Table S1: Functional characteristics of putative genomic islands identified BJG-01

GI-Number	insert site	Size (bp)	IS/transposase/integrase	Pathogenicity/antibiotic resistance	Description/Functional Annotation
GI-02	VC1582-VC1588	3,584	-	-	Oxidative Stress Response; Superoxide dismutase [Cu-Zn] precursor (EC 1.15.1.1)/Catalase (EC 1.11.1.6)
GI-03	VC1747-VC1753	4,866	-	-	membrane protein;corresponds to STY3950 from Accession AL513382: Salmonella typhi CT18;Small-conductance mechanosensitive channel
GI-04	VC1819-VC1828	9,486	-	-	Carbohydrates (PTS system, Mannose Metabolism)
GI-10	VCA0877-VCA0885	4,901	-/-/integrase-related protein	Non-hemolytic enterotoxin lytic component L1	
GI-19	VCA0569-VCA0570	9,497			
GI-47	VC0809-VC0848	15824, 51529(c)	-	-	Cell division protein ftsK; Exonuclease SbcC
GI-58	VCA0235-VCA0237	6,533	-/(Transposase)/-	-	Mu-like prophage FluMu I protein;Ferrichrome transport ATP-binding protein fhuC (TC 3.A.1.14.3);Iron (III) ABC transporter;Iron(III) dicitrate transport system permease protein fecD (TC 3.A.1.14.1);Isochorismatase (EC 3.3.2.1);LysR-family transcriptional regulator clustered with PA0057;
GI-61	VCA1064-VCA1067	6,421	-	-	Outer membrane lipoprotein-sorting protein; Predicted exporter of the RND superfamily; Transcriptional activator, LuxR/UhpA family of regulators
GI-64	VC1560-VC1563	5,541			Adenylosuccinate synthetase (EC 6.3.4.4); LuxC,; LuxD; LuxA,; LuxB; LuxE,; LuxG; extracellular solute-binding protein, family 3; 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomerase 2 (EC 5.3.1.16)
GI-67	VCA0734-VCA0735	37,871	-	Iron aquisition yersiniabactin synthesis enzyme (Irp1; polyketide synthetase, Irp2), 2,3-dihydroxybenzoate-AMP ligase (EC 2.7.7.58) # Vulnibactin-specific	Amino Acids and Derivatives(Choline dehydrogenase (EC 1.1.99.1),Betaine aldehyde dehydrogenase (EC 1.2.1.8),BetI,BetT); FyuA precursor; hypotetical anthranilate synthase; hypothetical thioesterase; putative reductase component; hypothetical transcriptional regulator
GI-79	VCA0990-VCA0991	10,459	-	-	2-dehydro-3-deoxyphosphogluconate aldolase (EC 4.1.2.14) / 4-Hydroxy-2-oxoglutarate aldolase (EC 4.1.3.16); Uronate isomerase (EC 5.3.1.12); D-mannonate oxidoreductase (EC 1.1.1.57); TRAP-type C4-dicarboxylate transport system; Uxu operon transcriptional regulator; Mannonate dehydratase (EC 4.2.1.8)
GI-85	VC1854-VC1835	15,489	-	TolA, tolB protein precursor, Tol biopolymer transport system, TolR protein, MotA/TolQ/ExbB proton channel family protein, 4-hydroxybenzoyl-CoA thioesterase family active site, Predicted signal transduction protein	Cytochrome d ubiquinol oxidase subunit I/II; Holliday junction DNA helicase RuvAB; Crossover junction endodeoxyribonuclease ruvC (EC 3.1.22.4); Cysteinyl-tRNA synthetase (EC 6.1.1.16); Peptidyl-prolyl cis-trans isomerase ppiB (EC 5.2.1.8); UDP-2,3-diacylglucosamine hydrolase (EC 3.6.1.-)
GI-86	VC1234-VC1235	5,574	-	-	hypothetical proteins
GI-87	VC1451-VC1479	5,347	-/-/Phage integrase / RstB phage-related integrase	-	FIG00072724: hypothetical protein, RstA phage-related replication protein
GI-88	VC1328-VC1329	3,431	-	Permease of the drug/metabolite transporter (DMT) superfamily, Membrane fusion component of tripartite multidrug resistance system	FIG01201931: hypothetical protein, Potassium channel protein/ homology with *Vibrio vulnificus* YJ016 chr.1 and *Shewanella loihica* PV-4
GI-89	VC2041-VC2042	2,899	ISSod22C transposase OrfAB/ COG2801: Transposase and inactivated derivatives	-	hypothetical proteins
GI-90	VCA0249-VCA0250	3,164	-	-	probable transcriptional regulator; Pirin-like; Nicotinamidase family protein YcaC; Antibiotic biosynthesis monooxygenase

Table S2: VNTR genotype of *V. cholerae* BJG-01. Allele number indicates the number of repeat units of each locus. The 11 repeat units of the MLVA loci are: AACAGA at VC0147, GACCCTA at VC0436-7, 12 GATAATCCA at VC1650, TGCTGT at VCA0171, and ACCAGA at VCA0283.

ID	Origin	Year	Source	Type	VC0147	VC0436-7*	VC1650	VCA0171	VCA0283
O395	India	1965	C	O1 OGCL	7	4	3	24	14
N16961	Bangladesh	1975	C	O1 INET	9	7	7	23	14
CIRS101	Bangladesh	2002	C	O1 OGET	9	3	6	16	11
CP1032	Mexico	1991	C	O1 OGET	8	7	8	13	17
CP1033	Mexico	2000	C	O1 OGET	8	7	8	13	24
CP1038	Zimbabwe	2009	C	O1 OGET	8	3	3	18	22
CP1041	Zambia	2004	C	O1 OGET	8	7	6	9	10
CP1042	Thailand	2010	C	O1 OGET	9	6	7	17	17
CP1048	Bangladesh	2010	C	O1 OGET	9	3	6	22	17
BJG-01	**MS, USA**	**2010**	**C**	**Non-O1/O139**	**12**	**12**	**5**	**10**	**NA**
HC-1A2	Haiti	2010	C	Non-O1/O139	12	8	7	16	NA
HC-2A1	Haiti	2010	C	Non-O1/O139	12	8	7	16	NA
HC-36A1	Haiti	2010	C	Non-O1/O139	12	8	7	15	NA
HE-09	Haiti	2010	E	Non-O1/O139	11	3	5	13	NA
HE39	Haiti	2010	E	Non-O1/O139	8	3	2	13	NA
HE48	Haiti	2010	E	Non-O1/O139	7	6	6	6	NA

C: Clinical, E: Environmental, *: Intergenic, NA; Not Applicable