

1 **SUPPLEMENTARY MATERIAL**

2 Supplementary tables

3 Table S1. Primers used in this study

	Primer name	Primers (5' – 3')	Reference
16S rRNA	V3F(341)	CCTACGGGAGGCAGCAG	(Klindworth et al., 2013)
	V4R(515)	TTACCGCGGCKGCTGGCAC	
Universal tags	CS1	ACACTGACGACATGGTTCTACA	
	CS2	TACGGTAGCAGAGACTTGGTCT	

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5 Table S2. Statistics from Dada2

Sample	Input	Filtered	Percentage of input passed filter	Denoised	Non- chimeric	Percentage of input non-chimeric
T[0]	107763	82964	77.0	69909	26267	24.4
T[0]	94175	72127	76.6	60914	22193	23.6
T[0]	97752	74775	76.5	66055	26182	26.8
T[R]	74478	49176	66.0	46514	24734	33.2
T[R]	73141	47935	65.5	45285	23453	32.1
T[R]	124251	81476	65.6	78429	49562	39.9
T[R]	102147	78114	76.5	68254	25093	24.6
T[R]	110406	85645	77.6	75962	28975	26.2
T[1]	94247	72267	76.7	63744	26572	28.2
T[1]	107731	83548	77.6	73493	27303	25.3
T[1]	96982	75308	77.7	67566	26508	27.3
T[1]	95525	71252	74.6	63172	22981	24.1
T[1]	90500	67764	74.9	64292	27474	30.4
T[2]	84648	63857	75.4	60608	25771	30.4
T[2]	96778	75662	78.2	66995	26245	27.1
T[2]	83749	63335	75.6	56952	25227	30.1
T[2]	92648	71470	77.1	65011	26239	28.3
T[2]	98388	77704	79.0	69728	26908	27.4
T[3]	92219	70652	76.6	61225	24567	26.6
T[3]	88140	67749	76.9	63081	28039	31.8
T[3]	85527	66739	78.0	58521	23282	27.2
T[3]	99090	75504	76.2	65145	23381	23.6
T[3]	102014	75994	74.5	65160	23004	22.6

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8 Table S3. List of the genes used for function prediction ordered by groups and subgroups.

Group	Metabolic traits	KEGG ID	Function
DNA conservation	Putative DNA-binding protein	K02524	K10; DNA binding protein (fs(1)K10, female sterile(1)K10)
	Putative DNA-binding protein	K03111	ssb; single-strand DNA-binding protein
	Putative DNA-binding protein	K03530	hupB; DNA-binding protein HU-beta
	Putative DNA-binding protein	K03622	ssh10b; archaea-specific DNA-binding protein
	Putative DNA-binding protein	K03746	hns; DNA-binding protein H-NS
	Putative DNA-binding protein	K04047	dps; starvation-inducible DNA-binding protein
	Putative DNA-binding protein	K04494	CHD8, HELSNF1; chromodomain helicase DNA binding protein 8 [EC:3.6.4.12]
	Putative DNA-binding protein	K04680	ID1; DNA-binding protein inhibitor ID1
	Putative DNA-binding protein	K05516	cbpA; curved DNA-binding protein
	Putative DNA-binding protein	K05732	ARHGAP35, GRLF1; glucocorticoid receptor DNA-binding factor 1
	Putative DNA-binding protein	K05787	hupA; DNA-binding protein HU-alpha
	Putative DNA-binding protein	K09061	GCF, C2orf3; GC-rich sequence DNA-binding factor
	Putative DNA-binding protein	K09423	BAS1; Myb-like DNA-binding protein BAS1
	Putative DNA-binding protein	K09424	REB1; Myb-like DNA-binding protein REB1
	Putative DNA-binding protein	K09425	K09425; Myb-like DNA-binding protein FlbD
	Putative DNA-binding protein	K09426	RAP1; Myb-like DNA-binding protein RAP1
	Putative DNA-binding protein	K10140	DDB2; DNA damage-binding protein 2
	Putative DNA-binding protein	K10610	DDB1; DNA damage-binding protein 1
	Putative DNA-binding protein	K10728	TOPBP1; topoisomerase (DNA) II binding protein 1
	Putative DNA-binding protein	K10748	tus, tau; DNA replication terminus site-binding protein
	Histone-like protein	K10752	RBBP4, HAT2, CAF1, MIS16; histone-binding protein RBBP4
	Putative DNA-binding protein	K10979	ku; DNA end-binding protein Ku
	Putative DNA-binding protein	K11367	CHD1; chromodomain-helicase-DNA-binding protein 1 [EC:3.6.4.12]
	Histone-like protein	K11495	CENPA; histone H3-like centromeric protein A

Putative DNA-binding protein	K11574	CBF2, CBF3A, CTF14; centromere DNA-binding protein complex CBF3 subunit A
Putative DNA-binding protein	K11575	CEP3, CBF3B; centromere DNA-binding protein complex CBF3 subunit B
Putative DNA-binding protein	K11576	CTF13, CBF3C; centromere DNA-binding protein complex CBF3 subunit C
Putative DNA-binding protein	K11642	CHD3, MI2A; chromodomain-helicase-DNA-binding protein 3 [EC:3.6.4.12]
Putative DNA-binding protein	K11643	CHD4, MI2B; chromodomain-helicase-DNA-binding protein 4 [EC:3.6.4.12]
Histone-like protein	K11659	RBBP7; histone-binding protein RBBP7
Putative DNA-binding protein	K11685	stpA; DNA-binding protein StpA
Putative DNA-binding protein	K12965	ZBP1, DAI; Z-DNA binding protein 1
Putative DNA-binding protein	K13102	KIN; DNA/RNA-binding protein KIN17
Putative DNA-binding protein	K13211	GCFC; GC-rich sequence DNA-binding factor
Putative DNA-binding protein	K14435	CHD5; chromodomain-helicase-DNA-binding protein 5 [EC:3.6.4.12]
Putative DNA-binding protein	K14436	CHD6; chromodomain-helicase-DNA-binding protein 6 [EC:3.6.4.12]
Putative DNA-binding protein	K14437	CHD7; chromodomain-helicase-DNA-binding protein 7 [EC:3.6.4.12]
Putative DNA-binding protein	K14438	CHD9; chromodomain-helicase-DNA-binding protein 9 [EC:3.6.4.12]
Putative DNA-binding protein	K14507	ORCA2_3; AP2-domain DNA-binding protein ORCA2/3
Histone-like protein	K15719	NCOAT, MGEA5; protein O-GlcNAcase / histone acetyltransferase [EC:3.2.1.169 2.3.1.48]
Putative DNA-binding protein	K16640	ssh7; DNA-binding protein 7 [EC:3.1.27.-]
Putative DNA-binding protein	K17693	ID2; DNA-binding protein inhibitor ID2
Putative DNA-binding protein	K17694	ID3; DNA-binding protein inhibitor ID3
Putative DNA-binding protein	K17695	ID4; DNA-binding protein inhibitor ID4
Putative DNA-binding protein	K17696	EMC; DNA-binding protein inhibitor ID, other
Histone-like protein	K18710	SLBP; histone RNA hairpin-binding protein
Putative DNA-binding protein	K18946	gp32, ssb; single-stranded DNA-binding protein
Putative DNA-binding protein	K19442	ICP8, DBP, UL29; Simplexvirus major DNA-binding protein
Histone-like protein	K19799	RPH1; DNA damage-responsive transcriptional repressor / [histone H3]-trimethyl-L-lysine36 demethylase [EC:1.14.11.69]
Putative DNA-binding protein	K20091	CHD2; chromodomain-helicase-DNA-binding protein 2 [EC:3.6.4.12]

	Putative DNA-binding protein	K20092	CHD1L; chromodomain-helicase-DNA-binding protein 1-like [EC:3.6.4.12]
	Putative DNA-binding protein	K22592	AHDC1; AT-hook DNA-binding motif-containing protein 1
	Putative DNA-binding protein	K23225	SATB1; DNA-binding protein SATB1
	Putative DNA-binding protein	K23226	SATB2; DNA-binding protein SATB2
	Putative DNA-binding protein	K23600	TARDBP, TDP43; TAR DNA-binding protein 43
DNA repair	DNA polymerase PolA (COG0258)	K02320	POLA1; DNA polymerase alpha subunit A [EC:2.7.7.7]
	DNA polymerase PolA (COG0258)	K02321	POLA2; DNA polymerase alpha subunit B
	DNA polymerase PolA (COG0258)	K02335	polA; DNA polymerase I [EC:2.7.7.7]
	DNA polymerase IV	K02346	dinB; DNA polymerase IV [EC:2.7.7.7]
	Exodeoxyribonuclease VII	K03601	xseA; exodeoxyribonuclease VII large subunit [EC:3.1.11.6]
	Exodeoxyribonuclease VII	K03602	xseB; exodeoxyribonuclease VII small subunit [EC:3.1.11.6]
	DNA polymerase IV	K04479	dbh; DNA polymerase IV (archaeal DinB-like DNA polymerase) [EC:2.7.7.7]
	Exodeoxyribonuclease VII	K10906	recE; exodeoxyribonuclease VIII [EC:3.1.11.-]
	DNA polymerase IV	K10981	POL4; DNA polymerase IV [EC:2.7.7.7]
	DNA polymerase IV	K16250	NRPD1; DNA-directed RNA polymerase IV subunit 1 [EC:2.7.7.6]
Lithotrophy	DNA polymerase IV	K16252	NRPD2, NRPE2; DNA-directed RNA polymerase IV and V subunit 2 [EC:2.7.7.6]
	DNA polymerase IV	K16253	NRPD7, NRPE7; DNA-directed RNA polymerase IV and V subunit 7
	NiFe hydrogenase	K00437	hydB ; [NiFe] hydrogenase large subunit [EC:1.12.2.1]
	NiFe hydrogenase	K02587	nifE; nitrogenase molybdenum-cofactor synthesis protein NifE
	CO-dehydrogenase CoxM & CoxS	K03518	coxS; aerobic carbon-monoxide dehydrogenase small subunit [EC:1.2.5.3]
	CO-dehydrogenase CoxM & CoxS	K03519	coxM, cutM; aerobic carbon-monoxide dehydrogenase medium subunit [EC:1.2.5.3]
	CO-dehydrogenase large subunit (coxL) Form I	K03520	CoxL, cutL ; aerobic carbon-monoxide dehydrogenase large subunit [EC:1.2.5.3]
	NiFe hydrogenase	K05586	hoxE ; bidirectional [NiFe] hydrogenase diaphorase subunit [EC:7.1.1.2]
	NiFe hydrogenase	K05587	hoxF; bidirectional [NiFe] hydrogenase diaphorase subunit [EC:7.1.1.2]
	NiFe hydrogenase	K05588	hoxU ; bidirectional [NiFe] hydrogenase diaphorase subunit [EC:7.1.1.2]
	SOX sulfur-oxidation system	K17218	sqr; sulfide:quinone oxidoreductase [EC:1.8.5.4]

	SOX sulfur-oxidation system	K17222	soxA; L-cysteine S-thiosulfotransferase [EC:2.8.5.2]
	SOX sulfur-oxidation system	K17223	soxX; L-cysteine S-thiosulfotransferase [EC:2.8.5.2]
	SOX sulfur-oxidation system	K17224	soxB; S-sulfosulfanyl-L-cysteine sulfohydrolase [EC:3.1.6.20]
	SOX sulfur-oxidation system	K17225	soxC ; sulfane dehydrogenase subunit SoxC
	SOX sulfur-oxidation system	K17226	soxY; sulfur-oxidizing protein SoxY
	SOX sulfur-oxidation system	K17227	soxZ; sulfur-oxidizing protein SoxZ
	NiFe hydrogenase	K18005	hoxF; [NiFe] hydrogenase diaphorase moiety large subunit [EC:1.12.1.2]
	NiFe hydrogenase	K18006	hoxU; [NiFe] hydrogenase diaphorase moiety small subunit [EC:1.12.1.2]
	NiFe hydrogenase	K18008	hydA; [NiFe] hydrogenase small subunit [EC:1.12.2.1]
	Propane monooxygenase (soluble)	K18223	prmA ; propane 2-monooxygenase large subunit [EC:1.14.13.227]
	Propane monooxygenase (soluble)	K18224	prmC; propane 2-monooxygenase small subunit [EC:1.14.13.227]
	Propane monooxygenase (soluble)	K18225	prmB; propane monooxygenase reductase component [EC:1.18.1.-]
	Propane monooxygenase (soluble)	K18226	prmD; propane monooxygenase coupling protein
	SOX sulfur-oxidation system	K22622	soxD; S-disulfanyl-L-cysteine oxidoreductase SoxD [EC:1.8.2.6]
	SOX sulfur-oxidation system	K24007	soxD; cytochrome aa3-type oxidase subunit SoxD
	SOX sulfur-oxidation system	K24008	soxC; cytochrome aa3-type oxidase subunit III
	SOX sulfur-oxidation system	K24009	soxB; cytochrome aa3-type oxidase subunit I [EC:7.1.1.4]
	SOX sulfur-oxidation system	K24010	soxA; cytochrome aa3-type oxidase subunit II [EC:7.1.1.4]
	SOX sulfur-oxidation system	K24011	soxM; cytochrome aa3-type oxidase subunit I/III [EC:7.1.1.4]
Organotrophy	ABC sugar transporters	K02025	ABC.MS.P; multiple sugar transport system permease protein
	ABC sugar transporters	K02026	ABC.MS.P1; multiple sugar transport system permease protein
	ABC sugar transporters	K02027	ABC.MS.S; multiple sugar transport system substrate-binding protein
	ABC sugar transporters	K02056	ABC.SS.A; simple sugar transport system ATP-binding protein [EC:7.5.2.-]
	ABC sugar transporters	K02057	ABC.SS.P; simple sugar transport system permease protein
	ABC sugar transporters	K02058	ABC.SS.S; simple sugar transport system substrate-binding protein

PTS sugar importers	K02777	crp; sugar PTS system EIIA component [EC:2.7.1.-]
Amino acid transporter	K03293	TC.AAT; amino acid transporter, AAT family
Peptide transporter	K03305	TC.POT; proton-dependent oligopeptide transporter, POT family
Amino acid transporter	K03311	TC.LIVCS; branched-chain amino acid:cation transporter, LIVCS family
Carboxylate transporters	K03326	TC.DCUC, dcuC, dcuD; C4-dicarboxylate transporter, DcuC family
Amino acid transporter	K03450	SLC7A; solute carrier family 7 (L-type amino acid transporter), other
Glycosyl hydrolases	K04844	ycjT; hypothetical glycosyl hydrolase [EC:3.2.1.-]
Amino acid transporter	K05048	SLC6A15S; solute carrier family 6 (neurotransmitter transporter, amino acid/orphan) member 15/16/17/18/20
Amino acid transporter	K05615	SLC1A4, SATT; solute carrier family 1 (neutral amino acid transporter), member 4
Amino acid transporter	K05616	SLC1A5; solute carrier family 1 (neutral amino acid transporter), member 5
Amino acid transporter	K07084	yuiF; putative amino acid transporter
Carboxylate transporters	K07791	dcuA ; anaerobic C4-dicarboxylate transporter DcuA
Carboxylate transporters	K07792	dcuB; anaerobic C4-dicarboxylate transporter DcuB
ABC sugar transporters	K10546	ABC.GGU.S, chvE; putative multiple sugar transport system substrate-binding protein
ABC sugar transporters	K10547	ABC.GGU.P, gguB; putative multiple sugar transport system permease protein
ABC sugar transporters	K10548	ABC.GGU.A, gguA; putative multiple sugar transport system ATP-binding protein [EC:7.5.2.-]
Carboxylate transporters	K11689	dctQ ; C4-dicarboxylate transporter, DctQ subunit
Carboxylate transporters	K11690	dctM; C4-dicarboxylate transporter, DctM subunit
Amino acid transporter	K13576	SLC38A3, SNAT3; solute carrier family 38 (sodium-coupled neutral amino acid transporter), member 3
Carboxylate transporters	K13577	SLC25A10, DIC; solute carrier family 25 (mitochondrial dicarboxylate transporter), member 10
Amino acid transporter	K13780	SLC7A5, LAT1; solute carrier family 7 (L-type amino acid transporter), member 5
Amino acid transporter	K13781	SLC7A8, LAT2; solute carrier family 7 (L-type amino acid transporter), member 8
Amino acid transporter	K13782	SLC7A10, ASC1; solute carrier family 7 (L-type amino acid transporter), member 10
Amino acid transporter	K13863	SLC7A1, ATRC1; solute carrier family 7 (cationic amino acid transporter), member 1
Amino acid transporter	K13864	SLC7A2, ATRC2; solute carrier family 7 (cationic amino acid transporter), member 2

Amino acid transporter	K13865	SLC7A3, ATRC3; solute carrier family 7 (cationic amino acid transporter), member 3
Amino acid transporter	K13866	SLC7A4; solute carrier family 7 (cationic amino acid transporter), member 4
Amino acid transporter	K13867	SLC7A7; solute carrier family 7 (L-type amino acid transporter), member 7
Amino acid transporter	K13868	SLC7A9, BAT1; solute carrier family 7 (L-type amino acid transporter), member 9
Amino acid transporter	K13869	SLC7A11; solute carrier family 7 (L-type amino acid transporter), member 11
Amino acid transporter	K13870	SLC7A13, AGT1; solute carrier family 7 (L-type amino acid transporter), member 13
Amino acid transporter	K13871	SLC7A14; solute carrier family 7 (cationic amino acid transporter), member 14
Amino acid transporter	K13872	SLC7A6; solute carrier family 7 (L-type amino acid transporter), member 6
Peptide transporter	K14206	SLC15A1, PEPT1; solute carrier family 15 (oligopeptide transporter), member 1
Amino acid transporter	K14207	SLC38A2, SNAT2; solute carrier family 38 (sodium-coupled neutral amino acid transporter), member 2
Amino acid transporter	K14209	SLC36A, PAT; solute carrier family 36 (proton-coupled amino acid transporter)
Amino acid transporter	K14210	SLC3A1, RBAT; solute carrier family 3 (neutral and basic amino acid transporter), member 1
Carboxylate transporters	K14388	SLC5A8_12, SMCT; solute carrier family 5 (sodium-coupled monocarboxylate transporter), member 8/12
Carboxylate transporters	K14445	SLC13A2_3_5; solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2/3/5
Peptide transporter	K14637	SLC15A2, PEPT2; solute carrier family 15 (oligopeptide transporter), member 2
Peptide transporter	K14638	SLC15A3_4, PHT; solute carrier family 15 (peptide/histidine transporter), member 3/4
Amino acid transporter	K14990	SLC38A1, SNAT1, GLNT; solute carrier family 38 (sodium-coupled neutral amino acid transporter), member 1
Amino acid transporter	K14991	SLC38A4, SNAT4; solute carrier family 38 (sodium-coupled neutral amino acid transporter), member 4
Amino acid transporter	K14992	SLC38A5, SNAT5; solute carrier family 38 (sodium-coupled neutral amino acid transporter), member 5
Amino acid transporter	K14993	SLC38A6, SNAT6; solute carrier family 38 (sodium-coupled neutral amino acid transporter), member 6
Amino acid transporter	K14994	SLC38A7_8; solute carrier family 38 (sodium-coupled neutral amino acid transporter), member 7/8
Amino acid transporter	K14995	SLC38A9; solute carrier family 38 (sodium-coupled neutral amino acid transporter), member 9

	Amino acid transporter	K14996	SLC38A10; solute carrier family 38 (sodium-coupled neutral amino acid transporter), member 10
	Amino acid transporter	K14997	SLC38A11; solute carrier family 38 (sodium-coupled neutral amino acid transporter), member 11
	Amino acid transporter	K15015	SLC32A, VGAT; solute carrier family 32 (vesicular inhibitory amino acid transporter)
	Carboxylate transporters	K15110	SLC25A21, ODC; solute carrier family 25 (mitochondrial 2-oxodicarboxylate transporter), member 21
	Amino acid transporter	K16261	YAT; yeast amino acid transporter
	Amino acid transporter	K16263	yjeH; amino acid efflux transporter
	Peptide transporter	K17938	sbmA, bacA; peptide/bleomycin uptake transporter
Phototrophy	RuBisCO	K01601	rbcl; ribulose-bisphosphate carboxylase large chain [EC:4.1.1.39]
	Chlorophyll synthesis	K01669	phrB; deoxyribodipyrimidine photo-lyase [EC:4.1.99.3]
	Chlorophyll synthesis	K02689	psaA; photosystem I P700 chlorophyll a apoprotein A1
	Chlorophyll synthesis	K02690	psaB; photosystem I P700 chlorophyll a apoprotein A2
	Chlorophyll synthesis	K02691	psaC; photosystem I subunit VII
	Chlorophyll synthesis	K02692	psaD; photosystem I subunit II
	Chlorophyll synthesis	K02693	psaE; photosystem I subunit IV
	Chlorophyll synthesis	K02694	psaF; photosystem I subunit III
	Chlorophyll synthesis	K02695	psaH; photosystem I subunit VI
	Chlorophyll synthesis	K02696	psaI; photosystem I subunit VIII
	Chlorophyll synthesis	K02697	psaJ; photosystem I subunit IX
	Chlorophyll synthesis	K02698	psaK; photosystem I subunit X
	Chlorophyll synthesis	K02699	psaL; photosystem I subunit XI
	Chlorophyll synthesis	K02700	psaM; photosystem I subunit XII
	Chlorophyll synthesis	K02701	psaN; photosystem I subunit PsaN
	Chlorophyll synthesis	K02702	psaX; photosystem I 4.8kDa protein
	Chlorophyll synthesis	K02703	psbA; photosystem II P680 reaction center D1 protein [EC:1.10.3.9]
	Chlorophyll synthesis	K02704	psbB; photosystem II CP47 chlorophyll apoprotein

Chlorophyll synthesis	K02705	psbC; photosystem II CP43 chlorophyll apoprotein
Chlorophyll synthesis	K02706	psbD; photosystem II P680 reaction center D2 protein [EC:1.10.3.9]
Chlorophyll synthesis	K02707	psbE; photosystem II cytochrome b559 subunit alpha
Chlorophyll synthesis	K02708	psbF; photosystem II cytochrome b559 subunit beta
Chlorophyll synthesis	K02709	psbH; photosystem II PsbH protein
Chlorophyll synthesis	K02710	psbI; photosystem II PsbI protein
Chlorophyll synthesis	K02711	psbJ; photosystem II PsbJ protein
Chlorophyll synthesis	K02712	psbK; photosystem II PsbK protein
Chlorophyll synthesis	K02713	psbL; photosystem II PsbL protein
Chlorophyll synthesis	K02714	psbM; photosystem II PsbM protein
Chlorophyll synthesis	K02716	psbO; photosystem II oxygen-evolving enhancer protein 1
Chlorophyll synthesis	K02717	psbP; photosystem II oxygen-evolving enhancer protein 2
Chlorophyll synthesis	K02718	psbT; photosystem II PsbT protein
Chlorophyll synthesis	K02719	psbU; photosystem II PsbU protein
Chlorophyll synthesis	K02720	psbV; photosystem II cytochrome c550
Chlorophyll synthesis	K02721	psbW; photosystem II PsbW protein
Chlorophyll synthesis	K02722	psbX; photosystem II PsbX protein
Chlorophyll synthesis	K02723	psbY; photosystem II PsbY protein
Chlorophyll synthesis	K02724	psbZ; photosystem II PsbZ protein
Chlorophyll synthesis	K03157	LTB, TNFC; lymphotoxin beta (TNF superfamily, member 3)
Chlorophyll synthesis	K03159	TNFRSF3, LTBR; lymphotoxin beta receptor TNFR superfamily member 3
Chlorophyll synthesis	K03541	psbR; photosystem II 10kDa protein
Chlorophyll synthesis	K03542	psbS; photosystem II 22kDa protein
Chlorophyll synthesis	K03716	splB; spore photoproduct lyase [EC:4.1.99.14]
Chlorophyll synthesis	K05468	LTA, TNFB; lymphotoxin alpha (TNF superfamily, member 1)
Chlorophyll synthesis	K06315	splA; transcriptional regulator of the spore photoproduct lyase operon
Chlorophyll synthesis	K06876	K06876; deoxyribodipyrimidine photolyase-related protein

	Chlorophyll synthesis	K08901	psbQ; photosystem II oxygen-evolving enhancer protein 3
	Chlorophyll synthesis	K08902	psb27; photosystem II Psb27 protein
	Chlorophyll synthesis	K08903	psb28; photosystem II 13kDa protein
	Chlorophyll synthesis	K08904	psb28-2; photosystem II Psb28-2 protein
	Chlorophyll synthesis	K08905	psaG; photosystem I subunit V
	Chlorophyll synthesis	K08928	pufL; photosynthetic reaction center L subunit
	Chlorophyll synthesis	K08929	pufM; photosynthetic reaction center M subunit
	Chlorophyll synthesis	K08940	pscA; photosystem P840 reaction center large subunit
	Chlorophyll synthesis	K08941	pscB; photosystem P840 reaction center iron-sulfur protein
	Chlorophyll synthesis	K08942	pscC; photosystem P840 reaction center cytochrome c551
	Chlorophyll synthesis	K08943	pscD; photosystem P840 reaction center protein PscD
	Chlorophyll synthesis	K11524	pixI ; positive phototaxis protein PixI
	Chlorophyll synthesis	K13991	puhA; photosynthetic reaction center H subunit
	Chlorophyll synthesis	K13992	pufC; photosynthetic reaction center cytochrome c subunit
	Chlorophyll synthesis	K13994	pufX; photosynthetic reaction center PufX protein
	Chlorophyll synthesis	K14332	psaO; photosystem I subunit PsaO
	Chlorophyll synthesis	K19016	IMPG1, SPACR; interphotoreceptor matrix proteoglycan 1
	Chlorophyll synthesis	K19017	IMPG2, SPACRCAN; interphotoreceptor matrix proteoglycan 2
	Chlorophyll synthesis	K20715	PHOT; phototropin [EC:2.7.11.1]
	Chlorophyll synthesis	K22464	FAP; fatty acid photodecarboxylase [EC:4.1.1.106]
	Chlorophyll synthesis	K22619	Aequorin; calcium-regulated photoprotein [EC:1.13.12.24]
	Chlorophyll synthesis	K24165	PCARE; photoreceptor cilium actin regulator
ROS-damage prevention	Cytochrome C oxidase	K00404	ccoN; cytochrome c oxidase cbb3-type subunit I [EC:7.1.1.9]
	Cytochrome C oxidase	K00405	ccoO; cytochrome c oxidase cbb3-type subunit II
	Cytochrome C oxidase	K00406	ccoP; cytochrome c oxidase cbb3-type subunit III
	Cytochrome C oxidase	K00407	ccoQ; cytochrome c oxidase cbb3-type subunit IV
	Cytochrome bd ubiquinol oxidase	K00424	cydX; cytochrome bd-I ubiquinol oxidase subunit X [EC:7.1.1.7]

Cytochrome C oxidase	K00424	cydX; cytochrome bd-I ubiquinol oxidase subunit X [EC:7.1.1.7]
Cytochrome bd ubiquinol oxidase	K00425	cydA; cytochrome bd ubiquinol oxidase subunit I [EC:7.1.1.7]
Cytochrome C oxidase	K00425	cydA; cytochrome bd ubiquinol oxidase subunit I [EC:7.1.1.7]
Cytochrome bd ubiquinol oxidase	K00426	cydB; cytochrome bd ubiquinol oxidase subunit II [EC:7.1.1.7]
Cytochrome C oxidase	K00426	cydB; cytochrome bd ubiquinol oxidase subunit II [EC:7.1.1.7]
Cytochrome C oxidase	K00428	E1.11.1.5; cytochrome c peroxidase [EC:1.11.1.5]
Cytochrome C oxidase	K02256	COX1; cytochrome c oxidase subunit 1 [EC:7.1.1.9]
Cytochrome C oxidase	K02258	COX11, ctaG; cytochrome c oxidase assembly protein subunit 11
Cytochrome C oxidase	K02259	COX15, ctaA; cytochrome c oxidase assembly protein subunit 15
Cytochrome C oxidase	K02260	COX17; cytochrome c oxidase assembly protein subunit 17
Cytochrome C oxidase	K02261	COX2; cytochrome c oxidase subunit 2
Cytochrome C oxidase	K02262	COX3; cytochrome c oxidase subunit 3
Cytochrome C oxidase	K02263	COX4; cytochrome c oxidase subunit 4
Cytochrome C oxidase	K02264	COX5A; cytochrome c oxidase subunit 5a
Cytochrome C oxidase	K02265	COX5B; cytochrome c oxidase subunit 5b
Cytochrome C oxidase	K02266	COX6A; cytochrome c oxidase subunit 6a
Cytochrome C oxidase	K02267	COX6B; cytochrome c oxidase subunit 6b
Cytochrome C oxidase	K02268	COX6C; cytochrome c oxidase subunit 6c
Cytochrome C oxidase	K02269	COX7; cytochrome c oxidase subunit 7
Cytochrome C oxidase	K02270	COX7A; cytochrome c oxidase subunit 7a
Cytochrome C oxidase	K02271	COX7B; cytochrome c oxidase subunit 7b
Cytochrome C oxidase	K02272	COX7C; cytochrome c oxidase subunit 7c
Cytochrome C oxidase	K02273	COX8; cytochrome c oxidase subunit 8
Cytochrome C oxidase	K02274	coxA, ctaD; cytochrome c oxidase subunit I [EC:7.1.1.9]
Cytochrome C oxidase	K02275	coxB, ctaC; cytochrome c oxidase subunit II [EC:7.1.1.9]
Cytochrome C oxidase	K02276	coxC, ctaE; cytochrome c oxidase subunit III [EC:7.1.1.9]
Cytochrome C oxidase	K02277	coxD, ctaF; cytochrome c oxidase subunit IV [EC:7.1.1.9]

Cytochrome C oxidase	K02297	cyoA; cytochrome o ubiquinol oxidase subunit II [EC:7.1.1.3]
Cytochrome C oxidase	K02298	cyoB; cytochrome o ubiquinol oxidase subunit I [EC:7.1.1.3]
Cytochrome C oxidase	K02299	cyoC; cytochrome o ubiquinol oxidase subunit III
Cytochrome C oxidase	K02300	cyoD; cytochrome o ubiquinol oxidase subunit IV
Cytochrome C oxidase	K02826	qoxA ; cytochrome aa3-600 menaquinol oxidase subunit II [EC:7.1.1.5]
Cytochrome C oxidase	K02827	qoxB; cytochrome aa3-600 menaquinol oxidase subunit I [EC:7.1.1.5]
Cytochrome C oxidase	K02828	qoxC; cytochrome aa3-600 menaquinol oxidase subunit III [EC:7.1.1.5]
Cytochrome C oxidase	K02829	qoxD; cytochrome aa3-600 menaquinol oxidase subunit IV [EC:7.1.1.5]
Mn2+ catalase	K07217	K07217; Mn-containing catalase
Cytochrome C oxidase	K15408	coxAC; cytochrome c oxidase subunit I+III [EC:7.1.1.9]
Cytochrome C oxidase	K15862	ccoNO; cytochrome c oxidase cbb3-type subunit I/II [EC:7.1.1.9]
Cytochrome C oxidase	K18173	COA1; cytochrome c oxidase assembly factor 1
Cytochrome C oxidase	K18174	COA2; cytochrome c oxidase assembly factor 2
Cytochrome C oxidase	K18175	CCDC56, COA3; cytochrome c oxidase assembly factor 3, animal type
Cytochrome C oxidase	K18176	COA3; cytochrome c oxidase assembly factor 3, fungi type
Cytochrome C oxidase	K18177	COA4; cytochrome c oxidase assembly factor 4
Cytochrome C oxidase	K18178	COA5, PET191; cytochrome c oxidase assembly factor 5
Cytochrome C oxidase	K18179	COA6; cytochrome c oxidase assembly factor 6
Cytochrome C oxidase	K18180	COA7, SELRC1, RESA1; cytochrome c oxidase assembly factor 7
Cytochrome C oxidase	K18181	COX14; cytochrome c oxidase assembly factor 14
Cytochrome C oxidase	K18182	COX16; cytochrome c oxidase assembly protein subunit 16
Cytochrome C oxidase	K18183	COX19; cytochrome c oxidase assembly protein subunit 19
Cytochrome C oxidase	K18184	COX20; cytochrome c oxidase assembly protein subunit 20
Cytochrome C oxidase	K18185	COX23; cytochrome c oxidase assembly protein subunit 23
Cytochrome C oxidase	K18189	TACO1; translational activator of cytochrome c oxidase 1
Cytochrome bd ubiquinol oxidase	K22501	appX; cytochrome bd-II ubiquinol oxidase subunit AppX [EC:7.1.1.7]
Cytochrome C oxidase	K22501	appX; cytochrome bd-II ubiquinol oxidase subunit AppX [EC:7.1.1.7]

	Cytochrome C oxidase	K24007	soxD; cytochrome aa3-type oxidase subunit SoxD
	Cytochrome C oxidase	K24008	soxC; cytochrome aa3-type oxidase subunit III
	Cytochrome C oxidase	K24009	soxB; cytochrome aa3-type oxidase subunit I [EC:7.1.1.4]
	Cytochrome C oxidase	K24010	soxA; cytochrome aa3-type oxidase subunit II [EC:7.1.1.4]
	Cytochrome C oxidase	K24011	soxM; cytochrome aa3-type oxidase subunit I/III [EC:7.1.1.4]
Sporulation	Glycogen synthesis	K00693	GYS; glycogen synthase [EC:2.4.1.11]
	Sporulation (Actinobacteria)	K02490	spo0F; two-component system, response regulator, stage 0 sporulation protein F
	Sporulation (Actinobacteria)	K02491	kinA; two-component system, sporulation sensor kinase A [EC:2.7.13.3]
	Glycogen synthesis	K03083	GSK3B; glycogen synthase kinase 3 beta [EC:2.7.11.26]
	Sporulation (Actinobacteria)	K03091	sigH; RNA polymerase sporulation-specific sigma factor
	Sporulation (Actinobacteria)	K04769	spoVT; AbrB family transcriptional regulator, stage V sporulation protein T
	Sporulation (Actinobacteria)	K06283	spoIIID; putative DeoR family transcriptional regulator, stage III sporulation protein D
	Sporulation (Actinobacteria)	K06348	kapD; sporulation inhibitor KapD
	Sporulation (Actinobacteria)	K06359	rapA, spo0L; response regulator aspartate phosphatase A (stage 0 sporulation protein L) [EC:3.1.-.-]
	Sporulation (Actinobacteria)	K06371	sda; developmental checkpoint coupling sporulation initiation to replication initiation
	Sporulation (Actinobacteria)	K06375	spo0B; stage 0 sporulation protein B (sporulation initiation phosphotransferase) [EC:2.7.-.-]
	Sporulation (Actinobacteria)	K06376	spo0E; stage 0 sporulation regulatory protein
	Sporulation (Actinobacteria)	K06377	spo0M; sporulation-barren protein
	Sporulation (Actinobacteria)	K06378	spoIIAA; stage II sporulation protein AA (anti-sigma F factor antagonist)
	Sporulation (Actinobacteria)	K06379	spoIIAB; stage II sporulation protein AB (anti-sigma F factor) [EC:2.7.11.1]
	Sporulation (Actinobacteria)	K06380	spoIIB; stage II sporulation protein B
	Sporulation (Actinobacteria)	K06381	spoIID; stage II sporulation protein D
	Sporulation (Actinobacteria)	K06382	spoIIE; stage II sporulation protein E [EC:3.1.3.16]
	Sporulation (Actinobacteria)	K06383	spoIIGA; stage II sporulation protein GA (sporulation sigma-E factor processing peptidase) [EC:3.4.23.-]
	Sporulation (Actinobacteria)	K06384	spoIIM; stage II sporulation protein M

Sporulation (Actinobacteria)	K06385	spoIIP; stage II sporulation protein P
Sporulation (Actinobacteria)	K06386	spoIIQ ; stage II sporulation protein Q
Sporulation (Actinobacteria)	K06387	spoIIR; stage II sporulation protein R
Sporulation (Actinobacteria)	K06388	spoIIISA ; stage II sporulation protein SA
Sporulation (Actinobacteria)	K06389	spoIISB; stage II sporulation protein SB
Sporulation (Actinobacteria)	K06390	spoIIIAA; stage III sporulation protein AA
Sporulation (Actinobacteria)	K06391	spoIIIAB; stage III sporulation protein AB
Sporulation (Actinobacteria)	K06392	spoIIIAC; stage III sporulation protein AC
Sporulation (Actinobacteria)	K06393	spoIIIAD; stage III sporulation protein AD
Sporulation (Actinobacteria)	K06394	spoIIIAE; stage III sporulation protein AE
Sporulation (Actinobacteria)	K06395	spoIIIAF; stage III sporulation protein AF
Sporulation (Actinobacteria)	K06396	spoIIIAG; stage III sporulation protein AG
Sporulation (Actinobacteria)	K06397	spoIIIAH; stage III sporulation protein AH
Sporulation (Actinobacteria)	K06398	spoIVA; stage IV sporulation protein A
Sporulation (Actinobacteria)	K06399	spoIVB; stage IV sporulation protein B [EC:3.4.21.116]
Sporulation (Actinobacteria)	K06401	spoIVFA; stage IV sporulation protein FA
Sporulation (Actinobacteria)	K06402	spoIVFB; stage IV sporulation protein FB [EC:3.4.24.-]
Sporulation (Actinobacteria)	K06403	spoVAA; stage V sporulation protein AA
Sporulation (Actinobacteria)	K06404	spoVAB; stage V sporulation protein AB
Sporulation (Actinobacteria)	K06405	spoVAC; stage V sporulation protein AC
Sporulation (Actinobacteria)	K06406	spoVAD; stage V sporulation protein AD
Sporulation (Actinobacteria)	K06407	spoVAE; stage V sporulation protein AE
Sporulation (Actinobacteria)	K06408	spoVAF; stage V sporulation protein AF
Sporulation (Actinobacteria)	K06409	spoVB; stage V sporulation protein B
Sporulation (Actinobacteria)	K06412	spoVG; stage V sporulation protein G
Sporulation (Actinobacteria)	K06413	spoVK; stage V sporulation protein K
Sporulation (Actinobacteria)	K06414	spoVM; stage V sporulation protein M

Sporulation (Actinobacteria)	K06415	spoVR; stage V sporulation protein R
Sporulation (Actinobacteria)	K06416	spoVS; stage V sporulation protein S
Sporulation (Actinobacteria)	K06417	spoVID; stage VI sporulation protein D
Sporulation (Actinobacteria)	K06437	yknT; sigma-E barrenled sporulation protein
Sporulation (Actinobacteria)	K06438	yqfD; similar to stage IV sporulation protein
Sporulation (Actinobacteria)	K07697	kinB; two-component system, sporulation sensor kinase B [EC:2.7.13.3]
Sporulation (Actinobacteria)	K07698	kinC; two-component system, sporulation sensor kinase C [EC:2.7.13.3]
Sporulation (Actinobacteria)	K07699	spo0A; two-component system, response regulator, stage 0 sporulation protein A
Sporulation (Actinobacteria)	K08293	SMK1; sporulation-specific mitogen-activated protein kinase SMK1 [EC:2.7.11.24]
Sporulation (Actinobacteria)	K08384	spoVD; stage V sporulation protein D (sporulation-specific penicillin-binding protein)
Glycogen synthesis	K08822	GSK3A; glycogen synthase kinase 3 alpha [EC:2.7.11.26]
Sporulation (Actinobacteria)	K12576	SPO12; sporulation-specific protein 12
Sporulation (Actinobacteria)	K12771	SPS1; sporulation-specific protein 1 [EC:2.7.11.1]
Sporulation (Actinobacteria)	K12772	SPS4; sporulation-specific protein 4
Sporulation (Actinobacteria)	K12773	SPR3; sporulation-regulated protein 3
Sporulation (Actinobacteria)	K12783	SSP1; sporulation-specific protein 1
Sporulation (Actinobacteria)	K13532	kinD; two-component system, sporulation sensor kinase D [EC:2.7.13.3]
Sporulation (Actinobacteria)	K13533	kinE; two-component system, sporulation sensor kinase E [EC:2.7.13.3]
Glycogen synthesis	K16150	K16150; glycogen synthase [EC:2.4.1.11]
Exopolysaccharide synthesis	K16566	exoY ; exopolysaccharide production protein ExoY
Exopolysaccharide synthesis	K16567	exoQ ; exopolysaccharide production protein ExoQ
Exopolysaccharide synthesis	K16568	exoZ ; exopolysaccharide production protein ExoZ
Sporulation (Actinobacteria)	K16947	SPR28; sporulation-regulated protein 28
Glycogen synthesis	K20812	glgA; glycogen synthase [EC:2.4.1.242]

11 Table S4. Chlorophyll concentration, (mg chla/ g soil)water content (%), total organic carbon (%),
 12 total nitrogen (%), and carbohydrates (µg/g soil) values in the biocrust at each sampling point and site.

Time	Chlorophyll concentration (mg chla/ g soil)	Water content (%)	Total organic carbon (%)	Total nitrogen (%)	Carbohydrates (µg/g soil)
T[0]	7.7	1.9	4.2	0.1	63.6
T[0]	8.6	2.7	4.1	0.1	69.4
T[0]	6.8	2.3	4.2	0.1	64.2
T[R]	10.1	13.6	3.0	0.1	54.3
T[R]	16.1	16.9	3.9	0.1	224.5
T[R]	15.7	16.6	3.8	0.1	134.8
T[R]	12.7	16.3	4.0	0.1	111.4
T[R]	14.2	17.5	4.0	0.1	157.1
T[1]	10.5	5.3	3.3	0.1	121.6
T[1]	16.0	5.6	3.2	0.1	82.6
T[1]	16.9	7.1	4.0	0.1	145.5
T[1]	15.3	6.2	4.0	0.1	168.9
T[1]	14.2	6.8	3.9	0.1	199.6
T[2]	10.1	3.9	3.9	0.1	78.4
T[2]	11.8	4.5	4.0	0.1	85.0
T[2]	11.8	4.5	4.2	0.1	133.3
T[2]	13.0	5.1	4.1	0.1	111.0
T[2]	13.0	6.9	4.1	0.1	59.8
T[3]	9.9	2.9	3.8	0.1	66.7
T[3]	12.8	3.7	3.7	0.1	78.4
T[3]	9.3	3.7	3.7	0.1	39.9
T[3]	9.4	4.3	4.5	0.1	75.7
T[3]	14.5	3.8	4.6	0.1	102.2

15 Table S5. Pairwise t-tests p-values for chlorophyll concentration, water content, total organic carbon
 16 content, total nitrogen, and carbohydrates in biocrust samples collected at the different sampling point.
 17 Bold numbers mark significant differences (<0.05).

Comparison	Chlorophyll	Water content	Total organic Carbon	Total Nitrogen	Carbohydrates
T[0] - T[1]	5.7E-02	5.4E-03	8.9E-01	1.7E-01	4.60E-02
T[0] - T[2]	3.6E-01	2.8E-02	6.4E-01	5.3E-01	7.34E-01
T[1] - T[2]	2.6E-02	2.6E-01	5.5E-01	4.5E-01	9.00E-02
T[0] - T[3]	2.0E-01	1.8E-01	7.5E-01	6.5E-02	6.93E-01
T[1] - T[3]	8.0E-03	5.3E-02	8.5E-01	6.1E-01	2.00E-02
T[2] - T[3]	3.2E-01	1.7E-01	4.3E-01	2.1E-01	4.64E-01
T[0] - T[R]	1.6E-01	3.6E-06	8.4E-01	7.2E-01	2.04E-01
T[1] - T[R]	2.8E-01	2.6E-02	9.5E-01	3.0E-01	4.26E-01
T[2] - T[R]	8.6E-02	4.9E-03	5.1E-01	7.8E-01	3.45E-01
T[3] - T[R]	3.3E-02	1.9E-04	9.0E-01	1.3E-01	1.02E-01
χ^2 /F-value	8.9	27.6	1.9	1.2	2.1

18

19 Table S6. Relative abundance (in %) of the taxa in the biocrust community at each time point.

Phylum	Order	Time Point	Relative abundance
Acidobacteriota	Bryobacterales	T[R]	0.62
		T[2]	0.63
Actinobacteriota	Frankiales	T[R]	4.94
		T[1]	1.55
		T[2]	4.03
		T[3]	2.36
	Gaiellales	T[0]	0.51
	IMCC26256	T[0]	36.68
		T[R]	0.78
		T[1]	1.60
		T[2]	1.48
		T[3]	0.89
	Micrococcales	T[R]	0.91
		T[2]	0.75
		T[3]	0.70
	Micromonosporales	T[R]	1.28
		T[3]	0.62
	Propionibacteriales	T[2]	0.55
	Rubrobacterales	T[0]	0.56
		T[R]	6.45
		T[1]	8.19
		T[2]	9.09
		T[3]	8.30
	Solirubrobacterales	T[0]	7.83
		T[R]	3.66
		T[1]	4.49
		T[2]	4.53
		T[3]	2.99
	uncultured	T[1]	0.63
		T[2]	0.72
Bacteroidota	Chitinophagales	T[0]	20.11
		T[2]	0.58
	Cytophagales	T[R]	11.12
		T[1]	11.38
		T[2]	7.97
Chloroflexi	Kallotenuales	T[3]	9.01
Cyanobacteria	Cyanobacteriales	T[R]	0.94
		T[2]	1.84
		T[3]	0.94
		T[0]	3.59
		T[R]	39.31
		T[1]	31.94
		T[2]	30.08
		T[3]	34.01

	Oxyphotobacteria_Incertae_Sedis	T[R]	1.82
		T[1]	2.44
		T[2]	2.10
		T[3]	2.44
Firmicutes	Lactobacillales	T[0]	2.08
Gemmatimonadota	Gemmatimonadales	T[0]	6.44
		T[2]	0.54
	Longimicrobiales	T[R]	1.49
Myxococcota	Haliangiales	T[R]	0.87
		T[1]	0.54
		T[2]	0.62
		T[3]	0.89
	Myxococcales	T[R]	2.34
		T[1]	1.30
		T[2]	1.78
		T[3]	1.93
	Nannocystales	T[R]	1.43
		T[1]	2.07
		T[2]	0.87
		T[3]	1.10
	Polyangiales	T[R]	0.63
		T[1]	0.94
		T[3]	0.62
Proteobacteria	Acetobacterales	T[R]	1.27
		T[1]	1.17
		T[2]	1.75
		T[3]	1.44
	Burkholderiales	T[0]	3.72
		T[R]	1.74
		T[1]	1.39
		T[2]	2.06
	Caulobacterales	T[3]	2.00
		T[R]	2.71
		T[1]	4.99
		T[2]	2.42
	Enterobacterales	T[3]	3.42
		T[0]	0.78
	Rhizobiales	T[0]	6.96
		T[R]	5.13
		T[1]	7.76
		T[2]	8.03
		T[3]	8.29
	Rhodobacterales	T[R]	1.44
		T[1]	2.54
		T[2]	3.09
		T[3]	2.09

	Sphingomonadales	T[0]	7.71
		T[R]	2.79
		T[1]	3.33
		T[2]	3.84
		T[3]	3.13
Verrucomicrobiota	Chthoniobacterales	T[0]	0.60
		T[R]	1.70
		T[1]	6.52
		T[2]	4.63
		T[3]	8.31

20

21

22 Table S7. P-values of the Dunn tests between time points on the relative abundance of the
 23 actinobacterial and cyanobacterial orders. Bold numbers are significant (<0.05).

Comparison	Cyanobacteria	Actinobacteria
T[0] - T[1]	1.85E-03	9.41E-03
T[0] - T[2]	3.02E-04	2.86E-02
T[0] - T[3]	2.72E-01	3.03E-01
T[0] - T[R]	6.25E-04	1.85E-03
T[1] - T[3]	3.54E-01	2.62E-01
T[1] - T[2]	4.08E-01	1.24E-01
T[1] - T[R]	1.03E-03	2.90E-02
T[2] - T[R]	4.19E-01	3.00E-01
T[3] - T[R]	3.44E-01	4.98E-01
T[2] - T[3]	4.33E-01	1.23E-01
χ^2	14.3	8.9

24

25 Table S8. Abundance (in copy number (CN)) of each time points within each group of gene.

Gene Group	Time points	Abundance
DNA conservation	T[0]	132553
	T[R]	128227
	T[1]	131306
	T[2]	124433
	T[3]	130391
DNA repair and degradation	T[0]	100256
	T[R]	77905
	T[1]	86459
	T[2]	82693
	T[3]	82154
Light energy or sensing	T[0]	0
	T[R]	94
	T[1]	193
	T[2]	126
	T[3]	119
Lithotrophy	T[0]	64266
	T[R]	52539
	T[1]	66879
	T[2]	72179
	T[3]	61058
Nitrogen	T[0]	87036
	T[R]	64445
	T[1]	84754
	T[2]	80353
	T[3]	81344
Organotrophy	T[0]	200506
	T[R]	191860
	T[1]	216236
	T[2]	230492
	T[3]	213249
Phototrophy	T[0]	82712
	T[R]	434046
	T[1]	394599
	T[2]	368618
	T[3]	411617
ROS-damage prevention	T[0]	255588
	T[R]	199315
	T[1]	229250
	T[2]	212687
	T[3]	217893
Sensing & motility	T[0]	248172
	T[R]	169291
	T[1]	214465
	T[2]	222854

	T[3]	197459
Sporulation capsule & C-storage	T[0]	38247
	T[R]	38125
	T[1]	39059
	T[2]	38962
	T[3]	38096

27 Table S9. Chi-square values and p-values of the Dunn tests between time points done on the functional
 28 prediction results. Bold numbers are significant (< 0.05)

Comparison	DNA Conservation	DNA Repair	Light energy	Lithotrophy	Nitrogen
T[0] - T[1]	4.61E-01	1.62E-01	4.65E-02	1.63E-01	1.05E-01
T[0] - T[2]	4.52E-01	3.26E-01	1.28E-03	2.91E-01	6.88E-02
T[0] - T[3]	4.75E-01	2.93E-01	2.26E-02	2.43E-01	8.02E-02
T[0] - T[R]	4.46E-01	2.23E-01	1.60E-02	4.33E-01	4.33E-02
T[1] - T[3]	4.01E-01	2.69E-01	6.15E-02	3.83E-02	3.95E-01
T[1] - T[2]	4.84E-01	3.06E-01	3.54E-01	2.62E-02	4.31E-01
T[1] - T[R]	3.94E-01	3.98E-01	2.95E-01	1.74E-01	2.98E-01
T[2] - T[3]	4.17E-01	4.57E-01	1.21E-01	4.33E-01	4.63E-01
T[2] - T[R]	4.93E-01	3.60E-01	1.57E-01	2.03E-01	3.96E-01
T[3] - T[R]	4.10E-01	4.02E-01	4.35E-01	1.59E-01	3.60E-01
χ^2	0.12	1.11	9.41	4.75	3.28

Comparisons	Organotrophy	Phototrophy	ROS	Motility	Sporulation
T[0] - T[1]	2.88E-01	6.92E-43	2.26E-01	1.22E-02	7.96E-04
T[0] - T[2]	2.21E-01	5.40E-30	4.43E-01	2.04E-01	5.09E-02
T[0] - T[3]	4.52E-01	3.95E-23	4.41E-01	2.72E-01	2.58E-03
T[0] - T[R]	3.27E-01	1.12E-32	4.71E-01	3.70E-01	8.65E-04
T[1] - T[3]	4.05E-01	3.21E-03	1.51E-01	1.89E-04	3.95E-02
T[1] - T[2]	3.06E-01	4.58E-06	2.43E-01	4.85E-04	3.38E-01
T[1] - T[R]	4.49E-01	1.73E-02	2.17E-01	1.34E-02	4.89E-01
T[2] - T[3]	2.27E-01	4.36E-02	3.68E-01	3.99E-01	9.02E-02
T[2] - T[R]	3.56E-01	2.70E-01	4.01E-01	9.02E-02	4.19E-02
T[3] - T[R]	3.53E-01	1.01E-02	4.65E-01	1.39E-01	3.49E-01
χ^2	0.90	209.59	1.23	15.85	14.10

30 Table S10. Shannon diversity index values for each time point

Time	Shannon
T[3]	4.67
T[3]	4.57
T[3]	4.59
T[3]	4.32
T[R]	4.31
T[R]	4.43
T[R]	4.36
T[R]	4.42
T[R]	4.52
T[0]	3.20
T[0]	3.37
T[0]	3.78
T[1]	4.61
T[1]	4.59
T[1]	4.73
T[1]	4.60
T[1]	4.63
T[2]	4.54
T[2]	4.72
T[2]	4.80
T[2]	4.41
T[2]	4.56
T[3]	4.36

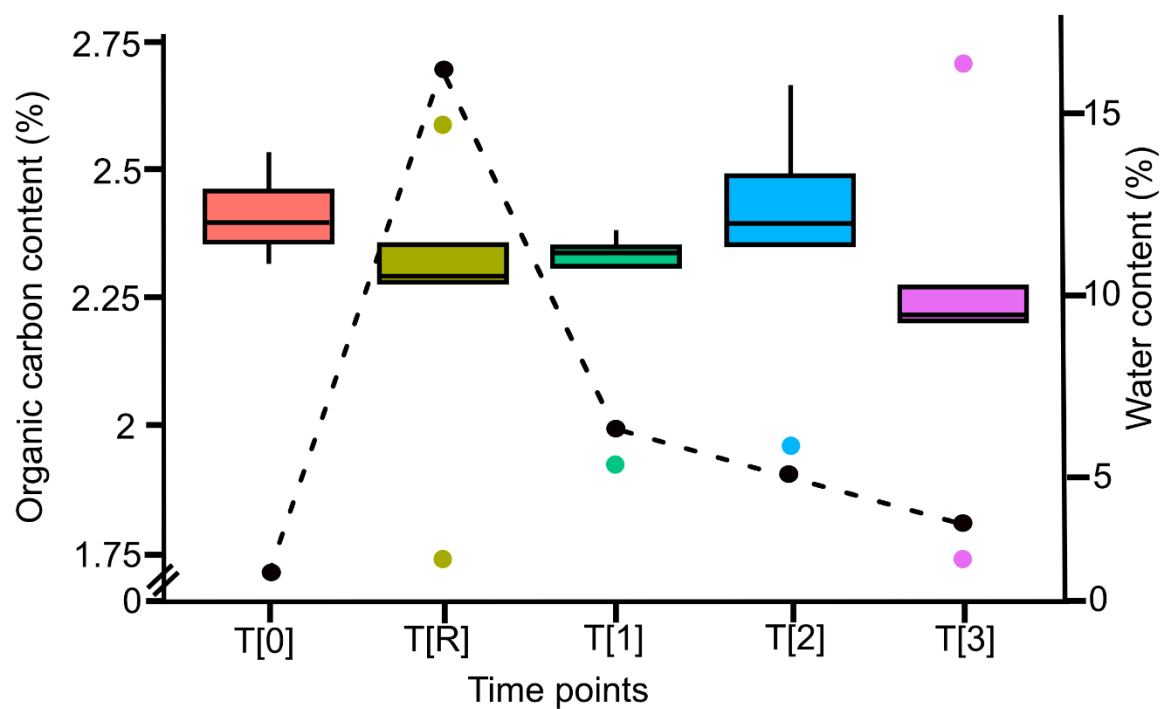
31

32 Table S11. P-values of the pairwise t-test of the different of the alpha diversity between each time
 33 point

Comparison	p-value
T[R]-T[0]	5.20E-07
T[1]-T[0]	3.20E-08
T[2]-T[0]	4.00E-08
T[3]-T[0]	1.50E-07
T[1]-T[R]	2.00E-01
T[2]-T[R]	2.80E-01
T[3]-T[R]	8.70E-01
T[2]-T[1]	8.70E-01
T[3]-T[1]	7.60E-01
T[3]-T[2]	8.70E-01
T-value	51.83

34

36



37

38 Figure S1. Organic carbon content (%) and water content (%) for each sampling point. Boxes

39 represent 25-75% of the data, solid lines the median, and the tips represent the minimum and

40 maximum values excluding the outliers (1.5 times lesser or greater than the lower or upper quantiles)

41 represented by dots outside of the boxes.

42

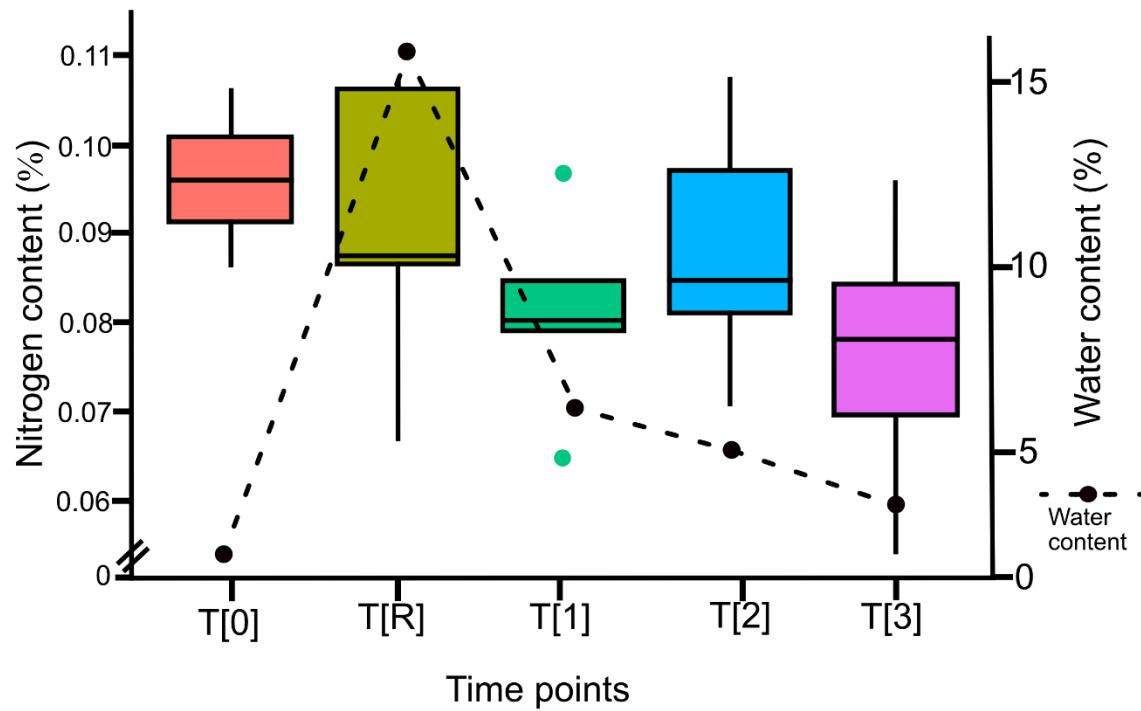
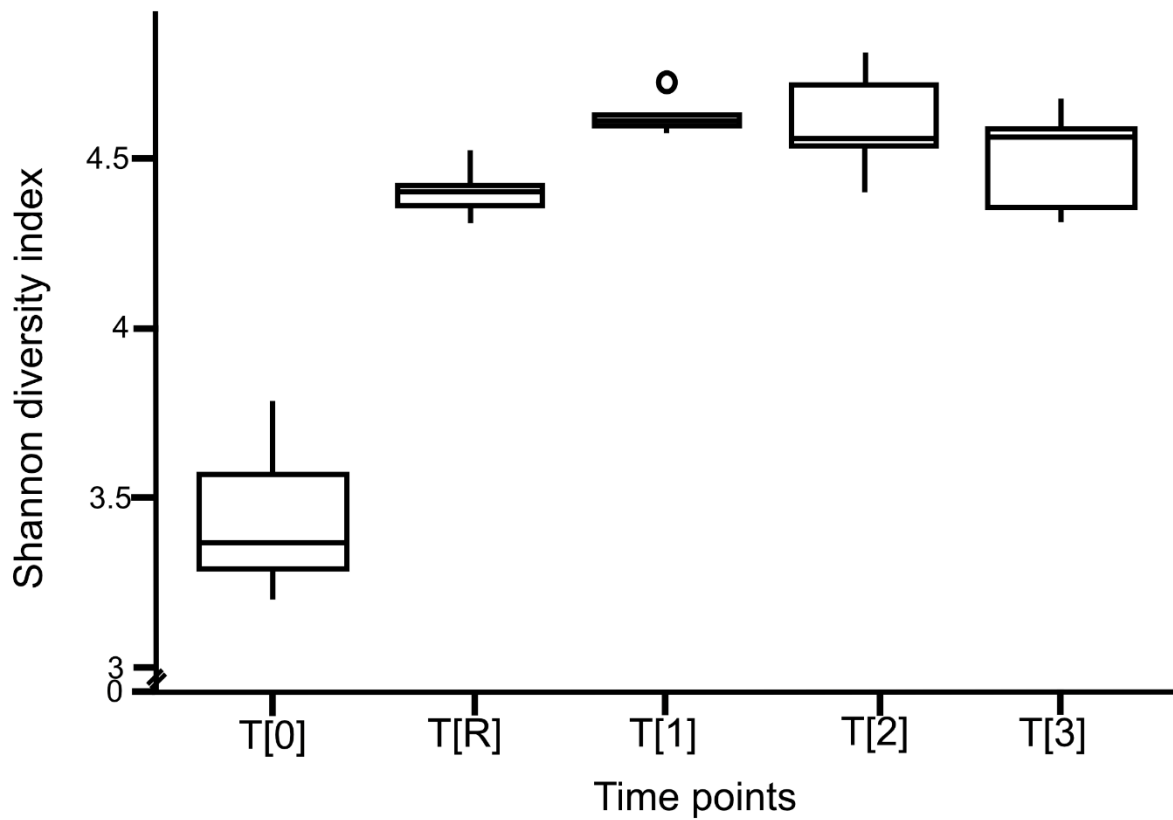


Figure S2. Nitrogen content (%) and water content (%) for each time point. Boxes represent 25-75% of the data, solid lines the median, and the tips represent the minimum and maximum values excluding the outliers (1.5 times lesser or greater than the lower or upper quantiles) represented by dots outside of the boxes.



49

50 Figure S3. Shannon diversity index for each timepoint. Boxes represent 25-75% of the data, solid lines

51 the median, the tips represent the minimum and maximum values excluding the outliers (1.5 times

52 lesser or greater than the lower or upper quantiles) represented by dots outside of the boxes.

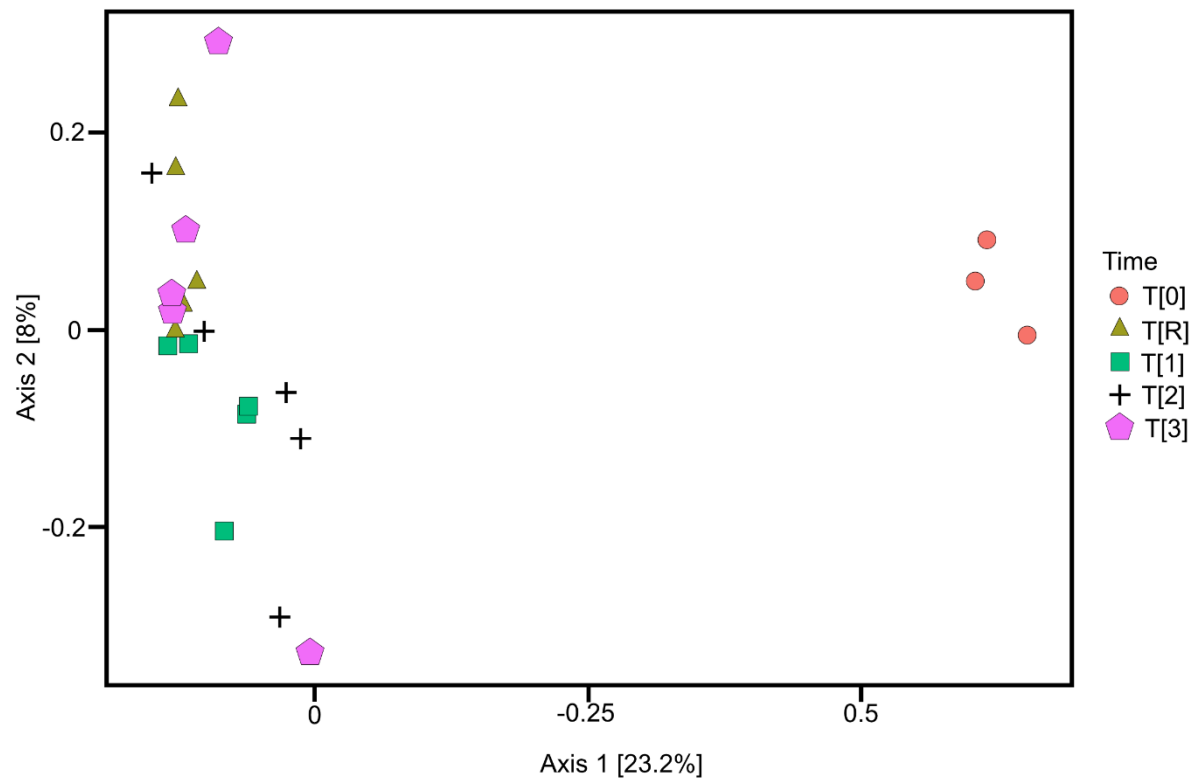


Figure S4. Principal Coordinate Analysis (PCoA) based on Bray-Curtis distance matrix of the bacterial distribution in biocrust samples taken at different timepoints.