

## Supplementary Information

**Table S1.** UPS genes selected for relative expression analysis in response to melatonin treatment. The cut off of fold change was >2. Values of mean of relative expression (in log<sub>2</sub>), SD standard deviation and N, number of isolated experiments are presented respectively.

PlasmoDB Accession Number	ID	Oligonucleotides	Gene Group	3 h	4 h	5 h	6 h
PF11_0177	ubiquitin C-terminal hydrolase	F TGGCGAGGGATAATGAAAAC R GAAATTTCTGTAGCACCCATACG	<b>Deubiquitinase</b>	0.36 ± 0.31; 3	1.09 ± 0.13; 4	1.48 ± 0.51; 3	0.20 ± 0.27; 4
PFL1790w	ubiquitin activating enzyme E1	F CAATGATCAATTGGAAATGCAC R CATATTTCTTCGACCTGCATA	<b>E1</b>	0.45 ± 0.41; 4	1.60 ± 0.72; 4	1.57 ± 0.45; 4	-0.24 ± 0.25; 4
PFL1245w	ubiquitin-activating enzyme E1	F TCAGGTGCTTTAGGATGTGAA R AGTTACCACAACAAGCCAAA		0.10 ± 0.57; 3	1.47 ± 1.13; 3	1.88 ± 0.18; 3	0.40 ± 0.29; 4
PFL0190w	ubiquitin conjugating enzyme E2	F CAGCAGGAGCAATATGTCTTGA R TGC GTTGGGGTCTGT TAGTA	<b>E2</b>	0.14 ± 0.12; 4	0.04 ± 0.64; 4	-0.03 ± 0.21; 3	-0.48 ± 0.52; 4
PFL1565c	hypothetical protein (F-box)	F AGTCAACGAAAGGTACCCAAA R TTCCTCATGTTACATTTTTTCG	<b>E3</b>	0.55 ± 0.78; 4	0.32 ± 0.18; 3	1.61 ± 0.28; 3	0.20 ± 0.86; 4
PF0960c	hipothetical protein (F-box)	F TGAATACAAACAGCGTAAAAGA R AGGTGCTACTTCTTCTCCACA		0.00 ± 0.10; 3	1.45 ± 0.26; 3	1.08 ± 0.41; 3	-0.38 ± 0.09; 3
PFC0845c	ubiquitin protein ligase	F GGGGGTATGTAATCATGCTTTTC R GGCTTTTTGAAATCCCAAGT		0.30 ± 0.07; 3	0.56 ± 0.18; 4	0.86 ± 0.26; 3	0.09 ± 0.12; 4
MAL8P1.23	ubiquitin protein ligase	F TGGCAATGGAGAAAATGATG R TGACTGGCGCAGATGTTAAA		0.39 ± 0.44; 3	2.11 ± 0.93; 4	1.71 ± 0.97; 3	-0.55 ± 0.13; 3
MAL13P1.337	skp1 family protein	F GCGTCAAATCTCTTGATATT R AAACCTCCGCTCGAATTTCTTC		0.09 ± 0.43; 3	-0.16 ± 0.62; 4	0.13 ± 0.35; 3	-0.32 ± 0.19; 4
PF08_0094	cullin-like protein	F GATCCAAATTTCAACGAATGC R TTTTCATCAACGCTGTTTTCA	<b>Preteasome subunit</b>	0.16 ± 0.32; 3	-0.01 ± 0.49; 3	2.28 ± 0.74; 3	0.13 ± 0.55; 4
PFF1445c	cullin-like protein	F TGATATGGGACCAACAACCTCA R TTCTTTCTGATGATTTTCCATTTG		-0.01 ± 0.67; 3	1.68 ± 0.99; 4	1.12 ± 0.49; 4	-0.34 ± 0.37; 4
PF14_0025	proteasome subunit	F GCCACATATGAGCGATGAGTT R TTGCATCACCTTCTCATTTCG		0.14 ± 0.19; 3	1.91 ± 0.56; 4	0.31 ± 2.07; 3	-0.10 ± 0.61; 4
PFA0400c	beta-3 proteasome subunit putative	F TGAACCTTATCTCACGGCATA R ACACATTCCAAAAAGCTGTTCA	0.29 ± 0.52; 3	-0.03 ± 0.70; 4	0.54 ± 0.49; 3	0.07 ± 0.33; 4	
PFI1085w	ubiquitin-like protein	F TCAACCCCTATGCCAAATA R CTTCATCGGGAACCTCTCA	<b>Ubiquitin-like</b>	0.03 ± 0.52; 3	0.57 ± 0.14; 3	0.50 ± 0.26; 3	-0.29 ± 0.16; 4

**Table S2.** Comparison of the analyzed UPS genes and the corresponding modulation in the various conditions in *P. falciparum*. Gray boxes refer to those genes that are positively modulated by the treatment. Melatonin 100 nM 5 h data were extracted from Koyama *et al.*, 2012 [16] (see article reference).

PlasmoDB Accession Number	Melatonin			NAS
	10 $\mu$ M 4 h	10 $\mu$ M 5 h	100 nM 5h	100 nM 5 h
PF11_0177	Gray	Gray	Gray	Gray
PFL1790w	Gray	Gray	Gray	Gray
PFL1245w	Gray	Gray	Gray	Gray
PFL0190w	Gray	Gray	Gray	Gray
PFL1565c	Gray	Gray	Gray	Gray
PFF0960c	Gray	Gray	Gray	Gray
PFC0845c	Gray	Gray	Gray	Gray
MAL8P1.23	Gray	Gray	Gray	Gray
MAL13P1.337	Gray	Gray	Gray	Gray
PF08_0094	Gray	Gray	Gray	Gray
PFF1445c	Gray	Gray	Gray	Gray
PF14_0025	Gray	Gray	Gray	Gray
PFA0400c	Gray	Gray	Gray	Gray
PFI1085w	Gray	Gray	Gray	Gray