

Table S2. Gene ontology enrichment and clustering of identified proteins in both Yucatan green dwarf (YGD) and Mexican pacific tall (MPT) (Core) or exclusively in YGD or MPT. For this analysis we used *Arabidopsis* protein homologs.

Core

WARNING - This exported Revigo data is only useful for the specific purpose of constructing a TreeMap visualization.

Do not use this table as a general list of non-redundant GO categories, as it sets an extremely permissive

threshold to detect redundancies ($c=0.10$) and fill the 'representative' column, while normally $c \geq 0.4$ is recommended.

To export a reduced-redundancy set of GO terms, go to the Scatterplot or Table tab, and export from there.

TermID	Name	Frequency	Value	Uniqueness	Dispensability	Representative
GO:0000226	microtubule cytoskeleton organization	0.340003	1.3678	0.988612	0.01040522	null
GO:0000278	mitotic cell cycle	0.386399	1.3678	0.988494	0.01052856	null
GO:0005975	carbohydrate metabolic process	5.826191	2.1907	0.933809	0.09069475	null
GO:0006096	glycolytic process	0.532551	22.149	0.648503	0	null
GO:0006108	malate metabolic process	0.054243	2.3475	0.884456	0.35081898	glycolytic process
GO:0010499	proteasomal ubiquitin-independent protein catabolic process	0.008394	6.7258	0.843223	0.37012795	glycolytic process
GO:0030388	fructose 1,6-bisphosphate metabolic process	0.012265	1.209	0.90986	0.36108737	glycolytic process
GO:0006457	protein folding	1.03808	12.777	0.987502	0.01158996	null
GO:0006734	NADH metabolic process	0.056712	1.4374	0.972475	0.0311262	null
GO:0007017	microtubule-based process	0.798415	1.9585	0.987781	0.01208936	null

GO:0015977	carbon fixation	0.050302	1.2859	0.96267	0.04453891	null
GO:0015979	photosynthesis	0.217587	1.4538	0.948841	0.06099619	null
GO:0045454	cell redox homeostasis	0.177877	2.7017	0.982087	0.00982244	null
GO:0032889	regulation of vacuole fusion, non-autophagic	0.000623	1.8008	0.992874	0.13563283	cell redox homeostasis
GO:0046686	response to cadmium ion	0.008823	41.215	0.804765	0	null
GO:0009408	response to heat	0.171454	5.7167	0.767998	0.21152305	response to cadmium ion
GO:0009615	response to virus	0.170613	1.7198	0.85991	0.26069386	response to cadmium ion
GO:0046685	response to arsenic-containing substance	0.01847	1.0885	0.815745	0.35730895	response to cadmium ion
GO:0051085	chaperone cofactor-dependent protein refolding	0.016725	8.2175	0.961239	0.00815552	null

Only Yucatan green dwarf (YGD)

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TermID	Name	Frequency	Value	Uniqueness	Dispensability	Representative
GO:0001558	regulation of cell growth	0.07213	1.28418	10.988	0	null
GO:0006457	protein folding	1.03808	7.60033	233745	0	null
GO:0006633	fatty acid biosynthetic process	0.75035	3.28483	0.74744286	0.01201001	null

GO:000		0.037	-	0.851		fatty acid
9298	GDP-mannose biosynthetic process	38	1.75	71838	0.2499	biosynthetic process
			374	8	6828	
GO:000		0.069	-			
6890	retrograde vesicle-mediated transport, Golgi to endoplasmic reticulum	58	1.00	1	0	null
				0.988		
GO:000		0.798	1.06	47352	0.0120	
7017	microtubule-based process	42	986	5	8936	null
GO:000		0.021	-			
9793	embryo development ending in seed dormancy	3	2.00	1	0	null
				0.931		
GO:004		0.092	3.93	44712	0.0098	
2026	protein refolding	36	554	1	3271	null
				0.788		
GO:004		0.008	17.5	62100		
6686	response to cadmium ion	82	331	6	0	null
				0.777		
GO:000		0.171	7.92	93993	0.2115	response to
9408	response to heat	45	082	7	2305	cadmium ion
				0.855		
GO:000		0.170	2.20	65905	0.2606	response to
9615	response to virus	61	337	1	9386	cadmium ion

Only Mexican pacific tall (MPT)

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TermID	Name	Frequency	Value	Uniqueness	Dispensability	Representative
			-			
			1.8	0.928		
GO:0005		5.8261	279	6656	0.090	
975	carbohydrate metabolic process	9	9	35	37153	null
			-			
			1.0	0.938		
GO:1901	carbohydrate derivative metabolic process	6.8137	690	3445	0.103	carbohydrate metabolic process
135		2	3	21	35243	

			-				
			4.4	0.863			
GO:0006099	tricarboxylic acid cycle	0.5173	762	8390			
		8	5	13	0	null	
			-	0.987			
GO:0006457	protein folding	1.0380	2.4	7121	0.012		
		8	677	61	32809	null	
			-				
			3.0	0.987			
GO:0007010	cytoskeleton organization	0.9577	710	7934	0.011		
		8	9	7	46205	null	
			-				
			1.8	0.946			
GO:0009793	embryo development ending in seed dormancy		105	0531			
		0.0213	6	88	0	null	
			-				
			1.0				
GO:0015031	protein transport	2.7257	707				
		1	7	1	0	null	
			-				
			1.2	0.943			
GO:0015979	photosynthesis	0.2175	812	4241	0.060		
		9	7	56	84153	null	
			-				
			1.4	0.833			
GO:0033356	UDP-L-arabinose metabolic process	0.0033	341	8947	0.047		
		3	4	42	03988	null	
			-				
			1.3	0.816			
GO:0006097	glyoxylate cycle	0.0538	685	4135	0.268	UDP-L-arabinose metabolic process	
		4	3	07	65503		
			-				
			1.3	0.822			
GO:0006101	citrate metabolic process	0.0108	685	7418	0.164	UDP-L-arabinose metabolic process	
		5	3	41	39007		
			-				
			1.2	0.784			
GO:0006536	glutamate metabolic process	0.2023	176	5563	0.325	UDP-L-arabinose metabolic process	
		5	4	98	9023		
			-				
			1.2	0.874			
GO:0015995	chlorophyll biosynthetic process	0.0477	306	9338	0.132	UDP-L-arabinose metabolic process	
		8	1	66	8704		
			-	0.839			
GO:0035999	tetrahydrofolate interconversion	0.1589	1.0	9656	0.205	UDP-L-arabinose metabolic process	
		1	482	81	20025		
			-				
			1.6	0.848			
GO:0042744	hydrogen peroxide catabolic process	0.1227	420	2478	0.057		
		2	2	04	92981	null	
				0.806			
GO:0046686	response to cadmium ion	0.0088	-	8122			
		2	23.	61	0	null	

			064				
			5				
			-				
			2.0	0.812			
GO:0009		0.0302	682	3304	0.190	response to cadmium	
651	response to salt stress	7	3	35	48836	ion	
			-				
			1.5	0.986			
GO:0080	negative regulation of response to	0.0001	119	8542			
148	water deprivation	8	8	61	0	null	
			-				
			1.4	0.969		negative regulation of	
GO:0045		0.1778	597	2513	0.116	response to water	
454	cell redox homeostasis	8	2	92	69074	deprivation	
			-				
			1.7	0.978		negative regulation of	
GO:0051		10.176	311	3476	0.288	response to water	
252	regulation of RNA metabolic process	5	5	48	32307	deprivation	