Supplementary Table 1. GenBank accessions and names of the *Mononegavirales* sequences used in this study.

GenBank Accession	Name
Avulavirus	
Newcastle disease virus	
AB524405	Goose/Alaska/415/91
AB524406	9a5b
AB534205	9a3b
AF077761	LaSota
AF309418	NDV-B1
AF375823	B1-Takaaki
AF431744	ZJ1
AY225110	HB92-V4
AY562985	Cockatoo/14698/90
AY562986	Anhinga/Fl/44083/93
AY562987	Gamefowl/211472/02
AY562988	Chicken/1083/72
AY562989	Dove/Italy/2736/00
AY562990	Mixedsp/US/Largo/71
AY562991	Chicken/Ulster/67
AY741404	Herts/33
AY865652	Sterna/Astr/2755
AY935489	01-1108
AY935490	02-1334
AY935491	98-154
AY935492	98-1249
AY935493	98-1252
AY935494	99-0655
AY935495	99-0868hi
AY935496	99-0868lo
AY935497	99-1997PR-32
AY935498	99-1435
AY935499	I-2
AY935500	I-2Progenitor
DQ060053	AQI-ND026
DQ097393	DE-R49/99
DQ097394	PHY-LMV42
DQ485229	Chicken/Guangxi7/02
DQ485230	Chicken/Guangxi9/02
DQ485231	Chicken/Guangxi11/02
DQ486859	GM
DQ659677	NA-1
EF026579	PPMV-1/0.025
EF026583	PPMV-1/1.3
EU167540	SRZ03
EU289028	VG/GA
EU289029	VG/GA
EU293914	Italien
EU546165	JL-1
FJ386392	NDV01
FJ386393	NDV02
FJ386394	NDV03
FJ386395	NDV04
FJ386396	NDV05
FJ410145	PPMV-1/NewYork/1984
FJ430159	JS/7/05/Ch
FJ430160	JS/9/05/Go
FJ436302	F48E8
FJ436303	ZJ/1/86/Ch
FJ436304	JS/1/85/Ch
FJ436305	JS/1/97/Ch
FJ436306	JS/1/02/Du
FJ751918	QH1
FJ751919	QH4
FJ766526	JS/07/22/Pi
FJ766527	JS/07/16/Pi
FJ766528	NDV05-029
FJ766529	ZhJ-3/97
FJ766530	JS/07/04/Pi
FJ766531	JS/07/03/Pi
FJ794269	NDV08-004
FJ872531	Muscovy duck/FP1/02
FJ939313	NDV/Chicken/Egypt/1/2005
FJ986192	2K3/Chennai/TamilNadu
GQ288377	Mallard/04-411
GQ288378	Pintail/87-486
GQ288379	Mallard/03-632
GQ288380	Mallard/86-233
GQ288381	Cormorant/D9704285
GQ288382	Cormorant/98CNN3-V1125
GQ288383	Cormorant/95DC02150
GQ288384	Cormorant/95DC2345
GQ288385	Cormorant/18719-03
GQ288386	Cormorant/19529-04
GQ288387	Cormorant/92-40140

EF065682	rAnhinga
EF201805	Mukteswar
EU140955	KBNP-C4152R2L
GQ288392	Mallard/MN00-39
GQ338309	ND/03/018
GQ338310	ND/03/044
GQ338311	ND/05/028
GQ429293	Dove/Italy/2736/00
GQ849007	JSD0812
GQ918280	BHG/Sweden/94
GQ994433	XD/Shandong/08
GQ994434	QG/Hebei/07
GU143550	Go/CH/HLJ/LL01/08
GU187941	NDV-2/chicken/Namakkal
GU564399	FMW
GU585905	Chicken/Sweden/97
GU978777	APMV-1/US(TX)/GB
HQ008337	JS10
HM063422	D3
HM063423	W4
HM063424	R8
HM063425	P4
HM117720	NDV-P05
HM125898	WDK/JX/7793/2004
HM188399	SDWF02
HM357251	NDV-4
NC_002617	B1

Bornavirus

Borna disease virus

AB032031	OL/Hu-BV
AB246670	Bo/04w
AB258389	huP2br
AJ311521	V/FR
AJ311522	He/80/FR
AJ311523	H1766
AJ311524	No/98
AY114161	CRNP3A
AY114162	CRNP3B
AY114163	CRNP5
NC_001607	bobe
U04608	V

GQ288388	Cormorant/92-23071
GQ288389	Mallard/99-376
GQ288390	Mallard/00-32

Ebolavirus

Ebola virus

AB050936	Reston
AF086833	Mayinga
AF272001	Mayinga
AF499101	Mayinga
AF522874	Pennsylvania
AY142960	Mayinga
AY354458	Zaire
AY729654	Gulu
AY769362	Pennsylvania
EU224440	Mayinga
EU338380	Yambio
FJ217161	Bundibugyo
FJ217162	Cote d'Ivoire
L11365	Zaire
NC_004161	Pennsylvania
NC_006432	Gulu
NC_014373	Bundibugyo
NC_002549	Mayinga

Henipavirus

Nipah virus

AF017149	Hendra virus
AF212302	Nipah virus
AJ564621	NV/MY/99/VRI-2794
AJ564622	NV/MY/99/VRI-1413
AJ564623	NV/MY/99/UM-0128
AJ627196	NV/MY/99/VRI-0626
AY029767	UMMC1
AY029768	UMMC2
AY988601	Bangladesh
FJ513078	Ind-Nipah-07-FG
NC_001906	Hendra virus
NC_002728	Nipah virus

Lyssavirus

Rabies virus

AB044824	Nishigahara
AB085828	HEP-Flury
AB128149	Ni-CE
AB362483	BR-Pfx1
AF499686	SRV9
AY705373	SHBRV-18

DQ875050	MRV
DQ875051	DRV
EF206707	ERA
EF206708	SAD Lysvulpen
EF206709	SAD B19
EF206710	SAD Bern var1
EF206711	SAD Bern var2
EF206712	SAD Bern var3
EF206713	SAD Bern var4
EF206714	SAD Bern var5
EF206715	SAD P5/88
EF206716	SAD VA1
EF206717	SAD1-3670var1
EF206718	SAD1-3670var2
EF206719	SAG 2
EF206720	SAD Bern
EF437215	NNV-RAB-H
EF564174	CTN181
EU182346	RB/E3-15
EU182347	Rb/E3-15-5
EU293111	8764THA
EU293113	9001FRA
EU293115	9147FRA
EU293116	9704ARG
EU293121	8743THA
EU311738	RRV ON-99-2
EU549783	BD06
EU643590	HN10
EU877067	SAD B19-4th
EU877068	SAD B19
EU877069	SAD B19-1st
EU877070	SAD B19-5th
EU877071	SAD B19-10th
FJ577895	Flury-LEP-C
FJ712193	D01
FJ712194	D02
FJ712195	F02
FJ712196	F04
FJ866835	FJ008
FJ866836	FJ009
FJ913470	ERA-VC
FJ959397	CTN-1
GQ918139	CVS-11
GU345746	CQ92
GU345747	J
AY956319	Serotype1
GU358653	GX4
GU565703	Flury-LEP
GU565704	Flury-HEP
GU647092	JX08-45
M13215	RAVMMGN
M31046	RAVCGA
NC_001542	RB

Metapneumovirus

Avian/human metapneumovirus

AB503857	Jpn03-1
AF371337	00-1
AY297748	CAN98-75
AY297749	CAN97-83
AY525843	NL/1/99
AY579780	USA
AY590688	Colorado
AY640317	LAH A
DQ009484	15a
DQ843658	BJ1816
DQ843659	BJ1887
EF199771	PL-1
EF199772	PL-2
EF535506	TW05-00125
FJ168778	NL/94/01
FJ168779	NL/00/17
FJ977568	aMPV/MN/turkey/2a/97
GQ153651	HMPVgz01
NC_004148	CAN97-83
NC_007652	15a

Morbilivirus

Canine distemper virus

AB474397	007Lm
AF014953	Onderstepoort
AF164967	A75/17
AF305419	Onderstepoort
AF378705	Onderstepoort-OS
AY386315	5804
AY386316	5804P
AY443350	00-2601
AY445077	98-2645
AY466011	98-2654

GU345748	SH06
AY649446	01-2689
EU716337	164071
GU138403	Snyder Hill
HM046486	Phoca/Caspian
HM063009	Shuskiy
HM852904	MKY-KM08
NC_001921	CDV

Measles virus

AB254456	SSPE-Kobe-1
AB481087	T11wild
AB481088	T11Ve-23
AF266286	AIK-C
AF266287	Moraten
AF266288	Edmonston
AF266289	Rubeovax
AF266290	Zagreb
AF266291	Schwarz
AY486083	EZD22
AY486084	EZD24 2/99
AY730614	Leningrad-4
DQ211902	CHN/7.05/4
DQ227318	CRO/47.02/[D6]
DQ227319	97-45881
DQ227320	CRO/08.03/SSPE
DQ227321	WA.USA/17.98
DQ345721	CAM-70
DQ345722	CAM-70
DQ345723	CAM-70
EF033071	Changchun-47
EU293548	D-V/S
EU293549	D-CEF
EU293550	Davis87
EU293551	D-VI
EU293552	D-VII
EU435017	Shanghai-191
FJ161211	IMB-1
FJ211583	0349U
FJ211589	MEV10016
FJ211590	AMJRB107B
FJ416067	Shanghai-191
FJ416068	Changchun-47
GQ376026	MV99Y
GQ376027	MV99YC7
K01711	Edmonston
AY542312	98-2646
NC_001498	Ichinose-B95a

Pneumovirus

Respiratory syncytial virus

AF013254	B1
AF013255	Cp52
AF035006	rA2cp
AY353550	9320
AY911262	ATCC VR-26
FJ948820	98-25147-X
NC_001781	HRSV
U39662	S2
U50362	Cp-RSV
U50363	Cpts-248
U63644	Cpts-248/404

Respirovirus

Sendai virus

AB005795	M1
AB039658	E0
AB195967	E-5
AB195968	Nagoya
AB275416	Cl.151
DQ219803	BB1
EF679198	Tianjin
M30202	Z
M69046	T-5
NC_001552	Ohita

Rubulavirus

Mumps virus

AB040874	Miyahara
AB470486	Hoshino
AB576764	Y213
AF201473	Jeryl Lynn
AF280799	Glouc1/UK96
AF314561	Biken
AF314562	87 1005
AF314558	SIPAR02
AF467767	88-1961
AY309060	Dg1062/Korea/98
AY508995	L3/Russia/Vector
AY669145	Drag94
AY681495	PetroNov

AY685921	L-Zagreb
DQ649478	SP
EU370206	9218/Zg98
EU370207	Du/CRO05
EU884413	SP
FJ375177	1004-10/2
FJ375178	Gw7
FJ556896	SP-A
GU980052	Enders
FN431985	JL2
NC_002200	Miyahara

Parainfluenza virus Type 3

AF178654	Kansas/15626/84
AF178655	Shipping Fever
D84095	910N
EU277658	Q5592
EU326526	ZHYMgz01
EU424062	14702
EU439428	92-7783_ISU-92
EU439429	81-19252_Texas
FJ455842	LZ22
NC_001796	HPIV3
NC_002161	HPIV3
U51116	Cp-45

Vesiculovirus

Vesicular stomatitis virus

AF473864	98COE
AF473865	85CLB
AF473866	94GUB
AM690337	Indiana
AM690336	Indiana
EF197793	MARMC
EU849003	Mudd-Summers
J02428	Indiana
NC_001560	Indiana

Supplementary Table 2. Relative mRNA and protein abundance for each *Mononegavirales* species and the associated source of information.

	Gene												
Virus	**NS1**	**NS2**	**N**	**P(V/C)**	**M**	**SH**	**F**	**G/H/HN**	**M2**	**VP30**	**VP24**	**L**	**Reference**
					mRNA abundance								
Newcastle disease virus	*	*	100	86.9	84.8	*	82.3	64.8	*	*	*	4.7	**4** (Fig 2. Lines a & d)
Borna disease virus	*	*	-	-	-	*	*	-	*	*	*	-	
Ebola virus	*	*	100	325.8	391	*	*	68.7	*	218.6	97	-	**14** (Fig 1. Line 4)
Nipah virus	*	*	-	-	-	*	-	-	*	*	*	-	
Rabies virus	*	*	100	70.2	42.6	*	*	21.2	*	*	*	1	**9** (Fig 5)
Avian/Human metapneumovirus	*	*	-	-	-	-	-	-	-	*	*	-	
Canine distemper virus	*	*	100	93.6	81.3	*	76.9	64.8	*	*	*	59.6	**18** (Fig 4. 56 days pi[†])
Measles virus	*	*	100	34	25	*	20	15	*	*	*	1.5	**3** (Fig 4. Panel E)
Respiratory syncytial virus	111.1	105.6	100	75.6	57.8	35.6	20	23.3	16.7	*	*	3.3	**1** (Fig 6)
Sendai virus	*	*	100	68	100	*	38	33	*	*	*	3	**10** (Table 1)
Mumps virus	*	*	100	39.2	62.6	-	31.5	6.6	*	*	*	0.6	**15** (Fig 2)
Parainfluenza virus type 3	*	*	100	31.6	-	*	20.9	19.3	*	*	*	14.2	**5** (Fig 4)
Vesicular stomatitis virus	*	*	100	75	50	*	*	36	*	*	*	5.6	**16** (Table 1)
					Protein abundance								
Newcastle disease virus	*	*	100	46.7	99.5	*	51	83.7	*	*	*	38.3	**8** (Fig 1. Panels A & B)
Borna disease virus	*	*	-	-	-	*	*	-	*	*	*	-	
Ebola virus	*	*	100	49.1	121.5	*	*	179.5	*	154.2	40.6	23.7	**14** (Fig 2. Line 2)
Nipah virus	*	*	-	-	-	*	-	-	*	*	*	-	
Rabies virus	*	*	100	86	52	*	*	64	*	*	*	1.9	**13** (Table 1)
Avian/Human metapneumovirus	*	*	-	-	-	-	-	-	-	*	*	-	
Canine distemper virus	*	*	100	58	62.3	*	43	62.3	*	*	*	-	**6** (Fig. 7)
Measles virus	*	*	100	51.8	86.6	*	-	44.7	*	*	*	8	**2** (Fig. 6. Panel b)
Respiratory syncytial virus	39.6	-	100	107.7	138.8	-	8.6	338.5	-	*	*	46.4	**12** (Fig 1. 16 hours pi[†], line I)
Sendai virus	*	*	100	88.7	47	*	61.3	68.6	*	*	*	9.1	**11** (Fig 1)
Mumps virus	*	*	100	137.1	99.7	-	56.2	87.1	*	*	*	54	**7** (Fig 2. Line g)
Parainfluenza virus type 3	*	*	100	49.3	127.4	*	116	144.9	*	*	*	55.2	**17** (Fig 1. 21 hours pi[†])
Vesicular stomatitis virus	*	*	100	77	53	*	*	34	*	*	*	6.9	**16** (Table 2)

* Gene not present in this species.

- No information available.

[†] post infection

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Supplementary Table 3. Calculation of relative mRNA abundance for the *Mononegavirales* genes.

Species	Gene	Measurement method[a]	Densitometry (Bg corrected)[b]	Gene length	mRNA abundance[c]	Relative mRNA abundance (%)[d]
Rabies virus	N	(^{3}H)Uridine	208.74	1353	0.1543	100
	P		96.82	894	0.1083	70.2
	M		41.98	639	0.0657	42.6
	G		51.50	1575	0.0327	21.2
	L		9.58	6387	0.0015	1
Vesicular stomatitis virus	N	Author's	-	NA	-	100
	P(NS)		-	NA	-	75
	M		-	NA	-	50
	G		-	NA	-	36
	L		-	NA	-	5.6
Ebola virus	N	(^{3}H)Uridine	8900	2220	2.99663	100
	VP35		13425	1023	9.76364	325.8
	VP40		17621	981	11.71609	391
	G		4949	2166	2.05779	68.7
	VP30		7119	867	6.54921	218.6
	VP24		4684	756	2.90751	97
Respiratory syncytial virus	NS1	Author's	-	NA	-	111.1
	NS2		-	NA	-	105.6
	N		-	NA	-	100
	P		-	NA	-	75.6
	M		-	NA	-	57.8
	SH		-	NA	-	35.6
	G		-	NA	-	20
	F		-	NA	-	23.3
	M2		-	NA	-	16.7
	L		-	NA	-	3.3
Canine distemper virus	N	Probe	1.192	NA	-	100
	P/V/C		1.116	NA	-	93.6
	M		0.969	NA	-	81.3
	F		0.917	NA	-	76.9
	H		0.772	NA	-	64.8
	L		0.711	NA	-	59.6
Newcasttle disease virus	N	(^{3}H)Uridine	137.67	1470	0.09365	100
	P/V		97.67	1200	0.08139	86.9
	M		87	1095	0.07945	84.8
	F		130.67	1695	0.07709	82.3
	HN		106.67	1758	0.06067	64.8
	L		29	6615	0.00438	4.7
Sendai virus	N	Author's	-	NA	-	100
	P/C/V		-	NA	-	68
	M		-	NA	-	100
	F		-	NA	-	38
	HN		-	NA	-	33
	L		-	NA	-	3
Mumps virus	N	(^{32}P)Phosphate	174.67	1650	0.10586	100
	P/V		48.67	1173	0.04149	39.2
	M		74.67	1127	0.06600	62.6
	F		39.67	1188	0.03339	31.5

	SH		-	1617	-	-
	HN		12.33	1749	0.0070	6.6
	L		4.67	6834	0.0007	0.6
Parainfluenza virus 3	N	Probe	49.3	NA	-	100
	P/C		15.6	NA	-	31.6
	M		10.3	NA	-	20.9
	F		9.5	NA	-	19.3
	HN		7.0	NA	-	14.2
	L					
Measles virus	N	Author’s	-	NA	-	100
	P/V/C		-	NA	-	34
	M		-	NA	-	25
	F		-	NA	-	20
	H		-	NA	-	15
	L		-	NA	-	1.5

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[a] Method used to detect the corresponding mRNA. (^{3}H)Uridine/(^{32}P)Phosphate: Addition of radiolabeling during infection/transcription. Probe: Hybridization with RNA probes specific for each mRNA. Author’s: Values given in the manuscript.

[b] Densitometry values obtained with ImageJ v1.45, automatically corrected for background intensity.

[c] Corrected for gene length = Densitometry/gene length, arbitrary units.

[d] % of mRNA abundance relative to that of the N gene: Corrected densitometry(N)/Corrected densitometry(gene)*100.

NA. Not applicable to the measurement method of mRNA abundance of the gene.

Supplementary Table 4. Calculation of relative protein abundance for the *Mononegavirales* genes.

Species	Gene	Measurement method[a]	Densitometry (Bg corrected)[b]	Number of labeled AA	Protein abundance[c]	Relative protein abundance (%)[d]
Rabies virus	N	Author's	-	NA	-	100
	P		-	NA	-	86
	M		-	NA	-	52
	G		-	NA	-	64
	L		-	NA	-	1.9
Vesicular stomatitis virus	N	Author's	-	NA	-	100
	P(NS)		-	NA	-	77
	M		-	NA	-	53
	G		-	NA	-	34
	L		-	NA	-	6.9
Ebola virus	N	(^{35}S) methionine	1152.18	20	57.609	100.0
	VP35		226.08	8	28.260	49.1
	VP40		560.15	8	70.019	121.5
	G		413.71	4	103.428	179.5
	VP30		266.46	3	88.820	154.2
	VP24		210.42	9	23.380	40.6
	L		517.84	38	13.627	23.7
Respiratory syncytial virus	NS1	(^{35}S) methionine	251.16	7	35.880	39.6
	NS2		-	5	-	-
	N		1267.73	14	90.552	100
	P		682.44	7	97.491	107.7
	M		1005.65	8	125.706	138.8
	SH		-	3	-	-
	G		612.95	2	306.475	338.5
	F		77.81	10	7.781	8.6
	M2		-	4	-	-
	L		1976.67	47	42.057	46.4
Canine distemper virus	N	(^{35}S) methionine	4756	17	279.78	100
	P/V/C		1623	10	162.36	58
	M		1917	11	174.29	62.3
	F		1445	12	120.42	43
	H		2092	12	174.38	62.3
	L		-	49	-	-
Newcastle disease virus	N	(^{35}S) methionine	3476.55	17	204.503	100.0
	P/V		1242.00	13	95.538	46.7
	M		1220.93	6	203.488	99.5
	F		1356.00	13	104.308	51.0
	HN		1711.12	10	171.112	83.7
	L		4696.65	60	78.278	38.3
Sendai virus	N	(^{35}S) methionine	17325.0	15	1155.000	100.0
	P/C/V		10242.0	10	1024.200	88.7
	M		4886.0	9	542.889	47.0
	F		7075.0	10	707.500	61.3
	HN		6336.0	8	792.000	68.6
	L		5142.8	49	104.955	9.1
Mumps virus	N	(^{3}H) leucine	172.15	52	3.311	100.0
	P/V		104.397	23	4.539	137.1

	M		105.656	32	3.302	99.7
	F		106.128	57	1.862	56.2
	SH		-	11	-	-
	HN		161.491	56	2.884	87.1
	L		517.106	289	1.789	54.0
Parainfluenza virus 3	N	(^{35}S) methionine	228.990	16	14.312	100.0
	P/C		91.728	13	7.056	49.3
	M		164.052	9	18.228	127.4
	F		149.460	9	16.607	116.0
	HN		228.098	11	20.736	144.9
	L		426.384	54	7.896	55.2
Measles virus	N	(^{35}S) methionine	1034	15	68.93	100
	P/V/C		357	10	35.7	51.8
	M		597	10	59.7	86.6
	F		-	12	-	-
	H		493	16	30.8	44.7
	L		286	52	5.5	8

[a] Method used to detect the corresponding mRNA. (^{35}S) methionine/(^{3}H) leucine: Addition of radiolabeled amino-acid during infection. Author's: Values given in the manuscript.

[b] Densitometry values obtained with ImageJ v1.45, automatically corrected for background intensity.

[c] Corrected for gene length = Densitometry/gene length, arbitrary units.

[d] % of protein abundance relative to that of the N gene: Corrected densitometry(N)/Corrected densitometry(protein)*100.

NA. Not applicable to the measurement method of protein abundance of the gene.

Supplementary Table 5. Analysis of the association between relative position in the genome and d_N/d_S, d_N and d_S in coding regions of the *Mononegavirales*.

		d_N/d_S			d_N			d_S			
Virus species	N[a]	r[b]	r_{mod}[c]	r_{nov}[d]	r	r_{mod}	r_{nov}[d]	r	r_{mod}	r_{nov}[d]	**Modification**[e]
Bornaviridae											
Borna disease virus	12	0.56	0.94*	0.85*	-0.28	0.99*	0.85*	0.73	0.36	-0.16	L
Rhabdoviridae											
Vesicular stomatitis virus	7	-0.04	0.92*	0.86*	-0.09	0.91*	0.77*	0.07	0.45	0.30	(P), L
Rabies virus	60	-0.33	0.99*	-	-0.33	0.89*	-	-0.77	-0.75	-	P, L
Filoviridae											
Ebola virus	18	-0.43	-	-	-0.44	-	-	0.17	-	-	-
Pneumoviridae											
A/H metapneumovirus	19	0.50	0.80*	-	0.33	0.77*	-	0.18	-0.43	-	L
Respiratory syncytial virus	11	0.17	0.20	-	0.15	0.09	-	0.10	-0.16	-	G, L
Paramyxoviridae											
Newcastle disease virus	110	-0.35	0.96*	0.98*	-0.28	0.99*	0.99*	0.12	-0.85	-0.82	(P), L
Sendai virus	6	-0.39	0.89*	0.71*	0.75*	0.85*	0.76*	0.47	0.58	0.37	(P), L
Mumps virus	23	0.12	0.41	0.57	-0.30	0.03	0.52	0.20	0.61	0.69	L
Parainfluenza virus 3	12	-0.37	0.78*	0.76*	-0.10	0.81*	0.88*	0.71	0.99*	-0.83*	(P), L
Canine distemper virus	18	-0.07	0.37	0.76*	0.01	0.47	0.82*	0.55	0.69	0.61	L
Measles virus	37	-0.38	0.95*	0.74*	0.07	0.89*	0.88*	-0.05	0.94*	-0.06	(P), L
Nipah virus	12	-0.32	0.91*	0.81*	0.26	0.76*	0.74*	0.57	0.47	-0.17	(P), L

[a] Number of sequences

[b] Pearson's Correlation coefficient

[c] Pearson's Correlation coefficient excluding P, G, and/or L

[d] Pearson's Correlation coefficient using non-overlapping regions of the P gene, and excluding L.

[e] Excluded gene(s)

*$P<0.05$

Cases in which values obtained using the full length P gene were substituted for those obtained considering only non-overlapping regions of this gene are shown in parentheses.

Supplementary Table 6. Analysis of the association between genetic diversity and length, and between relative position and length of non-coding regions in the *Mononegavirales*.

	***d* to Length**		**Length to Relative Position**		
Virus species	r^b	r_{modified}^c	r^b	r_{modified}^c	**Modification**[d]
Bornaviridae					
Borna disease virus	0.18 (0.730)	0.16 (0.794)	0.14 (0.785)	0.11 (0.857)	P
Rhabdoviridae					
Vesicular stomatitis virus	0.76 (0.079)	0.78 (0.112)	0.56 (0.249)	0.84 (0.076)	5’UTR
Rabies virus	0.15 (0.778)	0.24 (0.698)	0.53 (0.274)	0.53 (0.358)	G
Filoviridae					
Ebola virus	0.22 (0.605)	0.44 (0.318)	0.54 (0.169)	0.36 (0.431)	5’UTR
Pneumoviridae					
A/H metapneumovirus[e]	**0.88 (0.002)**	**0.96 (0.001)**	**0.85 (0.004)**	**0.90 (0.006)**	F, 5’UTR
Respiratory syncytial virus	**0.68 (0.021)**	-	**0.64 (0.034)**	-	-
Paramyxoviridae					
Newcastle disease virus	0.56 (0.189)	0.80 (0.053)	0.03 (0.948)	0.54 (0.270)	P
Sendai virus	0.21 (0.654)	0.36 (0.547)	0.01 (0.991)	0.21 (0.732)	L, 5’UTR
Mumps virus	-0.05 (0.897)	-	-0.23 (0.585)	-	-
Parainflueza virus 3	0.45 (0.368)	0.37 (0.546)	-0.03 (0.951)	0.12 (0.851)	F, 5’UTR
Canine distemper virus	0.56 (0.187)	0.58 (0.309)	0.03 (0.948)	0.44 (0.455)	L, 5’UTR
Measles virus	-0.29 (0.522)	-0.25 (0.680)	-0.32 (0.480)	-0.36 (0.550)	F, 5’UTR
Nipah virus	0.68 (0.109)	0.82 (0.100)	-0.02 (0.966)	0.83 (0.083)	P, 5’UTR
ALL	0.43 (0.169)	0.54 (0.099)	0.24 (0.229)	0.24 (0.183)	Outliers

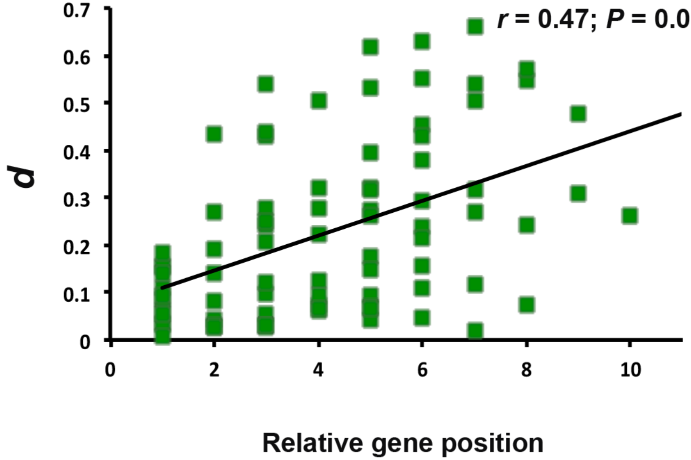
[a] Number of sequences

[b] Pearson correlation coefficient (*p*-value). Genetic distance calculated using all genes.

[c] Pearson correlation coefficient (*p*-value). Genetic distance calculated excluding outliers.

[d] Excluded non-coding region(s). Internal non-coding regions are named by the gene located downstream.

[e] Avian/Human metapneumovirus.


r = 0.47; P = 0.02
d
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
0
2
4
6
8
10
Relative gene position

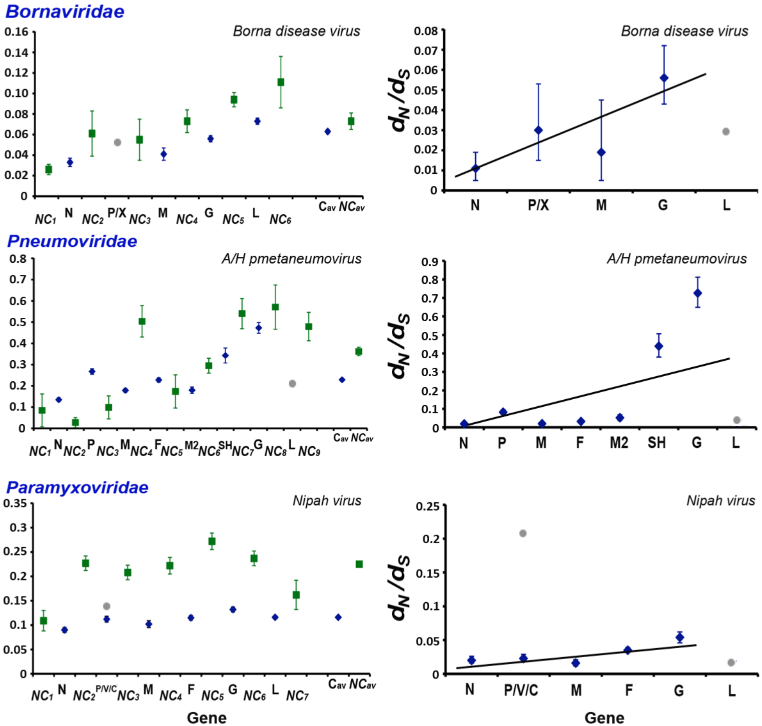

Bornaviridae
Borna disease virus
d
0.16
0.14
0.12
0.10
0.08
0.06
0.04
0.02
0
NC1 N NC2 P/X NC3 M NC4 G NC5 L NC6 Cav NCav
Borna disease virus
dN /dS
0.08
0.07
0.06
0.05
0.04
0.03
0.02
0.01
0
N P/X M G L
Pneumoviridae
A/H pmetaneumovirus
d
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
NC1 N NC2 P NC3 M NC4 F NC5 M2 NC6 SH NC7 G NC8 L NC9 Cav NCav
A/H pmetaneumovirus
dN /dS
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
N P M F M2 SH G L
Paramyxoviridae
Nipah virus
d
0.35
0.3
0.25
0.2
0.15
0.1
0.05
0
NC1 N NC2 P/V/C NC3 M NC4 F NC5 G NC6 L NC7 Cav NCav
Gene
Nipah virus
dN /dS
0.25
0.2
0.15
0.1
0.05
0
N P/V/C M F G L
Gene

Figure S1. Correlation between relative gene position and genetic distance (*d,* left) or selection pressures (d_N/d_S ratio, right) for those species with no available information on mRNA abundance. Upper panel represents the correlation between relative gene position and *d* considering all the *Mononegavirales* species together. Coding regions are represented by blue diamonds, and non-coding regions by green squares. Grey dots indicate outlier values. Values are the mean ± Standard Deviation for each data set. Note the different scale in each panel.