



Supplemental Material to:

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**Evidence for the widespread distribution of
CRISPR-Cas system in the Phylum Cyanobacteria**

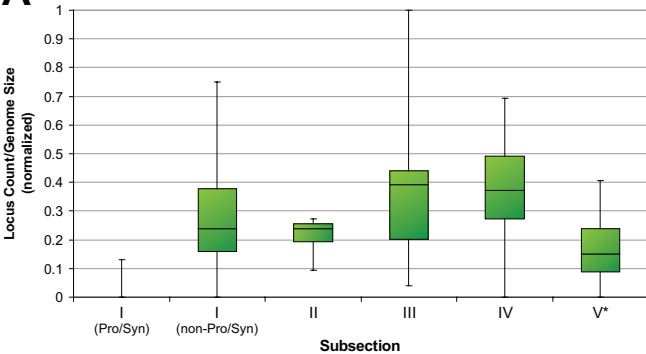
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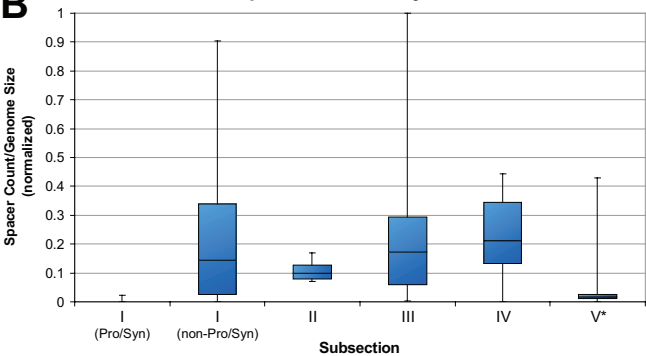
A

Normalized Locus Counts by Subsection



B

Normalized Spacer Counts by Subsection



Cluster
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Consensus Sequence

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Number of Sequences in Cluster	Number of Organisms with Cluster	Structure Predicted as Stem-loop	Rfam Hit
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refseq_genomic

NCBI GI	Domain	Top Hit Genome Name/Scaffold	Cyanobacterium Genome Name
256374160	Bacteria	<i>Actinosynnema mirum</i> DSM 43827 chromosome	<i>Synechocystis</i> sp. PCC 6308
211593993	Bacteria	<i>Aurantimonas manganoxydans</i> SI85-9A1 scf_1099451004081 genomic scaffold	<i>Oscillatoria</i> sp. PCC 10802
#####	Bacteria	<i>Burkholderiales</i> bacterium JOSHI_001 chromosome	<i>Synechococcus</i> sp. PCC 7002 plasmid pAQ6 <i>Synechococcus</i> sp. PCC 7002 plasmid pAQ6
403048614	Bacteria	<i>Clostridium</i> sp. JC122 JC122T genomic scaffold, scaffold00001	<i>Spirulina</i> sp. PCC 9445
134093294	Bacteria	<i>Herminiimonas arsenicoxydans</i> chromosome	<i>Pleurocapsa</i> sp. PCC 7327
148283997	Bacteria	<i>Orientia tsutsugamushi</i> str. Boryong	<i>Crinalium epipsammum</i> PCC 9333
319785620	Bacteria	<i>Pseudoxanthomonas suwonensis</i> 11-1 chromosome	<i>Microchaete</i> sp. PCC 7126
323356407	Bacteria	<i>Streptococcus vestibularis</i> ATCC 49124 genomic scaffold SCAFFOLD1	<i>Arthrospira platensis</i> NIES-39
313846893	Eukarya	<i>Anolis carolinensis</i> unplaced genomic scaffold, AnoCar2.0 chrUn0294	<i>Calothrix</i> sp. PCC 7507
347611422	Eukarya	<i>Oreochromis niloticus</i> unplaced genomic scaffold, Orenil1.0 scaffold00079	<i>Microcystis aeruginosa</i> PCC 7806
302809162	Eukarya	<i>Selaginella moellendorffii</i> unplaced genomic scaffold SELMOscaffold_72	<i>Calothrix</i> sp. PCC 6303
115304338	Viruses	Phormidium phage Pf-WMP4	<i>Leptolyngbya</i> sp. PCC 6306

env_nt

NCBI GI	Domain	Top Hit Genome Name/Scaffold	Cyanobacterium Genome Name
197449997	Metagenome	Freshwater sediment metagenome lwFormate_BCIX11460_g1	<i>Synechococcus</i> sp. PCC 7002 plasmid pAQ6 <i>Synechococcus</i> sp. PCC 7002 plasmid pAQ6
341908879	Metagenome	Hot springs metagenome ctg3753	<i>Synechococcus</i> sp. JA-2-3B'a(2-13)
341907640	Metagenome	Hot springs metagenome ctg5361	<i>Synechococcus</i> sp. JA-3-3Ab
341906534	Metagenome	Hot springs metagenome ctg6698	<i>Synechococcus</i> sp. JA-3-3Ab
341913414	Metagenome	Hot springs metagenome ctg6942	<i>Synechococcus</i> sp. JA-2-3B'a(2-13)
341913397	Metagenome	Hot springs metagenome ctg7937	<i>Synechococcus</i> sp. JA-3-3Ab <i>Synechococcus</i> sp. JA-3-3Ab <i>Synechococcus</i> sp. JA-3-3Ab <i>Synechococcus</i> sp. JA-3-3Ab
341905256	Metagenome	Hot springs metagenome ctg8228	<i>Synechococcus</i> sp. JA-3-3Ab
131104569	Metagenome	Marine metagenome ctg_1101667016826	<i>Calothrix</i> sp. PCC 6303
59978746	Metagenome	Metagenome 2662324_fasta.screen.Contig29817	<i>Nostoc</i> sp. PCC 7120
188050466	Metagenome	Microbial mat metagenome hsmat01_BHWG1956_x1	<i>Coleofasciculus chthonoplastes</i> PCC 7420 scf_1103659003789

188042672	Metagenome	Microbial mat metagenome hsmat01_BHWG6877_x1	<i>Coleofasciculus chthonoplastes</i> PCC 7420 scf_1103659003816
188042671	Metagenome	Microbial mat metagenome hsmat01_BHWG6877_y1	<i>Coleofasciculus chthonoplastes</i> PCC 7420 scf_1103659003816
188058376	Metagenome	Microbial mat metagenome hsmat02_BHWH11547_x1	<i>Coleofasciculus chthonoplastes</i> PCC 7420 scf_1103659003816
188058375	Metagenome	Microbial mat metagenome hsmat02_BHWH11547_y1	<i>Coleofasciculus chthonoplastes</i> PCC 7420 scf_1103659003816
188053976	Metagenome	Microbial mat metagenome hsmat02_BHWH14320_y1	<i>Coleofasciculus chthonoplastes</i> PCC 7420 scf_1103659003782
188063308	Metagenome	Microbial mat metagenome hsmat02_BHWH5666_y1	<i>Geitlerinema</i> sp. PCC 7105
188076061	Metagenome		<i>Coleofasciculus chthonoplastes</i> PCC 7420 scf_1103659003816
188071483	Metagenome	Microbial mat metagenome hsmat03_BHWI3562_y1	<i>Cylindrospermopsis raciborskii</i> CS-505 CS505_72
188067028	Metagenome	Microbial mat metagenome hsmat03_BHWI6525_x1	<i>Oscillatoria</i> sp. PCC 10802
364558569	Metagenome	Microbial mat metagenome MIS-Os_c1758	<i>Nostoc</i> sp. PCC 7107
364557817	Metagenome	Microbial mat metagenome MIS-Ph1_c587	<i>Tolypothrix</i> sp. PCC 9009
364547818	Metagenome	Microbial mat metagenome MIS-Unclassified_c11216	<i>Oscillatoria</i> sp. PCC 10802
364553671	Metagenome	Microbial mat metagenome MIS-Unclassified_c5315	<i>Microchaete</i> sp. PCC 7126
179808362	Metagenome	Stromatolite metagenome 54426327	<i>Leptolyngbya</i> sp. PCC 7104
179861119	Metagenome	Stromatolite metagenome 54461039	<i>Cylindrospermopsis raciborskii</i> CS-505 CS505_72
179831165	Metagenome	Stromatolite metagenome 54481267	<i>Cyanothece</i> sp. PCC 7425 plasmid pP742501
179800342	Metagenome	Stromatolite metagenome 54481595	<i>Fischerella</i> sp. JSC-11
gss			
NCBI GI	Domain	Top Hit Genome Name/Scaffold	Cyanobacterium Genome Name
315353639	Bacteria (uncultured)	1099893297741 M60 Mushroom Spring microbial mat library uncultured bacterium genomic clone MSU/Amplicon M60B005J21	<i>Synechococcus</i> sp. JA-3-3Ab

315341500	Bacteria (uncultured)	1119065707113 M60 Mushroom Spring microbial mat library uncultured bacterium genomic clone MSU/Amplicon M60B455A17	<i>Geitlerinema</i> sp. PCC 7105
329032525	Eukarya	P.MONODON-F2514E07.xg Tiger shrimp fosmid genomic library	<i>Calothrix</i> sp. PCC 6303

cyanobacterial plasmids

Scaffold Accession	Domain	Top Hit Genome Name/Scaffold	Cyanobacterium Genome Name
NC_009928	Bacteria	<i>Acaryochloris marina</i> MBIC11017 plasmid pREB3	<i>Fischerella</i> sp. JSC-11
NC_007412	Bacteria	<i>Anabaena variabilis</i> ATCC 29413 plasmid C	<i>Nostoc</i> sp. PCC 7524
NC_011880	Bacteria	<i>Cyanothece</i> sp. PCC 7425 plasmid pP742501	<i>Nostoc</i> sp. PCC 7107
NC_011885	Bacteria	<i>Cyanothece</i> sp. PCC 7425 plasmid pP742502	<i>Nostoc</i> sp. PCC 7107
NC_014533	Bacteria	<i>Cyanothece</i> sp. PCC 7822 plasmid Cy782201	<i>Coleofasciculus chthonoplastes</i> PCC 7420
NC_014533	Bacteria		<i>Leptolyngbya</i> sp. PCC 7104
NC_013160	Bacteria	<i>Cyanothece</i> sp. PCC 8802 plasmid pP880201	<i>Cyanothece</i> sp. PCC 8801
NC_010630	Bacteria	<i>Nostoc punctiforme</i> PCC 73102	<i>Calothrix</i> sp. PCC 7103
NC_010630	Bacteria	plasmid pNPUN03	<i>Calothrix</i> sp. PCC 7507
NC_003276	Bacteria	<i>Nostoc</i> sp. PCC 7120 plasmid pCC7120alpha	<i>Tolypothrix</i> sp. PCC 9009

Spacer Name	ID (%)	E-value
Syn6308DRAFT_JRD.1_8_10	94.87	2.E-08
Osc10802DRAFT_Contig7.7_32_195	96.88	1.E-06
NC_010480_1_36	89.47	3.E-09
NC_010480_1_44	89.47	3.E-09
Contig210_18_30	100.00	3.E-07
Ple7327_Contig355.1_5_31	92.68	4.E-07
Cepi9333_unknown1_1_32	97.30	7.E-08
Mic7126DRAFT_MPQ.3_15_12	94.44	1.E-06
AP011615_15_5	100.00	3.E-07
Contig86_12_49	100.00	9.E-07
MICAP_embl_AM778913_AM778913.73_1_65	100.00	1.E-12
Csp6303_Contig662_2_6	100.00	6.E-08
LepboDRAFT LPC.2 2 24	97.14	2.E-08

Spacer Name	ID (%)	E-value
NC_010480_1_36	89.47	6.E-09
NC_010480_1_44	89.47	6.E-09
NC_007776_1_3	97.06	1.E-07
NC_007775_7_1	100.00	9.E-12
NC_007775_9_9	99.91	0.E+00
NC_007776_5_1	100.00	9.E-12
NC_007775_7_16	100.00	6.E-13
NC_007775_7_15	100.00	2.E-13
NC_007775_7_14	100.00	1.E-10
NC_007775_7_13	97.67	8.E-13
NC_007775_2_33	100.00	2.E-07
Csp6303_Contig662_2_6	100.00	1.E-07
NC_003272_13_8	97.44	1.E-09
NZ_DS989880_1_19	89.05	2.E-115

NZ_DS989846_5_9	100.00	3.E-07
NZ_DS989846_5_5	91.07	7.E-11
NZ_DS989846_4_1	89.29	2.E-08
NZ_DS989846_5_7	96.23	3.E-16
NZ_DS989846_5_3	91.07	7.E-11
NZ_DS989846_5_2	92.86	3.E-13
NZ_DS989846_4_2	88.79	3.E-24
NZ_DS989846_4_3	88.68	1.E-06
NZ_DS989846_4_4	91.30	3.E-07
NZ_DS989861_1_5	86.14	2.E-32
Gei7105DRAFT_GPC.5_13_3	97.50	2.E-09
NZ_DS989846_5_4	96.17	3.E-94
NZ_DS989846_5_6	92.45	2.E-11
NZ_DS989846_5_8	92.86	3.E-13
NZ_ACYA01000074_1_25	83.17	2.E-07
Osc10802DRAFT_Contig7.7_15_8	95.35	1.E-08
Nsp7107_Contig281_23_21	96.97	5.E-07
Contig652_3_2	100.00	3.E-09
Osc10802DRAFT_Contig7.7_30_3	81.75	6.E-10
Mic7126DRAFT_MPQ.3_8_30	97.22	8.E-09
Lepto7104DRAFT_LPD.1_4_4	90.32	2.E-10
NZ_ACYA01000074_1_33	94.59	6.E-07
NC_011880_2_6	91.67	4.E-26
Contig115_2_44	95.29	4.E-29

Spacer Name	ID (%)	E-value
NC_007775_4_1	100.00	7.E-08

Gei7105DRAFT_GPC.5_13_3	91.67	1.E-06
Csp6303_Contig662_2_6	100.00	1.E-06

Spacer Name	ID (%)	E-value
Contig115_2_44	84.80	6.E-19
Nos7524_Contig213.1_2_35	95.12	2.E-10
Nsp7107_Contig281_11_20	79.31	7.E-22
Nsp7107_Contig281_23_2	88.52	1.E-08
NZ_DS989880_1_19	93.48	1.E-06
Lepto7104DRAFT_LPD.1_4_4	90.74	3.E-09
NC_011726_8_1	100.00	1.E-15
Cal7103DRAFT_CPM.6_4_3	84.21	2.E-08
Contig86_8_78	100.00	8.E-13
Contig652_3_2	100.00	6.E-20