

**Table S1:** List of variable genes identified in the genomes of *B. adolescentis* strains through CGH experiments

ORF	Product	6T	125B	145B	153B	22L	369B	703B
BAD_0003	recombination protein RecF	+	-	+	+	+	-	+
BAD_0006	DNA gyrase subunit A	+	+	+	+	+	-	+
BAD_0012	carbonic anhydrase	+	+	+	+	-	+	+
BAD_0014	PE family protein (fragment)	+	+	+	+	-	+	+
BAD_0015	SSU ribosomal protein S8P	+	+	+	-	-	+	+
BAD_0017	phage-associated protein	+	+	+	+	-	+	+
BAD_0019	hypothetical protein	+	+	+	-	+	+	+
BAD_0020	hypothetical protein	+	+	+	+	-	+	+
BAD_0021	hypothetical protein	+	+	+	-	+	+	-
BAD_0027	tryptophanyl-tRNA synthetase	+	+	+	-	+	+	+
BAD_0028	hypothetical protein	+	+	+	-	+	+	+
BAD_0038	serine-threonine protein kinase	+	+	+	+	-	+	-
BAD_0043	hypothetical protein	+	-	-	+	+	-	+
BAD_0048	hypothetical protein	+	+	-	+	+	-	+
BAD_0052	hypothetical protein	+	-	-	-	-	-	-
BAD_0053	hypothetical protein	+	+	-	-	-	-	-
BAD_0054	putative exodeoxyribonuclease V	+	+	+	-	-	+	-
BAD_0055	response regulator of two-component system	+	+	+	-	+	+	-
BAD_0056	queuine tRNA-ribosyltransferase	+	-	-	+	+	+	+
BAD_0060	hypothetical protein	+	+	-	-	-	+	+
BAD_0066	fructose-bisphosphate aldolase	+	+	+	+	+	-	+
BAD_0068	voltage gated channel protein	+	+	+	+	+	+	-
BAD_0070	branched-chain amino acid ABC-type transport system permease components	+	+	+	+	+	+	-
BAD_0071	branched-chain amino acid transport system permease protein	+	+	+	+	+	+	-
BAD_0072	branched-chain amino acid transport system ATP-binding protein	+	+	+	+	+	+	-
BAD_0073	ABC-type branched-chain amino acid transport systems ATPase component	+	+	+	+	+	+	-
BAD_0074	branched-chain amino acid transport system substrate-binding protein	+	+	+	+	+	+	-
BAD_0075	LacI-type transcriptional regulator	+	+	+	+	+	+	-
BAD_0076	4-amino-4-deoxychorismate lyase	+	+	+	+	+	+	-
BAD_0083	sialic acid-specific 9-O-acetyltransferase	+	+	+	+	-	+	+
BAD_0084	aromatic amino acid transport protein AroP	+	+	+	+	-	+	+
BAD_0088	amino acid permease	+	+	+	-	-	+	-
BAD_0090	thiamine biosynthesis protein ThiF	+	+	+	+	+	-	+
BAD_0093	ABC transporter permease	+	+	+	+	+	-	+
BAD_0096	hypothetical protein	+	+	-	-	+	+	+
BAD_0102	ATP binding protein of ABC transporter	+	+	+	-	+	+	-

BAD_0103	hypothetical protein	+	+	+	+	+	-	+
BAD_0108	dipeptidase	+	+	+	+	+	+	-
BAD_0110	TetR-type transcriptional regulator	+	+	+	+	+	-	+
BAD_0121	putative peptidoglycan bound protein	+	-	-	+	+	-	+
BAD_0122	sortase	+	-	+	+	+	+	+
BAD_0131	hypothetical protein	+	-	+	+	+	-	+
BAD_0134	hypothetical protein	+	+	+	+	+	-	+
BAD_0139	aspartokinase	+	+	+	+	+	+	-
BAD_0147	hypothetical protein	+	+	+	+	-	+	-
BAD_0152	exo-alpha-L-arabinofuranosidase II	+	+	+	+	-	+	-
BAD_0153	solute binding protein of ABC transporter system	+	+	+	-	+	+	-
BAD_0154	sugar permease of ABC transporter system	+	+	+	-	+	+	-
BAD_0155	sugar permease of ABC transporter system	+	+	+	-	-	+	-
BAD_0162	thymidylate kinase	+	-	-	+	+	-	+
BAD_0163	DNA polymerase III subunit delta'	+	-	-	+	+	+	+
BAD_0165	hypothetical protein	+	-	-	+	+	-	+
BAD_0172	hypothetical protein	+	+	+	+	+	+	-
BAD_0187	ABC transporter solute-binding protein	+	+	+	-	+	+	+
BAD_0188	ABC transporter permease	+	+	+	-	+	+	+
BAD_0189	ABC transporter permease	+	+	+	-	+	+	+
BAD_0190	ABC transporter ATP-binding protein	+	+	+	-	+	+	+
BAD_0191	hypothetical protein	+	+	+	-	+	+	+
BAD_0193	hypothetical protein	+	+	+	+	+	-	+
BAD_0194	hypothetical protein	+	+	+	-	+	+	+
BAD_0210	hypothetical protein	+	-	-	+	+	-	+
BAD_0213	amidotransferase	+	-	+	+	+	+	+
BAD_0218	transcription regulator ArsR	+	-	+	-	-	-	+
BAD_0226	hypothetical protein	+	+	-	+	+	-	+
BAD_0233	hypothetical protein	+	+	-	+	+	+	+
BAD_0236	hypothetical protein	+	+	+	+	+	-	+
BAD_0240	50S ribosomal protein L21	+	+	+	-	+	+	+
BAD_0250	hypothetical protein	+	-	+	+	+	+	+
BAD_0254	JadJ	+	-	-	+	+	+	+
BAD_0255	propionyl-CoA carboxylase beta chain	+	-	+	+	+	-	+
BAD_0257	putative holo-[acyl-carrier protein] synthase	+	+	-	+	+	-	+
BAD_0263	hypothetical protein	+	+	+	-	+	+	+
BAD_0272	aminopeptidase C	+	-	-	+	+	-	+
BAD_0275	5'-methylthioadenosine nucleosidase	+	-	+	+	+	+	+
BAD_0298	hypothetical protein	+	+	+	+	-	+	+
BAD_0301	pyridine nucleotide-disulphide oxidoreductase	+	-	+	+	+	-	+
BAD_0309	50S ribosomal protein L13	+	+	-	+	+	-	+

BAD_0311	glycogen operon protein GlgX	+	+	+	-	-	+	-
BAD_0312	hypothetical protein	+	-	+	+	+	+	+
BAD_0313	zinc-binding dehydrogenase	+	+	+	-	-	+	-
BAD_0334	30S ribosomal protein S14	+	+	+	+	+	-	+
BAD_0348	50S ribosomal protein L17	+	-	+	+	+	+	+
BAD_0355	ribosome-binding factor A	+	-	+	+	+	-	+
BAD_0382	hypothetical protein	+	-	-	+	+	-	+
BAD_0384	hypothetical protein	+	+	+	-	+	+	-
BAD_0393	nucleoside-diphosphate-sugar epimerase	+	+	+	+	+	+	-
BAD_0394	hypothetical protein	+	+	+	+	+	+	-
BAD_0395	hypothetical protein	+	+	+	+	+	+	-
BAD_0396	glycosyltransferase I	+	+	+	+	+	+	-
BAD_0397	hypothetical protein	+	+	+	+	+	+	-
BAD_0398	spore coat protein H	+	+	+	-	+	+	-
BAD_0400	hypothetical protein	+	+	-	+	+	+	-
BAD_0401	hypothetical protein	+	+	+	+	+	+	-
BAD_0402	putative 200 kDa antigen p200	+	+	+	+	+	+	-
BAD_0411	dihydropteroate synthase 1	+	+	+	+	+	-	+
BAD_0414	Acyl-CoA thioesterase II	+	-	-	+	+	+	+
BAD_0416	hypothetical protein	+	+	-	-	+	+	+
BAD_0423	alpha-L-arabinofuranosidase	+	+	-	+	+	+	+
BAD_0425	putative sugar transporter solute-binding protein	+	-	+	+	+	-	+
BAD_0430	putative esterase	+	+	+	+	+	-	+
BAD_0433	XylR-type repressor	+	+	+	+	-	+	+
BAD_0434	gamma-glutamyltranspeptidase	+	+	+	-	+	+	+
BAD_0435	beta-galactosidase	+	+	+	-	-	-	+
BAD_0436	transcriptional regulator	+	+	+	-	+	+	+
BAD_0437	TetR-type transcriptional regulator	+	+	+	-	-	+	+
BAD_0438	xylan esterase	+	+	+	-	+	+	-
BAD_0460	citrate synthase 1	+	-	-	+	+	-	+
BAD_0470	ABC transporter solute-binding protein	+	+	-	+	+	-	+
BAD_0478	phosphopantothencysteine decarboxylase	+	-	-	+	+	-	+
BAD_0479	solute binding protein of ABC transporter systemy for peptides	+	+	-	+	+	+	+
BAD_0480	peptide ABC transporter permease	+	+	+	-	+	+	-
BAD_0481	peptide ABC transporter permease	+	+	+	-	+	+	-
BAD_0482	peptide ABC transporter ATP-binding protein	+	+	+	-	+	+	-
BAD_0484	hypothetical protein	+	+	+	-	+	+	-
BAD_0485	hypothetical protein	+	+	+	+	+	+	-
BAD_0487	hypothetical protein	+	+	+	-	-	+	-
BAD_0488	ABC transporter	+	-	+	-	-	+	-
BAD_0489	hypothetical protein	+	+	+	-	+	+	-

BAD_0493	S-ribosylhomocysteinase	+	+	+	+	+	-	+
BAD_0508	hypothetical protein	+	+	+	-	-	+	+
BAD_0517	metal uptake regulator ferric uptake regulator protein	+	-	-	+	+	+	+
BAD_0521	amidophosphoribosyltransferase	+	+	+	+	+	+	-
BAD_0522	hypothetical protein	+	+	+	-	+	+	+
BAD_0528	Na <sup>+</sup> dependent nucleoside transporter	+	+	+	-	+	+	+
BAD_0552	DNA-binding protein HB1	+	-	-	+	+	-	+
BAD_0558	hypothetical protein	+	-	+	+	+	+	+
BAD_0562	magnesium chelatase family protein	+	-	+	+	+	+	+
BAD_0585	recombination factor protein RarA	+	+	+	-	+	+	+
BAD_0586	efflux-type transporter	+	+	+	-	+	+	+
BAD_0604	transport protein	+	+	+	-	+	+	+
BAD_0610	hypothetical protein	+	+	+	-	-	+	+
BAD_0635	two-component system sensor histidine kinase	+	-	-	+	+	-	+
BAD_0641	hypothetical protein	+	-	+	+	+	+	+
BAD_0659	WhiB-type transcription regulator	+	-	+	+	+	+	+
BAD_0677	hypothetical protein	+	+	+	+	+	+	-
BAD_0685	3-phosphoshikimate 1-carboxyvinyltransferase	+	+	+	-	+	+	-
BAD_0699	secreted protein	+	+	-	+	+	+	+
BAD_0702	hypothetical protein	+	+	-	+	+	+	+
BAD_0706	3-dehydroquinate dehydratase	+	+	-	-	+	+	+
BAD_0708	pullulanase	+	+	+	-	-	+	-
BAD_0714	hypothetical protein	+	-	+	+	+	+	+
BAD_0729	hypothetical protein	+	+	+	+	+	+	-
BAD_0730	hypothetical protein	+	+	+	+	+	+	-
BAD_0732	MarR family regulatory protein	+	+	+	+	+	+	-
BAD_0733	putative drug resistance transporter	+	+	+	+	+	+	-
BAD_0735	protein crcB homolog 3	+	-	-	+	+	-	-
BAD_0736	hypothetical protein	+	+	+	+	+	+	-
BAD_0737	cobalt ABC transporter permease	+	+	+	+	+	+	-
BAD_0738	ATP binding protein of ABC transporter	+	+	+	+	+	+	-
BAD_0739	hypothetical protein	+	+	+	+	+	+	-
BAD_0741	hypothetical protein	+	+	+	+	+	+	-
BAD_0753	hypothetical protein	+	-	+	+	+	-	+
BAD_0777	inosine 5-monophosphate dehydrogenase	+	+	+	-	+	+	+
BAD_0799	hypothetical protein	+	+	-	+	+	+	+
BAD_0807	adenine phosphoribosyltransferase	+	-	-	+	+	+	+
BAD_0821	anaerobic C4-dicarboxylate transport protein	+	+	+	+	+	-	+
BAD_0824	hypothetical protein	+	-	+	+	+	+	+
BAD_0826	hypothetical protein	+	-	+	+	+	+	+
BAD_0843	hypothetical protein	+	-	-	+	+	-	+

BAD_0850	putative ABC transporter	+	+	+	-	+	+	+
BAD_0855	regulatory protein	+	-	+	+	+	-	+
BAD_0860	hypothetical protein	+	+	-	+	+	+	+
BAD_0870	hypothetical protein	+	-	-	+	+	+	+
BAD_0875	CBS domain-containing protein	+	+	+	-	+	+	-
BAD_0877	hypothetical protein	+	+	+	-	+	+	-
BAD_0880	hypothetical protein	+	+	+	-	-	+	-
BAD_0881	type III restriction enzyme	+	+	+	-	-	+	-
BAD_0882	hypothetical protein	+	+	+	+	-	+	-
BAD_0883	hypothetical protein	+	+	+	-	-	+	-
BAD_0891	ABC transporter ATP-binding protein	+	+	+	+	+	-	+
BAD_0902	serine hydroxymethyltransferase	+	+	+	+	-	+	+
BAD_0905	GntR family transcriptional regulator	+	-	-	-	-	+	+
BAD_0906	hydrolyase	+	+	+	-	-	+	+
BAD_0907	DNA repair protein RecN	+	+	+	-	+	+	+
BAD_0908	inorganic polyphosphate/ATP-NAD kinase	+	+	+	+	+	+	-
BAD_0913	hypothetical protein	+	+	+	-	+	+	+
BAD_0917	hypothetical protein	+	-	+	+	+	+	+
BAD_0932	hypothetical protein	+	+	+	-	-	+	-
BAD_0933	acyl protein synthase	+	+	+	-	-	+	-
BAD_0935	3-oxoacyl-[acyl-carrier protein] reductase	+	+	+	+	-	+	+
BAD_0936	hypothetical protein	+	-	+	-	-	+	-
BAD_0937	hypothetical protein	+	+	+	+	+	+	-
BAD_0938	integral membrane protein	+	+	+	-	-	+	-
BAD_0939	phage integrase	+	+	+	-	+	+	-
BAD_0940	hypothetical protein	+	+	+	-	+	+	-
BAD_0941	putative endonuclease/exonuclease/phosphatase family protein	+	+	+	+	+	+	-
BAD_0942	putative ATP/GTP-binding protein	+	+	+	-	-	+	-
BAD_0972	ABC transporter solute-binding protein	+	+	+	-	-	+	-
BAD_0973	D-tyrosyl-tRNA(Tyr) deacylase	+	+	+	-	+	+	+
BAD_0974	hypothetical protein	+	+	+	-	+	+	-
BAD_0975	glycosyl transferase	+	-	-	-	-	-	-
BAD_0977	nucleotidyltransferase family protein	+	+	+	-	-	+	+
BAD_0978	hypothetical protein	+	+	+	-	-	+	+
BAD_0979	hypothetical protein	+	-	+	-	-	-	+
BAD_0984	hypothetical protein	+	+	+	-	+	+	+
BAD_0985	putative DNA polymerase III epsilon subunit	+	+	-	+	+	+	+
BAD_0986	homocysteine methyltransferase	+	+	+	-	+	+	+
BAD_0987	histidine permease	+	+	+	-	+	+	+
BAD_0994	glutamine-dependent NAD(+) synthetase	+	-	-	+	+	+	+
BAD_1001	peptidyl-prolyl cis-trans isomerase	+	-	-	-	+	-	+

BAD_1016	hypothetical protein	+	+	-	+	+	+	-
BAD_1019	anthranilate phosphoribosyltransferase	+	+	+	+	+	+	-
BAD_1030	mannan endo-1,4-beta-mannosidase precursor	+	+	+	-	-	+	+
BAD_1050	hypothetical protein	+	+	+	-	+	+	-
BAD_1056	hypothetical protein	+	+	+	+	+	-	+
BAD_1067	chorismate mutase	+	+	+	+	+	-	+
BAD_1093	peptide ABC transporter permease	+	-	+	+	+	+	+
BAD_1113	transcriptional regulator NrdR	+	+	+	+	+	-	+
BAD_1114	hypothetical protein	+	+	+	-	+	+	+
BAD_1122	hypothetical protein	+	+	+	-	-	+	+
BAD_1141	phosphate ABC transporter	+	+	+	-	-	+	+
BAD_1144	hydroxyethylthiazole kinase	+	+	-	+	-	+	+
BAD_1152	ABC transporter solute-binding protein	+	+	+	-	+	+	+
BAD_1153	inosine-uridine preferring nucleoside hydrolase	+	+	+	-	-	+	+
BAD_1159	hypothetical protein	+	+	+	+	+	-	+
BAD_1160	hypothetical protein	+	-	+	+	+	-	+
BAD_1169	hypothetical protein	+	-	-	+	+	+	+
BAD_1173	L-asparagineamidohydrolase	+	+	+	+	+	-	+
BAD_1176	hypothetical protein	+	+	+	-	+	+	-
BAD_1177	putative transposase	+	-	+	-	-	+	-
BAD_1179	CRISPR-associated Cas2 family protein	+	+	+	-	-	+	-
BAD_1180	CRISPR-associated DNA polymerase	+	+	+	-	+	+	-
BAD_1181	hypothetical protein	+	+	+	-	-	+	-
BAD_1183	CRISPR-associated Csd1 family protein	+	+	+	-	+	+	-
BAD_1184	CRISPR-associated Csd1 family protein	+	+	+	-	-	+	-
BAD_1185	CRISPR-associated Cas5d family protein	+	+	+	+	+	+	-
BAD_1186	putative CRISPR-associated helicase	+	+	+	-	-	+	-
BAD_1187	isoleucyl-tRNA synthetase	+	+	+	+	+	+	-
BAD_1195	TetR-type transcriptional regulator	+	+	+	-	+	+	+
BAD_1203	xylan beta-1,4-xylosidase	+	+	+	-	+	+	+
BAD_1205	alpha-L-arabinosidase	+	+	+	-	+	+	+
BAD_1207	TetR-type transcriptional regulator	+	+	+	-	-	+	+
BAD_1209	membrane protein with transport function	+	+	+	+	+	+	-
BAD_1211	beta-galactosidase I	+	-	+	-	-	+	-
BAD_1212	TetR-type transcriptional regulator	+	+	-	-	+	+	-
BAD_1218	hypothetical protein	+	+	-	-	+	-	+
BAD_1219	hypothetical protein	+	+	+	-	+	+	+
BAD_1221	hypothetical protein	+	+	+	-	+	+	+
BAD_1222	hypothetical protein	+	+	-	+	+	+	+
BAD_1223	hypothetical protein	+	+	+	-	+	+	+
BAD_1224	aspartate aminotransferase	+	+	+	+	+	-	+

BAD_1228	restriction endonuclease	+	+	+	-	+	+	-
BAD_1229	putative type II restriction enzyme Sau3AI	+	+	+	-	-	+	-
BAD_1230	helicase	+	+	+	-	-	+	-
BAD_1231	hypothetical protein	+	+	+	-	+	+	-
BAD_1232	type II restriction enzyme Sau3AI	+	+	+	-	+	+	-
BAD_1233	modification methylase Sau3AI	+	+	+	-	-	+	-
BAD_1234	hypothetical protein	+	+	+	-	+	+	+
BAD_1235	transmembrane protein	+	+	+	-	+	+	+
BAD_1236	hypothetical protein	+	-	+	+	+	+	+
BAD_1239	putative transcriptional regulator	+	+	+	-	+	+	-
BAD_1240	apolipoprotein N-acyltransferase	+	+	+	-	+	+	-
BAD_1241	replicase	+	+	+	-	+	+	-
BAD_1242	hypothetical protein	+	+	+	-	+	+	-
BAD_1243	hypothetical protein	+	+	+	+	+	+	-
BAD_1245	hypothetical protein	+	+	+	-	-	+	-
BAD_1247	two-component sensor histidine kinase involved in chemotaxis	+	+	+	+	+	+	-
BAD_1249	hypothetical protein	+	+	+	-	-	+	-
BAD_1250	hypothetical protein	+	+	+	-	-	+	-
BAD_1251	hypothetical protein	+	-	+	+	+	+	-
BAD_1254	hypothetical protein	+	-	-	-	-	-	-
BAD_1257	hypothetical protein	+	+	+	-	+	+	-
BAD_1258	hypothetical protein	+	+	+	-	-	+	-
BAD_1259	hypothetical protein	+	+	+	-	+	+	+
BAD_1260	glutamine ABC transporter ATP-binding protein	+	+	+	-	-	+	-
BAD_1262	hypothetical protein	+	+	+	-	+	+	-
BAD_1264	hypothetical protein	+	+	+	-	-	+	-
BAD_1267	DNA-binding response regulator	+	+	+	+	+	+	-
BAD_1268	DNA-binding response regulator	+	+	+	-	+	+	-
BAD_1269	hypothetical protein	+	+	+	-	+	+	-
BAD_1270	hypothetical protein	+	+	+	+	+	+	-
BAD_1273	hypothetical protein	+	+	+	-	+	+	-
BAD_1275	hypothetical protein	+	+	+	-	+	+	-
BAD_1276	hypothetical protein	+	+	+	-	-	+	-
BAD_1277	cobalt ABC transporter ATP-binding protein	+	+	+	-	+	+	-
BAD_1278	filamentous haemagglutinin	+	+	+	-	-	+	-
BAD_1280	type II restriction-modification systemrestriction subunit	+	-	-	-	-	-	-
BAD_1281	type II restriction-modification systemrestriction subunit	+	+	+	-	-	+	-
BAD_1282	restriction endonuclease RKpn2kI	+	+	+	-	-	+	-
BAD_1284	DNA invertase-like protein	+	+	+	-	+	+	-
BAD_1285	hypothetical protein	+	+	+	+	+	-	-
BAD_1287	beta-glucosidase	+	+	+	+	+	+	-

BAD_1289	ABC transporter sugar permease	+	+	+	+	+	+	-
BAD_1290	sugar ABC transporter binding protein	+	+	+	+	+	+	-
BAD_1291	ribose operon repressor	+	+	+	+	+	+	-
BAD_1292	DNA polymerase III	+	+	+	+	-	+	+
BAD_1308	putative beta-lactamase (class A) precursor	+	+	-	-	-	+	+
BAD_1309	hypothetical protein	+	+	+	-	-	+	+
BAD_1324	hypothetical protein	+	+	+	+	-	+	+
BAD_1326	LacI-type transcriptional regulator	+	+	+	-	+	+	+
BAD_1328	sugar ABC transporter permease	+	+	+	-	+	+	+
BAD_1329	polysaccharide ABC transporter permease	+	+	+	-	+	+	+
BAD_1330	ABC transporter	+	+	+	-	+	+	+
BAD_1339	hypothetical protein	+	+	+	+	+	+	-
BAD_1340	3-isopropylmalate dehydrogenase	+	+	+	+	+	+	-
BAD_1341	hypothetical protein	+	+	+	-	-	+	-
BAD_1349	thioredoxin	+	-	+	-	+	+	+
BAD_1351	prolipoprotein	+	-	-	-	-	-	-
BAD_1352	hypothetical protein	+	+	+	-	-	+	-
BAD_1354	hypothetical protein	+	+	+	-	-	+	-
BAD_1356	hypothetical protein	+	-	+	-	-	+	-
BAD_1357	hypothetical protein	+	+	+	-	+	+	-
BAD_1358	Etk-like tyrosine kinase	+	+	+	-	-	+	-
BAD_1359	hypothetical protein	+	+	+	-	-	+	-
BAD_1360	hypothetical protein	+	+	-	-	-	-	-
BAD_1361	ribonuclease	+	+	+	-	-	+	-
BAD_1362	hydroxymethylglutaryl-CoA synthase	+	-	+	-	-	+	-
BAD_1363	ABC transporter	+	+	+	-	+	+	-
BAD_1364	putative transcriptional regulator	+	+	+	-	+	+	-
BAD_1365	hypothetical protein	+	+	+	-	-	+	-
BAD_1366	hypothetical protein	+	+	-	-	+	+	-
BAD_1367	putative transposase	+	+	+	-	+	+	-
BAD_1368	phage AbiD protein	+	+	+	-	+	+	-
BAD_1369	ISSdy1_ transposase OrfB	+	+	+	+	+	+	-
BAD_1370	ImpB/MucB/SamB family protein	+	+	+	-	-	+	-
BAD_1371	Na <sup>+</sup> /H <sup>+</sup> -dicarboxylate symporter	+	+	+	-	+	+	-
BAD_1373	transposase subunit B	+	+	+	-	-	+	+
BAD_1374	IS3 family transposase	+	+	+	-	-	+	-
BAD_1375	putative transposase	+	+	-	-	-	-	-
BAD_1376	insertion element hypothetical protein	+	+	+	+	-	+	-
BAD_1377	insertion element IS6110 hypothetical protein	+	+	+	-	-	-	-
BAD_1379	hypothetical protein	+	+	+	-	-	-	-
BAD_1381	fhiA protein	+	+	+	-	+	+	-



BAD_1383	hypothetical protein	+	-	-	-	-	-	-
BAD_1384	hypothetical protein	+	+	+	-	+	+	-
BAD_1385	putative glycosyltransferase	+	+	+	-	+	+	-
BAD_1386	hypothetical protein	+	-	+	-	-	+	-
BAD_1387	spore coat protein	+	+	-	-	-	-	-
BAD_1388	capsular polysaccharide biosynthesis proteinCps4H	+	+	+	+	-	+	-
BAD_1389	galactosyl transferase CpsD	+	+	+	-	-	+	-
BAD_1390	hypothetical protein	+	+	+	-	+	+	-
BAD_1391	hypothetical protein	+	+	+	-	-	+	-
BAD_1392	regulatory protein	+	+	+	-	-	+	-
BAD_1394	putative 200 kDa antigen p200	+	+	+	+	-	+	-
BAD_1395	H(+)-stimulated manganese uptake system protein	+	-	-	+	+	-	+
BAD_1397	hypothetical protein	+	+	+	+	+	+	-
BAD_1398	hypothetical protein	+	+	+	+	-	+	+
BAD_1402	beta-galactosidase precursor	+	+	+	+	-	+	+
BAD_1404	ABC-type sugar transport systems, permease components	+	+	+	+	-	+	+
BAD_1405	putative periplasmic binding (signal peptide) ABC transporter protein	+	+	+	+	-	+	+
BAD_1425	hypothetical protein	+	-	-	+	+	-	+
BAD_1434	homoserine O-succinyltransferase	+	+	+	+	+	-	+
BAD_1436	ABC transporter	+	+	+	+	+	+	-
BAD_1438	cation efflux system protein	+	-	-	+	-	+	-
BAD_1439	hypothetical protein	+	-	+	+	-	+	-
BAD_1440	hypothetical protein	+	-	+	+	-	+	-
BAD_1442	two-component response regulator	+	+	+	+	-	+	+
BAD_1443	hypothetical protein	+	+	+	+	-	+	-
BAD_1452	chorismate mutase	+	+	+	+	+	-	+
BAD_1456	acetyltransferase	+	+	-	+	+	+	+
BAD_1462	hypothetical protein	+	+	+	+	+	-	+
BAD_1463	copper-transporting ATPase	+	+	-	+	+	+	+
BAD_1464	chaperone clpB	+	-	-	+	+	-	+
BAD_1467	cell surface protein fimafimbrial subunit	+	+	+	+	-	+	-
BAD_1468	hypothetical protein	+	+	+	+	+	+	-
BAD_1475	glycerol uptake facilitator protein	+	+	+	+	+	-	+
BAD_1476	hypothetical protein	+	-	+	+	+	-	+
BAD_1485	PfkB family sugar kinase	+	-	-	-	-	+	+
BAD_1486	putative nucleoside hydrolase protein	+	+	+	-	-	+	+
BAD_1488	hypothetical protein	+	-	+	-	-	-	+
BAD_1489	ATPase	+	+	+	-	-	+	+
BAD_1490	transcription regulator protein	+	+	+	-	+	+	+
BAD_1492	hypothetical protein	+	-	-	+	+	-	+
BAD_1494	putative acetyl CoA carboxylase beta subunit	+	-	-	-	-	+	+

BAD_1495	rhamnose biosynthesis dTDP-glucose 4,6-dehydratase	+	-	-	-	+	+	-
BAD_1496	hypothetical protein	+	-	+	-	+	+	-
BAD_1497	hypothetical protein	+	+	+	-	-	+	-
BAD_1498	hypothetical protein	+	+	+	+	+	+	-
BAD_1499	glycosyl transferase	+	+	+	-	-	+	-
BAD_1500	ATP-driven polysaccharide export protein	+	+	+	-	+	+	-
BAD_1501	polysaccharide ABC transporter permease	+	+	-	-	-	+	-
BAD_1502	hypothetical protein	+	+	+	-	-	+	-
BAD_1503	hypothetical protein	+	+	+	+	+	+	-
BAD_1504	hypothetical protein	+	+	+	-	-	+	-
BAD_1505	glycosyltransferase	+	+	+	-	+	+	-
BAD_1506	nucleoside-diphosphate-sugar epimerases-like	+	-	+	-	-	-	-
BAD_1507	rhamnose biosynthesis dTDP-glucose 4,6-dehydratase	+	+	-	-	+	-	-
BAD_1508	fused dTDP-4-keto-L-rhamnose reductase	+	+	-	-	-	+	-
BAD_1509	hypothetical protein	+	+	+	-	-	+	-
BAD_1510	proline symporter	+	+	+	+	+	+	-
BAD_1511	1,4-beta-N-acetylmuramidase	+	-	-	+	+	-	+
BAD_1516	hypothetical protein	+	+	+	-	+	+	-
BAD_1531	ABC transporter permease	+	+	+	-	+	+	+
BAD_1537	hypothetical protein	+	+	-	+	+	-	+
BAD_1539	hypothetical protein	+	+	+	+	+	-	+
BAD_1548	alkaline phosphatase	+	+	+	-	+	+	+
BAD_1549	hypothetical protein	+	+	-	+	+	+	-
BAD_1550	hypothetical protein	+	+	-	-	+	+	-
BAD_1551	sortase family protein	+	+	+	+	+	+	-
BAD_1553	putative diguanylate cyclase	+	+	+	-	+	+	+
BAD_1554	hypothetical protein	+	+	+	-	-	+	+
BAD_1555	putative death on curing protein	+	+	+	-	-	+	+
BAD_1556	LacI-type transcriptional regulator	+	+	+	-	+	+	+
BAD_1559	pullulanase precursor	+	+	+	-	-	+	-
BAD_1562	hypothetical protein	+	+	+	-	-	+	+
BAD_1568	NADPH-flavin oxidoreductase	+	+	+	+	+	-	+
BAD_1569	Sir2-type regulatory protein	+	+	+	+	-	+	-
BAD_1579	phospholipase/carboxylesterase	+	+	+	-	-	+	+
BAD_1583	hypothetical protein	+	+	+	+	+	-	+
BAD_1585	putative solute-binding lipoprotein	+	+	+	-	+	+	-
BAD_1586	ABC transporter membrane component	+	+	+	-	+	+	-
BAD_1587	sugar permeases	+	+	+	-	+	+	-
BAD_1588	hypothetical protein	+	+	+	+	+	-	+
BAD_1591	tRNA/rRNA methyltransferase protein	+	-	+	+	-	-	+
BAD_1595	two-component sensor histidine kinase	+	+	+	+	-	+	+

BAD_1600	transposase	+	+	-	+	-	-	+
BAD_1601	putative endonuclease/exonuclease/phosphatase family protein	+	+	-	-	+	-	+
BAD_1602	N-acetylglucosamine-6-phosphate deacetylase	+	+	+	+	+	+	-
BAD_1603	beta-galactosidase	+	+	+	+	+	+	-
BAD_1608	acetyltransferase	+	-	-	-	+	+	-
BAD_1610	beta-glucosidase	+	+	+	-	-	+	+
BAD_1615	dimethyladenosine transferase	+	-	-	+	+	-	+
BAD_1617	hypothetical protein	+	+	-	+	+	+	+
BAD_1623	thioredoxin reductase	+	+	-	+	+	-	+
BAD_1626	16S rRNA methyltransferase GidB	+	+	-	+	+	-	+