



Additional file 8. Clusters of genes co-expressed between Patient Groups 2 and 4. Normalised read counts from the *DESeq2* analysis were used to generate clusters of genes with positively correlated transcription profiles using *coseq*. 351 DEGs formed seven clusters; four clusters with dynamics that clearly distinguish the two patient groups are shown here. Boxplots (left) represent individual patient, shaded by Patient Group; the black line connecting boxplots is the mean expression value of all genes in the cluster. **a)** Two PvMSP-7H and -7I are co-expressed with 26 other genes including ETRAMP, rhostry neck protein 12 (RON12, PvP01_0602300), and membrane associated erythrocyte binding-like protein (MAEBL, PvP01_0948400). **b)** The schizont stage-specific marker SEA1 is co-expressed with 77 other genes such as parasite-infected erythrocyte surface protein (PIESP1, PvP01_0829800) and MOP. **c)** A gametocyte-specific marker, gamete antigen 27/25, clustered with 31 other genes including *Plasmodium* exported protein (PHIST, PvP01_0001440) and tryptophan-rich protein (TRAG24, PvP01_1470100). **d)** Another stage-specific marker, liver stage antigen 3, clustered with 69 other genes such as *Plasmodium* exported protein (PHIST, PvP01_0119200) and tryptophan-rich protein (TRAG28, PvP01_0000130), but was negatively correlated with PvMSP-7H.