Supplementary Table 2. Altered metabolic proficiencies of microbiota in SSc patients in the cecum (A) and Sigmoid (B) regions.

Table 2A. Differences of KEGG pathway and orthology in SSc versus healthy controls (Nrml) in the cecum region.*

KEGG Pathway			KEGG orthology			
KO Pathway ID	**Pathway (L2)**	**Pathway (L3)**	**KO Gene ID: Name**	**Gene increased in**	**Effect size**	***q* value**
ko00250	Amino Acid Metabolism	Alanine, aspartate and glutamate metabolism	K00266: glutamate synthase (NADPH/NADH) small chain	Nrml	2.38	0.002
ko00270	Amino Acid Metabolism	Cysteine and methionine metabolism	K00640: serine O-acetyltransferase	Nrml	2.05	0.048
ko00270	Amino Acid Metabolism	Cysteine and methionine metabolism	K01740: O-acetylhomoserine (thiol)-lyase	Nrml	2.00	0.019

ko00260	Amino Acid Metabolism	Glycine, serine and threonine metabolism	K01834: phosphoglycerate mutase	Nrml	2.26	0.013
ko00360	Amino Acid Metabolism	Phenylalanine metabolism	K01912: phenylacetate-CoA ligase	Nrml	2.04	0.098
ko00250	Amino Acid Metabolism	Alanine, aspartate and glutamate metabolism	K01955: carbamoyl-phosphate synthase large subunit	Nrml	2.11	0.009
ko00340	Amino Acid Metabolism	Histidine metabolism	K11755: phosphoribosyl-ATP pyrophosphohydrolase / phosphoribosyl-AMP	Nrml	2.00	0.003
ko00940	Biosynthesis of Other Secondary Metabolites	Phenylpropanoid biosynthesis	K05349: beta-glucosidase	Nrml	2.52	0.061
ko05230	Cancers	Central carbon metabolism in cancer	K00850: 6-phosphofructokinase	Nrml	2.02	0.066
ko05230	Cancers	Central carbon metabolism	K01834:	Nrml	2.26	0.013

		in cancer	phosphoglycerate mutase			
ko00020	Carbohydrate Metabolism	Citrate cycle (TCA cycle)	K00174: 2-oxoglutarate ferredoxin oxidoreductase subunit alpha	Nrml	2.05	0.061
ko00020	Carbohydrate Metabolism	Citrate cycle (TCA cycle)	K00175: 2-oxoglutarate ferredoxin oxidoreductase subunit beta	Nrml	2.05	0.084
ko00010	Carbohydrate Metabolism	Glycolysis / Gluconeogenesis	K00850: 6-phosphofructokinase	Nrml	2.02	0.066
ko00030	Carbohydrate Metabolism	Pentose phosphate pathway	K00850: 6-phosphofructokinase	Nrml	2.02	0.066
ko00051	Carbohydrate Metabolism	Fructose and mannose metabolism	K00850: 6-phosphofructokinase	Nrml	2.02	0.066
ko00052	Carbohydrate Metabolism	Galactose metabolism	K00850: 6-phosphofructokinase	Nrml	2.02	0.066
ko00030	Carbohydrate Metabolism	Pentose phosphate pathway	K00874: 2-dehydro-3-deoxygluconokinase	Nrml	2.04	0.004
ko00520	Carbohydrate	Amino sugar and nucleotide	K00983: N-	Nrml	2.01	0.001

	Metabolism	sugar metabolism	acylneuraminate cytidylyltransferase			
ko00040	Carbohydrate Metabolism	Pentose and glucuronate interconversions	K01051: pectinesterase	NrmI	2.08	0.021
ko00500	Carbohydrate Metabolism	Starch and sucrose metabolism	K01051: pectinesterase	NrmI	2.08	0.021
ko00052	Carbohydrate Metabolism	Galactose metabolism	K01187: alpha-glucosidase	NrmI	2.40	0.044
ko00500	Carbohydrate Metabolism	Starch and sucrose metabolism	K01187: alpha-glucosidase	NrmI	2.40	0.044
ko00052	Carbohydrate Metabolism	Galactose metabolism	K01190: beta-galactosidase	NrmI	2.73	0.021
ko00520	Carbohydrate Metabolism	Amino sugar and nucleotide sugar metabolism	K01209: alpha-N-arabinofuranosidase	NrmI	2.24	0.009
ko00620	Carbohydrate Metabolism	Pyruvate metabolism	K01572: oxaloacetate decarboxylase, beta subunit	NrmI	2.14	0.017
ko00040	Carbohydrate	Pentose and glucuronate	K01686: mannonate	NrmI	2.07	0.026

	Metabolism	interconversions	dehydratase			
ko00010	Carbohydrate Metabolism	Glycolysis / Gluconeogenesis	K01785: aldose 1-epimerase	Nrml	2.24	0.012
ko00052	Carbohydrate Metabolism	Galactose metabolism	K01785: aldose 1-epimerase	Nrml	2.24	0.012
ko00520	Carbohydrate Metabolism	Amino sugar and nucleotide sugar metabolism	K01791: UDP-N-acetylglucosamine 2-epimerase	Nrml	2.36	0.028
ko00010	Carbohydrate Metabolism	Glycolysis / Gluconeogenesis	K01834: phosphoglycerate mutase	Nrml	2.26	0.013
ko00500	Carbohydrate Metabolism	Starch and sucrose metabolism	K05349: beta-glucosidase	Nrml	2.52	0.061
ko00520	Carbohydrate Metabolism	Amino sugar and nucleotide sugar metabolism	K12373: beta-hexosaminidase	Nrml	2.42	0.072
ko02030	Cell Motility	Bacterial chemotaxis	K03406: methyl-accepting chemotaxis protein	Nrml	2.66	0.048
ko04974	Digestive System	Protein digestion and absorption	K01278: dipeptidyl-peptidase 4	Nrml	2.10	0.034

ko03320	Endocrine System	PPAR signaling pathway	K01897: long-chain acyl-CoA synthetase	NrmI	2.28	0.021
ko04920	Endocrine System	Adipocytokine signaling pathway	K01897: long-chain acyl-CoA synthetase	NrmI	2.28	0.021
ko00720	Energy Metabolism	Carbon fixation pathways in prokaryotes	K00174: 2-oxoglutarate ferredoxin oxidoreductase subunit alpha	NrmI	2.05	0.061
ko00720	Energy Metabolism	Carbon fixation pathways in prokaryotes	K00175: 2-oxoglutarate ferredoxin oxidoreductase subunit beta	NrmI	2.05	0.084
ko00910	Energy Metabolism	Nitrogen metabolism	K00266: glutamate synthase (NADPH/NADH) small chain	NrmI	2.38	0.002
ko00920	Energy Metabolism	Sulfur metabolism	K00640: serine O-acetyltransferase	NrmI	2.05	0.048
ko00680	Energy Metabolism	Methane metabolism	K00850: 6-phosphofructokinase	NrmI	2.02	0.066
ko00680	Energy	Methane metabolism	K01834:	NrmI	2.26	0.013

	Metabolism		phosphoglycerate mutase			
ko04122	Folding, Sorting and Degradation	Sulfur relay system	K00566: tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase	NrmI	2.05	0.066
ko03018	Folding, Sorting and Degradation	RNA degradation	K00850: 6-phosphofructokinase	NrmI	2.02	0.066
ko03060	Folding, Sorting and Degradation	Protein export	K03100: signal peptidase I	NrmI	2.23	0.056
ko03018	Folding, Sorting and Degradation	RNA degradation	K03654: ATP-dependent DNA helicase RecQ	NrmI	2.01	0.098
ko00511	Glycan Biosynthesis and Metabolism	Other glycan degradation	K01190: beta-galactosidase	NrmI	2.73	0.021

ko00511	Glycan Biosynthesis and Metabolism	Other glycan degradation	K01201: glucosylceramidase	Nrml	2.00	0.011
ko00511	Glycan Biosynthesis and Metabolism	Other glycan degradation	K12373: beta-hexosaminidase	Nrml	2.42	0.072
ko00531	Glycan Biosynthesis and Metabolism	Glycosaminoglycan degradation	K12373: beta-hexosaminidase	Nrml	2.42	0.072
ko00603	Glycan Biosynthesis and Metabolism	Glycosphingolipid biosynthesis - globo series	K12373: beta-hexosaminidase	Nrml	2.42	0.072
ko00604	Glycan Biosynthesis	Glycosphingolipid biosynthesis - ganglio	K12373: beta-hexosaminidase	Nrml	2.42	0.072

	and Metabolism	series				
ko00600	Lipid Metabolism	Sphingolipid metabolism	K01190: beta-galactosidase	Nrml	2.73	0.021
ko00600	Lipid Metabolism	Sphingolipid metabolism	K01201: glucosylceramidase	Nrml	2.00	0.011
ko00120	Lipid Metabolism	Primary bile acid biosynthesis	K01442: choloylglycine hydrolase	Nrml	2.01	0.013
ko00121	Lipid Metabolism	Secondary bile acid biosynthesis	K01442: choloylglycine hydrolase	Nrml	2.01	0.013
ko00061	Lipid Metabolism	Fatty acid biosynthesis	K01897: long-chain acyl-CoA synthetase	Nrml	2.28	0.021
ko00071	Lipid Metabolism	Fatty acid degradation	K01897: long-chain acyl-CoA synthetase	Nrml	2.28	0.021
ko01212	Lipid Metabolism	Fatty acid metabolism	K01897: long-chain acyl-CoA synthetase	Nrml	2.28	0.021
ko01200	Metabolism	Carbon metabolism	K00640: serine O-acetyltransferase	Nrml	2.05	0.048

ko01230	Metabolism	Biosynthesis of amino acids	K00640: serine O-acetyltransferase	NrmI	2.05	0.048
ko01200	Metabolism	Carbon metabolism	K00850: 6-phosphofructokinase	NrmI	2.02	0.066
ko01230	Metabolism	Biosynthesis of amino acids	K00850: 6-phosphofructokinase	NrmI	2.02	0.066
ko01200	Metabolism	Carbon metabolism	K00874: 2-dehydro-3-deoxygluconokinase	NrmI	2.04	0.004
ko01200	Metabolism	Carbon metabolism	K01834: phosphoglycerate mutase	NrmI	2.26	0.013
ko01230	Metabolism	Biosynthesis of amino acids	K01834: phosphoglycerate mutase	NrmI	2.26	0.013
ko01230	Metabolism	Biosynthesis of amino acids	K11755: phosphoribosyl-ATP pyrophosphohydrolase / phosphoribosyl-AMP	NrmI	2.00	0.003
ko00860	Metabolism of Cofactors and	Porphyrin and chlorophyll metabolism	K00595: precorrin-6Y C5,15-methyltransferase /	NrmI	2.10	0.016

	Vitamins		precorrin-8W decarboxylase			
ko00860	Metabolism of Cofactors and Vitamins	Porphyrin and chlorophyll metabolism	K02224: hydrogenobyrinic acid a,c-diamide synthase	Nrml	2.10	0.028
ko00460	Metabolism of Other Amino Acids	Cyanoamino acid metabolism	K05349: beta-glucosidase	Nrml	2.52	0.061
ko00240	Nucleotide Metabolism	Pyrimidine metabolism	K01955: carbamoyl-phosphate synthase large subunit	Nrml	2.11	0.009
ko03030	Replication and Repair	DNA replication	K03111: single-strand DNA-binding protein	Nrml	2.06	0.008
ko03430	Replication and Repair	Mismatch repair	K03111: single-strand DNA-binding protein	Nrml	2.06	0.008
ko03440	Replication and Repair	Homologous recombination	K03111: single-strand DNA-binding protein	Nrml	2.06	0.008
ko03440	Replication	Homologous recombination	K03655: ATP-dependent	Nrml	2.12	0.031

	and Repair		DNA helicase RecG			
ko04152	Signal transduction	AMPK signaling pathway	K00850: 6-phosphofructokinase	Nrml	2.02	0.066
ko02020	Signal Transduction	Two-component system	K03406: methyl-accepting chemotaxis protein	Nrml	2.66	0.048
ko04142	Transport and Catabolism	Lysosome	K01201: glucosylceramidase	Nrml	2.00	0.011
ko04146	Transport and Catabolism	Peroxisome	K01897: long-chain acyl-CoA synthetase	Nrml	2.28	0.021
ko04142	Transport and Catabolism	Lysosome	K12373: beta-hexosaminidase	Nrml	2.42	0.072
ko01200	Metabolism	Carbon metabolism	K00174: 2-oxoglutarate ferredoxin oxidoreductase subunit alpha	Nrml	2.05	0.061
ko00270	Amino Acid Metabolism	Cysteine and methionine metabolism	K01011: 3-mercaptopyruvate sulfurtransferase	SSc	2.03	0.098
ko00400	Amino Acid	Phenylalanine, tyrosine and	K01626: 3-deoxy-7-	SSc	2.03	0.023

	Metabolism	tryptophan biosynthesis	phosphoheptulonate synthase			
ko00280	Amino Acid Metabolism	Valine, leucine and isoleucine degradation	K01782: 3-hydroxybutyryl-CoA epimerase	SSc	2.02	0.003
ko00310	Amino Acid Metabolism	Lysine degradation	K01782: 3-hydroxybutyryl-CoA epimerase	SSc	2.02	0.003
ko00380	Amino Acid Metabolism	Tryptophan metabolism	K01782: 3-hydroxybutyryl-CoA epimerase	SSc	2.02	0.003
ko00630	Carbohydrate Metabolism	Glyoxylate and dicarboxylate metabolism	K00123: formate dehydrogenase, alpha subunit	SSc	2.04	0.044
ko00640	Carbohydrate Metabolism	Propanoate metabolism	K01782: 3-hydroxybutyryl-CoA epimerase	SSc	2.02	0.003
ko00650	Carbohydrate Metabolism	Butanoate metabolism	K01782: 3-hydroxybutyryl-CoA epimerase	SSc	2.02	0.003
ko02030	Cell Motility	Bacterial chemotaxis	K10439: ribose transport system substrate-binding protein	SSc	2.12	0.072

ko00680	Energy Metabolism	Methane metabolism	K00123: formate dehydrogenase, alpha subunit	SSc	2.04	0.044
ko00920	Energy Metabolism	Sulfur metabolism	K01011: 3-mercaptopyruvate sulfurtransferase	SSc	2.03	0.098
ko04122	Folding, Sorting and Degradation	Sulfur relay system	K01011: 3-mercaptopyruvate sulfurtransferase	SSc	2.03	0.098
ko00071	Lipid Metabolism	Fatty acid degradation	K01782: 3-hydroxybutyryl-CoA epimerase	SSc	2.02	0.003
ko01040	Lipid Metabolism	Biosynthesis of unsaturated fatty acids	K01782: 3-hydroxybutyryl-CoA epimerase	SSc	2.02	0.003
ko01212	Lipid Metabolism	Fatty acid metabolism	K01782: 3-hydroxybutyryl-CoA epimerase	SSc	2.02	0.003
ko02060	Membrane Transport	Phosphotransferase system (PTS)	K08483: phosphotransferase system, enzyme I, PtsI	SSc	2.01	0.009

ko02010	Membrane Transport	ABC transporters	K10439: ribose transport system substrate-binding protein	SSc	2.12	0.072
ko02010	Membrane Transport	ABC transporters	K10440: ribose transport system permease protein	SSc	2.05	0.034
ko01200	Metabolism	Carbon metabolism	K00123: formate dehydrogenase, alpha subunit	SSc	2.04	0.044
ko01200	Metabolism	Carbon metabolism	K01782: 3-hydroxybutyryl-CoA epimerase	SSc	2.02	0.003
ko00410	Metabolism of Other Amino Acids	beta-Alanine metabolism	K01782: 3-hydroxybutyryl-CoA epimerase	SSc	2.02	0.003
ko00281	Metabolism of Terpenoids and Polyketides	Geraniol degradation	K01782: 3-hydroxybutyryl-CoA epimerase	SSc	2.02	0.003
ko00903	Metabolism of	Limonene and pinene	K01782: 3-hydroxybutyryl-	SSc	2.02	0.003

	Terpenoids and Polyketides	degradation	CoA epimerase			
ko00930	Xenobiotics Biodegradation and Metabolism	Caprolactam degradation	K01782: 3-hydroxybutyryl-CoA epimerase	SSc	2.02	0.003
ko01230	Metabolism	Biosynthesis of amino acids	K01626: 3-deoxy-7-phosphoheptulonate synthase	SSc	2.03	0.023

* Certain KEGG gene names may appear more than once if they are associated with more than one KEGG pathway.

Table 2B. Differences of KEGG pathway and orthology in SSc versus healthy controls (Nrml) in the sigmoid region.*

KEGG pathway			KEGG orthology			
Ko Pathway ID	**Pathway (L2)**	**Pathway (L3)**	**KO Gene Name**	**Gene increased in**	**Effect size**	***q* value**
ko00250	Amino Acid Metabolism	Alanine, aspartate and glutamate metabolism	K00266: glutamate synthase (NADPH/NADH) small chain	Nrml	2.34	0.017
ko00250	Amino Acid Metabolism	Alanine, aspartate and glutamate metabolism	K01424: L-asparaginase	Nrml	2.13	0.001
ko00250	Amino Acid Metabolism	Alanine, aspartate and glutamate metabolism	K01955: carbamoyl-phosphate synthase large subunit	Nrml	2.14	0.004
ko00250	Amino Acid Metabolism	Alanine, aspartate and glutamate metabolism	K01915: glutamine synthetase	Nrml	2.01	0.056
ko00260	Amino Acid Metabolism	Glycine, serine and threonine metabolism	K01834: phosphoglycerate mutase	Nrml	2.23	0.004

ko00270	Amino Acid Metabolism	Cysteine and methionine metabolism	K00640: serine O-acetyltransferase	Nrml	2.11	0.015
ko00330	Amino Acid Metabolism	Arginine and proline metabolism	K01915: glutamine synthetase	Nrml	2.01	0.056
ko00340	Amino Acid Metabolism	Histidine metabolism	K11755: phosphoribosyl-ATP pyrophosphohydrolase / phosphoribosyl-AMP	Nrml	2.04	0.000
ko00360	Amino Acid Metabolism	Phenylalanine metabolism	K01912: phenylacetate-CoA ligase	Nrml	2.08	0.020
ko00521	Biosynthesis of Other Secondary Metabolites	Streptomycin biosynthesis	K01790: dTDP-4-dehydrorhamnose 3,5-epimerase	Nrml	2.02	0.011
ko00940	Biosynthesis of Other Secondary Metabolites	Phenylpropanoid biosynthesis	K05349: beta-glucosidase	Nrml	2.51	0.037

ko05230	Cancers	Central carbon metabolism in cancer	K01834: phosphoglycerate mutase	Nrml	2.23	0.004
ko00010	Carbohydrate Metabolism	Glycolysis / Gluconeogenesis	K01785: aldose 1-epimerase	Nrml	2.29	0.003
ko00010	Carbohydrate Metabolism	Glycolysis / Gluconeogenesis	K01834: phosphoglycerate mutase	Nrml	2.23	0.004
ko00020	Carbohydrate Metabolism	Citrate cycle (TCA cycle)	K00174: 2-oxoglutarate ferredoxin oxidoreductase subunit alpha	Nrml	2.13	0.015
ko00020	Carbohydrate Metabolism	Citrate cycle (TCA cycle)	K00175: 2-oxoglutarate ferredoxin oxidoreductase subunit beta	Nrml	2.12	0.014
ko00020	Carbohydrate Metabolism	Citrate cycle (TCA cycle)	K01960: pyruvate carboxylase subunit B	Nrml	2.03	0.010
ko00030	Carbohydrate Metabolism	Pentose phosphate pathway	K00874: 2-dehydro-3-deoxygluconokinase	Nrml	2.02	0.008
ko00040	Carbohydrate Metabolism	Pentose and glucuronate interconversions	K01051: pectinesterase	Nrml	2.15	0.015

ko00040	Carbohydrate Metabolism	Pentose and glucuronate interconversions	K01686: mannonate dehydratase	Nrml	2.14	0.022
ko00040	Carbohydrate Metabolism	Pentose and glucuronate interconversions	K01815: 4-deoxy-L-threo-5-hexosulose-uronate ketol-isomerase	Nrml	2.05	0.003
ko00052	Carbohydrate Metabolism	Galactose metabolism	K01187: alpha-glucosidase	Nrml	2.45	0.014
ko00052	Carbohydrate Metabolism	Galactose metabolism	K01190: beta-galactosidase	Nrml	2.79	0.007
ko00052	Carbohydrate Metabolism	Galactose metabolism	K01785: aldose 1-epimerase	Nrml	2.29	0.003
ko00052	Carbohydrate Metabolism	Galactose metabolism	K07407: alpha-galactosidase	Nrml	2.04	0.060
ko00052	Carbohydrate Metabolism	Galactose metabolism	K12308: beta-galactosidase	Nrml	2.04	0.020
ko00500	Carbohydrate Metabolism	Starch and sucrose metabolism	K01051: pectinesterase	Nrml	2.15	0.015
ko00500	Carbohydrate	Starch and sucrose	K01187: alpha-glucosidase	Nrml	2.45	0.014

	Metabolism	metabolism				
ko00500	Carbohydrate Metabolism	Starch and sucrose metabolism	K05349: beta-glucosidase	Nrml	2.51	0.037
ko00520	Carbohydrate Metabolism	Amino sugar and nucleotide sugar metabolism	K : N-acylneuraminate cytidylyltransferase	Nrml	2.07	0.001
ko00520	Carbohydrate Metabolism	Amino sugar and nucleotide sugar metabolism	K01209: alpha-N-arabinofuranosidase	Nrml	2.23	0.002
ko00520	Carbohydrate Metabolism	Amino sugar and nucleotide sugar metabolism	K01791: UDP-N-acetylglucosamine 2-epimerase	Nrml	2.42	0.015
ko00520	Carbohydrate Metabolism	Amino sugar and nucleotide sugar metabolism	K12373: beta-hexosaminidase	Nrml	2.52	0.040
ko00620	Carbohydrate Metabolism	Pyruvate metabolism	K01572: oxaloacetate decarboxylase, beta subunit	Nrml	2.19	0.006
ko00620	Carbohydrate Metabolism	Pyruvate metabolism	K01960: pyruvate carboxylase subunit B	Nrml	2.03	0.010

ko00630	Carbohydrate Metabolism	Glyoxylate and dicarboxylate metabolism	K01915: glutamine synthetase	Nrml	2.01	0.056
ko04974	Digestive System	Protein digestion and absorption	K01278: dipeptidyl-peptidase 4	Nrml	2.18	0.008
ko03320	Endocrine System	PPAR signaling pathway	K01897: long-chain acyl-CoA synthetase	Nrml	2.36	0.004
ko04920	Endocrine System	Adipocytokine signaling pathway	K01897: long-chain acyl-CoA synthetase	Nrml	2.36	0.004
ko00680	Energy Metabolism	Methane metabolism	K01834: phosphoglycerate mutase	Nrml	2.23	0.004
ko00720	Energy Metabolism	Carbon fixation pathways in prokaryotes	K00174: 2-oxoglutarate ferredoxin oxidoreductase subunit alpha	Nrml	2.13	0.015
ko00720	Energy Metabolism	Carbon fixation pathways in prokaryotes	K00175: 2-oxoglutarate ferredoxin oxidoreductase subunit beta	Nrml	2.12	0.014
ko00720	Energy Metabolism	Carbon fixation pathways in prokaryotes	K01960: pyruvate carboxylase subunit B	Nrml	2.03	0.010

ko00910	Energy Metabolism	Nitrogen metabolism	K00266: glutamate synthase (NADPH/NADH) small chain	Nrml	2.34	0.017
ko00910	Energy Metabolism	Nitrogen metabolism	K01915: glutamine synthetase	Nrml	2.01	0.056
ko00920	Energy Metabolism	Sulfur metabolism	K00640: serine O-acetyltransferase	Nrml	2.11	0.015
ko03018	Folding, Sorting and Degradation	RNA degradation	K03654: ATP-dependent DNA helicase RecQ	Nrml	2.06	0.013
ko03060	Folding, Sorting and Degradation	Protein export	K03100: signal peptidase I	Nrml	2.25	0.015
ko04122	Folding, Sorting and Degradation	Sulfur relay system	K00566: tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase	Nrml	2.13	0.007
ko00511	Glycan	Other glycan degradation	K01190: beta-	Nrml	2.79	0.007

	Biosynthesis and Metabolism		galactosidase			
ko00511	Glycan Biosynthesis and Metabolism	Other glycan degradation	K01201: glucosylceramidase	Nrml	2.06	0.006
ko00511	Glycan Biosynthesis and Metabolism	Other glycan degradation	K12373: beta-hexosaminidase	Nrml	2.52	0.040
ko00511	Glycan Biosynthesis and Metabolism	Other glycan degradation	K01206: alpha-L-fucosidase	Nrml	2.51	0.056
ko00531	Glycan Biosynthesis and	Glycosaminoglycan degradation	K12373: beta-hexosaminidase	Nrml	2.52	0.040

	Metabolism					
ko00603	Glycan Biosynthesis and Metabolism	Glycosphingolipid biosynthesis - globo series	K12373: beta-hexosaminidase	Nrml	2.52	0.040
ko00603	Glycan Biosynthesis and Metabolism	Glycosphingolipid biosynthesis - globo series	K07407: alpha-galactosidase	Nrml	2.04	0.060
ko00604	Glycan Biosynthesis and Metabolism	Glycosphingolipid biosynthesis - ganglio series	K12373: beta-hexosaminidase	Nrml	2.52	0.040
ko00061	Lipid Metabolism	Fatty acid biosynthesis	K01897: long-chain acyl-CoA synthetase	Nrml	2.36	0.004
ko00071	Lipid Metabolism	Fatty acid degradation	K01897: long-chain acyl-CoA synthetase	Nrml	2.36	0.004
ko00561	Lipid	Glycerolipid metabolism	K07407: alpha-	Nrml	2.04	0.060

	Metabolism		galactosidase			
ko00600	Lipid Metabolism	Sphingolipid metabolism	K01190: beta-galactosidase	Nrml	2.79	0.007
ko00600	Lipid Metabolism	Sphingolipid metabolism	K01201: glucosylceramidase	Nrml	2.06	0.006
ko00600	Lipid Metabolism	Sphingolipid metabolism	K07407: alpha-galactosidase	Nrml	2.04	0.060
ko01212	Lipid Metabolism	Fatty acid metabolism	K01897: long-chain acyl-CoA synthetase	Nrml	2.36	0.004
ko01200	Metabolism	Carbon metabolism	K00640: serine O-acetyltransferase	Nrml	2.11	0.015
ko01200	Metabolism	Carbon metabolism	K00874: 2-dehydro-3-deoxygluconokinase	Nrml	2.02	0.008
ko01200	Metabolism	Carbon metabolism	K01834: phosphoglycerate mutase	Nrml	2.23	0.004
ko01200	Metabolism	Carbon metabolism	K01960: pyruvate carboxylase subunit B	Nrml	2.03	0.010
ko01230	Metabolism	Biosynthesis of amino acids	K00640: serine O-	Nrml	2.11	0.015

			acetyltransferase			
ko01230	Metabolism	Biosynthesis of amino acids	K01834: phosphoglycerate mutase	NrmI	2.23	0.004
ko01230	Metabolism	Biosynthesis of amino acids	K11755: phosphoribosyl-ATP pyrophosphohydrolase / phosphoribosyl-AMP	NrmI	2.04	0.000
ko01230	Metabolism	Biosynthesis of amino acids	K01915: glutamine synthetase	NrmI	2.01	0.056
ko01230	Metabolism	Biosynthesis of amino acids	K01960: pyruvate carboxylase subunit B	NrmI	2.03	0.010
ko00860	Metabolism of Cofactors and Vitamins	Porphyrin and chlorophyll metabolism	K00595: precorrin-6Y C5,15-methyltransferase / precorrin-8W decarboxylase	NrmI	2.09	0.011
ko00860	Metabolism of Cofactors and Vitamins	Porphyrin and chlorophyll metabolism	K02224: hydrogenobyrinic acid a,c-diamide synthase	NrmI	2.06	0.040

ko00860	Metabolism of Cofactors and Vitamins	Porphyrin and chlorophyll metabolism	K01599: uroporphyrinogen decarboxylase	Nrml	2.01	0.056
ko00460	Metabolism of Other Amino Acids	Cyanoamino acid metabolism	K05349: beta-glucosidase	Nrml	2.51	0.037
ko00460	Metabolism of Other Amino Acids	Cyanoamino acid metabolism	K01424: L-asparaginase	Nrml	2.13	0.001
ko00523	Metabolism of Terpenoids and Polyketides	Polyketide sugar unit biosynthesis	K01790: dTDP-4-dehydrorhamnose 3,5-epimerase	Nrml	2.02	0.011
ko04724	Nervous System	Glutamatergic synapse	K01915: glutamine synthetase	Nrml	2.01	0.056
ko00230	Nucleotide Metabolism	Purine metabolism	K00951: GTP pyrophosphokinase	Nrml	2.01	0.002
ko00230	Nucleotide	Purine metabolism	K02342: DNA polymerase	Nrml	2.03	0.001

	Metabolism		III subunit epsilon			
ko00240	Nucleotide Metabolism	Pyrimidine metabolism	K01955: carbamoyl-phosphate synthase large subunit	Nrml	2.14	0.004
ko04727	Organismal Systems	GABAergic synapse	K01915: glutamine synthetase	Nrml	2.01	0.056
ko03030	Replication and Repair	DNA replication	K03111: single-strand DNA-binding protein	Nrml	2.02	0.013
ko03430	Replication and Repair	Mismatch repair	K03111: single-strand DNA-binding protein	Nrml	2.02	0.013
ko03440	Replication and Repair	Homologous recombination	K03111: single-strand DNA-binding protein	Nrml	2.02	0.013
ko03440	Replication and Repair	Homologous recombination	K03655: ATP-dependent DNA helicase RecG	Nrml	2.13	0.017
ko02020	Signal Transduction	Two-component system	K01915: glutamine synthetase	Nrml	2.01	0.056
ko02020	Signal Transduction	Two-component system	K07713: two-component system, NtrC family,	Nrml	2.03	0.022

			response regulator HydG			
ko04142	Transport and Catabolism	Lysosome	K01201: glucosylceramidase	Nrml	2.06	0.006
ko04142	Transport and Catabolism	Lysosome	K12373: beta-hexosaminidase	Nrml	2.52	0.040
ko04146	Transport and Catabolism	Peroxisome	K01897: long-chain acyl-CoA synthetase	Nrml	2.36	0.004
ko01200	#N/A	Carbon metabolism	K00174: 2-oxoglutarate ferredoxin oxidoreductase subunit alpha	Nrml	2.13	0.015
ko00270	Amino Acid Metabolism	Cysteine and methionine metabolism	K01011: 3-mercaptopyruvate sulfurtransferase	SSc	2.05	0.011
ko00280	Amino Acid Metabolism	Valine, leucine and isoleucine degradation	K01782: 3-hydroxybutyryl-CoA epimerase	SSc	2.04	0.004
ko00310	Amino Acid Metabolism	Lysine degradation	K01782: 3-hydroxybutyryl-CoA epimerase	SSc	2.04	0.004
ko00380	Amino Acid	Tryptophan metabolism	K01782: 3-hydroxybutyryl-	SSc	2.04	0.004

	Metabolism		CoA epimerase			
ko00400	Amino Acid Metabolism	Phenylalanine, tyrosine and tryptophan biosynthesis	K01626: 3-deoxy-7-phosphoheptulonate synthase	SSc	2.12	0.003
ko00630	Carbohydrate Metabolism	Glyoxylate and dicarboxylate metabolism	K00123: formate dehydrogenase, alpha subunit	SSc	2.00	0.022
ko00640	Carbohydrate Metabolism	Propanoate metabolism	K01782: 3-hydroxybutyryl-CoA epimerase	SSc	2.04	0.004
ko00650	Carbohydrate Metabolism	Butanoate metabolism	K01782: 3-hydroxybutyryl-CoA epimerase	SSc	2.04	0.004
ko02030	Cell Motility	Bacterial chemotaxis	K10439: ribose transport system substrate-binding protein	SSc	2.18	0.014
ko00680	Energy Metabolism	Methane metabolism	K00123: formate dehydrogenase, alpha subunit	SSc	2.00	0.022
ko00920	Energy	Sulfur metabolism	K01011: 3-	SSc	2.05	0.011

	Metabolism		mercaptopyruvate sulfurtransferase			
ko04122	Folding, Sorting and Degradation	Sulfur relay system	K01011: 3-mercaptopyruvate sulfurtransferase	SSc	2.05	0.011
ko00550	Glycan Biosynthesis and Metabolism	Peptidoglycan biosynthesis	K07258: D-alanyl-D-alanine carboxypeptidase (penicillin-binding protein 5/6)	SSc	2.08	0.037
ko00071	Lipid Metabolism	Fatty acid degradation	K01782: 3-hydroxybutyryl-CoA epimerase	SSc	2.04	0.004
ko01040	Lipid Metabolism	Biosynthesis of unsaturated fatty acids	K01782: 3-hydroxybutyryl-CoA epimerase	SSc	2.04	0.004
ko01212	Lipid Metabolism	Fatty acid metabolism	K01782: 3-hydroxybutyryl-CoA epimerase	SSc	2.04	0.004
ko02010	Membrane Transport	ABC transporters	K10439: ribose transport system substrate-binding protein	SSc	2.18	0.014

ko02010	Membrane Transport	ABC transporters	K10440: ribose transport system permease protein	SSc	2.03	0.018
ko02060	Membrane Transport	Phosphotransferase system (PTS)	K08483: phosphotransferase system, enzyme I, PtsI	SSc	2.03	0.001
ko03070	Membrane Transport	Bacterial secretion system	K02453: general secretion pathway protein D	SSc	2.03	0.003
ko01200	Metabolism	Carbon metabolism	K00123: formate dehydrogenase, alpha subunit	SSc	2.00	0.022
ko01200	Metabolism	Carbon metabolism	K01782: 3-hydroxybutyryl-CoA epimerase	SSc	2.04	0.004
ko00410	Metabolism of Other Amino Acids	beta-Alanine metabolism	K01782: 3-hydroxybutyryl-CoA epimerase	SSc	2.04	0.004
ko00281	Metabolism of Terpenoids and	Geraniol degradation	K01782: 3-hydroxybutyryl-CoA epimerase	SSc	2.04	0.004

	Polyketides					
ko00903	Metabolism of Terpenoids and Polyketides	Limonene and pinene degradation	K01782: 3-hydroxybutyryl-CoA epimerase	SSc	2.04	0.004
ko00930	Xenobiotics Biodegradation and Metabolism	Caprolactam degradation	K01782: 3-hydroxybutyryl-CoA epimerase	SSc	2.04	0.004
ko01230	Metabolism	Biosynthesis of amino acids	K01626: 3-deoxy-7-phosphoheptulonate synthase	SSc	2.12	0.003

* Certain KEGG gene names may appear more than once if they are associated with more than one KEGG pathway.