

Fig. S1

Klamath River watershed isolate LC16 is a member of the *Cyanobium gracile* cluster of *Synechococcus* sp. Consensus phylogenetic tree depicting relationships between ITS sequences from *Synechococcus* isolates, including selected marine *Synechococcus* and *Prochlorococcus* isolates that serve as hosts for characterized cyanomyophages (indicated next to host names). The indicated *Cyanobium gracile* cluster of mostly freshwater isolates follows the definition of Ernst et al. (2003). The tree was constructed by maximum likelihood analysis with a TN93 (Tamura-Nei) substitution model using the PhyML package (Guindon and Gascuel, 2003). Bootstrap values are indicated.

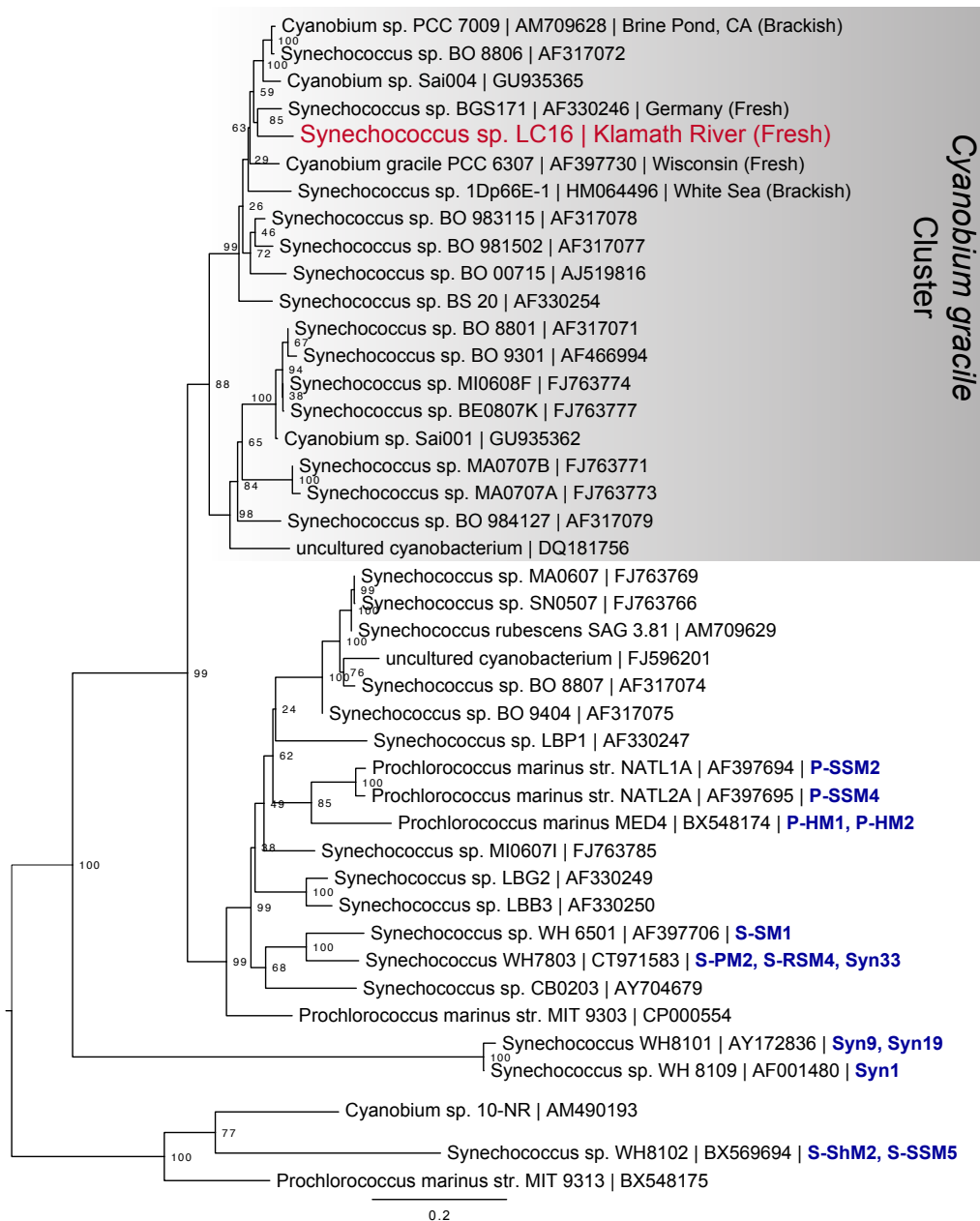


Fig. S2

Number of common genes among S-CRM01, marine cyanomyophages and T4-like phages. Gene similarities are based on BLAST hits with at least a 1e-5 E-value. Colors indicate levels of similarity.

	S-CRM01	Syn1	S-PM2	Syn19	syn9	S-SM2	S-SM1	S-ShM2	P-SSM2	P-SSM4	S-RSM4	P-RSM4	S-SSM5	Syn33	S-SSM7	KVP40	T4	Aeh1
S-CRM01	297																	
Syn1	66	232																
S-PM2	75	144	239															
Syn19	62	111	88	215														
syn9	64	117	97	164	228													
S-SM2	72	132	100	138	140	266												
S-SM1	65	110	93	173	166	130	234											
S-ShM2	63	120	94	147	161	110	152	229										
P-SSM2	73	105	86	105	104	131	104	101	329									
P-SSM4	60	96	85	141	121	98	130	120	116	198								
S-RSM4	66	142	125	109	118	109	121	110	114	91	235							
P-RSM4	64	101	88	144	142	104	152	136	125	152	105	238						
S-SSM5	65	111	94	172	159	119	187	150	124	138	114	176	225					
Syn33	62	124	90	161	161	111	161	171	109	129	116	143	154	227				
S-SSM7	66	102	93	105	100	131	107	105	168	111	105	124	110	101	318			
KVP40	37	34	36	34	35	35	37	40	36	34	34	37	36	34	39	380		
T4	34	32	34	35	37	36	39	40	34	34	32	37	37	34	32	96	272	
Aeh1	33	33	34	34	33	31	32	36	31	33	33	31	32	31	32	95	109	352

Fig. S3

Phylogenetic tree showing relationship of S-CRM01 *gp20* gene to other *gp20* sequences from freshwater or marine phage sources.

See Fig. S1 for tree construction details. Cyanophages whose genomes have been sequenced are labeled by name and with a red hexagon. The group designations are taken from Sullivan et al. (2008). EU715812, closest to S-CRM01, represents phage P-ShM1 (Sullivan et al. (2008)).

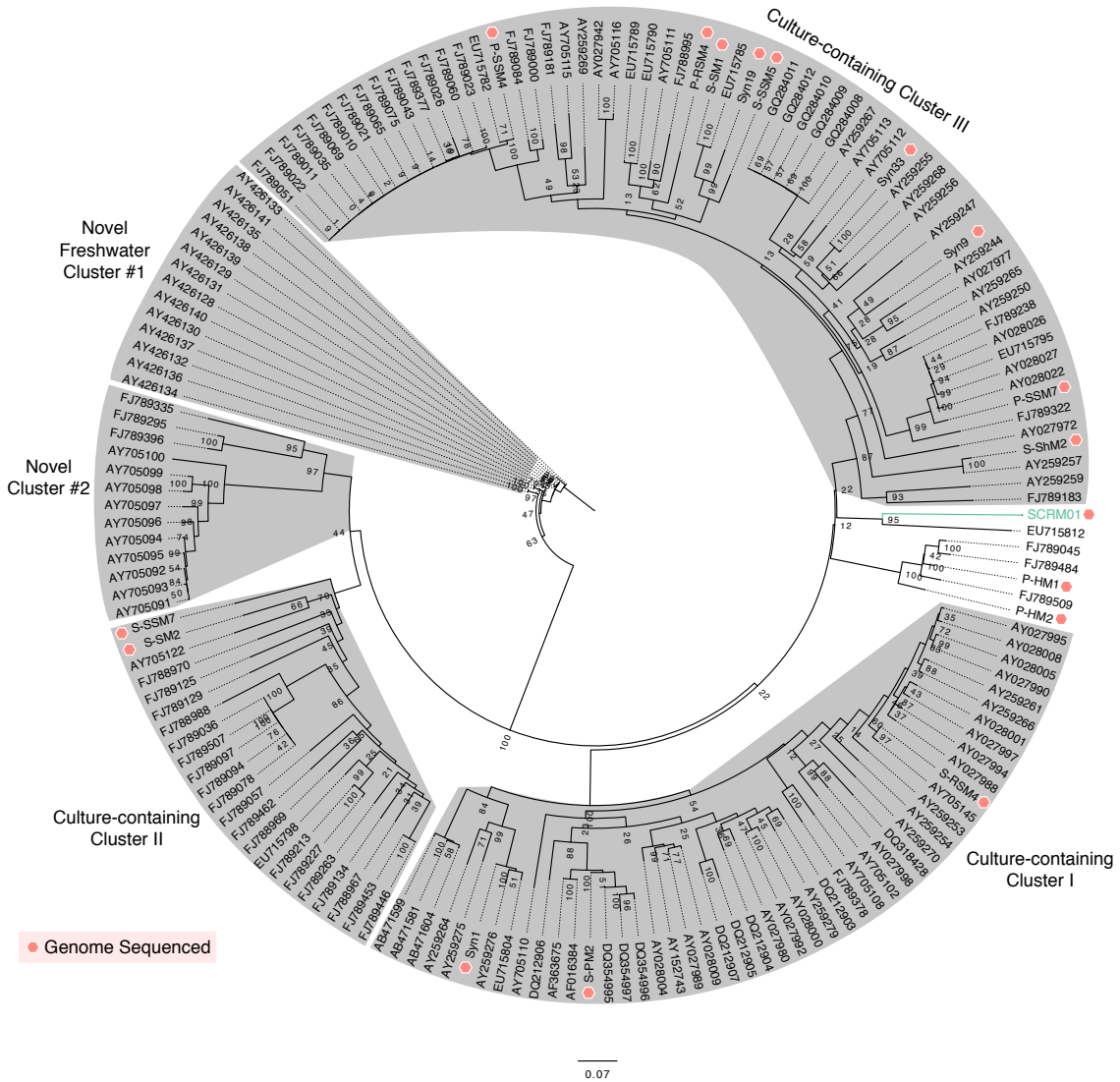


Fig. S4

Phylogenetic tree showing relationship of S-CRM01 *psbA* gene to other *psbA* sequences from freshwater or marine phage sources.

See Fig. S1 for tree construction details. Cyanophages whose genomes have been sequenced are labeled by name and with a red hexagon. The group designations are taken from Chénard and Suttle (2008). S-CRM01 sits between two a freshwater clade (EU258991-6 and EU404136) and a marine-dominated clade containing phage S-SSM7.

