

Table S2. Differential Gene Presence

Cluster	Group 1	Group 2	GeneID in ref. genome	Function or Pfam ¹	Fraction of group 1	Fraction of group 2
C2	A	B	(1)-00149	hypothetical protein	96%	0%
	A	B	(1)-00226	PF1291.2 RelB_N[Antitoxin of toxin-antitoxin stability system N-terminal]	98%	7%
C8	A	B	(1)-00227	PF06789.8 Plasmid_Txe[Plasmid encoded toxin Txe].PF05016.9[Plasmid_stabI[Plasmid stabilisation system protein]	98%	7%
	A	B	(1)-00228	hypothetical protein	98%	7%
	A	B	(1)-00229	hypothetical protein	91%	0%
	A	B	(1)-00329	PF13527.1 Acetyltransf_9[Acetyltransferase (GNAT) domain]	91%	0%
	A	B	(1)-00353	PF08279.7 HTH_11[HTH domain]	88%	0%
	A	B	(1)-00693	hypothetical protein	86%	0%
	A	B	(1)-00998	hypothetical protein	95%	0%
	A	B	(1)-01075	hypothetical protein	98%	0%
	A	B	(1)-01076	hypothetical protein	100%	0%
	A	B	(1)-01143	hypothetical protein	88%	0%
C10	A	B	(1)-01276	hypothetical protein	95%	0%
	A	B	(1)-01279	PTS system, IICBA component / PF00358.15 PTS_EIIA_1[Phosphoenolpyruvate-dependent sugar phosphotransferase system, EIIA 1];TIGR00830[PTBA: PTS system, glucose subfamily, IIA component]	100%	0%
	A	B	(1)-01280	glycosyl hydrolase family protein / PF02056.11 Glyco_hydro_4[Family 4 glycosyl hydrolase]	100%	0%
	A	B	(1)-01281	PTS system, N-acetylglucosamine-specific IIB component / PF02378.13 PTS_EIIC[Phosphotransferase system, EIIC]	100%	0%
	A	B	(1)-01282	PF04794.7 YjdC YjdC-like protein]	100%	0%
	A	B	(1)-01283	BglG family transcriptional antiterminator / PF00874.15 PRD[PRD domain]	98%	0%
C11	A	B	(1)-01493	PF13242.1 Hydrolase_like[HAD-hydrolase-like].PF00702.21 Hydrolase[haloacid dehalogenase-like hydrolase]	80%	13%
	A	B	(1)-01503	PF00389.25 2-Hacid_dh[D-isomer specific 2-hydroxyacid dehydrogenase, catalytic domain]	80%	13%
	A	B	(1)-01504	TIGR00872[gnd_rel: 6-phosphogluconate dehydrogenase (decarboxylating)]	80%	13%
	A	B	(1)-01505	PF13580.1 SIS_2[SIS domain].PF01380.17 SIS[SIS domain].PF01418.12 HTH_6[Helix-turn-helix domain, rpiI family]	80%	13%
	A	B	(1)-01516	PF00923.14 Transaldolase[Transaldolase]	84%	13%
C12	A	B	(1)-01517	PF03929.8 PTSA_4[PTS system, glucitol/sorbitol-specific IICa component].PF00923.14 Transaldolase[Transaldolase]	84%	13%
	A	B	(1)-01519	PF07863.6 EIIIC-GUT_C[Sorbitol phosphotransferase enzyme II C-terminus];TIGR00825 EIIIC-GUT_PTS system, glucitol/sorbitol-specific, IIB component].PF03612.9 EIIIC-GUT_N[Sorbitol phosphotransferase enzyme II N-terminus]	84%	13%
	A	B	(1)-01520	TIGR00821[EII-GUT_PTS system, glucitol/sorbitol-specific, IIC component].PF03608.8 EII-GUT PTS system enzyme II sorbitol-specific factor]	84%	13%
	A	B	(1)-01521	TIGR00821[EII-GUT_PTS system, glucitol/sorbitol-specific, IIC component].PF03608.8 EII-GUT PTS system enzyme II sorbitol-specific factor].PF06923.6 GutM[Glucitol operon activator protein (GutM)]	84%	13%
	A	B	(1)-01522	PF00874.15 PRD[PRD domain].PF05043.8 Mga[Mga Helix-turn-helix domain].PF00359.17 PTS_EIIA_2[Phosphoenolpyruvate-dependent sugar phosphotransferase system, EIIA 2]	84%	13%
	A	B	(1)-01523	PF13561.1 adh_short_C2 Enoyl-(Acyl carrier protein) reductase].PF08659.5 K R[KR domain].PF00106.20 adh_short[short chain dehydrogenase].PF01370.16 Epmirase[NAD dependent epimerase/dehydratase family]	84%	13%
	A	B	(1)-01677	hypothetical protein	100%	0%
	A	B	(1)-01684	hypothetical protein	98%	0%
C17	A	B	(1)-01766	PF02275.13 CBAH[Linear amide C-N hydrolases, choloylglycine hydrolase family]	96%	0%
	A	B	(1)-01798	hypothetical protein	91%	0%
	A	B	(1)-01889	PF13630.1 SdpI[SdpI/YhfL protein family]	80%	13%
	A	B	(1)-02231	PF00149.23 Metallophos[Caseinase-like phosphoesterase]	90%	0%
	A	B	(1)-02234	PF00805.17 Pentapeptide Pentapeptide repeats (8 copies)].PF13599.1 Pentapeptide_4 Pentapeptide repeats (9 copies)]	96%	0%
	A	B	(1)-02295	PF02517.11 Abj CAAX protease self-immunity]	91%	0%
	A	B	(1)-02306	PF00583.19 Acetyltransf_1[Acetyltransferase (GNAT) family]	100%	0%
	A	B	(1)-02463	PF01061.19 ABC2_membrane ABC-2 type transporter].PF12698.2 ABC2_membrane_3 ABC-2 family transporter protein]	100%	0%
	A	B	(1)-02464	PF12698.2 ABC2_membrane_3 ABC-2 family transporter protein]	100%	0%
	A	B	(1)-02465	PF00005.22 ABC_tran ABC transporter].PF13304.1 AAA_21 AAA domain]	100%	0%
	A	B	(1)-02466	PF07730.8 HiskA_3 Histidine kinase].PF02518.21 HATPase_c Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase]	100%	0%
	A	B	(1)-02467	PF00196.14 GerE Bacterial regulatory proteins, luxR family].PF00072.19 Response_reg Response regulator receiver domain]	100%	0%
C20	A	B	(1)-02468	hypothetical protein	100%	0%
	A	B	(1)-02508	hypothetical protein	96%	0%
	A	B	(1)-02509	PF00005.22 ABC_tran ABC transporter].PF13304.1 AAA_21 AAA domain].PF12848.2 ABC_tran_2 ABC transporter]	100%	0%
	A	B	(1)-02577	PF05738.8 Cna_B Cna protein B-type domain].TIGR01167 LPXTG_anchor: LPXTG-motif cell wall anchor domain]	98%	0%
C21	A	B	(1)-02578	hypothetical protein	82%	0%
	A	B	(1)-02582	PF02012.15 BNR Asp-box repeat]	95%	0%
	A	B	(1)-02673	PF13460.1 NAD_binding_10 NADH(P)-binding].PF08659.5 K R[KR domain].PF08643.5 DUF1776[Fungal family of unknown function (DUF1776)].PF13561.1 adh_short_C2 Enoyl-(Acyl carrier protein) reductase]	98%	0%
	A	B	(1)-02674	PF00132.19 Hexapep[Bacterial transferase hexapeptide (six repeats)]	98%	0%
	A	B	(1)-02675	PF03466.15 LysR_substrate LysR substrate binding domain]	98%	0%
	A	B	(1)-02696	PF12730.2 ABC2_membrane_4 ABC-2 family transporter protein]	98%	7%
	A	B	(1)-02697	PF12679.2 ABC2_membrane_2 ABC-2 family transporter protein].PF00005.22 ABC_tran ABC transporter].PF13304.1 AAA_21 AAA domain]	100%	7%
	A	B	(1)-02698	hypothetical protein	95%	7%
	A	B	(1)-02820	TIGR01990 BPGM: beta-phosphoglucomutase].PF13419.1 HAD_2 Haloacid dehalogenase-like hydrolase].PF13242.1 Hydrolase_like[HAD-hydrolase-like]	100%	0%
	A	B	(1)-02821	PF02595.10 Gly_kinase Glycerate kinase family].TIGR00045 Glycerate kinase]	100%	0%
C24	A	B	(1)-02822	PF02595.10 Gly_kinase Glycerate kinase family].PF03632.10 Glyco_hydro_65n Glycosyl hydrolase family 65 central catalytic domain]	100%	0%
	A	B	(1)-02823	PF01408.17 GFO_IDH_MocA Oxidoreductase family, NAD-binding Rossmann fold].PF03636.10 Glyco_hydro_65N Glycosyl hydrolase family 65, N-terminal domain]	100%	0%
	A	B	(1)-02824	PF01261.19 AP_endonuc_2 Xylose isomerase-like TIM barrel]	100%	0%
	A	B	(1)-02825	PF00107.21 ADH_zinc_N Zinc-binding dehydrogenase]	100%	0%
	A	B	(1)-02826	PF00528.17 BPD_transp_1 Binding-protein-dependent transport system inner membrane component]	100%	0%
	A	B	(1)-02827	PF00528.17 BPD_transp_1 Binding-protein-dependent transport system inner membrane component]	100%	0%
	A	B	(1)-02828	PF13531.1 SBP_bac_11 Bacterial extracellular solute-binding protein].PF13416.1 SBP_bac_8 Bacterial extracellular solute-binding protein]	100%	0%
	A	B	(1)-02829	PF00128.19 Alpha-amylase Alpha amylase, catalytic domain]	100%	0%
	A	B	(1)-02830	PF13377.1 Peripla_BP_3 Periplasmic binding protein-like domain].PF00356.16 LacI Bacterial regulatory proteins, lacI family]	100%	0%
	C30	B	A	(3)-00029	PF00652.17 Ricin_B_lectin[Ricin-type beta-trefoil lectin domain].PF00388.14 PI-PLC-X[Phosphatidylinositol-specific phospholipase C, X domain]	100%
B		A	(3)-00124	PF13443.1 HTH_26 Cro/C1-type HTH DNA-binding domain].PF01381.17 HTH_3 Helix-turn-helix].PF12844.2 HTH_19 Helix-turn-helix domain]	100%	4%
B		A	(3)-00125	PF13396.1 PLDc_N Phospholipase_D_nuclease N-terminal]	100%	4%
B		A	(3)-00126	PF00005.22 ABC_tran ABC transporter].PF13304.1 AAA_21 AAA domain]	100%	5%
B		A	(3)-00127	PF12730.2 ABC2_membrane_4 ABC-2 family transporter protein]	100%	4%
B		A	(3)-00159	hypothetical protein	100%	0%
B		A	(3)-00160	PF05543.8 Peptidase_C47 Staphopain peptidase C47]	100%	0%
B		A	(3)-00161	hypothetical protein	100%	0%
B		A	(3)-00162	TIGR01716 RGG_Cterm: transcriptional activator, Rgg/GadR/MutR family, C-terminal domain]	100%	0%
B		A	(3)-00257	hypothetical protein	100%	4%
C32	B	A	(3)-00258	hypothetical protein	100%	4%
	B	A	(3)-00259	hypothetical protein	100%	4%
	B	A	(3)-00278	PF13419.1 HAD_2 Haloacid dehalogenase-like hydrolase].PF13242.1 Hydrolase_like[HAD-hydrolase-like]	100%	9%
	B	A	(3)-00279	PF00004.24 AAA ATPase family associated with various cellular activities (AAA)].PF01078.16 Mg_chelatase[Magnesium chelatase, subunit CHL1].PF13401.1 AAA_22 AAA domain].PF00158.21 Sigma54_activat Sigma-54 interaction domain]	100%	9%
	B	A	(3)-00282	PF03609.9 EII-Sor PTS system sorbose-specific iic component]	100%	9%
	B	A	(3)-00283	PF03830.10 PTSIIb_sorb PTS system sorbose subfamily IIB component]	100%	9%
C33	B	A	(3)-00284	PF03830.10 PTSIIb_sorb PTS system sorbose subfamily IIB component].PF03610.11 EIIA-man PTS system fructose IIA component]	100%	9%
	B	A	(3)-00310	PF03806.8 ABG_transport AbgT putative transporter family]	100%	4%
	B	A	(3)-00311	TIGR01887 dipeptidase putative dipeptidase].PF01546.23 Peptidase_M20 Peptidase family M20/M25/M40]	100%	4%
	B	A	(3)-00373	PF00589.17 Phage_integrase Phage integrase family]	93%	5%
C35	B	A	(3)-00380	PF01418.12 HTH_9 Helix-turn-helix domain, rpiI family].PF01380.17 SIS[SIS domain]	87%	0%
	B	A	(3)-00391	PF02056.11 Glyco_hydro_4 Family 4 glycosyl hydrolase]	87%	0%
	B	A	(3)-00392	TIGR02005 PTS_IIB-alpha: PTS system, alpha-glucoside-specific IIB component].TIGR00826 EIIb_glc: PTS system, glucose-like IIB component]	93%	0%
	B	A	(3)-00431	PF01656.18 CbaI CobQ/CobB/MinD/ParA nucleotide binding domain].PF09140.6 MipZ ATPase MipZ].TIGR01007 eps_fam: capsular exopolysaccharide family].PF13614.1 AAA_31 AAA domain]	100%	4%
	B	A	(3)-00538	PF00583.19 Acetyltransf_1[Acetyltransferase (GNAT) family]	100%	0%
C34	B	A	(3)-00575	hypothetical protein	100%	0%
	B	A	(3)-00603	PF10022.4 DUF2264 Uncharacterized protein conserved in bacteria (DUF2264)]	100%	0%
	B	A	(3)-00604	hypothetical protein	100%	0%
	B	A	(3)-00605	PF01301.14 Glyco_hydro_35 Glycosyl hydrolases family 35].PF02449.10 Glyco_hydro_42 Beta-galactosidase]	100%	4%
	B	A	(3)-00606	PF07470.8 Glyco_hydro_88 Glycosyl Hydrolase Family 88]	100%	0%
	B	A	(3)-00607	PF00392.16 GntR Bacterial regulatory proteins, gntR family].PF07702.8 UTRA UTRA domain]	100%	0%

C36	B	A	(3)-00610	PF00874.15[PRD PRD domain];PF05043.8[Mga Mga helix-turn-helix domain];PF00359.17[PTS_EIIA_2 Phosphoenolpyruvate-dependent sugar phosphotransferase system, EIIA 2]	100%	0%
	B	A	(3)-00611	PF00359.17[PTS_EIIA_2 Phosphoenolpyruvate-dependent sugar phosphotransferase system, EIIA 2]	100%	0%
	B	A	(3)-00612	hypothetical protein	93%	0%
	B	A	(3)-00613	TIGR00848[ruA: PTS system, fructose subfamily, IIA component];PF00359.17[PTS_EIIA_2 Phosphoenolpyruvate-dependent sugar phosphotransferase system, EIIA 2]	93%	0%
	B	A	(3)-00614	hypothetical protein	100%	0%
	B	A	(3)-00615	TIGR01427[PTS_IIC_fructo: PTS system, Fru family, IIC component];PF02378.13[PTS_EIIC Phosphotransferase system, EIIC]	100%	0%
	B	A	(3)-00616	PF00834.14[Ribul_ P_3_epim Ribulose-phosphate 3 epimerase family]	100%	0%
	B	A	(3)-00617	PF03830.10[PTS_IIB_sorb PTS system sorbose subfamily IIB component];PF03610.11[EIIA-man PTS system fructose IIA component]	100%	0%
	B	A	(3)-00618	PF03809.9[EII-Sor PTS system sorbose-specific iic component]	100%	0%
	B	A	(3)-00619	PF03613.9[EIID-AGA PTS system mannose/fructose/sorbose family IID component]	100%	0%
C37	B	A	(3)-00620	PF08124.6[Lyase_8_N Polysaccharide lyase family 8, N terminal alpha-helical domain];PF02278.13[Lyase_8 Polysaccharide lyase family 8, super-sandwich domain]	100%	0%
	B	A	(3)-00850	PF02839.9[CBM_5_12 Carbohydrate binding domain];PF00041.16[fn3 Fibronectin type III domain];PF00704.23[Glyco_hydro_18 Glycosyl hydrolases family 18]	100%	5%
	B	A	(3)-00950	Chitinase C1 / PF02839.9[CBM_5_12 Carbohydrate binding domain];PF00041.16[fn3 Fibronectin type III domain];PF00704.23[Glyco_hydro_18 Glycosyl hydrolases family 18]	100%	0%
	B	A	(3)-00951	TIGR01716[RGG_Cterm: transcriptional activator, Rgg/GadR/MutR family, C-terminal domain];PF01381.17[HTH_3 Helix-turn-helix];PF12844.2[HTH_19 Helix-turn-helix domain]	100%	0%
C38	B	A	(3)-00952	PF03067.10[Chitin_bind_3 Chitin binding domain]	100%	0%
	B	A	(3)-00961	hypothetical protein	100%	0%
C39	B	A	(3)-00962	hypothetical protein	100%	0%
	B	A	(3)-00999	PF02018.12[CBM_4_9 Carbohydrate binding domain]	100%	5%
	B	A	(3)-01081	PF12840.2[HTH_20 Helix-turn-helix domain];PF01022.15[HTH_5 Bacterial regulatory protein, arsR family]	93%	0%
	B	A	(3)-01098	TIGR01167[LPXTG_anchor: LPXTG-motif cell wall anchor domain]	93%	2%
	B	A	(3)-01099	PF05043.8[Mga Mga helix-turn-helix domain];PF08280.6[HTH_Mga M protein trans-acting positive regulator (MGA) HTH domain]	93%	2%
	B	A	(3)-01102	agrC / hypothetical protein	93%	2%
	B	A	(3)-01103	agrA / PF04397.10[LytR LytR DNA-binding domain];PF00072.19[Response_reg Response regulator receiver domain]	93%	2%
	B	A	(3)-01104	agrB / PF04647.10[AggB Accessory gene regulator B]	93%	2%
	B	A	(3)-01105	agrD / cyclic lactone autoinducer peptide	93%	2%
	B	A	(3)-01300	PF03577.10[Peptidase_C69 Peptidase family C69]	100%	0%
C41	B	A	(3)-01359	hypothetical protein	93%	7%
	B	A	(3)-01362	hypothetical protein	100%	7%
	B	A	(3)-01533	hypothetical protein	93%	2%
	B	A	(3)-01605	PF01717.13[Meth_synt_2 Cobalamin-independent synthase, Catalytic domain]	93%	14%
	B	A	(3)-01634	PF12844.2[HTH_19 Helix-turn-helix domain];PF01381.17[HTH_3 Helix-turn-helix]	100%	14%
	B	A	(3)-01635	hypothetical protein	100%	14%
	B	A	(3)-01642	PF00005.22[ABC_tran ABC transporter]	100%	0%
	B	A	(3)-01660	PF12730.2[ABC2_membrane_4 ABC-2 family transporter protein]	100%	0%
	B	A	(3)-01661	PF13304.1[AAA_21 AAA domain]	100%	2%
	B	A	(3)-01684	hypothetical protein	93%	0%
C42	B	A	(3)-01695	hypothetical protein	87%	14%
	B	A	(3)-01784	PF00490.15[RC3 ROK family]	100%	7%
	B	A	(3)-01785	PF13377.1[Peripla_BP_3 Periplasmic binding protein-like domain];PF00356.16[LacI Bacterial regulatory proteins, lacI family];PF01381.17[HTH_3 Helix-turn-helix]	100%	5%
	B	A	(3)-01786	TIGR01322[scrB_fam: sucrose-6-phosphate hydrolase];PF08244.7[Glyco_hydro_32C Glycosyl hydrolases family 32 C terminal]	100%	5%
C43	B	A	(3)-01787	TIGR01996[PTS-II-BC-sucr: PTS system, sucrose-specific IIBC component];PF00358.15[PTS_EIIA_1 Phosphoenolpyruvate-dependent sugar phosphotransferase system, EIIA 1]	100%	7%
	B	A	(3)-01789	PF00128.19[Alpha-amylase Alpha amylase, catalytic domain]	100%	7%
	B	A	(3)-01805	PF00874.15[PRD PRD domain];PF05043.8[Mga Mga helix-turn-helix domain];PF00359.17[PTS_EIIA_2 Phosphoenolpyruvate-dependent sugar phosphotransferase system, EIIA 2]	93%	9%
	B	A	(3)-01806	PF00359.17[PTS_EIIA_2 Phosphoenolpyruvate-dependent sugar phosphotransferase system, EIIA 2]	93%	9%
C44	B	A	(3)-01807	PF02302.12[PTS_IIB PTS system, Lactose/Cellobiose specific IIB subunit]	93%	9%
	B	A	(3)-01808	PF03611.9[EIIC-GAT PTS system sugar-specific permease component]	93%	7%
	B	A	(3)-01809	PF13580.1[SIS_2 SIS domain]	93%	7%
	B	A	(3)-01860	PF02302.12[PTS_IIB PTS system, Lactose/Cellobiose specific IIB subunit]	93%	0%
C45	B	A	(3)-01861	PF00380.17[SIS(SIS domain)];PF01418.12[HTH_6 Helix-turn-helix domain, tpiR family]	93%	0%
	B	A	(3)-01862	TIGR02004[PTS_IIBC-malK: PTS system, maltose and glucose-specific IIBC component];TIGR00826[EIIB_glc: PTS system, glucose-like IIB component]	93%	0%
	B	A	(3)-01863	PF00155.16[Aminotran_1_2 Aminotransferase class I and II]	100%	0%
	B	A	(3)-01865	PF13671.1[AAA_33 AAA domain];PF06414.7[Zeta_toxin Zeta toxin]	100%	0%
C46	B	A	(3)-01866	PF00383.17[dCMP_cyt_deam_1 Cytidine and deoxycytidylate deaminase zinc-binding region]	100%	4%
	B	A	(3)-01908	hypothetical protein	93%	4%
	B	A	(3)-01909	PF09992.4[DUF2233 Predicted periplasmic protein (DUF2233)]	93%	4%
	B	A	(3)-01910	PF00535.21[Glycosyl_transf_2 Glycosyl transferase family 2];PF04138.9[GrA GrA-like protein]	93%	4%
C47	B	A	(3)-01944	PF13527.1[Acetyltransf_9 Acetyltransferase (GNAT) domain];PF00583.19[Acetyltransf_1 Acetyltransferase (GNAT) family]	100%	0%
	B	A	(3)-01947	hypothetical protein	100%	0%
	B	A	(3)-02009	hypothetical protein	93%	0%
	B	A	(3)-02010	PF11131.3[DUF2974 Protein of unknown function (DUF2974)]	100%	0%
C48	B	A	(3)-02012	hypothetical protein	100%	0%
	B	A	(3)-02023	hypothetical protein	100%	0%
	B	A	(3)-02056	PF00496.17[SBP_bac_5 Bacterial extracellular solute-binding proteins, family 5 Middle]	100%	5%
	B	A	(3)-02057	PF00528.17[BPD_transp_1 Binding-protein-dependent transport system inner membrane component]	100%	5%
C49	B	A	(3)-02058	PF00528.17[BPD_transp_1 Binding-protein-dependent transport system inner membrane component];PF12911.2[OppC_N N-terminal TM domain of oligopeptide transport permease C]	100%	5%
	B	A	(3)-02059	PF00005.22[ABC_tran ABC transporter];TIGR01727[oligo_HPY: oligopeptide/dipeptide ABC transporter, ATP-binding protein, C-terminal domain]	100%	5%
	B	A	(3)-02060	PF00005.22[ABC_tran ABC transporter];PF08352.7[oligo_HPY Oligopeptide/dipeptide transporter, C-terminal region]	100%	5%
	B	A	(3)-02061	PF01230.18[Hit HIT domain];PF11969.3[DcpS_C Scavenger mRNA decapping enzyme C-term binding]	100%	5%
C50	B	A	(3)-02065	PF00293.23[NUDIX NUDIX domain]	93%	0%
	B	A	(3)-02066	hypothetical protein	93%	0%
	B	A	(3)-02085	PF00228.26[DnaJ DnaJ domain]	100%	0%
	B	A	(3)-02086	PF00753.22[Lactamase_B Metallo-beta-lactamase superfamily];PF12706.2[Lactamase_B_2 Beta-lactamase superfamily domain]	100%	0%
C51	B	A	(3)-02260	hypothetical protein	100%	0%
	B	A	(3)-02302	hypothetical protein	87%	0%
	B	A	(3)-02464	PF05043.8[Mga Mga helix-turn-helix domain]	100%	0%
	B	A	(3)-02465	PF05043.8[Mga Mga helix-turn-helix domain]	100%	0%
C52	B	A	(3)-02474	hypothetical protein	100%	0%
	B	A	(3)-02475	hypothetical protein	87%	0%
	B	A	(3)-02477	hypothetical protein	100%	0%
	B	A	(3)-02478	hypothetical protein	93%	0%
C53	B	A	(3)-02509	hypothetical protein	93%	0%
	B	A	(3)-02510	PF06013.7[WXG100 Proteins of 100 residues with WXG];TIGR03930[WXG100_ESAT6: WXG100 family type VII secretion target];PF10824.3[DUF2580 Protein of unknown function (DUF2580)]	87%	0%
	B	A	(3)-02511	TIGR03929[T7_essa: Nterm: type VII secretion protein EsaA]	87%	0%
	B	A	(3)-02512	hypothetical protein	87%	0%
C54	B	A	(3)-02513	PF08817.5[YukD WXG100 protein secretion system (Wss), protein YukD]	87%	0%
	B	A	(3)-02515	TIGR03926[T7_EssB: type VII secretion protein EssB];PF10140.4[YukC WXG100 protein secretion system (Wss), protein YukC]	87%	0%
	B	A	(3)-02516	PF01580.13[FtsK_SpoIIIE FtsK/SpoIIIE family];PF12846.2[AAA_10 AAA-like domain];TIGR03928[T7_EssCb: FtsK type VII secretion protein EssC]	87%	0%
	B	A	(3)-02525	PF01832.15[Glucosaminidase Mannosyl-glycoprotein endo-beta-N-acetylglucosaminidase];PF07538.6[ChW Clostridial hydrophobic W]	100%	0%
C55	B	A	(3)-02550	PF04892.7[VanZ VanZ like family]	87%	4%
	B	A	(3)-02576	PF00004.24[AAA ATPase family associated with various cellular activities (AAA)];PF00158.21[Sigma54_activat Sigma-54 interaction domain];PF07724.9[AAA_2 AAA domain (Cdc48 subfamily)]	93%	13%
	B	A	(3)-02636	PF03009.12[GDPD Glycerophosphoryl diester phosphodiesterase family]	93%	4%
	B	A	(3)-02648	PF02525.12[Flavodoxin_2 Flavodoxin-like fold];PF03358.10[FMN_red NADPH-dependent FMN reductase]	93%	2%
	B	A	(3)-02690	hypothetical protein	100%	0%
	B	A	(3)-02688	PF01548.12[DEDD_Tnp_IS110 Transposase];PF02371.11[Transposase_20 Transposase IS116/IS110/IS902 family]	93%	9%
	B	A	(3)-02841	hypothetical protein	100%	0%
	B	A	(3)-02866	TIGR00410[lacE: PTS system, lactose/cellobiose family IIC component];PF02378.13[PTS_EIIC Phosphotransferase system, EIIC]	100%	0%
	B	A	(3)-02871	PF05043.8[Mga Mga helix-turn-helix domain];PF08280.6[HTH_Mga M protein trans-acting positive regulator (MGA) HTH domain]	100%	0%
	B	A	(3)-02872	hypothetical protein	100%	0%
C54	B	A	(3)-02873	hypothetical protein	100%	0%
	B	A	(3)-02874	hypothetical protein	100%	0%
	B	A	(3)-02875	hypothetical protein	100%	0%
	B	A	(3)-02875	hypothetical protein	100%	0%

	B	A	(3)-02876	PF11797.3[DUF3324[Protein of unknown function C-terminal (DUF3324)];PF06030.7[DUF916[Bacterial protein of unknown function (DUF916)]]	100%	0%
	B	A	(3)-02878	hypothetical protein	87%	4%
	B	A	(3)-02890	hypothetical protein	100%	0%
	B	A	(4)-01523	PF00874.15[PRD[PRD domain]]	87%	13%
	B	A	(4)-02162	PF00085.15[Thioredoxin[Thioredoxin]]	87%	0%
	B	A	(4)-04231	hypothetical protein	87%	18%
Cluster	Group 1	Group 2	GeneID in ref. genome	Function or Pfam*	Fraction of group 1	Fraction of group 2
	A1	A2	(1)-00507	PF02586.9[DUF159[Uncharacterised ACR, COG2135]]	95%	0%
	A1	A2	(1)-00584	hypothetical protein	81%	17%
	A1	A2	(1)-00676	PF00004.24[AAA[ATPase family associated with various cellular activities (AAA)];PF00158.21[Sigma54_activa[Sigma-54 interaction domain];PF00874.15[PRD[PRD domain]]	90%	17%
	A1	A2	(1)-00677	PF03610.11[EIIA-man[PTS system fructose IIA component]]	90%	17%
	A1	A2	(1)-00678	PF03830.10[PTSII sorb[PTS system sorbose subfamily IIB component]]	90%	17%
	A1	A2	(1)-00679	PF03609.9[EII-Sor[PTS system sorbose-specific ic component]]	90%	17%
	A1	A2	(1)-00680	PF03613.9[EIIID-AGA[PTS system mannose/fructose/sorbose family IID component]]	90%	17%
	A1	A2	(1)-00681	hypothetical protein	90%	17%
	A1	A2	(1)-00682	PF11175.3[DUF2961[Protein of unknown function (DUF2961)]]	90%	17%
	A1	A2	(1)-00683	PF00480.15[ROK[ROK family]]	90%	17%
	A1	A2	(1)-00684	PF01381.17[HTH_3[Helix-turn-helix];PF12844.2[HTH_19[Helix-turn-helix domain]]	90%	17%
	A1	A2	(1)-00685	PF01381.17[HTH_3[Helix-turn-helix]]	90%	0%
	A1	A2	(1)-00686	PF02486.14[Rep_trans[Replication initiation factor]]	90%	17%
	A1	A2	(1)-00687	PF11372.3[DUF3173[Domain of unknown function (DUF3173)]]	90%	17%
	A1	A2	(1)-00688	PF00847.15[AP2[AP2 domain];PF00589.17[Phage_integrase[Phage integrase family]]	90%	17%
	A1	A2	(1)-00793	PF00589.17[Phage_integrase[Phage integrase family]]	95%	14%
	A1	A2	(1)-00794	hypothetical protein	95%	0%
	A1	A2	(1)-00795	hypothetical protein	95%	0%
	A1	A2	(1)-00796	hypothetical protein	95%	0%
	A1	A2	(1)-00797	PF00851.4[SHC-T[Short C-terminal domain]]	95%	0%
	A1	A2	(1)-00803	PF05595.6[DUF771[Domain of unknown function (DUF771)]]	90%	9%
	A1	A2	(1)-00805	hypothetical protein	90%	14%
	A1	A2	(1)-01146	hypothetical protein	90%	0%
	A1	A2	(1)-01259	PF01548.12[DEDD_Tnp_IS110[Transposase];PF02371.11[Transposase_20[Transposase IS116/IS110/IS902 family]]	100%	14%
	A1	A2	(1)-01409	PF01527.15[HTH_Tnp_1[Transposase];PF13518.1[HTH_28[Helix-turn-helix domain];PF01710.11[HTH_Tnp_IS630[Transposase]]	95%	14%
	A1	A2	(1)-01451	PF06378.6[DUF1071[Protein of unknown function (DUF1071)]]	90%	17%
	A1	A2	(1)-01502	hypothetical protein	86%	3%
	A1	A2	(1)-01510	PF03960.10[ArsC[ArsC family];TIGR01617[arsC_related: transcriptional regulator, Spx/MgsR family]]	86%	17%
	A1	A2	(1)-01512	hypothetical protein	86%	14%
	A1	A2	(1)-01513	hypothetical protein	86%	17%
	A1	A2	(1)-01678	hypothetical protein	81%	17%
	A1	A2	(1)-01679	hypothetical protein	81%	17%
	A1	A2	(1)-01680	hypothetical protein	81%	17%
	A1	A2	(1)-01683	PF04276.7[DUF443[Protein of unknown function (DUF443)]]	81%	14%
	A1	A2	(1)-01685	hypothetical protein	81%	14%
	A1	A2	(1)-01806	PF00126.22[HTH_1[Bacterial regulatory helix-turn-helix protein, lysR family];PF01022.15[HTH_5[Bacterial regulatory protein, arsR family]]	86%	17%
	A1	A2	(1)-01809	PF05043.8[Mga[Mga helix-turn-helix domain];PF08279.7[HTH_11[HTH domain];PF08280.6[HTH_MgaM protein trans-acting positive regulator (MGA) HTH domain]]	86%	17%
	A1	A2	(1)-01810	hypothetical protein	86%	17%
	A1	A2	(1)-01811	hypothetical protein	86%	17%
	A1	A2	(1)-02179	PF07470.8[Glyco_hydro_88[Glycosyl Hydrolase Family 88]]	90%	6%
	A1	A2	(1)-02180	PF10222.4[DUF2264[Uncharacterized protein conserved in bacteria (DUF2264)]]	90%	6%
	A1	A2	(1)-02181	PF02470.8[Glyco_hydro_88[Glycosyl Hydrolase Family 88]]	90%	6%
	A1	A2	(1)-02182	PF00528.17[IBPD_transp_1[Binding-protein-dependent transport system inner membrane component]]	90%	6%
	A1	A2	(1)-02183	PF00528.17[IBPD_transp_1[Binding-protein-dependent transport system inner membrane component]]	90%	6%
	A1	A2	(1)-02184	PF13416.1[SBP_bac_8[Bacterial extracellular solute-binding protein];PF01547.20[SBP_bac_1[Bacterial extracellular solute-binding protein]]	90%	6%
	A1	A2	(1)-02185	PF12833.2[HTH_18[Helix-turn-helix domain];PF0165.18[HTH_AraC[Bacterial regulatory helix-turn-helix proteins, AraC family]]	90%	6%
	A1	A2	(1)-02683	PF10551.4[MULEE[MULE transposase domain];PF00872.13[Transposase_mut[Transposase, Mutator family]]	100%	14%
	A1	A2	(5)-00309	hypothetical protein	81%	9%
Cluster	Group 1	Group 2	GeneID in ref. genome	Function or Pfam*	Fraction of group 1	Fraction of group 2
	A1	B	(1)-00033	hypothetical protein	100%	7%
	A1	B	(1)-00034	hypothetical protein	100%	7%
	A1	B	(1)-00035	hypothetical protein	100%	7%
	A1	B	(1)-00036	hypothetical protein	100%	0%
	A1	B	(1)-00037	PF13242.1[Hydrolase_like[HAD-hydrolase-like];PF00702.21[Hydrolase[haloacid dehalogenase-like hydrolase]]	100%	7%
	A1	B	(1)-00038	PF00392.16[GntR[Bacterial regulatory proteins, gntR family];PF00455.17[DeoRC[DeoR C terminal sensor domain]]	100%	7%
	A1	B	(1)-00039	PF0232.13[Glyco_hydro_1[Glycosyl hydrolase family 1];TIGR01233[lacG: 6-phospho-beta-galactosidase]]	100%	7%
	A1	B	(1)-00040	PF02255.11[PTS_IIA[PTS system, Lactose/Cellobiose specific IIA subunit]]	100%	7%
	A1	B	(1)-00041	TIGR00853[pts-lac: PTS system, lactose/cellobiose family IIB component];PF02302.12[PTS_IIB[PTS system, Lactose/Cellobiose specific IIB subunit]]	100%	7%
	A1	B	(1)-00042	PF00150.13[Cellulase[Cellulase (glycosyl hydrolase family 5)];PF07745.8[Glyco_hydro_53[Glycosyl hydrolase family 53]]	100%	7%
	A1	B	(1)-00149	hypothetical protein	100%	0%
	A1	B	(1)-00226	PF12910.2[RelB_N[Antitoxin of toxin-antitoxin stability system N-terminal]]	100%	7%
	A1	B	(1)-00227	PF06769.8[Plasmid_Txe[Plasmid encoded toxin Txe];PF05016.9[Plasmid_stabil[Plasmid stabilisation system protein]]	100%	7%
	A1	B	(1)-00228	hypothetical protein	100%	7%
	A1	B	(1)-00229	hypothetical protein	100%	0%
	A1	B	(1)-00311	hypothetical protein	86%	0%
	A1	B	(1)-00329	PF13527.1[Acetyltransf_9[Acetyltransferase (GNAT) domain]]	86%	0%
	A1	B	(1)-00353	PF08279.7[HTH_11[HTH domain]]	95%	0%
	A1	B	(1)-00368	PF00232.13[Glyco_hydro_1[Glycosyl hydrolase family 1]]	95%	0%
	A1	B	(1)-00369	PF08279.7[HTH_11[HTH domain];PF08280.6[HTH_MgaM protein trans-acting positive regulator (MGA) HTH domain]]	95%	0%
	A1	B	(1)-00370	PF00358.15[PTS_EIIA_1[phosphoenolpyruvate-dependent sugar phosphotransferase system, EIIA 1];PF00232.13[Glyco_hydro_1[Glycosyl hydrolase family 1]]	95%	0%
	A1	B	(1)-00371	PF00232.13[Glyco_hydro_1[Glycosyl hydrolase family 1]]	95%	0%
	A1	B	(1)-00476	hypothetical protein	90%	0%
	A1	B	(1)-00507	PF02586.9[DUF159[Uncharacterised ACR, COG2135]]	95%	0%
	A1	B	(1)-00511	hypothetical protein	95%	0%
	A1	B	(1)-00512	hypothetical protein	95%	0%
	A1	B	(1)-00565	PF00589.17[Phage_integrase[Phage integrase family]]	95%	7%
	A1	B	(1)-00566	PF12844.2[HTH_19[Helix-turn-helix domain];PF01381.17[HTH_3[Helix-turn-helix]]	95%	7%
	A1	B	(1)-00567	TIGR01764[excise: DNA binding domain, excisionase family];PF12728.2[HTH_17[Helix-turn-helix domain]]	95%	7%
	A1	B	(1)-00568	hypothetical protein	95%	7%
	A1	B	(1)-00569	PF13560.1[HTH_31[Helix-turn-helix domain];PF01381.17[HTH_3[Helix-turn-helix];PF12844.2[HTH_19[Helix-turn-helix domain]]	90%	13%
	A1	B	(1)-00570	PF13443.1[HTH_26[Cro/C1-type HTH DNA-binding domain];PF01381.17[HTH_3[Helix-turn-helix];PF12844.2[HTH_19[Helix-turn-helix domain]]	95%	13%
	A1	B	(1)-00571	PF13248.1[zf-ribbon_3[Zinc-ribbon domain]]	95%	13%
	A1	B	(1)-00572	hypothetical protein	95%	13%
	A1	B	(1)-00573	hypothetical protein	95%	13%
	A1	B	(1)-00580 (1)-01762	PF05598.6[DUF772.2[Transposase domain (DUF772)];PF01609.16[DD_E_Tnp_1[Transposase DDE domain];PF13751.1[DD_E_Tnp_1_6[Transposase DDE domain]]	100%	0%
	A1	B	(1)-00584	hypothetical protein	81%	7%
	A1	B	(1)-00676	PF00004.24[AAA[ATPase family associated with various cellular activities (AAA)];PF00158.21[Sigma54_activa[Sigma-54 interaction domain];PF00874.15[PRD[PRD domain]]	90%	0%
	A1	B	(1)-00677	PF03610.11[EIIA-man[PTS system fructose IIA component]]	90%	0%
	A1	B	(1)-00678	PF03830.10[PTSII sorb[PTS system sorbose subfamily IIB component]]	90%	0%
	A1	B	(1)-00679	PF03609.9[EII-Sor[PTS system sorbose-specific ic component]]	90%	0%
	A1	B	(1)-00680	PF03613.9[EIIID-AGA[PTS system mannose/fructose/sorbose family IID component]]	90%	0%
	A1	B	(1)-00681	hypothetical protein	90%	0%

C6	A1	B	(1)-00682	PF11175.3[DUF2961[Protein of unknown function (DUF2961)]	90%	0%
	A1	B	(1)-00683	PF00480.15[ROK[ROK family]	90%	0%
A1	B	(1)-00684	PF01381.17[HTH_3[Helix-turn-helix];PF12844.2[HTH_19[Helix-turn-helix domain]	90%	7%	
A1	B	(1)-00685	PF01381.17[HTH_3[Helix-turn-helix]	90%	0%	
A1	B	(1)-00686	PF02486.14[Rep_trans[Replication initiation factor]	90%	0%	
A1	B	(1)-00687	PF11372.3[DUF3173[Domain of unknown function (DUF3173)]	90%	0%	
A1	B	(1)-00688	PF00847.15[AP2[AP2 domain];PF00589.17[Phage_integrase[Phage integrase family]	90%	0%	
A1	B	(1)-00693	hypothetical protein	100%	0%	
A1	B	(1)-00793 (1)-01466	PF00689.17[Phage_integrase[Phage integrase family]	95%	13%	
A1	B	(1)-00794 (1)-01465	hypothetical protein	95%	0%	
A1	B	(1)-00796 (1)-01463	hypothetical protein	95%	7%	
A1	B	(1)-00805 (1)-01454	hypothetical protein	90%	0%	
A1	B	(1)-00849 (1)-01410	PF13333.1[rve_2[Integrase core domain];PF00665.21[rve[Integrase core domain];PF13276.1[HTH_21[HTH-like domain]	90%	0%	
A1	B	(1)-00850	PF01527.15[HTH_Tnp_1[Transposase];PF13518.1[HTH_28[Helix-turn-helix domain];PF01710.11[HTH_Tnp_IS630[Transposase]	95%	0%	
A1	B	(1)-00944	hypothetical protein	95%	0%	
A1	B	(1)-00998	hypothetical protein	100%	0%	
A1	B	(1)-01075	hypothetical protein	95%	0%	
A1	B	(1)-01076	hypothetical protein	100%	0%	
A1	B	(1)-01143 (1)-01144	hypothetical protein	100%	0%	
A1	B	(1)-01146	hypothetical protein	90%	0%	
A1	B	(1)-01147	hypothetical protein	95%	0%	
A1	B	(1)-01259 (1)-01518	PF01548.12[DEDD_Tnp_IS110[Transposase];PF02371.11[Transposase_20[Transposase IS116/IS110/IS902 family]	100%	0%	
A1	B	(1)-01276	hypothetical protein	100%	0%	
A1	B	(1)-01279	PTS system, IICBA component / PF00358.15[PTS_EIIA_1[phosphoenolpyruvate-dependent sugar phosphotransferase system, EIIA 1];TIGR00830[PTBA: PTS system, glucose subfamily, IIA component]	100%	0%	
A1	B	(1)-01280	glycosyl hydrolase family protein / PF02056.11[Glyco_hydro_4[Family 4, glycosyl hydrolase]	100%	0%	
A1	B	(1)-01281	PTS system, N-acetylglucosamine-specific IIBC component / PF02378.13[PTS_EIIC[Phosphotransferase system, EIIC	100%	0%	
A1	B	(1)-01282	PF04794.7[YjC[17jC-like protein]	90%	0%	
A1	B	(1)-01283	BglG family transcriptional antiterminal / PF00874.15[PRD[PRD domain]	95%	0%	
A1	B	(1)-01384 (1)-01885	PF01610.12[DEE_Tnp_ISL3[Transposase]	100%	0%	
A1	B	(1)-01411 (1)-00848	PF01527.15[HTH_Tnp_1[Transposase];PF13518.1[HTH_28[Helix-turn-helix domain]	90%	0%	
A1	B	(1)-01451 (1)-00808	PF06378.6[DUF1071[Protein of unknown function (DUF1071)]	90%	13%	
A1	B	(1)-01456 (1)-00803	PF05595.6[DUF771[Domain of unknown function (DUF771)]	90%	13%	
A1	B	(1)-01462 (1)-01461	PF09851.4[SHOCT[Short C-terminal domain]	95%	7%	
A1	B	(1)-01464 (1)-00795	hypothetical protein	95%	0%	
A1	B	(1)-01489	hypothetical protein	95%	0%	
A1	B	(1)-01493	PF13242.1[Hydrolase_like[HAD-hydrolase-like];PF00702.21[Hydrolase[haloacetal dehalogenase-like hydrolase]	95%	13%	
A1	B	(1)-01494	TIGR00695[uxuA: mannuronate dehydratase];PF03786.8[UxuA[D-mannuronate dehydratase (UxuA)];PF01261.19[AP_endonuc_2[Xylose isomerase-like TIM barrel]	95%	13%	
A1	B	(1)-01496 (1)-01497	PF03610.11[EIIA_man[PTS system fructose IIA component]	95%	13%	
A1	B	(1)-01498	hypothetical protein	95%	13%	
A1	B	(1)-01498	PF03830.10[PTSIIb_sorb[PTS system sorbose subfamily IIB component]	95%	13%	
A1	B	(1)-01499	PF03613.9[EIID-AGA[PTS system mannose/fructose/sorbose family IID component]	95%	13%	
A1	B	(1)-01500	PF03609.9[EIIL-Sor[PTS system sorbose-specific iic component]	95%	13%	
A1	B	(1)-01501	PF13685.1[Fe-ADH_2[Iron-containing alcohol dehydrogenase];PF00465.14[Fe-ADH[Iron-containing alcohol dehydrogenase]	95%	13%	
A1	B	(1)-01502	hypothetical protein	86%	0%	
A1	B	(1)-01503	PF00389.25[2-Hacid_dh[D-isomer specific 2-hydroxyacid dehydrogenase, catalytic domain]	95%	13%	
A1	B	(1)-01504	TIGR00872[gnr_rel_6: phosphogluconate dehydrogenase (decarboxylating)]	95%	13%	
A1	B	(1)-01505	PF13580.1[SIS_2[SIS domain];PF01380.17[SIS[SIS domain];PF01418.12[HTH_6[Helix-turn-helix domain, rpiR family]	95%	13%	
A1	B	(1)-01512 (1)-01511	hypothetical protein	86%	13%	
A1	B	(1)-01516	PF00923.14[Transaldolase[Transaldolase]	95%	13%	
A1	B	(1)-01517	PF03829.8[PTSIIa_gutA[PTS system glucitol/sorbitol-specific IIA component];PF00923.14[Transaldolase[Transaldolase]	95%	13%	
A1	B	(1)-01519	PF07863.6[EIIBC-GUT_C[Sorbitol phosphotransferase enzyme II C-terminus];TIGR00825[EIIBC-GUT: PTS system, glucitol/sorbitol-specific, IIBC component];PF03612.9[EIIBC-GUT_N[Sorbitol phosphotransferase enzyme II N-terminus]	95%	13%	
A1	B	(1)-01520	TIGR00821[EIIL-GUT: PTS system, glucitol/sorbitol-specific, IIC component];PF03608.8[EIIL-GUT[PTS system enzyme II sorbitol-specific factor]	95%	13%	
A1	B	(1)-01521	TIGR00821[EIIL-GUT: PTS system, glucitol/sorbitol-specific, IIC component];PF03608.8[EIIL-GUT[PTS system enzyme II sorbitol-specific factor];PF06923.6[GuM[Glucitol operon activator protein (GuM)]	95%	13%	
A1	B	(1)-01522	PF00874.15[PRD[PRD domain];PF05043.8[Mga[Mga helix-turn-helix domain];PF00359.17[PTS_EIIA_2[Phosphoenolpyruvate-dependent sugar phosphotransferase system, EIIA 2]	95%	13%	
A1	B	(1)-01523	PF13561.1[adh_short_C2[Enoyl-(Acyl carrier protein) reductase];PF08659.5[KR[KR domain];PF00106.20[adh_short[short chain dehydrogenase];PF01370.16[Epimerase[NAD dependent epimerase/dehydratase family]	95%	13%	
A1	B	(1)-01595	PF01909.18[NTP_transf_2[Nucleotidyltransferase domain]	81%	0%	
A1	B	(1)-01677	hypothetical protein	100%	0%	
A1	B	(1)-01678	hypothetical protein	81%	0%	
A1	B	(1)-01679	hypothetical protein	81%	0%	
A1	B	(1)-01680	hypothetical protein	81%	0%	
A1	B	(1)-01683	PF04276.7[DUF443[Protein of unknown function (DUF443)]	81%	0%	
A1	B	(1)-01684	hypothetical protein	81%	0%	
A1	B	(1)-01685	hypothetical protein	81%	0%	
A1	B	(1)-01766 (1)-01763	PF02275.13[CBAH[Linear amide C-N hydrolases, choloylglycine hydrolase family]	100%	0%	
A1	B	(1)-01798	hypothetical protein	100%	0%	
A1	B	(1)-01806	PF00126.22[HTH_1[Bacterial regulatory helix-turn-helix protein, lysR family];PF01022.15[HTH_5[Bacterial regulatory protein, arsR family]	86%	0%	
A1	B	(1)-01889	PF13630.1[Sdp][Sdp/YhfL protein family]	90%	13%	
A1	B	(1)-01960 (1)-01827	hypothetical protein	90%	0%	
A1	B	(1)-01985 (1)-00014	PF03050.9[DEE_Tnp_IS66[Transposase IS66 family];PF13005.2[HTH_Tnp_IS66[putative Helix-turn-helix domain of transposase IS66]	90%	0%	
A1	B	(1)-01986 (1)-01959	PF05717.8[TnpB_IS66[IS66 Orf2 like protein]	86%	0%	
A1	B	(1)-02170	hypothetical protein	100%	0%	
A1	B	(1)-02171	PF00005.22[ABC_tran[ABC transporter];PF13304.1[AAA_21[AAA domain]	100%	0%	
A1	B	(1)-02179	PF07470.8[Glyco_hydro_88[Glucosyl Hydrolase Family 88]	90%	0%	
A1	B	(1)-02180	PF10022.4[DUF2264[Uncharacterized protein conserved in bacteria (DUF2264)]	90%	0%	
A1	B	(1)-02181	PF07470.8[Glyco_hydro_88[Glucosyl Hydrolase Family 88]	90%	0%	
A1	B	(1)-02182	PF00528.17[BPD_transp_1[Binding-protein-dependent transport system inner membrane component]	90%	0%	
A1	B	(1)-02183	PF00528.17[BPD_transp_1[Binding-protein-dependent transport system inner membrane component]	90%	0%	
A1	B	(1)-02184	PF13416.1[SBP_bac_8[Bacterial extracellular solute-binding protein];PF01547.20[SBP_bac_1[Bacterial extracellular solute-binding protein]	90%	0%	
A1	B	(1)-02185	PF12833.2[HTH_18[Helix-turn-helix domain];PF00165.18[HTH_AraC[Bacterial regulatory helix-turn-helix proteins, AraC family]	90%	0%	
A1	B	(1)-02294	PF00805.17[Pentapeptide repeats (8 copies)];PF13599.1[Pentapeptide_4[Pentapeptide repeats (9 copies)]	100%	0%	
A1	B	(1)-02295	PF02517.11[Abj[CAAX protease self-immunity]	100%	0%	
A1	B	(1)-02306 (1)-02305	PF00689.19[Acyl_transf_1[Acyltransferase (GNAT) family]	100%	0%	
A1	B	(1)-02414 (1)-01480	PF06114.8[DUF955[Domain of unknown function (DUF955)]	95%	13%	
A1	B	(1)-02430	bacteriocin-type signal sequence	100%	0%	
A1	B	(1)-02431	PF01721.13[Bacteriocin_II[Class II bacteriocin];PF08951.5[EntA_Imm[Enterocin A Immunity]	100%	0%	
A1	B	(1)-02432	PF01721.13[Bacteriocin_II[Class II bacteriocin]	100%	0%	
A1	B	(1)-02463	PF01061.19[ABC2_membrane[ABC-2 type transporter];PF12698.2[ABC2_membrane_3[ABC-2 family transporter protein]	100%	0%	
A1	B	(1)-02464	PF12698.2[ABC2_membrane_3[ABC-2 family transporter protein]	100%	0%	
A1	B	(1)-02465	PF00005.22[ABC_tran[ABC transporter];PF13304.1[AAA_21[AAA domain]	100%	0%	
A1	B	(1)-02466	PF07730.8[HiskA_3[Histidine kinase];PF02518.21[HatPase_c[Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase]	100%	0%	
A1	B	(1)-02467	PF00196.14[GerE[Bacterial regulatory proteins, luxR family];PF00072.19[Response_reg[Response regulator receiver domain]	100%	0%	
A1	B	(1)-02468	hypothetical protein	100%	0%	
A1	B	(1)-02498	hypothetical protein	90%	0%	
A1	B	(1)-02509	PF00005.22[ABC_tran[ABC transporter];PF13304.1[AAA_21[AAA domain];PF12848.2[ABC_tran_2[ABC transporter]	100%	0%	
A1	B	(1)-02577	PF05738.8[Cna_B[Cna protein B-type domain];TIGR01167[LPXTG_anchor.LPXTG-motif cell wall anchor domain]	100%	0%	
A1	B	(1)-02578	hypothetical protein	95%	0%	
A1	B	(1)-02582	PF02012.15[BNR[BNR/Asp-box repeat]	100%	0%	
A1	B	(1)-02673	PF13460.1[NAD_binding_10[NAD(PH)-binding];PF08659.5[KR[KR domain];PF08643.5[DUF1776[Fungal family of unknown function (DUF1776)];PF13561.1[adh_short_C2[Enoyl-(Acyl carrier protein) reductase]	100%	0%	
A1	B	(1)-02674	PF00132.19[Hexapep[Bacterial transferase hexapeptide (six repeats)]	100%	0%	
A1	B	(1)-02675	PF03466.15[LysR_substrate[LysR substrate binding domain]	100%	0%	
A1	B	(1)-02683 (1)-01890	PF10551.4[MULE[MULE transposase domain];PF00872.13[Transposase_mut[Transposase, Mutator family]	100%	0%	

C23	A1	B	(1)-02696	PF12730.2 ABC2 membrane_4 ABC-2 family transporter protein]		100%	7%	
	A1	B	(1)-02697	PF12679.2 ABC2 membrane_2 ABC-2 family transporter protein];PF00005.22 ABC_tran ABC transporter];PF13304.1 AAA_21 AAA domain]		100%	7%	
	A1	B	(1)-02698	hypothetical protein		100%	7%	
	A1	B	(1)-02820	TIGR01990 bPGM: beta-phosphoglucomutase];PF13419.1 HAD_2 Haloacid dehalogenase-like hydrolase];PF13242.1 Hydrolase_like HAD-hydrolase-like]		100%	0%	
	A1	B	(1)-02821	PF02595.10 Gly_kinase Glycerate kinase family];TIGR00045 TIGR00045: glycerate kinase]		100%	0%	
	A1	B	(1)-02822	PF02595.10 Gly_kinase Glycerate kinase family];PF03632.10 Glyco_hydro_65n Glycosyl hydrolase family 65 central catalytic domain]		100%	0%	
	A1	B	(1)-02823	PF01408.17 GFO_IDH_MocA Oxidoreductase family, NAD-binding Rossmann fold];PF03636.10 Glyco_hydro_65N Glycosyl hydrolase family 65, N-terminal domain]		100%	0%	
	A1	B	(1)-02824	PF01261.19 AP_endonuc_2 Xylose isomerase-like TIM barrel]		100%	0%	
	A1	B	(1)-02825	PF00107.21 ADH_zinc_N Zinc-binding dehydrogenase]		100%	0%	
	A1	B	(1)-02826	PF00528.17 BPD_transp_1 Binding-protein-dependent transport system inner membrane component]		100%	0%	
C24	A1	B	(1)-02827	PF00528.17 BPD_transp_1 Binding-protein-dependent transport system inner membrane component]		100%	0%	
	A1	B	(1)-02828	PF13531.1 SBP_bac_11 Bacterial extracellular solute-binding protein];PF13416.1 SBP_bac_8 Bacterial extracellular solute-binding protein]		100%	0%	
	A1	B	(1)-02829	PF00128.19 Alpha-amylase Alpha amylase, catalytic domain]		100%	0%	
	A1	B	(1)-02830	PF13377.1 Peripla_BP_3 Periplasmic binding protein-like domain];PF00356.16 LacI Bacterial regulatory proteins, lacI family]		100%	0%	
	A1	B	(1)-p1001	PF06970.6 RepA_N Replication initiator protein A (RepA) N-terminus]		90%	0%	
	A1	B	(1)-p1049	PF01797.11 Y1_Trg Transposase IS200 like]		86%	1%	
	A1	B	(1)-p1049	PF01385.14 OjB_IS605 Probable transposase];TIGR01766 SpaseT_teng_C: transposase, IS605 OrfB family];PF07282.6 OrfB_Zn_ribbon Putative transposase DNA-binding domain]		86%	13%	
	A1	B	(1)-p1050	PF12910.2 RelB_N Antitoxin of toxin-antitoxin stability system N-terminal];TIGR01552 phd_fam: prevent-host-death family protein];PF02604.14 PndYeFM_antitox Antitoxin Pnd_YeFM, type II toxin-antitoxin system]		86%	0%	
	A1	B	(1)-p1051	TIGR02116 toxin_Txe_YoeB: addiction module toxin, Txe/YoeB family];PF06769.8 PiPlasmid_Txe Plasmid encoded toxin Txe]		86%	0%	
	A1	B	(1)-p1060	hypothetical protein		81%	7%	
C26	A1	B	(1)-p1061	hypothetical protein		81%	0%	
	A1	B	(1)-p1062	PF06564.7 YhjQ YhjQ protein];PF00142.13 Fer4_NiH 4Fe-4S iron sulfur cluster binding proteins, NiH/frxC family];PF01656.18 CbiA CobQ/CobB/MinD/ParA nucleotide binding domain]		86%	0%	
	A1	B	(1)-p1063	hypothetical protein		86%	0%	
	A1	B	(2)-00980	PF05401.6 NodS Nodulation protein S (NodS)];PF12847.2 Methyltransf_18 Methyltransferase domain];PF00398.15 RnaAD Ribosomal RNA adenine dimethylase]		81%	7%	
C27	A1	B	(2)-01224	hypothetical protein		81%	0%	
	A1	B	(2)-01740	TIGR00826 EiIB_glc: PTS system, glucose-like IIB component];PF00367.15 PTS_EiIB phosphotransferase system, EiIB]		81%	0%	
	A1	B	(2)-01741	PF04131.9 NanE Putative N-acetylmannosamine-6-phosphate epimerase]		81%	7%	
	A1	B	(2)-01742	PF01380.17 SIS SIS domain];PF01418.12 HTH_6 Helix-turn-helix domain, rpiR family]		81%	0%	
Cluster	Group 1	Group 2	GeneID in ref. genome	Function or Pfam*	Fraction of group 1	Fraction of group 2		
C30	B	A1	(3)-00029	PF00652.17 Ricin_B_lectin Ricin-type beta-trefoil lectin domain];PF00388.14 PI-PLC-X Phosphatidylinositol-specific phospholipase C, X domain]		100%	0%	
	B	A1	(3)-00124	PF13443.1 HTH_26 Cro/C1-type HTH DNA-binding domain];PF01381.17 HTH_3 Helix-turn-helix];PF12844.2 HTH_19 Helix-turn-helix domain]		100%	0%	
	B	A1	(3)-00125	PF13396.1 PLDC_N Phospholipase_D-nuclease N-terminal]		100%	0%	
	B	A1	(3)-00126	PF00005.22 ABC_tran ABC transporter];PF13304.1 AAA_21 AAA domain]		100%	0%	
	B	A1	(3)-00127	PF12730.2 ABC2 membrane_4 ABC-2 family transporter protein]		100%	0%	
C31	B	A1	(3)-00159	hypothetical protein		100%	0%	
	B	A1	(3)-00160	PF05543.8 Penitidease_C47 Staphopain peptidase C47]		100%	0%	
	B	A1	(3)-00161	hypothetical protein		100%	0%	
	B	A1	(3)-00162	TIGR01716 RGG_Cterm: transcriptional activator, Rgg/GadR/MutR family, C-terminal domain]		100%	0%	
C32	B	A1	(3)-00257	hypothetical protein		100%	0%	
	B	A1	(3)-00258	hypothetical protein		100%	0%	
	B	A1	(3)-00259	hypothetical protein		100%	0%	
C33	B	A1	(3)-00278	PF13419.1 HAD_2 Haloacid dehalogenase-like hydrolase];PF13242.1 Hydrolase_like HAD-hydrolase-like]		100%	0%	
	B	A1	(3)-00279	PF00004.24 AAA ATPase family associated with various cellular activities (AAA)];PF01078.16 Mg_chelataase Magnesium chelataase, subunit CH1];PF13401.1 AAA_22 AAA domain];PF00158.21 Sigma54_activat Sigma-54 interaction domain]		100%	0%	
	B	A1	(3)-00282	PF03609.9 EiII-Sor PTS system sorbose-specific iic component]		100%	0%	
	B	A1	(3)-00283	PF03830.10 PTSiIB_sorb PTS system sorbose subfamily IIB component]		100%	0%	
	B	A1	(3)-00294	PF03830.10 PTSiIB_sorb PTS system sorbose subfamily IIB component];PF03610.11 EiIA-man PTS system fructose IIA component]		100%	0%	
C34	B	A1	(3)-00309	PF03830.9 ABG_Transport ABG transporter family]		100%	0%	
	B	A1	(3)-00311	TIGR01887 dipeptidase-like; putative dipeptidase];PF01546.23 Peptidase_M20 Peptidase family M20/M25/M40]		100%	0%	
	B	A1	(3)-00373	PF00589.17 Phage_integrase Phage integrase family]		93%	5%	
	B	A1	(3)-00375	PF06114.8 DUF955 Domain of unknown function (DUF955)]		93%	0%	
C35	B	A1	(3)-00390	PF01418.12 HTH_6 Helix-turn-helix domain, rpiR family];PF01380.17 SIS SIS domain]		87%	0%	
	B	A1	(3)-00391	PF02056.11 Glyco_hydro_4 Family 4 glycosyl hydrolase]		87%	0%	
	B	A1	(3)-00392	TIGR02005 PTS-IIB-alpha: PTS system, alpha-glucoside-specific IIBC component];TIGR00826 EiIB_glc: PTS system, glucose-like IIB component]		93%	0%	
	B	A1	(3)-00431	PF01656.18 CbiA CobQ/CobB/MinD/ParA nucleotide binding domain];PF09140.6 MipZ ATPase MipZ];TIGR01007 eps_fam: capsular exopolysaccharide family];PF13614.1 AAA_31 AAA domain]		100%	0%	
	B	A1	(3)-00538	PF00583.19 Acetyltransf_1 Acetyltransferase (GNAT) family]		100%	0%	
	B	A1	(3)-00575	(3)-02024	hypothetical protein		100%	0%
	B	A1	(3)-00603	PF10022.4 DUF2264 Uncharacterized protein conserved in bacteria (DUF2264)]		100%	0%	
C36	B	A1	(3)-00604	hypothetical protein		100%	0%	
	B	A1	(3)-00605	PF01301.14 Glyco_hydro_35 Glycosyl hydrolases family 35];PF02449.10 Glyco_hydro_42 Beta-galactosidase]		100%	0%	
	B	A1	(3)-00606	PF07470.8 Glyco_hydro_88 Glycosyl Hydrolase Family 88]		100%	0%	
	B	A1	(3)-00607	PF00392.16 GntR Bacterial regulatory proteins, gntR family];PF07702.8 UTRA UTRA domain]		100%	0%	
	B	A1	(3)-00610	PF00874.15 PRD PRD domain];PF05043.8 Mga Mga helix-turn-helix domain];PF00359.17 PTS_EiIA_2 Phosphoenolpyruvate-dependent sugar phosphotransferase system, EIIA 2]		100%	0%	
	B	A1	(3)-00611	PF00359.17 PTS_EiIA_2 Phosphoenolpyruvate-dependent sugar phosphotransferase system, EIIA 2]		100%	0%	
	B	A1	(3)-00612	hypothetical protein		93%	0%	
	B	A1	(3)-00613	TIGR00848 fruA: PTS system, fructose subfamily, IIA component];PF00359.17 PTS_EiIA_2 Phosphoenolpyruvate-dependent sugar phosphotransferase system, EIIA 2]		93%	0%	
	B	A1	(3)-00614	hypothetical protein		100%	0%	
	B	A1	(3)-00615	TIGR01427 PTS_IIC_fructo: PTS system, Fru family, IIC component];PF02738.13 PTS_EiIC Phosphotransferase system, EiIC]		100%	0%	
	B	A1	(3)-00616	PF00834.14 RbuU_P_3_epim Ribulose-phosphate 3 epimerase family]		100%	0%	
	B	A1	(3)-00617	PF03830.10 PTSiIB_sorb PTS system sorbose subfamily IIB component];PF03610.11 EiIA-man PTS system fructose IIA component]		100%	0%	
	B	A1	(3)-00618	PF03809.9 EiII-Sor PTS system sorbose-specific iic component]		100%	0%	
C37	B	A1	(3)-00619	PF03813.9 EiIID-AGA PTS system mannose/fructose/sorbose family IID component]		100%	0%	
	B	A1	(3)-00620	PF08124.6 Lyase_8_N Polysaccharide lyase family 8, N-terminal alpha-helical domain];		100%	0%	
	B	A1	(3)-00850	PF02839.9 CBM_5_12 Carbohydrate binding domain];PF00041.16 fn3 Fibronectin type III domain];PF00704.23 Glyco_hydro_18 Glycosyl hydrolases family 18]		100%	0%	
	B	A1	(3)-00950	Chitinase C1 / PF02839.9 CBM_5_12 Carbohydrate binding domain];PF00041.16 fn3 Fibronectin type III domain];PF00704.23 Glyco_hydro_18 Glycosyl hydrolases family 18]		100%	0%	
	B	A1	(3)-00951	TIGR01716 RGG_Cterm: transcriptional activator, Rgg/GadR/MutR family, C-terminal domain];PF01381.17 HTH_3 Helix-turn-helix];PF12844.2 HTH_19 Helix-turn-helix domain]		100%	0%	
	B	A1	(3)-00952	PF03067.10 Chitin_bind_3 Chitin binding domain]		100%	0%	
	C38	B	A1	(3)-00961	hypothetical protein		100%	0%
		B	A1	(3)-00962	hypothetical protein		100%	0%
		B	A1	(3)-00959	PF02018.12 CBM_4_9 Carbohydrate binding domain]		100%	0%
		B	A1	(3)-01091	PF12840.2 HTH_20 Helix-turn-helix domain];PF01022.15 HTH_5 Bacterial regulatory protein, arSR family]		93%	0%
B		A1	(3)-01098	(3)-01097	TIGR01167 LPXTG_anchor: LPXTG-motif cell wall anchor domain]		93%	0%
B		A1	(3)-01099	PF05043.8 Mga Mga helix-turn-helix domain];PF08280.6 HTH_Mga M protein trans-acting positive regulator (MGA) HTH domain]		93%	0%	
B		A1	(3)-01102	agrC / hypothetical protein		93%	0%	
B		A1	(3)-01103	agrA / PF04397.10 LyT LyT DNA-binding domain];PF00072.19 Response_reg Response regulator receiver domain]		93%	0%	
B		A1	(3)-01104	agrB / PF04647.10 AgrB Accessory gene regulator B]		93%	0%	
B		A1	(3)-01105	agrD / cyclic lactone autoinducer peptide		93%	0%	
C39	B	A1	(3)-01300	PF03577.10 Peptidase_C69 Peptidase family C69]		100%	0%	
	B	A1	(3)-01359	hypothetical protein		93%	19%	
	B	A1	(3)-01362	hypothetical protein		100%	19%	
	B	A1	(3)-01533	hypothetical protein		93%	0%	
	B	A1	(3)-01537	PF06987.6 TraX TraX protein]		93%	0%	
	B	A1	(3)-01538	PF06983.8 3-dmU-9_3-m 3-demethylubiquinone-9 3-methyltransferase]		87%	10%	
	B	A1	(3)-01539	PF13460.1 NAD_binding_10 NAD(P)-binding];PF04321.12 RmlD_sub_bind RmlD substrate binding domain];PF05368.8 NmA NmA-like family];PF01370.16 E epimerase NAD dependent epimerase/dehydratase family]		87%	10%	
	B	A1	(3)-01540	PF01965.19 DJ-1_Pfp DJ-1_Pfp family];PF13587.1 DJ-1_Pfp NIN-terminal domain of DJ-1_Pfp family]		87%	10%	
	B	A1	(3)-01541	PF12840.2 HTH_20 Helix-turn-helix domain];PF01022.15 HTH_5 Bacterial regulatory protein, arSR family];PF13587.1 DJ-1_Pfp NIN-terminal domain of DJ-1_Pfp family]		87%	10%	
	B	A1	(3)-01545	hypothetical protein		87%	10%	
C40	B	A1	(3)-01605	PF01717.13 Meth_synt_2 Cobalamin-independent synthase, Catalytic domain]		93%	0%	
	B	A1	(3)-01634	PF12844.2 HTH_19 Helix-turn-helix domain];PF01381.17 HTH_3 Helix-turn-helix]		100%	0%	
	B	A1	(3)-01635	hypothetical protein		100%	0%	
B	A1	(3)-01642	(3)-01641	PF00005.22 ABC_tran ABC transporter]		100%	0%	

C42	B	A1	(3)-01660	PF12730.2[ABC2_membrane_4[ABC-2 family transporter protein]	100%	0%	
	B	A1	(3)-01661	PF13304.1[AAA_21[AAA domain]	100%	0%	
C43	B	A1	(3)-01684	hypothetical protein	93%	0%	
	B	A1	(3)-01695	hypothetical protein	87%	19%	
	B	A1	(3)-01780	PF04226.8[Transgly_assoc[Transglycosylase associated protein]	87%	14%	
	B	A1	(3)-01781	PF02566.14[OsmC[OsmC-like protein];TIGR03561[organ_hyd_perox:peroxidase, Ohr subfamily]	100%	19%	
	B	A1	(3)-01782	hypothetical protein	100%	19%	
	B	A1	(3)-01783	PF01420.14[Methylase_S[Type I restriction modification DNA specificity domain]	93%	19%	
	B	A1	(3)-01784	PF00480.15[ROK[ROK family]	100%	5%	
	B	A1	(3)-01785	PF13377.1[Peripla_BP_3][Periplasmic binding protein-like domain];PF00356.16[LacI][Bacterial regulatory proteins, lacI family];PF01381.17[HTH_3][Helix-turn-helix]	100%	0%	
	B	A1	(3)-01786	TIGR01322[scrB_fam: sucrose-6-phosphate hydrolase];PF08244.7[Glyco_hydro_32C][Glycosyl hydrolases family 32 C terminal]	100%	0%	
	B	A1	(3)-01787	TIGR01996[PTS-II-BC_sucr: PTS system, sucrose-specific IIBC component];PF00358.15[PTS_EIIA_1][phosphoenolpyruvate-dependent sugar phosphotransferase system, EIIA 1]	100%	0%	
C44	B	A1	(3)-01789	PF00128.19[Alpha-amylase[Alpha amylase, catalytic domain]	100%	0%	
	B	A1	(3)-01805	PF00874.15[PRD[PRD domain];PF05043.8[Mga[Mga helix-turn-helix domain];PF00359.17[PTS_EIIA_2][Phosphoenolpyruvate-dependent sugar phosphotransferase system, EIIA 2]	93%	5%	
	B	A1	(3)-01806	PF00359.17[PTS_EIIA_2][Phosphoenolpyruvate-dependent sugar phosphotransferase system, EIIA 2]	93%	5%	
	B	A1	(3)-01807	PF02302.12[PTS_IIB[PTS system, Lactose/Cellobiose specific IIB subunit]	93%	0%	
	B	A1	(3)-01808	PF03611.9[IIc-GAT][PTS system sugar-specific permease component]	93%	0%	
	B	A1	(3)-01809	PF13580.1[SIS_2][SIS domain]	93%	0%	
	B	A1	(3)-01860	PF02302.12[PTS_IIB[PTS system, Lactose/Cellobiose specific IIB subunit]	93%	0%	
	B	A1	(3)-01861	PF01380.17[SIS][SIS domain];PF01418.12[HTH_6][Helix-turn-helix domain, rpiR family]	93%	0%	
	B	A1	(3)-01862	TIGR02004[PTS-IIBC-malX: PTS system, maltose and glucose-specific IIBC component];TIGR00826[EIIB_glc: PTS system, glucose-like IIB component]	93%	0%	
	B	A1	(3)-01863	PF00155.16[Aminotran_1_2][Aminotransferase class I and II]	100%	0%	
C45	B	A1	(3)-01865	PF13671.1[AAA_33[AAA domain];PF06414.7[Zeta_toxin[Zeta toxin]	100%	0%	
	B	A1	(3)-01866	PF00383.17[dCMP_cyt_deam_1][Cytidine and deoxycytidylate deaminase zinc-binding region]	100%	0%	
C46	B	A1	(3)-01908	hypothetical protein	93%	0%	
	B	A1	(3)-01909	PF09592.4[DUF2233[Predicted periplasmic protein (DUF2233)]	93%	0%	
C47	B	A1	(3)-01947	PF00355.21[Glycosyl_transf_2][Glycosyl transferase family 2];PF04138.9[GrA[GrA-like protein]	93%	0%	
	B	A1	(3)-01944	PF13527.1[Acetyltransf_9[Acetyltransferase (GNAT) domain];PF00583.19[Acetyltransf_1[Acetyltransferase (GNAT) family]	100%	0%	
	B	A1	(3)-01947	hypothetical protein	100%	0%	
	B	A1	(3)-02009	hypothetical protein	93%	0%	
	B	A1	(3)-02010	PF11187.3[DUF2974[Protein of unknown function (DUF2974)]	100%	0%	
C48	B	A1	(3)-02012	hypothetical protein	100%	0%	
	B	A1	(3)-02023	hypothetical protein	100%	0%	
	B	A1	(3)-02056	PF00496.17[SBP_bac_5][Bacterial extracellular solute-binding proteins, family 5 Middle]	100%	0%	
	B	A1	(3)-02057	PF00528.17[BPD_transp_1][Binding-protein-dependent transport system inner membrane component]	100%	0%	
	B	A1	(3)-02058	PF00528.17[BPD_transp_1][Binding-protein-dependent transport system inner membrane component];PF12911.2[OppC_N][N-terminal TM domain of oligopeptide transport permease C]	100%	0%	
C49	B	A1	(3)-02059	PF00005.22[ABC_tran[ABC transporter];TIGR01727[oligo_HPY: oligopeptide/dipeptide ABC transporter, ATP-binding protein, C-terminal domain]	100%	0%	
	B	A1	(3)-02060	PF00005.22[ABC_tran[ABC transporter];PF05352.7[oligo_HPY: oligopeptide/dipeptide transporter, C-terminal region]	100%	0%	
	B	A1	(3)-02061	PF01230.18[HTH[HTH domain];PF11969.3[DcpS_C[Scavenger mRNA decapping enzyme C-term binding]	100%	0%	
	B	A1	(3)-02065	PF00293.23[NUDX][NUDX domain]	93%	0%	
	B	A1	(3)-02066	hypothetical protein	93%	0%	
C50	B	A1	(3)-02085	PF00226.26[DnaJ][DnaJ domain]	100%	0%	
	B	A1	(3)-02086	PF00753.22[Lactamase_B][Metallo-beta-lactamase superfamily];PF12706.2[Lactamase_B_2][Beta-lactamase superfamily domain]	100%	0%	
C51	B	A1	(3)-02260	hypothetical protein	100%	0%	
	B	A1	(3)-02302	hypothetical protein	87%	0%	
	B	A1	(3)-02464	PF05043.8[Mga[Mga helix-turn-helix domain]	100%	0%	
	B	A1	(3)-02465	PF05043.8[Mga[Mga helix-turn-helix domain]	100%	0%	
	B	A1	(3)-02474	hypothetical protein	100%	0%	
C52	B	A1	(3)-02475	hypothetical protein	87%	0%	
	B	A1	(3)-02477	hypothetical protein	100%	0%	
	B	A1	(3)-02478	hypothetical protein	93%	0%	
	B	A1	(3)-02509	hypothetical protein	93%	0%	
	B	A1	(3)-02510	PF06013.7[WXG100[Proteins of 100 residues with WXG];TIGR03930[WXG100_ESAT6: WXG100 family type VII secretion target];PF10824.3[DUF2580[Protein of unknown function (DUF2580)]	87%	0%	
C53	B	A1	(3)-02511	TIGR03929[T7_esaA_Nterm: type VII secretion protein EsaA]	87%	0%	
	B	A1	(3)-02512	hypothetical protein	87%	0%	
	B	A1	(3)-02513	PF08817.5[YukD][WXG100 protein secretion system (Wss), protein YukD]	87%	0%	
	B	A1	(3)-02515 (3)-02514	TIGR03926[T7_EssB: type VII secretion protein EssB];PF10140.4[YukC][WXG100 protein secretion system (Wss), protein YukC]	87%	0%	
	B	A1	(3)-02516 (3)-02517	PF01580.13[FtsK_SpoIIIE][FtsK/SpoIIIE family];PF12846.2[AAA_10][AAA-like domain];TIGR03928[T7_EssCb: Firm: type VII secretion protein EssC]	87%	0%	
	B	A1	(3)-02525	PF01832.15[GaJA[Galactosaminidase[Mannosyl-glycoprotein endo-beta-N-acetylglucosaminidase];PF07538.6][Chv1][Clostridial hydrophobic W]	100%	0%	
	B	A1	(3)-02550	PF04896.7[VanZ][VanZ-like family]	93%	0%	
	B	A1	(3)-02576	PF00094.24[AAAT][Pase family associated with various cellular activities (AAA)];PF00158.21[Sigma54_activat][Sigma-54 interaction domain];PF07724.9[AAA_2][AAA domain (Cdc48 subfamily)]	93%	0%	
	B	A1	(3)-02636	PF03009.12[GDPD][Glycerophosphoryl diester phosphodiesterase family]	93%	0%	
	B	A1	(3)-02648	PF02525.12[Flavodoxin_2][Flavodoxin-like fold];PF03358.10[FMN_red][NADPH-dependent FMN reductase]	93%	0%	
C54	B	A1	(3)-02650	hypothetical protein	93%	0%	
	B	A1	(3)-02668	PF01548.12[DEDD_Tnp_IS110][Transposase];PF02371.11[Transposase_20][Transposase IS116/IS110/S902 family]	93%	5%	
	B	A1	(3)-02841	hypothetical protein	100%	0%	
	B	A1	(3)-02866	TIGR00410[lacE: PTS system, lactose/cellobiose family IIC component];PF02378.13[PTS_EIIC][Phosphotransferase system, EIIC]	100%	0%	
	B	A1	(3)-02871	PF05043.8[Mga[Mga helix-turn-helix domain];PF08280.6[HTH_Mga][Mga protein trans-acting positive regulator (MGA) HTH domain]	100%	0%	
	B	A1	(3)-02872	hypothetical protein	100%	0%	
	B	A1	(3)-02873	hypothetical protein	100%	0%	
	B	A1	(3)-02874	hypothetical protein	100%	0%	
	B	A1	(3)-02875	hypothetical protein	100%	0%	
	B	A1	(3)-02876	PF11797.3[DUF3324[Protein of unknown function C-terminal (DUF3324)];PF06030.7[DUF916[Bacterial protein of unknown function (DUF916)]	100%	0%	
C22	B	A1	(3)-02878	hypothetical protein	87%	0%	
	B	A1	(3)-02890	hypothetical protein	100%	0%	
	B	A1	(4)-01523	PF00874.15[PRD[PRD domain]	87%	5%	
	B	A1	(4)-02162	PF00085.15[Thioredoxin][Thioredoxin]	87%	0%	
	B	A1	(4)-04231	hypothetical protein	87%	0%	
	Cluster	Group 1	Group 2	GeneID in ref. genome	Function or Pfam ^a	Fraction of group 1	Fraction of group 2
	C24	A2	B	(1)-02830	PF13377.1[Peripla_BP_3][Periplasmic binding protein-like domain];PF00356.16[LacI][Bacterial regulatory proteins, lacI family]	100%	0%
		A2	B	(1)-02829	PF00128.19[Alpha-amylase[Alpha amylase, catalytic domain]	100%	0%
		A2	B	(1)-02828	PF13531.1[SBP_bac_11][Bacterial extracellular solute-binding protein];PF13416.1[SBP_bac_8][Bacterial extracellular solute-binding protein]	100%	0%
		A2	B	(1)-02306 (1)-02305	PF00583.19[Acetyltransf_1[Acetyltransferase (GNAT) family]	100%	0%
A2		B	(1)-02295	PF02517.11[Abi][CAAX protease self-immunity]	86%	0%	
C8	A2	B	(1)-01075	hypothetical protein	100%	0%	
	A2	B	(1)-01076	hypothetical protein	100%	0%	
C13	A2	B	(1)-01677	hypothetical protein	100%	0%	
	A2	B	(1)-01684	hypothetical protein	97%	0%	
C24	A2	B	(1)-02820	TIGR01990[bPGM: beta-phosphoglucomutase];PF13419.1[HAD_2][Haloacid dehalogenase-like hydrolase];PF13242.1[Hydrolase_like][HAD-hydrolase-like]	100%	0%	
	A2	B	(1)-02821	PF02595.10[Gly_kinase][Glycerate kinase family];TIGR00045[Glycerate kinase]	100%	0%	
	A2	B	(1)-02822	PF02595.10[Gly_kinase][Glycerate kinase family];PF03632.10[Glyco_hydro_65m][Glycosyl hydrolase family 65 central catalytic domain]	100%	0%	
	A2	B	(1)-02824	PF01408.17[ICF_IDH_MoxA][Oxidoreductase family, NAD-binding Rossmann fold];PF03636.10[Glyco_hydro_65N][Glycosyl hydrolase family 65, N-terminal domain]	100%	0%	
	A2	B	(1)-02824	PF01261.19[ATP_endonuc_2][Xylose isomerase-like TIM barre]	100%	0%	
	A2	B	(1)-02825	PF00107.21[ADH_zinc_N][Zinc-binding dehydrogenase]	100%	0%	
	A2	B	(1)-02826	PF00528.17[BPD_transp_1][Binding-protein-dependent transport system inner membrane component]	100%	0%	
	A2	B	(1)-02827	PF00528.17[BPD_transp_1][Binding-protein-dependent transport system inner membrane component]	100%	0%	
	A2	B	(1)-02675	PF03466.15[LysR_substrate][LysR substrate binding domain]	97%	0%	
	A2	B	(1)-02674	PF00132.19[Hexapep][Bacterial transferase hexapeptide (six repeats)]	97%	0%	
C22	A2	B	(1)-02673	PF13460.1[NAD_binding_10][NADH(P)-binding];PF08659.5[KR1][KR domain];PF08643.5[DUF1776][Fungal family of unknown function (DUF1776)];PF13561.1[adh_short_C2][Enoyl-(Acyl carrier protein) reductase]	97%	0%	
	A2	B	(1)-00229	hypothetical protein	84%	0%	

C2	A2	B	(1)-00228	hypothetical protein		95%	7%	
	A2	B	(1)-00227	PF06769.8 Plasmid_Txe Plasmid encoded toxin Txe].PF05016.9 Plasmid_stabil Plasmid stabilisation system protein]		95%	7%	
C10	A2	B	(1)-00226	PF12910.2 RelB_N Antitoxin of toxin-antitoxin stability system N-terminal]		95%	7%	
	A2	B	(1)-00329	PF13527.1 Acetyltransf_9 Acetyltransferase (GNAT) domain]		89%	0%	
	A2	B	(1)-01283	BaG family transcriptional antiterminal / PF00874.15 PRD PRD domain]		100%	0%	
	A2	B	(1)-01281	PTS system, N-acetylglucosamine-specific [IIBC component / PF02378.13 PTS_EIIC Phosphotransferase system, EIIC		100%	0%	
	A2	B	(1)-01280	glycosyl hydrolase family protein / PF02056.11 Glyco_hydro_4 Family 4 glycosyl hydrolase]		100%	0%	
	A2	B	(1)-01279	PTS system, IICBA component / PF00358.15 PTS_EIIA_1 phosphoenolpyruvate-dependent sugar phosphotransferase system, EIIA 1 TIGR00830 PTBA: PTS system, glucose subfamily, IIA component]		100%	0%	
	A2	B	(1)-02508	hypothetical protein		100%	0%	
	A2	B	(1)-02509	PF00005.22 ABC_tran ABC transporter].PF13304.1 AAA_21 AAA domain].PF12848.2 ABC_tran_2 ABC transporter]		100%	0%	
	A2	B	(1)-02468	hypothetical protein		100%	0%	
	A2	B	(1)-02467	PF00196.14 GerE Bacterial regulatory proteins, luxR family].PF00072.19 Response_reg Response regulator receiver domain]		100%	0%	
C19	A2	B	(1)-02466	PF07730.8 HiskA_3 Histidine kinase].PF02518.21 HATPase_c Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase]		100%	0%	
	A2	B	(1)-02465	PF00005.22 ABC_tran ABC transporter].PF13304.1 AAA_21 AAA domain]		100%	0%	
	A2	B	(1)-02464	PF12698.2 ABC2_membrane_3 ABC-2 family transporter protein]		100%	0%	
	A2	B	(1)-02463	PF01281.19 ABC2_membrane ABC-2 type transporter].PF12698.2 ABC2_membrane_3 ABC-2 family transporter protein]		100%	0%	
	A2	B	(1)-01786 (1)-01763	PF02275.13 CBAA Linear amide C-N hydrolases, cholestyglycine hydrolase family]		95%	0%	
	A2	B	(1)-02582	PF02012.15 BNR BNR/Asp-box repeat]		92%	0%	
	A2	B	(1)-01276	hypothetical protein		92%	0%	
	A2	B	(1)-02696	PF12730.2 ABC2_membrane_4 ABC-2 family transporter protein]		97%	7%	
	A2	B	(1)-02697	PF12679.2 ABC2_membrane_2 ABC-2 family transporter protein].PF00005.22 ABC_tran ABC transporter].PF13304.1 AAA_21 AAA domain]		100%	7%	
	A2	B	(1)-02698	hypothetical protein		92%	7%	
C23	A2	B	(1)-00998	hypothetical protein		92%	0%	
	A2	B	(1)-01143 (1)-01144	hypothetical protein		81%	0%	
	A2	B	(1)-02577	PF05738.8 Cna_B Cna protein B-type domain].TIGR01167 LPXTG_anchor: LPXTG-motif cell wall anchor domain]		97%	0%	
	A2	B	(1)-01798	hypothetical protein		86%	0%	
	A2	B	(1)-01282	PF04794.7 YjvC YjvC-like protein]		100%	0%	
	A2	B	(1)-02231	PF00149.23 Metallophos Calcineurin-like phosphoesterase]		84%	0%	
	A2	B	(1)-00149	hypothetical protein		92%	0%	
	Cluster	Group 1	Group 2	GeneID in ref. genome	Function or Pfam*	Fraction of group 1	Fraction of group 2	
	C30	B	A2	(3)-00029	PF00652.17 Ricin_B_lectin Ricin-type beta-trefoil lectin domain].PF00388.14 PI-PLC_X Phosphatidylinositol-specific phospholipase C, X domain]		100%	0%
		B	A2	(3)-00124	PF13443.1 HTH_26 Cro/C1-type HTH DNA-binding domain].PF01381.17 HTH_3 Helix-turn-helix].PF12844.2 HTH_19 Helix-turn-helix domain]		100%	5%
B		A2	(3)-00125	PF13396.1 PLDc_N Phospholipase_D-nuclease N-terminal]		100%	5%	
B		A2	(3)-00126	PF00005.22 ABC_tran ABC transporter].PF13304.1 AAA_21 AAA domain]		100%	8%	
B		A2	(3)-00127	PF12730.2 ABC2_membrane_4 ABC-2 family transporter protein]		100%	5%	
B		A2	(3)-00159	hypothetical protein		100%	0%	
B		A2	(3)-00160	PF05543.8 Peptidase_C47 Staphopain peptidase C47]		100%	0%	
B		A2	(3)-00161	hypothetical protein		100%	0%	
B		A2	(3)-00162	TIGR01716 RGG_Cterm: transcriptional activator, Rgg/GadR/MutR family, C-terminal domain]		100%	0%	
B		A2	(3)-00257	hypothetical protein		100%	5%	
C32	B	A2	(3)-00258	hypothetical protein		100%	5%	
	B	A2	(3)-00259	hypothetical protein		100%	5%	
	B	A2	(3)-00278	PF13419.1 HAD_2 Haloacid dehalogenase-like hydrolase].PF13242.1 Hydrolase_like HAD-hydrolyase-like]		100%	14%	
	B	A2	(3)-00279	PF00004.24 AAA ATPase family associated with various cellular activities (AAA).PF01078.16 Mg_chelatase Magnesium chelatase, subunit ChI].PF13401.1 AAA_22 AAA domain].PF00158.21 Sigma54_activat Sigma-54 interaction domain]		100%	14%	
	B	A2	(3)-00282	PF03609.9 EII-Sor PTS system sorbose-specific ic component]		100%	14%	
	B	A2	(3)-00283	PF03630.10 PTS IB sorb PTS system sorbose subfamily IIB component]		100%	14%	
	B	A2	(3)-00284	PF03630.10 PTS IB sorb PTS system sorbose subfamily IIB component].PF03610.11 EIIA-man PTS system fructose IIA component]		100%	14%	
	B	A2	(3)-00310 (3)-00309	PF03806.8 ABC_tran Aba1 putative transporter family]		100%	5%	
	B	A2	(3)-00311 (3)-00312	TIGR01887 dipeptidase-like: putative dipeptidase].PF01546.23 Peptidase_M20 Peptidase family M20/M25/M40]		100%	5%	
	B	A2	(3)-00373 (3)-00372	PF00589.17 Phage_integrase Phage integrase family]		93%	5%	
C35	B	A2	(3)-00390	PF01418.12 HTH_6 Helix-turn-helix domain, rpiR family].PF01380.17 SIS SIS domain]		87%	0%	
	B	A2	(3)-00391	PF02056.11 Glyco_hydro_4 Family 4 glycosyl hydrolase]		87%	0%	
	B	A2	(3)-00392	TIGR02005 PTS-IIBC-alpha: PTS system, alpha-glucoside-specific IIBC component].TIGR00826 EIIb_glc: PTS system, glucose-like IIB component]		93%	0%	
	B	A2	(3)-00431	PF01656.18 CobA CobB/CobD/ParA nucleotide binding domain].PF09140.6 MipZ ATPase MipZ].TIGR01007 eps_fam: capsular exopolysaccharide family].PF13614.1 AAA_31 AAA domain]		100%	5%	
	B	A2	(3)-00538	PF00583.19 Acetyltransf_1 Acetyltransferase (GNAT) family]		100%	3%	
	B	A2	(3)-00575 (3)-02024	hypothetical protein		100%	5%	
	B	A2	(3)-00603	PF10022.4 DUF2264 Uncharacterized protein conserved in bacteria (DUF2264)]		100%	0%	
	B	A2	(3)-00604	hypothetical protein		100%	0%	
	B	A2	(3)-00605	PF01301.14 Glyco_hydro_35 Glycosyl hydrolases family 35].PF02449.10 Glyco_hydro_42 Beta-galactosidase]		100%	0%	
	B	A2	(3)-00606	PF07470.8 Glyco_hydro_88 Glycosyl Hydrolase Family 88]		100%	0%	
C36	B	A2	(3)-00607	PF00392.16 GntR Bacterial regulatory proteins, gntR family].PF07702.8 UTRA UTRA domain]		100%	0%	
	B	A2	(3)-00610	PF00874.15 PRD PRD domain].PF05043.8 Mga Mga helix-turn-helix domain].PF00359.17 PTS_EIIA_2 Phosphoenolpyruvate-dependent sugar phosphotransferase system, EIIA 2]		100%	0%	
	B	A2	(3)-00611	PF00359.17 PTS_EIIA_2 Phosphoenolpyruvate-dependent sugar phosphotransferase system, EIIA 2]		100%	0%	
	B	A2	(3)-00612	hypothetical protein		93%	0%	
	B	A2	(3)-00613	TIGR00848 fruA: PTS system, fructose subfamily, IIA component].PF00359.17 PTS_EIIA_2 Phosphoenolpyruvate-dependent sugar phosphotransferase system, EIIA 2]		93%	0%	
	B	A2	(3)-00614	hypothetical protein		100%	0%	
	B	A2	(3)-00615	TIGR01427 PTS_IIC_fructo: PTS system, Fru family, IIC component].PF02378.13 PTS_EIIC Phosphotransferase system, EIIC]		100%	0%	
	B	A2	(3)-00616	PF00834.14 RbuL_P_3_epim Ribulose-phosphate 3 epimerase family]		100%	0%	
	B	A2	(3)-00617	PF03630.10 PTS IB sorb PTS system sorbose subfamily IIB component].PF03610.11 EIIA-man PTS system fructose IIA component]		100%	0%	
	B	A2	(3)-00618	PF03609.9 EII-Sor PTS system sorbose-specific ic component]		100%	0%	
C37	B	A2	(3)-00619	PF03613.9 EIID-AGA PTS system mannose/fructose/sorbose family IID component]		100%	0%	
	B	A2	(3)-00620 (3)-00621	PF08124.6 Lyase_8_N Polysaccharide lyase family 8, N terminal alpha-helical domain].PF00041.16 fn3 Fibronectin type III domain].PF00704.23 Glyco_hydro_18 Glycosyl hydrolases family 18]		100%	0%	
	B	A2	(3)-00850	PF02839.9 CBM_5_12 Carbohydrate binding domain].PF00041.16 fn3 Fibronectin type III domain].PF00704.23 Glyco_hydro_18 Glycosyl hydrolases family 18]		100%	11%	
	B	A2	(3)-00950	Chitinase C1 / PF02839.9 CBM_5_12 Carbohydrate binding domain].PF00041.16 fn3 Fibronectin type III domain].PF00704.23 Glyco_hydro_18 Glycosyl hydrolases family 18]		100%	0%	
	B	A2	(3)-00951	TIGR01716 RGG_Cterm: transcriptional activator, Rgg/GadR/MutR family, C-terminal domain].PF01381.17 HTH_3 Helix-turn-helix].PF12844.2 HTH_19 Helix-turn-helix domain]		100%	0%	
	B	A2	(3)-00952	PF03067.10 Chitin_bind_3 Chitin binding domain]		100%	0%	
	B	A2	(3)-00961	hypothetical protein		100%	0%	
	B	A2	(3)-00962	hypothetical protein		100%	0%	
	B	A2	(3)-00999	PF02018.12 CBM_4_9 Carbohydrate binding domain]		100%	11%	
	B	A2	(3)-01041	PF12844.2 HTH_20 Helix-turn-helix domain].PF1022.15 HTH_5 Bacterial regulatory protein, arsR family]		93%	3%	
C39	B	A2	(3)-01098 (3)-01097	TIGR01167 LPXTG_anchor: LPXTG-motif cell wall anchor domain]		93%	3%	
	B	A2	(3)-01099	PF05043.8 Mga Mga helix-turn-helix domain].PF08280.6 HTH_Mga M protein trans-acting positive regulator (MGA) HTH domain]		93%	3%	
	B	A2	(3)-01102	agrC / hypothetical protein		93%	3%	
	B	A2	(3)-01103	agrA / PF04397.10 LyT LyT DNA-binding domain].PF00072.19 Response_reg Response regulator receiver domain]		93%	3%	
	B	A2	(3)-01104	agrB / PF04647.10 AgrB Accessory gene regulator B]		93%	3%	
	B	A2	(3)-01105	agrD / cyclic lactone autoinducer peptide		93%	3%	
	B	A2	(3)-01300	PF03577.10 Peptidase_C69 Peptidase family C69]		100%	0%	
	B	A2	(3)-01359	hypothetical protein		93%	0%	
	B	A2	(3)-01362	hypothetical protein		100%	0%	
	B	A2	(3)-01533	hypothetical protein		93%	3%	
C42	B	A2	(3)-01642 (3)-01641	PF00005.22 ABC_tran ABC transporter]		100%	0%	
	B	A2	(3)-01660	PF12730.2 ABC2_membrane_4 ABC-2 family transporter protein]		100%	0%	
	B	A2	(3)-01661	PF13304.1 AAA_21 AAA domain]		100%	3%	
	B	A2	(3)-01684	hypothetical protein		93%	0%	
	B	A2	(3)-01695	hypothetical protein		87%	14%	
C43	B	A2	(3)-01784	PF00480.15 ROK ROK family]		100%	14%	
	B	A2	(3)-01785	PF13377.1 Peripla_BP_3 Periplasmic binding protein-like domain].PF00356.16 LacI Bacterial regulatory proteins, lacI family].PF01381.17 HTH_3 Helix-turn-helix]		100%	14%	
	B	A2	(3)-01786	TIGR01322 scrB_fam: sucrose-6-phosphate hydrolase].PF08244.7 Glyco_hydro_32C Glycosyl hydrolases family 32 C terminal]		100%	14%	
	B	A2	(3)-01787	TIGR01996 PTS-II-BC-sucr: PTS system, sucrose-specific IIBC component].PF00358.15 PTS_EIIA_1 phosphoenolpyruvate-dependent sugar phosphotransferase system, EIIA 1]		100%	16%	
	B	A2	(3)-01789 (3)-01788	PF00128.19 Alpha-amylase Alpha amylase, catalytic domain]		100%	16%	

C44	B	A2	(3)-01805	PF00874.15 PRD PRD domain PF05043.8 Mga[Mga helix-turn-helix domain] PF00359.17 PTS_EIIA_2[Phosphoenolpyruvate-dependent sugar phosphotransferase system, EIIA 2]	93%	16%
	B	A2	(3)-01806	PF00359.17 PTS_EIIA_2[Phosphoenolpyruvate-dependent sugar phosphotransferase system, EIIA 2]	93%	16%
	B	A2	(3)-01807	PF02302.12 PTS_IIB PTS system, Lactose/Cellobiose specific IIB subunit	93%	16%
	B	A2	(3)-01808	PF03611.9 EIIc-GAT PTS system sugar-specific permease component	93%	16%
C45	B	A2	(3)-01809	PF13580.1 SIS_2 SIS domain	93%	0%
	B	A2	(3)-01860	PF02302.12 PTS_IIB PTS system, Lactose/Cellobiose specific IIB subunit	93%	0%
	B	A2	(3)-01861	PF01380.17 SIS SIS domain PF01418.12 HTH_6 Helix-turn-helix domain, rpiR family	93%	0%
	B	A2	(3)-01862	TIGR02004 PTS-IIBC-malX: PTS system, maltose and glucose-specific IIBC component TIGR00826 EIIb_glc: PTS system, glucose-like IIB component	93%	0%
C46	B	A2	(3)-01863	PF00155.16 Aminotran_1_2 Aminotransferase class I and II	100%	0%
	B	A2	(3)-01865	PF13671.1 AAA_33 AAA domain PF06414.7 Zeta_toxin Zeta toxin	100%	0%
	B	A2	(3)-01866	PF00383.17 dCMP_cyt_deam_1 Cytidine and deoxycytidylate deaminase zinc-binding region	100%	5%
	B	A2	(3)-01908	hypothetical protein	93%	5%
C47	B	A2	(3)-01909	PF09992.4 DUF2233 Predicted periplasmic protein (DUF2233)	93%	5%
	B	A2	(3)-01910	PF00535.21 Glycosyl_transf_2 Glycosyl transferase family 2 PF04138.9 GtrA GtrA-like protein	93%	5%
	B	A2	(3)-01944	PF13527.1 Acetyltransf_9 Acetyltransferase (GNAT) domain PF00583.19 Acetyltransf_1 Acetyltransferase (GNAT) family	100%	5%
	B	A2	(3)-01947	hypothetical protein	100%	5%
C48	B	A2	(3)-02009	hypothetical protein	93%	5%
	B	A2	(3)-02010	PF11187.3 DUF2974 Protein of unknown function (DUF2974)	100%	5%
	B	A2	(3)-02012	hypothetical protein	100%	5%
	B	A2	(3)-02023	hypothetical protein	100%	5%
C49	B	A2	(3)-02056	PF00496.17 SBP_bac_5 Bacterial extracellular solute-binding proteins, family 5 Middle	100%	11%
	B	A2	(3)-02057	PF00528.17 BPD_transp_1 Binding-protein-dependent transport system inner membrane component	100%	11%
	B	A2	(3)-02058	PF00528.17 BPD_transp_1 Binding-protein-dependent transport system inner membrane component PF12911.2 OppC_N [N-terminal TM domain of oligopeptide transport permease C]	100%	11%
	B	A2	(3)-02059	PF00005.22 ABC_tran ABC transporter TIGR01727 oligo_HP_Y: oligopeptide/dipeptide ABC transporter, ATP-binding protein, C-terminal domain	100%	11%
C50	B	A2	(3)-02060	PF00005.22 ABC_tran ABC transporter PF08352.7 oligo_HP_Y Oligopeptide/dipeptide transporter, C-terminal region	100%	11%
	B	A2	(3)-02061	PF01230.18 HIT HIT domain PF11969.3 DcpS_C Scavenger mRNA decapping enzyme C-term binding	100%	11%
	B	A2	(3)-02065	PF00093.23 NUD NUDIX domain	93%	3%
	B	A2	(3)-02066	hypothetical protein	93%	3%
C51	B	A2	(3)-02085	PF00226.26 DnaJ DnaJ domain	100%	5%
	B	A2	(3)-02086	PF00753.22 Lactamase_B Metallo-beta-lactamase superfamily PF12706.2 Lactamase_B_2 Beta-lactamase superfamily domain	100%	5%
	B	A2	(3)-02260	hypothetical protein	100%	0%
	B	A2	(3)-02302	hypothetical protein	87%	0%
C52	B	A2	(3)-02464	PF05043.8 Mga[Mga helix-turn-helix domain]	100%	0%
	B	A2	(3)-02465	PF05043.8 Mga[Mga helix-turn-helix domain]	100%	0%
	B	A2	(3)-02474	hypothetical protein	100%	0%
	B	A2	(3)-02475	hypothetical protein	87%	0%
C53	B	A2	(3)-02477	hypothetical protein	100%	0%
	B	A2	(3)-02478	hypothetical protein	93%	0%
	B	A2	(3)-02509	hypothetical protein	93%	0%
	B	A2	(3)-02510	PF06013.7 WXG100 Proteins of 100 residues with WXG TIGR03930 WXG100_ESAT6: WXG100 family type VII secretion target PF10824.3 DUF2580 Protein of unknown function (DUF2580)	87%	0%
C54	B	A2	(3)-02511	TIGR03929 T7_esaA_Nterm: type VII secretion protein EsaA	87%	0%
	B	A2	(3)-02512	hypothetical protein	87%	0%
	B	A2	(3)-02513	PF08817.5 YukD WXG100 protein secretion system (Wss), protein YukD	87%	0%
	B	A2	(3)-02515 (3)-02514	TIGR03926 T7_EssB: type VII secretion protein EssB PF10140.4 YukC WXG100 protein secretion system (Wss), protein YukC	87%	0%
C55	B	A2	(3)-02516 (3)-02517	PF01580.13 FtsK_SpoIIIE FtsK/SpoIIIE family PF12846.2 AAA_10 AAA-like domain TIGR03928 T7_EssCb_Firm: type VII secretion protein EssC	87%	0%
	B	A2	(3)-02525	PF01832.15 Glucosaminidase Mannosyl-glycoprotein endo-beta-N-acetylglucosaminidase PF07538.6 ChW Clostridial hydrophobic W	100%	0%
	B	A2	(3)-02550	PF04892.7 VanZ VanZ like family	87%	5%
	B	A2	(3)-02576	PF00004.24 AAA ATPase family associated with various cellular activities (AAA) PF00158.21 Sigma54_activat Sigma-54 interaction domain PF07724.9 AAA_2 AAA domain (Cdc48 subfamily)	93%	19%
C56	B	A2	(3)-02636	PF03009.12 GDP Glycerophosphoryl diester phosphodiesterase family	93%	5%
	B	A2	(3)-02848	PF02525.12 Flavodoxin_2 Flavodoxin-like fold PF03368.10 FMN_red NADPH-dependent FMN reductase	93%	3%
	B	A2	(3)-02850	hypothetical protein	93%	3%
	B	A2	(3)-02868	PF01548.12 DEDD_Tnp_IS110 Transposase PF02371.11 Transposase_20 Transposase IS116/IS110/IS902 family	93%	14%
C57	B	A2	(3)-02841	hypothetical protein	100%	0%
	B	A2	(3)-02866	TIGR00410 IacE: PTS system, lactose/cellobiose family IIC component PF02378.13 PTS_EIIC Phosphotransferase system, EIIC	100%	0%
	B	A2	(3)-02871	PF05043.8 Mga[Mga helix-turn-helix domain] PF08280.6 HTH_Mga Mga protein trans-acting positive regulator (MGA) HTH domain	100%	0%
	B	A2	(3)-02872	hypothetical protein	100%	0%
C58	B	A2	(3)-02873	hypothetical protein	100%	0%
	B	A2	(3)-02874	hypothetical protein	100%	0%
	B	A2	(3)-02875	hypothetical protein	100%	0%
	B	A2	(3)-02876	PF11797.3 DUF3324 Protein of unknown function C-terminal (DUF3324) PF06030.7 DUF916 Bacterial protein of unknown function (DUF916)	100%	0%
C59	B	A2	(3)-02878	hypothetical protein	87%	5%
	B	A2	(3)-02890	hypothetical protein	100%	0%
	B	A2	(4)-02162	PF00085.15 Thioredoxin Thioredoxin	87%	0%

(1)- stands for EFAU004_in the AUS0004 reference genome, (2)- for EfmE4452_in the E4452 genome, (3)- for EfmE980_in the E980 genome, (4)- for EFGV_in the Com12 genome and (5)- for EfmE1162 in the E1162 genome

* Italicized annotations are from the reference genome