

**Table S3.** Number of total expressed genes in *Coffea arabica* cv. Icatu (Icatu) and *C. canephora* cv. CL153 (CL153), number of differentially expressed genes (DEGs) detected by DESeq2 and edgeR, with log2 fold-change (FC)  $\neq 0$  and false discovery rate (FDR)  $< 0.01$ , and number of overlapping DEGs from both analyses (% DEGs relative to the average of genes expressed by treated and control plants). Plants were grown in three different water conditions, well-watered (control), moderate water deficit (MWD), and severe water deficit (SWD), under either ambient air 380  $\mu\text{L L}^{-1}$  [ $\text{CO}_2$ ] (aCO<sub>2</sub>) or elevated 700  $\mu\text{L L}^{-1}$  [ $\text{CO}_2$ ] (eCO<sub>2</sub>), at 25/20 °C (day/night). DEGs represent the number of significant genes found to be differently expressed between each stress water treatment and the control (respectively, MWD vs. WW and SWD vs. WW) [overlap % is the proportion of DEGs detected by both edgeR and DESeq2 related to the average of genes expressed by control and treated plants].

Genotype	Water	[CO <sub>2</sub> ]	Expressed genes		DEGs					
			Control	Test	DESeq2	edgeR	Overlapped			
							Total	%	Up	Down
Icatu	MWD	aCO <sub>2</sub>	29519	29960	714	1026	548	1.84	66	482
		eCO <sub>2</sub>	31041	29223	47	227	35	0.12	27	8
	SWD	aCO <sub>2</sub>	29519	29199	2259	2436	1673	5.70	313	1360
		eCO <sub>2</sub>	31041	29222	3670	3810	2940	9.76	859	2081
CL153	MWD	aCO <sub>2</sub>	20463	20001	953	1165	704	3.48	295	409
		eCO <sub>2</sub>	19818	19912	71	284	47	0.24	17	30
	SWD	aCO <sub>2</sub>	20463	20348	3251	3150	2576	12.62	725	1851
		eCO <sub>2</sub>	19818	19558	2793	2691	2040	10.36	768	1272