

Table S1. Pacific Biosciences sequencing statistics.

Strain	Number of reads	Average read length (bp)	Total number of base reads (Mb)	Avg. insert length (bp)	N50 insert length (bp)	Avg. coverage	Number of circularized contigs¹
87-9-116	70 764	14 341	1014.81	10 565	12 639	180.5	2
JLL237	139 094	4 662	643	3 635	6 051	118.2	3
S3 4/9	32 981	12 412	409.4	9 521	12 268	84.4	2
CNEVA NB11008	83 091	13 548	1125.73	8 303	9 283	198.4	3
VIB43	86 652	14 551	1260.84	8 864	9 960	207.8	3
ATCC-68554	58 664	13 446	788.79	9 087	10 396	155.17	3
VIB12	64 225	10 633	683.92	8 430	11 094	113.7	3

¹ The number of circularised contigs is based on the result from Mimimus v.2 followed by correction by SMRT Analysis version v2.3.0. For strain CNEVA NB11008 and JLL237, the number of contigs does not correlate with the actual number of circular chromosomes and plasmids in the bacterium, and was corrected bioinformatically (see main text). VIB12 and VIB43 each harbour two chromosomes and two plasmids not reported before, 15 kB and 292 kB, respectively [the latter containing mainly the COG-classes “function unknown” (30,2%) and “replication and repair” (62,6%; also covering transposases), without blast-overlaps with the two chromosomes, except for a few IS-elements in common].

Table S2: Presence of pJM1-like plasmids and the occurrences of complete or truncated integrase VangIntIA in *V. anguillarum* genomes.

<i>Vibrio anguillarum</i> strains (complete ●/ partial genome ●) ¹		pJM1 (2×ISVa5)	VangIntIA in chr2 ² (truncated/complete)	Chr 2 size (Mb)	Superintegron position <i>attC</i> -span in chr2 (%:SI/chr2)	Number of <i>attC</i> -sites in chr2 ³
NB10 (O1)	●	+	ISVa5-Ntrunc	1.187342	437,197–584,697 (12.7%)	65
ATCC68554/775 (O1; USA)	●	+	ISVa5-Ntrunc	0.997600	475,118–594,260 (12.2%)	67
775CrosaNC15637 (O1, USA) (replication origo at 12h)	●	+	ISVa5-Ntrunc	0.988135	402,279–467,168 (<6.9%)	64
VIB93 (O1)	●	+	ISVa5-Ntrunc	-	-	(30)
90-11-287 (O1)	●	+	ISVa5-Ntrunc	-	-	(23)
VIB18 (O1)	●	+	ISVa5-Ntrunc	-	-	(38)
VA1 (O1; Greece)	●	+	ISVa5-Ntrunc	-	-	(23)
T265 (O1; United Kingdom)	●	+	ISVa5-Ntrunc	-	-	(28)
LMG 12010 (O1)	●	+	ISVa5-Ntrunc	-	-	(25)
91-8-178 (O1)	●	+	ISVa5-Ntrunc	-	-	(23)
91-7-154 O1)	●	+	ISVa5-Ntrunc	-	-	(27)
9014-8 (O1)	●	+	ISVa5-Ntrunc	-	-	(30)
87-9-117 (O1)	●	+	ISVa5-Ntrunc	-	-	(23)
6018-1 (O1)	●	+	ISVa5-Ntrunc	-	-	(30)
601-90 (O1)	●	+	ISVa5-Ntrunc	-	-	(24)
261-91 (O1; Italy)	●	+	ISVa5-Ntrunc	-	-	(24)
178-90 (O1; Italy)	●	+	ISVa5-Ntrunc	-	-	(23)
M3 (O1; China/Japan)	●	+	ISVa5-Ntrunc	0.988134	(replic.origo ±12) (<6.9%)	64
87-9-116 (O1)	●	-	ISVa5-Ntrunc	1.207200	424,099–572,143 (12.5%)	65
VIB12 (O2; Greece) – p292	●	-	VangIntIA	1.282503	532,187–748,997 (17.2%)	78
CNEVA/NB11008 (O3; France)	●	-	VangIntIA	1.123902	386,342–561,697 (15.9%)	145
VIB43 (O1; UK) – p15	●	-	VangIntIA	1.152744	390,188–644,182 (22.3%)	58
S3 4/9 (O1)	●	-	VangIntIA	1.227548	293,375–645,764 (28.9%)	147
JLL237 (O1)	●	-	VangIntIA	1.164167	392,055–529,604 (12.1%)	93
90-11-286 (O1)	●	-	VangIntIA	1.293370	(replic.origo ± 12) (14.1%)	106
PF4 (O3; Chile)	●	-	VangIntIA	-	-	(15)

HI 610 (O2a)	●	-	VangIntIA	-	-	(7)
PF430-3 (O3; Chile)	●	-	VangIntIA	-	-	(13)
PF7 (O3; Chile)	●	-	VangIntIA	-	-	(46)
S2-2-9 (O1)	●	-	VangIntIA	-	-	(1)
DEM21597 (O2)	●	-	VangIntIA	-	-	(3)

¹ Serovariant number in parenthesis (and geographical origin, if isolated outside Scandinavia). Strains VIB12 and VIB43 harbor specific plasmids, p292 and p15, respectively. None of these two plasmids contain ISVa5-elements, but both have several copies of ISVa11. The ISVa5-orf3 and ISVa11-orf3 transposases are 88,5% aminoacid-identical (similarity=94,6%; gaps=5/514), cfr.: <https://www-is.biotoul.fr/>. The p292-plasmid contains replication and repair genes, including transposases (>62%), and genes with unknown function (>30%).

² A complete VangIntIA consists of 690 bp/330aa; the ISVa5-truncated version: 501 bp/167aa. The N-term part/12aa in Crosa775-chr2-IntIAtruncated *annotated* 2017-version [VAA_RS18025: (LTSRPVGSWGGY)VRVWQ ..] belong to the C-term part of an ISVa5.

³ *Parenthetical* numbers represent *attC*-sites within *unfinished* genomes. Sizes of their respective published chromosome2s seem quite normal, i.e. between 975 – 1.110 kB, thus calling attention to putative missing or lost IS-cassette genes. A low number of *attC*-sites does also apply to the pr March 2018 published unfinished strains: A023 (24), 51-82-2 (25), 4299 (6) and Ba35 (26).

Table S3: IS-elements from *V. anguillarum* available in the ISfinder database.

N°	Name	Family	Group	Synonyms	Iso	Origin	Length	IR	DR	ORF	Accession Number
1	IS1358A	ISAs1			IS1358	<i>Vibrio anguillarum</i>	1326	16/17		377 (174-1307)	U93591
2	ISVa1	IS5	IS903	ISV-A1		<i>Vibrio anguillarum</i>	1041	27/39	9	302 (79-987)	L40497
3	ISVa10	ISL3				<i>Vibrio anguillarum</i>	1349	19/22	7	389 (167-1336)	
4	ISVa11	IS66				<i>Vibrio anguillarum</i>	2376	13/19		106 (81-401) 117 (398-751) 510 (811-2343)	
5	ISVa12	IS66				<i>Vibrio anguillarum</i>	2378	14/19	8	106 (81-401) 117 (398-751) 510 (811-2343)	
6	ISVa13	ISAs1				<i>Vibrio anguillarum</i>	1235	17/21		371 (93-1208)	
7	ISVa14	IS4	ISH8			<i>Vibrio anguillarum</i>	1390	18/24	10	422 (109-1377)	
8	ISVa15	IS630				<i>Vibrio anguillarum</i>	1097	19/24	2	347 (47-1090)	
9	ISVa16	IS4	IS4			<i>Vibrio anguillarum</i>	1412	16/18	11	435 (92-1399)	CP011460
10	ISVa17	IS1634				<i>Vibrio anguillarum</i>	1820	21/24	6	539 (181-1800)	
11	ISVa18	IS4	IS50			<i>Vibrio anguillarum</i>	1504	16/21	8	462 (105-1493)	WP_053411098
12	ISVa19	IS256				<i>Vibrio anguillarum</i>	1366	21/27	8	412 (99-1337)	
13	ISVa2	IS5	IS903	ISV-A2		<i>Vibrio anguillarum</i>	1054	21/25	9	306 (80-1000)	L40498
14	ISVa20	IS66				<i>Vibrio anguillarum</i>	2397	17/22	8	106 (82-402) 117 (399-753) 516 (812-2359)	
15	ISVa3	IS91				<i>Vibrio anguillarum</i>	1508			415 (105-1352)	AY255699
16	ISVa4	IS3	IS3			<i>Vibrio anguillarum</i>	1254	29/36		99 (69-368) 305 (308-1225) 385 (69-1225)	
17	ISVa5	IS66				<i>Vibrio anguillarum</i>	2381	15/19		105 (81-398) 117 (395-748) 513 (808-2349)	
18	ISVa6	IS30				<i>Vibrio anguillarum</i>	1091	22/27	3	322 (93-1061)	NZ_LK021130
19	ISVa7	ISL3				<i>Vibrio anguillarum</i>	1348	22		412 (97-1335)	
20	ISVa8	IS66	ISBst12			<i>Vibrio anguillarum</i>	1563	16	8	88 (102-368) 415 (281-1528) 475 (102-1528)	
21	ISVa9	IS66				<i>Vibrio anguillarum</i>	2372	14/19	8	106 (81-401) 117 (398-751) 510 (811-2343)	

<https://www-is.biotoul.fr>