

Supplementary Table 1 MaAslin2 analysis of microbial species associated with different PACS symptoms

Species	coef	pval	qval
s__Blautia_wexlerae	-0.26548	1.48E-11	6.16E-10
s__Bacteroides_galacturonicus	-0.25155	2.82E-09	9.35E-08
s__Blautia_obeum	-0.2906	6.71E-07	1.86E-05
s__Gemmiger_formicilis	-0.35336	1.08E-06	2.55E-05
s__Erysipelatoclostridium_ramosum	0.380782	3.98E-06	8.27E-05
s__Roseburia_hominis	-0.37007	1.55E-05	0.000257
s__Ruminococcus_gnavus	0.416571	1.40E-05	0.000257
s__Eubacterium_hallii	-0.2941	2.36E-05	0.000356
s__Faecalibacterium_prausnitzii	-0.26288	4.00E-05	0.000553
s__Sutterella_parvirubra	0.192596	9.32E-05	0.00119
s__Streptococcus_vestibularis	-0.18874	0.000184	0.002034
s__Anaerotignum_lactatifermentans	0.178486	0.000182	0.002034
s__Oscillibacter_sp_57_20	-0.26078	0.00022	0.002284
s__Bifidobacterium_adolescentis	-0.34435	0.000305	0.002788
s__Asaccharobacter_celatus	-0.26366	0.000319	0.002788
s__Eubacterium_ramulus	-0.22102	0.000298	0.002788
s__Agathobaculum_butyriciproducens	-0.16664	0.000376	0.003124
s__Bifidobacterium_pseudocatenulatum	-0.31041	0.000431	0.003251
s__Parabacteroides_gordonii	0.14744	0.000412	0.003251
s__Streptococcus_thermophilus	-0.18249	0.000604	0.004177
s__Turicimonas_muris	0.18501	0.00058	0.004177
s__Adlercreutzia_equolifaciens	-0.24308	0.00073	0.004845
s__Clostridium_bolteae	0.257505	0.000766	0.00489
s__Anaerostipes_hadrus	-0.17544	0.000859	0.005228
s__Bacteroides_fragilis	0.340827	0.000882	0.005228
s__Bacteroides_salyersiae	0.203681	0.000938	0.005369
s__Megamonas_funiformis	-0.29275	0.001108	0.006045
s__Dorea_formicigenerans	-0.23973	0.001159	0.006045
s__Coprobacillus_cateniformis	0.228054	0.001165	0.006045
s__Klebsiella_quasipneumoniae	-0.17647	0.001757	0.008837
s__Blautia_hansenii	0.19892	0.002074	0.010125
s__Streptococcus_pasteurianus	0.14305	0.002869	0.013605
s__Firmicutes_bacterium_CAG_83	-0.26549	0.003047	0.01405
s__Fusicatenibacter_saccharivorans	-0.2104	0.003403	0.015238
s__Blautia_producta	0.12797	0.00358	0.015238
s__Blautia_sp_CAG_257	0.224475	0.003547	0.015238
s__Parasutterella_excrementihominis	0.221376	0.004122	0.017107
s__Bacteroides_thetaiotaomicron	0.186053	0.004288	0.017362
s__Dorea_sp_CAG_317	0.141272	0.006602	0.026095

s_Dorea_longicatena	-0.18283	0.006868	0.026515
s_Veillonella_atypica	0.137401	0.007206	0.027187
s_Megamonas_hypermegale	-0.1937	0.007772	0.028046
s_Escherichia_coli	0.174986	0.007712	0.028046
s_Coprococcus_catus	-0.2139	0.008391	0.029636
s_Ruminococcus_torques	-0.16247	0.009056	0.031319
s_Eubacterium_rectale	-0.2057	0.011574	0.036652
s_Coprococcus_comes	-0.19018	0.011275	0.036652
s_Ruminococcaceae_bacterium_D16	0.117242	0.011702	0.036652
s_Tyzzereella_nexilis	0.137746	0.011386	0.036652
s_Proteobacteria_bacterium_CAG_139	0.192373	0.010923	0.036652
s_Clostridium_clostridioforme	0.129459	0.012045	0.037026
s_Flavonifractor_plautii	0.140405	0.012738	0.038445
s_Coprococcus_eutactus	-0.0913	0.015086	0.04472
s_Clostridium_symbiosum	0.145429	0.016076	0.046817
s_Bifidobacterium_longum	-0.16628	0.018345	0.052506
s_Bacteroides_dorei	-0.26398	0.020902	0.058809
s_Eubacterium_eligens	-0.17549	0.022148	0.060273
s_Haemophilus_sp_HMSC71H05	-0.10892	0.021923	0.060273
s_Bifidobacterium_dentium	0.099412	0.024297	0.065054
s_Hungatella_hathewayi	0.144427	0.028627	0.075431
s_Bacteroides_massiliensis	0.181702	0.030389	0.078822
s_Lactobacillus_rogosae	-0.12724	0.032074	0.081911
s_Clostridium_leptum	-0.15077	0.035766	0.089956
s_Collinsella_aerofaciens	-0.18485	0.037557	0.093052
s_Ruminococcus_bicirculans	-0.17667	0.043867	0.106759
s_Firmicutes_bacterium_CAG_110	-0.10287	0.044376	0.106759
s_Bacteroides_ovatus	-0.14322	0.053627	0.127172
s_Parabacteroides_merdae	-0.1732	0.059319	0.13869
s_Bacteroides_intestinalis	-0.13702	0.064098	0.147781
s_Veillonella_parvula	0.109276	0.066008	0.1501
s_Blautia_coccoides	0.088044	0.068756	0.154236
s_Olsenella_scotoligenes	-0.0971	0.074363	0.16459
s_Eubacterium_ventriosum	-0.14844	0.076974	0.168127
s_Fusobacterium_varium	0.082804	0.084288	0.180174
s_Collinsella_intestinalis	0.087697	0.08466	0.180174
s_Ruminococcus_lactaris	-0.11519	0.109584	0.230265
s_Roseburia_intestinalis	-0.14707	0.116356	0.241439
s_Oscillibacter_sp_CAG_241	-0.13649	0.118469	0.242788
s_Bacteroides_cellulosilyticus	-0.14088	0.121231	0.245418
s_Parabacteroides_goldsteinii	0.09897	0.126492	0.252984
s_Eisenbergiella_massiliensis	0.086093	0.135932	0.268628
s_Roseburia_inulinivorans	-0.12123	0.146931	0.286947

s__Ruminococcus_bromii	-0.13795	0.154571	0.295053
s__Parabacteroides_distasonis	0.067754	0.154636	0.295053
s__Streptococcus_parasanguinis	0.109304	0.165792	0.312744
s__Collinsella_stercoris	0.084802	0.18266	0.340692
s__Eubacterium_siraeum	-0.10855	0.186757	0.344463
s__Streptococcus_anginosus_group	0.062108	0.189877	0.346369
s__Clostridium_asparagiforme	0.075523	0.196034	0.353714
s__Gordonibacter_pamelaee	-0.07842	0.199015	0.355231
s__Eubacterium_sp_CAG_274	-0.07026	0.202944	0.35839
s__Bacteroides_clarus	0.093799	0.206413	0.360679
s__Clostridium_citroniae	0.083817	0.210247	0.363551
s__Enterobacter_cloacae_complex	-0.04973	0.231187	0.39564
s__Roseburia_sp_CAG_303	-0.04806	0.236531	0.400654
s__Klebsiella_pneumoniae	-0.09646	0.256924	0.426977
s__Bacteroides_vulgatus	0.094141	0.257215	0.426977
s__Klebsiella_variicola	-0.06732	0.264102	0.434068
s__Intestinimonas_butyrificiproducens	0.066269	0.282875	0.460365
s__Eubacterium_sp_CAG_38	-0.09739	0.286679	0.462026
s__Odoribacter_splanchnicus	-0.08006	0.304122	0.482719
s__Eisenbergiella_tayi	0.051791	0.305334	0.482719
s__Veillonella_dispar	0.031051	0.31008	0.485597
s__Eggerthella_lenta	0.069525	0.336095	0.521419
s__Acidaminococcus_intestini	-0.0761	0.351606	0.540431
s__Bacteroides_caccae	-0.0741	0.364483	0.555085
s__Ruthenibacterium_lactatiformans	0.05463	0.386924	0.583903
s__Alistipes_shahii	-0.07015	0.391179	0.585006
s__Paraprevotella_xylaniphila	-0.04313	0.398383	0.590461
s__Bacteroides_sp_OM05_12	0.052322	0.408592	0.600232
s__Bacteroides_coprocola	0.057408	0.415105	0.604451
s__Haemophilus_parainfluenzae	0.038761	0.440895	0.636422
s__Parabacteroides_johnsonii	0.041641	0.449089	0.642662
s__Phascolarctobacterium_succinatutens	0.032905	0.466907	0.662449
s__Clostridium_bolteae_CAG_59	-0.04257	0.479243	0.67419
s__Mitsuokella_multacida	0.03483	0.483996	0.675154
s__Alistipes_putredinis	-0.0635	0.511498	0.681439
s__Bacteroides_finegoldii	-0.05189	0.496964	0.681439
s__Bacteroides_stercoris	-0.05142	0.524994	0.681439
s__Streptococcus_salivarius	-0.04386	0.507025	0.681439
s__Enterococcus_faecalis	-0.03542	0.51281	0.681439
s__Desulfovibrio_piger	0.034767	0.524073	0.681439
s__Holdemanella_biformis	0.042333	0.52249	0.681439
s__Bacteroides_xylanisolvans	0.048445	0.525447	0.681439
s__Akkermansia_muciniphila	0.062866	0.503066	0.681439

s__Roseburia_faecis	-0.06331	0.53336	0.686339
s__Bacteroides_eggerthii	0.053877	0.547793	0.69949
s__Alistipes_finegoldii	0.048835	0.552116	0.699628
s__Firmicutes_bacterium_CAG_145	0.032346	0.566247	0.706744
s__Bacteroides_plebeius	0.048915	0.561991	0.706744
s__Eubacterium_sp_CAG_251	0.031862	0.575505	0.712938
s__Paraprevotella_clara	-0.02352	0.580379	0.713651
s__Cloacibacillus_porcorum	0.028121	0.587254	0.716795
s__Megasphaera_elsdenii	0.025074	0.605059	0.733138
s__Copro bacter fastidiosus	0.021388	0.620553	0.746462
s__Anaerotruncus_colihominis	0.029601	0.629174	0.751388
s__Barnesiella_intestinihominis	-0.04048	0.643395	0.762883
s__Clostridium_innocuum	0.031884	0.658854	0.775672
s__Alistipes_indistinctus	-0.03281	0.671073	0.784494
s__Faecalitalea_cylindroides	-0.01916	0.687234	0.797768
s__Bifidobacterium_bifidum	-0.02074	0.737787	0.840016
s__Bacteroides_uniformis	-0.01884	0.742294	0.840016
s__Butyricimonas_synergistica	0.021039	0.740916	0.840016
s__Lawsonibacter_asaccharolyticus	0.023716	0.74387	0.840016
s__Clostridium_sp_CAG_242	-0.02615	0.749908	0.841113
s__Butyricimonas_virosa	0.02299	0.767471	0.855035
s__Blautia_hydrogenotrophica	-0.01669	0.773783	0.85632
s__Eubacterium_sp_CAG_180	0.019705	0.785982	0.86406
s__Clostridium_sp_CAG_58	-0.01718	0.820181	0.895724
s__Anaeromassilibacillus_sp_An250	-0.01019	0.845401	0.911276
s__Lachnospira_pectinoschiza	0.022083	0.845146	0.911276
s__Clostridium_sp_CAG_299	-0.00907	0.854184	0.913817
s__Bilophila_wadsworthia	0.009688	0.858768	0.913817
s__Phascolarctobacterium_faecium	-0.01265	0.878988	0.92034
s__Clostridium_saccharolyticum	-0.00804	0.879019	0.92034
s__Holdemania_filiformis	0.007447	0.881531	0.92034
s__Sellimonas_intestinalis	-0.0082	0.909994	0.940744
s__Intestinibacter_bartlettii	-0.00671	0.918075	0.940744
s__Dialister_sp_CAG_357	0.01159	0.917331	0.940744
s__Oxalobacter_formigenes	-0.00429	0.935369	0.952584
s__Prevotella_copri	0.005813	0.954866	0.96651
s__Fusobacterium_mortiferum	-0.00221	0.963449	0.969288
s__Roseburia_sp_CAG_471	0.001193	0.987949	0.987949