Slope=-1.037e-05 AA p=0.0	slope=-3.585e-07 AB p=0.82	slope=-1.184e-05 AC p=0.021	slope AD p=0. 80 - 80 - 75 - 65 -	e=-1.056e-06 174		
3.0 3.5 4.0 Genome size, bp 1e6 slope=-2.054e-06 AF p=0.852 Actinobacillus (n=45) 85 -	5.75 6.00 6.25 6.50 6.75 7.00 7.25 Genome size, bp 1e6 slope=-3.302e-06 AG p=0.004	2.8 3.0 3.2 3.4 3.6 3.8 4.0 Genome size, bp 1e6 slope=3.764e-06 AH p=0.017		4.0 4.5 5.0 5.5 6.0 6.5 Genome size, bp 1e6 e=6.288e-06 326 Aggregatibacter (n=76)	slop	
2.2 2.3 2.4 2.5 Genome size, bp 1e6 slope=1.651e-06	4.00 4.25 4.50 4.75 5.00 5.25 Genome size, bp 1e6 slope=3.651e-06 AL p=0.165	4.00 4.25 4.50 4.75 5.00 5.25 Genome size, bp 1e6 slope=-1.509e-05	40 -	• • • • • • • • • • • • • • • • • • • •	60 · slop	5.0 5.5 6.0 6.5 Genome size, bp 1e6 0e=-3.097e-07 0.891 Alteromonas (n=64)
3.8 4.0 4.2 4.4 Genome size, bp 1e6 slope=1.398e-06 AP p=0.201	2.0 2.5 3.0 3.5 4.0 4.5 5.0 Genome size, bp 1e6 slope=-3.734e-05 AQ p=0.0 Anaplasma (n=45) 70	Genome size, bp 1e6 slope=-3.648e-06	slope AS p=0. 80 -	Genome size, bp 1e6 e=3.275e-06	slop	
75.0 75.0 70.0 4.5 5.0 5.5 6.0 6.5 7.0 Genome size, bp 1e6 Slope=-2.130e-05 AU p=0.032 Avibacterium (n=14)	1.2 1.3 1.4 1.5 1.6 1.7 1. Genome size, bp 1e6 slope=-7.354e-07 AV p=0.83 Azoarcus (n=10)	slope=-2.744e-07	slope AX p=0.	3.75 4.00 4.25 4.50 4.75 5.00 Genome size, bp 1e6 128 Azotobacter (n=14)	O 75.0 75.0 70.0 Slop AY p=0	4.25 4.50 4.75 5.00 5.25 5.50 Genome size, bp 1e6 0.412 Bacteriovorax (n=12)
% 80 -	% 80	75		4.9 5.0 5.1 5.2 5.3 5.4 5.5 Genome size, bp 1e6		3.2 3.4 3.6 3.8 Genome size, bp 1e6
80 - 80 - 90 - 90 - 90 - 90 - 90 - 90 -	••	slope=-1.011e-05 BB p=0.15	Slope BC p=0. % '80 -		BD p=0 80, 80 75 70	
1.4 1.6 1.8 2.0 2.2 2.4 Genome size, bp 1e6 slope=-2.721e-06 BE p=0.0 Bradyrhizobium (n=140) 75 - 8 70 - 9 00 us 65 - 9 00 do 60 - 9	3.0 3.2 3.4 3.6 3.8 4.0 Genome size, bp 1e6 slope=2.293e-06 BF p=0.221 Brenneria (n=11) % 80.0 -	3.9 4.0 4.1 4.2 4.3 4.4 Genome size, bp 1e6 slope=-4.652e-06 BG p=0.135 Brevundimonas (n=62)	slope	Genome size, bp 1e6 e=3.249e-05		
82.5 - 80.0 - 90	4.00 4.25 4.50 4.75 5.00 5.25 Genome size, bp 1e6 slope=-8.874e-07 BK p=0.0	slope=-2.348e-05	slope	3.24 3.26 3.28 3.30 3.32 3.34 Genome size, bp 1e6 e=1.958e-05 077 Candidatus Pelagibacter (n=25)	slop	6.5 7.0 7.5 8.0 Genome size, bp 1e6 0.596 Candidatus Thioglobus (n=12)
## 75.0 - 72.5 - 4.4	68 - 66 - 0.6 0.7 0.8 0.9 1.0 1.1 1. Genome size, bp 1e7 slope=-3.395e-06 BP p=0.329		slope BR p=0. % 80 -	Genome size, bp 1e6 e=-7.355e-06 0 Citrobacter (n=173)	slop	1.0 1.2 1.4 1.6 1.8 Genome size, bp 1e6 0.42
Slope=4.845e-07 BT 75.0 Slope=4.847 Collimonas (n=15) 8 72.5	4.0 4.2 4.4 4.6 4.8 5.0 Genome size, bp 1e6 slope=-6.107e-06 BU p=0.013	Genome size, bp 1e6 slope=-2.092e-06	u 75 - Genes in 9 70 -	4.6 4.8 5.0 5.2 5.4 5.6 5.3 Genome size, bp 1e6	slop	2.8 2.9 3.0 3.1 3.2 3.3 3.4 Genome size, bp 1e6 0.023
90 70.0	Siope=2.129e-05 BZ p=0.049 YO - 1.5	slope=-9.192e-06	slope CB p=0.	1.95 2.00 2.05 2.10 Genome size, bp 1e6 e=-1.677e-06 166 Desulfovibrio (n=66)	slop	4.3 4.4 4.5 4.6 4.7 Genome size, bp 1e6 0e=-6.196e-07
85	75 -	80 -	Genes in COGs, % - 09 - 09 - 09 - 09 - 09 - 09 - 09 -	3.0 3.5 4.0 4.5 5.0 Genome size, bp 1e6	% '800' 75' 70' 70' 70' 70' 70' 70' 70' 70' 70' 70	
slope=6.811e-06 CD p=0.008	slope=3.281e-06 CE p=0.335	slope=-1.046e-07	slope CG p=0.	e=-2.323e-06	slop	pe=1.01e-05 0.122
75	6.2 6.4 6.6 6.8 7.0 Genome size, bp 1e6 slope=-3.991e-07 CJ p=0.588	slope=-8.963e-06	slope	* • • •	slop	•
1.8 2.0 2.2 2.4 Genome size, bp 1e6 slope=1.586e-07 CN p=0.892	5.5 6.0 6.5 7.0 7.5 8.0 Genome size, bp 1e6 Slope=-3.866e-06 CO p=0.305	slope=-9.296e-06	slope	•••	slop	4.70 4.75 4.80 4.85 4.90 4.95 Genome size, bp 1e6 0.001 Gallibacterium (n=37)
Siope=-2.288e-06 CS p=0.476	2.6 2.8 3.0 3.2 3.4 3.6 Genome size, bp 1e6 Slope=-4.99e-06 CT p=0.012 Gilliamella (n=70)	slope=-4.501e-06 CU p=0.052	slope	1.80 1.85 1.90 1.9 Genome size, bp 1e6 488 Glaesserella (n=31)	ui 80 - 75 - 5 - Slop	2.3 2.4 2.5 2.6 2.7 Genome size, bp 1e6
30 40 4.5 5.0 Genome size, bp 1e6	% 80 -	slope=3.213e-06	Genes in COGs Genes in COGs 65 -	2.1 2.2 2.3 2.4 2. Genome size, bp 1e6 e=-1.467e-05 005 Helicobacter (n=550)	70 Genes in COGs	2.8 3.0 3.2 3.4 3.6 Genome size, bp 1e6 0.096 Henriciella (n=11)
% 80 -	% 80 -	80 - Genes in COGs in	% 70 - 60 - 50 - 40 -	1.55 1.60 1.65 1.70	% 77.5 % 75.0 % 72.5 70.0 67.5	3.2 3.4 3.6 3.8 4.0 4.2
Genome size, bp 1e6 slope=-4.007e-06 DC p=0.003	Slope=-3.250e-06 DD p=0.698	slope=-1.208e-05	slope	Genome size, bp 1e6 e=1.529e-06 582	slop DG p=0 70.0 % 67.5 65.0 62.5	
4.5 5.0 5.5 6.0 6.5 Genome size, bp 1e6 slope=-7.317e-06 DH p=0.013	2.0 2.1 2.2 2.3 Genome size, bp 1e6 Slope=5.286e-07 DI p=0.859 75 % 70	slope=-5.453e-06	L	• ••	slop	3.00 3.25 3.50 3.75 4.00 4.25 Genome size, bp 1e6 0.0 Klebsiella (n=1125)
2.2 2.4 2.6 2.8 3.0 Genome size, bp 1e6 slope=-1.33e-05 DM p=0.0	3.50 3.75 4.00 4.25 4.50 4.75 Genome size, bp 1e6 Slope=1.132e-06 DN p=0.805	slope=-2.252e-07		1.8 1.9 2.0 2.1 2.2 2.3 2.4 Genome size, bp 1e6 e=-7.507e-06 012	slop	5.0 5.2 5.4 5.6 5.8 6.0 6.2 Genome size, bp 1e6 0.004
3.4 3.6 3.8 4.0 4.2 Genome size, bp 1e6	4.8 5.0 5.2 5.4 5.6 5.8 Genome size, bp 1e6 slope=6.298e-07 DS p=0.85 Lelliottia (n=16)	Genome size, bp 1e6 slope=-2.118e-05	.⊆ 75.0 -	4.8 5.0 5.2 5.4 Genome size, bp 1e6 2=-3.048e-06 542	slop	3.2 3.4 3.6 3.8 Genome size, bp 1e6
65 - 4.6 4.8 5.0 5.2 Genome size, bp 1e6 slope=-1.087e-05	% 80 8	Genome size, bp 1e6 slope=-4.862e-06	90 80 - 90 75 - 70 -	2.5 3.0 3.5 4. Genome size, bp 1e6 2=-4.263e-06 0	y 75.0 ·	3.4 3.6 3.8 4.0 4.2 Genome size, bp 1e6
82 - \$\frac{\sqrt{30}}{\sqrt{90}} 80 - \frac{\sqrt{30}}{\sqrt{30}} 78 - \frac{\sqrt{30}}{\sqrt{30}}	74 - \$\frac{\sigma}{\sigma} 72 - \frac{\sigma}{\sigma} 68 - \frac{\sigma}{\sigma} 66 - \frac{\sigma}{\sigma} 4.2 4.4 4.6 4.8 \text{Genome size, bp} 1e6	80	80 - % 75 - 70 - 65 - 55 -	3 4 5 6 Genome size, bp 1e6	75 % 70 65 % 60 60 60 60 60 60 60 60 60 60 60 60 60	
slope=3.433e-06	slope=-6.140e-06 EC p=0.0	slope=-2.382e-07 ED p=0.855	slope EE p=0. 85 - % 80 -	e=-2.773e-06	slop	oe=-3.628e-06 0.127
O denes in 70 -	Genes in COGs, 50 - 50 -	Genes in COC 72	Genes in COG Genes in COG		Genes in COC	
2.5 2.6 2.7 Genome size, bp 1e6 slope=7.905e-07 EG p=0.39 Massilia (n=45) % 75 - \$\frac{\sigma}{9}\$ 70 - \$\frac{\sigma}{\sigma}\$	3.0 3.5 4.0 4.5 5.0 Genome size, bp 1e6 Slope=-9.187e-07 EH p=0.177 Mesorhizobium (n=141) 80 -	3.5 4.0 4.5 5.0 5.5 Genome size, bp le6 Slope=-4.885e-06 EI p=0.014 Methylobacter (n=14) % 62.5 % 62.5 % 67.5 % 67.5	O is slope slope p=0.		OS uses in COGs, % Soon Senes in COGs	1.5 2.0 2.5 3.0 Genome size, bp 1e6 0.452
2.5 2.6 2.7 Genome size, bp 1e6 slope=7.905e-07 EG p=0.39 Massilia (n=45) % 75 - % 90 70 Slope=9.369e-06 EL p=0.275 Methylophaga (n=14) % 75 - %	3.0 3.5 4.0 4.5 5.0 Genome size, bp 1e6 slope=-9.187e-07 EH p=0.177	3.5 4.0 4.5 5.0 5.5 Genome size, bp 1e6 Slope=-4.885e-06 EI	O ui saua9 65 - Slope EJ % 'SDO2 ii Saua9 50 - Slope EO 72.5 - 70.0 - 72.5 - 70.0 - 70	Genome size, bp 1e6 2=-3.829e-07 325	OD us about the contract of th	1.5 2.0 2.5 3.0 Genome size, bp 1e6 0.452
2.5 2.6 2.7 Genome size, bp 1e6 Slope=7.905e-07 EG	Slope=-9.187e-07 EH p=0.177	3.5 4.0 4.5 5.0 5.5 Genome size, bp 1e6 Slope=-4.885e-06 P=0.014 Methylobacter (n=14)	Slope EJ % Slope EJ % Slope EO 72.5 - Slope EO 72.5 - Slope ET 80 - Slop	Genome size, bp 1e6 2=-3.829e-07 325	OD US SIOPE OF SIOPE	1.5 2.0 2.5 3.0 Genome size, bp 1e6 0.452
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2.5 2.6 2.7 Genome size, bp 1e6 slope=7.905e-07 EG p=0.39 Massilia (n=45) % 75 60 5 6 7 8 Genome size, bp 1e6 slope=9.369e-06 EL p=0.275 Methylophaga (n=14) % 75 2.8 2.9 3.0 3.1 3.2 3.3 Genome size, bp 1e6 slope=-5.194e-06 EQ p=0.124 Microbulbifer (n=16) % 75 % 7	Slope=-9.187e-07 EH p=0.177 Mesorhizobium (n=141) 80 575 60 5.5 6.0 6.5 7.0 7.5 Genome size, bp 1e6 Slope=-3.419e-06 EM p=0.259 Methylophilus (n=17) 71 70 69 67 2.7 2.8 2.9 3.0 Genome size, bp 1e6 Results a slope size, bp 1e6 Results a slope size, bp 1e6 Slope=-3.905e-06 ER p=0.002 Microvirga (n=11) 80 80 80 67 68 69 67 69 69 50 60 60 60 60 60 60 60 60 60	Slope=-9.051e-06 EN p=0.007 Methylobacter (n=14) **62.5 **55.5 **5.25 5.50 5.75 6.00 6.25 6.50 6.75 Slope=-1.121e-05 ES p=0.0 **8 80.0 **1.8 2.0 2.2 2.4 2.6 2.8 Genome size, bp 1e6 **1.8 2.0 2.2 2.4 2.6 2.8 Genome size, bp 1e6 **1.8 2.0 2.2 2.4 2.6 2.8 **1.8 2.0 2.2 2.4 2.6 2.8 **1.8 2.0 2.2 2.4 2.6 2.8 **1.8 2.0 2.2 2.4 2.6 2.8 **1.8 2.0 2.2 2.4 2.6 2.8 **1.8 2.5 3.5 3.5 3.5 3.5 3.5 3.5 3.5 3.5 3.5 3	Oui sales Slope	Genome size, bp 1e6 2=-3.829e-07 325 Methylobacterium (n=97) 5 6 7 8 9 Genome size, bp 1e6 2=-6.005e-07 89 Methylotenera (n=15) 2.2 2.4 2.6 2.8 3.0 Genome size, bp 1e6 2=-1.617e-05 Morganella (n=42) 3.6 3.8 4.0 4.2 4.4 Genome size, bp 1e6 2=6.892e-08	OS used to the control of the contro	1.5 2.0 2.5 3.0 Genome size, bp 1e6 0.452
2.5	3.0 3.5 4.0 4.5 5.0 Genome size, bp 1e6 EH Slope=-9,187e-07 Mesorhizobium (n=141)	Slope=-4.885e-06 EI 65.0 4.25 4.50 4.75 5.00 5.25 5.50 Genome size, bp 1e6 8 62.5 4.25 4.50 4.75 5.00 5.25 5.50 Genome size, bp 1e6 8 57.5 9 55.0 4.25 5.50 5.75 6.00 6.25 6.50 6.75 Genome size, bp 1e6 8 80.0 8 80.0 9 70.5 1.8 2.0 2.2 2.4 2.6 2.8 Genome size, bp 1e6 8 80.0 9 70.5 8 80.0 7 8 80.0 7 8 80.0 7 9 7 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	Senes in Color of the color of	Genome size, bp 1e6 2=-3.829e-07 325	OS uis especial of the control of th	1.5 2.0 2.5 3.0 1e6 De=-4.796e-06 A.48 5.0 5.2 5.4 Genome size, bp 1e6 De=-9.208e-06 De=-9.208e-06 De=-9.208e-06 De=-5.281e-06 De=-8.838e-06 De=-8.838e-06 De=-8.838e-06 De=-1.463e-05 De=-1.4
2.5 2.6 2.7 Genome size, bp le6 slope=7.905e-07 EG p=0.39	Slope=-9.187e-07 EH p=0.177	Slope=-4.885e-06 El p=0.014 Methylobacter (n=14) % 62.5 Slope=-9.051e-06 En p=0.007 Methylorubrum (n=14) % 70 % 65 5.25 5.50 5.75 6.00 6.25 6.50 6.75 Genome size, bp Moraxella (n=93) % 80.0 Expected a solution of the strength	Senes in Color of the State of	Genome size, bp 1e6 2=-3.829e-07 325 Methylobacterium (n=97) 5 6 7 8 9 Genome size, bp 1e6 2=-6.005e-07 Methylotenera (n=15) 2.2 2.4 2.6 2.8 3.0 Genome size, bp 1e6 2=-1.617e-05 Morganella (n=42) 3.6 3.8 4.0 4.2 4.4 Genome size, bp 1e6 2=-6.892e-08 Mitratireductor (n=12) 3.6 3.8 4.0 4.2 4.4 Genome size, bp 1e6 3=-1.323e-06 Cohrobactrum (n=65) 4.25 4.50 4.75 5.00 5.25 5.50 Genome size, bp 1e6 3=-1.323e-06 4.25 4.50 4.75 5.00 5.25 5.50 Genome size, bp 1e6 3=-2.316e-06	OD US SIDE OF CORREST	1.5 2.0 2.5 3.0 Genome size, bp 1e6 1.5 2.0 2.5 3.0 1e6 1.5 2.0 2.5 3.0 1e7 1.5 2.0 2.5 3.0 1e6 1.5 2 5.4 Genome size, bp 1e6 1.5 2.0 2.5 2.5 2.5 2.5 2.7 2.8 2.9 Genome size, bp 1e6 1.5 2.0 2.5 3.0 3.5 4.0 Genome size, bp 1e6 1.5 2.0 2.0 2.0 2.5 2.5 2.5 2.5 2.5 2.5 2.5 2.5 2.5 2.5
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