Table S1. Differentially abundant proteins in *Eucalyptus urophylla* x *Eucalyptus grandis* polyploid plants (G1 to G5) against the isogenic diploid (G6).

Comparison [a]	Accession [b]	Description [c]	LFQ [d]	*p*-value [e]	FC [f]
G1xG6	Eucgr.B03166.3	Glycosyl transferase, family 35	18.10	1.84	1.27
G1xG6	Eucgr.C00990.1	6-phosphogluconate dehydrogenase family protein	17.96	1.38	1.46
G1xG6	Eucgr.E00233.1	Shikimate kinase like 2	19.11	1.41	1.01
G1xG6	Eucgr.I00535.2	Histone superfamily protein	19.63	1.49	1.01
G1xG6	Eucgr.G03258.4	Scarecrow-like 3	17.10	1.81	1.03
G1xG6	Eucgr.J01502.1	Ribulose bisphosphate carboxylase (small chain) family protein	22.44	1.31	1.13
G1xG6	Eucgr.J02986.1	Putative methyltransferase family protein	19.87	1.55	1.19
G1xG6	Eucgr.K01671.1	Mog1/PsbP/DUF1795-like photosystem II reaction center PsbP family protein	17.32	1.99	1.00
G2xG6	Eucgr.B03013.1	Ribulose bisphosphate carboxylase (small chain) family protein	21.14	1.47	1.60
G2xG6	Eucgr.H00726.1	Lactoylglutathione lyase / glyoxalase I family protein	20.08	1.47	1.42
G2xG6	Eucgr.J01354.1	Ribosomal protein S2	20.12	1.33	1.26
G2xG6	Eucgr.J02208.1	Formate dehydrogenase	18.70	1.53	1.24
G3xG6	Eucgr.C03953.1	ATP binding	16.87	2.41	1.05
G3xG6	Eucgr.E03981.1	Fibrillin	17.20	2.17	1.17
G3xG6	Eucgr.G02327.1	Alpha-xylosidase 1	16.38	1.41	1.15
G3xG6	Eucgr.H04692.1	Heat shock protein 21	15.04	1.82	4.84
G3xG6	Eucgr.I01263.1	Coatomer gamma-2 subunit, putative	17.25	1.40	1.07
G3xG6	Eucgr.I01982.1	Casein lytic proteinase B3	16.86	1.65	2.01
G3xG6	Eucgr.J00176.1	Ferritin 4	16.64	1.53	2.29
G3xG6	Eucgr.J00766.1	Chaperonin-like RbcX protein	17.55	1.39	1.13
G3xG6	Eucgr.J01823.1	ACD1-like	17.38	1.32	1.03
G3xG6	Eucgr.L02860.1	Heat shock protein	16.77	1.61	2.17
G5xG6	Eucgr.F01077.1	Light-harvesting chlorophyll B-binding protein 3	16.91	1.73	1.08
G5xG6	Eucgr.G00777.1	Light harvesting complex photosystem II subunit 6	18.28	1.35	1.47

[a] Pairwise comparison; [b] *Eucalyptus grandis* identifier in the Phytozome portal; [c] Functional annotation; [d] Normalized protein abundance (log_2). [e] -log *p*-value (t-test). [f] log_2 fold-change.

Table S2. Differentially abundant proteins in *Eucalyptus urophylla* x *Eucalyptus grandis* polyploid plants (G1 to G5) against the isogenic diploid (G6) upon cultivation in different CO_2-enriched (eCO_2) and high-temperature (HT) conditions for 30 days.

Accession[a]	**Description**[b]	**LFQ**[c]		
		eCO_2	**HT**	**eCO_2+HT**
Genotype G1				
Eucgr.B02310.1	Rubisco activase	-	14.66	14.04
Eucgr.E01107.1	Cinnamyl-alcohol dehydrogenase	-	-16.06	-14.83
Eucgr.H03983.1	MLP-like protein 423	-	-13.83	-13.42
Eucgr.J01502.1	Ribulose bisphosphate carboxylase (small chain) family protein	-	-16.37	-15.53
Eucgr.I00535.2	Histone superfamily protein	-15.89	-15.77	-
Eucgr.A01711.1	Ribosomal protein L6 family	-	-	15.95
Eucgr.B01744.1	O-methyltransferase 1	-	-	15.28
Eucgr.F02835.1	PfkB-like carbohydrate kinase family protein	-	-	14.23
Eucgr.F03538.1	SKU5 similar 5	-	-	17.13
Eucgr.J00819.1	Lipoxygenase 2	-	-	14.44
Eucgr.A00020.1	Homolog of carrot EP3-3 chitinase	-	-	-14.02
Eucgr.A00159.1	MLP-like protein 423	-	-	-13.14
Eucgr.B00144.1	Glyceraldehyde-3-phosphate dehydrogenase C subunit 1	-	-	-12.58
Eucgr.D01888.1	Osmotin 34	-	-	-13.73
Eucgr.H00972.1	Chaperone protein htpG family protein	-	-	-13.45
Eucgr.H02295.1	Acetamidase/Formamidase family protein	-	-	-12.91
Genotype G2				
Eucgr.J02986.1	Putative methyltransferase family protein	17.07	-	17.10

Eucgr.G01960.3	Acyl carrier protein 4	-15.38	-	-14.96
Eucgr.K03545.1	CP12 domain-containing protein 1	-14.15	-	-13.61
Eucgr.D01707.2	ARM repeat superfamily protein	-12.77	-12.83	-12.55
Eucgr.E01416.1	N-terminal nucleophile aminohydrolases (Ntn hydrolases) superfamily protein	-12.70	-11.92	-12.37
Eucgr.F01878.1	Ribosomal protein L31	-14.53	16.79	-
Eucgr.K00881.1	Terpene synthase 03	13.78	13.67	-
Eucgr.J00176.1	Ferritin 4	-14.80	-14.55	-
Eucgr.G03258.4	Scarecrow-like 3	-	-	14.60
Eucgr.H01629.1	Thioredoxin F2	-	-	14.55
Eucgr.H03041.1	NAD(P)-linked oxidoreductase superfamily protein	-	-	13.82
Eucgr.J00820.1	Lipoxygenase 2	-	-	14.14
Eucgr.K02223.1	Ribulose bisphosphate carboxylase (small chain) family protein	-	-	15.13
Eucgr.B01262.2	Acyl carrier protein 3	-	-	-14.08
Eucgr.D01888.1	Osmotin 34	-	-	-14.76
Eucgr.D02461.1	Ribosomal protein S13A	-	-	-13.99
Eucgr.F01428.1	Glutathione S-transferase TAU 19	-	-	-13.43
Eucgr.I00535.2	Histone superfamily protein	-	-	-14.75
Eucgr.H03865.1	Osmotin 34	-	-	-13.90
Genotype G3				
Eucgr.G03258.4	Scarecrow-like 3	14.33	-	14.49
Eucgr.K03545.1	CP12 domain-containing protein 1	-14.19	-	-13.87
Eucgr.J01502.1	Ribulose bisphosphate carboxylase (small chain) family protein	16.32	-	-15.20
Eucgr.J00431.1	Phosphoglycerate/bisphosphoglycerate mutase family protein	-	13.47	13.58
Eucgr.J00819.1	Lipoxygenase 2	-	14.42	14.66

Eucgr.J00820.1	Lipoxygenase 2	-	14.32	15.01
Eucgr.K01283.1	Lipid transfer protein 1	-	-15.40	-15.75
Eucgr.A01915.2	Phosphoenolpyruvate carboxylase 3	-	-	15.28
Eucgr.A02451.1	Plastid-lipid associated protein PAP / fibrillin family protein	-	-	15.14
Eucgr.B03573.1	Translation protein SH3-like family protein	-	-	15.47
Eucgr.B03013.1	Ribulose bisphosphate carboxylase (small chain) family protein	-	-	14.51
Eucgr.B03067.2	Phosphoenolpyruvate carboxylase 4	-	-	14.28
Eucgr.C01003.3	NADP-malic enzyme 3	-	-	14.42
Eucgr.C03415.3	Lycopene beta/epsilon cyclase protein	-	-	19.23
Eucgr.E00628.3	Plasma membrane intrinsic protein 1B	-	-	14.21
Eucgr.H00206.1	Sieve element occlusion B*	-	-	15.42
Eucgr.H01172.1	Glutathione S-transferase 6	-	-	16.77
Eucgr.H03041.1	NAD(P)-linked oxidoreductase superfamily protein	-	-	14.71
Eucgr.J00237.2	Plasma membrane intrinsic protein 1;4	-	-	12.96
Eucgr.K02223.1	Ribulose bisphosphate carboxylase (small chain) family protein	-	-	15.50
Eucgr.A00746.1	Lipid transfer protein 1	-	-	-15.20
Eucgr.B01262.2	acyl carrier protein 3	-	-	-14.22
Eucgr.B01760.1	Copper/zinc superoxide dismutase 1	-	-	-13.85
Eucgr.B02879.1	FAD/NAD(P)-binding oxidoreductase	-	-	-13.17
Eucgr.D01115.1	Ribosomal protein L3 family protein	-	-	-13.55
Eucgr.D02179.2	Single hybrid motif superfamily protein	-	-	-15.13
Eucgr.I00535.2	Histone superfamily protein	-	-	-14.93
Eucgr.H02279.1	Subtilase family protein	-	-	-12.56
Eucgr.J00657.1	Glutathione S-transferase, C-terminal-like;Translation elongation factor EF1B	-	-	-15.93
Eucgr.J01250.1	RNA-binding (RRM/RBD/RNP motifs) family protein	-	-	-14.54
Genotype G4				
Eucgr.B02495.1	4-hydroxy-3-methylbut-2-enyl diphosphate synthase	13.44	-	13.26

Eucgr.H01629.1	Thioredoxin F2	14.37	-	14.47
Eucgr.F01428.1	Glutathione S-transferase TAU 19	-13.81	-	-13.73
Eucgr.I01643.1	Ribosomal protein large subunit 27	-15.77	-	-15.94
Eucgr.A01241.1	Histone H2A 12	-	17.23	17.32
Eucgr.B00335.1	Aldehyde dehydrogenase 10A8	-	14.98	15.13
Eucgr.F02551.1	Rubredoxin-like superfamily protein	-	13.30	13.41
Eucgr.H00206.1	Sieve element occlusion B*	-	14.91	14.68
Eucgr.H01176.4	Glutathione S-transferase 6	-	14.88	15.07
Eucgr.K03300.3	Winged-helix DNA-binding transcription factor family protein	-	16.20	15.90
Eucgr.H02489.1	Mog1/PsbP/DUF1795-like photosystem II reaction center PsbP family protein	-	-13.74	-13.73
Eucgr.B02162.1	Photosystem I subunit E-2	-14.02	-14.79	-14.25
Eucgr.D00319.1	Chlorophyll A/B binding protein 1	-14.55	-15.54	-15.39
Eucgr.J01502.1	Ribulose bisphosphate carboxylase (small chain) family protein	-16.53	-15.73	-15.94
Eucgr.B01744.1	O-methyltransferase 1	-	-	14.49
Eucgr.H04433.2	Gamma histone variant H2AX	-	-	17.55
Eucgr.D01798.1	VIRB2-interacting protein 1	-	-	13.24
Eucgr.E00001.1	NmrA-like negative transcriptional regulator family protein	-	-	13.68
Eucgr.E03875.1	O-methyltransferase 1	-	-	13.83
Eucgr.H01235.1	Geranylgeranyl pyrophosphate synthase 1	-	-	12.55
Eucgr.H03423.1	Ribosomal protein S3Ae	-	-	15.19
Eucgr.I01803.1	Oxidoreductase, zinc-binding dehydrogenase family protein	-	-	16.42
Eucgr.I01807.1	Oxidoreductase, zinc-binding dehydrogenase family protein	-	-	12.83
Eucgr.K02223.1	Ribulose bisphosphate carboxylase (small chain) family protein	-	-	14.94
Eucgr.B01262.2	Acyl carrier protein 3	-	-	-14.05
Eucgr.D00322.1	Light-harvesting chlorophyll-protein complex II subunit B1	-	-	-18.10
Eucgr.D01115.1	Ribosomal protein L3 family protein	-	-	-13.68
Eucgr.D02588.1	Breast basic conserved 1	-	-	-14.92

Eucgr.F02754.1	Thioredoxin superfamily protein	-	-	-17.07
Eucgr.J01096.1	Photosystem I light harvesting complex gene 1	-	-	-15.49
Eucgr.K03545.1	CP12 domain-containing protein 1	-	-	-13.24
Genotype G5				
Eucgr.C00846.1	Pyridoxal-5\'-phosphate-dependent enzyme family protein	12.90	-	12.80
Eucgr.H01235.1	Geranylgeranyl pyrophosphate synthase 1	13.07	-	12.79
Eucgr.K01508.1	Cobalamin-independent synthase family protein	14.05	-	13.64
Eucgr.L03049.1	Thioredoxin M-type 4	-16.35	-	-15.88
Eucgr.L00271.3	Inorganic H pyrophosphatase family protein	-15.24	-	-15.39
Eucgr.B02310.1	Rubisco activase	-	14.58	14.22
Eucgr.J00176.1	Ferritin 4	-	16.59	16.72
Eucgr.J00820.1	Lipoxygenase 2	-	14.42	14.48
Eucgr.B01262.2	Acyl carrier protein 3	-	-14.50	-14.43
Eucgr.I00441.1	Ribosomal L29 family protein	-	-14.71	-14.27
Eucgr.B02294.2	Adenine nucleotide alpha hydrolases-like superfamily protein	14.80	15.08	15.01
Eucgr.B02495.1	4-hydroxy-3-methylbut-2-enyl diphosphate synthase	13.28	13.22	13.58
Eucgr.C03415.3	Lycopene beta/epsilon cyclase protein	18.51	18.55	18.76
Eucgr.F01428.1	Glutathione S-transferase TAU 19	-14.11	-13.66	-13.27
Eucgr.H03865.1	Osmotin 34	-14.48	-14.09	-
Eucgr.E03613.1	Plastid developmental protein DAG, putative	-	-	13.56
Eucgr.H01629.1	Thioredoxin F2	-	-	14.63
Eucgr.H02333.1	Thioredoxin superfamily protein	-	-	16.48
Eucgr.H02679.1	Serine hydroxymethyltransferase 4	-	-	14.82
Eucgr.J01372.1	UDP-glucose 6-dehydrogenase family protein	-	-	13.79
Eucgr.A00020.1	Homolog of carrot EP3-3 chitinase	-	-	-14.06

Eucgr.A02337.1	NADPH-dependent thioredoxin reductase C	-	-	-14.18
Eucgr.D02339.2	Uncharacterized protein	-	-	-16.28
Eucgr.F00208.1	Subtilisin-like serine endopeptidase family protein	-	-	-12.83
Eucgr.H00143.1	ATP citrate lyase (ACL) family protein	-	-	-14.41
Eucgr.H03983.1	MLP-like protein 423	-	-	-13.83
Eucgr.J01771.1	ARM repeat superfamily protein	-	-	-20.32
Genotype G6				
Eucgr.G03258.4	Scarecrow-like 3	-	13.58	9.27
Eucgr.B01747.2	O-methyltransferase 1	-	14.35	14.47
Eucgr.J00820.1	Lipoxygenase 2	-	-13.46	-13.18
Eucgr.F02130.1	G-box regulating factor 6	-	-15.43	-15.95
Eucgr.B03013.1	Ribulose bisphosphate carboxylase (small chain) family protein	-	-	15.55
Eucgr.C03415.3	Lycopene beta/epsilon cyclase protein	-	-	19.07
Eucgr.L00627.1	Temperature-induced lipocalin	-	-	10.09
Eucgr.G01289.2	SWIB/MDM2 domain superfamily protein	-	-	9.86
Eucgr.K02223.1	Ribulose bisphosphate carboxylase (small chain) family protein	-	-	15.58
Eucgr.E00872.1	UDP-D-glucose/UDP-D-galactose 4-epimerase 5	-	-	-12.70
Eucgr.E02058.1	Uncharacterized protein	-	-	-16.86
Eucgr.E02747.1	General regulatory factor 9	-	-	-14.20
Eucgr.F02017.1	Aldolase superfamily protein	-	-	-13.23
Eucgr.G01960.3	Acyl carrier protein 4	-	-	-14.71
Eucgr.H01016.1	CP12 domain-containing protein 2	-	-	-13.24
Eucgr.K03545.1	CP12 domain-containing protein 1	-	-	-13.29

[a] *Eucalyptus grandis* identifier in the Phytozome portal; [b] Functional annotation. [c] Normalized protein abundance (in $\log_2$). HT= 29°C vs 25°C; eCO_2: 680vs420 ppm. Negative values indicate down-regulation. Positive values indicate up-regulation.