Supplementary table 1.Genes with obviously changed methylation type in SMRT sequencing.

Virmbon	T 1 4	C6	706	CV2	TICD Common Nama	Gene	Mainuala	Cl1-
umber	Local tag	m4C	m6A	m4C m6A	A TIGR Common Name	Symbol	Mainrole	Subrole
1	VC_0025	+	+	+	hypothetical protein			
2	VC_0141	+	+	+	hypothetical protein			
3	VC_0367	+	+	+	primosomal replication protein N	priB	DNA metabolism	DNA replication, recombination, and repair
4	VC_0368	+	+	+	ribosomal protein S18	rpsR	Protein synthesis	Ribosomal proteins: synthesis and modification
5	VC_0686	+	+	+	hypothetical protein			
6	VC_0912	+	+	+	hypothetical protein			
7	VC_1007	+	+	+	hypothetical protein			
8	VC_1020	+	+	+	hypothetical protein			
9	VC_1109	+	+	+	hypothetical protein			
	VC_1142	+	+	+	cold shock-like protein CspD	cspD	Regulatory functions	Other
11	VC_1227	+	+	+	hypothetical protein	•	<i>.</i>	
12	VC_1247	+	+	+	hypothetical protein			
13	VC_1415	+	+	+	hcp protein	hcp-1	Unknown function	General
	VC_1441	+	+	+	cytochrome c oxidase, subunit CcoO	ccoO	Energy metabolism	Electron transport
	VC_1474	+	+	+	conserved hypothetical protein		Hypothetical proteins	Conserved
16	VC_1487	+	+	+	conserved hypothetical protein		Hypothetical proteins	Conserved
17	VC_1569	+	+	+	hypothetical protein			
	VC_1835	+	+	+	peptidoglycan-associated lipoprotein	pal	Cell envelope	Other
19	VC_1962	+	+	+	lipoprotein	•	Cell envelope	Other
	VC_2170	+	+	+	hypothetical protein		•	
	VC 2200	+	+	+	flagellar basal-body rod protein FlgB	flgB	Cellular processes	Chemotaxis and motility
22	VC_2423	+	+	+	fimbrial protein	pilA	Cell envelope	Surface structures
	VC_2575	+	+	+	ribosomal protein L36	rpmJ	Protein synthesis	Ribosomal proteins: synthesis and modification
	VC_2652	+	+	+	conserved hypothetical protein	r	Hypothetical proteins	Conserved
	VC_A0019	+	+	+	hypothetical protein		51 · · · · · · · · · · · · · · · · · · ·	
	VC_A0028	+	+	+	hypothetical protein			
	VC_A0045	+	+	+	protease-related protein		Protein fate	Degradation of proteins, peptides, and glycopeptides
	VC_A0100	+	+	+	phage shock protein E	pspE	Cellular processes	Adaptations to atypical conditions
	VC_A0138	+	+	+	hypothetical protein	F F	Francisco Programme Progra	
	VC_A0159	+	+	+	conserved hypothetical protein		Hypothetical proteins	Conserved
	VC_A0182	+	+	+	sigma-54 dependent transcriptional regulator		Regulatory functions	Other
	VC_A0313	+	+	+	MutT/nudix family protein		DNA metabolism	DNA replication, recombination, and repair
	VC_A0318	+	+	+	conserved hypothetical protein		Hypothetical proteins	Conserved
	VC_A0448	+	+	+	hypothetical protein)r	
	VC_A0480	+	+	+	hypothetical protein			
	VC_A0705	+	+	+	phosphoglycerate transport regulatory protein PgtB, putative		Regulatory functions	Other
	VC_A0729	+	+	+	hypothetical protein			
	VC_A0735	+	+	+	hypothetical protein			
	VC_A0844	+	+	+	hypothetical protein			
	VC_A0857	+	+	+	hypothetical protein			
	VC_A0859	+	+	+	oxidoreductase, aldo/keto reductase 2 family		Central intermediary metabolism	Other
	VC_A0889	+	+	+	transcriptional regulator, LysR family		Regulatory functions	Other
	VC_A0009 VC_A1019	+	+	+	conserved hypothetical protein		Hypothetical proteins	Conserved
	VC_A1019 VC_A1080	T		+	secretion protein, HlyD family		Protein fate	Protein and peptide secretion and trafficking
	VC_A1080 VC_t021	±	±	T	secretion protein, riny Diaminy		1 Totelli Tate	rotein and popule secretion and trafficking
	VC_t021 VC_t042		+	+				
4()	v C_1042	+	+	+				

N. 1	T 1.	C6706 CV2			V2	TIOD C N	Gene	M 1	Cubusla	
Number	Local tag	m4C	m6A	m4C	m6A	5A TIGR Common Name	Symbol	Mainrole	Subrole	
48	VC_t085	+	+	+						
49	VC_0001	+	+		+	hypothetical protein				
50	VC_1243	+	+		+	hypothetical protein				
51	VC_1379	+	+		+	hypothetical protein				
52	VC_2304	+	+		+	hypothetical protein				
53	VC_A0253	+	+		+	antibiotic acetyltransferase		Cellular processes	Toxin production and resistance	
54	VC_A0463	+	+		+	biphenyl-2,3-diol 1,2-dioxygenase III-related protein		Central intermediary metabolism	Other	
55	VC_A0541	+	+		+	hypothetical protein		•		
56	VC_A1091	+	+		+	chemotaxis protein methyltransferase CheR	cheR-3	Cellular processes	Chemotaxis and motility	
57	VC_t045	+	+		+					
58	VC_1030	+				hypothetical protein				
59	VC_1387	+				hypothetical protein				
60	VC_1648	+				hypothetical protein				
61	VC_2034	+				hypothetical protein				
62	VC_2230	+				phosphoheptose isomerase	lpcA	Cell envelope	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	
63	VC_2328	+				hypothetical protein				
64	VC_2648	+				hypothetical protein				
65	VC_2752	+				hypothetical protein				
66	VC_A0040	+				conserved hypothetical protein		Hypothetical proteins	Conserved	
67	VC_A0109	+				hypothetical protein				
68	VC_A0189	+				response regulator		Regulatory functions	Other	
69	VC_A0228	+				vibriobactin and enterobactin ABC transporter, permease protein	vctD	Transport and binding proteins	Cations	
70	VC_A0301	+				oxidoreductase, short-chain dehydrogenase/reductase family		Central intermediary metabolism	Other	
71	VC_A0326	+				hypothetical protein				
72	VC_A0342	+				hypothetical protein				
73	VC_A0578	+				conserved hypothetical protein		Hypothetical proteins	Conserved	
74	VC_A0625	+				heme receptor HasR	hasR	Transport and binding proteins	Cations	
75	VC_A0653	+				PTS system, sucrose-specific IIBC component	scrA	Transport and binding proteins	Carbohydrates, organic alcohols, and acids	
76	VC_A0672	+				hypothetical protein				
77	VC_A0752	+				thioredoxin 2	trxC	Energy metabolism	Electron transport	
78	VC_A0888	+				transcriptional regulator, LuxR family		Regulatory functions	Other	
79	VC_A0934	+				hypothetical protein				
80	VC_A1047	+				mannitol operon repressor	mtlR	Regulatory functions	Other	
81	VC_A1066		+			hypothetical protein				
82	VC_0107	+		+	+	hypothetical protein				
83	VC_0226	+		+	+	hypothetical protein				
84	VC_0479	+		+	+	hypothetical protein				
85	VC_0621	+		+	+	hypothetical protein				
86	VC_0805	+		+	+	hypothetical protein				
87	VC_0996	+		+	+	hypothetical protein				
88	VC_1027	+		+	+	molybdenum cofactor biosynthesis protein D	moaD	Biosynthesis of cofactors, prosthetic groups, and carriers	Molybdopterin	
89	VC_1239	+		+	+	cobinamide kinase/cobinamide phosphate guanylyltransferase	cobU	Biosynthesis of cofactors, prosthetic groups, and carriers	Heme, porphyrin, and cobalamin	
90	VC_1462	+		+	+	RstB2 protein	rstB2	Other categories	Prophage functions	
91	VC_1468	+		+	+	conserved hypothetical protein		Hypothetical proteins	Conserved	
92	VC_1498	+		+	+	conserved hypothetical protein		Hypothetical proteins	Conserved	

Number	Local tag	C6706		CV2		TIGR Common Name	Gene	Mainrole	Subrole
Nullibei	Local tag	m4C m6A m4C m6A				A TION Common Name	Symbol	Walliote	Subtoic
93	VC_1780	+		+	+	hypothetical protein			
94	VC_1913	+		+	+	conserved hypothetical protein		Hypothetical proteins	Conserved
95	VC_2663	+		+	+	hypothetical protein			
96	VC_A0007	+		+	+	3-hydroxyisobutyrate dehydrogenase, putative		Energy metabolism	Other
97	VC_A0292	+		+	+	hypothetical protein			
98	VC_A0419	+		+	+	hypothetical protein			
99	VC_A0456	+		+	+	hypothetical protein			
100	VC_A0483	+		+	+	hypothetical protein			
101	VC_A0540	+		+	+	formate transporter 1, putative		Transport and binding proteins	Carbohydrates, organic alcohols, and acids
102	VC_A0631	+		+	+	hypothetical protein			
103	VC_A0638	+		+	+	transporter, AcrB/D/F family		Transport and binding proteins	Cations
104	VC_A0658	+		+	+	methyl-accepting chemotaxis protein		Cellular processes	Chemotaxis and motility
105	VC_A0760	+		+	+	arginine ABC transporter, ATP-binding protein	artP	Transport and binding proteins	Amino acids, peptides and amines
106	VC_A0803	+		+	+	serine protease, putative		Protein fate	Degradation of proteins, peptides, and glycopeptides
107	VC_A1021	+		+	+	transcriptional regulator, LysR family		Regulatory functions	Other
108	VC_r003	+		+	+				
109	VC_r019	+		+	+				
110	VC_t046	+		+	+				
111	VC_t050	+		+	+				
112	VC_A0244		+	+	+	sugar isomerase SgaE, AraD/FucA family		Energy metabolism	Sugars
113	VC_A0399		+	+	+	hypothetical protein			
114	VC_A0635		+	+	+	transcriptional regulator, LysR family		Regulatory functions	Other
115	VC_A1015		+	+	+	Na+/H+ antiporter	nhaD	Transport and binding proteins	Cations
116	VC_A0698	+			+	hypothetical protein			