Suppl. Table 4: Significant metabolic pathways across the CAP group and the healthy group

Name	P-value	FDR
K00029_malate_dehydrogenase_(oxaloacetate_decarboxylating)(NADP+)_EC:1_1_1_40	1.08E-05	9.60E-04
K09800_translocation_and_assembly_module_TamB	1.10E-05	9.60E-04
K02014_iron_complex_outermembrane_recepter_protein	1.42E-05	9.60E-04
K00164_2_oxoglutarate_dehydrogenase_E1_component_EC:1_2_4_2	1.31E-04	0.005849
K03694_ATP_dependent_Clp_protease_ATP_binding_subunit_ClpA	1.63E-04	0.005849
K00990_protein_PII_uridylyltransferase_EC:2_7_7_59	2.05E-04	0.005849
K16087_hemoglobin_transferrin_lactoferrin_receptor_protein	2.18E-04	0.005849
K03303_lactate_permease	2.31E-04	0.005849
K00163_pyruvate_dehydrogenase_E1_component_EC:1_2_4_1	3.12E-04	0.006567
K04744_LPS_assembly_protein	3.23E-04	0.006567
K18138_multidrug_efflux_pump	5.18E-04	0.009565
K07277_outer_membrane_protein_insertion_porin_family	8.09E-04	0.013681
K03688_ubiquinone_biosynthesis_protein	0.0012315	0.019231
K07278_translocation_and_assembly_module_TamA	0.0013969	0.020256
K04079_molecular_chaperone_HtpG	0.0015117	0.020458

K01687_dihydroxy_acid_dehydratase_EC:4_2_1_9	0.0017276	0.020632
K00239_succinate_dehydrogenase___fumarate_reductase,_flavoprotein_subunit_EC:1_3_5_1_1_3_5_4	0.0017278	0.020632
K07090_uncharacterized_protein	0.0018916	0.021333
K09815_zinc_transport_system_substrate_binding_protein	0.0020066	0.021439
K01338_ATP_dependent_Lon_protease_EC:3_4_21_53	0.0029677	0.030122

This table illustrates metabolic pathways that showed significant differences in abundance between children with community-acquired pneumonia (CAP) and healthy controls.