

Supplementary Material

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Table 1S: The composition of sugarcane KQ228 internodes during different stages of development and in the presence of MODDUS. sd=standard deviation, nd = not determined.

Internode	Phenotype	Component									
		glucan	sd	pentan	sd	lignin	sd	sucrose	sd	hexoses	sd
1	fast_growth	271.41	7.82	111.39	3.21	86.69	2.99	102.25	1.71	166.40	15.29
1	moddus	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd
1	slow_growth	448.96	19.89	178.03	17.16	77.80	47.72	184.40	33.75	160.80	14.34
2	fast_growth	271.65	5.28	112.72	2.19	90.58	2.73	116.29	2.20	130.85	17.55
2	moddus	271.65	5.28	112.72	2.19	90.58	2.73	187.66	51.94	108.34	20.82
2	slow_growth	416.55	48.99	177.53	22.48	86.68	36.90	232.74	14.59	121.21	38.32
3	fast_growth	264.50	6.20	119.77	2.81	90.69	4.25	119.31	4.14	128.10	4.53
3	moddus	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd
3	slow_growth	398.41	55.72	178.91	15.25	102.38	45.40	275.92	13.79	93.50	3.32
4	fast_growth	260.74	6.71	102.25	2.63	81.95	4.92	158.20	13.03	99.00	6.48
4	moddus	260.74	6.71	102.25	2.63	112.10	4.08	430.82	220.42	77.60	4.93
4	slow_growth	426.33	50.12	152.63	15.58	89.79	34.48	389.92	48.07	83.40	7.68
5	fast_growth	248.12	3.75	98.26	1.48	86.34	1.93	188.10	5.59	83.40	4.45
5	moddus	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd
5	slow_growth	383.74	19.37	127.71	3.90	88.36	21.28	513.67	31.29	60.75	3.77
6	fast_growth	238.70	4.28	95.26	2.83	101.95	4.73	280.60	14.07	66.10	2.52
6	moddus	242.78	1.22	96.22	1.91	101.19	8.37	584.25	60.06	54.60	4.40
6	slow_growth	269.07	9.71	111.98	5.25	106.85	5.04	645.66	21.08	48.65	4.71
8	fast_growth	234.18	8.74	101.50	1.91	116.19	3.53	406.00	16.17	57.48	2.48
8	moddus	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd
8	slow_growth	367.87	55.57	170.27	23.71	118.36	5.72	772.12	49.21	39.00	2.93
10	fast_growth	219.99	3.24	89.61	2.27	124.41	4.60	501.25	13.77	48.25	4.91
10	moddus	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd
10	slow_growth	326.69	43.22	142.95	23.59	130.92	7.19	801.41	54.48	41.20	3.13
12	fast_growth	214.81	8.78	94.18	2.36	118.86	3.12	486.00	14.05	40.00	1.73
12	moddus	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd
12	slow_growth	395.03	48.05	163.70	5.83	123.94	8.01	795.51	31.30	34.04	2.35

Table S2: Structure of the Mapman mapping file for the identified metabolites.

BINCODE	NAME	IDENTIFIER	TYPE
1	Sucrose		
1.1	Sucrose.storage		
1.1.1	Sucrose.storage.dryweight	dryweight	
1.1.2	Sucrose.storage.length	length	
1.1.3	Sucrose.storage.sucrose	sucrose	M
1.2	Sucrose.breakdown		
1.2.1	Sucrose.breakdown.fructose	fructose	M
1.2.2	Sucrose.breakdown.glucose	glucose	M
2	Sugars		
2.1	Sugars.other		
2.1.1	Sugars.other.gentibiose	gentibiose	M
2.1.2	Sugars.other.trehalose	trehalose	M
2.1.3	Sugars.other.mannose	raffinose	M
2.1.4	Sugars.other.raffinose	mannose	M
2.1.5	Sugars.other.1-kestose	1-kestose	M
2.1.6	Sugars.other.ribose	ribose	M
2.2	Sugar alcohols		
2.2.1	Sugar alcohols.galactitol	galactitol	M
2.2.2	Sugar alcohols.galactinol	galactinol	M
2.2.3	Sugar alcohols.galactitol	erythritol	M
2.2.4	Sugar alcohols.mannitol	mannitol	M
2.2.5	Sugar alcohols.erythritol	erythritol	M
3	Cell wall		M
3.1	Cell wall.cellulose	glucan	M
3.2	Cell wall.hemicellulose		
3.2.1	Cell wall.hemicellulose.rhamnose	rhamnose	M
3.2.2	Cell wall.hemicellulose.arabinose	arabinose	M
3.2.3	Cell wall.hemicellulose.arabitol	arabitol	
3.2.4	Cell wall.hemicellulose.galactose	galactose	M
3.2.5	Cell wall.hemicellulose.glucarate	glucarate	M
3.2.6	Cell wall.hemicellulose.xylitol	xylitol	M
3.2.7	Cell wall.hemicellulose.gluconate	gluconate	M
3.2.8	Cell wall.hemicellulose.xylose	xylose	M
3.2.9	Cell wall.hemicellulose.glucuronate	glucuronate	M
3.2.10	Cell wall.hemicellulose.myoinisitol	myoinisitol	M
3.3	Cell wall.ascobate		
3.3.1	Cell wall.ascobate.ascorbate	ascorbate	M
3.3.2	Cell wall.ascobate.erythrose	erythrose	M
3.3.3	Cell wall.ascobate.threonate	threonate	M
3.3.4	Cell wall.ascobate.threonate lactone	threonate lactone	M
3.3.5	Cell wall.ascobate.glycolate	glycolate	M
3.3.6	Cell wall.ascobate.oxalate	oxalate	M
3.3.7	Cell wall.ascobate.myoinisitol	myoinisitol	M
4	Glycolysis		

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BINCODE	NAME	IDENTIFIER	TYPE
4.1	Glycolysis.hexoses		
4.1.1	Glycolysis.hexoses.glucose6P	glucose6P	M
4.1.2	Glycolysis.hexoses.fructose6P	fructose6P	M
4.2	Glycolysis.trioseP		
4.2.1	Glycolysis.trioseP.glycerol	glycerol	M
4.2.2	Glycolysis.trioseP.glycerol3P	glycerol3P	M
4.2.3	Glycolysis.trioseP.glycerate	glycerate	M
4.2.4	Glycolysis.trioseP.pyruvate	pyruvate	M
4.3	Glycolysis.fermentation		
4.3.1	Glycolysis. fermentation.lactate	lactate	
5	Organic acids		
5.1	Organic acids.TCA		
5.1.1	Organic acids.TCA.citrate	citrate	M
5.1.2	Organic acids.TCA.aconitate	aconitate	M
5.1.3	Organic acids.TCA.isocitrate	isocitrate	M
5.1.4	Organic acids.TCA.succinate	succinate	M
5.1.5	Organic acids.TCA.fumarate	fumarate	M
5.1.6	Organic acids.TCA.malate	malate	M
5.1.7	Organic acids.TCA.oxaloacetate	oxaloacetate	M
5.2	Organic acids.other		
5.2.1	Organic acids.other2-oxoglutarate	2-oxoglutarate	M
6	Aminoacids		
6.1	Aminoacids.glucogenic		
6.1.1	Aminoacids.glucogenic.serine	serine	M
6.1.2	Aminoacids.glucogenic.glycine	glycine	M
6.1.3	Aminoacids.glucogenic.cysteine	cysteine	M
6.1.4	Aminoacids.glucogenic.alanine	alanine	M
6.2	Aminoacids.ketogenic		
6.2.1	Aminoacids.ketogenic.aspartate	aspartate	M
6.2.2	Aminoacids.ketogenic.asparagine	asparagine	M
6.2.3	Aminoacids.ketogenic.glutamate	glutamate	M
6.2.4	Aminoacids.ketogenic.glutamine	glutamine	M
6.2.5	Aminoacids.ketogenic.arginine	arginine	M
6.2.6	Aminoacids.ketogenic.methionine	methionine	M
6.2.7	Aminoacids.ketogenic.lysine	lysine	M
6.2.8	Aminoacids.ketogenic.proline	proline	M
6.2.9	Aminoacids.ketogenic.isoleucine	isoleucine	M
6.2.10	Aminoacids.ketogenic.threonine	threonine	M
6.2.11	Aminoacids.ketogenic.valine	valine	M
6.3	Aminoacids.aromatic		
6.3.1	Aminoacids.aromatic.phenylalanine	phenylalanine	M
6.3.2	Aminoacids.aromatic.tryptophan	tryptophan	M
6.3.3	Aminoacids.aromatic.tyrosine	tyrosine	M
6.4	Aminoacids.GABA.		
6.4.1	Aminoacids.GABA.aminobutyrate	aminobutyrate	
7	Secondary metabolism		
7.1	Secondary metabolism.shikimate		

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Table S2 – continued from previous page

BINCODE	NAME	IDENTIFIER	TYPE
7.1.1	Secondary metabolism.shikimate.shikimate	shikimate	M
7.1.2	Secondary metabolism.shikimate.tyrosine	tyrosine	M
7.1.3	Secondary metabolism.shikimate.shikimate	tryptophan	M
7.1.4	Secondary metabolism.shikimate.shikimate	phenylalanine	M
7.1.5	Secondary metabolism.shikimate.quininate	quininate	M
7.1.6	Secondary metabolism.shikimate.chlorogenate	chlorogenate	M
7.2	Secondary metabolism.phenylpropanoid		
7.2.1	Secondary metabolism.phenylpropanoid.coumaroylquininate	coumaroylquininate	M
7.2.2	Secondary metabolism.phenylpropanoid.hydroxymethoxybenzoate	hydroxymethoxybenzoate	M
7.2.3	Secondary metabolism.phenylpropanoid.caffeoylquininate	caffeoylquininate	M
7.3	Secondary metabolism.lignin		
7.3.1	Secondary metabolism.lignin.caffeate	caffeate	M
7.3.2	Secondary metabolism.lignin.sinapinate	sinapinate	M
7.3.3	Secondary metabolism.lignin.ferulate	ferulate	M
7.3.4	Secondary metabolism.lignin.hydroxycinnamate	hydroxycinnamate	M
7.3.5	Secondary metabolism.lignin.ferulate	ferulate	M
7.3.6	Secondary metabolism.lignin.vanillate	vanillate	M
8	Lipid		M
8.1	Lipid.sterols		M
8.1.1	Lipid.sterols.sitosterol	sitosterol	M
8.1.2	Lipid.sterols.campesterol	campesterol	M
8.1.3	Lipid.sterols.stigmasterol	stigmasterol	M
8.2	lipid.other		M
8.2.1	lipid.other.ethanolamine	ethanolamine	M
8.2.2	lipid.other.palmitate	palmitate	
8.2.3	lipid.other.stearate	stearate	
9	Signaling		M
9.1	Signaling.defence		M
9.1.1	Signaling.defence.putrescine	putrescine	M
9.1.2	Signaling.defence.pipicolate	pipicolate	M
9.2	Signaling.regulation		M

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Table S2 – continued from previous page

BINCODE	NAME	IDENTIFIER	TYPE
9.2.1	Signaling.regulation.glycolate	glycolate	M
9.2.2	Signaling.regulation.pyroglutamate	pyroglutamate	M
9.3	Signaling.other		M
9.3.1	Signaling.other.cyanoalanine	cyanoalanine	M
9.3.2	Signaling.other.nicotinate	nicotinate	M
9.3.3	Signaling.other.uracil	uracil	M
9.3.4	Signaling.other.phosphoric.acid	phosphoric.acid	M
9.3.5	Signaling.other.itaconate	itaconate	M
9.3.6	Signaling.other.erythronate	erythronate	M
9.3.7	Signaling.other.monomethylphosphate	monomethylphosphate	M

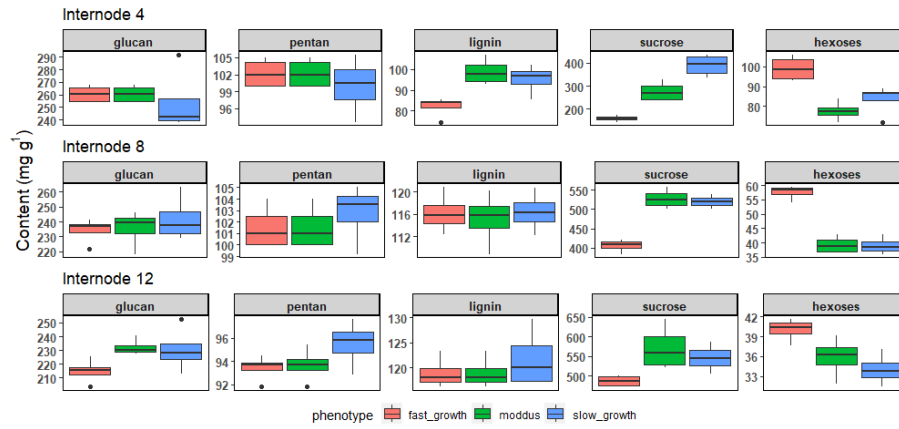


Figure S1: Biomass composition of internodes 4, 8 and 12 from fast-growing, slow-growing and in the presence of MODDUS.

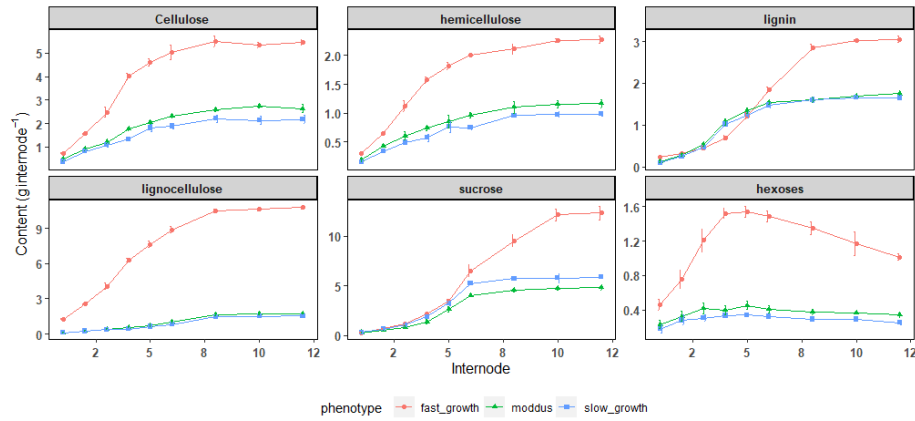


Figure S2: Changes in the biomass components of sugarcane internodes at fast growth, slow growth and in the presence of MODDUS.

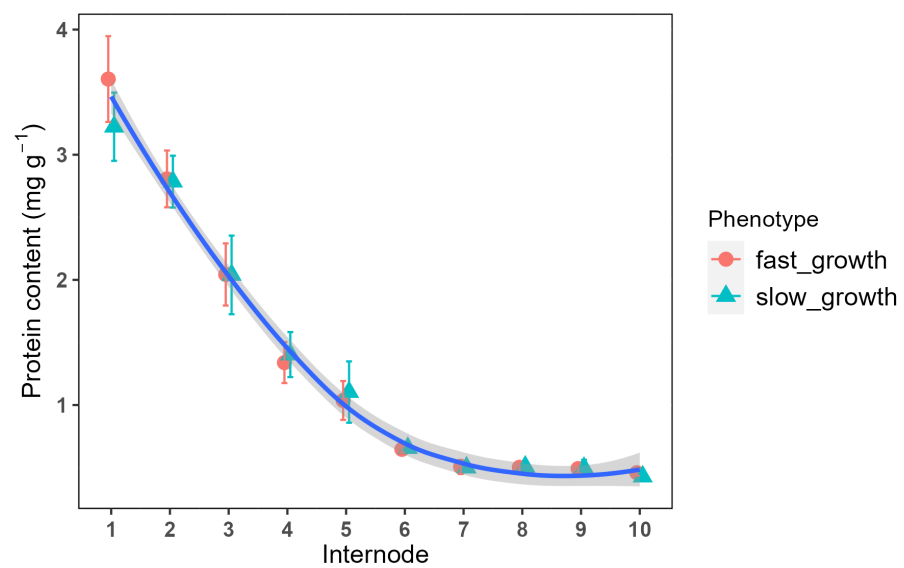


Figure S3: The water-soluble protein content of sugarcane internodes.

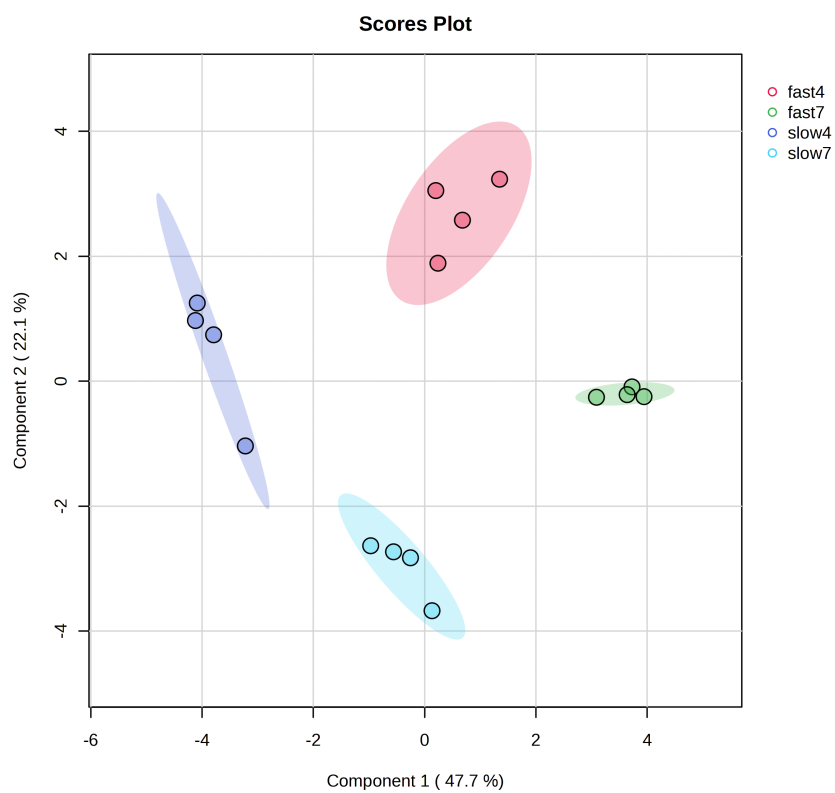


Figure S4: PLS-DA from metabolomic data of internodes at the biomass and sucrose accumulation peak rate. Scores plot generated using MetaboAnalyst.

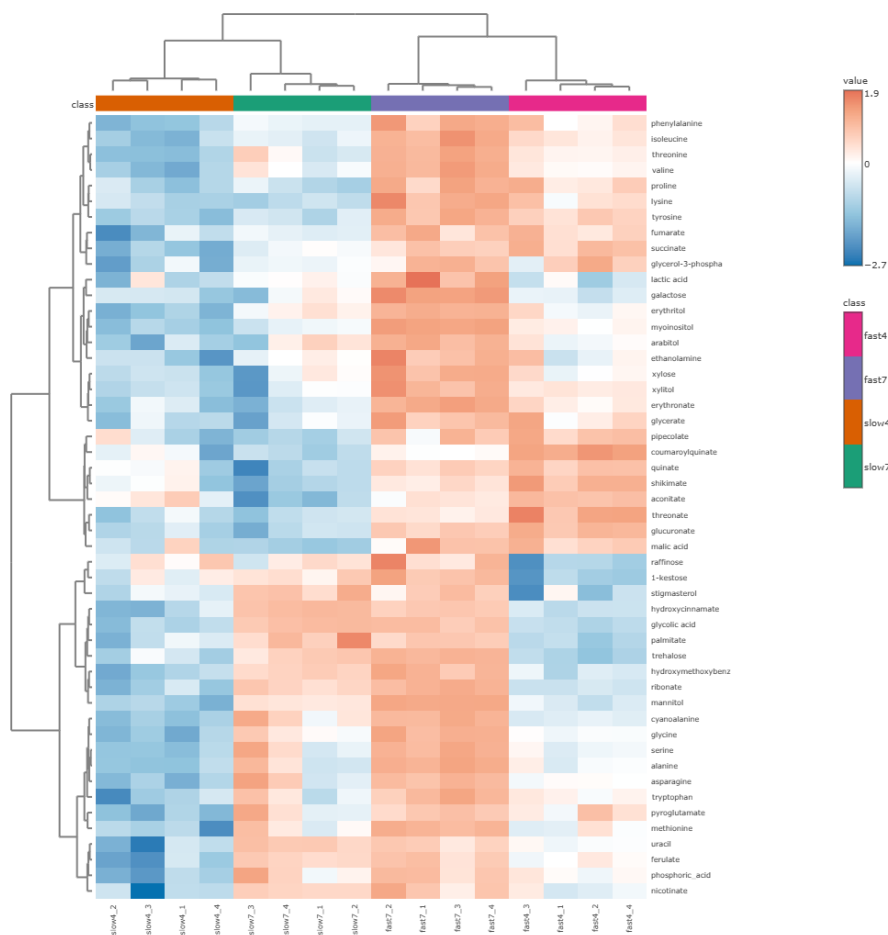


Figure S5: Heatmap profiling of the top 50 metabolites in the presence and absence of MODDUS. Values were normalised through log transformation and mean centring. The log2 fold changes in the relative metabolite abundance were subjected to a Benjamini Hochberg test and a fold change cutoff on 1.2 and then displayed using Pageman. Metabolite BINS in blue are significantly down-regulated, whereas BINS coloured in red are up-regulated. F = fast growth, S = slow growth, FM = fast growth and MODDUS. Biomass = internodes at peak biomass accumulation and sucrose - internodes with peak sucrose accumulation. Blue implies higher expression in the biomass accumulation phase and red higher expression during sucrose accumulation.

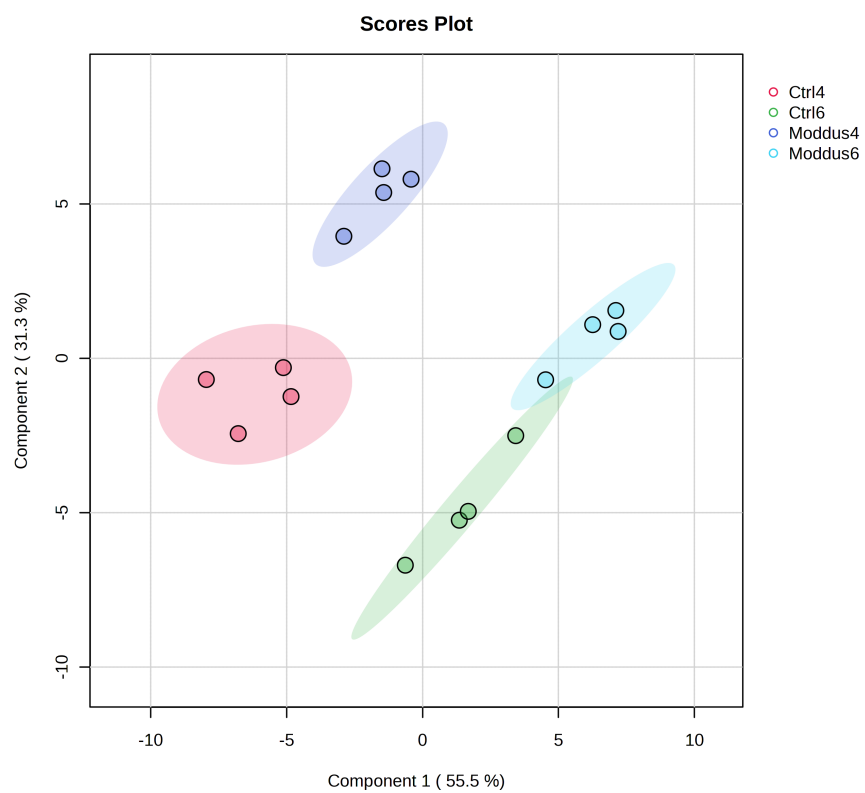


Figure S7: PLS-DA from proteome data of internodes in the presence and absence of MODDUS. Scores plot generated using MetaboAnalyst.

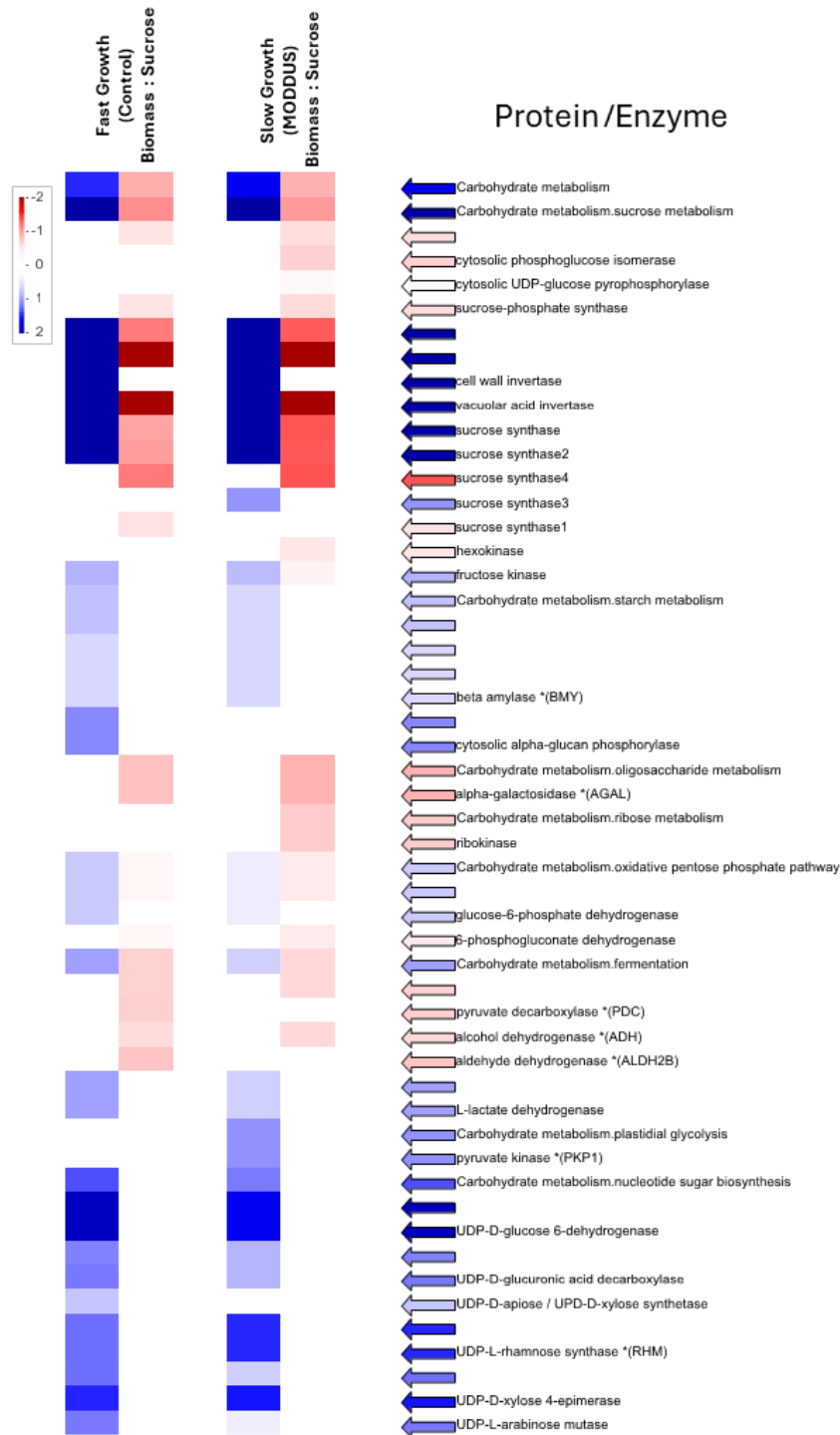


Figure S8: PageMan Analysis of the differential expression of proteins associated with carbohydrate metabolism (Mapman BINCode 3) at different stages internode development. The significant log2 fold change in expression values were used as input (FDR $p < 0.05$). Comparison is between internodes at peak biomass and sucrose accumulation in the control and MODDUS treated tissue. Blue implies higher expression in the biomass accumulation phase and red higher expression during sucrose accumulation.

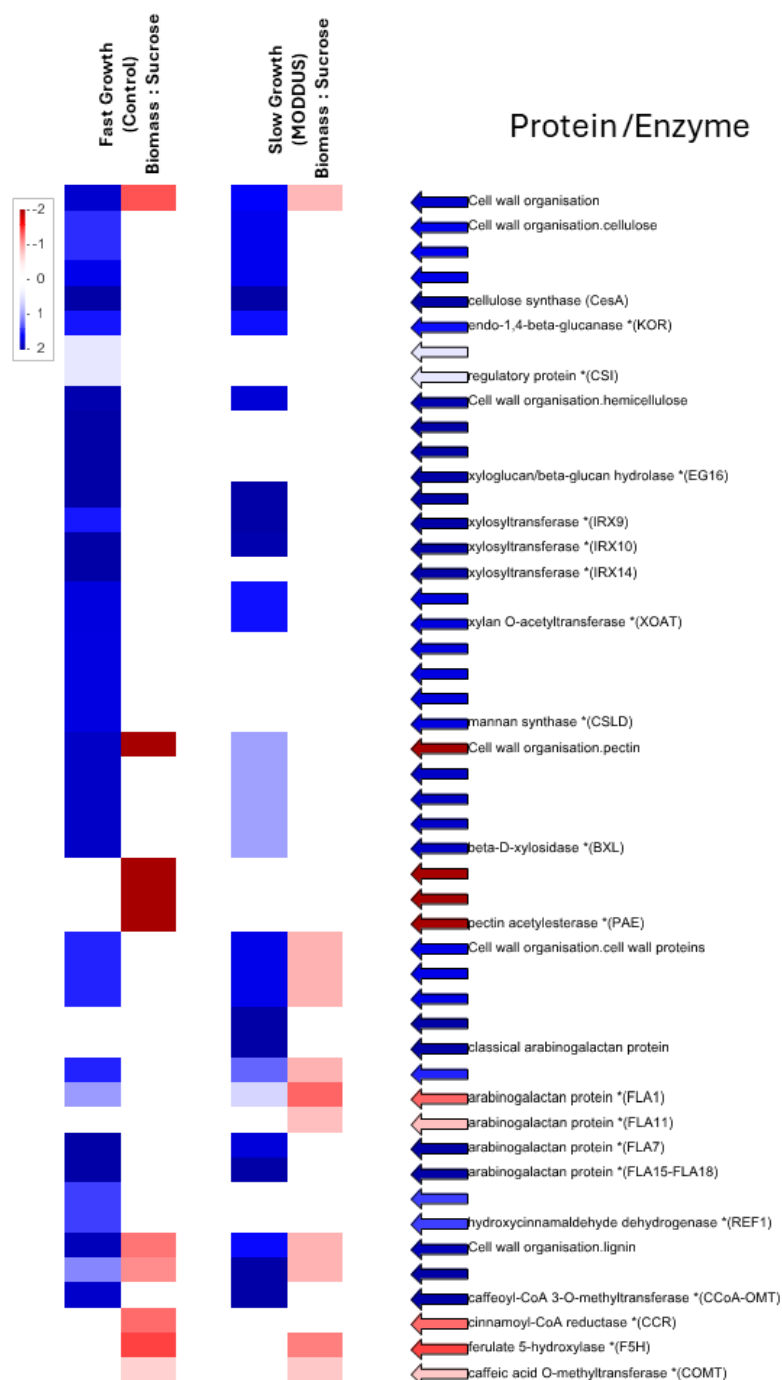


Figure S9: PageMan Analysis of the differential expression of proteins associated with cell wall metabolism (Mapman BINCode 21) at different stages of internode development. The significant log₂ fold change in expression values were used as input (FDR $p < 0.05$). Comparison is between internodes at peak biomass and sucrose accumulation in the control and MODDUS treated tissue. Blue implies higher expression in the biomass accumulation phase and red higher expression during sucrose accumulation.

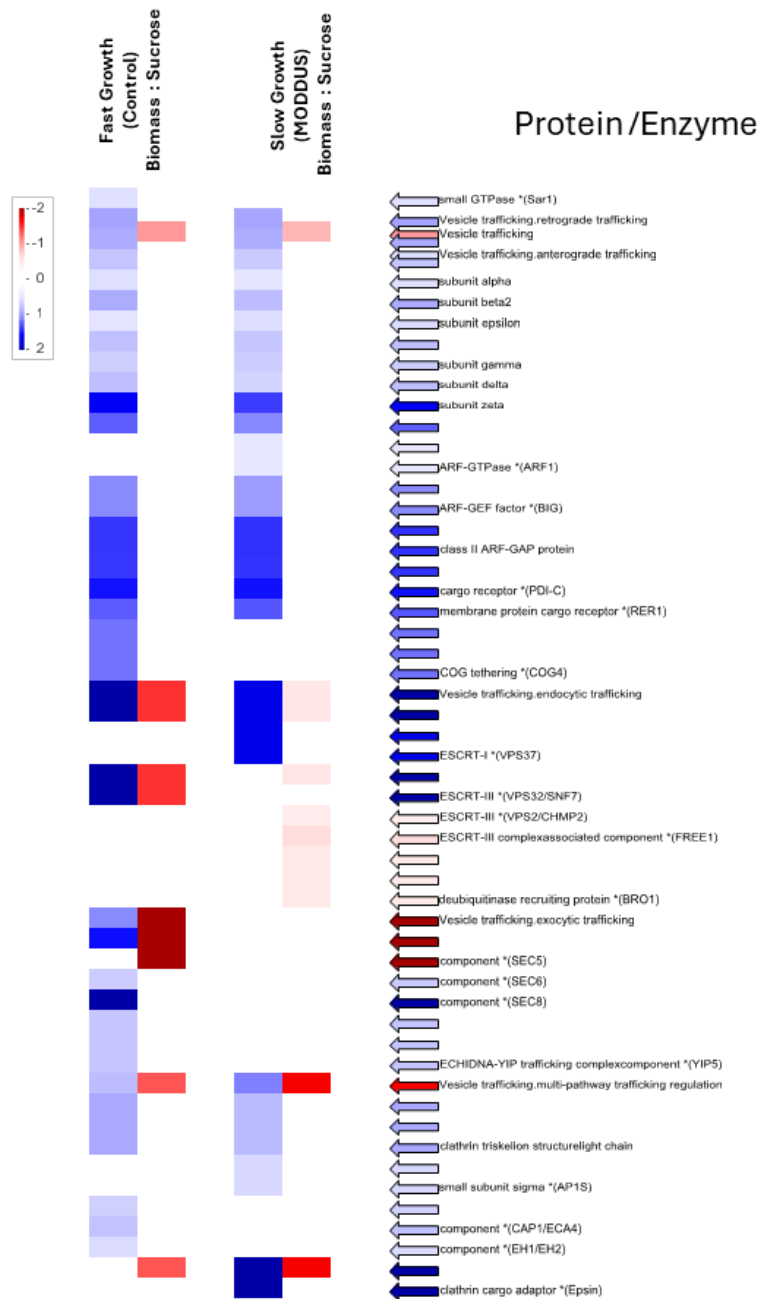


Figure S10: PageMan Analysis of the differential expression of proteins associated with vesicle trafficking metabolism (Mapman BINCode 22) at different stages of internode development. The significant log2 fold change in expression values were used as input (FDR $p < 0.05$). Comparison is between internodes at peak biomass and sucrose accumulation in the control and MODDUS treated tissue. Blue implies higher expression in the biomass accumulation phase and red higher expression during sucrose accumulation.

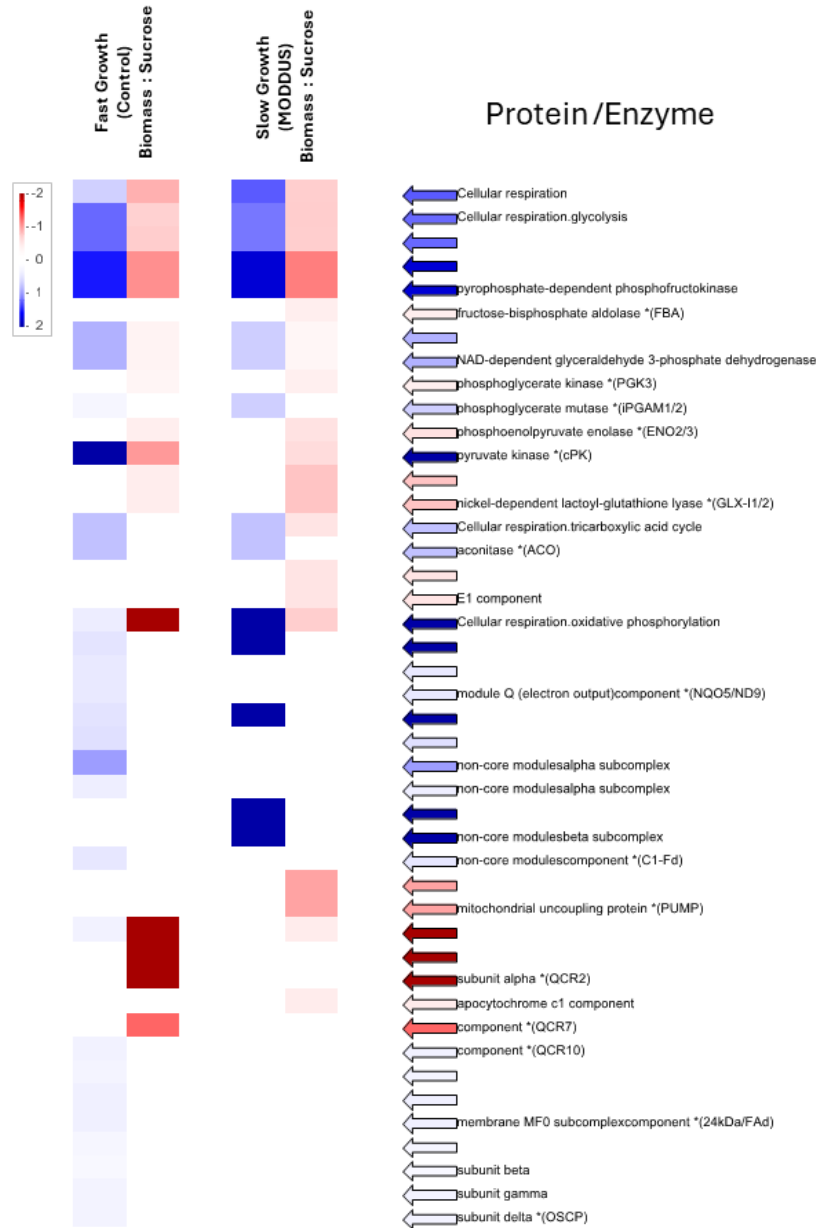


Figure S11: PageMan Analysis of the differential expression of proteins associated with respiratory metabolism (Mapman BINCode 2) at different stages internode development. The significant log2 fold change in expression values were used as input (FDR $p < 0.05$). Comparison is between internodes at peak biomass and sucrose accumulation in the control and MODDUS treated tissue. Blue implies higher expression in the biomass accumulation phase and red higher expression during sucrose accumulation.

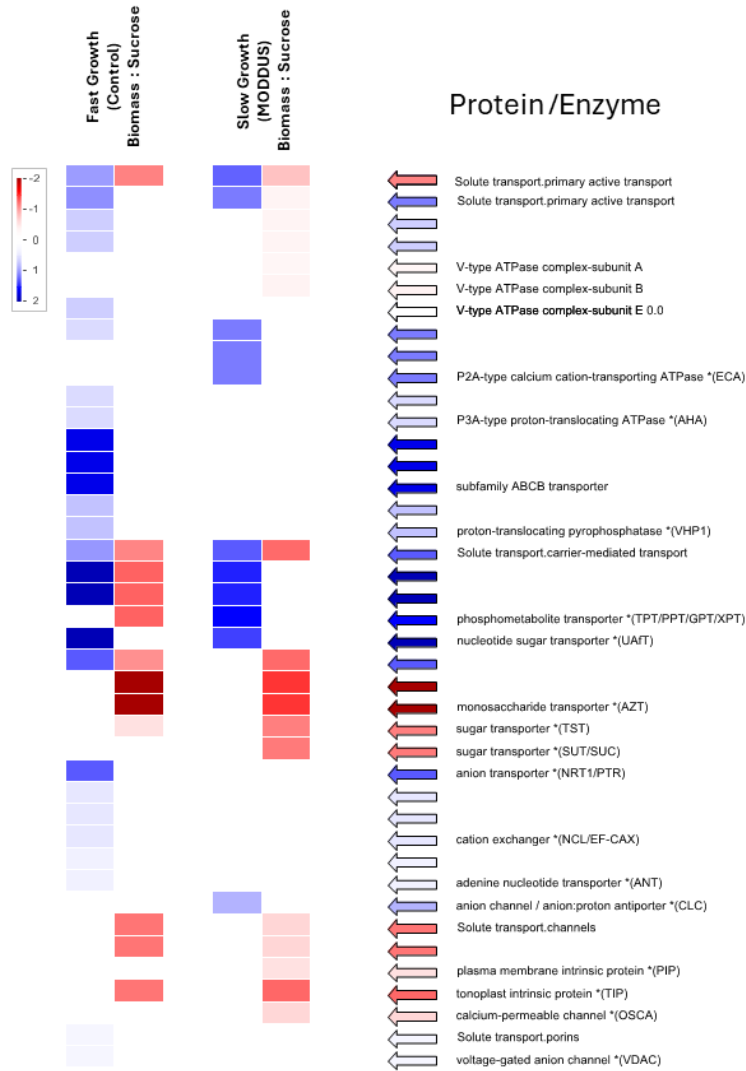


Figure S12: PageMan Analysis of the differential expression of proteins associated with vacuolar metabolism (Mapman BINCode 2) at different stages of internode development. The significant log2 fold change in expression values were used as input (FDR $p < 0.05$). Comparison is between internodes at peak biomass and sucrose accumulation in the control and MODDUS treated tissue. Blue implies higher expression in the biomass accumulation phase and red higher expression during sucrose accumulation.