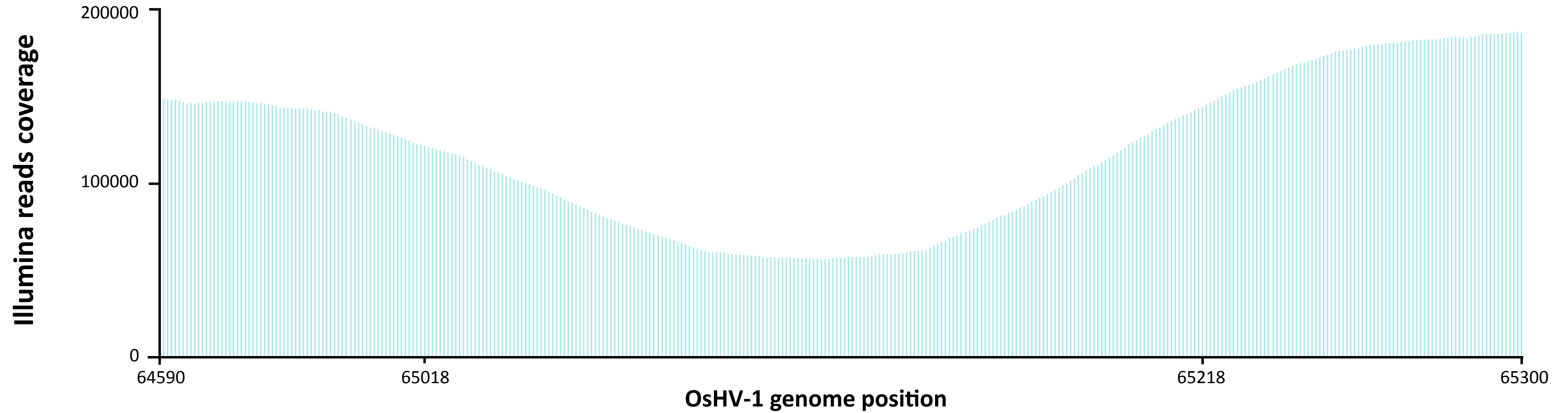


Figure Suppl 1

A



B

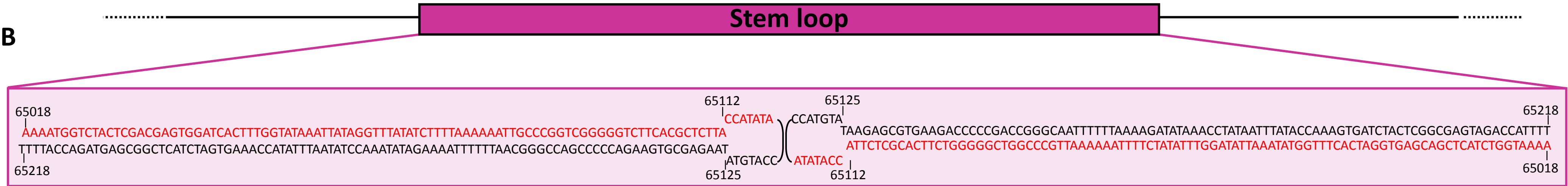


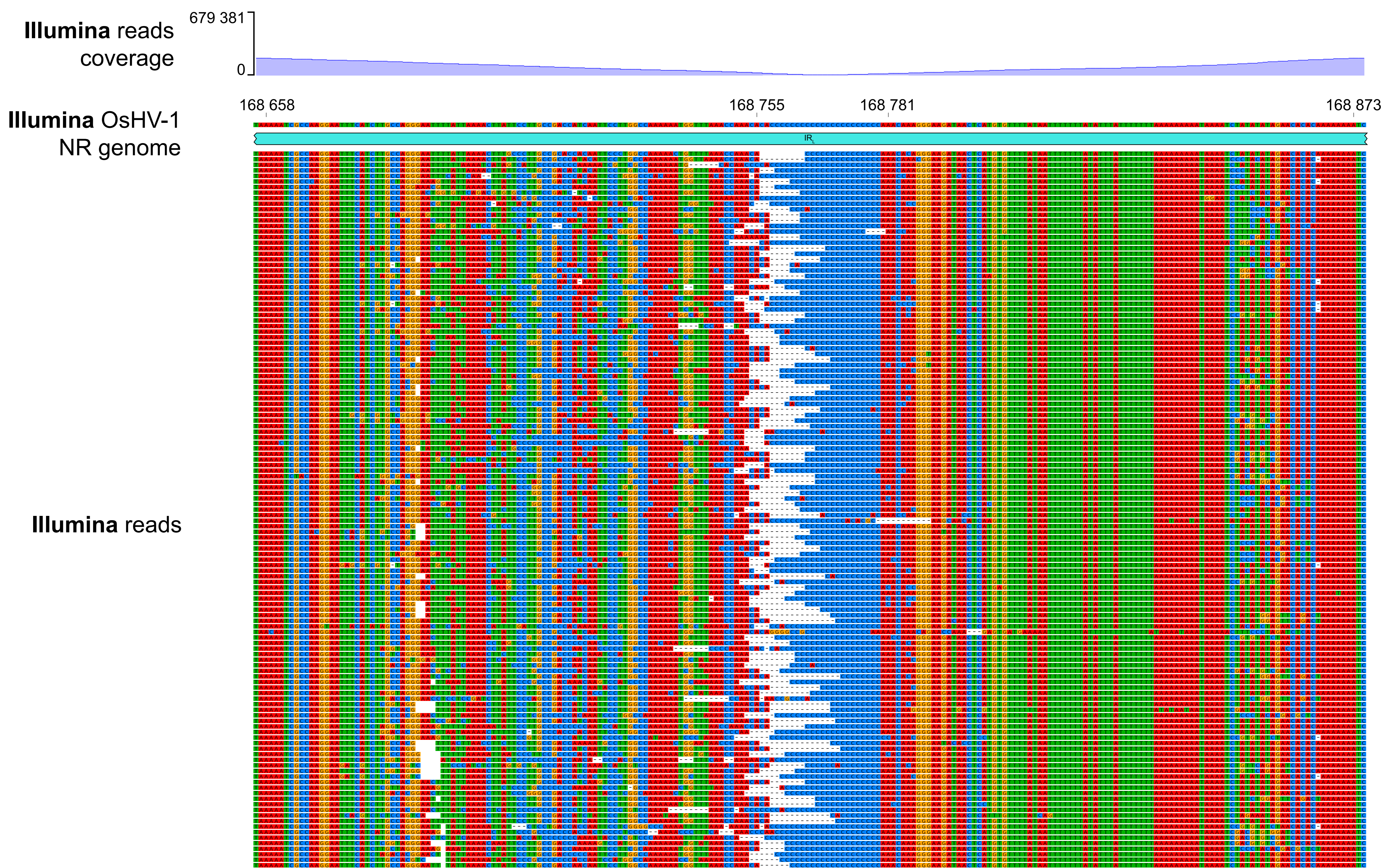
Figure Suppl 1: Read coverage analysis in the stem-loop region of the Illumina OsHV-1 NR genome.

(A) Illumina short-read coverage between position 64590 and 65300.

(B) Schematic representation of the palindromic region inside the stem-loop. Sequence color-coded in red correspond to the complementary strand forming the stem-loop.

Figure Suppl 2

A



B

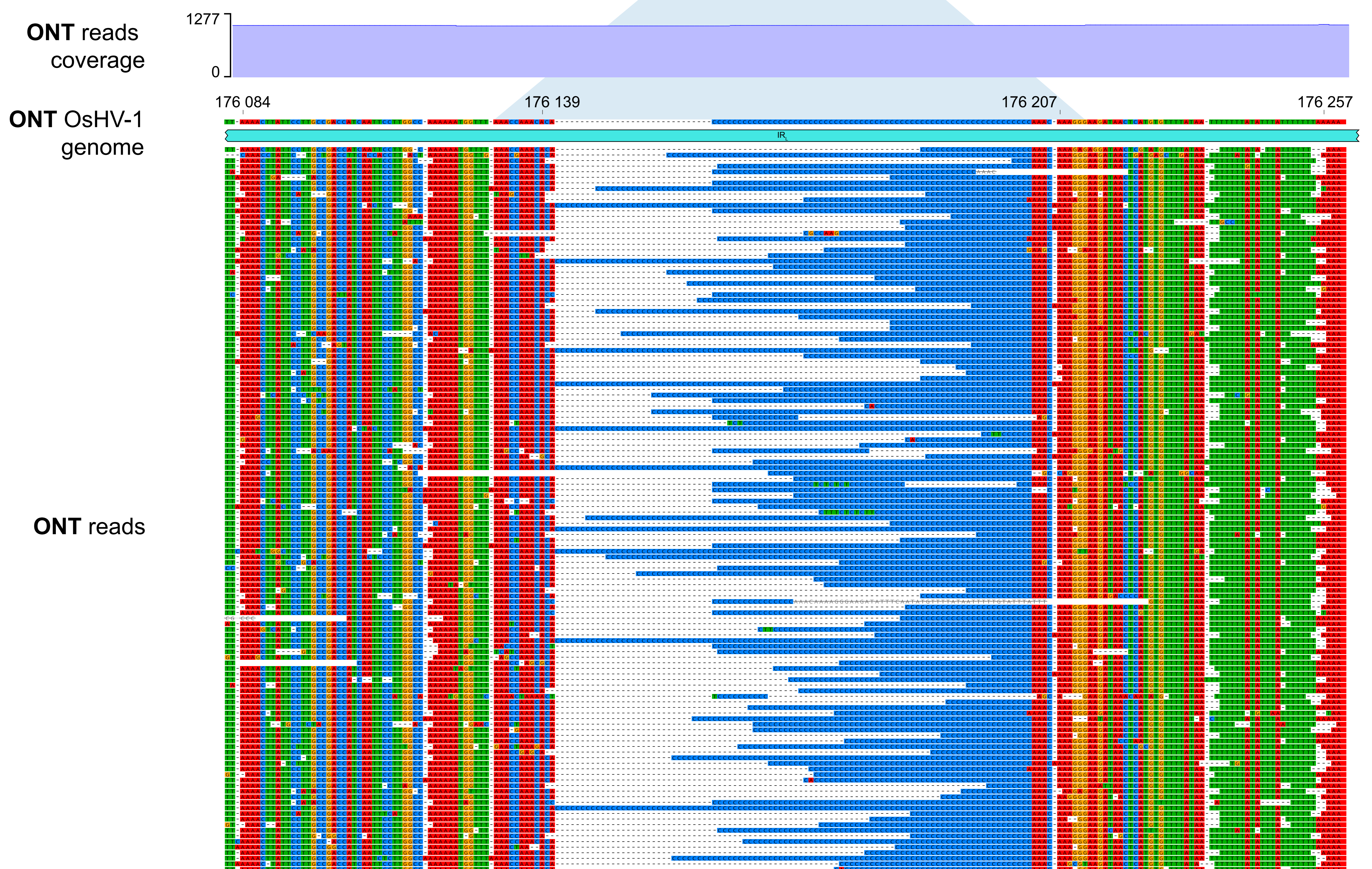


Figure Suppl 2: Large homopolymer read analysis.

(A) Snapshot of Illumina short-read aligned in the large homopolymer in the IRL region of the Illumina OsHV-1 NR genome.

(B) Snapshot of ONT long-read aligned in the large homopolymer in the IRL region of the ONT OsHV-1 genome.

Figure Suppl 3

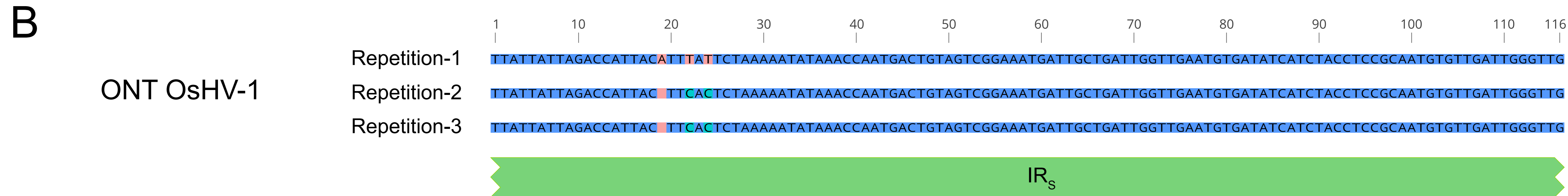
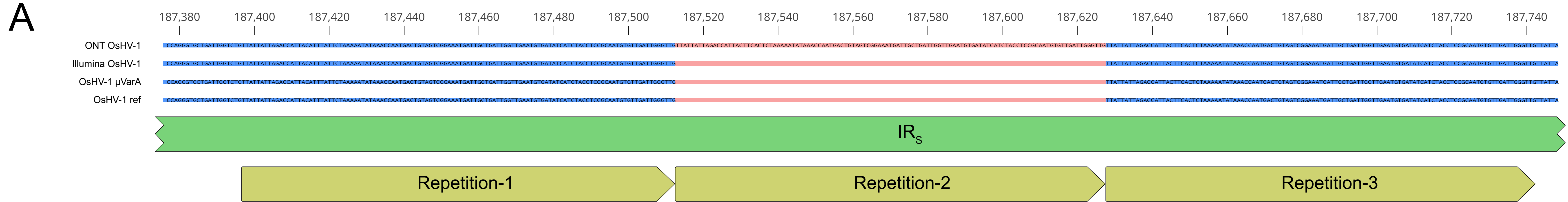


Figure Suppl 3: Schematic representation of the 115 bp structural variation present in the IRS region.

(A) Multiple alignment of the structural variation region from the 2005 OsHV-1 genome [7] the 2017 OsHV-1 μ Var A genome [31], the Illumina OsHV-1 NR genome and the ONT OsHV-1 genome. In red is highlighted the missing repetition.

(B) Multiple alignment of the three copies of the repetition.

Table Suppl 1: Description of the methodologies used to date to sequence OshV-1 genomes.

Reference	Strain	Genbank Accession	Publication Date	Origin	Host	Sampling Date	Tissue Type	Virus Isolation	DNA Extraction	% virus DNA (reads)	Amplification	Sequencing Library	Sequencing Technology	Assembly Type
Davison et al.	OshV-1 Ref	AY509253	2005	France	<i>C. gigas</i>	1992-1993	Virions purified from infected <i>C. gigas</i> larvae	Ultra centrifugation + sucrose gradient	Phenol-chloroform	99%	/	M3mp19 library	Sanger	GGG / Ptrans / BLAST / FastA / PRED-TMR2
Ren et al.	AVNV	GQ153938	2013	China	<i>C. farreri</i>	2007	Virions purified from infected <i>C. farreri</i>	Ultra centrifugation + sucrose gradient	Takara MiniBEST DNA Extraction Kit Ver. 3.0	no data	Tiling PCR based on 2005 genome	pGEM-T	Sanger	DNASTAR
Xia et al.	OshV-1 SB	KP412538	2015	China	<i>S. broughtonii</i>	2012	Virions purified from infected <i>S. broughtonii</i>	Ultra centrifugation + sucrose gradient	TIANampTM Marine Animals DNA Kit	no data	Tiling PCR based on 2005 genome	pEASYTM-T5 Zero Cloning Vector	Sanger	DNASTAR 7.1
Buridi et al.	OshV-1 μVar A and B	KY242785 and KY271630	2017	France and Ireland	<i>C. gigas</i>	2010	Virions purified from infected <i>C. gigas</i> spat / minced spat tissues	Ultra centrifugation + sucrose gradient / no isolation	QIAamp DNA Mini kit	From ultracentrifugation + sucrose gradient = 1% to 66% (pPCR) / Tissue samples = no data	Pre-capture PCR for library enrichment	SPRIworks HT Fragment library kit × 150 bp Mid Output kit.	illumina® NextSeq® 500 system with a 2 × 150 bp Mid Output kit.	Reference-based (2005 genome) Bowtie2 / Sambtools / MindTheGap
Abbadati et al.	OshV-1 PT	MS561751	2018	Italy	<i>C. gigas</i>	2016	Gills and mantle from infected <i>C. gigas</i>	no isolation	QIAamp DNA Mini Kit	2,60%	Sequencing library amplification + Gap closing by PCR	Nextera XT DNA sample preparation kit	illumina MiSeq + Sanger for finishing	Herpesvirales reads / denovo assembly IDBA-UD v1.1.1 / MUMmer v3.1 (2005 genome)
Bai et al.	OshV-1 ZK0118	MF509813	2019	China	<i>C. farreri</i>	2001	Gills and mantle from infected <i>C. farreri</i>	no isolation	QIAGEN DNeasy Blood and Tissue kit	no data	Tiling LR-PCR based on 2005 genome	9-13kb SMRTBell library / illumina TruSeq	PacBio RS II / illumina HiSeq 4000 / Sanger	PacBio: denovo Celera assembler + Quiver / illumina: denovo SOAPdenovo + gapclose
	VW46-2-m			France, Charente-maritime	<i>C. gigas</i>	2017				3,04%			HiSeq 4000, Paired-end 150bp	
	VW56-10-m			France, Charente-maritime	<i>C. gigas</i>	2017				2,76%			HiSeq 4000, Paired-end 150bp	
	VW48-4-m			France, Charente-maritime	<i>C. gigas</i>	2017				2,87%			HiSeq 4000, Paired-end 150bp	
	VW49-5-m88			France, Charente-maritime	<i>C. gigas</i>	2017				1,92%			HiSeq 4000, Paired-end 150bp	
	VW58-12-m			France, Charente-maritime	<i>C. gigas</i>	2017				1,19%			HiSeq 4000, Paired-end 150bp	
	VW47-3-m			France, Charente-maritime	<i>C. gigas</i>	2017				3,19%			HiSeq 4000, Paired-end 150bp	
	VW57-11-m99			France, Charente-maritime	<i>C. gigas</i>	2017				0,36%			HiSeq 4000, Paired-end 150bp	
	Posi-Harbour_UK_summer_2015			United-Kingdom	<i>C. gigas</i>	2015				3,53%			HiSeq 4000, Paired-end 150bp	
	LI			France, Charente-maritime	<i>C. gigas</i>	2010				2,00%			HiSeq 2500, Paired-end 100bp	
	PR			France, Port en Bessin	<i>C. gigas</i>	2008	Gills or mantle from infected spat-juveniles-	no isolation	QIAamp DNA Mini Kit	10,13%			HiSeq 2500, Single-end 100bp	
	MV	PRJNA721248	2021	France, Charente-maritime	<i>C. gigas</i>	2010	adults <i>C. gigas</i> or pool of larvae			11,62%			HiSeq 2500, Single-end 100bp	Reference mapping (2005 genome) BWA-MEM + consensus with bcftools and bedtools
	NZ			New-Zealand	<i>C. gigas</i>	2010				3,61%			HiSeq 2500, Single-end 100bp	
	NZ16			New-Zealand	<i>C. gigas</i>	2011				0,61%			HiSeq 2500, Paired-end 100bp	
	NZ17			New-Zealand	<i>C. gigas</i>	2011				0,88%			HiSeq 2500, Paired-end 100bp	
	NZ18			New-Zealand	<i>C. gigas</i>	2011				0,92%			HiSeq 2500, Paired-end 100bp	
	IRL15			Ireland	<i>C. gigas</i>	2011				0,01%			HiSeq 2500, Paired-end 100bp	
	JP2			Japan	<i>C. gigas</i>	na				0,01%			HiSeq 2500, Paired-end 100bp	
	JP6			Japan	<i>C. gigas</i>	na				0,01%			HiSeq 2500, Paired-end 100bp	
	NL4			Netherlands	<i>C. gigas</i>	na				0,02%			HiSeq 2500, Paired-end 100bp	
	SP16			Spain	<i>C. gigas</i>	na				0,01%			HiSeq 2500, Paired-end 100bp	
	SW3			Sweden	<i>O. edulis</i>	2012				0,01%			HiSeq 2500, Paired-end 100bp	
	SW6			Sweden	<i>O. edulis</i>	2012				2,12%			HiSeq 2500	
	OshV-1 Br ind2	OM811577								1,85%				
	OshV-1 Br ind4	OM811578								1,73%				
	OshV-1 Br ind6	OM811579		France, Bay of Brest (Br) (Logonna-Ouelias, lat.: 48.335 long.: -4.318)						1,09%				
	OshV-1 Br ind9	OM811580								1,10%				
	OshV-1 Br ind10	OM811581								3,19%				
	OshV-1 MO ind1	OM811582								5,29%				
	OshV-1 MO ind3	OM811583								0,66%				
	OshV-1 MO ind4	OM811584								5,26%				
	OshV-1 MO ind7	OM811585		France, Marennes-Oléron Bay (MO) (La Flotte, lat.: 45.803 and long.: -1.153)						2,77%				
	OshV-1 MO ind8	OM811586								2,73%				
	OshV-1 MO ind9	OM811587								5,91%				
	OshV-1 MO ind10	OM811588								2,02%				
	OshV-1 Th ind1	OM811589								3,10%				
	OshV-1 Th ind3	OM811590								2,78%				
	OshV-1 Th ind4	OM811591								2,85%				
	OshV-1 Th ind5	OM811592								2,21%				
	OshV-1 Th ind6	OM811593								4,30%				
	OshV-1 Th ind7	OM811594		France, Thau Lagoon (Th) (Meze, lat. 43.379 long. 3.571)						9,88%				
	OshV-1 Th ind8	OM811595								6,05%				
	OshV-1 Th ind9	OM811596								4,05%				
	OshV-1 Th ind10	OM811597								13,21%				
Delmotte et al.			2022		<i>C. gigas</i>	2018	Whole tissue from a single oyster spat	no isolation	MagAttract HMW DNA kit			Shotgun PCR-free library preparation kit	illumina NovaSeq 6000	Viral read extraction with Kraken and <i>C. gigas</i> reference mapping / Denovo assembly with SPAdes / Scaffolding with SSPACE using OshV-1 μVar A as reference

Table Suppl 2A: Taxonomic classification of non-OsHV-1 contigs. (A) Non-OsHV-1 contig identified in the ONT sequencing. Contig name in bold correspond to contigs also identified in the Illumina data.

Flye		Canu		Read Coverage (Flye all reads)	Lenght	GC%	Tool	Description	Accession
Name (all reads) (n=24)	Name (top10%) (n=9)	Name (all reads) (n=4)	Name (top10%) (n=5)						
Contig_01				6,4	41 032	52,9	PHASTER	Ralstonia phage RSK1 DNA	NC_022915.1
Contig_02	Contig_05			3,2	39 124	33,6	PHASTER	Flavobacterium phage FpV4	NC_041872.1
Contig_03				7,1	35 245	43,9	PHASTER	Pseudomonas phage tf	NC_017971.2
Contig_04				11,8	18 738	49,5	PHASTER	Cellulophaga phage phi39:1	NC_021804.1
Contig_05				4	45 019	37,5	PHASTER	Pseudoalteromonas phage B55	NC_031917.1
Contig_06				5,1	24 004	31,5	BlastX	Phage	
Contig_07				4,7	27 938	36,5	BlastN	Vibrio phage pVp-1	NC_019529.1
Contig_08				6,4	29 804	31,7	PHASTER	Persicivirga phage P12024L	NC_018272.1
Contig_09				6,2	27 288	48,1	BlastN	Vibrio phage 1.151.O_10N.222.46.B1	MG592520.1
Contig_10				5,4	25 934	47,5	PHASTER	Lentibacter virus vB_LenP_ICBM2	NC_048671.1
Contig_15				7,3	32 985	34,9	PHASTER	Cellulophaga phage phi38:1	NC_021796.1
Contig_16				5,7	28 718	39,9	PHASTER	Flavobacterium phage vB_FspS_hemulen6-1	NC_048833.1
Contig_17	Contig_06	tig00000003		65,4	41 592	42	PHASTER	Vibrio phage pYD21-A	NC_020846.1
Contig_18	Contig_04			9,9	18 201	36,6	BlastN	C. gigas mitochondrial DNA	AF177226.1
Contig_19	Contig_12			5	64 902	67,5	PHASTER	Gordonia phage Bachita	NC_030936.1
Contig_21				4,1	35 292	44,8	PHASTER	Pseudoalteromonas phage Pq0	NC_029100.1
Contig_22		tig00000001		182,8	14 374	37	BlastN	Eukaryotic Circular Rep-Encoding Single-Stranded DNA (CRESS DNA) Viruses	MH617489.1
Contig_23				3,6	34 661	42,1	BlastN	Myoviridae sp. isolate ct2701	BK025998.1
Contig_25	Contig_09			30,3	59 544	44,6	PHASTER	Vibrio phage douglas 12A4	NC_021068.1
Contig_26	Contig_10			22,6	163 592	33	PHASTER	Bacteroides phage crAss001	NC_049977.1
Contig_27	Contig_11			8,6	51 757	47,8	PHASTER	Vibrio phage VpKK5	NC_026610.2
Contig_28				4,9	29 738	43,3	BlastN	Uncultured Caudovirales phage genome assembly	LR798326.1

