

**Table S5. Classification of less abundant (>2 fold) protein in *XooΔfleQ* using clusters of orthologous groups from the comparison between *XooΔfleQ* and *Xoo***

COG function	Accession	locus tag	Predicted function	fold change ( <i>XooΔfleQ</i> / <i>Xoo</i> )	P-value	included in other group
C (Energy production and conversion)	188574291	PXO_03463	L-lactate dehydrogenase	0.50	0.0043	K
	188577685	PXO_01298	NADH-quinone oxidoreductase chain I	0.47	0.0040	
	188578714	PXO_03110	atpH ATP synthase F1 and delta subunit	0.48	0.0014	
	188574429	PXO_03330	avirulence protein AvrBs2	*		
	188574660	PXO_03815	cytochrome C5	*		
	188575437	PXO_04578	nitroreductase family	*		
	188576377	PXO_00718	twin-arginine translocation pathway signal	*		
	188577687	PXO_01296	NADH-ubiquinone oxidoreductase Nqo10 subunit	*		
	188577758	PXO_01901	glutamate symport protein	*		
	188578533	PXO_02734	glycerophosphodiester phosphodiesterase	*		
	188578925	PXO_02893	acetyltransferase, gnat family	*		
E (Amino acid transport and metabolism)	188574441	PXO_03319	glutamate synthase	0.44	0.0044	
	188575123	PXO_04132	prolyl oligopeptidase family protein	0.46	0.0086	
	188575946	PXO_00126	dapA dihydrodipicolinate synthase	0.45	0.0004	
	188576104	PXO_00463	glutamine synthetase	0.36	0.0108	
	188576283	PXO_00528	L-lysine 6-aminotransferase	0.42	0.0173	
	188578413	PXO_02519	kbl 2-amino-3-ketobutyrate coenzyme A ligase	0.33	0.0008	
	188574714	PXO_03755	5-methyltetrahydropteroyltriglutamate- homocysteine methyltransferase	*		
	188575357	PXO_04660	acyl-CoA thioesterase I	*		
	188575891	PXO_00179	serine carboxypeptidase	*		
	188576920	PXO_06127	hypothetical protein	*		
	188576965	PXO_06174	nucleotide sugar transaminase	*		
	188577042	PXO_06257	metX homoserine O-acetyltransferase	*		
	188577253	PXO_01746	leucine dehydrogenase	*		
	188577712	PXO_01272	trpA tryptophan synthase, alpha subunit	*		
F (Nucleotide metabolism and transport)	188578397	PXO_02504	purF amidophosphoribosyltransferase	0.45	0.0097	
	188575371	PXO_04647	bis(5'-nucleosyl)-tetraphosphatase (symmetrical)	*		
	188576902	PXO_06108	GTP-binding protein	*		
	188578974	PXO_02846	tmk thymidylate kinase	*		
G (Carbohydrate transport and metabolism)	188574285	PXO_03469	fbp fructose-1 and 6-bisphosphatase	0.49	0.0011	
	188578278	PXO_02384	rpiA ribose 5-phosphate isomerase A	0.50	0.0328	
	188578403	PXO_02509	phosphoglycerate mutase	0.47	0.0063	
	188574298	PXO_03455	2-keto-3-deoxygluconate kinase	*		
	188575748	PXO_04867	otsB trehalose-phosphatase	*		
	188577271	PXO_01728	beta-hexosaminidase	*		
	188577698	PXO_01285	tpiA triosephosphate isomerase	*		
	188578122	PXO_02219	ptsI phosphoenolpyruvate-protein phosphotransferase	*		
H (Coenzyme transport and metabolism)	188575142	PXO_04274	ubiE ubiquinone/menaquinone biosynthesis methyltransferase UbiE	0.43	0.0024	
	188575172	PXO_04292	bifunctional NMN adenyllyltransferase/Nudix hydrolase	0.40	0.0119	
	188579029	PXO_02788	panE 2-dehydropantoate 2-reductase	0.43	0.0149	
	188579047	PXO_02769	ubiB 2-polyprenylphenol 6-hydroxylase	0.31	0.0099	
	188574497	PXO_03630	bioC biotin biosynthesis protein BioC	*		
	188574888	PXO_04009	ubiquinone biosynthesis protein	*		
	188575036	PXO_04216	hppD 4-hydroxyphenylpyruvate dioxygenase	*		
	188575239	PXO_04425	glutamate--cysteine ligase	*		
	188576405	PXO_00690	panB 3-methyl-2-oxobutanoate hydroxymethyltransferase	*		
	188577962	PXO_02016	ispb polyprenyl synthetase	*		
	188578154	PXO_02183	pyridoxamine 5'-phosphate oxidase	*		
	188578945	PXO_02874	bioB biotin synthase	*		
	188579217	PXO_03535	foIE GTP cyclohydrolase I	*		
I (Lipid metabolism)	188574520	PXO_03607	glycerol-3-phosphate acyltransferase	0.43	0.0015	
	188575774	PXO_05537	ispH 4-hydroxy-3-methylbut-2-en-yl diphosphate reductase	0.41	0.0295	
	188576594	PXO_00800	ispG 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	0.43	0.0021	
	188577289	PXO_01709	fatty oxidation complex alpha subunit	0.49	0.0153	
	188575391	PXO_04626	P-hydroxycinnamoyl CoA hydratase	*		
	188575902	PXO_00168	ispF 2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	*		
	188576967	PXO_06176	3-oxoacyl- synthase	*		
	188577115	PXO_01178	streptomyces cyclase/dehydrase superfamily	*		
	188577167	PXO_01127	uppS undecaprenyl diphosphate synthase	*		
	188577293	PXO_01706	enoyl-CoA hydratase	*		
	188578040	PXO_01931	pvsA vibrioferrin biosynthesis protein PvsA	*		
	188578683	PXO_03138	fabA beta-hydroxyacyl-(acyl-carrier-protein) dehydratase FabA	*		
	188578914	PXO_02905	pcaF beta-ketoadipyl CoA thiolase	*		
	188574926	PXO_04048	Sua5/YciO/YrdC family protein	0.42	0.0178	
	188575407	PXO_04610	glnS glutaminyl-tRNA synthetase	0.48	0.0040	
	188575465	PXO_04548	prfA peptide chain release factor 1	0.33	0.0151	
	188576122	PXO_00446	miaB tRNA-I(6)A37 thiotransferase enzyme MiaB	0.37	0.0089	

J (Translation)	188577725	PXO_01259	hemK modification methylase and HemK family	0.49	0.0374	
	188578564	PXO_02705	rpmF ribosomal protein L32	0.43	0.0008	
	188578611	PXO_02657	valS valyl-tRNA synthetase	0.27	0.0024	
	188575498	PXO_04513	rpmC ribosomal protein L29	*		
	188575910	PXO_00160	hypothetical protein	*		
	188575911	PXO_00159	rrmJ ribosomal RNA large subunit methyltransferase J	*		
	188576927	PXO_06135	infA translation initiation factor IF-1	*		
	188577228	PXO_01770	fmcC oxacillin resistance-associated protein fmcC	*		
K (Transcription)	188575056	PXO_04197	N-acetyltransferase	*		
	188575920	PXO_00150	lexA LexA repressor	*		
	188575985	PXO_00085	transcriptional elongation factor	*		
	188576615	PXO_00918	iron dependent repressor	*		
	188576658	PXO_00875	morphogene BolA protein	*		
	188577059	PXO_01234	transcriptional regulator	*		
	188577216	PXO_01782	RNA polymerase sigma factor	*		
	188577282	PXO_01717	rnc ribonuclease III	*		
L (Replication, recombination and repair)	188574927	PXO_04049	topA DNA topoisomerase I	0.31	0.0147	
	188575614	PXO_04745	mfd transcription-repair coupling factor	0.45	0.0023	
	188575308	PXO_04356	dgtp-pyrophosphohydrolase; thiamine phosphate synthase	*		
	188576161	PXO_00410	mutL DNA mismatch repair protein MutL	*		
	188577414	PXO_01578	hrpA ATP-dependent helicase HrpA	*		
	188577974	PXO_02001	hypothetical protein	*		
M (Cell wall/membrane /envelope biogenesis)	188575294	PXO_04370	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D- alanine ligase	0.23	0.0255	
	188578620	PXO_02649	soluble lytic murein transglycosylase	0.39	0.0021	
	188574278	PXO_03476	TonB protein	*		
	188575153	PXO_04259	penicillin-binding protein 2	*		
	188575781	PXO_00004	Rhs element Vgr protein, putative	*		
	188577221	PXO_01777	cyclopropane-fatty-acyl-phospholipid synthase	*		
	188577583	PXO_01399	gumI exopolysaccharide xanthan biosynthesis glycosyltransferase GumI	*		
	188578251	PXO_02356	penicillin-binding protein 1A (PBP-1a) (PBP1a)	*		
N (Cell motility)	188576036	PXO_00027	OmpA family protein,chemotaxis protein MotB	*		
	188576956	PXO_06165	flagellar protein	*		
O (Post-translational modification, protein turnover, and chaperones)	188577468	PXO_01524	gntY protein GntY	0.47	0.0069	
	188575906	PXO_00164	pcm protein-L-isoaspartate O-methyltransferase	*		
	188577116	PXO_01177	smpB SsrA-binding protein	*		
P (Inorganic ion transport and metabolism)	188577777	PXO_01883	TonB-dependent outer membrane Receptor	0.46	0.0100	
	188577853	PXO_02129	TonB-dependent receptor	0.45	0.0126	
	188578039	PXO_01932	TonB-dependent outer membrane Receptor	0.37	0.0148	
	188574966	PXO_04088	TonB-dependent outer membrane Receptor	*		
	188576273	PXO_00302	TonB-dependent receptor	*		
	188578214	PXO_02317	beta-lactamase	*		
	188579174	PXO_03245	alkaline phosphatase	*		
Q (Secondary metabolites biosynthesis, transport, and catabolism)	188578041	PXO_01930	pvsB vibrioferrin biosynthesis protein PvsB	*		
	188578635	PXO_03182	ABC transporter ATP-binding protein	*		
	188578689	PXO_03132	copA copper resistance protein A	*		
	188579087	PXO_03209	toluene tolerance protein	*		
	188574437	PXO_03322	lipoprotein, putative	0.45	0.0224	
	188577927	PXO_02052	hypothetical protein	0.43	0.0112	
	188574893	PXO_04014	ISXo5 transposase	*		
	188575111	PXO_04142	ISXoo13 transposase	*		
	188575568	PXO_04700	Rhs element Vgr protein	*		
	188575572	PXO_05513	Sulfatase modifying factor 1 precursor-like protein (C-alpha-formylglycine-generating enzyme 1)	*		
	188575784	PXO_05538	rhs RHS Repeat family	*		
	188575802	PXO_00272	hypothetical protein	*		
	188575878	PXO_00193	hypothetical protein	*		
	188576343	PXO_00751	hypothetical protein	*		
	188576458	PXO_00634	ISXoo8 transposase	*		
	188577477	PXO_05663	ISXoo12 transposase	*		
	188578617	PXO_02738	ISXo1 transposase	*		
	188579095	PXO_03202	ISXo2 putative transposase	*		
	188575565	PXO_04697	hypothetical protein	0.48	0.0259	
	188576618	PXO_00916	methyl-accepting chemotaxis protein	0.13	0.0034	
	188577094	PXO_01199	acetyltransferase and gnat family	0.42	0.0175	
	188578392	PXO_02499	lpxH UDP-2 and 3-diacetylglucosamine hydrolase	0.46	0.0230	
	188574374	PXO_03381	ABC transporter substrate binding protein	*		
	188574433	PXO_03326	hypothetical protein	*		
	188574475	PXO_03654	hypothetical protein	*		

S (Function unknown)	188574484	PXO_03644	Rhs element Vgr protein	*		
	188574495	PXO_03632	hypothetical protein	*		
	188574513	PXO_03615	5'-nucleotidase, lipoprotein e(P4) family	*		
	188574538	PXO_03588	hypothetical protein	*		
	188574572	PXO_03554	hemagglutinin-like protein	*		
	188574654	PXO_03824	ATPase	*		
	188574656	PXO_03819	hypothetical protein	*		
	188574813	PXO_03933	hypothetical protein	*		
	188574837	PXO_03958	lipoprotein, putative	*		
	188575178	PXO_04298	hypothetical protein	*		
	188575232	PXO_04431	GTP-binding protein	*		
	188575334	PXO_04687	phosphoanhydride phosphohydrolase	*		
	188575364	PXO_04653	lemA LemA family protein	*		
	188575536	PXO_04472	inner membrane protein	*		
	188575626	PXO_04733	hypothetical protein	*		
	188575757	PXO_04858	EF hand domain protein	*		
	188575967	PXO_00103	3-hydroxyacyl-CoA dehydrogenase type II	*		
	188576022	PXO_00043	chemotaxis protein	*		
	188576647	PXO_00886	beta-alanine synthetase	*		
	188576966	PXO_06175	acyl carrier protein	*		
	188576973	PXO_06182	fkfM methyltransferase, FkbM family protein	*		
	188577156	PXO_01138	protein U	*		
	188577219	PXO_01779	dehydrogenase	*		
	188577682	PXO_01301	yhbC YhbC family protein	*		
	188577782	PXO_01878	domain of unknown function superfamily	*		
	188577946	PXO_02034	hypothetical protein	*		
	188577947	PXO_02033	hypothetical protein	*		
	188577957	PXO_02024	hydrolase	*		
	188578105	PXO_02236	hypothetical protein	*		
	188578111	PXO_02230	hypothetical protein	*		
	188578150	PXO_02187	hypothetical protein	*		
	188578313	PXO_02422	hypothetical protein	*		
	188578328	PXO_02436	methanol dehydrogenase regulator	*		
	188578355	PXO_02463	hypothetical protein	*		
	188578399	PXO_02506	hypothetical protein	*		
	188578950	PXO_02868	hydrolase	*		
T (Signal transduction mechanisms)	188574562	PXO_03565	two-component system sensor protein	*		
	188575184	PXO_04304	two-component system sensor protein	*		
	188575701	PXO_04836	two-component system regulatory protein	*		
	188576011	PXO_00054	methyl-accepting chemotaxis protein	*		
	188576018	PXO_00047	chemotaxis protein	*		
	188576019	PXO_00046	chemotaxis protein	*		
	188576021	PXO_00045	chemotaxis protein	*		
	188576023	PXO_00041	chemotaxis protein	*		
	188576031	PXO_00032	cheA chemotaxis protein CheA	*		
	188576936	PXO_06145	Putative signal protein with PAS(PAC), GGDEF and EAL domains	*		
	188577287	PXO_01712	regulatory protein	*		
	188578023	PXO_01951	hrpG HrpG	*		
	188578297	PXO_02404	transcriptional regulator LuxR/uhpA family	*		
	188578874	PXO_02943	two-component system sensor protein	*		
U (Intracellular trafficking, secretion, and vesicular transport)	188576289	PXO_00522	secD protein-export membrane protein SecD	0.38	0.0019	
	188576287	PXO_00524	yajC preprotein translocase, YajC subunit	*		
	188577284	PXO_01715	lepB signal peptidase I	*		
	188577659	PXO_01325	type IV pilin	*		
V (Defense mechanisms)	188577137	PXO_01156	multidrug resistance efflux pump	*		
	188578532	PXO_02735	hypothetical protein	*		

\* indicates that the protein is unique to Xoo