

MAGs IDs	Completeness	Contamination	Contigs	N50	Season	Specificity(indval)	p-value
BL_0902_bin.full.136	77.11	4.19	13	431366	Winter/Spring	0.88	0.001
BL_0908_bin.full.20	80.68	7.95	9	1189765	Summer/Autumn	0.97	0.001
BL_0908_bin.full.418	93.05	0.8	7	1028904	Others	NA	NA
BL_0908_bin.full.436	99.25	0	2	2919795	Others	NA	NA
BL_0908_bin.full.522	73.63	8.79	3	450935	Summer/Autumn	0.76	0.001
BL_0908_bin.full.528	99.47	0.73	6	1809632	Others	NA	NA
BL_0908_bin.full.559	98.64	0.77	4	2498219	Others	NA	NA
BL_0908_bin.full.759	99.1	0	6	881846	Others	NA	NA
BL_0908_bin.full.869	77.85	0.27	2	637273	Summer/Autumn	0.62	0.004
BL_1001_bin.full.234	82.58	8.04	11	277874	Others	NA	NA
BL_pooled_bin.circ.35	76.92	0	1	1013495	Summer/Autumn	0.92	0.001
BL_pooled_bin.circ.36	97.04	0	1	2408581	Summer/Autumn	0.98	0.001
BL_pooled_bin.full.145	75.88	3.37	5	760863	Others	NA	NA
BL_pooled_bin.full.1551	79.91	1.42	14	286836	Others	NA	NA
BL_pooled_bin.full.596	72.25	8.86	1	1558692	Summer/Autumn	0.93	0.001
BL_pooled_bin.full.761	81.04	1.74	4	1353826	Winter/Spring	0.86	0.001
s1032.ctg0011321_BL_0908sc	74.4	0	1	807564	Summer/Autumn	0.94	0.001
s111.ctg000126c_BL_0902sc	98.58	0	1	2319832	Winter/Spring	0.87	0.001
s131.ctg000151c_BL_0908sc	90.37	0	1	4491150	Others	NA	NA
s215.ctg000240l_BL_0908sc	68.31	0.37	1	1245483	Summer/Autumn	0.76	0.001
s2266.ctg002461l_BL_0908sc	62.07	0	1	641599	Summer/Autumn	0.62	0.001
s23.ctg000345l_BL_0902sc	75.07	0	1	1282429	Winter/Spring	0.95	0.001
s249.ctg000277l_BL_0908sc	83.78	0	1	1777046	Summer/Autumn	1.00	0.001
s266.ctg000297l_BL_0908sc	95.01	0	1	1086608	Summer/Autumn	0.57	0.001
s325.ctg000366c_BL_0908sc	98.9	1.1	1	1567908	Summer/Autumn	0.81	0.001
s35.ctg000041c_BL_0902sc	98.93	0.46	1	2639517	Winter/Spring	0.91	0.001
s388.ctg000435l_BL_0908sc	56.94	0	1	987645	Summer/Autumn	0.78	0.001
s44.ctg000052l_BL_0902sc	98.4	0	1	2268659	Winter/Spring	0.90	0.001
s7.ctg000447l_BL_0908sc	89.01	0	1	1572606	Summer/Autumn	0.72	0.001
s96.ctg000111c_BL_0908sc	99.68	0	1	2775026	Others	NA	NA

Supplementary Table 1: The 30 long-read MAGs investigated in this study. MAGs IDs: The identification of the 30 long-read MAGs. Completeness: the entirety of a particular microbial genome, shown in percentage. Contamination: The presence of genetic material from organisms other than the target microbe within a MAG, shown in percentage. Contigs: Segments of genetic information derived from different organisms present in a complex microbial community. N50: The length at which half of the total genome sequence is contained. Season: Assignation of MAGs to specific seasons based on abundance ( RPKG) and the “Indicator Value” indval. Specificity: indval value for each season and MAG. P-value: statistical measurement of indval.

MAGs IDs	Taxonomy
BL_0902_bin.full.136	d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Flavobacteriales;f_Flavobacteriaceae;g_Polaribacter;s_
BL_0908_bin.full.20	d_Bacteria;p_Plantomycetota;c_Phycisphaerae;o_Phycisphaerales;f_SMIA02;g_UBA8653;s_UBA8653 sp002168105
BL_0908_bin.full.418	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacterales;f_Alteromonadaceae;g_Alteromonas;s_Alteromonas macleodii
BL_0908_bin.full.436	d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Alteriqipengyuania;s_Alteriqipengyuania bathymarina
BL_0908_bin.full.522	d_Bacteria;p_Marinisomatota;c_Marinisomatia;o_Marinisomatales;f_Marinisomataceae;g_Marinisoma;s_Marinisoma sp902525615
BL_0908_bin.full.528	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_Mitsularia;s_
BL_0908_bin.full.559	d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Erythrobacter_A;s_Erythrobacter_A pelagi
BL_0908_bin.full.759	d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Chitinophagales;f_Chitinophagaceae;g_Sediminibacterium;s_
BL_0908_bin.full.869	d_Bacteria;p_Cyanobacteria;c_Cyanobacteria;o_PCC-6307;f_Cyanobiaceae;g_Prochlorococcus_A;s_Prochlorococcus_A pastoris
BL_1001_bin.full.234	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacterales;f_Alteromonadaceae;g_Glaciecola;s_
BL_pooled_bin.circ.35	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_SAR86;f_TMED112;g_TMED112;s_
BL_pooled_bin.circ.36	d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Flavobacteriales;f_UA16;g_UBA8752;s_UBA8752 sp002172485
BL_pooled_bin.full.145	d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Rhodobacteraceae;g_s_
BL_pooled_bin.full.1551	d_Bacteria;p_Cyanobacteria;c_Vampirovibrionia;o_Obscuribacteriales;f_Obscuribacteraceae;g_Ga0077546;s_
BL_pooled_bin.full.596	d_Bacteria;p_Actinobacterota;c_Actinomycetia;o_Actinomycetales;f_Microbacteriaceae;g_Pontimonas;s_Pontimonas sp002172585
BL_pooled_bin.full.761	d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales_B;f_TMED25;g_MED-G09;s_MED-G09 sp002704345
s1032.ctg0011321_BL_0908sc	d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Pelagibacterales;f_Pelagibacteraceae;g_HIMB114;s_HIMB114 sp008638005
s111.ctg000126c_BL_0902sc	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Porticoccaceae;g_HTCC2207;s_
s131.ctg000151c_BL_0908sc	d_Bacteria;p_Actinobacterota;c_Actinomycetia;o_Propionibacteriales;f_Nocardioidaceae;g_Nocardioides;s_Nocardioides sp001627335
s215.ctg000240l_BL_0908sc	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_SAR86;f_D2472;g_SCGC-AAA076-P13;s_
s2266.ctg002461l_BL_0908sc	d_Bacteria;p_Actinobacterota;c_Acidimicrobia;o_Actinomarinales;f_Actinomarinaceae;g_Actinomarina;s_
s23.ctg000345l_BL_0902sc	d_Archaea;p_Thermoplasmata;c_Posidonia_A;o_Posidoniales;f_Thalassarchaeace;g_MGIIb-O2;s_MGIIb-O2 sp002498985
s249.ctg000277l_BL_0908sc	d_Bacteria;p_Verrucomicrobiota;c_Verrucomicrobia;o_Opitutes;f_DSM-45221;g_UBA7445;s_
s266.ctg000297l_BL_0908sc	d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Pelagibacterales;f_Pelagibacteraceae;g_Pelagibacter;s_
s325.ctg000366c_BL_0908sc	d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_TMED127;f_TMED127;g_TMED13;s_TMED13 sp002167825
s35.ctg000041c_BL_0902sc	d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Rhodobacteraceae;g_Amylibacter;s_
s388.ctg000435l_BL_0908sc	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_SAR86;f_D2472;g_SCGC-AAA076-P13;s_SCGC-AAA076-P13 sp902610905
s44.ctg000052l_BL_0902sc	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Porticoccaceae;g_HTCC2207;s_
s7.ctg000447l_BL_0908sc	d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Flavobacteriales;f_Flavobacteriaceae;g_UBA7446;s_
s96.ctg000111c_BL_0908sc	d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Caulobacterales;f_Caulobacteraceae;g_Brevundimonas;s_

Supplementary Table 2: The taxonomy of 30 long-read MAGs investigated in this study.

MAGs IDs	BBMO	SOLA	Number of Genes	Difference between time series
BL_0902_bin.full.136	18	12	1880	0.32%
BL_0908_bin.full.20	78	62	2068	0.77%
BL_0908_bin.full.418	1	11	3908	0.26%
BL_0908_bin.full.436	12	NA	3158	NA
BL_0908_bin.full.522	5	5	832	0.00%
BL_0908_bin.full.528	NA	NA	5530	NA
BL_0908_bin.full.559	48	8	3016	1.33%
BL_0908_bin.full.759	NA	NA	3535	NA
BL_0908_bin.full.869	24	21	1444	0.21%
BL_1001_bin.full.234	48	20	2350	1.19%
BL_pooled_bin.circ.35	8	8	1050	0.00%
BL_pooled_bin.circ.36	147	117	2007	1.50%
BL_pooled_bin.full.145	9	9	2017	0.00%
BL_pooled_bin.full.1551	NA	NA	2506	NA
BL_pooled_bin.full.596	40	39	1630	0.06%
BL_pooled_bin.full.761	6	3	1608	0.19%
s1032.ctg0011321_BL_0908sc	3	2	917	0.11%
s111.ctg000126e_BL_0902sc	15	11	2144	0.19%
s131.ctg000151c_BL_0908sc	17	NA	4406	0.39%
s215.ctg000240l_BL_0908sc	4	7	1340	0.22%
s2266.ctg0024611_BL_0908sc	2	2	724	0.00%
s23.ctg000345l_BL_0902sc	7	5	1167	0.17%
s249.ctg000277l_BL_0908sc	84	76	1611	0.50%
s266.ctg000297l_BL_0908sc	4	3	1207	0.08%
s325.ctg000366e_BL_0908sc	15	11	1648	0.24%
s35.ctg000041c_BL_0902sc	1	NA	2757	0.04%
s388.ctg000435l_BL_0908sc	9	8	1083	0.09%
s44.ctg000052l_BL_0902sc	17	30	2121	0.61%
s7.ctg000447l_BL_0908sc	16	10	1427	0.42%
s96.ctg000111c_BL_0908sc	26	NA	2775	0.94%

Supplementary Table 3: The number of adaptive genes for each of the 30 MAGs. The table shows the number of adaptive genes we found in each time series, the number of total genes in each MAGs ,and the difference in the number of adaptive genes we found between both time series.

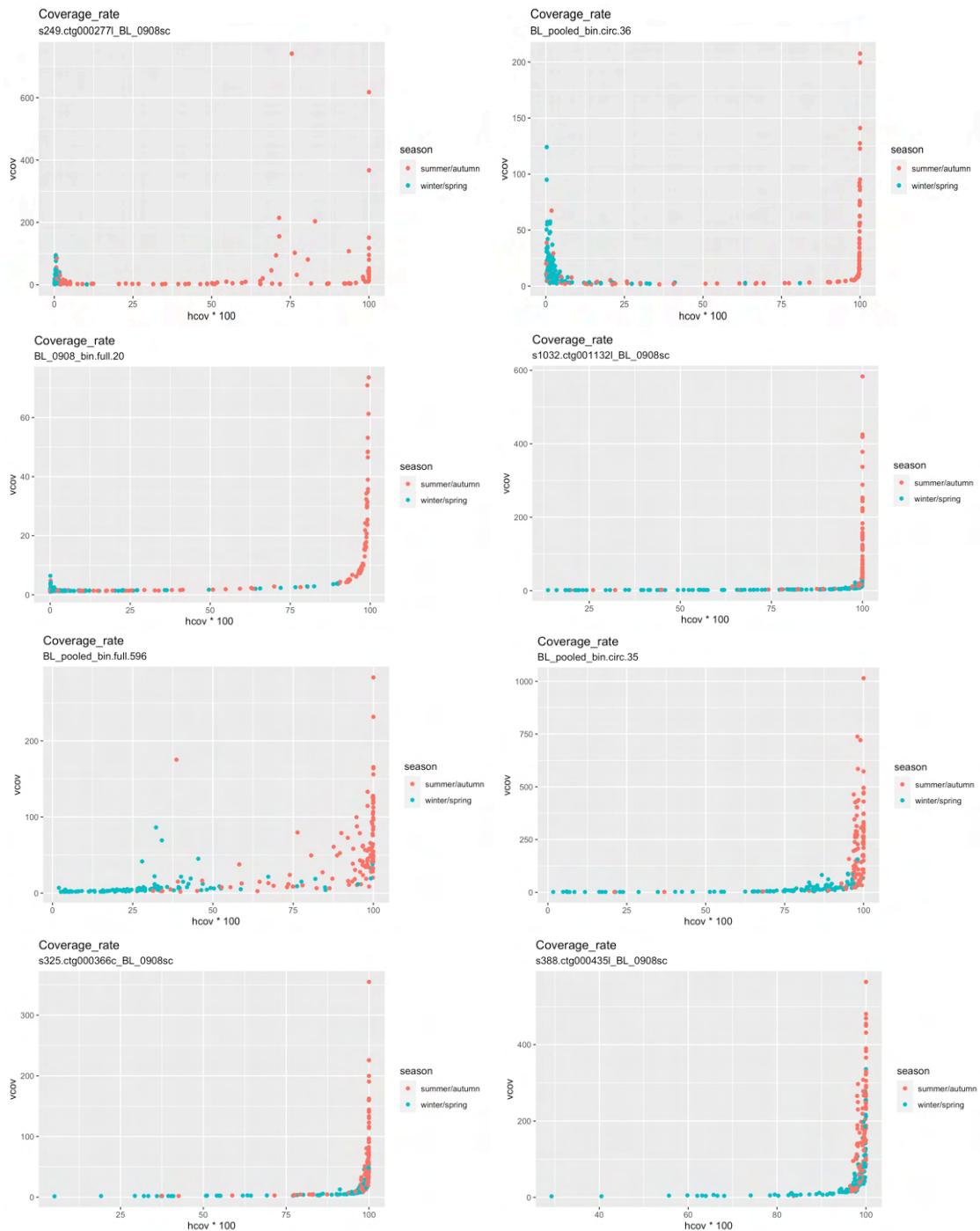
MAGs IDs	Shared Gene	Number
BL_0902_bin.full.136	"1_141" "1_322" "5_191"	3
BL_0908_bin.full.20	"1_82" "1_104" "1_109" "1_117" "1_266" "1_369" "1_480" "1_623" "1_705" "1_709" "1_714" "1_898" "1_900" "1_908" "1_935" "1_936" "1_937" "1_1095" "1_1122" "1_1127" "2_63" "2_77" "2_115" "2_159" "2_161" "2_165" "2_209" "2_446" "2_492" "2_568" "2_575" "2_584" "2_593" "3_9" "3_21" "3_22" "3_52"	37
BL_0908_bin.full.418	NA	NA
BL_0908_bin.full.436	NA	NA
BL_0908_bin.full.522	"1_101" "1_456" "2_86" "3_1" "3_7"	5
BL_0908_bin.full.528	NA	NA
BL_0908_bin.full.559	"1_161" "1_165" "1_263" "1_292"	4
BL_0908_bin.full.759	NA	NA
BL_0908_bin.full.869	1_130 "1_170" "1_323" "1_640" "2_29" "2_33" "2_150" "2_166" "2_199" "2_234" "2_236" "2_525" "2_527" "2_540" "2_541" "2_543" "2_574"	17
BL_1001_bin.full.234	"1_91" "2_194" "2_259" "5_246" "8_62"	5
BL_pooled_bin.circ.35	"1_360" "1_411" "1_520" "1_521" "1_555" "1_878" "1_922"	7
BL_pooled_bin.circ.36	"1_51" "1_83" "1_118" "1_129" "1_135" "1_140" "1_156" "1_159" "1_178" "1_185" "1_194" "1_201" "1_206" "1_232" "1_274" "1_316" "1_326" "1_331" "1_415" "1_471" "1_560" "1_564" "1_581" "1_590" "1_599" "1_663" "1_673" "1_689" "1_716" "1_736" "1_780" "1_795" "1_889" "1_912" "1_929" "1_935" "1_944" "1_958" "1_966" "1_982" "1_983" "1_1020" "1_1035" "1_1042" "1_1064" "1_1126" "1_1211" "1_1230" "1_1232" "1_1243" "1_1267" "1_1286" "1_1368" "1_1379" "1_1386" "1_1397" "1_1404" "1_1410" "1_1412" "1_1467" "1_1480" "1_1484" "1_1502" "1_1525" "1_1598" "1_1651" "1_1671" "1_1672" "1_1677" "1_1691" "1_1728" "1_1735" "1_1748" "1_1767" "1_1815" "1_1816" "1_1866" "1_1881" "1_1885" "1_1930" "1_1950" "1_1982"	82
BL_pooled_bin.full.145	"1_79" "3_127"	2
BL_pooled_bin.full.1551	NA	NA
BL_pooled_bin.full.596	"1_397" "1_521" "1_554" "1_555" "1_646" "1_663" "1_843" "1_855" "1_1130" "1_1171" "1_1194" "1_1245" "1_1247" "1_1318" "1_1326" "1_1328" "1_1329" "1_1342" "1_1343" "1_1362" "1_1375" "1_1392" "1_1401" "1_1406" "1_1480" "1_1493" "1_1498" "1_1508" "1_1577" "1_1626"	30
BL_pooled_bin.full.761	"1_216"	1
s1032.ctg00011321_BL_0908sc	"1_676" "1_700"	2
s111.ctg000126e_BL_0902sc	"1_3" "1_444" "1_591" "1_955" "1_959" "1_1915" "1_1951"	7
s131.ctg000151c_BL_0908sc	NA	NA
s215.ctg000240l_BL_0908sc	"1_58" "1_971" "1_1088" "1_1259"	4
s2266.ctg0024611_BL_0908sc	"1_157"	1
s23.ctg000345l_BL_0902sc	"1_158" "1_342" "1_805" "1_821" "1_1152"	5
s249.ctg000277l_BL_0908sc	"1_17" "1_250" "1_254" "1_331" "1_332" "1_402" "1_406" "1_436" "1_437" "1_477" "1_504" "1_505" "1_578" "1_582" "1_599" "1_647" "1_695" "1_696" "1_725" "1_727" "1_728" "1_732" "1_752" "1_792" "1_795" "1_845" "1_849" "1_856" "1_857" "1_858" "1_883" "1_885" "1_891" "1_892" "1_930" "1_931" "1_932" "1_935" "1_937" "1_938" "1_939" "1_940" "1_941" "1_947" "1_948" "1_955" "1_971" "1_1041" "1_1067" "1_1126" "1_1133" "1_1136" "1_1200" "1_1206" "1_1207" "1_1208" "1_1215" "1_1290" "1_1308" "1_1318" "1_1319" "1_1374" "1_1398" "1_1399" "1_1424" "1_1437" "1_1451" "1_1487" "1_1513" "1_1586"	70
s266.ctg000297l_BL_0908sc	"1_69" "1_994"	2
s325.ctg000366c_BL_0908sc	"1_67" "1_83" "1_512" "1_536" "1_812" "1_1241" "1_1303" "1_1403"	8
s35.ctg000041c_BL_0902sc	NA	NA
s388.ctg000435l_BL_0908sc	"1_124" "1_129" "1_272" "1_439" "1_772" "1_831" "1_1031"	7
s44.ctg000052l_BL_0902sc	"1_507" "1_807" "1_1104" "1_1513" "1_1515" "1_1520" "1_1673" "1_1708" "1_1936"	9
s7.ctg000447l_BL_0908sc	"1_110" "1_147" "1_309" "1_581" "1_736" "1_739" "1_829" "1_842" "1_1293"	9
s96.ctg000111c_BL_0908sc	NA	NA

Supplementary Table 4: The Gene ID and the number of adaptive genes we found in both time series for each of the 30 MAGs.

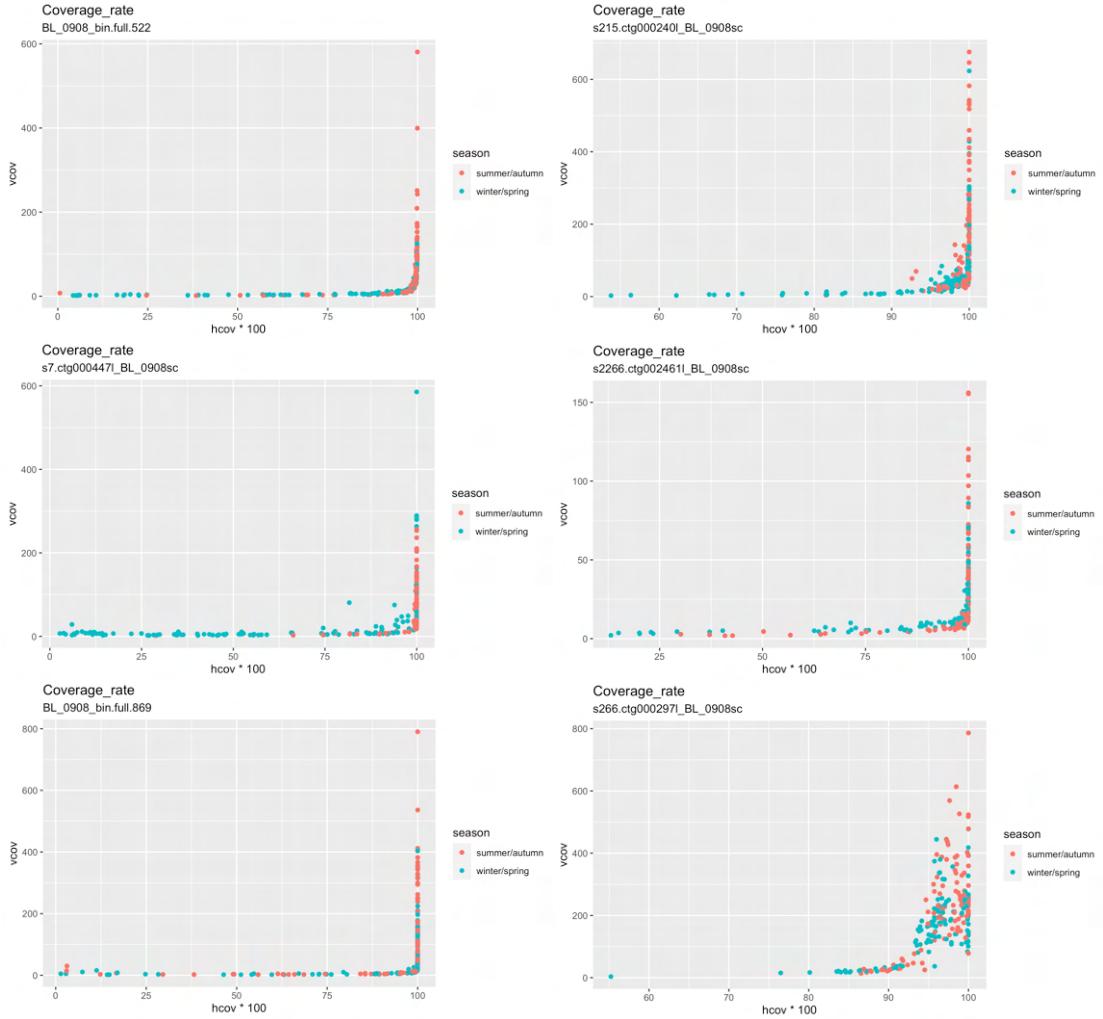
MAGs IDs	Shared Gene Annotation
BL_0902_bin.full.136	I_141:PF11827.7, I_322:PF12867.6,PF07606.10, 5_191:PF14114.5
BL_0908_bin.full.20	I_117:PF01041.16, I_714:PF00884.22 I_900:K00605,PF01571.20,PF08669.10, I_1127:PF04390.11, 2_446:K02003,PF00005.26, 2_492:PF03965.15, 2_568:PF00498.25,PF16697.4
BL_0908_bin.full.418	NA
BL_0908_bin.full.436	NA
BL_0908_bin.full.522	I_101:PF01073.18,PF01370.20,PF16363.4,PF13460.5, PF07993.11,PF04321.16,PF03435.17
BL_0908_bin.full.528	NA
BL_0908_bin.full.559	I_263:PF03061.21, I_292:K18586,PF05019.12
BL_0908_bin.full.759	NA
BL_0908_bin.full.869	I_130:PF06080.11, 2_234:PF08241.11,PF13649.5
BL_1001_bin.full.234	I_91:K03524,PF02237.16,PF03099.18,PF08279.11, 2_259:PF03550.13, 5_246:K07001,PF01734.21
BL_pooled_bin.circ35	hypothetical_protein
BL_pooled_bin.circ36	I_51:PF01476.19, I_129:PF02230.15,PF00135.27,PF12146.7, I_135:PF13579.5, I_159:PF05036.12, I_178:K02843,PF01075.16,GT9, I_194:K18703,PF02515.16, I_201:PF01551.21,PF01551.21, I_316:PF13585.5, I_326:PF13585.5,PF00801.19, I_331:K03321,PF01740.20,PF00916.19, I_415:K01911,PF00501.27, I_471:K13019,PF02350.18, I_581:PF02272.18,PF01411.18,PF07973.13, I_590:PF01025.18, I_663:PF13585.5,PF01364.17, I_673:K03470,PF01351.17, I_689:PF08665.11,PF00072.23, I_716:PF04389.16, I_763:K07052,PF02517.15, I_780:K00602,PF01808.17,PF02142.21, I_795:K04075,PF01171.19,PF11734.7, I_889:K02031&K02032,PF00005.26,PF00005.26,PF08352.11, I_912:K19304,PF01551.21, I_929:PF11751.7, I_935:PF00892.19,PF00892.19, I_966:PF04199.12, I_983:K04564,PF02777.17,PF00081.21, I_1035:PF13585.14, I_1042:PF01066.20, I_1126:K08968,PF13185.5, I_1211:K07058,PF03631.14, I_1230:K14742,PF00814.24, I_1232:K12340,PF02321.17,PF02321.17, I_1286:PF00639.20,PF00639.20,PF13145.5,PF13145.5,PF13616.5,PF13616.5, I_1368:PF16271.4, I_1404:K00588,PF13578.5,PF01596.16, I_1467:PF06271.11, I_1480:K06953,PF00149.27, I_1525:K01448,PF01520.17, I_1651:PF03160.13, I_1671:K12373,PF00754.24,PF00728.21,PF02838.14, I_1677:PF15902.4, I_1691:K01953,PF00733.20,PF00733.20,PF12481.7,PF13522.5,PF13537.5 I_1728:PF04932.14, I_1735:K02558,PF01225.24,PF08245.11, I_1748:PF13439.5,PF13692.5,PF13579.5, I_1767:01468,PF01979.19,PF07969.10, I_1815:PF13180.5,PF04389.16, I_1866:PF09822.8, I_1885:PF00171.21, I_1930:K00872,PF08544.12,PF00288.25, I_1950:PF00801.19,PF00801.19, I_1982:K00626,PF00109.25,PF02803.17,PF00108.22
BL_pooled_bin.full.145	hypothetical_protein
BL_pooled_bin.full.151	NA
BL_pooled_bin.full.596	I_1343:K09005,PF02643.14, I_1375:PF13602.5, I_1392:PF00583.24,PF13673.6,PF13508.6,PF08445.9, I_1401:PF03453.16, I_1508:PF01230.22
BL_pooled_bin.full.761	K07636,PF02518.25,PF14501.5,PF00512.24
s1032.ctg0011321_BL_0908sc	hypothetical_protein
s111.ctg000126e_BL_0908sc	I_955:K05785,PF02357.18, I_959:PF01370.20,PF16363.4, I_1915:PF07715.14,PF00593.23, I_1951:K01895,PF16177.4,PF00501.27,PF13193.5
s131.ctg000151c_BL_0908sc	NA
s215.ctg000240l_BL_0908sc	I_971:PF13464.5,PF13413.5
s226.ctg0024611_BL_0908sc	I_157:PF01471.17

s23.ctg0003451_BL_0902sc	1_1152:PF03030.15
s249.ctg000271_BL_0908sc	1_582:PF01850.20, 1_935:PF02604.18, 1_1126:PF14312.5,PF14312.5,PF14312.5,PF14312.5, PF14312.5,PF14312.5,PF14312.5
s266.ctg0002971_BL_0908sc	hypothetical_protein
s325.ctg000366c_BL_0908sc	1_67:K00568,PF05219.11,PF08241.11,PF08242.11,PF13489.5, PF13649.5,PF13847.5,PF13679.5,PF07021.11 1_512:PF13472.5
s35.ctg000041c_BL_0902sc	NA
s388.ctg0004351_BL_0908sc	1_124:PF14333.5, 1_129:K01673,PF00484.18, 1_272:K00537,PF03960.14, 1_439:PF01915.21, 1_1031:K03641,PF08662.10,PF07676.11,PF04052.12 1_807:K08968,PF13185.5, 1_1104:PF00162.18, 1_1708:PF00144.23 1_1515:K15727,PF00364.21,PF13533.5,PF13437.5,PF16576.4,PF16576.4, 1_1520:PF02321.17,PF02321.17, 1_1673:PF13443.5,PF01381.21,PF13560.5,
s44.ctg0000521_BL_0902sc	1_309:PF11146.7, 1_581:PF13884.5
s7.ctg0004471_BL_0908sc	NA
s96.ctg000111c_BL_0908sc	

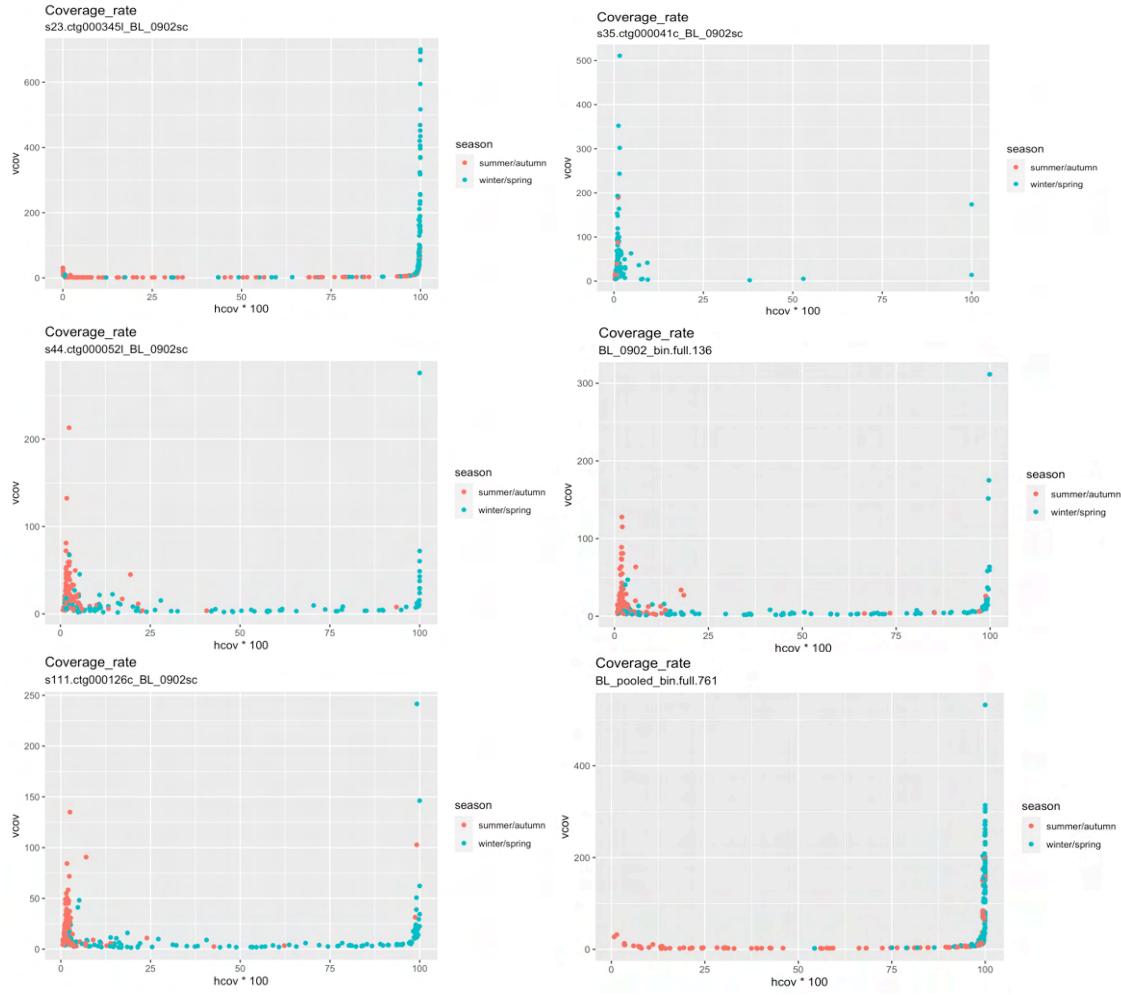
Supplementary Table 5: The annotation of the adaptive genes we found in both time series for each of the 30 MAGs.



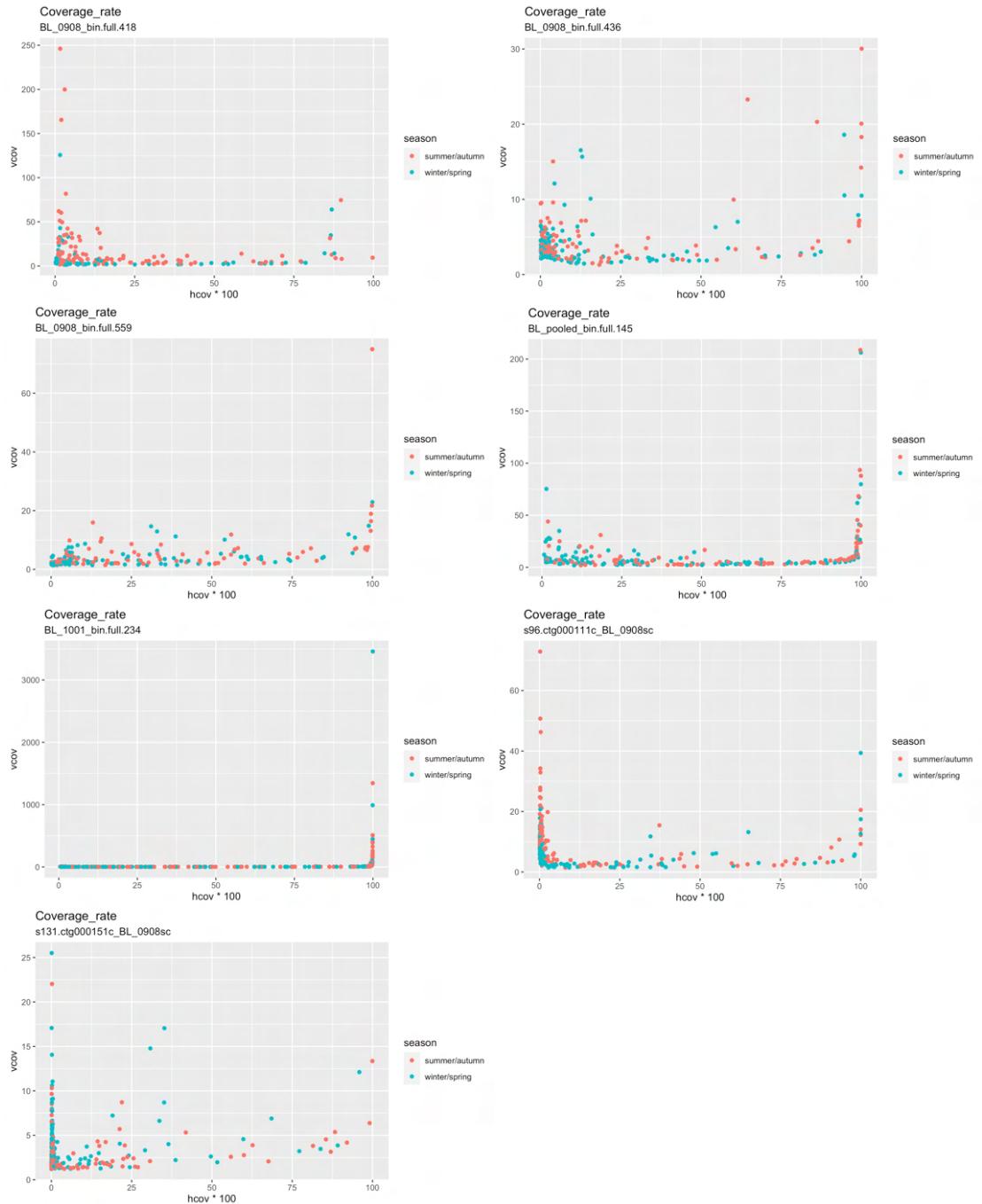
Supplementary Figure 1: The covering percentage of hits on MAGs (Horizontal coverage) and the average hits number per nucleotide in the mapped region of MAG (vertical coverage) for 8 MAGs from the Summer/Autumn group. The samples were plotted in different colors depending on their collected season.



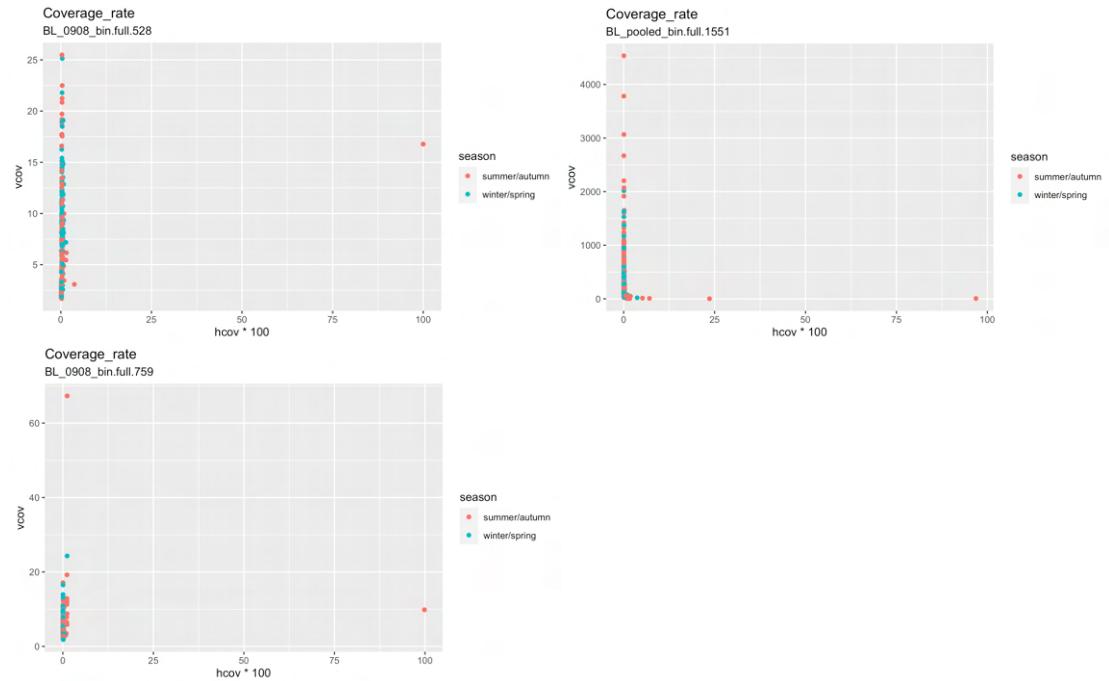
Supplementary Figure 2: The covering percentage of hits on MAGs (Horizontal coverage) and the average hits number per nucleotide in the mapped region of MAG (vertical coverage) for 6 MAGs from the Summer/Autumn group. The samples were plotted in different colors depending on their collected season.



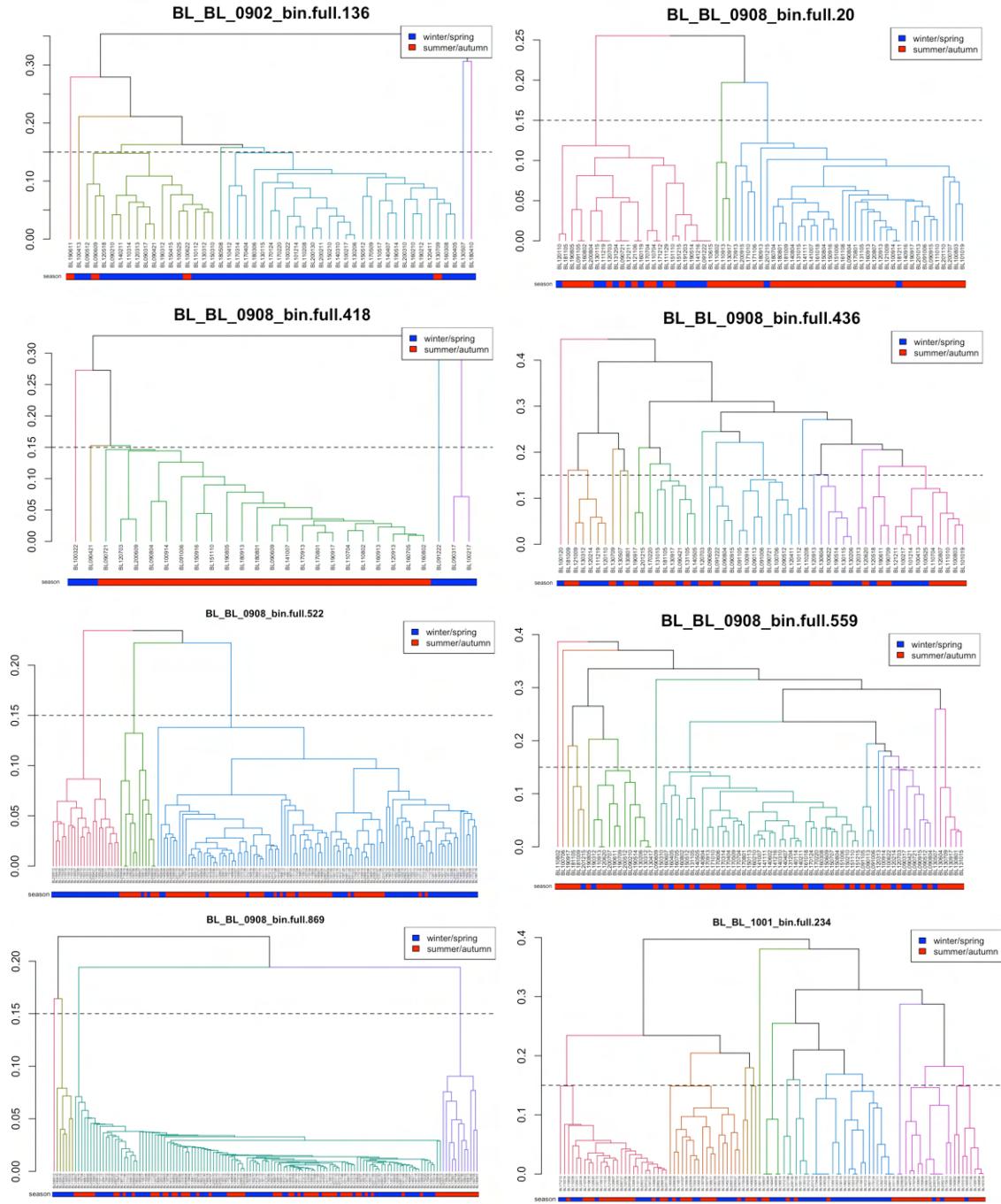
Supplementary Figure 3: The covering percentage of hits on MAGs (Horizontal coverage) and the average hits number per nucleotide in the mapped region of MAG (vertical coverage) for 6 MAGs from the Winter/Spring group. The samples were plotted in different colors depending on their collected season.



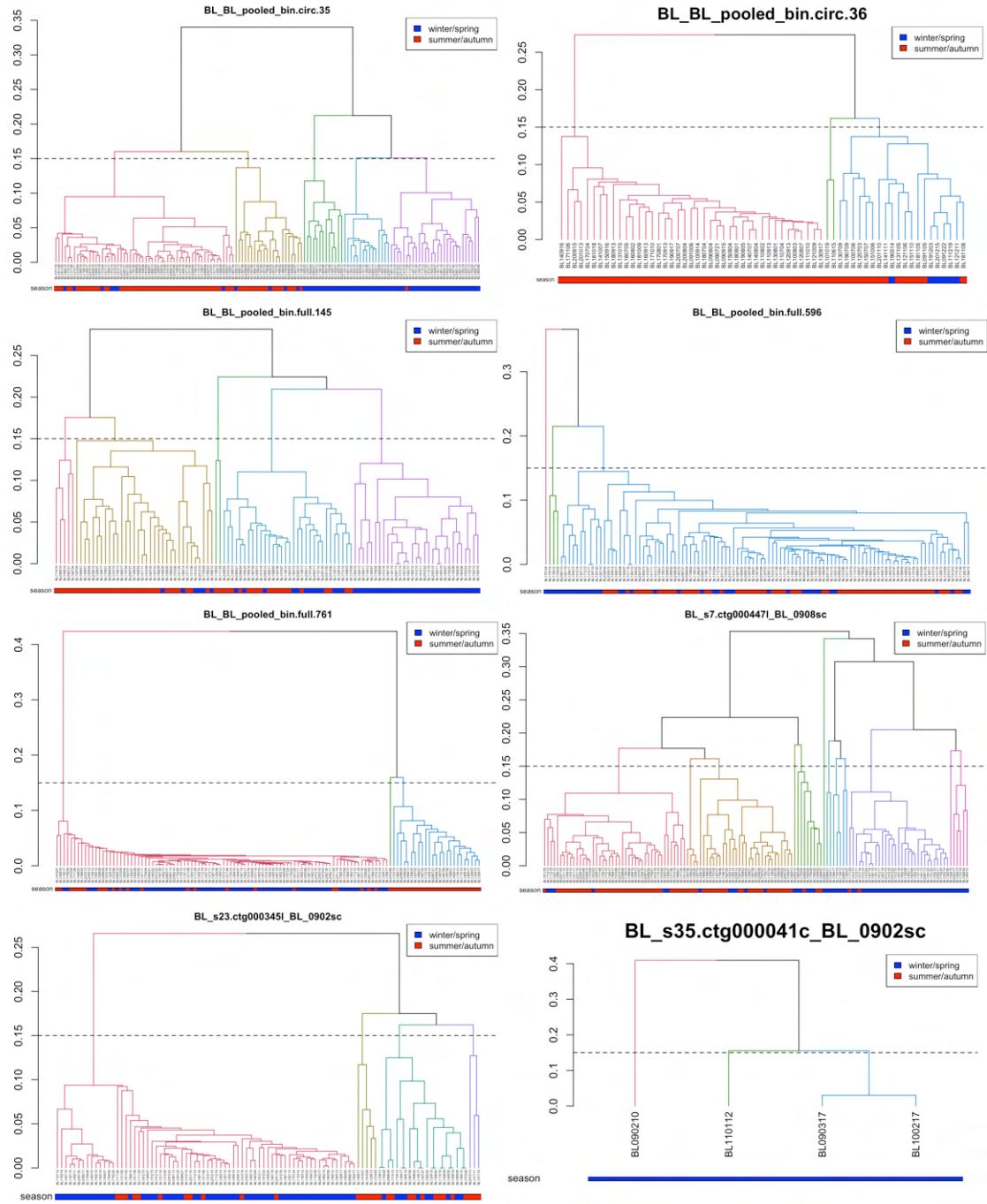
Supplementary Figure 4: The covering percentage of hits on MAGs (Horizontal coverage) and the average hits number per nucleotide in the mapped region of MAG (vertical coverage) for 7 MAGs from the Others group. The samples were plotted in different colors depending on their collected season.



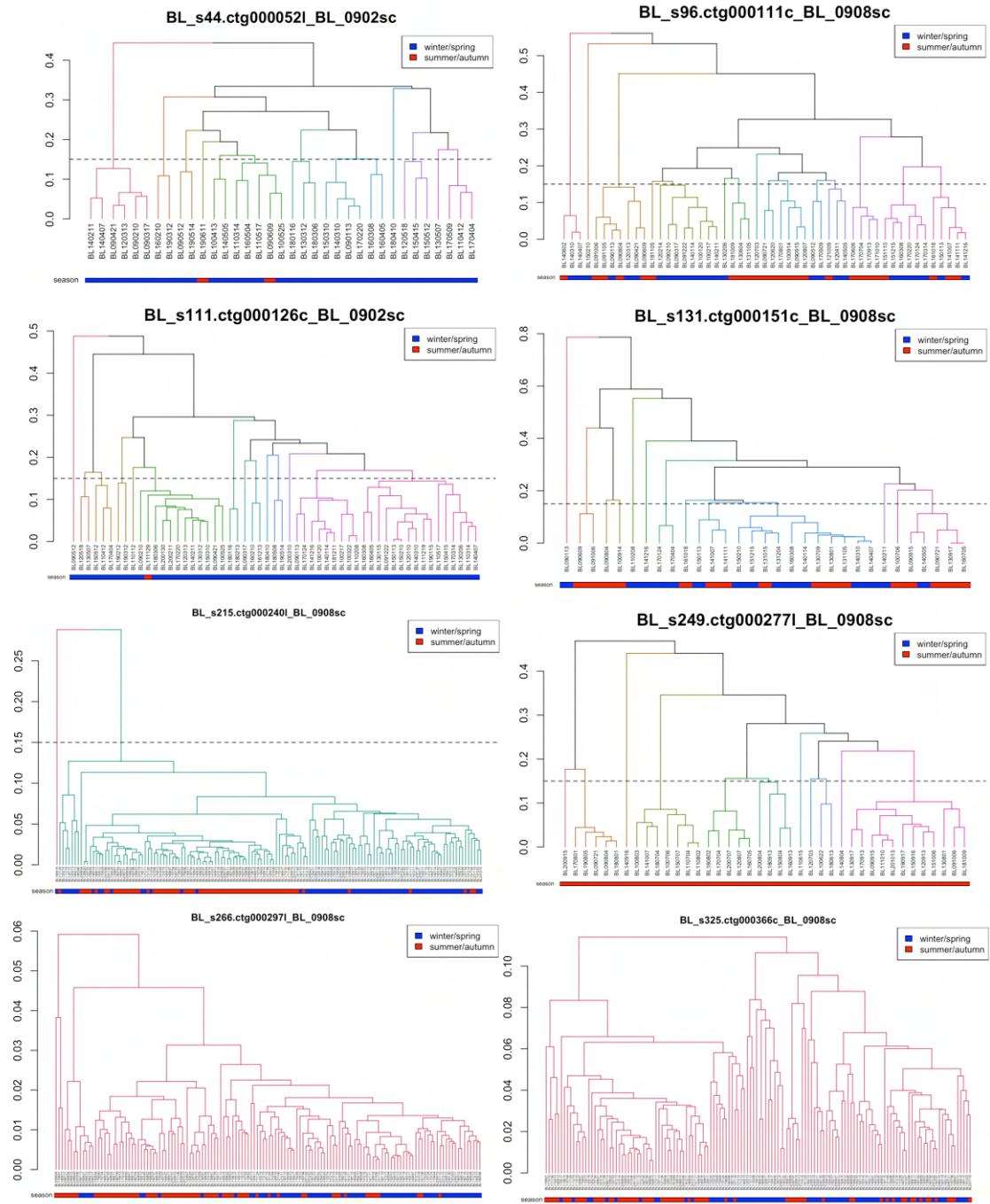
Supplementary Figure 5: The covering percentage of hits on MAGs (Horizontal coverage) and the average hits number per nucleotide in the mapped region of MAG (vertical coverage) for 3 MAGs from the Others group. The samples were plotted in different colors depending on their collected season.



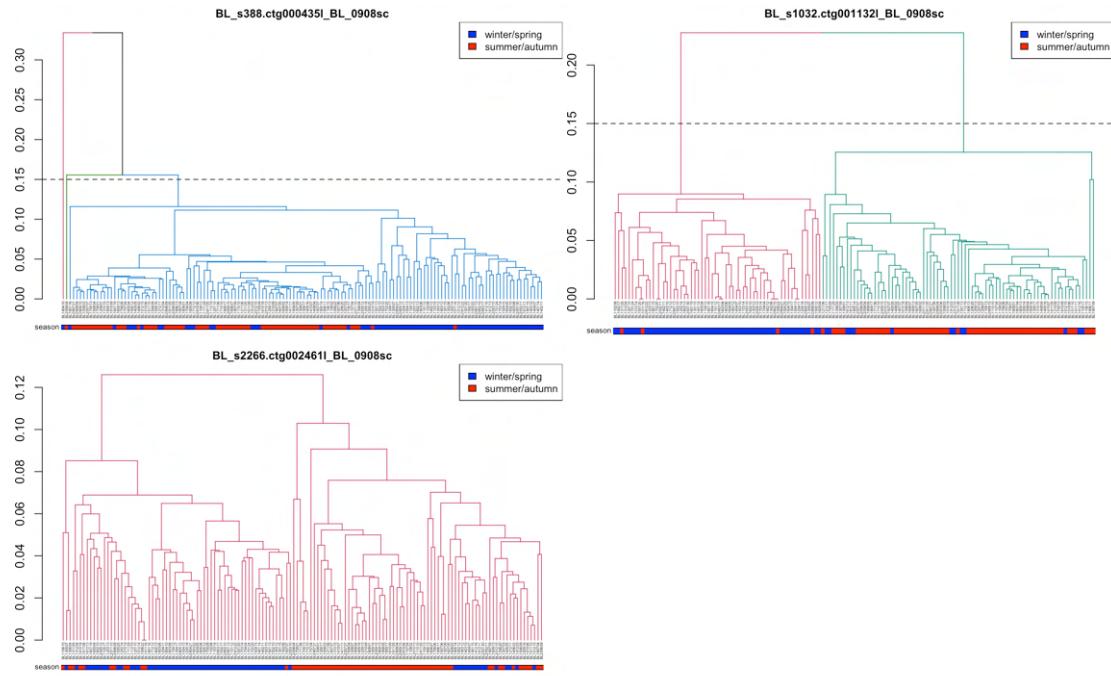
Supplementary Figure 6: Fixation Index (Fst) distance dendograms for 8 MAGs from BBMO time series. The tree was cut at 0.15 Fst and subtrees were colored differently according to the varying populations. The color bar shows the season when these short-read genome samples were collected. Any sample with a covering percentage of hits on MAGs less than 25% was excluded.



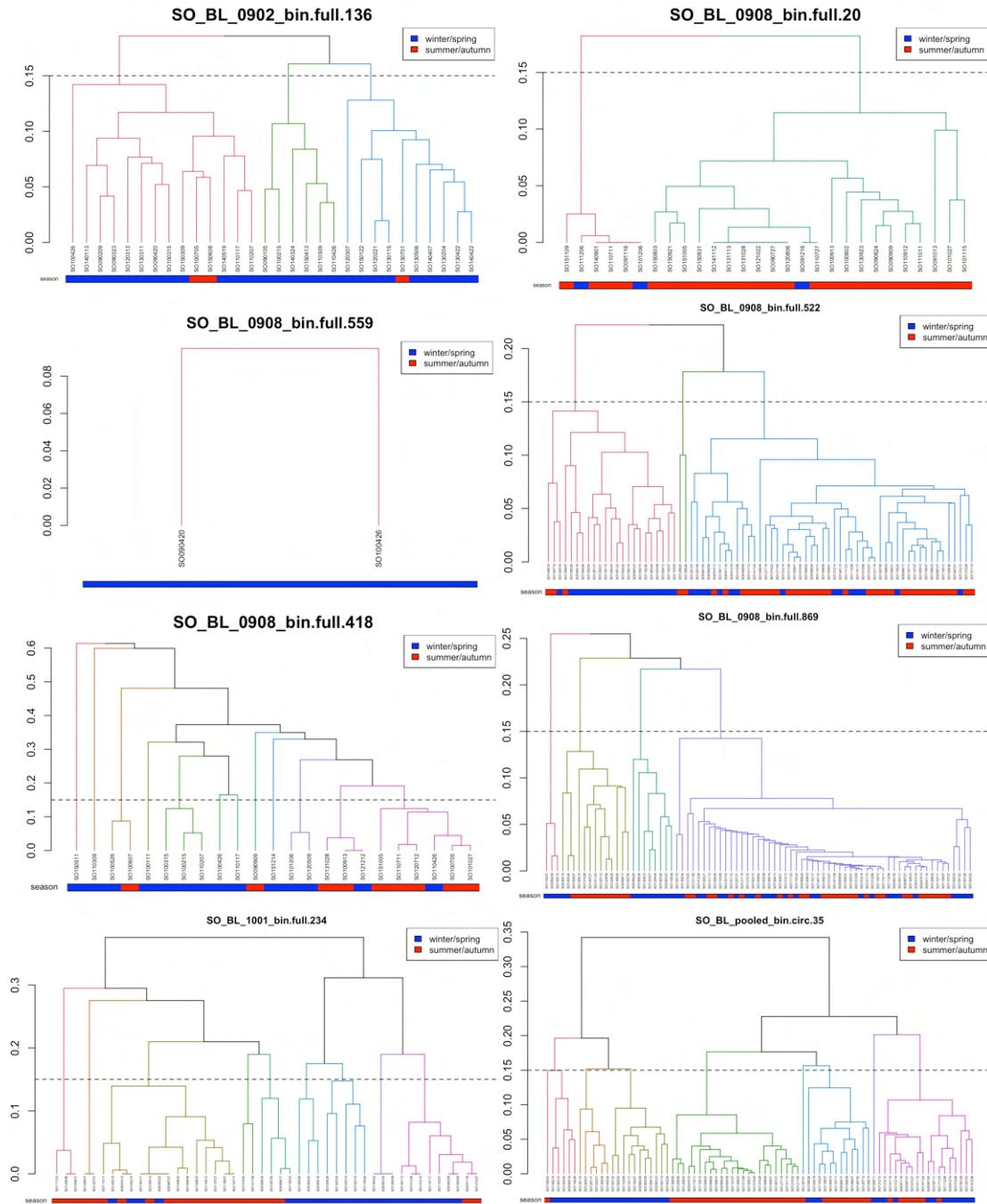
Supplementary Figure 7: Fixation Index (Fst) distance dendograms for 8 MAGs from BBMO time series. The tree was cut at 0.15 Fst and subtrees were colored differently according to the varying populations. The color bar shows the season when these short-read genome samples were collected. Any sample with a covering percentage of hits on MAGs less than 25% was excluded.



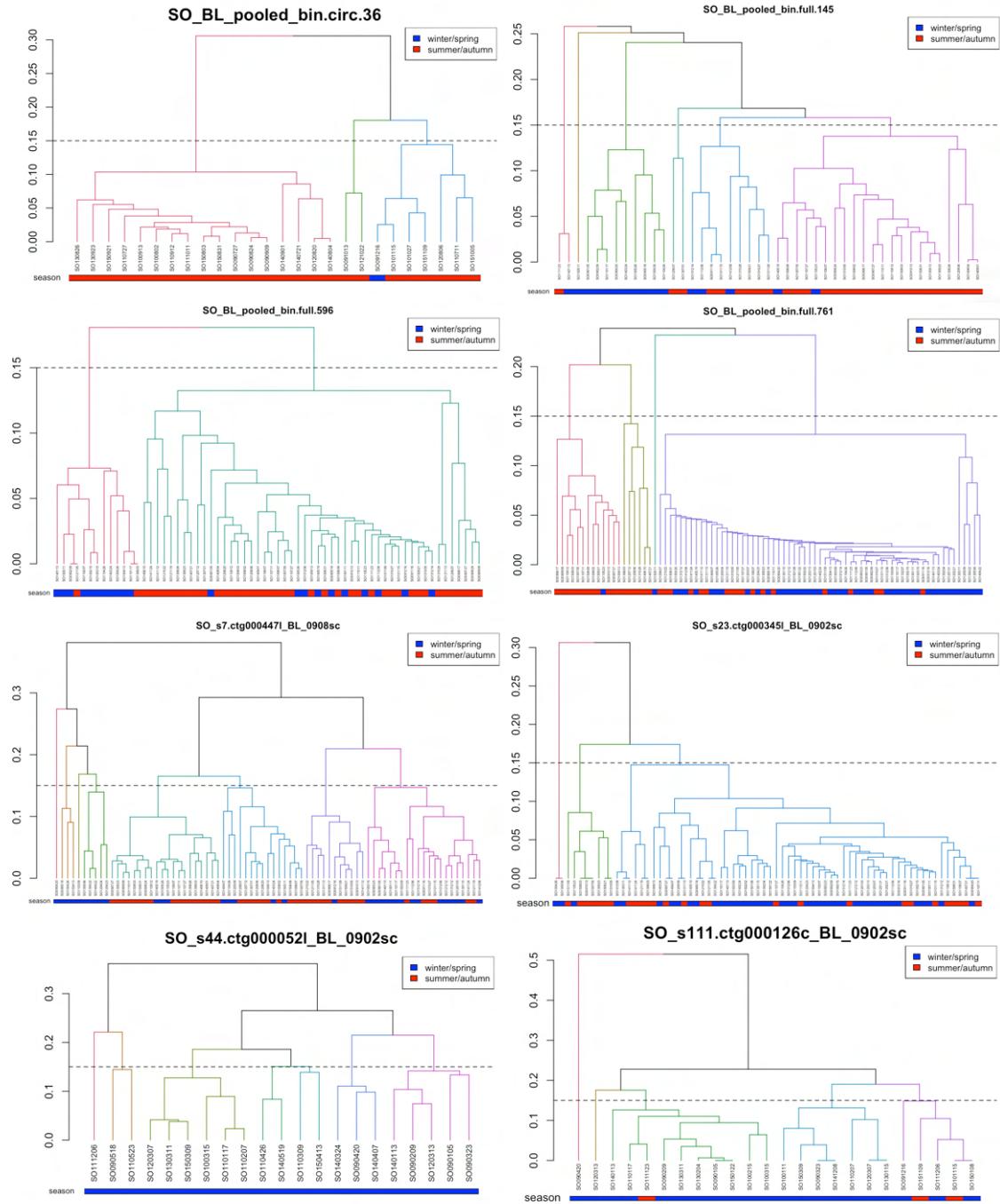
Supplementary Figure 8: Fixation Index (Fst) distance dendograms for 8 MAGs from BBMO time series. The tree was cut at 0.15 Fst and subtrees were colored differently according to the varying populations. The color bar shows the season when these short-read genome samples were collected. Any sample with a covering percentage of hits on MAGs less than 25% was excluded.



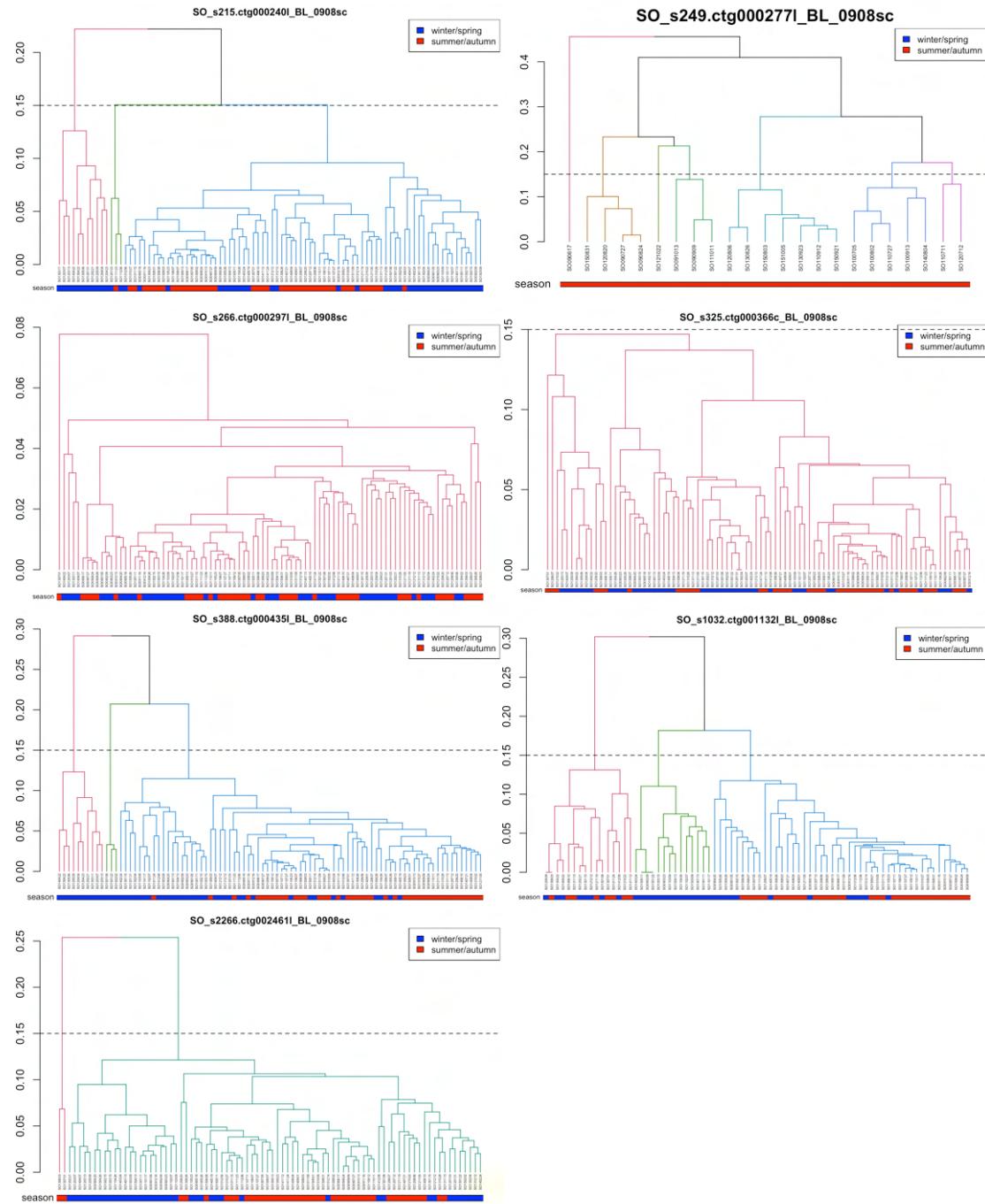
Supplementary Figure 9: Fixation Index (Fst) distance dendograms for 3 MAGs from BBMO time series. The tree was cut at 0.15 Fst and subtrees were colored differently according to the varying populations. The color bar shows the season when these short-read genomes samples were collected. Any sample with a covering percentage of hits on MAGs less than 25% was excluded.



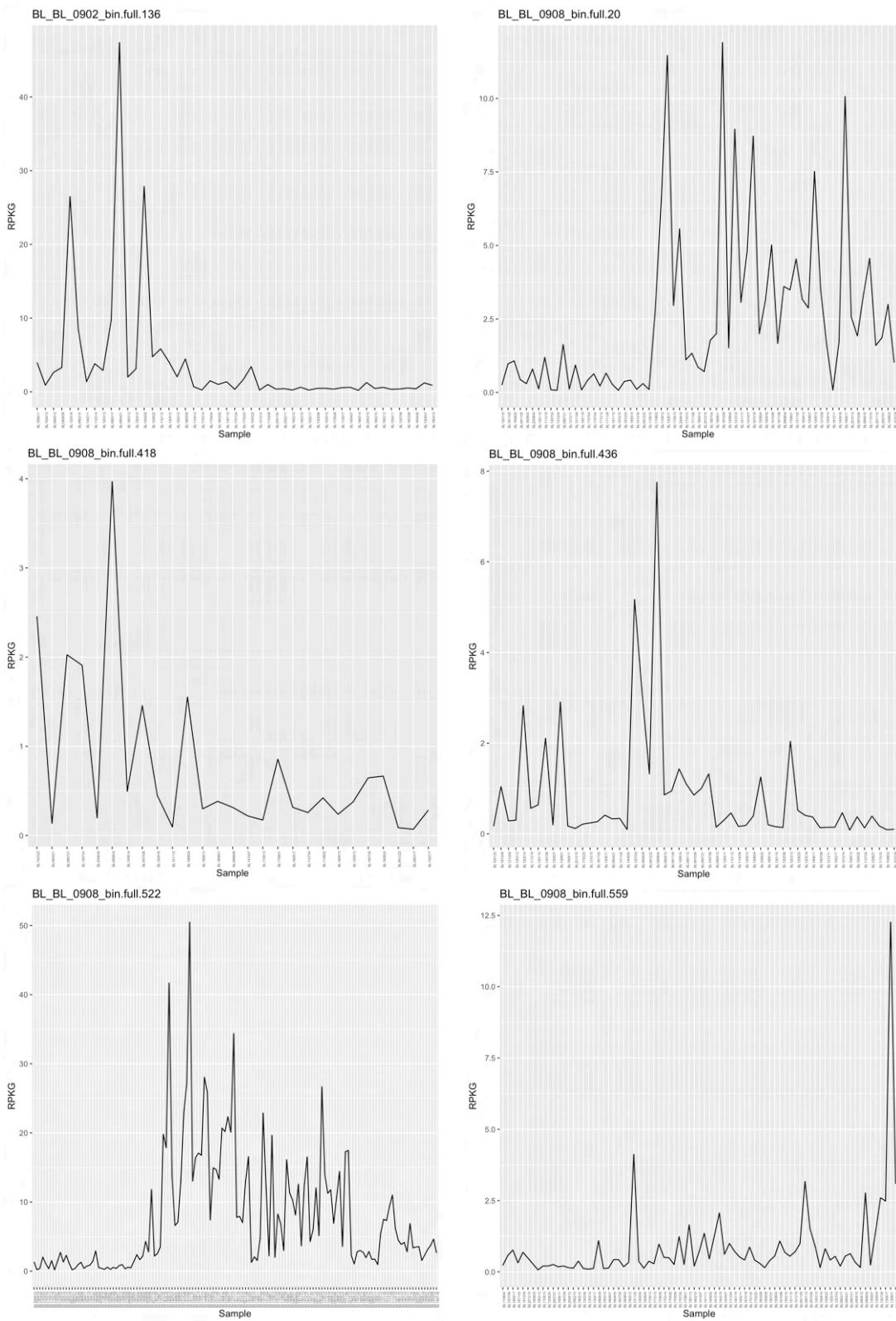
Supplementary Figure 10: Fixation Index (Fst) distance dendograms for 8 MAGs from SOLA time series. The tree was cut at 0.15 Fst and subtrees were colored differently according to the varying populations. The color bar shows the season when these short-read genome samples were collected. Any sample with a covering percentage of hits on MAGs less than 25% was excluded.



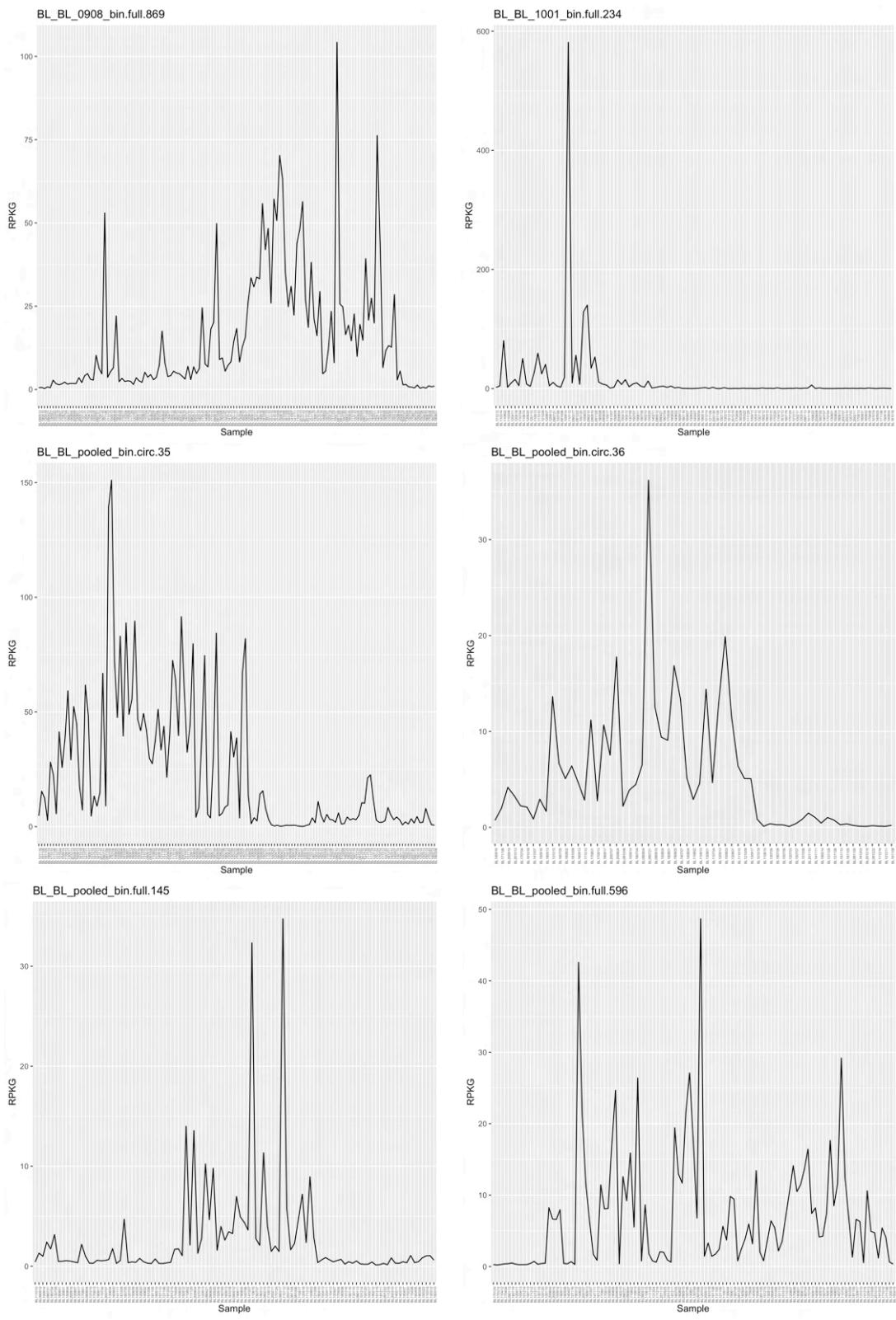
Supplementary Figure 11: Fixation Index (Fst) distance dendograms for 8 MAGs from SOLA time series. The tree was cut at 0.15 Fst and subtrees were colored differently according to the varying populations. The color bar shows the season when these short-read genome samples were collected. Any sample with a covering percentage of hits on MAGs less than 25% was excluded.



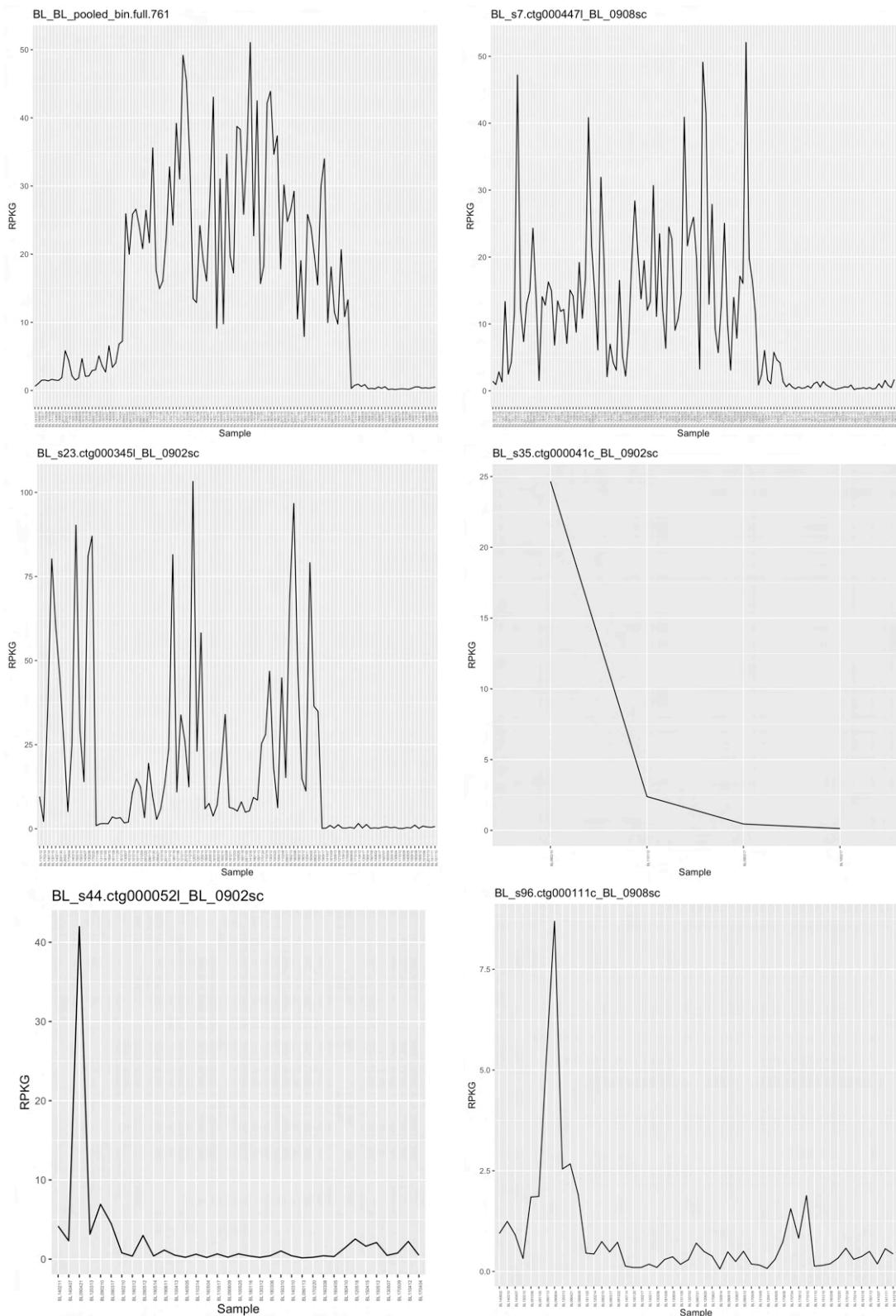
Supplementary Figure 12: Fixation Index (Fst) distance dendograms for 7 MAGs from SOLA time series. The tree was cut at 0.15 Fst and subtrees were colored differently according to the varying populations. The color bar shows the season when these short-read genomes samples were collected. Any sample with a covering percentage of hits on MAGs less than 25% was excluded.



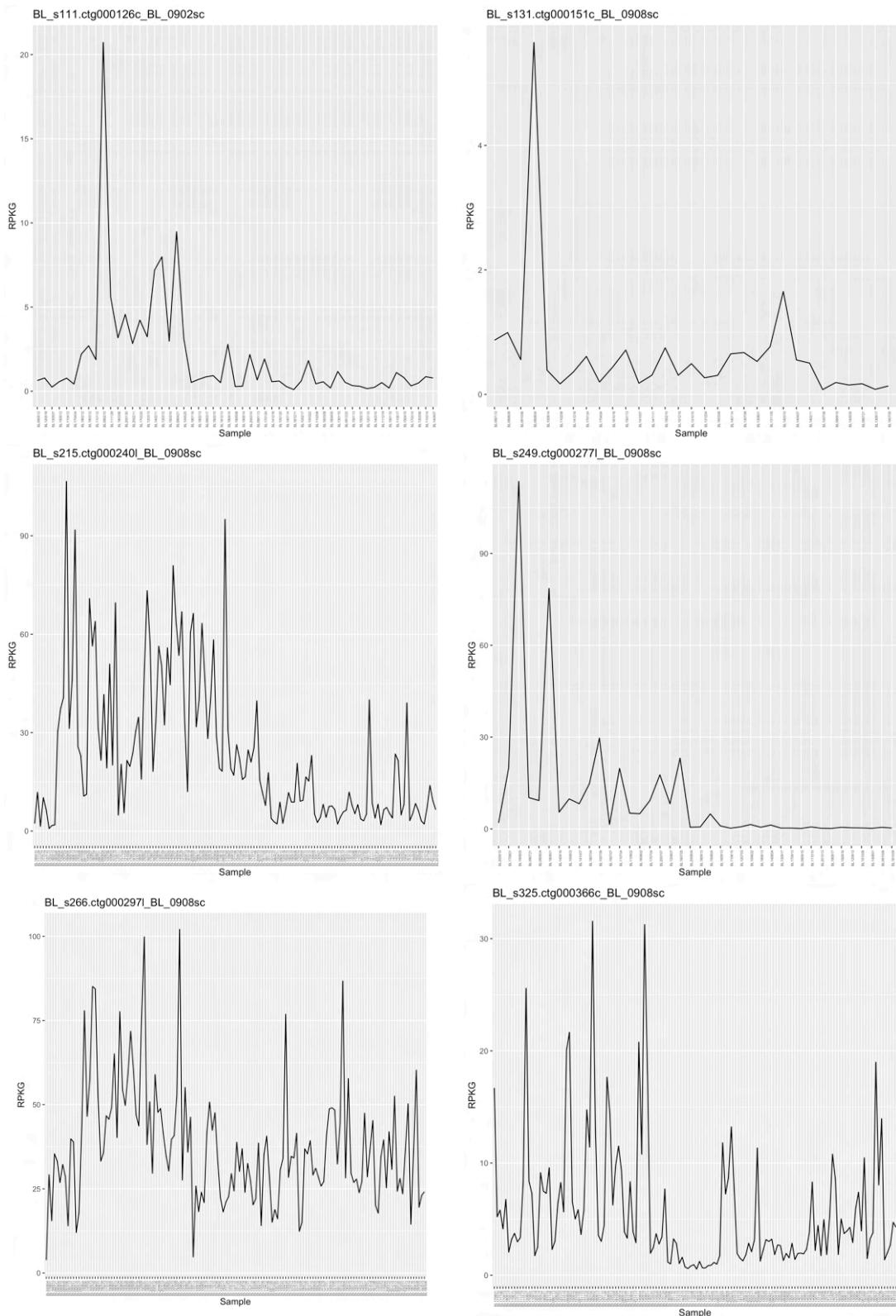
Supplementary Figure 13: Relative abundance of 6 MAGs across the 140 samplings for 12 years from 2009-2020 (BBMO). Along the x-axis is the sequence of sampling months from the 1st to the 140th. RPKG values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded.



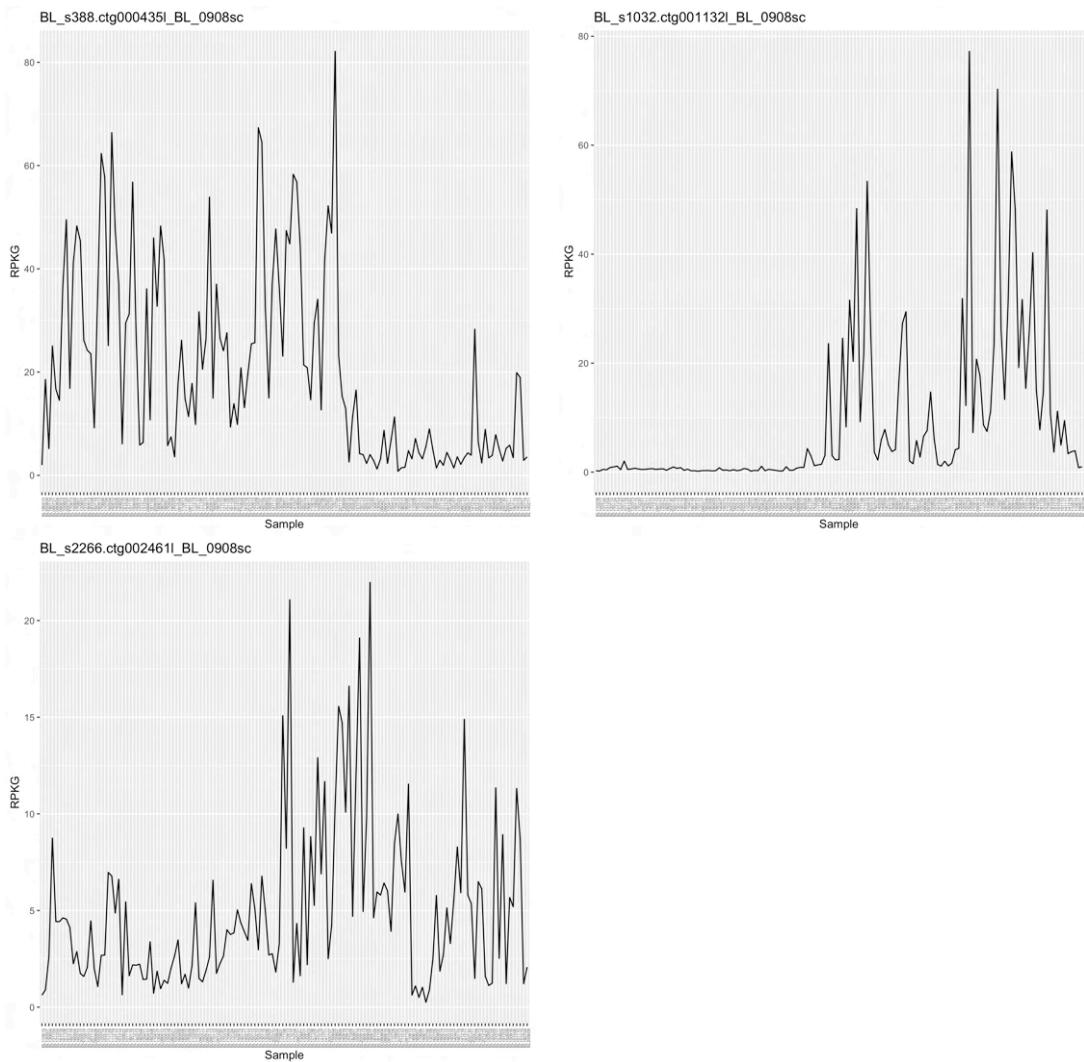
Supplementary Figure 14: Relative abundance of 6 MAGs across the 140 samplings for 12 years from 2009-2020 (BBMO). Along the x-axis is the sequence of sampling months from the 1st to the 140th. RPKG values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded.



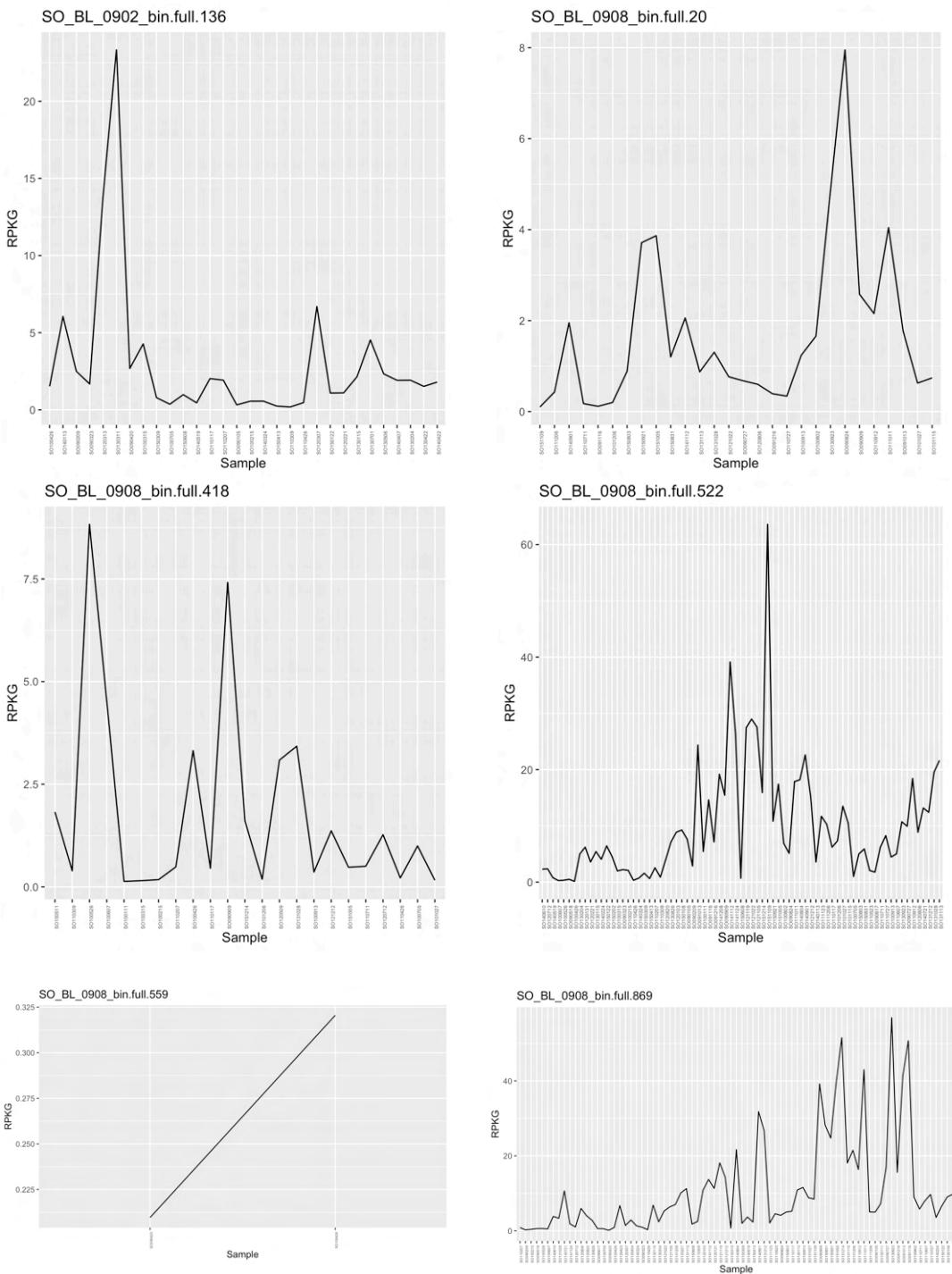
Supplementary Figure 15: Relative abundance of 6 MAGs across the 140 samplings for 12 years from 2009-2020 (BBMO). Along the x-axis is the sequence of sampling months from the 1st to the 140th. RPKG values are measured along the y-axis. Any sample with a covering percentage on MAGs less than 25% was excluded.



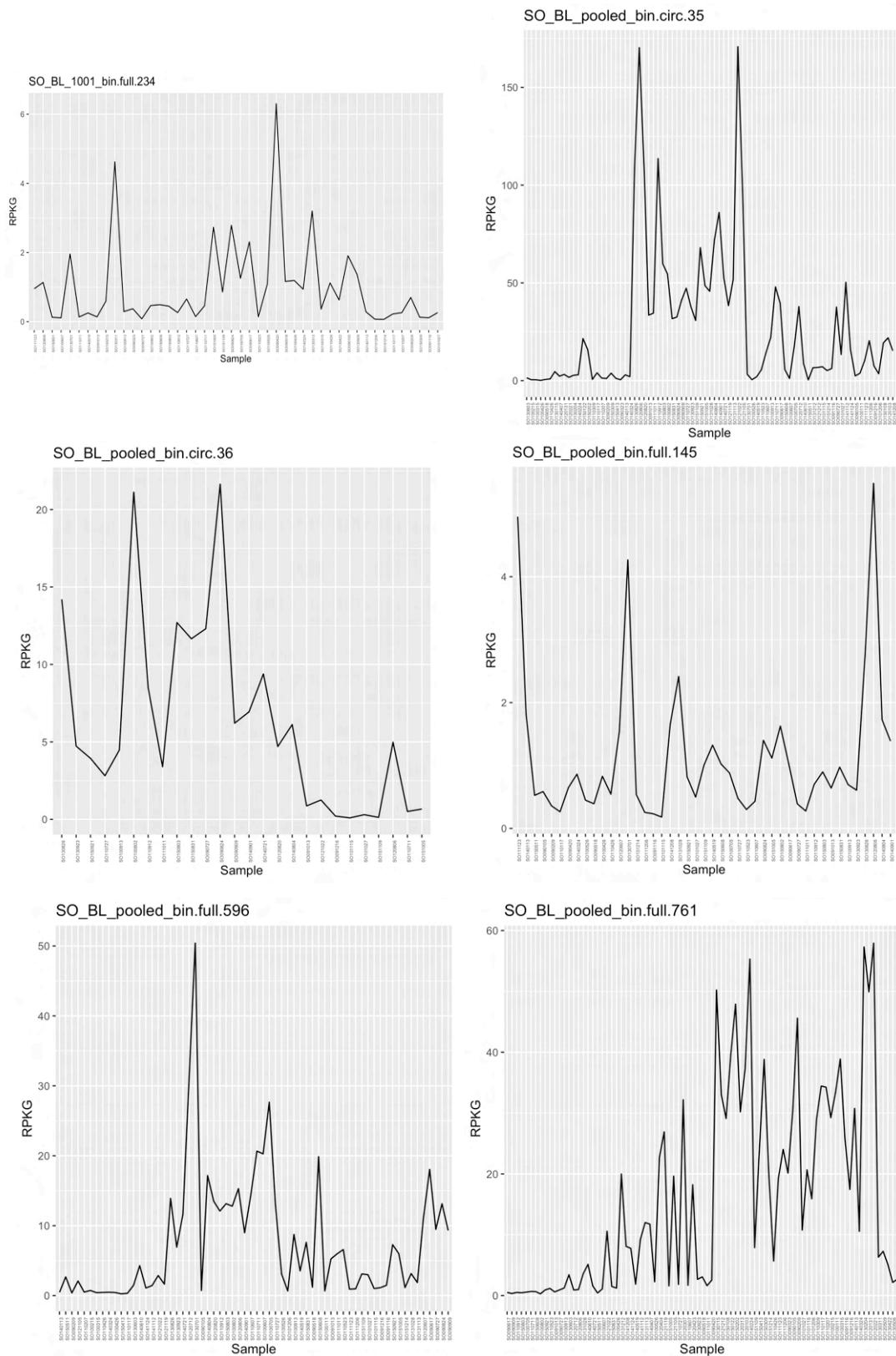
Supplementary Figure 16: Relative abundance of 6 MAGs across the 140 samplings for 12 years from 2009-2020 (BBMO). Along the x-axis is the sequence of sampling months from the 1st to the 140th. RPKG values are measured along the y-axis. Any sample with a covering percentage on MAGs less than 25% was excluded.



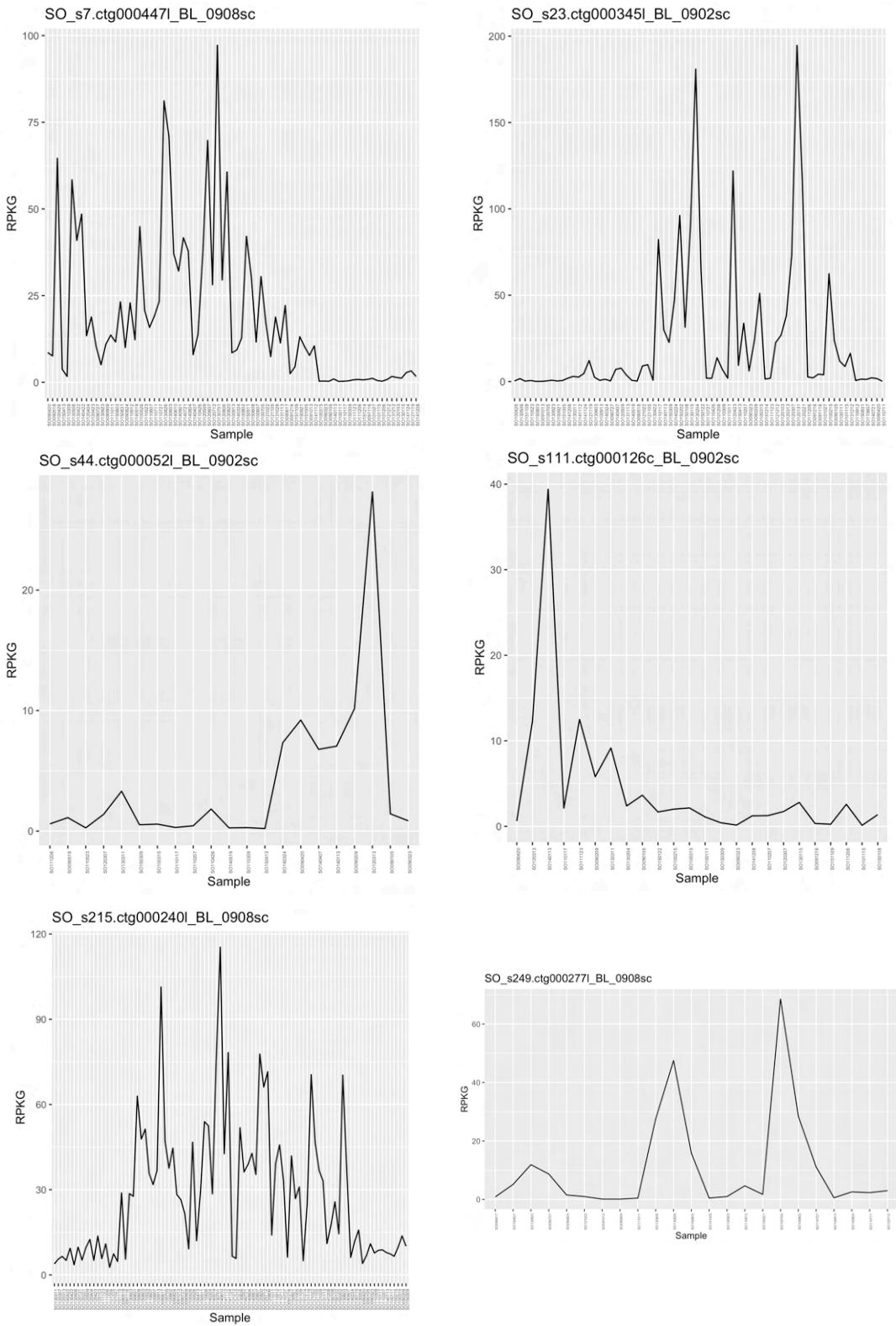
Supplementary Figure 17: Relative abundance of 3 MAGs across the 140 samplings for 12 years from 2009-2020 (BBMO). Along the x-axis is the sequence of sampling months from the 1st to the 140th. RPKG values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded.



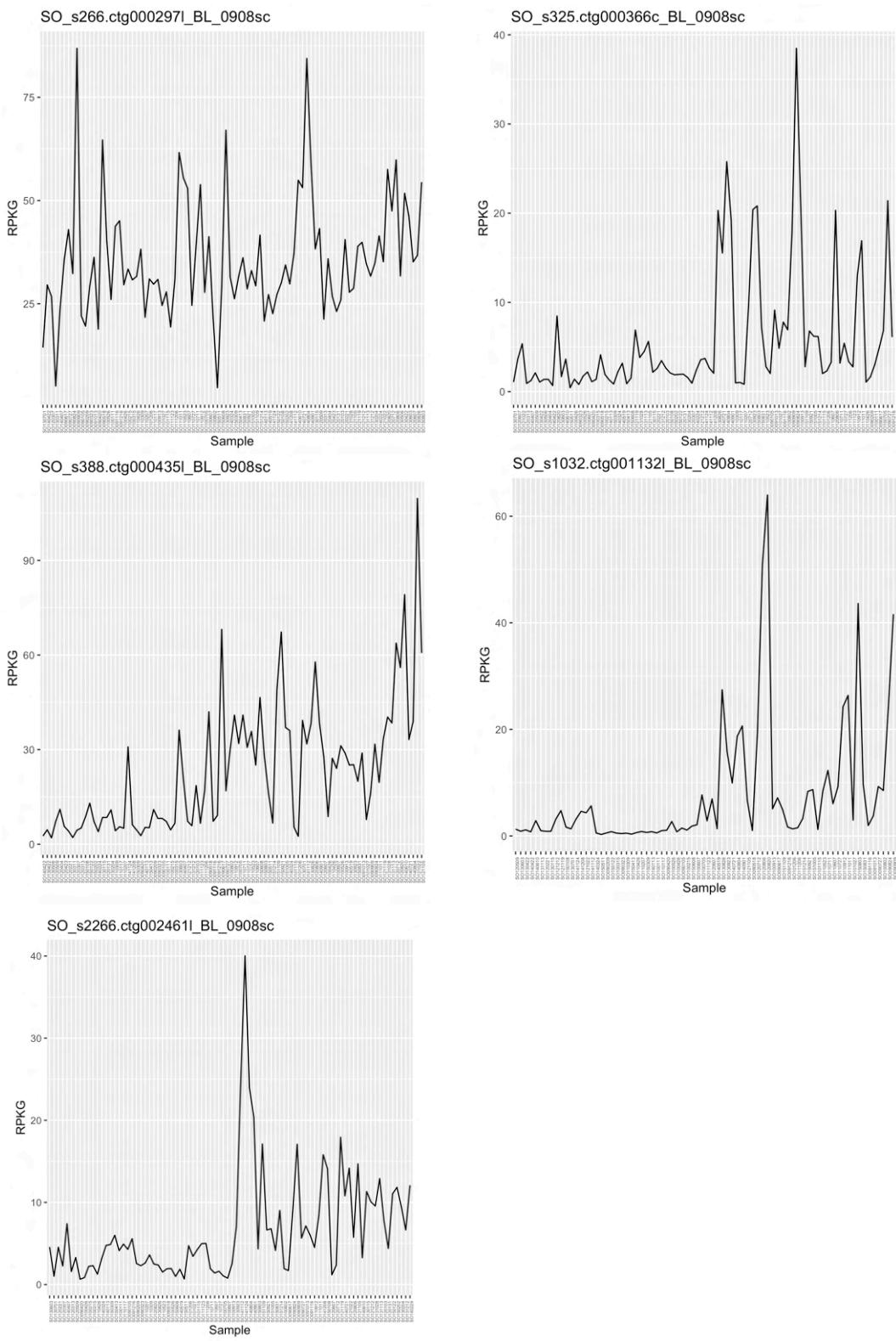
Supplementary Figure 18: Relative abundance of 6 MAGs across the 90 samplings for 7 years from 2009-2015 (SOLA). Along the x-axis is the sequence of sampling months from the 1st to the 90th. RPKG values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded.



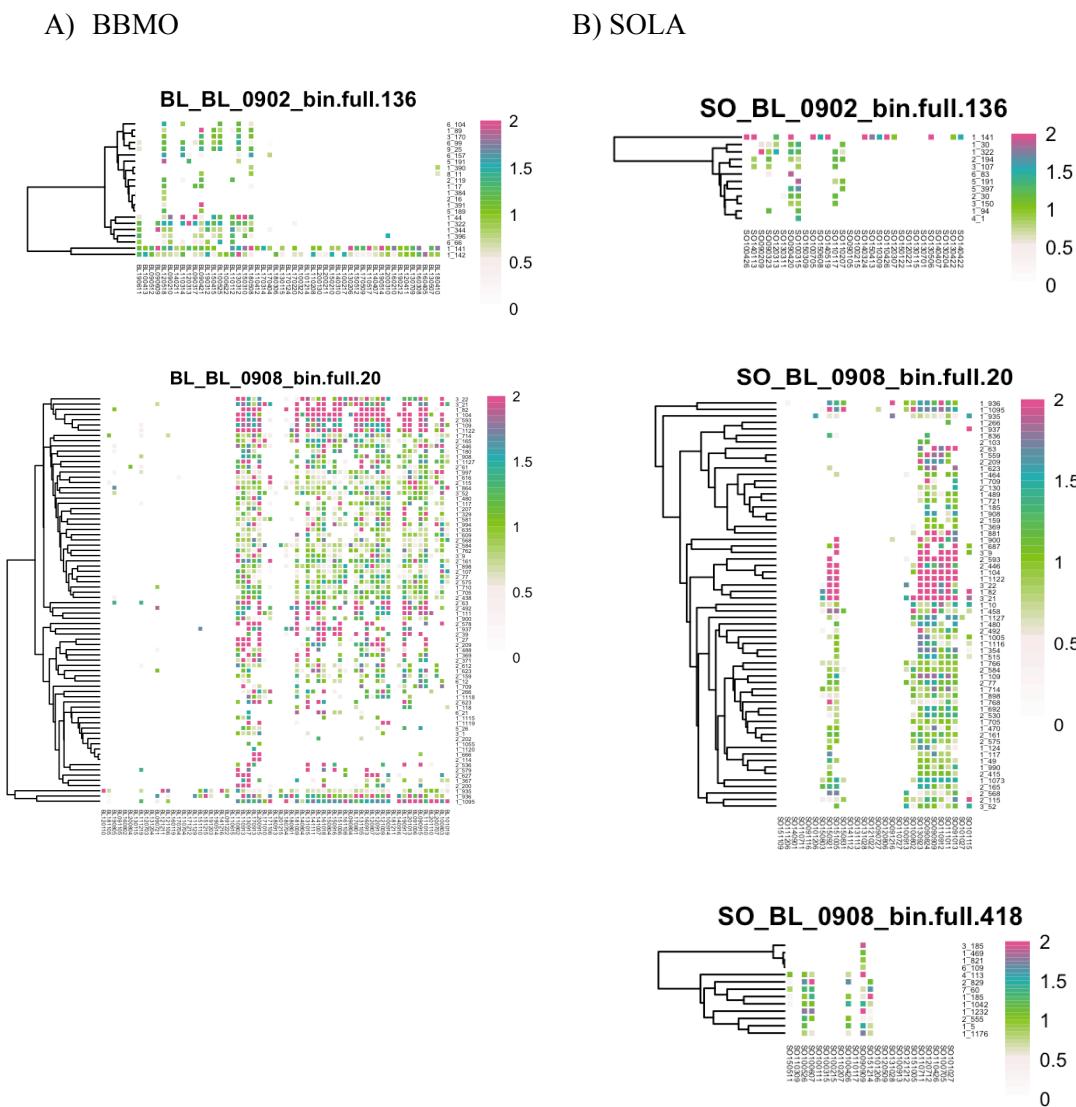
Supplementary Figure 19: Relative abundance of 6 MAGs across the 90 samplings for 7 years from 2009-2015 (SOLA). Along the x-axis is the sequence of sampling months from the 1st to the 90th. RPKG values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded.



Supplementary Figure 20: Relative abundance of 6 MAGs across the 90 samplings for 7 years from 2009-2015 (SOLA). Along the x-axis is the sequence of sampling months from the 1st to the 90th. RPKG values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded.

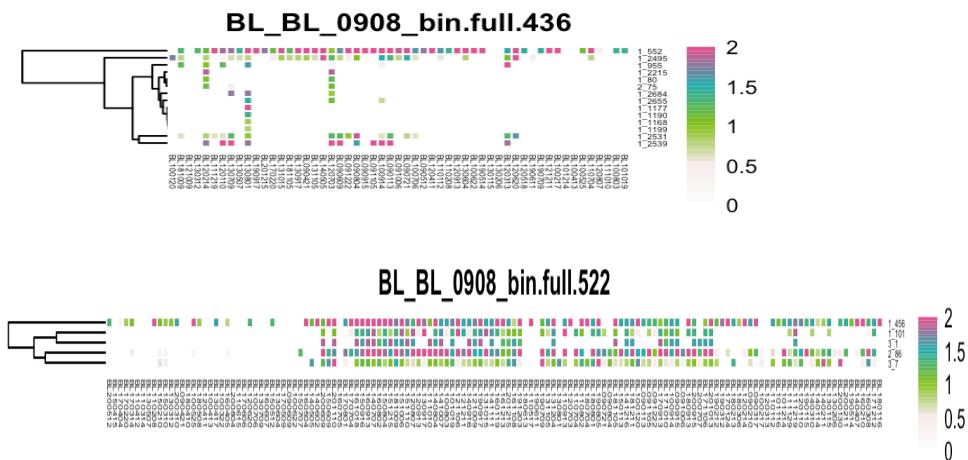


Supplementary Figure 21: Relative abundance of 5 MAGs across the 90 samplings for 7 years from 2009-2015 (SOLA). Along the x-axis is the sequence of sampling months from the 1st to the 90th. RPKG values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded.

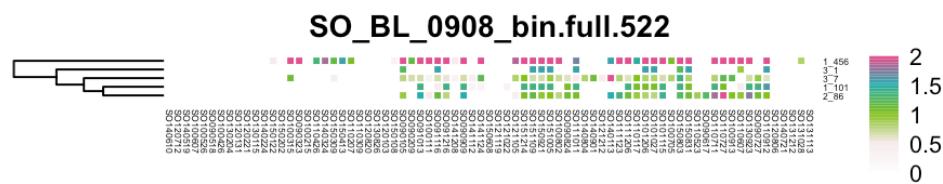


Supplementary Figure 22: Genes from 2 MAGs in both A) BBMO and B) SOLA time series exhibit positive selection patterns with a mean pN/pS ratio greater than 0.8. The color of cells represents the pN/pS ratio of a gene in a specific sample. White tails indicate NA values (pS = 0 in pN/pS calculations) due to missing mapping in those samples. The mean pN/pS ratio is calculated by excluding NA values, which leads to genes found in a limited number of samples (e.g., 1 sample) having a mean pN/pS ratio greater than 0.8. The genome “BL\_0908\_bin.full.418” has no adaptive gene found in the BBMO time series.

A) BBMO

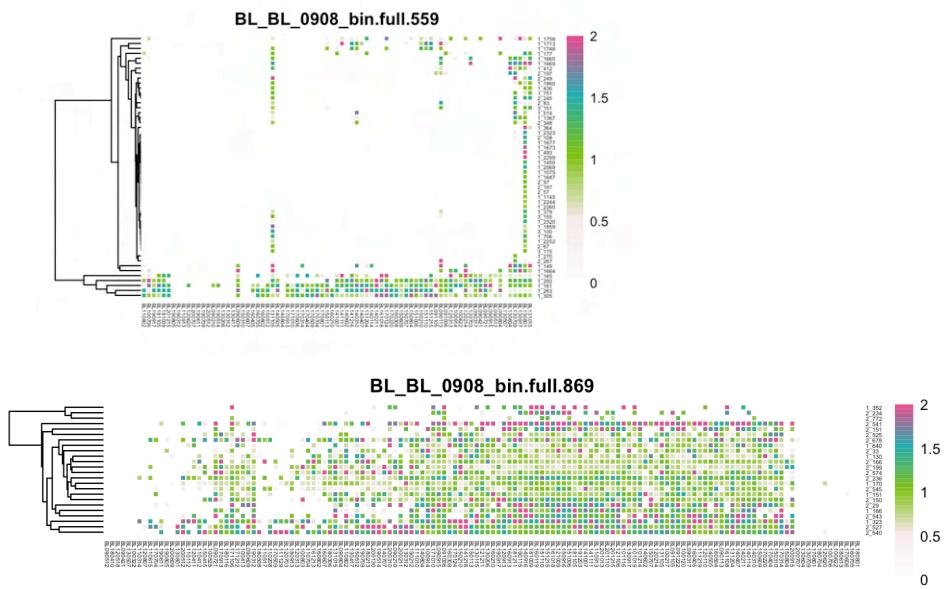


B) SOLA

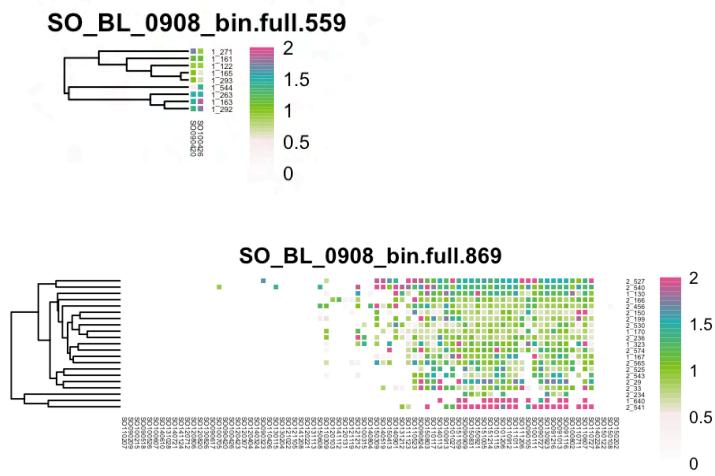


Supplementary Figure 23: Genes from MAG “BL\_0908\_bin.full.522” in both A) BBMO and B) SOLA time series exhibit positive selection patterns with a mean pN/pS ratio greater than 0.8. The color of cells represents the pN/pS ratio of a gene in a specific sample. White tails indicate NA values ( $pS = 0$  in pN/pS calculations) due to missing mapping in those samples. The mean pN/pS ratio is calculated by excluding NA values, which leads to genes found in a limited number of samples (e.g., 1 sample) having a mean pN/pS ratio greater than 0.8. The genome “BL\_0908\_bin.full.436” has no adaptive gene found in the SOLA time series.

A) BBMO

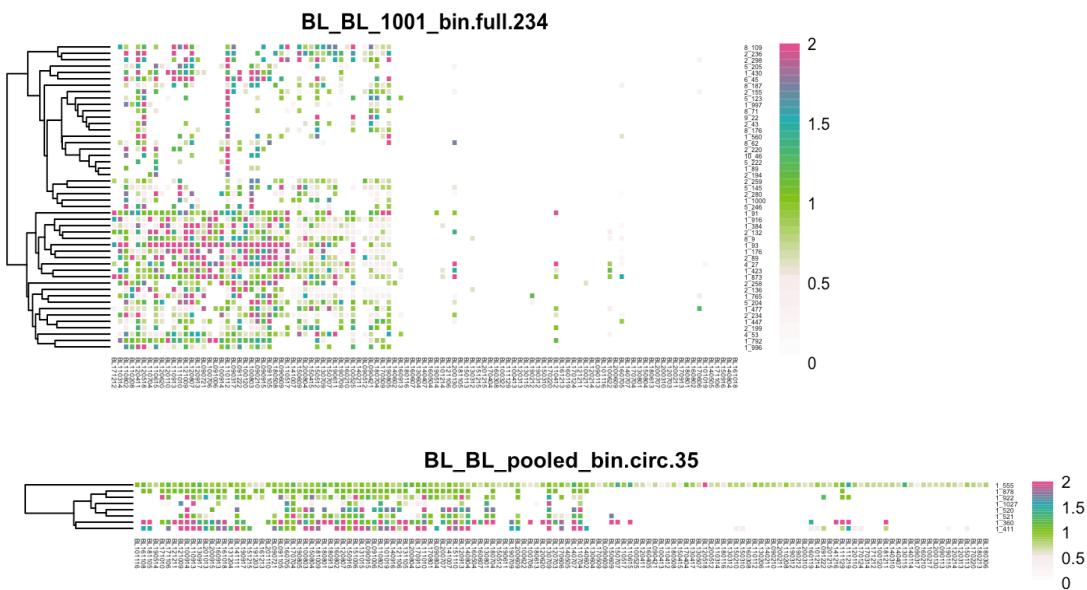


B) SOLA

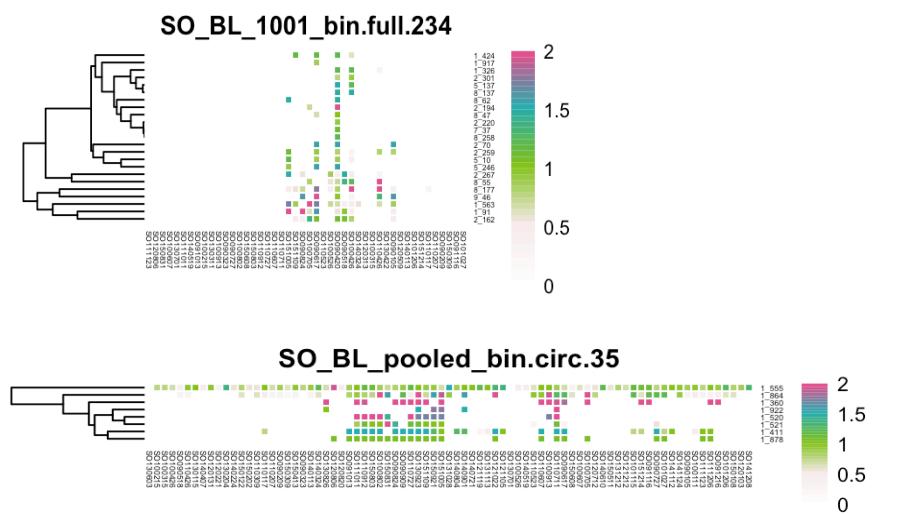


Supplementary Figure 24: Genes from 2 MAGs in both A) BBMO and B) SOLA time series exhibit positive selection patterns with a mean pN/pS ratio greater than 0.8. The color of cells represents the pN/pS ratio of a gene in a specific sample. White tails indicate NA values (pS = 0 in pN/pS calculations) due to missing mapping in those samples. The mean pN/pS ratio is calculated by excluding NA values, which leads to genes found in a limited number of samples (e.g., 1 sample) having a mean pN/pS ratio greater than 0.8.

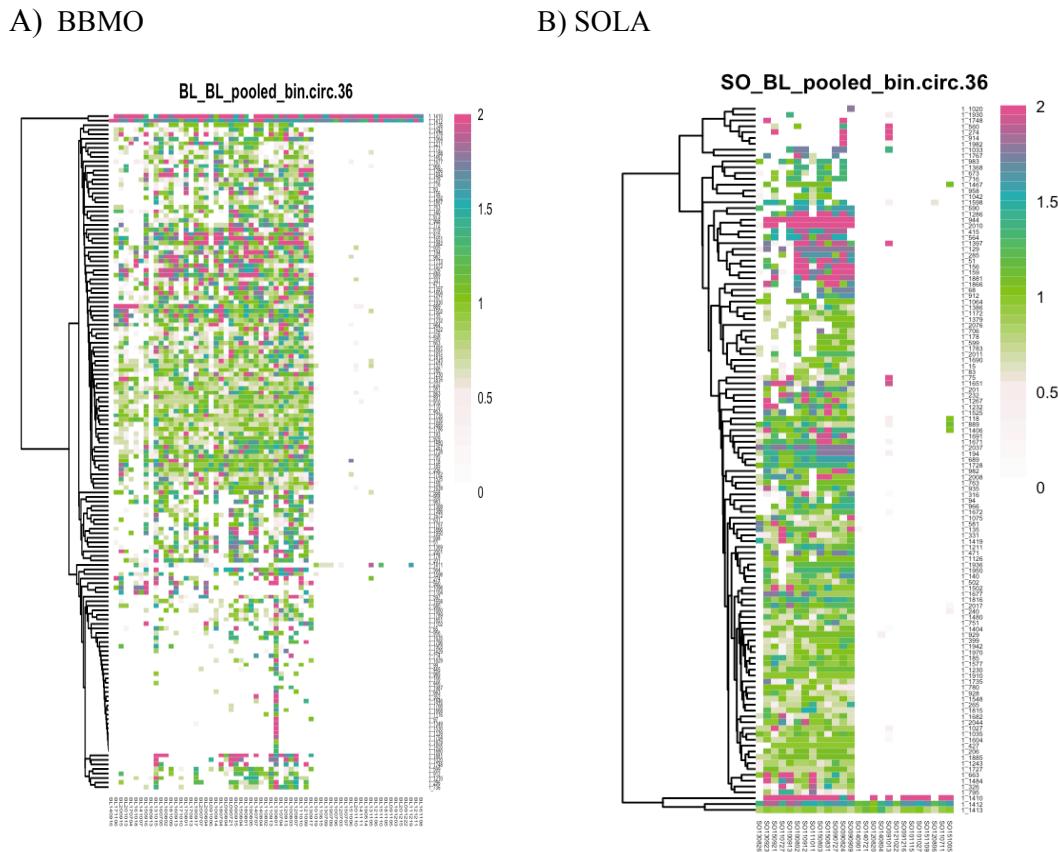
### A) BBMO



### B) SOLA

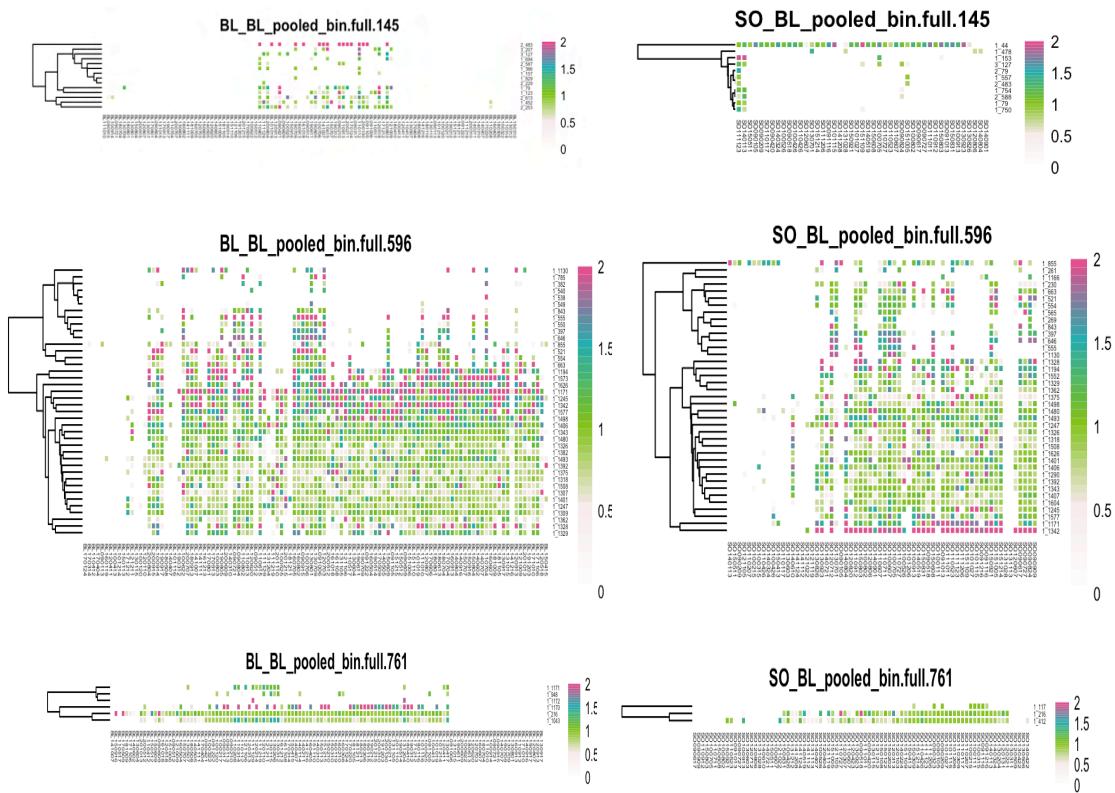


Supplementary Figure 25: Genes from 2 MAGs in both A) BBMO and B) SOLA time series exhibit positive selection patterns with a mean pN/pS ratio greater than 0.8. The color of cells represents the pN/pS ratio of a gene in a specific sample. White tails indicate NA values (pS = 0 in pN/pS calculations) due to missing mapping in those samples. The mean pN/pS ratio is calculated by excluding NA values, which leads to genes found in a limited number of samples (e.g., 1 sample) having a mean pN/pS ratio greater than 0.8.



Supplementary Figure 26: Genes from MAG “BL\_pooled\_bin.circ.36” in both A)BMMO and B)SOLA time series exhibit positive selection patterns with a mean pN/pS ratio greater than 0.8. The color of cells represents the pN/pS ratio of a gene in a specific sample. White tails indicate NA values ( $pS = 0$  in pN/pS calculations) due to missing mapping in those samples. The mean pN/pS ratio is calculated by excluding NA values, which leads to genes found in a limited number of samples (e.g., 1 sample) having a mean pN/pS ratio greater than 0.8.

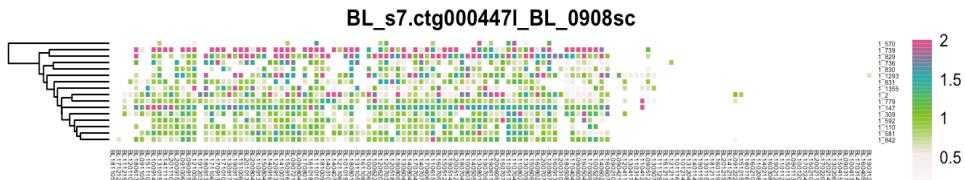
A) BBMO



B) SOLA

Supplementary Figure 27: Genes from 3 MAGs in both A) BBMO and B) SOLA time series exhibit positive selection patterns with a mean pN/pS ratio greater than 0.8. The color of cells represents the pN/pS ratio of a gene in a specific sample. White tails indicate NA values (pS = 0 in pN/pS calculations) due to missing mapping in those samples. The mean pN/pS ratio is calculated by excluding NA values, which leads to genes found in a limited number of samples (e.g., 1 sample) having a mean pN/pS ratio greater than 0.8.

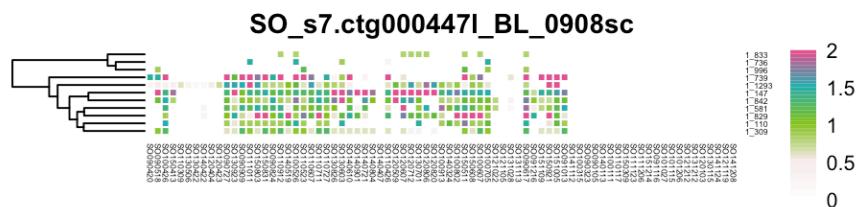
A) BBMO



BL\_s23.ctg000345I\_BL\_0902sc



B) SOLA

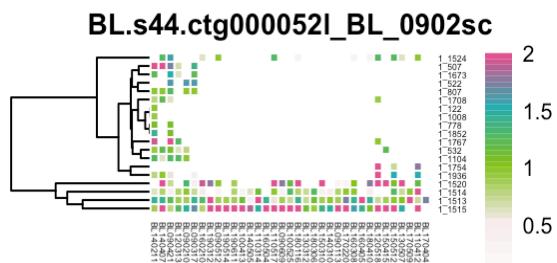


SO\_s23.ctg000345I\_BL\_0902sc

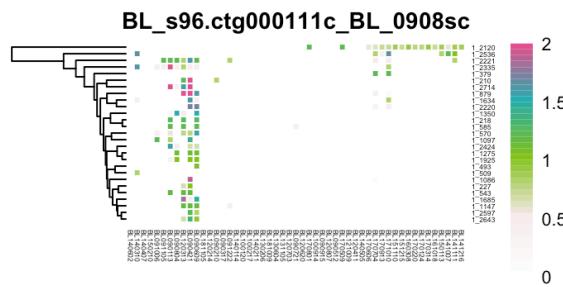
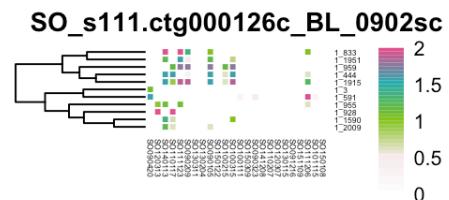
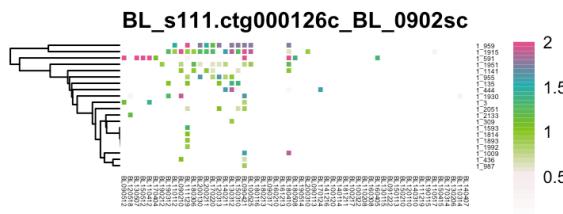
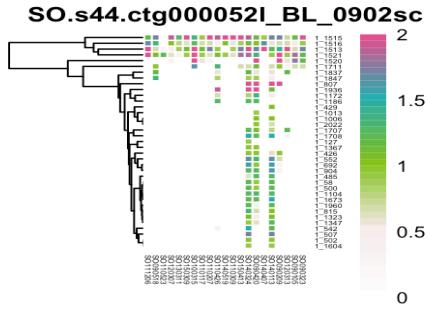


Supplementary Figure 28: Genes from 2 MAGs in both A) BBMO and B) SOLA time series exhibit positive selection patterns with a mean pN/pS ratio greater than 0.8. The color of cells represents the pN/pS ratio of a gene in a specific sample. White tails indicate NA values (pS = 0 in pN/pS calculations) due to missing mapping in those samples. The mean pN/pS ratio is calculated by excluding NA values, which leads to genes found in a limited number of samples (e.g., 1 sample) having a mean pN/pS ratio greater than 0.8.

A) BBMO

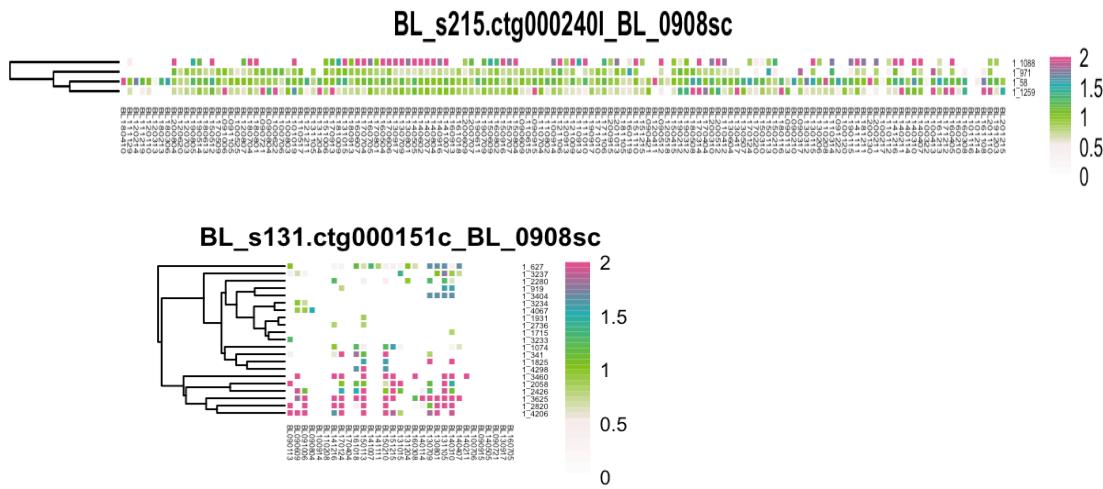


B) SOLA

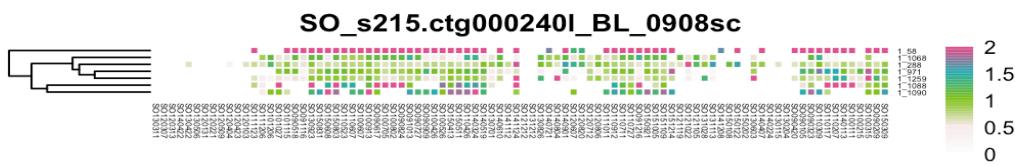


Supplementary Figure 29: Genes from MAGs “s44.ctg000052I\_BL\_0902sc” and “s111.ctg000126c\_BL\_0902sc” in both A) BBMO and B) SOLA time series exhibit positive selection patterns with a mean pN/pS ratio greater than 0.8. The color of cells represents the pN/pS ratio of a gene in a specific sample. White tails indicate NA values ( $pS = 0$  in pN/pS calculations) due to missing mapping in those samples. The mean pN/pS ratio is calculated by excluding NA values, which leads to genes found in a limited number of samples (e.g., 1 sample) having a mean pN/pS ratio greater than 0.8. The genome “s96.ctg000111c\_BL\_0908sc” has no adaptive gene found in the SOLA time series.

A) BBMO

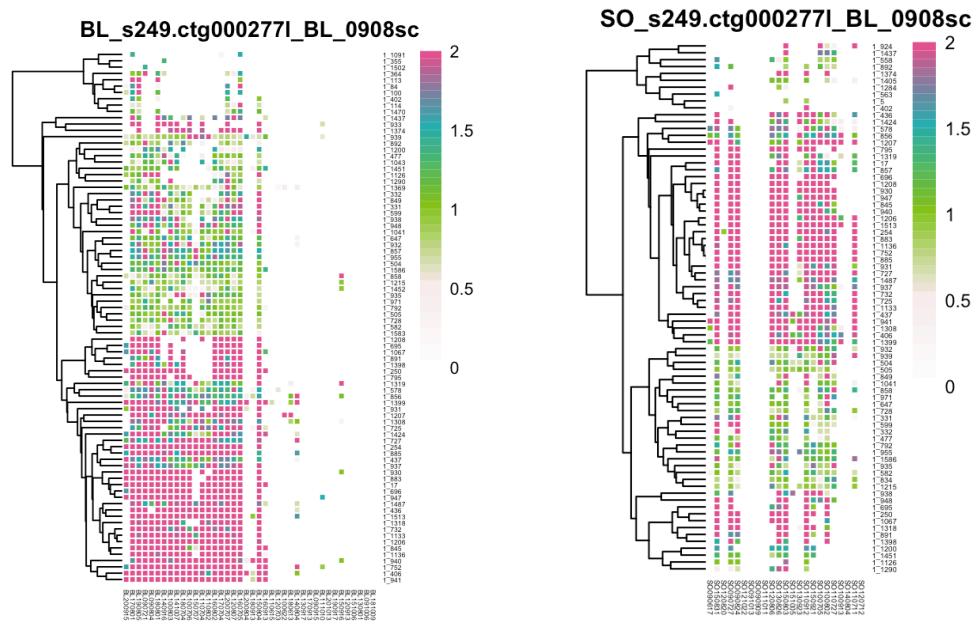


B) SOLA



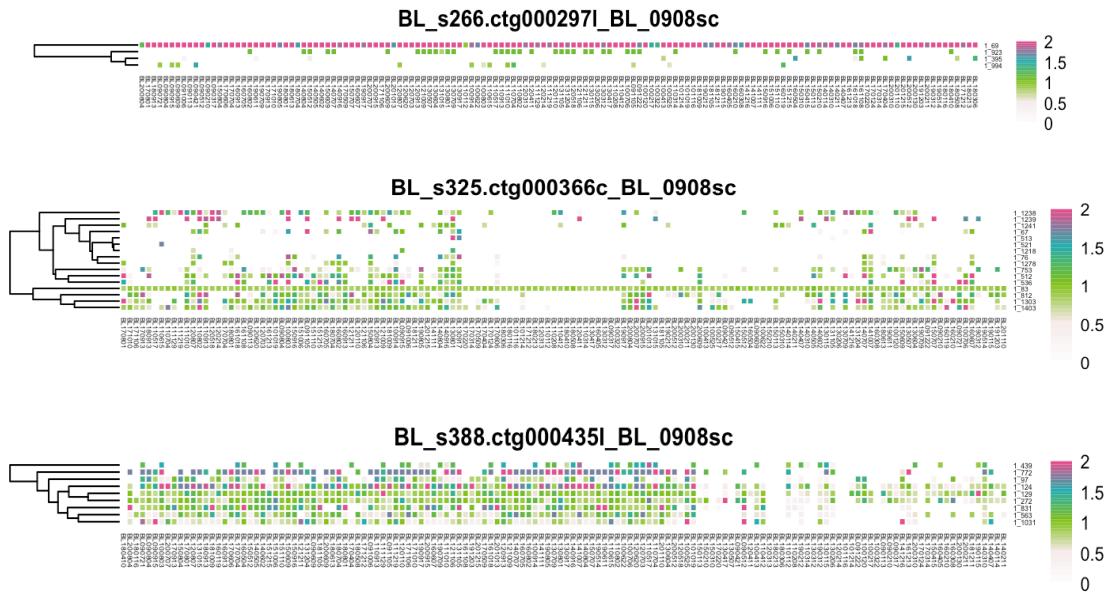
Supplementary Figure 30: Genes from MAGs “s215.ctg000240I\_BL\_0908sc” in both A) BBMO and B) SOLA time series exhibit positive selection patterns with a mean pN/pS ratio greater than 0.8. The color of cells represents the pN/pS ratio of a gene in a specific sample. White tails indicate NA values (pS = 0 in pN/pS calculations) due to missing mapping in those samples. The mean pN/pS ratio is calculated by excluding NA values, which leads to genes found in a limited number of samples (e.g., 1 sample) having a mean pN/pS ratio greater than 0.8. The genome “s131.ctg000151c\_BL\_0908sc” has no adaptive gene found in the SOLA time series.

A) BBMO

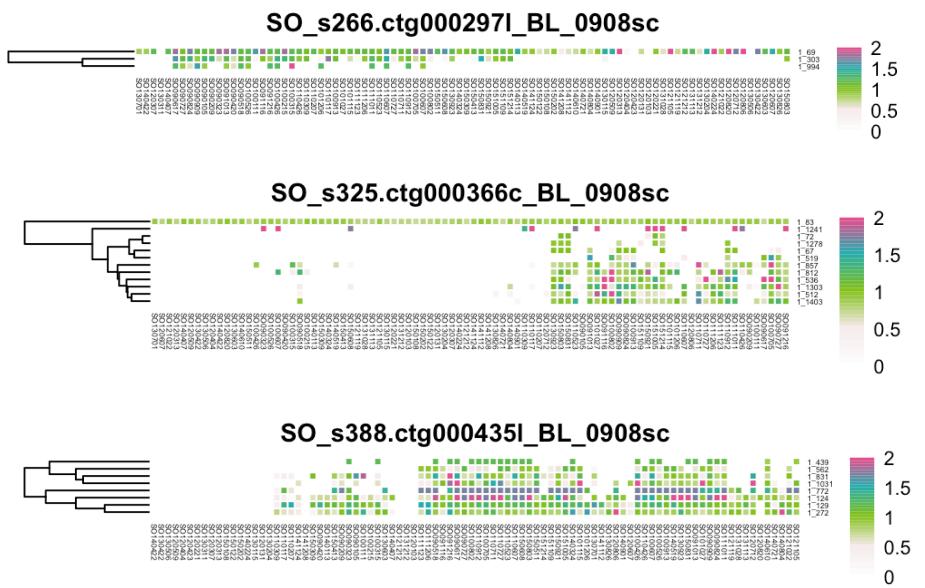


Supplementary Figure 31: Genes from MAGs “s249.ctg000277I\_BL\_0908sc” in both A) BBMO and B) SOLA time series exhibit positive selection patterns with a mean pN/pS ratio greater than 0.8. The color of cells represents the pN/pS ratio of a gene in a specific sample. White tails indicate NA values ( $pS = 0$  in pN/pS calculations) due to missing mapping in those samples. The mean pN/pS ratio is calculated by excluding NA values, which leads to genes found in a limited number of samples (e.g., 1 sample) having a mean pN/pS ratio greater than 0.8.

A) BBMO

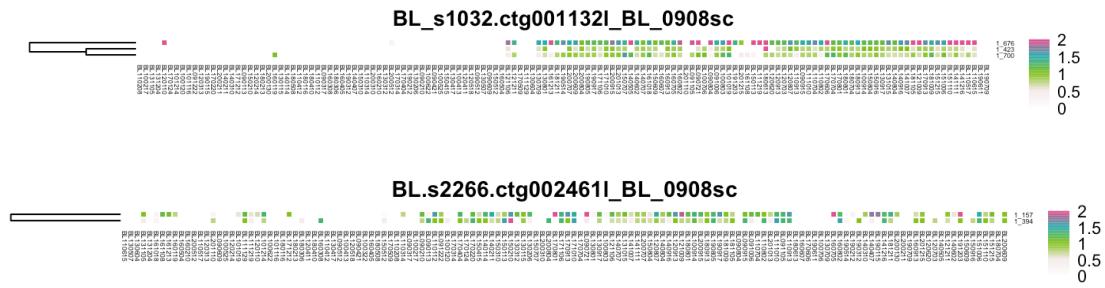


B) SOLA

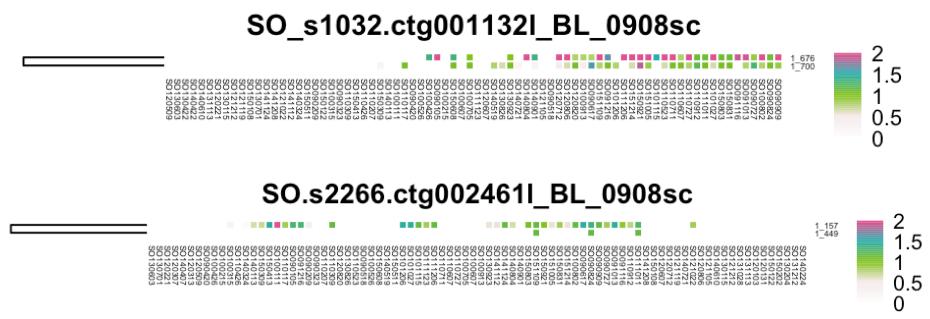


Supplementary Figure 32: Genes from 3 MAGs in both A) BBMO and B) SOLA time series exhibit positive selection patterns with a mean pN/pS ratio greater than 0.8. The color of cells represents the pN/pS ratio of a gene in a specific sample. White tails indicate NA values ( $pS = 0$  in pN/pS calculations) due to missing mapping in those samples. The mean pN/pS ratio is calculated by excluding NA values, which leads to genes found in a limited number of samples (e.g., 1 sample) having a mean pN/pS ratio greater than 0.8.

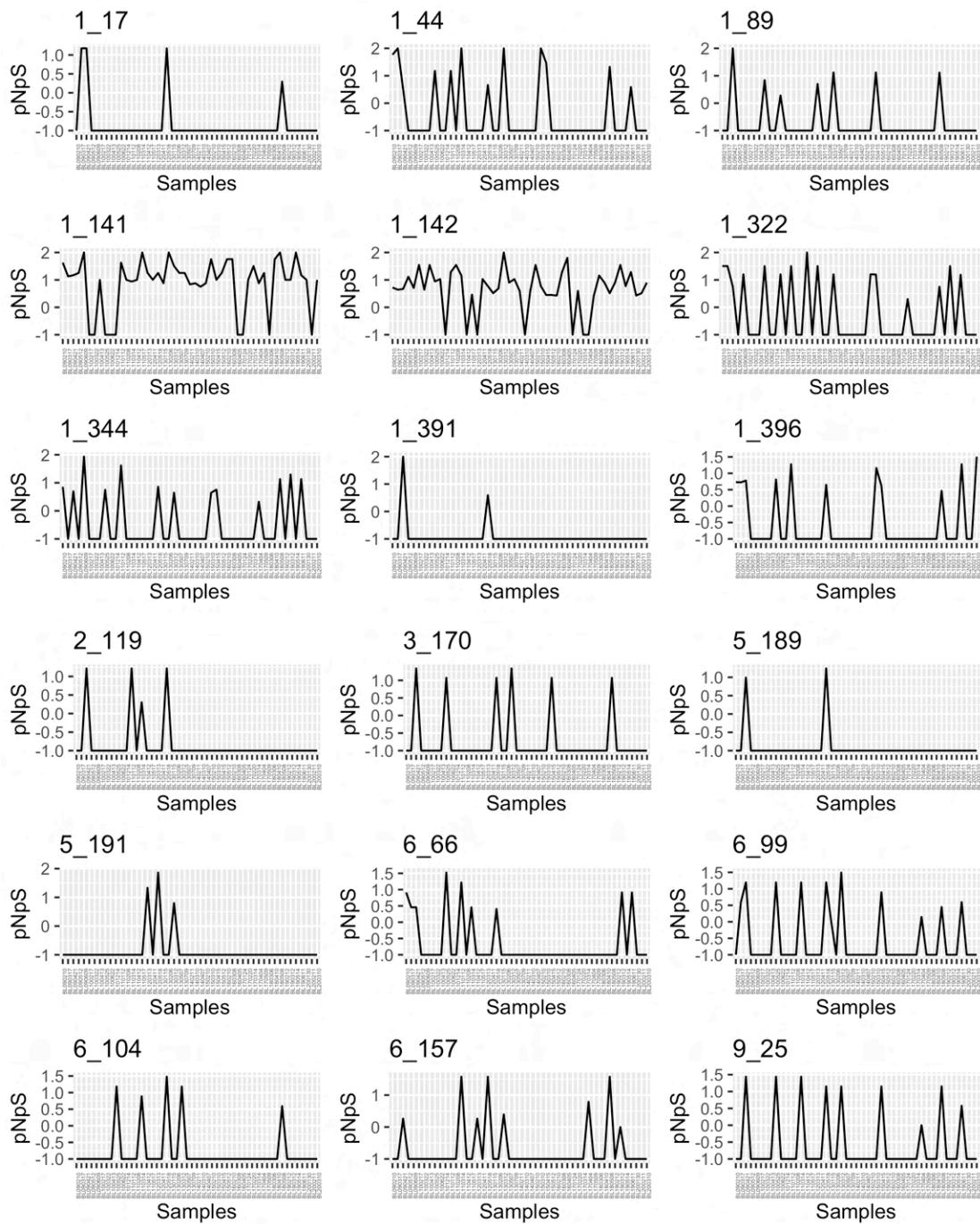
A) BBMO



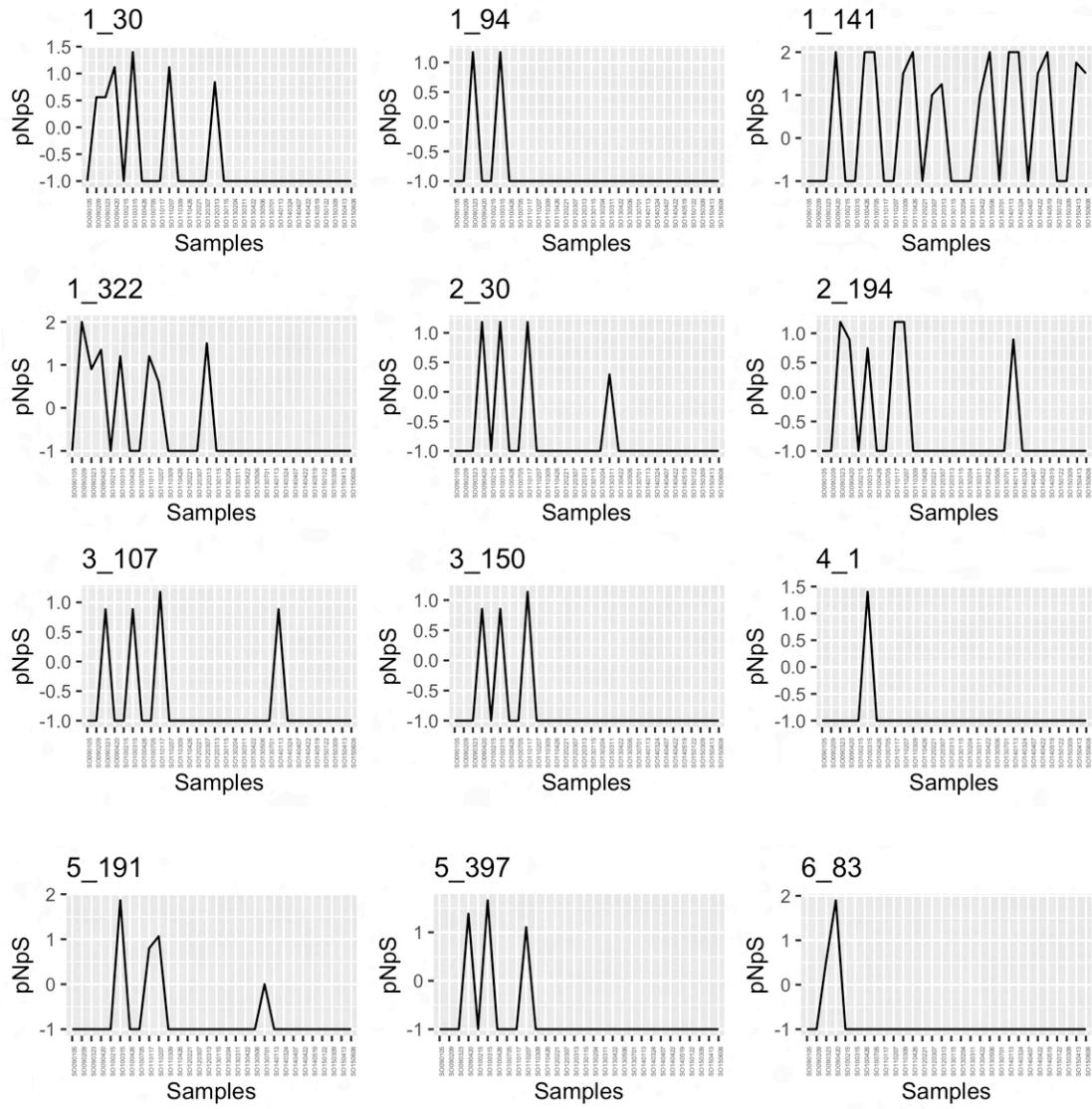
B) SOLA



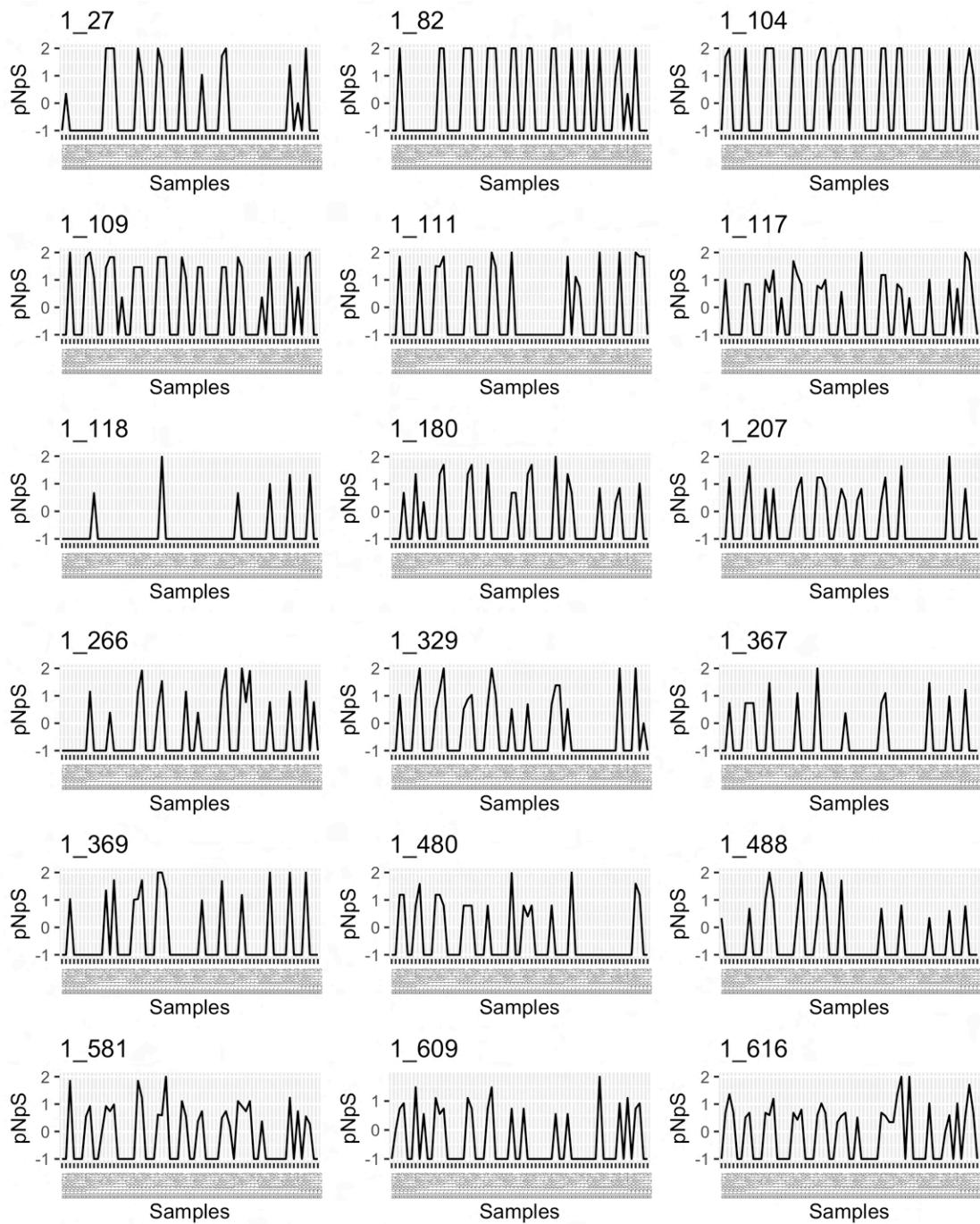
Supplementary Figure 33: Genes from 2 MAGs in both A) BBMO and B) SOLA time series exhibit positive selection patterns with a mean pN/pS ratio greater than 0.8. The color of cells represents the pN/pS ratio of a gene in a specific sample. White tails indicate NA values (pS = 0 in pN/pS calculations) due to missing mapping in those samples. The mean pN/pS ratio is calculated by excluding NA values, which leads to genes found in a limited number of samples (e.g., 1 sample) having a mean pN/pS ratio greater than 0.8.



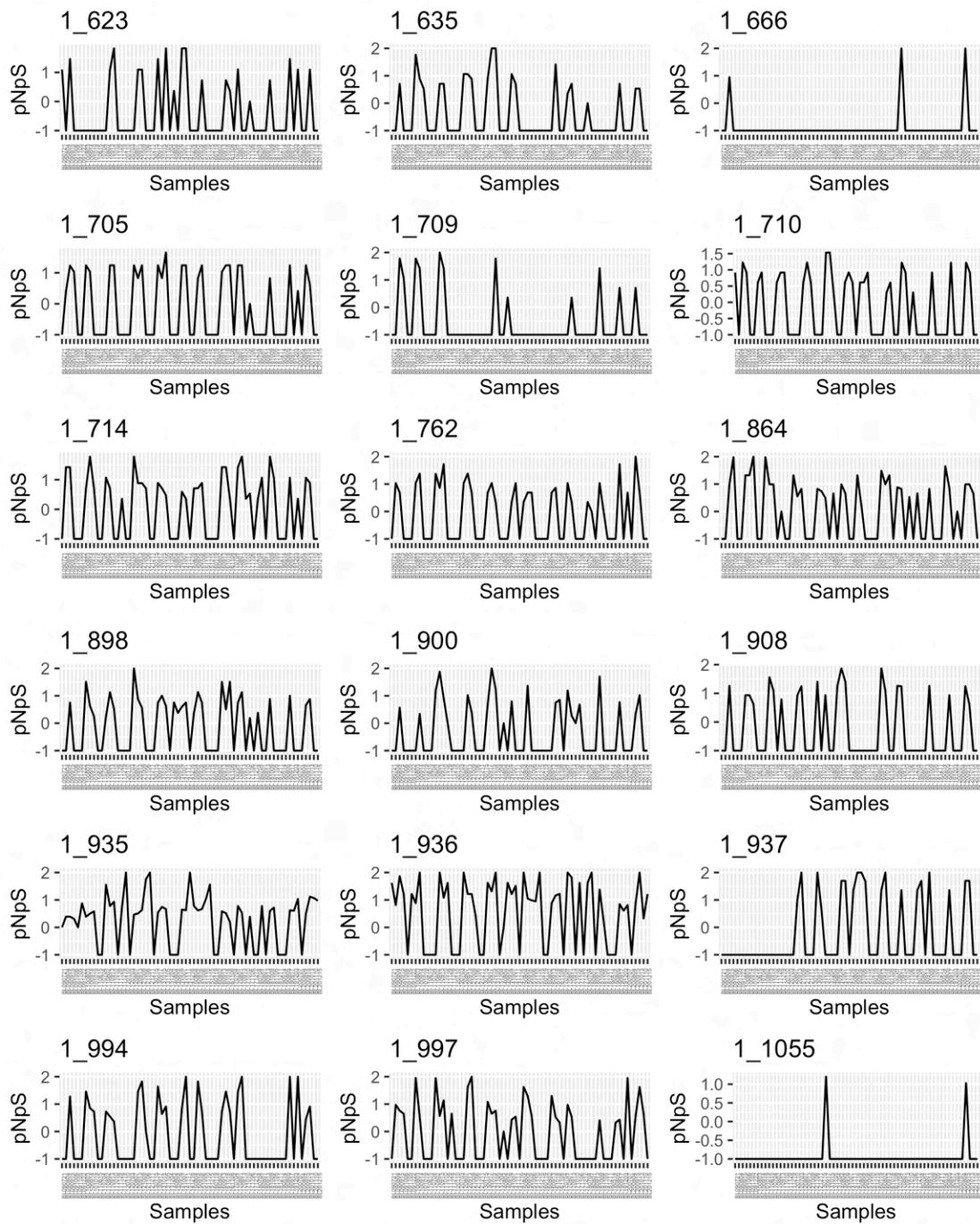
Supplementary Figure 34: The change of pNpS value of adaptive genes from MAG “BL\_0902\_bin.full.136” over time in BBMO. Along the x-axis is the sequence of sampling months from the 1st to the 140th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



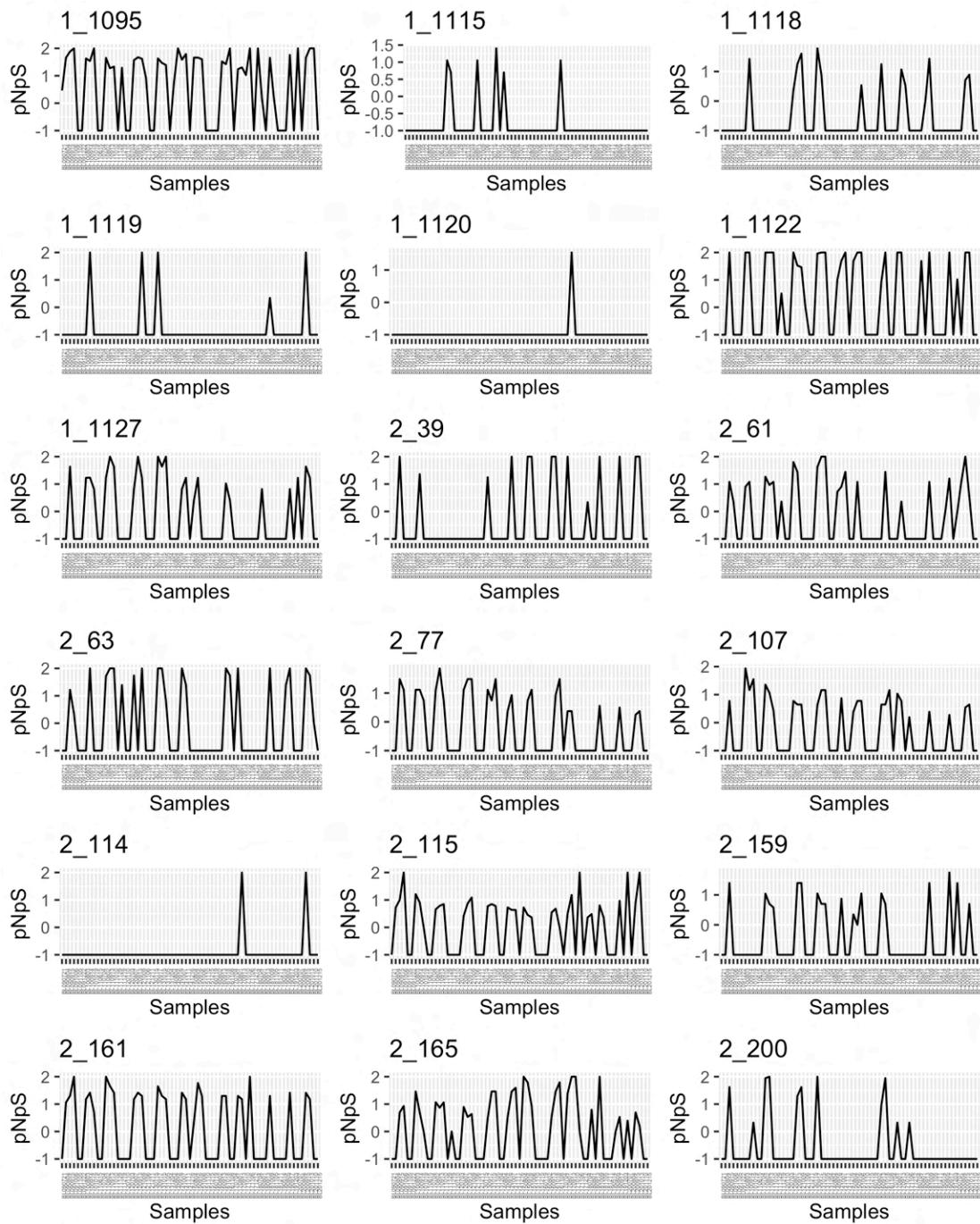
Supplementary Figure 35: The change of pNpS value of adaptive genes from MAG “BL\_0902\_bin.full.136” over time in SOLA. Along the x-axis is the sequence of sampling months from the 1st to the 90th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



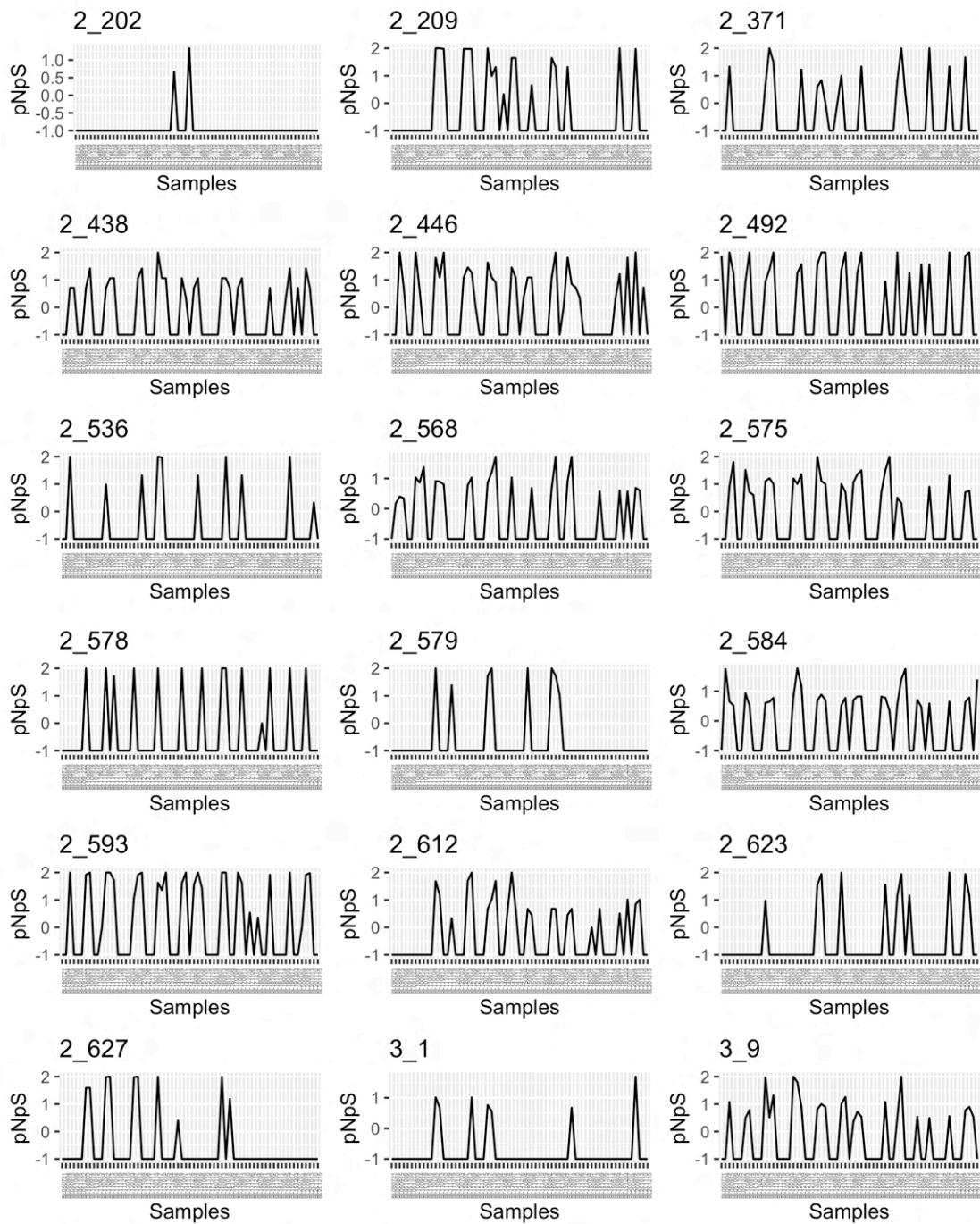
Supplementary Figure 36.1: The change of pNpS value of adaptive genes from MAG “BL\_0908\_bin.full.20” over time in BBMO. Along the x-axis is the sequence of sampling months from the 1st to the 140th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



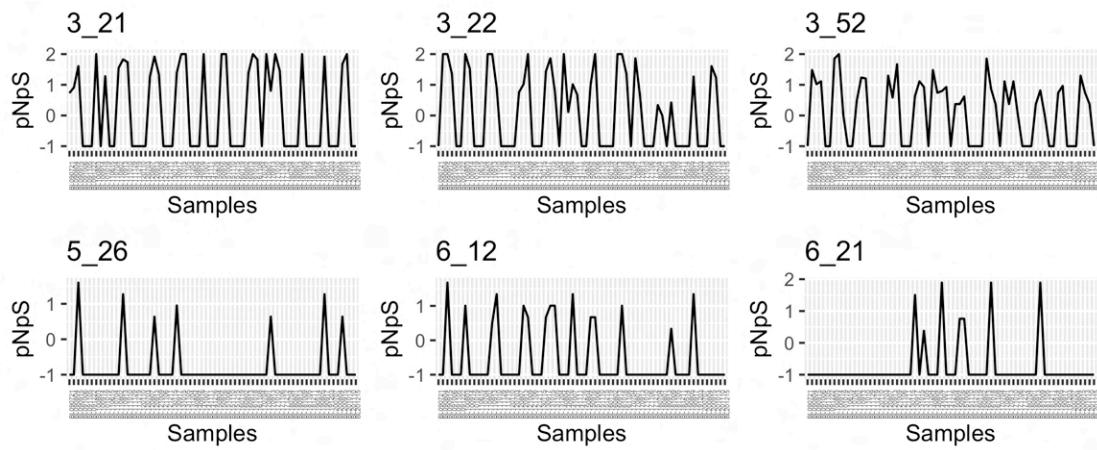
Supplementary Figure 36.2: The change of pNpS value of adaptive genes from MAG “BL\_0908\_bin.full.20” over time in BBMO. Along the x-axis is the sequence of sampling months from the 1st to the 140th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



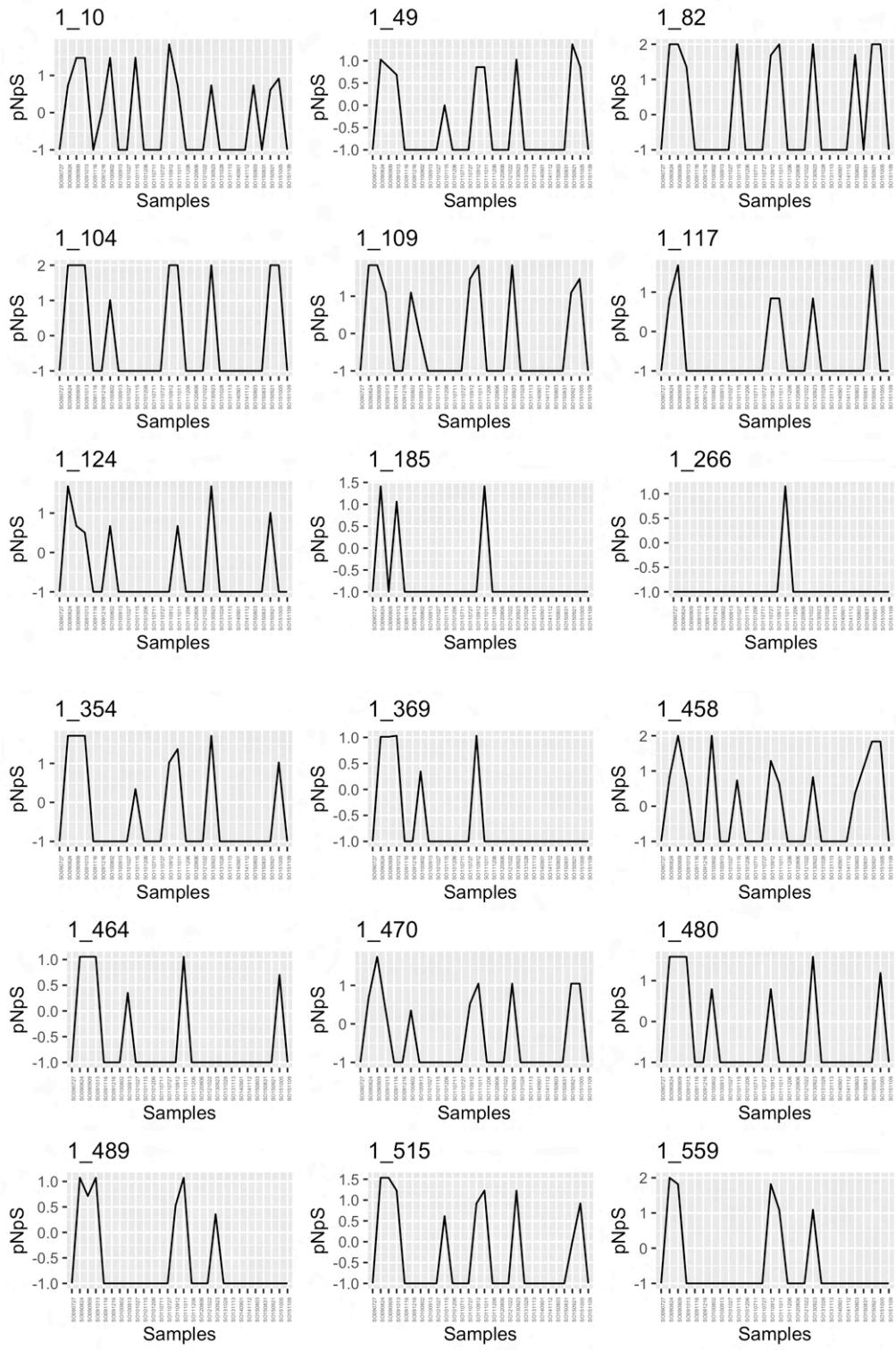
Supplementary Figure 36.3: The change of pNpS value of adaptive genes from MAG “BL\_0908\_bin.full.20” over time in BBMO. Along the x-axis is the sequence of sampling months from the 1st to the 140th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



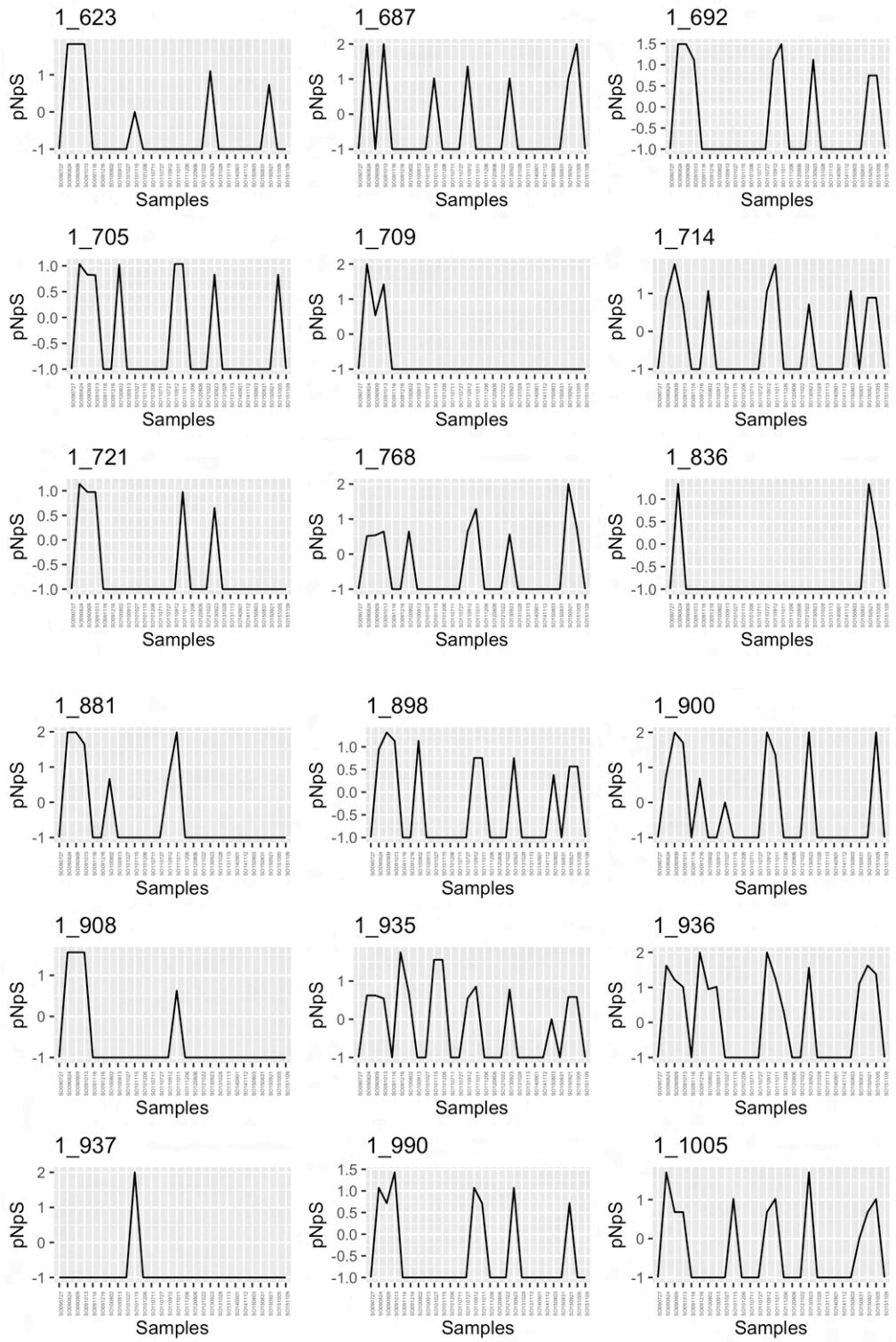
Supplementary Figure 36.4: The change of pNpS value of adaptive genes from MAG “BL\_0908\_bin.full.20” over time in BBMO. Along the x-axis is the sequence of sampling months from the 1st to the 140th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



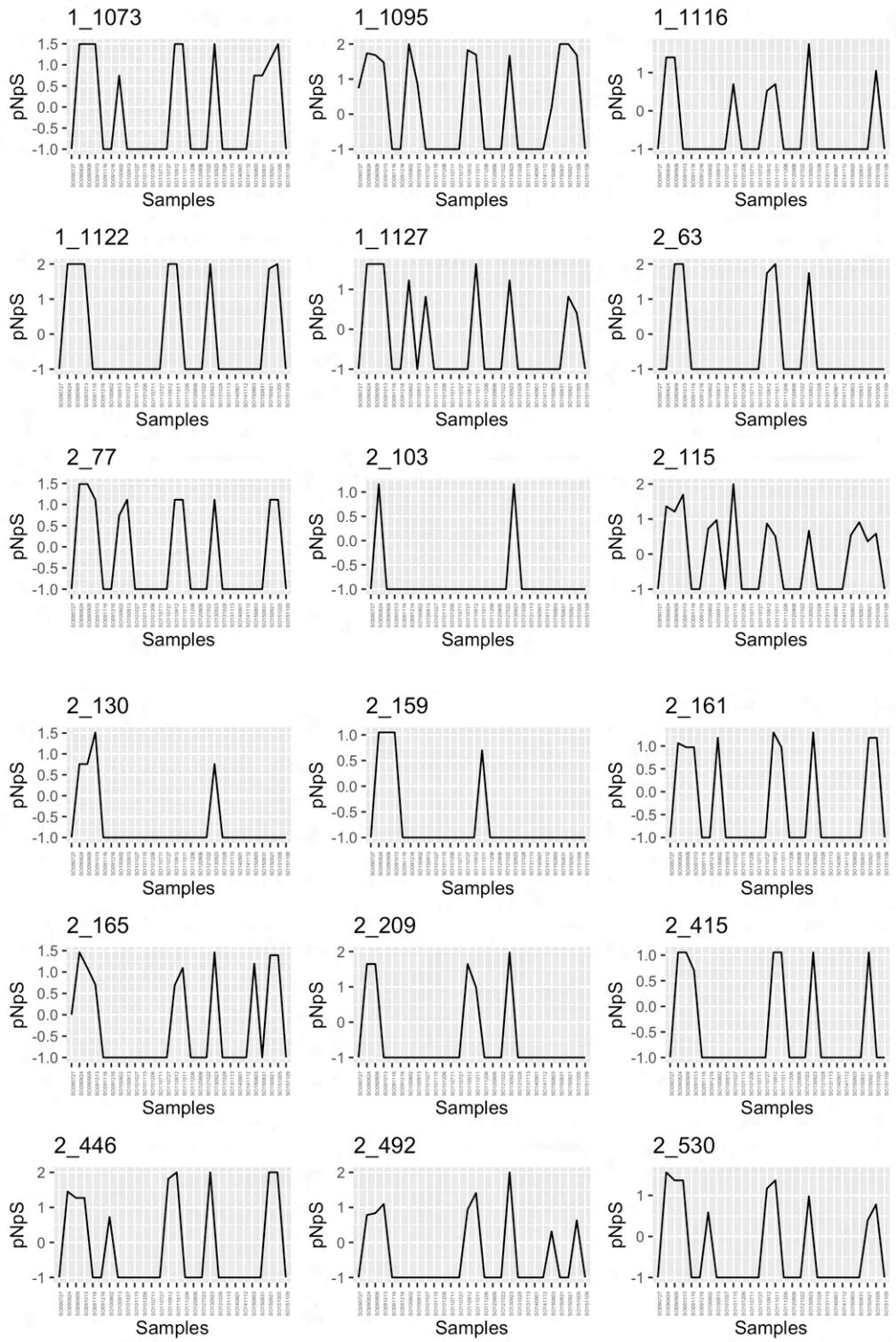
Supplementary Figure 36.5: The change of pNpS value of adaptive genes from MAG “BL\_0908\_bin.full.20” over time in BBMO. Along the x-axis is the sequence of sampling months from the 1st to the 140th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



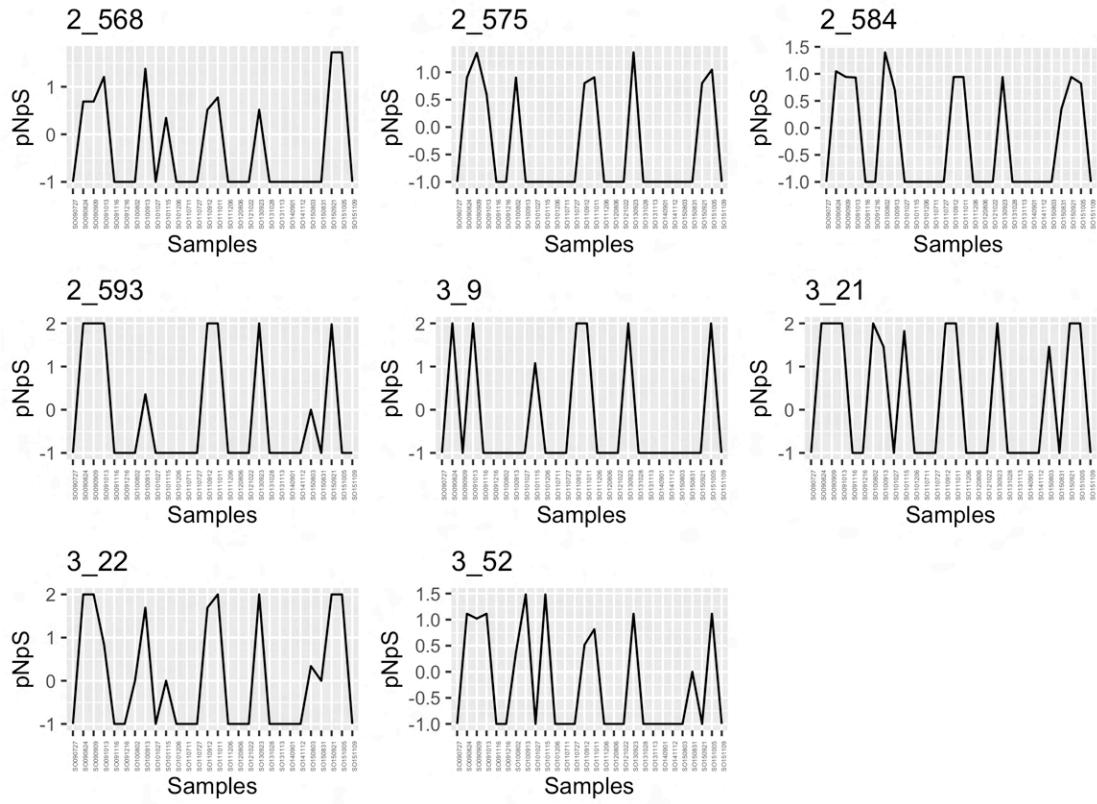
Supplementary Figure 37.1: The change of pNpS value of adaptive genes from MAG “BL\_0908\_bin.full.20” over time in SOLA. Along the x-axis is the sequence of sampling months from the 1st to the 90th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



Supplementary Figure 37.2: The change of pNpS value of adaptive genes from MAG “BL\_0908\_bin.full.20” over time in SOLA. Along the x-axis is the sequence of sampling months from the 1st to the 90th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.

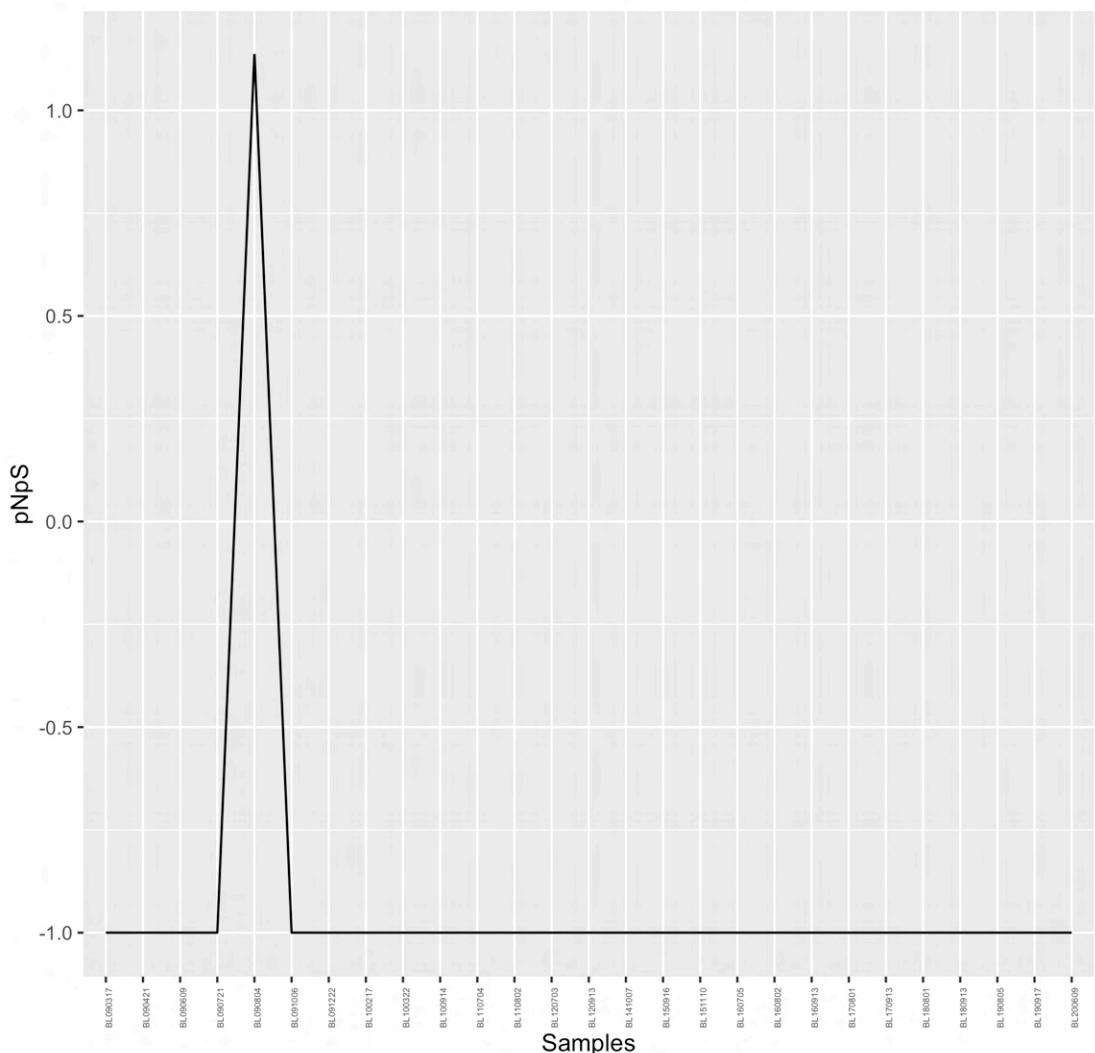


Supplementary Figure 37.3: The change of pNpS value of adaptive genes from MAG “BL\_0908\_bin.full.20” over time in SOLA. Along the x-axis is the sequence of sampling months from the 1st to the 90th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.

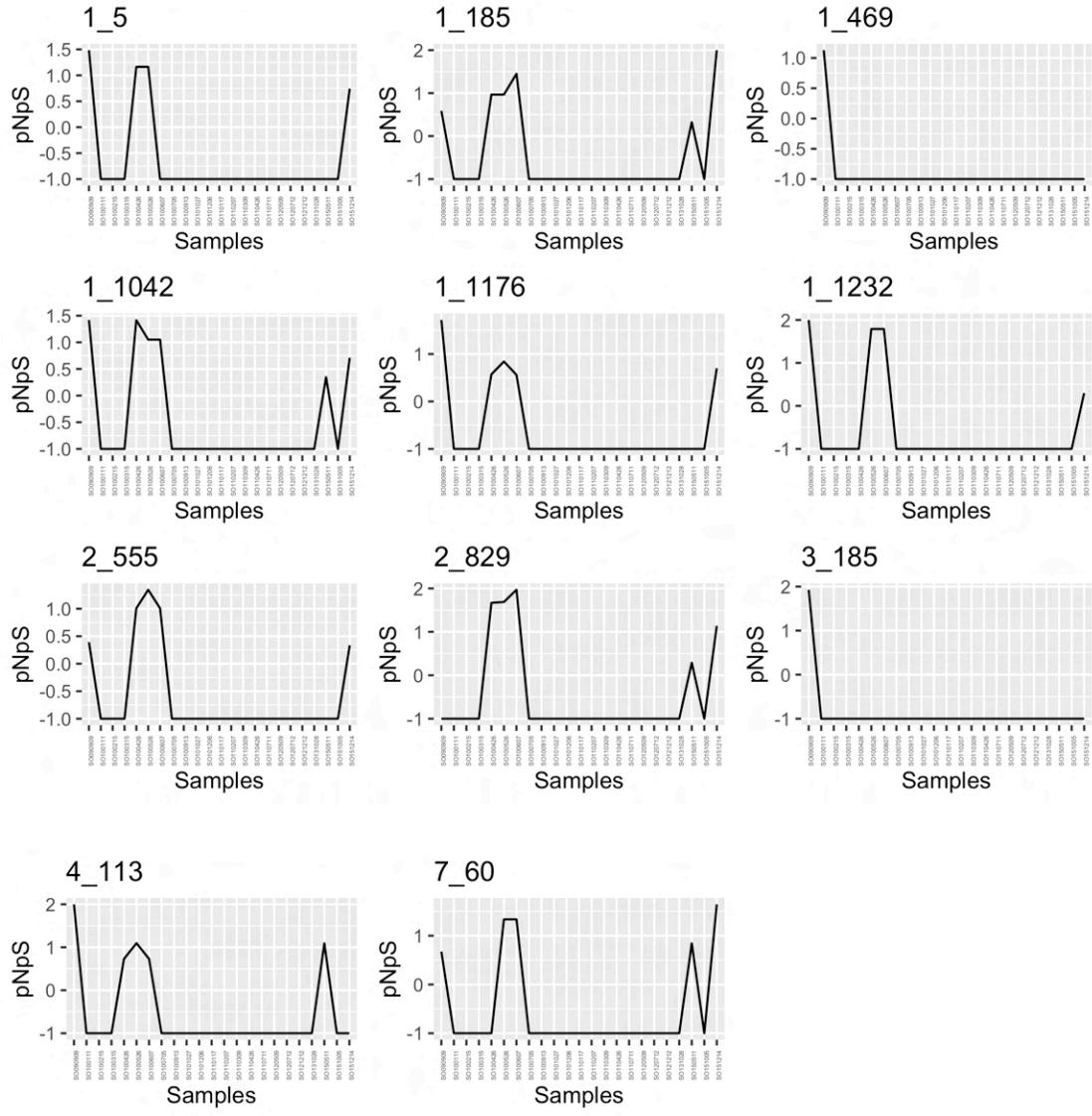


Supplementary Figure 37.4: The change of pNpS value of adaptive genes from MAG “BL\_0908\_bin.full.20” over time in SOLA. Along the x-axis is the sequence of sampling months from the 1st to the 90th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.

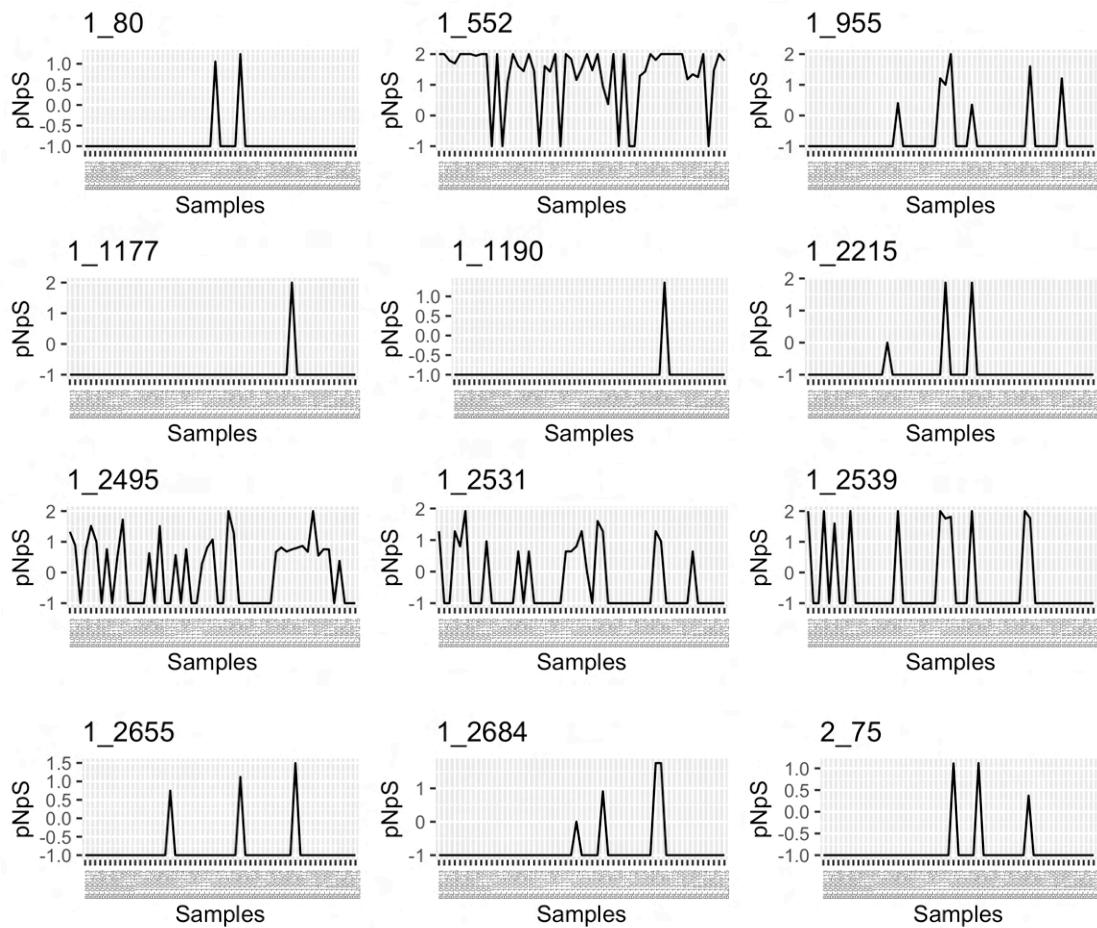
1\_1035



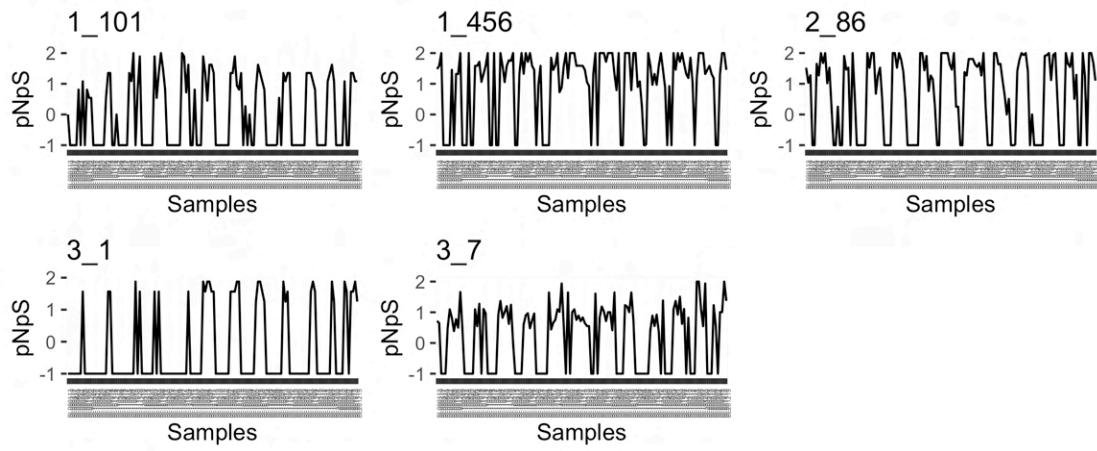
Supplementary Figure 38: The change of pNpS value of adaptive genes from MAG “BL\_0908\_bin.full.418” over time in BBMO. Along the x-axis is the sequence of sampling months from the 1st to the 140th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



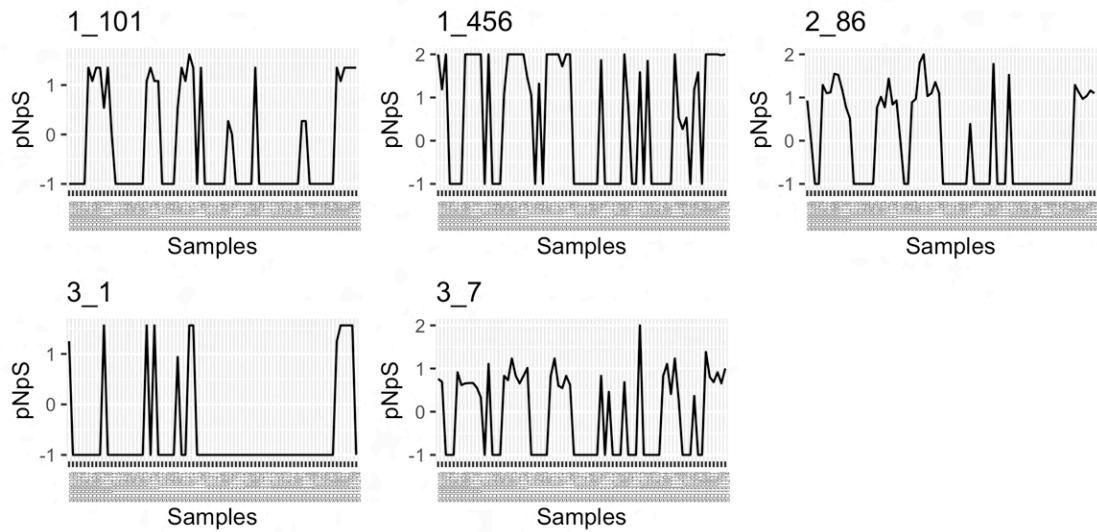
Supplementary Figure 39: The change of pNpS value of adaptive genes from MAG “BL\_0908\_bin.full.418” over time in SOLA. Along the x-axis is the sequence of sampling months from the 1st to the 90th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



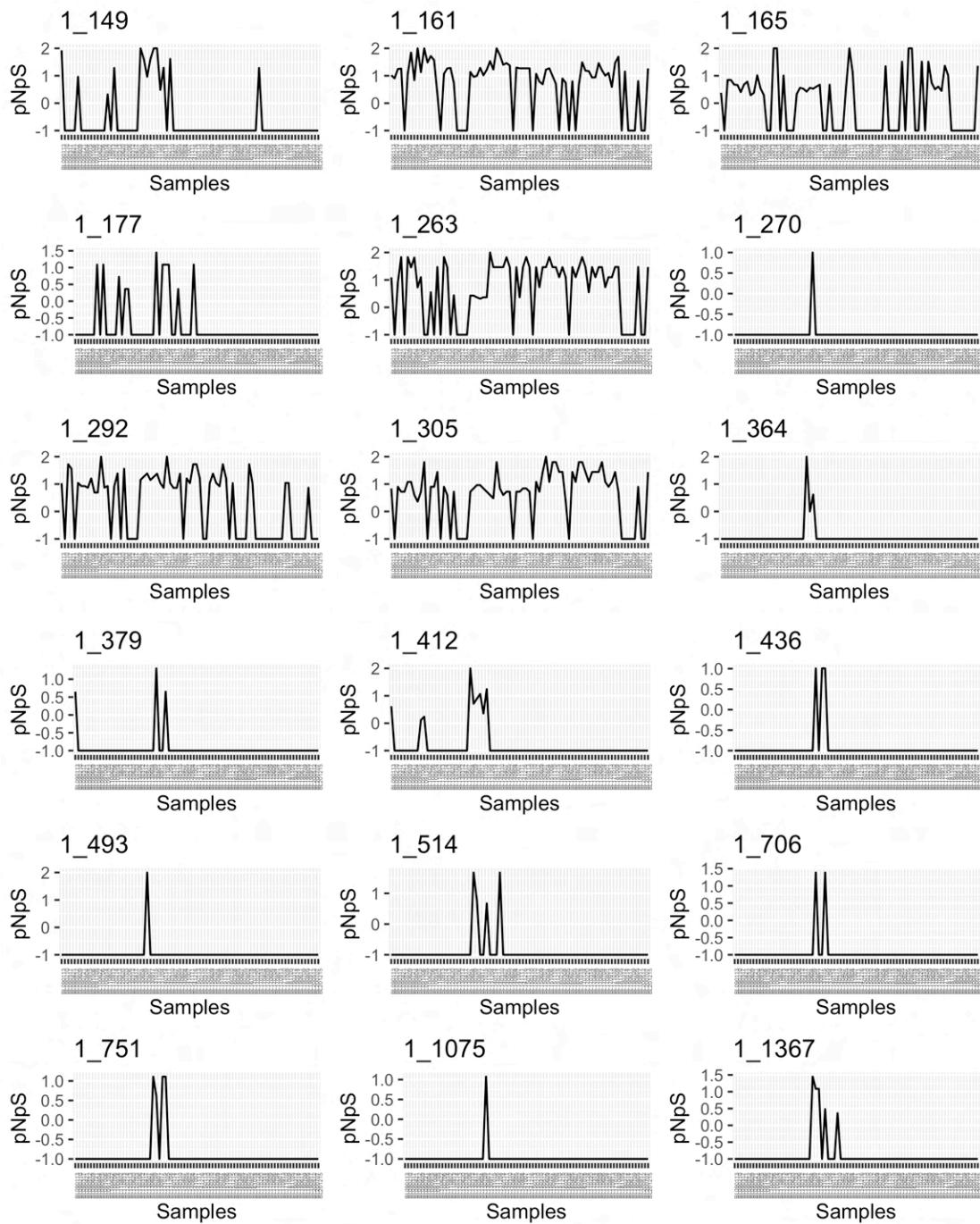
Supplementary Figure 40: The change of pNpS value of adaptive genes from MAG “BL\_0908\_bin.full.436” over time in BBMO. Along the x-axis is the sequence of sampling months from the 1st to the 140th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



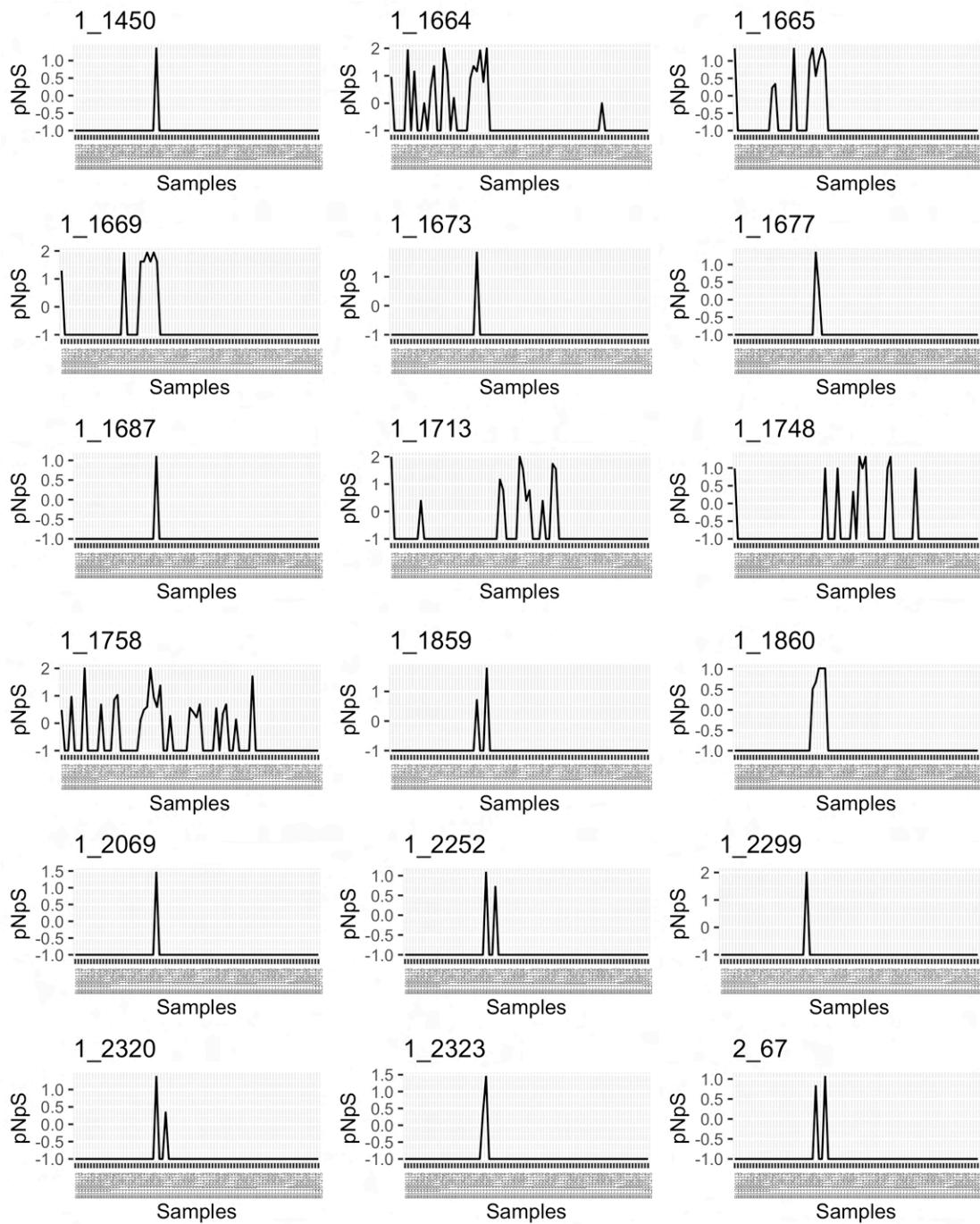
Supplementary Figure 41: The change of pNpS value of adaptive genes from MAG “BL\_0908\_bin.full.522” over time in BBMO. Along the x-axis is the sequence of sampling months from the 1st to the 140th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



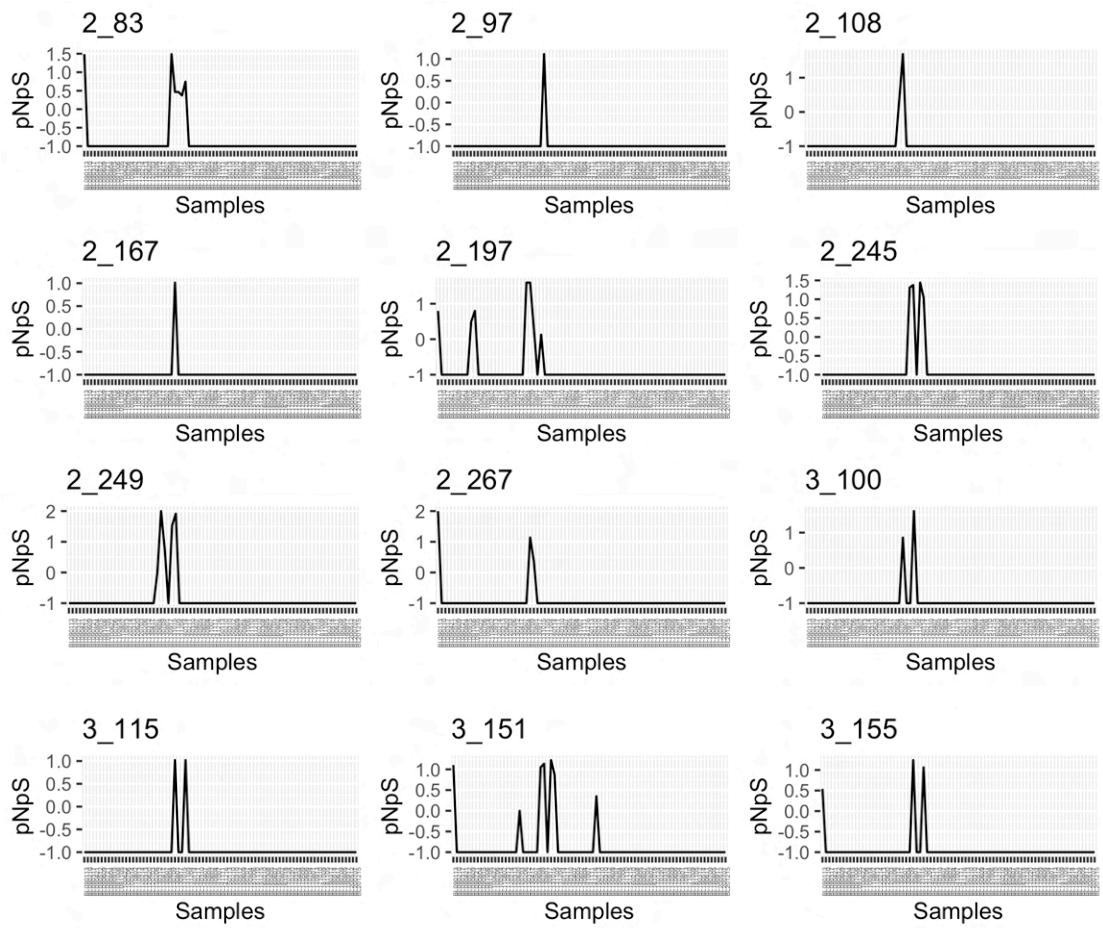
Supplementary Figure 42: The change of pNpS value of adaptive genes from MAG “BL\_0908\_bin.full.522” over time in SOLA. Along the x-axis is the sequence of sampling months from the 1st to the 90th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



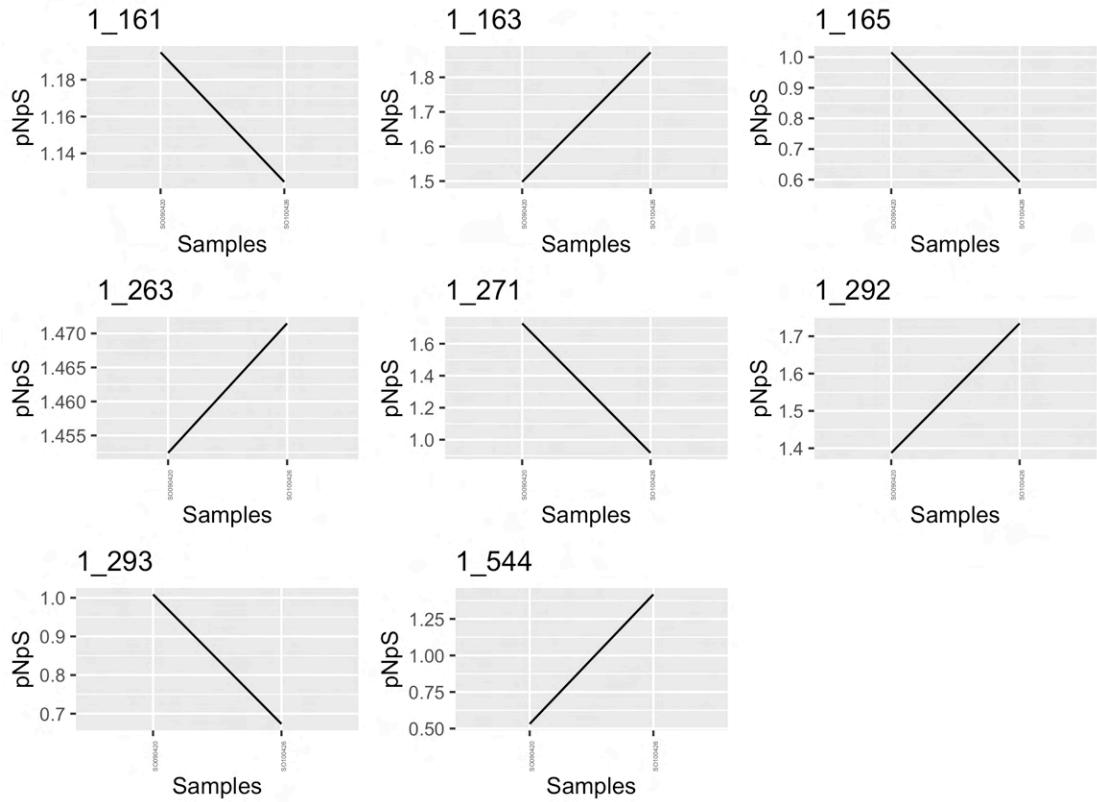
Supplementary Figure 43.1: The change of pNpS value of adaptive genes from MAG “BL\_0908\_bin.full.559” over time in BBMO. Along the x-axis is the sequence of sampling months from the 1st to the 140th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



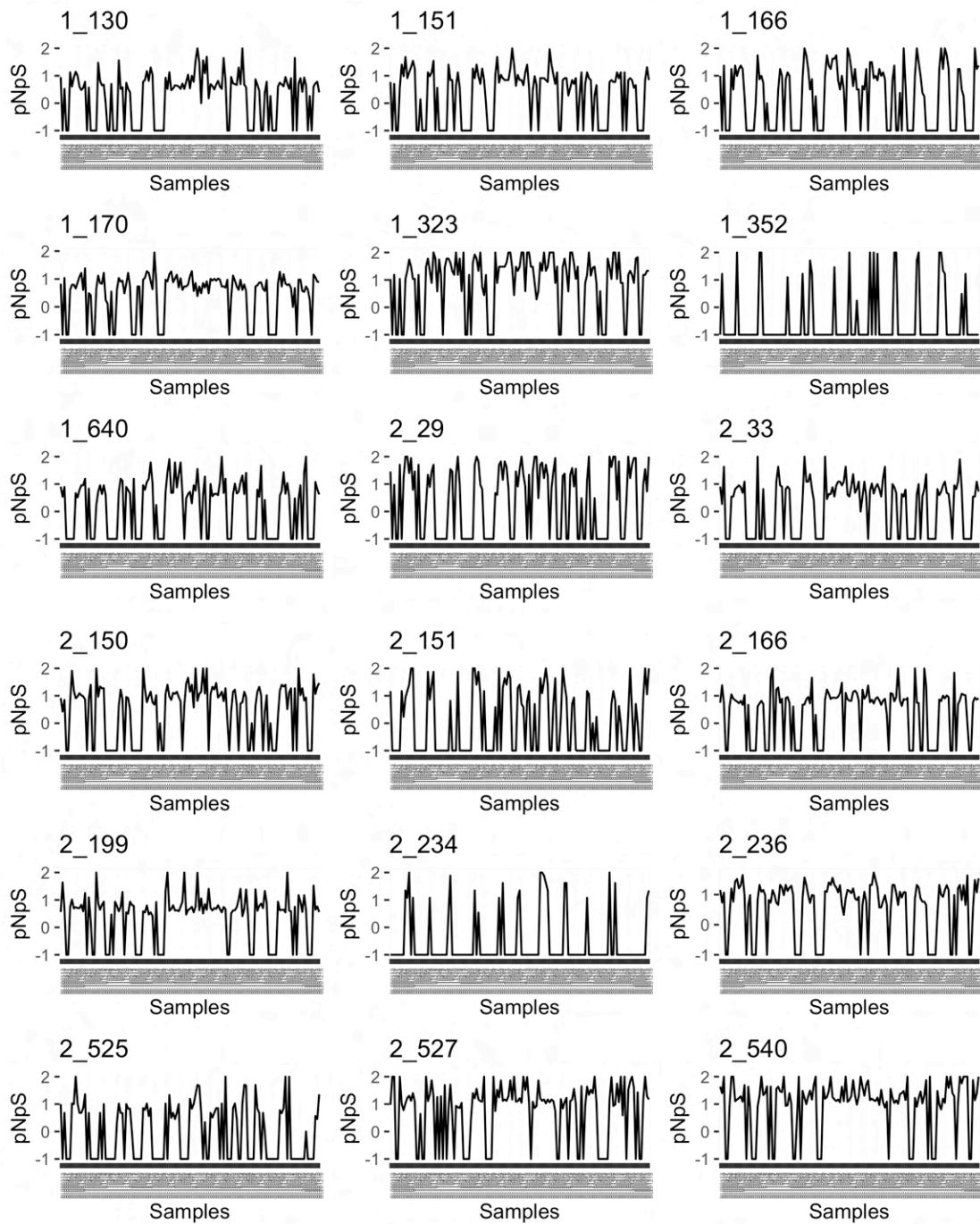
Supplementary Figure 43.2: The change of pNpS value of adaptive genes from MAG “BL\_0908\_bin.full.559” over time in BBMO. Along the x-axis is the sequence of sampling months from the 1st to the 140th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



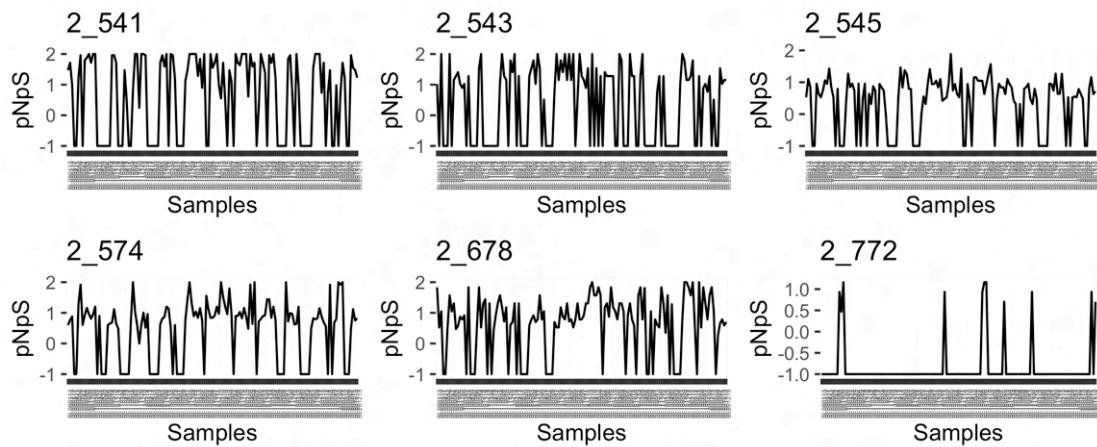
Supplementary Figure 43.3: The change of pNpS value of adaptive genes from MAG “BL\_0908\_bin.full.559” over time in BBMO. Along the x-axis is the sequence of sampling months from the 1st to the 140th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



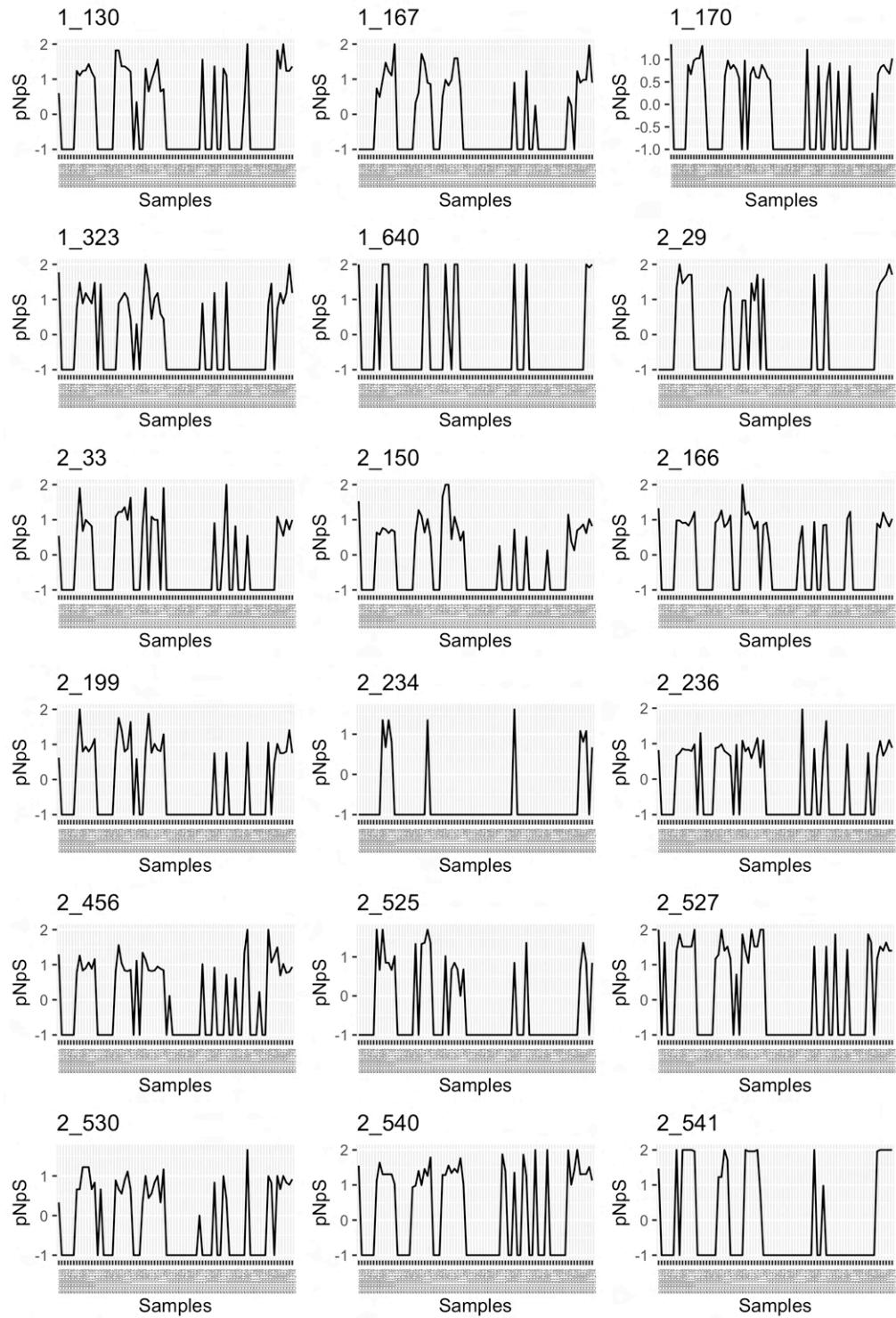
Supplementary Figure 44: The change of pNpS value of adaptive genes from MAG “BL\_0908\_bin.full.559” over time in SOLA. Along the x-axis is the sequence of sampling months from the 1st to the 90th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



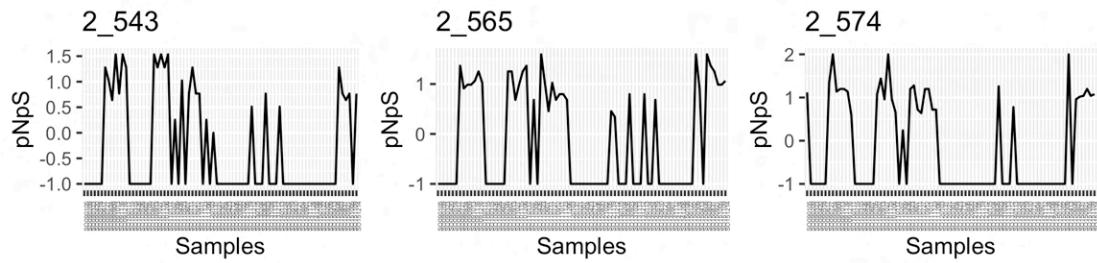
Supplementary Figure 45.1: The change of pNpS value of adaptive genes from MAG “BL\_0908\_bin.full.869” over time in BBMO. Along the x-axis is the sequence of sampling months from the 1st to the 140th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



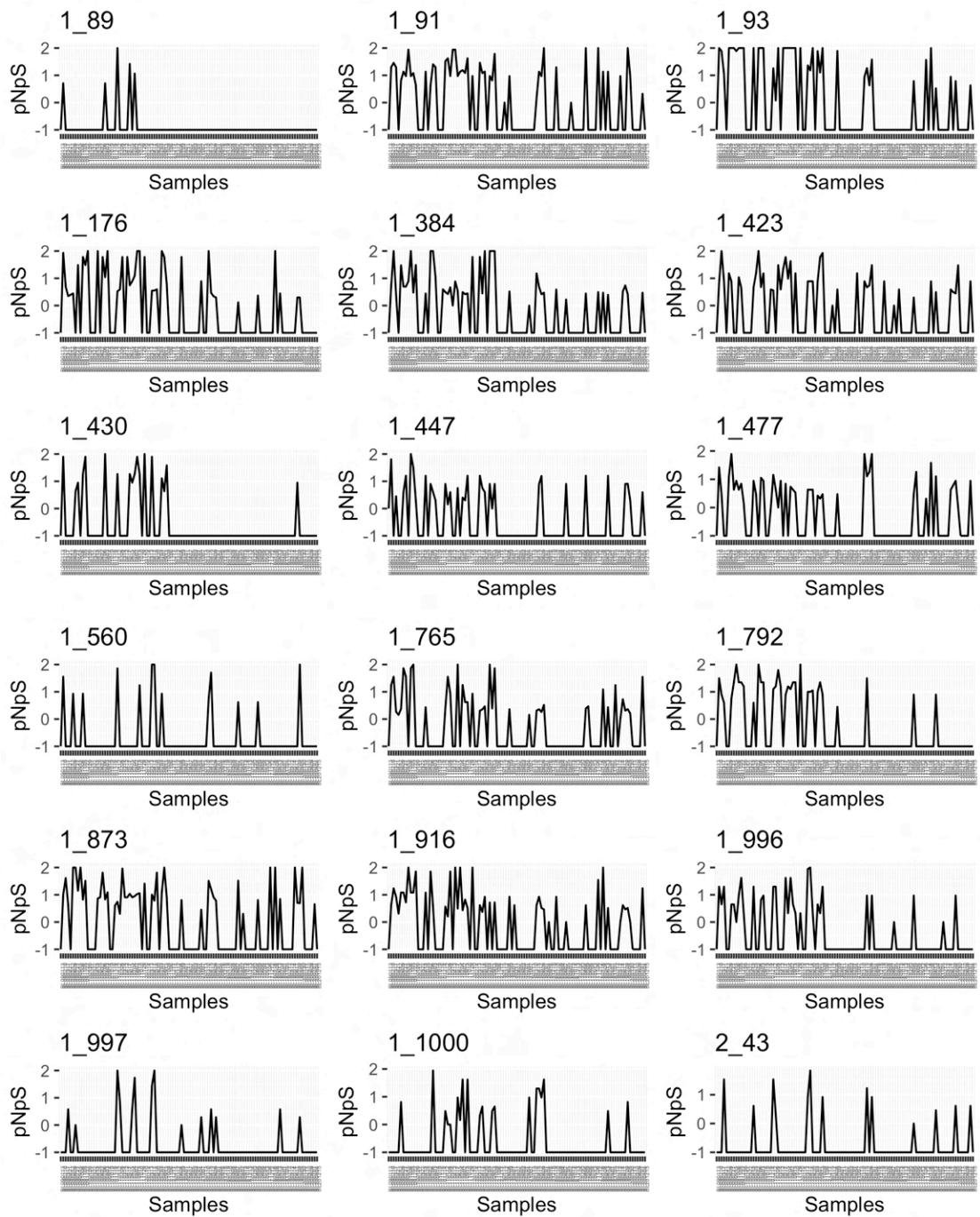
Supplementary Figure 45.2: The change of pNpS value of adaptive genes from MAG “BL\_0908\_bin.full.869” over time in BBMO. Along the x-axis is the sequence of sampling months from the 1st to the 140th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



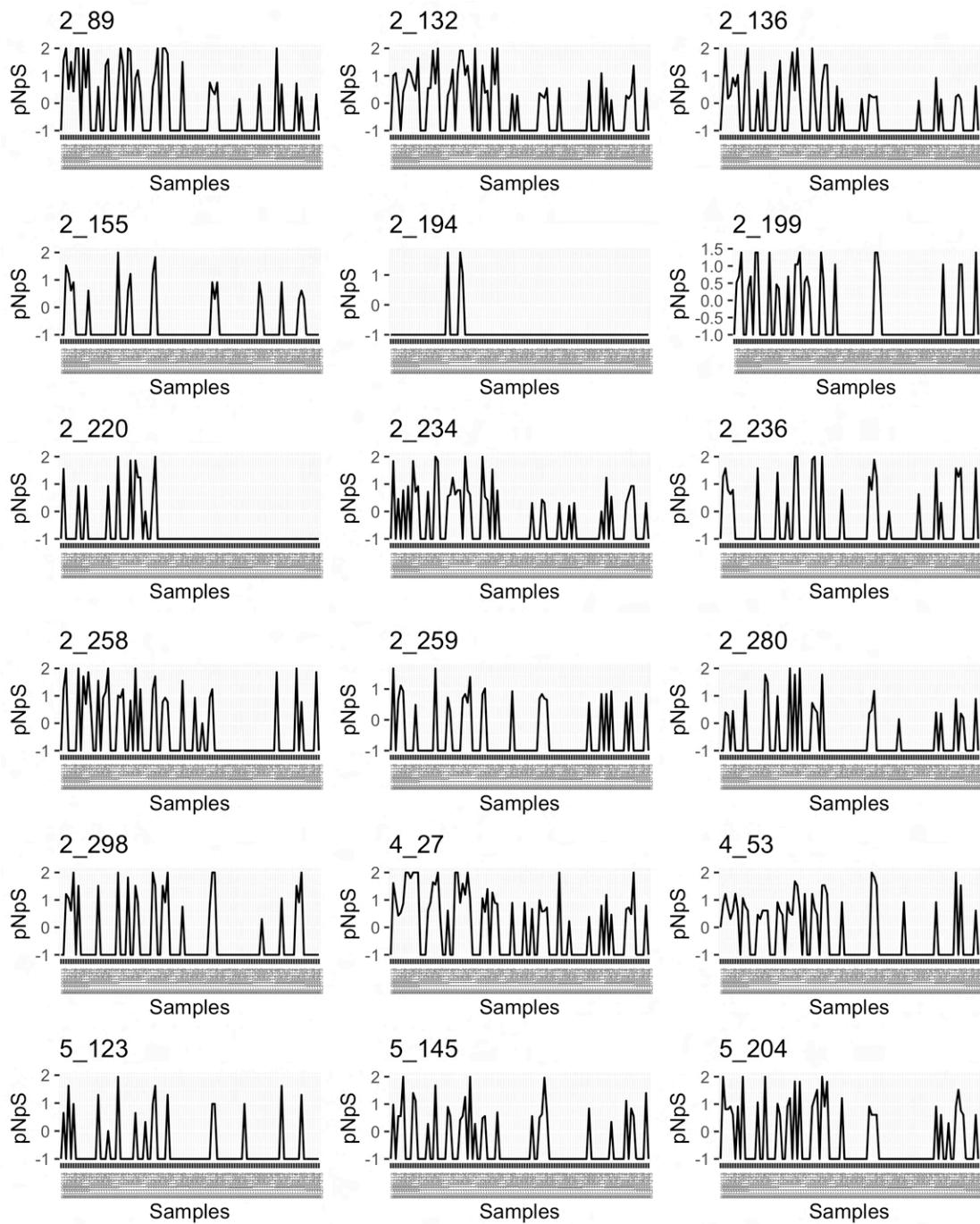
Supplementary Figure 46.1: The change of pNpS value of adaptive genes from MAG “BL\_0908\_bin.full.869” over time in SOLA. Along the x-axis is the sequence of sampling months from the 1st to the 90th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



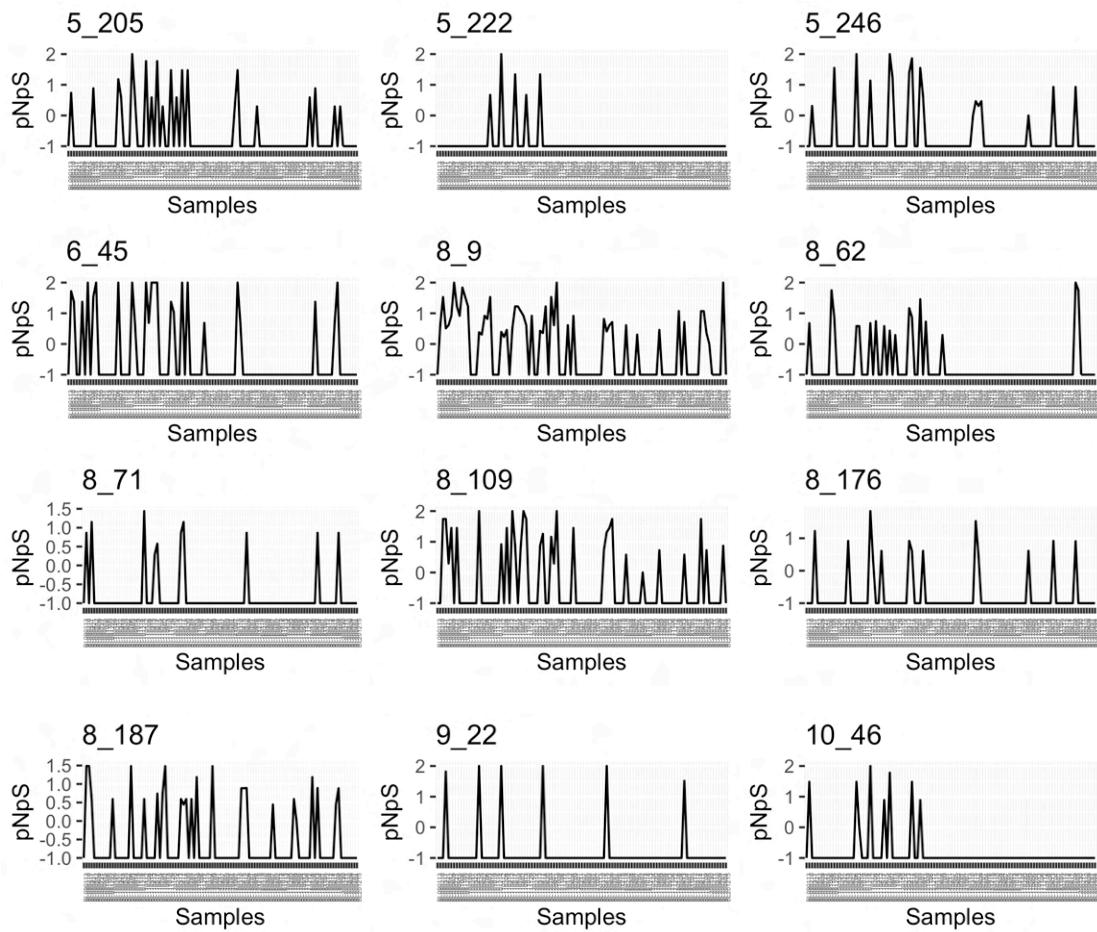
Supplementary Figure 46.2: The change of pNpS value of adaptive genes from MAG “BL\_0908\_bin.full.869” over time in SOLA. Along the x-axis is the sequence of sampling months from the 1st to the 90th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



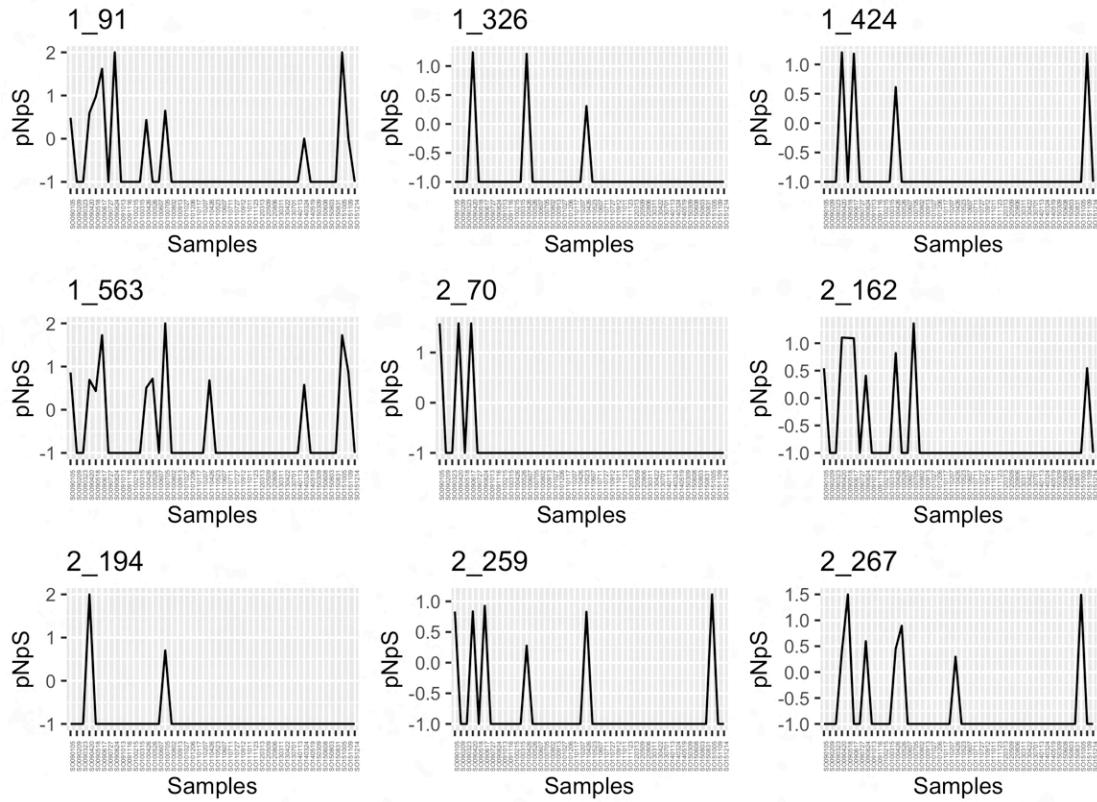
Supplementary Figure 47.1: The change of pNpS value of adaptive genes from MAG “BL\_1001\_bin.full.234” over time in BBMO. Along the x-axis is the sequence of sampling months from the 1st to the 140th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



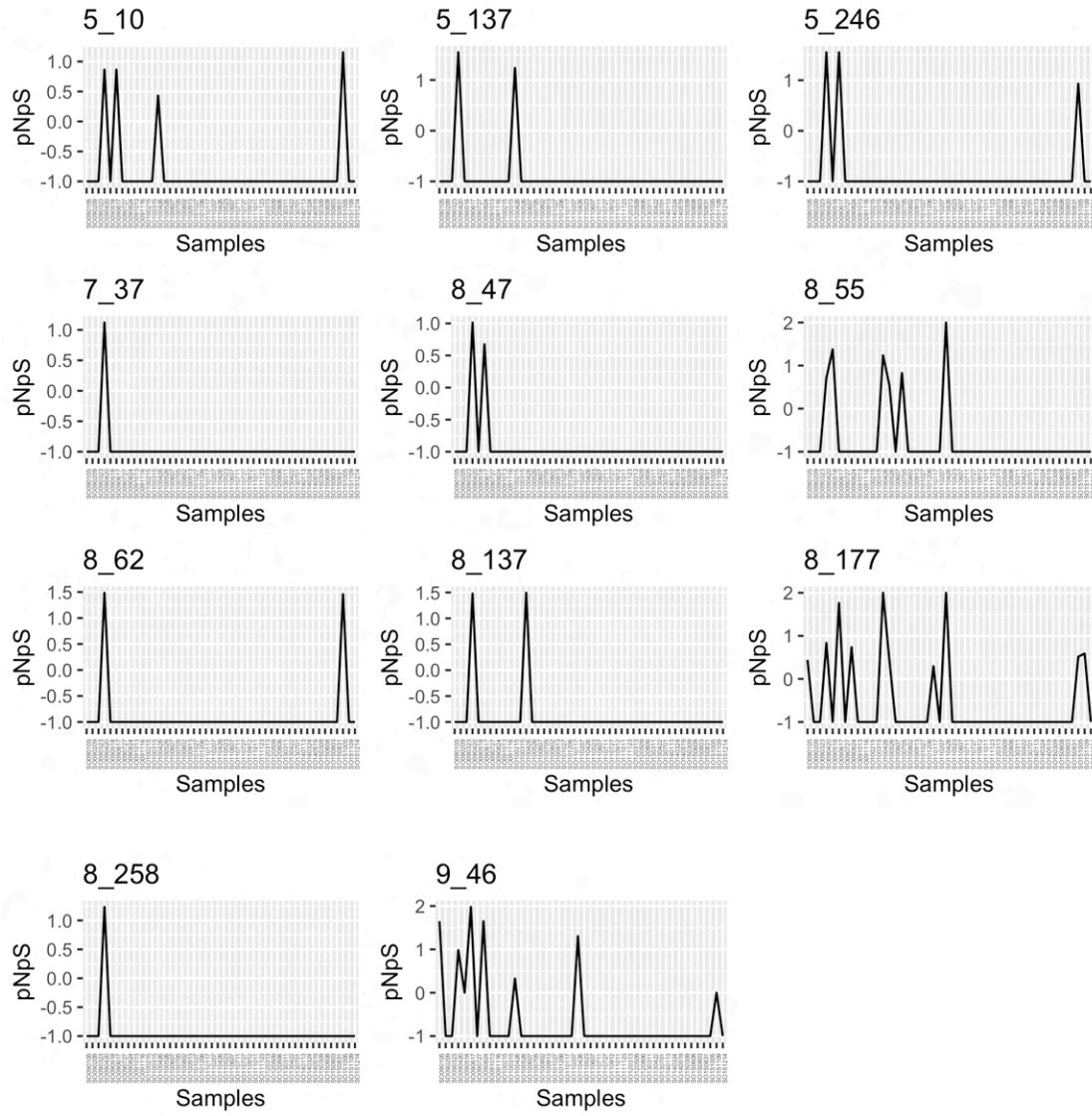
Supplementary Figure 47.2: The change of pNpS value of adaptive genes from MAG “BL\_1001\_bin.full.234” over time in BBMO. Along the x-axis is the sequence of sampling months from the 1st to the 140th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



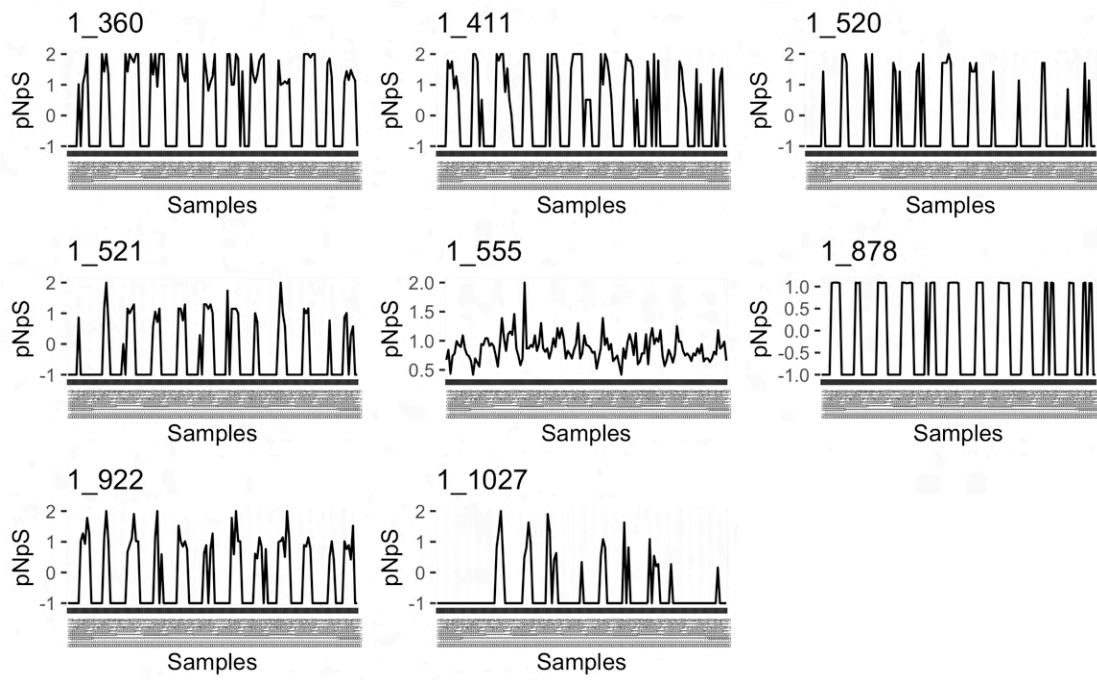
Supplementary Figure 47.3: The change of pNpS value of adaptive genes from MAG “BL\_1001\_bin.full.234” over time in BBMO. Along the x-axis is the sequence of sampling months from the 1st to the 140th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



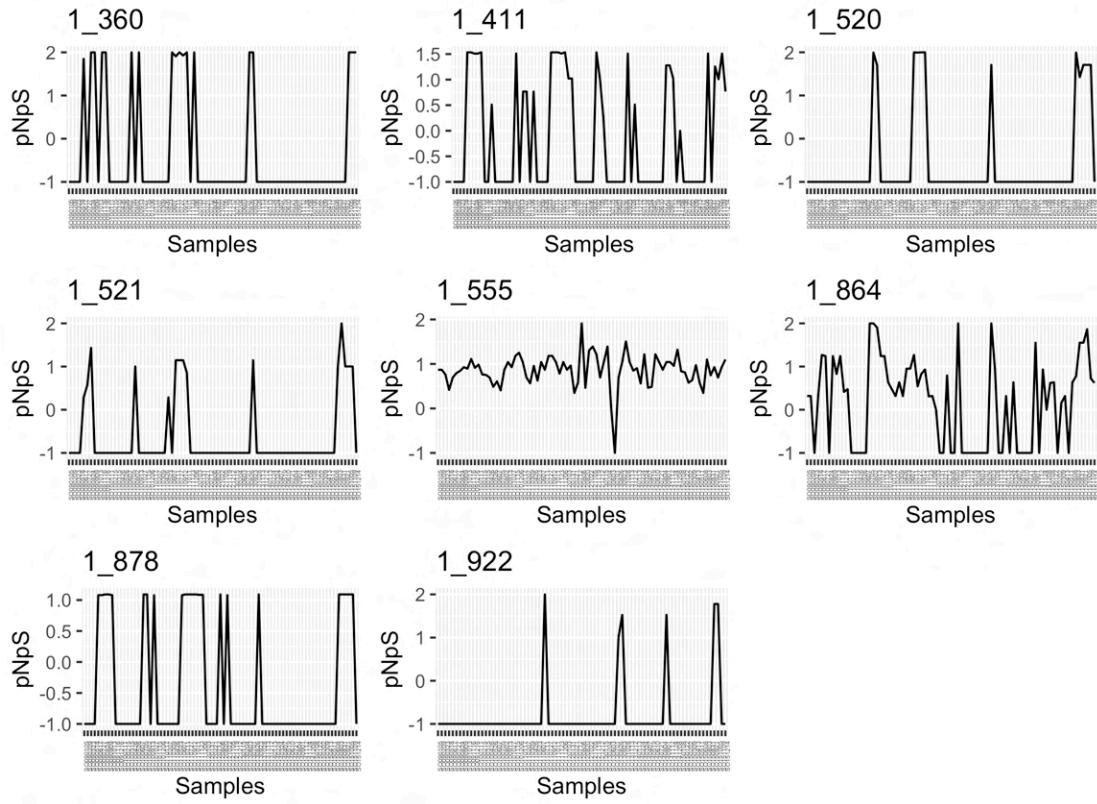
Supplementary Figure 48.1: The change of pNpS value of adaptive genes from MAG “BL\_1001\_bin.full.234” over time in SOLA. Along the x-axis is the sequence of sampling months from the 1st to the 90th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



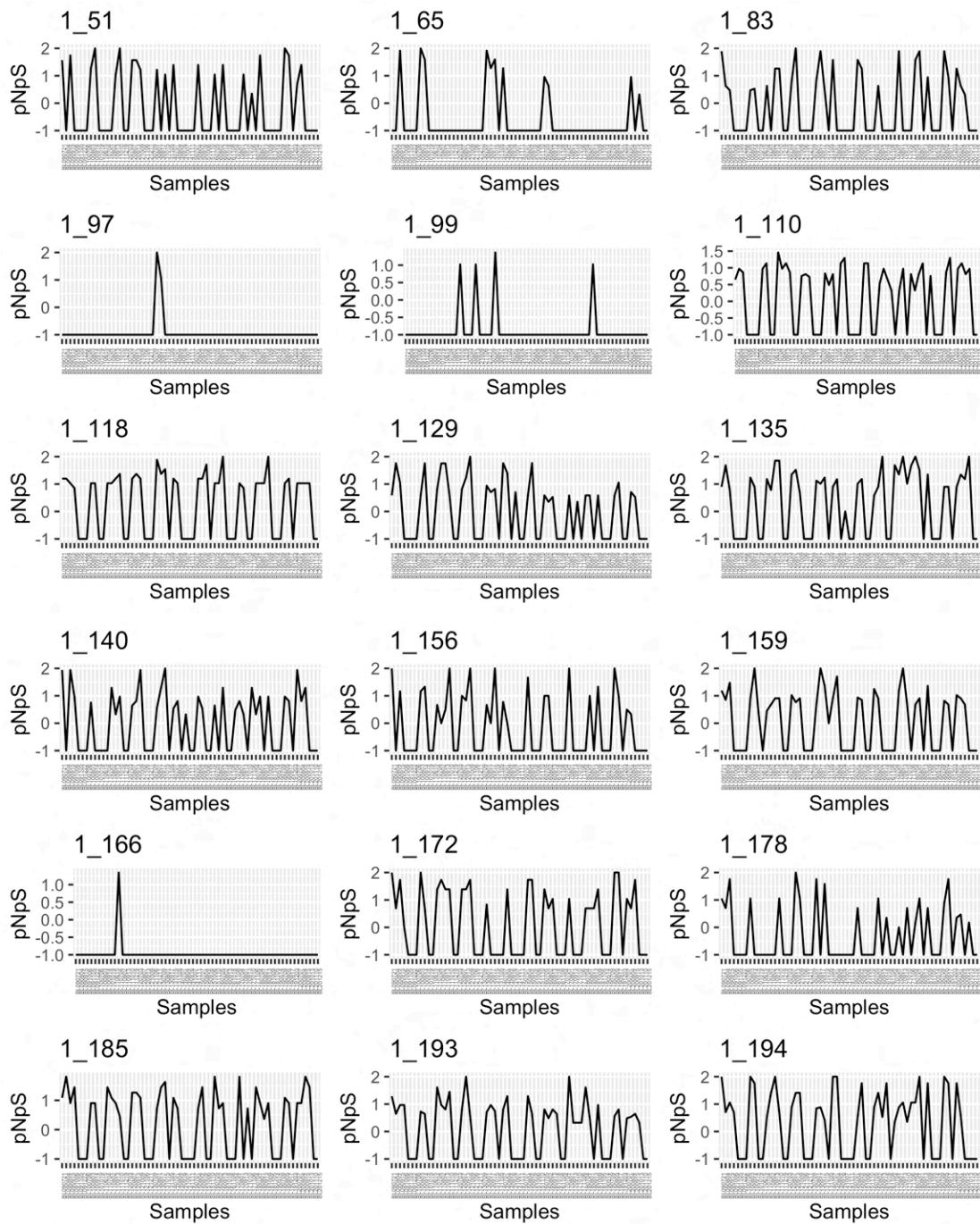
Supplementary Figure 48.2: The change of pNpS value of adaptive genes from MAG “BL\_1001\_bin.full.234” over time in SOLA. Along the x-axis is the sequence of sampling months from the 1st to the 90th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



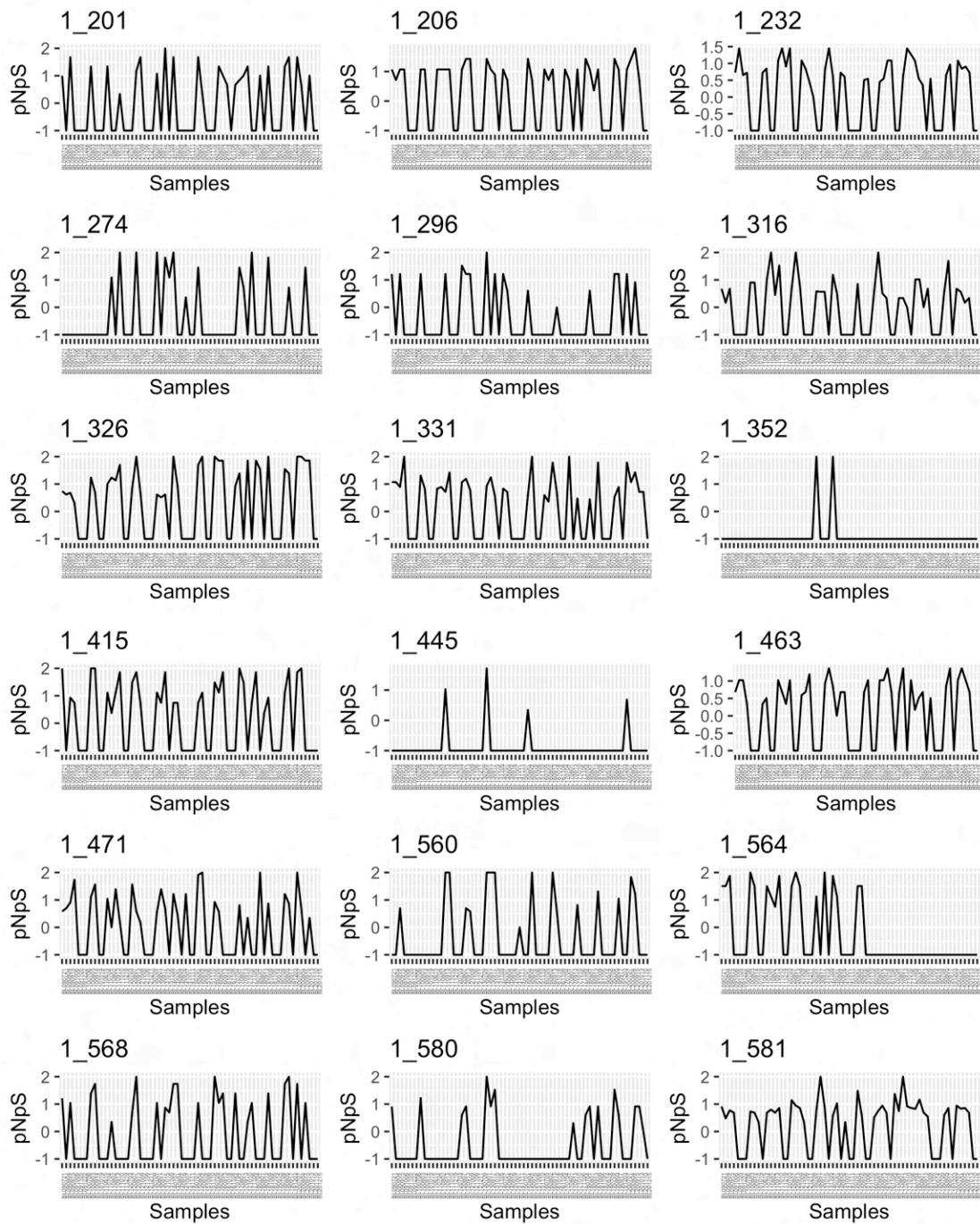
Supplementary Figure 49: The change of pNpS value of adaptive genes from MAG “BL\_pooled\_bin.circ.35” over time in BBMO. Along the x-axis is the sequence of sampling months from the 1st to the 140th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



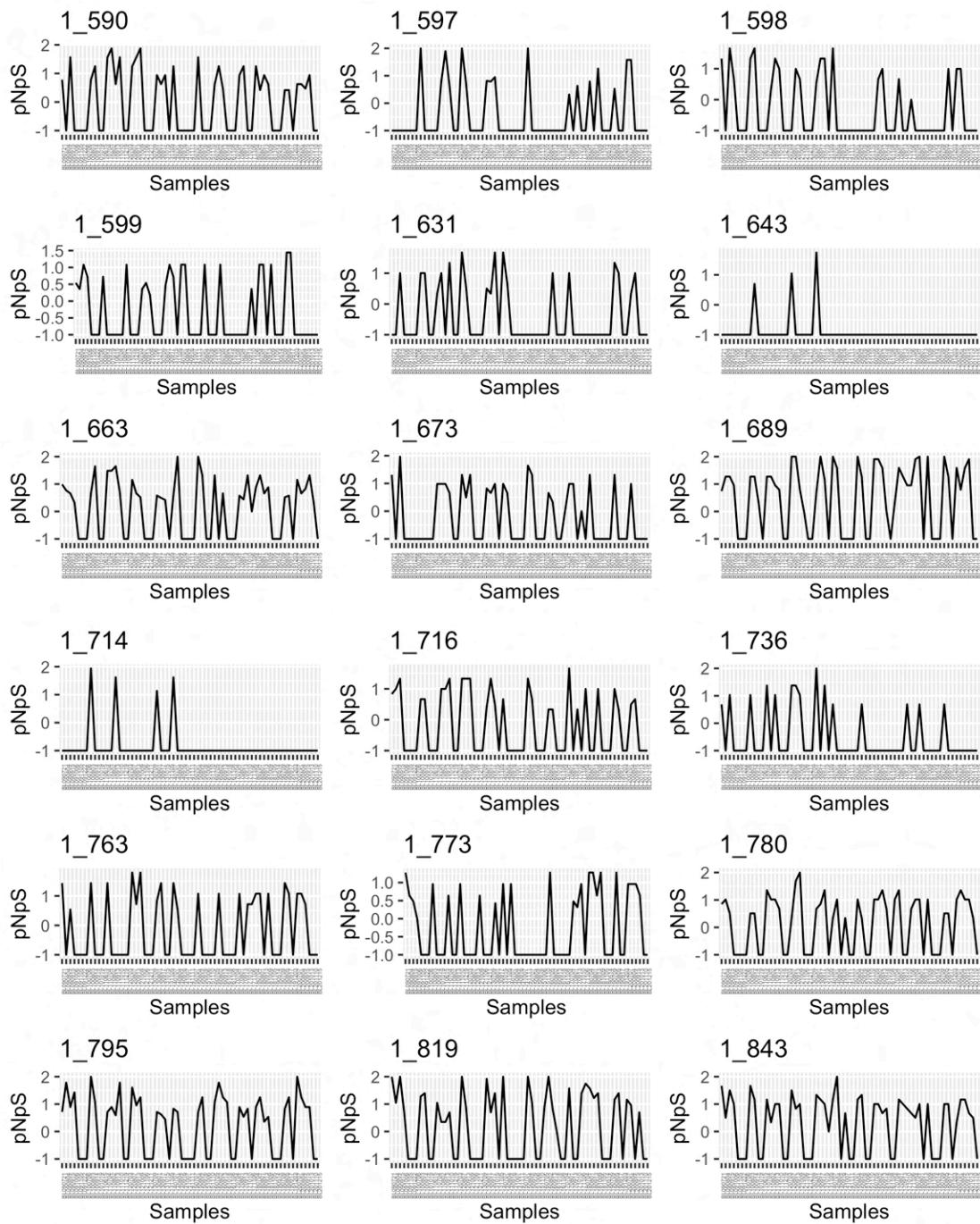
Supplementary Figure 50: The change of pNpS value of adaptive genes from MAG “BL\_pooled\_bin.circ.35” over time in SOLA. Along the x-axis is the sequence of sampling months from the 1st to the 90th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



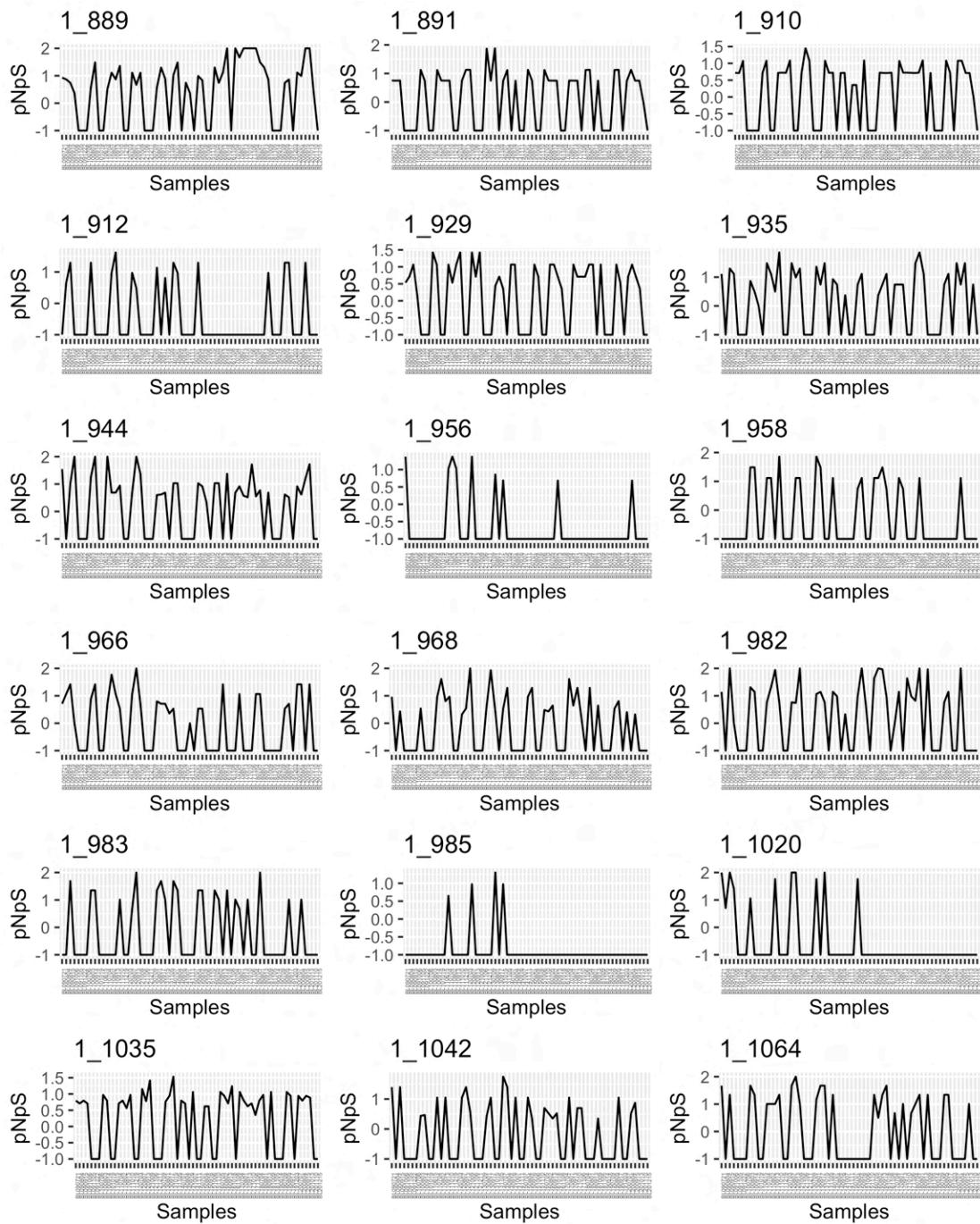
Supplementary Figure 51.1: The change of pNpS value of adaptive genes from MAG “BL\_pooled\_bin.circ.36” over time in BBMO. Along the x-axis is the sequence of sampling months from the 1st to the 140th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



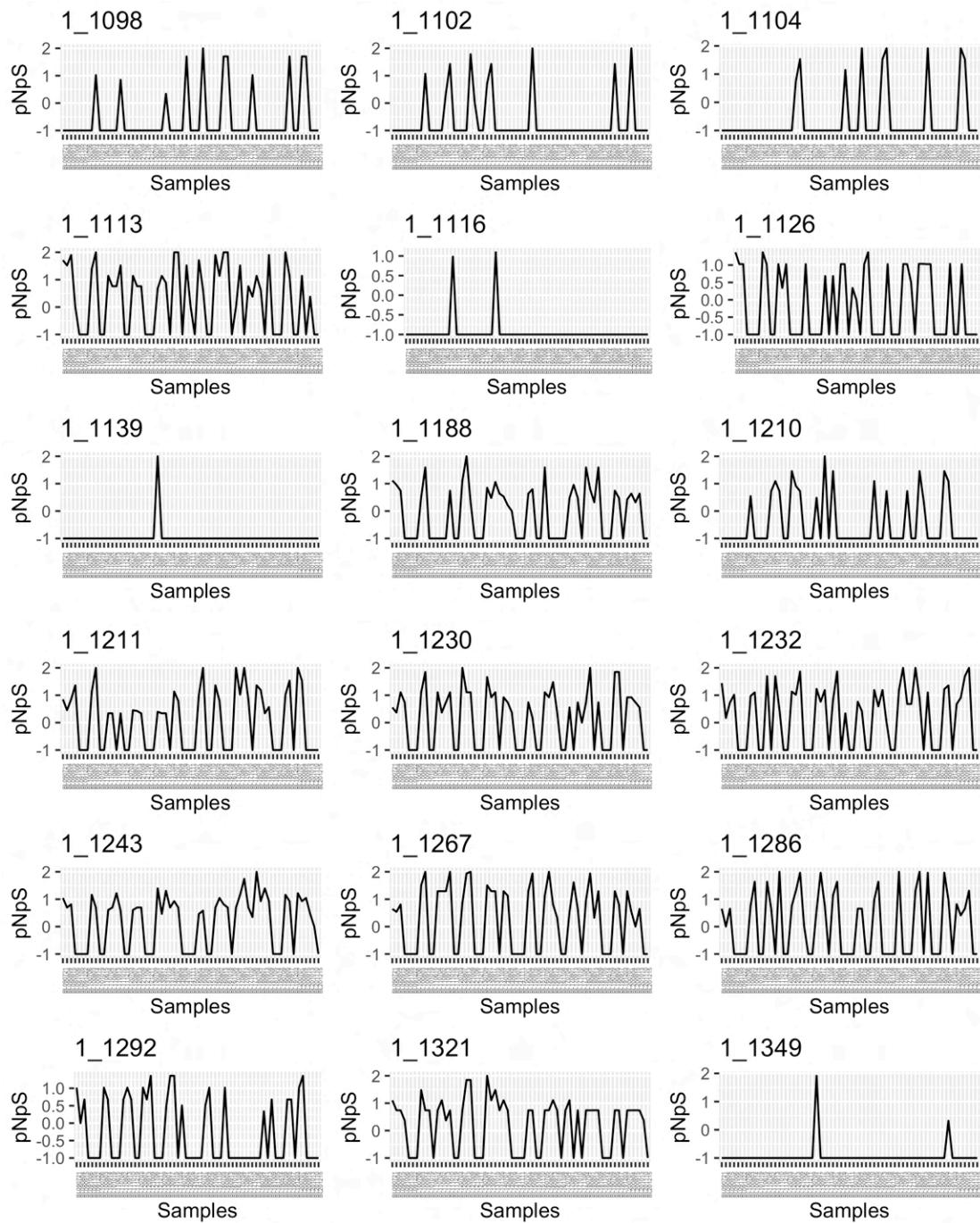
Supplementary Figure 51.2: The change of pNpS value of adaptive genes from MAG “BL\_pooled\_bin.circ.36” over time in BBMO. Along the x-axis is the sequence of sampling months from the 1st to the 140th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



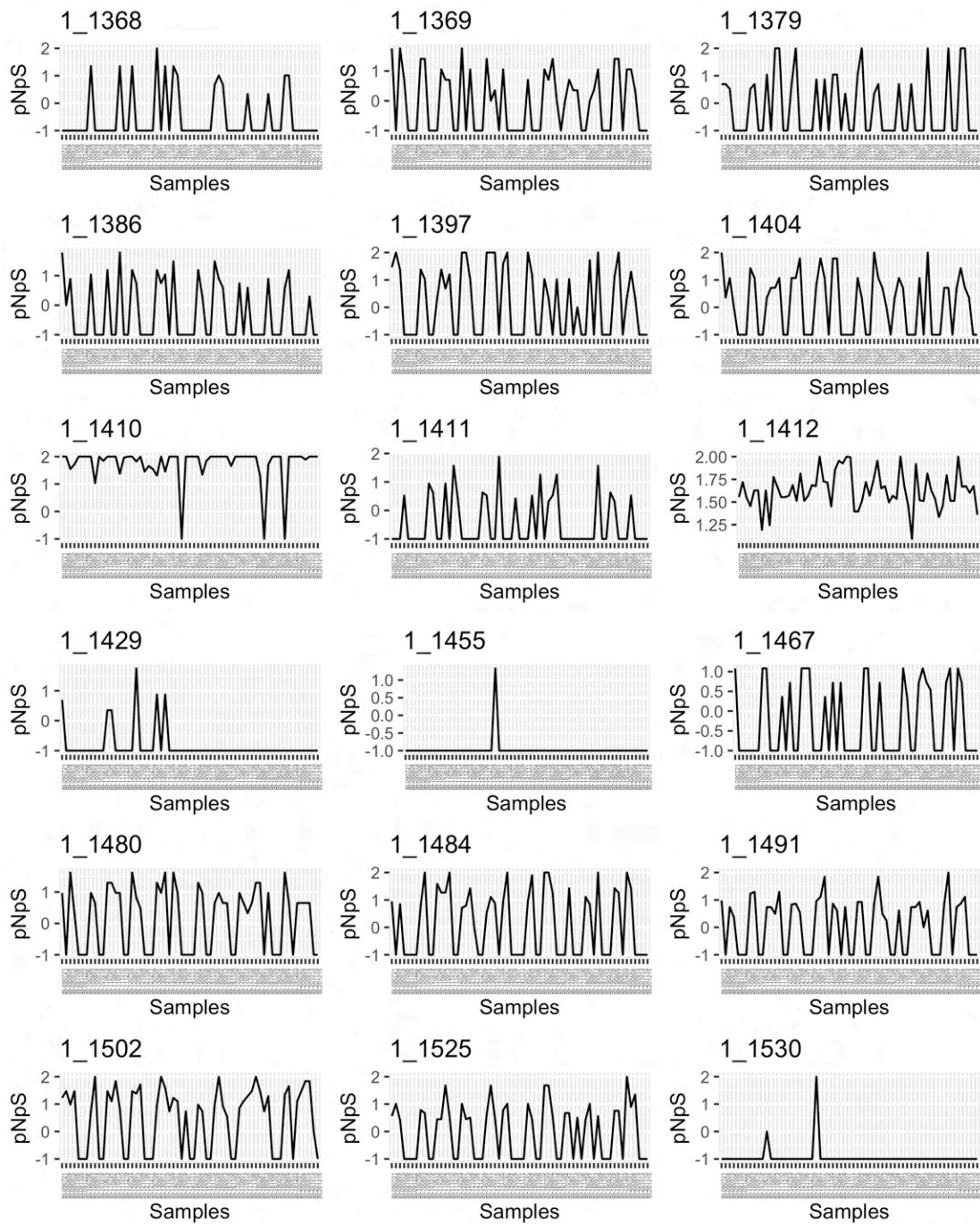
Supplementary Figure 51.3: The change of pNpS value of adaptive genes from MAG “BL\_pooled\_bin.circ.36” over time in BBMO. Along the x-axis is the sequence of sampling months from the 1st to the 140th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



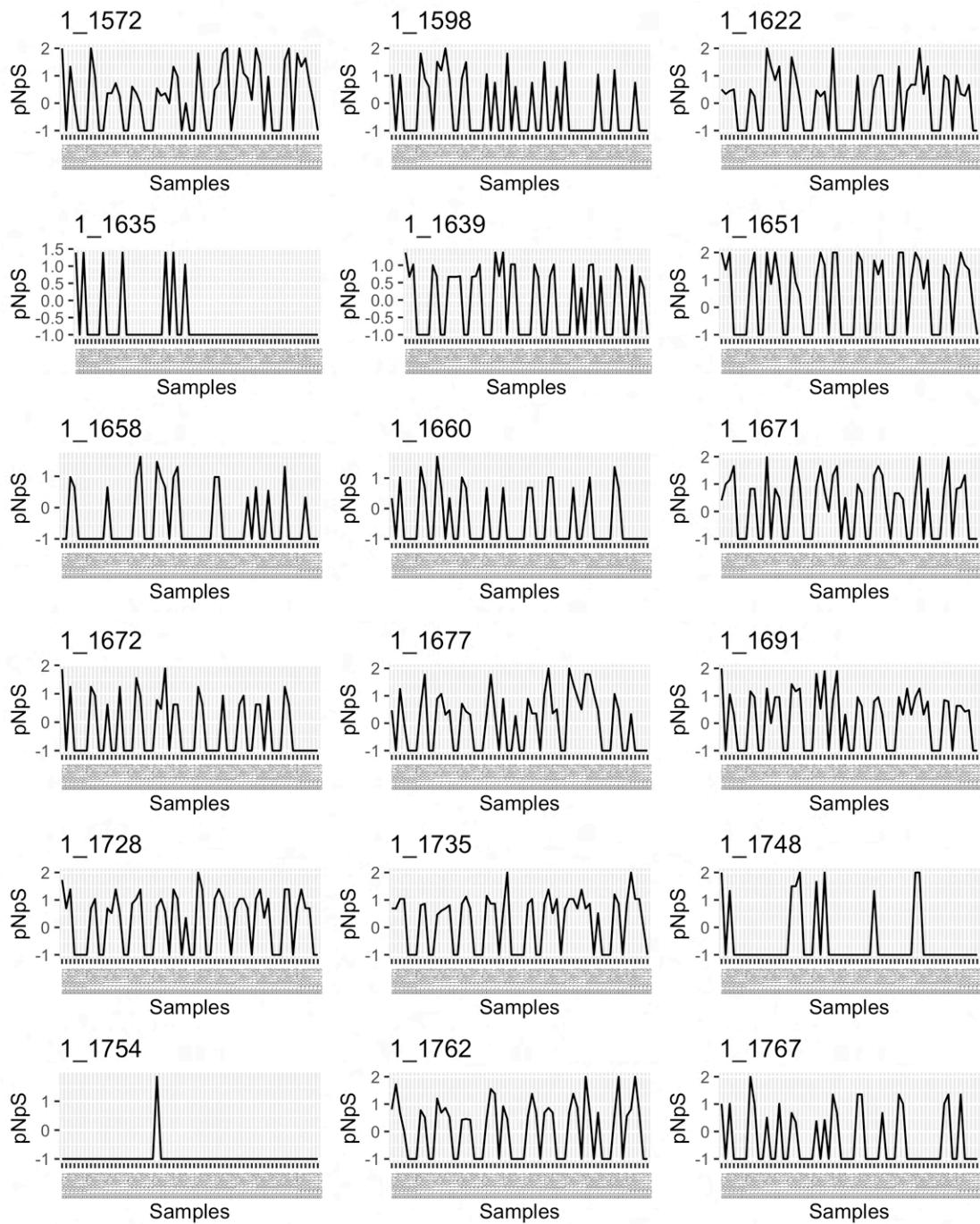
Supplementary Figure 51.4: The change of pNpS value of adaptive genes from MAG “BL\_pooled\_bin.circ.36” over time in BBMO. Along the x-axis is the sequence of sampling months from the 1st to the 140th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



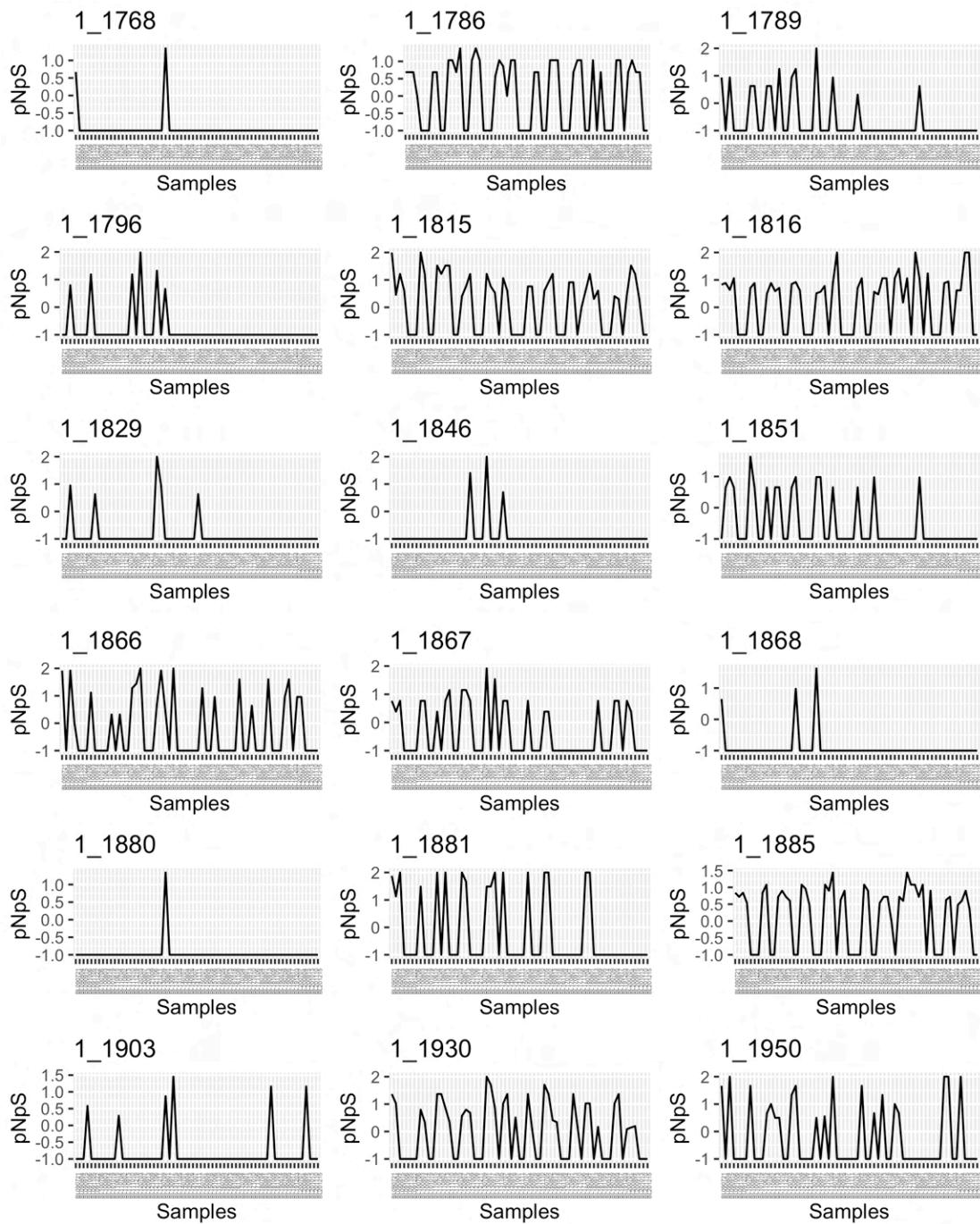
Supplementary Figure 51.5: The change of pNpS value of adaptive genes from MAG “BL\_pooled\_bin.circ.36” over time in BBMO. Along the x-axis is the sequence of sampling months from the 1st to the 140th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



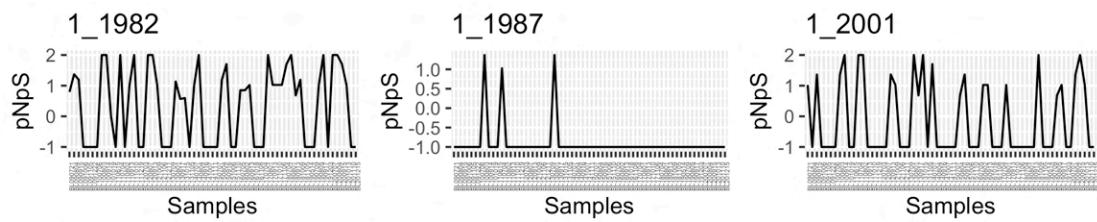
Supplementary Figure 51.6: The change of pNpS value of adaptive genes from MAG “BL\_pooled\_bin.circ.36” over time in BBMO. Along the x-axis is the sequence of sampling months from the 1st to the 140th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



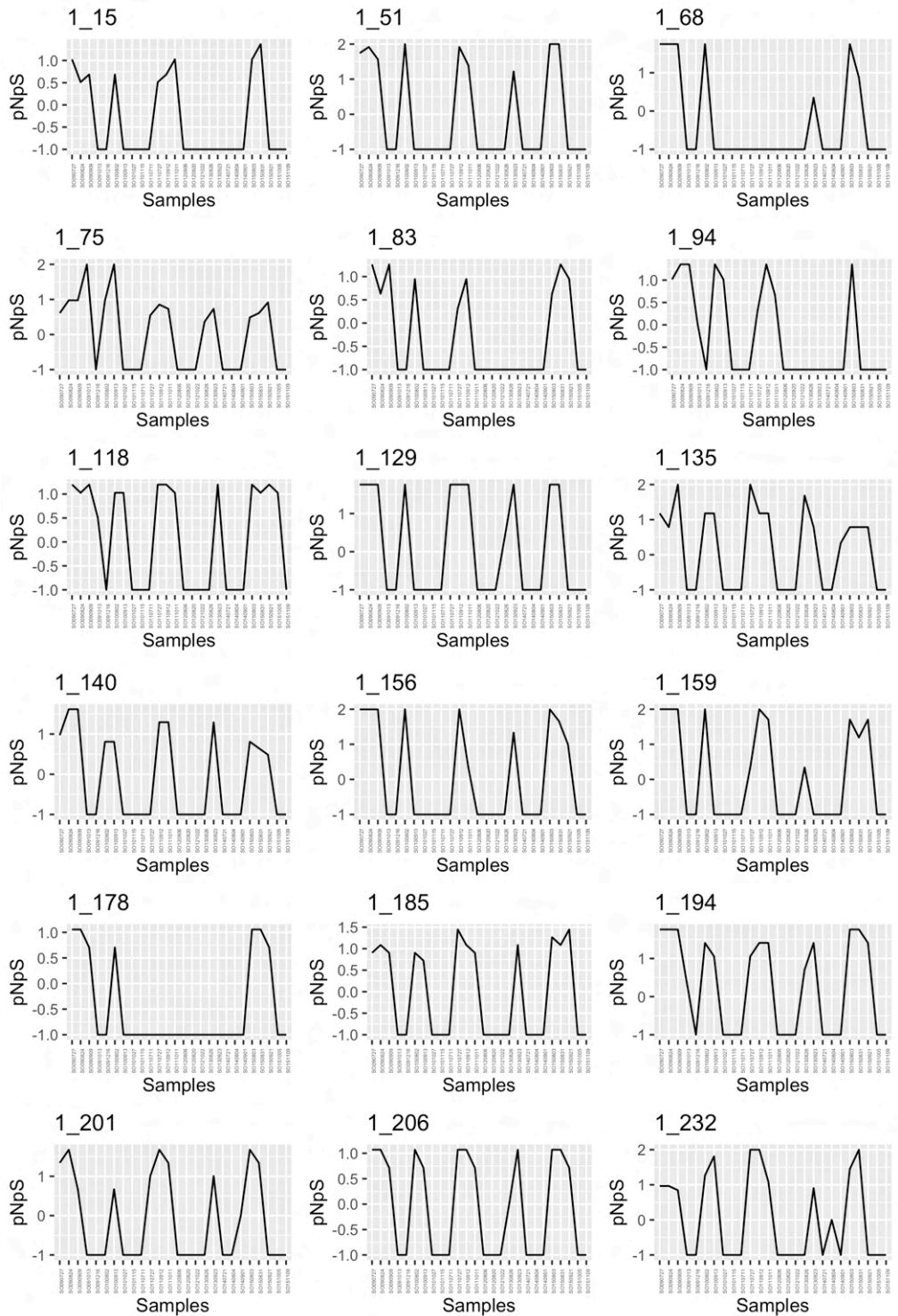
Supplementary Figure 51.7: The change of pNpS value of adaptive genes from MAG “BL\_pooled\_bin.circ.36” over time in BBMO. Along the x-axis is the sequence of sampling months from the 1st to the 140th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



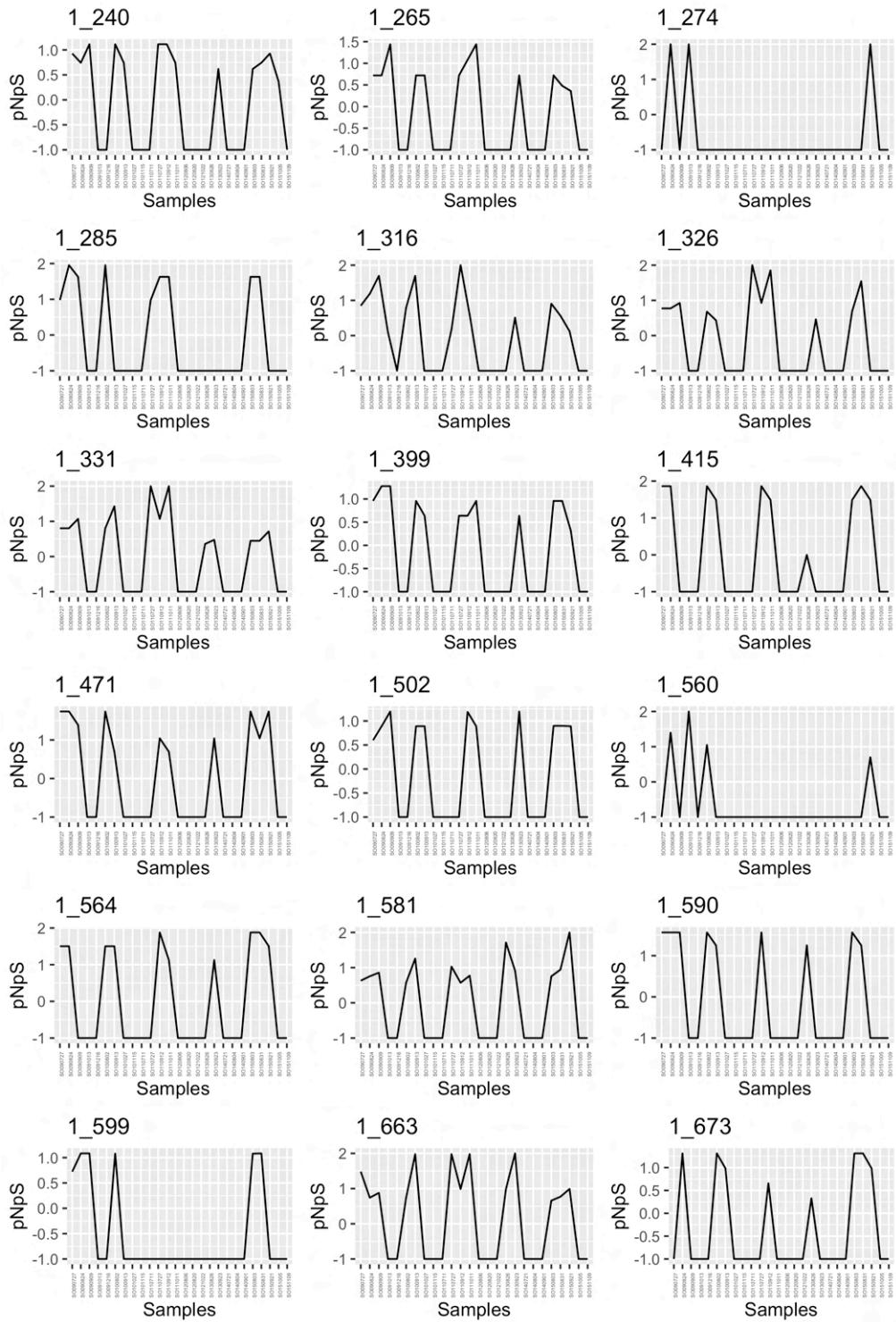
Supplementary Figure 51.8: The change of pNpS value of adaptive genes from MAG “BL\_pooled\_bin.circ.36” over time in BBMO. Along the x-axis is the sequence of sampling months from the 1st to the 140th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



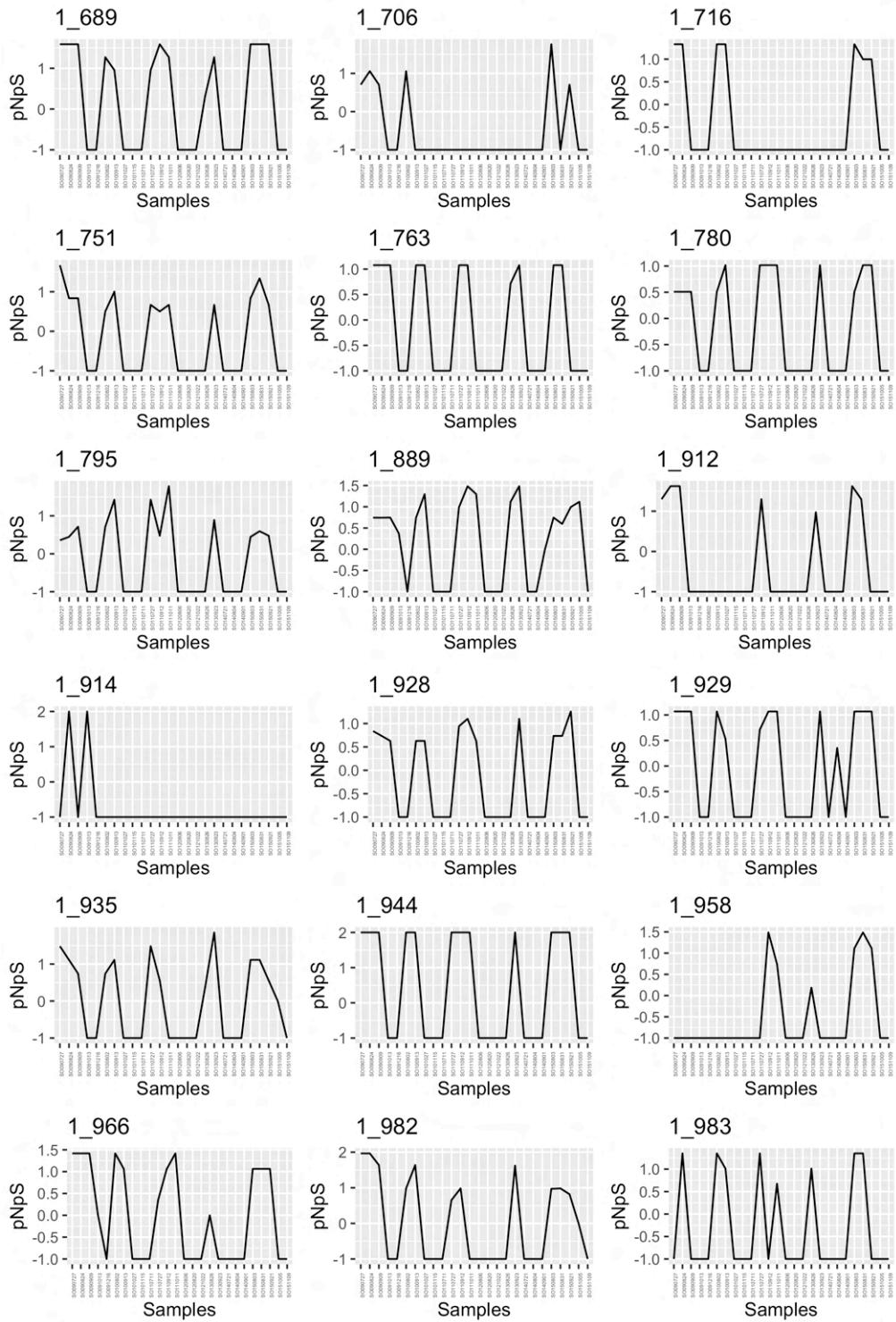
Supplementary Figure 51.9: The change of pNpS value of adaptive genes from MAG “BL\_pooled\_bin.circ.36” over time in BBMO. Along the x-axis is the sequence of sampling months from the 1st to the 140th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



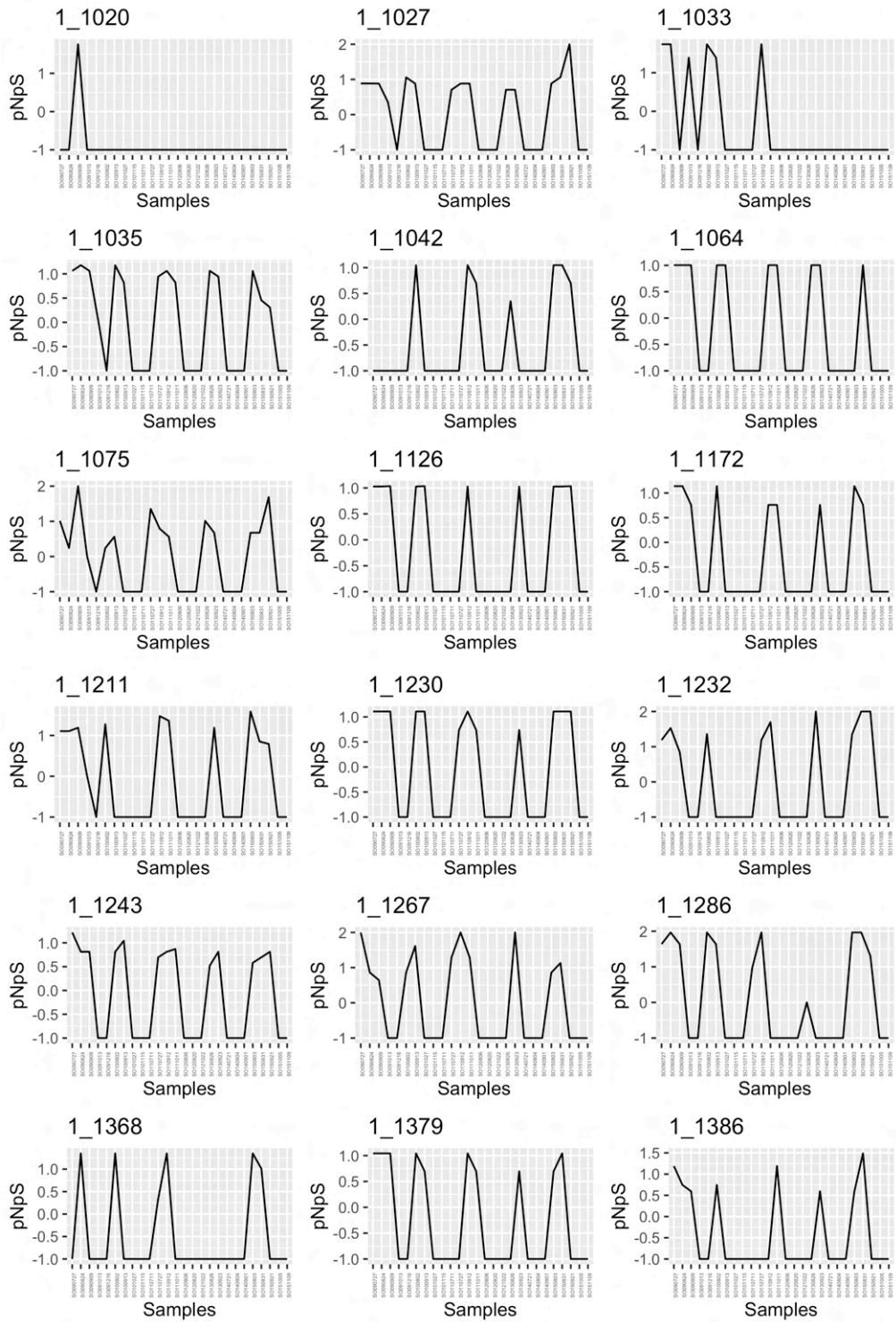
Supplementary Figure 52.1: The change of pNpS value of adaptive genes from MAG “BL\_pooled\_bin.circ.36” over time in SOLA. Along the x-axis is the sequence of sampling months from the 1st to the 90th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



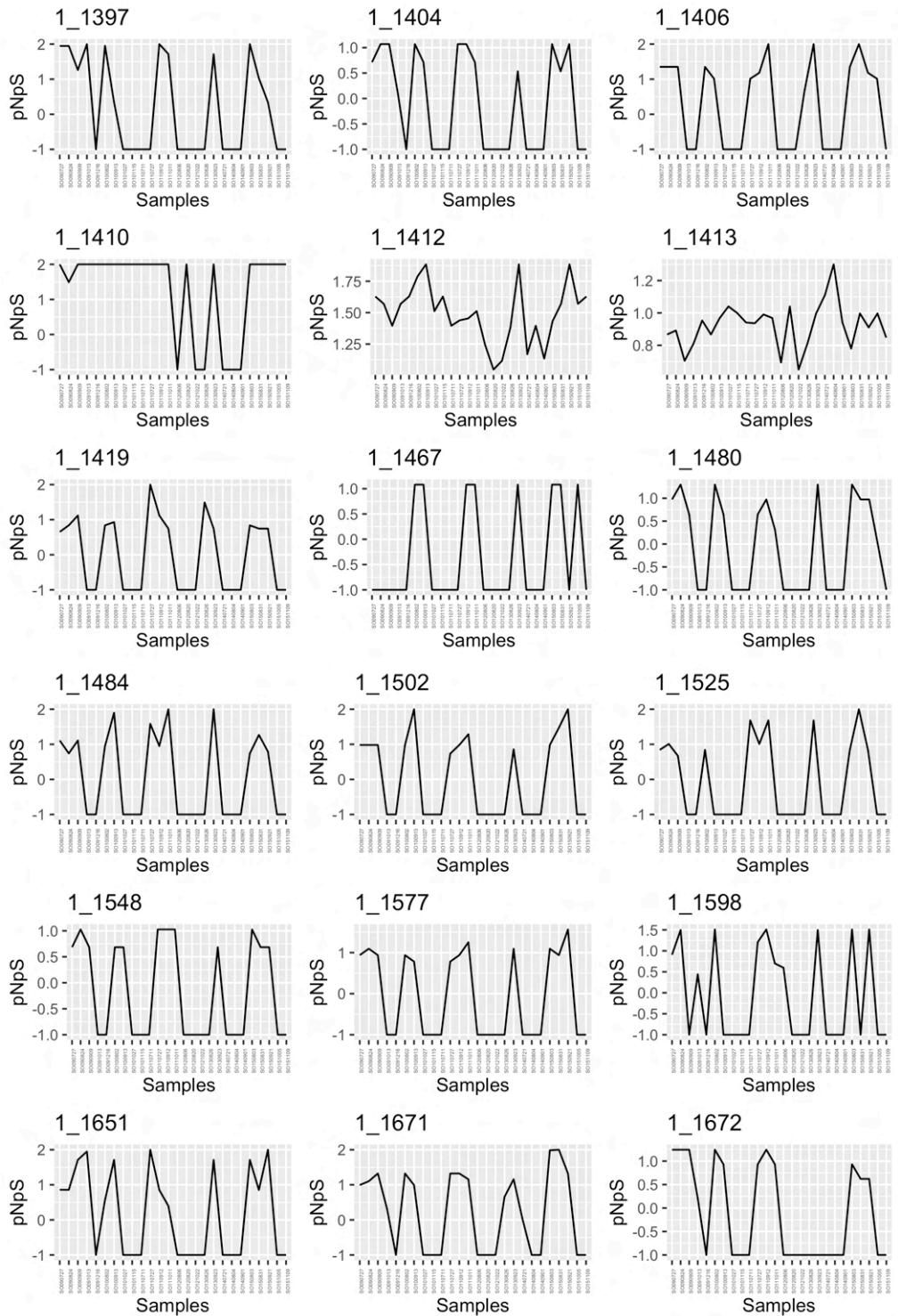
Supplementary Figure 52.2: The change of pNpS value of adaptive genes from MAG “BL\_pooled\_bin.circ.36” over time in SOLA. Along the x-axis is the sequence of sampling months from the 1st to the 90th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



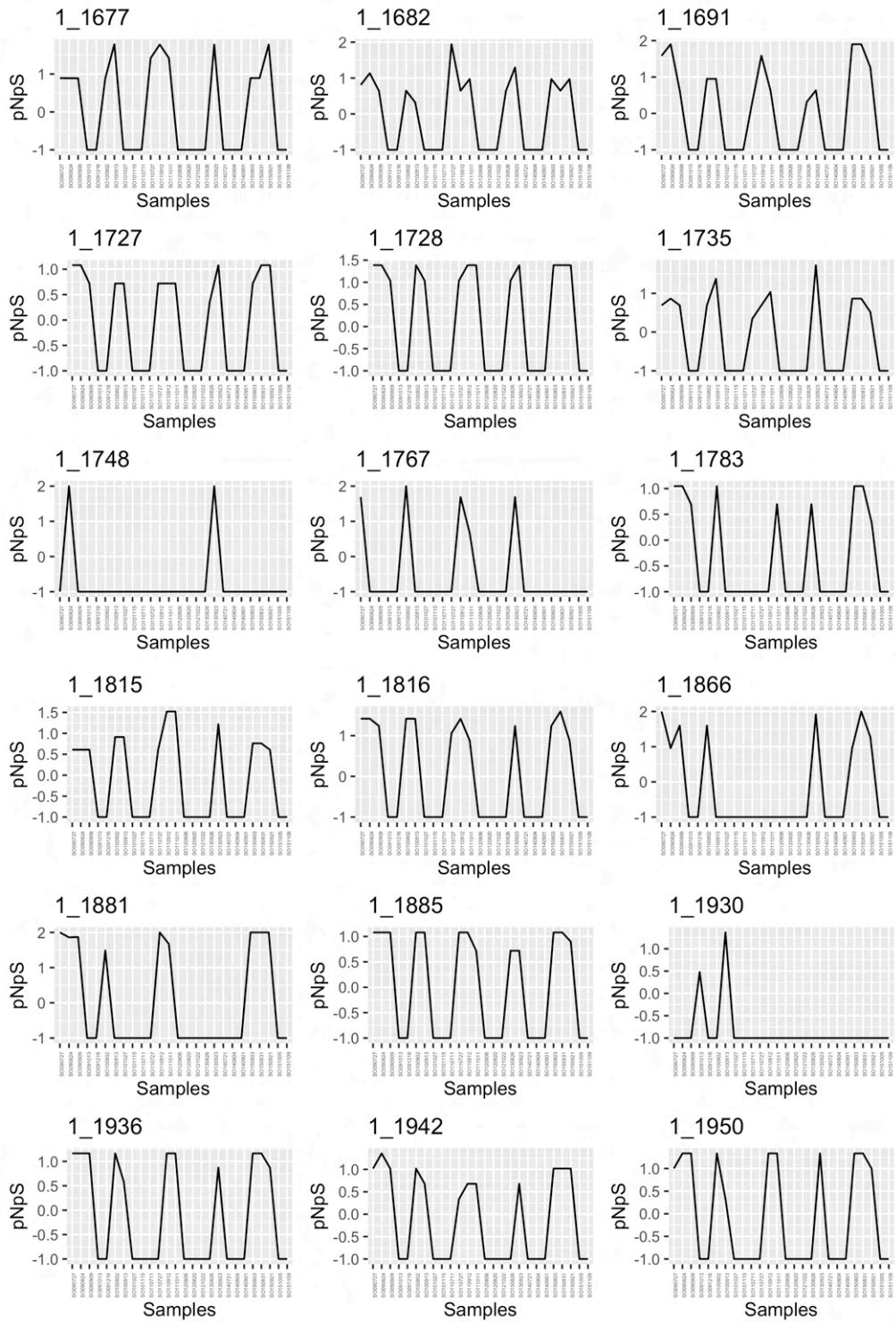
Supplementary Figure 52.3: The change of pNpS value of adaptive genes from MAG “BL\_pooled\_bin.circ.36” over time in SOLA. Along the x-axis is the sequence of sampling months from the 1st to the 90th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



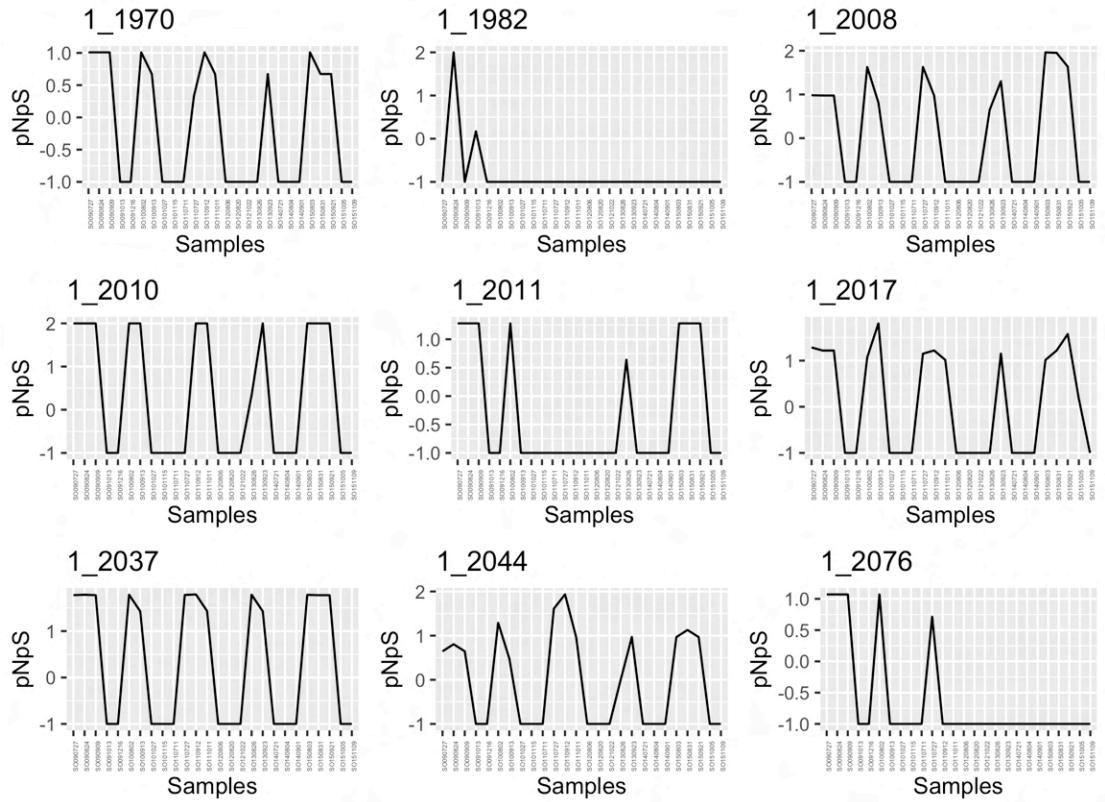
Supplementary Figure 52.4: The change of pNpS value of adaptive genes from MAG “BL\_pooled\_bin.circ.36” over time in SOLA. Along the x-axis is the sequence of sampling months from the 1st to the 90th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



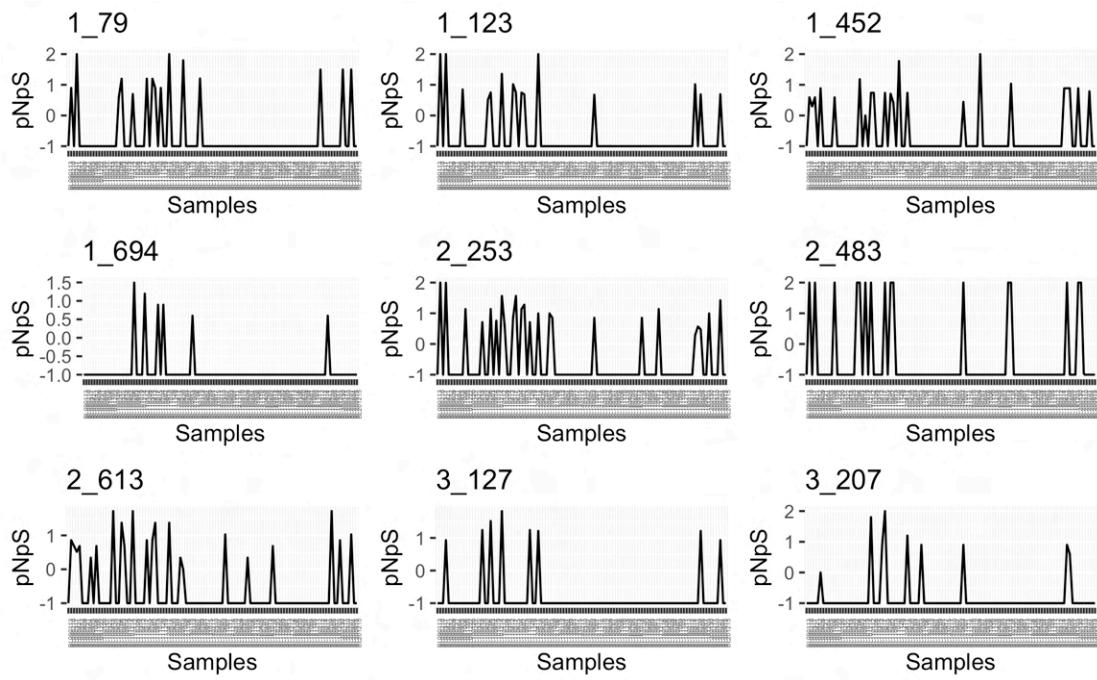
Supplementary Figure 52.5: The change of pNpS value of adaptive genes from MAG “BL\_pooled\_bin.circ.36” over time in SOLA. Along the x-axis is the sequence of sampling months from the 1st to the 90th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



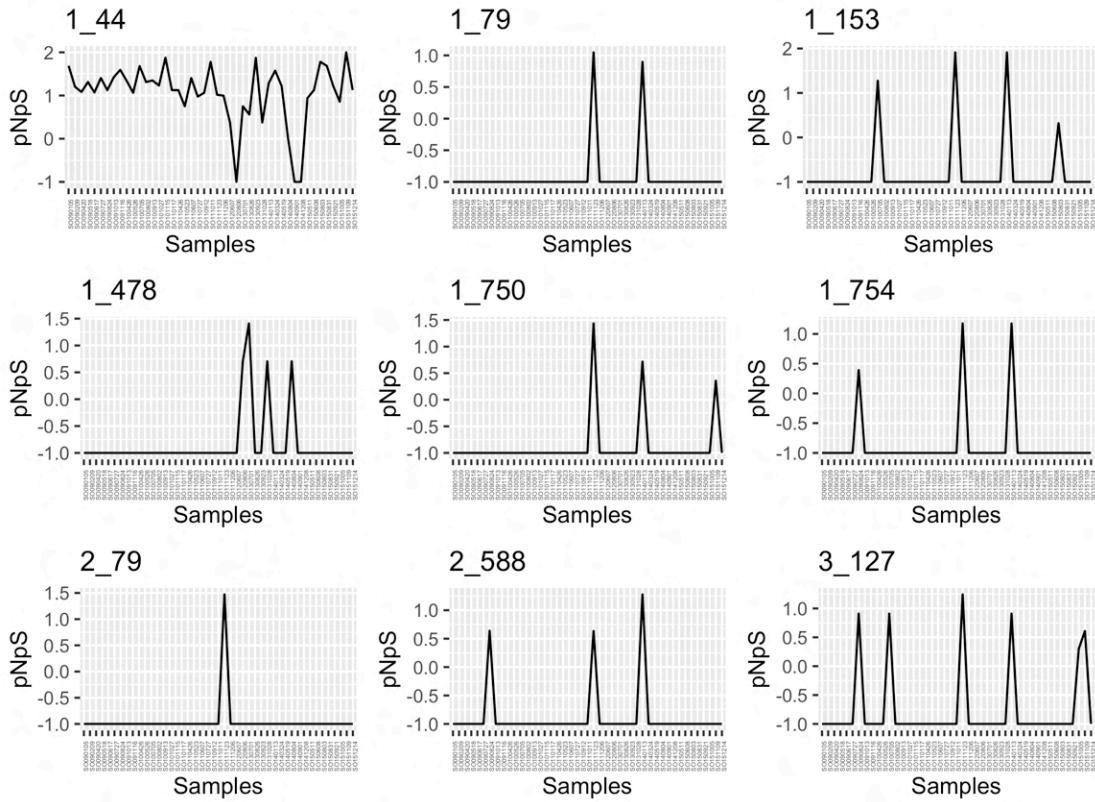
Supplementary Figure 52.6: The change of pNpS value of adaptive genes from MAG “BL\_pooled\_bin.circ.36” over time in SOLA. Along the x-axis is the sequence of sampling months from the 1st to the 90th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



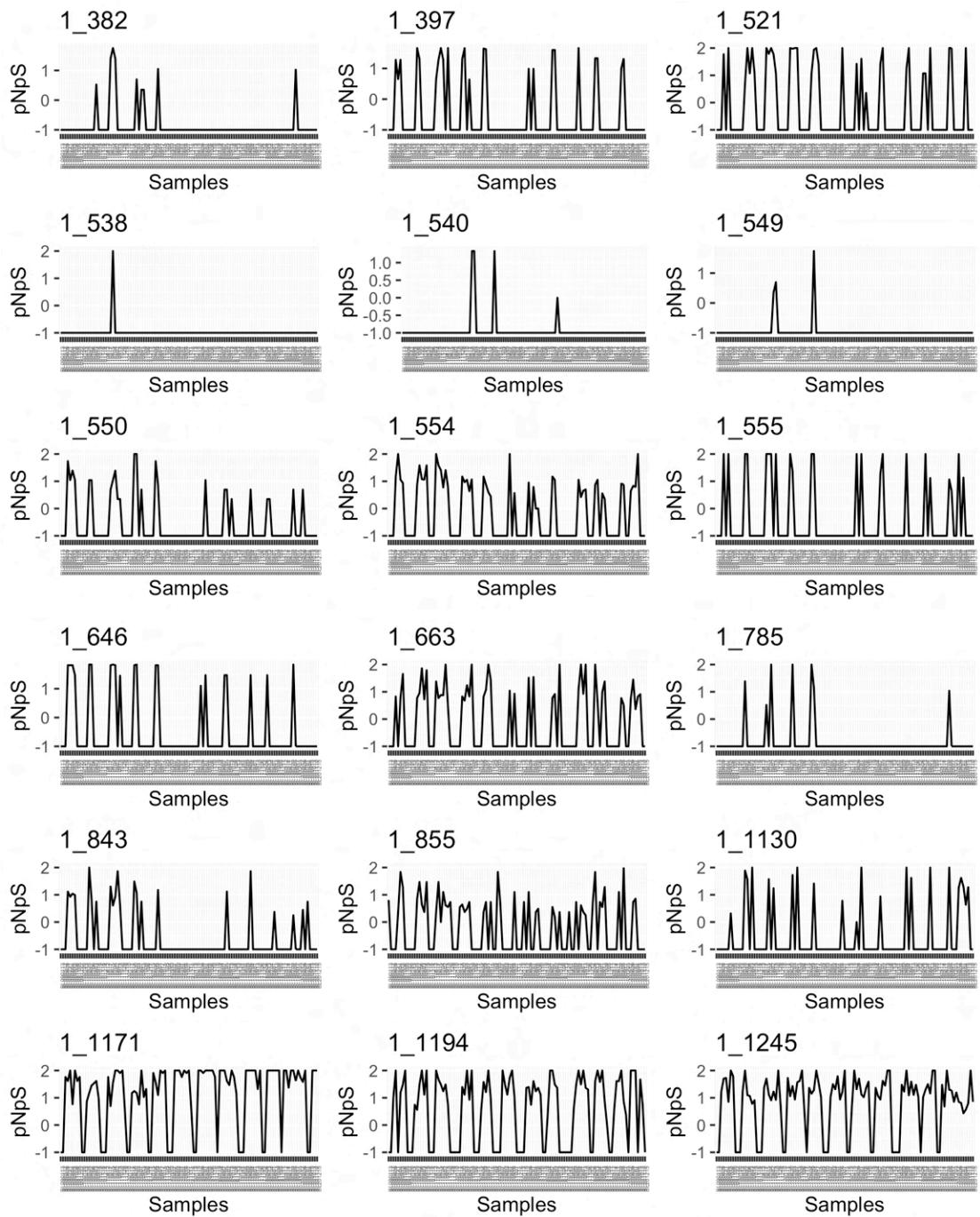
Supplementary Figure 52.7: The change of pNpS value of adaptive genes from MAG “BL\_pooled\_bin.circ.36” over time in SOLA. Along the x-axis is the sequence of sampling months from the 1st to the 90th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



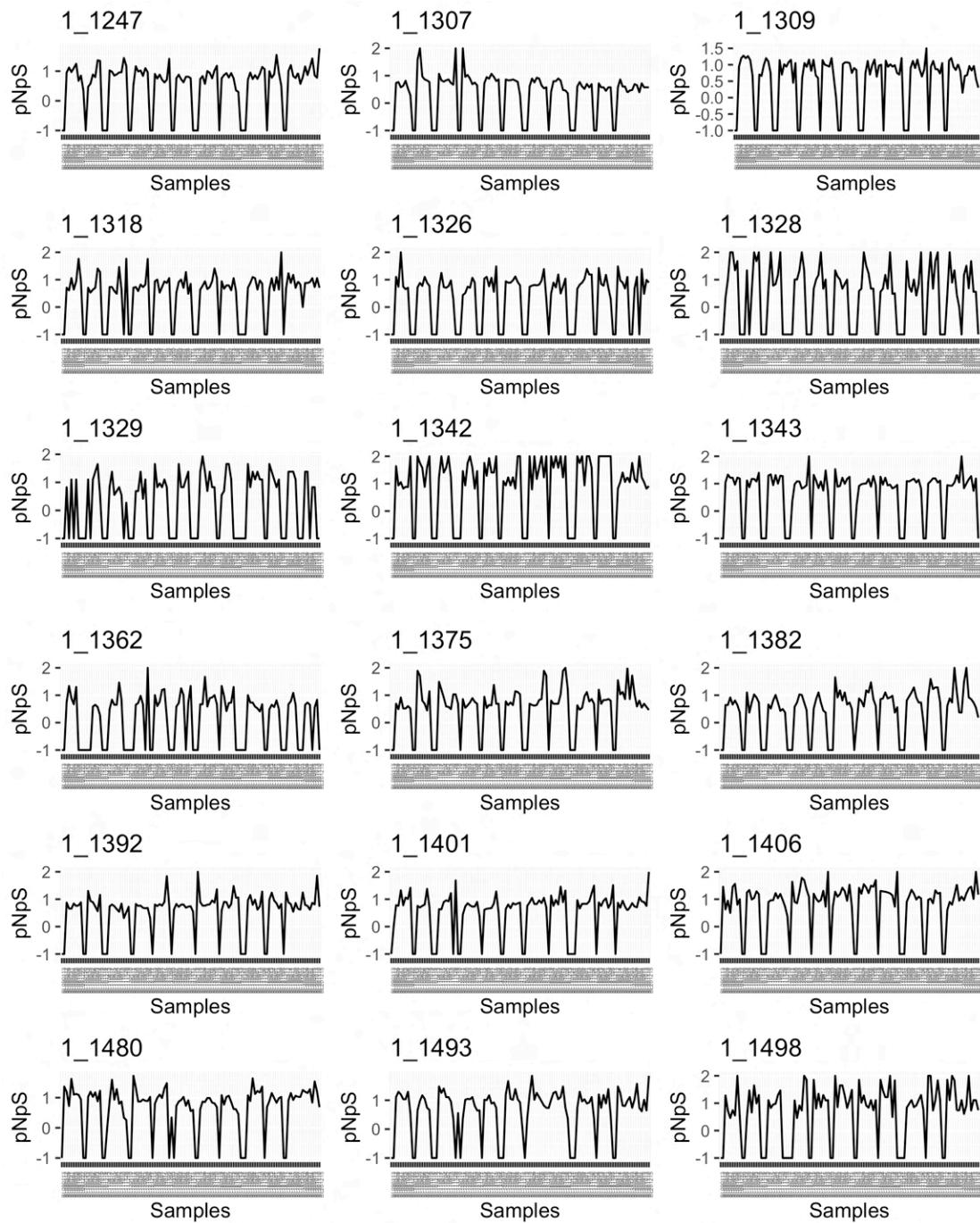
Supplementary Figure 53: The change of pNpS value of adaptive genes from MAG “BL\_pooled\_bin.full.145” over time in BBMO. Along the x-axis is the sequence of sampling months from the 1st to the 140th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



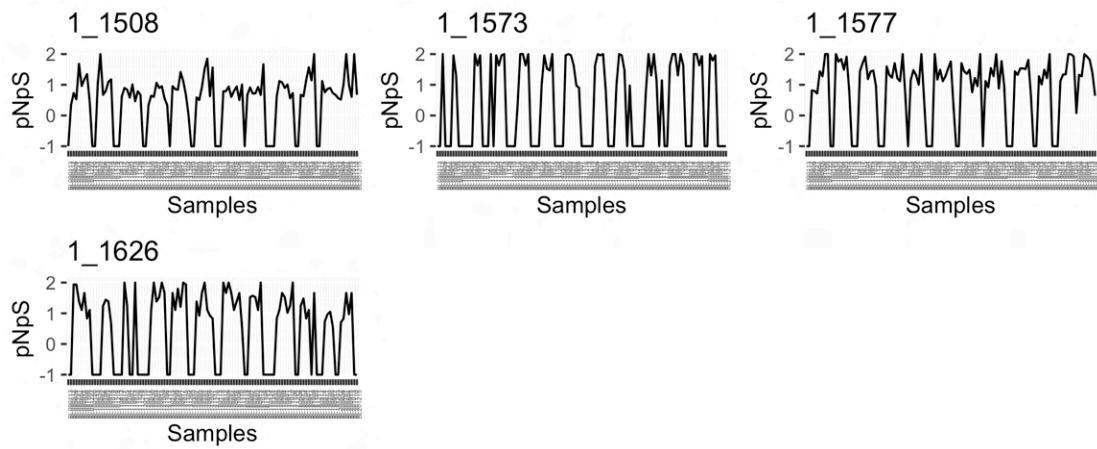
Supplementary Figure 54: The change of pNpS value of adaptive genes from MAG “BL\_pooled\_bin.full.145” over time in SOLA. Along the x-axis is the sequence of sampling months from the 1st to the 90th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



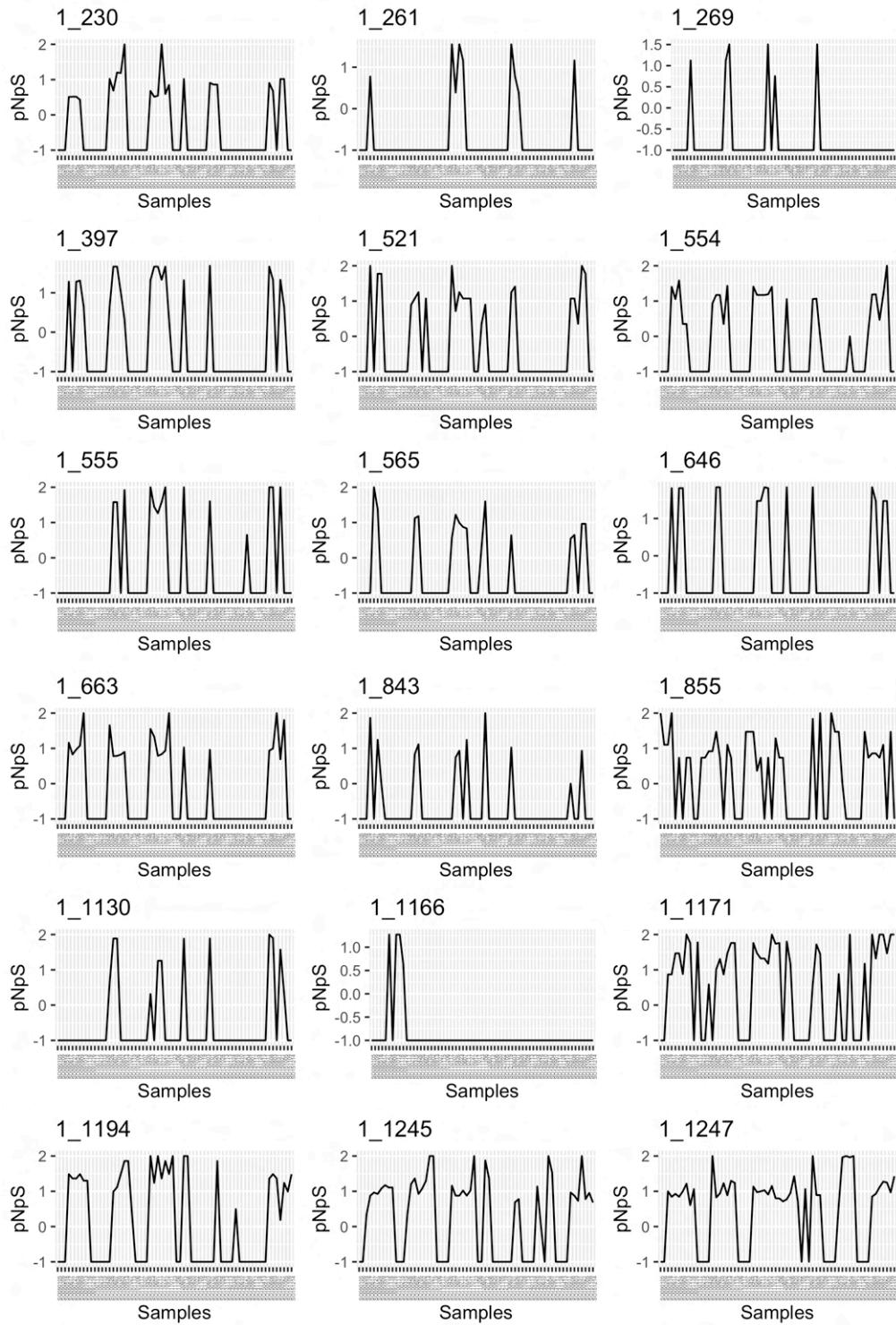
Supplementary Figure 55.1: The change of pNpS value of adaptive genes from MAG “BL\_pooled\_bin.full.596” over time in BBMO. Along the x-axis is the sequence of sampling months from the 1st to the 140th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



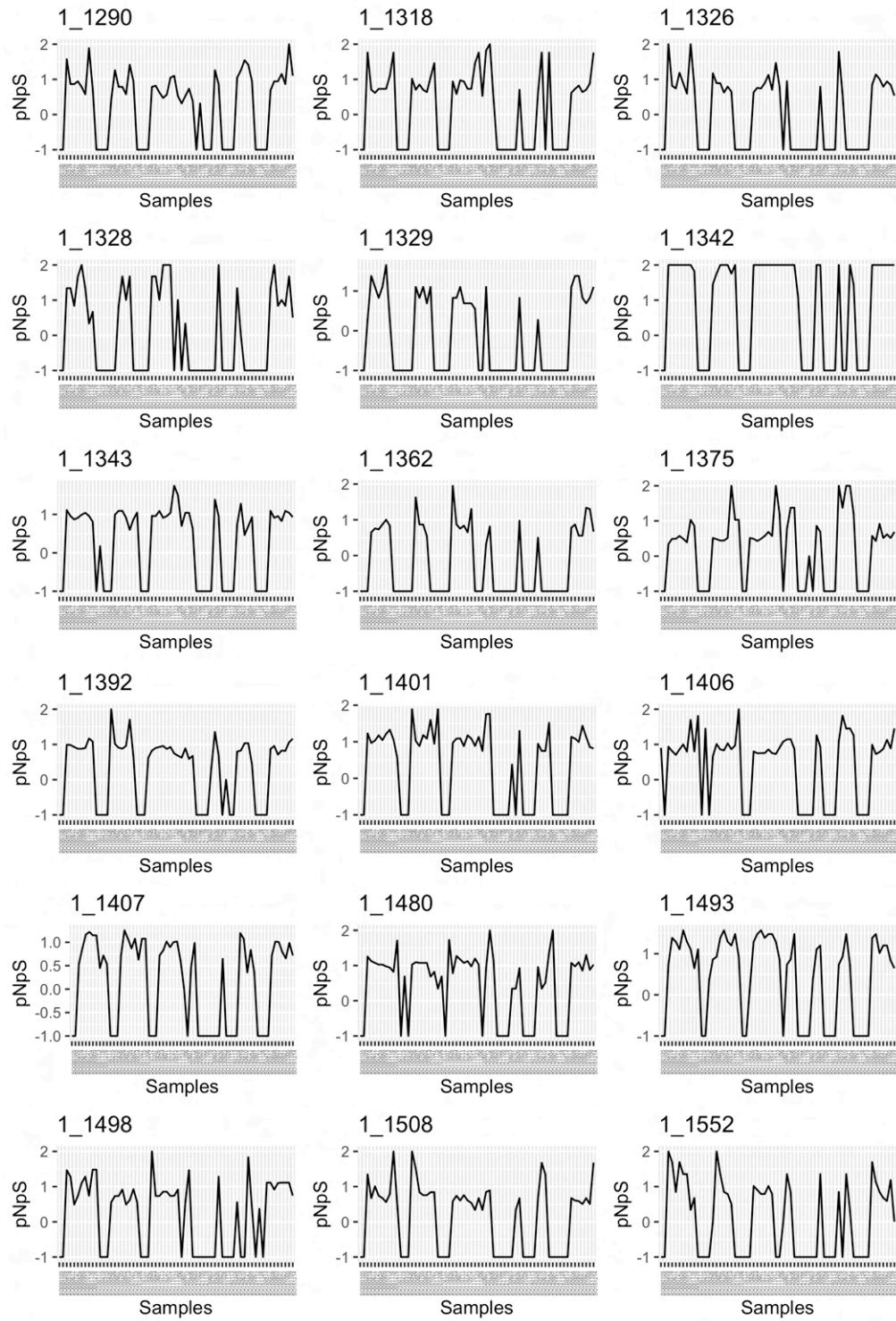
Supplementary Figure 55.2: The change of pNpS value of adaptive genes from MAG “BL\_pooled\_bin.full.596” over time in BBMO. Along the x-axis is the sequence of sampling months from the 1st to the 140th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



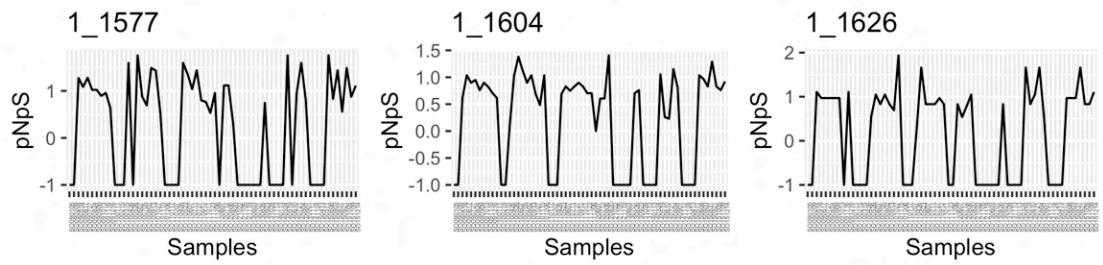
Supplementary Figure 55.3: The change of pNpS value of adaptive genes from MAG "BL\_pooled\_bin.full.596" over time in BBMO. Along the x-axis is the sequence of sampling months from the 1st to the 140th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



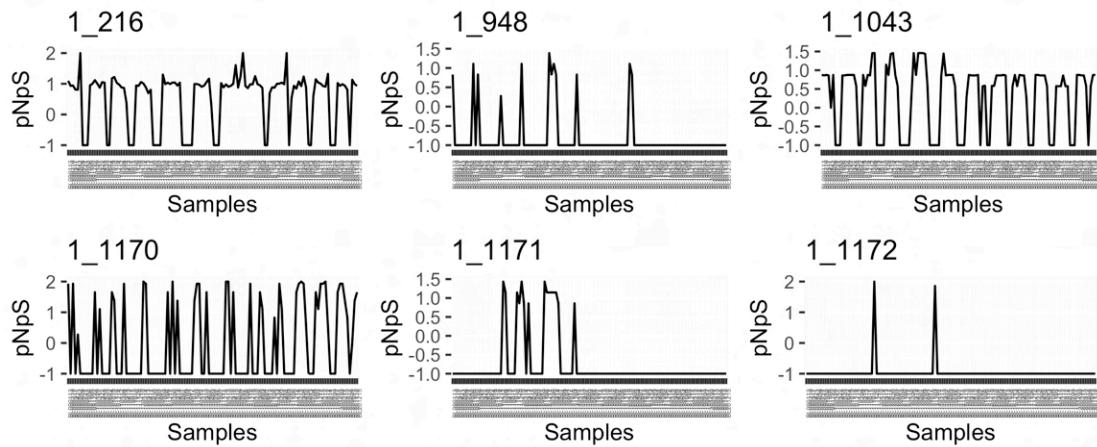
Supplementary Figure 56.1: The change of pNpS value of adaptive genes from MAG “BL\_pooled\_bin.full.596” over time in SOLA. Along the x-axis is the sequence of sampling months from the 1st to the 90th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



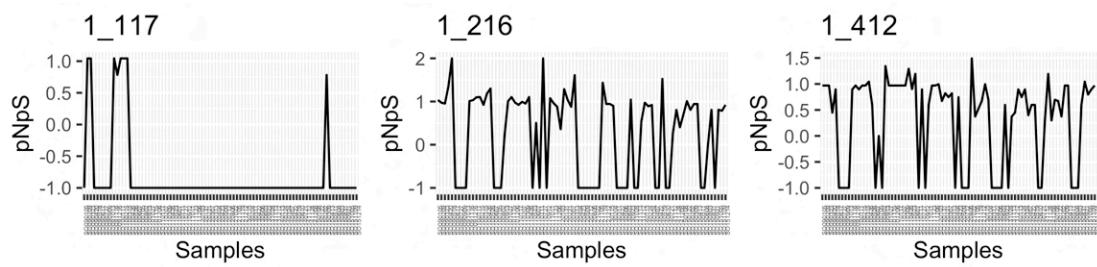
Supplementary Figure 56.2: The change of pNpS value of adaptive genes from MAG “BL\_pooled\_bin.full.596” over time in SOLA. Along the x-axis is the sequence of sampling months from the 1st to the 90th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



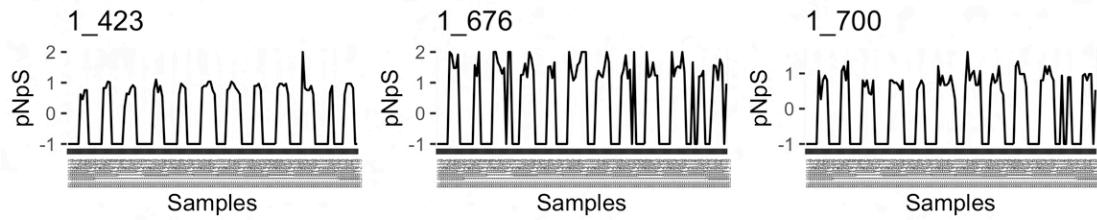
Supplementary Figure 56.3: The change of pNpS value of adaptive genes from MAG “BL\_pooled\_bin.full.596” over time in SOLA. Along the x-axis is the sequence of sampling months from the 1st to the 90th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



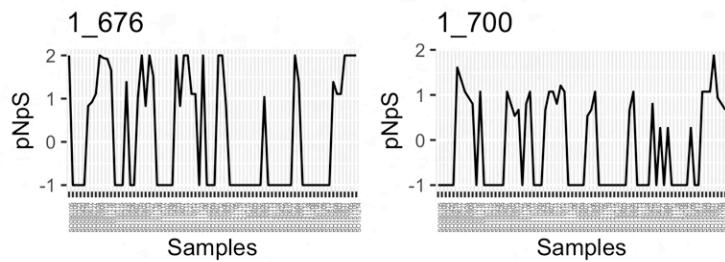
Supplementary Figure 57: The change of pNpS value of adaptive genes from MAG “BL\_pooled\_bin.full.761” over time in BBMO. Along the x-axis is the sequence of sampling months from the 1st to the 140th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



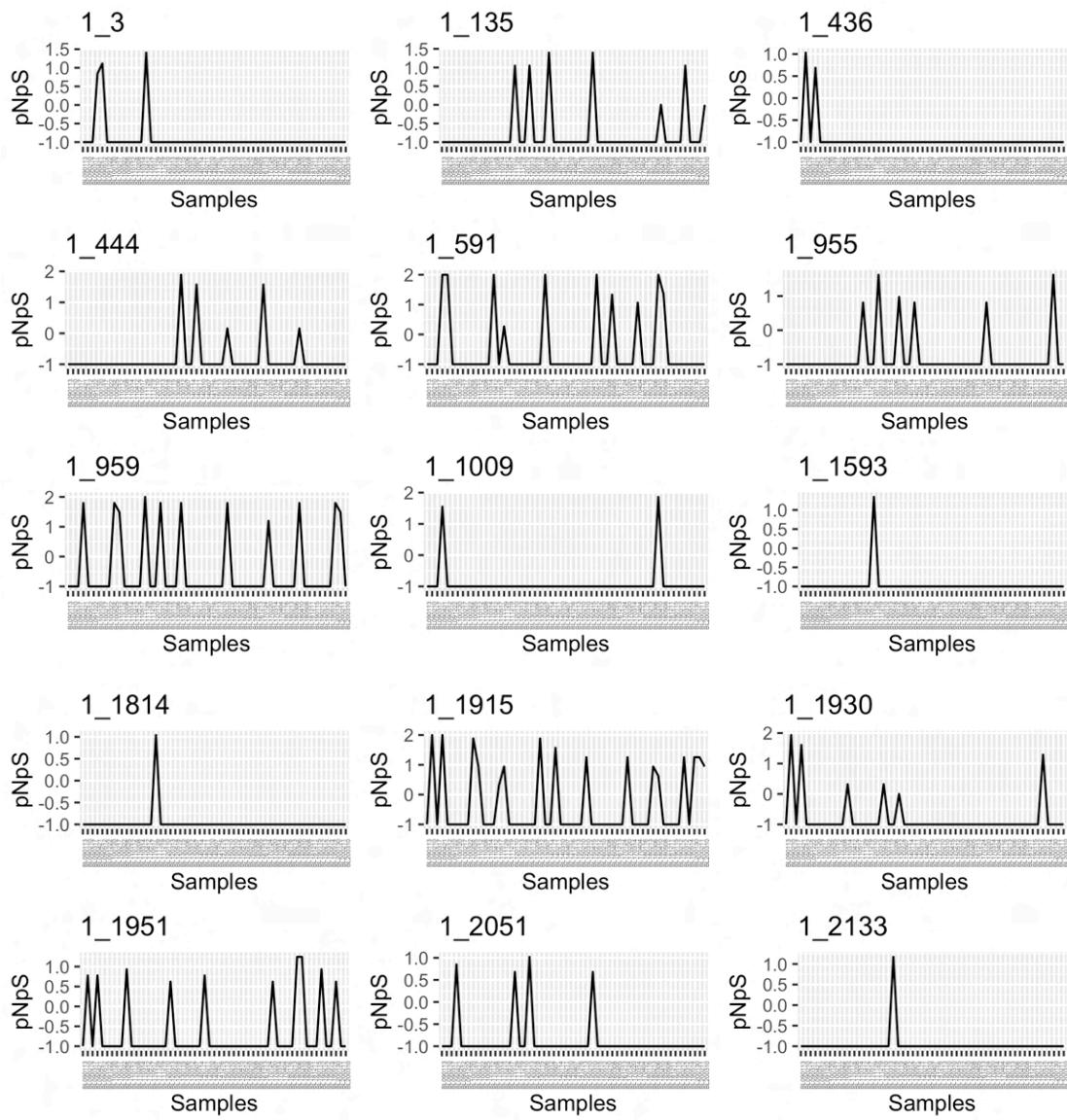
Supplementary Figure 58: The change of pNpS value of adaptive genes from MAG “BL\_pooled\_bin.full.761” over time in SOLA. Along the x-axis is the sequence of sampling months from the 1st to the 90th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



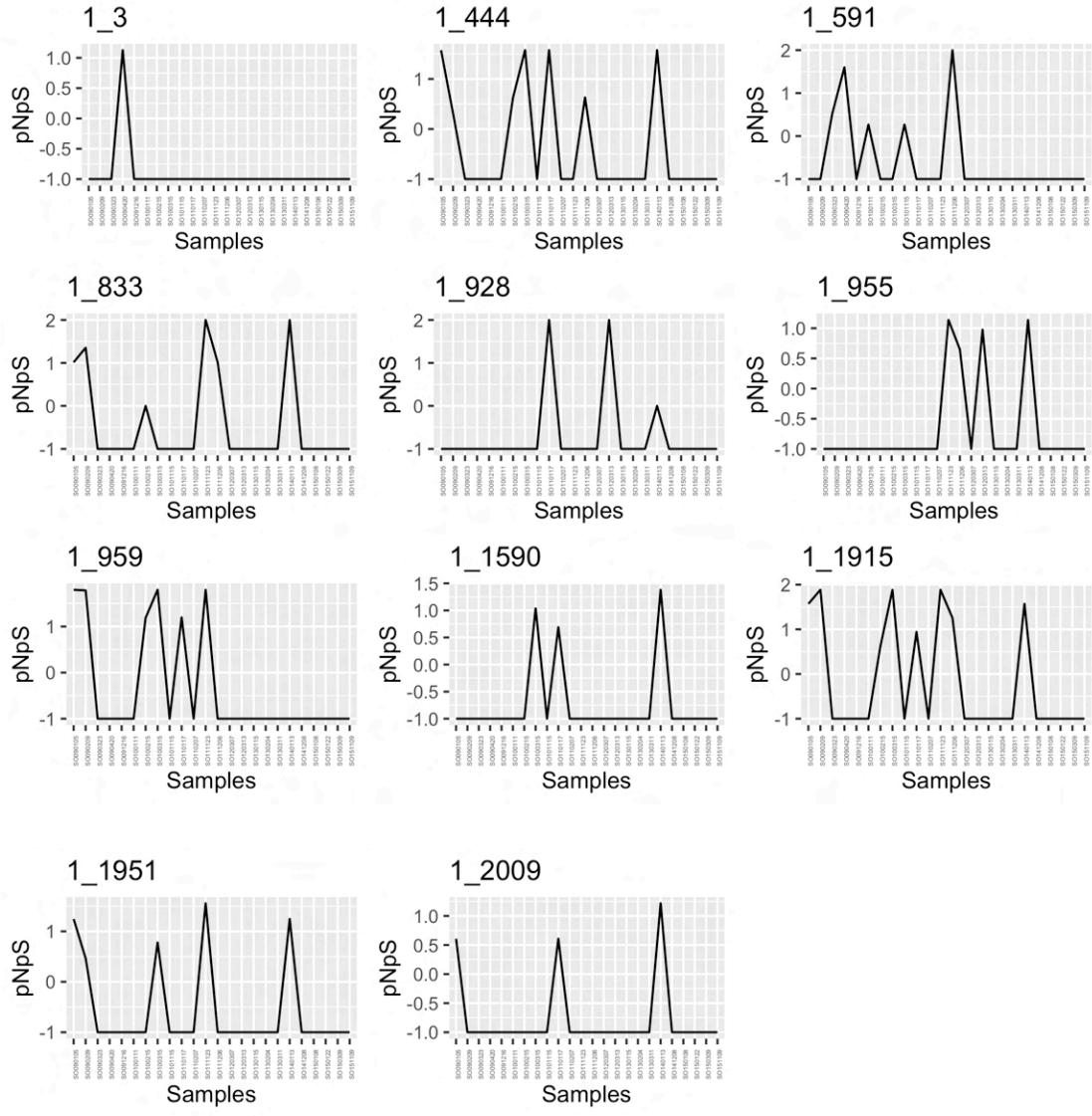
Supplementary Figure 59: The change of pNpS value of adaptive genes from MAG “s1032.ctg001132l\_BL\_0908sc” over time in BBMO. Along the x-axis is the sequence of sampling months from the 1st to the 140th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



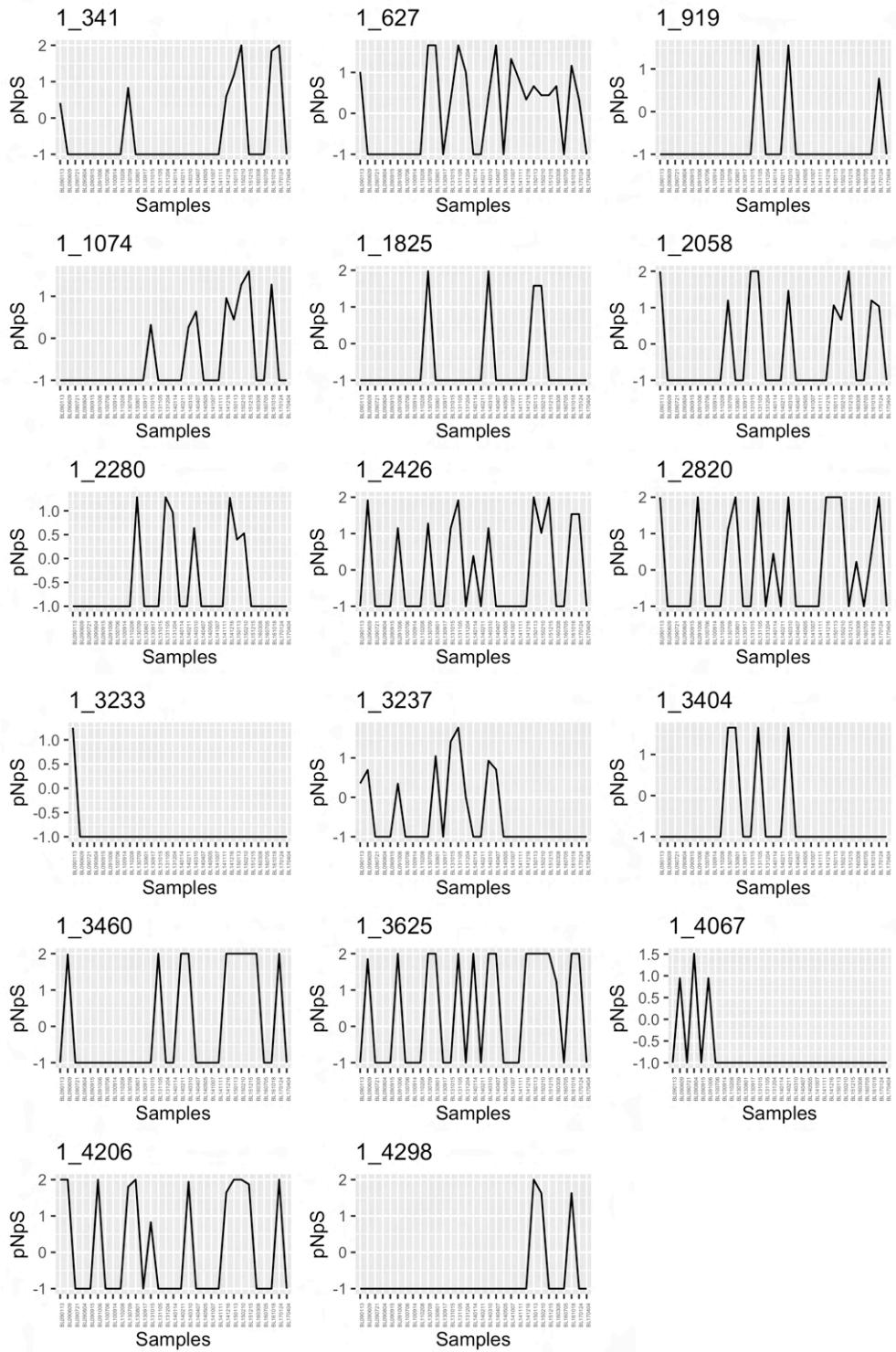
Supplementary Figure 60: The change of pNpS value of adaptive genes from MAG “s1032.ctg001132l\_BL\_0908sc” over time in SOLA. Along the x-axis is the sequence of sampling months from the 1st to the 90th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



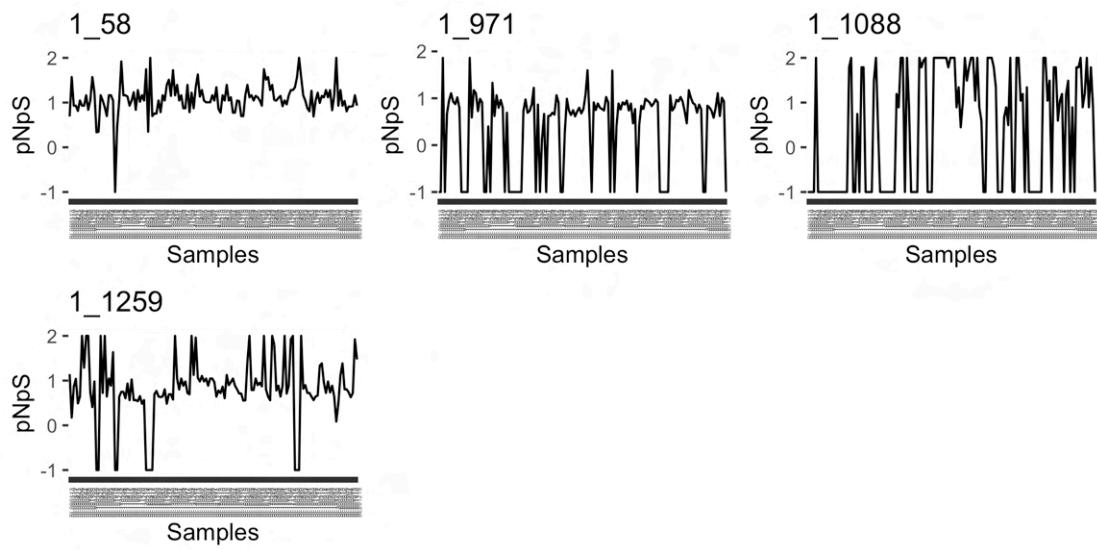
Supplementary Figure 61: The change of pNpS value of adaptive genes from MAG “s111.ctg000126c\_BL\_0902sc” over time in BBMO. Along the x-axis is the sequence of sampling months from the 1st to the 140th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



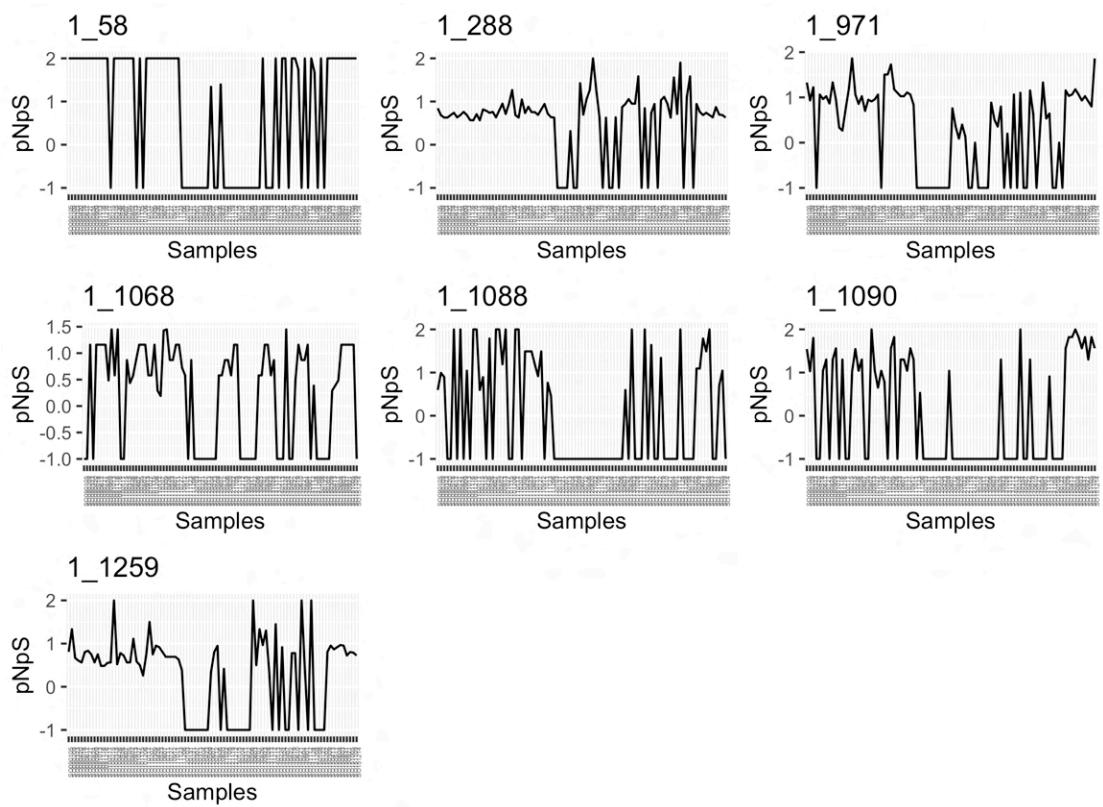
Supplementary Figure 62: The change of pNpS value of adaptive genes from MAG “s111.ctg000126c\_BL\_0902sc” over time in SOLA. Along the x-axis is the sequence of sampling months from the 1st to the 90th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



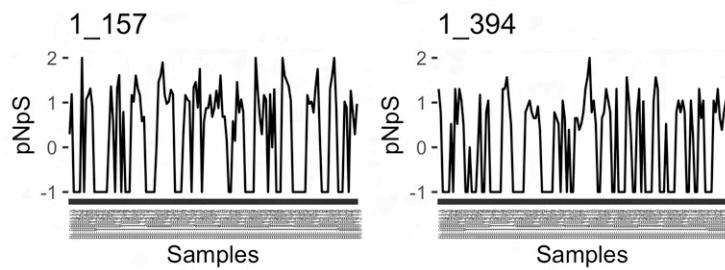
Supplementary Figure 63: The change of pNpS value of adaptive genes from MAG “s131.ctg000151c\_BL\_0908sc” over time in BBMO. Along the x-axis is the sequence of sampling months from the 1st to the 140th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



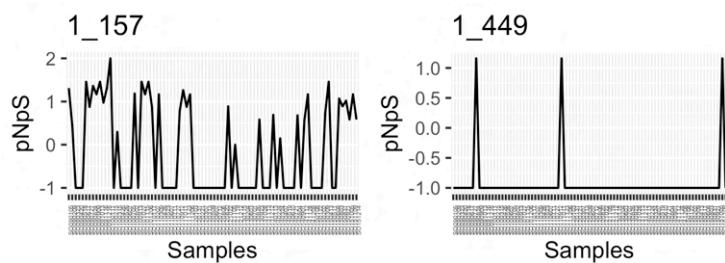
Supplementary Figure 64: The change of pNpS value of adaptive genes from MAG “s215.ctg0002401\_BL\_0908sc” over time in BBMO. Along the x-axis is the sequence of sampling months from the 1st to the 140th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



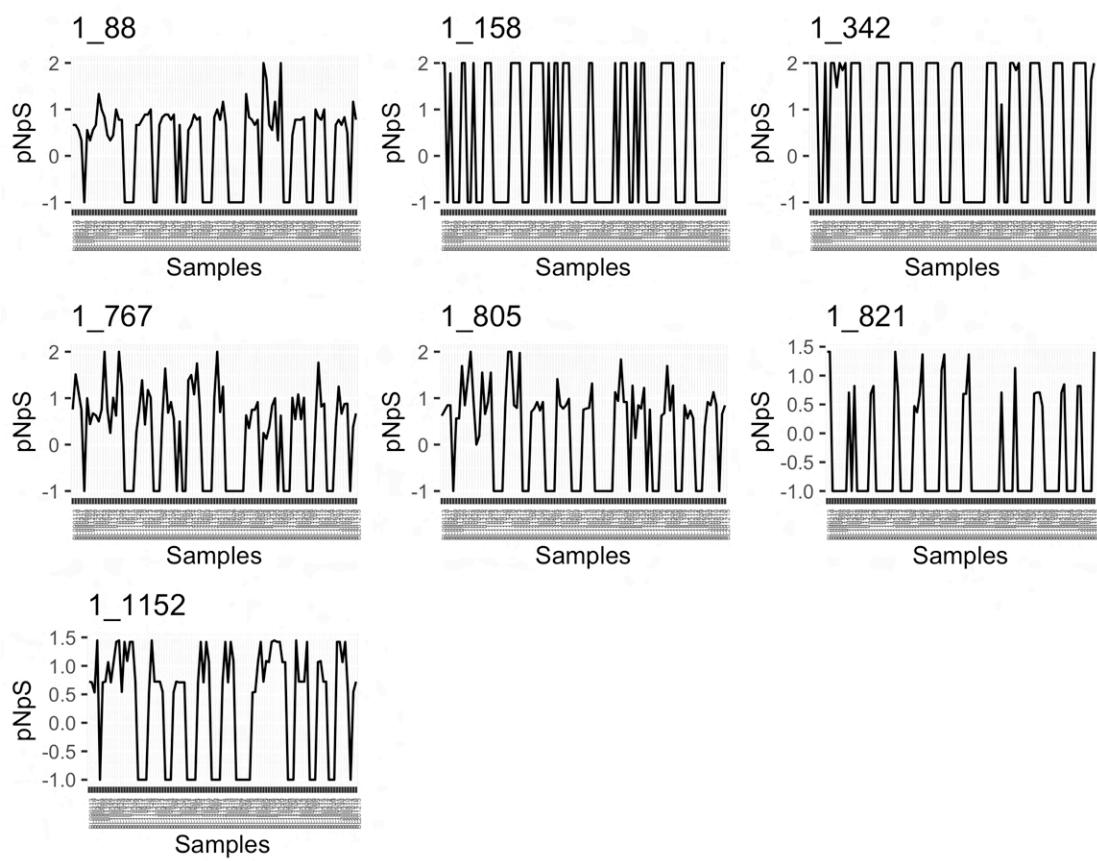
Supplementary Figure 65: The change of pNpS value of adaptive genes from MAG "s215.ctg0002401\_BL\_0908sc" over time in SOLA. Along the x-axis is the sequence of sampling months from the 1st to the 90th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



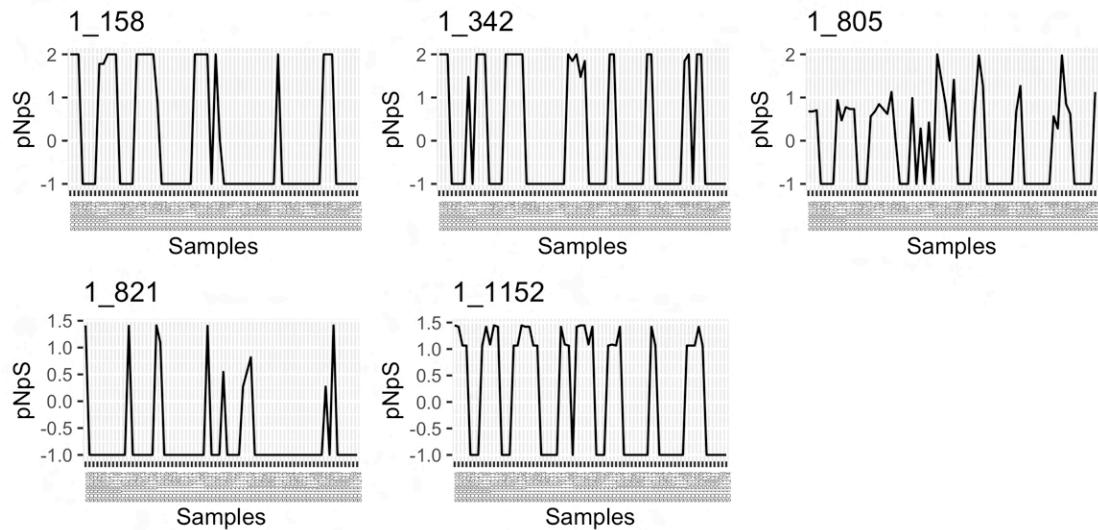
Supplementary Figure 66: The change of pNpS value of adaptive genes from MAG “s2266.ctg0024611\_BL\_0908sc” over time in BBMO. Along the x-axis is the sequence of sampling months from the 1st to the 140th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



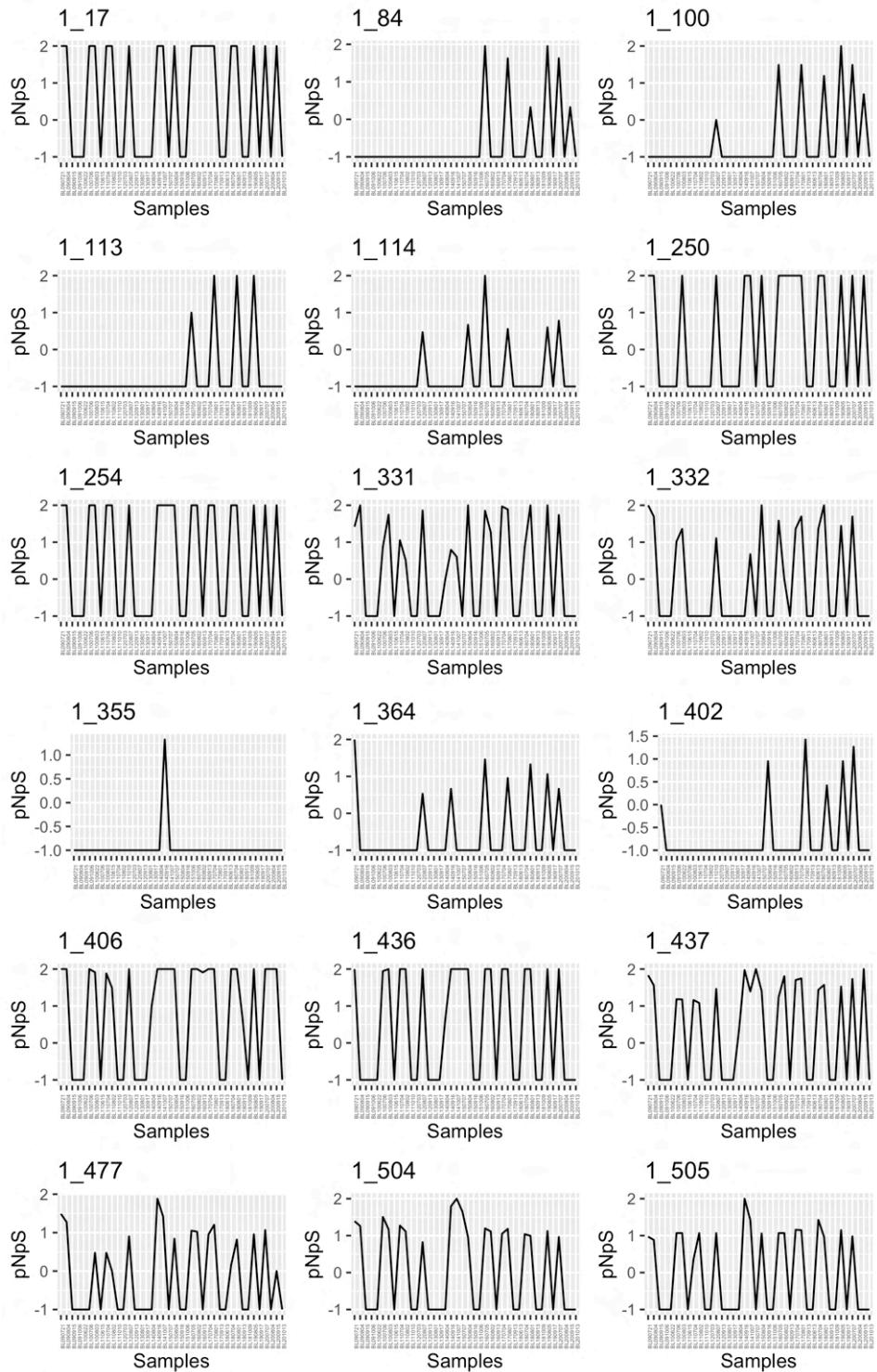
Supplementary Figure 67: The change of pNpS value of adaptive genes from MAG “s2266.ctg0024611\_BL\_0908sc” over time in SOLA. Along the x-axis is the sequence of sampling months from the 1st to the 90th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



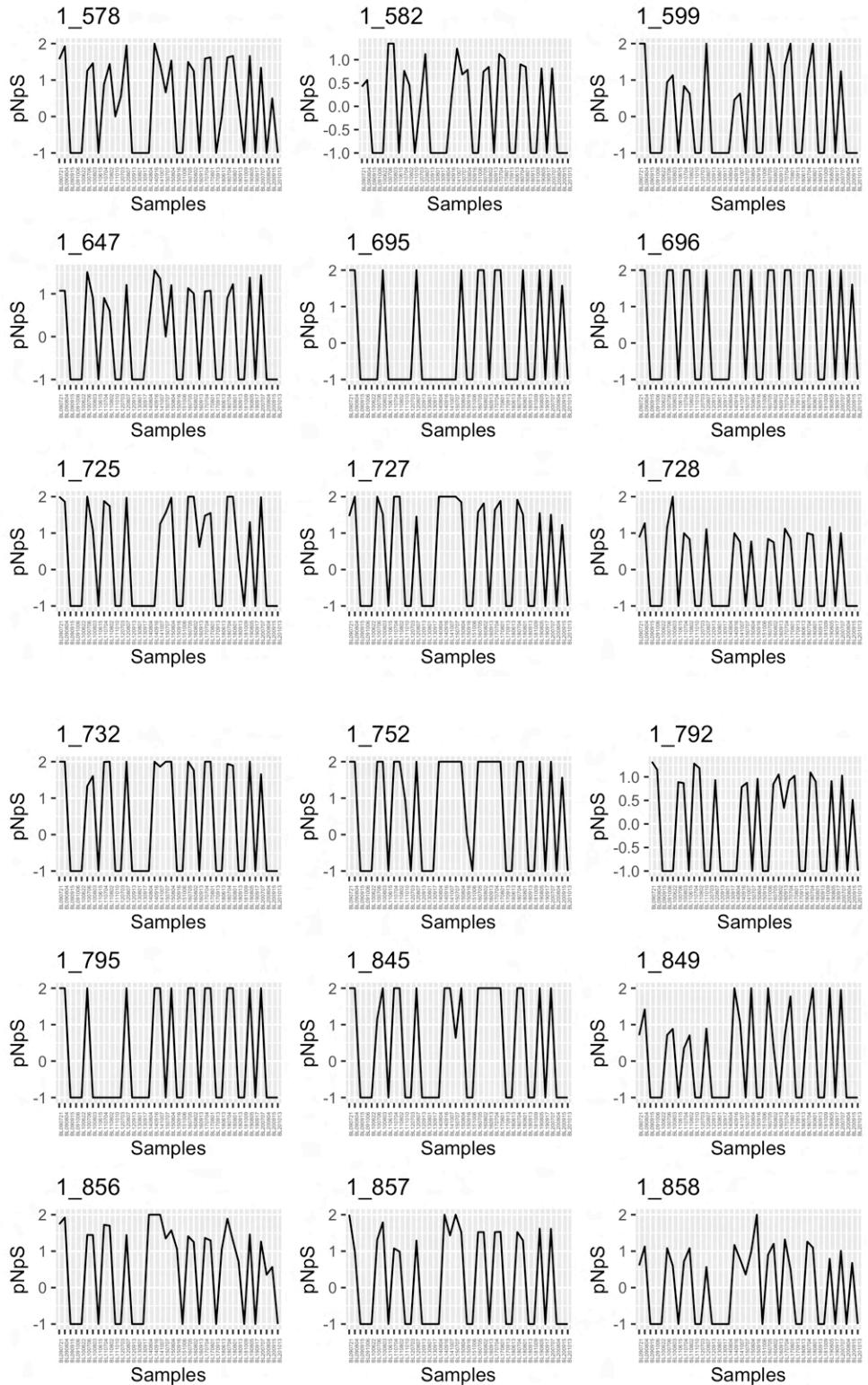
Supplementary Figure 68: The change of pNpS value of adaptive genes from MAG “s23.ctg000345l\_BL\_0902sc” over time in BBMO. Along the x-axis is the sequence of sampling months from the 1st to the 140th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



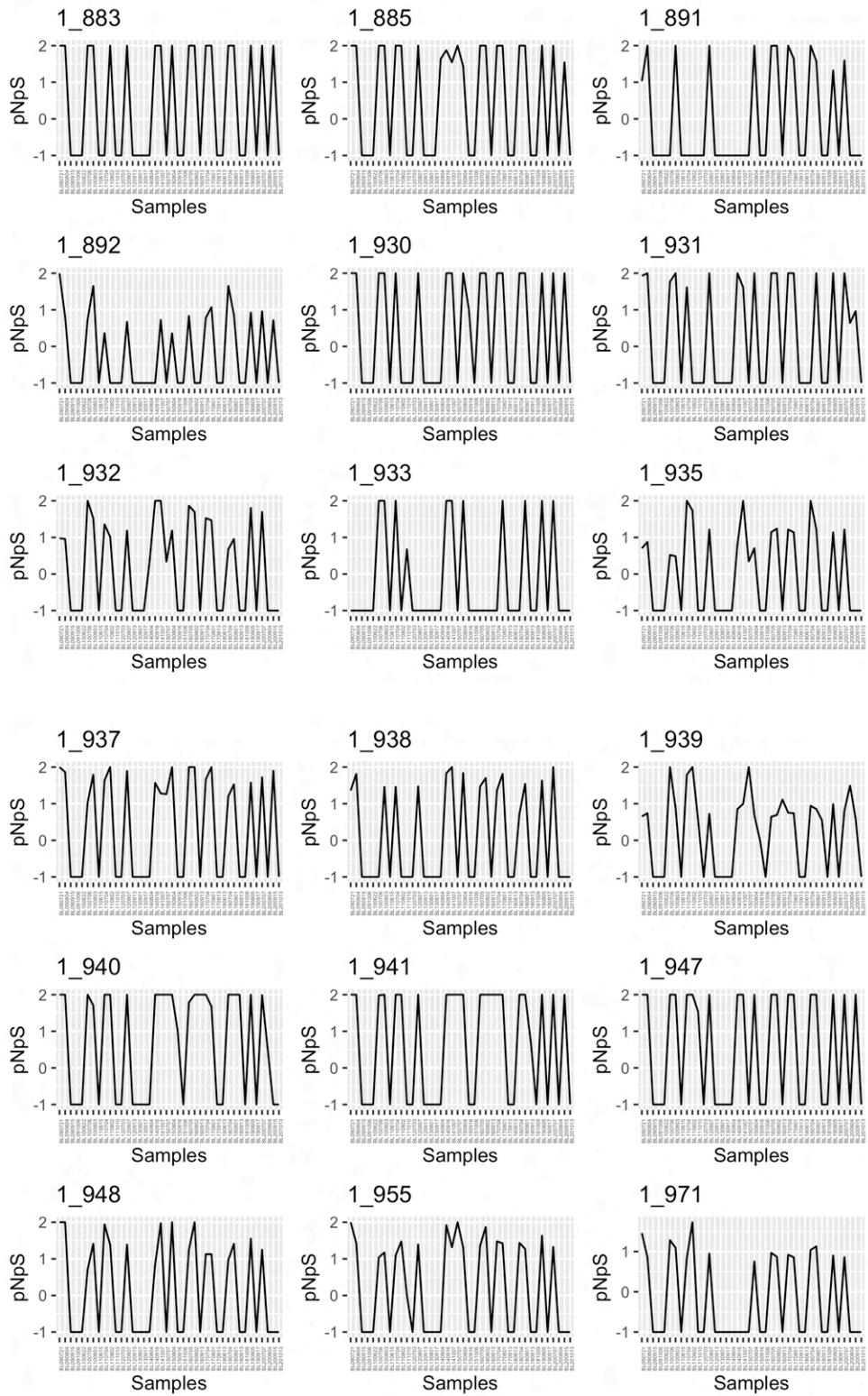
Supplementary Figure 69: The change of pNpS value of adaptive genes from MAG “s23.ctg0003451\_BL\_0902sc” over time in SOLA. Along the x-axis is the sequence of sampling months from the 1st to the 90th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



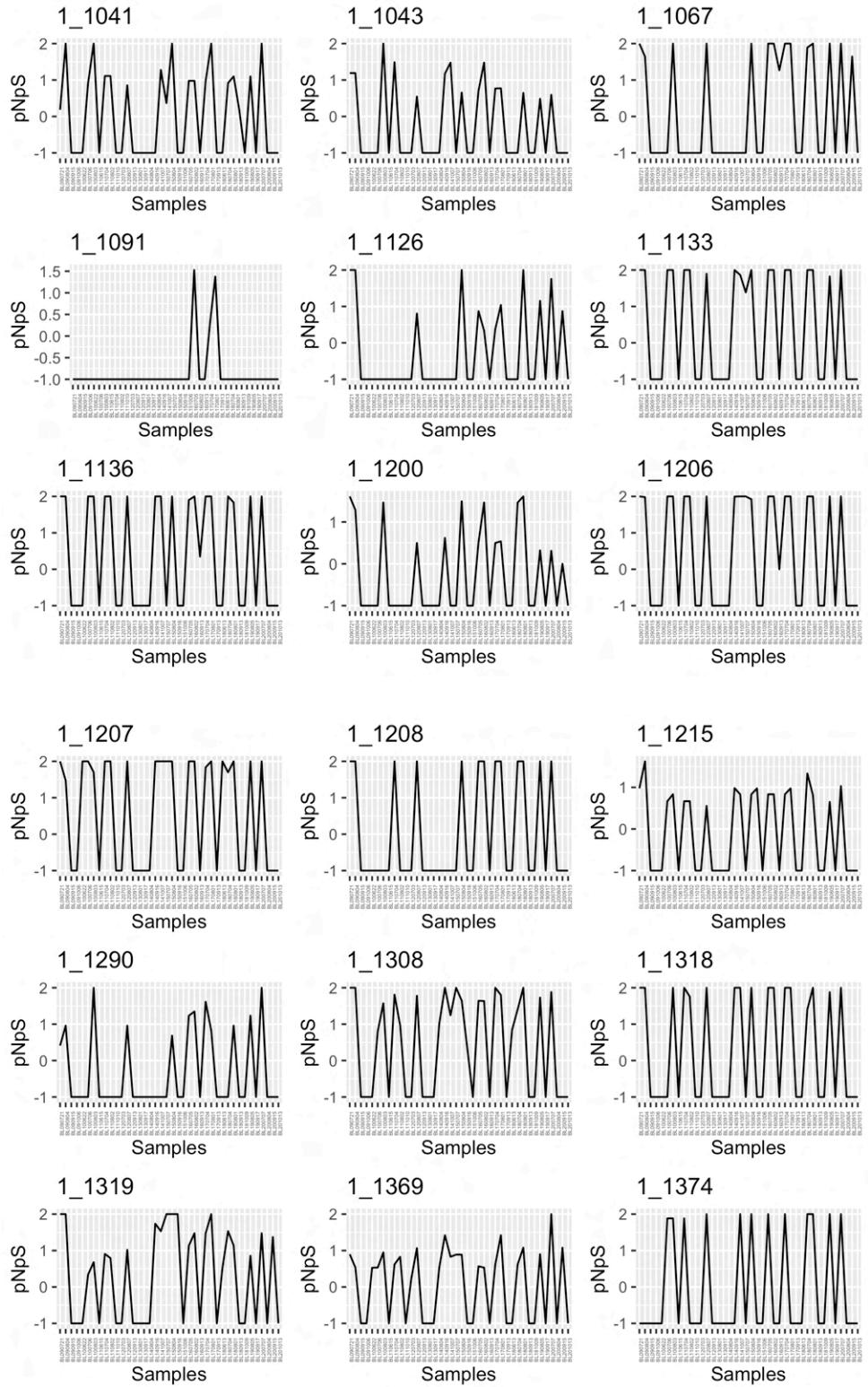
Supplementary Figure 70.1: The change of pNpS value of adaptive genes from MAG “s249.ctg000277l\_BL\_0908sc” over time in BBMO. Along the x-axis is the sequence of sampling months from the 1st to the 140th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



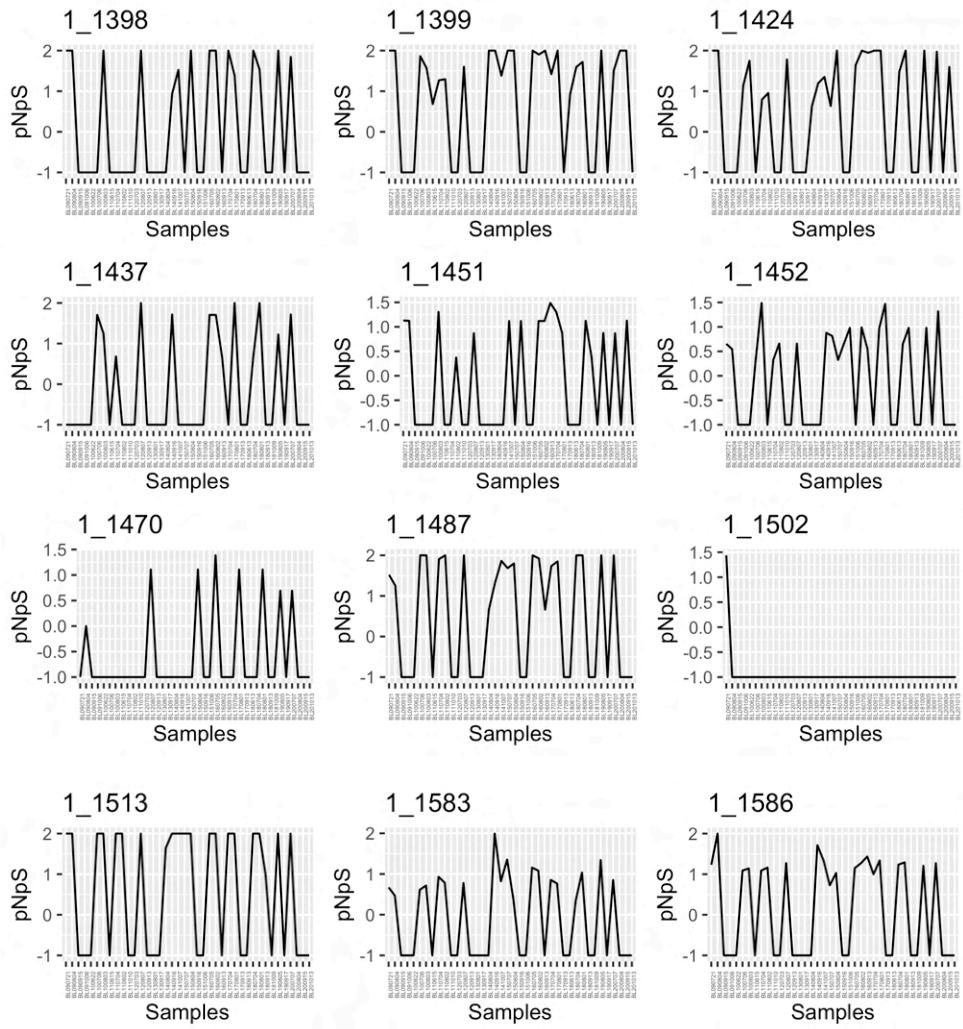
Supplementary Figure 70.2: The change of pNpS value of adaptive genes from MAG “s249.ctg000277l\_BL\_0908sc” over time in BBMO. Along the x-axis is the sequence of sampling months from the 1st to the 140th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



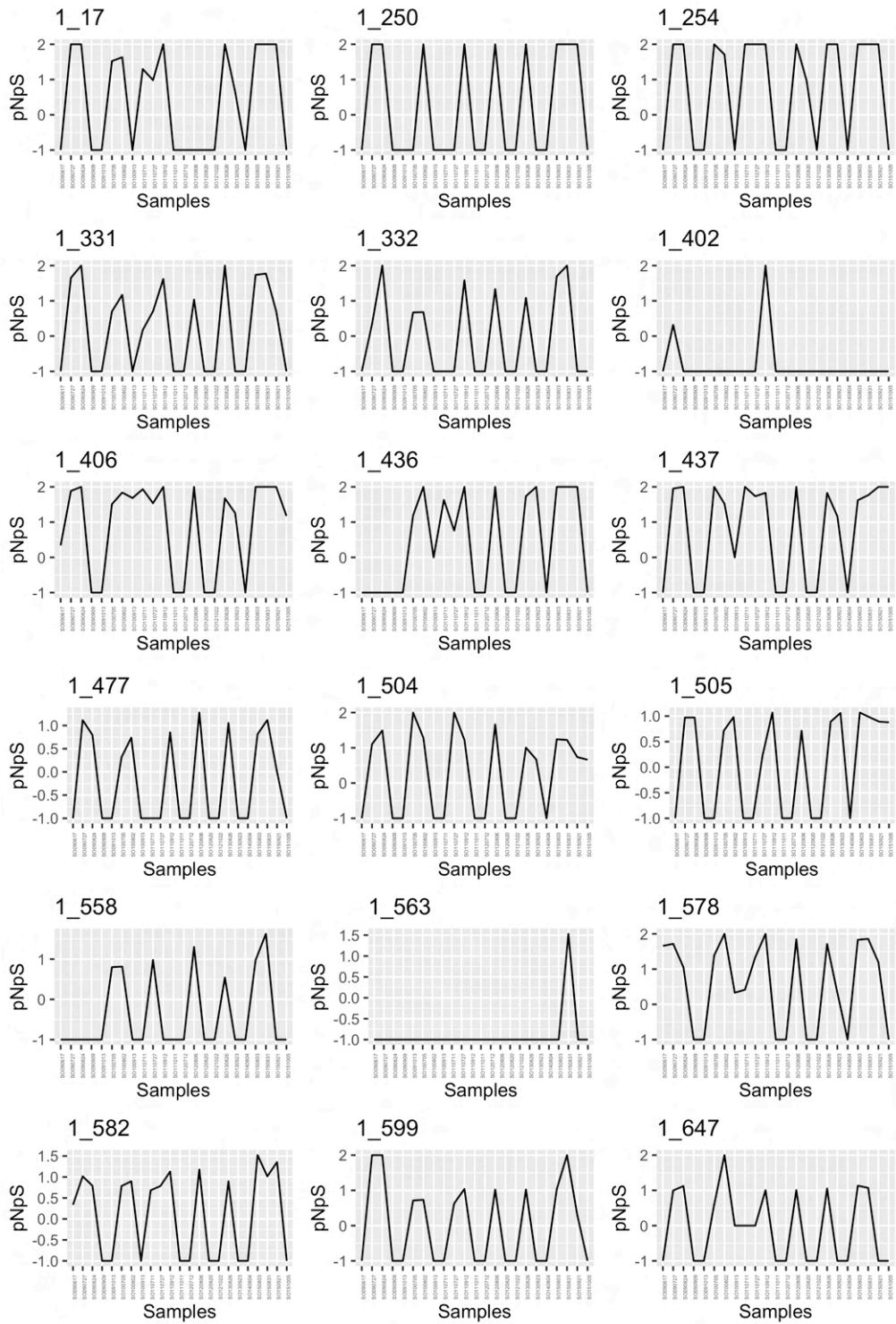
Supplementary Figure 70.3: The change of pNpS value of adaptive genes from MAG “s249.ctg000277l\_BL\_0908sc” over time in BBMO. Along the x-axis is the sequence of sampling months from the 1st to the 140th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



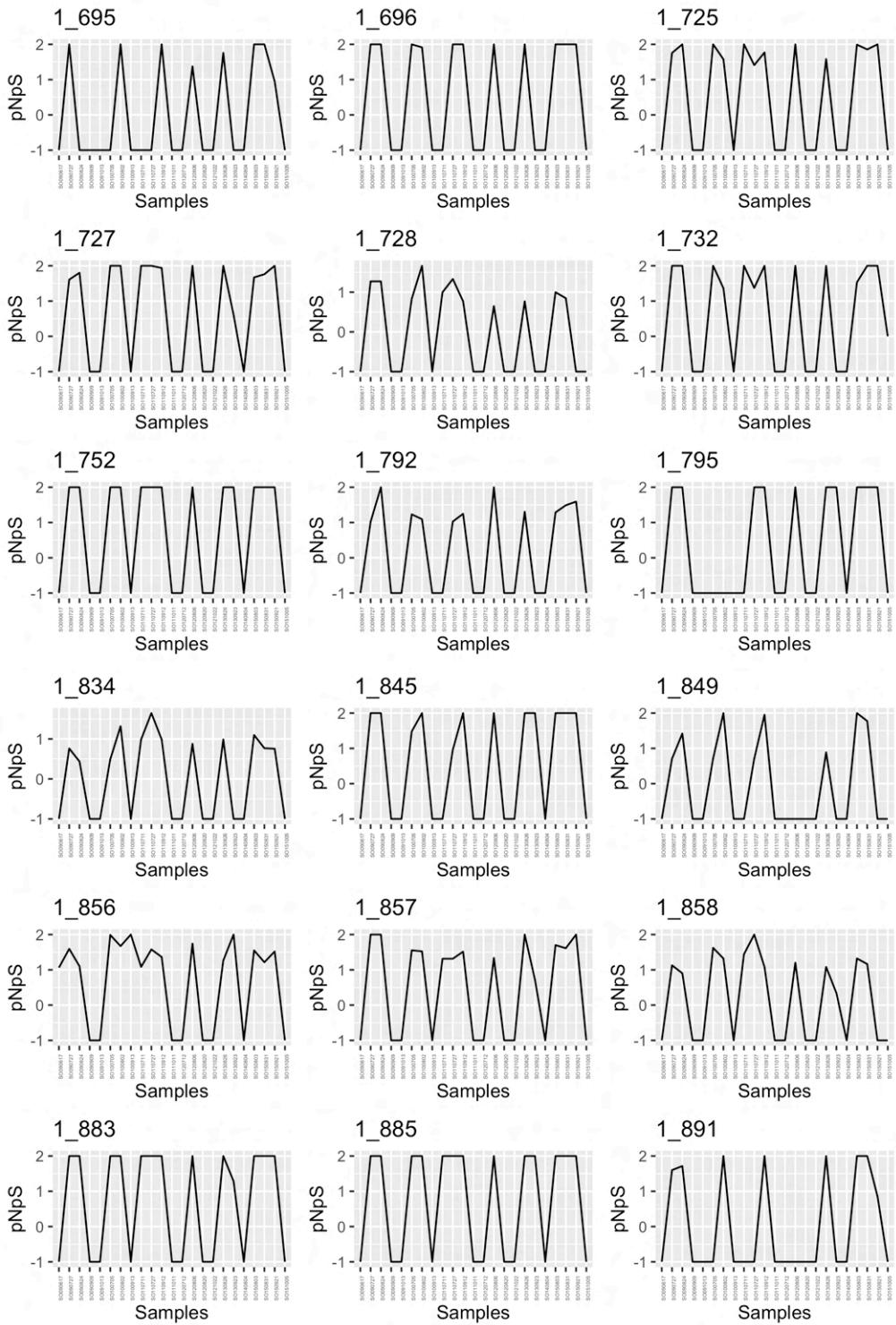
Supplementary Figure 70.4: The change of pNpS value of adaptive genes from MAG “s249.ctg000277l\_BL\_0908sc” over time in BBMO. Along the x-axis is the sequence of sampling months from the 1st to the 140th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



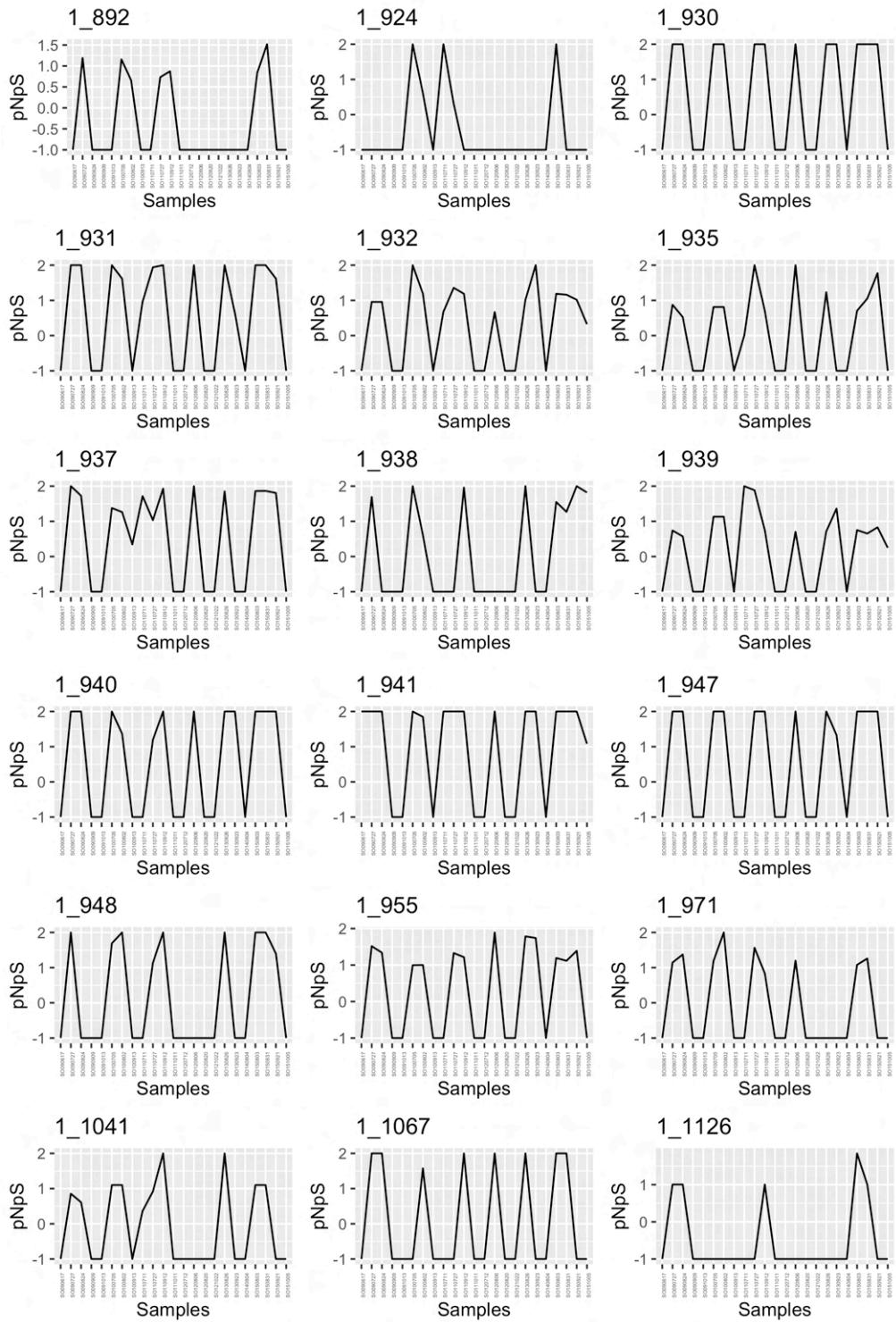
Supplementary Figure 70.5: The change of pNpS value of adaptive genes from MAG “s249.ctg000277l\_BL\_0908sc” over time in BBMO. Along the x-axis is the sequence of sampling months from the 1st to the 140th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



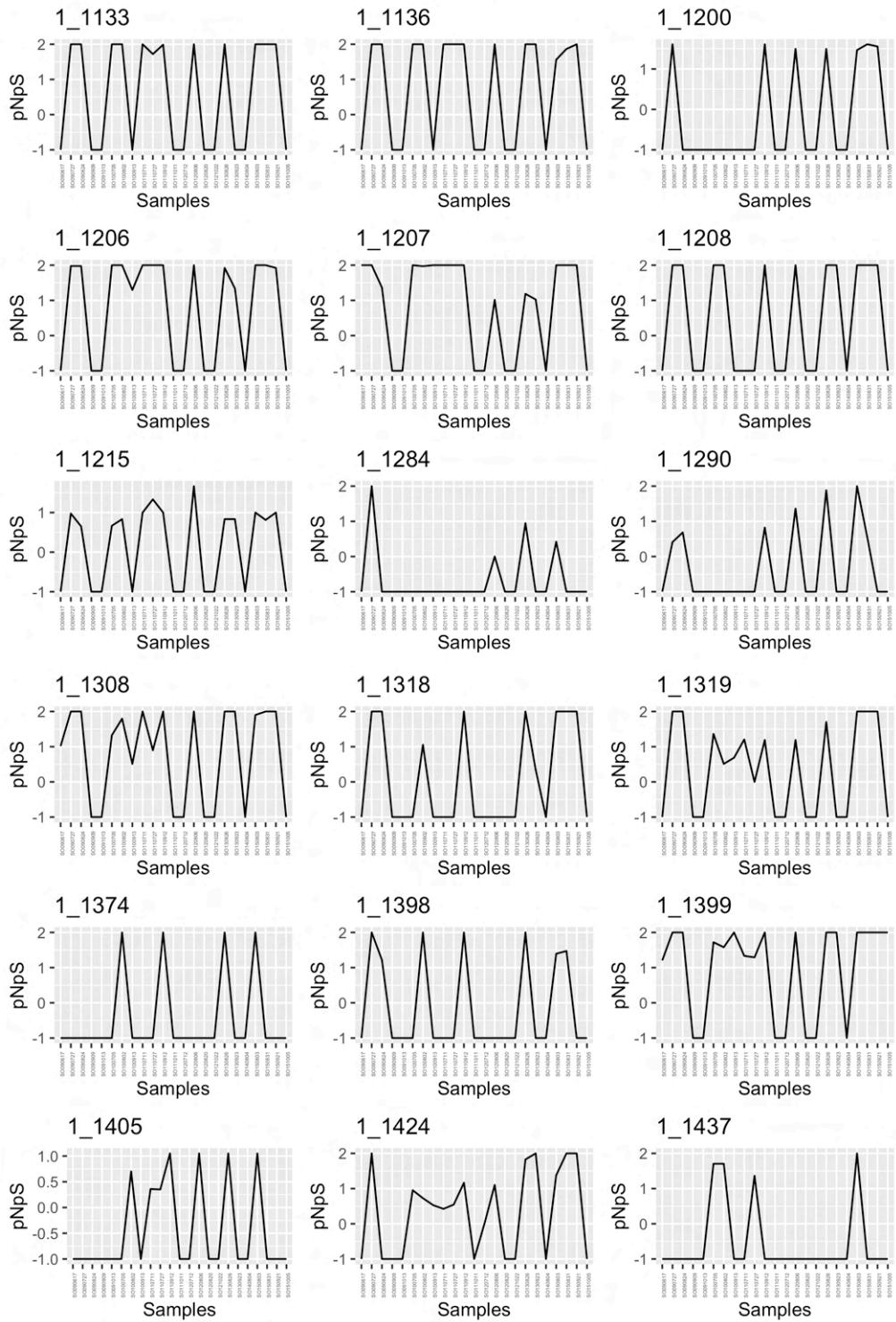
Supplementary Figure 71.1: The change of pNpS value of adaptive genes from MAG “s249.ctg000277l\_BL\_0908sc” over time in SOLA. Along the x-axis is the sequence of sampling months from the 1st to the 90th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



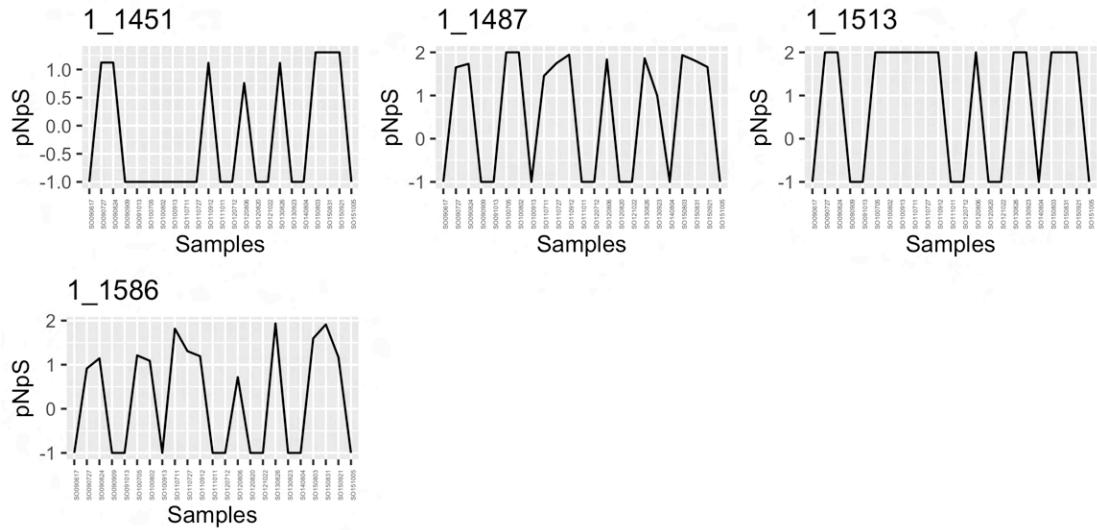
Supplementary Figure 71.2: The change of pNpS value of adaptive genes from MAG “s249.ctg000277l\_BL\_0908sc” over time in SOLA. Along the x-axis is the sequence of sampling months from the 1st to the 90th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



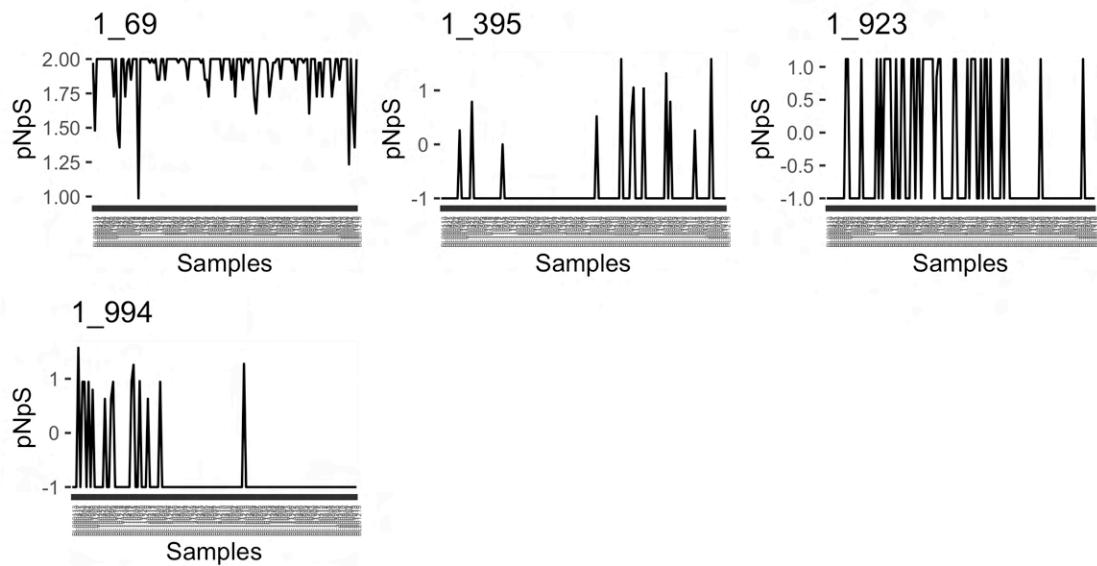
Supplementary Figure 71.3: The change of pNpS value of adaptive genes from MAG “s249.ctg000277l\_BL\_0908sc” over time in SOLA. Along the x-axis is the sequence of sampling months from the 1st to the 90th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



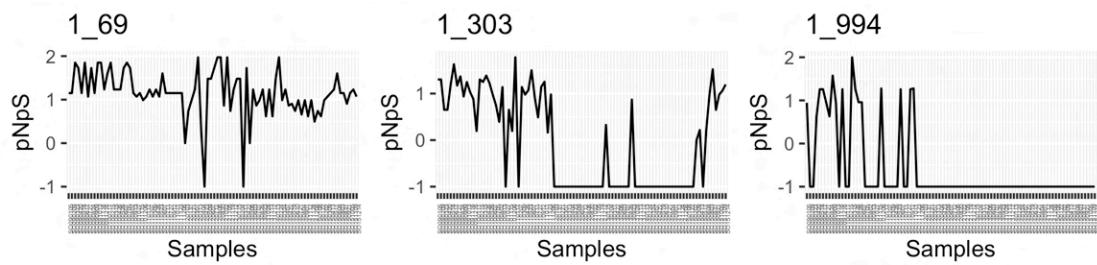
Supplementary Figure 71.4: The change of pNpS value of adaptive genes from MAG “s249.ctg000277l\_BL\_0908sc” over time in SOLA. Along the x-axis is the sequence of sampling months from the 1st to the 90th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



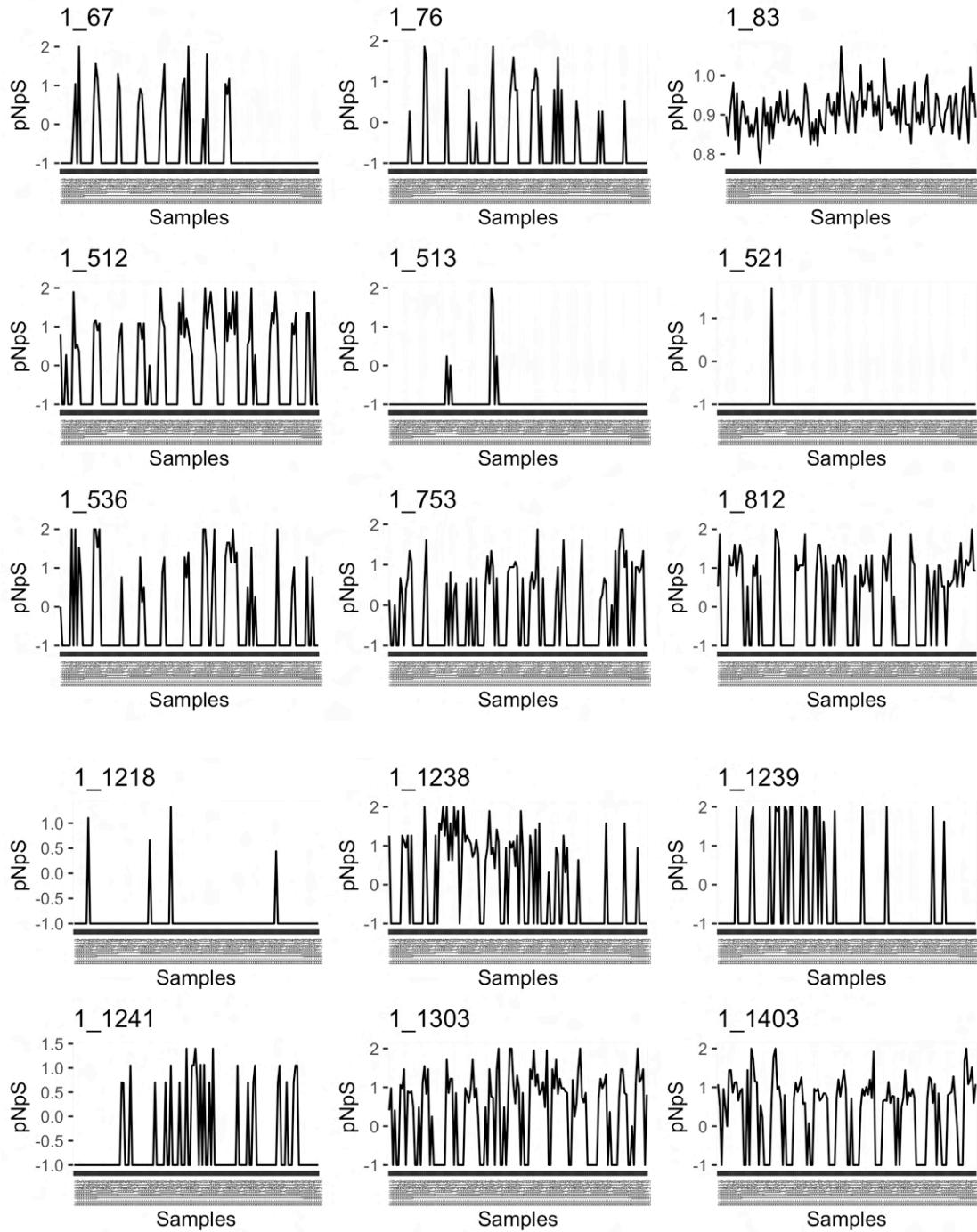
Supplementary Figure 71.5: The change of pNpS value of adaptive genes from MAG “s249.ctg0002771\_BL\_0908sc” over time in SOLA. Along the x-axis is the sequence of sampling months from the 1st to the 90th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



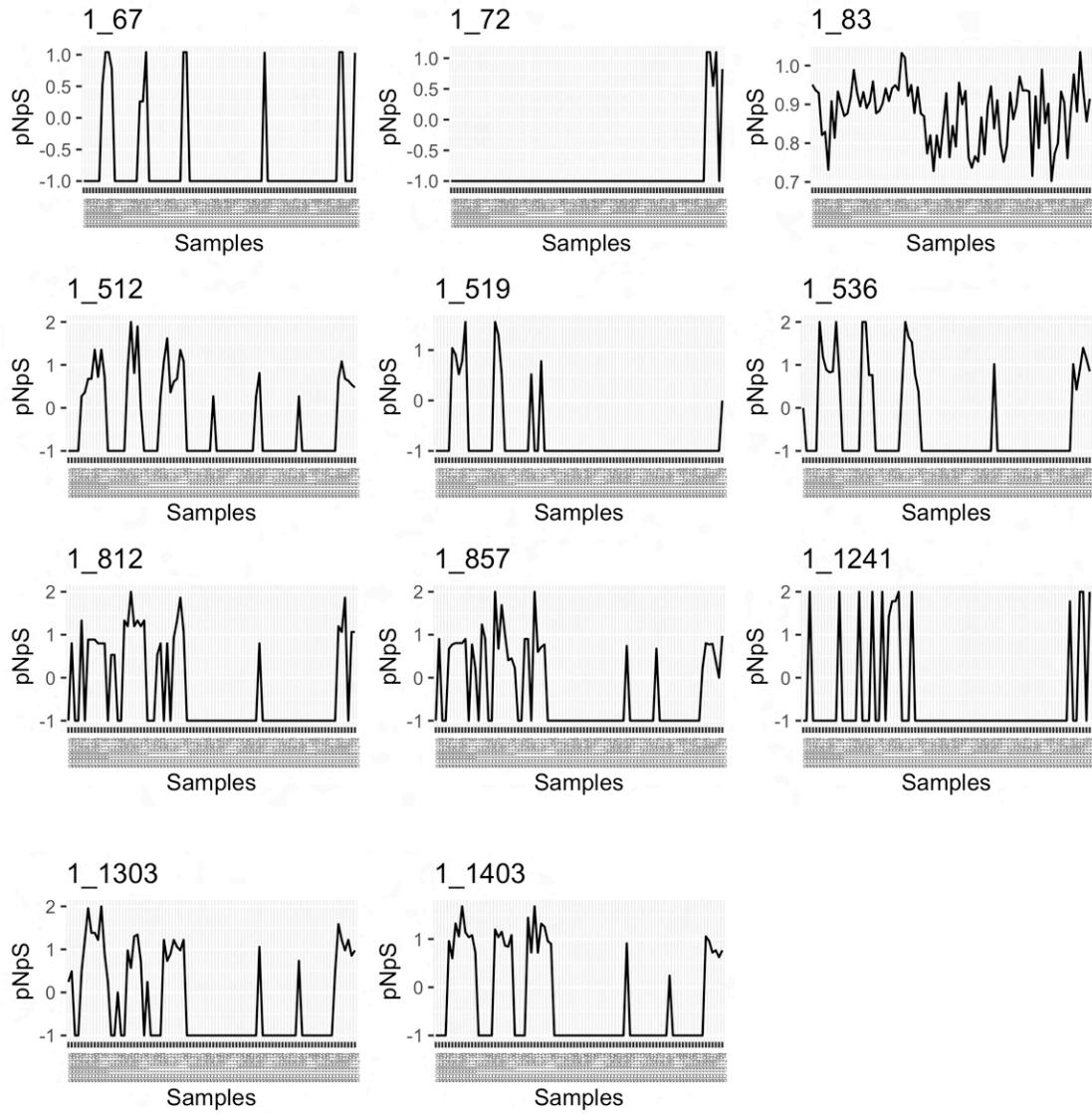
Supplementary Figure 72: The change of pNpS value of adaptive genes from MAG “s266.ctg0002971\_BL\_0908sc” over time in BBMO. Along the x-axis is the sequence of sampling months from the 1st to the 140th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



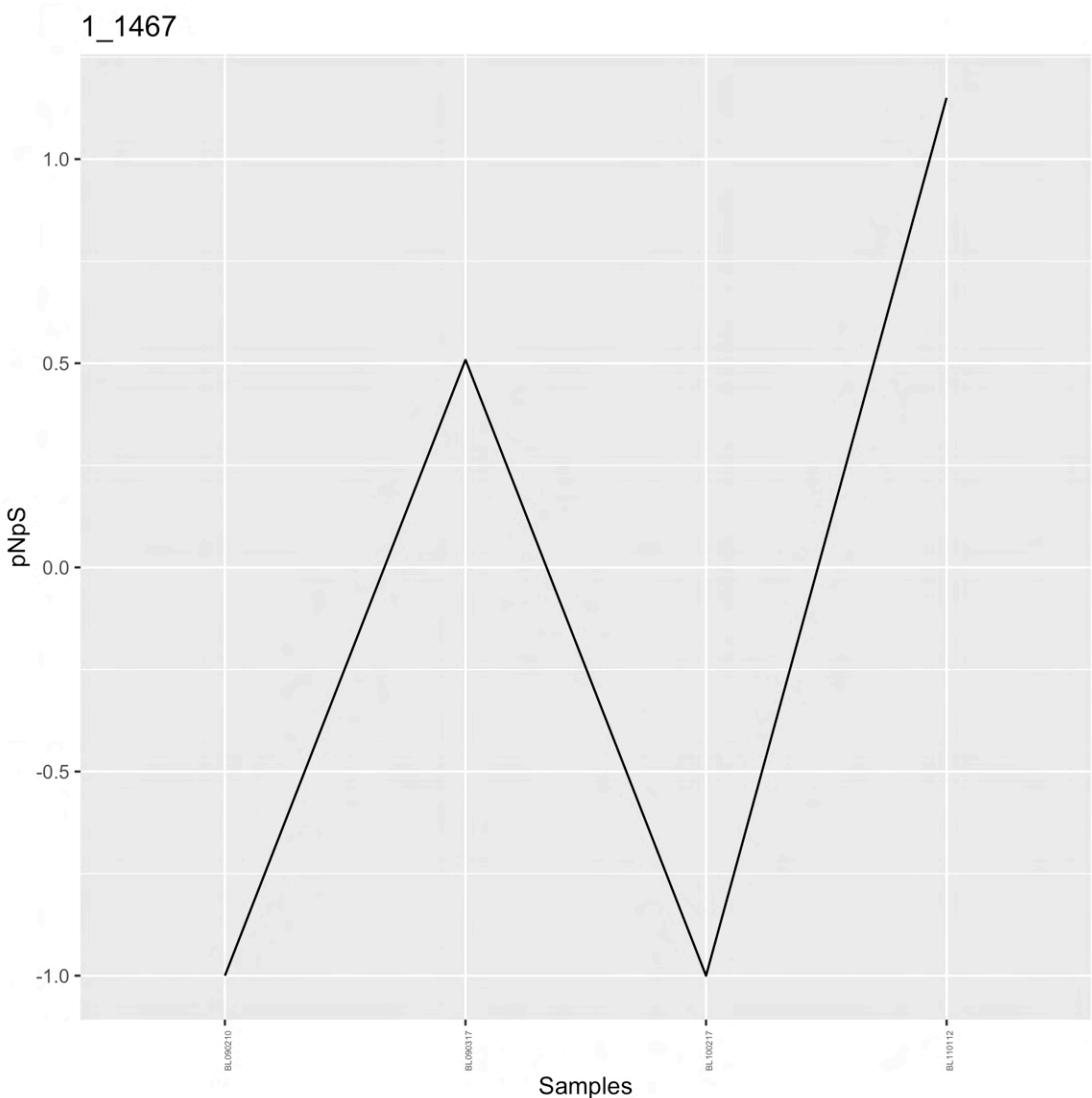
Supplementary Figure 73: The change of pNpS value of adaptive genes from MAG “s266.ctg0002971\_BL\_0908sc” over time in SOLA. Along the x-axis is the sequence of sampling months from the 1st to the 90th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



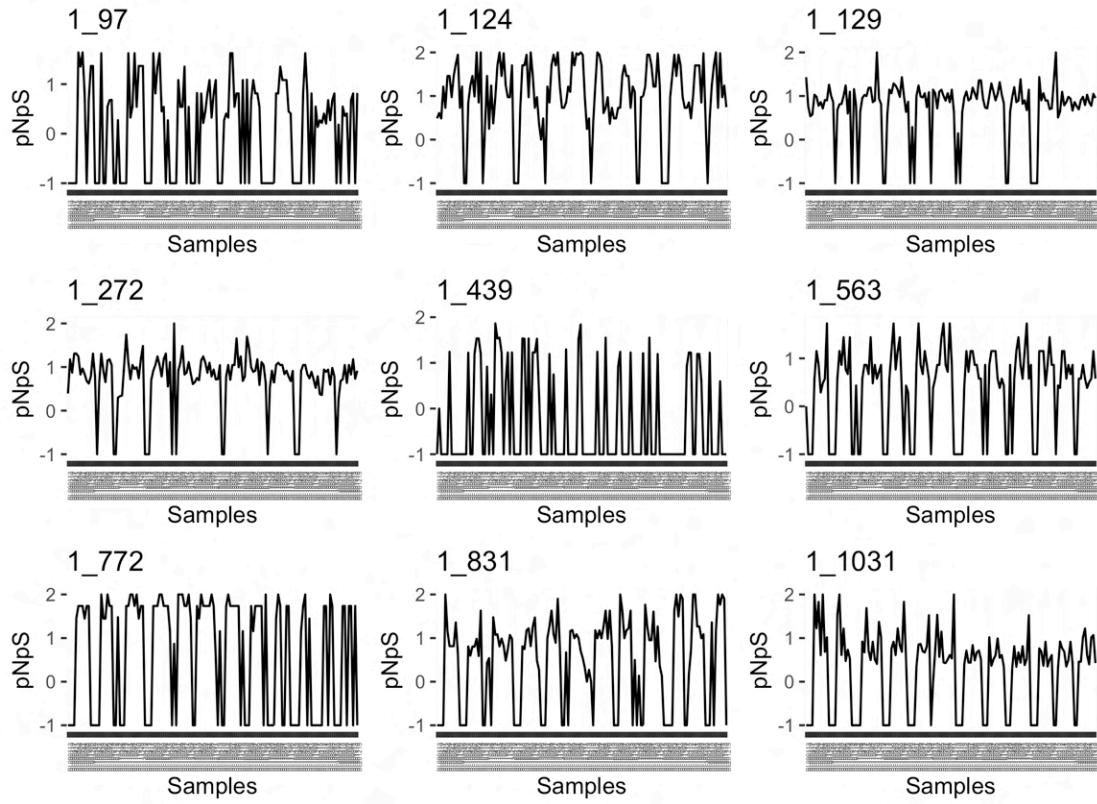
Supplementary Figure 74: The change of pNpS value of adaptive genes from MAG “s325.ctg000366c\_BL\_0908sc” over time in BBMO. Along the x-axis is the sequence of sampling months from the 1st to the 140th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



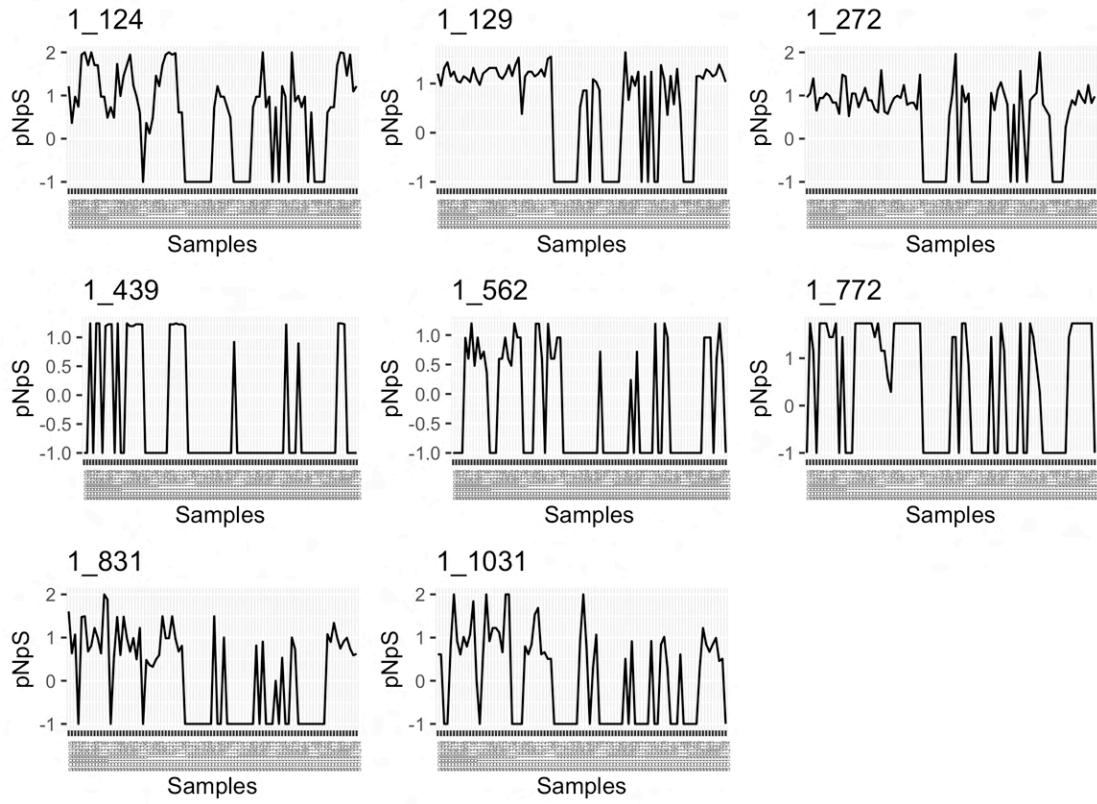
Supplementary Figure 75: The change of pNpS value of adaptive genes from MAG “s325.ctg000366c\_BL\_0908sc” over time in SOLA. Along the x-axis is the sequence of sampling months from the 1st to the 90th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



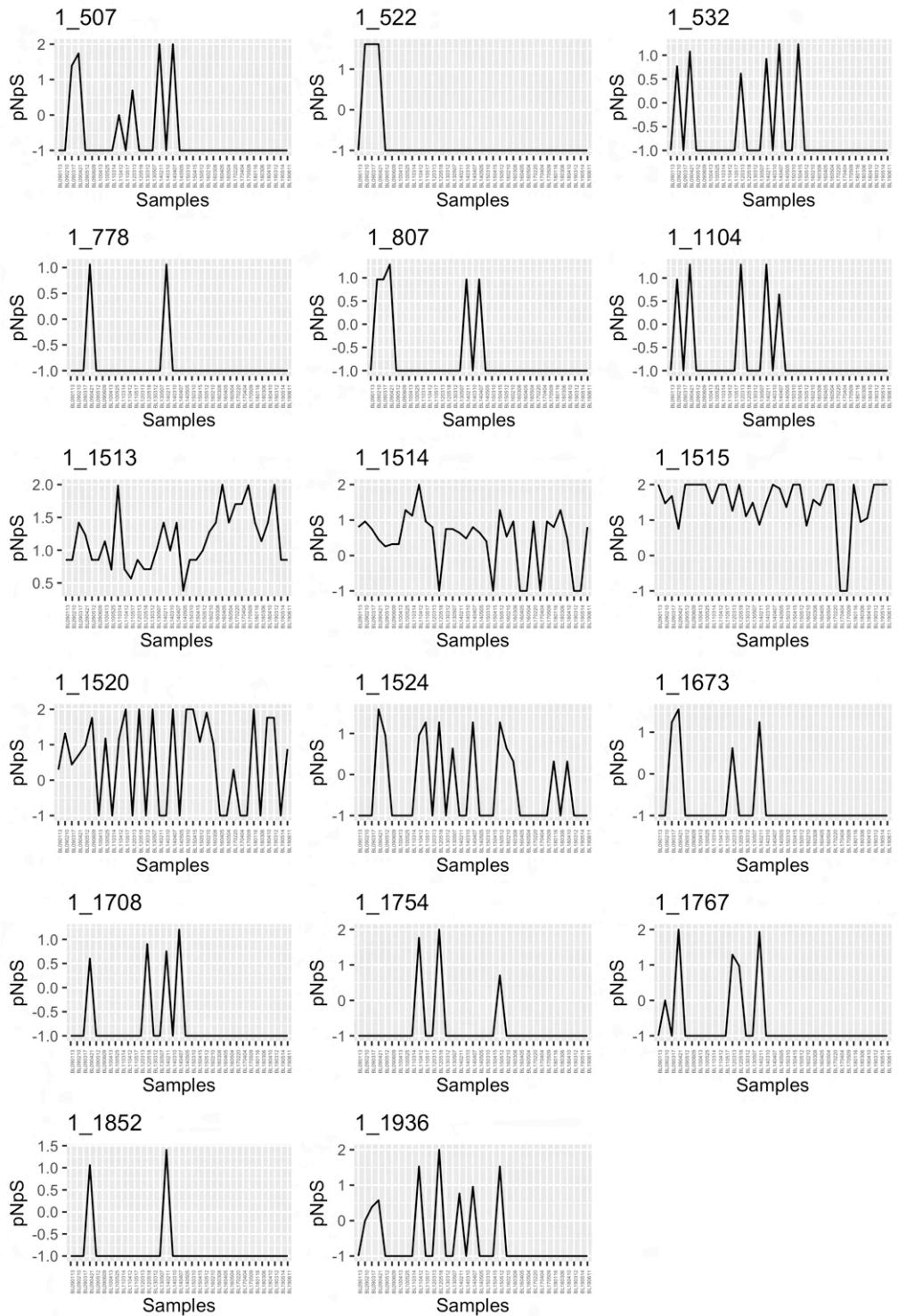
Supplementary Figure 76: The change of pNpS value of adaptive genes from MAG “s35.ctg000041c\_BL\_0902sc” over time in BBMO. Along the x-axis is the sequence of sampling months from the 1st to the 140th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



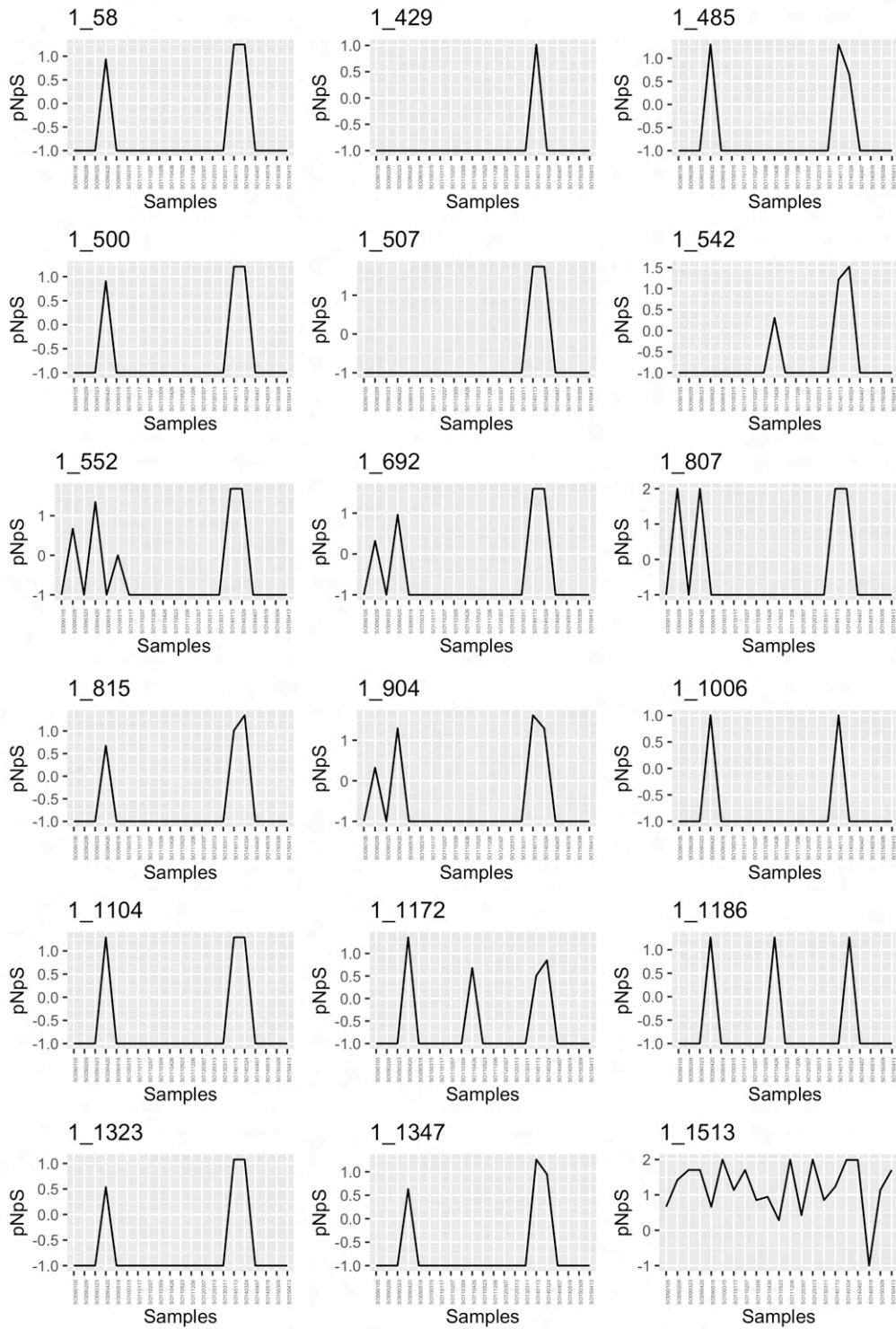
Supplementary Figure 77: The change of pNpS value of adaptive genes from MAG “s388.ctg0004351\_BL\_0908sc” over time in BBMO. Along the x-axis is the sequence of sampling months from the 1st to the 140th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



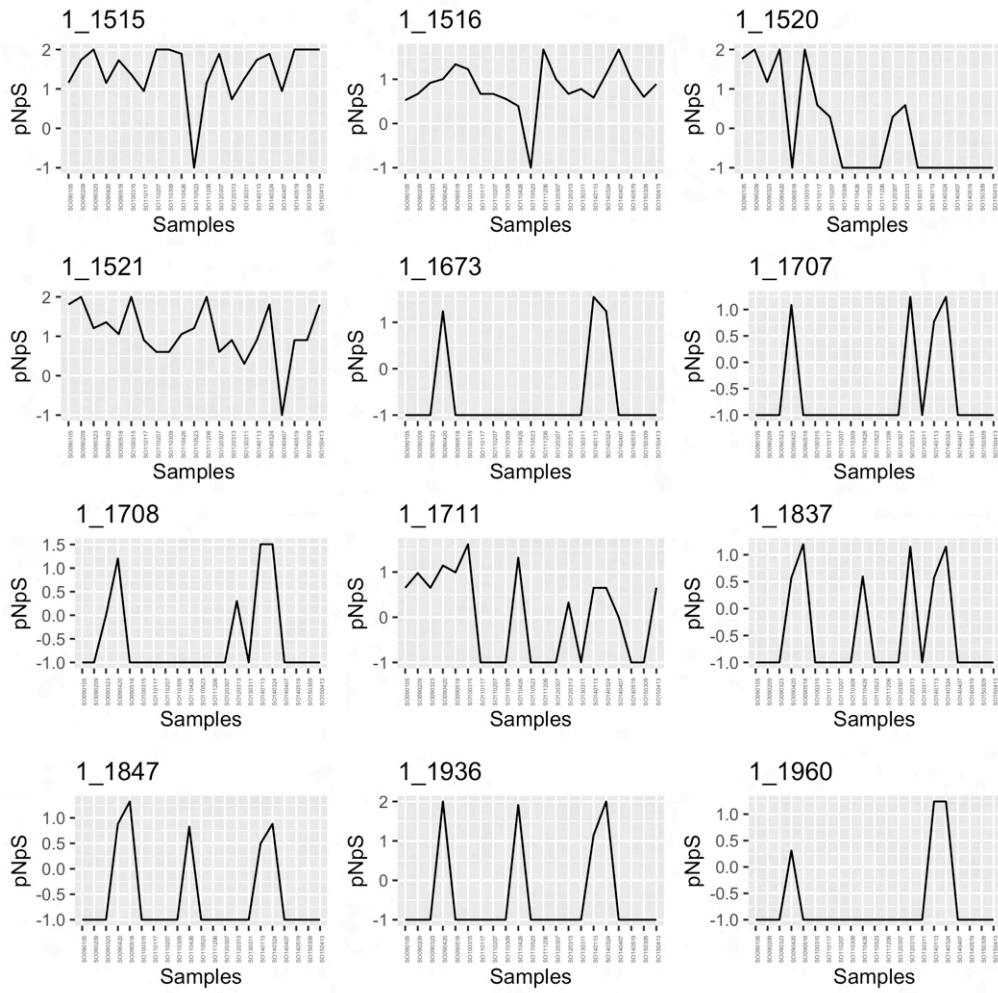
Supplementary Figure 78: The change of pNpS value of adaptive genes from MAG “s388.ctg0004351\_BL\_0908sc” over time in SOLA. Along the x-axis is the sequence of sampling months from the 1st to the 90th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



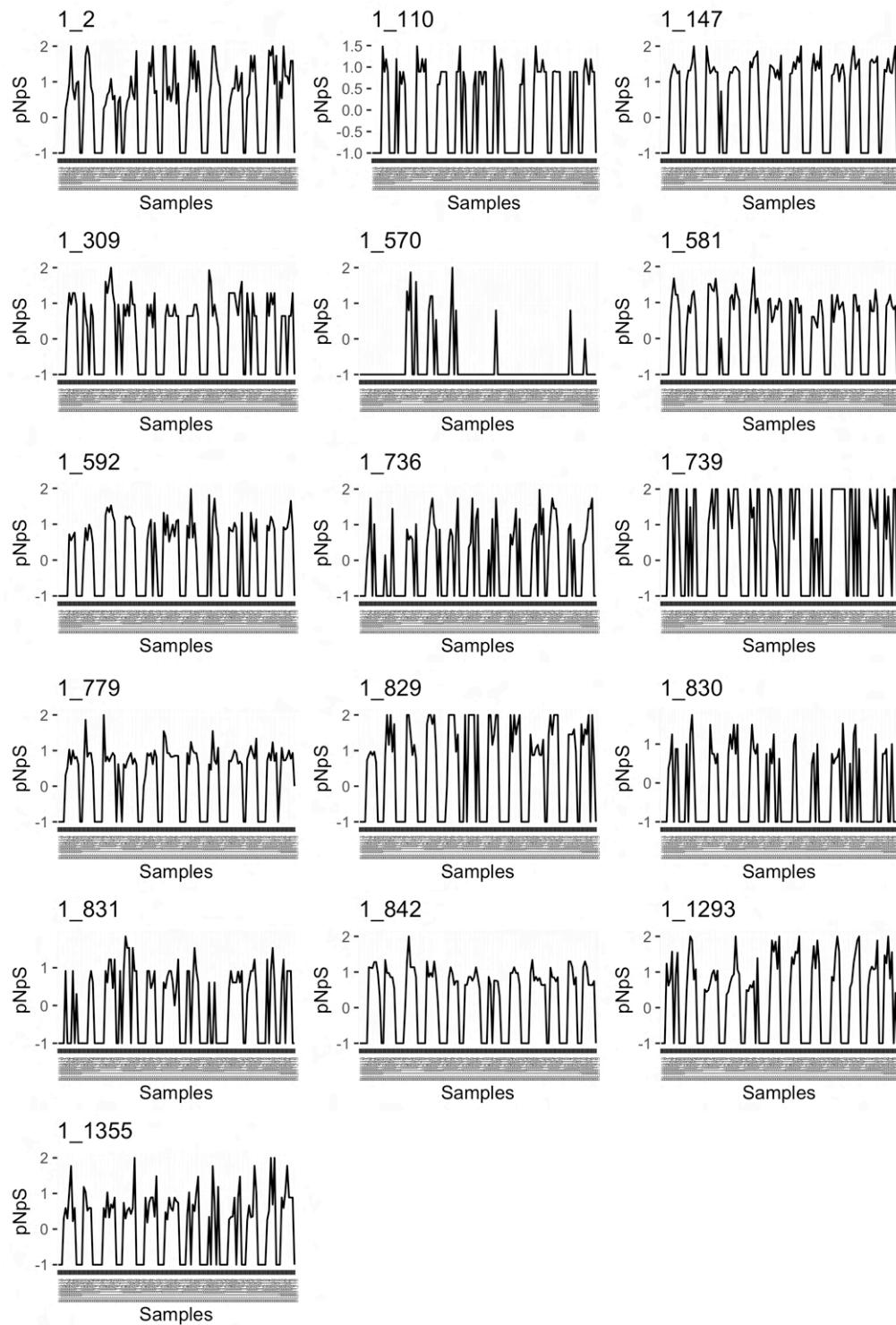
Supplementary Figure 79: The change of pNpS value of adaptive genes from MAG “s44.ctg000052l\_BL\_0902sc” over time in BBMO. Along the x-axis is the sequence of sampling months from the 1st to the 140th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



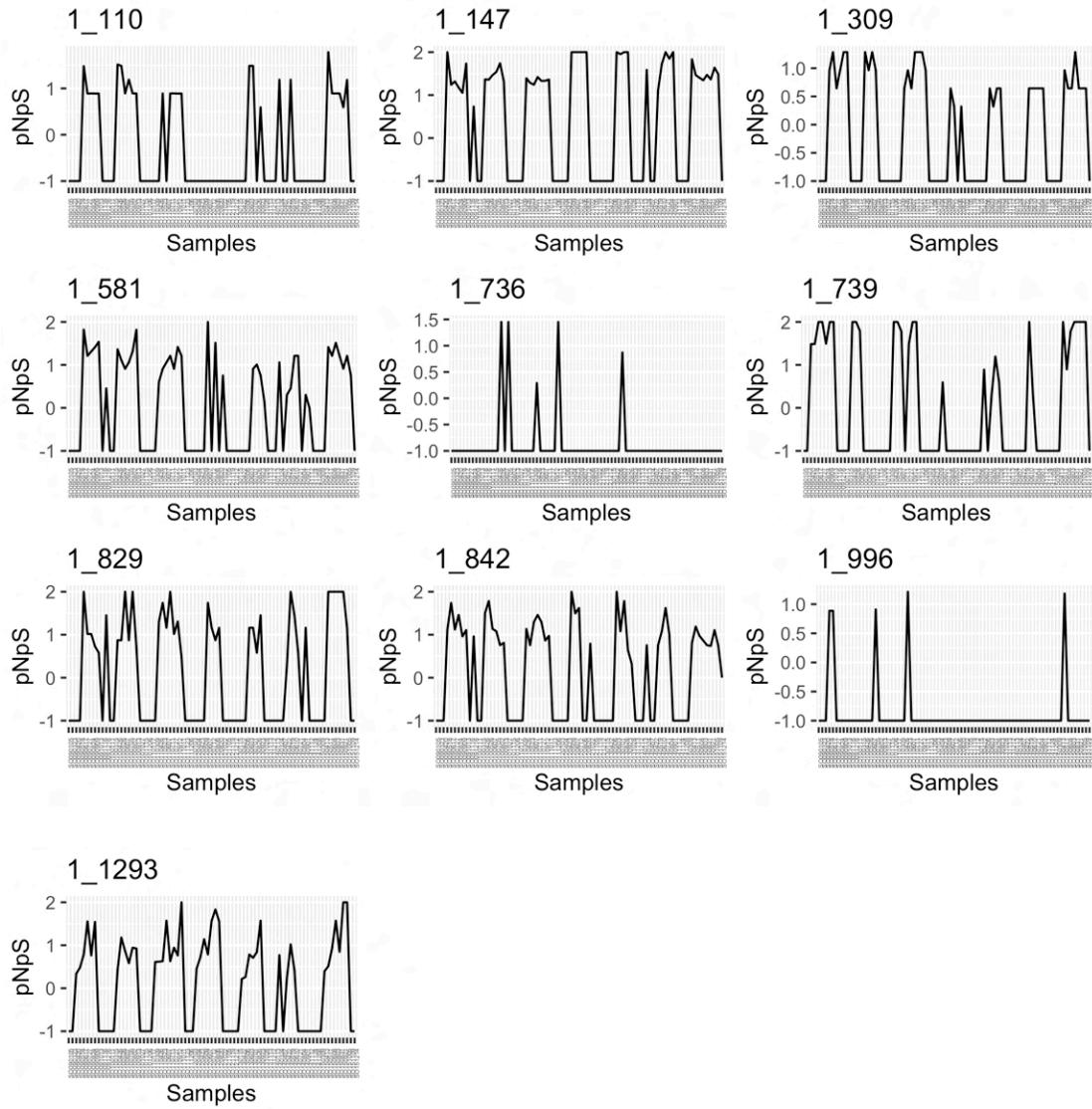
Supplementary Figure 80.1: The change of pNpS value of adaptive genes from MAG "s44.ctg000052l\_BL\_0902sc" over time in SOLA. Along the x-axis is the sequence of sampling months from the 1st to the 90th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



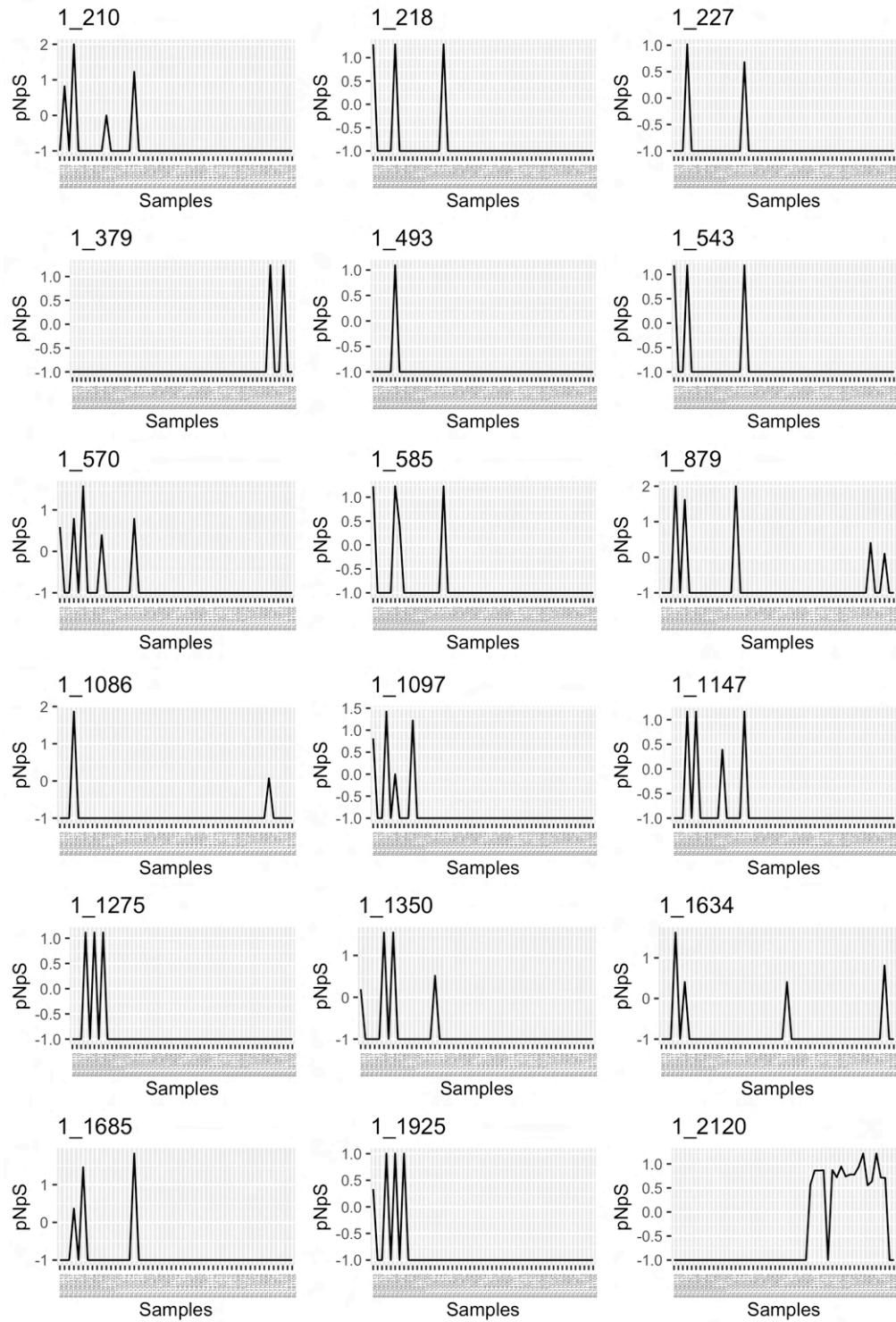
Supplementary Figure 80.2: The change of pNpS value of adaptive genes from MAG “s44.ctg000052l\_BL\_0902sc” over time in SOLA. Along the x-axis is the sequence of sampling months from the 1st to the 90th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



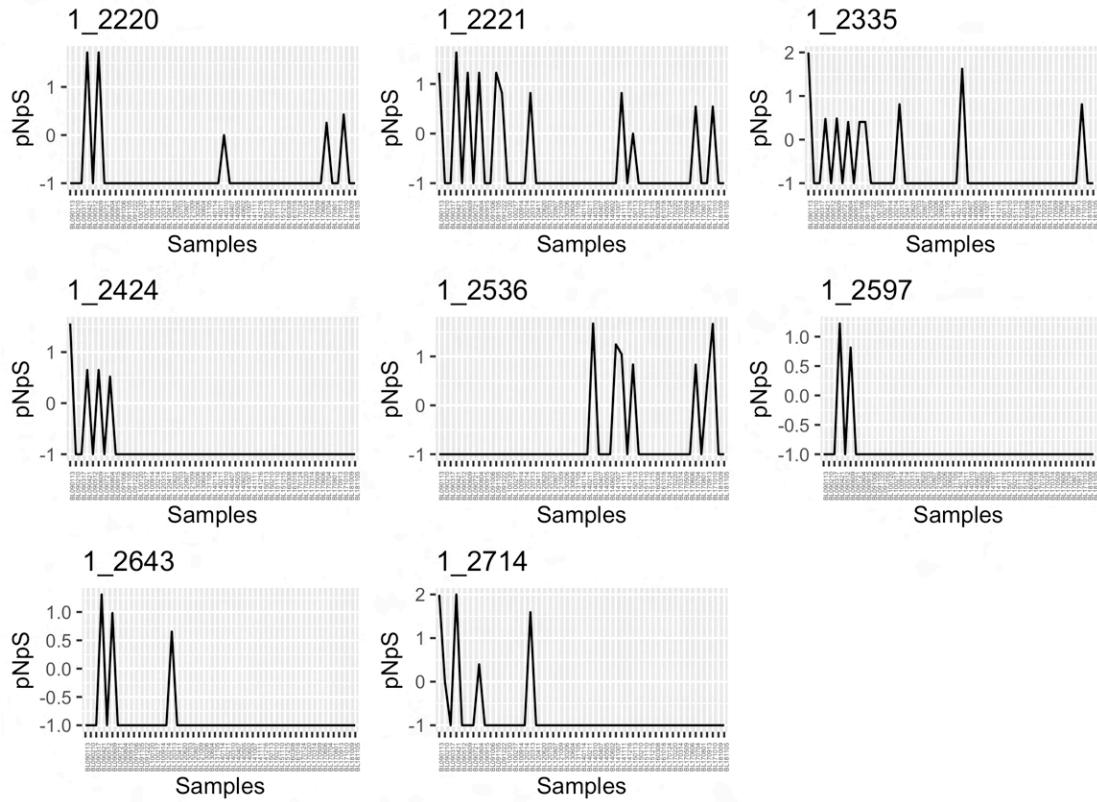
Supplementary Figure 81: The change of pNpS value of adaptive genes from MAG “s7.ctg000447l\_BL\_0908sc” over time in BBMO. Along the x-axis is the sequence of sampling months from the 1st to the 140th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



Supplementary Figure 82: The change of pNpS value of adaptive genes from MAG “s7.ctg000447l\_BL\_0908sc” over time in SOLA. Along the x-axis is the sequence of sampling months from the 1st to the 90th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



Supplementary Figure 83: The change of pNpS value of adaptive genes from MAG “s96.ctg000111c\_BL\_0908sc” over time in BBMO. Along the x-axis is the sequence of sampling months from the 1st to the 140th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.



Supplementary Figure 84: The change of pNpS value of adaptive genes from MAG “s96.ctg000111c\_BL\_0908sc” over time in BBMO. Along the x-axis is the sequence of sampling months from the 1st to the 140th. pNpS values are measured along the y-axis. Any sample with a covering percentage of hits on MAGs less than 25% was excluded. The pNpS values exceeding 2 were uniformly assigned a value of 2 and the missing pNpS value in the sample was assigned a value of -1.