorylethanolamine transferase [Haemophilus influenzae str. 86-028NP (nontypeable)]
T. forsythia	VBITanFor42681_0765	ABC transporter ATP-binding protein	alpha-hemolysin translocation ATP-binding protein HlyB [Escherichia coli str. 536 (UPEC)]
T. forsythia	VBITanFor42681_0797	putative transcriptional regulatory protein RprY	two component response transcriptional regulatory protein prra [Mycobacterium intracellulare str. MOTT 64]
T. forsythia	VBITanFor42681_0824	Pleiotropic regulatory protein	probable aminotransferase WbpE [Pseudomonas aeruginosa str. PAO1]
T. forsythia	VBITanFor42681_0931	Arabinose 5-phosphate isomerase EC 5.3.1.13	arabinose-5-phosphate isomerase [Campylobacter jejuni str. 269.97 (subsp. doylei)]
T. forsythia	VBITanFor42681_0937	Glycosyl transferase 2C group 2 family protein	hypothetical protein [Mycobacterium avium str. K-10 (subsp. paratuberculosis)]
T. forsythia	VBITanFor42681_0943	UDP-N-acetylglucosamine 2-epimerase EC 5.1.3.14	UDP-N-acetylglucosamine 2-epimerase [Vibrio cholerae str. O395 chromosome II]
T. forsythia	VBITanFor42681_0955	UDP-N-acetylglucosamine 2-epimerase EC 5.1.3.14	UDP-N-acetylglucosamine 2-epimerase [Pseudomonas aeruginosa str. PA7]
T. forsythia	VBITanFor42681_0956	N-acetylneuraminate synthase EC 2.5.1.56	N-acetylneuraminic acid synthetase [Campylobacter jejuni str. NCTC 11168 (subsp. jejuni)]
T. forsythia	VBITanFor42681_1095	putative transcriptional regulatory protein afsQ1	two component response transcriptional regulatory protein prra [Mycobacterium intracellulare str. MOTT 64]
T. forsythia	VBITanFor42681_1156	probable bacteriocin lantibiotic ABC transporter 2C ATP-binding protein	hemolysin B [Escherichia coli str. Sakai (EHEC O157:H7) plasmid pO157]
T. forsythia	VBITanFor42681_1232	Acyl-acyl-carrier-protein--UDP-N-acetylglucosamine O-acyltransferase EC 2.3.1.129	UDP-N-acetylglucosamine acyltransferase [Haemophilus ducreyi str. 35000HP]
T. forsythia	VBITanFor42681_1233	N-acetylglucosamine deacetylase EC 3.5.1.- 3R-hydroxymyristoyl-acyl carrier protein dehydratase EC 4.2.1.-	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase [Haemophilus influenzae str. Rd KW20 (serotype d)]
T. forsythia	VBITanFor42681_1234	UDP-3-O-3-hydroxymyristoyl glucosamine N-acyltransferase EC 2.3.1.-	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase [Haemophilus somnus str. 129PT]
T. forsythia	VBITanFor42681_1265	putative bactoprenol glucosyl transferase-like protein	putative bactoprenol glucosyl transferase [Shigella flexneri str. 301 (serotype 2a)]
T. forsythia	VBITanFor42681_1283	ABC transporter ATP-binding protein	hemolysin secretion protein HlyB [Escherichia coli str. UTI89 (UPEC)]
T. forsythia	VBITanFor42681_1301	di-trans 2Cpoly-cis-decaprenylcistransferase	undecaprenyl diphosphate synthase [Enterococcus faecalis str. V583]
T. forsythia	VBITanFor42681_1324	GTP pyrophosphokinase EC 2.7.6.5 2C pppGpp synthetase I	RelASpoT family (p)ppGpp synthetase [Mycobacterium gilvum str. Spyr1]
T. forsythia	VBITanFor42681_1339	NAD-dependent 4-hydroxybutyrate dehydrogenase EC 1.1.1.61	hypothetical protein [Listeria innocua str. Clip11262 (serovar 6a)]
T. forsythia	VBITanFor42681_1340	Succinate-semialdehyde dehydrogenase 2C CoA-dependent	hypothetical protein [Listeria innocua str. Clip11262 (serovar 6a)]
T. forsythia	VBITanFor42681_1430	putative coproporphyrinogen dehydrogenase	coproporphyrinogen III oxidase [Haemophilus influenzae str. PittGG (nontypeable)]

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T. forsythia	VBITanFor42681_1471	ABC transporter ATP-binding protein	lipoprotein inner membrane ABC-transporter [Yersinia pestis str. Pestoides F]
T. forsythia	VBITanFor42681_1473	ABC transporter 2C ATP-binding protein	ABC transporter ATP-bindingpermease protein [Pseudomonas syringae str. 1448A (pv. phaseolicola)]
T. forsythia	VBITanFor42681_1538	Putative dipeptidase 2C pyoverdin biosynthesis	dipeptidase putative [Pseudomonas putida str. KT2440]
T. forsythia	VBITanFor42681_1541	ABC transporter ATP-binding protein	Hemolysin B [Escherichia coli str. CFT073 (UPEC)]
T. forsythia	VBITanFor42681_1576	hypothetical protein	transport protein ysiA [Clostridium perfringens str. SM101]
T. forsythia	VBITanFor42681_1635	exopolysaccharide biosynthesis polyprenyl glycosylphosphotransferase	putative capsular polysaccharide biosynthesis glycosyltransferase [Vibrio cholerae str. O395 chromosome II]
T. forsythia	VBITanFor42681_1707	Phosphomannomutase EC 5.4.2.8 Phosphoglucosamine mutase EC 5.4.2.10	phosphomannomutase [Pseudomonas putida str. KT2440]
T. forsythia	VBITanFor42681_1745	Superoxide dismutase Fe EC 1.15.1.1	[Mn] superoxide dismutase [Mycobacterium smegmatis str. MC2 155]
T. forsythia	VBITanFor42681_1751	3-deoxy-D-manno-octulosonic-acid transferase EC 2.-.-.-	3-deoxy-D-manno-octulosonic-acid transferase [Haemophilus ducreyi str. 35000HP]
T. forsythia	VBITanFor42681_1794	glycosyltransferase 2C group 2 family protein	Putative glycosyl transferase [Bordetella avium str. 197N]
T. forsythia	VBITanFor42681_1799	putative membrane protein	putative O-unit flippase [Yersinia pseudotuberculosis str. IP32953 (serotype I)]
T. forsythia	VBITanFor42681_1804	Alpha-D-GlcNAc alpha-1 2C2-L-rhamnosyltransferase EC 2.4.1.-	rhamnosyltransferase putative [Streptococcus gordonii str. Challis (substr. CH1)]
T. forsythia	VBITanFor42681_1819	Transcriptional regulatory protein rprY	response regulator mprA [Mycobacterium indicus pranii str. MTCC 9506]
T. forsythia	VBITanFor42681_1856	Ferrous iron transport protein B	ferrous iron transporter B [Legionella pneumophila str. Lens]
T. forsythia	VBITanFor42681_1876	Enolase EC 4.2.1.11	enolase [Streptococcus gordonii str. Challis (substr. CH1)]
T. forsythia	VBITanFor42681_1884	TonB-dependent receptor	iron-regulated outer membrane virulence protein TonB receptor family [Vibrio cholerae str. N16961 (O1 biovar eltor) chromosome I]
T. forsythia	VBITanFor42681_1932	dTDP-glucose 4 2C6-dehydratase EC 4.2.1.46	dTDP-glucose 4 6-dehydratase [Vibrio fischeri str. ES114 chromosome I]
T. forsythia	VBITanFor42681_1951	Phosphoglucomutase EC 5.4.2.2	probable phosphomannomutase [Haemophilus ducreyi str. 35000HP]
T. forsythia	VBITanFor42681_1961	Glycosyltransferase	putative bactoprenol glucosyl transferase [Shigella flexneri str. 301 (serotype 2a)]
T. forsythia	VBITanFor42681_1976	3-oxoacyl-acyl-carrier protein reductase EC 1.1.1.100	hypothetical protein [Streptococcus agalactiae str. NEM316 (serotype III)]
T. forsythia	VBITanFor42681_1991	Adenylate cyclase EC 4.6.1.1	Multi-sensor Hybrid Histidine Kinase [Pseudomonas fluorescens str. Pf0-1]
T. forsythia	VBITanFor42681_2037	dTDP-glucose 4 2C6-dehydratase EC 4.2.1.46	hypothetical protein [Campylobacter jejuni str. 81116 (NCTC11828)]
T. forsythia	VBITanFor42681_2078	gluconate 5-dehydrogenase	cylG protein [Streptococcus agalactiae str. A909 (serotype Ia)]
T. forsythia	VBITanFor42681_2241	peptidyl-prolyl cis-trans isomerase 2C FKBP-type	macrophage infectivity potentiator [Legionella pneumophila str. Paris]
T. forsythia	VBITanFor42681_2242	outer membrane protein MIP	macrophage infectivity potentiator [Legionella pneumophila str. Paris]
T. forsythia	VBITanFor42681_2499	gliding motility-associated protein GldE	CBStransporter associated domain protein [Clostridium perfringens str. ATCC 13124]
T. forsythia	VBITanFor42681_2530	UDP-glucose dehydrogenase EC 1.1.1.22	UDP-glucoseGDP-mannose dehydrogenase-like protein [Pseudomonas aeruginosa str. LESB58]
T. forsythia	VBITanFor42681_2531	Mannose-1-phosphate guanylyltransferase GDP EC 2.7.7.22	Mannose-1-phosphate guanylyltransferase ManC protein [Yersinia enterocolitica str. 105.5R(r) (subsp. palearctica)]
T. forsythia	VBITanFor42681_2537	Phosphoribosylaminoimidazole-succinocarboxamide synthase EC 6.3.2.6	phosphoribosylaminoimidazole-succinocarboxamide synthase [Mycobacterium sp. str. JLS]
T. forsythia	VBITanFor42681_2565	hypothetical protein	hypothetical protein [Listeria innocua str. Clip11262 (serovar 6a)]
T. forsythia	VBITanFor42681_2619	Protein export cytoplasm protein SecA ATPase RNA helicase TC 3.A.5.1.1	preprotein translocase subunit SecA [Mycobacterium abscessus str. ATCC 19977]
T. forsythia	VBITanFor42681_2619	Protein export cytoplasm protein SecA ATPase RNA helicase TC 3.A.5.1.1	preprotein translocase subunit SecA [Mycobacterium abscessus str. ATCC 19977]
T. forsythia	VBITanFor42681_2624	Glycosyltransferase	Sugar transferase involved in lipopolysaccharide synthesis [Vibrio vulnificus str. CMCP6 chromosome II]
T. forsythia	VBITanFor42681_2661	GDP-mannose 4 2C6 dehydratase EC 4.2.1.47	GDP-mannose 4 6-dehydratase [Brucella suis str. 1330 chromosome I]

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T. forsythia	VBITanFor42681_2676	ABC transporter 2C ATP-binding protein	lipid A export ATP-binding protein MsbA [Haemophilus influenzae str. 86-028NP (nontypeable)]
T. forsythia	VBITanFor42681_2888	Malonyl CoA-acyl carrier protein transacylase EC 2.3.1.39	polyketide synthase [Mycobacterium leprae str. TN]
T. denticola	VBITreDen150577_0077	sensor histidine kinase response regulator	two component response transcriptional regulatory protein MprA [Mycobacterium intracellulare str. MOTT36Y]
T. denticola	VBITreDen150577_0191	Ferric iron ABC transporter 2C ATP-binding protein	ABC transporter related [Haemophilus somnus str. 2336]
T. denticola	VBITreDen150577_0210	ABC transporter 2C ATP-binding permease protein	lipid A export ATP-binding protein MsbA [Haemophilus influenzae str. 86-028NP (nontypeable)]
T. denticola	VBITreDen150577_0211	ABC transporter 2C ATP-binding permease protein	fused lipid transporter subunits of ABC superfamily: membrane componentATP-binding component [Haemophilus influenzae str. PittEE (nontypeable)]
T. denticola	VBITreDen150577_0230	methyl-accepting chemotaxis protein	accessory colonization factor AcfB [Vibrio cholerae str. N16961 (O1 biovar eltor) chromosome I]
T. denticola	VBITreDen150577_0257	hypothetical protein	transporter HlyCCorC family [Clostridium botulinum str. Langeland (serotype F)]
T. denticola	VBITreDen150577_0258	hypothetical protein	transporter HlyCCorC family [Clostridium botulinum str. Okra (serotype B1)]
T. denticola	VBITreDen150577_0263	ABC transporter 2C ATP-binding protein	putative ABC transporter protein [Escherichia coli str. UTI89 (UPEC)]
T. denticola	VBITreDen150577_0296	Transport ATP-binding protein CydC	ABC transporter ATP-bindingpermease protein [Pseudomonas syringae str. 1448A (pv. phaseolicola)]
T. denticola	VBITreDen150577_0320	transporter	ABC transporter ATP-bindingpermease protein [Pseudomonas syringae str. DC3000 (pv. tomato)]
T. denticola	VBITreDen150577_0322	Lipid A export ATP-binding permease protein MsbA	ABC transporter ATP-bindingpermease protein [Pseudomonas syringae str. 1448A (pv. phaseolicola)]
T. denticola	VBITreDen150577_0335	ABC transporter 2C ATP-binding protein	ABC transporter ATP-bindingpermease protein [Pseudomonas syringae str. DC3000 (pv. tomato)]
T. denticola	VBITreDen150577_0336	ABC transporter ATP-binding protein	ABC transporter ATP-bindingpermease protein [Pseudomonas syringae str. DC3000 (pv. tomato)]
T. denticola	VBITreDen150577_0345	Transport ATP-binding protein CydC	ABC transporter ATP-binding protein MsbA [Haemophilus ducreyi str. 35000HP]
T. denticola	VBITreDen150577_0397	Putrescine transport ATP-binding protein PotA TC 3.A.1.11.1	iron(III) ABC transporter ATP-binding protein [Haemophilus influenzae str. PittEE (nontypeable)]
T. denticola	VBITreDen150577_0493	UDP-N-acetylenolpyruvoylglucosamine reductase EC 1.1.1.158	MurB family protein [Enterococcus faecalis str. V583]
T. denticola	VBITreDen150577_0511	RNA polymerase sigma factor RpoD	stationary phase specific sigma factor RpoS [Legionella pneumophila str. Philadelphia 1]
T. denticola	VBITreDen150577_0527	Flagellar biosynthesis protein FlhB	flagellar biosynthetic protein FlhB [Campylobacter jejuni str. RM1221]
T. denticola	VBITreDen150577_0540	Acyl-coenzyme A synthetases AMP-fatty acid ligases	pyochelin biosynthesis protein PchD [Pseudomonas aeruginosa str. PA7]
T. denticola	VBITreDen150577_0541	3-oxoacyl-acyl-carrier-protein synthase 2C KASII EC 2.3.1.41	3-oxoacyl-(acyl carrier protein) synthase II [Mycobacterium sp. str. JDM601]
T. denticola	VBITreDen150577_0551	hypothetical protein	hypothetical protein [Mycobacterium avium str. K-10 (subsp. paratuberculosis)]
T. denticola	VBITreDen150577_0586	methyl-accepting chemotaxis protein	accessory colonization factor AcfB [Vibrio cholerae str. O395 chromosome II]
T. denticola	VBITreDen150577_0587	hypothetical protein	hemolysin B [Escherichia coli str. Sakai (EHEC O157:H7) plasmid pO157]
T. denticola	VBITreDen150577_0588	ABC transporter 2C ATP-binding permease protein	fused lipid transporter subunits of ABC superfamily: membrane componentATP-binding component [Haemophilus influenzae str. PittEE (nontypeable)]
T. denticola	VBITreDen150577_0597	Flagellar hook protein FlgE	flagellar hook protein [Pseudomonas aeruginosa str. PA7]
T. denticola	VBITreDen150577_0599	Flagellar motor rotation protein MotA	flagellar motor protein [Vibrio parahaemolyticus str. RIMD 2210633 chromosome I]
T. denticola	VBITreDen150577_0600	Flagellar motor rotation protein MotB	OmpAMotB domain protein [Pseudomonas mendocina str. ymp]
T. denticola	VBITreDen150577_0602	Flagellar motor switch protein FliM	hypothetical protein [Helicobacter acinonychis str. Sheeba]
T. denticola	VBITreDen150577_0605	Flagellar biosynthesis protein FliP	flagellar biosynthetic protein FliP [Campylobacter fetus str. 82-40 (subsp. fetus)]
T. denticola	VBITreDen150577_0670	Flagellar synthesis regulator FleN	ParA family protein [Vibrio cholerae str. O395 chromosome II]

Supplementary Table S7. Up-regulated putative virulence factors of the 'red-complex' in disease. These virulence factors were identified bibliographically or by BLAST alignment to the VFDB as described in the methods section. In red are proteins with potential protease or peptidase activities. In green are proteins probably involved in iron metabolism.

T. denticola	VBITreDen150577_0672	RNA polymerase sigma factor SigB	RNA polymerase sigma factor for flagellar operon [Yersinia enterocolitica str. 8081 (biotype 1B)]
T. denticola	VBITreDen150577_0685	Undecaprenyl-phosphate N-acetylglucosaminyl 1-phosphate transferase EC 2.7.8.-	putative glycosyl transferase N-acetylglucosaminyltransferase) RgpG [Streptococcus mutans str. UA159]
T. denticola	VBITreDen150577_0708	ABC transporter 2C ATP-binding protein	ABC transporter related [Haemophilus somnus str. 2336]
T. denticola	VBITreDen150577_0711	Glycerol-3-phosphate dehydrogenase EC 1.1.5.3	hypothetical protein [Shigella flexneri str. 2457T (serotype 2a)]
T. denticola	VBITreDen150577_0726	Transport ATP-binding protein CydD	ABC transporter ATP-bindingpermease protein [Pseudomonas syringae str. DC3000 (pv. tomato)]
T. denticola	VBITreDen150577_0728	Transport ATP-binding protein CydC	ABC transporter ATP-bindingpermease protein [Pseudomonas syringae str. 1448A (pv. phaseolicola)]
T. denticola	VBITreDen150577_0796	hypothetical protein	fused lipid transporter subunits of ABC superfamily: membrane componentATP-binding component [Haemophilus influenzae str. PittEE (nontypeable)]
T. denticola	VBITreDen150577_0797	ABC transporter ATP-binding protein	putative ATP binding cassette (ABC) transporter [Escherichia coli str. 536 (UPEC)]
T. denticola	VBITreDen150577_0840	hypothetical protein	fused lipid transporter subunits of ABC superfamily: membrane componentATP-binding component [Haemophilus influenzae str. PittEE (nontypeable)]
T. denticola	VBITreDen150577_0841	Lipid A export ATP-binding permease protein MsbA	fused lipid transporter subunits of ABC superfamily: membrane componentATP-binding component [Haemophilus influenzae str. PittEE (nontypeable)]
T. denticola	VBITreDen150577_0934	Oligopeptide transport ATP-binding protein OppF TC 3.A.1.5.1	oligopeptide ABC transporter permease component [Mycoplasma mycoides str. PG1]
T. denticola	VBITreDen150577_0934	Oligopeptide transport ATP-binding protein OppF TC 3.A.1.5.1	oligopeptide ABC transporter permease component [Mycoplasma mycoides str. PG1]
T. denticola	VBITreDen150577_0999	Flagellar hook-associated protein FlgK	flagellar hook-associated protein FlgK [Campylobacter fetus str. 82-40 (subsp. fetus)]
T. denticola	VBITreDen150577_1008	Undecaprenyl pyrophosphate synthetase EC 2.5.1.31	undecaprenyl diphosphate synthase [Enterococcus faecalis str. V583]
T. denticola	VBITreDen150577_1011	membrane-associated zinc metalloprotease	putative membrane-associated zinc metalloprotease [Pseudomonas aeruginosa str. UCBPP-PA14]
T. denticola	VBITreDen150577_1025	ClpB protein	type VI secretion ATPase ClpV1 family [Pseudomonas putida str. GB-1]
T. denticola	VBITreDen150577_1036	COG1272 Predicted membrane protein hemolysin III homolog	hemolysin III [Clostridium botulinum str. Okra (serotype B1)]
T. denticola	VBITreDen150577_1042	sigma-54 dependent transcriptional regulator 2C putative	flagellar regulator FleQ [Pseudomonas syringae str. 1448A (pv. phaseolicola)]
T. denticola	VBITreDen150577_1050	Outer membrane stress sensor protease DegS	alginate biosynthesis negative regulator serine protease AlgY [Pseudomonas putida str. KT2440]
T. denticola	VBITreDen150577_1065	FKBP-type peptidyl-prolyl cis-trans isomerase FkpA precursor EC 5.2.1.8	macrophage infectivity potentiator [Legionella pneumophila str. Paris]
T. denticola	VBITreDen150577_1084	ABC transporter 2C ATP-binding permease protein	lipid A export ATP-bindingpermease protein [Haemophilus somnus str. 129PT]
T. denticola	VBITreDen150577_1143	Zinc ABC transporter 2C periplasmic-binding protein ZnuA	putative laminin adhesion [Streptococcus pyogenes str. SSI-1 (serotype M3)]
T. denticola	VBITreDen150577_1176	2-amino-3-ketobutyrate coenzyme A ligase EC 2.3.1.29	aminotransferase class II [Vibrio cholerae str. O395 chromosome I]
T. denticola	VBITreDen150577_1244	ATP-dependent Clp protease ATP-binding subunit ClpA	clpB protein [Vibrio cholerae str. O395 chromosome I]
T. denticola	VBITreDen150577_1285	sigma-54 dependent transcriptional regulator	putative two-component system response regulator [Pseudomonas fluorescens str. SBW25]
T. denticola	VBITreDen150577_1315	Oligopeptide ABC transporter 2C periplasmic oligopeptide-binding protein OppA TC 3.A.1.5.1	oligopeptide ABC transporter oligopeptide-binding protein [Listeria monocytogenes str. F2365 (serovar 4b)]
T. denticola	VBITreDen150577_1357	Transport ATP-binding protein CydC	ABC transporter ATP-bindingpermease protein [Pseudomonas syringae str. DC3000 (pv. tomato)]
T. denticola	VBITreDen150577_1359	Transport ATP-binding protein CydD	lipoprotein inner membrane ABC-transporter [Yersinia pestis str. CO92 (biovar Orientalis)]
T. denticola	VBITreDen150577_1384	Flagellar basal-body rod protein FlgC	flagellar basal body rod protein FlgC [Helicobacter pylori str. P12]
T. denticola	VBITreDen150577_1386	Flagellar M-ring protein FliF	flagellar M-ring protein FliF [Campylobacter jejuni str. 269.97 (subsp. doylei)]
T. denticola	VBITreDen150577_1387	Flagellar motor switch protein FliG	flagellar motor protein [Pseudomonas fluorescens str. Pf0-1]
T. denticola	VBITreDen150577_1389	Flagellum-specific ATP synthase FliI	type III secretion system ATPase [Bordetella pertussis str. Tohama I]

Supplementary Table S7. Up-regulated putative virulence factors of the 'red-complex' in disease. These virulence factors were identified bibliographically or by BLAST alignment to the VFDB as described in the methods section. In red are proteins with potential protease or peptidase activities. In green are proteins probably involved in iron metabolism.

T. denticola	VBITreDen150577_1396	Manganese ABC transporter 2C ATP-binding protein SitB	Iron transport protein ATP-binding component [Shigella flexneri str. 8401 (serotype 5b)]
T. denticola	VBITreDen150577_1411	Magnesium and cobalt efflux protein CorC	transporter HlyCCorC family [Clostridium botulinum str. Okra (serotype B1)]
T. denticola	VBITreDen150577_1428	Cholinephosphate cytidylyltransferase EC 2.7.7.15 Choline kinase EC 2.7.1.32	lic-1 operon protein [Haemophilus influenzae str. PittEE (nontypeable)]
T. denticola	VBITreDen150577_1439	Oligopeptide transport ATP-binding protein OppD TC 3.A.1.5.1	ABC transporter related [Haemophilus somnus str. 2336]
T. denticola	VBITreDen150577_1514	FIG01187002 hypothetical protein	protease Do [Pseudomonas putida str. GB-1]
T. denticola	VBITreDen150577_1518	RNA polymerase sigma factor RpoD	sigma factor MysA [Mycobacterium smegmatis str. MC2 155]
T. denticola	VBITreDen150577_1587	Phosphoenolpyruvate phosphomutase EC 5.4.2.9	hypothetical protein [Campylobacter jejuni str. 81116 (NCTC11828)]
T. denticola	VBITreDen150577_1588	Phosphonopyruvate decarboxylase EC 4.1.1.82	hypothetical protein [Campylobacter jejuni str. 81116 (NCTC11828)]
T. denticola	VBITreDen150577_1591	ABC transporter 2C ATP-binding protein	polysaccharide ABC exporter ATP-binding protein [Streptococcus thermophilus str. LMG 18311 (nonpathogenic)]
T. denticola	VBITreDen150577_1604	UDP-glucose dehydrogenase EC 1.1.1.22	UDP-glucose 6-dehydrogenase putative [Streptococcus pneumoniae str. D39 (serotype 2)]
T. denticola	VBITreDen150577_1627	dTDP-glucose 4 2C6-dehydratase EC 4.2.1.46	dTDP-glucose 4 6-dehydratase [Vibrio fischeri str. ES114 chromosome I]
T. denticola	VBITreDen150577_1665	Flagellin protein FlaA	flagellin FliC [Pseudomonas fluorescens str. Pf-5]
T. denticola	VBITreDen150577_1667	Flagellin protein FlaA	flagellin FliC [Pseudomonas fluorescens str. Pf-5]
T. denticola	VBITreDen150577_1678	NAD-dependent glyceraldehyde-3-phosphate dehydrogenase EC 1.2.1.12	glyceraldehyde-3-phosphate dehydrogenase [Streptococcus pneumoniae str. CGSP14 (serotype 14)]
T. denticola	VBITreDen150577_1684	Chemotaxis regulator - transmits chemoreceptor signals to flagelllar motor components CheY	Chemotaxis response regulator CheY [Listeria welshimeri str. SLCC5334 (serovar 6b)]
T. denticola	VBITreDen150577_1707	ABC transporter 2C ATP-binding protein 2C putative	iron-uptake permease ATP-binding protein [Neisseria meningitidis str. Z2491 (serogroup A)]
T. denticola	VBITreDen150577_1735	Lipoate-protein ligase A	hypothetical protein [Listeria monocytogenes str. EGD-e (serovar 12a)]
T. denticola	VBITreDen150577_1861	Cell division trigger factor EC 5.2.1.8	trigger factor [Streptococcus agalactiae str. A909 (serotype Ia)]
T. denticola	VBITreDen150577_1872	V-type ATP synthase subunit B EC 3.6.3.14	type III secretion system ATPase [Vibrio parahaemolyticus str. RIMD 2210633 chromosome I]
T. denticola	VBITreDen150577_1873	V-type ATP synthase subunit A EC 3.6.3.14	ATP synthase (predicted TTSS protein) [Chlamydia trachomatis str. 434Bu (serovar L2)]
T. denticola	VBITreDen150577_1879	ABC transporter 2C ATP-binding protein	daunorubicin resistance ABC transporter ATPase subunit [Mycobacterium vanbaalenii str. PYR-1]
T. denticola	VBITreDen150577_1945	UDP-glucose 4-epimerase EC 5.1.3.2	UDP-glucose 4-epimerase [Bacillus cereus str. ATCC 10987]
T. denticola	VBITreDen150577_2016	ABC transporter ATP-binding protein	iron(III) ABC transporter ATP-binding protein [Haemophilus influenzae str. Rd KW20 (serotype d)]
T. denticola	VBITreDen150577_2070	Protein export cytoplasm protein SecA ATPase RNA helicase TC 3.A.5.1.1	SecA DEAD domain protein [Mycobacterium vanbaalenii str. PYR-1]
T. denticola	VBITreDen150577_2109	ABC transporter 2C ATP-binding protein	daunorubicin-DIM-transport ATP-binding protein ABC transporter DrrA [Mycobacterium marinum str. M]
T. denticola	VBITreDen150577_2129	Response regulator of zinc sigma-54-dependent two-component system	putative two-component system response regulator [Pseudomonas fluorescens str. SBW25]
T. denticola	VBITreDen150577_2155	ABC-type multidrug transport system 2C ATPase and permease components	ABC transporter ATP-binding protein MsbA [Haemophilus ducreyi str. 35000HP]
T. denticola	VBITreDen150577_2177	internalin-related protein	hypothetical protein [Listeria monocytogenes str. EGD-e (serovar 12a)]
T. denticola	VBITreDen150577_2177	internalin-related protein	hypothetical protein [Listeria monocytogenes str. EGD-e (serovar 12a)]
T. denticola	VBITreDen150577_2177	internalin-related protein	hypothetical protein [Listeria monocytogenes str. EGD-e (serovar 12a)]
T. denticola	VBITreDen150577_2177	internalin-related protein	hypothetical protein [Listeria monocytogenes str. EGD-e (serovar 12a)]
T. denticola	VBITreDen150577_2180	3-oxoacyl-acyl-carrier protein reductase EC 1.1.1.100	cylG protein [Streptococcus agalactiae str. A909 (serotype Ia)]
T. denticola	VBITreDen150577_2223	Chemotaxis protein methyltransferase CheR EC 2.1.1.80	chemotaxis methyltransferase CheR [Vibrio parahaemolyticus str. RIMD 2210633 chromosome I]
T. denticola	VBITreDen150577_2224	Chemotaxis response regulator protein-glutamate methylesterase CheB EC	protein-glutamate methylesterase CheB [Vibrio cholerae str. O395 chromosome II]

Supplementary Table S7. Up-regulated putative virulence factors of the 'red-complex' in disease. These virulence factors were identified bibliographically or by BLAST alignment to the VFDB as described in the methods section. In red are proteins with potential protease or peptidase activities. In green are proteins probably involved in iron metabolism.

		3.1.1.61	
T. denticola	VBITreDen150577_2264	Phosphoribosylaminoimidazole-succinocarboxamide synthase EC 6.3.2.6	phosphoribosylaminoimidazolesuccinocarboxamide synthase [Mycobacterium gilvum str. Spyr1]
T. denticola	VBITreDen150577_2291	capsular polysaccharide biosynthesis protein	Extracellular polysaccharide biosynthesis [Streptococcus gordonii str. Challis (substr. CH1)]
T. denticola	VBITreDen150577_2298	UDP-4-amino-4-deoxy-L-arabinose--oxoglutarate aminotransferase EC 2.6.1.-	lipopolysaccharide biosynthesis protein [Bordetella avium str. 197N]
T. denticola	VBITreDen150577_2319	Vitamin B12 ABC transporter 2C permease component BtuC	putative permease of iron compound ABC transport system [Escherichia coli str. O1 (APEC)]
T. denticola	VBITreDen150577_2326	Translation elongation factor Tu	elongation factor Tu [Mycoplasma penetrans str. HF-2]
T. denticola	VBITreDen150577_2380	ABC transporter 2C ATP-binding permease protein	ABC transporter ATP-bindingpermease protein [Pseudomonas syringae str. DC3000 (pv. tomato)]
T. denticola	VBITreDen150577_2381	ABC transporter 2C ATP-binding permease protein	ABC transporter ATP-bindingpermease protein [Pseudomonas syringae str. DC3000 (pv. tomato)]
T. denticola	VBITreDen150577_2462	ABC transporter ATP-binding protein	ABC transporter ATP-bindingpermease protein [Pseudomonas syringae str. 1448A (pv. phaseolicola)]
T. denticola	VBITreDen150577_2477	ABC transporter 2C ATP-binding permease protein	lipoprotein inner membrane ABC-transporter [Yersinia pestis str. CO92 (biovar Orientalis)]
T. denticola	VBITreDen150577_2481	ABC transporter 2C ATP-binding permease protein	lipid A export ATP-bindingpermease protein [Haemophilus somnus str. 129PT]
T. denticola	VBITreDen150577_2482	ABC transporter 2C ATP-binding permease protein	ABC transporter ATP-binding protein MsbA [Haemophilus ducreyi str. 35000HP]
T. denticola	VBITreDen150577_2483	ABC transporter ATP-binding protein	ABC transporter ATP-bindingpermease protein [Pseudomonas syringae str. 1448A (pv. phaseolicola)]
T. denticola	VBITreDen150577_2489	Ornithine carbamoyltransferase EC 2.1.3.3	phaseolotoxin-insensitive ornithine carbamoyltransferase [Pseudomonas syringae str. 1448A (pv. phaseolicola)]
T. denticola	VBITreDen150577_2496	RNA polymerase sigma factor RpoD	sigma factor MysA [Mycobacterium smegmatis str. MC2 155]
T. denticola	VBITreDen150577_2507	Enolase EC 4.2.1.11	phosphopyruvate hydratase [Streptococcus pneumoniae str. TIGR4 (serotype 4)]
T. denticola	VBITreDen150577_2549	Oligopeptide transport ATP-binding protein OppF TC 3.A.1.5.1	oligopeptide ABC transporter permease component [Mycoplasma mycoides str. PG1]
T. denticola	VBITreDen150577_2564	Flagellin protein FlaA	flagellin FliC [Pseudomonas fluorescens str. Pf-5]
T. denticola	VBITreDen150577_2566	Flagellar basal-body rod protein FlgF	flagellar basal body rod protein FlgG [Helicobacter pylori str. Shi470]
T. denticola	VBITreDen150577_2567	Flagellar basal-body rod protein FlgG	flagellar distal rod protein FlgG [Helicobacter hepaticus str. ATCC 51449]
T. denticola	VBITreDen150577_2621	ABC transporter 2C ATP-binding permease protein	ABC transporter ATP-binding protein MsbA [Haemophilus ducreyi str. 35000HP]
T. denticola	VBITreDen150577_2626	Oligopeptide transport ATP-binding protein OppF TC 3.A.1.5.1	oligopeptide ABC transporter permease component [Mycoplasma mycoides str. PG1]
T. denticola	VBITreDen150577_2627	Oligopeptide transport ATP-binding protein OppD TC 3.A.1.5.1	oligopeptide ABC transporter permease component [Mycoplasma mycoides str. PG1]
T. denticola	VBITreDen150577_2635	Dipeptide transport ATP-binding protein DppF TC 3.A.1.5.2	oligopeptide ABC transporter permease component [Mycoplasma mycoides str. PG1]
T. denticola	VBITreDen150577_2662	hypothetical protein	ABC transporter related [Haemophilus somnus str. 2336]
T. denticola	VBITreDen150577_2665	Lipid A export ATP-binding permease protein MsbA	lipid A ABC exporter fused ATPase and inner membrane subunits MsbA [Haemophilus somnus str. 2336]
T. denticola	VBITreDen150577_2699	Heat shock protein 60 family chaperone GroEL	chaperonin GroEL [Clostridium perfringens str. 13]
T. denticola	VBITreDen150577_2701	Hypothetical radical SAM family enzyme 2C NOT coproporphyrinogen III oxidase 2C oxygen-independent	putative oxygen independent coproporphyrinogen III oxidase [Escherichia coli str. 536 (UPEC)]
T. denticola	VBITreDen150577_2703	iron compound ABC transporter	ferric enterobactin transport ATP-binding protein FepC [Mycobacterium smegmatis str. MC2 155]
T. denticola	VBITreDen150577_2704	Ferrichrome transport system permease protein FhuB TC 3.A.1.14.3	putative permease of iron compound ABC transport system [Shigella dysenteriae str. 197 (serotype 1)]
T. denticola	VBITreDen445_0030	ABC transporter 2C ATP-binding protein	ABC transporter related [Yersinia pseudotuberculosis str. PB1+ (serotype IB)]
T. denticola	VBITreDen445_0035	DNA-binding response regulator	DNA-binding response regulator LytTr family [Clostridium perfringens str. ATCC 13124]
T. denticola	VBITreDen445_0040	3-oxoacyl-acyl-carrier-protein synthase 2C KASII EC 2.3.1.41	3-oxoacyl-(acyl carrier protein) synthase II [Mycobacterium sp. str. JDM601]
T. denticola	VBITreDen445_0042	Acyl-coenzyme A synthetases AMP-fatty acid ligases	pyochelin biosynthesis protein PchD [Pseudomonas aeruginosa str. PA7]

Supplementary Table S7. Up-regulated putative virulence factors of the 'red-complex' in disease. These virulence factors were identified bibliographically or by BLAST alignment to the VFDB as described in the methods section. In red are proteins with potential protease or peptidase activities. In green are proteins probably involved in iron metabolism.

T. denticola	VBITreDen445_0056	Flagellar biosynthesis protein FlhB	flagellar biosynthetic protein FlhB [Campylobacter jejuni str. RM1221]
T. denticola	VBITreDen445_0057	Flagellar biosynthesis protein FlhA	flagellar biosynthesis protein [Bordetella avium str. 197N]
T. denticola	VBITreDen445_0239	Lipid A export ATP-binding permease protein MsbA	ABC transporter ATP-bindingpermease protein [Pseudomonas syringae str. 1448A (pv. phaseolicola)]
T. denticola	VBITreDen445_0240	transporter	ABC transporter ATP-bindingpermease protein [Pseudomonas syringae str. DC3000 (pv. tomato)]
T. denticola	VBITreDen445_0264	Transport ATP-binding protein CydC	ABC transporter ATP-bindingpermease protein [Pseudomonas syringae str. 1448A (pv. phaseolicola)]
T. denticola	VBITreDen445_0266	ABC-type multidrug transport system 2C ATPase and permease components	ABC transporter ATP-bindingpermease protein [Pseudomonas syringae str. DC3000 (pv. tomato)]
T. denticola	VBITreDen445_0304	ABC transporter 2C ATP-binding protein	putative ABC transporter protein [Escherichia coli str. UTI89 (UPEC)]
T. denticola	VBITreDen445_0309	hypothetical protein	transporter HlyCCorC family [Clostridium botulinum str. Okra (serotype B1)]
T. denticola	VBITreDen445_0310	hypothetical protein	transporter HlyCCorC family [Clostridium botulinum str. Langeland (serotype F)]
T. denticola	VBITreDen445_0336	methyl-accepting chemotaxis protein	accessory colonization factor AcfB [Vibrio cholerae str. O395 chromosome II]
T. denticola	VBITreDen445_0348	ABC transporter 2C ATP-binding permease protein	fused lipid transporter subunits of ABC superfamily: membrane componentATP-binding component [Haemophilus influenzae str. PittEE (nontypeable)]
T. denticola	VBITreDen445_0349	ABC transporter 2C ATP-binding permease protein	lipid A export ATP-binding protein MsbA [Haemophilus influenzae str. 86-028NP (nontypeable)]
T. denticola	VBITreDen445_0573	internalin-related protein	hypothetical protein [Listeria monocytogenes str. EGD-e (serovar 12a)]
T. denticola	VBITreDen445_0573	internalin-related protein	hypothetical protein [Listeria monocytogenes str. EGD-e (serovar 12a)]
T. denticola	VBITreDen445_0573	internalin-related protein	hypothetical protein [Listeria monocytogenes str. EGD-e (serovar 12a)]
T. denticola	VBITreDen445_0573	internalin-related protein	hypothetical protein [Listeria monocytogenes str. EGD-e (serovar 12a)]
T. denticola	VBITreDen445_0573	internalin-related protein	hypothetical protein [Listeria monocytogenes str. EGD-e (serovar 12a)]
T. denticola	VBITreDen445_0578	3-oxoacyl-acyl-carrier protein reductase EC 1.1.1.100	cylG protein [Streptococcus agalactiae str. A909 (serotype Ia)]
T. denticola	VBITreDen445_0603	ABC transporter 2C ATP-binding protein	iron-enterobactin transporter ATP-binding protein [Shigella boydii str. CDC 3083-94 (serotype 18)]
T. denticola	VBITreDen445_0626	Chemotaxis protein methyltransferase CheR EC 2.1.1.80	chemotaxis methyltransferase CheR [Vibrio parahaemolyticus str. RIMD 2210633 chromosome I]
T. denticola	VBITreDen445_0627	Chemotaxis response regulator protein-glutamate methylesterase CheB EC 3.1.1.61	protein-glutamate methylesterase CheB [Vibrio cholerae str. O395 chromosome II]
T. denticola	VBITreDen445_0673	ABC-type multidrug transport system 2C ATPase component	daunorubicin-DIM-transport ATP-binding protein ABC transporter DrrA [Mycobacterium marinum str. M]
T. denticola	VBITreDen445_0691	capsular polysaccharide biosynthesis protein	Extracellular polysaccharide biosynthesis [Streptococcus gordonii str. Challis (substr. CH1)]
T. denticola	VBITreDen445_0701	UDP-4-amino-4-deoxy-L-arabinose--oxoglutarate aminotransferase EC 2.6.1.-	lipopolysaccharide biosynthesis protein [Bordetella avium str. 197N]
T. denticola	VBITreDen445_0722	Vitamin B12 ABC transporter 2C permease component BtuC	putative permease of iron compound ABC transport system [Shigella dysenteriae str. 197 (serotype 1)]
T. denticola	VBITreDen445_0731	Vitamin B12 ABC transporter 2C ATPase component BtuD	ATP-binding component of ferric enterobactin transport [Shigella sonnei str. 046]
T. denticola	VBITreDen445_0732	Vitamin B12 ABC transporter 2C permease component BtuC	putative permease of iron compound ABC transport system [Escherichia coli str. O1 (APEC)]
T. denticola	VBITreDen445_0790	ABC transporter 2C ATP-binding permease protein	ABC transporter ATP-bindingpermease protein [Pseudomonas syringae str. DC3000 (pv. tomato)]
T. denticola	VBITreDen445_0791	ABC transporter 2C ATP-binding permease protein	ABC transporter ATP-bindingpermease protein [Pseudomonas syringae str. DC3000 (pv. tomato)]
T. denticola	VBITreDen445_0867	ABC transporter 2C ATP-binding permease protein	ABC transporter ATP-bindingpermease protein [Pseudomonas syringae str. DC3000 (pv. tomato)]
T. denticola	VBITreDen445_0868	ABC transporter ATP-binding protein	ABC transporter ATP-bindingpermease protein [Pseudomonas syringae str. 1448A (pv. phaseolicola)]
T. denticola	VBITreDen445_0879	ABC transporter 2C ATP-binding permease protein	lipoprotein inner membrane ABC-transporter [Yersinia pestis str. CO92 (biovar Orientalis)]

Supplementary Table S7. Up-regulated putative virulence factors of the 'red-complex' in disease. These virulence factors were identified bibliographically or by BLAST alignment to the VFDB as described in the methods section. In red are proteins with potential protease or peptidase activities. In green are proteins probably involved in iron metabolism.

T. denticola	VBITreDen445_0886	ABC transporter 2C ATP-binding permease protein	ABC transporter related [Yersinia pseudotuberculosis str. PB1+ (serotype IB)]
T. denticola	VBITreDen445_0889	ABC transporter 2C ATP-binding permease protein	lipid A export ATP-bindingpermease protein [Haemophilus somnus str. 129PT]
T. denticola	VBITreDen445_0890	ABC transporter 2C ATP-binding permease protein	ABC transporter ATP-binding protein MsbA [Haemophilus ducreyi str. 35000HP]
T. denticola	VBITreDen445_0891	ABC transporter ATP-binding protein	ABC transporter ATP-bindingpermease protein [Pseudomonas syringae str. 1448A (pv. phaseolicola)]
T. denticola	VBITreDen445_0892	ABC transporter ATP-binding protein	lipoprotein inner membrane ABC-transporter [Yersinia pestis str. CO92 (biovar Orientalis)]
T. denticola	VBITreDen445_0897	Ornithine carbamoyltransferase EC 2.1.3.3	phaseolotoxin-insensitive ornithine carbamoyltransferase [Pseudomonas syringae str. 1448A (pv. phaseolicola)]
T. denticola	VBITreDen445_0903	RNA polymerase sigma factor RpoD	sigma factor MysA [Mycobacterium smegmatis str. MC2 155]
T. denticola	VBITreDen445_0948	Oligopeptide transport ATP-binding protein OppD TC 3.A.1.5.1	oligopeptide ABC transporter permease component [Mycoplasma mycoides str. PG1]
T. denticola	VBITreDen445_0964	Flagellin protein FlaA	flagellin FliC [Pseudomonas fluorescens str. Pf-5]
T. denticola	VBITreDen445_0967	Flagellar basal-body rod protein FlgG	flagellar distal rod protein FlgG [Helicobacter hepaticus str. ATCC 51449]
T. denticola	VBITreDen445_1022	ABC transporter 2C ATP-binding permease protein	ABC transporter ATP-binding protein MsbA [Haemophilus ducreyi str. 35000HP]
T. denticola	VBITreDen445_1027	Oligopeptide transport ATP-binding protein OppF TC 3.A.1.5.1	oligopeptide ABC transporter permease component [Mycoplasma mycoides str. PG1]
T. denticola	VBITreDen445_1028	Oligopeptide transport ATP-binding protein OppD TC 3.A.1.5.1	oligopeptide ABC transporter permease component [Mycoplasma mycoides str. PG1]
T. denticola	VBITreDen445_1036	Dipeptide transport ATP-binding protein DppF TC 3.A.1.5.2	oligopeptide ABC transporter permease component [Mycoplasma mycoides str. PG1]
T. denticola	VBITreDen445_1133	Heat shock protein 60 family chaperone GroEL	chaperonin GroEL [Clostridium perfringens str. 13]
T. denticola	VBITreDen445_1134	Hypothetical radical SAM family enzyme 2C NOT coproporphyrinogen III oxidase 2C oxygen-independent	putative oxygen independent coproporphyrinogen III oxidase [Escherichia coli str. 536 (UPEC)]
T. denticola	VBITreDen445_1137	Ferrichrome transport system permease protein FhuB TC 3.A.1.14.3	putative permease of iron compound ABC transport system [Shigella dysenteriae str. 197 (serotype 1)]
T. denticola	VBITreDen445_1168	Flagellar basal-body rod protein FlgC	flagellar basal body rod protein FlgC [Helicobacter pylori str. P12]
T. denticola	VBITreDen445_1171	Flagellar motor switch protein FliG	flagellar motor protein [Pseudomonas fluorescens str. Pf0-1]
T. denticola	VBITreDen445_1173	Flagellum-specific ATP synthase FliI	type III secretion system ATPase [Bordetella pertussis str. Tohama I]
T. denticola	VBITreDen445_1195	Magnesium and cobalt efflux protein CorC	transporter HlyCCorC family [Clostridium botulinum str. Okra (serotype B1)]
T. denticola	VBITreDen445_1212	Cholinephosphate cytidylyltransferase EC 2.7.7.15 Choline kinase EC 2.7.1.32	lic-1 operon protein [Haemophilus influenzae str. PittEE (nontypeable)]
T. denticola	VBITreDen445_1223	Oligopeptide transport ATP-binding protein OppD TC 3.A.1.5.1	ABC transporter related [Haemophilus somnus str. 2336]
T. denticola	VBITreDen445_1235	Flagellar motor switch protein FliG	flagellar motor switch protein FliG [Pseudomonas mendocina str. ymp]
T. denticola	VBITreDen445_1283	Probable polybeta-D-mannuronate O-acetylase EC 2.3.1.-	membrane bound O-acyl transferase MBOAT family protein [Pseudomonas mendocina str. ymp]
T. denticola	VBITreDen445_1291	FIG01187002 hypothetical protein	protease Do [Pseudomonas putida str. GB-1]
T. denticola	VBITreDen445_1294	RNA polymerase sigma factor RpoD	sigma factor MysA [Mycobacterium smegmatis str. MC2 155]
T. denticola	VBITreDen445_1355	Phosphoenolpyruvate phosphomutase EC 5.4.2.9	hypothetical protein [Campylobacter jejuni str. 81116 (NCTC11828)]
T. denticola	VBITreDen445_1356	Phosphonopyruvate decarboxylase EC 4.1.1.82	hypothetical protein [Campylobacter jejuni str. 81116 (NCTC11828)]
T. denticola	VBITreDen445_1359	ABC transporter 2C ATP-binding protein	polysaccharide ABC transporter ATP-binding protein [Streptococcus thermophilus str. CNRZ1066 (nonpathogenic)]
T. denticola	VBITreDen445_1367	aminotransferase 2C DegT DnrJ EryC1 StrS family	hypothetical protein [Campylobacter jejuni str. 81116 (NCTC11828)]
T. denticola	VBITreDen445_1374	glycosyltransferase	lipooligosaccharide biosynthesis galactosyltransferase putative [Campylobacter jejuni str. RM1221]
T. denticola	VBITreDen445_1380	UDP-glucose 4-epimerase EC 5.1.3.2	NAD-dependent epimerasedehydratase [Yersinia pseudotuberculosis str. YPIII (serotype O:3)]
T. denticola	VBITreDen445_1382	dTDP-glucose 4 2C6-dehydratase EC 4.2.1.46	dTDP-glucose 4 6-dehydratase [Vibrio fischeri str. ES114 chromosome I]

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T. denticola	VBITreDen445_1415	Flagellin protein FlaA	flagellin FliC [Pseudomonas fluorescens str. Pf-5]
T. denticola	VBITreDen445_1416	Flagellin protein FlaA	flagellin FliC [Pseudomonas fluorescens str. Pf-5]
T. denticola	VBITreDen445_1427	NAD-dependent glyceraldehyde-3-phosphate dehydrogenase EC 1.2.1.12	glyceraldehyde-3-phosphate dehydrogenase [Streptococcus pneumoniae str. CGSP14 (serotype 14)]
T. denticola	VBITreDen445_1433	Chemotaxis regulator - transmits chemoreceptor signals to flagelllar motor components CheY	Chemotaxis response regulator CheY [Listeria welshimeri str. SLCC5334 (serovar 6b)]
T. denticola	VBITreDen445_1455	ABC transporter 2C ATP-binding protein 2C putative	iron-uptake permease ATP-binding protein [Neisseria meningitidis str. Z2491 (serogroup A)]
T. denticola	VBITreDen445_1480	mannosyltransferase 2C putative	Mannosyltransferase [Brucella suis str. ATCC 23445 chromosome I]
T. denticola	VBITreDen445_1597	Cell division trigger factor EC 5.2.1.8	trigger factor [Streptococcus agalactiae str. A909 (serotype Ia)]
T. denticola	VBITreDen445_1609	V-type ATP synthase subunit B EC 3.6.3.14	type III secretion system ATPase [Vibrio parahaemolyticus str. RIMD 2210633 chromosome I]
T. denticola	VBITreDen445_1610	V-type ATP synthase subunit A EC 3.6.3.14	ATP synthase (predicted TTSS protein) [Chlamydia trachomatis str. 434Bu (serovar L2)]
T. denticola	VBITreDen445_1616	ABC transporter 2C ATP-binding protein	daunorubicin resistance ABC transporter ATPase subunit [Mycobacterium vanbaalenii str. PYR-1]
T. denticola	VBITreDen445_1676	UDP-glucose 4-epimerase EC 5.1.3.2	UDP-glucose 4-epimerase [Bacillus cereus str. ATCC 10987]
T. denticola	VBITreDen445_1757	ABC transporter ATP-binding protein	iron(III) ABC transporter ATP-binding protein [Haemophilus influenzae str. Rd KW20 (serotype d)]
T. denticola	VBITreDen445_1797	Protein export cytoplasm protein SecA ATPase RNA helicase TC 3.A.5.1.1	translocase [Mycobacterium avium str. K-10 (subsp. paratuberculosis)]
T. denticola	VBITreDen445_1861	Response regulator of zinc sigma-54-dependent two-component system	putative two-component system response regulator [Pseudomonas fluorescens str. SBW25]
T. denticola	VBITreDen445_1862	Chemotaxis regulator - transmits chemoreceptor signals to flagelllar motor components CheY	flagellar regulatory protein B [Vibrio cholerae str. O395 chromosome II]
T. denticola	VBITreDen445_1895	Transport ATP-binding protein CydD	ABC transporter ATP-bindingpermease protein [Pseudomonas syringae str. DC3000 (pv. tomato)]
T. denticola	VBITreDen445_1896	Transport ATP-binding protein CydC	ABC transporter ATP-bindingpermease protein [Pseudomonas syringae str. DC3000 (pv. tomato)]
T. denticola	VBITreDen445_1921	ClpB protein	type VI secretion ATPase ClpV1 family [Pseudomonas putida str. GB-1]
T. denticola	VBITreDen445_1935	Oligopeptide ABC transporter 2C periplasmic oligopeptide-binding protein OppA TC 3.A.1.5.1	oligopeptide ABC transporter oligopeptide-binding protein [Listeria monocytogenes str. F2365 (serovar 4b)]
T. denticola	VBITreDen445_1964	sigma54 specific transcriptional regulator 2C Fis family	putative two-component system response regulator [Pseudomonas fluorescens str. SBW25]
T. denticola	VBITreDen445_2007	ATP-dependent Clp protease ATP-binding subunit ClpA	clpB protein [Vibrio cholerae str. O395 chromosome I]
T. denticola	VBITreDen445_2071	2-amino-3-ketobutyrate coenzyme A ligase EC 2.3.1.29	aminotransferase class II [Vibrio cholerae str. O395 chromosome I]
T. denticola	VBITreDen445_2102	Zinc ABC transporter 2C periplasmic-binding protein ZnuA	putative laminin adhesion [Streptococcus pyogenes str. SSI-1 (serotype M3)]
T. denticola	VBITreDen445_2109	Vitamin B12 ABC transporter 2C permease component BtuC	putative hemin permease [Escherichia coli str. Sakai (EHEC O157:H7)]
T. denticola	VBITreDen445_2136	ABC transporter 2C ATP-binding permease protein	lipid A export ATP-bindingpermease protein [Haemophilus somnus str. 129PT]
T. denticola	VBITreDen445_2157	FKBP-type peptidyl-prolyl cis-trans isomerase FkpA precursor EC 5.2.1.8	macrophage infectivity potentiator (Mip) [Legionella pneumophila str. Philadelphia 1]
T. denticola	VBITreDen445_2170	Outer membrane stress sensor protease DegS	protease Do [Pseudomonas putida str. F1]
T. denticola	VBITreDen445_2179	sigma-54 dependent transcriptional regulator 2C putative	flagellar regulator FleQ [Pseudomonas syringae str. 1448A (pv. phaseolicola)]
T. denticola	VBITreDen445_2196	ClpB protein	type VI secretion ATPase ClpV1 family [Pseudomonas putida str. W619]
T. denticola	VBITreDen445_2209	Membrane-associated zinc metalloprotease	putative membrane-associated zinc metalloprotease [Pseudomonas aeruginosa str. UCBPP-PA14]
T. denticola	VBITreDen445_2212	Undecaprenyl diphosphate synthase EC 2.5.1.31	undecaprenyl diphosphate synthase [Enterococcus faecalis str. V583]
T. denticola	VBITreDen445_2220	Flagellar hook-associated protein FlgK	flagellar hook-associated protein FlgK [Campylobacter fetus str. 82-40 (subsp. fetus)]
T. denticola	VBITreDen445_2225	ABC-type Fe3+-siderophore transport system 2C permease component	cobalaminFe3+-siderophores transport system permease component [Corynebacterium glutamicum str. ATCC 13032

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			(Bielefeld)]
T. denticola	VBITreDen445_2231	Branched-chain amino acid transport ATP-binding protein LivF TC 3.A.1.4.1	daunorubicin resistance ABC transporter ATP-binding subunit [Mycobacterium sp. str. MCS]
T. denticola	VBITreDen445_2369	Signal transduction histidine kinase	multi-sensor hybrid histidine kinase [Pseudomonas mendocina str. ymp]
T. denticola	VBITreDen445_2386	ABC transporter 2C ATP-binding protein	RtxB protein [Vibrio cholerae str. O395 chromosome II]
T. denticola	VBITreDen445_2388	ABC transporter 2C ATP-binding protein	putative ABC transporter protein [Escherichia coli str. UTI89 (UPEC)]
T. denticola	VBITreDen445_2412	ABC transporter related	ABC-type bacteriocinlantibiotic exporter [Vibrio vulnificus str. CMCP6 chromosome II]
T. denticola	VBITreDen445_2417	ABC transporter ATP-binding protein	lipoprotein inner membrane ABC-transporter [Yersinia pestis str. CO92 (biovar Orientalis)]
T. denticola	VBITreDen445_2432	Glucose-6-phosphate isomerase EC 5.3.1.9	glucose-6-phosphate isomerase [Haemophilus influenzae str. Rd KW20 (serotype d)]
T. denticola	VBITreDen445_2451	Response regulator of zinc sigma-54-dependent two-component system	two-component response regulator PilR [Pseudomonas aeruginosa str. UCBPP-PA14]
T. denticola	VBITreDen445_2459	Outer membrane protein assembly factor YaeT precursor	surface antigenouter membrane protein OMP85 family [Bartonella bacilliformis str. KC583ATCC 35685]
T. denticola	VBITreDen445_2483	Transport ATP-binding protein CydD	ABC transporter ATP-bindingpermease protein [Pseudomonas syringae str. DC3000 (pv. tomato)]
T. denticola	VBITreDen445_2502	Lipoate-protein ligase A	lipoyltransferase and lipoate-protein ligase family protein [Listeria monocytogenes str. F2365 (serovar 4b)]
T. denticola	VBITreDen445_2535	RNA polymerase sigma factor SigB	RNA polymerase sigma factor for flagellar operon [Yersinia enterocolitica str. 8081 (biotype 1B)]
T. denticola	VBITreDen445_2537	Flagellar synthesis regulator FleN	ParA family protein [Vibrio cholerae str. O395 chromosome II]
T. denticola	VBITreDen445_2538	Flagellar biosynthesis protein FlhF	flagellar biosynthesis protein [Campylobacter jejuni str. 81116 (NCTC11828)]
T. denticola	VBITreDen445_2601	Oligopeptide ABC transporter 2C periplasmic oligopeptide-binding protein OppA TC 3.A.1.5.1	oligopeptide ABC transporter oligopeptide-binding protein [Listeria monocytogenes str. HCC23 (serotype 4a)]
T. denticola	VBITreDen445_2607	Flagellar motor switch protein FliM	hypothetical protein [Helicobacter acinonychis str. Sheeba]
T. denticola	VBITreDen445_2609	Flagellar motor rotation protein MotB	OmpAMotB domain protein [Pseudomonas mendocina str. ymp]
T. denticola	VBITreDen445_2610	Flagellar motor rotation protein MotA	flagellar motor protein [Vibrio parahaemolyticus str. RIMD 2210633 chromosome I]
T. denticola	VBITreDen445_2612	Flagellar hook protein FlgE	flagellar hook protein [Pseudomonas aeruginosa str. PA7]
T. denticola	VBITreDen445_2626	methyl-accepting chemotaxis protein	accessory colonization factor AcfB [Vibrio cholerae str. O395 chromosome II]