

Table S7. Regulation pattern of among differentially expressed genes (DEGs) related to photosynthesis and biochemical processes. in plants of *Coffea canephora* cv. Conilon Clone CL153 (CL153) and *C. arabica* cv. Icatu (Icatu) submitted to moderate water deficit (MWD) and severe water deficit (SWD) relative to the control, well-watered (WW) plants. DEGs were selected if annotated with the direct or respective child Gene Ontology (GO) terms “antioxidant activity” (GO:0016209) and/or “response to oxidative stress” (GO:0006979) [Antioxidant activity], “cellular respiration” (GO:0045333), “mitochondrion” (GO:0005739), “malate dehydrogenase activity” (GO:0016615), “pyruvate kinase activity” (GO:0004743) [Cellular respiration], “fatty acid metabolic process” (GO:0006631), LOX (GO:0004051, GO:0016702) [Lipid metabolism], “photosynthesis” (GO:0015979), “photosystem” (GO:0009521), “photosynthetic electron transport chain” (GO:0009767), “photorespiration” (GO:0009853) and/or “chlorophyll biosynthetic process” (GO:0015995) [Photosynthesis]. Red represent up-regulated DEGs and blue represent down-regulated DEGs.

Gene ID	Homolog		log ₂ FC			
	Gene Name	Protein Name	CL153		Icatu	
			MWD	SWD	MWD	SWD
Antioxidant activity						
Cc06_g21030		Peroxidase 44	7,72			
Cc07_g14740	AT2G22420	Peroxidase 17	4,48	5,41		
Cc00_g17550	AT1G05260	Peroxidase 3	4,2			
Cc06_g12610		Peroxiredoxin Q, chloroplastic	-2,05	-2,18		-2,22
Cc10_g15150	AT1G71695	Peroxidase 12		5,02		
Cc06_g03490	AT3G09640	L-ascorbate peroxidase 2, cytosolic		3,65		
Cc00_g17550	AT1G05260	Peroxidase 3		2,86		
Cc10_g12080		L-ascorbate peroxidase T, chloroplastic		1,2		1,23
Cc04_g06610		alpha dioxygenase		-1,36		
Cc08_g00640		Putative L-ascorbate peroxidase 2, cytosolic		-1,38		
Cc09_g01700	AT4G21960	Peroxidase 42		-1,92	-3,08	-5,57
Cc06_g00570	AT1G14550	Cationic peroxidase 1		-2,21	-4,57	
Cc07_g02590	AT5G40150	Peroxidase 63		-2,51	-3,05	-2,14
Cc02_g21960		Peroxidase 43		-2,57	-2,87	-4,08

Cc05_g08480	AT5G05340	Peroxidase 4	-2,59	-2,48	-5,46
Cc07_g06870	AT5G67400	Peroxidase 73	-2,62	-3,88	
Cc06_g13090	AT2G18980	Peroxidase 16	-3,35		
Cc07_g11210	AT5G42180	Peroxidase 64	-4,36	-9,85	-10,37
Cc06_g08460		Peroxidase 25		-2,71	
Cc01_g15110		Peroxidase 4		-3,55	
Cc00_g00940		Peroxidase 47		-5,09	
Cc07_g17340		Peroxidase 5		-6,87	
Cc07_g02500	AT3G01420	Peroxidase superfamily protein			2,94
Cc10_g06720	AT4G09010	Thylakoid lumenal 29 kDa protein. chloroplastic			-2,35
Cc01_g10280	AT2G28190	Superoxide dismutase [Cu-Zn], chloroplastic			-2,38
Cc03_g02460	AT1G08830	Superoxide dismutase [Cu-Zn]			-2,61
Cc02_g03550		Peroxidase 66			-9,1
Cc07_g11210	AT5G42180	Peroxidase 64			
Cc06_g08070	AT3G57520	Probable galactinol--sucrose galactosyltransferase 6	3,52	2,84	2,47
Cc04_g04320		Putative Tetratricopeptide repeat (TPR)-like superfamily protein	-1,3		
Cc03_g02760	AT4G21860	Peptide methionine sulfoxide reductase B3, chloroplastic	-2,68	-3,5	
Cc01_g04080		Putative Long-chain-fatty-acid--AMP ligase FadD28		5	
Cc10_g00570	AT4G35090	Catalase		3,32	
Cc09_g02320		Elongator complex protein 6		1,62	1,96
Cc04_g03820		Putative Monoglyceride lipase	-1,53	-1,5	-1,75
Cc11_g10330		Putative uncharacterized protein	-1,67		
Cc00_g20670	AT5G43750	NAD(P)H dehydrogenase 18	-1,72		
Cc08_g11220		peptidyl-prolyl cis-trans isomerases	-2,92		-2,65
Cc07_g13330		15.7 kDa heat shock protein. peroxisomal		2,59	
Cc07_g02770	AT3G28340	Probable galacturonosyltransferase-like 9		3,86	
Cc06_g16900		GTP-binding protein TypA/BipA homolog			-2,09

Cellular respiration					
Cc05_g11180	AT3G14940	Phosphoenolpyruvate carboxylase	-3,82	-3,7	-4,08
Cc04_g10080	AT5G03860	Malate synthase, glyoxysomal	2,79		
Cc03_g02560	AT5G18800	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8-B	-1,5		
Cc11_g10810	AT1G68750	Phosphoenolpyruvate carboxylase 4	-1,66		-1,79
Cc06_g20970		Succinate dehydrogenase [ubiquinone] iron-sulfur subunit 2, mitochondrial	-1,25		
Cc06_g13830	AT2G18700	Probable alpha.alpha-trehalose-phosphate synthase [UDP-forming] 11	3,01	4	2,57
Cc03_g02940	AT5G35630	Glutamine synthetase leaf isozyme, chloroplastic	-1,66	-1,9	-1,83
Cc09_g01490	AT1G11860	Aminomethyltransferase, mitochondrial	-2,81	-3,36	-3,16
Cc08_g01750	AT4G28060	Cytochrome c oxidase subunit 6b-3	-5,71	-5,32	
Cc04_g15520		Putative Mitochondrial outer membrane protein porin of 36 kDa	-5,75	-10,93	
Cc07_g05130	AT2G23790	Putative Protein of unknown function (DUF607)		2,94	
Cc11_g17430	AT5G50850	Pyruvate dehydrogenase E1 component subunit beta. mitochondrial		2,83	
Cc06_g11140	AT4G26180	Putative Graves disease carrier protein		2,19	
Cc02_g00270		Putative ATPase family AAA domain-containing protein 3-A		2,02	
Cc00_g21200	AT3G06500	Plant neutral invertase family protein		1,94	
Cc02_g21470	AT5G09420	Outer envelope protein 64, mitochondrial		1,83	
Cc07_g07860	AT5G09590	Heat shock 70 kDa protein, mitochondrial		1,83	
Cc02_g09270		Mitochondrial glycoprotein family protein		1,7	
Cc02_g27440	AT5G48030	Putative Chaperone protein dnaJ 1, mitochondrial		1,65	
Cc08_g05000		Anamorsin homolog		1,56	
Cc09_g03060		Solanesyl diphosphate synthase 3, chloroplastic/mitochondrial		1,51	
Cc05_g13790		CRS2-associated factor 2, mitochondrial		1,5	
Cc09_g01900		Putative Cardiolipin synthase		1,45	
Cc05_g14280		Co-chaperone GrpE family protein		1,41	
Cc11_g00600		Dihydroorotate dehydrogenase (quinone), mitochondrial		1,37	
Cc04_g15410		Probable aldehyde dehydrogenase		1,32	

Cc11_g14960		Transaldolase		1,3	
Cc03_g07290		3-ketoacyl-CoA thiolase 2. peroxisomal		1,1	
Cc06_g12530		20 kDa chaperonin. chloroplastic		-1,19	
Cc07_g14260	AT2G22500	Putative Probable mitochondrial 2-oxoglutarate/malate carrier protein		-1,79	
Cc01_g13710	AT5G58970	Putative Mitochondrial uncoupling protein 3		-1,9	
Cc04_g07800	AT5G23060	Calcium sensing receptor, chloroplastic	-2,06	-1,47	
Cc09_g06160	AT5G14780	Formate dehydrogenase, mitochondrial		-2,45	
Cc04_g04190		Putative Pentatricopeptide repeat-containing protein Atlg52620			3,32
Cc11_g04410		Pyridine nucleotide-disulfide oxidoreductase domain-containing protein 2			1,14
Cc00_g08170		Putative Heat shock protein 90			1
Cc07_g01900		Cytochrome c oxidase subunit 5C			3,36
Cc06_g11140	AT4G26180	Putative Graves disease carrier protein			2,36
Cc01_g15620		Protein of unknown function (DUF607)			-1,49
Cc11_g15490		Alpha-glucan water dikinase, chloroplastic			-1,73
Cc08_g02390	AT1G32470	Glycine cleavage system H protein, mitochondrial			-2,2
Cc06_g10370		NADP-dependent malic enzyme			1,55
Cc02_g20400	AT2G22780	Malate dehydrogenase, glyoxysomal			-2,41
Cc02_g20400	AT2G22780	Malate dehydrogenase, glyoxysomal	-2,25		
Cc04_g09680		Pyruvate kinase, cytosolic isozyme	-6,34		
Cc02_g02100		Plastidial pyruvate kinase 2	1,46		
Cc11_g00360	AT4G26390	Pyruvate kinase, cytosolic isozyme	-1,42		
Cc08_g02330		Pyruvate kinase isozyme G, chloroplastic	-1,24		
Lipid metabolism					
Cc11_g10180	AT1G68530	3-ketoacyl-CoA synthase 6	8,39	9,65	
Cc06_g09070	AT2G26640	3-ketoacyl-CoA synthase 11	2,35	3,47	
Cc05_g07170		Two pore calcium channel protein 1A	1,84		
Cc01_g16760	AT3G25110	Oleoyl-acyl carrier protein thioesterase, chloroplastic (Fragment)	-1,34		

Cc02_g39890	AT1G01120	3-ketoacyl-CoA synthase 1	-1,38		
Cc04_g04380	AT3G15850	Palmitoyl-monogalactosyldiacylglycerol delta-7 desaturase, chloroplastic	-1,64	-1,18	
Cc08_g07790	AT2G26250	3-ketoacyl-CoA synthase 10	-2,06		
Cc11_g17510	AT1G54630	Acyl carrier protein 1, chloroplastic	-2,7		
Cc07_g08840	AT1G68530	3-ketoacyl-CoA synthase 6	-3,07		
Cc03_g04570	AT1G04220	3-ketoacyl-CoA synthase 17	-3,84	-4,6	
Cc08_g11520	AT4G24510	Putative HXXXD-type acyl-transferase family protein	-4,34		
Cc11_g10190	AT1G68530	3-ketoacyl-CoA synthase 6	-5,18		
Cc00_g14020	AT5G04530	3-ketoacyl-CoA synthase 21	-5,66		
Cc04_g01940	AT1G72970	Protein HOTHEAD	-9,61	-5,86	
Cc02_g22540		3-ketoacyl-CoA synthase 7		5,1	
Cc03_g04540	AT1G04220	3-ketoacyl-CoA synthase 17		4,19	
Cc02_g37010	AT2G45670	Putative Lysophosphatidylcholine acyltransferase 2		1,48	
Cc00_g17690		rhomboid-like protein 11		1,28	
Cc01_g16760	AT3G25110	Oleoyl-acyl carrier protein thioesterase, chloroplastic (Fragment)	-1,53		-2,62
Cc02_g39890	AT1G01120	3-ketoacyl-CoA synthase 1	-1,9		-1,87
Cc01_g19410	AT3G63170	Chalcone-flavanone isomerase family protein	-1,96		
Cc11_g17510	AT1G54630	Acyl carrier protein 1, chloroplastic	-2,38		-4,62
Cc01_g16740		Oleoyl-acyl carrier protein thioesterase, chloroplastic (Fragment)	-2,61		
Cc08_g07790	AT2G26250	3-ketoacyl-CoA synthase 10	-2,64		-1,79
Cc11_g10190	AT1G68530	3-ketoacyl-CoA synthase 6	-4,69	-2,16	
Cc07_g08840	AT1G68530	3-ketoacyl-CoA synthase 6	-5,26	-1,75	
Cc00_g14020	AT5G04530	3-ketoacyl-CoA synthase 21	-6,77	-3,62	
Cc08_g11520	AT4G24510	Putative HXXXD-type acyl-transferase family protein	-9,84		-6,68
Cc07_g08840	AT1G68530	3-ketoacyl-CoA synthase 6			-5,96
Cc11_g10190	AT1G68530	3-ketoacyl-CoA synthase 6			-7,39
Cc00_g14020	AT5G04530	3-ketoacyl-CoA synthase 21			-8,88
Cc07_g03350		Myb-related protein 306		-4,66	-4,11

Cc10_g05850		Acetyl-CoA carboxylase 1				-1,68
Cc11_g01680		3-ketoacyl-CoA synthase 11				-2,05
Cc07_g14130		3-hydroxyacyl-CoA dehydratase PASTICCINO 2				-2,71
Cc03_g04550		3-ketoacyl-CoA synthase 17				-6,75
Cc02_g33320	AT1G55020	Probable linoleate 9S-lipoxygenase 5	3,82		-1,98	-4,25
Cc03_g03580	AT3G22400	Linoleate 9S-lipoxygenase 5, chloroplastic				-2,98
Cc02_g13400		Linoleate 13S-lipoxygenase 3-1, chloroplastic				-7,8
Cc01_g04060	AT3G45140	Linoleate 13S-lipoxygenase 2-1, chloroplastic		-3,37		
Cc02_g33790	AT1G55020	Probable linoleate 9S-lipoxygenase 5		3,07		
Photosynthesis						
Cc00_g15710	AT1G67090	Ribulose biphosphate carboxylase small chain SSU11A, chloroplastic	-2,23	-2,76		-2,39
Cc10_g12590		Photosystem I reaction center subunit N, chloroplastic		-3,91		-3,04
Cc06_g22740	AT3G56940	Magnesium-protoporphyrin IX monomethyl ester [oxidative] cyclase, chloroplastic		-3,54		-2,96
Cc04_g03050	AT3G16140	Photosystem I reaction center subunit VI, chloroplastic		-2,34		-2,45
Cc09_g08490	AT1G30380	Photosystem I reaction center subunit psaK, chloroplastic		-5,08		-2,4
Cc07_g18500	AT5G45930	Magnesium-chelatase subunit chlI, chloroplastic				-2,28
Cc08_g01300		photosystem II subunit X		-3,99		-2,28
Cc01_g15890	AT4G12800	Photosystem I reaction center subunit XI, chloroplastic		-2,69		-2,08
Cc10_g14740	AT1G43670	Fructose-1.6-bisphosphatase, cytosolic				-2,23
Cc03_g03590	AT1G03130	Photosystem I reaction center subunit II, chloroplastic		-2,7		-1,94
Cc01_g18800	AT2G30570	Photosystem II reaction center W protein, chloroplastic		-2,97		-2,11
Cc02_g09420		Unknown protein		-3,17		-2,09
Cc11_g16230	AT1G67740	Photosystem II core complex proteins psbY, chloroplastic		-2,84		-1,87
Cc01_g06000		Magnesium-chelatase subunit chlD, chloroplastic				-1,3
Cc01_g17500	AT2G20260	Photosystem I reaction center subunit IV A, chloroplastic		-2,09		-1,5
Cc05_g06850	AT1G03630	Protochlorophyllide reductase, chloroplastic		-2,7		-1,63
Cc05_g12370	AT5G54190	Protochlorophyllide reductase, chloroplastic		-2,36		

Cc10_g04190	AT1G45474	Chlorophyll a-b binding protein P4, chloroplastic	-3,96	-5,37	-5,13
Cc10_g16210	AT4G10340	Chlorophyll a-b binding protein CP26, chloroplastic		-4,15	-3,24
Cc09_g09500	AT2G05100	Chlorophyll a-b binding protein 36, chloroplastic		-3,31	-2,42
Cc09_g09010		Chlorophyll a-b binding protein 21, chloroplastic			-3,8
Cc02_g21720	AT1G45474	Chlorophyll a-b binding protein CP24 10A, chloroplastic		-3,58	-2,76
Cc07_g00260	AT5G54270	Chlorophyll a-b binding protein 13, chloroplastic			-4,01
Cc09_g09020	AT1G29930	Chlorophyll a-b binding protein 21, chloroplastic		-5,71	-2,8
Cc05_g09650	AT1G29930	Chlorophyll a-b binding protein 1, chloroplastic			-6,82
Cc09_g02010	AT3G54890	Chlorophyll a-b binding protein 6A, chloroplastic		-3,99	-2,33
Cc04_g16410	AT3G47470	Chlorophyll a-b binding protein 4, chloroplastic		-5,78	-2,81
Cc11_g16910	AT3G61470	Chlorophyll a-b binding protein, chloroplastic		-3	-1,5
Cc05_g09930	AT1G61520	Chlorophyll a-b binding protein 8, chloroplastic		-2,89	-1,7
Cc06_g01460	AT3G08940	Chlorophyll a-b binding protein CP29.2, chloroplastic		-3,06	-1,72
Cc09_g09030	AT1G29930	Chlorophyll a-b binding protein 21, chloroplastic		-4,48	
Cc05_g12720	AT5G54270	Chlorophyll a-b binding protein 13, chloroplastic		-5,28	-3,52
Cc01_g17770		Photosystem II reaction center PSB28 protein. chloroplastic	-2,08		
Cc02_g35130	AT4G15510	PsbP domain-containing protein 1. chloroplastic	-1,59	-1,83	-1,77
Cc02_g11770	AT4G05180	Oxygen-evolving enhancer protein 3-2. chloroplastic		-4,19	-4,44
Cc05_g00840	AT1G06680	Oxygen-evolving enhancer protein 2. chloroplastic		-2,47	-2,12
Cc05_g15930	AT1G79040	Photosystem II 10 kDa polypeptide. chloroplastic		-2,56	-2,05
Cc07_g05350	AT3G50820	Oxygen-evolving enhancer protein 1. chloroplastic		-2,07	-1,86
Cc11_g04720		PsbP-like protein 1. chloroplastic			-2,24
Cc01_g17770		Photosystem II reaction center PSB28 protein. chloroplastic		-1,94	-1,92
Cc02_g31060	AT3G05410	Photosystem II reaction center PsbP family protein		-2,05	-1,74
Cc02_g33910	AT2G28605	Predicted protein (Fragment)			-1,71
Cc02_g32670	AT1G54780	UPF0603 protein At1g54780. chloroplastic	-1,94	-2,38	-1,55
Cc07_g02170	AT3G27925	Protease Do-like 1. chloroplastic		-1,57	-1,56
Cc05_g11580		Putative Predicted protein	-2,96	-2,7	-3,63

Cc05_g06070	AT2G20890	Protein THYLAKOID FORMATION1. chloroplastic		-2,22	-1,41
Cc05_g06750	AT1G03600	Thylakoid lumenal protein At1g03610. chloroplastic		-2,19	-1,63
Cc08_g05240	AT4G19100	Protein PAM68. chloroplastic		-2,27	
Cc01_g08780	AT1G08380	photosystem I subunit O		-4,74	-2,83
Cc04_g03080		Putative Glyoxylate reductase		-1,28	
Cc06_g17100	AT5G13630	Putative Magnesium-chelatase subunit H		-3,35	-3
Cc05_g12410		Putative COP1-interacting protein 7			-1,7
Cc01_g19080	AT1G19670	Putative Chlorophyllase-1	-4,39	-6,7	-3,88
Cc10_g00150		Hypothetical protein		-1,4	