Table S1. List of *Streptomyces* type strains and their 16S rRNA gene accession numbers used for phylogenetic analysis.

Scientific name	Type strain	Accession numbers	Taxonomy	Database
Streptomyces sp. ZE1316R2A	-	PZ007821	Bacteria ; Actinomycetota ; Actinomycetia ; Streptomycetales ; Streptomycetaceae ; Streptomyces	NCBI database
Streptomyces albidoflavus	DSM 40455^T	Z76676	Bacteria ; Actinomycetota ; Actinomycetia ; Streptomycetales ; Streptomycetaceae ; Streptomyces	EzBioCloud 16S database
Streptomyces daghestanicus	NRRL B-5418^T	DQ442497	Bacteria ; Actinomycetota ; Actinomycetia ; Streptomycetales ; Streptomycetaceae ; Streptomyces	EzBioCloud 16S database
Streptomyces violascens	ISP 5183^T	AY999737	Bacteria ; Actinomycetota ; Actinomycetia ; Streptomycetales ; Streptomycetaceae ; Streptomyces	EzBioCloud 16S database
Streptomyces koyangensis	VK-A60^T	CP031742	Bacteria ; Actinomycetota ; Actinomycetia ; Streptomycetales ; Streptomycetaceae ; Streptomyces	EzBioCloud 16S database
Streptomyces cadmiisoli	ZFG47^T	CP030073	Bacteria ; Actinomycetota ; Actinomycetia ; Streptomycetales ; Streptomycetaceae ; Streptomyces	EzBioCloud 16S database
Streptomyces purpurascens	NBRC 13077^T	AB184859	Bacteria ; Actinomycetota ; Actinomycetia ; Streptomycetales ; Streptomycetaceae ; Streptomyces	EzBioCloud 16S database
Streptomyces pyxinicus	LP11^T	OL765279	Bacteria ; Actinomycetota ; Actinomycetia ; Streptomycetales ; Streptomycetaceae ; Streptomyces	EzBioCloud 16S database
Streptomyces hawaiiensis	NBRC 12784^T	AB184143	Bacteria ; Actinomycetota ; Actinomycetia ; Streptomycetales ; Streptomycetaceae ; Streptomyces	EzBioCloud 16S database
Streptomyces luteogriseus	NBRC 13402^T	AB184379	Bacteria ; Actinomycetota ; Actinomycetia ; Streptomycetales ; Streptomycetaceae ; Streptomyces	EzBioCloud 16S database
Streptomyces cupreus	PSKA01^T	JACMSF010000162	Bacteria ; Actinomycetota ; Actinomycetia ; Streptomycetales ; Streptomycetaceae ; Streptomyces	EzBioCloud 16S database
Streptomyces fumigatiscleroticus	NBRC 12999^T	AB184248	Bacteria ; Actinomycetota ; Actinomycetia ; Streptomycetales ; Streptomycetaceae ; Streptomyces	EzBioCloud 16S database
Streptomyces levis	NBRC 15423^T	AB184670	Bacteria ; Actinomycetota ; Actinomycetia ; Streptomycetales ; Streptomycetaceae ; Streptomyces	EzBioCloud 16S database
Streptomyces violaceus	NRRL B-2867^T	KL569104	Bacteria ; Actinomycetota ; Actinomycetia ; Streptomycetales ; Streptomycetaceae ; Streptomyces	EzBioCloud 16S database
Streptomyces venetus	CMU-AB225^T	LC073310	Bacteria ; Actinomycetota ; Actinomycetia ; Streptomycetales ; Streptomycetaceae ; Streptomyces	EzBioCloud 16S database
Streptomyces sennicomposti	RCPT1-4^T	OM661191	Bacteria ; Actinomycetota ; Actinomycetia ; Streptomycetales ; Streptomycetaceae ; Streptomyces	EzBioCloud 16S database
Streptomyces spinoverrucosus	NBRC 14228^T	AB184578	Bacteria ; Actinomycetota ; Actinomycetia ; Streptomycetales ; Streptomycetaceae ; Streptomyces	EzBioCloud 16S database
Streptomyces massasporeus	NBRC 12796^T	AB184152	Bacteria ; Actinomycetota ; Actinomycetia ; Streptomycetales ; Streptomycetaceae ; Streptomyces	EzBioCloud 16S database
Streptomyces roseoviolaceus	ISP 5277^T	AJ399484	Bacteria ; Actinomycetota ; Actinomycetia ; Streptomycetales ; Streptomycetaceae ; Streptomyces	EzBioCloud 16S database
Streptomyces jeddahensis	G25^T	LOHS01000151	Bacteria ; Actinomycetota ; Actinomycetia ; Streptomycetales ; Streptomycetaceae ; Streptomyces	EzBioCloud 16S database
Streptomyces diastaticus	NBRC 3714^T	AB184785	Bacteria ; Actinomycetota ; Actinomycetia ; Streptomycetales ; Streptomycetaceae ; Streptomyces	EzBioCloud 16S database
Streptomyces janthinus	ISP 5206^T	AJ399478	Bacteria ; Actinomycetota ; Actinomycetia ; Streptomycetales ; Streptomycetaceae ; Streptomyces	EzBioCloud 16S database
Streptomyces carpinensis	NRRL B-16921^T	MUBM01000291	Bacteria ; Actinomycetota ; Actinomycetia ; Streptomycetales ; Streptomycetaceae ; Streptomyces	EzBioCloud 16S database
Streptomyces intermedius	NBRC 13049^T	AB184277	Bacteria ; Actinomycetota ; Actinomycetia ; Streptomycetales ; Streptomycetaceae ; Streptomyces	EzBioCloud 16S database
Streptomyces spiralis	NBRC 14215^T	AB184575	Bacteria ; Actinomycetota ; Actinomycetia ; Streptomycetales ; Streptomycetaceae ; Streptomyces	EzBioCloud 16S database
Streptomyces pluripotens	MUSC 135^T	CP021080	Bacteria ; Actinomycetota ; Actinomycetia ; Streptomycetales ; Streptomycetaceae ; Streptomyces	EzBioCloud 16S database
Streptomyces cinerochromogenes	NBRC 13822^T	AB184507	Bacteria ; Actinomycetota ; Actinomycetia ; Streptomycetales ; Streptomycetaceae ; Streptomyces	EzBioCloud 16S database
Streptomyces parvulus	NBRC 13193^T	AB184326	Bacteria ; Actinomycetota ; Actinomycetia ; Streptomycetales ; Streptomycetaceae ; Streptomyces	EzBioCloud 16S database
Streptomyces coeruleofuscus	NBRC 12757^T	AB184840	Bacteria ; Actinomycetota ; Actinomycetia ; Streptomycetales ; Streptomycetaceae ; Streptomyces	EzBioCloud 16S database
Streptomyces naganishii	NBRC 12892^T	AB184224	Bacteria ; Actinomycetota ; Actinomycetia ; Streptomycetales ; Streptomycetaceae ; Streptomyces	EzBioCloud 16S database
Streptomyces muensis	MBRL 179^T	JN560155	Bacteria ; Actinomycetota ; Actinomycetia ; Streptomycetales ; Streptomycetaceae ; Streptomyces	EzBioCloud 16S database
Streptomyces tibetensis	XZ 46^T	MH988793	Bacteria ; Actinomycetota ; Actinomycetia ; Streptomycetales ; Streptomycetaceae ; Streptomyces	EzBioCloud 16S database
Streptomyces coeruleorubidus	ISP 5145^T	AJ306622	Bacteria ; Actinomycetota ; Actinomycetia ; Streptomycetales ; Streptomycetaceae ; Streptomyces	EzBioCloud 16S database
Streptomyces ferrugineus	HV38^T	KF767859	Bacteria ; Actinomycetota ; Actinomycetia ; Streptomycetales ; Streptomycetaceae ; Streptomyces	EzBioCloud 16S database
Streptomyces misionensis	DSM 40306^T	FNTD01000004	Bacteria ; Actinomycetota ; Actinomycetia ; Streptomycetales ; Streptomycetaceae ; Streptomyces	EzBioCloud 16S database
Streptomyces andamanensis	KC-112^T	LC008305	Bacteria ; Actinomycetota ; Actinomycetia ; Streptomycetales ; Streptomycetaceae ; Streptomyces	EzBioCloud 16S database
Streptomyces cinereospinus	NBRC 15397^T	AB184648	Bacteria ; Actinomycetota ; Actinomycetia ; Streptomycetales ; Streptomycetaceae ; Streptomyces	EzBioCloud 16S database
Streptomyces tuirus	NBRC 15617^T	AB184690	Bacteria ; Actinomycetota ; Actinomycetia ; Streptomycetales ; Streptomycetaceae ; Streptomyces	EzBioCloud 16S database
Streptomyces phaeoluteichromatogenes	NRRL 5799^T	AJ391814	Bacteria ; Actinomycetota ; Actinomycetia ; Streptomycetales ; Streptomycetaceae ; Streptomyces	EzBioCloud 16S database

Table S1 (continued). List of *Streptomyces* type strains and their 16S rRNA gene accession numbers used for phylogenetic analysis.

Scientific name	Type strain	Accession numbers	Taxonomy	Database
Streptomyces coerulescens	ISP 5146^T	AY999720	Bacteria ; Actinomycetota ; Actinomycetia ; Streptomycetales ; Streptomycetaceae ; Streptomyces	EzBioCloud 16S database
Streptomyces nogalater	JCM 4799^T	AB045886	Bacteria ; Actinomycetota ; Actinomycetia ; Streptomycetales ; Streptomycetaceae ; Streptomyces	EzBioCloud 16S database
Streptomyces azureus	ATCC 14921^T	DF968281	Bacteria ; Actinomycetota ; Actinomycetia ; Streptomycetales ; Streptomycetaceae ; Streptomyces	EzBioCloud 16S database
Streptomyces tacrolimicus	ATCC 55098^T	FN429653	Bacteria ; Actinomycetota ; Actinomycetia ; Streptomycetales ; Streptomycetaceae ; Streptomyces	EzBioCloud 16S database
Streptomyces fabae	T66^T	KM229360	Bacteria ; Actinomycetota ; Actinomycetia ; Streptomycetales ; Streptomycetaceae ; Streptomyces	EzBioCloud 16S database
Streptomyces malaysiense	MUSC 136^T	LBDA02000093	Bacteria ; Actinomycetota ; Actinomycetia ; Streptomycetales ; Streptomycetaceae ; Streptomyces	EzBioCloud 16S database
Streptomyces nigra	452^T	MG572975	Bacteria ; Actinomycetota ; Actinomycetia ; Streptomycetales ; Streptomycetaceae ; Streptomyces	EzBioCloud 16S database
Streptomyces griseomycini	NBRC 12778^T	AB184137	Bacteria ; Actinomycetota ; Actinomycetia ; Streptomycetales ; Streptomycetaceae ; Streptomyces	EzBioCloud 16S database
Streptomyces prasinosporus	NRRL B-12431^T	DQ026655	Bacteria ; Actinomycetota ; Actinomycetia ; Streptomycetales ; Streptomycetaceae ; Streptomyces	EzBioCloud 16S database
Streptomyces afghaniensis	NBRC 12831^T	AB184847	Bacteria ; Actinomycetota ; Actinomycetia ; Streptomycetales ; Streptomycetaceae ; Streptomyces	EzBioCloud 16S database
Streptomyces flavofungini	NBRC 13371^T	AB184359	Bacteria ; Actinomycetota ; Actinomycetia ; Streptomycetales ; Streptomycetaceae ; Streptomyces	EzBioCloud 16S database
Streptomyces poonensis	NBRC 13485^T	AB184437	Bacteria ; Actinomycetota ; Actinomycetia ; Streptomycetales ; Streptomycetaceae ; Streptomyces	EzBioCloud 16S database
Kitasatospora setae	NBRC 14216^T	NR037063	Bacteria; Actinomycetota; Actinomycetia; Streptomycetales; Streptomycetaceae; Kitasatospora	EzBioCloud 16S database

Table S2. List of whole-genome assemblies employed in this study, including scientific names, strain designations, genome assembly accession numbers, and taxonomic affiliations.

Scientific name	Type strain	Genome Assembly Accession	Taxonomy
Streptomyces sp. ZE1316R2A	-	GCA_055693065	Bacteria; Actinomycetota; Actinomycetia; Streptomycetales; Streptomycetaceae; Streptomyces
Streptomyces pyixinicus	LP11^T	GCA_024753135	Bacteria; Actinomycetota; Actinomycetia; Streptomycetales; Streptomycetaceae; Streptomyces
Streptomyces naganishii	JCM 4654^T	GCA_014650575	Bacteria; Actinomycetota; Actinomycetia; Streptomycetales; Streptomycetaceae; Streptomyces
Streptomyces daghestanicus	JCM 4365^T	GCA_014649475	Bacteria; Actinomycetota; Actinomycetia; Streptomycetales; Streptomycetaceae; Streptomyces
Streptomyces vinaceudrappus	JCM 4529^T	GCA_014650215	Bacteria; Actinomycetota; Actinomycetia; Streptomycetales; Streptomycetaceae; Streptomyces
Streptomyces pilosus	JCM 4403^T	GCA_014649835	Bacteria; Actinomycetota; Actinomycetia; Streptomycetales; Streptomycetaceae; Streptomyces
Streptomyces resistomycificus	DSM 40133^T	GCA_001514265	Bacteria; Actinomycetota; Actinomycetia; Streptomycetales; Streptomycetaceae; Streptomyces
Streptomyces massasporeus	JCM 4139^T	GCA_014648995	Bacteria; Actinomycetota; Actinomycetia; Streptomycetales; Streptomycetaceae; Streptomyces
Streptomyces violascens	JCM 4424^T	GCA_014649955	Bacteria; Actinomycetota; Actinomycetia; Streptomycetales; Streptomycetaceae; Streptomyces
Streptomyces rutgersensis	NBRC 12819^T	GCA_011170105	Bacteria; Actinomycetota; Actinomycetia; Streptomycetales; Streptomycetaceae; Streptomyces
Streptomyces diastaticus	JCM 4128^T	GCA_014648935	Bacteria; Actinomycetota; Actinomycetia; Streptomycetales; Streptomycetaceae; Streptomyces
Streptomyces gougerotii	NBRC 13043^T	GCA_011170145	Bacteria; Actinomycetota; Actinomycetia; Streptomycetales; Streptomycetaceae; Streptomyces
Streptomyces gougerotii	JCM 4136^T	GCA_014648955	Bacteria; Actinomycetota; Actinomycetia; Streptomycetales; Streptomycetaceae; Streptomyces
Streptomyces intermedicus	JCM 4483^T	GCA_039532785	Bacteria; Actinomycetota; Actinomycetia; Streptomycetales; Streptomycetaceae; Streptomyces
Streptomyces koyangensis	VK-A60^T	GCA_003428925	Bacteria; Actinomycetota; Actinomycetia; Streptomycetales; Streptomycetaceae; Streptomyces
Streptomyces albidoflavus	DSM 40455^T	GCA_004195735	Bacteria; Actinomycetota; Actinomycetia; Streptomycetales; Streptomycetaceae; Streptomyces
Streptomyces sampsonii	NBRC 13083^T	GCA_004195755	Bacteria; Actinomycetota; Actinomycetia; Streptomycetales; Streptomycetaceae; Streptomyces
Streptomyces limosus	NBRC 12790^T	GCA_004195885	Bacteria; Actinomycetota; Actinomycetia; Streptomycetales; Streptomycetaceae; Streptomyces
Kitasatospora setae	NBRC 14216^T	GCA_000269985	Bacteria; Actinomycetota; Actinomycetia; Streptomycetales; Streptomycetaceae; Kitasatospora

Table S3. Prediction of Biosynthetic Gene Clusters encoding for secondary metabolites in *Streptomyces* sp. ZE1316R2A^T.

antiSMASH Region id	Begin	End	Length	Region type	MIBiG	Completion	Product
1	81543	370759	289217	T1PKS, NRPS, terpene	BGC0001012	1	meridamycin
2	552846	629448	76603	terpene, NRPS-like, NRPS	BGC0002318	0.285714	canucin A/canucin B
3	758750	808157	49408	T1PKS, NRPS	BGC0002365	1	10-epi-HSAF/10-epi-3-deOH-HSAF/10-epi-maltophilin/10-epi-xanthobaccin C/10-epi-hydroxymaltophilin/10-epi-FI-2
4	841871	868418	26548	terpene	BGC0000663	0.769231	hopene
5	948138	958353	10216	RiPP-like	BGC0002497	0.0454545	hexacosalactone A
7	1664138	1697212	33075	NI-siderophore	BGC0002633	0.25	schizokinen
8	1936268	1958568	22301	terpene	BGC0001181	1	geosmin
9	2314597	2335571	20975	terpene	BGC0000660	1	albaflavenone
10	2834304	2869002	34699	LAP, thiopeptide, RRE-containing	BGC0001596	0.0465116	fluostatins M-Q
11	3191354	3213933	22580	lanthipeptide-class-iii	BGC0000551	1	SapB
12	**3443744**	**3466031**	**22288**	**Lasso peptide**	**BGC0000704**	**0.075**	**kanamycin**
13	3526519	3588751	62233	NRPS	BGC0002358	0.208333	cyclofaulknamycin
14	**4199097**	**4209543**	**10447**	**RiPP-like**	**BGC0000973**	**0.0740741**	**collismycin A**
15	4262748	4371391	108644	NRPS, LAP	BGC0001792	0.952381	surugamide A/surugamide D
16	5063590	5093410	29821	NI-siderophore	BGC0001478	1	desferrioxamine E
17	5992397	6002795	10399	ectoine	BGC0002052	1	ectoine
18	6793433	6820745	27313	RiPP-like, terpene	BGC0000664	0.857143	isorenieratene
19	6905561	6916928	11368	RiPP-like	BGC0002115	0.75	streptamidine
20	6918110	7244104	325995	T3PKS, T1PKS, NRPS-like, NRPS, lanthipeptide-class-ii, terpene	BGC0000958	1	antimycin

In bold: Product specific to ZE1316R2A^T

Table S4. Prediction of Biosynthetic Gene Clusters encoding potentially novel secondary metabolites in *Streptomyces* sp. ZE1316R2A^{T}.

antiSMASH Region id	Begin	End	Length	Region type
6	1366916	1378244	11329	RiPP-like

Table S5. Prediction of Biosynthetic Gene Clusters encoding for secondary metabolites in strain *Streptomyces albidoflavus* DSM 40455^T.

antiSMASH Region id	Begin	End	Length	Region type	MIBiG	Completion	Product
2	257826	294621	36796	NRPS	BGC0002358	0.75	cyclofaulknamycin
3	339072	416572	77501	terpene, NRPS-like, NRPS	BGC0002318	0.285714	canucin A/canucin B
4	581777	604268	22492	NRPS	BGC0002358	0.291667	cyclofaulknamycin
5	710418	743449	33032	NI-siderophore	BGC0002633	0.25	schizokinen
6	1242419	1272160	29742	NRPS	BGC0001792	0.47619	surugamide A/surugamide D
7	1272261	1308569	36309	NRPS	BGC0001792	0.190476	surugamide A/surugamide D
8	1308670	1343516	34847	NRPS, LAP	BGC0001792	0.47619	surugamide A/surugamide D
9	2136459	2171144	34686	LAP, thiopeptide, RRE-containing	BGC0001596	0.0465116	fluostatins M-Q
10	2448111	2469946	21836	lanthipeptide-class-iii	BGC0000551	1	SapB
11	**2495532**	**2555992**	**60461**	**NRPS**	**BGC0000388**	**0.518519**	**mannopeptimycin**
13	3847587	3857985	10399	Ectoine	BGC0002052	1	Ectoine
15	**4109193**	**4153023**	**43831**	**NRPS-like**	**BGC0002295**	**0.8**	**minimycin**
16	4173152	4200465	27314	RiPP-like, terpene	BGC0000664	0.857143	isorenieratene
17	4288434	4299801	11368	RiPP-like	BGC0002115	0.75	streptamidine
18	**4316691**	**4357788**	**41098**	**T3PKS**	**BGC0001310**	**1**	**naringenin**
19	4362758	4468416	105659	T1PKS	BGC0001012	1	meridamycin
20	4468517	4597992	129476	T1PKS, NRPS-like, NRPS, lanthipeptide-class-ii	BGC0000958	1	antimycin
21	**4855298**	**4905587**	**50290**	**NRPS**	**BGC0000325**	**0.363636**	**coelichelin**
22	5132758	5155043	22286	terpene	BGC0001181	1	geosmin
23	5492554	5513528	20975	terpene	BGC0000660	1	Albaflavenone
24	**5873092**	**5917441**	**44350**	**NRPS**	**BGC0002359**	**0.173913**	**dudomycin A**
25	6462778	6492598	29821	NI-siderophore	BGC0001478	1	desferrioxamine E
27	6728226	6777636	49411	NRPS, T1PKS	BGC0002365	1	10-epi-HSAF/10-epi-3-deOH-HSAF/10-epi-maltophilin/10-epi-xanthobaccin C/10-epi-hydroxymaltophilin/10-epi-FI-2
28	6812146	6838710	26565	terpene	BGC0000663	0.769231	hopene
29	6904243	6914458	10216	RiPP-like	BGC0002497	0.0454545	hexacosalactone A

In bold: Product specific to DSM 40455^T

Table S6. Prediction of Biosynthetic Gene Clusters encoding potentially novel secondary metabolites in *Streptomyces albidoflavus* DSM 40455^{T}.

antiSMASH Region id	Begin	End	Length	Region type
1	6005	17333	11329	RiPP-like
12	3102688	3109320	6633	transAT-PKS
14	3933927	3936412	2486	NRPS
26	6665084	6690102	25019	T1PKS

Table S7. Functional comparison of lipid metabolic pathways in *Streptomyces* sp. ZE1316R2A^T and *S. albidoflavus* 40455^T based on KEGG and MicroCyc annotations, including conserved lipid metabolic cores and accessory lipid-related reactions.

Pathway / Reaction	ZE1316R2A^T	DSM 40455^T	Database	Notes
Fatty acid biosynthesis	✓	✓	KEGG	Conserved core
Fatty acid elongation	✓	✓	KEGG	Conserved core
Fatty acid degradation (β-oxidation)	✓	✓	KEGG	Conserved core
Glycerolipid metabolism	✓	✓	KEGG	Conserved core
Glycerophospholipid metabolism	✓	✓	KEGG	Conserved core
Farnesyl-PP → presqualene-PP → squalene	Present	Absent	KEGG	Part of triterpenoid precursor branch (annot. under "steroid biosynthesis")
Acetone → acetoacetate	Partial	Absent	MicroCyc	Acetone degradation II (fragment)
Acetoacetate → acetyl-CoA	Present (partial)	Reduced	MicroCyc	Fragment of acetoacetate degradation
Cutin/suberin/wax biosynthesis (KEGG)	Present (1 gene)	Absent	KEGG	Likely spurious; bacterial relevance limited
Ether lipid metabolism	Present (1 gene)	Present (2 genes)	KEGG	Minimal difference

KEGG: Kyoto Encyclopedia of Genes and Genomes
MicroCyc: Collection of microbial Pathway/Genome Databases

Table S8. Comparative Analysis of CAZyme Families and Their Functional Profiles in *Streptomyces* sp. ZE1316R2A^T and *Streptomyces albidoflavus* DSM 40455^T.

Famille CAZyme	Principal function	*Streptomyces* sp. ZE1316R2A^T	*S. albidoflavus* DSM 40455^T
AA (Auxiliary Activities)	Oxidation, lignocellulose degradation	AA1(1), AA2(1), **AA3(3)**, **AA4(2)**, AA5(2), AA6(1), AA9(1), AA10(4)	AA1(1), AA2(1), **AA3(4)**, **AA4(1)**, AA5(2), AA6(1), AA9(1), AA10(4)
CBM (Carbohydrate Binding Modules)	Binding to polysaccharides	**CBM2(2)**, CMB3(2), CBM4(2), **CMB5(2)**, CBM6(3), **CMB12(4)**, **CBM13(12)**, CBM16(1), CMB20(1), **CMB32(7)**, CMB35(2), **CMB38(2)**, CMB42(1), CMB48(7), **CMB50(7)**, CMB51(1)	**CBM2(3)**, CMB3(2), CBM4(2), **CMB5(4)**, CBM6(3), **CMB12(5)**, **CBM13(9)**, CBM16(1), CMB20(1), **CMB32(6)**, CMB35(2), **CMB38(1)**, CMB42(1), CMB48(7), **CMB50(13)**, CMB51(1), CMB92(1) *, CMB96(1) *
CE (Carbohydrate Esterases)	Deacylation, modification of polysaccharides	**CE1(4)**, CE3(1), **CE4(11)**, CE7(2), **CE8(1)**, **CE9(3)**, CE12(2), CE**14(3)**	**CE1(5)**, CE3(1), **CE4(10)**, CE7(2), **CE8(2)**, **CE9(4)**, CE12(2), **CE14(4)**
GH (Glycoside Hydrolases)	Hydrolysis of glycosidic bonds	GH0(3), **GH1(7)**, **GH2(2)**, **GH3(6)**, **GH4(3)**, **GH5(3)**, GH6(2), GH9(1), GH**13(14)**, GH15(2), **GH16(1)**, **GH18(4)**, GH19(2), GH20(3), **GH23(15)**,GH25(3), **GH28(2),** GH29(1) *, GH31(2), GH32(2),GH33(1), **GH38(2)**,GH39(2),GH43(1)*,GH46(2),GH47(2),GH63(1),GH64(1),GH65(2)*,**GH71(2)**,GH75(2)*,GH76(3),GH77(1),GH81(1),GH84(2),GH87(1),**GH101(3)**,GH109(1)*,**GH114(1)**,GH131(1),GH132(1),GH135(1),GH171(1),GH176(1),GH178(1),GH179(2),GH183(2), GH184(2), **GH188(3)**	GH0(3), **GH1(5)**, **GH2(3)**, **GH3(7)**, **GH4(4)**, **GH5(1)**, GH6(2), GH9(1), **GH13(15)**, GH15(2), **GH16(2)**, **GH18(5)**,GH19(2), GH20(3), **GH23(10)**, GH25(3), GH27(1) *,**GH28(3)**, GH31(2), GH32(2), GH33(1), GH35(1) *, **GH38(4)**,GH39(2), GH46(2), GH47(2), GH63(1), GH64(1), **GH71(3)**, GH76(3), GH77(1), GH81(1), GH84(2), GH87(1),**GH101(2)**, **GH114(2)**, GH127(1) *, GH131(1), GH132(1),GH135(1), GH144(1) *, GH152(1) *, GH171(1), GH176(1),GH178(1), GH179(2), GH183(2), GH184(2), **GH188(2)**
GT (Glycosyltransferases)	Biosynthesis and modification of polysaccharides	**GT1(14)**, **GT2(52)**, **GT4(16)**, GT9(2) *, GT20(1), **GT28(4)**, GT35(1), GT39(1), **GT47(1)**, **GT49(1)**, **GT51(4)**, GT76(2), **GT81(1)**, GT83(1), GT87(4), GT119(5)	**GT1(21)**, **GT2(36)**, **GT4(18)**, GT20(1), GT22(1) *, **GT28(3)**, GT30(1) *, GT34(1) *, GT35(1), GT39(1), GT41(1) *, GT44(1) *, **GT47(2)**, **GT49(3)**, GT50(1) *, **GT51(5)**, GT76(2), **GT81(2)**, GT83(1), GT87(4), GT119(5)
PL (Polysaccharide Lyases)	Non-hydrolytic cleavage of polysaccharides	PL31 (1)	PL4(1) *, PL31 (1)

In bold: Indicates differences in CAZyme numbers between strain ZE1316R2A and strain DSM 40455^T

*: Indicates the presence of the CAZyme in only one strain

Table S9. Growth responses of *Streptomyces* sp. ZE1316R2A^T and *Streptomyces albidoflavus* DSM 40455^T under different salinity, temperature and pH conditions after 14 days of incubation

	Condition	*Streptomyces* sp. ZE1316R2A^T	*S. albidoflavus* DSM 40455^T
Salinity (%)	0	++++	++++
	5	+	+
	10	-	-
	15	-	-
	20	-	-
Temperature (°C)	5	-	-
	16	+++	+++
	28	++++	++++
	30	++++	++++
	37	++	++++
	50	-	-
pH	5.5	-	-
	6.5	++++	++++
	7	++++	++++
	7.5	++++	++++
	8.5	++++	++++

Growth code legend: (-): No growth; (+) Poor growth; (++) Moderate growth; (+++): Good growth; (++++): Abundant growth

Table S10. Differential carbohydrate utilisation patterns of *Streptomyces* sp. ZE1316R2A^T and closely related strain *Streptomyces albidoflavus* DSM 40455^T.

Carbohydrate	***Streptomyces* sp. ZE1316R2A^T**	***S. albidoflavus* DSM 40455^T**
D-Arabinose	-	+
L-Arabinose	-	+
D-Ribose	-	+
D-Glucose	-	+
D-Fructose	-	+
D-Mannose	+	-
D-Mannitol	-	+
Amygdalin	-	+
D-Cellobiose	-	+
D-Lactose	-	+
D-Melezitose	-	+
D-Fucose	-	+

(+), positive reaction ; (–), negative reaction.