OTU ID	SG1-TOP-201S	G1-TOP-201	SG1-TOP-201	SG1-TOP-201	SG1-TOP-201
HM127296.1.1462	1	1	1	0	0
AB072814.1.1472	3	1	0	1	2
AF142880.1.991	9	15	0	4	5
FJ890991.1.1350	0	0	0	0	0
CU467262.1.1344	0	0	0	0	0
AM947482.1.1343	0	0	4	0	0
KC465591.1.1355	4	1	0	14	0
HQ400505.1.919	0	0	0	0	0
AB533880.1.1504	0	0	0	0	0
FN391244.1.1346	0	0	0	0	0
KC354385.1.904	0	0	0	0	0
GQ374969.1.1442	0	0	0	0	1
HG475319.1.907	94	613	9	52	17
KF798423.1.1453	0	0	0	0	0
FN391290.1.1341	0	3	0	1	1
EF690638.1.1440	23	11	13	6	4
JX882083.1.1474	7	8	35	46	2
AB534005.1.1513	0	0	0	0	0
KJ534549.1.1470	5	3	1	9	2
JX883654.1.1487	0	0	0	0	0
JX883143.1.1486	2	0	0	0	0
FN391257.1.1346	0	9	3	7	5
KF452253.1.942	0	0	0	0	1
JX884946.1.1470	0	0	1	0	0
CU467120.1.1342	10	44	73	12	76
HM186329.1.1369	0	0	0	0	0
HQ400517.1.919	0	0	15	0	0
JX882977.1.1481	18	19	44	10	11
JN436038.1.1347	0	42	4	0	0
HQ400533.1.919	2	2	0	1	0
AM947471.1.1342	1	1	0	4	0
KM496558.1.1391	0	0	0	0	0
HQ400523.1.914	2	3	2	0	0
JX884092.1.1463	0	0	1	0	0
HE604526.1.919	0	0	0	0	0
AB735496.1.1471	12	5	4	2	4
KC463678.1.1437	0	0	0	0	0
JX883000.1.1462	0	0	0	0	0
FJ891047.1.1360	0	0	0	0	0
JX883674.1.1474	2	1	0	0	2
JX883125.1.1467	0	0	1	0	0
JN863500.1.1245	0	0	0	0	0
AYLJ01000015.6615.807		6	7	9	6
HQ400525.1.920	37	9	19	6	12

JN714404.1.1473	0	0	0	0	0
EU722669.1.1444	24	50	3	33	26
JX882498.1.1479	0	0	2	0	0
JF196762.1.1375	0	0	1	0	0
AB533838.1.1509	0	1	2	0	0
JX883869.1.1481	0	0	0	0	0
EU722658.1.1435	1	0	0	2	0
GQ861373.1.917	3	1	0	0	4
HQ425149.1.1433	133	134	127	57	103
FN391240.1.1345	2	0	0	1	0
HQ425152.1.1427	0	0	10	3	2
JQ684501.1.1404	0	0	0	0	0
JN714407.1.1472	4	5	0	1	9
JN714431.1.1473	0	0	1	0	0
AB534154.1.972	5	2	1	3	4
AM947502.1.1345	0	6	5	18	0
GQ374923.1.1446	19	0	0	2	4
EF106117.1.1342	3	5	1	1	5
FN391292.1.1351	0	0	6	0	0
EU869368.1.1233	0	0	0	0	12
HQ425095.1.932	0	1	3	0	3
BARE01000094.345.181	1	0	0	0	2
AB588757.1.1474	74	151	21	39	36
GQ375027.1.1443	0	0	0	0	0
CU467127.1.1340	0	0	12	1	11
KF650689.1.1017	7	1	0	0	4
JX882124.1.1468	6	16	14	8	6
HQ400507.1.919	0	0	0	1	0
FJ790610.1.1311	0	0	0	0	0
HM240871.1.1312	0	0	0	0	0
EU365395.1.1098	2	1	2	1	4
JX883469.1.1474	0	0	0	0	0
CU467136.1.1339	2	10	22	2	19
HQ425172.1.1426	0	0	0	0	0
FN391188.1.1354	0	0	0	1	0
KF591561.1.1041	0	0	0	0	0
EU869375.1.1415	5	3	12	6	9
KJ588897.1.998	0	0	1	0	0
AJ969889.1.918	0	0	0	0	0
AJ344317.1.917	0	0	0	0	0
EF106654.1.937	18	5	26	9	24
AB534051.1.1519	0	0	0	0	1
HF968436.1.1211	0	0	0	0	0
GU951430.1.1473	20	54	2	57	57
FJ192058.1.1399	1	1	0	0	0

AJ969930.1.919	0	0	0	0	0
EU911994.1.1223	1	0	6	0	4
HQ876207.1.1478	0	0	0	0	0
FR869801.1.1333	0	0	0	0	0
JX881926.1.1475	0	0	0	0	0
KF620446.1.1362	0	0	0	1	0
JN714424.1.1473	5	8	4	2	4
AB696386.1.1319	0	0	0	0	0
EU869390.1.1440	9	45	40	15	25
HM127111.1.1468	42	47	54	15	18
HQ400513.1.919	63	47	13	9	16
KM068159.1.1473	3	5	0	5	4
EF106659.1.938	41	17	24	45	46
KJ917626.1.1376	1	1	0	0	0
HQ400465.1.919	16	26	7	11	14
JX883895.1.1471	0	0	0	0	2
HQ400562.1.919	1	1	0	1	0
EF106671.1.999	62	33	64	11	26
KC003257.1.1346	0	0	0	1	1
JN714457.1.1469	7	2	1	7	2
KC465587.1.1353	4	0	0	0	1
CU915217.1.1386	0	0	0	0	0
HG475330.1.920	1	1	0	0	0
JX883459.1.1476	6	14	3	15	8
JX884089.1.1458	0	1	4	0	0
KC465592.1.1351	881	919	244	762	543
AB533910.1.1502	11	29	36	7	12
AF142882.1.992	2	7	0	1	4
HQ157614.1.921	0	0	1	0	0
DQ432537.1.1395	1	0	40	0	0
HQ400480.1.920	64	10	10	5	9
KF717637.1.955	8	0	1	0	15
GQ861389.1.920	0	0	0	0	0
AB725662.1.1441	3	0	0	0	0
GQ249213.1.1360	0	0	0	0	0
KJ689297.1.1389	0	0	0	0	0
KF234338.1.1355	21	21	4	9	12
GQ861378.1.924	1	0	1	6	0
JQKV01000030.1.1156	1	0	0	0	1
HM159604.1.1374	27	38	0	18	27
JX882215.1.1483	0	0	1	0	0
Z76654.1.1494	0	0	0	0	0
EF105755.1.1364	1	0	0	0	0
EU869371.1.1242	1	1	0	0	0
AY987828.1.1441	162	234	5	90	94

AB533952.1.1522	0	0	2	0	0
AB454050.1.1425	4	1	0	0	0
CU467357.1.1354	0	0	0	0	0
HQ400452.1.918	5	23	0	10	1
JX884811.1.1468	0	0	3	0	1
KF814464.1.1356	1	0	0	0	0
HQ400559.1.919	12	18	22	3	3
APHM01017498.1.1009	0	1	1	0	0
AB766179.1.1471	6	26	4	28	18
JN714446,1.1471	0	0	0	1	1
JQ627427.1.1343	0	0	0	0	0
JX883832.1.1478	1783	2169	1194	1017	1101
AGNT01000024.7597.90	0	0	0	0	1
CU467404.1.1354	3	8	4	1	2
GU363383.1.1142	0	19	0	0	0
AB454051.1.1420	0	0	0	0	0
KC756198.1.1430	0	0	0	0	0
HM126809.1.1479	2	3	1	0	0
EF690598.1.1438	0	0	0	0	0
EF690625.1.1441	1	1	1	0	0
FN994978.1.1345	17	28	0	8	4
HQ400553.1.914	13	16	23	12	5
EF522229.1.1329	0	0	1	0	0
FN391185.1.1355	0	1	15	0	3
LN649992.1.1350	5	11	1	17	23
GQ016413.1.1310	0	0	0	0	0
FN994970.1.1343	0	0	0	0	0
HQ400485.1.919	2	0	1	0	0
AY862793.1.1400	0	1	0	0	0
HQ425165.1.1418	0	2	0	0	0
AB533937.1.1485	5	1	19	4	0
HQ425161.1.1358	63	72	241	32	54
FJ891036.1.1214	0	0	0	0	0
APHM01010977.3.1297	29	35	0	35	50
JN038033.1.1058	0	2	5	0	2
JX883112.1.1463	44	54	103	17	21
JX883736.1.1463	1	2	16	1	13
CP001688.1954831.1956	12	11	0	4	1
GQ281067.1.1414	0	0	0	0	1
FN391286.1.1344	1	0	1	0	0
FJ891051.1.1349	0	0	0	0	0
HQ425186.1.1501	0	0	0	0	0
EF106039.1.1370	3	2	0	2	2
HE604442.1.919	5	0	1	1	0
KF234372.1.1441	0	0	3	0	0

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FN391194.1.1355	3	2	2	3	1
JX523749.1.1206	0	0	0	0	0
AJ969892.1.919	14	14	0	1	2
JN714439.1.1469	0	2	1	2	3
HF677567.1.1352	2	1	0	0	1
JX883165.1.1465	0	0	0	0	0
KC465611.1.1352	0	7	0	3	2
KF452248.1.954	3	0	0	1	0
JN714420.1.1471	22	7	8	3	5
JX882784.1.1485	0	0	0	4	2
KF814650.1.1483	0	0	1	0	0
FN393530.1.1361	0	19	22	4	7
CU467261.1.1348	0	0	0	0	0
KC465599.1.1248	2	0	0	0	0
LN649829.1.1060	0	0	0	0	0
AJ344314.1.918	0	1	0	2	0
AB576127.1.1467	2	0	1	0	1
JX883276.1.1475	2	1	0	0	0
KM496562.1.1381	7	9	6	5	0
HM241039.1.1314	0	0	2	0	0
AB533842.1.1259	0	0	3	0	0
HQ425153.1.1433	190	216	121	94	141
KF673170.1.1386	25	66	5	53	39
JX075128.1.1271	0	0	0	0	0
KJ145789.1.1365	0	0	0	0	0
EU869373.1.1239	0	2	5	2	0
JN714423.1.1470	10	33	8	24	22
JN714460.1.1472	9	6	0	3	4
AB108676.1.1473	1	0	0	0	1
FN391272.1.1348	6	11	125	2	1
HQ425162.1.1424	41	72	113	17	21
JN714448.1.1473	5	17	0	7	6
EU440677.1.1465	0	0	0	0	0
KM258096.1.1031	0	1	0	0	0
AJ969840.1.917	18	16	11	14	23
JX884312.1.1480	1	0	0	0	0
AJ277204.1.1325	1	0	0	0	0
JQ937358.1.1388	1	0	1	1	1
GQ861367.1.915	77	49	22	81	87
AB663392.1.1473	18	25	0	3	11
KF234305.1.919	0	0	0	0	0
DD437355.1.1511	0	0	0	0	1
HQ400502.1.918	4	0	0	0	0
CP007060.191367.19284	9	14	0	7	201
FJ716048.1.1407	0	0	0	0	0

EF106448.1.1390	0	21	42	2	0
KC465612.1.1351	12	26	0	5	10
AJ278931.1.918	0	0	0	1	2
HQ425209.1.1500	3	7	5	0	6
AB074301.1.1473	0	1	0	0	0
EU869382.1.1429	0	0	0	0	0
JN038029.1.1050	1	0	0	0	0
LN649952.1.1383	46	114	2	27	24
CU467121.1.1342	0	0	3	0	1
HQ400506.1.919	1	0	0	0	0
AF280796.1.1488	0	0	0	0	0
EF468473.1.1470	2	19	73	6	26
JX883445.1.1493	2	0	0	0	1
FJ595635.1.1313	0	0	0	0	0
JX882356.1.1454	1	1	26	0	3
KM453695.1.1471	3	5	0	9	1
EF690614.1.1438	0	0	2	1	0
KM258031.1.1042	0	1	0	0	0
GQ861363.1.919	1	0	0	0	0
EF690585.1.1438	5	3	1	1	3
AJ878084.1.1345	0	0	0	0	1
GQ861355.1.915	10	6	3	8	5
FR733704.1.1480	0	0	4	0	0
KF452281.1.954	13	10	0	3	3
EU869367.1.1235	1	0	0	1	0
KF037375.1.1456	0	0	0	0	0
AM981378.1.1352	1	0	0	0	0
HQ400520.1.919	4	0	1	0	0
EU506287.1.1363	0	0	0	0	0
KF582944.1.1471	19	73	3	31	46
AB454049.1.1426	0	2	0	0	0
AJ344311.1.918	46	15	2	22	24
KF673189.1.1469	0	1	1	0	0
EU869377.1.1432	0	0	1	0	0
JQ421328.1.1454	0	0	0	0	0
HE604599.1.919	0	0	0	0	0
FJ978723.1.1421	0	0	0	0	0
JX884358.1.1470	0	2	1	0	0
EU911982.1.1222	0	1	0	0	0
AM947496.1.1351	8	11	2	11	13
KF814306.1.920	0	0	1	1	0
CU467128.1.1345	0	0	0	0	0
CU467266.1.1348	13	4	0	1	18
KC918821.1.1386	0	0	0	0	0
HQ400554.1.919	0	2	0	1	1

HM126955.1.1468	10	18	144	4	5
HQ425053.1.1367	0	0	0	0	0
EF106688.1.996	2	3	2	1	2
HQ400414.1.919	0	0	0	0	0
FJ891032.1.1350	0	0	0	0	0
HQ425148.1.1427	0	1	2	0	0
JN038019.1.1053	0	1	0	1	1
DQ432015.1.1454	83	60	18	28	22
HQ157635.1.921	8	1	62	1	4
HQ425146.1.1450	386	475	386	200	264
KF591573.1.1094	7	4/3	13	4	30
EF106050.1.1350	0	0	0	0	0
JX881516.1.1465	0	0	0	0	0
HQ425189.1.1455	1	0	0	2	0
FN391291.1.1344	2	22	1	5	3
JN714464.1.1470	56	34	4	13	11
HQ400459.1.915	1	0	0	0	0
HQ400439.1.919	0	0	0	0	0
FN994968.1.1344	3	0	2	0	3
GQ169802.1.1389	0	0	0	1	0
AF015964.1.1050	20	21	2	26	2
FN393497.1.1351	0	0	2	0	0
GQ374958.1.1442	2	1	19	1	0
KC465608.1.1353	4	1	0	0	0
KF673167.1.1439	114	161	32	34	84
KC465602.1.1348	1	0	1	1	1
KC465586.1.1352	3	6	3	10	14
FN391256.1.1340	0	1	1	0	0
HQ215546.1.1474	0	1	0	0	0
EF535046.1.974	15	44	0	3	7
CU467116.3.1355	0	0	0	0	0
JX884060.1.1469	0	4	2	2	3
GQ032594.1.1348	0	0	0	0	0
AY862785.1.1360	0	0	0	3	0
EF106344.1.1451	0	1	0	0	0
KJ817648.1.1496	0	0	0	0	0
EF459702.1.1440	2	2	0	2	1
JQ237116.1.1471	5	2	10	7	2
FN391294.1.1347	0	1	1	2	0
JF832329.1.1413	0	0	0	0	0
JX883632.1.1475	1	0	2	0	0
HM152714.1.1486	0	0	0	0	0
New.ReferenceOTU290	64	48	23	36	39
New.ReferenceOTU179	15	18	0	8	9
New.ReferenceOTU79	13	0	0	0	0
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New.ReferenceOTU71	342	276	215	175	172
New.ReferenceOTU75	2	2	3	0	0
New.ReferenceOTU76	16	25	25	9	18
New.ReferenceOTU77	0	0	1	0	0
New.ReferenceOTU200	21	39	15	10	15
New.ReferenceOTU206	0	0	0	0	0
New.ReferenceOTU207	24	77	84	14	13
New.ReferenceOTU110	159	232	369	125	133
New.ReferenceOTU111	3	10	8	20	29
New.ReferenceOTU112	199	179	159	157	159
New.ReferenceOTU3	12	23	3	9	4
New.ReferenceOTU4	373	584	166	355	350
New.ReferenceOTU5	4	4	10	1	0
New.ReferenceOTU6	1	4	16	24	1
New.ReferenceOTU7	1581	1431	680	1159	1292
New.ReferenceOTU289	4	3	1	9	8
New.ReferenceOTU131	0	1	1	0	0
New.ReferenceOTU0	289	163	153	96	145
New.ReferenceOTU136	0	0	2	0	0
New.ReferenceOTU284	6	1	4	2	2
New.ReferenceOTU286	0	2	0	0	0
New.ReferenceOTU177	0	0	0	0	0
New.ReferenceOTU95	0	0	0	0	0
New.ReferenceOTU47	7	30	131	7	56
New.ReferenceOTU89	2	5	5	2	2
New.ReferenceOTU68	2	1	0	2	3
New.ReferenceOTU67	7	16	22	30	3
New.ReferenceOTU66	6	7	3	3	0
New.ReferenceOTU65	160	381	0	54	13
New.ReferenceOTU63	10	10	0	12	1
New.ReferenceOTU61	1	3	1	0	1
New.ReferenceOTU60	65	29	38	23	27
New.ReferenceOTU234	4	15	50	8	11
New.ReferenceOTU237	0	0	0	0	0
New.ReferenceOTU231	79	218	8	208	77
New.ReferenceOTU233	8	5	107	7	19
New.ReferenceOTU239	151	280	109	77	171
New.ReferenceOTU123	76	20	9	72	35
New.ReferenceOTU122	37	54	85	32	30
New.ReferenceOTU325	113	1	31	26	3
New.ReferenceOTU322	35	17	33	7	13
New.ReferenceOTU230	0	1	0	5	2
New.ReferenceOTU18	11	21	32	5	15
New.ReferenceOTU19	308	275	725	75	121
New.ReferenceOTU118	0	1	0	0	0

New.ReferenceOTU12	92	329	72	126	145
New.ReferenceOTU13	17	32	3	13	24
New.ReferenceOTU10	3	9	0	4	1
New.ReferenceOTU11	549	375	2	181	194
New.ReferenceOTU16	112	191	10	91	106
New.ReferenceOTU17	5	2	1	1	3
New.ReferenceOTU14	2	0	0	0	0
New.ReferenceOTU15	174	123	22	44	43
New.ReferenceOTU181	53	37	11	13	23
New.ReferenceOTU271	68	14	2	114	88
New.ReferenceOTU228	45	16	4	52	66
New.ReferenceOTU229	5	1	2	1	2
New.ReferenceOTU270	2	2	1	1	1
New.ReferenceOTU222	57	110	12	130	46
New.ReferenceOTU223	0	0	0	0	0
New.ReferenceOTU220	0	0	0	0	0
New.ReferenceOTU221	76	37	120	23	85
New.ReferenceOTU227	4	3	1	13	4
New.ReferenceOTU224	15	0	46	0	0
New.ReferenceOTU225	0	0	0	0	0
New.ReferenceOTU92	0	1	4	0	0
New.ReferenceOTU175	17	62	8	78	27
New.ReferenceOTU9	32	37	77	21	14
New.ReferenceOTU161	1	4	0	1	2
New.ReferenceOTU160	10	24	5	6	5
New.ReferenceOTU52	3	1	1	1	4
New.ReferenceOTU108	9	3	0	4	0
New.ReferenceOTU98	24	6	4	4	17
New.ReferenceOTU121	3	1	8	1	0
New.ReferenceOTU162	8	6	3	0	0
New.ReferenceOTU256	1	2	1	1	2
New.ReferenceOTU255	21	10	4	5	18
New.ReferenceOTU254	30	28	2	38	46
New.ReferenceOTU252	4	13	0	4	7
New.ReferenceOTU83	0	0	0	0	0
New.ReferenceOTU144	0	1	36	0	1
New.ReferenceOTU85	12	4	4	4	7
New.ReferenceOTU142	59	62	2	15	11
New.ReferenceOTU141	7	5	1	2	5
New.ReferenceOTU301	3	6	1	5	8
New.ReferenceOTU88	9	21	56	10	9
New.ReferenceOTU328	27	6	3	4	31
New.ReferenceOTU307	9	2	6	5	6
New.ReferenceOTU113	0	0	0	0	0
New.ReferenceOTU36	2	2	1	0	5

New.ReferenceOTU37	14	53	95	24	109
New.ReferenceOTU32	0	4	0	2	0
New.ReferenceOTU115	8	7	0	10	7
New.ReferenceOTU80	84	16	5	14	19
New.ReferenceOTU248	10	15	32	3	8
New.ReferenceOTU130	16	17	1	2	16
New.ReferenceOTU245	0	0	1	3	1
New.ReferenceOTU156	25	17	12	9	9
New.ReferenceOTU157	0	0	1	1	0
New.ReferenceOTU153	0	2	2	0	2
New.ReferenceOTU317	0	0	1	0	0
New.ReferenceOTU312	38	24	8	11	9
New.ReferenceOTU311	12	14	51	111	9
New.ReferenceOTU318	6	10	21	0	64
New.ReferenceOTU208	0	62	198	0	1
New.ReferenceOTU33	3	3	2	1	2
New.ReferenceOTU23	0	0	0	0	0
New.ReferenceOTU21	11	44	0	39	71
New.ReferenceOTU27	640	525	15	293	235
New.ReferenceOTU26	0	2	0	1	0
New.ReferenceOTU183	755	677	521	629	514
New.ReferenceOTU209	6	4	3	3	1
New.ReferenceOTU182	5	2	5	5	2
New.ReferenceOTU158	10	52	282	2	7
New.ReferenceOTU258	24	7	9	5	6
New.ReferenceOTU159	23	155	1	27	13
New.ReferenceOTU273	184	232	167	200	161
New.ReferenceOTU272	10	38	4	14	7
New.ReferenceOTU274	21	12	3	14	14
New.ReferenceOTU163	43	15	2	11	15
New.ReferenceOTU165	0	1	0	0	2
New.ReferenceOTU164	36	50	2	33	6
New.ReferenceOTU167	57	39	9	7	16
New.ReferenceOTU166	5	22	3	14	31
New.ReferenceOTU218	26	18	28	25	58
New.ReferenceOTU50	7	32	50	12	4
New.ReferenceOTU184	88	23	11	19	94
New.ReferenceOTU46	28	18	1	60	6
New.ReferenceOTU54	10	17	13	24	34
New.ReferenceOTU180	2	20	2	15	13
New.ReferenceOTU53	1	0	0	0	0
New.ReferenceOTU185	0	4	0	0	0
New.ReferenceOTU189	1	1	0	0	1
New.ReferenceOTU81	5	4	1	1	2
New.ReferenceOTU291	0	0	0	0	0

New.ReferenceOTU308	1	1	1	0	0	
New.ReferenceOTU266	71	103	16	18	51	
New.ReferenceOTU267	34	22	22	18	14	
New.ReferenceOTU265	0	0	0	0	0	
New.ReferenceOTU176	55	74	25	42	44	
New.ReferenceOTU59	0	0	0	0	0	
New.ReferenceOTU173	4	5	1	2	3	
New.ReferenceOTU40	0	2	2	0	0	
New.ReferenceOTU304	0	0	0	0	3	
New.ReferenceOTU192	0	0	0	1	0	
New.ReferenceOTU193	6	5	1	2	2	
New.ReferenceOTU99	6	8	30	15	11	
New.ReferenceOTU196	0	0	0	0	0	
New.ReferenceOTU178	0	1	0	0	1	
New.ReferenceOTU199	3	3	1	0	3	
New.ReferenceOTU219	26	13	1	5	7	
New.ReferenceOTU212	0	0	0	0	1	
New.ReferenceOTU217	1	1	0	0	0	
New.ReferenceOTU215	0	0	4	0	0	
New.ReferenceOTU43	0	1	0	0	0	
New.ReferenceOTU102	178	103	92	70	90	
New.ReferenceOTU101	9	9	2	5	17	
New.ReferenceOTU100	80	31	31	6	22	
New.ReferenceOTU107	293	63	3	18	17	
New.ReferenceOTU106	1	6	0	0	6	
New.ReferenceOTU129	1	7	2	3	0	
New.ReferenceOTU299	0	0	0	0	1	
New.ReferenceOTU20	17	8	1	0	3	
New.ReferenceOTU186	5	8	1	8	4	
New.ReferenceOTU149	0	2	5	0	0	
New.ReferenceOTU103	12	16	3	5	2	
New.ReferenceOTU306	26	37	18	19	13	
New.ReferenceOTU297	1	0	0	0	0	
New.ReferenceOTU296	0	1	0	0	1	

SG1-TOP-201SG1	L-TOP-201SG1-	TOP-201SG1	-TOP-201SG1-	-TOP-201SG1-	TOP-201SG1	-TOP-201
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0	0	2	0	0	0	0
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1	0	11	15	0	2	5
2	3	0	0	0	0	0
0	0	2	4	0	6	2
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0	1	23	6	14	8	5
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0	0	14	5	2	5	1
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7	1	36	9	13	19	13
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0	1	1	0	1	0	1
0	0	0	0	0	4	8
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0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	1	0	0	0	1
0 0	0	3 0	11 0	1 0	8 0	2 0
	0	0				
0 0	0 0	0	0 0	0 4	0 0	0 0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	1	0	0
0	0	9	1	0	17	2
1	1	6	6	27	12	13
±	_	J	J	۷,	16	10

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3	6	32	24	1	22	21
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0	0	0	0	3	0	0
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0	0	1	2	0	2	0
30	30	245	45	47	74	35
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0	0	0	2	1	0	0
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1	1	13	0	0	19	2
1	5	0	0	1	31	44
1	0	0	8	0	1	1
1	0	1	0	2	4	1
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0	0	17	10	1	0	2
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7	5	2	11	12	11	10
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0	0	2	0	0	0	3
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1	2	0	0	0	0	0
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16	22	14	61	5	26	5
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1	3	59	37	0	71	29

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0	0	4	0	0	0	0
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163	226	3031	990	702	1912	988
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0	0	1	3	5	4	1
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2	0	53	9	1	24	37
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0	0	0	0	0	1	0
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1	2	10	7	1	12	16
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0	0	0	1	0	2	1
0	0	2	0	1	0	0
0	0	0	0	1	3	0
U	U	U	U	1	3	U

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1	1	9	6	0	19	5
1	3	8	3	1	5	5
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1	0	26	1	0	2	2
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0	0	7	13	3	6	7
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0	0	0	0	0	0	0
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0	0	0	0	0	0	1
1	0	1	0	0	1	1
0	0	7	0	1	8	3
0	0	0	0	11	0	0
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12	22	179	130	84	292	149
0	4	79	38	6	100	24
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0	0	54	18	1	16	2
0	1	1	10	0	18	8
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3	9	30	2	0	2	11
6	16	63	27	26	45 10	0
1 6	5 4	10 0	10 0	2 0	10 0	9 0
	0	0	0	0	0	0
0 3	8	48	19	4	34	19
0	0	40	0	0	0	0
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0	0	0	1	0	2	0
35	55	73	59	49	100	20
0	1	22	7	0	16	16
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0	1	0	0	0	0	0
0	0	7	1	0	0	0
1	0	2	15	0	10	23
0	0	0	0	0	0	0
J	U	U	U	U	U	U

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0	0	0	1	0	0	1
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3	8	29	9	0	44	36
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0	1	0	3	2	2	1
5	6	4	11	1	3	1
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0	2	5	3	0	9	5
0	0	0	0	0	0	0
0	1	4	0	2	4	2
0	0	0	0	0	0	0
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0	0	0	0	0	0	0
0	0	1	0	2	1	1
0	0	3	0	0	2	3
0	0	0	0	0	0	0
0	0	46	37	3	76	39
0	0	4	0	0	0	0
0	5	54	9	0	25	28
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0	0	0	0	0	1	0
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0	0	0	0	0	0	0
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0	0	0	0	0	0	1
0	0	0	0	1	0	0
1	10	10	8	0	15	23
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0	1	3	2	0	4	5
0	0	0	0	0	0	0
0	0	0	2	0	0	1

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43	69	511	289	196	598	287
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0	0	4	0	0	1	0
0	0	0	0	0	0	0
3	5	13	10	0	6	11
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25	29	116	42	18	88	52
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0	1	9	2	0	13	13
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0	0	12	2	1	5	9
0	1	0	1	0	7	4
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9	12	63	24	49	38	67
1	5	37	7	0	22	11
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54	61	366	354	211	284	178
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26	34	201	142	219	269	164
5	14	80	23	10	28	19
32	31	409	100	124	129	165
3	4	29	12	11	24	4
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466	461	3015	722	461	999	980
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54	72	252	50	76	61	96
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37	35	14	16	15	24	4
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7	6	84	40	1	172	88
4	3	62	18	56	47	22
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4	1	57	24	19	11	5
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3	3	13	9	19	16	12
13	28	89	88	228	132	98
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0	0	334	65	3	407	37
30	55	160	179	62	314	167
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5	7	16	15	2	30	23
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10	19	225	19	4	328	19
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0	0	4	9	0	0	4
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0	0	2	2	4	1	0
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3	3	34	21	5	20	7
18	38	111	29	2	78	122
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0	1	5	3	4	6	4
7	9	29	6	4	6	16
2	4	7	20	2	17	16
0	0	17	7	1	5	3
4	3	23	3	24	11	9
1	2	2	6	0	9	7
3	0	12	10	3	3	1
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0	0	3	0	0	5	0
•	J	9	J	J	9	•

1	3	52	58	29	86	19
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8	13	4	31	61	18	28
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21	38	210	73	31	85	40
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10	22	302	257	106	395	141
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8	11	14	7	6	34	25
5	3	12	48	7	27	29
0	0	0	1	0	1	0
2	1	31	34	0	19	15
5	1	18	17	8	18	12
0	12	96	7	5	4	69
0	0	29	40	3	22	5
0	0	8	16	1	9	10
3	4	21	24	9	27	30
0	4	179	9	0	37	55
4	17	52	33	17	60	41
0	0	27	11	0	58	11
0	0	1	1	0	1	0
0	0	2	0	1	2	2
0	0	0	0	0	1	0
0	1	4	0	0	4	3
0	0	0	0	0	0	0
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0	0	2	0	0	2	0
12	10	33	28	14	31	42
6	2	40	26	16	32	19
0	0	0	0	1	0	0
3	5	121	35	14	59	31
0	0	2	0	0	0	0
0	0	7	6	0	1	0
0	0	16	3	1	0	4
0	0	0	3	0	0	2
0	0	0	0	0	0	0
0	1	8	5	2	8	3
0	1	41	17	7	20	3
1	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	1	1	1	4	0
0	0	12	4	0	3	7
0	0	0	0	0	0	0
4	5	0	1	1	0	2
0	0	6	2	0	7	0
0	0	0	0	0	0	0
20	18	130	203	74	137	73
4	5	39	9	6	29	3
3	4	10	45	14	17	12
1	4	5	144	0	12	37
1	4	6	3	0	3	3
0	0	1	2	2	0	3
0	0	0	0	0	0	0
1	3	5	10	2	11	2
0	0	3	3	1	5	10
0	0	0	0	1	0	0
3	4	7	1	7	2	12
3	1	32	18	12	41	27
0	0	0	0	0	0	2
1	2	0	0	3	1	1

SG1-TOP-2015	SG1-TOP-201SG	i1-TOP-201SG1	L-TOP-201SG	1-TOP-201S0	G1-TOP-201S	G1-TOP-201
0	0	0	0	0	0	0
1	0	0	0	0	0	0
0	25	2	3	10	10	1
0	0	0	0	1	0	0
0	0	0	0	0	0	0
1	1	0	0	0	0	0
1	3	0	1	2	7	0
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0	0	0	0	0	0	0
0	0	0	0	3	0	0
0	0	0	0	0	0	0
0	0	0	0	1	0	0
9	18	0	3	18	3	1
0	0	0	5	0	0	0
0	1	0	0	0	2	0
5	19	0	1	15	34	6
7	18	0	0	1	7	0
0	0	0	3	0	0	2
0	4	0	1	11	9	0
0	0	0	0	0	0	0
1	0	0	0	0	0	0
1	4	0	0	3	10	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
29	98	0	0	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	0
16	23	1	0	27	31	0
0	4	0	0	0	0	0
1	2	0	0	0	1	1
0	3	0	0	20	11	0
1	0	0	0	0	0	0
0	0	0	0	0	0	0
1	0	0	0	0	0	0
0	0	0	0	0	0	0
4	12	0	0	2	15	0
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0	0	0	0	0	0	0
1	0	0	0	0	0	0
0	0	0	0	0	0	0
3	0	0	0	0	0	0
5	13	0	0	8	3	0
15	6	0	1	2	39	4

0	0	0	0	0	0	0
2	50	5	3	16	24	9
0	0	0	0	0	0	0
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0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	1	0	0	3	3	0
0	1	0	0	0	3	0
62	118	3	19	35	98	74
0	1	0	0	0	0	0
0	0	0	0	1	0	0
0	0	0	0	1	0	0
3	2	0	0	5	3	0
0	0	0	1	0	0	0
0	6	0	1	8	4	0
0	29	0	0	151	65	0
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2	1	1	0	1	0	0
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0	0	0	0	0	0	0
0	0	0	0	3	0	0
0	0	0	0	0	0	0
30	81	58	410	188	169	138
1	1	0	0	0	0	0
0	4	0	0	0	0	0
2	2	1	0	3	2	0
3	12	0	0	3	12	2
0	0	0	0	1	0	0
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0	0	0	0	0	0	0
0	3	0	0	1	0	0
0	0	0	0	0	0	0
10	10	0	0	0	0	0
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0	1	0	3	1	1	0
0	0	0	0	0	0	0
0	0	0	1	1	0	0
0	0	0	0	0	0	0
20	8	0	0	5	2	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
1	161	2	3	80	202	1
0	0	0	0	0	0	0

0	0	0	0	0	0	0
6	0	0	0	0	0	0
0	0	0	0	0	0	0
4	0	0	0	0	0	0
0	0	0	0	0	0	0
0	1	0	0	10	2	0
0	5	0	1	4	6	0
0	0	0	0	0	0	0
31	19	1	0	10	32	0
17	41	0	0	35	46	2
16	4	0	18	50	43	19
0	14	0	0	5	8	0
14	44	0	6	26	46	6
0	0	0	0	1	0	0
1	13	0	1	46	18	2
0	0	0	1	0	1	1
0	0	3	2	5	0	1
55	26	1	21	67	41	7
0	0	0	0	0	0	0
4	7	0	2	2	29	2
0	0	0	0	0	1	0
0	1	0	2	0	0	0
0	0	0	0	0	2	0
73	42	0	7	74	13	5
1	0	0	0	1	0	0
154	1163	41	342	1978	1780	260
11	6	0	0	12	28	3
1	9	0	0	5	1	1
0	0	0	0	0	0	0
1	1	0	0	0	0	0
6	8	0	5	3	3	5
0	10	0	1	11	6	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
3	0	0	0	0	0	0
0	0	0	0	1	0	0
7	34	4	30	41	11	6
2	15	0	6	5	2	0
0	0	0	0	0	0	0
1	64	0	1	10	20	0
1	0	0	0	0	0	0
0	1	0	0	0	0	0
0	0	0	0	5	1	0
1	1	0	0	0	0	0
3	352	1	14	44	124	1
3	332	7	14	44	124	T

0	0	0	0	0	0	0
0	5	0	0	2	0	0
0	0	0	0	1	0	1
0	22	0	0	78	9	0
3	0	0	0	0	0	0
0	0	0	0	0	0	0
6	14	0	1	8	10	0
0	0	0	0	0	1	0
1	17	0	0	6	21	1
0	0	0	0	0	3	0
0	0	0	0	0	0	0
588	1863	36	201	2372	2055	306
0	1	0	0	0	0	0
6	2	0	1	1	1	1
0	1	0	0	0	0	0
0	2	0	0	2	1	0
0	0	0	0	0	0	0
0	2	0	0	0	6	0
0	0	0	0	0	0	0
0	1	0	0	0	0	0
0	35	0	0	6	14	1
12	13	1	1	10	21	2
0	0	0	0	0	0	0
6	6	0	0	0	0	0
2	30	0	0	14	12	1
0	0	0	0	0	0	0
0	0	0	0	1	0	0
0	2	0	3	0	1	2
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0	1	0	0	0	4	0
0	0	0	0	0	5	0
43	80	0	0	19	36	0
0	0	0	0	0	0	0
1	46	1	0	83	53	1
6	1	0	1	0	1	1
24	31	0	5	37	42	4
23	4	0	0	1	3	0
0	6	0	0	8	5	0
0	0	0	0	0	0	0
0	0	0	1	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	2	0	0	1	0
0	0	0	0	0	0	0
4	1	0	0	1	0	0

6	3	0	0	1	3	0
0	0	1	0	0	0	0
0	11	1	2	18	3	2
1	4	0	0	3	4	0
0	1	0	0	3	1	0
0	0	0	0	0	0	0
0	14	0	0	3	5	0
0	0	0	0	0	1	0
5	1	0	0	13	13	4
1	3	0	0	2	1	0
0	0	0	0	0	0	0
11	5	0	0	2	9	0
0	0	0	0	0	0	0
0	2	0	0	2	6	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	1	0	0
0	2	0	2	0	1	0
0	3	0	0	1	3	0
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0	0	0	0	1	1	0
71	155	6	17	266	275	67
11	43	0	0	18	80	1
0	0	0	0	0	0	0
0	0	0	2	0	0	0
0	1	0	0	3	1	1
3	23	0	0	9	52	0
0	4	0	4	17	3	2
0	1	0	0	0	3	0
5	9	0	2	1	0	0
34	26	0	5	20	25	21
0	16	0	3	26	14	1
0	0	0	4	0	0	1
0	1	0	0	1	1	0
4	25	0	0	28	55	1
0	0	0	0	0	1	0
0	0	0	0	1 0	0 0	0
0	1	0 6	0			0
34 0	195 24	0	128 1	56 14	91 22	14 0
				14		
0 0	1 0	0 0	0 2	0 0	0 0	0 0
0	1	0	0	1	0	0
7		0	0			0
0	17			17 0	13	
U	0	0	0	U	0	0

0	1	0	0	0	0	0
14	12	1	0	69	25	5
0	0	0	0	8	14	0
2	3	0	0	3	3	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
2	88	3	3	74	115	0
1	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	3	0	0	0
43	82	0	0	0	0	0
1	0	0	0	0	0	0
0	0	0	0	0	0	0
2	0	0	1	1	0	0
0	55	0	2	138	10	1
0	0	0	1	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
8	5	0	3	5	6	3
0	0	0	0	8	0	0
1	4	0	2	31	7	4
0	0	0	0	0	0	0
1	14	0	11	9	2	2
0	3	0	0	1	1	0
0	0	0	0	0	0	0
1	1	0	0	0	0	0
2	2	0	1	0	5	0
1	0	0	0	0	0	0
2	37	0	0	12	41	0
0	2	0	0	0	0	0
1	74	1	7	9	127	2
0	0	0	0	0	0	0
0	0	0	0	2	0	0
0	0	0	1	0	0	0
0	0	0	1	0	1	0
0	0	0	2	0	0	0
5	0	0	0	0	0	0
0	0	0	0	0	0	0
0	21	0	0	23	8	2
0	1	0	0	0	0	0
0	0	0	0	0	0	0
0	2	0	1	1	4	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0

12	3	0	0	1	0	0
0	0	0	0	1	0	0
0	0	0	0	0	0	0
0	0	0	0	1	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	4	1	1	2	0	0
11	48	0	0	25	52	0
16	1	1	9	5	0	3
161	408	12	64	415	531	164
3	4	0	0	3	14	1
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	1	0
2	5	2	2	1	10	3
5	14	0	18	2	24	5
0	0	0	0	0	0	1
1	0	0	0	0	0	0
2	1	0	0	0	0	0
0	0	0	0	0	0	0
0	26	2	11	14	15	1
0	0	0	0	0	1	0
5	0	1	1	1	0	0
0	1	0	0	0	1	1
31	89	5	39	80	121	25
0	3	1	3	2	1	0
0	19	0	0	16	15	0
0	0	0	0	0	0	0
0	3	0	0	0	0	0
0	22	0	2	27	24	1
0	0	0	0	0	0	0
1	1	0	0	1	11	0
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0	1	0	0	0	1	0
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0	1	0	0	5	1	0
1	12	0	4	3	14	0
0	5	0	0	24	6	0
0	0	0	0	0	0	0
0	0	0	0	0	1	0
0	0	0	0	0	0	0
23	49	3	12	175	106	37
0	48	0	0	19	47	0
0	1	0	0	2	3	0

145	281	4	45	490	566	228
145	0	0	43	490	2	1
12	24	1	4	10	15	3
0	0	0	0	0	0	0
3	21	1	0	29	39	2
0	0	0	0	0	0	0
40	45	1	29	21	72	25
143	166	5	34	187	250	83
3	60	0	0	66	45	3
115	186	6	52	384	330	43
15	18	1	19	131	11	38
243	670	4	131	1312	984	187
243	10	0	0	4	10	1
4	44	0	0	182	66	0
407	1682	68	429	2741	2550	560
0	4	0	0	8	13	0
2	0	0	0	1	3	0
72	144	5	41	313	317	90
1	0	0	0	2	1	0
1	0	1	1	3	1	0
0	0	0	0	0	2	0
0	0	0	0	1	2	0
0	0	0	0	0	0	0
66	127	0	0	0	0	0
0	2	0	0	8	2	0
1	4	0	0	17	7	0
7	28	0	1	28	27	1
2	2	0	0	9	8	0
5	19	5	21	42	20	5
1	8	0	1	10	14	1
0	0	0	0	1	2	0
39	24	0	6	129	78	8
7	9	0	0	7	12	1
0	0	0	0	1	0	0
5	158	1	6	80	90	1
17	9	0	1	7	5	1
80	202	0	0	32	144	0
1	287	4	42	102	98	5
63	47	0	6	52	51	5
22	1	0	0	0	19	0
24	10	0	1	8	17	3
0	6	0	0	3	2	0
12	14	4	10	18	14	13
355	232	7	15	317	242	15
0	0	0	0	0	2	0

			_			_
49	259	0	4	268	313	2
12	10	0	0	15	30	0
2	5	0	1	2	3	0
13	519	0	0	247	348	0
35	234	23	50	221	205	74
7	6	0	0	0	4	0
0	0	0	0	0	0	0
10	67	5	19	152	109	10
6	17	0	8	39	106	25
1	28	1	8	219	0	0
7	255	0	1	121	62	6
1	3	0	1	1	7	1
0	0	0	1	4	2	0
0	164	1	3	83	96	1
0	0	0	0	0	0	0
0	0	0	0	0	0	1
30	22	0	0	41	22	1
5	2	0	3	24	6	1
68	0	0	0	2	5	0
1	0	0	0	0	0	0
1	1	0	0	1	1	0
3	174	0	1	43	267	0
25	15	2	1	25	53	2
0	2	0	0	5	6	1
2	8	0	1	11	7	0
1	2	0	0	3	2	0
0	0	0	0	0	0	0
2	13	0	6	7	12	7
4	3	0	0	1	1	0
2	2	0	0	2	7	1
1	1	0	0	2	4	0
2	16	0	2	14	9	0
6	76	1	7	148	83	6
0	23	2	1	10	37	0
0	0	0	0	0	0	0
8	1	0	0	0	1	3
2	3	0	0	12	12	1
4	47	1	21	69	24	3
0	78	0	0	8	9	1
8	5	0	0	4	3	0
30	16	1	1	20	13	1
1	4	0	0	4	11	0
3	10	0	1	5	8	3
0	0	0	0	0	0	0
0	0	0	0	0	0	0

28	59	0	0	10	133	1
1	6	0	0	4	3	0
0	14	0	0	2	4	0
9	6	0	7	97	146	5
9	13	0	0	8	12	2
7	4	0	1	5	9	0
0	1	0	0	1	3	0
18	14	2	1	11	22	3
1	1	0	0	0	0	0
3	3	0	0	1	0	0
0	0	0	0	0	0	0
15	3	0	1	0	47	0
10	163	0	0	89	113	23
82	1	0	0	1	7	0
2	5	0	0	0	1	0
1	1	0	0	0	4	0
0	0	0	0	0	0	0
5	69	0	0	51	48	2
21	782	0	9	340	677	2
2	0	0	0	3	3	0
236	717	13	110	1126	1464	137
2	2	2	1	12	10	0
4	1	0	0	4	9	1
44	108	0	1	5	4	0
5	6	0	3	8	21	5
1	35	0	0	30	49	0
84	232	3	12	300	326	39
4	5	5	9	36	15	9
9	18	2	5	16	26	4
8	27	2	16	27	27	5
0	0	0	0	0	1	0
1	63	0	0	116	43	2
4	16	2	4	23	41	10
5	96	0	1	18	63	0
9	12	0	0	7	58	0
34	12	0	0	6	5	0
3	19	0	2	14	36	7
2	106	2	1	22	26	1
18	68	0	2	64	28	10
3	9	1	0	4	21	0
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0	1	0	0	1	6	0
0	0	0	0	1	0	0
2	3	1	5	20	4	9
0	0	0	0	0	0	0
U	U	U	U	U	U	U

0	0	0	0	0	1	0
27	45	4	41	75	76	11
16	20	3	6	84	122	8
0	0	0	0	0	0	0
15	59	0	2	82	51	3
0	0	0	0	0	0	0
1	2	0	0	0	2	0
2	4	0	0	0	0	0
0	3	0	0	1	0	0
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0	4	0	1	4	5	0
15	29	0	0	10	27	3
0	0	0	0	1	0	1
0	0	0	0	0	2	0
0	1	0	0	4	2	0
1	3	1	2	19	18	1
0	0	0	0	0	1	0
0	0	1	18	3	1	7
1	2	0	0	1	1	0
0	2	0	0	0	1	0
56	110	1	23	195	247	74
4	16	0	2	7	9	24
12	22	2	18	12	34	11
0	37	0	8	12	6	15
0	1	0	0	11	36	0
1	2	0	0	0	2	0
0	0	0	0	1	1	0
3	4	0	3	3	5	0
1	8	2	0	1	12	0
1	0	0	0	0	0	0
5	5	0	13	39	7	4
8	24	0	1	42	54	4
0	0	1	0	0	1	0
1	1	0	0	2	4	0

SG1-TOP-201	SG1-TOP-201SG1-TOP-201SG1-TOP-201SG1-TOP-201SG1-TOP-201SG1-TOP-201							
0	0	0	0	0	0	0		
0	0	0	0	0	0	0		
4	5	13	4	1	4	1		
0	0	0	0	0	1	0		
0	0	0	0	1	0	0		
3	0	0	0	0	0	0		
1	2	2	4	0	0	0		
0	0	0	1	0	0	0		
0	0	0	0	0	0	0		
0	0	0	0	0	0	0		
0	1	0	0	0	0	1		
0	0	0	0	0	0	0		
8	2	0	0	3	3	0		
0	2	0	2	0	4	4		
0	0	3	0	0	0	0		
4	0	13	3	19	1	1		
146	0	6	0	28	0	1		
1	2	0	0	0	6	0		
1	0	4	0	0	0	0		
0	0	0	0	0	0	0		
0	0	0	0	12	0	0		
3	0	1	1	2	0	0		
0	0	0	0	0	0	0		
0	0	0	0	0	0	0		
5	0	2	0	14	0	0		
0	0	0	0	0	0	0		
0	0	0	0	0	0	0		
27	0	10	1	31	0	2		
0	0	1	0	0	0	0		
0	4	0	5	0	1	2		
1	0	3	0	0	0	0		
0	0	0	0	5	0	0		
0	0	0	0	1	0	0		
0	0	0	0	0	0	0		
0	0	0	0	0	0	0		
3	0	6	0	5	0	0		
0	0	0	0	1	0	0		
0	0	0	0	0	0	1		
0	0	0	0	0	0	0		
0	0	0	0	0	0	0		
1	0	0	0	0	0	0		
0	0	0	0	0	0	0		
2	0	10	0	15	0	0		
23	0	49	1	8	2	2		

2	0	0	0	0	0	0
4	14	29	17	0	3	3
0	0	1	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	1
0	0	0	0	2	0	0
161	51	195	33	65	20	33
0	0	0	0	0	0	0
0	0	0	0	0	0	1
0	0	0	0	0	0	1
1	0	3	1	1	0	2
0	0	0	0	0	0	0
0	0	1	1	0	0	1
0	0	23	1	0	0	3
0	3	1	7	0	1	0
0	0	2	0	3	0	1
2	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	1	0	0
0	0	0	0	0	0	0
224	567	160	230	74	489	115
0	0	0	0	0	0	0
1	0	0	0	1	0	0
0	2	1	2	0	1	1
12	2	6	0	8	0	0
0	0	0	2	0	0	0
0	1	0	0	0	0	0
0	0	0	0	0	0	0
0	0	1	0	2	0	0
0	0	0	0	0	0	0
0	0	0	0	10	0	0
3	0	2	0	0	0	0
0	0	2	0	0	0	0
0	0	0	0	0	0	0
5	0	2	0	4	1	0
0	0	0	0	0	0	0
0	0	0	0	0	1	0
0	0	0	0	0	0	0
25	0	8	0	25	0	0
0	0	0	0	3	0	0
0	0	0	0	0	0	2
4	4	75	1	3	6	1
0	0	0	0	0	0	0

0	0	0	0	0	0	0
2	0	10	0	1	0	0
0	0	0	0	0	1	1
0	0	0	0	0	0	0
0	0	0	0	0	0	0
1	0	0	0	0	0	1
3	1	5	0	1	2	0
0	0	0	0	0	0	0
12	0	27	0	18	0	3
33	3	38	1	32	1	3
8	5	12	1	10	7	2
0	1	3	1	0	0	0
19	5	31	5	17	3	8
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9	6	10	15	18	2	7
0	0	0	0	1	0	0
0	3	1	5	0	4	0
42	17	132	15	17	11	10
1	0	0	0	0	0	0
7	0	11	1	2	1	2
1	0	0	0	0	0	0
0	2	0	0	0	0	3
0	0	1	0	0	0	0
8	0	31	25	20	6	16
0	0	0	0	1	0	0
356	339	1036	207	263	540	321
15	4	7	0	12	4	3
0	1	2	2	0	0	0
0	0	0	0	1	0	0
0	0	0	0	0	0	0
5	1	22	2	1	3	3
0	1	2	7	2	0	1
13	0	21	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
4	34	9	113	4	22	20
2	9	1	14	3	5	3
0	0	0	0	1	0	0
1	1	3	1	1	1	0
0	0	0	0	1	0	0
0	0	0	0	0	0	0
1	0	0	1	3	1	1
2	0	0	0	1	0	0
4	41	26	30	1	15	6

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0	0	0	0	0	0	0
0	2	6	1	0	0	0
0	0	0	0	0	0	0
3	1	9	2	2	0	0
1	0	4	0	4	0	0
0	0	0	0	0	0	1
0	1	5	3	11	1	0
2	0	0	0	0	0	0
0	0	10	0	1	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
1132	294	1706	169	1124	223	251
5	0	0	0	0	0	0
1	0	1	0	2	0	0
1	0	0	0	0	1	0
0	0	1	0	0	0	0
0	0	0	0	0	0	0
5	0	0	0	0	0	0
0	1	0	0	0	0	0
0	0	0	0	0	0	0
0	1	0	0	0	1	0
2	1	9	0	14	0	1
1	0	0	0	1	0	0
0	0	0	0	0	0	0
31	0	18	1	0	1	5
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	4	0	0	1	0	2
0	0	0	0	0	0	0
0	0	0	0	0	0	0
2	0	1	0	15	2	0
39	0	33	2	331	0	2
0	0	0	0	1	0	0
45	2	49	1	4	0	1
2	2	1	0	2	5	0
59	1	26	2	60	1	3
5	0	29	0	3	0	0
2	0	5	1	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
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0	0	0	0	0	0	0
1	0	0	0	3	0	1
0	0	0	0	3	0	0
1	0	0	0	1	0	0
	-		-	=	=	-

3		0	0	7	0	0
0		0	0	0	0	0
8		22	2	1	2	0
6		6	0	0	0	0
0	0	2	0	0	0	0
0	0	0	0	0	0	0
0		0	1	1	0	1
0		0	0	0	0	1
1		2	1	4	1	4
3		1	1	7	2	1
0		0	0	0	0	0
9	0	8	0	10	0	1
0	0	0	0	0	0	0
0	0	1	1	0	0	0
0	0	0	0	1	0	0
0	0	0	0	0	0	0
1	0	0	1	0	0	0
2	0	1	0	0	0	0
3	0	6	0	4	0	0
0	0	0	0	1	1	0
1	0	0	0	2	0	1
110	20	220	18	58	13	18
13	0	28	1	0	1	1
0	0	0	0	0	2	1
0	0	0	0	0	2	3
1	0	2	0	1	0	1
11	0	11	0	6	0	0
1	24	2	5	4	8	0
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44	1	2	1	23	1	4
31	3	39	7	150	3	11
2	7	9	1	0	1	4
0	7	1	0	0	7	7
0	0	0	0	0	0	0
8	1	19	7	7	0	4
3	0	0	0	1	0	0
0	0	0	0	0	0	0
1	0	0	0	1	0	0
14	69	28	145	37	65	42
0	1	9	1	0	0	3
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	5	1	0	0	0
2	0	5	0	0	0	0
0	0	0	0	0	0	0

0	0	2	0	0	0	0
1	5	10	8	2	0	2
0	0	0	0	0	0	0
0	0	3	0	4	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	1	0	0	0	0
1	11	53	7	1	7	5
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	3	0	2	0	2	2
1	0	2	1	2	0	0
1	0	0	0	13	0	0
1	0	0	0	0	0	0
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0	0	1	0	0	0	0
0	0	0	0	0	0	0
1	5	8	7	1	0	5
0	0	0	0	0	2	0
0	1	13	1	0	1	2
0	0	0	0	0	0	0
0	15	3	14	0	6	1
0	0	1	0	0	0	2
0	0	0	0	0	0	0
1	0	0	0	1	0	0
0	2	2	1	0	2	1
0	0	0	0	0	0	0
4	0	23	0	1	0	0
0	0	0	0	0	0	0
2	4	26	6	0	4	9
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0	1	0	0	0	1	0
0	5	0	0	1	3	6
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0	0	0	0	0	0	0
20	3	11	8	2	2	7
0	0	0	0	0	0	0
0	0	0	0	0	0	0
13	1	5	1	0	0	0
0	0	0	1	0	1	0
0	0	0	0	0	0	0
						_

		_	•		•	
25	0	4	0	6	0	0
0	0	0	0	0	0	0
2	0	1	0	0	0	0
0	1	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
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11	0	59	0	19	0	0
47	11	1	28	36	4	17
305	43	415	103	184	35	79
1	0	6	0	10	0	1
0	0	0	0	1	0	0
0	0	2	0	0	0	0
0	0	3	0	0	0	0
2	5	4	19	4	1	2
6	3	11	4	1	11	0
0	0	0	0	0	0	0
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0	0	2	0	0	0	0
0	0	0	0	0	0	0
1	21	8	16	0	8	5
0	0	0	0	1	0	0
14	7	1	4	14	0	5
5	0	2	0	0	0	0
61	76	- 74	27	26	53	18
1	0	0	1	1	1	0
14	1	17	4	7	0	4
0	0	0	0	0	0	0
0	0	0	0	0	0	0
3	4	11	6	1	1	1
0	0	0	0	0	0	0
13	0	1	0	0	0	0
0	0	0	1	0	0	0
1	0	0	0	0	0	0
0	0	0	0	0	0	0
0				2	0	0
	0	0 1	0			
3	1 2		2	1	0	0
0		19	4	0	4	0
2	0	0	2	0	0	1
1	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
22	16	88	19	22	25	12
2	2	13	16	0	1	3
2	0	1	0	14	0	0

190	34	312	90	151	29	72
0	0	0	0	2	0	0
32	4	20	6	25	2	5
0	0	0	0	0	0	0
2	4	29	0	8	2	3
0	0	0	0	0	1	1
18	12	29	6	28	21	10
251	19	196	29	109	7	27
2	0	38	5	3	0	6
179	36	231	32	176	74	39
6	23	44	23	4	11	6
201	76	480	137	405	122	94
3	0	5	0	20	2	0
8	2	23	2	2	1	9
671	487	1649	383	713	624	509
3	0	4	1	0	0	0
1	0	1	0	2	0	0
75	45	164	29	137	71	59
1	0	1	0	0	0	0
1	0	1	0	0	0	0
9	0	0	0	0	0	0
0	0	1	0	0	0	0
0	0	0	0	0	0	0
1	0	1	0	12	0	0
2	0	8	1	1	0	2
0	0	2	0	0	1	0
10	0	40	1	11	0	0
1	0	7	0	2	0	0
11	42	10	4	2	41	2
0	2	3	0	0	0	1
1	0	0	0	1	0	0
33	4	33	7	63	16	7
14	1	16	2	19	2	2
0	0	0	0	0	0	0
3	17	71	13	2	4	10
115	8	9	1	32	0	47
82	0	107	0	89	0	1
6	56	134	37	6	53	4
88	5	55	3	77	6	4
0	0	4	0	30	0	0
44	5	11	3	17	3	0
6	0	5	0	3	0	0
16	14	13	7	16	14	3
667	15	114	12	222	29	21
0	0	0	0	0	0	0

138	2	156	3	47	7	6
10	0	14	0	7	1	0
0	0	3	2	2	3	1
5	0	220	0	20	0	0
142	83	184	81	23	54	58
13	2	6	1	23	0	5
0	0	0	0	0	0	0
12	21	85	10	22	20	12
15	10	19	8	5	12	6
65	21	116	5	2	9	1
6	11	41	81	8	3	26
0	3	0	14	11	1	2
0	0	1	0	1	1	0
1	9	69	2	4	2	13
0	0	0	0	0	0	0
0	0	0	0	0	0	0
16	3	39	5	47	0	13
1	0	5	6	8	0	8
54	0	1	0	20	0	0
0	0	0	0	0	0	0
3	0	2	0	2	0	0
16	3	86	4	8	4	2
12	1	28	2	17	0	0
1	1	1	0	0	0	0
5	0	3	0	7	0	0
0	0	2	0	0	0	1
0	0	6	0	0	0	0
31	3	10	4	14	4	0
1	0	2	1	2	0	0
1	0	3	0	3	0	1
0	0	1	0	0	0	1
3	3	10	0	13	0	1
4	37	34	37	4	9	43
4	1	7	0	2	0	0
0	0	0	0	1	0	0
0	0	0	0	36	1	2
0	0	8	2	8	2	1
10	24	27	12	0	12	3
2	1	12	0	1	0	3
7	0	5	1	1	0	1
43	1	10	3	41	1	3
20	0	9	0	0	0	0
4	1	6	0	1	1	0
0	0	0	0	0	0	0
1	0	3	0	3	0	0

	_		_		_	_
139	1	14	5	46	2	5
0	0	1	0	0	0	0
0	0	2	0	0	0	0
53	5	31	2	24	10	17
23	0	10	0	23	2	0
15	0	9	0	99	1	1
1	0	0	0	1	0	1
12	3	11	5	8	2	4
0	0	1	1	0	0	1
0	0	0	0	0	0	0
0	0	0	0	0	0	0
39	0	112	0	10	0	0
25	22	77	17	17	3	37
0	0	0	0	3	0	0
0	0	6	0	0	0	0
0	0	1	0	5	0	0
0	0	0	0	2	0	0
80	1	44	3	13	0	4
41	14	331	7	37	5	11
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457	90	679	105	339	134	113
1	2	6	1	0	0	1
4	0	7	0	2	0	1
1	0	4	0	159	0	0
10	5	8	1	2	0	2
0	0	15	0	2	0	0
	10	240	20			
170				89	16	15
16	3	23	8	12	15	4
11	4	42	8	25	4	10
13	8	50	7	5	1	2
0	0	0	0	0	0	0
8	2	17	1	2	0	2
14	5	16	2	5	5	3
0	0	16	3	21	2	26
10	0	20	1	28	0	1
8	0	8	0	14	0	0
94	3	41	1	13	6	3
1	5	8	2	34	0	4
42	10	13	17	5	0	23
2	0	8	0	2	0	0
0	0	0	0	0	0	0
1	0	1	0	0	0	0
0	0	0	0	0	0	0
5	0	7	3	2	2	2
0	0	1	0	0	0	0

0	0	1	0	0	0	0	
20	55	53	17	6	44	8	
33	8	36	6	23	11	2	
0	0	0	0	0	0	0	
32	1	70	2	23	3	4	
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0	0	2	0	1	0	0	
0	0	0	0	2	0	0	
1	0	0	0	0	0	0	
0	0	0	0	0	0	0	
0	0	1	0	0	1	1	
5	0	32	0	19	0	0	
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0	0	0	0	0	0	0	
0	1	1	1	0	0	0	
16	2	13	2	4	1	1	
0	0	0	0	0	0	0	
4	18	6	6	2	24	5	
0	0	2	0	2	0	0	
0	1	0	0	0	0	0	
54	17	120	31	86	9	20	
41	16	17	17	35	2	9	
53	75	14	10	16	29	6	
0	22	17	72	0	8	11	
1	5	5	9	0	2	4	
5	0	1	0	2	0	0	
0	0	0	0	0	0	0	
5	4	1	2	0	1	5	
0	0	1	0	0	0	0	
0	0	0	0	0	0	0	
16	9	6	15	1	7	3	
14	0	19	1	11	0	3	
0	2	1	0	0	0	0	
1	0	2	0	1	1	0	

SG1-TOP-201SG	1-TOP-201SG1-	TOP-201SG1-	TOP-201SG1-	TOP-201SG1-	TOP-201SG1-	-TOP-201
0	0	0	0	0	0	0
0	0	0	0	0	0	0
2	3	23	1	1	1	6
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	1	0	0
0	1	10	0	0	2	0
0	0	0	0	0	0	0
0	0	1	0	1	0	0
0	0	0	0	0	1	0
0	0	0	0	0	0	0
0	0	5	0	0	0	0
0	6	2	0	3	0	13
0	1	0	3	0	0	0
0	2	0	0	0	0	5
3	14	8	4	13	4	13
0	12	12	0	22	1	55
5	0	0	6	0	0	0
0	16	2	2	2	0	2
0	0	0	0	0	0	0
0	0	2	0	0	0	0
0	1	4	0	1	0	5
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	50	75	0	3	0	29
0	0	0	0	0	0	0
0	0	0	0	0	0	0
2	11	15	1	39	0	25
0	1	37	0	0	0	7
0	0	0	0	1	0	1
0	3	4	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	16	7	0	0	0	5
1	0	0	0	0	0	0
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0	0	0	0	0	0	0
0	0	0	0	1	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	5	16	0	4	0	6
1	18	8	1	9	1	32

0	0	0	0	0	0	0
0 5	0 22	41	0 1	0 6	0 0	0 17
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75 0	0	89 0	55 0	116 0	14	82 0
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0	3 17	20	0	0	3	33
0	3	0	0	0	0	33 0
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153	62	81	173	141	21	23
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2	2	5	1	17	3	9
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1	7	2	0	13	0	1
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8	35	57	6	19	3	34
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9	23	8	7	7	8	7
1	2	1	2	3	6	2
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1 8	8	12 2	0		0	15 5
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2	26 16	4	1	1	2	25 1
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0	22	7	0	1	1	10
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1	4	0	1	1	9	1
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0	0	0	0	0	0	1
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0	0	16	0	0	4	2
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0	2	4	2	0	1	0
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0	37	33	0	10	0	80
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0	0	1	0	2	0	3
0	0	0	0	0	0	0
1	13	16	2	3	8	4
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0	6	3	0	0	0	3
0	0	0	0	0	0	0
0	0	0	0	0	0	1

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0	0	0	0	2	0	0
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131	398	427	107	330	20	503
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0	3	17	3	3	2	1
2	6	9	7	9	1	4
0	0	0	0	1	0	0
0	0	0	0	0	0	4
0	0	3	0	0	0	1
0	0	0	0	0	0	0
2	3	29	0	2	3	6
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0	0	1	0	0	0	2
29	76	123	31	36	7	59
0	1	3	0	0	0	1
0	11	11	1	1	3	7
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0	0	0	0	0	0	0
2	3	9	1	0	0	9
0	1	0	0	0	0	0
0	1	1	0	0	0	7
0	0	0	0	0	0	0
0	0	1	0	0	0	1
0	0	1	0	0	0	0
0	0	0	0	0	0	0
2	3	3	1	0	1	2
1	13	10	0	3	0	10
0	1	4	0	0	0	2
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0	0	0	0	0	0	0
22	69	78	22	68	15	29
0	10	16	1	2	0	7
0	0	1	0	4	0	0

147	436	207	139	445	21	199
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3	32	36	1	2	1	43
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6	67	25	22	150	5	33
64	183	241	46	305	15	291
4	35	22	1	2	5	4
30	204	287	36	103	43	214
27	13	18	43	17	13	13
271	589	152	225	561	53	253
0	1	4	0	5	0	8
0	30	29	0	5	6	33
409	1287	2461	470	424	527	2029
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40	124	192	71	104	67	186
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0	0	0	0	0	0	0
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1	2	9	0	0	1	10
0	3	3	0	0	1	5
1	7	20	0	18	2	7
0	3	11	2	3	0	8
4	21	13	7	14	0	5
0	1	2	0	0	0	1
0	0	0	0	0	0	3
5	55	64	11	85	9	43
1	13	15	0	16	0	20
0	0	0	0	0	0	0
1	89	63	0	30	8	69
1	23	14	0	37	29	45
0	185	137	0	17	0	126
8	151	79	8	16	5	44
2	17	37	5	90	5	57
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4	12	20	2	44	1	35
0	5	5	0	3	0	3
16	5	21	17	35	6	9
19	105	156	17	640	7	123
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3	87	124	4	169	0	84	
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83	169	127	60	35	38	98	
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6	77	110	11	40	8	64	
12	43	20	19	22	0	31	
1	170	7	0	1	0	25	
1	45	20	1	10	15	35	
1	6	1	0	1	1	2	
0	1	1	0	0	0	3	
2	62	48	1	5	4	51	
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2	40	132	2	81	11	114	
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1	42	42	1	7	5	83	
5	37	34	1	30	0	33	
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0	5	6	0	1	0	6	
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0	4	1	0	5	0	4	
0	9	6	0	14	0	5	
0	5	2	0	1	1	2	
0	12	21	1	2	1	24	
4	68	31	5	13	47	19	
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2	8	53	1	0	9	11	
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5	8	15	3	51	3	26	
0	7	5	2	1	0	3	
1	4	7	4	2	1	2	
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3	27	60	2	19	5	94
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3	7	56	8	74	13	60
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0	7	3	0	32	0	4
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0	0	1	0	0	0	3
0	0	0	0	1	0	0
0	28	26	1	10	0	40
16	150	86	7	6	14	29
0	4	35	0	0	0	30
0	5	107	0	0	0	109
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0	84	95	1	23	8	126
0	3	2	0	0	1	0
83	646	881	130	334	127	968
2	7	4	1	0	1	7
0	5	1	0	15	1	3
0	9	9	0	6	0	102
9	17	14	5	7	2	9
0	12	2	0	0	0	7
53	214	250	41	332	3	358
7	4	12	7	5	2	15
2	16	21	3	15	9	20
5	33	12	7	7	3	33
0	1	1	0	1	0	1
0	40	21	2	6	1	3
9	15	19	10	32	1	16
1	21	74	0	8	4	25
1	25	23	0	22	0	20
0	2	15	0	10	0	9
2	22	15	7	11	1	12
1	93	39	3	3	2	27
6	64	78	7	5	14	18
0	6	16	0	8	0	21
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7	17	26	6	54	3	24
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0	0	0	0	0	0	0
1	5	3	1	0	0	15
3	20	14	0	11	0	15
0	0	1	0	0	0	0
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2	1	5	1	7	1	6
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5	0	1	8	0	0	0
0	1	0	0	1	0	3
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61	184	72	35	144	8	118
16	13	5	20	19	3	12
6	23	22	13	26	0	18
6	32	16	9	2	5	11
0	6	73	0	1	2	1
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0	8	2	1	2	0	5
0	2	2	0	1	1	5
0	0	2	0	0	0	7
11	2	4	3	17	0	0
3	22	36	4	10	1	53
1	0	0	0	0	0	0
1	0	0	0	1	1	0

SG1-TOP-201SG	1-TOP-201SG1-1	ГОР-201SG1- ⁻	TOP-201SG1-	TOP-201SG1-1	ГОР-201SG1-	TOP-201
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0	2	0	0	0	0	1
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0	0	0	0	0	0	0
0	0	0	0	0	0	0
2	3	1	0	1	0	9
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0	2	0	0	0	0	0
5	7	0	3	0	2	2
0	22	0	1	0	2	54
0	0	1	0	0	0	0
1	1	1	0	0	1	3
0	2	0	0	0	0	0
0	0	0	0	0	0	0
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0	0	0	0	0	1	0
0	0	0	0	0	0	1
0	24	0	0	0	2	76
0	0	0	0	0	0	1
0	0	0	0	0	0	2
0	13	2	3	0	0	34
0	0	0	0	0	1	0
1	0	1	0	1	0	3
1	0	0	0	0	0	0
0	2	0	0	0	0	0
0	0	0	0	0	0	0
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0	0	0	0	0	0	1
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1	0	0	3	1	5	8

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0	0	0	0	0	0	1
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52	65	35	33	18	25	224
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1	0	1	0	0	0	0
0	7	0	1	0	0	1
0	0	5	0	2	0	0
1	0	0	0	0	3	1
0	0	0	0	0	1	1
0	0	0	0	0	0	0
0	0	0	0	0	0	3
0	0	0	0	0	0	0
108	169	257	14	406	28	54
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0	7	0	0	0	0	12
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3	6	3	0	0	1	5
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0	1	0	0	0	0	0
0	0	0	0	0	0	2
0	0	0	0	0	1	4
0	1	0	0	0	0	1
0	11	0	0	0	2	42
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0	1	0	1	0	0	0
0	0	0	0	0	0	0
1	8	0	0	0	2	60
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0	19	0	0	0	6	9
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4	13	4	1	3	7	1
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0	0	0	0	0	0	0
0	1	0	0	0	2	6
0	0	0	0	0	0	0
0	0	0	0	0	0	1
0	0	0	0	0	0	0
0	1	0	1	0	0	0
2	3	1	0	0	0	2
1	0	0	0	0	0	0
0	19	0	1	0	5	39
0	18	0	7	1	9	22
5	5	8	4	0	3	17
0	0	0	2	0	0	0
20	21	4	5	3	1	20
1	0	0	0	0	0	0
3	11	11	2	4	2	7
1	0	0	0	0	0	0
3	0	2	0	13	0	0
8	17	14	10	5	12	33
0	0	0	0	0	0	0
0	3	2	0	0	0	13
0	0	0	0	0	0	0
0	0	1	0	1	0	0
0	0	0	0	0	1	0
9	56	1	2	2	2	20
0	0	0	0	0	0	0
173	251	242	49	207	90	344
1	18	6	0	1	5	19
0	0	1	0	0	0	0
0	0	0	0	0	0	1
0	0	0	0	0	6	0
4	1	0	2	0	0	4
1	0	2	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	1
0	0	0	0	0	0	0
26	22	34	0	63	1	4
2	5	1	0	0	0	2
0	0	0	0	0	0	0
1	2	1	0	3	0	1
0	3 0	0	0	0	0	1
0 0	0	0 1	0 0	0 0	0 0	0
0					0	0
0 5	0 4	0 20	0	0 17		0 8
Э	4	29	9	17	16	ð

				_		_
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0	0	1	0	1	0	0
0	0	0	0	0	0	1
0	1	1	2	2	0	3
0	0	0	0	0	0	0
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1	3	0	1	2	2	1
0	1	0	0	0	0	1
0	13	0	1	0	1	8
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226	699	246	211	93	251	1304
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0	10	1	0	0	0	3
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0	6	0	1	0	0	1
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1	0	0	0	0	0	0
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2	33	0	0	0	16	63
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5	0	1	0	1	1	2
3	30	6	5	1	12	62
0	8	0	3	0	1	10
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0	1	0	0	0	0	0
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0	1	0	0	0	1	0
-	-	-	-	-	=	-

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2	9	0	1	0	1	23
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0	1	0	2	0	0	0
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0	1	0	0	0	0	0
0	2	0	0	0	0	3
45	110	13	20	4	10	157
0	23	0	2	0	4	17
0	0	0	0	0	0	0
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1	0	0	0	0	4	1
1	8	0	1	0	1	3
1	4	6	0	7	0	1
0	0	0	0	0	0	0
7	35	0	1	0	3	34
46	31	3	6	1	12	58
0	4	5	3	7	0	0
0	0	3	0	6	0	0
0	0	0	0	0	0	0
0	12	4	2	3	2	42
0	2	0	1	0	0	0
0	0	0	0	0	0	0
0	1 54	0	0	0	0	1
42 0		26	4 2	39 2	4	48
	0	0			0	1
0 0	0 0	0 0	0 0	0 1	0 0	0 0
0	0	1	0	0	0	0
0				0		
0	0	1	1		0	3
U	0	0	0	0	0	0

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0	0	0	0	3	0	0
0	15	0	0	0	1	43
0	0	0	0	0	0	4
0	0	0	0	0	0	0
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2	0	6	0	3	0	2
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0	0	0	0	0	0	0
1	1	0	0	4	1	3
0	0	0	0	0	0	0
2	2	2	0	0	0	3
0	0	0	0	0	0	0
2	0	4	1	3	0	1
0	0	0	0	1	0	0
0	0	0	0	0	0	0
0	1	0	0	0	0	2
2	0	2	0	0	1	0
0	0	0	0	0	0	0
0	22	0	3	0	0	21
0	0	0	0	0	0	0
3	3	4	1	15	0	3
0	0	0	0	0	0	0
0	0	0	0	0	0	2
0	0	0	0	1	0	0
0	0	0	0	0	0	0
1	0	2	0	2	0	0
0	0	0	0	0	0	2
0	0	0	0	0	0	1
1	10	2	0	1	0	8
0	0	0	0	0	0	0
0	2	0	0	0	0	1
1	2	0	2	0	0	4
0	0	0	0	0	0	0
0	0	0	0	0	0	0

	_	_		_	_	
0	4	0	0	0	1	27
0	0	0	0	0	0	0
7	0	1	0	0	1	0
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0	1	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	16	0	4	0	7	8
4	28	26	0	10	6	24
107	237	77	77	15	66	456
0	1	0	1	0	0	1
0	0	0	0	0	0	0
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0	0	0	0	0	1	2
4	17	19	0	3	0	3
2	9	2	3	0	2	13
0	0	0	0	0	0	0
2	0	0	1	0	0	0
0	0	0	0	0	0	0
0	1	0	0	0	0	0
3	0	9	2	0	0	0
0	0	0	1	0	0	0
0	9	5	0	4	2	6
0	14	0	0	0	0	0
34	36	47	8	45	7	61
0	0	0	0	1	0	0
1	3	3	2	1	0	6
0	0	0	0	0	0	0
0	0	0	0	0	0	0
1	3	4	2	5	0	2
0	0	0	0	0	0	1
0	6	1	1	0	0	1
0	0	1	0	0	0	0
0	1	0	0	0	0	2
0	0	0	0	0	0	0
0	0	0	0	0	0	0
1	2	4	0	1	0	2
0	6	0	4	1	2	1
0	2	0	3	0	1	0
0	0	0	0	0	0	0
0	0	0	0	0	0	1
0	0	0	0	0	0	0
32	33	5	4	4	14	30
1	1	1	1	0	0	0
0	3	0	0	0	1	1

114	140	28	53	31	62	125
0	0	0	1	0	0	1
5	13	3	8	3	2	66
0	1	0	0	0	0	0
3	9	4	0	3	1	5
1	0	0	0	0	0	0
32	16	12	3	2	14	14
74	247	19	82	8	44	341
4	14	1	6	1	1	9
30	111	40	29	31	24	213
32	12	6	5	2	3	19
58	393	18	42	21	87	450
1	2	0	0	0	0	5
0	17	0	21	0	1	0
299	468	385	118	253	103	669
0	0	0	2	0	0	3
0	0	0	0	0	0	3
59	75	29	22	18	13	123
0	0	0	0	0	0	2
2	38	0	0	0	1	5
0	8	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	37	0	0	0	1	115
0	1	2	0	0	0	4
0	0	0	0	0	0	3
3	7	2	4	2	5	27
1	1	0	2	0	0	5
2	7	10	2	1	1	12
0	1	0	2	0	0	0
0	2	0	0	0	0	0
6	26	4	7	1	10	22
1	19	0	0	0	4	19
0	1	0	0	0	0	0
2	6	25	18	1	2	11
1	10	2	1	0	7	28
0	89	0	14	0	26	134
11	17	31	17	18	3	3
5	46	3	10	1	10	102
0	0	0	0	0	18	70
2	19	2	2	0	3	42
2	1	0	2	0	0	1
9	33	6	1	2	8	18
11	357	12	28	15	72	527
0	0	0	0	0	0	0

0	Г1	1	10	г	1.4	167
0 0	51 8	1 0	18 0	5 0	14 1	167 5
1	3	0	0	0	1	4
0	20	0	41	0	2	37
46	83	89	13	93	13	32
0	1	0	1	0	0	0
0	0	0	0	0	0	0
14	15	13	8	5	2	21
14	13	10	2	0	0	2
0	18	4	4	0	8	16
23	20	16	7	8	1	14
4	16	21	0	5	0	0
1	0	0	0	0	0	1
2	3	11	13	3	2	8
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0	0	0	0	0	0	0
2	25	0	7	0	3	17
2	14	1	1	6	2	9
0	0	0	1	0	2	84
0	0	0	0	0	0	0
0	3	1	1	0	0	7
1	8	0	12	11	4	21
2	13	1	1	0	5	20
0	0	0	0	0	0	0
1	6	0	0	0	0	7
1	3	0	0	0	0	0
0	14	1	2	0	0	0
4	21	1	3	0	2	14
1	4	0	0	0	0	7
5	3	0	0	0	1	0
0	1	1	1	0	1	4
3	2	0	6	0	1	20
11	8	113	6	48	3	8
0	2	1	1	0	5	0
0	0	0	0	0	0	0
6	0	1	0	0	4	0
1	1	0	2	0	0	3
0	0	10	6	1	2	5
0 1	1 3	0 0	1 0	0 0	0 0	14 0
3	30	2	3	0	5	61
0	6	2	0	0	0	7
3	1	0	0	2	0	5
0	1	0	0	0	0	0
0	0	0	0	0	0	0
U	U	U	U	U	U	U

0	268	2	47	4	18	46
0	0	0	0	1	0	0
0	0	0	0	1	0	0
15	104	1	9	1	2	40
0	12	1	1	0	1	33
0	14	1	0	0	1	8
0	0	0	0	0	0	1
7	20	2	1	0	1	19
0	0	0	0	0	0	0
0	1	0	0	0	0	2
0	1	0	0	0	0	2
1	1	0	27	0	7	20
3	28	10	22	4	18	112
0	3	0	0	0	5	29
0	1	0	0	0	2	0
0	0	0	1	0	0	0
0	0	0	0	0	0	0
2	10	0	8	0	2	5
3	29	4	43	11	6	67
0	0	0	0	0	0	1
98	415	99	47	66	54	549
0	1	0	0	0	0	4
0	5	0	1	0	2	7
2	4	0	1	0	7	4
4	7	1	2	1	3	6
0	1	0	3	0	1	4
54	247	24	32	2	31	265
7	10	3	1	0	1	61
4	3	3	0	2	0	14
7	3	2	7	13	6	2
0	0	0	0	0	0	0
2	4	3	7	0	0	2
10	8	4	5	0	2	3
0	1	0	3	0	2	7
0	17	0	3	0	6	11
0	14	1	0	0	4	41
3	15	1	4	0	3	36
3	19	2	6	1	1	0
5	30	10	2	10	0	27
0	18	0	3	0	0	20
0	0	0	0	0	0	0
0	1	0	0	0	0	0
0	0	0	0	0	0	1
4	2	3	1	0	0	7
0	0	0	0	0	0	0

0	0	0	0	0	0	0
11	21	46	5	42	5	36
11	34	3	5	4	15	34
0	0	0	0	0	0	1
2	21	1	1	1	4	33
0	0	0	0	0	0	0
0	0	0	0	0	0	1
0	0	0	0	0	0	3
0	0	0	0	0	0	0
0	0	0	0	0	0	1
2	0	1	0	0	0	1
0	9	1	3	0	3	19
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	1
2	4	0	3	0	1	8
0	0	0	0	0	0	0
4	1	11	0	15	2	0
0	2	0	0	0	0	0
0	0	0	0	0	0	0
33	49	23	18	9	23	51
2	3	12	1	5	0	5
12	23	89	13	1	9	35
11	0	101	15	18	0	5
2	0	13	4	4	0	3
0	0	0	0	0	0	2
0	0	0	0	0	0	0
0	1	1	0	0	0	3
0	0	0	0	0	0	0
0	0	0	0	0	0	0
4	11	4	0	25	1	10
8	12	3	2	0	1	11
0	0	1	0	1	0	0
0	0	0	0	0	1	0

SG1-TOP-2015	SG1-TOP-201SG	i1-TOP-201S	G1-TOP-201	SG1-TOP-201:	SG1-TOP-201	SG1-TOP-201
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
1	1	1	1	0	0	0
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0	0	0	0	0	0	0
0	0	0	0	0	0	0
4	2	0	1	1	1	1
0	0	0	0	0	0	0
0	1	0	0	0	0	0
22	0	1	22	0	0	5
96	51	16	15	3	2	0
0	0	0	0	0	0	4
1	0	2	2	0	0	0
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0	0	0	0	0	0	0
3	0	0	6	0	0	1
0	0	0	0	0	0	0
0	0	0	0	0	0	0
26	23	16	12	2	7	0
0	0	2	0	0	0	0
9	1	3	3	0	0	0
65	5	10	29	5	5	2
0	0	2	0	0	0	0
1	0	0	1	0	0	1
0	0	0	0	0	0	0
0	1	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
7	2	0	10	1	1	0
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1	0	0	0	0	0	0
0	1	0	0	0	0	0
0	0	0	0	0	0	0
1	0	0	0	0	2	0
7	3	1	7	1	0	0
23	3	0	16	0	3	1

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0	1	0	0	0	0	0
0	0	0	0	0	1	0
0	0	0	0	0	1	0
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1	0	0	0	0	0	0
175	114	29	109	34	35	36
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5	0	1	0	0	0	0
0	0	0	0	0	0	0
3	1	0	3	0	1	0
0	0	0	0	0	1	0
1	0	0	2	0	0	0
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1	0	0	0	1	0	0
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64	32	8	152	30	22	171
1	0	0	0	0	0	0
3	2	1	0	0	1	0
0	0	0	2	0	0	1
14	8	4	13	1	5	1
0	0	0	0	1	0	0
0	0	0	1	0	0	0
0	0	0	1	0	0	0
4	1	0	0	0	0	0
1	0	0	0	0	0	0
13	35	12	6	5	5	0
0	0	0	0	0	0	0
1	0	0	1	0	0	0
0	0	0	0	0	0	0
10	41	5	21	2	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
39	8	5	45	2	7	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
5	0	2	32	3	0	1
0	0	0	0	0	0	0

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0	3	1	6	0	9	0
0	0	0	0	0	0	0
0	1	1	0	0	2	0
0	1	0	0	0	0	0
0	0	0	1	0	0	0
5	0	2	2	0	2	1
0	0	0	0	0	0	0
11	26	15	12	7	28	0
47	7	25	15	5	8	0
42	7	10	21	4	15	9
1	0	0	1	0	0	0
65	10	5	21	14	4	6
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32	1	0	7	5	0	0
0	0	0	0	0	1	0
0	0	0	1	0	0	0
49	13	8	58	5	15	5
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13	4	1	6	1	3	1
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0	0	0	0	0	0	0
97	6	1	24	16	29	4
1	1	1	1	0	4	0
547	143	66	309	91	85	358
30	5	10	29	2	3	1
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0	0	0	0	0	0	0
0	1	10	31	1	0	0
7	0	3	7	1	2	0
0	0	0	1	0	0	0
0	0	0	3	0	0	0
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0	0	0	0	0	0	0
12	7	2	4	1	2	8
0	0	1	3	0	1	3
0	0	0	0	0	0	0
0	0	0	11	0	0	0
1	0	1	0	0	0	0
0	0	1	0	0	0	0
0	0	0	0	0	0	0
1	0	0	0	0	0	0
2	1	3	68	21	1	1
_	±	3	30	- +	±	_

0	0	0	0	0	1	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
5	0	0	2	1	1	0
3	0	0	9	0	1	0
0	0	0	0	0	0	0
10	1	3	7	3	1	1
0	0	0	0	0	0	0
1	5	0	3	0	1	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
1968	711	395	1199	278	351	186
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T	U	U	U	U	U	U

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127	101	389	96	292	122	104
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81	107	72	27	267	88	67
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1	3	9	11	8	1	5
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3	3	1	0	17	4	9
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SG1-TOP-201

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1 0

4 35

0

0 0

0 0

5 0

6

5 0

0

8

1 10

17

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taxonomy
D 0 Bacteria; D 1 Proteobacteria; D 2 Gammaproteobacteria; D 3 Chromatiales; D 4 Ectothio
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Bacteria; D 1 Cyanobacteria; D 2 Cyanobacteria; D 3 uncultured
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Bacteria; D_1_Proteobacteria; D_2_Deltaproteobacteria; D_3_Desulfuromonadales; D_4 GR-
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Nanohaloarchaeota
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Bacteria; D_1_Proteobacteria; D_2_Gammaproteobacteria; D_3_Alteromonadales; D_4_Shev
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Bacteria; D 1 Proteobacteria; D 2 Gammaproteobacteria; D 3 Chromatiales; D 4 Ectothio
D 0 Bacteria; D 1 Proteobacteria; D 2 Deltaproteobacteria; D 3 Desulfuromonadales; D 4 GR
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Bacteria; D 1 Bacteroidetes; D 2 Cytophagia; D 3 Order II; D 4 Rhodothermaceae; D 5
D 0 Bacteria; D 1 Proteobacteria; D 2 Deltaproteobacteria; D 3 Desulfuromonadales; D 4 GR-
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Bacteria; D 1 Bacteroidetes; D 2 Cytophagia; D 3 Order II; D 4 Rhodothermaceae; D 5
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4 Halobacteriacea
D 0 Bacteria; D 1 Bacteroidetes; D 2 Cytophagia; D 3 Order II; D 4 Rhodothermaceae; D 5
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D_0_Bacteria; D_1_Bacteroidetes; D_2_Cytophagia; D_3_Order II; D_4_Rhodothermaceae; D_5_:
D 0 Bacteria; D 1 Cyanobacteria; D 2 Cyanobacteria; D 3 SubsectionIII; D 4 FamilyI; D 5 un
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Bacteria; D_1_Bacteroidetes; D_2_Cytophagia; D_3_Order II; D_4_Rhodothermaceae; D_5_:
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Bacteria; D 1 Cyanobacteria; D 2 Cyanobacteria; D 3 SubsectionIV; D 4 FamilyI; D 5 Scy
D 0 Bacteria; D 1 Bacteroidetes; D 2 Cytophagia; D 3 Order II; D 4 Rhodothermaceae; D 5
D_0_Bacteria; D_1_Cyanobacteria; D_2_Cyanobacteria; D_3_SubsectionII; D 4 FamilyII; D 5 Ch
D_0_Bacteria; D_1_Bacteroidetes; D_2 Cytophagia; D_3 Order II; D_4 Rhodothermaceae; D_5
D 0 Bacteria; D 1 Proteobacteria; D 2 Gammaproteobacteria; D 3 Chromatiales; D 4 Ectothio
D_0_Bacteria; D_1_Proteobacteria; D_2_Alphaproteobacteria; D_3_Rhizobiales; D_4_Methylobac
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D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea

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D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Bacteria; D_1_Bacteroidetes; D_2_Cytophagia; D_3_Order II; D_4_Rhodothermaceae; D_5_:
D 0 Bacteria; D 1 Firmicutes; D 2 Bacilli; D 3 Bacillales; D 4 Staphylococcaceae; D 5 Staphyl
D 0 Bacteria; D 1 Proteobacteria; D 2 Deltaproteobacteria; D 3 Desulfuromonadales; D 4 GR-
D 0 Bacteria; D 1 Bacteroidetes; D 2 Cytophagia; D 3 Order II; D 4 Rhodothermaceae; D 5
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Bacteria; D 1 Proteobacteria; D 2 Gammaproteobacteria; D 3 Pseudomonadales; D 4 Pse
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Nanohaloarchaeota; D 2 uncultured haloarchaeon; D 3 uncultured haloarchae
D 0 Bacteria; D 1 Bacteroidetes; D 2 Cytophagia; D 3 Order II; D 4 Rhodothermaceae; D 5
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
\label{eq:decomposition} D\_0\_Bacteria; D\_1\_Proteobacteria; D\_2\_Alphaproteobacteria; D\_3\_Sphingomonadales; D\_4\_Sphingomonadales; D\_
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Bacteria; D 1 Bacteroidetes; D 2 Cytophagia; D 3 Order II; D 4 Rhodothermaceae; D 5
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Bacteria; D_1_Cyanobacteria; D_2_Cyanobacteria; D_3_SubsectionII; D_4_FamilyII; D_5_Ch
D_0_Bacteria; D_1_Cyanobacteria; D_2_Cyanobacteria; D_3_SubsectionI; D_4_FamilyI; D_5_Cyar
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Bacteria; D 1 Bacteroidetes; D 2 Cytophagia; D 3 Order II; D 4 Rhodothermaceae; D 5
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D_4_Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Bacteria; D 1 Bacteroidetes; D 2 Cytophagia; D 3 Order II; D 4 Rhodothermaceae; D 5
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Bacteria; D 1 Proteobacteria; D 2 Deltaproteobacteria; D 3 Desulfuromonadales; D 4 GR-
D_0_Bacteria; D_1_Proteobacteria; D_2_Gammaproteobacteria; D_3_Alteromonadales; D_4_Shev
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Bacteria; D 1 Proteobacteria; D 2 Alphaproteobacteria; D 3 Sphingomonadales; D 4 Sphi
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D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Bacteria; D 1 Bacteroidetes; D 2 Cytophagia; D 3 Order II; D 4 Rhodothermaceae; D 5
D_0_Bacteria; D_1_Proteobacteria; D_2_Gammaproteobacteria; D_3_Alteromonadales; D_4_Shev
D 0 Bacteria; D 1 Proteobacteria; D 2 Alphaproteobacteria; D 3 Rhizobiales; D 4 Methylobac
D_0_Bacteria; D_1_Bacteroidetes; D_2_Cytophagia; D_3_Order II; D_4_Rhodothermaceae; D_5_:
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Bacteria; D 1 Cyanobacteria; D 2 Cyanobacteria; D 3 SubsectionII; D 4 FamilyII; D 5 Ch
D 0 Bacteria; D 1 Bacteroidetes; D 2 Cytophagia; D 3 Order II; D 4 Rhodothermaceae; D 5
D 0 Bacteria; D 1 Bacteroidetes; D 2 Cytophagia; D 3 Order II; D 4 Rhodothermaceae; D 5
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Bacteria; D 1 Proteobacteria; D 2 Deltaproteobacteria; D 3 Desulfuromonadales; D 4 GR-
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Bacteria; D 1 Proteobacteria; D 2 Alphaproteobacteria; D 3 Sphingomonadales; D 4 Sphi
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Bacteria; D_1_Proteobacteria; D_2_Gammaproteobacteria; D_3_Oceanospirillales; D_4_Halo
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Bacteria; D_1_Bacteroidetes; D_2_Cytophagia; D_3_Order II; D_4_Rhodothermaceae; D_5_:
D 0 Bacteria; D 1 Bacteroidetes; D 2 Cytophagia; D 3 Order II; D 4 Rhodothermaceae; D 5
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Bacteria; D 1 Bacteroidetes; D 2 Cytophagia; D 3 Order II; D 4 Rhodothermaceae; D 5
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Bacteria; D_1_Proteobacteria; D_2_Alphaproteobacteria; D_3_Rhizobiales; D_4 Methylobac
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Bacteria; D_1_Bacteroidetes; D_2_Cytophagia; D_3_Order II; D_4_Rhodothermaceae; D_5_:
D 0 Bacteria; D 1 Proteobacteria; D 2 Gammaproteobacteria; D 3 Pseudomonadales; D 4 Pse
D_0_Bacteria; D_1_Proteobacteria; D_2_Gammaproteobacteria; D_3_Chromatiales; D_4_Ectothio
D 0 Archaea; D 1 Nanohaloarchaeota; D 2 uncultured archaeon; D 3 uncultured archaeon; D 4
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
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D 0 Bacteria; D 1 Proteobacteria; D 2 Deltaproteobacteria; D 3 Desulfuromonadales; D 4 GR-
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Bacteria; D_1_Bacteroidetes; D_2_Cytophagia; D_3_Order II; D_4_Rhodothermaceae; D_5_:
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Bacteria; D_1_Proteobacteria; D_2_Deltaproteobacteria; D_3_Desulfuromonadales; D_4 GR-
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Bacteria; D_1_Cyanobacteria; D_2_Cyanobacteria; D_3_uncultured; D_4_uncultured bacteriu
D 0 Bacteria; D 1 Bacteroidetes; D 2 Cytophagia; D 3 Order II; D 4 Rhodothermaceae; D 5
D 0 Archaea; D 1 Nanohaloarchaeota
D 0 Bacteria; D 1 Bacteroidetes; D 2 Cytophagia; D 3 Order II; D 4 Rhodothermaceae; D 5
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Bacteria; D 1 Proteobacteria; D 2 Gammaproteobacteria; D 3 Oceanospirillales; D 4 Halo
D 0 Bacteria; D 1 Bacteroidetes; D 2 Cytophagia; D 3 Order II; D 4 Rhodothermaceae; D 5
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D_0_Bacteria; D_1_Cyanobacteria; D_2_Chloroplast; D_3_uncultured Chlorophyta; D_4_unculture
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Bacteria; D 1 Cyanobacteria; D 2 Cyanobacteria; D 3 SubsectionIV; D 4 FamilyI
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Bacteria; D_1_Bacteroidetes; D_2_Sphingobacteriia; D_3_Sphingobacteriales; D_4_Chitinoph
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Bacteria; D 1 Bacteroidetes; D 2 Cytophagia; D 3 Order II; D 4 Rhodothermaceae; D 5
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Bacteria; D_1_Cyanobacteria; D_2_Cyanobacteria; D_3_ SubsectionII; D 4 FamilyII; D 5 Ch
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D_0_Bacteria; D_1_Bacteroidetes; D_2_Cytophagia; D_3_Order II; D_4_Rhodothermaceae; D_5_:
D 0 Bacteria; D 1 Bacteroidetes; D 2 Cytophagia; D 3 Order II; D 4 Rhodothermaceae; D 5
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Bacteria; D 1 Proteobacteria; D 2 Alphaproteobacteria; D 3 Rhizobiales; D 4 Methylobac
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Bacteria; D_1_Cyanobacteria; D_2_Cyanobacteria; D_3 SubsectionII; D_4 FamilyII; D_5 Ch
D 0 Bacteria; D 1 Bacteroidetes; D 2 Cytophagia; D 3 Order II; D 4 Rhodothermaceae; D 5
D_0_Bacteria; D_1_Bacteroidetes; D_2_Cytophagia; D_3_Order II; D_4_Rhodothermaceae; D_5_:
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4 Halobacteriacea
D 0 Bacteria; D 1 Cyanobacteria; D 2 Chloroplast
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D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Bacteria; D 1 Cyanobacteria; D 2 Cyanobacteria; D 3 uncultured; D 4 uncultured bacteria
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Bacteria; D 1 Proteobacteria; D 2 Betaproteobacteria; D 3 Burkholderiales; D 4 Comamo
D 0 Bacteria; D 1 Proteobacteria; D 2 Deltaproteobacteria; D 3 Desulfuromonadales; D 4 GR-
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Bacteria; D 1 Proteobacteria; D 2 Deltaproteobacteria; D 3 Desulfuromonadales; D 4 GR
D_0_Bacteria; D_1_Bacteroidetes; D_2_Sphingobacteriia; D_3_Sphingobacteriales; D_4_Chitinoph
D 0 Bacteria; D 1 Bacteroidetes; D 2 Cytophagia; D 3 Order II; D 4 Rhodothermaceae; D 5
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Bacteria; D 1 Bacteroidetes; D 2 Cytophagia; D 3 Order II; D 4 Rhodothermaceae; D 5
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Bacteria; D 1 Cyanobacteria; D 2 Cyanobacteria; D 3 SubsectionII; D 4 FamilyII; D 5 Ch
D 0 Bacteria; D 1 Bacteroidetes; D 2 Cytophagia; D 3 Order II; D 4 Rhodothermaceae; D 5
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Bacteria; D_1_Proteobacteria; D_2_Gammaproteobacteria; D_3_Oceanospirillales; D_4_Halo
D 0 Bacteria; D 1 Proteobacteria; D 2 Gammaproteobacteria; D 3 Oceanospirillales; D 4 Halo
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Bacteria; D 1 Proteobacteria; D 2 Gammaproteobacteria; D 3 Oceanospirillales; D 4 Halo
D_0_Archaea; D_1_Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D_0_Bacteria; D_1_Bacteroidetes; D_2_Cytophagia; D_3_Order II; D_4_Rhodothermaceae; D_5_:
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Bacteria; D 1 Proteobacteria; D 2 Gammaproteobacteria; D 3 Alteromonadales; D 4 Shev
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Bacteria; D 1 Proteobacteria; D 2 Gammaproteobacteria; D 3 Enterobacteriales; D 4 Enterobacteria
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D 0 Bacteria; D 1 Cyanobacteria; D 2 Cyanobacteria; D 3 SubsectionIII; D 4 FamilyI; D 5 un
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D_0_Bacteria; D_1_Bacteroidetes; D_2_Cytophagia; D_3_Order II; D_4_Rhodothermaceae; D_5_:
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Bacteria; D 1 Proteobacteria; D 2 Deltaproteobacteria; D 3 Desulfuromonadales; D 4 GR-
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Bacteria; D 1 Proteobacteria; D 2 Gammaproteobacteria; D 3 Oceanospirillales; D 4 Halo
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Bacteria; D 1 Proteobacteria; D 2 Deltaproteobacteria; D 3 Desulfuromonadales; D 4 GR-
D 0 Bacteria; D 1 Cyanobacteria; D 2 Cyanobacteria; D 3 uncultured; D 4 uncultured bacteria
D_0_Bacteria; D_1_Bacteroidetes; D_2_Cytophagia; D_3_Order II; D_4_Rhodothermaceae; D_5_:
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Bacteria; D 1 Proteobacteria; D 2 Alphaproteobacteria; D 3 Rhodospirillales; D 4 Rhodos
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Bacteria; D 1 Cyanobacteria; D 2 Cyanobacteria; D 3 uncultured bacterium; D 4 uncultur
D 0 Bacteria; D 1 Bacteroidetes; D 2 Cytophagia; D 3 Order II; D 4 Rhodothermaceae; D 5
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Bacteria; D_1_Proteobacteria; D_2_Alphaproteobacteria; D_3_Rhizobiales; D_4_Methylobac
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Bacteria; D 1 Bacteroidetes; D 2 Cytophagia; D 3 Order II; D 4 Rhodothermaceae; D 5
D_0_Bacteria; D_1_Proteobacteria; D_2_Gammaproteobacteria; D_3 Oceanospirillales; D_4 Halo
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Bacteria; D 1 Proteobacteria; D 2 Gammaproteobacteria; D 3 Oceanospirillales; D 4 Halo
D 0 Bacteria; D 1 Bacteroidetes; D 2 Cytophagia; D 3 Order II; D 4 Rhodothermaceae; D 5
D 0 Bacteria; D 1 Bacteroidetes; D 2 Cytophagia; D 3 Order II; D 4 Rhodothermaceae; D 5
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
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D 0 Bacteria; D 1 Proteobacteria; D 2 Gammaproteobacteria; D 3 Chromatiales; D 4 Ectothio
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Bacteria; D 1 Cyanobacteria; D 2 Cyanobacteria; D 3 SubsectionII; D 4 FamilyII; D 5 Ch
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Bacteria; D 1 Bacteroidetes; D 2 Cytophagia; D 3 Order II; D 4 Rhodothermaceae; D 5
D 0 Bacteria; D 1 Bacteroidetes; D 2 Cytophagia; D 3 Order II; D 4 Rhodothermaceae; D 5
D 0 Bacteria; D 1 Bacteroidetes; D 2 Cytophagia; D 3 Order II; D 4 Rhodothermaceae; D 5
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Bacteria; D 1 Proteobacteria; D 2 Alphaproteobacteria; D 3 Sphingomonadales; D 4 Sphi
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Bacteria; D_1_Bacteroidetes; D_2_Cytophagia; D_3_Order II; D_4_Rhodothermaceae; D_5_
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Bacteria; D 1 Bacteroidetes; D 2 Cytophagia; D 3 Order II; D 4 Rhodothermaceae; D 5
D 0 Bacteria; D 1 Actinobacteria; D 2 Actinobacteria; D 3 Propionibacteriales; D 4 Propioniba
D 0 Bacteria; D 1 Proteobacteria; D 2 Gammaproteobacteria; D 3 Chromatiales; D 4 Ectothio
D_0_Bacteria; D_1_Planctomycetes; D_2_Phycisphaerae; D_3_Phycisphaerales; D_4_Phycisphaera
D_0_Bacteria; D_1_Proteobacteria; D_2_Deltaproteobacteria; D_3_Desulfuromonadales; D_4_GR-
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Bacteria; D 1 Proteobacteria; D 2 Alphaproteobacteria; D 3 Rhodospirillales; D 4 Acetobacteria
D_0_Bacteria; D_1_Bacteroidetes; D_2_Cytophagia; D_3_Order II; D_4_Rhodothermaceae; D_5_:
D 0 Bacteria; D 1 Actinobacteria; D 2 Actinobacteria; D 3 Corynebacteriales; D 4 Nocardiacea
Unassigned
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
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D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D_0_Bacteria; D_1_Bacteroidetes; D_2_Cytophagia; D_3_Order II; D_4_Rhodothermaceae; D_5_:
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
Unassigned
D 0 Archaea; D 1 Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
Unassigned
D 0 Bacteria; D 1 Cyanobacteria; D 2 Cyanobacteria; D 3 SubsectionIII; D 4 FamilyI; D 5 un
D_0_Bacteria; D_1_Bacteroidetes; D_2_Cytophagia; D_3_Order II; D_4 Rhodothermaceae; D_5
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Bacteria; D_1_Bacteroidetes; D_2_Cytophagia; D_3_Order II; D_4_Rhodothermaceae; D_5_:
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Bacteria; D 1 Bacteroidetes; D 2 Cytophagia; D 3 Order II; D 4 Rhodothermaceae; D 5
D 0 Bacteria; D 1 Proteobacteria; D 2 Deltaproteobacteria; D 3 Desulfuromonadales; D 4 GR-
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D_0_Bacteria; D_1_Cyanobacteria; D_2_Chloroplast
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Bacteria; D 1 Actinobacteria; D 2 Nitriliruptoria; D 3 Euzebyales; D 4 Euzebyaceae; D 5
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Bacteria; D 1 Bacteroidetes; D 2 Cytophagia; D 3 Order II; D 4 Rhodothermaceae; D 5
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Bacteria; D_1_Bacteroidetes; D_2_Cytophagia; D_3_Order II; D_4_Rhodothermaceae; D_5_:
D 0 Bacteria; D 1 Cyanobacteria; D 2 Chloroplast
D 0 Bacteria; D 1 Bacteroidetes; D 2 Cytophagia; D 3 Order II; D 4 Rhodothermaceae; D 5
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D 0 Bacteria; D 1 Cyanobacteria; D 2 Chloroplast
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
Unassigned
Unassigned
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
Unassigned
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Bacteria; D 1 Bacteroidetes; D 2 Cytophagia; D 3 Order II; D 4 Rhodothermaceae; D 5
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D_0_Bacteria; D_1_Bacteroidetes; D_2_Cytophagia; D_3_Order II; D_4_Rhodothermaceae; D_5_:
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Bacteria; D_1_Planctomycetes; D_2_Phycisphaerae; D_3_Phycisphaerales; D_4_Phycisphaera
D_0_Bacteria; D_1_Bacteroidetes; D_2_Cytophagia; D_3_Order II; D_4_Rhodothermaceae; D_5_:
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Bacteria; D_1_Bacteroidetes; D_2_Cytophagia; D_3_Order II; D_4_Rhodothermaceae; D_5_:
D_0_Bacteria; D_1_TM6; D_2_uncultured bacterium; D_3_uncultured bacterium; D_4_uncultured
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Nanohaloarchaeota
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Bacteria; D 1 Bacteroidetes; D 2 Cytophagia; D 3 Order II; D 4 Rhodothermaceae; D 5
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Bacteria; D 1 Bacteroidetes; D 2 Cytophagia; D 3 Order II; D 4 Rhodothermaceae; D 5
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
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D 0 Bacteria; D 1 Bacteroidetes; D 2 Cytophagia; D 3 Order II; D 4 Rhodothermaceae; D 5
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Bacteria; D 1 Proteobacteria; D 2 Gammaproteobacteria; D 3 Chromatiales; D 4 Ectothio
D_0_Bacteria; D_1_Bacteroidetes; D_2_Cytophagia; D_3_Order II; D_4_Rhodothermaceae; D_5_:
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Bacteria; D_1_Bacteroidetes; D_2_Cytophagia; D_3_Order II; D_4_Rhodothermaceae; D_5_:
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Bacteria; D 1 Cyanobacteria; D 2 Cyanobacteria; D 3 SubsectionIII; D 4 FamilyI
D_0_Bacteria; D_1_Cyanobacteria; D_2_Cyanobacteria; D_3_SubsectionIII; D_4_FamilyI; D_5_un
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Bacteria; D_1_Bacteroidetes; D_2_Cytophagia; D_3_Order II; D_4_Rhodothermaceae; D_5_:
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Bacteria; D 1 Bacteroidetes; D 2 Cytophagia; D 3 Order II; D 4 Rhodothermaceae; D 5
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Nanohaloarchaeota; D 2 uncultured haloarchaeon; D 3 uncultured haloarchae
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D_0_Bacteria; D_1_Bacteroidetes; D_2_Cytophagia; D_3_Order II; D_4_Rhodothermaceae; D_5_:
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Bacteria; D_1_Bacteroidetes; D_2_Cytophagia; D_3_Order II; D_4_Rhodothermaceae; D_5_:
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D_0_Bacteria; D_1_Bacteroidetes; D_2_Cytophagia; D_3_Order II; D_4_Rhodothermaceae; D_5_:
D 0 Bacteria; D 1 Bacteroidetes; D 2 Cytophagia; D 3 Order II; D 4 Rhodothermaceae; D 5
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D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
Unassigned
Unassigned
D 0 Archaea; D 1 Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Bacteria; D 1 Planctomycetes; D 2 Phycisphaerae; D 3 Phycisphaerales; D 4 Phycisphaera
Unassigned
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
Unassigned
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Archaea; D_1_Nanohaloarchaeota; D_2_uncultured archaeon; D_3_uncultured archaeon; D_4
D 0 Archaea; D 1 Nanohaloarchaeota; D 2 uncultured haloarchaeon; D 3 uncultured haloarchae
D 0 Bacteria; D 1 Cyanobacteria; D 2 Chloroplast
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4 Halobacteriacea
D 0 Bacteria; D 1 Cyanobacteria; D 2 Cyanobacteria; D 3 SubsectionII; D 4 uncultured; D 5
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Sequence

ACGTGCCAGCAGCCGCGGTAATACGGAGGGCGCAAGCGTTAATCGGAATTACTGGGCGTAAAGTGCGC(GTGCCAGCCGCGCGGTAATACCGGCAGCACAAGTGATGGCCGATTTTATTGGGCCTAAAGCGTCCGTA(ACGTGTCAGCCGCCGCGGTAATACCGGCAGCTCGAGTGATGACCGATCTTATTGGGCCTAAAGCGTCCG1 CACTCCTACGGGGGCAGCAGTGGGGAATTTTCCGCAATGGGCGAAAGCCTGACGGAGCAATACCGCGT(GTGTCAGCCGCCGCTAATACCGGAAGCCCGAGTGATGGCCGATATTATTGGGCCTAAAGCGTCCGTA GTGTCAGCCGCCGCGGTAATACCGGCAGCCCGAGTGATGGCCGATATTATTGGGCCTAAAGCGTCCGTA+ GTGTCAGCCGCCGCGGTAATACCGGCAGCTCGAGTGATCGACCGATTTTATTGGGCCTAAAGCGTCCGTA(GTGTCAGCAGCCGCGGTAATACCGGCAGCGCGAGTGATGGCCGATCTTATTGGGCCTAAAGCGTCCGTA CGTGCCAGCAGCCGCGGTAAGACGGAGGGTGCAAGCGTTGTTCGGAATCATTGGGCGTACAGGGCGCG CGTGTCAGCCGCCGCGGTAACACCGGCAGCCCGAGTGATGGCCGATCTTATTGGGCCTAAAGCGTCCGT/ GTGTCAGCCGCCGCGGTAATACCGGCAGTCCGAGTGATGGCCGATATTATTGGGCCTAAAGCGTCCGTA(GTGTCAGCCGCCGCGGTAATAGCAGAACCCCGAGTGGTAGTCATTATTATTGGGTTTAAAGTGTTCGTAG ACGTGTCAGCAGCCGCGGTAATACCGGCAGCCCGAGTGATGGCCGCTATTATTGGGCCTAAAAGCGTCCG ACGTGCCAGCCGCCGCTAATACGGAGGGTGCGAGCGTTAATCGGAATTACTGGGCGTAAAGCGTGC(GTGCCAGCCGCGCGGTAATACCGGCAGCACGAGTGATCGATTTTATTGGGCCTAAAGCGTCCGTA(ACGTGTCAGCCGCCGCGGTAATACCGGCAGCACGAGTGATGGCCGATATTATTGGGCCTAAAGCGTCCG CGTGTCAGCCGCCGCGGTAATACGGAGGGTGCAAGCGTTAATCGGAATCACTGGGCGTAAAGGGCACG GTGCCAGCAGCCGCGGTAAGACGGAGGGTGCAAGCGTTGTTCGGAATCATTGGGCGTAAAGGGCACGC CGTGCCAGCCGCCGCGGTAATACCGGCAGCACGAGTGATGGCCGATCTTATTGGGCCTAAAGCGTTCGT/ CCGCCAATTTCTTTGAGTTTCAACCTTGCGATCGTACTCCCCAGGTGGAATGCTTAACGCGTTAACTTAGC(CGTGCCAGCAGCCGCGGTAAGACGGAGGGTGCAAGCGTTGTTCGGAATCATTGGGCGTACAGGGTGCG ACGTGTCAGCCGCCGCGGTAATACCGGCAGCACGAGTGATGGCCGATATTATTGGGCCTAAAGCGTCCG GTGGCTGCAGCCGCGGTAATACCGGCAGCACGAGTGATGGCCGATATTATTGGGCCTAAAGCGTCCGTA GCCGTCAATTCCTTTGAGTTTCAACCTTGCGATCGTACTCCCCAGGCGGAATGCTTAACGCGTTAGCTTAG ACGTGTCAGCCGCCGGTAATACCGGCAGCCCGAGTGATGGCCGATCTTATTGGGCCTAAAGCGTCCG⁻ GCCGTCAATTTATTTAAGTTTCAACCTTGCGATCGTACTCCCCAGGCGGAATGCTTAACGCGTTAACTTAG GTGTCAGCCGCCGCGGTAATACCGGCAGCTCGAGTGATGGCCGCTATTATTGGGCCTAAAGCGTCCGTA(CGTGTCAGCAGCCGCGGTAATACGGAGGGTGCAAGCGTTGTCCGGAATCACTGGGCGTAAAGGGTGTG GTGTCAGCAGCCGCGGTAATACGGAGGAGGCAAGCGTTATTCGGAATTATTGGGCGTAAAGCGTCCGCA GTGCCAGCCGCCGCTAATACCGGCAGCACAAGTGATGGCCGCTTTTATTGGGCCTAAAGCGTCCGTA(CGTGCCAGCAGCCGCGGTAATACCGGCAGCCCAAGTGATGGCCGATCTTATTGGGCCTAAAGCGTCCGT/ CGTGCCAGCCGCGCGGTAATACCGGCAGCACGAGTGATGGCCGATCTTATTGGGCCTAAAGCGTTCGT/ ACGTGTCAGCCGCCGCGGTAACACCCGGCAGCCCAAGTGATGGCCGCTATTATTGGGCCTAAAGCGTCCG ACGTGCCAGCCGCCGGTAATACGGAGGGTGCAAGCGTTGTCCGGAATCACTGGGCGTAAAGGGTGC GTGCCAGCCGCGGTAATACCGGCAGCCCGAGTGATGGCCGATATTATTGGGCCTAAAGCGTCCGTA GTGTCAGCCGCCGCGGTAATACCGGCAGCTCGAGTGATGGCCGATCTTATTGGGCCTAAAGCGTCCGTA(CACTCCTACGGGAGGCAGCAGTGGGGAATTTTCCGCAATGGGCGAAAGCCTGACGGAGCAATACCGCG1 ACGTGCCAGCCGCCGCTAATACGGAGGGTCCAAGCGTTGTCCGGAATCACTGGGCGTAAAGTGTGTC TACACTCCTACGGAGGCAGCAGTGGGGAATTTTCCGCAATGGGCGAAAGCCTGACGGAGCAATACCGCC ACGTGTCAGCCGCCGCGGTAATACGGAGGGTCCAAGCGTTGTCCGGAATCACTGGGCGTAAAGGGTGT(TTGCCAGCCGCGCGGTAATACGGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGGGCACGC/ CGTGCCAGCAGCCGCGGTAATACGAAGGGGGCTAGCGTTGCTCGGAATCACTGGGCGTAAATGGCGCGC ACGTGTCAGCCGCCGCGGTAATACCGGCAGCACAAGTGATGGCCAATATTATTGGGCCTAAAGCGTCCG⁻ GTGTCAGCCGCCGCGGTAATACCGGCAGCCCGAGTGATGGCCGCTGTTATTGGGCCTAAAGCGTCCGTA+

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GTGTCAGCCGCCGCGGTAATACGGAGGAGGCAAGCGTTATTCGGAATTATTGGGCGTAAAGCGTCCGCA GTGTCAGCCGCCGCTAACACCGGCAGCCCGAGTGATGGCCGATATTATTGGGCCTAAAGCGTCCGTA GTGTCAGCAGCCGCGGTAACACCGGCAGCCCGAGTGATGGCCGATATTATTGGGCCTAAAGCGTCCGTA ACGTGTCAGCCGCCGCGGTAATACGGAGGGTGCAAGCGTTGTCCGGAATCACTGGGCGTAAAGGGTGT(CGTGTCAGCAGCCGCGGTAATACCGGCAGTCCGAGTGATGGCCGATTTTATTGGGCCTAAAGCGTCCGT/ CGTGTCAGCAGCCGCGGTAAGACGGAGGGTGCAAGCGTTGTTCGGAATCATTGGGCGTAAAGGGCGCG GTGCCAGCCGCGGGTAACACCGGCAGCCCGAGTGATGGCCGATATTATTGGGCCTAAAGCGTCCGTA GTGTCAGCCGCCGCGGTAATACCGGCAGCTCAAGTGATCACCGATCTTATTGGGCCTAAAGCGTCCGTA(CGTGCCAGCCGCGCGGTAATACCGGCAGCCCGAGTGATGGCCGATCTTATTGGGCCTAAAGCGTCCGT/ ACGTGCCATCCGCCGCGGTAATACCGGCAGCGCAAGTGATGGCCGATCTTATTGGGCCTAAAGCGTCCG GTGTCAGCCGCCGCGTAATACGGAGGGTGCGAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGT/ GTGTCAGCCGCCGCTAATACCGGCAGCCCGAGTGATGGCCGATCTTATTGGGCCTAAAGCGTCCGTA(ACGTGCCAGCCGCCGCTAAGACGGAGGGTGCAAGCGTTGTTCGGAATCATTGGGCGTACAGGGTGC ACTCCTAGGGAGGCAGCAGTGGGGAATTTTCCGCAATGGGCGCAAGCCTGACGGAGCAATACCGCGTG(CGTGTCAGCAGCCGCGGTAATACGGAGGGTCCAAGCGTTGTCCGGAATCACTGGGCGTAAAGGGTGTG(GTGTCAGCCGCCGCGGTAATACCGGCAGTCCGAGTGATGGCCGCTATTATTGGGCCTAAAGCGTCCGTA(CCGTGCCAGCCGCCGGTAATACCGGCAGCACAAGTGATGGCCGATATTATTGGGCCTAAAGCGTCCG GTGCCAGCAGCCGCGTAACACCGGCAGCCCGAGTGATGGCCGATATTATTGGGCCTAAAGCGTCCGTA GTGTCAGCCGCCGCGGTAATACCGGCAGCCCGAGTGATGGCCGCTATTATTGGGCCTAAAGCGTCCGTA(GTGCCAGCCGCGGTAATACCGGCAGCACGAGTGATGGCCGCTATTATTGGGCCTAAAGCGTCCGTA GTGTCAGCCGCCGCTAACACCGGCAGCCCGAGTGATGGCCGATATTATTGGGCCTAAAGCGTCCGTA ACGTGTCAGCCGCCGGTAACACCGGCAGCCCAAGTGATGGCCGCTGTTATTGGGCCTAAAGCGTTCG⁻ CGTGTCAGCAGCCGCGGTAATACGGAGGGGGCTAGCGTTGTTCGGAATCACTGGGCGTAAAGGGCGCG ACGTGTCAGCCGCCGCGGTAATACCGGCAGCTCGAGTGATGACCGATGTTATTGGGCCTAAAGCGTCCG⁻ GTGTCAGCCGCCGCTAACACCGGCAGCCCGAGTGATGGCCGATATTATTGGGCCTAAAGCGTCCGTA TACACTCCTACGGAGGCAGCAGTGGGGAATTTTCCGCAATGGGCGAAAGCCTGACGGAGCAATACCGCC GTGTCAGCAGCCGCGGTAATACGGAGGGTCCAAGCGTTGTCCGGAATCACTGGGCGTAAAGGGTGTGC/ CGTGTCAGCCGCCGCGGTAATACCGGCAGCACAAGTGATGGCCGCTTTTATTGGGCCTAAAGCGTCCGT/ ACGTGCCAGCCGCCGGTAATACGTAGGGGGCTAGCGTTGCTCGGAATCACTGGGCGTAAAGGGCGC(ACGTGCCAGCCGCCGCGGTAATACCGGCAGCACGAGTGATGGCCGATTTTATTGGGCCTAAAGCGTCCG CGTGTCAGCAGCCGCGGTAATACCGGCAGTCCGAGTGATGGTCGATATTATTGGGCCTAAAGCGTCCGT/ GTGTCAGCCGCCGCGGTAATACCGGCAGTCCAAGTGATGGCCGCTATTATTGGGCCTAAAGCGTTCGTA(CGTGTCAGCCGCCGCGGTAATACCGGCAGCCCGAGTGATGGCCGATTTTATTGGGCCTAAAGCGTCCGT/ ACGTGTCAGCAGCCGCGGTAATACGGAGGGTGCAAGCGTTGTCCGGAATCACTGGGCGTAAAGGGTGT(ACGTGTCAGCCGCCGCGGTAATACGGAGGGTGCGAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCC GTGTCTGCCGCCGCGGTAATACCGGCAGCTCAAGTGATGGCCGATATTATTGGGCCTAAAGCGTCCGTA(GTGTCAGCAGCCGCGGTAATACGGAGGGTGCGAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGT/ ACGTGTCAGCTGCCGCGGTAATACGGAGGGTCCAAGCGTTGTCCGGAATCACTGGGCGTAAAGGGTGTC CGTGCCAGCCGCCGCGGTAATACGGAGGGTCCAAGCGTTGTCCGGAATCACTGGGCGTAAAGGGTGTG(GTGTCAGCCGCCGCTAATACCGGCAGCACGAGTGATGGCCGATATTATTGGGCCTAAAGCGTCCGTA CGTGCCAGCCGCGCGGTAATACCGGCAGCCCGAGTGATGGCCGATATTATTGGGCCTAAAGCGTTCGT/ CTTGCCAGCCGCGGGTAATACCGGCAGCCCGAGTGATGGCCGATCTTATTGGGCCTAAAGCGTCCGT/ GTGTCAGCCGCCGCGGTAATACCGGCAGCACGAGTGATGGCCGCTATTATTGGGCCTAAAGCGTCCGTA ACGTGCCAGCCGCCGCTAATACCGGCAGTCCAAGTGATGGCCGCTGTTATTGGGCCTAAAGCGTCCG⁻ GTGCCAGCCGCGGGTAATACCGGCAGCACGAGTGATGACCGATTTTATTGGGCCTAAAGCGTCCGTA(

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ACGTGCCAGCCGCCGGTAATACCGGCAGCACGAGTGATGGCCGATTTTATTGGGCCTAAAGCGTCCG CGTGTAAGCCGCCGCGGTAATACCGGCAGCACGAGTGATGGCCGATATTATTGGGCCTAAAGCGTCCGT ACGTGTCAGCAGCCGCGGTAATACCGGCAGCCCGAGTGATGGCCGATATTATTGGGCCTAAAGCGTCCG GTGTCAGCCGCCGCGGTAATACGGAGGGTGCAAGCGTTGTCCGGAATCACTGGGAGTAAAGGGTGTGC GTGCGAGCAGACGCGGTAACACCGGCAGCACGAGTGATGGCAGATATTATTGGGCCTAAAGCGACCGT/ TCGTGTCAGCCGCCGGTAACACCGGCAGCCCGAGTGATGGCCGATATTATTGGGCCTAAAGCGTCCG⁻ ACGTGCCAGCCGCCGGTAATACCGGCAGCACGAGTGATGGCCGATATTATTGGGCCTAAAGCGTCCG CCTGTCAGCAGCCGCGGTAATACCGGCAGCACAAGTGATGGCCGATATTATTGGGCCTAAAGCGTCCGT/ CGTGTCAGCAGCCGCGGTAATACCGGCAGCACGAGTGATGGCCGATATTATTGGGCCTAAAGCGTTCGT/ GTGTCAGCAGCCGCGGTAACACCGGCAGCCCGAGTGATGGCCGATATTATTGGGCCTAAAGCGTCCGTA ACGTGTCAGCAGCCGCGGTAATACGGAGGGTCCAAGCGTTGTCCGGAATCACTGGGTGTAAAGGTTGTC GTGTCAGCCGCCGCGGTAATACGGAGGAGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGCGTCCGC/ ACGTGTCAGCCGCCGCGGTAATACGGAGGGTGCAAGCGTTGTCCGGAATCACTGGGCGTAAAGGGTGT(ACGTGTCAGCAGCCGCGGTAATACCGGCAGCCCAAGTGATGGCCGATCTTATTGGGCCTAAAGCGTCCG⁻ CGTGCCAGCCGCGGGTAACACCGGCAGCCCGAGTGATGGCCGATATTATTGGGCCTAAAGCGTCCGT CGTGTCAGCCGCCGCGGTAATACCGGCAGCCCGAGTGATGGCCGCTATTATTGGGCCTAAAGCGTCCGT/ TGCCGCCAATTTATTTAAGTTTCAACCTTGCGATCGTACTCCCCAGGCGGAATGCTTAACGCGTTAGCTTAI ATGTCAGCCGCCGCGGTAACACCCGGCAGCCCGAGTGATGGCCGATATTATTGGGCCTAAAGCGTCCGTA GTGCCATCCGCCGCGGTAATACCGGCAGCACAAGTGATGGCCGATATTATTGGGCCTAAAGCGTCCGTA(ACGTGTCATCAGCCGCGGTAATACGGAGGGTGCAAGCGTTGTCCGGAATCACTGGGTGTAAAGGGTGTC TTGTCAGCAGCCGGGGTAATACCGGCAGCACGAGTGATGGCCGATCTTATTGGGCCTAAAGCGTCCGTA GCCGTCAATTTCTTTAAGTTTCACTCTTGCGATCGTACTTCCCAGGCGGGAGACTTAACGCGTTAACTTCG/ ACGTGCCAGCAGCCGCGTAATACCGGCAGCCCGAGTGATGGCCGATCTTATTGGGCCTAAAGCGTCCG TGCCGTCAATTCATTTGAGTTTCATCCTTGCAGACGTACTTCCCAGGCGGCTCGCTTCACGGCTTCCCTGC(GCCGTCAATTTCTTTAAGTTTCATCCTTGCAGACGTACTTCCCAGGCGGCTCGCTTCACGGCTTCCCTGCG(ACGTGTCAGCAGCCGCGGTAACACCGGCAGCCCAAGTGATGGCCGCTGTTATTGGGCCTAAAGCGTCCG ACGTGTCAGCCGCCGCGGTAATACCGGCAGCACAAGTGATGGCCGATATTATTGGGCCTAAAGCGTCCG GTGTCAGCAGCCGCGGTAATACCGGCAGCTCGAGTGATGGCCGCTATTATTGGGCCTAAAGCGTCCGTA(GCCGTCAATTTCTTTGAGTTTCATCCTTGCAGACGTACTTCCCAGGCGGCTCGCTTATCGTCTTCACTTCGG ACGTGTCAGCAGCCGCGGTAATACGTAGGGTCCGAGCGTTGTCCGGAATTATTGGGCCGTAAAGGGCTCG CGTGTCAGCAGCCGCGGTAATACCGGCAGCCCAAGTGATGGCCGATATTATTGGGCCTAAAGCGTCCGT/ GCCGTCAATTTATTTAAGTTTCATCCTTGCAGACGTACTTCCCAGGCGGTCTGCTTCACGGCTTCCCTACG(GTGCCAGCCGCGCGGTAATACCGGCAGTCCAAGTGATGGCCGATCTTATTGGGCCTAAAGCGTCCGTA(CGTGTCAGCCGCCGCGGTAATACCGGCAGCACAAGTGATGGCCGATATTATTGGGCCTAAAGCGTTCGT/ ACGTGTCAGCAGCCGCGGTAATACCGGCAGCTCGAGTGATGGCCGATCTTATTGGGCCTAAAGCGTCCG CGTGTCAGCCGCCGCGGTAATACCGGCAGCCCGAGTGATGGCCGCTGTTATTGGGCCTAAAGCGTCCGT/ ACGTGTCAGCCGCCGCGGTAATACGGAGGGTGCAAGCGTTGTCCGGAATCACTGGGCGTAAAGGGTGT(GTGCCAACAGCCGCGGTAATACCGGCAGCTCGAGTGATGGCCGCTATTATTGGGCCTAAAGCGTCAGTA+ ACGTGCCAGCAGCCGCGTAATACCGGCAGCACGAGTGATGGCCGATGTTATTGGGCCTAAAGCGTCCG GTGTCAGCCGCCGCGGTAATACCGGCAGCACGAGTGATGACCGATATTATTGGGCCTAAAGCGTCCGTA CGTGCCAGCCGCCGCGGTAATACGGAGGGTGCAAGCGTTGTCCGGAATCACTGGGCGTAAAGGGTGTG ACGTGTCAGCCGCCGCGGTAACACGAGGAATGCAAGCGTTATCCAGAATTATTGGGCGTAAAGAGCCTG CCGTAAATTTCTTTAAGTTTCAACCTTGCGATCGTACTCCCCAGGCGGAATGCTTAACGCGTTAGCTTAGC ACGTGCCAGCAGCCGCGGTAACACGAGGAATGCAAGCGTTATCCAGAATTATTGGGCGTAAAGGGCCTC ACGTGTCAGCAGCCGCGGTAATACCGGCAGCACGAGTGATGGCCGATATTATTGGGCCTAAAGCGTCCG CGTGTCAGCCGCCGCGGTAATACCGGCAGCACGAGTGATGGCCGATATTATTGGGCCTAAAGCGTCCGT/ GTGTCAGCCGCCGCGGTAATACCGGCAGCACAAGTGATGGCCGCTATTATTGGGCCTAAAGCGTCCGTA(CGTGTCAGCCGCCGCGGTAATACCGGCAGCACGAGTGATGGCCGATCTTATTGGGCCTAAAGCGTCCGT/ CGTGTCAGCCGCCGCGGTAATAGCAGGACCCCAAGTGGTGGCCGATATTACTGGGCTTAAAGCGTTCGT/ CGTGTCAGCCGCCGCGGTAACACGTGAACCCCAAGCGTTATCCGAAATCATTGGGCGTAAAGGGTGCGT ACGTGCCAGCCGCCGGTAACACCGGCAGCCCGAGTGATGGACGATCTTATTGGGCCTAAAGCGTCCG GTGTCAGCCGCCGCGGTAATACCGGCAGCCCGAGTGATGGCCAATCTTATTGGGCCTAAAGCGTTCGTA(CATGCCAGCCGCGGGTAATACCGGCAGTTCGAGTGATGGCCGTTCTTATTGGGCCTAAAGCGTCCGTA CGTGTCAGCAGCCGCGGTAATACCGGCAGCTCGAGTGATGGCCGATCTTATTGGGCCTAAAGCGTCCGT/ ACGTGTCAGCCGCCGTAATACCGGCAGCACGAGTGATGGCCGATATTATTGGGCCTAAAGCGTCCG⁻ GTGTCAGCCGCCGCGGTAACACCGGCAGCCCGAGTGATGGCCGATATTATTGTGCCTAAAGCGTCCGTA(CGTGTCAGCAGCCGCGGTAATACCGGCAGTCCGAGTGATGGCCGATCTTATTGGGCATAAAGCGTCCGT/ GTGTCAGCCGCCGCTAACACCGGCAGCCCGAGTGATGGCCGATATTATTGGGCCTAAAGCGTCCGTA GCCGTCAATTTATTTGAGTTTCAGCCTTGCGGACGTACTTCCCAGGCGGCCCGCTTCTCGGCTTCCCTACG+ ACGTGCCGGCAGCCGCGAATACCGGCAGCTCGAGTGATGGCCGCTGTTATTGGGCCTAAAGCGTCCG CGTGTCAGCAGCCGCGGTAATACCGGCAGCCCGAGTGATCGCCGCTATTATTGGGCCTAAAGCGTCCGT/ ACGTGTCAGCCGCCGCGGTAACACCGGCAGCCCGAGTGATGGCCGATATTATTGGGCCTAAAGCGTCCG ACGTGTCAGCCGCCGGTAATACCGGCAGCACAAGTGATGGCCGATTTTATTGGGCCTAAAGCGTCCG⁻ TGCCGTCAATTTCTTTAAGTTTCAACCTTGCGATCGTACTCCCCAGGCGGAATGATTAACGCGTTAGCTTA(GTGTCAGCAGCCGCGGTAATACCGGCAGCACGAGTGATGGCCGCTATTATTGGGCCTAAAGCGTCCGTA CGTGCCAGCCGCCGCGGTAATACCGGCAGCACGAGTGATGGCCGATCTTATTGGGCCTAAAGCGTTCGT/ GTGCCAGCCGCCGCTAATACGGAGGGTGCAAGCGTTGTCCGGAATCACTGGGCGTAAAGGGTGTGC CGTGCCAGCAGCCGCGTAATACCGGCAGCCCGAGTGATGGCCGCTATTATTGGGCCTAAAGCGTCCGT. GCCGCCAATTTATTTGAGTTTCATTCTTGCGGACGTACTTCCCAGGCGGTCTGCTTCACGGCTTCCCTACG(CGTGTCATCAGCCGCGGTAATACCGGCAGCACGAGTGATGGCCGATATTATTGGGCCTAAAGCGTCCGT/ GTGTCAGCAGCCGCGGTAATACGGAGGGTCCAAGCGTTAATCGGAATTACTGGGCTTAAAGGGTGCGTA GTGTCAGCCGCCGCGTAATACGGAGGGTGCAAGCGTTGTCCGGAATCACTGGGCGTAAAGGGTGTGC/ ACGTCCCAGCCGCCGCGGTAATACCGGCAGCCCGAGTGATGGCCAATATTATTGGGCCTAAAGCGTCCGT ACGTGCCAGCCGCCGGTAATACCGGCAGCCCGAGTGATGGCCAATCTTATTGGGCCTAAAGCGTTCG⁻ GTGTCAGCCGCCGCTAACACCGGCAGCCCGAGTGATGGCCGATATTATTGGGCCTAAAGCGTCCGTA ACGTGTCAGCCGCCGCGGTAATACCGGCAGCTCGAGTGATGACCGATCTTATTGGGCCTAAAGCGTTCG1 ACGTGTCAGCAGCCGCGGTAACACCGGCAGCCCGAGTGATGGCCGATATTATTGGGCCTAAAGCGTCCG GTGCCAGCAGCCGCGGTAATACGGAGGGTGCAAGCGTTGTCCGGAATCACTGGGCGTAAAGGGTGTTC/ GTGCCAGCAGCCGCGTAATACGAAGGGTGCTAGCGTTATCCGGAATCATTGGGCGTAAAGGGGGCGCA GTGTCAGCCGCCGCTAACACCGGCAGCCCGAGTGATGGCCGATATTATTGGGCCTAAAGCGTCCGTA ACGTGTCAGCCGCCGGTAATACCGGCAGCTCGAGTGATGACCGATCTTATTGGGCCTAAAGCGTCCG CGTGCCAGCCGCCGCGGTAATAGCCGCACCCCAAGTGGTAGTCATTGTTATTGGGCTTAAAGTGTTCGTA CGTGTCAGCCGCCGCGGTAATACCGGCAGCACAAGTGATGGCCGCTATTATTGGGCCTAAAGCGTCCGT/ TGCCGTCAATTTCTTTGAGTTTCAACCTTGCGATCGTACTCCCCAGGCGGAATGCTTAACGCGTTAGCTTA(ACGTGTCAGCCGCCGCGGTAATACCGGCAGCACGAGTGATGGCCGCTATTATTGGGCCTAAAGCGTCCG GTGTCAGCCGCCGCGGTAATACCGGCAGCACGAGTGATGGCCGCTCTTATTGGGCCTAAAGCGTCCGTA GTGTCAGCAGCCGCGGTAATACGGAGGGTGCAAGCGTTGTCCGGAATCACTGGGCGTAAAGGGTGTGC TGCCGTCAATTTATTTGAGTTTCATCCTTGCGGACGTACTTCCCAGGCGGCTCGCTTCACGGCTTCCCTAC(

GTGTCAGCCGCCGCGGTAATACGGAGGGTGCAAGCGTTGTCCGGAATCACTGGGCGTAAAGGGTGCGC, CCGTCAATTTATTTAAGTTTCATCCTTGCAGACGTACTTCCCAGGCGGCTCGCTTCACGGCTTCCCTGCGG(GCCGTCAATTCCTTTAAGTTTCATCCTTGCAGACGTACTTCCCAGGCGGTCCGCTTCTCGGCTTCCCTACG@ ACGTGTCAGCAGCCGCGGTAATACGGAGGGTGCAAGCGTTAATCGGATTTACTGGGCGTAAAGTGCGCC CCGTCAATTTATTTAAGTTTCAACCTTGCGATCGTACTCCCCAGGCGGAATGCTTAACGCGTTAGCTTAGC CGTGTCCGCCGCCGTGGTAATACCGGCAGCCCGAGTGATGGCCGATCTTATTGGGCCTAAAGCGTTCGT/ GCCGCCAATTCATTTGAGTTTCATTCTTGCGGACGTACTTCCCAGGCGGTCTGCTTCACGGCTTCCCTACG(GTGCCAGCCGCCGCTAATACCGGCAGCCCGAGTGATGACCGCTATTATTGGGCCTAAAGCGTCCGTA(GTGTAAGCCGCCGCGGTAATACCGGCAGCCCGAGTGATGGCCGCTGTTATTGGGCCTAAAGCGTTCGTAI TGCCGCCAATTTATTTGAGTTTCATCCTTGCGGACGTACTTCCCAGGCGGTCTGCTTAGCGGCTTCCCTGC TGCCGTCAATTTATTTGAGTTTCAACCTTGCGATCGTACTCCCCAGGCGGAATGCTTAACGCGTTAGCTTA CGTGTCAGCAGCCGCGGTAATACCGGCAGCCCGAGTGATGGCCGCTGTTATTGGGCCTAAAGCGTCCGT CGTGTCAGCCGCCGCGGTAATACCGGCAGCCCGAGTGATGGCCGATCTTATTGGGCCTAAAGCGTCCGT/ CGTGTCAGCCGCCGCGGTAATACGGAGGAGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGCGTCCGC GTGTCAGCAGCCGCGGTAATACGGAGGAGGCAAGCGTTATTCGGAATTATTGGGCGTAAAGCGTCCGC/ TGCCGTCAATTCATTTAAGTTTCATCCTTGCGGACGTACTTCCCAGGCGGCTCGCTTCACGGCTTCCCTAC(GCCGTCAATTTCTTTGAGTTTCAACCTTGCGATCGTACTCCCCAGGCGGAATGCTTAACGCGTTAGCTTAG TTGTCAGCCGCCGCTGTAATACCGGCAGCACGAGTGATGACCGATATTATTGGGCCTAAAGCGTCCGTAC GTGTCAACAGCCGCGGTAATACCGGCAGTCCAAGTGATGGCCGCTATTATTGGGCCTAAAGCGTCCGTA(GCCGCCAATTTATTTGAGTTTCATCCTTGCAGACGTACTTCCCAGGCGGCTCGCTTCACGGCTTCCCTGCG(GTGTCAGCAGCCGCGGTAACACCGGCAGCCCAAGTGATGGCCGATATTATTGGGCCTAAAGCGTCCGTA GCCGTCAATTCATTTAAGTTTCATCCTTGCAGACGTACTTCCCAGGCGGCTCGCTTCACGGCTTCCCTGCG(GTGTCAGCAGCCGCGGTAACACCGGCAGCCCAAGTGATGGCCGCTGTTATTGGGCCTAAAGCGTCCGTA CGTGTCAGCAGCCGCGGTAATACCGGCAGCCCAAGTGATGGCCGATCTTATTGGGCCTAAAGCGTTCGT/ GTGTCAGCAGCCGCGGTAATACCGGCAGCCCGAGTGATGGCCGATGTTATTGGGCCTAAAGCGTCCGTA CGTGCCAGCAGCCGCGGTAATACCGGCAGTCCGAGTGATGGCAGATCTTATTGGGCCTAAAGCGTCCGT. CGTGCCAGCAGCCGCGGTAATACCGGCAGCACGAGTGATGGCCGATATTATTGGGCCTAAAGCGTCCGT ACGTGTCAGCAGCCGCGGTAATACGGAGGGTCCAAGCGTTGTCCGGAATCACTGGGTGTAAAGGGTGT(ACGTGTCAGCCGCCGCGGTAATACCGGCAGCACGAGTGATGGCCGCTGTTATTGGGCCTAAAGCGTCCG CGTGTCAGCCGCCGCGGTAATACCGGCAGCACGAGTGATGGCCGTTTTTATTGGGCCTAAAGCGTCCGT/ GTGCCAGCAGCCGCGTAATACCGGCAGCACGAGTGATGGCCGATCTTATTGGGCCTAAAGCGTTCGTA ACGTGTCAGCAGCCGCGGTAATACCGGCAGCTCAAGTGATGGCCGCTATTATTGGGCCTAAAGCGTTCG1 CGTGTCAGCAGCCGCGGTAATACCGGCAGCACGAGTGATGGACAATCTTATTGGGCCTAAAGCGTTCGT/ GTGCCAGCCGCGGGTAATAGCAGCATCCCGAGTGGTAGTCATTATTATTGGGCTTAAAGTGTCCGTAG CGTGCCAGCCGCCGCTAATACCGGCAGCCCGAGTGATGGCCGATATTATTGGGCCTAAAGCGTCCGT/ ACGTGTCAGCAGCCGCGGTAATACGGAGGGTGCAAGCGTTGTCCGGAATCACTGGGCGTAAAGGGTGC+ ACGTGCCAACAGCCGCGGTAATACCGGCAGCACGAGTGATGGCCGCTATTATTGGGCCTAAAAGCGTCCG CGTGTCAGCAACCGCGGTAATACCGGCAGCTCAAGTGATGGCCGATCTTATTGGGCCTAAAGCGTCCGT/ CGTGTCAGCAGCCGCGGTAATACCGGCAGCACGAGTGATGGCCGATATTATTGGGCCTAAAGCGTCCGT ACGTTTCAGCCGCCGCGGTAATACCGGCAGCACGAGTGATGGCCGATTTTATTGGGCCTAAAGCGTCCG1 GCCGTCAATTTATTTGAGTTTCAACCTTGCGATCGTACTCCCCAGGCGGAATGCTTAACGCGTTAGCTTAG CGTGTCAGCAGCCGCGGTAATACCGGCAGCTCGAGTGATGGCCGATCTTATTGGGCCTAAAGCGTCCGT/ CCGTCAATTCCTTTAAGTTTCATCCTTGCGGACGTACTTCCCAGGCGGTCTGCTTCACGGCTTCCCTACGG(CCGTGCCAGCCGCCGCGTAATACGGAGGGTCCAAGCGTTGTCCGGAATCACTGGGTGTAAAGGGTGTC GTGTCAGCAGCCGCGGTAATACGGAGGGTGCAAGCGTTGTCCGGAATCACTGGGCGTAAAGGGTGTGC

TGCCGCCAATTTATTTGAGTTTCATTCTTGCGGACGTACTTCCCAGGCGGTCTGCTTCACGGCTTCCCTACC CGTGTCAGCTGCCGCGGTAATACCGGCAGCCCGAGTGATGGCCGATGTTATTGGGCCTAAAGCGTCCGT/ GTGCCAGCCGCGGTAATACCGGCAGCCCGAGTGATGGCCGATATTATTGGGCCTAAAGCGTCCGTA CCGTCAATTCATTTAAGTTTCATCCTTGCAGACGTACTTCCCAGGCGGCTCGCTTCACGGCTTCCCTACGG(ACGTGTCAGCCGCCGCGGTAATACGGAGGGTGCAAGCGTTGTCCGGAATCACTGGGCGTAAAGGGTGT(TGCCGTCAATTTATTTGAGTTTCATCCTTGCAGACGTACTTCCCAGGCGGCTCGCTTCACGGCTTCCCTGCC CGTGCCAGCAGCCGCGGTAATACCGGCAGCACGAGTGATGGCCGCTATTATTGGGCCTAAAGCGTCCGT GCCGTCAATTTATTTAAGTTTCATCCTTGCGGACGTACTTCCCAGGCGGTCTGCTTAGCGGCTTCCCTGCG GCCGTCAATTCATTTAAGTTTCATCCTTGCAGACGTACTTCCCAGGCGGTCTGCTTCACGGCTTCCCTACG(GCCGTCAATTTATTTGAGTTTCATCCTTGCAGACGTACTTCCCAGGCGGCTCGCTTCTCGGCTTCCCTAGG(GCCGTCAATTCATTTAAGTTTCATTCTTGCGGACGTACTTCCCAGGCAGTCTGCTTCACGGCTTCCCTACG(ACGTGTCAGCAGCCGCGGTAATACCGGCAGCCCGAGTGATGGCCGATCTTATTGGGCCTAAAGCGTCCG 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CCGCCAATTTCTTTGAGTTTCATCCTTGCAGACGTACTTCCCAGGCGGCTCGCTTCACGGCTTCCCTGCGG(CGTGTCAGCCGCCGCGGTAATACCGGCAGCCCGAGTGATGGCCGCTGTTATTGGGCCTAAAGCGTCCGT/ ACGTGTCACCCGCCGCGGTAACACCGGCAGCCCAAGTGATGGCCGATATTATTGGGCCTAAAGCGTCCG⁻ GTGCCAGCCGCGGGTAATACCGGCAGCCCGAGTGATGGCCGATATTATTGGGCCTAAAGCGTCCGTA GTGTCAGCAGCCGCGGTAATACCGGCAGCTCGAGTGATGGCCGATCTTATTGGGCCTAAAGCGTCCGTA(GCCGTCAATTCCTTTAAGTTTCATTCTTGCGGACGTACTTCCCAGGCGGTCTGCTTCACGGCTTCCCTACG(TGCCGTCAATTTATTTGAGTTTCATCCTTGCGGACGTACTTCCCAGGCGGTCCGCTTCTCGGCTTCCCTAC GCCGTCAATTCATTTAAGTTTCATGATTGCGCACGTACTCCCCAGGCGGGATACTTAACGCGTTGGCTTCG GTAGGCGGTCGAGTAAGTCGGATGTGAAAGCCCTGGGCTCAACCTAGGAATTGCATTCGATACTGCTT GCTCGCCGAGCAAGTCCGTCGGGAAATCCAGTGGCTCAACCTCTGGGCTTCCGGCGGAAACTGTTCGC TAGCTGGCCATGCAAGTCCGTCGGGAAATCCACCTGCTTAACAGGTGGGCGTCCGGCGGAAACTGCA(3AGGGAGGAAGGCTCTTGGGTTGTAAACCTCTTTTCTCAGGGAAGAATACAATGACGGTACCTGAGG/ GCTGGCCAGACAAGTCTGTTGGGAAATCCACGAGCTCAACGCGTGGGCGTCCAGCGGAAACTGTCTG GCTGGCCAGACAAGTCTGTTGGGAAATCCACGCGCTCAACGCGTGGGCGTCCAGCGGAAACTGTCTG 3CTGGCCATGCAAGTCCGTCGGGAAATCCACCCGCTTAACGGGTGGGCGTCCGGCGGAAACTGCACG(GCTGGCCGGCAAGTCCATCGGGAAATCCACCCACTCAACGGGTGGGCGCCCGGTGGAAACTGCCCC ICAGGCGGCCGAGCAAGTCCGGTGTGAAAGCCCGGGGCTCAACCCCGGAATGGCATCGGAAACTGGT AGCTGGCCGCAAGTCCACCGGAAAATCCACCCGCCCAACGGGTGGGCGTCCGGTGGAAACTGCGT GCTGGCTAAACAAGTCCGTTGGGAAATCTGCCCGCTTAACGGGCAGGCGTCCAGCGGAAACTGTCTA(3CCGGATCTGCAAGTCTGCTGTGAAATCCACCTGCTTAACAGATGGGCGTGCAGCGGATACTGCAGGT(TAGCCGGCCAGACAGGTCCGTCGGGAAATCCAGTGGCTTAACCACTGGGCGTCCGGCGGAAACCAGC GCAGGCGGTTTGTTAAGCGAGATGTGAAAGCCCCGGGCTCAACCTGGGAACCGCATTTCGAACTGGC/ GCCGGCCGGACAAGTCCGTTGGGAAATCGACGCGCTCAACGCGTCGGCGTCCAGCGGAAACTGTCCG TAGCCGGCCGGACAAGTCCGTTGGGAAATCCACGCGCTCAACGCGTGGGCGTCCAGCGGAAACTGTC CAGGCGGTTGGATAAGTCGGGTGTGAAAGCCCCGGGCTCAACCTGGGAACGGCATTCGATACTGTCC AGGCGGCCGTCCAAGTCTGATGTGAAAGTCCGGGGCTCAACTCCGGAAGCGCATCGGAAACTGGTTC AGCCGGCCGGACAAGTCCGTTGGGAAATCCACGCGCTCAACGCGTGGGCGTCCAGCGGAAACTATCC CACTGCCCCTAACGAGGCAACGGCGAGCATTCATCGTTTACTGCGTGGACTACCAGGGTATCTAATC(CAGGCGGCCTGGCATGTCCGATGTGAAAGCCCGGGGCTCAACTCCGGAATCGCATTGGAAACTGTCA TAGCCGGCCGGACAAGTCCGTTGGGAAATCGACGTGCCTAACACGTCGGCGTCCAGCGGAAACTGTC GCTGGCCGGACAAGTACGTTGGGAAATCCACCCGCTTAACGGGTGGGCGTCCAGCGGAAACTGTCCG CCACTGCCCCTAACGAGGCAACGGCGAGCATTCATCGTTTACGGCGTGGACTACCAGGGTATCTAAT TAGCTGGCCACGCAAGTCCACCGGGAAATCCACCTGCCCAACAGGTGGACGCCCGGTAGAAACTGCG CCACTATTCCTTAGGCGGAATAACGGCGAGCATTCATCGTTTACGGCGTGGACTACCAGGGTATCTAA GCCGGCCGAACAAGTCCGTCGGGAAATCCATCGGCTTAACCGATGGGCGTCCGGCGGAAACTGTTCG(CAGGCGGGCAGCAAGTCGGAGGTGAAAGCCCACGGCTCAACCGTGGAAGTGCCTTCGAAACTGTT@ \GGGGGCTCATCAAGTCTGCTGTCAAAGGTCGGAGCTCAACTCCGGTTCGGCAGTGGAAACTGGTGG(GCCGGCCGAACAAGTCCGTCGGGAAATCCATCCGCCCAACGGATGGGCGTCCGGCGGAAACTGTTCG AGCTGGCCGCGAAGTCCACCGGAAAATCCACCCGCCCAACGGGTGGGCGTCCGGTGGAAACTGCGT 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GCTGGCCGAGCAAGTCTGTCGGGAAATCCAGTGGCTCAACCACTGGGCTGCCGGCGGAAACTGTTCG TAGCTGGCCGAGCAAGTCCGTTGGGAAATCGACGTGCCTAACACGTCGGCGTCCAGCGGAAACTGTT AGGCGGGGCAGCAAGTCGGAGGTGAAAGCCCGTGGCTCAACCACGGAAGTGCCTTCGAAACTGCTG(\GGCGGTTTTTTAAGTCTGATGGGAAAGCCCACGGCTCAACCGTGGAGGGTCCTTGGAAACTGGAAAA GCAGGCGGCCTTGCAAGTCCGGTGTGAAAGCCCGGGGCTCAACTCCGGAAGCGCATCGGAAACTGTC iCCACTGCCCCTAACGAGGCAACGGCGAGCATTCATCGTTTACGGCATGGACTACCAGGGTATCTAAT TAGCTGGCCGAGCAAGTTCGTCGGGAAATCCACGCGCCCAACGTGTGGGCGTCCGGCGAAAACTGTT TAGCCGGCCGGACAAGTCCGTTGGGAAATCGACGCGCCTAACGCGTCGGCGTCCAGCGGAAACTGTC TAGCTGGCCGAACAGTCCGTCGGGAAATCCACGTGCTTAACGCGTGGGCGACCGGCGGAAACTGTT GCTGGCCTCGCAAGTCCGTCGGAAATCCAGTAGCCCAACTACTGGGCGTCCGGCGGAAACTCCGAG(AGCCGGCCAGCCAAGTCCGTTGGGAAATCCACGTGCTCAACGCGTGGGCGTCCAGCGGAAACTGTCT(AGGTGGTTTGTTAAGTTGGATGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATCCAAAACTGGCAAG GCCGGCCGGTCGAGTTCGTCGGGAAATCTGCCCGCTTAACGGGCAGGCGTCCGGCGAAAACTGATCG AGCCGGCCGCAAGTCCGTCGGGAAATCCACCCGCCTAACGGGTGGGCGTCCGGCGGAAACTGTGC GCTGGCCTCACAAGTCCGTCGGGAAATCCACCCGCTCAACGGGTGGGCGTCCGGCGGAAACTGTGAA TAGCTGGCCGCAAGTCCACCGGAAAATCCACCCGCCCAACGGGTGGGCGTCCGGTGGAAACTGCG \GCCTGCCGTGCAAGTCCGCTGTGAAATCCACGCGCTCAACGTGTGGGCGTGCAGCGGATACTGTATG CAGGCGGGGCAGCAAGTCGGAGGTGAAAGCCCACGGCTCAACCATGGAAGTGCCTTCGAAACTGTTC AGCTGGCCAGACAAGTCTGTTGGGAAATCCACGCGCTCAACGCGTGGGCGTCCAGCGGAAACTGTCT AGCTGGCCAGTCAAGTCTGTCGGGAAACCTGCTCGCTCAACGAGCAGCCGTCTGGCGGAAACTGACT@ GCTGGCCGCGAAGTCCCCCGGGAAATCCACCTGCCCAACAGGTGGACGCCCGGTAGAAACTGCACG 3TAGGCGGCGATTTAAGTCAGAGGTGAAAGCCCGGGGCTCAACCCCGGAACTGCCTTTGAGACTGGA FAGCTGGCCGAACGGGTCCGTCGGGAAATCCACCCGCTCAACGGGTGGGCGTCCGGCGGAAACCAGT CACAGCACCCACTCGTAGTGGGAGCCACACCTAGCAGACATCGTTTACGGCCAGGACTACCCGGGTA1 TAGCTGGCCACGCAAGTCCACCGGGAAATCCACCTGCCCAACAGGTGGACGCCCGGTAGAAACTGTG AGCTGGCCATGCAAGTCCGTCGGGAAATCCACCCGCTTAACGGGTGGGCGTCCGGCGGAAACTGCAC(AGGCGGGGCAGCAAGTCGGAGGTGAAAGCCCACGGCTCAACCGTGGAAGTGCCTTCGAAACTGTTG(TAGCTGGCCATGCAAGTCCGTCGGGAAATCCACCCGCTTAACGGGTGGGCGTCCGGCGGAAACTGCA CGTGAGGGAGGAAGGCTCTTGGGTTGTAAACCTCTTTTCTCAGGGAAGAACAAAATGACGGTACCTGA CONTRACTOR C GCTGGCCGCGAAGTCCACCGGGAAATCCACCTGCCCAACAGGTGGACGCCCGGTAGAAACTGCGCG AGGTGGGGCAGCAAGTCCAAGGTGAAAGCCCGTGGCTTAACCACGGAAGTGCCTTTGAAACTGCTGC AGCTGGCCGCAAGTCCACCGGGAAATCCACCTGCCCAACAGGTGGACGCCCGGTAGAAACTGCGC TAGCCGGCCAAACAAGTCCGTTGGGAAATCGACGCGCTCAACGCGTCGGCGTCCGGCGGAAACTGTT AGCTGGCCGCAAGTCCACCGGAAAATCCACCCGCCCAACGGGTGGGCGTCCGGTGGAAACTGCGT GCCGGTCACGGAAGTCCGTTGGGAAATCTGCTCGCTCAACGAGCAGGCGTCCGGCGGAAACTCCGTG AGGTGGGGCAGCAAGTCAAAGGTGAAAGCCCGTGGCTTAACCACGGAAGTGCCTTTGAAACTGCTGC GCCGGCCGAACGGGTCCGTCGGGAAATCCACTCGCTTAACGAGTGGGCGTCCGGCGGAAACTGTTCG GCCAGCCAGACAGGTCCGTCGGGAAATCCACTCGCTCAACGAGTGGGCGTCCGGCGGAAACCAGCTG TAGCTGGCCGCGAAGTCCGTCGGGAAATCCACCCGCTTAACGGGTGGGCGTCCGGCGGAAACTGCA AGCTGGCCGGACAAGTCCGTTGGGAAATCCACCCGCTTAACGGGTGGGCGTCCAGCGGAAACTGTCC \GGCGGCCTGGCATGTCCGATGTGAAAGCCCGGGGCTCAACTCCGGAATCGCATTGGAAACTGTCAGC AGGCGGTTTGTTAAGCGAGATGTGAAAGCCCCGGGCTCAACCTGGGAACCGCATTTCGAACTGGCAA TAGCCAGCTGAACAGGTCCGTCGGGAAATCTGCTCGCTCAACGAGCAGGCGTCCGGCGGAAACCAGT AGGCGGCGATTTAAGTCAGAGGTGAAAGCCCGGGGCTCAACCCCGGAACTGCCTTTGAGACTGGATT(

AGGCGGGGCAGCAAGTCGGAGGTGAAAGCCCATGGCTCAACCATGGAAGTGCCTTCGAAACTGTTGC GCAGGCGGTTTGTTAAGCGAGATGTGAAAGCCCCGGGCTCAACCTGGGAACCGCATTTCGAACTGGC AGGCGGCGTTTAAGTCGGGGGTGAAAGCCTGTGGCTCAACCACAGAATGGCCTTCGATACTGGGACG AGGTGGGGCAGCAAGTCAAAGGTGAAAGCCCGTGGCTTAACCACGGAAGTGCCTTTGAAACTGCTGC AGCTGGCCGCAAGTCCACCGGAAAATCCACCGCCCAACGGGTGGGCGTCCGGTGGAAACTGCGT GCCGGCCGGCAAGTCCGTCGGGAAATCCACCCGCTTAACGGGTGGGCGACCGGCGAAACTGCTCC 3TGAGGGAGGAAGGCTCTTGGGTTGTAAACCTCTTTTCTCAGGGAAGAAAAAAATGACGGTACCTCAC GCAGGCGGGCAGCAAGTCGGAGGTGAAAGCCCGTGGCTCAACCACGGAAGTGCCTTCGAAACTGCT GCAGGCGGGCAGCAAGTCGGAGGTGAAAGCCCACGGCTCAACCGTGGAAGTGCCTTCGAAACTGTT GCCGGCCGAACGAGTCCGTCGGGAAATCGACGCGCCCAACGCGTCGGCGTCCGGCGGAAACTGTTCG GCCGGCCAGGCAAGTTCGTCGGGAAATCCACCCGCCCAACGGGTGGGCGTCCGGCGAAAACTGTCTG TAGCCGGCCGGACAAGTCCGTTGGGAAATCTGCGCGCTTAACGCGCAGGCGGCCAGCGGAAACTGTC 3CTGGCCGCACAAGTCCGTCGGGAAATCCACCCGCTTAACGGGTGGGCGTCCGGCGGAAACTGTGCG TAGCTGGCCGGGCAAGTCCGTCGGGAAATCCACGCGCCCAACGCGTGGGCGTCCGGCGGAAACTGTT AGGCGGCCTCCCATGTCCGATGTGAAAGCCCGGGGCTCAACTCCGGAGGCGCATTGGAAACTGGGTC AGCCGGCTAGACAGGTCCGTCGGGAAATCCACCCGCTCAACGGGTGGGCGACCGGCGGAAACCAGCT GCCGGCCGGACAAGTCCGTTGGGAAATCCACGCGCTCAACGCGTGGGCGTCCAGCGGAAACTGTCCG GAGTGATGAAGGCCTTAGGGTTGTAAAGCTCTTTTACCCGGGATGATAATGACAGTACCGGGAGAAT/ TAGCCGGCCGGACGGTCCATCGGGAAATCCACGTGCTCAACGCGTGGGCCGACCGGTGGAAACCATC GCTGGCCAGACAAGTCCGTTGGGAAATCCACGTGCCTAACATGTGGGCGTCCAGCGGAAACTGTCTG(AGGTGGCTTGATAAGCCGGTTGTGAAAGCCCCGGGCTCAACCTGGGAACGGCATCCGGAACTGTCAG .GCCAGCCAGACAGGTCTGTCGGGAAATCCACGCGCTCAACGCGTGGGCGGCCGACAGAAACCAGCT(AGGTGGGGCAGCAAGTCAGAGGTGAAAGCCCGTGGCTTAACCACGGACGTGCCTTTGAAACTGTTGC GCAGGCGGGCAGCAAGTCGGAGGTGAAAGCCCGTGGCTCAACCACGGAAGTGCCTTCGAAACTGC AGCTGGCCGAGCAAGTTCGTCGGGAAATCCACGCGCCCAACGTGTGGGCGTCCGGCGAAAACTGTTC GCAGGCGGGCAGCAAGTCGGAGGTGAAAGCCCACGGCTCAACCGTGGAAGTGCCTTCGAAACTGTT GCTGGCCATGCAAGTCCGTCGGGAAATCCACCTGCTTAACAGGTGGGCGTCCGGCGGAAACTGCACG(AGCCTGCCGTACGGGTCCGTCGGGAAATCCGCCCGCTCAACGGGCGGACGTCCGGCGGAAACCATAC TAGCCTGCCGGACAAGTCCGTTGGGAAATCCACGCGCTCAACGCGTGGGCGTCCAGCGGAAACTGTC TAGCCGGCCGAACAAGTCTGTCGGGAAATCCATCCGCCTAACGGATGGGCGTCCGGCAGAAACTGTT(AGCTGGCCTCACAAGTCCATCGGGAAATCCACCCGCCCAACGGGTGGGCGTCCGGTGGAAACTGTAA(AGCTGGCCAGGCAAGTCCGTTGGGAAATCTGCTCGCTTAACGAGCAGGCGTCCAGCGGAAACTGCTT@ AGCTGGCCGAGAGGGTCCGTCGGGAAATCTGCTCGCTCAACGAGCAGGCGTCCGGCGGAAACCAATC GTAGGCGGCGTTTTAAGTCGGGGGTGAAAGCCTGTGGCTCAACCACAGAATGGCCTTCGATACTGGG TAGCTGGCCGCACAAGTCCGTCGGGAAATCCACCCGCTTAACGGGTGGGCGTCCGGCGAAAACTGTG TAGCTGGCCGGGGAAGTCCGTCGGGAAATCCACTCGCTCAACGAGTGGGCGTCCGGCGGAAACTCTC AGCTGGCCGCGTAGGTCCGTCGGGAAATCTACTGGCTCAACCAGTAGGCGTCCGGCGGAAACCTCGT GCTGGCCGCGAAGTCCACCGGGAAATCCACCTGCCCAACAGGTGGACGCCCGGTAGAAACTGCGCG GCTGGCTAGACAAGTCCGTTGGGAAATCTGCCCGCTTAACGGGCAGGCGTCCAGCGGAAACTGTCTA(GCCACTGCCCCCTAACGAGGCAACGGCGAGCATTCATCGTTTACGGCGTGGACTACCAGGGTATCTAA AGGTGGTTTGTTAAGTTGAATGTGAAATCCCCGGGCTCAACCTGGGAACTGCATCCAAAACTGGCAAG 3TAGGCGGTCAAGTAAGTTGGGTGTGAAAGCCCCGGGCTCAACCTGGGAATTGCATCCAATACTGCTT 3CCGGCCATGTAAGTCCGCTGTGAAATCCACGCGCTCAACGTGTGGAAGTGCAGCGGATACTGCATGG TAGCTGGCTAGACAAGTCCGTTGGGAAATCTGCCCGCTTAACGGGCAGGCGTCCAGCGGAAACTGTC

GCAGGCGGCCCGGCAAGTCCGATGTGAAACCCCGAGGCTCAACCTCGGAGGCGCATTGGAAACTGTC GCCGGCCAGACAAGTCCGTTGGGAAATCGACGCGCTCAACGCGTCGGCGTCCAGCGGAAACTGTCTG GCAGGCGGGCAGCAAGTCGGAGGGGAAAGCCCATGGCTCAACCATGGAAGTGCCTTCGAAACTGTT TAGCTGGCCAGGAAGGTCCGTCGGGAAATCCACTCGCTTAACGAGTGGGCGTCCGGCGGATACCTCT GCAGGCGGCCGTGCAAGTCTGGTGTGAAAGCCCGGGGCTCAACCCCGGAACTGCATTGGAAACTGTA GCCGGCCGAGCGGGTCCGTCGGAAAATCCACGCGCTCAACGCGTGGGCGTCCGGCGGAAACCACTCG GCCGGCCGGACAAGTCCGTTGGGAAATCCACGCGCTCAACGCGTGGGCGTCCAGCGGAAACTGTCCG GCTGGCCAGACAAGTCTGTTGGGAAATCCACGCGCTCAACGCGTGGGCGTCCAGCGGAAACTGTCTG GCCGGCCGGACAAGTCCGTTGGGAAATCGACGCGCTCAACGCGTCGGCGTCCAGCGGAAACTGTCCG AGCTTGCTGTGTAAGTCCATCGGGAAATCGACGCGCTCAACGCGTCGGCGTCCGGTGGAAACTACACC GGGGGAGGAAGGCTCTTGGGTCGTAAACCTCTTTTCTCAGGGAAGAACACAATGACGGTACCTGAGG GCAGGCGGGCAGCAAGTCGGAGGTGAAAGCCCACGGCTCAACCGTGGAAGTGCCTTCGAAACTGTT ragccggccgtgtaagtccgctgtgaaatccaggcgcttaacgtctgggcgtgcagcggatactgcac CAGGCGGGCAGCAAGTCGGGGGTGAAAGCCCAAGGCTCAACCGTGGAAGTGCCTTCGAAACTGTT(GCCGGCCAGACAGGTCCGTCGGGAAATCCAGTGGCTTAACCACTGGGCGTCCGGCGGAAACCAGCTG GCTGGCTGGCAAGTCCGTTGGGAAATCTGTTCGCTTAACGAGCAGCGTCCAGCGGAAACTGTTCG(AGGTGGCTTGATAAGCCGGTTGTGAAAGCCCCGGGCTCAACCTGGGAACGGCATCCGGAACTGTCAG CAGGCGGGCAGCAAGTCGGAGGTGAAAGCCCGTGGCTCAACCACGGAAGTGCCTTCGAAACTGCT(AGCCTGCCAGACAGGTCCGTCGGGAAATCTGCACGCCCAACGTGCAGGCGTCCGGCGGAAACCAGCT GCCGGCCGGACAAGTCCGTTGGGAAATCCACGCGCTCAACGCGTGGGCGTCCAGCGGAAACTGTCCG TAGCTGGCTAGACAAGTCCGTTGGGAAATCTGCCCGCTTAACGGGCAGGCGTCCAGCGGAAACTGTC TAGCCGGCCGGGCAGGTCCGTCGGGAAATCCACTGGCTCAACCAGTGGGCGTCCGGCGGAAACCGC GGAGGATGACAGCCTATGGGTCGTAAACTCCTTTTCTTGGAGAAGAAATTTTGACGGTATCTGAGGAA GCTGGCCACGCAAGTCCACCGGGAAATCCACCTGCCCAACAGGTGGACGCCCGGTAGAAACTGCGCG TAGCTGGCCAAGCAAGTCCATCGGGAAATCGACGTGCTCAACGCGTCGGCGTCCGGTGGAAACTGTT CGTGAGGGAGGAAGGCTCTTGGGTTGTAAACCTCTTTTCTCAGGGAAGAACAAAATGACGGTACCTGA \GCTGGCCGCGCAAGTCCACCGGAAAATCCACCGCCCAACGGGTGGGCGTCCGGTGGAAACTGCGT(GCTGGCCGGCAAGTCCATCGGGAAATCCACCCGCTCAACGGGTGGGCGGCCGGTGGAAACTGCCCC iCAGGCGGCTAAGTAAGTCAGTGGTGAAAGCCTTCGGCTCAACCGGAGAATTGCCATTGAAACTACTT/ AGCCGGCCGGACAAGTCCGTTGGGAAATCGACGCGCTCAACGCGTCGGCGTCCAGCGGAAACTGTCC GCAGGTGGGGCAGCAAGTCAAAGGTGAAAGCCCGTGGCTTAACCACGGAAGTGCCTTTGAAACTGCT TAGCCGGCCGGACAAGTCCGTTGGGAAATCCACCCGCCTAACGGGTGGGCGTCCAGCGGAAACTGTC 3GGGGAGGAAGGCTCTTGGGTCGTAAACCCCTTTTCTCAGGGAAGAACACAATGACGGTACCTGAGG, TAGCTTGCTGTAAGTCCATTGGGAAATCCACGCGCTCAACGCGTGGGCGTCCGGTGGAAACTACAC TAGCCGGCCAGTCAAGTTCGTCGGGAAATCTGCCCGCTTAACGGGCAGGCGTCCGGCGAAAACTGAT GCCACTGCCCCTAACGAGGCAACGGCGAGCATTCATCGTTTACGGCGTGGACTACCAGGGTATCTAA CAGGCGGAGCGGCAAGTCGGAGGTGAAAGCCCGTGGCTCAACCATGGAAGTGCCTTCGAAACTGCTC TAGCTCGCCGTGCAAGTCCATCGGGAAATCGACGCGCTCAACGCGTCGGCTTCCGGTGGAAACTGCA(GTAGGCGGCGTTTTAAGTCGGGGGTGAAAGCCTGTGGCTCAACCACAGAATGGCCTTCGATACTGGG GCCAGCCGAACAGGTCCGTTGGGAAATCTGCTCGCTCAACGAGCAGGCGTCCGGCGGAAACCAGTCC :AGGTGGCTTTTCAAGTCTGCTGTCAAAGCCCGGGGCTCAACCCTGGAGAGGCAGTGGAAACTGAGG/ CAGGCGGGCAACAAGTCGGGGGTGAAAGCCCACGGCTCAACCGTGGAAGTGCCTTCGAAACTGTT(AGGCGGGGCAGCAAGTCGGAGGTGAAAGCCCGTGGCTCAACCACGGAAGTGCCTTCGAAACTGCTG GCCGGCCGGACAAGTCCGTCGGGAAATCCACGTGCTCAACGCGTGGGGGTCCGGCGGAAACTGTTCG \GGTGGCCTTCAAAGTCTTTTGTGAAAGGGTACGGCTCAACCGTACATGCGCAAGAGAAACTCGAAGG

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\GGGGGCTCATCAAGTCTGCTGTCAAAGGTTGGAGCTCAACTCCGGTTCGGCAGTGGAAACTGGTGGC GCCAGCTGAACAGGTCCGTCGGGAAATCTGCTCGCTCAACGAGCAGCGTCCGGCGGAAACCCGTCA .GCCGGTCACGAAAGTCCGTTGGGAAATCTGCTCGCTCAACGAGCAGACGTCCGGCGGAAACTACGTG GCAGGCGGGCAGCAAGTCGGGGGTGAAAACCTGCGGCTCAACCGCAGAGGTGCCTTCGAAACTGC1 AGCTGGCTGGACAAGTCCGTTGGGAAATCTGCCCGCTTAACGGGCAGGCGTCCAGCGGAAACTGTTC/ CAGGCGGCCTCCCATGTCCGATGTGAAAGCCCGGGGCTCAACTCCGGAGGCGCATTGGAAACTGGGT GCCGGCCGAGTAAGTCCGTCGGGAAATCCACGCGCTCAACGCGTGGGCGTCCGGCGGAAACTGCTCC 3CTGGCCGCACAAGTCCGTCGGGAAATCCACCCGCTTAACGGGTGGGCGTCCGGCGGAAACTGTGCA(AGCTGGCCGCAAGTCCACCGGGAAATCCACCTGCCCAACAGGTGGACGCCCGGTAGAAACTGCGC TAGCTGGCCGGGCAAGTCCATCGGGAAATCCACCCGCTCAACGGGTGGACGGCCGGTGGAAACTGCC AGGTGGCTTGATAAGCCGGTTGTGAAAGCCCCGGGCTCAACCTGGGAACGGCATCCGGAACTGTCAG GCTGGCCACGCAAGTCCACCGGGAAATCCACCTGCCCAACAGGTGGACGCCCGGTAGAAACTGCGCG GCAGGCGGCCTGGCATGTCCGATGTGAAAGCCCGGGGCTCAACTCCGGAATCGCATTGGAAACTGTC GGGGAGGAAGGCTCTTGGGTCGTCAACCTCTTTTCTCATGGAAGAACACAATGACGGTACCTGAGGA/ CAGGTGGGACAGCAAGTCAGAGGTGAAAACCCGCGGCTTAACCGCGGAAGTGCCTTTGAAACTGCTG GCCGGCCGGCAAGTTCGTCGGGAAATCCACCCGCCCAACGGGTGGGCGTCCGGCGAAAACTGCCTG TAGCTGGCCGGACAAGTCCGTTGGGAAATCCACGCGCTCAACGCGTGGGCGTCCAGCGGAAACTGTC IGCTGGCCGAGCAAGTTCGTCGGGAAATCCACGCGCCCAACGTGTGGGCGTCCGGCGAAAACTGTTCG GCCGGCCGAACAAGTCCGTCGGGAAATCCGCGCGCCTAACGCGCGGGCGTCCGGCGGAAACTGTCCG GCCGGCCGAGCAAGTCCGTCGGGAAATCTGCCCGCTTAACGGGCAGGCGTCCGGCGGAAACTGTTCG GCTGGCCGAGCAAGTTCGTCGGGAAATCCACGCGCCCAACGTGTGGGCGTCCGGCGAAAACTGTTCG TAGCCGGCCGAGCAGGTCCGTCGGGAAATCCATCCGCTTAACGGATGGGCGTCCGGCGGATACCGTT TAGGCGGACCACCAAGTCAGGGGTGAAAGCCCTGGGCTAAACCTAGGAAGTGCCCTTGAAACTGATG TAGCTGGCCATGCAAGTCCGTCGGGAAATCCACCTGCTTAACAGGTGGGCGTCCGGCGGAAACTGCAI GCTGGCCGCGTAGGTCCGTCGGGAAATCTACTGGCTCAACCAGTAGGCGTCCGGCGGAAACCTCGTG 3TGAGGGAGGAAGGCTCTTGGGTTGTAAACCTCTTTTCTCAGGGAAGAAAAAAATGACGGTACCTGAC AGGTGGGGCAGCAAGTCAGAGGTGAAAGCCCGTGGCTTAACCACGGACGTGCCTTTGAAACTGTTGC AGCCGGCCGAACAAGTCCGTCGGGAAATCCATCCGCCCAACGGATGGGCGTCCGGCGGAAACTGTTC(GTAGGCGGCGTTTTAAGTCGGGGGTGAAAGCCTGTGGCTCAACCACAGAATGGCCTTCGATACTGGG. TAGCCGGCCGGACAAGTCCGTTGGGAAATCGACGCGCTCAACGCGTCCGGCGCACAACTGTC AGCTGGCCGAGCAAGTCTGTCGGGAAATCCAGCAGCTCAACTGCTGGACGTCCGGTGGAAACTGTTC(3CCAGCCAGGCAAGTTCGTCGGGAAATCCACCCGCTCAACGGGTGGGCGTCCGGCGAAAACTGTCTG(AGCCGGCCAGACAAGTCCGTTGGGAAATCCACGCGCTCAACGCGTGGGCGTCCAGCGGAAACTGTCT(GCAGGCGGGCAGCAAGTCGGAGGTGAAAGCCCACGGCTCAACCGTGGAAGTGCCTTCGAAACTGT1 GTAGGTGGCTTGATAAGCCGGTTGTGAAAGCCCCGGGCTCAACCTGGGAACGGCATCCGGAACTGTC/ 3CCGGCCGGACAAGTCCGTCGGGAAATCCACGCGCTCAACGCGTGGGCGTCCGGCGGAAACTATCCG AGGTGGCTTGATAAGCCGGTTGTGAAAGCCCCGGGCTCAACCTGGGAACGGCATCCGGAACTGTCAG 3CAGGTGGGGCAGCAAGTCAGAGGTGAAAGCCCGTGGCTTAACCACGGACGTGCCTTTGATACTGCT(CAGGTGGGGCAACAAGTCAGAGGTGAAAGCCCGCGGCTTAACCGCGGAAGCGCCTTTGAAACTGTTG GCTTGCTGTTAGTCCATCGGGAAATCCACGCGCTCAACGCGTGGGCGTCCGGTGGAAACTGCACA(AGCCGGCCAGACAAGTCTGTTGGGAAATCCACGCGCTCAACGCGTGGGCGTCCAGCGGAAACTGTCT(AGCTGGCCACGCAAGTCCACCGGGAAATCCACCTGCCCAACAGGTGGACGCCCGGTAGAAACTGCGC(GCCGGCCGAGCAAGTCCGTCGGGAAATCTGCCCGCTTAACGGGCAGGCGTCCGGCGGAAACTGTTCG TAGCCAGCCAGACAGGTCCGTCGGGAAATCCACTCGCTCAACGAGTGGGCGTCCGGCGGAAACCAGC GCCGGCCGGACAAGTCCGTTGGGAAATCGACGCGCTCAACGCGTCGGCGTCCAGCGGAAACTGTCCG

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CGGGCTCGAGTCCGAGAGGGGCCCGTGGAATTCCCGGTGTAGGGGTGAAATCCGTAGAGATCGGGAC GCTTGGGGCCGGAAGACCTGAGGGGTACGTCCGGGGTAGGAGTGAAATCCCGTAATCCTGGACGGA TGCTCTTGAGTCCCGGAGAGGCTGTCGGAATTCGTGGTGTAGCGGTGAAATGCGTAGAGATCACGAG TGGCTTGGGACCGAGAGACCAGAGGGGTACGTCCGGGGTAGGAGTGAAATCCTGTAATCCTGGACG(\CGGCTTGAGTCCGGGAGGGCCAGTGGAATTCCTGGTGTAGGGGTGAAATCCGTAGATATCAGGAG 3GCTTGGGGCCGGAGGACTCGAGGGGTACGTCTGGGGTAGGAGTGAAATCCCGTAATCCTGGACGGA 3GCTTGGGGCCGGAGGACTCGAGGGGTACGTCCGGGGTAGGAGTGAAATCCCGTAATCCTGGACGGA GCTTGGGGCCGGAGGACTCGAGGGGTACGTCCGGGGTAGGAGTGAAATCCCGTAATCCTGGACGGA GCTTGGGGCCGGAAGACCTGGGGGGTACGTCCGGGGTAGGAGTGAAATCCTGTAATCCTGGACGGA 3GCTTGGGGCCGAGAGACTCGACGGGTACGTCCGGGGTAGGAGTGAAATCCTGTAATCCTGGACGGA 3AATCAGCATCTGCTAACTCCGTGCCAGCAGCCGCGGTAATACGGAGTATGCAAGCGTTATCCGGAAT(FGCTCTTGAGTCCCGGAGAGGCTGCCGGAATTCGTGGTGTAGCGGTGAAATGCGTAGAGATCACGAG TGGCTAGGGACCGGACGGTGTCGAGGCTATTCCAGGAGTAGGGGTGAAATCCTAAAATTCCTGGAGC GCTCTTGAGTCCCGGAGAGGCTGTCGGAATTCGTGGTGTAGCGGTGAAATGCGTAGAGATCACGAGG 3GCTTGGGGCCGGAAGATCTGAGGGGTACGTCCGGGGTAGGAGTGAAATCCTGTAATCCTGGACGGA GCTTGGGACCGGAAGACCTGAGGGGTACGTCCGGGGTAGGAGTGAAATCCCGTAATCCTGGACGGA(GCTAGAGTGCAGGAGGAAGGTAGAATTCCCGGTGTAGCGTGAAATGCGTAGAGATCGGGAGG/ GCTCTTGAGTCCCGGAGAGGTTGCCGGAATTCGTGGTGTAGCGGTGAAATGCGTAGATATCACGAGG GGCTTGGGGCCGGAAGACCCAGGGGGTACGTCCGGGGTAGGAGTGAAATCCCGTAATCCTGGACGG 3GCTTGGGGCCGGAGGACTCGAGGGGTACGTCCGGGGTAGGAGTGAAATCCAGTAATCCTGGACGG/ TAGCTTGGGACCGGAAGACCTGAGGGGTACGTCTGGGGTAGGAGTGAAATCCCGTAATCCTGGACGC TCGGCTTGGGACCGGGAGACCAGAGGGGTACGTCCGGGGTAGGAGTGAAATCCCGTAATCCTGGACC TAAGCATCGGCTAACTCCGTGCCAGCAGCCGCGGTAATACGGAGGATGCAAGCGTTGTCCGGAATCA GCTTGGGACCGGAAGGCGCGACGGGTACGTCCGGGGTAGGAGTGAAATCCCGTAATCCTGGACGGA TGGCTTGGGGCCAGAAGACCTGAGGGGTACGTCCGGGGTAGGAGTGAAATCCCGTAATCCTGGACG(\GGAATAAGCATCGGCTAACTCCGTGCCAGCAGCCGCGGTAATACGGAGGATGCAAGCGTTATCCGG/ GGCTTGGGACCGGAGGCGCGACGGGTACGTCCGGGGTAGGAGTGAAATCCCGTAATCCTAGACGG. 3GCTCGGGACCGGAAGACCCAACGGGTACGTCCAGGGTAGGAGTGAAATCCCGTAATCCTGGACGGA AGCTTGAGTGCAGAAGAGGTAGGCGGAATGTAGCATGTAGCTGTGAAATGCATAGATATGTTACAGA. 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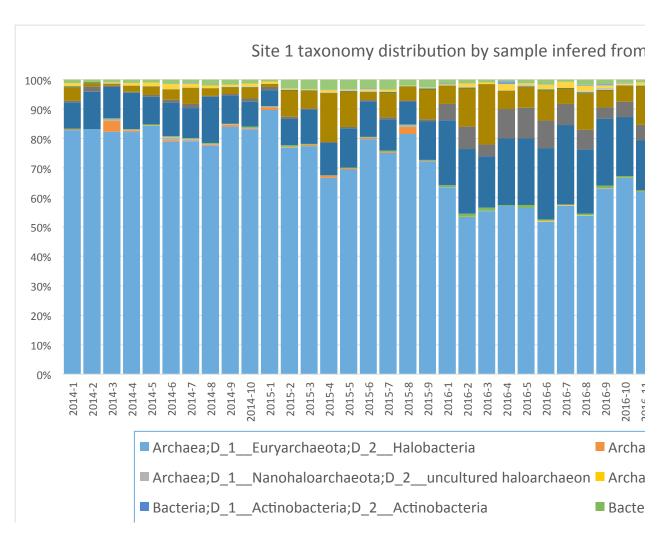
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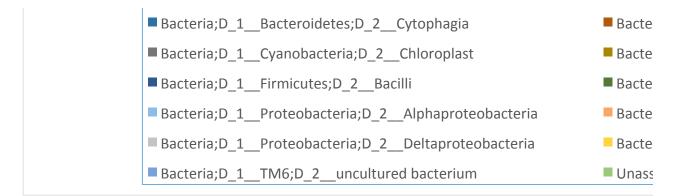
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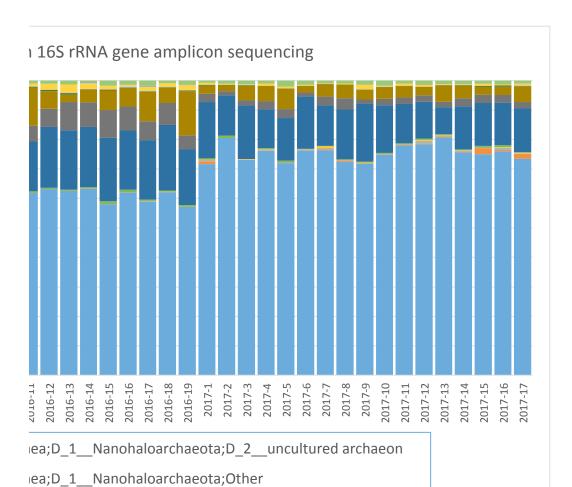
ACTTAAATGAATTGACGGCA ACTTAAAGGAATTGACGG

Taxa	2014-1	2014-2	2014-3
Archaea;D_1Euryarchaeota;D_2Halobacteria	0.82864095	0.83173077	0.82270549
Archaea;D_1_Nanohaloarchaeota;D_2_uncultured archaeon	0.00278067	0	0.03722816
Archaea;D_1_Nanohaloarchaeota;D_2_uncultured haloarchaeon	0.00034758	0	0.00663472
Archaea;D_1Nanohaloarchaeota;Other	0	0	0
Bacteria;D_1Actinobacteria;D_2Actinobacteria	0.00034758	0	0.0003686
Bacteria;D_1Actinobacteria;D_2Nitriliruptoria	0.00208551	0	0.00147438
Bacteria;D_1_Bacteroidetes;D_2_Cytophagia	0.08759124	0.12740385	0.10615555
Bacteria;D_1_Bacteroidetes;D_2_Sphingobacteriia	0	0	0
Bacteria;D_1Cyanobacteria;D_2Chloroplast	0.0066041	0.01682692	0.00479174
Bacteria;D_1Cyanobacteria;D_2Cyanobacteria	0.04553354	0.01201923	0.00663472
Bacteria;D_1_Firmicutes;D_2_Bacilli	0	0	0
Bacteria;D_1Planctomycetes;D_2Phycisphaerae	0.00278067	0.00240385	0.0003686
Bacteria;D_1Proteobacteria;D_2Alphaproteobacteria	0	0	0
Bacteria;D_1Proteobacteria;D_2Betaproteobacteria	0	0	0
Bacteria;D_1Proteobacteria;D_2Deltaproteobacteria	0.00139034	0	0.00073719
Bacteria;D_1Proteobacteria;D_2Gammaproteobacteria	0.00973236	0	0.00368596
Bacteria;D_1_TM6;D_2_uncultured bacterium	0	0	0.0003686
Unassigned;Other;Other	0.01216545	0.00961538	0.0088463





2014-4	2014-5	2014-6	2014-7	2014-8	2014-9	2014-10
0.82220367	0.84212985	0.78941525	0.79018547	0.77551985	0.84036057	0.83158211
0.00375626	0.00046707	0.00407106	0.0015456	0.00283554	0.00639721	0.00240168
0.0033389	0.00093414	0.01110289	0.00618238	0.00283554	0.00232626	0.00150105
0	0.00093414	0.00111029	0.0015456	0	0.00029078	0
0	0	0	0	0	0	0
0.00250417	0.0032695	0.00259067	0.00193199	0.00425331	0.00116313	0.00480336
0.12353923	0.09388136	0.11361954	0.10239567	0.15595463	0.09566735	0.08495947
0	0	0	0	0	0	0
0.00375626	0.006539	0.0099926	0.01313756	0.00330813	0.0049433	0.01080757
0.01961603	0.02895843	0.03478905	0.05448223	0.02551985	0.02268101	0.03752627
0	0	0	0	0	0	0
0.00083472	0	0.0003701	0.0007728	0.00094518	0.00145391	0.00150105
0	0.00046707	0	0	0	0	0
0	0	0	0	0	0	0
0	0.00046707	0.0003701	0.0007728	0	0.00087235	0.00240168
0.00918197	0.01167679	0.01813472	0.01313756	0.00897921	0.00697877	0.00960672
0.00083472	0.00046707	0.00074019	0.0015456	0.00047259	0	0.00030021
0.01043406	0.0098085	0.01369356	0.01236476	0.01937618	0.01686537	0.01260883



ria;D_1__Actinobacteria;D_2__Nitriliruptoria

```
ria;D_1__Bacteroidetes;D_2__Sphingobacteriia
ria;D_1__Cyanobacteria;D_2__Cyanobacteria
ria;D_1__Planctomycetes;D_2__Phycisphaerae
ria;D_1__Proteobacteria;D_2__Betaproteobacteria
ria;D_1__Proteobacteria;D_2__Gammaproteobacteria
signed;Other;Other
```

2015-1	2015-2	2015-3	2015-4	2015-5	2015-6	2015-7	
0.89655172	0.7683838	0.77417323	0.66714559	0.69514563	0.79750645	0.75147275	
0.00940439	0.00275265	0.00472441	0.00670498	0.00355987	0.00472915	0.0033137	
0.0031348	0.00117971	0.00031496	0.00047893	0.00032362	0.00085985	0	
0	0	0.00031496	0	0	0	0	
0	0	0	0	0	0	0	
0.00052247	0.00511207	0.00251969	0.00143678	0.00194175	0.00257954	0.00405007	
0.05485893	0.08926465	0.11527559	0.10871648	0.13398058	0.12037833	0.10530191	
0	0	0	0	0	0	0	
0.01044932	0.00707825	0.00535433	0.00335249	0.0038835	0.00472915	0.00773196	
0.01097179	0.08887141	0.05889764	0.16618774	0.11941748	0.02536543	0.08284242	
0	0	0	0	0	0	0	
0	0.00314589	0.00251969	0.00191571	0.0038835	0.00257954	0.00257732	
0	0.00039324	0	0	0	0	0	
0	0	0	0	0	0	0	
0	0.00157295	0.00094488	0.00047893	0.00161812	0.00171969	0.00257732	
0.00783699	0.00275265	0.00188976	0.00814176	0.00291262	0.00730868	0.0062592	
0	0.00039324	0.00094488	0.00047893	0.00032362	0.00257954	0.00036819	
0.00626959	0.02909949	0.03212598	0.03496169	0.03300971	0.02966466	0.03350515	

2015-8	2015-9	2016-1	2016-2	2016-3	2016-4	2016-5
0.81506165	0.72290048	0.63358779	0.53358925	0.55335787	0.57153502	0.56413399
0.023992	0.00221976	0	0	0	0	0
0.00633122	0.00036996	0.00127226	0.00076775	0.00091996	0	0.0004085
0	0	0	0.00038388	0	0	0.0004085
0.00033322	0	0	0	0	0	0
0.00233256	0.0018498	0.00636132	0.00998081	0.01103956	0.00298063	0.00980392
0.07597468	0.12985572	0.22073791	0.21919386	0.17433303	0.22690015	0.22589869
0	0	0	0	0	0.00037258	0
0.00499833	0.0081391	0.05534351	0.07600768	0.03955842	0.09798808	0.10334967
0.04565145	0.10099889	0.06170483	0.13013436	0.20561178	0.06184799	0.07189542
0	0	0	0	0	0	0.0004085
0.00199933	0.00295967	0.0019084	0.00307102	0.00045998	0.00037258	0.00122549
0	0	0	0.00076775	0	0.00074516	0.00204248
0	0	0	0	0	0	0
0.00033322	0.00221976	0	0.00153551	0	0	0.00163399
0.00233256	0.00147984	0.00318066	0.01151631	0.00459982	0.02235469	0.00653595
0	0.00147984	0.00254453	0	0	0.00894188	0.00081699
0.02065978	0.02552719	0.01335878	0.01305182	0.0101196	0.00596125	0.01143791

2016-6	2016-7	2016-8	2016-9	2016-10	2016-11	2016-12
0.51664753	0.57154109	0.53772017	0.62882279	0.66681194	0.61848011	0.63152401
0.00114811	0.00105014	0	0.00013965	0	0.00015477	0
0.00153081	0.00078761	0.00066467	0.00293255	0.00021791	0.00046432	0.00014912
0.00153081	0.00052507	0.00066467	0.00013965	0.00032687	0.0006191	0.00044736
0	0	0	0	0.00010896	0.00015477	0
0.00497512	0.00236282	0.00598205	0.00879765	0.00435825	0.00464324	0.00387712
0.24225029	0.26988711	0.21834497	0.22636503	0.20156897	0.16916886	0.20742619
0	0	0	0	0	0.00046432	0.00029824
0.09299656	0.07140982	0.06613493	0.03812317	0.05153628	0.05293298	0.06113928
0.101416	0.05145708	0.12429379	0.05767351	0.05469601	0.12908219	0.05964808
0	0	0	0	0	0	0
0.00382702	0.00236282	0.00299103	0.00251362	0.00130747	0.00355982	0.003728
0.0003827	0.00026254	0.00166168	0	0.00032687	0.00046432	0.00014912
0	0	0	0	0	0	0
0.0007654	0.00026254	0.00199402	0.0058651	0.00141643	0.00077387	0.00164032
0.01492537	0.02074035	0.01927551	0.00865801	0.00414034	0.00944126	0.01953475
0.00153081	0	0.00265869	0.00502723	0.00217912	0.00046432	0
0.01607348	0.00735101	0.01761383	0.01494205	0.01100458	0.00913171	0.01043841

2016-13	2016-14	2016-15	2016-16	2016-17	2016-18	2016-19
0.6251186	0.63337431	0.57947757	0.62026066	0.58941836	0.62056213	0.57117246
0.00023719	0.00030731	0.00023427	0.00019747	0.00035039	0.00052832	0
0.0001186	0.00030731	0.00105423	0.00098736	0.00105116	0.00105664	0.00089638
0.00083017	0.00010244	0	0	0.00077085	0.00147929	0.00035855
0	0	0	0	0	0	0
0.00391366	0.00389264	0.00995666	0.00770142	0.0049054	0.0023246	0.00466117
0.20125712	0.2052858	0.21459529	0.20161927	0.20119131	0.22379544	0.19074937
0	0.00010244	0	0	0	0.00052832	0
0.09629981	0.08225773	0.09523252	0.08076619	0.06426069	0.07354184	0.04661169
0.02419355	0.04435566	0.06606536	0.06477093	0.09950946	0.05092984	0.15023306
0	0.00010244	0	0	0	0	0
0.005574	0.00051219	0.00281129	0.00059242	0.00280308	0.0023246	0.00197203
0.00023719	0.00040975	0	0.0021722	0.00021023	0.00021133	0.00017928
0	0	0	0	0	0	0
0.00177894	0.00071707	0.00152278	0.00118483	0.00063069	0.00052832	0.00197203
0.02692125	0.01905347	0.01194799	0.00552923	0.01450596	0.01299662	0.01595554
0	0.00368777	0	0.00157978	0.00294324	0	0.0007171
0.01351992	0.00553165	0.01710203	0.01263823	0.01744919	0.00919273	0.01452133

2017-1	2017-2	2017-3	2017-4	2017-5	2017-6	2017-7	
0.71698113	0.80517381	0.7311007	0.76139887	0.7193851	0.76200807	0.76367199	
0.00943396	0.00080841	0.00090717	0.00030499	0.00062533	0.00035318	0.00232715	
0.00440252	0	0.00060478	0.00503228	0.0015112	0.00514632	0.00600159	
0.00062893	0	0.00143635	0.00045748	0.00046899	0.00075681	0.00483802	
0	0	0	0	0	0	0	
0.00440252	0.00727567	0.00037799	0.00396482	0.00672225	0.00085772	0.00146978	
0.19119497	0.13662086	0.18037496	0.13094088	0.14450234	0.17663976	0.13742421	
0	0	0	0	0	0	0	
0.02893082	0.01455133	0.0190505	0.02831292	0.03053674	0.0136226	0.03025292	
0.02641509	0.01940178	0.0489114	0.05062776	0.06857738	0.02199798	0.04176618	
0	0	0	0	0	0	0	
0.00377358	0.00242522	0.00173874	0.00152493	0.00135487	0.00095863	0.00097985	
0	0	0	0	0	0	0	
0	0	0	5.08E-05	0.00015633	0.00010091	6.12E-05	
0	0	0.00128515	0.00020332	0.00010422	0.00030272	0.00024496	
0.00628931	0.00323363	0.00211672	0.00787882	0.0054716	0.00292634	0.00183722	
0	0	7.56E-05	5.08E-05	0	0	6.12E-05	
0.00754717	0.0105093	0.01201996	0.00925126	0.02058364	0.01432896	0.00906363	

2017-8	2017-9	2017-10	2017-11	2017-12	2017-13	2017-14	
0.724493	0.71781278	0.74780289	0.78047196	0.78340236	0.80767804	0.75725594	
0.00401833	0.00083308	0.00133396	0.00194847	0.00122718	0.00296736	0.00172519	
0.00175802	0.0019691	0.0017263	0.00173198	0.01127474	0.0027819	0.00416075	
0.00031393	0.00159043	0.00094162	0.0002165	0.00276116	0.00055638	0.00071037	
0	0	0	0	0	0	0	
0.00182081	0.00325659	0.00258945	0.00248972	0.00490873	0.00510015	0.00274	
0.16983738	0.19494093	0.16250785	0.13347045	0.12478908	0.09124629	0.14674244	
6.28E-05	0	0	0	0	0	0	
0.03836253	0.0157528	0.02126491	0.0220827	0.02162908	0.01789688	0.02699411	
0.04520625	0.03279309	0.03852793	0.03864473	0.02822519	0.05563798	0.04221636	
0	0	0	0	0	0	0	
0.00125573	0.00098455	0.00180477	0.00097424	0.00069029	0.00083457	0.00243556	
6.28E-05	0	0	0.0002165	0	0	0.00040593	
6.28E-05	0.00015147	0.00015694	0	7.67E-05	9.27E-05	0.00010148	
0.00018836	0.00045441	0.00039234	0.00043299	0.00053689	0.00083457	0.00071037	
0.00269982	0.01529839	0.00329567	0.00725265	0.00628931	0.00213279	0.00274	
6.28E-05	0	0	0	7.67E-05	0	0.00010148	
0.00979469	0.01416238	0.01765537	0.01006711	0.01411259	0.01224036	0.01096002	

2017-15	2017-16	2017-17
0.75061451	0.75966562	0.73520744
0.02064752	0.00429583	0.01632283
0.00175574	0.00847556	0.00204035
0.00049161	0.00197376	0.00226706
0	0	0
0.00456493	0.00626959	0.00068012
0.14551584	0.14396842	0.15007935
0	0	0.00022671
0.02816209	0.02681992	0.02063024
0.02661704	0.02821317	0.05259578
0	0	0
0.00351148	0.00371531	0.00181365
0.00014046	0	0
0.00014046	0	0
0.00028092	0.0001161	0.00340059
0.00723365	0.00394752	0.00510088
0	0	0
0.01032376	0.01253918	0.009635

OTU ID	SG1-BOT-201SG1-F	3OT-201SG1-	BOT-201SG1-B	OT-201SG1-	BOT-201
EF106537.1.904	1	1	0	0	0
CU467404.1.1354	3	2	1	0	0
CU467121.1.1342	0	0	0	0	0
KC465608.1.1353	3	1	1	4	2
AB454051.1.1420	0	0	0	0	0
GQ861389.1.920	2	0	1	2	1
AB663427.1.1471	0	0	0	0	0
KF100432.1.1345	0	0	0	0	0
JX883654.1.1487	2	0	0	0	0
FJ890991.1.1350	0	0	0	0	0
JX883445.1.1493	0	0	0	0	0
HM126809.1.1479	1	0	0	0	0
EU869375.1.1415	1	1	0	0	0
JX882356.1.1454	0	0	0	0	0
CU467262.1.1344	1	0	0	0	0
AJ969889.1.918	0	0	0	0	0
HQ400553.1.914	2	4	1	0	0
EF690614.1.1438	2	0	0	0	0
FN391185.1.1355	0	0	0	0	0
GQ375041.1.1370	0	0	0	0	0
KC758946.1.1404	0	0	0	0	0
KC354385.1.904	1	0	0	0	0
HQ400485.1.919	0	1	0	0	1
GQ374969.1.1442	0	0	0	1	0
HQ425095.1.932	0	0	0	0	0
GQ861355.1.915	3	3	0	0	0
KF798423.1.1453	0	0	0	0	0
FN391290.1.1341	3	0	0	0	0
AB108676.1.1473	0	0	0	0	0
AB663392.1.1473	5	0	0	0	0
EU869367.1.1235	1	0	0	0	0
HQ400502.1.918	5	0	0	0	1
AM981378.1.1352	7	0	0	0	0
JX882083.1.1474	5	0	0	1	0
JX884811.1.1468	0	0	0	0	0
AB534005.1.1513	10	0	0	0	0
KF620446.1.1362	5	0	0	1	1
FN391257.1.1346	0	0	0	0	1
KF582944.1.1471	36	1	0	0	0
FN391286.1.1344	0	0	0	0	0
EU869373.1.1239	3	4	2	0	1
KM068159.1.1473	3	0	1	1	0
KJ917626.1.1376	1	0	0	0	0
EU869377.1.1432	3	0	0	0	0

CP007060.191367.192843	24	0	1	0	0
JX882977.1.1481	35	5	2	2	1
HQ400533.1.919	1	0	0	0	0
JX883895.1.1471	1	0	0	1	0
AM947496.1.1351	41	6	4	4	3
KC003257.1.1346	2	0	0	0	0
HQ400507.1.919	0	0	0	1	0
JN714439.1.1469	17	1	0	0	2
HE604526.1.919	0	0	0	0	0
EF106039.1.1370	2	1	0	0	0
KC918821.1.1386	0	0	0	1	0
AB735496.1.1471	18	0	0	0	0
CU915217.1.1386	0	0	0	0	0
HM126955.1.1468	1	0	0	0	0
KF452248.1.954	6	0	0	0	0
HG475330.1.920	0	0	0	0	0
JX882784.1.1485	4	1	0	0	3
AJ969892.1.919	30	0	3	4	0
FN391194.1.1355	1	3	0	0	0
FN393530.1.1361	16	0	0	0	0
JX884089.1.1458	1	0	0	0	0
JX882971.1.1478	1	0	0	0	0
CU467261.1.1348	1	0	0	0	0
DQ432015.1.1454	103	0	6	0	2
HQ157635.1.921	3	4	2	7	0
AB533937.1.1485	1	1	4	0	1
JX883276.1.1475	3	0	2	0	0
HQ425152.1.1427	3	0	0	0	1
AB533842.1.1259	2	1	2	0	0
AM947482.1.1343	0	0	0	0	0
JN714404.1.1473	0	0	0	0	0
HQ425189.1.1455	0	0	0	0	0
JN714464.1.1470	4	1	0	1	0
KF673170.1.1386	97	4	1	3	2
CU467266.1.1348	3	0	0	0	0
AJ344317.1.917	1	0	0	0	0
JN714460.1.1472	10	1	0	0	1
FN391272.1.1348	66	10	21	0	1
CP001688.1954831.19563(3	0	0	0	0
AB454050.1.1425	8	0	0	3	1
HQ425172.1.1426	4	0	0	0	0
EF105755.1.1364	7	0	0	0	1
EU869371.1.1242	1	0	0	0	1
KF234379.1.1501	0	0	0	0	0
AJ344314.1.918	0	0	0	0	1

HQ425162.1.1424	43	4	17	5	7
FN391256.1.1340	1	0	0	0	0
KF717637.1.955	6	2	0	0	1
AB534154.1.972	5	0	1	0	0
CU467357.1.1354	0	0	0	0	0
HQ215546.1.1474	2	0	0	0	0
HQ400452.1.918	3	1	0	0	0
EF535046.1.974	8	0	0	0	0
JQ237116.1.1471	5	0	2	0	1
GQ374923.1.1446	0	0	0	0	0
JN714407.1.1472	1	0	0	0	0
CU467127.1.1340	0	0	0	0	0
KC465586.1.1352	25	1	1	5	1
JX884060.1.1469	12	1	0	0	0
FN391294.1.1347	9	0	0	0	3
GQ032594.1.1348	0	0	0	0	0
JQ937358.1.1388	1	0	0	0	0
CU467410.1.1354	0	0	0	0	0
GQ861367.1.915	58	88	14	19	25
HF677567.1.1352	0	0	0	0	0
EF106344.1.1451	0	0	1	0	0
HE604458.1.916	0	0	0	2	0
AJ315073.1.1441	0	0	0	0	0
JX882124.1.1468	26	2	4	3	1
KC465612.1.1351	9	2	0	1	0
FJ978723.1.1421	0	0	0	0	0
JN714448.1.1473	24	5	1	5	2
JN714420.1.1471	4	0	4	2	1
AB766179.1.1471	15	0	0	0	0
AB072814.1.1472	0	0	0	0	0
FJ696371.1.1397	0	0	0	0	0
CU467136.1.1339	0	0	0	0	3
FN391291.1.1344	3	1	1	0	0
GQ374958.1.1442	1	3	0	4	0
KF234338.1.1355	14	5	4	10	3
DQ432537.1.1395	0	0	0	0	1
GQ861378.1.924	4	3	1	0	1
HQ400414.1.919	0	0	0	0	0
JX883832.1.1478	3580	544	301	208	141
JX883632.1.1475	4	0	0	0	0
New.ReferenceOTU74	4	0	0	1	0
New.ReferenceOTU75	24	1	1	0	0
New.ReferenceOTU76	72	9	3	3	5
New.ReferenceOTU8	0	0	0	114	1
New.ReferenceOTU9	0	0	0	1	0

New.ReferenceOTU111	128	6	0	5	11
New.ReferenceOTU2	179	19	1	83	9
New.ReferenceOTU3	762	82	54	60	74
New.ReferenceOTU6	0	0	0	1	0
New.ReferenceOTU7	255	0	13	30	17
New.ReferenceOTU91	545	69	23	31	6
New.ReferenceOTU177	25	6	3	2	0
New.ReferenceOTU135	1	0	0	0	1
New.ReferenceOTU63	53	1	1	2	0
New.ReferenceOTU19	343	48	68	8	68
New.ReferenceOTU12	80	13	9	3	6
New.ReferenceOTU13	2604	413	349	188	132
New.ReferenceOTU10	849	166	131	38	43
New.ReferenceOTU11	65	3	1	0	2
New.ReferenceOTU17	79	0	2	21	3
New.ReferenceOTU14	247	5	18	20	20
New.ReferenceOTU90	48	3	1	6	2
New.ReferenceOTU95	19	0	0	2	0
New.ReferenceOTU92	45	4	2	15	9
New.ReferenceOTU52	17	0	0	0	0
New.ReferenceOTU0	113	0	2	7	12
New.ReferenceOTU1	27	1	3	5	1
New.ReferenceOTU89	21	2	4	0	4
New.ReferenceOTU88	1	4	0	0	1
New.ReferenceOTU112	109	4	33	6	5
New.ReferenceOTU113	6	1	0	0	0
New.ReferenceOTU30	154	15	5	11	14
New.ReferenceOTU31	59	2	36	4	1
New.ReferenceOTU32	386	11	29	5	7
New.ReferenceOTU5	76	4	3	4	1
New.ReferenceOTU116	17	4	4	0	1
New.ReferenceOTU152	403	39	145	33	27
New.ReferenceOTU114	230	14	18	11	31
New.ReferenceOTU23	296	82	29	145	22
New.ReferenceOTU20	3	0	0	1	0
New.ReferenceOTU27	1719	144	165	120	157
New.ReferenceOTU26	249	8	141	44	30
New.ReferenceOTU25	11	6	2	0	0
New.ReferenceOTU24	32	1	4	0	1
New.ReferenceOTU29	4	0	0	0	0
New.ReferenceOTU28	147	6	19	3	5
New.ReferenceOTU57	64	10	6	1	5
New.ReferenceOTU54	431	32	27	24	4
New.ReferenceOTU50	138	19	15	4	29
New.ReferenceOTU184	2	0	0	1	0

New.ReferenceOTU53	141	2	1	4	5
New.ReferenceOTU188	0	1	0	0	0
New.ReferenceOTU58	230	59	14	22	19
New.ReferenceOTU59	2	0	0	0	0
New.ReferenceOTU87	19	4	2	4	0
New.ReferenceOTU86	15	0	0	2	0
New.ReferenceOTU196	187	41	12	15	32
New.ReferenceOTU49	93	26	3	16	73
New.ReferenceOTU108	108	9	3	4	2
New.ReferenceOTU102	136	16	24	16	15
New.ReferenceOTU107	32	0	0	20	1
New.ReferenceOTU106	121	6	0	34	1
New.ReferenceOTU105	0	0	0	0	0

SG1-BOT-2019	G1-BOT-201SG1-F	3OT-201SG1-	BOT-201SG1-	BOT-201SG1-	BOT-201SG1-	BOT-201
0	0	0	0	0	0	0
82	3	3	5	1	5	1
0	0	0	0	0	0	0
1	2	0	0	1	1	2
0	0	0	1	0	0	0
77	2	6	27	1	80	0
0	1	8	0	0	3	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	1	0
3	0	0	0	0	0	0
12	0	0	0	0	4	0
2	1	0	2	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	5	0	0	3	0
4	0	0	9	1	7	0
1	0	1	0	0	1	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
2	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	5	2	0	0	0
1	0	0	0	0	0	0
0	0	0	0	0	1	0
9	0	5	14	0	23	0
0	0	0	0	0	0	0
1	0	0	0	0	1	0
0	0	0	0	0	0	0
5	1	1	2	0	10	0
2	0	0	0	0	0	0
0	1	7	4	0	3	0
0	0	0	1	0	1	0
4	1	14	0	0	0	0
0	0	0	1	0	1	0
2	0	0	3	0	0	4
3	1	0	0	0	2	0
1	0	1	1	0	3	0
15	0	1	1	0	12	0
0	1	3	0	0	0	0
1	0	1	1	0	0	0
11	2	3	8	1	11	0
0	0	1	0	0	0	0
3	0	1	1	0	2	0

7	0	13	10	0	2	0
33	4	12	12	4	20	4
2	3	2	0	0	0	0
2	1	1	1	1	0	0
26	6	13	17	6	30	1
1	0	0	0	0	0	0
0	2	23	0	0	0	0
2	2	1	1	0	13	0
0	0	1	0	0	0	0
6	0	0	0	0	0	0
0	0	3	0	0	2	0
5	0	0	21	0	3	0
0	0	1	0	0	0	0
1	0	0	0	0	0	0
1	1	0	0	0	0	0
0	0	6	0	0	1	0
16	3	10	3	2	3	1
18	7	26	4	3	31	3
2	0	1	1	0	2	0
5	0	0	0	0	4	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
11	6	1	47	0	18	0
1	1	3	1	0	3	2
1	0	0	0	0	1	0
0	0	0	1	1	1	0
0	0	0	0	1	1	0
0	0	0	0	0	2	0
0	1	0	0	0	0	0
1	0	0	0	0	0	0
2	0	1	1	0	1	0
10	0	2	4	0	10	2
50	11	16	22	2	41	1
7	0	7	1	0	1	3
0	0	32	0	0	0	0
8	0	38	15	5	1	8
38	10	4	6	0	8	0
3	1	0	0	0	3	0
5	5	15	2	0	9	2
2	2	1	0	0	2	0
7	1	3	3	2	1	0
0	1	0	1	0	0	1
0	0	0	0	0	0	0
0	1	12	0	0	1	0

142	3	2	14	4	19	6
0	0	0	0	0	0	0
2	0	1	0	1	3	0
0	0	2	0	0	4	0
1	0	0	0	0	0	0
1	0	1	1	0	4	0
5	2	3	7	0	12	0
14	1	7	2	1	2	0
4	2	5	1	0	14	0
0	0	0	0	0	1	0
1	0	1	0	0	1	0
0	0	0	0	0	0	0
25	6	3	6	0	22	0
25	0	0	1	0	5	0
1	3	2	2	0	1	0
0	1	0	0	2	0	0
0	0	0	0	0	0	0
0	0	1	0	1	0	0
26	35	155	9	5	23	50
3	0	0	0	0	1	0
0	0	1	0	0	0	0
0	0	1	0	0	1	0
0	0	0	2	0	0	0
11	6	12	15	5	17	6
4	0	13	4	0	5	1
0	0	0	1	0	0	0
47 12	10	50	21	4	34	0
13 9	2	4	20 0	2	15 3	3 0
0	0 0	0	0	0		0
0	0	0	0	0 0	1 0	0
0	0	1	0	0	0	0
1	0	6	0	0	0	0
1	1	15	0	0	2	0
5	8	53	14	6	5	13
0	0	0	0	0	1	0
3	1	10	0	1	1	4
0	0	0	0	0	1	0
3225	497	1020	1932	458	2035	206
0	0	0	0	0	0	0
6	0	1	3	0	1	1
15	0	2	18	2	19	0
70	0	10	21	28	35	7
0	3	1470	0	23	0	1
4	3	309	0	1	0	0

120	25	45	16	7	57	2
92	66	943	92	133	86	22
1560	132	377	1199	181	987	124
0	132	13	0	0	0	0
317	32	202	259	9	676	5
378	50	92	136	82	107	137
66	2	23	22	2	15	11
1	0	0	0	0	2	0
41	0	3	7	8	23	8
41	185	78	44	231	36	7
76	14	22	38	8	43	6
1799	308	1282	597	285	765	169
649	119	238	437	134	352	81
47	2	236	43 <i>7</i> 62	2	47	0
51	13	131	183	0	673	0
186	33	101	103	6	380	3
65	2	101	31	1	123	0
32	3	7	13		123	0
				0		
82 4	13	26	48	5	164	1
	0	1	0	0	4	0
107	23	37	44	3	85	5
37	5	35	18	3	13	2
96	0	0	9	2	16	3
1	1	0		0	2	0
152	23	73	45	7	42	11
1	0	1	14	0	10	0
184	7	11	8	0	32	0
56	9	10	128	14	50	8
359	14	21	212	19	169	13
38	7	78	14	0	13	16
19	3	6	26	1	13	1
312	90	95	201	106	159	65
231	574	204	76	31	58	7
315	84	623	174	81	253	39
2	5	1	0	0	0	0
3110	245	794	2037	237	1809	259
183	336	94	97	121	191	7
2	0	13	10	0	0	2
115	16	28	67	1	25	2
1	0	1	1	0	0	0
114	9	12	67	11	58	14
51	12	13	37	7	28	6
341	27	162	143	49	301	83
58	46	51	44	7	79	1
3	1	1	3	0	2	0

96	4	6	15	1	141	0
1	0	0	0	0	0	0
256	26	46	138	81	216	39
0	0	0	0	0	4	0
12	3	26	7	3	15	1
3	1	21	5	6	21	1
80	78	86	62	24	124	0
41	38	160	1	3	19	10
133	7	10	78	31	51	14
162	43	60	107	16	55	31
89	9	193	328	0	25	1
259	12	97	170	16	131	22
0	0	0	0	0	0	0

SG1-BOT-201SG1	1-BOT-201SG1-F	3OT-201SG1-I	BOT-201SG1-I	3OT-201SG1-	BOT-201SG1-	BOT-201
0	0	0	0	0	0	0
1	1	1	1	1	1	1
1	0	0	0	0	0	0
7	0	0	1	0	0	2
0	0	0	0	0	0	0
3	0	0	0	6	30	18
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	1	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
4	0	2	1	1	0	0
0	0	2	0	0	0	0
0	0	0	0	0	0	0
0	0	0	2	0	0	0
0	2	0	1	0	1	1
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6	0	0	0	0	1	0
0	0	0	0	0	1	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	1	1
8	0	0	0	0	1	0
1	0	0	0	0	1	0
3	0	0	0	0	0	17
0	0	1	1	0	0	0
0	0	0	0	0	0	1
0	0	0	0	0	1	0
0	0	1	1	0	0	3
0	0	0	0	0	1	0
5	1	0	0	0	0	0
0	0	0	0	0	1	0
1	0	0	0	0	0	0
0	0	0	0	0	0	0
0	3	0	0	0	0	1
12	0	0	0	2	1	0
0	0	0	0	0	0	0
3	0	0	0	0	0	11
0	0	0	0	0	0	0
2	1	1	1	0	0	0
2	1	0	0	1	0	7
0	0	0	0	0	0	0
0	0	0	0	0	0	0

1	0	0	0	2	4	27
14	3	6	3	2	3	17
1	0	0	0	0	0	1
0	1	1	0	1	0	0
30	1	1	3	4	4	37
0	0	0	0	0	0	0
0	0	0	0	0	0	1
12	0	0	0	2	1	10
0	0	0	0	0	0	1
18	0	0	0	0	0	0
0	0	0	0	0	0	0
1	0	0	0	0	0	0
0	0	2	1	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	1
0	0	0	0	0	0	0
10	4	0	2	4	2	4
2	5	2	1	2	3	36
0	0	0	0	0	0	2
0	0	0	1	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
32	0	2	0	5	4	0
1	3	0	3	0	1	1
3	0	0	2	0	1	0
1	1	1	0	0	0	0
12	1	0	1	2	1	0
1	0	0	1	0	0	0
0	0	1	0	0	1	0
0	0	0	0	0	0	1
0	0	0	0	0	1	2
1	4	1	1	0	2	11
16	1	1	7	2	6	16
1	2	0	0	0	0	3
0	0	0	0	0	0	0
0	15	0	4	0	4	121
20	1	5	1	3	7	1
1	1	0	0	0	0	3
1	0	0	0	0	2	14
0	0	0	0	0	0	0
0	2	0	0	1	0	1
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0

16	5	9	11	1	6	14
0	0	0	0	0	0	0
2	1	0	0	0	2	1
1	0	0	0	0	0	1
0	0	0	0	0	0	0
0	0	0	0	0	0	1
0	1	0	0	0	0	47
9	2	0	0	1	1	4
2	1	2	0	0	1	3
0	0	0	0	0	0	0
0	0	0	0	0	0	0
1	0	0	0	0	0	0
15	0	1	4	1	3	32
0	0	0	0	0	1	0
33	0	0	1	3	0	0
1	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
41	30	2	30	3	27	66
0	0	0	0	0	0	2
0	0	0	0	0	0	1
0	0	0	0	0	0	0
0	0	0	0	0	0	0
13	5	1	6	1	1	5
1	2	0	2	0	4	12
0	0	1	0	0	0	0
7	4	1	3	4	16	30
7	5	0	0	1	1	11
2	0	1	0	0	0	1
0	0	0	0	0	0	0
0	0	0	0	2	0	0
16	0	0	0	2	0	0
0	0	1	1	0	0	3
1	0	0	4	0	1	0
3	20	3	3	2	19	131
0	0	0	0	0	0	0
2	1	0	1	0	0	4
0	0	0	0	0	0	0
1862	343	230	361	93	282	1409
0	0	0	0	0	0	0
0	1	0	0	0	2	3
1	0	0	0	0	1	8
22	47	9	4	0	3	368
55	0	0	298	0	0	0
0	0	0	0	0	0	0

80	9	5	8	3	12	22
60	97	90	83	5	18	924
107	280	37	27	21	95	1294
0	0	0	0	0	93	0
225	7	15	20	99	61	417
					6	
12	191	195	75	1		132
1 0	14 0	2	1 0	0	0	18
		0		0	0	0
0	35	21	0	0	0	15
1300	44	47	42	160	43	69
30	8	2	4	0	6	38
929	350	478	328	204	294	1461
260	123	74	69	17	65	901
2	2	0	0	0	3	14
53	0	1	0	3	11	25
50	10	10	9	12	25	408
24	1	1	2	4	6	77
6	0	0	2	0	0	5
51	0	3	3	12	8	66
1	0	0	0	0	1	1
14	5	6	1	30	11	59
4	2	1	3	0	2	22
4	4	8	2	0	2	8
0	1	0	1	0	1	0
12	9	1	3	7	5	51
0	5	0	0	0	2	9
26	1	7	0	0	4	6
26	7	1	4	0	3	55
39	39	12	6	2	13	102
1	15	4	0	0	5	11
0	5	2	0	0	1	17
208	173	51	40	14	45	162
166	15	16	17	256	57	2988
104	116	94	111	11	37	1793
2	0	0	0	0	2	1
329	423	70	73	45	195	2251
252	29	14	7	191	80	1503
0	1	4	3	0	0	9
5	0	0	0	1	1	62
0	0	0	0	0	0	0
22	17	8	5	2	6	26
31	5	5	2	3	2	13
18	137	15	7	1	20	219
186	5	3	19	6	16	112
0	0	1	0	0	0	1

17	1	0	2	0	3	48
0	2	0	0	0	0	0
108	37	69	110	3	12	27
1	1	0	1	1	0	2
6	8	0	3	2	1	66
0	5	2	0	0	0	43
186	7	5	29	13	42	142
62	14	5	25	11	16	28
12	13	5	2	1	8	49
67	51	10	9	3	9	166
2	21	1	0	0	10	165
5	20	6	21	0	5	178
0	1	0	0	0	0	0

SG1-BOT-201SG1	1-BOT-201SG1-	BOT-201SG1-	BOT-201SG1-	BOT-201SG1-I	BOT-201SG1-	BOT-201
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1	3	1	1	2	1	2
0	0	0	0	0	0	0
0	1	3	0	1	0	0
0	1	2	0	0	0	0
5	0	13	0	0	0	4
1	0	0	0	0	0	0
0	0	0	0	0	0	0
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0	4	0	0	1	0	0
0	1	0	1	0	0	0
1	0	0	1	0	0	0
1	0	1	0	0	0	0
0	0	3	3	3	0	0
1	0	0	1	0	0	0
2	0	0	1	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
1	1	0	0	0	0	7
0	0	0	0	0	0	0
1	0	1	0	0	0	0
1	2	4	2	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	1	0	0	0
1	0	0	0	0	0	0
0	0	0	0	0	0	0
1	0	0	0	0	0	5
0	0	3	1	0	0	0
5	1	0	0	0	2	0
0	4	0	0	0	0	0
0	0	0	0	0	0	0
11	0	6	0	0	0	1
0	0	0	0	0	0	0
0	9	1	0	2	0	0
0	0	0	0	0	0	0
0	0	0	5	0	0	6
0	1	5	0	0	0	0
0	1	0	0	0	0	1
0	0	1	0	0	1	0

2	0	3	0	0	0	0
9	2	3	18	2	1	2
0	1	0	0	0	0	0
0	0	0	0	1	1	0
9	0	32	8	0	5	5
0	0	1	0	0	0	0
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1	0	1	0	0	0	0
0	0	0	0	0	0	0
6	0	0	0	9	0	0
0	0	0	0	0	0	0
0	1	0	0	0	0	0
1	2	2	3	0	1	10
3	0	15	3	1	5	5
			2			
0	0	0		0	1	0
2	1	0	0	0	0	0
0	0	0	0	1	0	0
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0	0	0	0	0	0	0
3	0	1	1	3	0	0
0	0	1	10	2	1	1
0	3	0	7	2	0	0
0	1	0	0	0	0	0
1	0	0	0	0	0	1
0	0	0	1	0	0	1
0	0	0	0	2	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	1	0	1	0	0	0
0	16	28	6	1	3	1
0	0	0	0	1	0	0
0	0	0	0	0	0	0
2	0	13	0	1	2	38
7	11	0	10	13	2	2
0	0	0	0	1	0	1
5	0	4	0	0	0	3
1	1	1	0	0	0	0
0	0	0	0	0	0	1
0	1	0	0	0	1	1
1	0	0	0	0	0	0
0	0	0	0	0	1	0
-	•	J	J	J	-	9

7	10	9	4	21	5	0	
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0	0	0	1	0	0	2	
0	0	0	1	0	0	0	
0	0	0	0	0	0	1	
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0	0	0	1	0	0	0	
0	1	0	0	0	0	0	
2	2	8	7	1	3	0	
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20	1	16	0	0	0	0	
1	0	0	0	0	0	0	
0	0	0	0	0	0	0	
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6	11	7	122	8	17	21	
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0	0	0	0	0	0	0	
0	0	0	0	0	0	0	
2	2	8	3	7	1	9	
2	0	4	1	0	8	7	
0	1	0	0	0	0	0	
6	1	46	8	1	1	2	
1	1	2	1	1	0	1	
0	8	3	1	0	0	0	
0	0	0	0	0	0	0	
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0	3	0	1	0	1	1	
0	0	0	2	0	2	1	
5	5	11	6	5	5	78	
0	0	1	0	0	0	0	
0	1	0	7	0	0	0	
0	0	1	0	0	0	0	
415	344	959	715	288	207	356	
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2	1	2	0	0	1	1	
0	0	40	0	0	0	1	
2	8	29	13	0	14	36	
65	2	0	0	0	143	43	
1	0	0	0	0	0	4	

25	11	38	5	0	2	39
57	16	286	40	3	104	129
68	62	1166	181	57	76	70
0	0	0	0	0	0	0
107	9	397	1	1	5	13
16	14	139	116	85	134	38
0	2	15	5	11	6	0
1	0	0	0	0	0	0
5	3	12	1	0	1	8
149	18	376	78	14	41	72
11	8	16	44	7	8	9
342	147	1431	688	151	377	787
94	54	393	288	73	59	128
1	1	45	3	2	1	1
52	14	74	0	0	1	0
130	26	201	3	0	5	15
5	1	43	10	2	4	5
0	0	16	1	0	3	1
19	4	74	5	2	0	13
0	0	0	0	0	3	0
15	4	103	0	0	0	1
8	5	17	4	1	3	1
4	11	5	5	9	1	0
0	0	0	3	2	1	0
64	23	25	4	2	10	14
2	0	77	1	1	0	0
13	16	10	17	22	8	1
8	1	25	5	9	2	3
22	9	102	26	26	5	14
2	2	10	2	0	1	7
2	0	2	2	5	9	2
67	56	101	62	108	33	57
87	303	972	41	0	22	69
59	71	610	154	13	176	155
3	2	1	0	0	0	0
177	125	1756	267	142	129	164
267	154	668	16	0	45	75
0	1	1	3	8	2	1
14	4	12	0	0	0	14
0	0	0	0	0	0	0
5	5	56	17	11	5	6
4	2	10	44	13	3	8
18	16	111	48	44	42	86
35	3	76	41	3	8	17
0	0	1	1	1	0	0

5	5	10	4	3	1	2
0	0	0	0	0	0	2
30	39	223	76	16	115	1
0	0	0	1	0	1	1
6	2	25	5	0	3	5
0	1	11	2	2	3	3
46	4	120	70	2	21	17
5	6	37	57	13	9	24
5	4	82	17	3	3	6
40	25	71	32	12	7	38
5	5	156	0	0	3	1
4	7	72	6	2	30	37
0	0	0	0	0	1	0

604 DOT 0044		04 507 004				
	SG1-BOT-201S					
0	0	0	0	0	0	0
1	0	0	0	0	0	0
0	1	0	0	0	0	0
1	1	1	4	5	0	0
0	0	0	0	0	1	0
4	4	0	0	1	0	1
0	0	0	0	0	1	0
0	0	0	0	0	0	1
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	1	0	0	0	0
0	0	0	0	0	0	0
2	1	0	4	0	0	0
0	0	0	0	0	0	0
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0	0	0	1	0	0	1
0	0	0	0	0	0	0
0	0	0	3	0	0	1
0	0	0	0	0	0	0
0	0	1	0	0	0	0
0	0	0	0	0	0	0
0	0	1	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
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0	1	0	2	0	0	0
0	0	0	0	0	0	0
2	0	1	6	0	0	0
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0	0	1	2	0	0	0

0	1	0	0	0	1	0
3	5	0	2	3	5	3
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0	1	0	1	0	0	1
5	2	1	1	1	11	5
0	0	0	0	0	0	0
0	0	0	0	0	0	0
1	0	0	5	1	2	2
0	0	0	0	0	0	0
0	4	0	2	0	0	0
0	0	0	0	0	0	0
3	0	0	0	0	0	0
0	0	0	0	0	0	0
0	8	3	3	0	0	0
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1	5	0	1	2	4	0
0	1	0	0	0	0	0
1	3	4	2	0	0	0
0	0	1	0	0	0	0
0	0	0	0	0	0	1
0	1	0	0	0	0	0
7	4	1	1	0	0	0
3	0	1	4	0	0	3
4	2	0	4	0	0	0
0	0	0	0	0	1	0
1	1	0	0	0	0	0
1	1	1	0	0	0	0
2	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	1	0	0	0	0
1	1	4	0	0	3	0
3	12	2	8	5	8	17
0	1	0	0	0	0	0
0	0	0	0	0	0	0
1	4	0	1	4	6	0
16	10	4	13	2	0	5
0	0	0	0	0	0	0
0	1	0	0	2	0	1
0	0	0	0	0	0	0
1	5	0	0	0	0	1
1	0	0	0	1	0	0
0	0	0	0	1	0	0
0	0	0	0	0	6	0

25	25	12	23	0	0	9
0	0	0	0	0	0	0
1	0	1	0	0	0	0
0	0	1	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	1	0	0	2	0
1	0	1	0	0	0	1
3	2	0	0	2	0	0
0	0	0	0	0	0	0
0	1	0	0	0	0	0
0	0	0	0	0	0	0
4	1	0	3	1	8	6
0	2	0	0	0	0	0
0	0	0	0	0	0	0
0	1	0	0	0	0	0
0	1	0	0	0	0	0
0	0	0	0	0	0	1
7	6	16	10	37	116	6
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0	0	0	0	0	0	0
0	0	0	0	0	0	0
2	8	2	2	1	4	12
1	1	2	0	2	0	0
0	0	0	0	0	0	0
2	7	2	1	1	20	7
15	13	0	1	0	1	2
0	0	0	0	0	0	0
0 0	0	2 0	1 0	0 0	0	0
2	1 7	0	0	0	0 0	0 5
0	2	1	0	1	1	0
1	0	1	3	1	1	1
0	15	1	1	15	24	1
0	0	0	0	0	0	0
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567	465	182	333	186	379	250
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0	0	0	1	0	0	0
12	5	4	3	13	12	11
0	17	15	1	0	451	2
0	0	0	0	0	0	0

2	20	4	2	3	3	4
2	9	19	13	118	337	19
72	175	49	90	52	17	111
0	0	1	0	0	0	0
21	28	1	4	17	36	31
33	27	68	147	48	24	16
5	9	5	3	2	2	4
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0	5	4	4	4	0	0
113	16	17	8	18	145	77
13	6	3	6	3	8	7
848	151	194	279	241	283	363
185	141	51	52	34	75	88
2	3	2	2	0	1	2
3	32	2	2	1	0	3
34	22	1	5	11	2	41
3	6	2	1	6	7	1
0	0	0	0	0	0	0
5	3	2	1	8	6	3
0	1	0	0	0	0	0
4	10	3	2	3	0	5
1	5	1	4	0	1	1
7	4	13	11	0	2	3
1	3	0	0	0	0	0
35	16	5	7	8	1	12
0	1	0	0	0	1	0
9	64	11	41	2	0	4
25	51	3	7	0	3	5
49	34	7	10	2	4	12
6	7	4	14	6	0	0
9	1	4	14	2	0	2
210	172	40	70	11	13	58
24	64	7	5	50	29	64
45	41	45	38	127	234	79
3	0	0	1	0	0	0
166	300	107	163	120	35	193
273	27	5	21	13	11	140
0	6	25	2	3	9	9
8	16	2	2	9	0	19
0	1	0	0	0	0	0
19	18	3	8	1	2	9
18	14	8	9	8	10	6
41	39	31	34	24	4	23
20	11	4	1	8	18	24
0	2	0	0	0	0	1

0	11	2	18	4	1	1
0	0	0	0	0	0	0
24	30	18	60	3	88	81
0	0	1	1	0	2	0
1	1	2	1	3	11	2
2	1	0	3	3	2	3
24	16	9	14	12	51	41
1	16	4	0	12	75	7
6	6	4	3	6	0	6
60	26	4	12	7	7	33
7	11	0	2	3	1	7
2	5	10	8	8	2	3
0	0	0	0	0	0	0

SG1-BOT-201SG	61-BOT-201SG1-B	OT-201SG1-	BOT-201SG1-I	BOT-201SG1-I	BOT-201SG1-	BOT-201
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
1	1	0	0	0	0	0
0	0	0	0	0	0	0
0	0	1	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
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0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	3	1	0	0	0	0
0	0	0	1	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
1	0	0	0	0	0	0
0	0	0	0	1	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	2
0	5	0	0	0	1	3
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
1	0	0	0	0	0	0
0	0	0	0	0	0	1
0	1	1	1	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	2	0	1	3	0	0
0	0	1	0	1	0	3
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	1	0	0	0	0
0	0	1	2	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0

_	_	_		_	_	
4	7	1	0	2	0	1
2	1	6	1	2	5	1
0	1	0	1	0	0	0
0	2	0	0	0	1	0
4	2	5	5	1	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	1	2	0	2	1
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0	0	0	0	0	0	0
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0	0	0	0	0	0	0
1	1	2	0	1	0	0
3	6	0	5	14	0	2
0	0	0	0	0	0	0
0	0	1	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	1	0	2	0	0	
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0	0	0	0	0	0	0
1	5	0	0	4	0	0
3	1	1	0	0	0	1
0	0	1	0	0	1	0
0	0	1	0	1	0	0
8	14	1	1	10	0	2
0	1	3	2	0	0	0
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3	0	1	3	0	0	0
1	0	0	0	0	0	0
0	3	1	1	2	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	1	0	0	0

3	8	4	0	3	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	1	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
5	12	0	0	7	0	11
2	0	1	3	0	0	0
1	0	0	0	0	0	1
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
2	1	2	0	0	2	0
0	0	0	0	0	0	0
0	0	3	0	0	0	3
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	1	0
9	1	25	1	4	10	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
1	2	1	3	3	2	0
0	1	3	0	1	1	0
0	0	0	0	0	0	0
3	15	1	6	7	0	2
1	4	0	0	2	0	0
2	0	0	0	0	0	0
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0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
11	18	4	4	8	1	0
0	0	0	1	0	0	0
1	0	1	0	0	0	0
0	0	0	0	0	0	0
189	192	264	228	115	169	86
0	0	0	0	0	0	0
3	3	0	0	3	0	0
4	0	1	0	0	0	5
37	13	12	12	9	2	1
0	0	0	104	0	0	0
0	0	0	0	0	0	0
J	J	J	J	J	J	J

_	1	C	22	1	1	2
5	1	6	22	1	1	3
129	47	70	24	66	6	32
176	250	94	75	163	54	115
0	0	0	0	0	0	0
42	3	22	89	6	10	44
17	322	58	3	314	117	14
1	11	6	2	15	1	2
0	0	2	0	0	0	0
2	3	10	5	3	0	2
10	1	33	32	3	0	40
1	7	4	7	6	6	3
229	337	508	207	168	226	142
120	201	71	105	114	65	37
1	1	1	0	2	0	5
7	0	0	1	0	2	8
57	4	33	3	5	25	22
14	2	5	2	0	1	4
0	1	0	3	1	0	4
11	5	5	3	3	3	4
0	0	1	0	0	0	0
10	1	7	5	0	0	8
2	44	16	1	23	1	1
3	7	2	0	0	0	1
0	0	0	0	0	2	1
13	8	6	25	14	3	3
2	0	0	0	0	6	4
0	0	7	0	0	3	0
4	16	6	5	8	6	2
10	9	11	10	6	4	6
1	20	2	2	8	1	1
3	9	6	0	2	0	0
45	55	47	62	33	25	15
485	46	102	33	32	1	101
277	57	102	138	48	34	57
0	0	0	136	0	0	0
320		152	157	408	80	166
	542					
113	18	45	41	13	0	93
0	2	1	0	0	0	0
15	22	3	0	17	0	1
0	0	0	0	0	0	0
5	3	5	8	3	4	2
3	4	4	6	2	4	1
44	48	38	12	29	9	12
12	0	10	12	0	1	6
0	0	0	1	1	0	0

10	5	3	0	1	8	2
0	0	0	0	0	1	0
4	6	12	9	5	132	33
0	0	0	1	0	0	0
15	0	7	0	0	1	6
4	2	1	1	3	0	1
13	0	14	12	1	11	17
1	0	5	4	0	5	3
5	16	2	2	6	3	6
21	13	22	18	14	30	7
28	161	2	12	72	25	13
38	19	33	52	3	0	3
0	0	0	2	1	0	0

taxonomy D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea

D_0_Bacteria; D_1_Bacteroidetes; D_2_Cytophagia; D_3_Order II; D_4_Rhodothermaceae; D_5_: D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea D 0 Bacteria; D 1 Actinobacteria; D 2 Actinobacteria; D 3 Propionibacteriales; D 4 Propioniba D 0 Bacteria; D 1 Bacteroidetes; D 2 Cytophagia; D 3 Order II; D 4 Rhodothermaceae; D 5 D_0_Bacteria; D_1_Cyanobacteria; D_2_Cyanobacteria; D 3 uncultured; D 4 uncultured bacteriu D 0 Bacteria; D 1 Proteobacteria; D 2 Deltaproteobacteria; D 3 Desulfuromonadales; D 4 GR D 0 Bacteria; D 1 Bacteroidetes; D 2 Cytophagia; D 3 Order II; D 4 Rhodothermaceae; D 5 D 0 Bacteria; D 1 Bacteroidetes; D 2 Cytophagia; D 3 Order II; D 4 Rhodothermaceae; D 5 D_0_Bacteria; D_1_Bacteroidetes; D_2_Cytophagia; D_3_Order II; D_4_Rhodothermaceae; D_5_: D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea D_0_Bacteria; D_1_Proteobacteria; D_2_Gammaproteobacteria; D_3_Xanthomonadales; D_4_Xar D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea D 0 Archaea; D 1 Nanohaloarchaeota D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea D 0 Bacteria; D 1 Proteobacteria; D 2 Gammaproteobacteria; D 3 Alteromonadales; D 4 Shev D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea D 0 Bacteria; D 1 Bacteroidetes; D 2 Cytophagia; D 3 Order II; D 4 Rhodothermaceae; D 5 D_0_Bacteria; D_1_Proteobacteria; D_2_Gammaproteobacteria; D_3_Chromatiales; D_4_Ectothio D_0_Bacteria; D_1_Proteobacteria; D_2_Deltaproteobacteria; D_3_Desulfuromonadales; D_4_GR-D 0 Bacteria; D 1 Proteobacteria; D 2 Deltaproteobacteria; D 3 Desulfuromonadales; D 4 GR-D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea D 0 Bacteria; D 1 Bacteroidetes; D 2 Cytophagia; D 3 Order II; D 4 Rhodothermaceae; D 5

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D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Bacteria; D 1 Bacteroidetes; D 2 Cytophagia; D 3 Order II; D 4 Rhodothermaceae; D 5
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Bacteria; D 1 Proteobacteria; D 2 Deltaproteobacteria; D 3 Desulfuromonadales; D 4 GR
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Bacteria; D 1 Proteobacteria; D 2 Alphaproteobacteria; D 3 Sphingomonadales; D 4 Sphi
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Bacteria; D 1 Bacteroidetes; D 2 Cytophagia; D 3 Order II; D 4 Rhodothermaceae; D 5
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Bacteria; D 1 Proteobacteria; D 2 Gammaproteobacteria; D 3 Oceanospirillales; D 4 Halo
D 0 Bacteria; D 1 Proteobacteria; D 2 Gammaproteobacteria; D 3 Chromatiales; D 4 Ectothio
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Bacteria; D 1 Proteobacteria; D 2 Deltaproteobacteria; D 3 Desulfuromonadales; D 4 GR
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Bacteria; D 1 Bacteroidetes; D 2 Cytophagia; D 3 Order II; D 4 Rhodothermaceae; D 5
D_0_Bacteria; D_1_Bacteroidetes; D_2_Cytophagia; D_3_Order II; D_4_Rhodothermaceae; D_5_:
D_0_Bacteria; D_1_Bacteroidetes; D_2_Cytophagia; D_3_Order II; D_4_Rhodothermaceae; D_5_:
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Bacteria; D 1 Bacteroidetes; D 2 Cytophagia; D 3 Order II; D 4 Rhodothermaceae; D 5
D 0 Bacteria; D 1 Bacteroidetes; D 2 Cytophagia; D 3 Order II; D 4 Rhodothermaceae; D 5
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D_0_Bacteria; D_1_Bacteroidetes; D_2_Cytophagia; D_3_Order II; D_4_Rhodothermaceae; D_5_:
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Bacteria; D 1 Bacteroidetes; D 2 Cytophagia; D 3 Order II; D 4 Rhodothermaceae; D 5
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D_4_Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Bacteria; D 1 Proteobacteria; D 2 Gammaproteobacteria; D 3 Chromatiales; D 4 Ectothio
D_0_Archaea; D_1_Nanohaloarchaeota; D_2_uncultured archaeon; D_3_uncultured archaeon; D_4
D 0 Bacteria; D 1 Proteobacteria; D 2 Deltaproteobacteria; D 3 Desulfuromonadales; D 4 GR-
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
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D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Bacteria; D 1 Bacteroidetes; D 2 Cytophagia; D 3 Order II; D 4 Rhodothermaceae; D 5
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Nanohaloarchaeota; D 2 uncultured archaeon; D 3 uncultured archaeon; D 4
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Bacteria; D 1 Bacteroidetes; D 2 Cytophagia; D 3 Order II; D 4 Rhodothermaceae; D 5
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Bacteria; D 1 Actinobacteria; D 2 Actinobacteria; D 3 Propionibacteriales; D 4 Propioniba
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Bacteria; D 1 Bacteroidetes; D 2 Cytophagia; D 3 Order II; D 4 Rhodothermaceae; D 5
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Bacteria; D 1 Proteobacteria; D 2 Betaproteobacteria; D 3 Burkholderiales; D 4 Comamo
D 0 Bacteria; D 1 Planctomycetes; D 2 Phycisphaerae; D 3 Phycisphaerales; D 4 Phycisphaera
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D_0_Bacteria; D_1_Proteobacteria; D_2_Alphaproteobacteria; D_3_Rhodospirillales; D_4_Acetobacteria; D_0_Bacteria; D_1_Proteobacteria; D_2_Alphaproteobacteria; D_3_Rhodospirillales; D_4_Acetobacteria; D_0_Bacteria; D_1_Proteobacteria; D_2_Alphaproteobacteria; D_3_Rhodospirillales; D_4_Acetobacteria; D_0_Bacteria; D_1_Proteobacteria; D_0_Bacteria; D_0_
D_0_Bacteria; D_1_Bacteroidetes; D_2_Cytophagia; D_3_Order II; D_4_Rhodothermaceae; D_5_:
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Bacteria; D 1 Proteobacteria; D 2 Gammaproteobacteria; D 3 Oceanospirillales; D 4 Halo
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Bacteria; D 1 Bacteroidetes; D 2 Cytophagia; D 3 Order II; D 4 Rhodothermaceae; D 5
D_0_Bacteria; D_1_Bacteroidetes; D_2_Cytophagia; D_3_Order II; D_4_Rhodothermaceae; D_5_:
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
Unassigned
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
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D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
Unassigned
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Bacteria; D 1 Cyanobacteria; D 2 Chloroplast
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
Unassigned
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Bacteria; D_1_Bacteroidetes; D_2_Cytophagia; D_3_Order II; D_4_Rhodothermaceae; D_5_:
D 0 Bacteria; D 1 Cyanobacteria; D 2 Cyanobacteria; D 3 SubsectionIII; D 4 FamilyI; D 5 un
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Bacteria; D 1 Bacteroidetes; D 2 Cytophagia; D 3 Order II; D 4 Rhodothermaceae; D 5
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Bacteria; D 1 Planctomycetes; D 2 Phycisphaerae; D 3 Phycisphaerales; D 4 Phycisphaera
Unassigned
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
Unassigned
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D_0_Bacteria; D_1_Bacteroidetes; D_2_Cytophagia; D_3_Order II; D_4_Rhodothermaceae; D_5_:
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Bacteria; D 1 Bacteroidetes; D 2 Cytophagia; D 3 Order II; D 4 Rhodothermaceae; D 5
Unassigned
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
D 0 Archaea; D 1 Euryarchaeota; D 2 Halobacteria; D 3 Halobacteriales; D 4 Halobacteriacea
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D_O_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea D_O_Bacteria; D_1_Bacteroidetes; D_2_Cytophagia; D_3_Order II; D_4_Rhodothermaceae; D_5_DO_Bacteria; D_1_Cyanobacteria; D_2_Chloroplast
D_O_Bacteria; D_1_Bacteroidetes; D_2_Cytophagia; D_3_Order II; D_4_Rhodothermaceae; D_5_DO_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea Unassigned
D_0_Archaea; D_1_Euryarchaeota; D_2_Halobacteria; D_3_Halobacteriales; D_4_Halobacteriacea Unassigned
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sequence

GTGCCAGCCGCGGGTAATACCGGCAGCACAAGTGATGGCCAATCTTATTGGGCCTAAAGCGTCC ACGTGTCAGCAGCCGCGGTAATACGGAGGGTGCAAGCGTTGTCCGGAATCACTGGGCGTAAAGGC CGTGCCAGCCGCCGCGGTAATACCGGCAGCCCGAGTGATGGCCGATCTTATTGGGCCTAAAGCGT(GTGTCAGCCGCCGCGGTAATACCGGCAGCACGAGTGATGGCCGATATTATTGGGCCTAAAGCGTC(GTGTCAGCCGCCGCGGTAATACCGGCAGCCCGAGTGATGGCCGATATTATTGGGCCTAAAGCGTC(ACGTGTCAGCCGCCGCGGTAATACCGGCAGCTCGAGTGATGGCCGATCTTATTGGGCCTAAAGCGT GTGCCAGCCGCCGGTAATACCGGCAGTCCAAGTGATGGCCGCTCTTATTGGGCCTAAAGCGTCC GTGCCAGCCGCCGGTGATACGTAGGGTGCGAGCGTTGTCCGGATTTATTGGGCGTAAAGGGCT CGTGCCAGCAGCCGCGTAATACGGAGGGTGCAAGCGTTGTCCGGAATCACTGGGTGTAAAGGGT TACACTCCTACGGGAGGCAGCAGTGGGGAATTTTCCGCAATGGGCGAAAGCCTGACGGAGCAATA ACGTGTCAGCAGCCGCGGTAAGACGGAGGGTGCAAGCGTTGTTCGGAATCATTGGGCGTACAGGC GTGTCAGCAGCCGCGGTAATACGGAGGGTGCAAGCGTTGTCCGGAATCACTGGGCGTAAAGGGTC CGTGCCAGCAGCCGCGGTAATACGGAGGGTCCAAGCGTTGTCCGGAATCACTGGGCGTAAAGGGT CGTGCCAGCAGCCGCGGTAATACGGAGGGTCCAAGCGTTGTCCGGAATCACTGGGCGTAAAGGGT GTGTCAGCAGCCGCGGTAATACCGGCAGCTCGAGTGATGGCCGATCTTATTGGGCCTAAAGCGTCC GTGTCAGCCGCCGCGGTAATACCGGCAGTCCAAGTGATGGCCGCTCTTATTGGGACTAAAGCGTAC CGTGCCAGCCGCCGGTAACACCGGCAGCCCAAGTGATGGCCGCTGTTATTGGGCCTAAAGCGT(CGTGTCAGCCGCCGCGGTAATACCGGCAGCACGAGTGATGGCCGATATTATTGGGCCTAAAGCGT(GTGCCGGCCGCGGTAATACCGGCAGCCCGAGTGATGGCCGATCTTATTGGGCCTAAAGCGTC(CGTGCCAGCCGCGCGGTAATACCGGCAGCACGAGTGATGGCCGCTCTTATTGGGCCTAAAGCGTC GTGACAGCCGCCGGTAATACGAAGGGTGCAAGCGTTACTCGGAATTACTGGGCGTAAAGTGTG GTGTCGGCCGCCGGTAATACCGGCAGTCCGAGTGATGGCCGATATTATTGGGCCTAAAGCGTC(CGTGTCAGCCGCCGCGGTAATACCGGCAGCGCAAGTGATGGCCGATCTTATTGGGCCTAAAGCGT(CGTGTCAGCAGCCGCGGTAATAGCAGAACCCCAAGTGGTAGTCATTATTATTGGGTTTAAAGTGTT(GTGCCAGCAGCCGCGTAATACCGGCAGCCCAAGTGATGGCCGATCTTATTGGGCCTAAAGCGTC(GTGTCAGCCGCCGCGGTAACACCGGCAGCCCAAGTGATGGCCGCTGTTATTGGGCCTAAAGCGTTC GTGTCAGCAGCCGCGGTAATACGGAGGGTGCGAGCGTTAATCGGAATTACTGGGCGTAAAGCGTG GTGTCAGCCGCCGCGGTAATACCGGCAGCACAAGTGATGGCCGATTTTATTGGGCCTAAAGCGTCC GTGTCAGCCGCCGCGGTAATACCGGCAGCACAAGTGATGGCCGATTTTATTGGGCCTAAAGCGTCC CGTGCCAGCCGCCGCGGTAATACCGGCAGCACGAGTGATGGCCGCTATTATTGGGCCTAAAGCGTT CGTGCCAGCCGCCGCGGTAACACCGGCAGCCCGAGTGATGGCCGATATTATTGGGCCTAAAGCGT(ACGTGTCAGCCGCCGCGGTAATACCGGCAGTCCGAGTGATGGTCGATATTATTGGGCCTAAAGCGT CGTGTCAGCCGCCGCGGTAATACGGAGGGTCCAAGCGTTGTCCGGAATCACTGGGCGTAAAGGGT GTGTCAGCCGCCCGGTAATACGGAGGGTGCAAGCGTTAATCGGAATCACTGGGCGTAAAGGGCA CGTGCCAGCAGCCGCGGTAAGACGGAGGGTGCAAGCGTTGTTCGGAATCATTGGGCGTAAAGGG1 CGTGCCAGCCGCGCGGTAATACGGAGGGTGCAAGCGTTGTTCGGAATCATTGGGCGTAAAGGGC CGTGTCAGCCGCCGCGGTAATACCGGCAGCCCAAGTGATGGCCGATCTTATTGGGCCTAAAGCGTC GTGTCAGCCGCCGCGGTAATACCGGCAGCACGAGTGATGGCCGATATTATTGGGCCTAAAGCGTC(CGTGTCAGCAGCCGCGGTAATACCGGCAGCACAAGTGATGGCCGATTTTATTGGGCCTAAAGCGTC CGTGCCAGCCGCGCGGTAACACCGGCAGCCCGAGTGATGGCCGATATTATTGGGCCTAAAGCGT(CGTGTCAGCCGCCGCGGTAATACCGGCAGCTCGAGTGATGGCCGCTGTTATTGGGCCTAAAGCGTC GTGTCAGCCGCCGCGGTAATACCGGCAGTCCAAGTGATGGCCGCTCTTATTGGGCCTAAAGCGTCC CGTGCCAGCCGCCACGGTAATACCGGCAGCTCGAGTGATCACCGATCTTATTGGGCCTAAAGCGTC CGTGCCAGCAGCCGCGGTAATACGGAGGGTGCAAGCGTTGTCCGGAATCACTGGGCGTAAAGGGT

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FACGAGCCTGCGCTGTGCCGTAGGGAAGCCGAGAAGCGGGCCGCCTGGGAAGTACGTCTGCAAGGAT \GGGGGCAGTGGCTAAGCTAACGCGTTAAGCATTCCGCCTGGGGAGTACGATCGCAAGGTTGAAACT CONTROL OF THE PROPERTY OF THE CAAACCGCGCCGTTTCGAAGCTAACGCGTTAAGTGAACCGCCTGGGGAGTACGGCCGCAAGGATAAA \TGAGCGCGTGATGTGCCGCAGTGAAGACGAGAAGCGAGCCGCCTGGGAAGTACGTCCGCAAGGAT(AAATTCGTAGATATTCGGAAGAACACCAGTGGCGAAGGCGGCTCACTGGAATGGTATTGACGCTGAG \CGAGTGAGTGATGTGCCGCAGGGAAGCCGCTAAACGGACCGCCTGGGAAGTACGTCTGCAAGGATG GAGCCTGCGCTGCGCCATAGGGAAGCCGAGAAGCGAGCCGCCTGGGAAGTACGTCCGCAAGGATGA CGAGCCTGCGCTGTGCCGTAGGGAAGCCGAGAAGCGGGCCGCCTGGGAAGTACGTCTGCAAGGATG/ ragggggcagtggctaagttaacgcgttaagcattccacctggggagtacgatcgcaaggttgaaact 'ACGAGTGTGTGCTGTGCTGTAGTGAAGACGAGAGCGAGCCGCCTGGGAAGTACGTCCGCAAGGAT 3AGTGGGTGCTGTGCCGCAGGGAAGCCGCTAAGCAGACCGCCTGGGAAGTACGTCCGCAAGGATGAA |AGCACTTAGTGGCGCAGTTAACGCGATAAGTCGACCGCCTGGGGAGTACGGCCGCAAGGTTAAAACT "AAAGGGTTTAGTGGCGCAGCTAACGCGATAAGTTCTCCGCCTGGGGAGTACGACCGCAAGGTTGAA!" ACGAGCCTGCGCTGTGCCGTAGGGAAGCCGTGAAGCGAGCCGCCTGGGAAGTACGTCTGCAAGGATC :GAGCCAGCGCTGTGCCGTAGGGAAGCCGAGAAGCGAGCCGCCTGGGAAGTACGTCCGCAAGGATG/ CAAACCGCGCAGTGTCGAAGCTAACGCGTTAAGTGAACCGCCTGGGGAGTACGGCCGCAAGGCTAAA CGAGCCTGCGCTGTGCCGTAGGGAAGCCGTGAAGCGAGCCGCCTGGGAAGTACGTCTGCAAGGATG/ 'ACGAGCCTGCGCTGTGCCGTAGGGAAGCCGTGAAGCGAGCCGCCTGGGAAGTACGTCCGCAAGGAT AAGGAATAGTGGCTAAGTTAACGCGTTAAGCATTCCGCCTGGGGAGTACGATCGCAAGGTTGAAACT 'AAGGAATAGTGGCTAAGTTAACGCGTTAAGCATTCCGCCTGGGGAGTACGATCGCAAGGTTGAAACT 3GGACAGTGGCTAAGCTAACGCGTTAAGCATCCCGCCTGGGGAGTACGATCGCAAGGTTGAAACTCA/ CGAGCCTGCGCTGTGCCGCAGGGAAGCCGTGAAGCAGACCGCCTGGGAAGTACGTCCGCAAGGATG/ :GAGTGGGTGCTGTGCCGCAGGGAAGCCGCTAAGCAGACCGCCTGGGAAGTACGTCCGCAAGGATGA ACGAGCCTGCGCTGTGCCAAAGGGAAGCCACGAAGCGAGCCGCCTGGGAAGTACGTCTGCAAGGATC 3GGACAGTGGCTAAGCTAACGCGTTAAGCATTCCGCCTGGGGAGTACGATCGCAAGGTTGAAACTTA/ GGGCAGTGGCTAAGCTAACGCGTTAAGCATTCCGCCTGGGGAGTACGATCGCAAGGTTGAAACTCA/ CGAGCCTGCGCTGTGCCGTAGGGAAGCCGTGAAGCAGACCGCCTGGGAAGTACGTCTGCAAGGATGA AGGGGGCAGTGGCTAAGCTAACGCGTTAAGCATTCCGCCTGGGGAGTACGATCGCAAGGTTGAAACT! .CGAGCCTGCGCTGTGCCGCAGGGAAGCCGTGAAGCGGACCGCCTGGGAAGTACGTCTGCAAGGATG. 3AGCCTGTGCTGCGCCACAGTGAAGACGCAAGCGAGCCGCCTGGGAAGTACGTCCGCAAGGATGAAA GGGGGCAGTGGCCAAGCTAACGCGTTAAGCATTCCGCCTGGGGAGTACGATCGCAAGGTTGAAACTC CGAGCCTGCGCTGTGCCGTAGGGAAGCCGTGAAGCGAGCCGCCTGGGAAGTACGTCCGCAAGGATG TGAGCACGTGATGTGCCGTAGTGAAGACGATAAGCGAGCCGCCTGGGAAGTACGTCCGCAAGGATG/ 'ACGAGCCTGCGCTGTGCCGTAGGGAAGCCGTGAAGCGAGCCGCCTGGGAAGTACGTCTGCAAGGAT(3AGTGAGTGATGTGCCGCAGGGAAGCCGCTAAACGGACCGCCTGGGAAGTACGTCTGCAAGGATGAA ACGAGCCTGTGCTGTGCCGTAGGGAAGCCGTGAAGCGAGCCGCCTGGGAAGTACGTCCGCAAGGAT(CGAGCCTGCGCTGTGCCGCAGGGAAGCCGTGAAGCGGACCGCCTGGGAAGTACGTCTGCAAGGATG/ AGTGCACGGTGAGCCGAAGTGAAGACGATAAACGAGCCGCCTGGGAAGTACGTCCGCAAGGATGAA 'ACGAGCCTGCGCTGTGCCGTAGGGAAGCCGTGAAGCGAGCCGCCTGGGAAGTACGTCTGCAAGGAT(CAGCCTGTGCTGTGCCCTAGGGAAGCCGAGAAGCGAGCCGCCTGGGAAGTACGTCCGCAATGATGA AAAGGGTTTGGTGGCGCAGCTAACGCGATAAGTTCTCCGCCTGGGGAGTACGACCGCAAGGTTGAAA AGGTTAGCCGGTGCCGAAGTAAAAACGTTAAACGGACCGCCTGGGTAGTACGGTCGCAAGGCTGAA/ CAAACCGCGCAGTGTCGAAGCTAACGCGTTAAGTGAACCGCCTGGGGAGTACGGCCGCAAGGCTAAA .CGAGCCAGCGCTGTGCCGTAGGGAAGCCGAGAAGCGAGCCGCCTGGGAAGTACGTCCGCAAGGATG

TACGAGCCTGCGCTGTGCCGTAGGGAAGCCGTGAAGCGAGCCGCCTGGGAAGTACGTCCGCAAGGA CGAGCCTGCGCTGTGCCGCAGGGAAGCCGTGAAGCAGACCGCCTGGGAAGTACGTCCGCAAGGATG/ GAGTGGTGTTGTGCCGTAGGGAAGCCGCTAAACAGGCCGCCTGGGAAGTACGTCTGCAAGGATGA/ 3AGTGGGTGTTGTGCCGTAGGGAAGCCGCTAAACAGGCCGCCTGGGAAGTACGTCTGCAAGGATGAA 3GGTCAGTGGCTAAGCTAACGCGTTAAGCATTCCGCCTGGGGAGTACGATCGCAAGGTTGAAACTCAA CAGCCTGCGCTGTGCCGTAGGGAAGCCGTGAAGCGAGCCGCCTGGGAAGTACGTCCGCAAGGATGA ACGAGCCTGCGCTGTGCCGTAGGGAAGCCGTGAAGCGAGCCGCCTGGGAAGTACGTCTGCAAGGAT(ACGCGTGAGTGTTGTGCCGCAGGGAAGCCGCTAAGCGAACCGCCTGGGAAGTACGTCCGCAAGGATG CGAGCCAGCGCTGTGCCGTAGGGAAGCCGAGAAGCGAGCCGCCTGGGAAGTACGTCCGCAAGGATG 3AGGTTAGCCGGTGCCGAAGTGAAAACGTTAAACGGACCGCCTGGGAAGTACGGTCGCAAGGCTGAA TACGAGCCTGCGCTGTGCCGTAGGGAAGCCGTGAAGTGAGCCGCCTGGGAAGTACGTCCGCAAGGAT CGAGTGGGTGCTGTGCCGCAGGGAAGCCGCTAAGCAGACCGCCTGGGAAGTACGTCCGCAAGGATG ATGAGCGCGTGATGTGCCGCAGTGAAGACGAGAAGCGAGCCGCCTGGGAAGTACGTCCGCAAGGAT(GGGGGTAGTGGCTAAGTTAACGCGTTAAGCATTCCGCCTGGGGAGTACGATCGCAAGGTTGAAACTT GAGTGGGTGCTGTGCCGCAGGGAAGCCGCTAAACAGACCGCCTGGGAAGTACGTCCGCAAGGATGA CGGGTTCCGTGCCGTAGCTAACGCTTTAAGTACCCCGCCTGGGGAGTACGGCCGCAAGGCTAAAACTT TACGAGCCTGCGCTGTGCCGTAGGGAAGCCGTGAAGCAGACCGCCTGGGAAGTACGTCTGTAAGGAT GGGGCAGTGGCTAAGCTAACGCGTTAAGCATTCCGCCTGGGGAGTACGATCGCAAGGTTGAAACTCA. CGAGCCTGCGCTGTGCCGTAGGGAAGCCGTGAAACGAGCCGCCTGGGAAGTACGTCTGCAAGGATG/ FCTCAGTAACGAAGCTAACGCGTGAAGTTGACCGCCTGGGGAGTACGGCCGCAAGGTTGAAACTTAA/ CCCGTCTCGGTCGAAGCGAAAGCGATAAGTGCACCGCCTGGGGATTACGGTCGCAAGGCTAAAACTC iagtgagtgatgtgccgcagggaagccgctaagcgaaccgcctgggaagtacgtctgcaaggatgaa TCACTCAGTGTCGTAGCTAACGCGATAAGCGCACCGCCTGGGGAGTACGTCCGCAAGGATGAAACTC/ 3GGGCAGTGGCTAAGCTAACGCGTTAAGCATTCCGCCTGGGGAGTACGATCGCAAGGTTGAAACTTA/ CGAGCCAGTGCTGTGCCGTAGGGAAGCCGTGAAGTGAGCCGCCTGGGAAGTACGTCCGCAAGGATG |AGCACTTAGTGGCGCAGTTAACGCGATAAGTCGACCGCCTGGGGAGTACGGCCGCAAGGTTAAAACT \CGAGCCTGCGCTGTGCCGTAGGGAAGCCGAGAAGCGGGCCGCCTGGGAAGTACGTCTGCAAGGATC TACGAGCCTGCGCTGTGCCGTAGGGAAGCCGTGAAGCGGACCGCCTGGGAAGTACGTCTGCAAGGAT CAGCCTGTGCTGCGCCCTAGGGAAGCCGAGAAGCGAGCCGCCTGGGAAGTACGTCTGCAAGGATGA 3AGCCTGTGCCGCGCCTCAGTGAAGACGTAAGCGGGCCGCCTGGGAAGTACGTCCGCAAGGATGAAA TACGAGCCTGTGCTGCCGCAGGGAAGCCGTGAAGCAGACCGCTTGGGAAGTACGTCCGCAAGGA1 LCGAGTGGTGCTGTGCCGCAGGGAAGCCGCTAAGCAGACCGCCTGGGAAGTACGTCCGCAAGGATG CAGCCTGCGCTGTGCCGTAGGGAAGCCGTGAAGCGGACCGCCTGGGAAGTACGTCTGCAAGGATGA CGAGCCTGCGCTGTGCCAAAGGGAAGCCACGAAGCGAGCCGCCTGGGAAGTACGTCTGCAAGGATGA ACGAGCCTGTGCTGTGCCGTAGGGAAGCCGTGAAGCGAGCCGCCTGGGAAGTACGTCCGCAAGGAT(CGAGCCTGCGCTGTGCCGTAGGGAAGCCGAGAAGCGGGCCGCCTGGGAAGTACGTCTGCAAGGATG CGAGCCTGCGCTGTGCCGTAGGGAAGCCGTGAAACGAGCCGCCTGGGAAGTACGTCCGCAAGGATGA CAGCCAGTGCTGTGCCGTAGGGAAGCCGTGAAGTGAGCCGCCTGGGAAGTACGTCCGCAAGGATGA 3GGGCAGTGGCTAAGCTAACGCGTTAAGCATTCCGCCTGGGGAGTACGATCGCAAGGTTGAAACTTAA 3GGGCAGTGGTTAAGCTAACGCGTTAAGCATTCCGCCTGGGGAGTACGATCGCAAGGTTGAAACTTA/ ACGAGCCTGCGCTGTGCCGTAGGGAAGCCGTGAAGCGGCCGCCTGGGAAGTACGTCTGCAAGGAT(CGAGCCTGTGCTGTGCCGCAGGGAAGCCCAGAAGCGAGCCGCCTGGGAAGTACGTCTGCAAGGATGA ACGGGCCAGCGCTGTGCCGTAGGGAAGCCGTGAAGCGAGCCGCCTGGGAAGTACGTCCGCAAGGAT(TTGAGTGCCGAAGCTAACGCGTTAATTCTCCCGCCTGGGGAGTACGCTCGCAAGAGTGAAACTTAAAG ACGAGTGTGTGCTGTGCTGTAGTGAAGACGTGAAGCGAGCCGCCTGGGAAGTACGTCCGCAAGGATC

CGCGTGAGTGTTGTGCCGCAGGGAAGCCGCTAAGCGAACCGCCTGGGAAGTACGTCCGCAAGGATGA \CGAGCCAGCGCTATGCCGTAGGGAAGCCGAGAAGCGAGTCGCCTGGGAAGTACGTCCGCAAGGATG TACGAGCCTGTGCTGCCGCAGGGAAGCCGTGAAGCGAGCCGCCTGGGAAGTACGTCTGCAAGGAT CAGGATGTCTGGTGCCAAAGTGAAAACATTAAGCGGGCCGCCTGGGTAGTACGGTCGCAAGGCTGA GAGCCTGTGCTGCCGCAGGGAAGCCGCGAAGCGAGCCGCCTGGGAAGTACGTCTGCAAGGATGA/ \ATTTTTCAGTGTCGAAGTTAACGCGTTAAGTCTCCCGCCTGGGAAGTACGCTCGCAAGAGTGAAACTC TACGAGACTGCGCTGTGCCGCAGGGAAGCCGTGAAGCGGGCCGCCTGGGAAGTACGTCTGCAAGGA CGAGCCTGTGCTGTGCCGCAGGGAAGCCGTGAAGCGAGCCGCCTGGGAAGTTCGTCTGCAAGGATG/ \TCGGGGCAGTGTTCAAGCTAACGCGGTAAGCATTCCACCTGGGGAGTACGTTCGCAAGGATGAAACT TACGAGCCTGTGCTGTGCCGTAGGGAAGCCGTGAAGCAGCCGCCTGGGAAGTACGTCTGCAAGGAT GGGCAGTGGCTAAGCTAACGCGTTAAGCATTCCGCCTGGGGAGTACGATCGCAAGGTTGAAACTCA/ CACCCCAGCCGTGCCGAAGCCAACGCGTTAAGTATCCCGCCTGGGGAGTACGTGCGCAAGCATGAAA 'ACGAGCCTGCGCTGTGCCGTAGGGAAGCCGAGAAGCGGGCCGCCTGGGAAGTACGTCTGCAAGGAT TACGAGCCTGCGCTGTGCCGTAGGGAAGCCGAGAAGCGGGCCGCCTGGGAAGTACGTCTGCAAGGA TACGAGCCTGTGCTGTGCCGCAGTGAAGACGCTAAACGGACCGCCTGGGAAGTACGTCCGCAAGGAT TACGAGCCAGCGCTGTGCCGTAGGGAAGCCGAGAAGCGAGCCGCCTGGGAAGTACGTCCGCAAGGA CGAGCCTGCGCTGTGCCGTAGGGAAGCCGTGAAGCGAGCCGCCTGGGAAGTACGTCTGCAAGGATGA TACGAGCCTGCGCTGTGCCGTAGGGAAGCCGAGAAGCGAGCCGCCTGGGAAGTACGTCCGCAAGGA IAGCGCATGGTGAGCCGAAGTGAAGACGATAAGCGAGCCGCCTGGGAAGTACGTCTGCAAGGATGAA SAGTGGGTGCTGTTCCGCAGGGAAGCCGCTAAACAGACCGCCTGGGAAGTACGTCCGCAAGGATTAA 'ACGAGCCTGTGCTGTGCCGCAGGGAAGCCGCGAAGCGAGCCGCCTGGGAAGTACGTCTGCAAGGAT TACGAGCCTGCGCTGTGCCGTAGGGAAGCCGTGAAGCGGACCGCCTGGGAAGTACGTCTGCAAGGA1 `TACGAGCCTGCGCTGTGCCGTAGGGAAGCCGTGAATCGAGCCGCCTGGGAAGTACGTCCGCAAGGA CTACGAGCCTGCGCTGTGCCGTAGGGAAGCCGAGAAGCGGGCCGCCTGGGAAGTACGTCTGCAAGG! CTACGAGCCTGCGCTGTGCCGTAGGGAAGCCGTGAAGCGGCCCCCTGGGAAGTACGTCCGCAAGG/ CAGCCTGCGCTGTGCCGTAGGGAAGCCGTGAAGCGAGCCGCCTGGGAAGTACGTCTGCAAGGATGA GGGGTAGTGGCTAAGTTAACGCGTTAAGCATTCCGCCTGGGGAGTACGATCGCAAGTTTGAAACTTA/ FACGAGCCTGCGCTGTGCCGTAGGGAAGCCGTGAAGCGGACCGCCTGGGAAGTACGTCTGCAAGGAT CTACGAGCCTGCGCTGTGCCGTAGGGAAGCCGTGAAGCAGACCGCCTGGGAAGTACGTCTGCAAGGA 3ACGCCTTCACGGTTGCAGCGAAAGCATTAAGTGCACCGCCTGGGGATTACGGTCGCAAGGCTAAAAC 3TGGTTGTTTGGTGCCGAAGGAAAACCGTTAAACGCACCGCCTGGGGAGTACGGTCGCAAGGCTGAA/ CGAGCCTGCGCTGTGCCGTAGGGAAGCCGTGAAGCAGACCGCCTTGGAAGTACGTCCGCAAGGATG/ *ACGAGCCAGCGCTGTGCTGTAGGGAAGCCGAGAAGCAGACCGCCTGGGAAGTACGTCTGCAAGGAT TACGAGCCAGCGCTGTGCCGTAGGGAAGCCGAGAAGCGAGCCGCCTGGGAAGTACGTCCGCAAGGA FACGAGCTTGCGCTGTGCCGTAGCGAAGGCGCGAAACGGGCCGCCTGGGAAGTACGTCTGCAAGGAT TACGAGCCTGTGCTGCCGCAGGGAAGCCGCGAAGCGAGCCGCCTGGGAAGTACGTCTGCAAGGAT TACGAGCCTGTGCTGCCGCATGGAAGCCCAGAAGCGAGCCGCCTGGGAAGTACGTCTGCAAGGAT \TGAGTCCGTGCCGTGCCACAGTGAAGACGCTAAGCGGGCCGCCTGGGAAGTACGTCTGCAAGGATG TACGAGCCAGCGCTGTGCCGTAGGGAAGCCGAGAAGCGAGCCGCCTGGGAAGTACGTCCGCAAGGA TAGGGGGCAGTGGCTAAGCTAACGCGTTAAGCATTCCGCCTGGGGAGTACGATCGCAAGGTTGAAAC ACGTGCCTGTGCTGTGCCGTAGGGAAGCCGTGAAGCGAGCCGCCTGGGAAGTACGTCTGCAAGGATG \GGAGGCAGTGGCTAAGCTAACGCGTTAAGCATTCCGCCTGGGGAGTACGATCGCAAGGTTGAAACT 「AGAGGGGCAGTGTTCAAGCTAACGCGGTAAGCATTCCACCTGGGGAGTACGTTCGCAAGGATGAAA(3AGCGCGTGATGTGCCGCAGTGAAGACGAGAAGCGAGCCGCCTGGGAAGTACGTCCGCACGGATGA/ *ACGAGCCTGTGCTGTGCCGCAGGGAAGCCGCGAAGCGAGCCGCCTGGGAAGTACGTCTGCAAGGAT

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\AACTCAAATAAATTGGCGGC

AATAAATTGACGGCA

AAGGAATTGACGGCA

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\AACTTAAATGAATTGGCGGC

3AAACTCAAATGAATTGGCGGCA

GAATTGACGG

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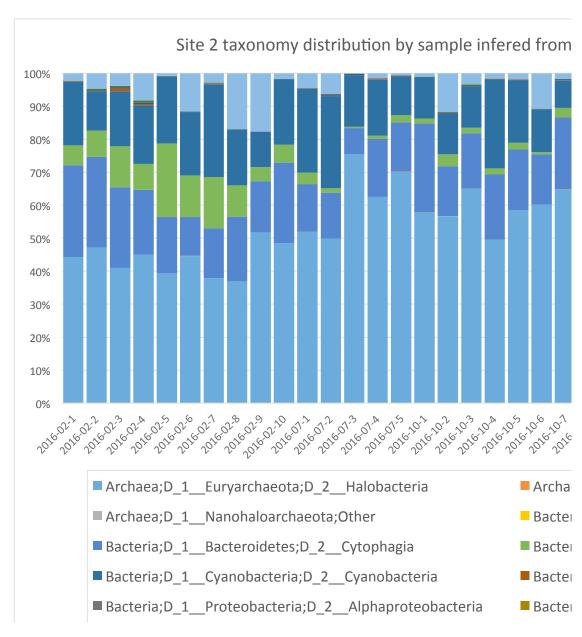
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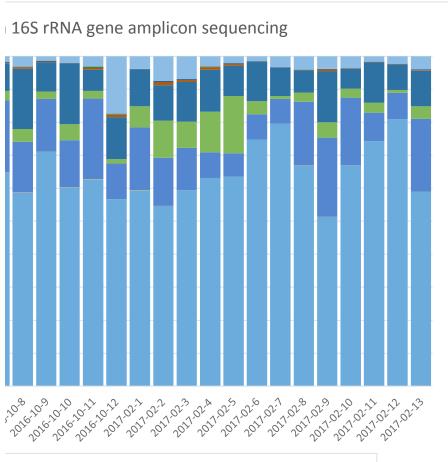
Taxa	2016-02-1	2016-02-2
Archaea;D_1Euryarchaeota;D_2Halobacteria	0.44299065	0.47235387
Archaea;D_1_Nanohaloarchaeota;D_2_uncultured archaeon	0	0
Archaea;D_1Nanohaloarchaeota;Other	0	0
Bacteria; D_1Actinobacteria; D_2Actinobacteria	0	0
Bacteria;D_1_Bacteroidetes;D_2_Cytophagia	0.27897196	0.27409163
Bacteria; D_1_Cyanobacteria; D_2_Chloroplast	0.05981308	0.07977883
Bacteria;D_1Cyanobacteria;D_2Cyanobacteria	0.19299065	0.1192733
Bacteria; D_1Planctomycetes; D_2Phycisphaerae	0.00186916	0
Bacteria; D_1Proteobacteria; D_2Alphaproteobacteria	0	0
Bacteria; D_1Proteobacteria; D_2Betaproteobacteria	0	0
Bacteria;D_1Proteobacteria;D_2Deltaproteobacteria	0.00046729	0.00078989
Bacteria; D_1Proteobacteria; D_2Gammaproteobacteria	0	0.007109
Unassigned;Other;Other	0.0228972	0.04660348



■ Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria ■ Bacter

Unassigned;Other;Other

2016-02-9	2016-02-8	2016-02-7	2016-02-6	2016-02-5	2016-02-4	2016-02-3
0.51783005	0.36909651	0.37933059	0.44619289	0.39336918	0.4496337	0.40982624
0	0	0	0.00050761	0	0	0
0	0	0	0	0	0	0.00059916
0	0	0	0	0	0	0
0.15515933	0.19661191	0.15149736	0.1177665	0.17114695	0.19688645	0.24445776
0.04248862	0.0949692	0.15502055	0.12639594	0.22311828	0.07875458	0.12402636
0.10735964	0.16837782	0.28068115	0.19137056	0.20250896	0.17765568	0.16716597
0	0	0.0023488	0.00050761	0.00089606	0.003663	0.00838826
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0.00037936	0.00102669	0.0005872	0.00101523	0.00089606	0.00457875	0.00239664
0	0.00102669	0.0023488	0.00101523	0	0.00641026	0.00539245
0.176783	0.16889117	0.02818555	0.11522843	0.00806452	0.08241758	0.03774715



ea;D_1__Nanohaloarchaeota;D_2__uncultured archaeon

ria;D_1__Actinobacteria;D_2__Actinobacteria

ria;D_1__Cyanobacteria;D_2__Chloroplast

 $ria; D_1_Planctomycetes; D_2_Phycisphaerae$

 ${\tt ria;D_1_Proteobacteria;D_2_Betaproteobacteria}$

 ${\tt ria;D_1_Proteobacteria;D_2_Gammaproteobacteria}$

2016-02-10	2016-07-1	2016-07-2	2016-07-3	2016-07-4	2016-07-5	2016-10-1
0.48437052	0.51953908	0.49911442	0.75596613	0.62507221	0.70132159	0.57717581
0	0	0.00035423	0	0	0.00088106	0
0	0	0	0	0.0005777	0	0.00107282
0	0.000501	0	0	0	0	0.0001341
0.24462289	0.14378758	0.13885937	0.07852194	0.17504333	0.14889868	0.26887488
0.05506166	0.03507014	0.01381509	0.00307929	0.01039861	0.02202643	0.01609226
0.19730427	0.25450902	0.27878144	0.15704388	0.16984402	0.11629956	0.12458093
0.00057356	0.001002	0.00247963	0	0.0028885	0.00088106	0.0001341
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0.00086034	0.001002	0.00354233	0.00384911	0.0011554	0.00264317	0.00134102
0	0.000501	0.00035423	0.00076982	0	0.00088106	0.0001341
0.01720677	0.04408818	0.06269926	0.00076982	0.01502022	0.0061674	0.01045997

2016-10-2	2016-10-3	2016-10-4	2016-10-5	2016-10-6	2016-10-7	2016-10-8	
0.56628914	0.65032919	0.49634805	0.58605664	0.60173697	0.64801343	0.58667676	
0	0.00036576	0.00031756	0	0	0.0005596	0.000757	
0.00066622	0	0	0	0	0	0	
0	0.00036576	0	0	0	0	0	
0.15189873	0.16715435	0.19720546	0.18300654	0.15260546	0.21712367	0.15367146	
0.03530979	0.01682516	0.01810098	0.02015251	0.00744417	0.02965865	0.03860712	
0.12524983	0.12509144	0.26929184	0.19008715	0.12841191	0.08226077	0.18243755	
0.00266489	0.00073153	0.00190537	0.00217865	0.00124069	0.00111919	0.00454201	
0	0	0	0	0	0	0	
0	0	0	0	0	0	0	
0.00066622	0.00073153	0	0	0.00062035	0.00391718	0.001514	
0.00066622	0.00402341	0.00031756	0	0.00062035	0.00111919	0.000757	
0.11658894	0.03438186	0.01651318	0.01851852	0.1073201	0.01622832	0.03103709	

2016-10-9	2016-10-10	2016-10-11	2016-10-12	2017-02-1	2017-02-2	2017-02-3	
0.7114094	0.60171198	0.62664404	0.56724512	0.59349275	0.54643766	0.59452909	
0.0002918	0	0	0	0	0.00063613	0	
0	0.00050352	0	0	0	0	0	
0.0002918	0.00050352	0.00042427	0	0.00078401	0	0	
0.15873942	0.14300101	0.24437845	0.10816407	0.19012152	0.1456743	0.12811634	
0.02217683	0.04884189	0.02418328	0.01360678	0.06389651	0.11195929	0.07894737	
0.08987453	0.18277946	0.06406449	0.12640505	0.11172089	0.10750636	0.12119114	
0.0020426	0	0.00296988	0.00778939	0	0.01017812	0.00519391	
0	0	0	0	0	0	0	
0	0	0	0	0	0	0	
0.0011672	0.00251762	0.00084854	0.0010846	0.00117601	0.00318066	0.00277008	
0.0005836	0.00050352	0.00551549	0.0017748	0.00078401	0	0.00069252	
0.01342282	0.01963746	0.03097157	0.17393019	0.0380243	0.07442748	0.06855956	

2017-02-4	2017-02-5	2017-02-6	2017-02-7	2017-02-8	2017-02-9	2017-02-10	
0.63144039	0.63546798	0.74745763	0.79666161	0.66960776	0.51414558	0.66975863	
0	0	0	0	8.74E-05	5.98E-05	9.97E-05	
0	0	0	0	0	0	0	
0	0	0	0	0	0	0	
0.07747273	0.07006021	0.07711864	0.07473445	0.19262689	0.23948801	0.20496709	
0.12335464	0.17460317	0.03983051	0.00796662	0.028217	0.04635445	0.02732894	
0.12673938	0.09195402	0.12033898	0.08687405	0.0669171	0.15575094	0.05954518	
0.00752162	0.00437876	0.00084746	0.00037936	0.00113567	0.00454573	0.00139637	
0	0	0	0	0	0.00011962	0.00019948	
0	0	0	0	8.74E-05	0	0	
0.00188041	0.00218938	0	0.00037936	0.00034944	0.00089718	0.00079793	
0.00112824	0.00109469	0	0	8.74E-05	0.00077756	0.00039896	
0.03046258	0.02025178	0.01440678	0.03300455	0.04088407	0.03786112	0.03550768	