Aved_18-Q3-R54-62_BAT3C.540 Proteobacteria Deltaproteobacteria Myxococcales P30B-42	Percent_identity 20 25 30 35 40 Function Export GT MOD Polymerization NA
midas_g_6017 midas_s_601 Aved_18-Q3-R54-62_BATAC.192 Chloroflexi Anaerolineae Ardenticatenales	GT Weet TagA/CPS F family no domain super transferase of the polysaccharide big transferase domain super transferase domain linner membrane edmpone fit of the polysaccharide big transferase domain super transferase domain
Ca_Promineofilaceae midas_g_461 midas_s_46 Aved_18-Q3-R54-62_BATAC.253 Proteobacteria Alphaproteobacteria	
Sphingomonadales Sphingomonadaceae midas_g_59 midas_s_35	gumD
	35% 20% 23% 25% gumb guml guml gumb GT [4] GT g1 GT [2] Polysaccharide biographic protein Protein Polysaccharide biographic point protein Polysaccharide biographic polysaccharide
Aved_18-Q3-R54-62_BATAC.601 Acidobacteria Blastocatellia (Subgroup 4) Blastocatellales Blastocatellaceae Stenotrophobacter midas_s_118	29% 28% 25% gumb gumb CoA-bugging of Sugar transferase Polysaccharide bieses in law port protein Polysaccharide bieses in law port protein Polysaccharide bipsyntess of the polysaccharide bipsynte
Aved_18-Q3-R54-62_MAXAC.392 Proteobacteria Alphaproteobacteria Micavibrionales Micavibrionaceae midas_g_2943 midas_s_294	21% 28% 21% 23% GumC gumD gumD gumD VanZ like larfilly beta-barrel porlin 2 Chain langth determinant protein Polysaccharide his method for the polysaccharide by the polysaccharide
Bjer_18-Q3-R1-45_BAT3C.347 Proteobacteria Gammaproteobacteria Betaproteobacteriales B1-7BS midas_g_190 midas_s_48	26% 22% 24% 24% Qumb Qumb Qumb Qumb Qumb Qumb Qumb Qumb
Bjer_18-Q3-R1-45_MAXAC.024 Bacteroidetes Bacteroidia Chitinophagales midas_f_536 midas_g_536 midas_s_53	1000 2000 30000 22% 21% gumb OurrAighta and domain DegT/Opter 1000 2000 GT 14 GT 9 Bacterial transaction logical logical transaction logical transaction logical
Bjer_18-Q3-R1-45_MAXAC.141 Proteobacteria Gammaproteobacteria Betaproteobacteriales Burkholderiaceae Candidatus Symbiobacter	0 5000 10000 15000 20000 32% 21% 22% 20% 25% 21% 27% gumb gumC gumJ gumb gumD gumb gumD gumb gumD gumb gumD gumD gumD gumD gumD gumD gumD gumD
midas_s_30 Bjer_18-Q3-R1-45_MAXAC.222 Bacteroidetes Bacteroidia Chitinophagales Chitinophagaceae	PROFESIOR PROBLEM PROB
Chitinophagaceae Niabella midas_s_71 Damh_18-Q3-R51-60_MAXAC.008 Chloroflexi Anaerolineae Ardenticatenales	GT g1 GT 14 GT g1 Bacterial transferase hekapeptide (six repeats) Polysaccharide biosynthesis protein Transcription ter miniation factor nusc Gerich domain and domain of Gerich
Ardenticatenales Ca_Promineofilaceae midas_g_461 midas_s_46 Ega_18-Q3-R5-49_BATAC.118 Bacteroidetes	gum gum gum Carboxypes das a superior s
Ignavibacteria Kryptoniales BSV26 midas_g_627 midas_s_62	gumC gumB gumD gumD gumD gumD gumD gumD gumD gumD
Proteobacteria Gammaproteobacteria Betaproteobacteriales B1-7BS midas_g_190 midas_s_48	24% Qum Qum Qum Qum Qum Qum Qum Qu
Ega_18-Q3-R5-49_MAXAC.075 Bacteroidetes Bacteroidia Sphingobacteriales AKYH767 midas_g_283 midas_s_28	22% SprB [apeat] SprB [apeat
Ejby_18-Q3-R6-50_BAT3C.362 Proteobacteria Deltaproteobacteria Bdellovibrionales Bdellovibrionaceae OM27_clade midas_s_81	23% 23% 24% 25% gumD gumD gumC
EsbE_18-Q3-R3-47_BAT3C.110 Proteobacteria Deltaproteobacteria Syntrophobacterales Syntrophaceae midas_g_134 midas_s_126	22% 21% 21% 20% gumB gumC gumJ gumJ gumJ AAL domain Hu domain Polysactharide biosynthesis of G-rich domain on gutative Trains in Polysactharide biosynthesis of G-rich domain on gutative Trains in Polysactharide biosynthesis of DuF based on E. rectale Gene description (DuF3880)
EsbE_18-Q3-R3-47_BATAC.463 Proteobacteria Alphaproteobacteria Sphingomonadales Sphingomonadaceae midas_g_59 midas_s_5	0 5000 10000 15000 34% 22% 25% gumb gumb gumb gumb gumb gumb
EsbE_18-Q3-R3-47_MAXAC.131 Proteobacteria Gammaproteobacteria Betaproteobacteriales Rhodocyclaceae Propionivibrio	5000 10000 38% 23% 30% 38% gumC gumD gumD
midas_s_42 EsbW_18-Q3-R4-48_BAT3C.113 Ca_Fermentibacterota Ca_Fermentibacteria midas_o_753	Adultransferase Tampily O-Antigen illuses of Wect TagA/CDSF family CobQ/CobB/MinD/ParA nucleptide binding domain Putative beta-barrel print? Bacterial transferase Not rase hexapeptide (six ref. G-rich dpmginach and six ref. Bacterial transferase hexapeptide (six ref. Bacterial transferase hexapeptide) 39% 21% 22% 32% 30% 30% 30% 30% 30%
EsbW_18-Q3-R4-48_BAT3C.4_cln Acidobacteria Thermoanaerobaculia	ein of unknown function (DUF3485) O 5000 10000 15000 20000 34% 25% 20% 20% 21% 21% 33%
Thermoanaerobaculales Thermoanaerobaculaceae Subgroup_10 midas_s_408 EsbW_18-Q3-R4-48_MAXAC.012_A	gumb gumb gumb gumb gumb gumb gumb gumb
Nitrospirae Nitrospira Nitrospirales Nitrospiraceae <i>Nitrospira</i> <i>defluvi</i>	21% 27% 24% 32% gum
EsbW_18-Q3-R4-48_MAXAC.012_B Nitrospirae Nitrospirales Nitrospiraceae Nitrospiraceae Official defluvi	21% 27% 23% 37% Quml Quml
Fred_18-Q3-R57-64_BAT3C.529_sub Chloroflexi Anaerolineae Ardenticatenales Ca_Promineofilaceae midas_g_461 midas_s_46	Polysacon Chamber Basici S
Fred_18-Q3-R57-64_BAT3C.6 Gemmatimonadetes Gemmatimonadates Gemmatimonadales Gemmatimonadaceae midas_g_395 midas_s_39	5000 10000 15000 21% 22% 29% 23% 22% 21% gumb gumb gumb gumb gumb gumb gumb gumb
Fred_18-Q3-R57-64_BAT3C.705 Acidobacteria Blastocatellia (Subgroup 4) Blastocatellales Blastocatellaceae Stenotrophobacter midas s_118	15000 15000 20000 29% 28% 24% 25% gumb gumb gumb gumb gumb gumb gumb gumb
midas_s_118 Fred_18-Q3-R57-64_BATAC.274 Bacteroidetes Bacteroidia Sphingobacteriales AKYH767 midas q 283	O South State Control of the Control
midas_g_283 midas_s_28 Fred_18-Q3-R57-64_BATAC.422 Proteobacteria Gammaproteobacteria Betaproteobacteriales Nitrosomonadaceae	henvlanelly beginner policy of the policy of
Betaproteobacteriales Nitrosomonadaceae oc32 midas_s_288 Fred_18-Q3-R57-64_BATAC.601 Proteobacteria Alphaproteobacteria	PPRETABLE domain COA- Base Polysaccharide of Coal-Base Pol
Alphaproteobacteria Rhizobiales Devosiaceae Devosia midas_s_98 Fred_18-Q3-R57-64_MAXAC.274 Proteobacteria	gumC gumB gumH gumD
Proteobacteria Alphaproteobacteria Dongiales Dongiaceae Dongia midas_s_405	28% 29% 31% 21% gumD gumD gumH gumH gumJ gumH gumJ gumH gumJ gumH polysaccharide biosynthesis protein CoA-bigging a gump and the polysaccharide biosynthesis protein Polysaccharide biosynthesis protein To Sooo 10000
Fred_18-Q3-R57-64_MAXAC.276 Proteobacteria Deltaproteobacteria Myxococcales Sandaracinaceae midas_g_4101 midas_s_410	29% 21% 20% 38% gumb gumb gumb gumb gumb gumb gumb gumb
Fred_18-Q3-R57-64_MAXAC.330_cln Planctomycetes Phycisphaerae Phycisphaerales Phycisphaeraceae SM1A02 midas_s_491	28% 20% 21% gumb
Hade_18-Q3-R52-61_BATAC.316 Proteobacteria Gammaproteobacteria Betaproteobacteriales B1-7BS midas_g_190 midas_s_51	10000 20000 300000 30% 20% 21% 23% 34% 37% guml/guml guml Methylen light for the guml guml guml guml guml guml guml guml
Hade_18-Q3-R52-61_MAXAC.056 Proteobacteria Alphaproteobacteria Sphingomonadales Sphingomonadaceae Sphingomonadaceae	0 5000 10000 15000 20000 25000 21% 26% 31% 34% gumD gumC gumB
Hade_18-Q3-R52-61_MAXAC.304 Proteobacteria Gammaproteobacteria Betaproteobacteriales Rhodocyclaceae	Bacterial sugar transferase GT 4-like do Tear g1 O 5000 10000 38% 30% 23% 37% gumD gumD gumB gumC gumD gumB gumC
Propionivibrio midas_s_42 Hirt_18-Q3-R61-65_BATAC.102 Bacteroidetes Bacteroidia	erial transferase hekapeptics in repeats) O 5000 To Antigen lipase CobO/CobB/MinD/P transcerase Published Publishe
Flavobacteriales NS9_marine_group midas_g_385 midas_s_455 Hirt_18-Q3-R61-65_MAXAC.142 Chloroflexi	AAAAVCGAA OR DESTRICTION OF THE PROTECTION OF TH
Anaerolineae Ardenticatenales Ca_Promineofilaceae midas_g_1951 midas_s_195	Helix-ture by the state of the
Proteobacteria Deltaproteobacteria Myxococcales	20% 36% Qum gum gum Qum gum gum
Hirt_18-Q3-R61-65_MAXAC.231 Proteobacteria Gammaproteobacteria Betaproteobacteriales B1-7BS midas_g_190 midas_s_48	21% 21% 23% 24% 22% Superfamily and on the s
Hjor_18-Q3-R7-51_BAT3C.155_A Proteobacteria Alphaproteobacteria Rhizobiales Beijerinckiaceae midas_g_534 midas_s_529	31% 20% 27% 21% GumD gumD gumC gumD gumH HTHIdd Mini Con binging do nain Con bin binging do nain Con binging do nain Con binging do nain Con bin
Hjor_18-Q3-R7-51_BAT3C.155_B Proteobacteria Alphaproteobacteria Rhizobiales Beijerinckiaceae midas_g_534 midas_s_529	500 1000 15000 33% 20% 32% 22% gumD gumH gumB gumC Methyltransferase domain O-Antigen ligase Col-binding domain Bacterial sugar transferase Grich domain on putative tyrosine kinase G-rich domain on putative tyrosine kinase G-rich domain on putative tyrosine kinase Acetyltransferase (GNAT) domain Polysaccharide deacetylase
Hjor_18-Q3-R7-51_BAT3C.262_A Proteobacteria Alphaproteobacteria Rhizobiales Hyphomicrobiaceae <i>Hyphomicrobium</i> <i>midas_s_59</i>	0 2500 5000 7500 10000 33% 21% 31% 20% gumD gumD gumH gumB gumC
Hjor_18-Q3-R7-51_BAT3C.262_B Proteobacteria Alphaproteobacteria Rhizobiales Hyphomicrobiaceae	O Antigen ligase Coa-binding domain Bacterial sugar transferase GT 14 GT g1 Polysaccharide biosential sugar transferase GT 14 GT g1 Polysaccha
Hyphomicrobium midas_s_59	Cellulase (GH5) GICNAC-PI de-N-acetylase GT g1 Acetyltransfer ase (GNAT) domain on rula in the control of the
Hjor_18-Q3-R7-51_BAT3C.262_C Proteobacteria Alphaproteobacteria	0 5000 10000 15000 2000 33% 32% 22% 21% 20%
Proteobacteria Alphaproteobacteria Rhizobiales Hyphomicrobiaceae Hyphomicrobium midas_s_59 Hjor_18-Q3-R7-51_BAT3C.262_D Proteobacteria	
Proteobacteria Alphaproteobacteria Rhizobiales Hyphomicrobiaceae Hyphomicrobium midas_s_59 Hjor_18-Q3-R7-51_BAT3C.262_D Proteobacteria Alphaproteobacteria Alphaproteobacteria Rhizobiales Hyphomicrobiaceae Hyphomicrobium midas_s_59 Hjor_18-Q3-R7-51_MAXAC.072	asponse square from the contract of the contra
Proteobacteria Alphaproteobacteria Rhizobiales Hyphomicrobiaceae Hyphomicrobium midas_s_59 Hjor_18-Q3-R7-51_BAT3C.262_D Proteobacteria Alphaproteobacteria Rhizobiales Hyphomicrobiaceae Hyphomicrobium midas_s_59	esponse standard de
Proteobacteria Alphaproteobacteria Rhizobiales Hyphomicrobiaceae Hyphomicrobium midas_s_59 Hjor_18-Q3-R7-51_BAT3C.262_D Proteobacteria Alphaproteobacteria Alphaproteobacteria Rhizobiales Hyphomicrobiaceae Hyphomicrobium midas_s_59 Hjor_18-Q3-R7-51_MAXAC.072 Proteobacteria Gammaproteobacteria Betaproteobacteria Betaproteobacteriales Rhodocyclaceae	gumb gumb gumb gumb protein at unlargen turcian (OUF1194) coporate significance statement of the control of th
Proteobacteria Alphaproteobacteria Rhizobiales Hyphomicrobiaceae Hyphomicrobium midas_s_59 Hjor_18-Q3-R7-51_BAT3C.262_D Proteobacteria Alphaproteobacteria Alphaproteobacteria Rhizobiales Hyphomicrobiaceae Hyphomicrobiaceae Hyphomicrobiaceae Hyphomicrobiaceae Hyphomicrobiaceae Hyphomicrobiaceae Hyphomicrobiaceae Proteobacteria Gammaproteobacteria Betaproteobacteriales Rhodocyclaceae Propionivibrio midas_s_42 Kalu_18-Q3-R12-55_BAT3C.181 Proteobacteria Gammaproteobacteria Betaproteobacteriales Burkholderiaceae midas_g_81	gumb gumb gumb gumb gumb gumb gumb gumb
Proteobacteria Alphaproteobacteria Rhizobiales Hyphomicrobium midas_s_59 Hjor_18-Q3-R7-51_BAT3C.262_D Proteobacteria Alphaproteobacteria Alphaproteobacteria Rhizobiales Hyphomicrobium Rhizobiales Hyphomicrobium midas_s_59 Hjor_18-Q3-R7-51_MAXAC.072 Proteobacteria Gammaproteobacteria Betaproteobacteriales Rhodocyclaceae Propionivibrio midas_s_42 Kalu_18-Q3-R12-55_BAT3C.181 Proteobacteria Gammaproteobacteria Betaproteobacteria	gumb gumb gumb gumb gumb gumb gumb gumb
Proteobacteria Alphaproteobacteria Rhizobiales Hyphomicrobium midas_s_59 Hjor_18-Q3-R7-51_BAT3C.262_D Proteobacteria Alphaproteobacteria Alphaproteobacteria Rhizobiales Hyphomicrobium Rhizobiales Hyphomicrobium midas_s_59 Hjor_18-Q3-R7-51_MAXAC.072 Proteobacteria Gammaproteobacteria Betaproteobacteriales Rhodocyclaceae Propionivibrio midas_s_42 Kalu_18-Q3-R12-55_BAT3C.181 Proteobacteria Gammaproteobacteria Betaproteobacteria	Qumb Qumb Qumb Qumb Qumb Qumb Qumb Qumb
Hjor_18-Q3-R7-51_BAT3C.262_D Proteobacteria Rhizobiales Hyphomicrobiaceae Proteobacteria Betaproteobacteriales Rhodocyclaceae Propionivibrio midas_s_42 Kalu_18-Q3-R12-55_BAT3C.181 Proteobacteria Betaproteobacteriales Burkholderiaceae midas_g_81 midas_s_815 Kalu_18-Q3-R12-55_BATAC.116 Proteobacteria Deltaproteobacteria Deltaproteobacteria Deltaproteobacteria Deltaproteobacteria Myxococcales Birii41 midas_g_3573 midas_s_674 Kalu_18-Q3-R12-55_BATAC.47 Chloroflexi Anaerolineae Ardenticatenales Ca_Promineofilaceae midas_g_461 midas_s_461 midas_s_461 midas_s_465 Kalu_18-Q3-R12-55_MAXAC.026 Proteobacteria Alphaproteobacteria Al	
Proteobacteria Alphaproteobacteria Rhizobiales Hyphomicrobiaceae Hyphomicrobiaceae Hyphomicrobiaceae Hyphomicrobiaceae Alphaproteobacteria Alphaproteobacteria Rhizobiales Hyphomicrobiaceae Hyphomicrobiaceae Hyphomicrobiaceae Hyphomicrobiaceae Hyphomicrobiaceae Hyphomicrobiaceae Hyphomicrobiaceae Hyphomicrobiaceae Hyphomicrobiaceae Propionivibrio midas_s_59 Kalu_18-Q3-R12-55_BAT3C.181 Proteobacteria Betaproteobacteria Myxococcales Briri41 midas_g_815 Kalu_18-Q3-R12-55_BATAC.47 Chloroflexi Anaerolineae Ardenticatenales Ca_Promineofilaceae midas_g_461 midas_s_461 Kalu_18-Q3-R12-55_MAXAC.026 Proteobacteria Alphaproteobacteria Sphingomonadales	Total gumb gum
Proteobacteria Alphaproteobacteria Alphaproteobacteria Rhizobiales Hyphomicrobium midas_s_59 Hjor_18-Q3-R7-51_BAT3C.262_D Proteobacteria Rhizobiales Hyphomicrobium Rhizobiales Hyphomicrobium Rhizobiales Hyphomicrobium midas_s_59 Hjor_18-Q3-R7-51_MAXAC.072 Proteobacteria Rhizobiales Hyphomicrobium midas_s_59 Hjor_18-Q3-R7-51_MAXAC.072 Proteobacteria Betaproteobacterials Betaproteobacterials Betaproteobacterials Betaproteobacterials Burkholderiaceae midas_g_81 midas_s_815 Kalu_18-Q3-R12-55_BATAC.116 Proteobacteria Deltaproteobacterial Deltaproteobacterial Deltaproteobacterial Deltaproteobacterial Deltaproteobacteria Anaerolineae Ardenticatenales Ca_Promineofilaceae Ardenticatenales Ca_Promineofilaceae Ardenticatenales Ca_Promineofilaceae Ardenticatenales Ca_Promineofilaceae Midas_g_461 midas_s_461 Kalu_18-Q3-R12-55_MAXAC.026 Proteobacteria Alphaproteobacteria Sphingomonadaceae midas_g_5midas_s_35 Kalu_18-Q3-R12-55_MAXAC.049_cln Actinobacteria Acidimicrobials Ilumatobacteriaceae midas_g_462 midas_s_35 Kalu_18-Q3-R12-55_MAXAC.049_cln Actinobacteria Acidimicrobiale Ilumatobacteriaceae midas_g_462 midas_s_35 Kalu_18-Q3-R12-55_MAXAC.049_cln Actinobacteria Acidimicrobiale Ilumatobacteriaceae midas_g_462 midas_s_35	
Proteobacteria Alphaproteobacteria Alphaproteobacteria Alphaproteobacteria Hyphomicrobiaceae Hyphomicrobiaceae Hyphomicrobiaceae Alphaproteobacteria Alphaproteobacteria Alphaproteobacteria Alphaproteobacteria Alphaproteobacteria Rhizobiales Hyphomicrobiaceae Hyphomicrobiaceae Hyphomicrobiaceae Hyphomicrobiaceae Hyphomicrobiaceae Hyphomicrobiaceae Hyphomicrobiaceae Proteobacteria Betaproteobacteria Betaproteobacteria Betaproteobacteria Betaproteobacteria Betaproteobacteria Burkholderiaceae midas_s_42 Kalu_18-Q3-R12-55_BAT3C.181 Proteobacteria Deltaproteobacteria Deltaproteobacteria Myxococcales Birii41 midas_s_674 Kalu_18-Q3-R12-55_BATAC.47 Chloroffexi Anaerolineae Ardenticatenales Ca_Promineofilaceae midas_g_461 midas_s_461 Kalu_18-Q3-R12-55_MAXAC.026 Proteobacteria Alphaproteobacteria Alphaproteobacteria Sphingomonadales Sphingomonadaceae midas_g_462 midas_s_35 Kalu_18-Q3-R12-55_MAXAC.049_cln Actindbictorbia Alphaproteobacteria Alphaproteobacteria Deltaproteobacteria Sphingomonadales	
Proteobacteria Alphaproteobacteria Betaproteobacteria Gammaproteobacteria Betaproteobacteria Betaproteobacteria Betaproteobacteria Gammaproteobacteria Betaproteobacteria Alphaproteobacteria Myxococcales Birii41 midas g. 81 Kalu_18-Q3-R12-55 BATAC_17 Chloroflexi Anaerolineae Ardenticatenales Ca_Promineofilaceae midas_g. 46 Kalu_18-Q3-R12-55 MAXAC.026 Proteobacteria Alphaproteobacteria Aphaproteobacteria Aphaproteoba	
Proteobacteria Alphaproteobacteria Alphaproteobacteria Alphaproteobacteria Hyphomicrobiaceae Hyphomicrobiaceae Hyphomicrobiaceae Alphaproteobacteria Alphaproteobacteria Alphaproteobacteria Alphaproteobacteria Alphaproteobacteria Alphaproteobacteria Betaproteobacteria Betaproteobacteria Betaproteobacteriales Rhodocyclaceae Propionivibrio midas_s_42 Kalu_18-Q3-R12-55_BAT3C.181 Proteobacteria Betaproteobacteriales Burkholderiaceae midas_g_81 midas_s_815 Kalu_18-Q3-R12-55_BATAC.116 Proteobacteria Betaproteobacteria Ca_midas_g_81 midas_s_674 Kalu_18-Q3-R12-55_BATAC.17 Chloroflexi Anaerolineae Ardenticatenales Ca_Promineofilaceae midas_g_367 Kalu_18-Q3-R12-55_MAXAC.026 Proteobacteria Sphingomonadaceae midas_g_461 midas_s_46 Kalu_18-Q3-R12-55_MAXAC.026 Proteobacteria Alphaproteobacteria Sphingomonadaceae midas_g_59 midas_s_35 Kalu_18-Q3-R12-55_MAXAC.049_cln Actinobacteria Actinobacteria Alphaproteobacteria Sphingomonadaceae polyangum midas_s_592 Lyne_18-Q3-R50-59_BAT3C.1 Proteobacteria Alphaproteobacteria Alphaproteobacteria Sphingomonadaceae Polyangum midas_s_592 Lyne_18-Q3-R50-59_BAT3C.1 Proteobacteria Alphaproteobacteria Sphingomonadaceae Polyangum midas_s_592 Lyne_18-Q3-R50-59_BAT3C.16 Bacteroidales	
Aphaproteobacteria Alphaproteobacteria Alphaproteobacteria Alphaproteobacteria Alphaproteobacteria Alphaproteobacteria Alphaproteobacteria Alphaproteobacteria Alphaproteobacteria Alphaproteobacteria Betaproteobacteria Cammaproteobacteria Betaproteobacteria Betaproteobacteria Betaproteobacteria Betaproteobacteria Alphaproteobacteria Betaproteobacteria Alphaproteobacteria Alphaproteobacteria Alphaproteobacteria Alphaproteobacteria Betaproteobacteria Alphaproteobacteria Alphaproteobacteria Betaproteobacteria Alphaproteobacteria Betaproteobacteria Alphaproteobacteria Alphaproteobacteria Betaproteobacteria Alphaproteobacteria Betaproteobacteria Alphaproteobacteria Betaproteobacteria Betaproteobacteria Alphaproteobacteria Betaproteobacteria Betaproteobacteria Betaproteobacteria Alphaproteobacteria Betaproteobacteria Betaprote	
Alphaproteobacteria Alphaproteobacteria Alphaproteobacteria Hyphomicrobiaceae Hyphomicrobiaceae Hyphomicrobiaceae Alphaproteobacteria Rhizobiales Hyphomicrobiaceae Proplonivibrio midas_s_59 Kalu_18-Q3-R12-55_BATAC_172 Betaproteobacteria Alphaproteobacteria Alphaprot	
Profeebacteria Rhizobiales Hyphomicrobiara Rhizobiales Hyphomicrobiara Mides. s. 58 Hjor_18-Q3-R7-51_BAT3C_262_D Proteobacteria Alphaproteobacteria Rhizobiales Hyphomicrobiara Alphaproteobacteria Rhizobiales Hyphomicrobiara Rhizobiales Hyphomicrobiara Rhizobiales Hyphomicrobiara Midas. s. 59 Hjor_18-Q3-R7-51_MAXAC_072 Proteobacteria Betaproteobacteriales Rhodocyclaceae Proplonivbrio midas. s. 42 Kalu_18-Q3-R12-55_BAT3C_181 Proteobacteriales Burkholderiaceae Proteobacteriales Burkholderiaceae Midas_g. 815 Kalu_18-Q3-R12-55_BATAC_176 Proteobacteria Deltaproteobacteriale Deltaproteobacteria Alphaproteobacteria Alphaproteobacteria Alphaproteobacteria Alphaproteobacteria Alphaproteobacteria Alphaproteobacteria Sphingomonadaceae Midas_g. 461 Midas_s_36 Kalu_18-Q3-R12-55_MAXAC_026 Proteobacteria Alphaproteobacteria Alphaproteobacteria Sphingomonadaceae Midas_g. 461 Midas_s_36 Kalu_18-Q3-R12-55_MAXAC_026 Proteobacteria Alphaproteobacteria Sphingomonadaceae Midas_g. 461 Midas_s_36 Kalu_18-Q3-R12-55_MAXAC_036 Acidimicrobia Burkotocateria Alphaproteobacteria Sphingomonadaceae Midas_g. 462 Midas_s_36 Kalu_18-Q3-R12-55_MAXAC_036 Acidimicrobia Burkotocateria Alphaproteobacteria Alphaproteobact	
Profeebacteria Rhapprofeebacteria Rhapprofeebacteria Rhapprofeebacteria Rhapprofeebacteria Profeebacteria Aphaprofeebacteria Aphaprofeebacteria Aphaprofeebacteria Aphaprofeebacteria Aphaprofeebacteria Hyphomicrobium midas. s. 59 Hjor_18-Q3-R7-51_MAXAC_072_Profeebacteria Gammaprofeebacteria Betaprofeebacteria Poltaprofeebacteria Poltaprofeebacteria Poltaprofeebacteria Anaerolineae Ardenticatenales Ca_Promineofiliaceae midas_g_482 midas_s_462 midas_s_6144 midas_s_61	
Profeebacteria Aphaprofeebacteria (Propositional Propositional Profesional Pro	
Proteobacteria Aphaprocobacteria Hyphomicrobia mides 5.99 Hjor 18-03-R7-51 BAT3C.262 D Proteobacteria Aphapricrobia mides 5.99 Hjor 18-03-R7-51 BAT3C.262 D Proteobacteria Bethoprocobacteria Myxoxococales mides g. 461 mide	
Proteobacteria Alphaproteobacteria Hyphomicrobia Hyphomicrobia midsa. S. 99 Hjor. 18–03–R7–51 BAT3C-262 D Hyphomicrobia midsa. S. 93 Hjor. 18–03–R7–51 BAT3C-262 D Hyphomicrobia midsa. S. 93 Hjor. 18–03–R7–51 MAXAC. 972 Froteobacteria Hyphomicrobia midsa. S. 93 Hjor. 18–03–R7–51 MAXAC. 972 Froteobacteria Betaproteobacteria Betaproteobacteria Betaproteobacteria Betaproteobacteria Gammaroteobacteria Gammaroteobacteria Betaproteobacteria Betaproteobacteria Betaproteobacteria Delaproteobacteria Sphingomonadales Sphingomonadales Sphingomonadales Sphingomonadales Sphingomonadales Sphingomonadales Sphingomonadales Sphingomonadales Sphingomonadales Sphingomonadaes Polyargia midsa. 9, 467 Kalu_18–Q3–R12–55 MAXAC.049 chartinobacteria Acidmicrobia delaproteobacteria Sphingomonadaes Polyargia Midsa. 9, 467 Kalu_18–Q3–R12–55 MAXAC.049 chartinobacteria Acidmicrobia Belaproteobacteria Sphingomonadaes Polyargia Midsa. 9, 467 Kalu_18–Q3–R12–55 MAXAC.049 chartinobacteria Sphingomonadaese Polyargia Midsa. 9, 468 Lyne_18–Q3–R50–59 BAT3C.16 Lyne_18–Q3–R50–59 BAT3C.262 Bacterioteobacteria Sphingomonadaese Polyargia Midsa. 9, 468 Lyne_18–Q3–R50–59 BAT3C.262 Bacterioteobacteria Sphingomonadaese Polyargia Midsa. 9, 468 Lyne_18–Q3–R50–59 BAT3C.262 Lyne_18–Q3–R50–59 BAT3C.262 Lyne_18–Q3–R50–59 BAT3C.262 Bacterioteobacteria Sphingomonadaese Polyargia Midsa. 9, 468 Mari_18–Q3–R50–59 BAT3C.262 Lyne_18–Q3-R50–59 BAT3C.262 Lyne_18–Q3-R50–59 BAT3C.262 Bacterioteobacteria Sphingomonadaese Polyargia Midsa. 9, 468 Mari_18–Q3-R50–59 BAT3C.262 Lyne_18–Q3-R50–59 BAT3C.262 Lyne_18–Q3-R50–59 BAT3C.262 Lyne_18–Q3-R50–59 BAT3C.262 Lyne_18–Q3-R50–59 BAT3C.262 Bacterioteobacteria Sphingomonadaese Polyargia Midsa. 9, 264 Mari_18–Q3-R50–69 BAT3C.294 Mari_18–Q3-R50–69 BAT3C.294 Mari_18–Q3-R50–69 BAT3C.294	
Protebolacteria Alphaprotechacteria Alphaprotechacteria Hyphomicrobiane Hyphomicrobiane Hyphomicrobiane Myhomicrobiane Hyphomicrobiane Hyphomi	
Proteobacteria Hyphomicrobiace Froteobacteria Betappianhibrio Indias_s_42 Kalu_18-Q3-R12-55_BAT3C_181 Froteobacteria Betappianhibrio Indias_s_815 Kalu_18-Q3-R12-55_BAT3C_181 Froteobacteria Betappianhibrio Indias_s_815 Kalu_18-Q3-R12-55_BAT3C_181 Froteobacteria Deltapproteobacteria Myxococcales Indias_s_674 Kalu_18-Q3-R12-55_BAT3C_182 Hyphomicrobiace Indias_s_674 Kalu_18-Q3-R12-55_BAT3C_183 Froteobacteria Sphingomonaclales Indias_s_674 Kalu_18-Q3-R12-55_BAT3C_186 Sphingomonaclales Indias_s_674 Kalu_18-Q3-R12-55_BAT3C_186 Indias_s_674 Lyne_18-Q3-R50-59_BAT3C_286 Indias_s_674 Lyne_18-Q3-R50-59_BAT3C_346 Indias_s_674	
Proteobacteria Hyphomicrobiace	
Proteobacteria Alphaprotocolecteria Hyphomicrobice Hiphomicrobice Hiphomicrobice Hyphomicrobice	
Frotebotacteria Alphapmicrobiaces Hyphomicrobiaces Hyphom	
Figure 18-Q3-R50-59 BAT3C. 16 Figure 18-Q3-R50-59 BAT3C. 26 Figure 18-Q3-R50-59 BAT3C. 26 Kalu_18-Q3-R12-55_MAXAC. 097 Figure 18-Q3-R12-55_BATAC. 18-Q3-R12-55_BAT	
Protectionace designation of the comment of the com	
High Productional field in the production of the	
### A Company of the	
Higher 18-Q3-R75-SB BATSC 1842 BATSC	
## Professional Coloration	
### 18-03-R75-51 PMT3C 262-D ### 18-03-R75-11 PMT3C 262-D ### 18-03-R75-13	
Professionation Professionationation Professionationation Professionationation Professionationation Professionationationationationationationationat	
Higher 18-03-R2-56 BATACC-18-18-03-R2-56 BATACC-18-18-18-03-R2-56 BATACC-18-18-03-R2-56 BA	
Proceedings	
### 19-03-RT-51-8470C-256-8 ### 19-03-RT-51-	
### 18-02-R2-19-19-19-19-19-19-19-19-19-19-19-19-19-	
National Color Nati	
History Hist	
### 19-03-17-05-05-05-05-05-05-05-05-05-05-05-05-05-	
### 19-03-17-18-18-17-29-18-18-18-18-18-18-18-18-18-18-18-18-18-	
### 18-03-#7-1 Hard Colf of Proposed Col	
Hand G	
Part	