

Supplementary figure legends.

Supplementary Figure 1:

Real-time quantitative RT-PCR verifies down-regulation of genes differentially expressed between WT and *Δpyhmgb2* in microarray experiments.

Real-time quantitative RT-PCR data is represented by the black bars. The microarray data is represented by grey bars. The ratio of transcript expression in the WT parasites to transcript expression in KO is represented for the genes listed at the bottom of the graph. Differential expression was verified for 9 genes whose expression was downregulated in *Δpyhmgb2* (Table III) along with genes with ubiquitous expression (*Pyppp*, *PytubI*, *Pyhmgb1*, *Pyada*) or selected gametocyte specific genes whose expression was not affected in the KO (*PytubII*, *Pywarp*, *Pys36*, PY06600, *pys48/45*, PY00415, *Pynima*). Array data only (grey bars) are shown for 5 additional sexual stage specific genes (*Cpk4*, *CCp1*, *CCp3*, *CTRP*, chitinase) that have been well-characterized in the literature. Primers used for qRT-PCR are in the supplementary materials.

Supplementary Figure 2:

Distribution of the of the expression profile during the gametocytogenesis of the 3D7 strain for the *P. falciparum* homologues of the downregulated genes in the *Δpyhmgb2* for which expression data was available (n=27) on PlasmoDB (www.plasmodb.org) and (3). Accession numbers and other identifiers of the genes are in Table III and Supplementary Table I. Absolute expression signal numbers are plotted against the number of days of the gametocytogenesis of the 3D7 strain.

Supplementary Figure 3:

A protein interaction network with PfHMGB2. The yeast two hybrid data is available at www.plasmodb.org or in (36). Red letters indicate proteins interacting with HMGB2. Proteins with AP2 domains are putative members of the AP2 family of plant-like transcription factors. A

black line accounts for direct interactions. A dashed blue line accounts for indirect interaction (i.e. an interaction partner in common).

Supplementary table legends.

Supplementary Table I

Plasmodium homologues for the genes downregulated in the $\Delta pyhmgb2$.

^a: FC= fold change calculated as normalized signal intensity of the WT divided by normalized signal intensity of the KO (two clones).

^b: As reported by Le Roch *et al.* (2) (data publicly available at www.plasmodb.org).

^c: Upregulated in gametocytes as reported by Hall *et al.*(4)

^d: As reported by Hall *et al.*(4) (data publicly available at www.plasmodb.org).

^e: Fold change in *P. berghei* $\Delta DOZI$ parasites as reported in Mair *et al* (7).

^f: PlasmoDB accession number.

Supplementary material legends.

Supplementary material 1: sequence of the primers used in real-time quantitative RT-PCR.