

Chirico et al. Supplementary Methods and Results

Table S1. Mean family overlap proportions and capsid description

Taxon	Total Species	Validated Species	Species with overlap	Genome length (ln)	Overlap proportion (ln)	Capsid type	Capsid flexible?
DNA viruses							
Acanthamoeba-polyphaga-mimivirus	1	0					
Adenoviridae	44	12	12	10.47	-3.71	icosahedral	no
Anellovirus	5	1	1	8.26	-1.78	icosahedral	no
Ascoviridae	3	0					
Asfarviridae	1	0					
Bacillus-phage-GIL-sixteen-c	1	1	1	9.61	-3.05	no description	?
Bacillus-virus-one	1	0					
Baculoviridae	43	1	1	11.78	-4.79	rod shaped	yes ^a
Bicaudaviridae	2	0					
Circoviridae	16	3	3	7.65	-1.78	icosahedral	no
Clostridium-phage-phiC-two	1	0					
Corticovirus	1	1	1	9.22	-4.76	icosahedral	no
Fuselloviridae	5	3	3	9.69	-3.22	lemon-shaped	yes ^b
Geminiviridae	199	82	80	8.23	-1.54	icosahedral	no
Geobacillus-phage-GBSVone	1	1	1	10.45	-4.69	no description	?
Globuloviridae	2	0					
Gryllus-bimaculatus-nudivirus	1	0					
Heliothis-zea-virus-one	1	0					
Herpesviridae	47	26	26	11.97	-4.44	icosahedral	no
His-one-virus	1	0					
His-two-virus	1	0					
Inoviridae	25	18	17	8.88	-4.64	filamentous	yes
Iridoviridae	8	1	1	11.54	-5.31	icosahedral	no
Lipothrixviridae	8	2	2	10.62	-4.34	rod shaped	yes
Microviridae	55	13	12	8.56	-2.23	icosahedral	no
Myoviridae	71	35	35	11.37	-4.89	icosahedral	no
Nanoviridae	6	1	0				

Nimaviridae	1	0					
Papillomaviridae	66	13	13	8.97	-3.11	icosahedral	no
Parvoviridae	44	8	6	8.56	-2.14	icosahedral	no
Phycodnaviridae	8	1	1	12.72	-5.95	icosahedral	no
Plasmaviridae	1	1	1	9.39	-8.00	quasi-spherical	yes
Podoviridae	62	32	32	10.59	-3.58	icosahedral	no
Polydnaviridae	5	0					
Polyomaviridae	17	2	2	8.57	-2.67	icosahedral	no
Poxviridae	25	7	7	12.12	-4.22	ovoid or brick	yes
Rudiviridae	4	0					
Salmonella-phage-ST-seventyfour-B	1	1	1	10.60	-5.02	no description	?
Sinorhizobium-phage-PBCfive	1	0					
Siphoviridae	180	106	106	10.77	-4.55	icosahedral	no
Streptococcus-phage-SMP	1	0					
Tectiviridae	2	1	1	9.61	-3.60	icosahedral	no
Xanthomonas-phage-OP-two	1	1	1	10.75	-4.78	no description	?
Xanthomonas-phage-Xp-fiveteen	1	0					
RNA viruses							
Acyrtosiphon pisum virus	1	0					
Arenaviridae	18	2	1	9.24	-4.25	spherical/pleomorphic	yes
Arteriviridae	4	3	3	9.59	-3.18	icosahedral ^c	no
Astroviridae	6	4	4	8.83	-6.37	isometric	no ^d
Barnaviridae	1	0					
Beet western yellows ST9-associated virus	1	0					
Benyvirus	2	0					
Birnaviridae	7	3	3	8.69	-2.68	icosahedral	no
Bornaviridae	1	1	1	9.09	-3.39	spherical	yes
Botrytis virus F	1	0					
Botrytis virus X	1	0					
Bromoviridae	25	9	4	9.05	-4.00	varies between genera	?
Bunyaviridae	24	4	0				
Caliciviridae	16	9	9	8.96	-6.78	icosahedral	no
Caulimoviridae	28	7	7	8.96	-4.77	varies between genera	?
Cheravirus	2	1	0				
Chrysoviridae	3	0					
Closteroviridae	21	7	7	9.73	-5.78	rod shaped	yes

Comoviridae	18	7	1	9.33	-6.93	icosahedral	no
Coronaviridae	17	9	9	10.29	-4.36	icosahedral ^e	no
Cystoviridae	4	3	3	9.54	-5.60	icosahedral	no
Cytoplasmic citrus leprosis virus	1	0					
Diaporthe ambigua RNA virus 1	1	0					
Dicistroviridae	14	0					
Endornavirus	5	1	0				
Filoviridae	4	0					
Flaviviridae	42	26	1	9.30	-6.31	icosahedral ^f	no
Flexiviridae	70	22	22	8.93	-3.56	rod shaped	yes
Furovirus	5	3	0				
Fusarium graminearum dsRNA mycovirus 1	1	0					
Hepadnaviridae	10	1	1	8.08	-0.68	icosahedral	no
Hepeviridae	1	0					
Heterocapsa circularisquama RNA virus	1	0					
Hordeivirus	1	1	1	9.23	-3.83	rod shaped	yes
Hypoviridae	4	0					
Idaeovirus	1	1	0				
Iflavirus	8	0					
Kelp fly virus	1	0					
Leviviridae	9	6	3	8.24	-3.74	icosahedral	no
Luteoviridae	18	8	8	8.64	-1.46	icosahedral	no
Marnaviridae	1	0					
Narnaviridae	8	0					
Nodaviridae	9	2	2	8.40	-2.87	icosahedral	no
Nora virus	1	0					
Ophiovirus	3	0					
Orthomyxoviridae	5	1	1	9.52	-3.30	spherical/pleomorphic	yes
Oyster mushroom spherical virus	1	0					
Paramyxoviridae	33	3	3	9.65	-3.25	spherical/pleomorphic	yes
Partitiviridae	19	2	0				
Pecluvirus	2	1	1	9.25	-3.97	rod shaped	yes
Picobirnavirus	1						
Picornaviridae	46	12	0				
Pomovirus	4	0					
Potyviridae	69	42 ^g	60	9.17	-3.65	filamentous	yes

Reoviridae	33	8 ^g	13	10.03	-4.57	icosahedral	no
Retroviridae	47	11	11	9.19	-3.47	spherical	yes
Rhabdoviridae	22	4	0				
Roniviridae	1	0					
Schizochytrium single-stranded RNA virus	1	1	0				
Sclerophthora macrospora virus A	1	1	1	8.68	-1.91	no description	?
Sequiviridae	6	4 ^g	2	9.40	-3.81	isometric	no
Sobemovirus	9	9	9	8.34	-1.85	icosahedral	no
Solenopsis invicta virus 2	1	0					
Tenuivirus	2	0					
Tetraviridae	4	0					
Thielaviopsis basicola dsRNA virus 1	1	0					
Tobamovirus	21	6	5	8.76	-4.91	rod shaped	yes
Tobravirus	3	1	1	9.25	-7.87	rod shaped	yes
Togaviridae	15	9	1	9.34	-6.36	icosahedral	no
Tomato torrado virus	1	0					
Tombusviridae	41	9	9	8.42	-2.55	icosahedral	no
Totiviridae	24	3	3	8.74	-4.40	icosahedral ^h	no
Tymoviridae	14	5	5	8.76	-1.16	icosahedral ^h	no
Umbravirus	4	2	2	8.32	-1.65	none ⁱ	yes
White bream virus	1	0					

^aVirion is within an occlusion body that may be polyhedral.

^bLemon-shaped and flexible according to ICTV website.

^cCore shell probably icosahedral.

^dRound with polyhedral symmetry. They have a distinctly star shape on the capsid.

^eCore shell possibly icosahedral.

^fCore is icosahedral.

^gNumber of validated species includes those in the Firth papers (see main text).

^hSome show some general isometric symmetry.

ⁱNo conventional virion.

Supplementary Methods

The larger bacteriophages that we use for illustration in Figure 1 share the so-called HK97 fold (Baker et al. 2005; Jiang et al. 2003; Wikoff et al. 2000) (Agirrezabala et al. 2007; Duda et al. 2006; Effantin et al. 2006; Jiang et al. 2006; Lander et al. 2008; Morais et al. 2005). In our choice among dsDNA bacteriophages which share the HK 97-fold (Casjens 2008), we considered only species whose capsid is isometric (see below) and have a T number which is known and has been confirmed (Duda 2008). For each T number, where more than one example was available, only one representative of each genus has been chosen (Duda 2008; van Regenmortel et al. 2000). The selected ssDNA viruses are ones with similar capsid molecular weight that represent different genera and a wide range of genome length. Among dsDNA viruses sharing the HK 97-fold, all the theoretically possible T numbers from 3 to 16 have been observed except for 9 and 12. One explanation put forward to explain these missing T numbers is that the coat proteins of the dsDNA viruses sharing HK97 have a tendency to form skewed hexons, which are hexameric clusters of the coat protein itself (Thuman-Commike et al. 1999). Such skewed hexons are present in the procapsids as shown by 3D structure reconstructions both at medium and high resolution (Conway et al. 1995; Dokland & Murialdo 1993; Gertsman et al. 2009; Jiang et al. 2003; Lander et al. 2008; Prasad et al. 1993; Trus et al. 1996) and show a twofold symmetry instead of the sixfold symmetry observed in mature viruses. Because of symmetry principles, a hexon with only a twofold symmetry must contain either three or six different conformations and this would lead to a restriction of possible T numbers, according to the quasi-equivalence rules (Caspar & Klug 1962) to the series $T = 3n + 1$, where n is any integer (Thuman-Commike et al. 1999). The only known apparent exception to this generalization is a T=3 capsid structure belonging to phage $\phi 29$

(Morais et al. 2005), in which a tendency of the coat protein to form skewed hexons has been shown (Choi et al. 2006). However, $\phi 29$ (and therefore $T = 3$) has not been included in our analysis for Figure 1 since it has a prolate (anisometric) head and can be expected to have more relaxed constraints with respect to genome packaging, as it has been shown for another similar phage, T4 (Earnshaw et al. 1978). A relatedness between capsids with T numbers of 4, 7 and 13 was also suggested on the basis of the so-called “local rule” switching mechanism for icosahedral shell geometry (Berger et al. 2000). These local rules specify local interaction patterns that can direct the self-assembly of viral coat and scaffolding subunits into different capsid geometries (Berger et al. 1994; Dokland 2000).

Table S2. Relative increase in capsid volume compared to genome length

Family	Genus	Species	Abbrev. Name	T-number (Ti)	Next T-number (Tf)	$\sqrt{(Tf)/\sqrt{(Ti)}} = Rf/Ri$ (R = Radius)	Relative increase in volume = $(Rf/Ri)^3$	ln (Relative increase in volume)	Genome length (bases)	ln (Genome length)	Major capsid protein mol. wht	Source
Myoviridae	T4-like	Synechococcus phage Syn9	Syn9	16	19	1.09	1.29	0.26	177300.00	12.09	48.7	a
Myoviridae	SPO1-like	Bacillus phage SPO1	SPO1	16	19	1.09	1.29	0.26	132500.00	11.79	45	b
Siphoviridae	T5-like	Enterobacteria phage T5	T5	13	16	1.11	1.37	0.31	121750.00	11.71	44	c
Myoviridae	P2-like	Enterobacteria phage P2	P2	7	13	1.36	2.53	0.93	33593.00	10.42	36.5	d
Siphoviridae	lambda-like	Enterobacteria phage λ	λ	7	13	1.36	2.53	0.93	48500.00	10.79	38	e
Podoviridae	T7-like	Enterobacteria phage T7	T7	7	13	1.36	2.53	0.93	39937.00	10.60	44	f
Podoviridae	P22-like	Enterobacteria phage P22	P22	7	13	1.36	2.53	0.93	41724.00	10.64	38	g
Myoviridae	P2-like	Enterobacteria phage P4	P4	4	7	1.32	2.32	0.84	11624.00	9.36	36.5	h
Circoviridae	Circovirus	Porcine circovirus-1 and -2 (average)	PCV	1	4	2.00	8.00	2.08	1763.00	7.47	27.4	i
Microviridae	Microvirus	ϕ X174	ϕ X174	1	4	2.00	8.00	2.08	5400.00	8.59	48.4	j
Parvoviridae	Brevidensovirus	Anopheles gambiae densovirus	AgDENV	1	4	2.00	8.00	2.08	4139.00	8.33	40.5	k
Circoviridae	Gyrovirus	Chicken Anemia Virus	CAV	1	4	2.00	8.00	2.08	2309.00	7.74	51.6	l

- ^a(Weigele et al. 2007)
- ^b(Duda et al. 2006; Parker et al. 1983)
- ^c(Effantin et al. 2006)
- ^d(Dokland et al. 1992)
- ^e(Lander et al. 2008; Williams & Richards 1974)
- ^f(Agirrezabala et al. 2007; Steven et al. 1983)
- ^g(Jiang et al. 2003; Prasad et al. 1993)
- ^h(Dokland et al. 1992)
- ⁱ(Bennett et al. 2008; Crowther et al. 2003; van Regenmortel et al. 2000)
- ^j(McKenna et al. 1992)
- ^k(Bennett et al. 2008; Cheng et al. 2004; van Regenmortel et al. 2000)
- ^l(Crowther et al. 2003; van Regenmortel et al. 2000)

Table S3. Virus mutation rates

Type	Family	Overlap Proportion	Species ^a	Mutation rate ^b	Reference used
RNA	Cystoviridae	0.0037	φ6	2.7x10 ⁻⁶	(Chao et al. 2002)
	Flaviridae	0.0018	HCV	1.2x10 ⁻⁴	(Cuevas et al. 2009b)
	Hepadnaviridae	0.5051	DHBV	2.7x10 ⁻⁵	(Pult et al. 2001) ^c
	Leviviridae	0.0238	Qβ	1.54x10 ⁻³	(Drake 1993)
	Orthomyxoviridae	0.0368	FLUAV	7.26x10 ⁻⁵	(Drake 1993)
				2x10 ⁻⁶	(Nobusawa & Sato 2006) ^d
				1.9x10 ⁻⁵	(Stech et al. 1999) ^e
			FLUBV	6x10 ⁻⁷	(Nobusawa & Sato 2006)
	Picornaviridae	0.0000	HRV-16	9.40x10 ⁻⁵	(Drake & Holland 1999) ^f
			Polio	1.75x10 ⁻⁵	(Drake & Holland 1999) ^f
				2.42x10 ⁻⁵	(Drake & Holland 1999) ^f
				1.02x10 ⁻⁵	(Drake & Holland 1999) ^f
				1.18x10 ⁻⁵	(Drake & Holland 1999) ^f
	Paramyxoviridae	0.0389	MeV	6.29x10 ⁻⁵	(Drake & Holland 1999) ^f
	Retroviridae	0.0311	BLV	3.3x10 ⁻⁶	(Drake et al. 1998) ^g
			HIV-1	1.8x10 ⁻⁵	(Drake et al. 1998) ^g
				2.38x10 ⁻⁵	(Drake et al. 1998) ^g
			MLV	3.77x10 ⁻⁷	(Drake 1993)
				>6.62x10 ⁻⁶	(Drake 1993)
				3.13x10 ⁻⁵	(Drake et al. 1998) ^{g,h}
			RSV	4.6x10 ⁻⁵	(Drake 1993)
			SNV	4.71x10 ⁻⁶	(Drake 1993)
				3.61x10 ⁻⁵	(Drake 1993)
1.2x10 ⁻⁵				(Mansky & Temin 1994)	
Rhabdoviridae	0.0000	VSV	9.59x10 ⁻⁵	(Drake & Holland 1999) ⁱⁱ	

				1.03x10 ⁻⁴	(Drake & Holland 1999) ^{fi}
				1.00x10 ⁻⁵	(Sanjuan et al. 2007)
				5.56x10 ⁻⁶	(Sanjuan et al. 2007)
				6.18x10 ⁻⁶	(Furio et al. 2005)
	Tobamovirus	0.0074	TMV	9.1x10 ⁻⁶	(Malpica et al. 2002)
ssDNA	Inoviridae	0.0048	M13	7.23x10 ⁻⁷	(Drake 1991)
	Microviridae	0.1511	φχ174	1.9x10 ⁻⁶	(Raney et al. 2004) ^j
				1.0x10 ⁻⁶	(Cuevas et al. 2009a)
dsDNA	Herpesviridae	0.01174	HSV-1	1.76x10 ⁻⁸	(Drake & Hwang 2005)
	Myoviridae	0.0075	T2	2.70x10 ⁻⁸	(Drake 1991)
			T4	2.02x10 ⁻⁸	(Drake 1991)
	Siphoviridae	0.0106	λ	7.74 x10 ⁻⁸	(Drake 1991)

^aEach entry for a species is from a separate study or method.

^bMutation rates in these publications are typically expressed as the number of substitutions per nucleotide site per round of genome replication. However, the values for HCV, φχ174 and the two Sanjuán VSV estimates are expressed as per cell infection cycle (there may be multiple rounds of genome replication within a single infection cycle).

^cMiddle of the range of values given (0.8x10⁻⁵ to 4.5x10⁻⁵).

^dWe have summed the data from H1N1 and H3N2 strains.

^eMeans of values for strains H2N2 and H1N1.

^fValues in Table 1 of reference (divided by genome length; where more than one μ_g value is given the mean was used).

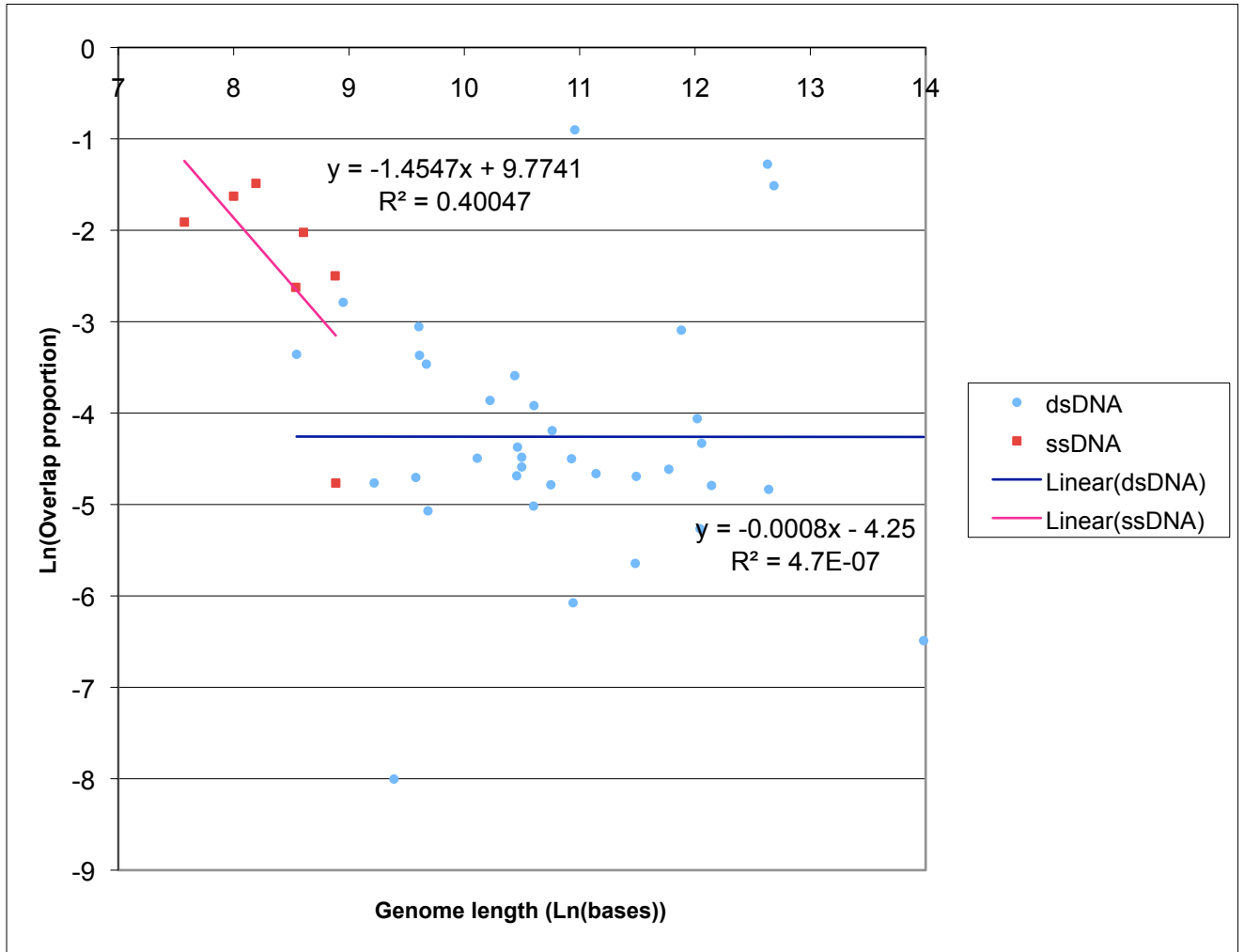
^gValues in Table 3 of reference.

^hThis value, in Table 3, is from a different study to that given in (Drake 1993).

ⁱThe other value, 3.83x10⁻⁴, may be unreliable, and we present two separate values for the experiments that were summed in the 2.47x10⁻⁴ value (Sanjuán, pers. comm.).

^jCalculated from the phenotypic mutant frequency given in the original reference (Cuevas et al. 2009a).

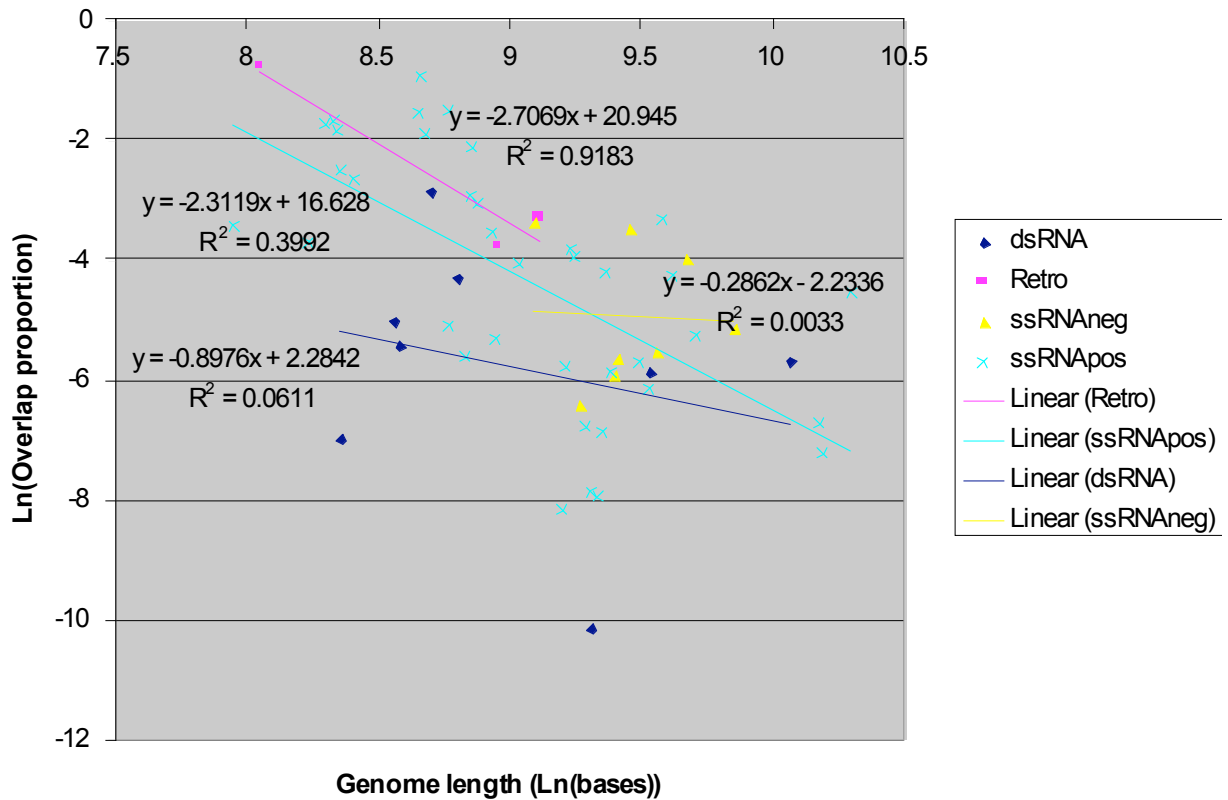
Figure S1. Relationship between overlap proportion and genome length in DNA viruses with all RefSeq entries included (i.e. not only validated ones as in Figures 2 and 3 of the main text).



dsDNA
Significance P = 0.996834

ssDNA
Significance P = 0.127169

Figure S2. Relationship between overlap proportion and genome length in the four types of RNA virus: single stranded positive sense, single stranded negative sense, double stranded and retrotranscribing.



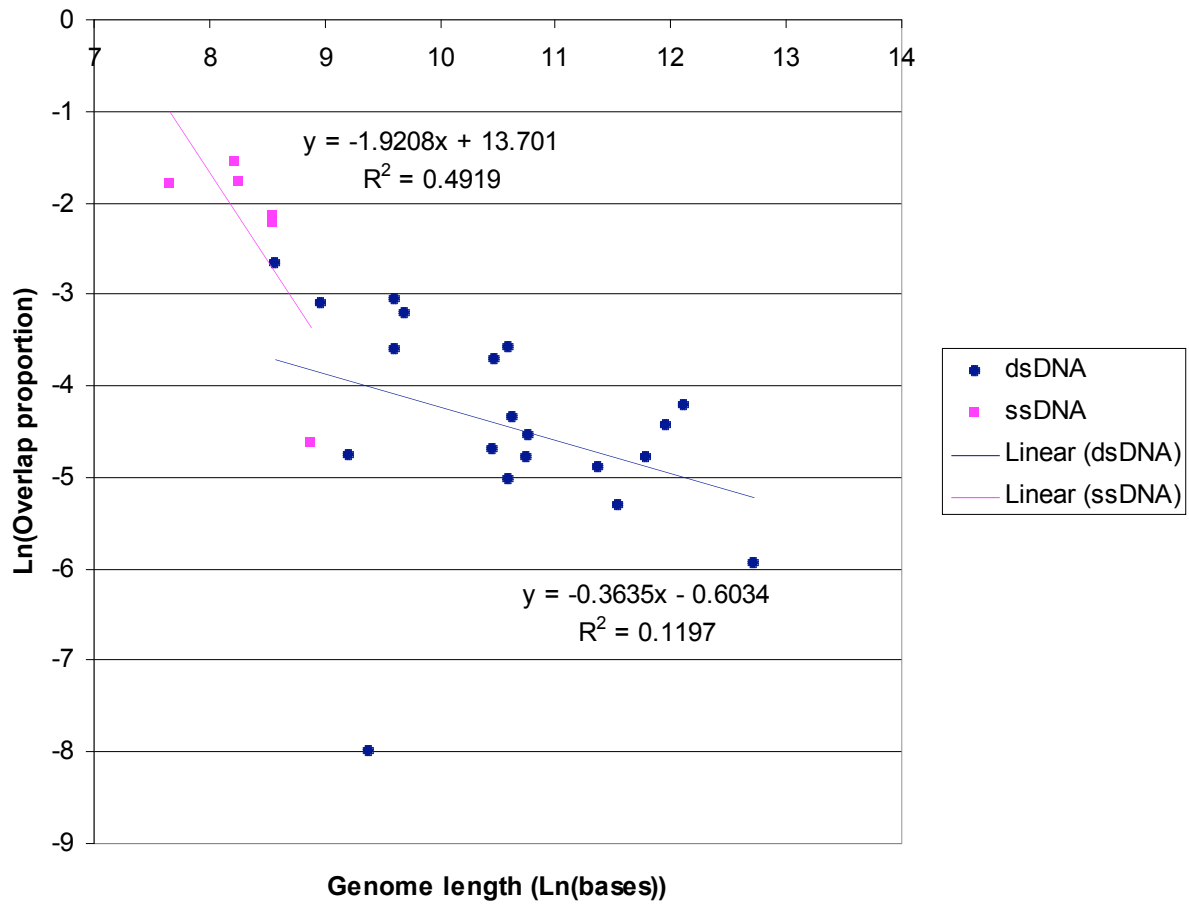
dsRNA
Significance P = 0.555201

Retroviridae
Significance P = 0.184485

ssRNAneg
Significance P = 0.893153

ssRNApos
Significance P = 2.74E-05

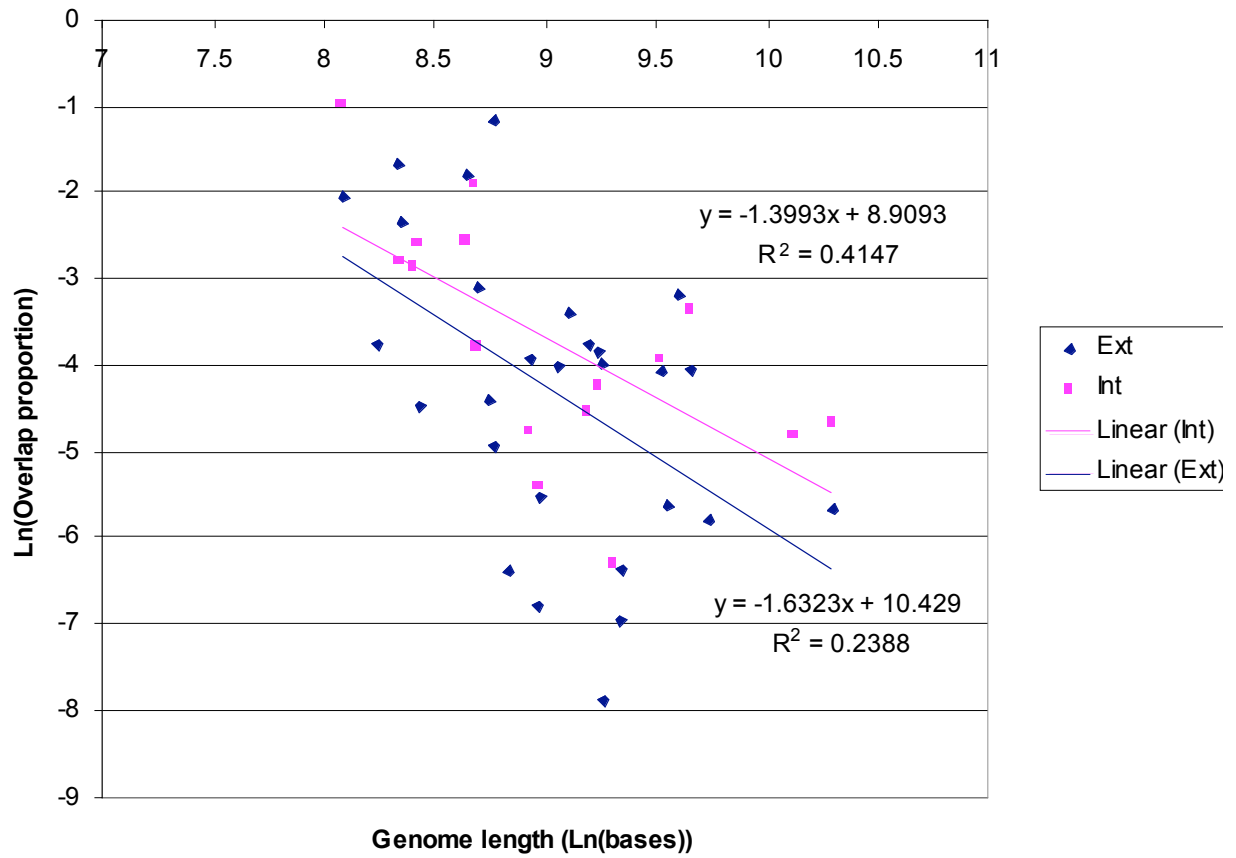
Figure S3. Relationship between overlap proportion and genome length in the two types of DNA virus: single stranded and double stranded.



dsDNA
Significance P = 0.135061

ssDNA
Significance P = 0.12046

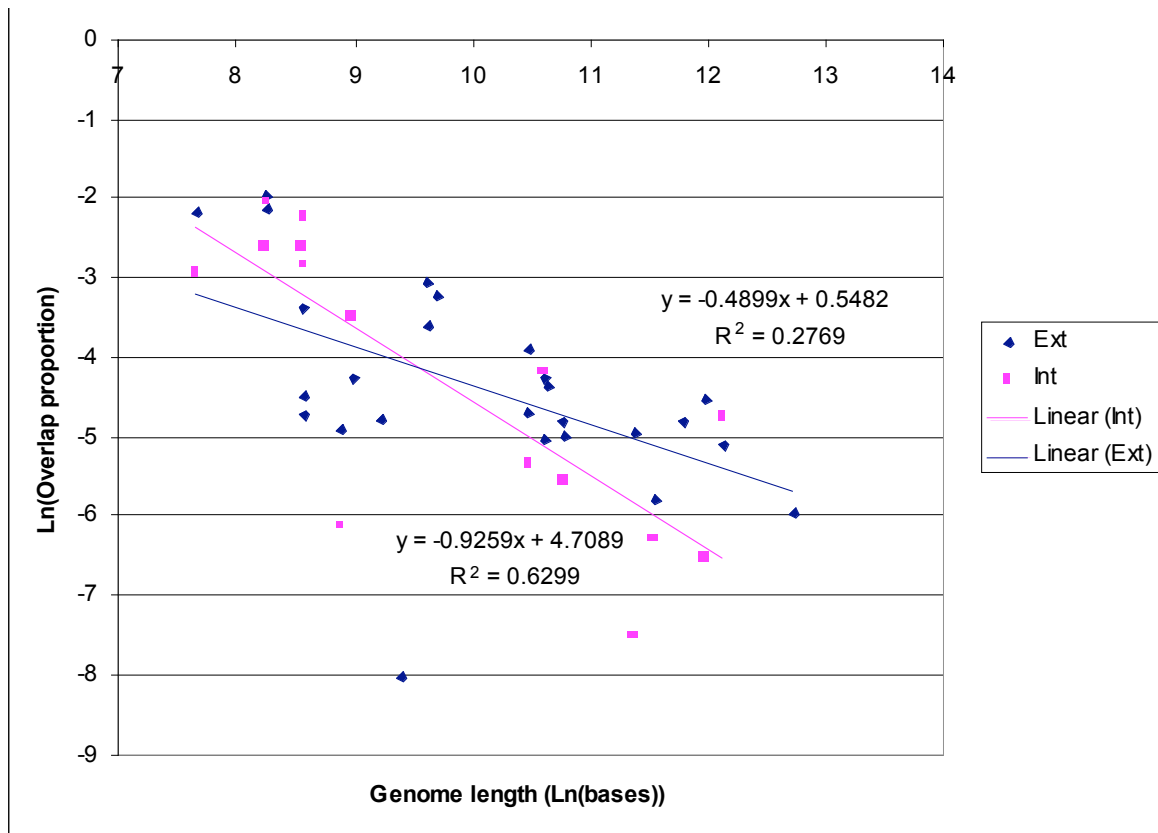
Figure S4. Relationship between overlap proportion and genome length in RNA viruses. Overlaps categorised as *Internal* (Int), where one gene is completely within another, and *External* (Ext), where two genes overlap for only part of their lengths.



Ext
Significance P = 0.008321

Int
Significance P = 0.007094

Figure S5. Relationship between overlap proportion and genome length in DNA viruses. Overlaps categorised as *Internal* (Int), where one gene is completely within another, and *External* (Ext), where two genes overlap for only part of their lengths.



Ext
Significance P = 0.00576

Int
Significance P = 0.000412

Figure S6. Relationship between mean number of overlaps compared to genome length. Open circles are family means for DNA viruses, closed circles are family means for RNA viruses

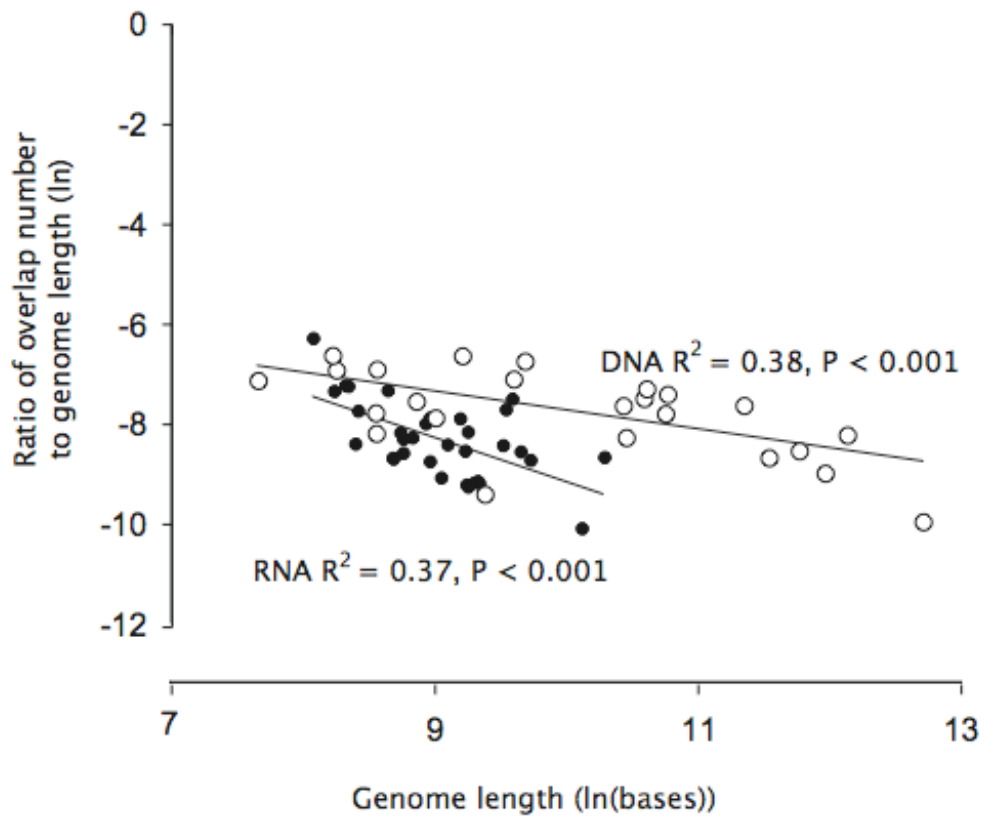


Figure S7. Relationship between mean overlap length and genome length. Circles: mean values for families of RNA viruses; squares: mean values for families of DNA viruses.

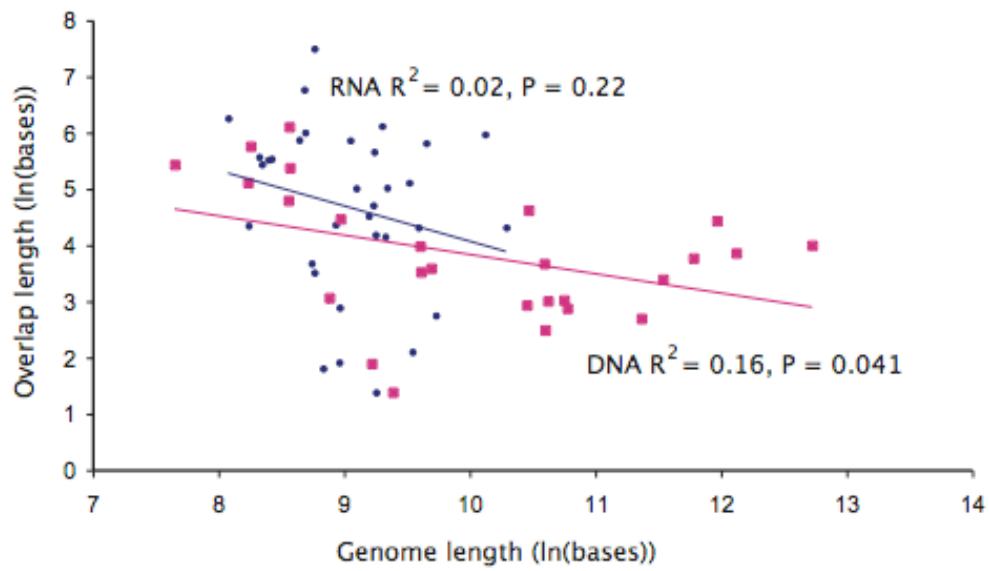


Figure S8. Relationship between the ratio of number of overlaps compared to number of genes (y axis), and genome length (x axis). Family means of overlap and gene number are used. Open circles are DNA viruses, closed circles are RNA viruses.

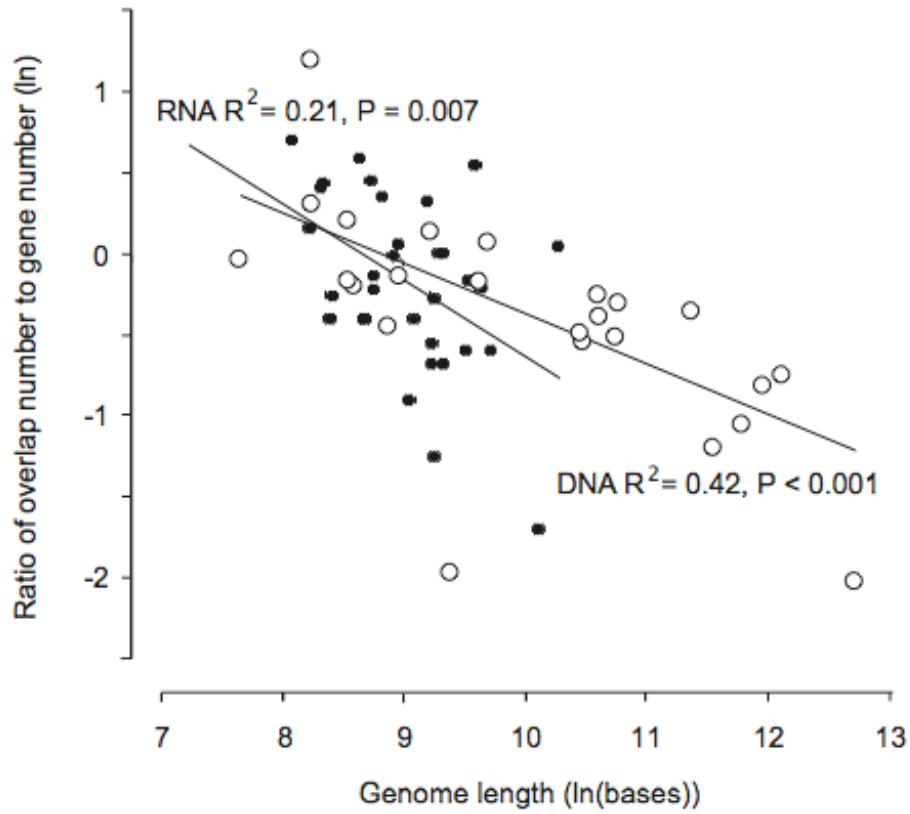


Figure S9. Relationship between overlap proportion and genome length excluding very short terminal overlaps (less than 60bp).

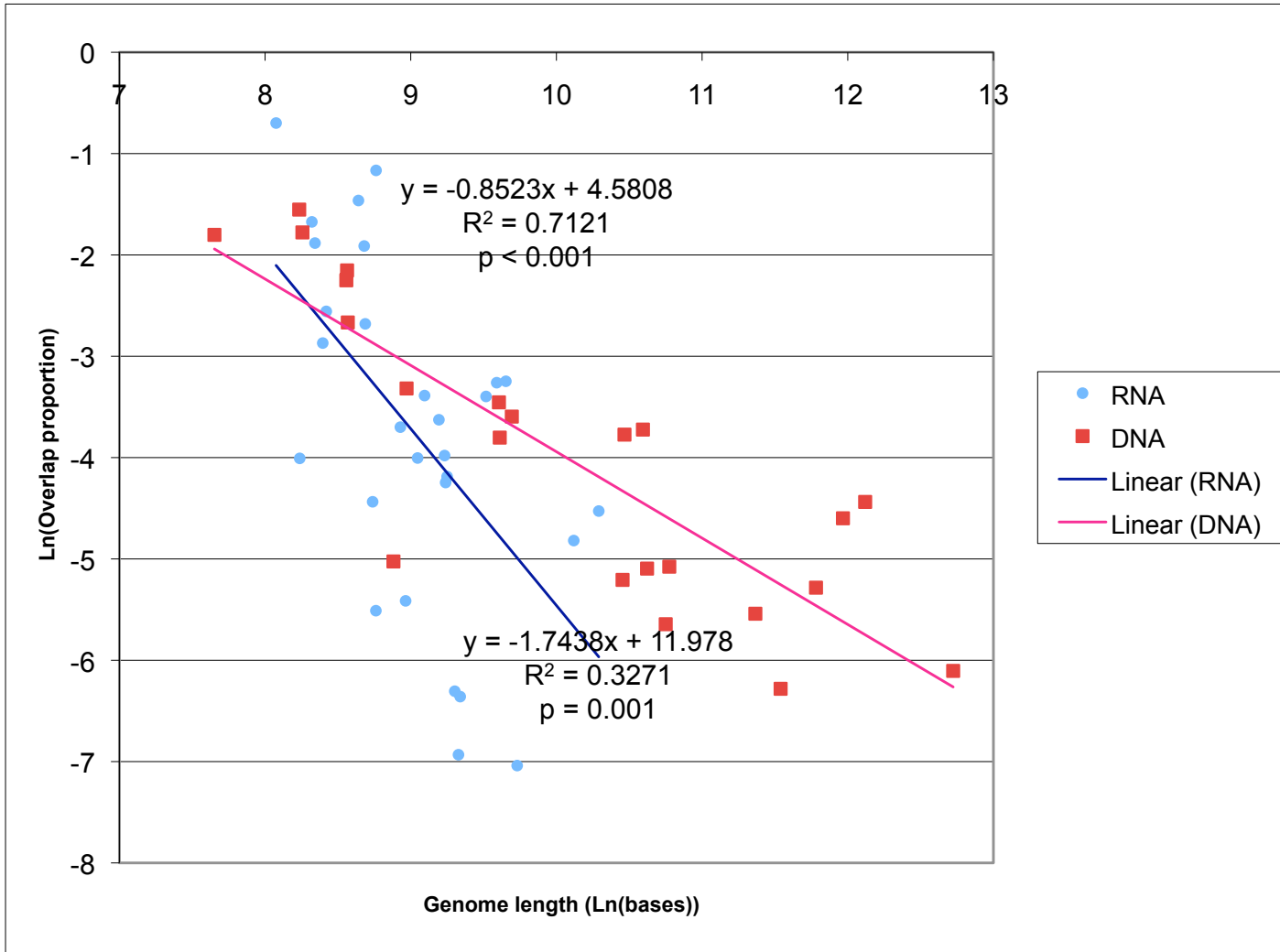


Figure S10. RNA virus within-family relationship between overlap proportion and genome length. Only families with at least eight genomes are included.

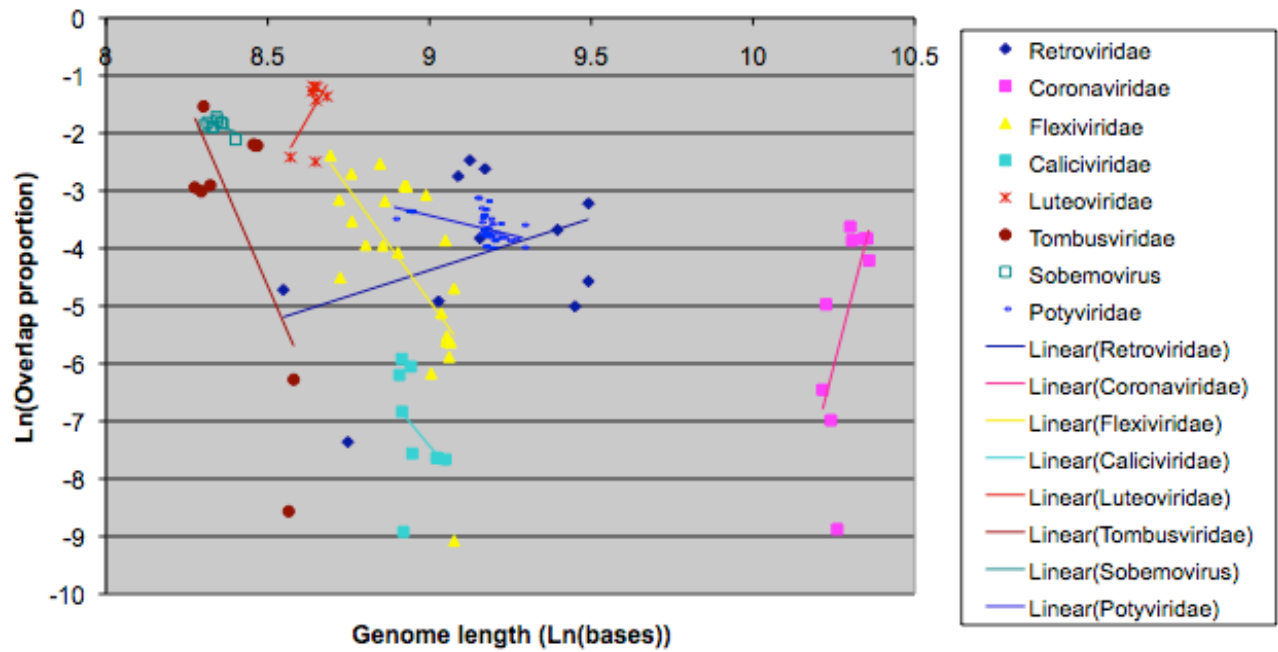
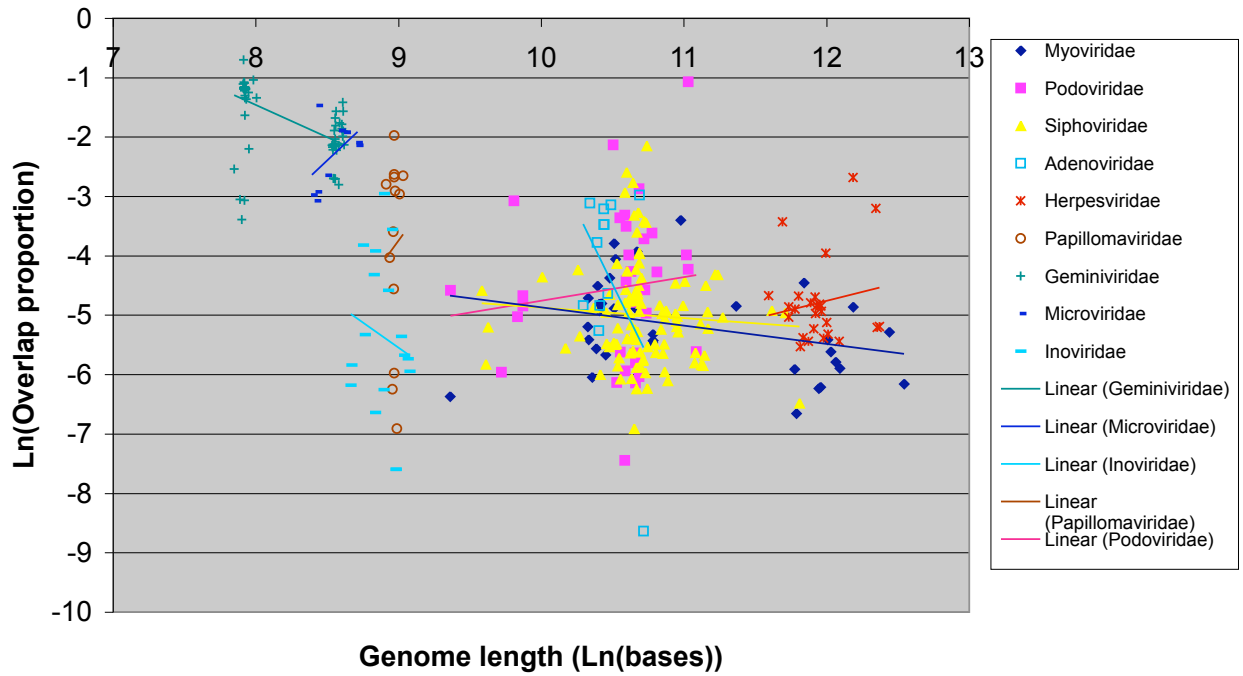


Figure S11. DNA virus within-family relationship between overlap proportion and genome length. Only families with at least eight genomes are included.



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