Table S1. Subcellular location prediction of *E. gracilis* marker proteins using TargetP 1.1.

Location	Marker enzyme name	EC number	EG transcript	LOC Plant	LOC nonPlant	LOC Plant (signal cut)
Chloroplast	ribulose-biphosphate carboxylase (small subunit)	4.1.1.39	7123	_	_	
			43244	S	S	Chl
			13866	_	_	
			59484	S	S	_
	NADP- glyceraldehyde-3-phosphate dehydrogenase	1.2.1.9	4454	Mt	Mt	
			5575	Mt	Mt	
			9413	Mt	Mt	
			7552	_	_	
			15045	Mt	Mt	
	fructose-biphosphate aldolase (chloroplastic)	4.1.2.13	15855	_	_	
			25832	Mt	Mt	
			7827	Chl	S	
			5279	Mt	Mt	
	pyruvate Pi dikinase (C4)	2.7.9.1	1635	_	_	
	photosystem II D1 subunit		13288	S	S	_
			10715	_	_	
	photosystem II D2 subunit		13288	S	S	_
			10715	_	_	
	photosystem II CP47 protein		899	Mt	S	_
	photosystem II CP43 protein		13640	S	S	_
	cytochrome b6f		5228	_	_	
			23844	_	Mt	
	photosystem I A1 subunit		158	Mt	Mt	
	photosystem I A2 subunit		158	Mt	Mt	
Mitochondria	fumarase	4.2.1.2	4764	Mt	Mt	
	succinic semialdehyde dehydrogenase	1.2.1.16	7552	_	_	
			5575	Mt	Mt	

			3780	Mt	Mt	
			5750	Mt	Mt	
	isocitrate dehydrogenase	1.1.1.41, 1.1.1.42	6875	_	_	
			10115	Mt	Mt	
			10872	Mt	Mt	
			10979	Mt	Mt	
	NADPH:glyoxylate reductase	1.1.1.79	5154	Mt	Mt	
			13699	_	S	
Cytosol	glutamate dehydrogenase	1.4.1.2	11196	_	_	
			10682	_	_	
			7536	Mt	_	
			791	_	_	
	NAD-lactate dehydrogenase	1.1.1.27	11571	_	_	
	thiosulfate sulfurtransferase	2.8.1.1	32721	_	_	
			19233	Mt	S	
			10931	_	_	
			27480	Mt	Mt	
			18090	_	_	
			46995	_	_	
			1438	Mt	S	
Secretory pathway	alpha-1,3-mannosyltransferase	2.4.1.258	11655	S	S	_
	alpha-1,2-mannosyltransferase	2.4.1.259/261	44449	S	S	_
			15548	Mt	S	
	alpha-1,6-mannosyltransferase	2.4.1.260	9095	S	S	_
	dolichol phosphate mannose synthase	2.4.1.83	21418	_	_	
	dolichyl-phosphate beta-glucosyltransferase	2.4.1.117	15275	S	S	_
	alpha-1,3-glucosyltransferase	2.4.1.267/265	22866	_	S	
			24290	Mt	S	
			22282	S	S	_
	alpha-1,2-glucosyltransferase	2.4.1.256	20467	Mt	Mt	

	dolichyl-diphosphooligosaccharide--protein glycosyltransferase	2.4.99.18	2741	Mt	S
			10761	_	_
			2733	_	_

Location	Reliability class*				
Mt: mitochondria	1	2	3	4	5
Chl: chloroplast	1	2	3	4	5
S: secretory pathway	1	2	3	4	5
_: other locations	1	2	3	4	5

*Reliability class is rated from 1 to 5, where 1 indicates the strongest prediction and 5 indicates the weakest.

Table S2. TargetP 1.1 subcellular location prediction of *E. gracilis* metabolic pathway components.

Pathway	Enzyme name	EC number	EG transcript	LOC Plant	LOC nonPlant	LOC Plant (signal cut)
Paramylon synthesis	1,3-β-glucan synthase	2.4.1.34	73	S	S	_
			11758	_	_	
			183	S	S	Chl
	endo-1,3-β-glucanases	3.2.1.6	2352	Chl	_	
		3.2.1.39	11364	S	S	_
			11498	_	_	
			3590	_	_	
			6201	_	_	
	exo-1,3-β-glucanases	3.2.1.58	11628	_	S	
			7060	_	_	
Trehalose synthesis	trehalose-phosphate synthase	2.4.1.15	2409	Chl	Mt	
	trehalose-phosphate phosphatase	3.1.3.12	2409	Chl	Mt	
	trehalose synthase	2.4.1.245	8134	_	_	
			10436	_	_	
			3686	Mt	_	
Glycolysis	hexokinase	2.7.1.1	26449	Mt	Mt	
			31789	_	_	
	glucokinase	2.7.1.2	8623	_	_	
			22400	_	_	
	fructokinase	2.7.1.4	15309	_	_	
			19345	S	S	_
			13564	Mt	Mt	
			14390	_	_	
	phosphoglucoisomerase	5.3.1.9	5108	_	_	
			17737	_	_	
			8453	_	_	
			19460	S	_	_

phosphofructokinase	2.7.1.11	6957	_	_	
		6970	_	_	
		12862	_	_	
		7619	_	_	
		7325	_	_	
		1546	_	_	
diphosphate-fructose-6-phosphate 1-phosphotransferase	2.7.1.90	7325	_	_	
		12862	_	_	
		6970	_	_	
fructose-bisphosphate aldolase	4.1.2.13	15855	_	_	
		7827	Chl	S	
		5279	Mt	Mt	
		25832	Mt	Mt	
triosephosphate isomerase	5.3.1.1	14120	Mt	Mt	
		18179	_	_	
		30563	_	_	
		44253	_	_	
		30456	Chl	Mt	
glyceraldehyde 3-phosphate dehydrogenase	1.2.1.12	16406	_	S	
		12332	_	_	
		8042	S	S	Chl
phosphoglycerate kinase	2.7.2.3	10778	_	_	
		12260	_	_	
		12119	_	_	
		32014	S	Mt	_
phosphoglycerate mutase	5.4.2.1	10778	_	_	
		12260	_	_	
		12119	_	_	
		32014	S	Mt	_
enolase	4.2.1.11	7256	Mt	S	

			12376	_	_	
			6665	_	_	
	pyruvate kinase	2.7.1.40	7941	_	_	
			6211	Mt	Mt	
			2957	_	_	
			6124	_	_	
	pyruvate dehydrogenase	1.2.1.51	9827	Mt	Mt	
			8975	Mt	Mt	
			14931	Mt	_	
			14495	Mt	Mt	
Gluconeogenesis	phosphoenolpyruvate synthase	2.7.9.2	1653	_	_	
	phosphoenolpyruvate carboxykinase	4.1.1.32	535	_	_	
			4483	Mt	S	
			14414	_	_	
	fructose-1,6-bisphosphatase	3.1.3.11	8727	S	S	Chl
			15632	_	_	
			7683	Chl	_	
			13690	Chl	_	
			4570	_	S	
TCA cycle	citrate synthase	4.1.3.7	10302	_	_	
			6849	_	_	
			11595	_	_	
			2898	Mt	Mt	
	aconitase	4.2.1.3	2608	_	_	
			1951	Mt	Mt	
	isocitrate dehydrogenase	1.1.1.41, 1.1.1.42	6875	_	_	
			10115	Mt	Mt	
			10872	Mt	Mt	
			10979	Mt	Mt	
	2-oxoglutarate decarboxylase	4.1.1.71	121	_	_	

	succinic semialdehyde dehydrogenase	1.2.1.16	7552	_	_	
			5575	Mt	Mt	
			3780	Mt	Mt	
			5750	Mt	Mt	
	succinate dehydrogenase	1.3.5.1	7873	_	_	
	fumarase	4.2.1.2	4764	Mt	Mt	
	malate dehydrogenase	1.1.1.37	12212	_	_	
			15919	_	_	
Dicarboxylic acid bypass	malate dehydrogenase (NADP-specific oxaloacetate-decarboxylating)	1.1.1.40	8836	Mt	S	
			7652	_	_	
	NAD-specific malic enzyme	1.1.1.39	5925	_	_	
			7652	_	_	
	phosphoenolpyruvate carboxylase	4.1.1.31	1597	_	S	
	pyruvate carboxylase	6.4.1.1	12535	_	_	
			23270	_	_	
			724	_	_	
			36271	_	_	
			97	Mt	Mt	
C2 metabolism	alcohol dehydrogenase	1.1.1.1	13473	_	_	
			21676	_	_	
	acetaldehyde dehydrogenase	1.2.1.10	8156	Mt	Mt	
	acetyl-CoA synthetase	6.2.1.1	3254	_	_	
			4603	_	_	
			9669	_	_	
			3515	S	_	_
Glyoxylate	isocitrate lyase	4.1.3.1	715	Mt	Mt	
	malate synthase	2.3.3.9	729	_	_	
			2530	_	_	
Oxidative PPP	glucose-6-phosphate 1-dehydrogenase	1.1.1.49	10052	_	_	
	6-phosphogluconolactonase	3.1.1.31	4334	_	_	

	6-phosphogluconate dehydrogenase	1.1.1.44	7631	S	_	_
Nonoxidative PPP	pentose-5-phosphate-3-epimerase	5.1.3.1	19182	_	_	
			23949	_	Mt	
	ribose 5-phosphate isomerase	5.3.1.6	15619	_	_	
			20009	_	_	
	transketolase	2.2.1.1	2997	S	_	_
			3894	_	_	
			4605	_	_	
	transaldolase	2.2.1.2	13075	_	_	
			8390	_	_	
Glycolate	glycolate dehydrogenase	1.1.99.14	8383	Mt	Mt	
			11827	Mt	Mt	
Methionine synthesis	cobalamin-dependent methionine synthase	2.1.1.13	3052	_	_	
			904	_	_	
			1784	_	_	

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S: secretory pathway	1	2	3	4	5
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