slope=-4.387e-01 AA p=0.0 80 % % % 60 Li 40 80 20	slope=-2.638e-02 AB p=0.82		• •		e=-7.204e-02 .174	AE p=0 80 70 80 80 70 60 50 40	ne=-4.095e-01 O.0 Acinetobacter (n=1269)
70 80 90 100 Genome size, % slope=-5.139e-02 AF p=0.852 Actinobacillus (n=45) % % % % % 75 - % 49 70 - 65 -	80 85 90 95 100 Genome size, % slope=-1.744e-01 AG p=0.004 Aeromonas (n=190) 80 -) Slop	70 75 80 85 90 95 100 Genome size, % e=2.005e-01 .017	Genes in COGs, % 80 -	60 70 80 90 100 Genome size, % e=1.69e-01 .326	slop	
85.0 87.5 90.0 92.5 95.0 97.5 100.0 Genome size, % slope=7.338e-02 AK p=0.763 85 - Alcaligenes (n=26) % % % 80 - Market Sign Sign Sign Sign Sign Sign Sign Sign	Genome size, % slope=1.799e-01	slop	, , ,	slope	0 75 80 85 90 95 100 Genome size, % e=9.826e-02 .311	slop	
85.0 87.5 90.0 92.5 95.0 97.5 100.0 Genome size, % slope=9.63e-02 AP 82.5 80.0 80.0 87.5 90.0 92.5 95.0 97.5 100.0 Genome size, % Aminobacter (n=17) 80.0 80.0 80.0 80.0 80.0 80.0 80.0 80.	40 50 60 70 80 90 100 Genome size, % Slope=-6.617e-01 Anaplasma (n=45)	slop	85.0 87.5 90.0 92.5 95.0 97.5 100. Genome size, % e=-1.271e-01 .113	0 slope	70 80 90 100 Genome size, % e=1.651e-01 3	slop AT p=0 80.0 % 77.5 75.0	
70.0 60 70 80 90 100 Genome size, % slope=-6.113e-01 AU p=0.032	70 80 90 100 Genome size, % slope=-4.279e-02 AV p=0.83 Azoarcus (n=10) 8 80 - 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	slop AW p=0 80 - % 75 - 00 70 -		slope	75 80 85 90 95 100 Genome size, % e=3.178e-01 .128	slop	75 80 85 90 95 100 Genome size, % De=-1.251e-01 D.412 Bacteriovorax (n=12)
Slope=-3.238e-01 AZ p=0.0 Slope=-3.238e-01 AZ p=0.0 Slope=-3.238e-01 Bartonella (n=105) 80 75 70 Bartonella (n=105)	70 80 90 100 Genome size, % Slope=-4.464e-01 BA p=0.144 65 - Bdellovibrio (n=13) 65 - S 60 - S	slop	75 80 85 90 95 100 Genome size, % e=-4.452e-01 .15 Blastomonas (n=20)	slope	90 92 94 96 98 100 Genome size, % e=8.304e-02 .068 Bordetella (n=200)	9 42 40 Slop BD 9 80 80 80	85 90 95 100 Genome size, % 0e=1.084e-01 0.143 Bosea (n=35)
Slope=-2.850e-01 BE p=0.0 Bradyrhizobium (n=140)	Slope=1.233e-01 BF p=0.221 80.0 - Slope=1.233e-01 BF p=0.221 Brenneria (n=11) 80.0 - Slope=1.233e-01	9 70.0 · Slop	88 90 92 94 96 98 100 Genome size, % e=-1.716e-01 .135 Brevundimonas (n=62)	slope		slop	70 80 90 100 Genome size, %
Siope=-4.292e-01 BJ p=0.003 Buttiauxella (n=13) 82.5	75.0	SO 60 - Slop BL p=0	70 75 80 85 90 95 100 Genome size, % e=-4.591e-01 .0	BM p=0	97 98 99 100 Genome size, % e=2.853e-01 .077 <i>Candidatus Pelagibacter (n=25)</i>	slop BN p=0	80 85 90 95 100 Genome size, % De=-5.992e-02 D.596 Candidatus Thioglobus (n=12)
80 85 90 95 100 Genome size, % slope=-1.002e-01 BO p=0.095 Caulobacter (n=45)	8 74 - 90 72 - 100 70 80 90 100 Genome size, % slope=-1.687e-01 BP p=0.329	slop	75 80 85 90 95 100 Genome size, % e=8.480e-02 .64	slope	80 85 90 95 100 Genome size, %	slop	60 70 80 90 100 Genome size, %
80 - 80 - 75 - 75 - 70 - 70 - 70 - 70 - 70 - 7	80 - 80 - 80 - 80 - 80 - 80 - 80 - 80 -	slop	85 90 95 100 Genome size, % e=-1.268e-01 .001	slope	80 85 90 95 100 Genome size, % e=5.518e-02	slop	85 90 95 100 Genome size, %
% 72.5	% 75 -	80 - 80 - 75 - 70 - 65 - 65 - 65 - 65 - 65 - 65 - 65 - 6	60 70 80 90 100 Genome size, %	70 - 60 - 50 - 40 -	92 94 96 98 100 Genome size, %	Genes in COGs, %	90 92 94 96 98 100 Genome size, %
Slope=-2.504e-01 BY p=0.002	slope=5.653e-01 BZ p=0.049	CA p=0 80 · 80 · 80 · 70 · 80 · 50 ·	e=-6.614e-01 .128	CB p=0.	Desulfovibrio (n=66) Desulfovibrio (n=66) 00 60 70 80 90 100 Genome size, %	CC p=0 % 80 75 70 70	
slope=3.481e-01 CD p=0.008	slope=2.316e-01 CE p=0.335	CF p=0 80 · 80 · 80 · 80 · 80 · 80 · 80 · 80	e=-5.647e-03 .968	Genes in COGs, % 60 - 60 - 60 - 60 - 60 - 60 - 60 - 60	e=-9.327e-02 .803	Genes in COGs, % 65 60 55	De=1.531e-01 D.122 Ehrlichia (n=22)
85.0 87.5 90.0 92.5 95.0 97.5 100.0 Genome size, % Slope=1.301e-01	Genome size, % slope=-3.296e-02	slop	70 75 80 85 90 95 100 Genome size, % e=-4.96e-01 .0	slope	**.	slop	
75 80 85 90 95 100 Genome size, % Slope=9.096e-03 CN p=0.892 80 80 80 80 60 10 Erwinia (n=63)	70 80 90 100 Genome size, % Slope=-1.393e-01 p=0.305 Erythrobacter (n=43) % 75 - % 75 - % 65 - % 66 - % 60 -	slop	80 85 90 95 100 Genome size, % e=-5.360e-01 .0	slope	88 90 92 94 96 98 100 Genome size, % e=7.643e-01 .043	slop	
70 80 90 100 Genome size, % Slope=-1.207e-01 p=0.476 80 70 Geobacter (n=25) 80 60 50 60 60 60 60 60 60 60 6	55 - 70 75 80 85 90 95 100 Genome size, % Slope=-1.765e-01 Gilliamella (n=70) 8 80 - 90 95 100 Genome size, % Gilliamella (n=70) 75 - 90 95 100	slop CU p=0 80 · % 75 ·	-	50 -	92 94 96 98 100 Genome size, % e=1.981e-01 .488	slop CW p=0 % 75 '\$907 u.s	85 90 95 100 Genome size, % 0e=-1.662e-01 0.042
30 - 70 80 90 100 Genome size, % Slope=2.059e-01 CX p=0.031 Haemophilus (n=176) 80 90 100 Genome size, %	65 - 60 70 80 90 100 Genome size, % Slope=-7.229e-01 Hafnia (n=33) 8 80 - 90 100 Hafnia (n=33)	slop	• •••	ສິງ 65 -	85.0 87.5 90.0 92.5 95.0 97.5 100. Genome size, % e=-2.546e-01 .005	slop DB p=0 % 77.5 % 75.0	
75 80 85 90 95 100 Genome size, % Slope=-2.603e-01 p=0.003 85 -	To - 90 92 94 96 98 100 Genome size, % Slope=-7.698e-02 Histophilus (n=24)	slop	40 50 60 70 80 90 100 Genome size, % e=-6.695e-01	slope	88 90 92 94 96 98 100 Genome size, % e=7.276e-02 .582 <i>Hyphomicrobium (n=14)</i>	slop DG p=0 70.0 % % 67.5	75 80 85 90 95 100 Genome size, % De=6.859e-02 D.295
75 - 70 - 75 80 85 90 95 100 Genome size, % Slope=-2.270e-01 p=0.013 Idiomarina (n=46) 85 - 880	Siope=2.560e-02 DI p=0.859 75- 35.0 Siope=2.560e-02 DI p=0.859 75- 36.0 Siope=2.560e-02 Siope=2.560e-02 Siope=2.560e-02 Siope=2.560e-02 Siope=2.560e-02	slop	85 90 95 100 Genome size, % e=-3.687e-01	DK 90 - 80 - 90 - 90 - 90 - 90 - 90 - 90 -	70 80 90 100 Genome size, % e=-2.421e-01 .239	slop	70 75 80 85 90 95 100 Genome size, % De=-3.648e-01
Siope=-5.561e-01 DM p=0.0 Komagataeibacter (n=38)	75 80 85 90 95 100 Genome size, % slope=6.545e-02 DN p=0.805 80 - • • • •	slop) DO p=0	•	slope DP p=0	75 80 85 90 95 100 Genome size, % e=-4.063e-01 .012	slop	80 85 90 95 100 Genome size, % De=-2.126e-01 D.004 Legionella (n=360)
% 75 -	\$\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\	slop	70 75 80 85 90 95 100 Genome size, % e=-2.78e-01	slope	87.5 90.0 92.5 95.0 97.5 100. Genome size, % e=-1.203e-01 .542 Limnohabitans (n=11)	Genes in COGs, %	85 90 95 100 Genome size, %
85.0 87.5 90.0 92.5 95.0 97.5 100.0 Genome size, %	84 -		90 92 94 96 98 100 Genome size, % e=-2.089e-01		60 70 80 90 100 Genome size, %		
DW p=0.001		0 DY p=0 80 - 80 75 75 76 76 76 76 76 76 76 76 76 76 76 76 76		80 - 80 - % 75 - 70 - 65 - 55 -	Lysobacter (n=43,	Genes in COGs, % 20 60	Magnetospirillum (n=14)
slope=9.429e-02 EB p=0.742 80 -	slope=-3.198e-01 EC p=0.0	% 74 · % 72 · 70 · 68 · 68 ·	e=-1.326e-02 .855	EE p=0. 85 - 85 - 80 - 75 - 65 -	e=-1.496e-01 .076	genes in COGs, % 25	De=-1.222e-01 D.127 Marinovum (n=16)
Genome size, % slope=6.711e-02 EG p=0.39 Massilia (n=45) % 75 -	Genome size, % slope=-7.218e-02 EH p=0.177	slop	Genome size, % e=-2.682e-01 .014	slope	Genome size, % e=-3.384e-02 .325 <i>Methylobacterium (n=97)</i>	slop	Genome size, % De=-2.63e-01 D.452 Methylomonas (n=17)
60 70 80 90 100 Genome size, % slope=3.098e-01 EL p=0.275	70 80 90 100 Genome size, % slope=-1.053e-01 EM p=0.259	slop		slope		slop	
85 90 95 100 Genome size, % slope=-2.511e-01 EQ p=0.124	87.5 90.0 92.5 95.0 97.5 100. Genome size, % Slope=-3.762e-01 ER p=0.002	0 slop	80 85 90 95 100 Genome size, % e=-3.262e-01 .0	slope ET p=0 % 75 -	70 75 80 85 90 95 100 Genome size, % e=-7.295e-01 .0	slop	50 60 70 80 90 100 Genome size, % De=2.805e-01 D.316 Moritella (n=18)
## 60 - For the image of the im	80 - % 70 - 00 60 - 	slop EX p=0 82.5 % 80.0	60 70 80 90 100 Genome size, % e=-4.650e-02 .801	slope	80 85 90 95 100 Genome size, % e=3.533e-03	slop	88 90 92 94 96 98 100 Genome size, % De=-3.595e-01 Nitrosomonas (n=51)
96 97 98 99 100 Genome size, % slope=-2.751e-01 FA p=0.001	85.0 87.5 90.0 92.5 95.0 97.5 100. Genome size, % slope=1.950e-01 PB p=0.131 Novosphingobium (n=89) 80 -	slop	85 90 95 100 Genome size, % e=-1.789e-01 .102	slope	70 75 80 85 90 95 100 Genome size, % e=-7.339e-02 .445	slop	50 60 70 80 90 100 Genome size, % De=-4.250e-01 0.046 Oligella (n=14)
Slope=1.620e-01 FF p=0.509	FG p=0.773 Pandoraea (n=23) 82.5	slop FH p=0	70 75 80 85 90 95 100 Genome size, % e=-5.757e-02 .78	slope FI p=0 80 -	75 80 85 90 95 100 Genome size, % e=-1.243e-01 .146	slop FJ p=0 80 %	80 85 90 95 100 Genome size, % 0e=-1.493e-01 0.0 Paraburkholderia (n=152)
Siope=4.801e-02 FK p=0.462	90-	slop) FM p=0	75 80 85 90 95 100 Genome size, % e=-8.284e-02 .498	slope FN p=0	85 90 95 100 Genome size, % e=-1.916e-01 .063	slop FO p=0	•
\$\frac{1}{50} \frac{1}{50} \fra	•	slop	87.5 90.0 92.5 95.0 97.5 100. Genome size, % e=-3.417e-02 .756 Phyllobacterium (n=23)	slope	85 90 95 100 Genome size, % e=3.185e-01 .239 <i>Piscirickettsia</i> (n=19)	slop	70 80 90 100 Genome size, % 0.007 Pluralibacter (n=14)
80 -	70 - 8 65 - 90.0 92.5 95.0 97.5 100. Genome size, % slope=2.413e-01 FV p=0.067 Polynucleobacter (n=47)	% 80 - 75 - 76 - 76 - 76 - 76 - 76 - 76 - 76	75 80 85 90 95 100	nes in COGs, % 0 2 2 9		% 80	
FU p=0.25	FV p= 0.067 Polynucleobacter (n= 47)	slop	Genome size, % e=1.065e-01 301 Porphyrobactor (n=17)	slope	85 90 95 100 Genome size, % e=-1.176e-01	ອີ້ 74 slop	94 96 98 100 Genome size, %
80 85 90 95 100 Genome size, %	% 70	77.5 · % 75.0 · % 70.0 · % 70.0 · % 70.0 · % 70.5 · % 70.0 · % 70.5 · % 70.0 · % 70.	e=1.065e-01 .301 Porphyrobacter (n=17)	slope FX p=0 80 - % 70 - 60 - 40 -	Genome size, % e=-1.176e-01 .512	Genes in COGs, % 250 100 100 100 100 100 100 100 100 100 1	94 96 98 100 Genome size, % De=-2.418e-02 D.841 Providencia (n=49)
	50 60 70 80 90 100 Genome size, %	FW p=0 77.5 · 77.5 · 77.5 · 77.5 · 70.0 · 80.0 · 80.0 · 80.0 · 77.5 · 70.0 · 9 Filter of the period	e=1.065e-01 .301 Porphyrobacter (n=17) 70 80 90 100 Genome size, % e=-8.258e-02 .753 Pseudooceanicola (n=11) 85 90 95 100	slope FX p=0 80 - 80 - 80 - 80 - 90 - 90 - 90 - 90 - 90 - 90 - 90 - 9	Genome size, % e=-1.176e-01 .512 Proteus (n=94, 85.0 87.5 90.0 92.5 95.0 97.5 100. Genome size, % e=-6.177e-01 .085 Pseudovibrio (n=19, **	Genes in COGs, % 250 10 10 10 10 10 10 10 10 10 10 10 10 10	94 96 98 100 Genome size, % De=-2.418e-02 D.841 Providencia (n=49) To 75 80 85 90 95 100 Genome size, % De=-4.264e-02 D.528 Pseudoxanthomonas (n=25)
Genome size, % slope=-2.856e-01 FZ p=0.0	Genome size, % slope=-8.379e-02 Feeudomonas (n=1965) 80 90 100 Genome size, % Slope=-9.781e-02 Genome size, % Slope=-9.781e-02 Fusillimonas (n=14) 85 90 100 Genome size, %	FW p=0 77.5 · 8 75.0 · 8 75.0 · 9 72.5 · 9 67.5 · 9 680.0 · 9 80.0 · 9 82.5 · 9 80.0 · 9 82.5 · 9 72.5	Porphyrobacter (n=17) 70 80 90 100 Genome size, % e=-8.258e-02 .753 Pseudooceanicola (n=11) 85 90 95 100 Genome size, % e=-1.509e-01 .745 Rahnella (n=22)	45 - 45 - 45 - 45 - 45 - 45 - 45 - 45 -	Genome size, % e=-1.176e-01 512	9 74 FY % 'SDO2 Uses in COG's 'SDO2 Uses in Sope Sope Sope Sope Sope Sope Sope Sope	94 96 98 100 Genome size, % De=-2.418e-02 D.841 Providencia (n=49) 70 75 80 85 90 95 100 Genome size, % De=-4.264e-02 D.528 Pseudoxanthomonas (n=25) 70 80 90 100 Genome size, % De=-3.516e-01 D.0 Raoultella (n=61)
Slope=-2.856e-01 Pseudoalteromonas (n=156)	GA p=0.0	FW p=0 77.5 · 77	Porphyrobacter (n=17) 70 80 90 100 Genome size, % e=-8.258e-02 753 Pseudooceanicola (n=11) 85 90 95 100 Genome size, % e=-1.509e-01 745 Rahnella (n=22) 95 96 97 98 99 100 Genome size, % e=-1.267e-02	45 - 45 - 45 - 45 - 45 - 45 - 45 - 45 -	Genome size, % e=-1.176e-01 512 Proteus (n=94, 85.0 87.5 90.0 92.5 95.0 97.5 100. Genome size, % e=-6.177e-01 085 Pseudovibrio (n=19, 88 90 92 94 96 98 100 Genome size, % e=1.864e-02 873 Ralstonia (n=146, 6 95 100 Genome size, % e=2.267e-01	Genes in COGs, 25 to be compared by the compar	94 96 98 100 Genome size, % De=-2.418e-02 D.841
Genome size, % Slope	GA p=0.0 Feedomonas (n=1965) 80 80 80 80 80 80 80 80 80 8	FW p=0 77.5 · 75.0 · 77.5 · 75.0 · 77.5 · 77	Porphyrobacter (n=17) Porphyrobacter (n=17) Porphyrobacter (n=17) Roll	45 - 45 - 45 - 45 - 45 - 45 - 45 - 45 -	Genome size, % e=-1.176e-01 512 Proteus (n=94, 85.0 87.5 90.0 92.5 95.0 97.5 100. Genome size, % e=-6.177e-01 085 Pseudovibrio (n=19, 88 90 92 94 96 98 100 Genome size, % e=1.864e-02 873 Ralstonia (n=146, 002 Rhodobacter (n=55, 002 Rodentibacter (n=25, 003 Rodentibacter (n=25, 004 Rodentibacter (n=25, 005 Rodentibacter (n=25, 006 Rodentibacter (n=25, 007 Rodentibacter (n=25, 0	74 Slope 75 70 65 P 80 75 70 65 Slope 80 75 70 67.5 Slope 80 75 70	94 96 98 100 Genome size, % 0e=-2.418e-02 0.841
Genome size, % FZ p=0.0 Pseudoalteromonas (n=156)	Slope=-9.781e-02 Genome size, % Slope=-9.781e-02 For p=0.616 Slope=-9.781e-02 For p=0.616	FW p=0 77.5 · 75.0 · 77.5 · 77	e=1.065e-01 .301 Porphyrobacter (n=17) 70 80 90 100 Genome size, % e=-8.258e-02 .753 Pseudooceanicola (n=11) 85 90 95 100 Genome size, % e=-1.509e-01 .745 Rahnella (n=22) 95 96 97 98 99 100 Genome size, % e=-1.267e-02 .918 Rhodanobacter (n=29) 80 85 90 95 100 Genome size, % e=-9.486e-01 .0 Rickettsia (n=97) 60 85 90 95 100 Genome size, % e=-9.214e-02	45 - 45 - 45 - 45 - 45 - 45 - 45 - 45 -	Genome size, % 2=-1.176e-01 512 Proteus (n=94, 85.0 87.5 90.0 92.5 95.0 97.5 100. Genome size, % 2=-6.177e-01 085 Pseudovibrio (n=19, Residence size, % 2=1.864e-02 873 Ralstonia (n=146, 0075 80 85 90 95 100 Genome size, % 2=2.267e-01 002 Rhodobacter (n=55, 70 80 90 95 100 Genome size, % 2=2.267e-01 002 Rodentibacter (n=25, Rodentibacter (n=25, Residence size, % 2=8.978e-02 Ruegeria (n=29, Ruegeria (n=20, Rue	Sence of the sence	94 96 98 100 Genome size, % De=-2.418e-02 De341
Genome size, % Slope=-2.856e-01 8 75 9 70 6 60 8 75 60 70 80 90 100 Genome size, % Slope=-2.796e-01 8 80 75 80 85 90 95 100 Genome size, % Slope=-8.336e-02 Rheinheimera (n=12) 8 75 80 85 90 95 100 Genome size, % Slope=-2.823e-01 Genome size, % Slope=-2.823e-01 Rhodopseudomonas (n=30) 8 75 80 85 90 85 90 95 100 Genome size, % Slope=-2.823e-01 Genome size, % Slope=-2.823e-01 Slope=-2.823e-02 Slope	GO 70 60 70 80 90 100 Gonome size, % Slope=-8.379e-02 Frequencial formula for the first of th	FW p=0 77.5 77.7	e=1.065e-01 301 Porphyrobacter (n=17) 70 80 90 100 Genome size, % e=3.258e-02 .753 Pseudooceanicola (n=11) 85 90 95 100 Genome size, % e=-1.509e-01 .745 Rahnella (n=22) 95 96 97 98 99 100 Genome size, % e=-1.267e-02 .918 Rhodanobacter (n=29) 80 85 90 95 100 Genome size, % e=-9.214e-02 .373 Roseovarius (n=33) 70 80 90 100 Genome size, % e=-9.214e-02 .373 Roseovarius (n=33) 70 80 90 100 Genome size, % e=-2.33e-01	45 - 45 - 45 - 45 - 45 - 45 - 45 - 45 -	Genome size, % 85.0 87.5 90.0 92.5 95.0 97.5 100. 85.0 87.5 90.0 92.5 95.0 97.5 100. Genome size, % 88 90 92 94 96 98 100. 88 90 92 94 96 98 100. 8873 Ralstonia (n=146, 2=1.864e-02 Rhodobacter (n=55, 6=2.267e-01 Rhodobacter (n=55, 70 80 90 100. 9=6.023e-01 Rodentibacter (n=25, 75 80 85 90 95 100. 9=8.978e-02 Ruegeria (n=29, 482 Ruegeria (n=29, 75 80 85 90 95 100. 9=8.978e-02 Ruegeria (n=29, 75 80 85 90 95 100. 9=1.179e-01 Shigella (n=167, 2=1.179e-01 Shigella (n=1	Series in Cock, spool of the Sipe of the S	94 96 98 100 Genome size, % De=-2.418e-02 .341 Providencia (n=49) 70 75 80 85 90 95 100 Genome size, % De=-4.264e-02 .528 Pseudoxanthomonas (n=25) 70 80 90 100 Genome size, % De=-3.516e-01 Raoultella (n=61) 85 90 95 100 Genome size, % De=-3.516e-02 .359 Rhodoferax (n=12) 80 85 90 95 100 Genome size, % De=-1.805e-02 .836 Roseivivax (n=11) 80 85 90 95 100 Genome size, % De=-1.805e-02 .836 Roseivivax (n=11) Sinorhizobium (n=91) Sinorhizobium (n=91)
Genome size, % Slope=-2.856e-01 8 75 60 70 80 90 100 Genome size, % Slope=-2.796e-01 Fig. 60 Fi	GA Slope=-8.379e-02 Pseudomonas (n=1965) 80 90 100 Genome size, % Slope=-9.781e-02 Pusillimonas (n=144) 85 86 65 70 75 80 80 90 100 Genome size, % Slope=-6.541e-02 Rhizobium (n=433) 85 86 67 65 65 66 70 78 80 90 100 Genome size, % GR P=0.02 Rhizobium (n=433) 87 880 675 680 690 70 800 90 100 Genome size, % GR P=0.01 Rhodovulum (n=23) 81 82 83 84 85 86 87 87 87 88 88 89 80 80 80 80 80 67 67 80 80 90 100 Genome size, % Genome size, % Genome size, % Genome size, % Slope=-3.502e-01 Roseomonas (n=18) 80 67 67 67 67 67 67 680 90 100 Genome size, % Genome size, % Slope=-3.502e-01 Serratia (n=161) 880 90 100 Genome size, % Slope=-3.502e-01 Serratia (n=161) 880 90 100 Genome size, % Slope=-3.502e-01 Serratia (n=161) Sphingobium (n=98)	FW p=0 77.5 do p=0	e=1.065e-01 301 Porphyrobacter (n=17) 70 80 90 100 Genome size, % e=-8.258e-02 753 Pseudooceanicola (n=11) 85 90 95 100 Genome size, % e=-1.509e-01 Rahnella (n=22) 80 80 85 90 95 100 Genome size, % e=-1.267e-02 918 Rhodanobacter (n=29) 80 80 85 90 95 100 Genome size, % e=-9.486e-01 Rickettsia (n=97) 70 75 80 85 90 95 100 Genome size, % e=-9.486e-01 Rickettsia (n=97) 70 75 80 85 90 95 100 Genome size, % e=-9.486e-01 Shewanella (n=110) 70 80 90 100 Genome size, % e=-2.33e-01 Shewanella (n=110)	A Solution of the control of the con	Genome size, % 25.12	FY % 'SDO2 vis Senes in COG's % 'SDO2 vis Senes	94 96 98 100 Genome size, % 0e=-2.418e-02 .841 Providencia (n=49) 70 75 80 85 90 95 100 Genome size, % 10e=-4.264e-02 .9:28 Pseudoxanthomonas (n=25) 70 80 90 100 Genome size, % 10e=-3.516e-01 Raoultella (n=61) 85 90 95 100 Genome size, % 10e=-1.805e-02 .836 Roseivivax (n=11) 80 85 90 95 100 Genome size, % 10e=-1.805e-02 .836 Roseivivax (n=11) 80 85 90 95 100 Genome size, % 10e=-7.394e-02 .511 Sinorhizobium (n=91) 80 85 90 95 100 Genome size, % 10e=-7.394e-02 .511 Sinorhizobium (n=91) 80 85 90 95 100 Genome size, % 10e=-7.394e-02 .511 Sinorhizobium (n=91) 80 85 90 95 100 Genome size, % 10e=-7.394e-02 .511 Sinorhizobium (n=91) 80 85 90 95 100 Genome size, % 10e=-7.394e-02 .511 Sinorhizobium (n=91)
Genome size, % slope=-2.856e-01 FZ p=0.0 Pseudoalteromonas (n=156) 80 75 60 70 80 90 100 Genome size, % slope=-2.796e-01 FS p=0.072 Psychrobacter (n=56) 80 85 90 95 100 FS p=0.0788 Rheinheimera (n=12) FS p=0.0788 Rheinheimera (n=12) FS p=0.0614 Rhodopseudomonas (n=30) FS p=0.614 Slope=-2.778e-01 FS p=0.616 Slope=-2.778e-02 FS p=0.616	Siope== 8.379e-02 From the size of the si	FW 77.5	e=1.065e-01 301 Porphyrobacter (n=17) 70 80 90 100 Genome size, % e=-8.258e-02 Pseudooceanicola (n=11) 85 90 95 100 Genome size, % e=-1.509e-01 Rahnella (n=22) 80 85 90 95 100 Genome size, % e=-1.267e-02 318 Rhodanobacter (n=29) 80 85 90 95 100 Genome size, % e=-9.486e-01 Rickettsia (n=97) 70 80 90 100 Genome size, % e=-9.214e-02 373 Roseovarius (n=33) 70 80 90 100 Genome size, % e=-9.214e-02 373 Roseovarius (n=110) 50 60 70 80 90 100 Genome size, % e=-2.32e-01 Shewanella (n=110) 50 60 70 80 90 100 Genome size, % e=-2.4.637e-03 Sphingomonas (n=186) 50 60 70 80 90 100 Genome size, % e=-3.4.838e-01 Sulfurimonas (n=21)	TX % 'SDO2 vi saves by CG % 'SDO2 vi saves by	Genome size, % 25-1.176e-01 Proteus (n=94, 85.0 87.5 90.0 92.5 95.0 97.5 100. Genome size, % 26-6.177e-01 27 80 85 90 95 100. Genome size, % 28-1.864e-02 88 90 92 94 96 98 100. Genome size, % 28-1.864e-02 88 890 92 94 96 98 100. Genome size, % 28-1.864e-02 88 890 92 94 96 98 100. Genome size, % 28-1.864e-02 88 890 90 95 100. Genome size, % 28-2.267e-01 Rodentibacter (n=25, 30 85 90 95 100. Genome size, % 28-1.179e-01 Rodentibacter (n=25, 30 85 90 95 100. Genome size, % 28-1.179e-01 Shigella (n=167, 219 Shigella (n=167, 219 Shigella (n=65, 219 Shigella (n=65, 219 Sphingopyxis (n=65, 219 Sphingopyxis (n=65, 219 Sphingopyxis (n=65, 219 Genome size, % 28-1.519e-02 Sphingopyxis (n=65, 29-1.519e-02	74 open 75 70 65 open 75 70 65 open 75 70 65 open 75 70 65 open 80 75 70 open 80 open 80 75 70 open 80 75 70 open 80 open 80 open 80 75 70 open 80 ope	94 96 98 100 94 96 98 100 96 98 100 96 98 100 97 75 80 85 90 95 100 Genome size, % 98 99 100 Genome size, % 98 99 100 Genome size, % 98 99 100 98 99 100 98 99 100 98 99 100 98 99 100 98 99 100 99 95 100 90 90 90 10
Siope=2.796e-01 Psychrobacter (n=156)	Slope=-8.379e-02 GA p=0 To genome size, % Slope=-9.781e-02 From the period of the	FW % 'SDO2 ui sauab F % 'SDO3 ui	e=1.065e-01 301 Porphyrobacter (n=17) 301 Porphyrobacter (n=17) 301 Possible of the properties of the	TX % 'SDO2 ui sauab G % 'SDO3 ui	Genome size, % 2=-1.176e-01 85.0 87.5 90.0 92.5 95.0 97.5 100. Genome size, % 2=-6.177e-01 88 90 92 94 96 98 100. Genome size, % 2=1.864e-02 873 Ralstonia (n=146. 70 80 95 90 95 100. Genome size, % 2=2.267e-01 Rhodobacter (n=55. 70 80 85 90 95 100. Genome size, % 2=-6.023e-01 Rodentibacter (n=25. 75 80 85 90 95 100. 2=-6.023e-01 Rodentibacter (n=29. 75 80 85 90 95 100. 2=-1.179e-01 Shigella (n=167. 75 80 85 90 95 100. 2=-1.179e-01 Shigella (n=167. 75 80 85 90 95 100. 2=-1.179e-01 Shigella (n=167. 2=-1.179e-02 Sphingopyxis (n=65. 30 75 80 85 90 95 100. 30 85 90 95 100.	74 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	94 96 98 100 Genome size, % 70 75 80 85 90 95 100 Genome size, % 70 75 80 85 90 95 100 Genome size, % 85 90 95 100 Genome size, % 85 90 95 100 Genome size, % 86 85 90 95 100 Genome size, % 87 86 87 90 95 100 Genome size, % 88 85 90 95 100 Genome size, % 89 85 90 95 100 Genome size, % 80 85 90 95 100 Genome size, % 81 85 90 95 100 Genome size, % 81 85 90 95 100 Genome size, % 82 85 90 95 100 Genome size, % 83 85 90 95 100 Genome size, % 84 85 90 95 100 Genome size, % 85 85 90 95 100 Genome size, % 86 85 90 95 100 Genome size, % 87 86 87 90 95 100 Genome size, % 88 85 90 95 100 Genome size, % 89 85 90 95 100 Genome size, % 80 85 90 95 100 Genome size, % 81 85 90 95 100 Genome size, % 82 85 90 95 100 Genome size, % 83 85 90 95 100 Genome size, % 84 90 90 100 Genome size, % 85 90 95 100 Genome size, % 86 85 90 95 100 Genome size, % 87 90 95 100 Genome size, % 88 90 95 100 Genome size, % 89 85 90 95 100 Genome size, % 80 85 90 95 100 Genome size, % 8
Solution	Slope=8.379e-02 From the state of the state	FW 'SDO2 ui sauab F 'SDO3 ui sauab F 'SD	e=1.065e-01 301 Porphyrobacter (n=17) 301 Porphyrobacter (n=17) 70 80 90 100 Genome size, % e=-8.258e-02 Pseudooceanicola (n=11) 85 90 95 100 Genome size, % e=-1.267e-02 918 Rhodanobacter (n=29) 70 75 80 85 90 95 100 Genome size, % e=-9.486e-01 Rickettsia (n=97) 70 80 90 90 100 Genome size, % e=-9.214e-02 Roseovarius (n=33) 70 80 90 90 100 Genome size, % e=-9.214e-02 Roseovarius (n=32) 70 80 90 90 100 Genome size, % e=-1.775e-01 Thalassospira (n=110) 87.5 90.0 92.5 95.0 97.5 100. Genome size, % e=-1.775e-01 88.5 90 95 100 Genome size, % e=-1.267e-03 Roseovarius (n=32) 70 80 90 90 100 Genome size, % e=-1.775e-01 Roseovarius (n=32) 88.5 90 95 100 Genome size, % e=-1.775e-01 Roseovarius (n=32) 88.5 90 95 100 Genome size, % e=-1.775e-01 Roseovarius (n=32) 88.5 90 95 100 Genome size, % e=-1.775e-01 Roseovarius (n=32)	The state of the s	Genome size, % 85.0 87.5 90.0 92.5 95.0 97.5 100. Genome size, % =-6.177e-01	The contraction of the contracti	94 96 98 100 Genome size, % 70 80 95 90 95 100 Genome size, % 70 80 99 100 Genome size, % 10.0 35 90 95 100 Genome size, % 10.0 36 90 95 100 Genome size, % 10.0 370 80 90 100 Genome size, % 10.0 380 95 100 Genome siz
Sione = 2.856c 01 Pseudoalteromonas (n=156) Ref	Sispe—9.781e-02 From Sispe—9.781e-03 From Sispe—9.781e-03 From Sispe—9.781e-03 From Sispe—9.781e-03 From Sispe—9.781e-03 From Sispe—9.781e-03 From Sispe—1.837e-01 From	FW % 'SOO III Salpage 10	e=1.065c-01 301 Porphyrobacter (n=17) 301 Porphyrobacter (n=17) 70 80 90 100 Seneme size, % e=8.258e-02 Pseudooceanicola (n=11) 85 90 95 100 Senome size, % e=-1.509e-01 Rahnella (n=22) 80 85 90 95 100 Senome size, % e=-1.267e-02 918 Phodanobacter (n=29) 80 85 90 95 100 Senome size, % e=-1.267e-02 918 Rhodanobacter (n=29) 80 85 90 95 100 Senome size, % e=-9.486e-01 Prophyrobacter (n=17) 80 85 90 95 100 Senome size, % e=-3.463re-03 Sphingomonas (n=186) 70 80 85 90 95 100 Senome size, % e=-4.637e-03 Sphingomonas (n=186) 70 80 85 90 95 100 Senome size, % e=-1.775e-01 Suffurimonas (n=21) 70 80 90 100 Senome size, % e=-1.775e-01 Variovorax (n=69) 70 80 90 100 Senome size, % e=-3.926e-01 Variovorax (n=69)	Senes in COGs, 2000 in Sanababababababababababababababababababa	Genome size, % ==1.176-01 Proteus (n=94, 1512 Proteus (n=19, 1512 Ralstonia (n=146, 1512 Ralstonia (n=146, 1512 Ralstonia (n=146, 1512 Rodentibacter (n=25, 1512 Rodentibacter (n=25, 1512 Ruegeria (n=29, 1512 Proteus (n=19, 1512 Ralstonia (n=146, 1512 Ruegeria (n=29, 1512 Proteus (n=19, 1512 Ralstonia (n=146, 1512 Ruegeria (n=29, 1512 Proteus (n=19, 1512 Ralstonia (n=146, 1512 Ruegeria (n=29, 1512 Sphingopyxis (n=65, 1512 Sphingopyxis (n=65, 1512 Sphingopyxis (n=1418, 1512 S	74 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	94 96 98 100 Cenome size, % ce-2.418c-02
Senome size, % Senome 2.856e-01 Pseudoalteromonas (n=156) \$ 75 60 70 80 70 60 70 80 90 100 Genome size, % 80 61 75 80 80 75 60 75 80 80 80 75 60 75 80 80 60 75 80 80 60 75 80 80 60 75 80 80 60 75 80 80 60 75 80 80 60 75 80 80 60 75 80 80 60 75 80 80 80 60 75 80 80 80 80 80 80 80 80 80 8	Single = 4.781e 02 From the state of the st	FW 75.0 0.5 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	==1.055e-01 70 80 90 100 6enome size, % ==-1.509e-01 Rahnella (n=22) 95 96 97 98 99 100 Genome size, % ==-1.509e-01 Rahnella (n=22) 95 96 97 98 99 100 Genome size, % ==-1.267e-02 Rhodanobacter (n=29) 80 85 90 95 100 Genome size, % ==-1.267e-02 Rhodanobacter (n=29) 80 85 90 95 100 Genome size, % ==-9.486e-01 Rickettsia (n=97) 70 80 85 90 95 100 Genome size, % ==-4.637e-03 Sphingomonas (n=186) 50 60 70 80 90 100 Genome size, % ==-4.637e-03 Sphingomonas (n=186) 70 80 90 95 100 Genome size, % ==-1.637e-03 Sphingomonas (n=21) 70 80 90 95 100 Genome size, % ==-1.637e-03 Sphingomonas (n=21) 70 80 90 95 100 Genome size, % ==-1.637e-03 Sphingomonas (n=22) 70 80 90 95 100 Genome size, % ==-1.637e-03 Sphingomonas (n=22) 70 80 90 95 100 Genome size, % ==-1.637e-03 Sphingomonas (n=24) 70 80 90 90 100 Genome size, % ==-1.775e-01 Xanthomonas (n=483) 70 80 90 90 100 Genome size, % ==-1.775e-01 Xanthomonas (n=483) 70 80 90 90 100 Genome size, % ==-1.775e-01 Xanthomonas (n=483) 70 80 90 90 100 Genome size, % =-1.775e-01 Xanthomonas (n=483)	45 - 10 - 10 - 10 - 10 - 10 - 10 - 10 - 1	Genome size, % ==1.176-01 Proteus (n=94, 1512 Proteus (n=19, 1512 Ralstonia (n=146, 1512 Ralstonia (n=146, 1512 Ralstonia (n=146, 1512 Rodentibacter (n=25, 1512 Rodentibacter (n=25, 1512 Ruegeria (n=29, 1512 Proteus (n=19, 1512 Ralstonia (n=146, 1512 Ruegeria (n=29, 1512 Proteus (n=19, 1512 Ralstonia (n=146, 1512 Ruegeria (n=29, 1512 Proteus (n=19, 1512 Ralstonia (n=146, 1512 Ruegeria (n=29, 1512 Sphingopyxis (n=65, 1512 Sphingopyxis (n=65, 1512 Sphingopyxis (n=1418, 1512 S	74	94 96 98 100 Genome size, % 20=2.418e-02