Table	S5 .	Maior	indels	in	the 3	genomes
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Indels	Location [*]	Size(bp)	Lineage [†]	Main properties	Additional properties [‡]
phage					
B6	12202971254162	33866	O, O/NM	Mu-like prophage	B6 and B7 are 100% identical and more homologous to
B7	12974101331275	33866	O, O/NM	Mu-like prophage	the <i>Shewanella</i> Mu-like prophage than the original Mu phage.
S 1	214245249127	34883	O, O/NM	K139-like phage	251 bp DRs.
ctx related					-
B9	15641331573773	9641	NO, delM	ctx phage	18 bp imperfect DRs.
B10	15641331566857	2725	N, O/NM	RS1 in N	
B11	16526121655299	2688	O, O/NM	RS2 in O	
S 3	696316703355	7040	O, insO	ctx phage	
island with i	ntegrase				
B1	582331424	25602	O, O/NM	Novel O island	has recombinase/integrase as last gene;2 Transposase (VC395_0018, VC395_0019) and 1 DNA-invertase; low GC, no DRs.
B2	175198189466	14269	N, insN	VSP-I	1 putative integrase(VC0185); low GC and no DRs. Within a region that has undergone recombination.
B4	332373349315	16943	O, O/NM	Novel O island	1 VINT_BPPH8 (P06155) Integrase;16 bp DRs, and regions of low GC.
B5	522863550186	27324	N, insN	VSP-II	an integrase gene as last gene and tRNA gene downstream; low GC in parts, imperfect DRs.
Insertion sec	quence (IS) and IS as	sociated			
S 4	686227687260	1034	O, O/NM	ISVch1	VC395_A0738, IS481 family; 7 bp DRs. At the end of a region that has undergone recombination.
B14	18131341813755	622	O, O/NM	IS1004	VC395_1731, 8 bp imperfect DRs.
B17	19562981956919	622	M, insM	IS1004	VC66-2_1798, 8 bp DRs.

B18	24170612417682	622	O, O/NM	IS1004	VC395_2301, 9 bp DRs.
B19	28350842835705	622	O, O/NM	IS1004	IS1004 (VC395_2681), 8 bp imperfect DRs.
B12	15831251584394	1270	MN, O/MN	ISVch4	orfAB (VC66-2_1420/VC66-2_1421) in TLC element.
B3	262291263551	1261	N, insN	ISVch4	orfAB (VC0256/VC0257), 6 bp DRs.
S 2	292398293659	1261	M, insM	ISVch4	orfAB (VC66-2_A0272/VC66-2_A0273),.no DRs.
S 6	637261639633	2373	O, O/NM	ISVch5	VC395_A0686 (ISVch5) and 3 hypothetical proteins;
					same site as S5; No DRs. Within recombinant region.
B16	19387691949510	10742	NO, delM	Partial VPI-2	VPI-2 includes 2 Mu related genes; low GC, no DRs.
S 9	465338469823	4486	O, O/NM	ISVch4+5 genes	Starts with ISVch4 with 8 bp DRs., and adjacent to the
					ISVch4 at end of big inversion. Effectively 2 ISs with 5 hypothetical proteins between.
rrn					
B20	29278852933644	5760	NO, delM	rrn operon	2 16S-23S <i>rrn</i> segments in N16961 and O395, but only one in M66-2.
others					
B8	15479141555781	7868	MN, delO	Partial RTX region deletion	Part of <i>rtxB</i> gene, <i>rtxC</i> , VC66-2_1405 equivalent and part of <i>rtxA</i> gene are absence in O395.
B13	16655191670354	4836	O, O/NM	TLC element	3rd copy of toxin-linked cryptic (TLC) element in CTX region.
B15	19065191907323	805	O, O/NM	Hypothetical ORF	1 hypothetical protein (VC395_1807). Low GC, no
					DRs. Within a region that has undergone recombination.
S 5	563579566177	2599	MN.O/NM	a hypothetical	Present in MN: located at same site as S6.
~~				protein	,
S 7	672301677746	5446	MN, O/NM	3 unknown ORF	Present in MN; located at same site as S8; Within a
					region that has undergone recombination.
S8	527797530766	2970	O, O/NM	1 ATPase gene	Present in O; same site as S7.

* For deletions the location given is N16961 genome positions for M66-2 and O395 deletions, and O395 genome positions for deletions in N16961.

[†] Symbol before comma indicates the strain where the indel is present: O, O395; N, N16961; M, M66-2.

Abbreviation after comma indicates lineage to which the insertion (ins) or deletion (del) is attributed.

[‡] DR, direct repeat;