A.

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FDLV                1    MIRTRIYKPTYTTTTPPTCHTPIKMEEDPREKMHPQSMWRLVRLRAQRLLSYSESTDLSTREFLEDVSKS
AnaPV(1110RN043)    1    ------------------------..V....R....................ND...........AI.R.
AnaPV(1110RN047)    1    ------------------------..V....R....................ND...........AI.R.
AnaPV(1201RN001)    1    ------------------------..V....R....................ND...........AI.R.
AnaPV(1201RN003)    1    ------------------------..V....R....................ND...........AI.R.
AnaPV(1203RN009)    1    ------------------------..V....R....................ND...........AI.R.
Biti-CA98           1    ---MYT..SVHI.A.SS....S....V....R.Y..................ND............I.R.
Dasy-GER00          1    ------------------------..V....R.Y..................ND............I.R.
Xeno-USA99          1    ------------------------..V.L..R.Y..................ND............I...
Gono-GER85          1    ..N.HTS.T.H..AKS.R....V...V.L..................K.....D................
PanGut-GER09        1    ------------------------..I............................A..........I.G.
HoBuc-HUN09         1    ------------------------..I....R...........M.........D.A..........I.G.
Orth-GER05          1    ------------------------..A.MK.S...........S..RK....ND.A.P..K.....I.R.
Igu-GER00           1    ------------------------..T.MK.A...........S..RK....ND.A.P..K.....I.E.

FDLV                71   VVVLFNRDGMSSISQWRTEDCAARRLGNLSKFAWDAVTKGRMDPCRLAFKMVTELGNDVAIRAEILTVVW
AnaPV(1110RN043)    47   ............TP..H.........E........VI.R....................I..........
AnaPV(1110RN047)    47   ............TP..H.........E........VI.R....................I..........
AnaPV(1201RN001)    47   ............TP..H.........E........VI.R....................I..........
AnaPV(1201RN003)    47   ............TP..H.........E........VI.R....................I..........
AnaPV(1203RN009)    47   ............TP..H.........E........VI.R....................I..........
Biti-CA98           68   ..I.........TP..H.........E.........IIR....................T..........
Dasy-GER00          47   ..I.........TP..H.........E.........IIR....................T..........
Xeno-USA99          47   ................H.........E.........I...........V..........T..........
Gono-GER85          71   ................H.........V.............K.............................
PanGut-GER09        47   .........IN.MK.RH.........E..........I...................SMI..V...MI..
HoBuc-HUN09         47   .........AA.MI.QH.R.....................K................NAIV.V...MI..
Orth-GER05          47   M........VN.TI.QH......K................K...R...........S.MIV.V.....I.
Igu-GER00           47   M........VN.TI.QH.G....K................K...R...........S.MIV.V.....I.

FDLV                141  LITGWSTIPRTLHKDLWSSAIYRRLSL-
AnaPV(1110RN043)    117  ......S..Q.................-
AnaPV(1110RN047)    117  ......S..Q.................-
AnaPV(1201RN001)    117  ......S..Q.................-
AnaPV(1201RN003)    117  ......S..Q.................-
AnaPV(1203RN009)    117  ......S..Q.................-
Biti-CA98           138  ......S..Q.................-
Dasy-GER00          117  ......S..Q.................-
Xeno-USA99          117  ......S..Q.................-
Gono-GER85          141  ...................T.......-
PanGut-GER09        117  ......S..K...N.........K...E
HoBuc-HUN09         117  ......S..KN..N.............-
Orth-GER05          117  ......S..KG..N..R..S.....P--
Igu-GER00           117  ......S..KG..N..R..S.....P--
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B.

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FDLV                1    --------MVMAIPQHLHRTTPSRAMLIKSRNLAKRSRTKRRNLNRCNSRIGAKSKKATLQ---- 53
AnaPV(1110RN043)    1    ---------M.VVLP.PPH.....IR.R...DPVT------------------------------ 26
AnaPV(1110RN047)    1    ---------M.VVLP.PPH.....IR.R...DPVT------------------------------ 26
AnaPV(1201RN001)    1    ---------M.VVLP.PPH.....IR.R...DPVT------------------------------ 26
AnaPV(1201RN003)    1    ---------M.VVLP.PPH.....IR.R...DPVT------------------------------ 26
AnaPV(1203RN009)    1    ---------M.VVLP.PPH.....IR.R...DPVT------------------------------ 26
HeV                 1    MDLGGEEISQNLLLEVMSIW.A..FT.RTT.MKISW.MRMSLPKAQVRLSLTLLLRTMI.STRRK 65
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FIG S1 Multiple alignments of (A) U protein and (B) putative SB protein in the genomes of FDLV, AnaPV and other reptilian paramyxoviruses. Biti-CA98, Reptilian paramyxovirus (AAS45836.1); Dasy-GER00, Snake paramyxovirus (ACT63842.1); Xeno-USA99, Lizard paramyxovirus (ACT63860.1); Gono-GER85 Reptilian paramyxovirus (AAS45835.1); PanGut-GER09 Snake paramyxovirus (ADT91317.1); HoBuc-HUN09, Snake paramyxovirus (AFQ32570.1); Orth-GER05, Snake paramyxovirus (ACT63852.1); Igu-GER00, Lizard paramyxovirus (ACT63854.1).

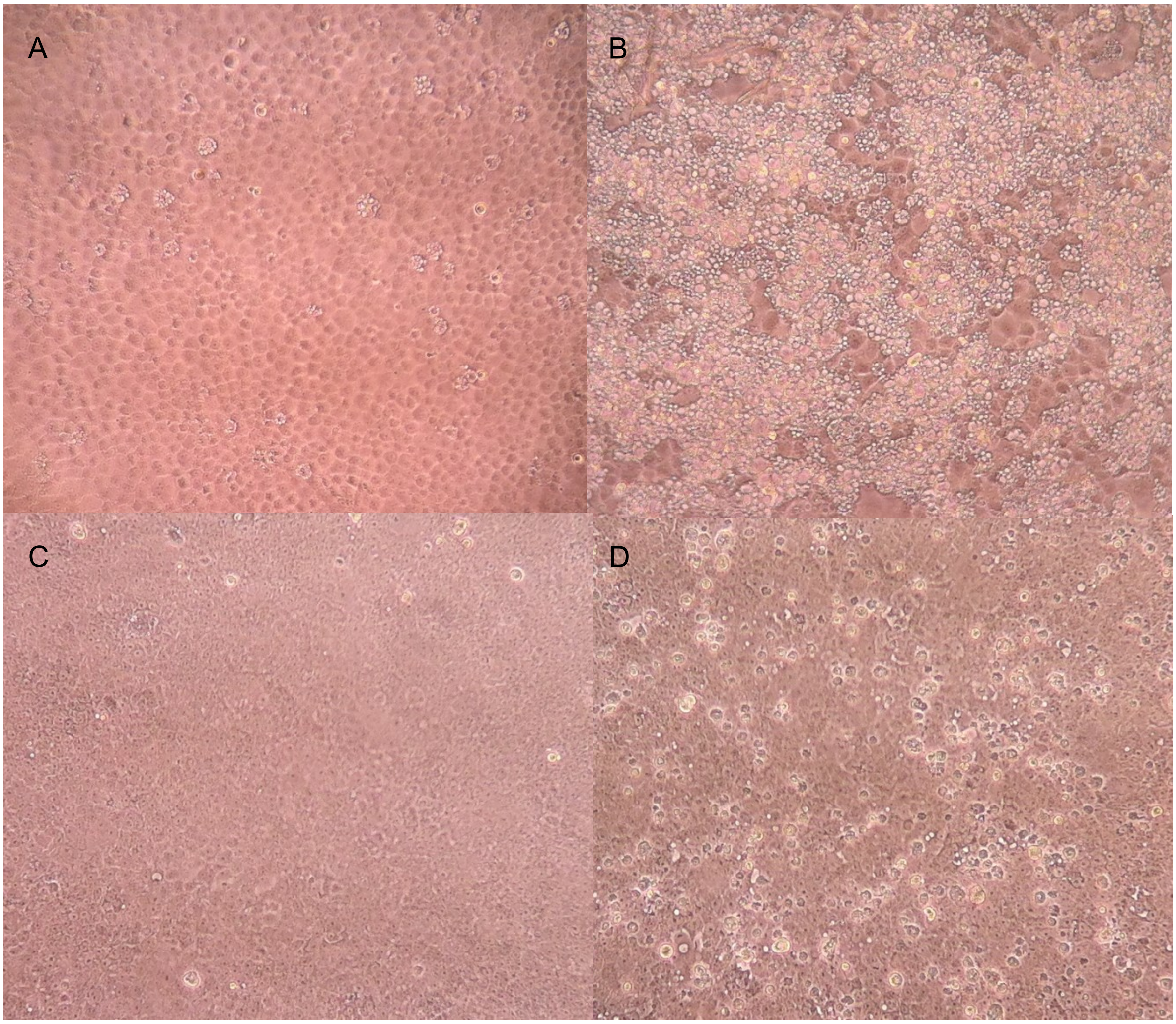

FIG S2 Panel A, Normal RK13 cells. Panel B, CPEs of AnaPV on RK13 cells. Panel C, Normal Vero cells. Panel D, CPEs of AnaPV on Vero cells.

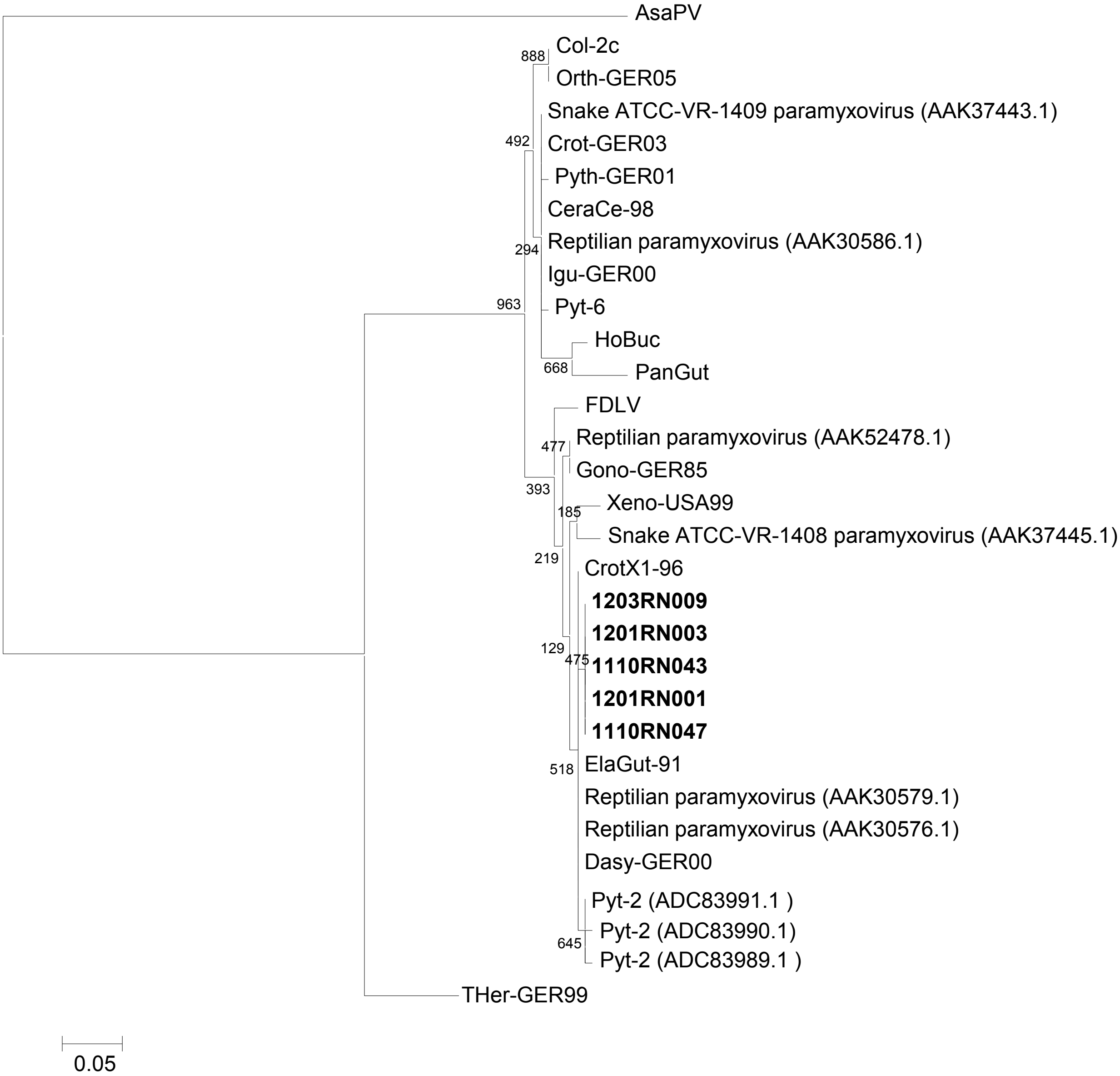

FIG S3 Phylogenetic analysis of amino acid sequences of partial L protein of AnaPV and other snake and reptilian paramyxoviruses. The trees were constructed by maximum likelihood method with bootstrap values calculated from 1,000 trees and rooted on midpoint. The scale bars indicates the branch length that corresponds to 0.05 substitutions per site. Five strains from AnaPV were named as 1201RN001, 1110RN043, 1110RN047, 1201RN003, and 1203RN009. AsaPV, Atlantic salmon paramyxovirus strain ASPV-Ro (EF646380.1); HoBuc-HUN09, Snake paramyxovirus (AFQ32572.1); PanGut-GER09, Snake paramyxovirus

(ADT91314.1); Col-2c, Snake paramyxovirus(ADC83992.1); Pyt-6, Snake paramyxovirus (ADC83993.1); Dasy-GER00, Snake paramyxovirus (ACT63842.1); Crot-GER03, Snake paramyxovirus (ACT63840.1); Orth-GER05, Snake paramyxovirus (ACT63845.1); Pyth-GER01, Snake paramyxovirus (ACT63841.1); THer-GER99, Tortoise paramyxovirus (ACT63844.1); Igu-GER00, Lizard paramyxovirus (ACT63846.1); Xeno-USA99, Lizard paramyxovirus (ACT63843.1); ElaGut-91, Reptilian paramyxovirus (AF349408.1); Gono-GER85, Reptilian paramyxovirus (AAS45835.1); CrotX1-96, Reptilian paramyxovirus (AF349405.1); CeraCe-98, Reptilian paramyxovirus (AF351137.1)

TABLE S1 Replication of AnaPV in 27 cell lines of different origins

Cell line			Viral load, $\log_{10}$ copies/ml, mean±SD						
Organism and anatomic site	Abbreviation	Source	Day 0	Day 1	*P*	Day 3	*P*	Day 5	*P*
Human									
Respiratory tract									
Embryonic lung fibroblasts	HFL	In-house development	5.81±0.01	7.95±0.01	<0.001	8.46±0.14	0.023	8.82±0.05	0.007
Lung adenocarcinoma	Calu-3	ATCC no. HTB-55	5.49±0.02	7.82±0.00	0.004	7.87±0.02	<0.001	8.22±0.05	0.002
Lung adenocarcinoma	A549	ATCC no. CCL-185	6.12±0.04	8.00±0.09	0.010	8.10±0.03	<0.001	8.29±0.00	0.007
Laryngeal epidermoid carcinoma	Hep-2	ATCC no. CCL-23	6.16±0.03	8.31±0.07	0.004	8.73±0.03	<0.001	8.91±0.09	0.006
Gastrointestinal tract									
Colorectal adenocarcinoma	Caco-2	ATCC no. HTB-37	6.20±0.15	8.20±0.02	0.017	9.73±0.10	<0.001	9.98±0.03	0.007
Ileocecal colorectal adenocarcinoma	HRT-18G	ATCC no. CRL-11663	6.30±0.15	7.98±0.01	0.040	8.70±0.04	0.02	9.13±0.06	0.011
Liver									
Hepatocellular carcinoma	Huh-7	JCRB0403, JCRB cell bank of Okayama University	6.45±0.01	7.92±0.01	<0.001	8.63±0.08	0.015	9.38±0.07	0.010
Genitourinary tract									
Cervical adenocarcinoma	HeLa	ATCC no. CCL-2.2	6.60±0.17	8.35±0.01	0.043	9.27±0.06	0.015	9.48±0.15	0.003
Fetal kidney	HEK	In-house development	6.88±0.03	8.54±0.18	0.041	9.11±0.36	0.070	9.39±0.55	0.100
Neuromuscular cells									
Neuron-committed teratocarcinoma	NT2	ATCC no. CRL-1973	6.56±0.10	8.60±0.06	0.004	8.88±0.03	0.012	9.44±0.04	0.006
Rhabdomyosarcoma	RD	ATCC no. CCL-136	5.73±0.05	7.85±0.05	<0.001	8.38±0.09	0.004	8.85±0.00	0.007
Central nervous system	SF268	Kindly provided by Prof. S. R. Shih	6.70±0.03	8.27±0.01	0.003	9.25±0.04	<0.001	9.41±0.01	0.004
Immune cell									
Malignant histiocytoma	His-1	In-house development	6.50±0.05	8.25±0.01	0.012	8.98±0.00	0.009	9.21±0.01	0.006
Non-human									
Mammals									
Madin-Darby canine kidney	MDCK	ATCC no. CCL-34	5.67±0.06	8.12±0.02	0.006	8.78±0.03	0.002	9.06±0.04	<0.001

Bovine kidney	MDBK	ATCC no. CCL-22	5.93±0.00	8.39±0.01	<0.001	9.28±0.01	<0.001	9.71±0.10	0.012
Rabbit kidney	RK13	ATCC no. CCL-37	6.26±0.02	8.14±0.01	<0.001	8.22±0.04	0.002	8.14±0.02	<0.001
Primary mouse embryonic fibroblasts	3T3	ATCC no. CCL-92	5.84±0.02	8.31±0.00	0.004	8.59±0.03	<0.001	8.73±0.03	<0.001
Camel skin	Dubca	ATCC no. CRL-2276	6.31±0.12	7.74±0.15	0.010	7.77±0.15	0.009	7.86±0.01	0.033
Rhesus monkey kidney	LLC-MK2	ATCC no. CCL-7	6.14±0.07	7.61±0.07	0.002	7.96±0.02	0.009	8.59±0.17	0.012
African green monkey kidney	Vero	ATCC no. CCL-81	5.97±0.11	7.71±0.02	0.024	8.39±0.02	0.015	9.00±0.01	0.015
African green monkey kidney (clone of Vero-76)	VeroE6	ATCC no. CRL-1586	5.78±0.08	7.72±0.03	0.009	8.66±0.02	0.009	9.19±0.02	0.008
Feline kidney	CRFK	ATCC no. CCL-94	5.74±0.02	7.70±0.04	0.003	7.90±0.04	0.003	7.88±0.00	0.003
Porcine kidney	PK-15	ATCC no. CCL-33	6.67±0.05	8.21±0.01	0.007	8.45±0.01	0.008	8.56±0.00	0.011
Rattus norvegicus kidney	RK3E	ATCC no. CRL-1895	6.72±0.05	8.37±0.08	0.004	8.53±0.05	<0.001	8.47±0.02	0.004
Rattus norvegicus kidney	RMC	ATCC no. CRL-2573	5.80±0.09	7.93±0.04	0.009	8.06±0.00	0.018	8.11±0.17	0.009
Chicken									
Chicken fibroblasts	DF-1	ATCC no. CRL-12203	6.73±0.16	8.17±0.01	0.033	8.56±0.06	0.015	8.75±0.07	0.010
Insect									
Aedes albopictus	C6/36	ATCC no. CRL-1660	6.51±0.15	7.65±0.02	0.056	7.80±0.01	0.052	7.71±0.04	0.045

TABLE S2 Comparison of genome characteristics between AnaPV and other members in *Paramyxovirinae*

Genus	Virus	Genome features		Pairwise percent amino acid identities of AnaPV proteins with analogous proteins in *Paramyxovirinae*								
		genome size	G+C content	N	U	P	V	I	M	F	HN	L
Ferlavirus	FDLV	15,378 bp	43.13%	97.2	75.4	87.2	83.7	79.4	97.4	95.6	93.3	96.8
Aquaparamyxovirus	AsaPV	16,965 bp	45.88%	18.5	NA	17.8	18.6	NA	35.8	40.8	38.6	43.9
Morbillivirus	CDV	15,690 bp	42.98%	27.9	NA	19.5	NA	NA	36.3	23.9	19.0	39.7
	MeV	15,894 bp	47.43%	26.7	NA	20.0	41.8	NA	34.2	32.0	19.2	39.5
	PPRV	15,948 bp	48.10%	28.0	NA	20.3	34.2	NA	35.2	28.6	18.1	40.0
Respirovirus	BPIV-3	15,456 bp	35.96%	26.7	NA	18.6	NA	NA	36.1	30.8	36.2	41.9
	HPIV-1	15,600 bp	37.24%	25.4	NA	18.0	NA	NA	37.4	29.8	39.1	43.6
	HPIV-3	15,462 bp	34.52%	25.6	NA	17.0	NA	NA	35.3	31.3	36.4	42.4
	SeV	15,384 bp	46.09%	26.3	NA	18.2	30.6	NA	36.6	30.2	40.3	43.4
Rubulavirus	MuV	15,384 bp	42.49%	22.7	NA	18.1	41.0	20.0	21.6	26.6	28.4	31.1
	HPIV4a	17,052 bp	36.23%	22.8	NA	19.4	22.4	NA	23.4	26.7	28.5	29.5
	HPIV4b	17,304 bp	36.40%	23.7	NA	19.3	21.4	NA	23.2	26.5	29.3	29.5
	PoRV	15,180 bp	46.70%	24.4	NA	19.6	39.8	NA	19.7	27.7	27.8	30.4
Henipavirus	HeV	15,882 bp	48.00%	29.7	NA	15.4	27.4	NA	34.9	28.5	21.8	40.0
	NiV	18,246 bp	38.17%	28.9	NA	17.1	27.5	NA	36.3	28.5	22.5	40.7
	CedPV	18,162 bp	37.20%	27.6	NA	16.5	NA	NA	33.6	29.2	21.1	36.1
Avulavirus	APMV6	16,236 bp	46.35%	23.6	NA	20.5	NA	NA	22.6	28.5	24.0	29.1
	NDV	15,186 bp	46.18%	25.5	NA	16.3	24.7	NA	19.7	25.0	29.0	28.2
	GooPV	15,192 bp	46.55%	27.1	NA	19.2	NA	NA	21.7	24.7	27.9	28.6
Unclassified Paramyxovirinae	BeiPV	19,212 bp	42.78%	26.7	NA	18.4	36.0	NA	39.2	35.3	25.5	40.7
	JPV	18,954 bp	40.95%	27.3	NA	20.8	38.4	NA	39.5	36.1	26.9	40.6
	TlmPV	19,152 bp	39.62%	27.7	NA	18.9	34.6	NA	37.5	34.5	17.7	42.4

NA, not available

TABLE S3 Molecular features and predicted gene products of AnaPV

Genome region	mRNA features, nt						Deduced protein			
	Total length	5'UTR	ORF	3'UTR	Hexamer phase	Intergenic regions, nt	Size, aa	MW, kDa	pI	Coding frame
Leader	55	-	-	-	-	(ATT)	-	-	-	-
N	1,550	55	1,416	79	2	CCT	471	51.4	5.52	3
U	604	86	432	86	1	CTT	143	16.8	9.23	3
P/V/I (P)	1,435	30	1,290	115	2	CTT	429	46.9	5.34	2
P/V/I (V)	1,433	30	684	719	2	CTT	227	25	6.01	2
P/V/I (I)	4,134	30	483	921	2	CTT	160	17.3	5.09	2
M	1,310	26	1,056	228	4	CTT	351	38.6	9.63	3
F	1,794	63	1,638	93	3	CTT	545	58.4	6.25	3
HN	1,938	29	1,695	214	6	CCT	564	61.8	5.13	2
L	6,640	24	6,546	70	3	(CTT)	2,181	247.2	6.26	3
Trailer	36	-	-	-	-	-	-	-	-	-