

**TABLE S1.** Homology of CN1 GDH1 gene regions with GenBank sequences.

Marker/ Primers	BLAST Hit #	NCBI Database Strain for Sequence Comparison	GenBank Accession Number	Base Pairs	Alignment Results		
					Max Score	Query Coverage	Sequence Identity
SuGDH1 Open Reading Frame  SugdhU SugdhL	1	<i>S. uvarum</i> Strain LZSP5L.2	KF892169.1	899/901	1652	100%	99.78%
	2	<i>S. uvarum</i> Strain LLFM11L.1	KF892165.1	899/901	1652	100%	99.78%
	3	<i>S. uvarum</i> Strain CLIB 251	AJ627640.1	899/901	1652	100%	99.78%
	4	<i>S. uvarum</i> GDH1 gene for glutamate dehydrogenase 1 and intergenic spacer (IGS)	AJ418037.1	899/901	1652	100%	99.78%
	5	<i>S. uvarum</i> Strain CLIB 398	AJ627874.1	777/781	1428	100%	99.67%
	6	<i>S. eubayanus</i> Strain CBS12357	CP030952. 1	777/781	1428	99%	96.22%
	12	<i>S. bayanus</i> Strain CLIB 181 <sup>T</sup> (=CBS380)	AJ627639.1	866/900	1472	99%	96.22%
SuGDH1 Open Reading Frame  SugdhF1 SugdhR1	1	<i>S. uvarum</i> Strain LZSP5L.2	KF892169.1	653/653	1206	99%	100%
	2	<i>S. bayanus</i> Strain LLFM11L.1	KF892165.1	653/653	1206	99%	100%
	3	<i>S. uvarum</i> Strain CLIB 251	AJ627640.1	653/653	1206	99%	100%
	4	<i>S. uvarum</i> GDH1 gene for glutamate dehydrogenase 1 and intergenic spacer (IGS)	AJ418037.1	653/653	1206	99%	100%
	5	<i>S. uvarum</i> Strain CLIB 398	AJ627874.1	652/653	1201	99%	99.85%
	6	<i>S. pastorianus</i> Strain 1483	CP049005. 1	627/653	1062	99%	96.02%
	16	<i>S. bayanus</i> Strain NBRC 1948	FR845792.1	625/650	1062	99%	96.15%
SuGDH1 Open Reading Frame	1	<i>S. uvarum</i> Strain LZSP5L.2	KF892169.1	222/224	401	97%	99.11%
	2	<i>S. uvarum</i> Strain LLFM11L.1	KF892165.1	222/224	401	97%	99.11%
	3	<i>S. uvarum</i> Strain CLIB 398	AJ627874.1	222/224	401	97%	99.11%
	4	<i>S. uvarum</i>	AJ627640.1	222/224	401	97%	99.11%

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SbgdhF1 SbgdhR1	5	<i>S. uvarum</i> GDH1 gene for glutamate dehydrogenase 1 and intergenic spacer (IGS)	AJ418037.1	222/224	401	97%	99.11%
	6	<i>S. aff. eubayanus</i> Strain LZSP1L.4	KF892156.1	211/224	340	99%	95.92%
	24	<i>S. bayanus</i> Strain NBRC 1948	FR845792.1	210/224	335	97%	93.75%
SuGDH1 Promoter  SugPrU SugPrL	1	<i>S. uvarum</i> Strain CLIB 251	AJ627640.1	452/452	835	98%	100%
	2	<i>S. uvarum</i> GDH1 gene for glutamate dehydrogenase 1 and intergenic spacer (IGS)	AJ418037.1	452/452	835	98%	100%
	3	<i>S. uvarum</i> Strain CLIB 398	AJ627874.1	451/452	830	98%	99.78%
	4	<i>S. uvarum</i> Strain LLFM11L.1	KF892165.1	346/346	640	75%	100%
	5	<i>S. uvarum</i> Strain LZSP5L.2	KF892169.1	345/346	632	75%	99.71%
	6	<i>S. uvarum</i> Strain CBS 7001	KF530435.1	292/296	521	63%	98.65%
	11	<i>S. bayanus</i> Strain CLIB 181 <sup>T</sup> (=CBS380)	AJ627639.1	385/454	435	98%	84.80%
SuGDH1 Intergenic Spacer  SugIgU SugIgL	1	<i>S. uvarum</i> Strain CLIB 398	AJ627874.1	219/225	392	92%	97.33%
	2	<i>S. uvarum</i> Strain CLIB 251	AJ627640.1	219/225	392	92%	97.33%
	3	<i>S. uvarum</i> GDH1 gene for glutamate dehydrogenase 1 and intergenic spacer (IGS)	AJ418037.1	219/225	392	92%	97.33%
	4	<i>S. eubayanus</i> Strain CBS12357	CP030952. 1	161/167	276	68%	96.41%
	5	<i>S. pastorianus</i> Strain CLIB 176	AJ627641.1	157/167	248	68%	94.01%
	6	<i>S. bayanus</i> Strain CLIB 181 <sup>T</sup> (=CBS380)	AJ627639.1	157/167	248	68%	94.01%