

Figure S1: LC/Corona-CAD results of total lipid content in *Streptomyces antibioticus* DSM 41481 and *Streptomyces sp.* DSM 40868 grown for 72h on solid R2YE glucose medium limited in phosphate. TAG stands for TriAcylGlycerol, DAG for DiAcylGlycerol, FA for Fatty Acids, PE for PhosphatidylEthanolamine, PA for Phosphatidic Acid, PI for Phosphatidyl Inositol, PIMs for PhosphatidylInositol Mannosides and CL for CardioLipid.

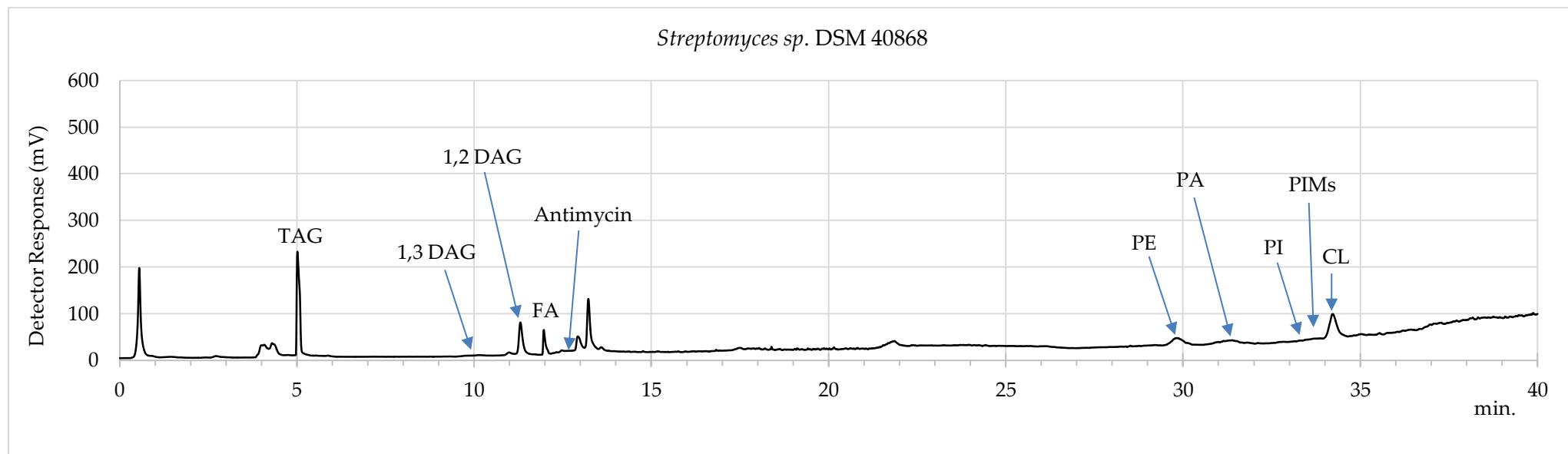
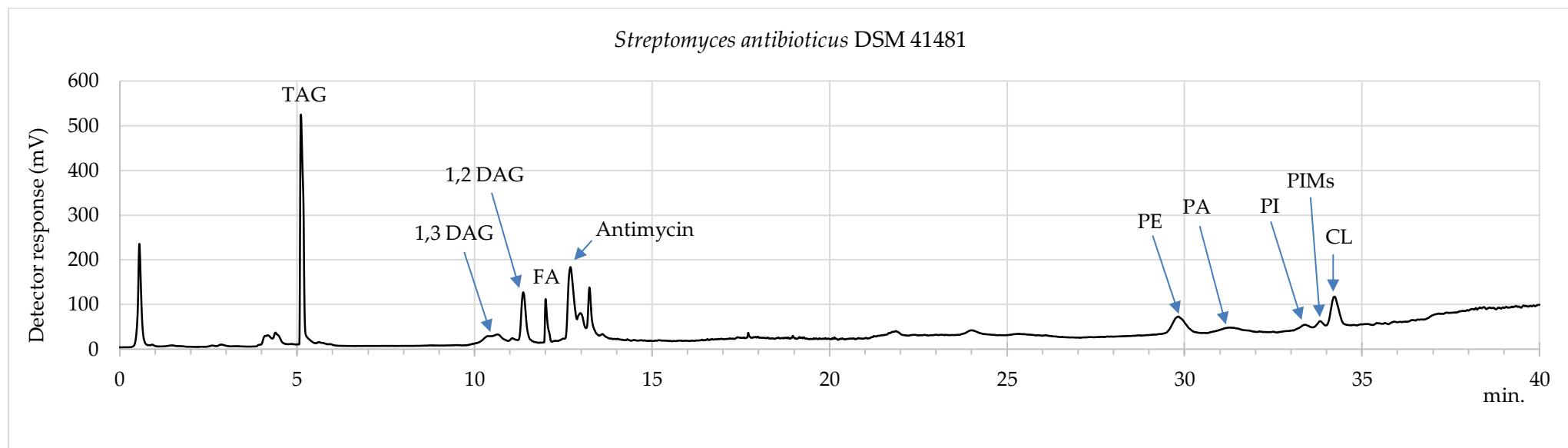


Figure S2 : Anti-Smash analysis of the genome of *Streptomyces antibioticus* DSM 41481 (8,473,575 bp).

Region	Type	From	To	Most similar known cluster	Similarity	
Region 1	bacteriocin ↗	216,990	226,748			
Region 2	lanthipeptide ↗, terpene ↗	327,516	361,829	Isorenieratene ↗	terpene	100%
Region 3	terpene ↗, melanin ↗	686,666	707,133	Melanin ↗	other	71%
Region 4	NRPS ↗, T1PKS ↗	731,747	800,687	Foxicins A-D ↗	nrps-t1pk	12%
Region 5	other ↗, CDPS ↗, NRPS ↗	1,217,807	1,292,777	Diisonitrile antibiotic SF2768 ↗	NRPS	50%
Region 6	terpene ↗, NRPS-like ↗, T1PKS ↗, T2PKS ↗	1,320,700	1,451,170	Spore pigment ↗	t2pk	83%
Region 7	NRPS-like ↗	1,943,835	1,985,314	Octacosamicin ↗	nrps-t1pk	12%
Region 8	ectoine ↗	2,173,921	2,184,325	Ectoine ↗	other	100%
Region 9	melanin ↗	3,218,444	3,228,956	Istamycin ↗	saccharide	5%
Region 10	siderophore ↗	3,311,605	3,322,761	Desferrioxamine ↗	other	83%
Region 11	T2PKS ↗	3,825,239	3,897,733	Fredericamycin ↗	t2pk	81%
Region 12	furan ↗, butyrolactone ↗	4,452,480	4,476,188	Methylenomycin ↗	other	14%
Region 13	terpene ↗	5,656,885	5,677,058	Albaflavenone ↗	terpene	100%
Region 14	NRPS-like ↗	5,732,586	5,775,707	Chloramphenicol ↗	NRPS	17%
Region 15	siderophore ↗	6,330,896	6,342,710			
Region 16	bacteriocin ↗	6,531,965	6,542,189			
Region 17	terpene ↗, butyrolactone ↗	6,571,015	6,592,442	Gamma-butyrolactone ↗	other	100%
Region 18	siderophore ↗	6,730,014	6,743,257	Grincamycin ↗	t2pk-saccharide	5%
Region 19	NRPS ↗, T1PKS ↗	6,832,866	6,889,853	Antimycin ↗	nrps-t1pk	100%
Region 20	indole ↗	6,981,746	7,002,897	Terfestatin ↗	other	23%
Region 21	terpene ↗	7,194,476	7,221,197	Hopene ↗	terpene	92%
Region 22	T1PKS ↗, hglE-KS ↗	7,247,598	7,298,972	Divergolide ↗	t1pk	13%
Region 23	bacteriocin ↗	7,520,677	7,530,892	Informatipeptin ↗	lanthipeptide	42%
Region 24	NRPS ↗	7,678,965	7,736,702	Scabichelin ↗	NRPS	80%
Region 25	NRPS-like ↗	7,929,006	7,970,314			
Region 26	other ↗, NRPS ↗	8,157,649	8,227,375	Actinomycin ↗	NRPS	89%

Figure S3 : Anti-smash analysis of the genome of *Streptomyces* sp. DSM 40868 (registered in gene bank as *Streptomyces antibioticus* DSM 40868 or ATCC 11891) (9,195,693 bp).

Region	Type	From	To	Most similar known cluster		Similarity
Region 1	NRPS	54,676	133,284	Azioemicin	t2pk	13%
Region 2	lantipeptide	142,326	165,105			
Region 3	NRPS	280,799	326,337	Paenibacitin	NRPS	83%
Region 4	beta-lactone , NRPS-like , nucleoside	370,187	417,072	Nikkomycin	other	100%
Region 5	terpene	417,600	440,735	Carotenoid	terpene	63%
Region 6	lassopeptide , NRPS	546,976	606,763	Achromosin	other	100%
Region 7	lassopeptide	623,914	646,589	SSV-2083	lantipeptide	37%
Region 8	butyrolactone	647,972	657,972			
Region 9	lantipeptide , phenazine	684,123	720,741	Primycin	t1pk	8%
Region 10	T1PKS	950,214	1,062,317	Scopoliholactam	t1pk	92%
Region 11	melanin	1,207,953	1,217,563	Melanin	other	57%
Region 12	T3PKS	1,645,922	1,685,386	Herboxidiene	t1pk+3pk	6%
Region 13	terpene	1,721,550	1,740,878	4-Z-annimycin	t1pk	22%
Region 14	ectoine	2,346,568	2,355,857	Ectoine	other	100%
Region 15	terpene	2,673,584	2,693,584	Calcium-dependent antibiotic	NRPS	5%
Region 16	T2PKS	2,711,900	2,783,355	Spore pigment	t2pk	83%
Region 17	ectoine	2,801,259	2,810,728	Showdomycin	other	52%
Region 18	melanin	3,354,806	3,365,330	Istamycin	saccharide	4%
Region 19	siderophore	3,472,780	3,483,385	Desferrioxamine B	other	83%
Region 20	terpene	3,931,030	3,950,571			
Region 21	T1PKS , NRPS	4,694,531	4,750,189	Thuggacin	nrps-t1pk	12%
Region 22	T2PKS	4,803,448	4,873,883	Oviedomycin	t2pk	95%
Region 23	NRPS	5,093,311	5,144,937	Ikarugamycin	nrps-t1pk	12%
Region 24	NRPS	5,593,128	5,666,806	Marinopyrrole	nrps-t1pk	16%
Region 25	terpene	5,802,574	5,823,000	Alfaflavonenone	terpene	100%
Region 26	bacteriocin	5,999,330	6,007,931			
Region 27	siderophore	6,427,302	6,439,209	Ficellomycin	NRPS	3%
Region 28	NRPS	6,592,191	6,634,621	Meilingmycin	t1pk	6%
Region 29	bacteriocin	6,694,119	6,703,498	Streptonigrin	other	5%
Region 30	butyrolactone	6,710,173	6,720,639	Rabelomycin	t2pk-saccharide	6%
Region 31	terpene	6,730,307	6,749,776	Geosmin	terpene	100%
Region 32	siderophore	6,889,179	6,902,589			
Region 33	butyrolactone	6,928,260	6,936,962	Griseoviridin / viridogrisein	nrps-transatpk	5%
Region 34	T1PKS	6,938,971	7,013,546	Erythromycin	t1pk	38%
Region 35	butyrolactone , arylpolyene	7,066,089	7,108,766	Rabelomycin	t2pk-saccharide	6%
Region 36	terpene	7,348,015	7,372,444	Hopene	terpene	92%
Region 37	T2PKS , NRPS	7,389,180	7,503,550	Erdacin	t2pk	44%
Region 38	bacteriocin	7,567,823	7,578,178			
Region 39	bacteriocin , NRPS , terpene	7,892,210	7,990,946	Informatipeptin	lantipeptide	42%
Region 40	NRPS-like	8,207,244	8,249,798	Livipeptin	NRPS	100%
Region 41	NRPS	8,357,875	8,400,853	Disorazole	nrps-transatpk	14%
Region 42	T3PKS	8,451,398	8,492,519	Balhimycin	NRPS	5%
Region 43	nucleoside	8,524,885	8,545,799			
Region 44	ectoine	8,697,094	8,707,507	Ectoine	other	75%
Region 45	lantipeptide , NRPS	8,940,409	9,046,443	Paulomycin	other	7%
Region 46	fused	9,126,473	9,150,066			

Figure S4: Chromosomal position of the biosynthetic gene clusters predicted by antiSMASH along the chromosome of *Streptomyces* sp. DSM 40868 and *Streptomyces antibioticus* DSM 41481. Metabolites synthetized by similar biosynthetic pathways are signaled by a vertical bar and named.

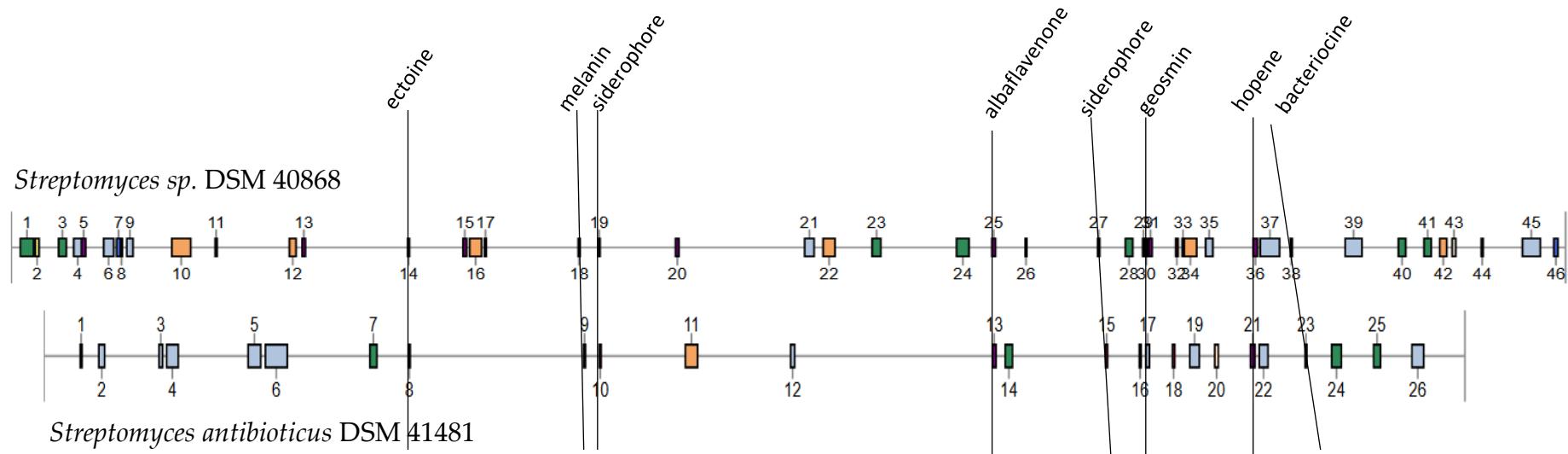
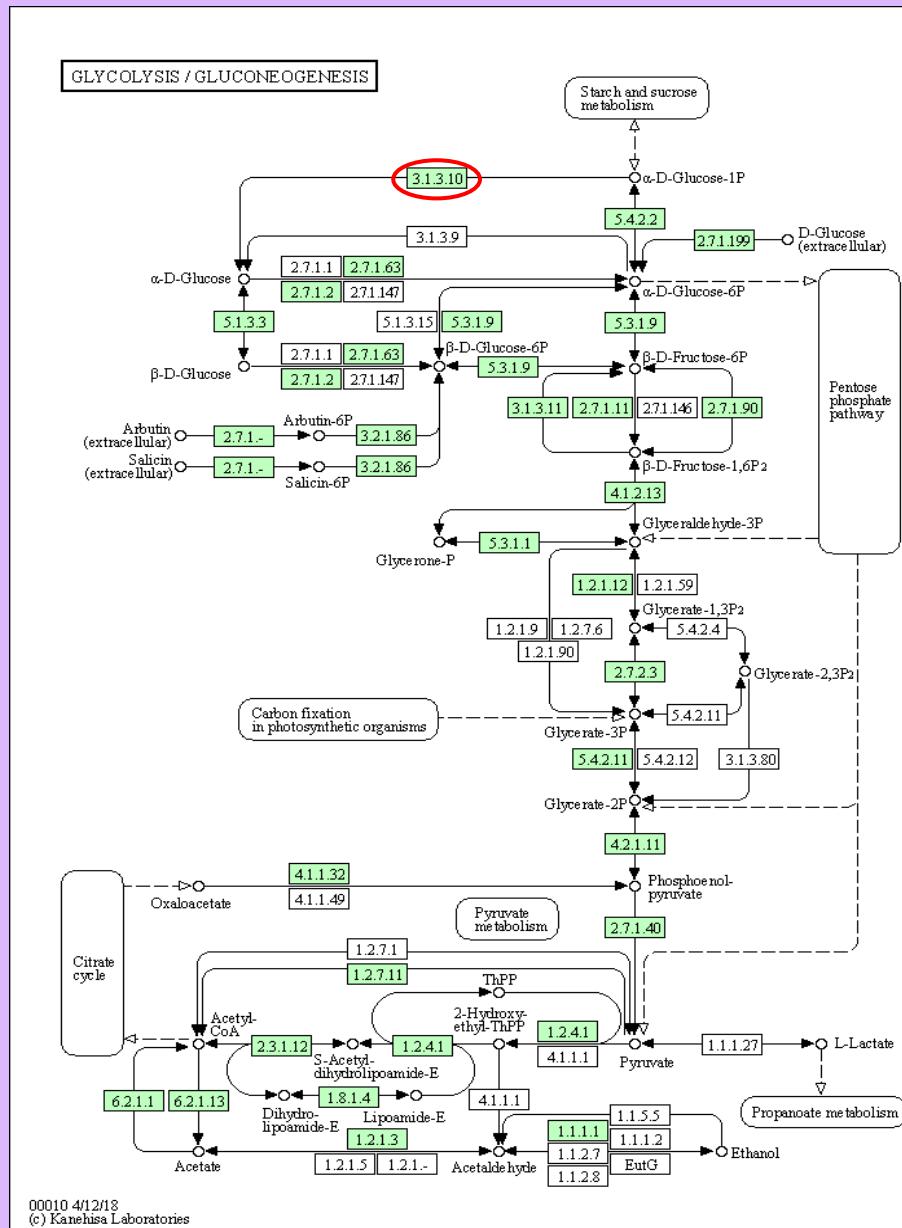


Figure S5 : Comparative analysis of glycolysis/gluconeogenesis pathway of DSM 40868 and DSM 41481.

Streptomyces sp. DSM 40868



Streptomyces antibioticus DSM 41481

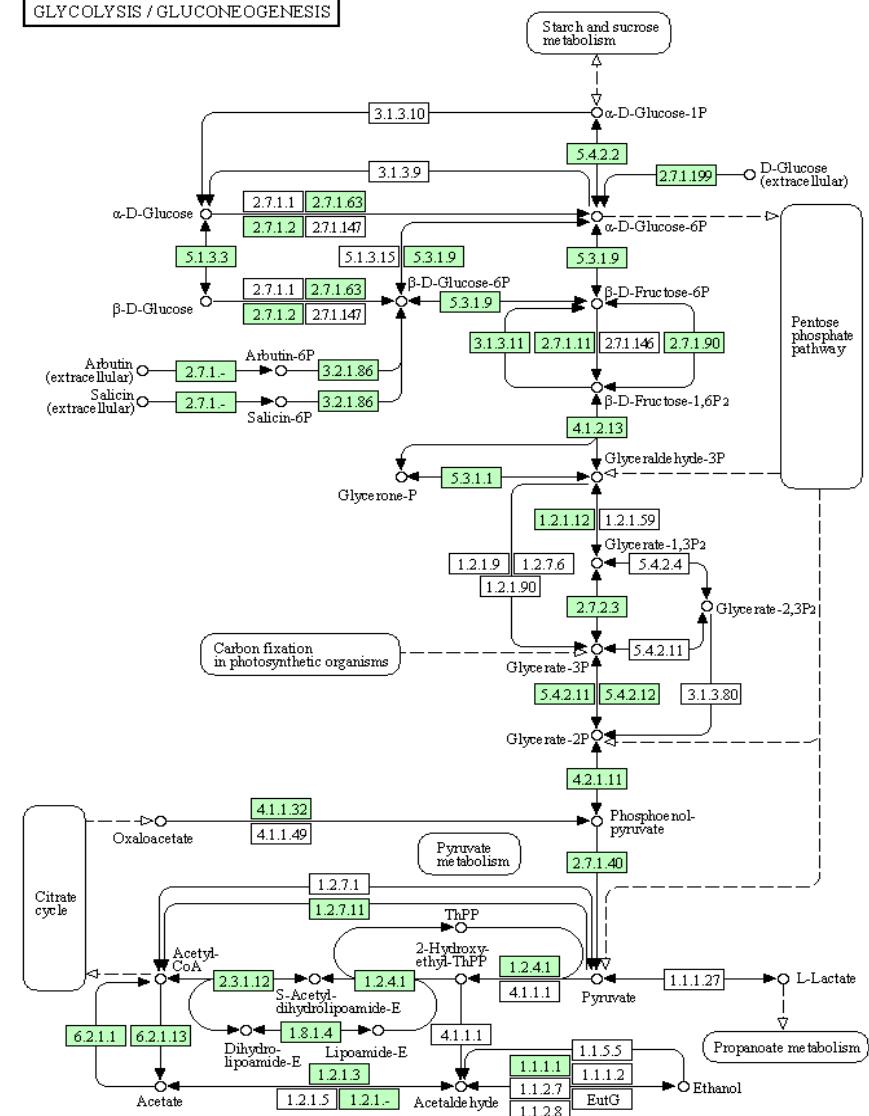
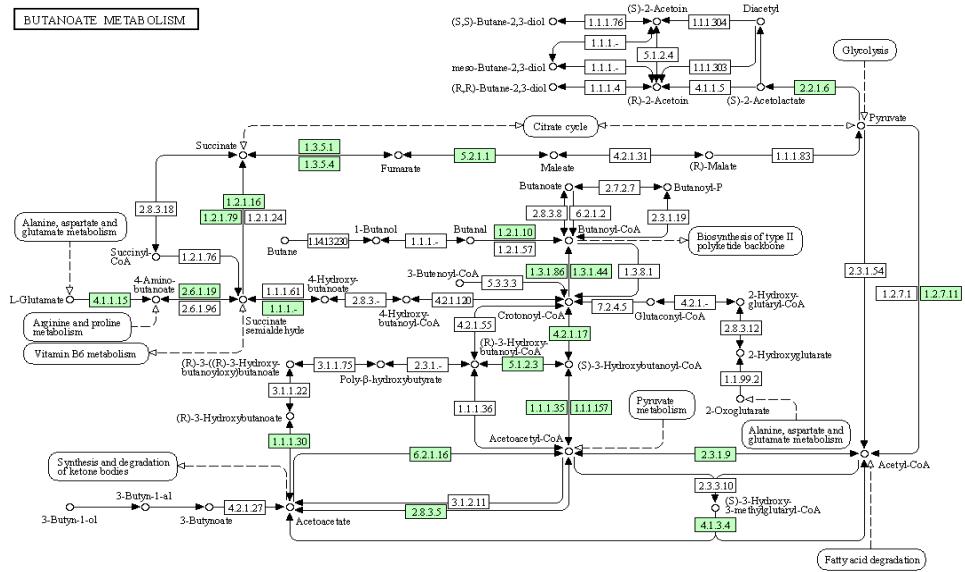


Figure S6 : Comparative analysis of butanoate metabolism of DSM 40868 and DSM 41481.

Streptomyces sp. DSM 40868



Streptomyces antibioticus DSM 41481

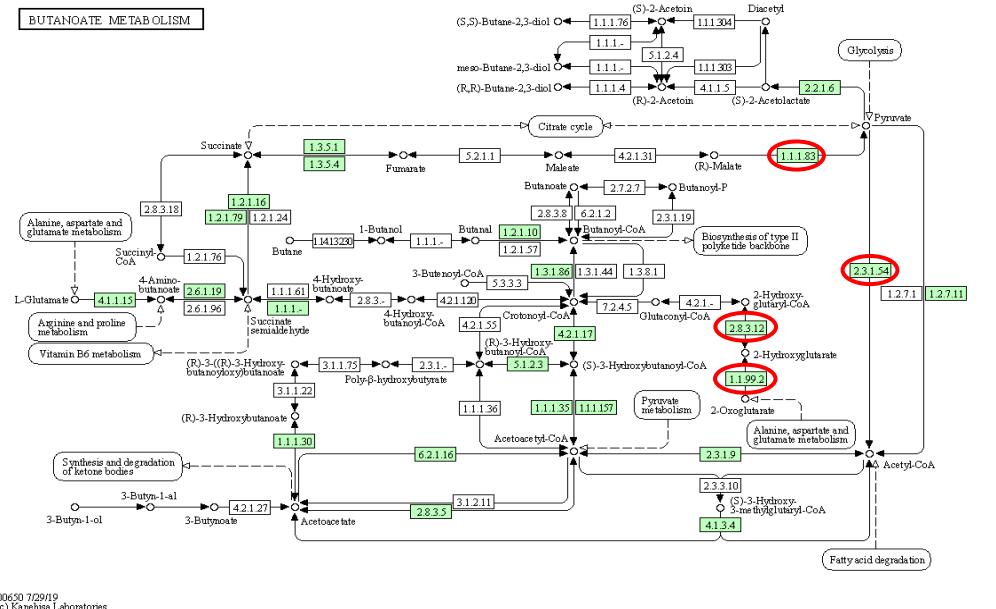
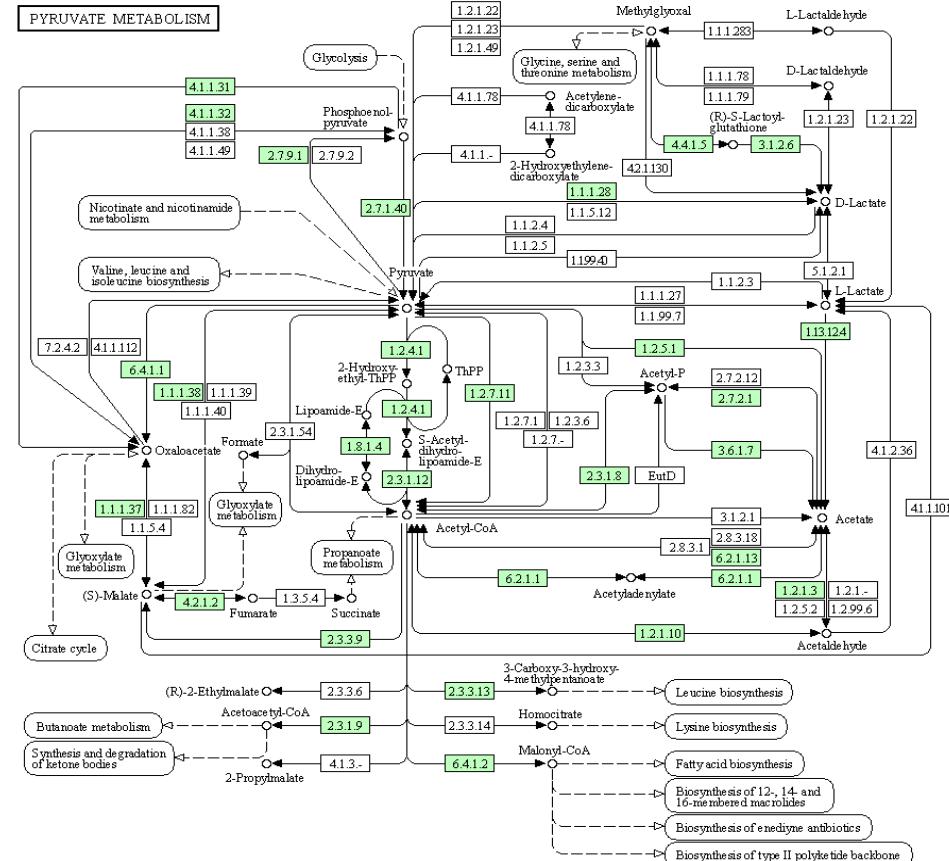


Figure S7 : Comparative analysis of pyruvate metabolism of DSM 40868 and DSM 41481.

Streptomyces sp. DSM 40868



Streptomyces antibioticus DSM 41481

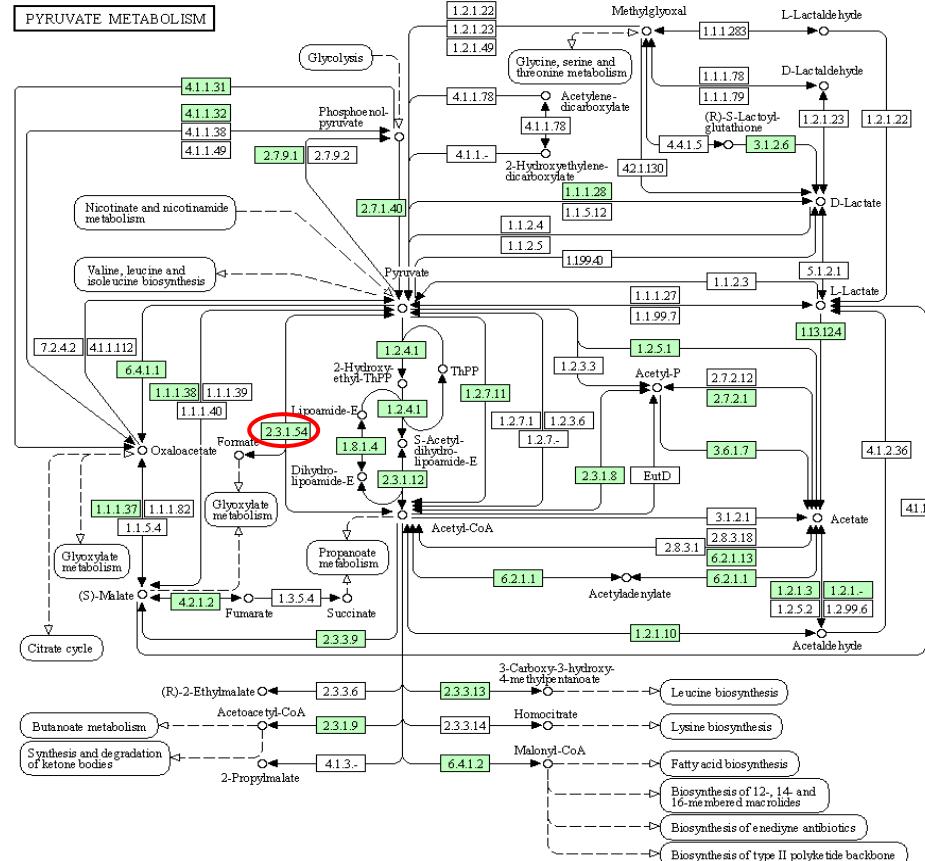
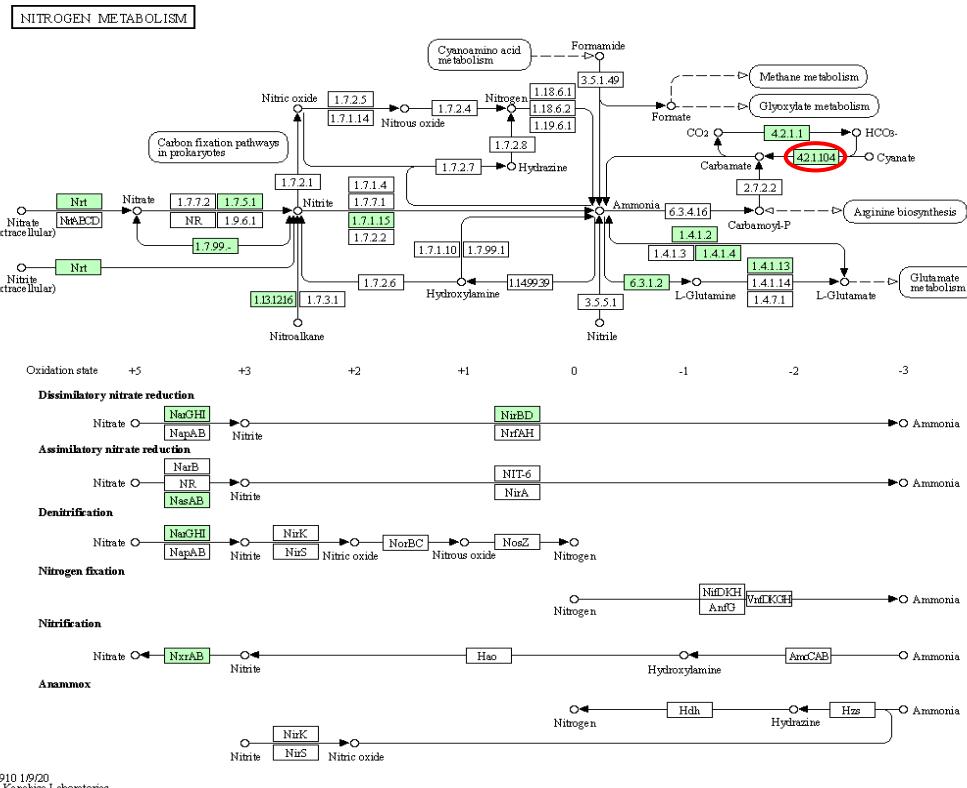


Figure S8 : Comparative analysis of nitrogen metabolism of DSM 40868 and DSM 41481.

Streptomyces sp. DSM 40868



Streptomyces antibioticus DSM 41481

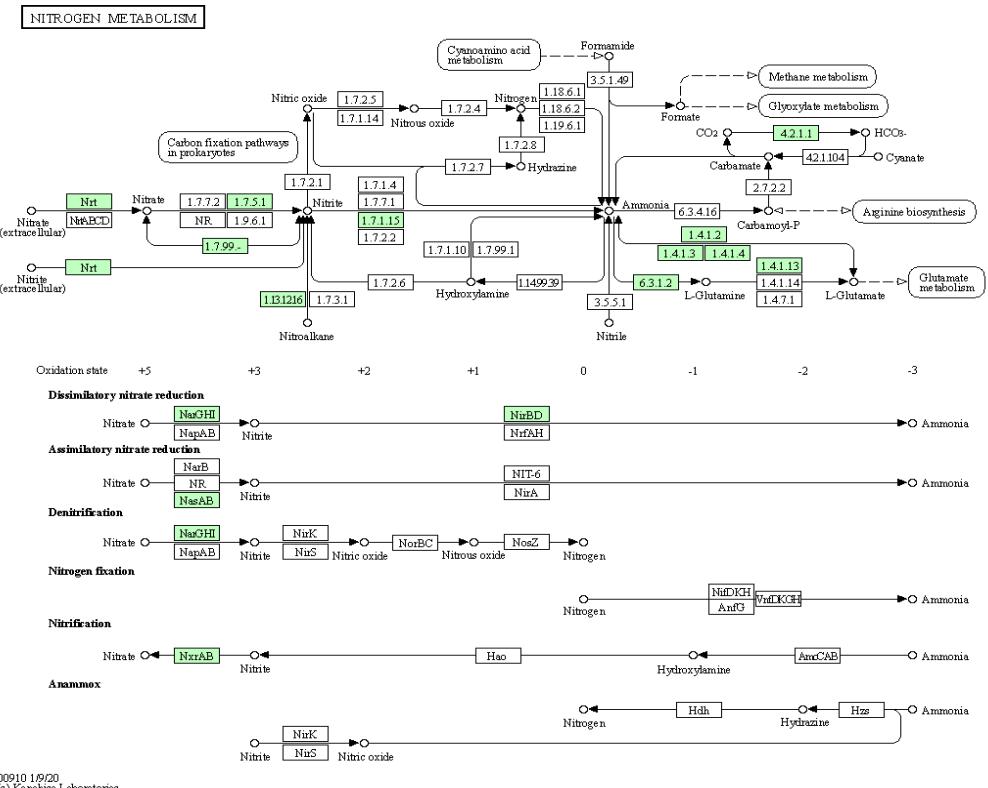
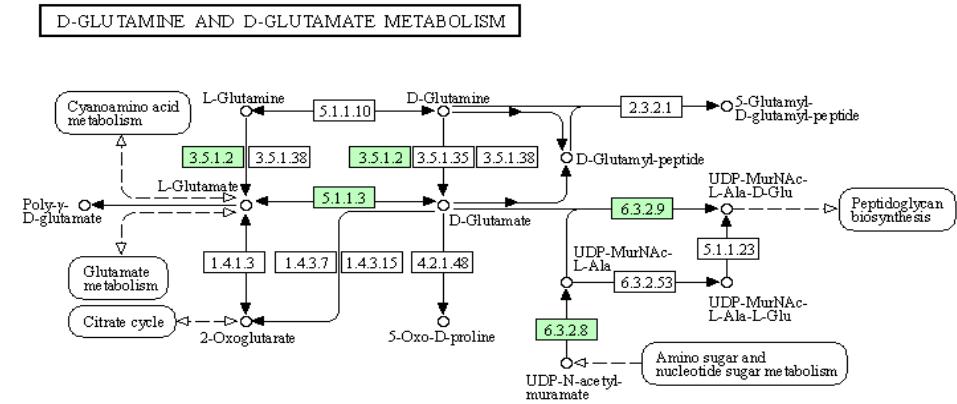


Figure S9: Comparative analysis of glutamine/glutamate metabolism of DSM 40868 and DSM 41481.

Streptomyces sp. DSM 40868



Streptomyces antibioticus DSM 41481

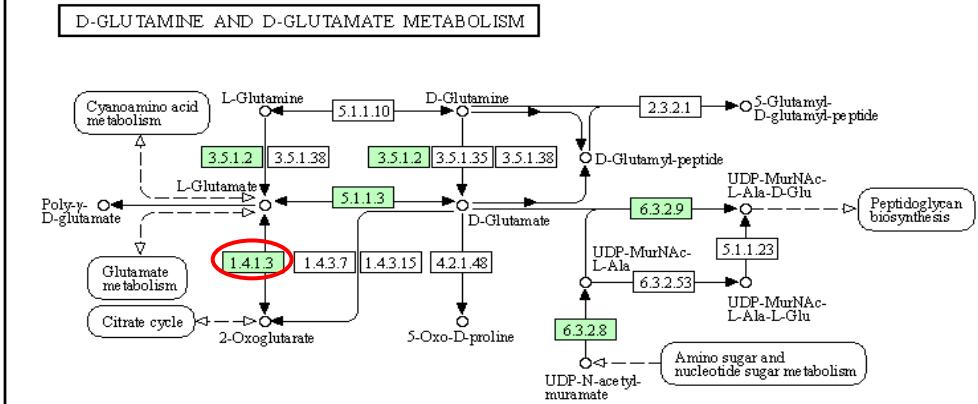
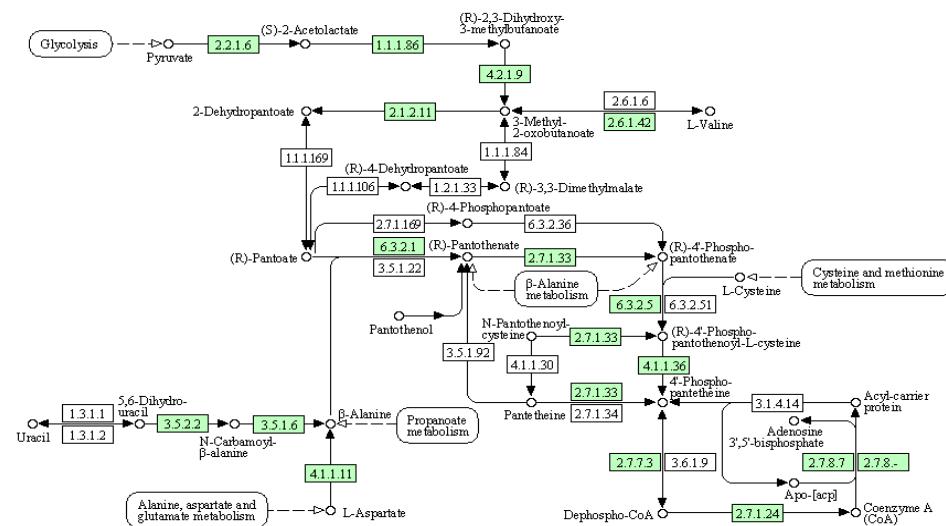


Figure S10 : Comparative analysis of pantothenate and CoA biosynthetic pathways of DSM 40868 and DSM 41481.

Streptomyces sp. DSM 40868

PANTOTHENATE AND CoA BIOSYNTHESIS



Streptomyces antibioticus DSM 41481

PANTOTHENATE AND CoA BIOSYNTHESIS

