Transcriptional regulation of the glucose-6-phosphate/Phosphate translocator 2 is related to carbon exchange across the chloroplast envelope

Supplementary Tables and Figures

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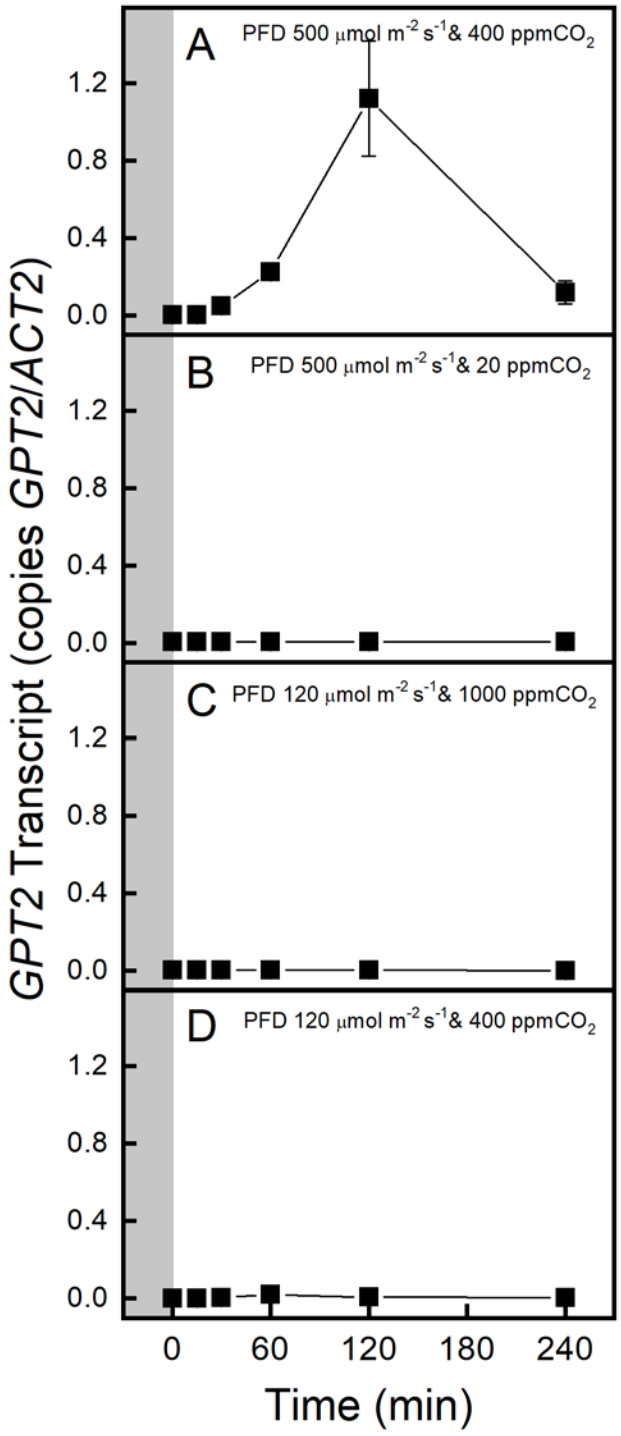
Supplementary Table S1. Primer sequences used in this study

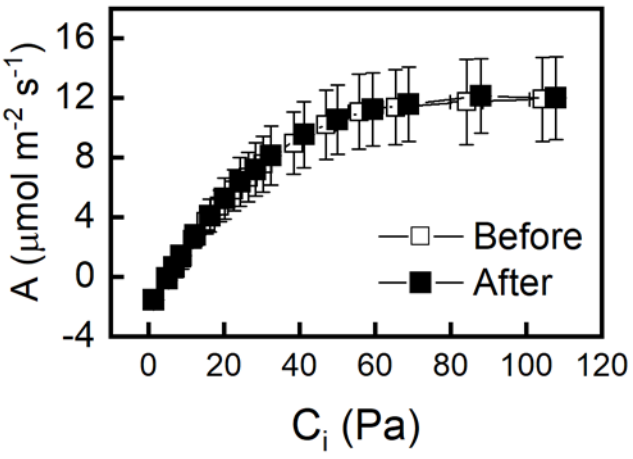
Gene	Gene Locus	Standard Generating Primers	qPCR primers
ACT2	At3g18780	GGTGATGAAGCACAATCCAA CAGTAAGGTCACGTCCAGCA	CAAAGGCCAACAGAGAGAAGA ATCACCAGAATCCAGCACAA
IDI2	At3g02780	CCGAATTTTCGTGCTTTCTC TGCAGCATTCCTCACACCTA	GTATGAGTTGCTTCTCCAGCAAAG GAGGATGGCTGCAACAAGTGT
GPT2	At1g61800	CGTGGAAGGTCCTCAAATGT TCACTGCTTCGCCTGTGAGT	AGACCAGATTTCGCCGTTAACT ACTGCTTCGCCTGTGAGTAGAG
XPT	At5g17630	AGGATCACATTGGGTTCCAG CTTTGCAGTGGCCTGAGAAT	CATTGCATCTGTTGGGACAC TGGACTGATCTCGTCGAGTG
G6PDH1	At5g35790	GAGAATGGCTGGACAAGGGT GCCGGTGTGAATAGATCCCA	ATTTCGGAACAGAAGGGCGT CAACCACATCTTCAAGCCGC
G6PDH2	At5g13110	TGGAAGAATCTCAAACCGCCT AGCCTCTCATATGCATCTGGT	ATTTCGGCACTGAAGGACGT GCGTTTCCATGGCAAAGAGG
G6PDH3	At1g24280	GAGTCTGATGGCGGTGAACA CTGCAAATGTCGGGGTCAGA	TGCATTGGACGAGAAGCTCA CACATTTCACCGCGTCAACA
RRTF1	At4g34410	CCCAACCCGGTATCAAAAGGA CTTGGCCCACGGAATCCAAT	GCCTCGGTTGGATTCAGACA TGATTTTCCCGCCACCTTCC

Supplementary Table S2. Specific differentially expressed *Arabidopsis* genes and loci used in heat maps in figure 4 and supplementary figure S5.

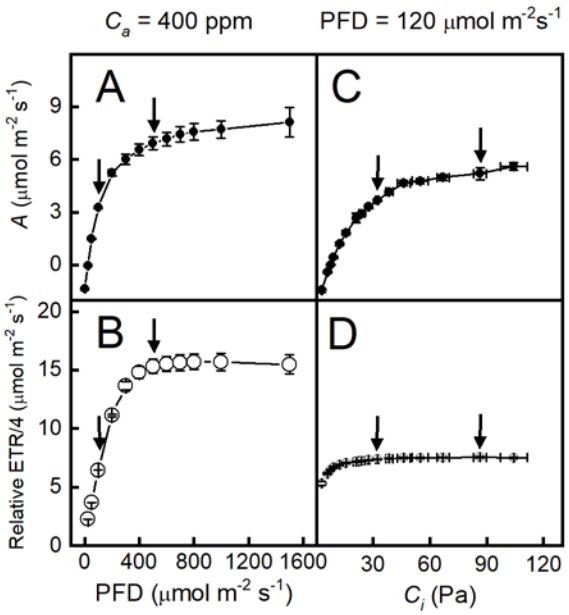
Gene	Locus	Gene	Locus
Calvin-Benson Cycle		**TP to G6P**	
RBCS1A	At1g67090	*TPT*	At5g46110
RBCS1B	At5g38430	*TPI*	At3g55440
RBCS2B	At5g38420	*FBA5*	At4g26530
RBCS3B	At5g38410	*FBA6*	At2g36460
RCA	At2g39730	*FBA7*	At4g26520
GAPA	At3g26650	*GPT2*	At1g61800
GAPA2	At1g12900	**G6P to TP**	
FBA2	At4g38970	*PFPβ1*	At4g04040
CFBP2	At5g64380	**G6P to Sucrose**	
SBPASE	At3g55800	*UGP2*	At5g17310
PRK	At1g32060	*SPS3*	At1g04920
CP12-2	At3g62410	*SPS4*	At4g10120
Starch Synthesis		*SPP2*	At2g35840
APL2	At1g27680	*G6PDH1*	At5g35790
APL3	At4g39210	*G6PDH2*	At5g13110
APL4	At2g21590	*G6PDH3*	At1g24280
SS2	At3g01180	*GAPN*	At2g24270
SS3	At1g11720		
SS4	At4g18240		
GBSS1	At1g32900		
SBE1	At3g20440		
SBE3	At2g36390		
PHS1	At3g29320		
GWD	At1g10760		
PWD	At5g26570		



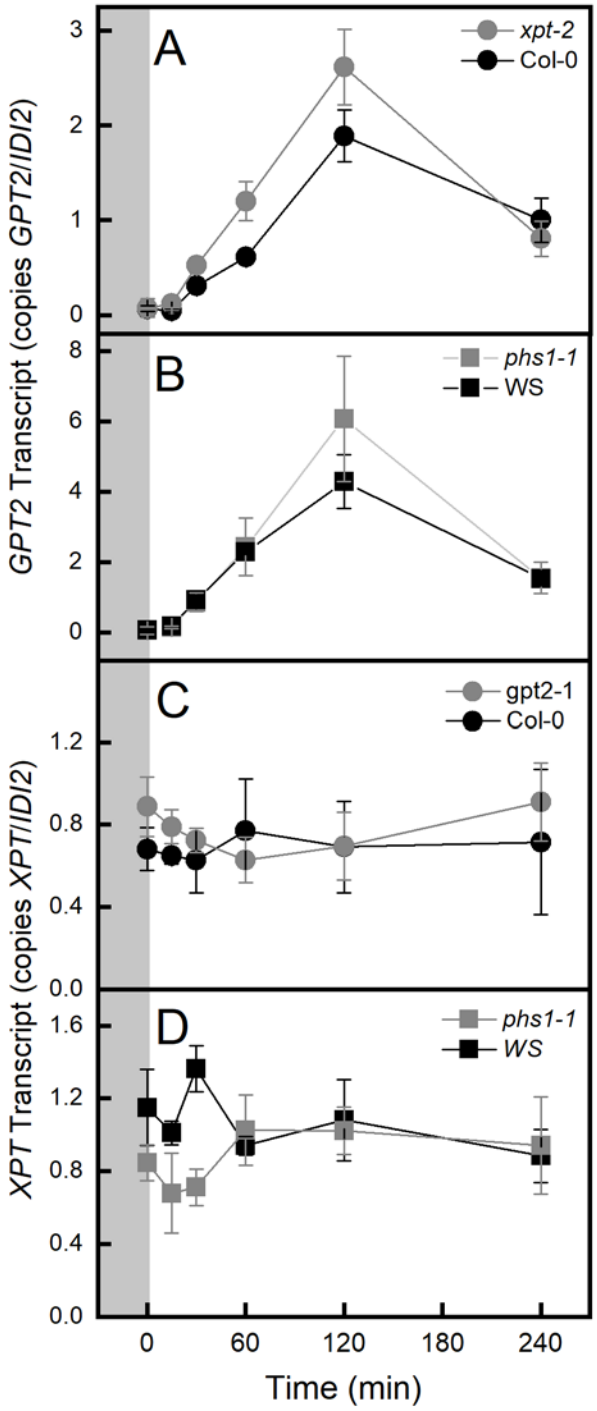
Supplementary Figure S1. Expression of *GPT2* in WS before and after transfer to an altered light or CO_2 environment. The grey block indicates sampling in growth conditions, PFD 120 µmol m^{-2} s^{-1} and 400 ppm CO_2. n = 5



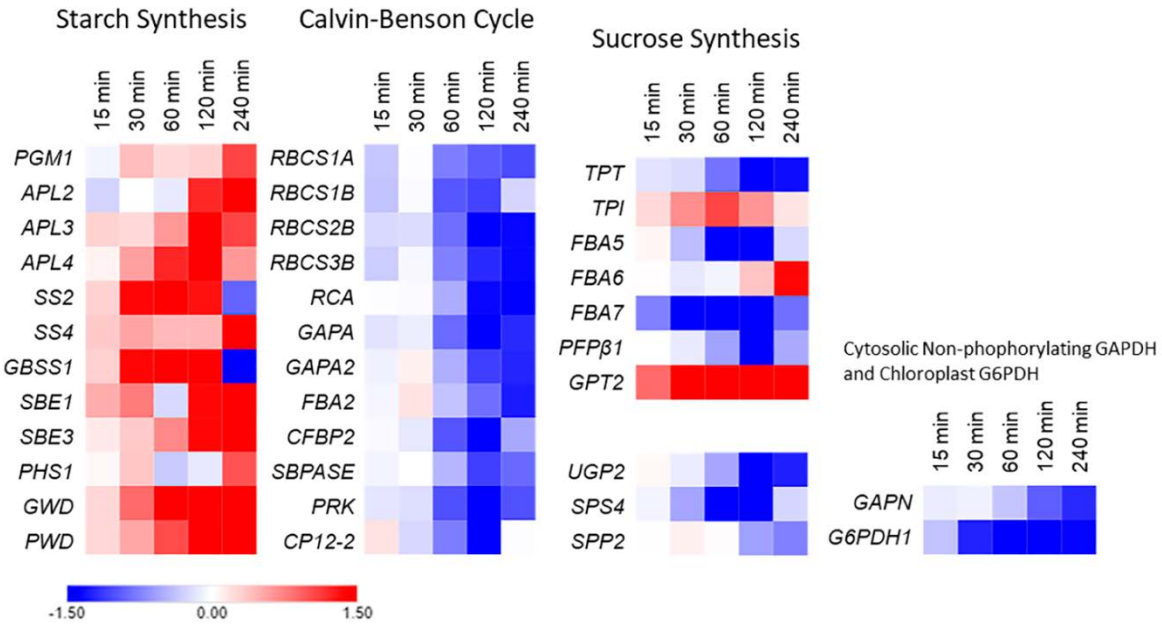
Supplementary Figure S2. A – C_i curves of WS taken before and after 4 hr incubation at a PFD of 500 µmol m_{-2} s^{-1} and C_a of 400 ppm. A – C_i curves were done at a PFD of 500 µmol m^{-2} s^{-1} n=5



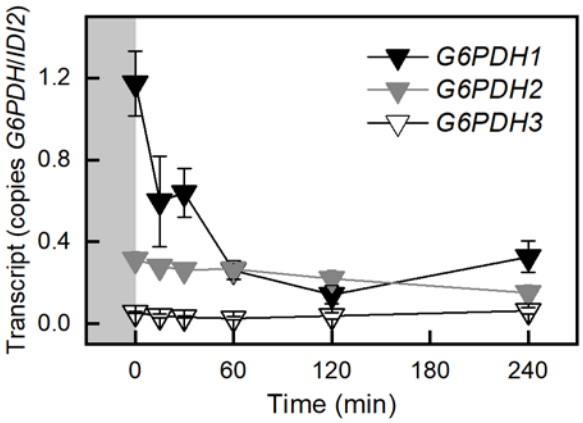
Supplementary Figure S3. Photosynthetic and relative electron transport (ETR) rates in Col-0 in varying light and CO_2 environments. Arrows indicate the PFD or average C_i values that correspond to the PFD or C_a values used in transcript experiments. ETR/4 is taken as the relative approximate rate of the Calvin-Benson cycle turnover. n=5



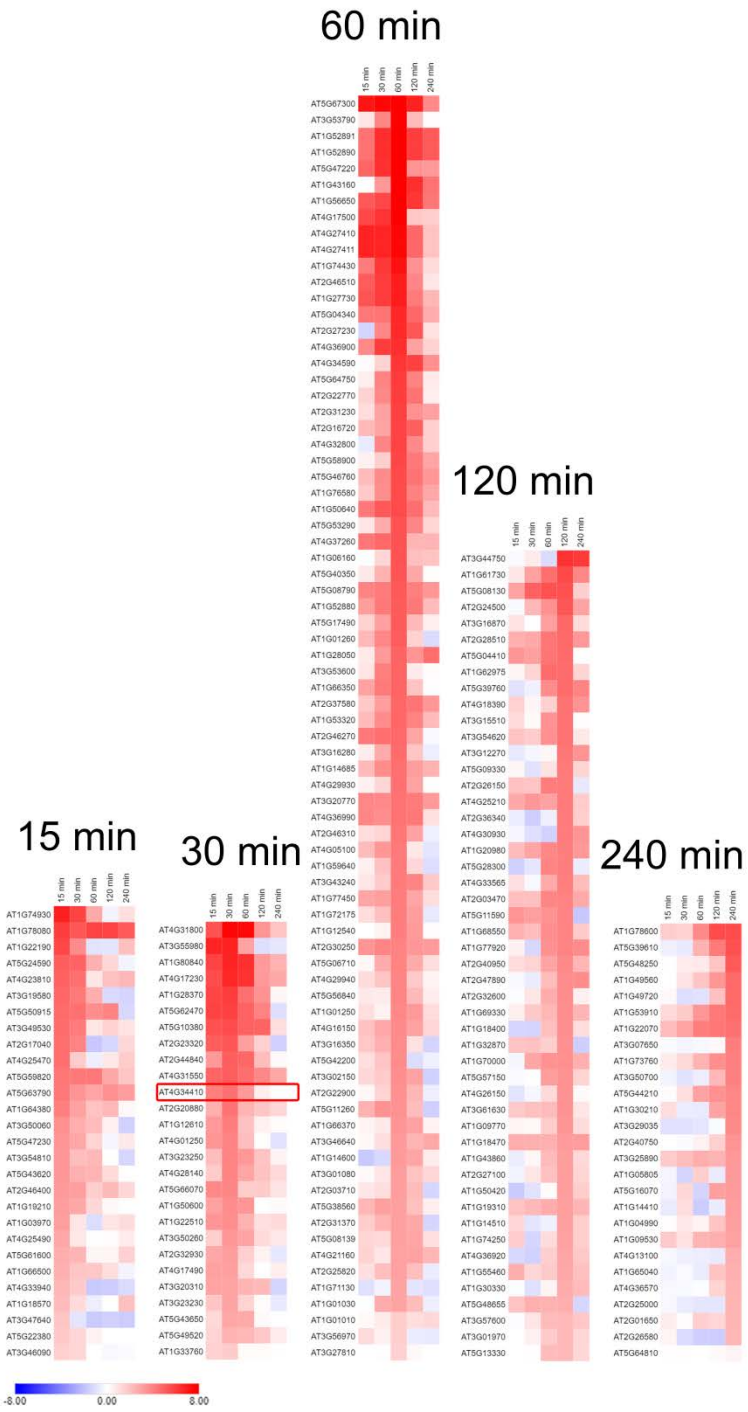
Supplementary Figure S4. Expression of *GPT2* and *XPT* in *xpt-2*, *gpt2-1*, and *phs1-1* mutants in response to a PFD of 500 µmol m^{-2} s^{-1} C_a of 400 ppm. The grey block indicates sampling in growth conditions, PFD 120 µmol m^{-2} s^{-1} and 400 ppm CO_2. n = 5



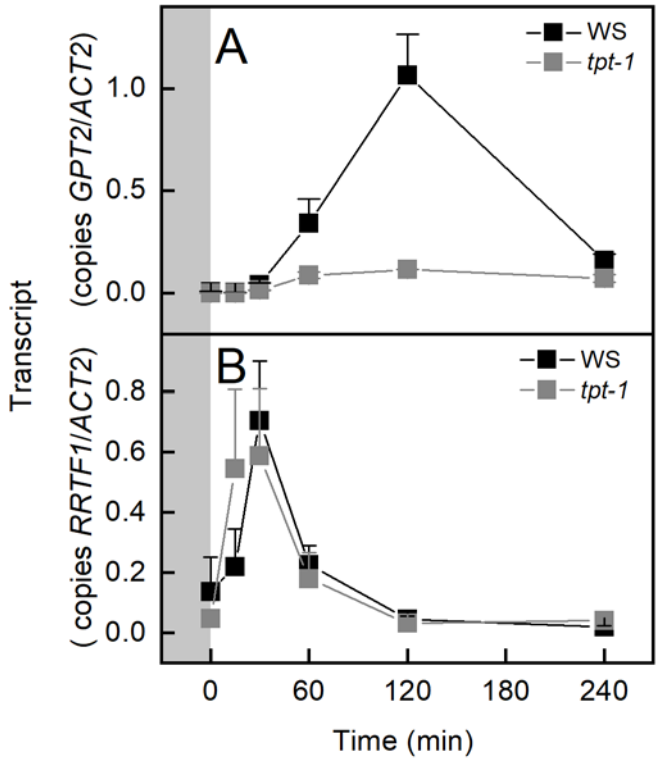
Supplementary Figure S5. Changes in transcription in WS in response to an increase in PFD from 120 to 500 µmol m^{-2} s^{-1}. Red boxes represent an increase in transcription and blue a decrease. Expression values shown had a $\log_2$ RPKM fold change greater than1 and are on an absolute scale of -1.5 to 1.5 n=3



Supplementary Figure S6. Changes in transcription of the plastid *G6PDH*s in WS in response to a PFD of 500 µmol m^{-2} s^{-1} C_a 400 ppm. Grey block indicates sampling in growth conditions, PFD 120 µmol m^{-2} s^{-1} and 400 ppm CO_2. n=5



Supplementary Figure S7. Transcription factors in WS whose expression was increased in response to an increase in PFD from 120 to 500 µmol m^{-2} s^{-1}. Transcription factors are grouped according to the time they had the highest transcript abundance after transfer to high light. The red box is around the *RRTF1* transcription factor. Expression values used for heat map generation are the $\log_2$ ΔRPKM + 1 and are on an absolute scale of -8 to 8. n=3



Supplementary Figure S8. Expression of *GPT2* and *RRTF1* in response to an increase in PFD from 120 to 500 µmol m^{-2} s^{-1} C_a 400 ppm in WS and the *tpt-1* mutant. Grey block indicates sampling in growth conditions, PFD 120 µmol m^{-2} s^{-1} and 400 ppm CO_2. n=5