Table 2. ORFs identified in the pC2C203U28

ORF	Position (start)	(stop)	Strand	Length (aa)	Product	Note
C2P001	101	1,585	+	494	putative replication protein	Similar to putative replication protein[Clostridium tetani E88](gi|28373132|ref|NP_783730.1|)57.8% identity in overlap 483aa
C2P002	1,833	2,573	+	246	putative two-component response regulator	Similar to VirR protein[Clostridium perfringens](gi|86559596|ref|YP_473417.1|)26.8% identity in overlap 239aa
C2P003	2,599	3,849	+	416	putative two-component response regulator	Similar to VirS protein[Clostridium perfringens](gi|86559597|ref|YP_473418.1|)24.8% identity in overlap 447aa
C2P004	4,543	4,058	-	161	putative agrB	Weakly similar to accessory gene regulator B[Staphylococcus aureus RF122](gi|82751638|ref|YP_417379.1|)27.6% identity in overlap 163aa. Probably truncated C-terminus
C2P005	5,243	6,130	+	295	putative ABC transporter, ATP-binding protein	Similar to ABC transporter ATP-binding protein[Clostridium tetani E88](gi|28210375|ref|NP_781319.1|)43.1% identity in overlap 297aa
C2P006	6,114	7,355	+	413	conserved hypothetical protein	Similar to hypothetical protein NT01CX_1309[Clostridium novyi NT](gi|118444312|ref|YP_877392.1|)29.3% identity in overlap 410aa
C2P007	7,382	7,621	+	79	hypothetical protein	
C2P008	7,705	7,944	+	79	hypothetical protein	
C2P009	8,215	7,997	-	72	conserved hypothetical protein	Similar to hypothetical protein NT01CX_0737[Clostridium novyi NT](gi|118445123|ref|YP_879203.1|)32.4% identity in overlap 71aa
C2P010	8,444	8,229	-	71	conserved hypothetical protein	Similar to hypothetical protein NT01CX_0738[Clostridium novyi NT](gi|118444037|ref|YP_879204.1|)37.5% identity in overlap 72aa
C2P011	8,828	8,511	-	105	hypothetical protein	N-terminus is similar to middle of putative N-acetylmuramoyl-L-alanine amidase[Clostridium tetani E88](gi|28373183|ref|NP_783826.1|)56.9% identity in overlap 58aa. C-terminus is similar to hypothetical protein pE88_03[Clostridium tetani E88](gi|28373134|ref|NP_783732.1|)58.0% identity in overlap 50aa
C2P012	8,868	9,080	+	70	hypothetical protein	
C2P013	9,328	9,089	-	79	putative UviB	Similar to uviB homologous protein[Clostridium tetani E88](gi|28373135|ref|NP_783733.1|)67.6% identity in overlap 74aa

C2P014	11,278	10,583	-	231	conserved hypothetical protein	Similar to hypothetical protein NT01CX_0694[Clostridium novyi NT](gi|118443237|ref|YP_879160.1|)37.2% identity in overlap 226aa
C2P015	11,670	12,110	+	146	putative RNA polymerase sigma factor	Similar to putative RNA polymerase sigma factor[Clostridium tetani E88](gi|28373140|ref|NP_783738.1|)53.9% identity in overlap 141aa, also similar to putative RNA polymerase sigma factor[Clostridium tetani E88](gi|28373141|ref|NP_783739.1|)32.2% identity in overlap 149aa. Probably truncated C-terminus
C2P016	12,183	13,496	+	437	conserved hypothetical protein	Similar to hypothetical protein CLC_1691[Clostridium botulinum A str. Hall](gi|153935200|ref|YP_001387547.1|)31.3% identity in overlap 291aa
C2P017	13,999	14,742	+	247	conserved hypothetical protein	Similar to membrane-spanning protein[Clostridium tetani E88](gi|28373170|ref|NP_783813.1|)29.5% identity in overlap 251aa
C2P018	14,792	15,511	+	239	hypothetical protein	
C2P019	15,527	16,174	+	215	putative ABC transporter, ATP-binding protein	Similar to ABC transporter ATP-binding protein[Clostridium tetani E88](gi|28373165|ref|NP_783765.1|)47.3% identity in overlap 201aa
C2P020	16,325	16,747	+	140	putative replication protein	Similar to putative replication protein[Clostridium tetani E88](gi|28373173|ref|NP_783816.1|)57.5% identity in overlap 127aa. Probably truncated N- and C-terminus
C2P021	17,217	17,918	+	233	conserved hypothetical protein	Weakly similar to hypothetical protein CAC0207[Clostridium acetobutylicum ATCC 824](gi|15893500|ref|NP_346849.1|)25.5% identity in overlap 204aa
C2P022	18,185	17,952	-	77	conserved hypothetical protein	Similar to C-terminus of putative phage lysozyme[Clostridium botulinum B str. Eklund 17B](gi|187934460|ref|YP_001887135.1|)50.7% identity in overlap 77aa. Probably truncated N-terminus
C2P023	18,323	18,652	+	109	hypothetical protein	
C2P024	19,455	18,730	-	241	conserved hypothetical protein	Similar to hypothetical protein NT01CX_0694[Clostridium novyi NT](gi|118443237|ref|YP_879160.1|)62.5% identity in overlap 237aa
C2P025	20,353	21,870	+	505	conserved hypothetical protein	Weakly similar to hypothetical protein CKL_3069[Clostridium kluyveri DSM 555](gi|153955683|ref|YP_001396448.1|)22.3% identity in overlap 476aa
C2P026	22,505	21,882	-	207	conserved hypothetical protein	N-terminus is similar to cell wall biogenesis enzyme(N-terminal domain related to N-Acetylmuramoyl-L-alanine amidase and C-terminal domain related to L-alanoyl-D-glutamate peptidase); peptodoglycan-binding domain[Clostridium acetobutylicum ATCC 824](gi|15894296|ref|NP_347645.1|)36.4% identity in overlap 110aa

C2P027	22,704	24,281	+	525	conserved hypothetical protein	N-terminus is similar to hypothetical protein NT01CX_1069[Clostridium novyi NT](gi|118444156|ref|YP_877153.1|)34.4% identity in overlap 294aa, C-terminus is similar to hypothetical protein NT01CX_1069[Clostridium novyi NT](gi|118444156|ref|YP_877153.1|)30.4% identity in overlap 306aa
C2P028	24,438	24,893	+	151	putative transposase OrfA	Similar probable transposase[Clostridium perfringens str. 13](gi|18309121|ref|NP_561055.1|)73.8% identity in overlap 149aa
C2P029	25,800	25,000	-	266	conserved hypothetical protein	N-terminus is similar to gamma-D-glutamyl-L-diamino acid endopeptidase I[Clostridium tetani E88](gi|28210330|ref|NP_781274.1|)32.8% identity in overlap 131aa
C2P030	26,263	26,811	+	182	putative RNA polymerase sigma factor	Similar to putative RNA polymerase sigma factor[Clostridium tetani E88](gi|28373140|ref|NP_783738.1|)46.8% identity in overlap 173aa, also to putative RNA polymerase sigma factor[Clostridium tetani E88](gi|28373141|ref|NP_783739.1|)30.2% identity in overlap 179 aa
C2P031	26,986	27,441	+	151	putative replication protein	Weakly similar to N-terminus of initiator RepB protein family[Clostridium perfringens SM101](gi|110803274|ref|YP_697644.1|)20.3% identity in overlap 153aa
C2P032	27,419	27,892	+	157	putative replication protein	Similar to C-terminus of initiator RepB protein family[Clostridium perfringens SM101](gi|110803274|ref|YP_697644.1|)34.8% identity in overlap 118aa
C2P033	27,941	28,402	+	153	conserved hypothetical protein	Similar to hypothetical protein NT01CX_1173[Clostridium novyi NT](gi|118444583|ref|YP_877256.1|)46.7% identity in overlap 135aa
C2P034	28,588	29,349	+	253	putative ParA protein	Similar to chromosome partitioning protein parA[Clostridium tetani E88](gi|28209873|ref|NP_780817.1|)33.6% identity in overlap 253aa
C2P035	29,469	29,747	+	92	conserved hypothetical protein	Similar to hypothetical protein CA_P0176[Clostridium acetobutylicum ATCC 824](gi|15004879|ref|NP_149339.1|)43.5% identity in overlap 92aa
C2P036	30,050	30,598	+	182	hypothetical protein	
C2P037	30,583	30,750	+	55	hypothetical protein	
C2P038	30,784	31,005	+	73	Putative replication protein	Similar to putative replication protein[Clostridium tetani E88](gi|28373173|ref|NP_783816.1|)66.7% identity in overlap 30aa. Probably truncated N- and C-terminus
C2P039	31,104	31,877	+	257	conserved hypothetical protein	Similar to membrane-spanning protein[Clostridium tetani E88](gi|28373170|ref|NP_783813.1|)33.9% identity in overlap 254 aa
C2P040	31,855	32,682	+	275	conserved hypothetical protein	Similar to hypothetical protein CPR_0051[Clostridium perfringens SM101](gi|110802027|ref|YP_697393.1|)39.8% identity in overlap 269aa

C2P041	32,679	33,434	+	251	conserved hypothetical protein	Similar to hypothetical protein CPR_0052[Clostridium perfringens SM101](gi|110802620|ref|YP_697394.1|)40.6% identity in overlap 249aa
C2P042	33,457	34,101	+	214	putative ABC transporter, ATP-binding protein	Similar to ABC transporter ATP-binding protein[Clostridium tetani E88](gi|28373165|ref|NP_783765.1|)51.9% identity in overlap 208aa
C2P043	34,638	34,471	-	55	hypothetical protein	
C2P044	34,658	34,960	+	100	hypothetical protein	
C2P045	35,426	35,214	-	70	hypothetical protein	
C2P046	36,100	36,846	+	248	conserved hypothetical protein	Similar to hypothetical protein CTC00614[Clostridium tetani E88](gi|28210346|ref|NP_781290.1|)38.2% identity in overlap 246aa
C2P047	37,357	37515	+	52	putative transposase OrfB	Similar to C-terminus of transposase[Clostridium tetani E88](gi|28210547|ref|NP_781491.1|)51.9% identity in overlap 52aa. Probably truncated N-terminus
C2P048	37,602	38,006	+	134	hypothetical protein	
C2P049	38,747	38,370	-	125	hypothetical protein	
C2P050	38,993	39,463	+	156	hypothetical protein	
C2P051	39,583	40,449	+	288	hypothetical protein	
C2P052	40,837	41,379	+	180	putative RNA polymerase sigma factor	Similar to putative RNA polymerase sigma factor[Clostridium tetani E88](gi|28373140|ref|NP_783738.1|)47.7% identity in overlap 172aa, also similar to putative RNA polymerase sigma factor[Clostridium tetani E88](gi|28373141|ref|NP_783739.1|)28.7% identity in overlap 181aa
C2P053	41,573	41,905	+	110	putative transcriptional regurator	Similar to transcriptional regulator, PadR family[Clostridium perfringens SM101](gi|110801733|ref|YP_697976.1|)46.1% identity in overlap 102aa
C2P054	41,908	42,654	+	248	hypothetical protein	N terminus is similar to hypothetical protein CPF_0700[Clostridium perfringens ATCC 13124](gi|110800270|ref|YP_695152.1|)44.7% identity in overlap 94 aa
C2P055	43,082	43,414	+	110	hypothetical protein	
C2P056	43,919	45,214	+	431	C2 toxin, component I	Identical to C2 toxin(component-I)[Clostridium botulinum](gi|3478671|ref|BAA32536.1|)
C2P057	45,460	47,625	+	721	C2 toxin, component II	Identical to C2 toxin(component-II)[Clostridium botulinum](gi|3478672|ref|BAA32537.1|)
C2P058	48,497	49,084	+	195	putative resolvase	Similar to resolvase[Clostridium perfringens SM101](gi|110804008|ref|YP_699911.1|)36.8% identity in overlap 193 aa

C2P059	49,541	49,206	-	111	hypothetical protein	
C2P060	49,909	49,577	-	110	hypothetical protein	
C2P061	50,213	51,259	+	348	putative replication protein	Similar to initiator RepB protein family[Clostridium perfringens SM101](gi|110803274|ref|YP_697644.1|)27.9% identity in overlap 280aa
C2P062	51,692	51,351	-	113	hypothetical protein	
C2P063	52,173	51,832	-	113	hypothetical protein	
C2P064	52,657	53,427	+	256	putative transcriptional regurator	Similar to chromosome partitioning protein; transcriptional regulator[Bacillus subtilis subsp. subtilis str. 168](gi|16081149|ref|NP_391977.1|)39.2% identity in overlap 250aa
C2P065	53,417	53,740	+	107	hypothetical protein	
C2P066	54,015	54,959	+	314	conserved hypothetical protein	Similar to hypothetical protein MAE_39620[Microcystis aeruginosa NIES-843](gi|166366703|ref|YP_001658976.1|)29.9% identity in overlap 291aa
C2P067	55,267	57,033	+	588	putative transcriptional regurator	Similar to signal-transduction and transcriptional-control protein[Clostridium tetani E88](gi|28209846|ref|NP_780790.1|)59.2% identity in overlap 585aa
C2P068	57,231	58,523	+	430	putative guanine deaminase	Similar to amidohydrolase[Thermosipho melanesiensis BI429](gi|150020028|ref|YP_001305382.1|)51.8% identity in overlap 427aa, also weakly similar to probable guanine deaminase[Thermococcus kodakarensis KOD1](gi|57160150|ref|BAD86080)28.0% identity in overlap 404aa
C2P069	58,550	59,638	+	362	putative dihydroorotate dehydrogenase family protein	Similar to dihydroorotate dehydrogenase family protein[Thermosipho melanesiensis BI429](gi|150020029|ref|YP_001305383.1|)61.8% identity in overlap 356aa
C2P070	59,658	60,443	+	261	putative xanthine dehydrogenase, FAD binding subunit	Similar to putative FAD-binding subunit of oxidoreductase[Clostridium difficile 630](gi|126699718|ref|YP_001088615.1|)42.3% identity in overlap 260aa, also similar to xanthine dehydrogenase[Bacillus subtilis subsp. subtilis str. 168](gi|16080302|ref|NP_391129.1|)24.4% identity in overlap 238aa
C2P071	60,443	60,892	+	149	putative xanthine dehydrogenase family protein, iron-sulfur-binding subunit	Similar to xanthine dehydrogenase family protein, iron-sulfur-binding subunit[Clostridium botulinum B1 str. Okra](gi|170756562|ref|YP_001779908.1|)43.3% identity in overlap 150aa, also similar to xanthine dehydrogenase[Bacillus subtilis subsp. subtilis str. 168](gi|16080300|ref|NP_391127.1|)34.7% identity in overlap 150aa
C2P072	60,901	63,204	+	767	putative xanthine dehydrogenase family protein, molybdopterin-binding subunit	Similar to xanthine dehydrogenase family protein, molybdopterin-binding subunit[Clostridium botulinum B1 str. Okra](gi|170755646|ref|YP_001780908.1|)34.4% identity in overlap 777aa, also similar to xanthine dehydrogenase[Bacillus subtilis subsp. subtilis str. 168](gi|16080301|ref|NP_391128.1)27.2% identity in overlap 765aa

C2P073	63,245	63,829	+	194	putative molybdopterin-guanine dinucleotide synthase	Similar to molybdopterin-guanine dinucleotide biosynthesis protein A[Clostridium tetani E88](gi|28212056|ref|NP_783000.1|)51.3% identity in overlap 195aa. N-terminus is similar to N-terminus of xanthine dehydrogenase[Bacillus subtilis subsp. subtilis str. 168](gi|16080303|ref|NP_391130.1|)30.5% identity in overlap 59aa
C2P074	63,839	65,980	+	713	putative xanthine dehydrogenase family protein, molybdopterin-binding subunit	Similar to xanthine dehydrogenase family protein, molybdopterin-binding subunit[Clostridium botulinum A3 str. Loch Maree](gi|170759696|ref|YP_001788204.1|)30.9% identity in overlap 712aa. N-terminus is similar to xanthine dehydrogenase[Bacillus subtilis subsp. subtilis str. 168](gi|16080301|ref|NP_391128.1)31.4% identity in overlap 519aa
C2P075	65,967	66,446	+	159	putative xanthine dehydrogenase family protein, iron-sulfur-binding subunit	Similar to xanthine dehydrogenase family protein, iron-sulfur binding subunit[Clostridium botulinum A3 str. Loch Maree](gi|170758476|ref|YP_001786676.1|)41.5% identity in overlap 147 aa, also similar to xanthine dehydrogenase[Bacillus subtilis subsp. subtilis str. 168](gi|16080300|ref|NP_391127)42.1% identity in overlap 159aa
C2P076	66,440	67,279	+	279	putative xanthine dehydrogenase, FAD-binding subunit	Similar to medium FAD-binding subunit of molybdenum enzyme[Clostridium botulinum B str. Eklund 17B](gi|187935032|ref|YP_001887512.1|)32.7% identity in overlap 275aa, also similar to xanthine dehydrogenase[Bacillus subtilis subsp. subtilis str. 168](gi|16080302|ref|NP_391129.1)23.3% identity in overlap 193aa
C2P077	67,475	68,293	+	272	putative xanthine dehydrogenase accessory factor	Similar to putative xanthine dehydrogenase accessory factor[Clostridium botulinum A3 str. Loch Maree](gi|170759749|ref|YP_001788216.1|)31.0% identity in overlap 258aa. C-terminus is similar to C-terminus of xanthine dehydrogenase[Bacillus subtilis subsp. subtilis str. 168](gi|16080304|ref|NP_391131.1)25.2% identity in overlap 147aa
C2P078	68,515	69,726	+	403	putative diaminopropionate ammonia-lyase	Similar to diaminopropionate ammonia-lyase[Clostridium tetani E88](gi|28209845|ref|NP_780789.1|)62.3% identity in overlap 401aa
C2P079	69,779	71,167	+	462	putative dihydropyrimidinase	Similar to dihydropyrimidinase[Clostridium tetani E88](gi|28211428|ref|NP_782372.1|)50.7% identity in overlap 456aa
C2P080	71,195	72,415	+	406	putative peptidase	Similar to peptidase, M20/M25/M40 family[Clostridium botulinum A str. Hall](gi|153937611|ref|YP_001388614.1|)85.4% identity in overlap 404aa
C2P081	72,457	73,440	+	327	putative ornithine carbamoyltransferase	Similar to aspartate/ornithine carbamoyltransferase family protein[Clostridium botulinum A str. Hall](gi|153936984|ref|YP_001388617.1|)35.2% identity in overlap 358aa
C2P082	73,853	73,521	-	110	hypothetical protein	
C2P083	74,661	75,065	+	134	hypothetical protein	
C2P084	75,449	75,144	-	101	hypothetical protein	
C2P085	75,608	76,006	+	132	hypothetical protein	

C2P086	76,139	76,558	+	139	putative transposase OrfA(ISCbt*5*-a)	Similar to transposase[Clostridium tetani E88](gi|28210546|ref|NP_781490.1|)92.1% identity in overlap 139aa
C2P087	76,561	77,475	+	304	putative transposase OrfB(ISCbt*5*-a)	Similar to transposase[Clostridium tetani E88](gi|28210547|ref|NP_781491.1|)93.8% identity in overlap 304aa
C2P088	77,881	77,537	-	114	hypothetical protein	
C2P089	79,675	77,996	-	559	conserved hypothetical protein	Similar to hypothetical protein pE88_20[Clostridium tetani E88](gi|28373149|ref|NP_783748.1|)43.9% identity in overlap 570aa
C2P090	81,393	80,788	-	201	putative superoxide dismutase	Similar to superoxide dismutase, Mn/Fe family[Clostridium botulinum A str. Hall](gi|153936872|ref|YP_001386477.1|)48.7% identity in overlap 193aa
C2P091	82,063	81,632	-	143	hypothetical protein	
C2P092	82,317	82,739	+	140	hypothetical protein	
C2P093	82,968	84,221	+	417	putative voltage gated chloride channel family protein	Similar to voltage gated chloride channel family[Clostridium perfringens SM101](gi|110803970|ref|YP_697884.1|)71.4% identity in overlap 392aa
C2P094	85,142	84,222	-	306	conserved hypothetical protein	Similar to hypothetical protein Noc_1844[Nitrosococcus oceani ATCC 19707](gi|77165316|ref|YP_343841.1|)35.8% identity in overlap 307aa
C2P095	86,137	85,217	-	306	conserved hypothetical protein	Similar to hypothetical protein Noc_1844[Nitrosococcus oceani ATCC 19707](gi|77165316|ref|YP_343841.1|)32.7% identity in overlap 306aa
C2P096	87,093	86,173	-	306	conserved hypothetical protein	Similar to hypothetical protein Noc_1844[Nitrosococcus oceani ATCC 19707](gi|77165316|ref|YP_343841.1|)33.3% identity in overlap 306aa
C2P097	88,381	87,458	-	307	conserved hypothetical protein	Similar to hypothetical protein Noc_1844[Nitrosococcus oceani ATCC 19707](gi|77165316|ref|YP_343841.1|)34.3% identity in overlap 306aa
C2P098	88,585	88,923	+	112	conserved hypothetical protein	Similar to hypothetical protein CPF_0409[Clostridium perfringens ATCC 13124](gi|110799856|ref|YP_694866.1|)42.5% identity in overlap 106aa
C2P099	89,063	89,452	+	129	hypothetical protein	
C2P100	90,881	89,517	-	454	putative guanine deaminase	Similar to hydroxydechloroatrazine ethylaminohydrolase[Clostridium botulinum B str. Eklund 17B](gi|187932710|ref|YP_001884832.1|)50.9% identity in overlap 442aa, also similar to putative guanine deaminase[Gluconacetobacter diazotrophicus PAl 5](gi|162147516|ref|YP_001601977.1|)41.9% identity in overlap 415aa
C2P101	91,253	91,690	+	145	putative MOSC domain-containing protein	MOSC domain-containing protein[Clostridium botulinum A str. Hall](gi|153934901|ref|YP_001387738.1|)74.8% identity in overlap 143aa

C2P102	91,776	93,119	+	447	putative ABC transporter, xanthine/uracil permease protein	Similar to xanthine/uracil permease family protein[Clostridium botulinum A str. Hall](gi|153934932|ref|YP_001386269.1|)49.6% identity in overlap 421aa
C2P103	93,233	93,667	+	144	hypothetical protein	
C2P104	94,065	93,718	-	115	hypothetical protein	
C2P105	94,457	95,407	+	316	putative carbamate kinase	Similar to carbamate kinase[Clostridium botulinum A str. Hall](gi|153937097|ref|YP_001388306.1|)76.8% identity in overlap 314aa
C2P106	95,654	96,673	+	339	putative molybdopterin biosynthesis protein	Similar to molybdopterin biosynthesis protein[Clostridium botulinum B1 str. Okra](gi|170755241|ref|YP_001780592.1|)47.8% identity in overlap 339aa
C2P107	96,742	97,539	+	265	putative ABC transporter, periplasmic molybdate-binding protein	Similar to molybdate ABC transporter, periplasmic molybdate-binding protein[Clostridium botulinum B str. Eklund 17B](gi|187932635|ref|YP_001885587.1|)43.2% identity in overlap 266aa
C2P108	97,563	98,366	+	267	putative ABC transporter, permease protein	Similar to putative anion ABC transporter, permease protein[Clostridium botulinum A str. Hall](gi|153937035|ref|YP_001386886.1|)47.1% identity in overlap 257aa
C2P109	98,399	99,136	+	245	putative ABC transporter, ATP-binding protein	Similar to ABC transporter, ATP-binding protein[Clostridium botulinum A str. Hall](gi|153936170|ref|YP_001387066.1|)47.5% identity in overlap 238aa
C2P110	99,186	99,920	+	244	conserved hypothetical protein	Similar to hypothetical protein CLC_1020[Clostridium botulinum A str. Hall](gi|153935100|ref|YP_001386888.1|)44.7% identity in overlap 237aa
C2P111	99,945	100,433	+	162	putative molybdopterin biosynthesis enzyme Mog	Similar to molybdopterin biosynthesis enzyme Mog[Clostridium botulinum A str. Hall](gi|153934484|ref|YP_001387743.1|)69.8% identity in overlap 162aa
C2P112	100,470	101,432	+	320	putative molybdenum cofactor biosynthesis protein A	Similar to molybdenum cofactor biosynthesis protein A[Clostridium botulinum A str. Hall](gi|153937083|ref|YP_001387740.1|)59.4% identity in overlap 320aa
C2P113	101,436	101,918	+	160	putative molybdenum cofactor biosynthesis protein C	Similar to molybdenum cofactor biosynthesis protein C[Clostridium botulinum A str. Hall](gi|153937145|ref|YP_001387739.1|)68.6% identity in overlap 156aa
C2P114	102,035	102,289	+	84	hypothetical protein	
C2P115	102,502	102,720	+	72	hypothetical protein	
C2P116	103,361	102,756	-	201	putative integrase/recombinase	Similar to integrase/recombinase[Clostridium tetani E88](gi|28373178|ref|NP_783821.1|)66.8% identity in overlap 202aa

C2P117	103,506	103,913	+	135	putative transposase OrfA(ISCbt6-a)	Similar to transposase[Clostridium tetani E88](gi|28210352|ref|NP_781296.1|)72.7% identity in overlap 132aa
C2P118	103,915	105,012	+	365	putative transposase OrfB(ISCbt6-a)	Similar to ISCpe2, transposase orfB[Clostridium perfringens SM101](gi|110802662|ref|YP_698899.1|)54.3% identity in overlap 385aa
C2P119	105,140	105,334	+	64	hypothetical protein	
C2P120a	105,350	105,502	+	50	putative ABC transporter, ATP-binding protein	Similar to N-terminus of ABC transporter ATP-binding protein[Clostridium tetani E88](gi|28373165|ref|NP_783765.1|)52.3% identity in overlap 44aa
C2P120b	105,543	105,680	+	45	putative ABC transporter ATP-binding protein	Similar to C-terminus of ABC transporter ATP-binding protein[Clostridium tetani E88](gi|28373165|ref|NP_783765.1|)46.2% identity in overlap 39aa
C2P121	105,681	106,073	+	130	conserved hypothetical protein	Similar to lipoprotein, putative[Clostridium novyi NT](gi|118444739|ref|YP_878536.1|)52.0% identity in overlap 123aa
C2P122	106,554	106,282	-	90	hypothetical protein	
C2P123	106,868	106,671	-	65	hypothetical protein	