

Table S1

Size fraction	Lineage	Clade (SILVA annotation)	Percent abundance in 16S libraries (experiment and control) per size fraction	BD shift	Percent of genomes in clade or lineage that encode TonB receptor proteins	
0.2 - 0.8	Euryarchaeota (MGII)	MGII.A	0.1656	0.012	No representative genome	
		MGII.C	0.1523	0.012		
	Actinobacteria	Sva0096	0.9712	0.018	100% (1/1)	
			0.0339	0.012		
	Actinobacteria	Sva0096	0.0160	0.012	62% (13/21)	
	Flavobacteria	NS9 marine group	0.0290	0.018	100% (7/7)	
	Gammaproteobacteria	SAR86	0.0142	0.018	88% (7/8)	
			5.3838	0.012		
			0.0412	0.036		
	Alphaproteobacteria	Uncultured Rhodobacteraceae	0.5947	0.012	100% (2/2)	
0.0712			0.018			
Verrucomicrobia	Uncultured Puniceicoccaceae	0.6991	0.012	35% (48/136)		
		0.1873	0.024			
0.8 - 3	Euryarchaeota (MGII)	MGII.A	0.1504	0.012	100% (1/1)	
		0.0043	0.012			
	Flavobacteria	Uncultured Flavobacteriaceae	0.0096	0.012	No representative genome	
			0.0155	0.030		
			0.0038	0.018		
			<i>Formosa</i> sp.	0.0048		0.030
			<i>Marinoscillum</i> sp.	0.0018		0.030
			NS11-12 marine group	0.0005		0.042
			NS7 marine group	0.0407		0.030
	Cyanobacteria	<i>Prochlorococcus</i>	0.1111	0.024	100% (7/7)	
1.4927			0.012			
Planctomycetes	CL500-3	0.3434	0.012	25% (6/24)		
		0.0009	0.018			
Alphaproteobacteria	SAR116 clade	0.0943	0.024	25% (1/4)		
		0.0109	0.018			
Deltaproteobacteria	Uncultured Rhodobacteraceae	0.0022	0.012	50% (4/8)		
		0.0022	0.018			
Gammaproteobacteria	GR-WP33-58	0.0008	0.012	35% (48/136)		
		0.0439	0.012			
Verrucomicrobia	OM60 clade	0.0628	0.018	No representative genome		
		0.0467	0.024			
Deltaproteobacteria	<i>Bdellovibrio</i> (OM27 clade)	0.0017	0.018	100% (5/5)		
		0.1218	0.012			
Gammaproteobacteria	KI89A clade	0.0030	0.012	100% (1/1)		
		0.0066	0.030			
Verrucomicrobia	Uncultured Puniceicoccaceae	0.0089	0.012	100% (1/1)		
		0.0020	0.012			
Verrucomicrobia	<i>Roseibacillus</i> sp.	0.0015	0.012	100% (1/1)		
		0.3558	0.024			
Actinobacteria	OCS155 marine group	0.1492	0.018	100% (1/1)		
		0.0012	0.018			
Actinobacteria	OCS155 marine group	0.6234	0.012	62% (13/21)		
		0.0430	0.012			
Flavobacteria	<i>Fluviicola</i> sp.	7.3527	0.024	100% (1/1)		
		0.0694	0.024			
Flavobacteria	<i>Formosa</i> sp.	0.0131	0.024	100% (2/2)		
		0.0052	0.018			
Flavobacteria	NS2b marine group	0.0031	0.018	100% (7/7)		
		0.0018	0.024			
Flavobacteria	NS9 marine group	0.0106	0.018	100% (1/1)		
		0.0068	0.018			
Flavobacteria	NS9 marine group	0.0103	0.018	100% (7/7)		
		1.9789	0.018			
Flavobacteria	NS9 marine group	1.4731	0.024	100% (7/7)		
		0.0061	0.024			
Flavobacteria	NS9 marine group	0.0051	0.018	100% (1/1)		
		0.0022	0.018			
Flavobacteria	<i>Owenweeksia</i> sp.	1.0545	0.012	100% (1/1)		
		0.9138	0.018			
Planctomycetes	CL500-3	0.2098	0.012	25% (1/4)		
		0.0327	0.012			
Alphaproteobacteria	Erythrobacteraceae	0.0122	0.012	100% (8/8)		
		0.0042	0.012			
Deltaproteobacteria	<i>Oceanicola</i> sp. YCWB25	0.0055	0.012	100% (1/1)		
		0.0055	0.012			
Deltaproteobacteria	Myxococcales	0.0055	0.012	100% (4/4)		
		0.0055	0.012			
Deltaproteobacteria	<i>Bdellovibrio</i> (OM27 clade)	0.0915	0.012	100% (5/5)		
		0.0915	0.012			
Verrucomicrobia	Puniceicoccaceae	0.0037	0.012	100% (1/1)		
		0.0030	0.012			
Verrucomicrobia	<i>Roseibacillus</i> sp.	0.7732	0.018	66% (11/16)		
		0.0030	0.018			
Verrucomicrobia	<i>Roseibacillus</i> sp.	0.0015	0.018	66% (11/16)		
		0.0050	0.012			
Verrucomicrobia	<i>Roseibacillus</i> sp.	0.0044	0.012	66% (11/16)		
		3.4850	0.012			