Figure S1: One-way ANOVA analysis of sizes of ORF in CAGs and core genes.

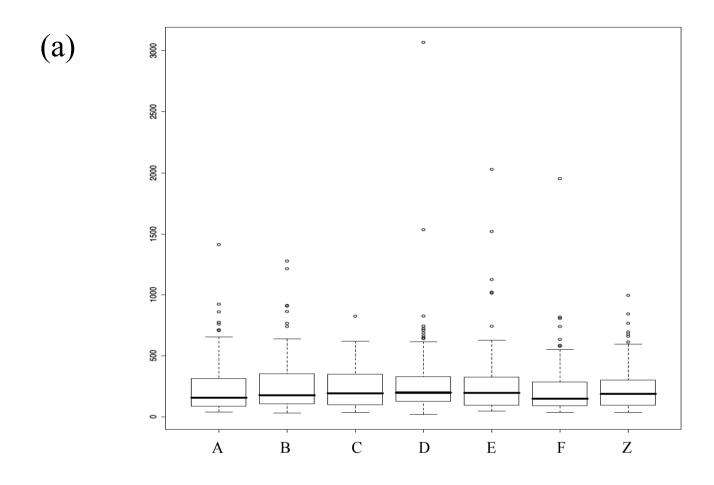
(a) ORF sizes from different categories of CAGs and core genes. The meaning of letters are as follows: A, sizes of ORFs included in CAGs having between 4-10 ORFs; B, sizes of ORFs included in CAGs having between 11-20 ORFs; C, sizes of ORFs included in CAGs having between 21-30 ORFs; D, sizes of ORFs included in CAGs having between 31-40 ORFs; E, sizes of ORFs included in CAGs having between 41-50 ORFs; F, sizes of ORFs included in CAGs having more than 50 ORFs; Z, core genes sizes. (b) Data had a normal distribution and a one-way ANOVA was applied. The result shows that no significant differences between the analyzed groups.

Figure S2: One-way ANOVA analysis of gene sizes of ORFans against ORFs from different categories.

(a) ORFs and ORFans sizes. (b) Data had a normal distribution and a one-way ANOVA was applied. The result is significant and means that at least one analyzed group is different from the others. (c) TukeyHSD test confirms that ORFans are smaller than ORFs. Significant difference between groups are denoted by asterisks: '***' if p-value is below 0.001, '**' if p-value is below 0.05.

Figure S3: ORFans in CAGs.

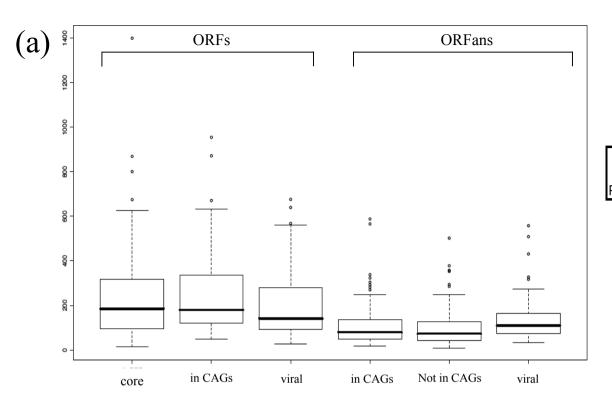
(a) expected (blue) and observed (red) average frequencies of ORFans included in CAGs. ORFans are overrepresented in CAGs. (b) Details of the Chi-squared analysis made with the expected and observed frequencies of the 122 analyzed genomes. It confirms that ORFans are more abundant in CAGs than that expected by chance only.



(b)

one-way ANOVA

Df Sum Sq Mean Sq F value Pr(>F) **6 384147 64024 0.9773 0.4395** Residuals 686 44938694 65508



(b)

Df Sum Sq Mean Sq F value Pr(>F) **5 1771792 354358 17.707 2.308e-16 *****Residuals 588 11767395 20013

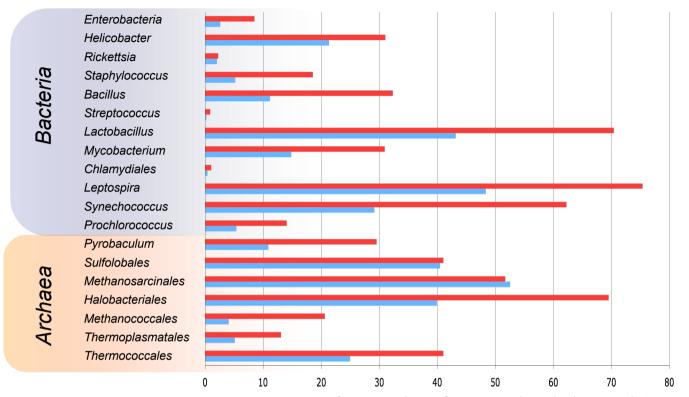
(c)

Tukey multiple comparisons of means 95% family-wise confidence level Fit: aov(formula = V2 ~ V1, data = ORF-ORFans-sizes)

V1	V2	diff	lwr	upr	р	
ORFs in CAGs	Core	6.616162	-50.87282	64.105140	0.9994883	
ORFs in	Core	-36.909091	-94.39807	20.579887	0.4435674	
viruses	_					
ORFans in CAGs	Core	-117.080808	-174.56979	-59.591830	0.0000001	*
ORFans not	Core	-128.404040	-185.89302	-70.915062	0.0000000	
in CAGs						*
ORFans in viruses	Core	-97.666667	-155.15564	-40.177689	0.0000225	*
ORFs in	ORFs in	-43.525253	-101.01423	13.963726	0.2560365	
viruses	CAGs					
ORFans in CAGs	ORFs in CAGs	-123.696970	-181.18595	-66.207992	0.0000000	*
ORFans not	ORFs in	-135.020202	-192.50918	-77.531224	0.0000000	
in CAGs	CAGs					*
ORFans in	ORFs in	-104.282828	-161.77181	-46.793850	0.0000044	*:
viruses	CAGs					•
ORFans in CAGs	ORFs in viruses	-80.171717	-137.66070	-22.682739	0.0010575	*
ORFans not	ORFs in	-91.494949	-148.98393	-34.005971	0.0000949	
in CAGs	viruses					*
ORFans in viruses	ORFs in	-60.757576	-118.24655	-3.268598	0.0312893	*
ORFans	ORFans in	-27.707071		6.251498	0.1342823	-
okrans nont in	CAGS	-27.707071	61.66563943	0.231498	0.1342823	
CAGs	CAGS		01.00303943			
ORFans in	ORFans in	6.323232	-	40.281801	0.8994311	
viruses	CAGs		27.63533640			
ORFans in	ORFans not	34.030303	0.07173431	67.988872	0.0493830	
viruses	in CAGs					

Figure S2

(a)



Average frequencies of expected and observed ORFans included in CAGs

(b) Chi-squared test for given probabilities

X-squared =1397.102, df = 102, p-value < 2.2e-16 ***