

Table 2. ORFs in and around ϕ 7401PVL and their similarities to ϕ Sa2mw

ORF and special structure	Start (bp)	End (bp)	Size (bp)	aa	Gene	Function	ϕ Sa2mw	
							% identities to ϕ Sa2mw genome	Corresponding ORF(size in bp)
<i>attB</i> -L	1459	1483	25			Attachment site on chromosome		
core	1484	1512	29			Core sequence		
<i>attP</i> -L	1513	1537	25			Attachment site on phage		
TUP01	1596	1925	330	110	<i>int</i>	integrase1	100.0%	int-MW1442(1206)
TUP02	2029	2802	774	258	<i>int</i>	integrase2	97.3%	int-MW1442(1206)
TUP03	2928	3542	615	205		Na/K ATPase	50.5%	
TUP04	3775	4170	396	132		hypothetical protein	99.7%	MW1439(396)
TUP05	4199	4633	435	145		putative lipoprotein	96.3%	MW1438(435)
TUP06	4650	5111	462	154		hypothetical protein	93.3%	MW1437(402)
TUP07	5124	5447	324	108	<i>rep</i>	repressor	99.1%	MW1436(324)
TUP08	5611	5859	249	83		hypothetical protein	99.2%	MW1435(249)
TUP09	6089	6454	366	122		hypothetical protein	100.0%	MW1433(366)
TUP10	7266	7589	324	108		hypothetical protein	91.0%	MW1429(324)
TUP11	7604	7966	363	121		hypothetical protein	96.1%	MW1428(363)
TUP12	7963	9177	1215	405		hypothetical protein	96.4%	MW1427(1167)
TUP13	9155	9712	558	186		hypothetical protein	98.6%	MW1426(558)
TUP14	9772	11733	1962	654		phage encoded DNA polymerase I	98.2%	MW1425(1962)
TUP15	11931	12332	402	134		hypothetical protein	97.8%	MW1423(402)
TUP16	13664	14209	546	182	<i>dut</i>	dUTPase	49.5%	
TUP17	15274	17721	2448	816	<i>virE</i>	virulence-associated protein E	99.3%	MW1408(2448)
TUP18	18062	18352	291	97		hypothetical protein	100.0%	MW1406(198)
TUP19	18333	19700	1368	456		helicase	100.0%	MW1405(1359)
TUP20	19713	20150	438	146		hypothetical protein	99.8%	MW1404(438)
TUP21	20307	20621	315	105		HNH endonuclease	97.5%	MW1403(315)
TUP22	20730	21053	324	108	<i>terS</i>	terminase-small subunit	98.0%	MW1402(306)
TUP23	21034	22734	1701	567	<i>terL</i>	terminase-large subunit	92.7%	MW1401(1692)
TUP24	22739	23977	1239	413	<i>por</i>	portal protein	99.0%	MW1400(1239)
TUP25	23961	24734	774	258	<i>pro</i>	protease	99.6%	MW1399(774)
TUP26	24701	25909	1209	403		phage major capsid protein	99.9%	MW1398(1164)
TUP27	25978	26256	279	93		hypothetical protein	98.2%	MW1397(279)
TUP28	26601	27002	402	134		hypothetical protein	96.3%	MW1395(402)
TUP29	27003	27398	396	132		hypothetical protein	97.2%	MW1394(396)
TUP30	27433	28074	642	214		major tail protein1	99.8%	MW1393(642)
TUP31	28166	28621	456	152		major tail protein2	100.0%	MW1392(456)
TUP32	28679	29020	342	114		hypothetical protein	100.0%	MW1391(342)
TUP33	29243	35419	6177	2059	<i>mip</i>	phage tail tape measure protein	93.5%	MW1390(6201)
TUP34	35419	36243	825	275		hypothetical protein	97.7%	MW1389(825)
TUP35	36252	37835	1584	528		hypothetical protein	95.8%	MW1388(1584)
TUP36	37835	38125	291	97		hypothetical protein	97.6%	MW1387(291)
TUP37	38141	40051	1911	637		hypothetical protein	94.0%	MW1386(1911)
TUP38	40018	41331	1314	438		hypothetical protein	92.5%	MW1385(1467)
TUP39	41516	41905	390	130		hypothetical protein	100.0%	MW1384(390)
TUP40	42108	42407	300	100		hypothetical protein	100.0%	MW1382(300)
TUP41	42543	42845	303	101	<i>hol</i>	holin	100.0%	hol-MW1381(303)
TUP42	42856	44310	1455	485	<i>ami</i>	amidase	99.9%	ami-MW1380(1455)
TUP43	44700	45638	939	313	<i>lukS-PV</i>	Panton-Valentine leukocidin chain S precursor	99.6%	LukS-PV-MW1379(939)
TUP44	45640	46617	978	326	<i>lukF-PV</i>	Panton-Valentine leukocidin chain F precursor	99.9%	LukF-PV-MW1378(978)
<i>attP</i> -R	46822	46846	25			Attachment site on phage		
coreR	46847	46875	29			Core sequence		
<i>attB</i> -R	46876	46900	25			Attachment site on chromosome		