



Supplementary materials

Table S1. Correlation values according to Guilford [69] between the transcription level of the evaluate genes related to different processes under normal white light.

	T abl e S1	Photorecep- tors				Circadian clock			Redox-re- sponsive TFs			Nitrate reduction				Glutathione metabolism				Antioxidant enzymes						Thiols						
		P h y A	C r y 1 a	C r y 1 b	C r y 2	C C A 1	T O C 1	P R R 73	O X S 2	A R F - lik e	m T R E F	N R	G L N a	G L N b	G L N d	G L N e	A P S R	γ- E C S	G S T	G R	A P X 1	A P X 4	C A T 1	C A T 2	C A T 4	P R X	C y S	C y S S	Ec yS/ Cys s	G S H	G S S G	EG SH/ GSSG
Photoreceptors	Ph yA		0.20	0.08	0.036	-0.022	0.070	-0.006	0.016	0.41	0.12	-0.06	-0.011	0.017	0.014	0.039	0.099	0.037	0.022	0.060	0.011	0.012	0.051	0.036	0.017	0.048	0.011	0.019	0.014	0.010	0.023	0.011
	Cr yl a			0.095	-0.006	0.054	0.006	-0.005	0.047	0.16	0.84	0.074	0.014	0.061	0.071	0.022	0.006	0.033	0.024	0.006	0.067	0.050	0.001	0.031	0.062	0.016	0.006	0.026	0.018	0.020	0.027	0.007
	Cr yl b				-0.008	0.064	0.004	-0.001	0.050	0.15	0.89	0.079	0.013	0.064	0.071	0.011	0.006	0.030	0.010	0.022	0.067	0.051	0.007	0.030	0.067	0.008	0.021	0.038	0.029	0.008	0.028	0.002

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A RF - lik e										0. 26	- 0 . 2 8	0. 1 9	0. 2 8	0. 3 5	0. 4 9	0. 1 7	0. 6 2	0 . 7 9	0 . 8 3	0 . 6 7	0. 5 7	- 0 . 1 4	0 . 1 5	0 . 2 0	0. 0 8	- 0 . 0 8	0 . 3 0	- 0 . 2 7	- 0 . 3 3	
	m T R EF									0 . 6 3	0. 2 3	0. 6 3	0. 7 3	0. 0 7	0. 1 0	0. 3 9	0 . 1 0	0 . 1 9	0. 6 5	0. 6 0	0. 0 5	0. 5 8	0 . 1 8	0 . 1 3	- 0 . 3 0	0. 0 17	- 0 . 1 8	- 0 . 3 4	0.0 7	
Nitrate reduction	N R											0. 1 1	0. 6 3	0. 6 0	- 0 . 1 2	0. 1 0	0. 1 6	- 0 . 1 5	0 . 1 1	0. 4 1	0. 3 4	- 0 . 4 4	0 . 0 8	0 . 1 0	- 0 . 2 9	0. 0 22	- 0 . 2 3	0. 0 2	0.1 6	
	G L Na												0. 2 7	0. 3 5	0. 6 5	0. 2 5	0. 4 4	0 . 1 7	0 . 3 7	0. 6 2	0. 3 0	0. 2 9	0. 4 8	0 . 4 4	- 0 . 0 7	0. 0 2	- 0 . 0 04	- 0 . 1 5	0. 1 0	0.1 1
	G L Nb													0. 9 1	0. 1 8	0. 0 0	0. 7 9	0 . 2 6	0 . 3 9	0. 7 4	0. 0 2	0. 7 7	0. 6 9	0 . 5 1	0 . 2 0	- 0 . 3 4	0. 0 28	- 0 . 1 2	0. 1 7	0.0 0
	G L Nd															0. 2 4	0. 0 9	0. 8 1	- 0 . 0 .	0 . 0 5	0. 8 6	0. 0 7	0. 7 0	0. 7 2	0 . 0 .	0 . 0 .	- 0 . 0 .	0 . 0 .	0.1 1	

[illegible]

Antioxidant enzymes	AP X1																			0. 8 2	- 0 5	0. 6 8	0. 7 7	0 6 1	0 1 9	- 0 3	- 0 28	- 0 1 0	- 0 3 0	- 0 0 3
	AP X4																			0. 0 7	0. 5 6	0. 6 3	0 5 3	0 0 7	0. 4 3	- 0 18	- 0 2 0	- 0 3 2	0.0 7	
	C A T1																				0. 4 1	0. 1 7	0 0 9	0 0 9	0. 2 9	0. 16	- 0 3	- 0 1	0.0 2	
	C A T2																					0. 3 4	0. 5 0	0 2 0	0. 9	- 0 25	0 0 3	0. 2 5	- 0 4	
	C A T4																						0 4 3	0 2 0	0. 3	- 0 31	0 1 4	- 0 9	0.0 6	
	PR X																								0 0 .	0. 6	0. 03	- 0 .	0. 1 4	0.1 5

[illegible]

* If correlation value is: < 0.20 - slight; almost negligible relationship; 0.20 - 0.40 - low correlation; definite but small relationship; 0.40 - 0.70 - moderate correlation; substantial relationship (green cells); 0.70 - 0.90 - high correlation; marked relationship (brown cells); 0.90 - 1.00 - very high correlation; very dependable relationship (black cells).

Table S2. Correlation values according to Guilford [69] between the transcription level of the evaluate genes related to different processes under additional blue light.

Table S2	Photoreceptors				Circadian clock				Redox-responsive TFs			Nitrate reduction				Glutathione metabolism				Antioxidant enzymes						Thiols					
	PhyA	Cry1a	Cry1b	Cry2	CYC1	CYC2	PRR73	ORF2	ARF-like	mTRF	NR	GLN	GLN	GLN	GLN	APSR	γ-EC	GST	GR	APX1	APX4	CAT1	CAT2	CAT4	PXR	CysS	CysS	ECS/CysS	GSH	GS SG	ECS H/GSSG
Photoreceptors	PhyA	0.81	0.80	0.14	0.17	-0.10	0.12	0.09	0.64	0.63	0.14	-0.05	0.34	0.36	0.15	-0.04	0.30	0.03	-0.28	0.23	0.00	0.14	0.40	-0.32	0.06	0.03	-0.08	0.03	-0.33	0.06	0.00
	Cry1a		0.98	0.01	0.54	-0.29	0.09	0.04	0.31	0.75	0.26	-0.03	0.53	0.55	0.15	-0.04	0.24	0.03	-0.44	0.42	0.05	0.21	0.00	0.11	0.03	0.00	0.00	0.00	0.40	-0.01	0.12
	Cry1b			0.01	0.62	-0.34	0.10	0.08	0.34	0.75	0.31	-0.04	0.49	0.57	0.16	-0.05	0.24	0.03	-0.38	0.47	0.11	0.21	0.11	0.10	0.03	0.13	0.30	0.00	0.42	-0.04	0.13
	Cry2				-0.32	0.33	0.65	0.26	0.28	-0.12	0.31	0.00	0.21	0.31	0.20	-0.05	0.41	0.00	-0.42	0.41	0.05	0.51	0.24	0.66	0.09	0.01	0.13	0.00	0.03	-0.07	0.05
Circadian	CC1					-0.58	-0.20	0.10	-0.35	0.33	0.49	-0.03	0.40	0.42	0.20	-0.07	0.11	0.08	-0.42	0.45	0.45	0.43	0.13	0.43	0.01	0.17	0.25	0.02	0.45	-0.06	0.20

	TO C1							- 0.0 6	0.2 4		- 0.25 03	- 0.1 6	- 0.0 4	- 0.0 5	0.1 0	0.3 6	0.4 0	0. 15	0. 65	- 0.2 8	- 0.1 9	0.4 3	0.2 5	- 0.4 7	- 0. 08	- 0. 07	0. 32	0.1 9	0. 28	0.3 7	- 0.03
								- 0.4 1		- 0. 08	- 0.02 30	0.3 6	0.3 3	0.3 3	0.1 9	0.1 2	0.0 5	0. 36	0. 10	0.3 2	0.1 0	0.3 3	0.0 7	0.2 3	0. 20	0. 05	0. 18	0.0 1	0. 37	0.1 8	0.00
Redox-responsive FEs	OX S2									- 0. 77	- 0.08	- 0.0 9	0.5 7	0.4 4	0.8 0	0.2 5	0.4 8	- 0. 22	0. 14	0.1 1	0.0 6	- 0.0 7	0.3 0	0.2 7	0. 05	- 0. 42	0. 09	0.3 5	0. 22	0.1 4	0.31
	AR F- like									0.51	- 0. 19	- 0.2 5	0.1 4	0.0 8	0.1 4	- 0.4 0	0.2 2	0. 09	0. 09	0.1 8	- 0.2 5	0.3 8	0.3 4	- 0.5 5	- 0. 26	0. 08	- 0. 06	0.1 4	0. 10	0.1 7	- 0.16
	mT REF										0. 03	0.2 3	0.4 5	0.4 0	0.0 0	0.4 8	0.0 4	0. 06	0. 47	0.4 3	0.0 7	- 0.0 9	0.0 8	0.1 1	0. 49	0. 06	0. 12	0.0 5	0. 22	0.2 2	0.09
												- 0.1 1	0.7 1	0.7 0	0.9 2	0.2 1	0.2 4	- 0. 04	0. 09	0.1 5	0.2 1	0.3 1	0.0 8	0.4 1	- 0. 06	- 0. 34	0. 08	0. 7	0.3 26	0.0 5	0.23
Nitrate reduction	GL Na												- 0.2 7	- 0.2 5	- 0.0 3	- 0.0 4	- 0.0 8	- 0. 32	- 0.0 12	0.3 4	0.3 3	0.1 3	0.3 4	0. 07	- 0. 08	0. 24	0.1 5	0. 08	0.1 3	0.10	
	GL Nb													0.8 7	0.6 1	0.2 6	0.4 8	- 0. 14	0. 26	0.6 0	0.2 1	- 0.1 6	0.1 2	0.2 0	- 0. 29	- 0. 41	0. 00	0.3 9	0. 38	0.35	
	GL Nd														0.6 2	0.2 4	0.3 5	0. 11	0. 25	0.6 1	0.2 5	- 0.2 8	0.0 0	0.2 8	0. 18	- 0. 28	0. 10	0.3 5	0. 28	0.0 2	0.19

	GL Ne																0.2 6	0.3 6	- 04	- 09	0.0 2	- 4	- 0	0.0 1	0.3 4	- 16	- 42	0. 22	0.4 4	- 24	0. 8	0.35
Glutathione metabolism	APS R																	- 0.3 2	0. 16	0. 17	- 0.5 3	- 0.1 8	- 0.0 1	- 0.1 5	0.2 1	0. 09	- 0.1 10	0. 36	0.1 9	0. 29	0.3 7	0.02
	γ- ECS																	0. 01	0. 29	0.1 0	0.0 8	0.3 5	0.4 3	0.3 1	0. 22	0. 27	0. 02	0.1 8	0. 15	0.0 6	0.24	
	GST																	0. 03	0.2 5	0.0 8	0.0 5	0.0 8	0.1 7	0. 04	0. 33	0. 03	0.2 3	0. 29	0.0 5	- 0.40		
	GR																	0.2 2	0.0 8	0.3 0	0.6 6	0.2 9	0. 22	0. 10	0. 30	0.1 6	0. 32	0.3 5	- 0.03			
Antioxidant enzymes	AP X1																					0.4 7	- 0.3 0	0.0 8	0.2 5	- 0.1 12	- 0.1 24	0. 05	0.2 6	0. 24	0.0 2	0.25
	AP X4																						0.2 4	0.0 4	0.3 8	0. 02	- 0.1 32	0. 08	0.3 8	0. 06	0.0 7	0.17
	CA T1																							0.1 4	0.4 8	0. 19	0. 18	0. 15	0.1 2	0. 03	0.0 7	0.14
	CA T2																									- 0.2 9	- 0.1 14	- 0.1 21	- 0.1 02	0.0 4	0. 06	0.0 0

Thiol	CA T4																							0. 18	- 21	0. 11	0.2 9	- 04	0.1 1		0.14
	PR X																								0. 28	0. 08	0.2 0	0. 10	0.0 2	-	0.23
	CyS																									0. 46	- 0	0.9 30	0. 8	-	0.88
	CyS S																										0.7 3	0. 52	0.9 2		0.48
	E _{CyS} / CySS																											- 02	0.7 3		0.81
	GS H																												0.5 4	-	0.35
	GSS G																														0.53
	E _{GSH} / /GSSG																														

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Table S3. Correlation values according to Guilford [69] between the transcription level of the evaluate genes related to different processes under additional far-red light.

	Table S3	Photoreceptors				Circadian clock			Redox-responsive TFs			Nitrate reduction				Glutathione metabolism				Antioxidant enzymes						Thiols						
		PhyA	Cry1a	Cry1b	Cry2	CcA1	ToC1	PR73	OXS2	ARF-like	mTRF	NR	GLNa	GLNb	GLNd	GLNe	APSR	γ-EC	GS	GR	APX1	APX4	CAT1	CAT2	CAT4	Perox	CysS	CysS	ECysS	GSH	GS SG	EGSHGSSG
Photoreceptors	PhyA		0.21	0.26	0.34	0.15	0.02	0.15	0.03	0.20	0.18	0.02	0.22	0.05	0.06	0.09	0.41	0.04	0.14	0.04	0.10	0.10	0.13	0.01	0.14	0.20	0.47	0.10	0.37	0.16	0.26	0.31
	Cry1a			0.92	0.04	0.47	0.08	0.06	0.39	0.08	0.63	0.44	0.24	0.43	0.25	0.02	0.26	0.19	0.20	0.16	0.43	0.30	0.10	0.24	0.42	0.16	0.21	0.48	0.40	0.10	0.28	0.09
	Cry1b				0.11	0.49	0.21	0.02	0.45	0.04	0.64	0.50	0.23	0.47	0.23	0.18	0.16	0.19	0.01	0.13	0.51	0.31	0.07	0.29	0.47	0.13	0.45	0.55	0.05	0.47	0.30	
	Cry2					0.24	0.04	0.60	0.31	0.13	0.06	0.41	0.16	0.33	0.19	0.29	0.06	0.09	0.72	0.03	0.33	0.14	0.28	0.23	0.22	0.16	0.11	0.00	0.02	0.25	0.20	
Circadian clock	CC A1						0.29	0.15	0.42	0.22	0.36	0.48	0.25	0.44	0.28	0.24	0.63	0.13	0.13	0.03	0.37	0.38	0.25	0.19	0.52	0.31	0.14	0.23	0.33	0.21	0.25	0.05
	TO C1							0.09	0.52	0.44	0.08	0.27	0.30	0.52	0.68	0.37	0.19	0.76	0.06	0.74	0.53	0.54	0.16	0.66	0.28	0.41	0.05	0.01	0.06	0.17	0.14	

[illegible]

Glutathione metabolism	APSR																0.40	0.10	0.50	0.33	0.46	0.10	0.33	0.59	0.54	-09	-35	-00	-02	-01	-003
	γ-ECS																-08	0.091	0.87	0.93	0.28	0.96	0.74	0.56	-06	-24	-05	0.09	0.26	0.18	
	GST																0.02	0.36	0.09	0.26	0.25	0.17	0.09	0.37	0.18	0.04	0.17	0.28	0.34		
	GR																		0.71	0.78	0.50	0.84	0.72	0.67	0.01	-27	-04	0.15	0.27	0.19	
Antioxidant enzymes	APX1																			0.89	0.04	0.94	0.79	0.48	-10	-26	-06	0.10	0.42	0.30	
	APX4																			0.12	0.93	0.85	0.58	-08	-33	-07	0.06	0.31	0.18		
	CAT1																				0.21	0.13	0.23	-11	-11	-09	0.36	0.29	0.31		
	CAT2																					0.80	0.57	-06	-26	-06	0.14	0.39	0.28		
	CAT4																						0.74	-10	-42	-05	0.08	0.44	0.25		

[illegible]

* If correlation value is: < 0.20 - slight; almost negligible relationship; 0.20 - 0.40 - low correlation; definite but small relationship; 0.40 - 0.70 - moderate correlation; substantial relationship (green cells); 0.70 - 0.90 - high correlation; marked relationship (brown cells); 0.90 - 1.00 - very high correlation; very dependable relationship (black cells).

Table S4. Primer sequences of the target genes and their origin used for qPCR analysis.

Target Gene	Gene ID (NCBI nr)	Ensembl Plants ID	Strand	Primer Sequences (5' → 3')
<i>HvCyclophilin*</i>	AK253120.1	HORVU6Hr1G01257 0	Forward	CCTGTCGTGTCGTCTCTAA A
			Reverse	ACGCAGATCCAGCAGCCTAA AG
<i>HvPHYA</i>	DQ201139.1 DQ201140.1, GU994113.1, GU994114.1	HORVU4Hr1G00861 0	Forward	TGCAGCACATTCAGAGAGGG
			Reverse	CCCTAGTGCCTTGTGCAGAG
<i>HvCRY1a</i>	DQ201149.1 DQ201150.1 DQ201151.1	not available	Forward	CACATGGAAGTGGACCGTGC
			Reverse	CGCTGGCAACTTGTTCCTG
<i>HvCRY1b</i>	DQ201152.1 DQ201153.1 DQ201154.1	not available	Forward	GATGGAAGTCCATTGGGAACC
			Reverse	CATACGGTGCTGAGGTTGCTG
<i>HvCRY2</i>	DQ201155.1 DQ201156.1	HORVU6Hr1G05874 0	Forward	GGCTCGCGAGTGCTTAGATG
			Reverse	GGAGCACTTGGAGATAGTTCC TTC
<i>HvCCA1</i>	JN603242.1	HORVU7Hr1G07087 0	Forward	AATAAGACTGGGGCAACTGG C
			Reverse	TAGTTGTGGGAAAGGGCTG
<i>HvTOC1</i>	JN603243.1	HORVU6Hr1G05763 0	Forward	AGGCAGAAAAGGAAGGACCG
			Reverse	TGCCTAACAACTGACCCCG
<i>HvPRR73</i>	AK356430.1	HORVU5Hr1G08162 0	Forward	GGTGAAGGGTCAGTTTGT
			Reverse	ACGACAAGTTAGCGTATACAA
<i>HvOXS2</i>	AK375304.1	HORVU4Hr1G00577 0	Forward	TCTGGGTCGCCAATGAATC
			Reverse	GCTCCTCATTGTCTGCTGGT
<i>HvARF-like</i>	AK358522.1	HORVU4Hr1G01174 0	Forward	GATGGGTGTATGTGTGTA
			Reverse	CTTGCTCTGAGGCTGTTAT
<i>HomTREF</i>	AK360739.1	HORVU5Hr1G10338 0	Forward	CGACCATGGTTTGTGATGTA
			Reverse	CCTATACACATGGCACATCC
<i>HvNR</i>	AK365506.1		Forward	ACGTGGAGCTGCTCATCAAG

		HORVU6Hr1G07970 0	Reverse	TCGAGGTACTGCGACATGAG
<i>HvGLN_a</i>	AK252215.1	HORVU1Hr1G03806 0	Forward	TTTGATGGGTGCGCAAATCC
			Reverse	GGTGAATGAGATCGCCAAAT GC
<i>HvGLN_b</i>	AK365634.1	HORVU2Hr1G11130 0	Forward	ATTTGCGCACATTGCTCTGC
			Reverse	CAGCGCATCCTTCAAGTTGTT G
<i>HvGLN_d</i>	JX878490.1	HORVU4Hr1G06686 0	Forward	TCGACATCAGGAGCAAAGCA AG
			Reverse	CTGAACGGGTCTTGAATAATG G
<i>HvGLN_e</i>	KF815944.1	HORVU6Hr1G07403 0	Forward	TATTTTGCTGACGGCGAACG
			Reverse	ATTCAGGAGCAAGAAGGCCA AG
<i>HvAPSR</i>	not available	not available	Forward	TCGCCTCTGAGATCATGGA
			Reverse	GTCCAGTCAGCTTCGCGTAT
<i>Hvγ-ECS</i>	AK353769.1	HORVU1Hr1G01559 0	Forward	TGCCCCACTTTGAACGATTGG
			Reverse	TCCCGGAATGGTGTCTTCAAA C
<i>HvGST</i>	AK251838.1	HORVU5Hr1G10343 0	Forward	CGGAAGGAAGCTACAGATAA A
			Reverse	GACACATGACACACACATAG A
<i>HvGR</i>	AK376974.1	HORVU6Hr1G08978 0	Forward	TGGAGGCTACTTGCTTTGCT
			Reverse	AGATAGCGGCGGAATACAGA
<i>HvAPX1</i>	MF804856.1	HORVU7Hr1G05743 0	Forward	CAGTGGCCCAGCATCTACAA
			Reverse	TAGCCCGCGATAACTACAGC
<i>HvAPX4</i>	AK356559.1	HORVU2Hr1G10173 0	Forward	AGGCCCCATTTCAATTTGCAG
			Reverse	CGCCCGAATATTTGTCTGAAG
<i>HvCAT1</i>	AF021939.1	HORVU6Hr1G00864 0	Forward	AAGTGC GGCTTCAAGAACAA CC

			Reverse	TCGTCTTCTCCCTCTTTCCAAC C
<i>HvCAT2</i>	AK366177.1	HORVU7Hr1G12170 0	Forward	CGCGGAAAATGAACAGCTTG
			Reverse	GAGCACATTTCGGGGCATTC
<i>HvCAT4</i>	AK357533.1	HORVU4Hr1G08204 0	Forward	CAACCGCAACATCGACAACCTT C
			Reverse	TTGTTGTGGTGGGAGCACTTG
<i>HvPRX1</i>	AK248281.1	HORVU3Hr1G07758 0	Forward	AGGCAACAAGAAGGACGAAA CG
			Reverse	ACGTACGCGCTGCAGATTTTC

* kindly provided by Morran *et al.* [78].

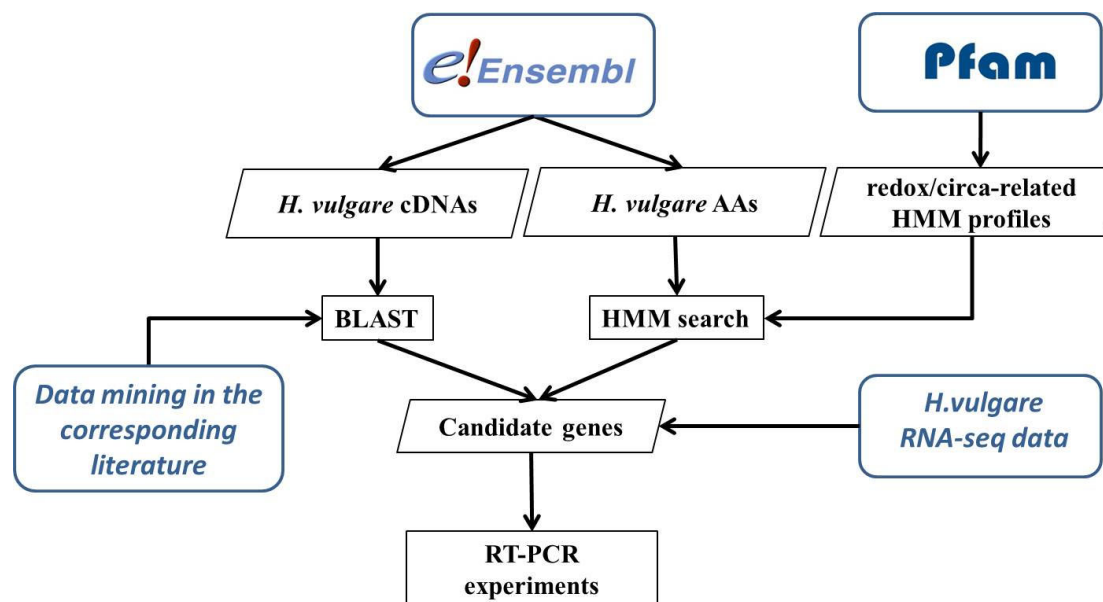


Figure S1. Selection procedure of redox-, circadian rhythm- and far-red-dependent genes. The *Hordeum vulgare* reference proteome was retrieved from Ensembl Plants FTP server ([ftp.ensemblgenomes.org](ftp://ftp.ensemblgenomes.org); release-41). The whole protein collection was subsequently scanned with the Hidden Markov Model (HMM)-based HMMER 3.0 software package (<http://eddylib.org/software/hmmer/>) [74] using redox and circadian-related HMM profiles of the Pfam 32.0 database (<ftp://ftp.ebi.ac.uk>) [75]. We also performed selection of genes responsive to far-red light with high expression changes (Galiba and Cattivelli, unpublished RNA-seq data).

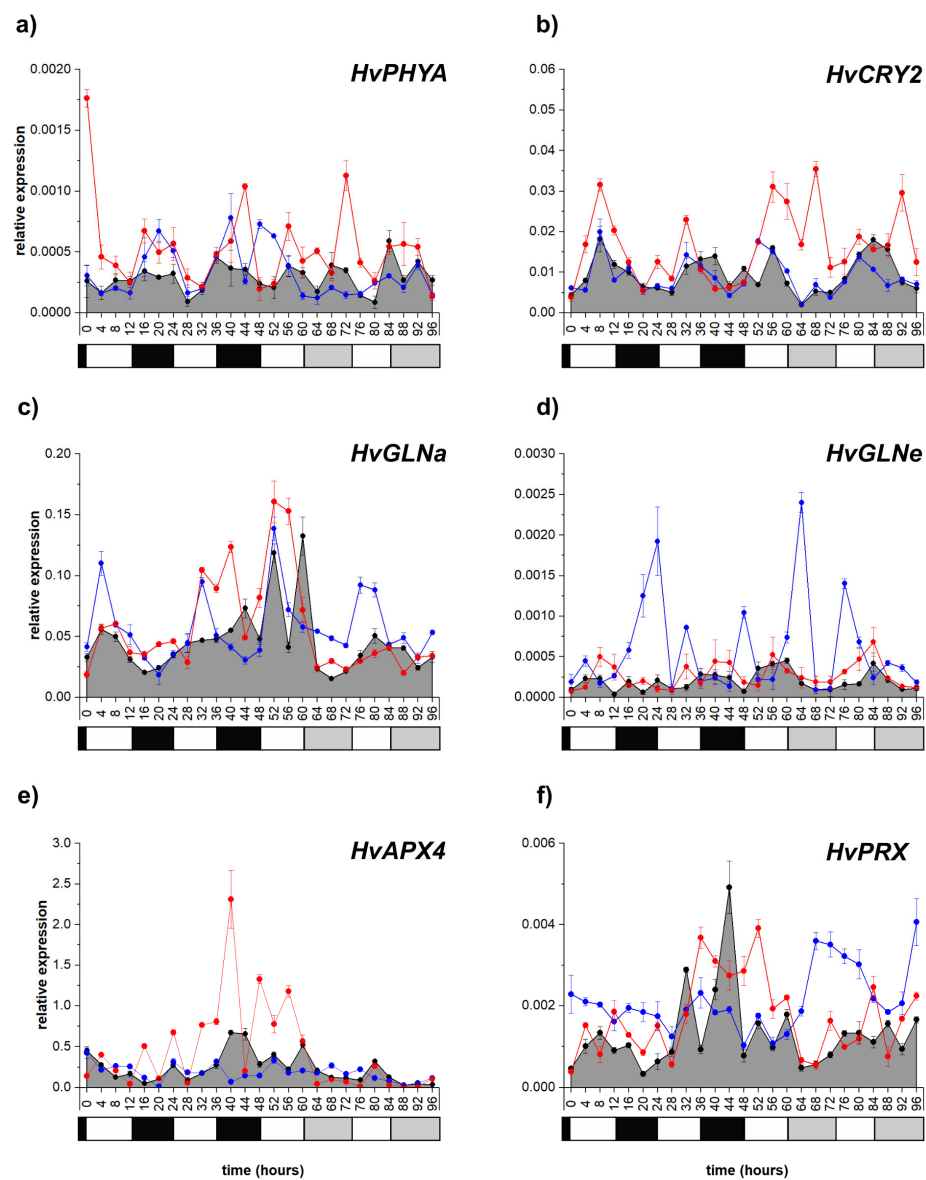


Figure S2. Expression patterns of *H. vulgare* phytochrome A (*HvPHYA*) (a), cryptochrome 2 (*HvCRY2*) (b), glutamine synthetase-a (*HvGLNa*) (c), glutamine synthetase-e (*HvGLNe*) (d), ascorbate peroxidase 4 (*HvAPX4*) (e) and peroxiredoxin (*HvPRX*) (f) coding genes under white, blue and far-red light illumination. Transcript levels were calculated with ΔCt method, expression data and error bars indicating standard deviations were calculated using three biological replicates. The following significant differences were calculated at $p \leq 5\%$ level: *HvPHYA* — 0.00012; *HvCRY2* — 0.0035; *HvGLNa* — 0.013; *HvGLNe* — 0.00019; *HvAPX4* — 0.21; *HvPRX* — 0.00016.

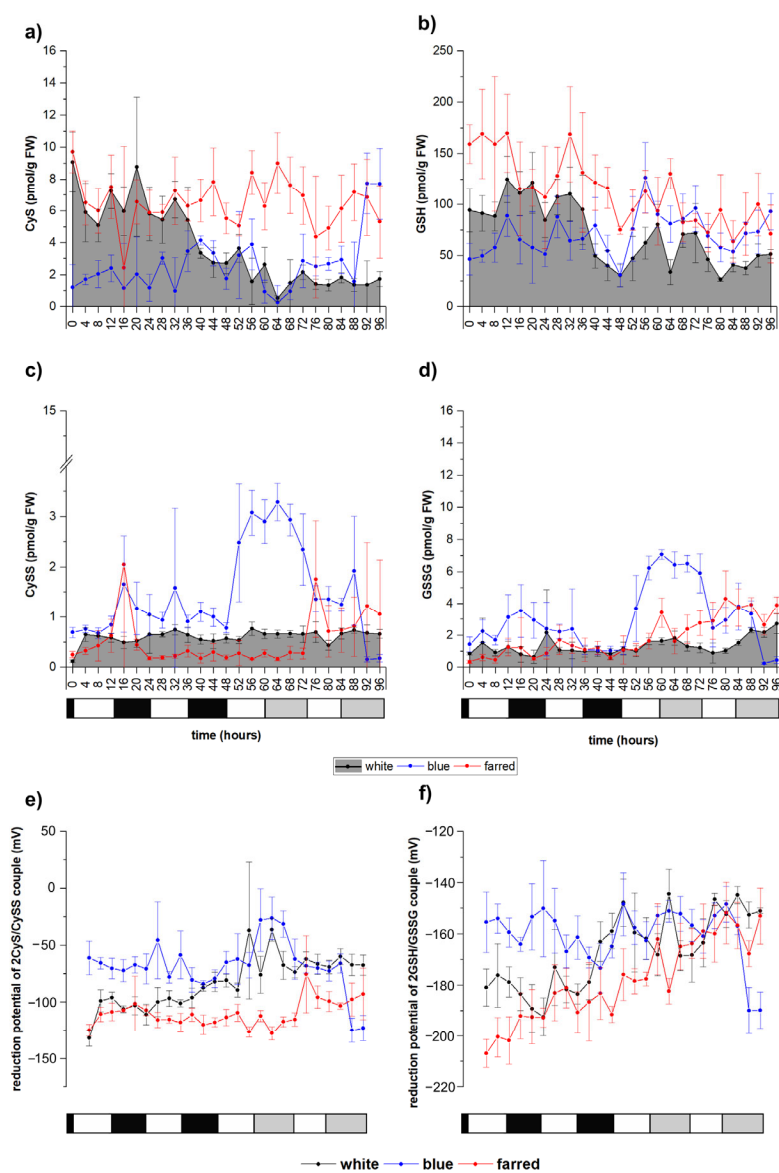


Figure S3. Changes in cysteine (a), glutathione (b), oxidized cysteine (c) and glutathione disulfide (d) content and reduction potential (E) of Cys/CySS (e) and GSH/GSSG (f) redox-couples in response to additional B/FR light treatment. Values on the X-axes show the time in hours after the start of the experiment; white and black bars below them indicate the light and dark periods, while grey bars indicate the subjective “night” period during constant light conditions. Data and error bars indicating standard deviations were calculated using three biological replicates. The following significant differences were calculated at $p \leq 5\%$ level: Cys: -0.56 ; GSH: -12.4 ; CySS -0.16 ; GSSG -0.23 ; $E_{2\text{Cys/CySS}} - 24.2$; $E_{2\text{GSH/GSSG}} - 21.9$.