Var family expression by upstream promoter classification

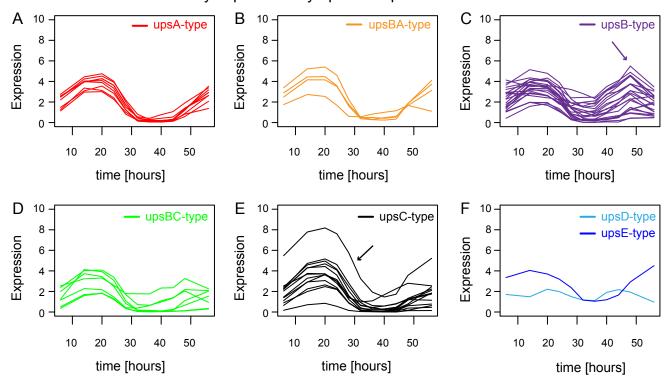


Figure S24. A central upsC-type var gene is the dominant var transcript, and subtelomeric upsB-type var genes produce the most non-coding transcripts. (A/B/C/D/E/F) Expression during the 56-hour time course of upsA-type (red), upsBA-type (orange), upsB-type (purple), upsBC-type (green), upsC-type (black), upsD-type (light blue) and upsE-type (dark blue) var genes, respectively [1]. This analysis indicated that an upsC-type gene, *Pf3D7 0412700*, was the dominant *var* transcript in the parasite population (black arrow). We also noted that the transcription of non-coding transcripts varied by upstream promoter (ups) type. Interestingly, the majority of upsB-type var genes transcribed non-coding transcripts during parasite invasion (purple arrow), whereas the majority of upsA-type and upsC-type var genes did not. Expression is plotted in units of log2(FPKM+1). upsA-type: Pf3D7 0425800, Pf3D7 1150400, Pf3D7 1300300, Pf3D7 0800200, Pf3D7 1100200, Pf3D7 0400400, Pf3D7 0100300, Pf3D7 0937600, Pf3D7 0600400; upsBA-type: Pf3D7 0800300, Pf3D7 1200400, Pf3D7 0600200, Pf3D7 0632500; upsB-type: Pf3D7 1100100, Pf3D7 0800100, Pf3D7 0500100, Pf3D7 0100100, Pf3D7 0115700, Pf3D7 0324900, Pf3D7 0400100, Pf3D7 0900100, Pf3D7 0223500, Pf3D7 1041300, Pf3D7 1200100, Pf3D7 0200100, Pf3D7 0300100, Pf3D7 1255200, Pf3D7 0426000, Pf3D7 0937800, Pf3D7 1000100, Pf3D7 1219300, Pf3D7 0632800, Pf3D7 1373500, Pf3D7 0733000, Pf3D7 0700100, Pf3D7 1300100, Pf3D7 0833500; upsBC-type: Pf3D7 0413100, Pf3D7_1240400, Pf3D7_0808700, Pf3D7_0712800, Pf3D7_0712400, Pf3D7_0421100, Pf3D7_1240300; upsC-type: Pf3D7 0712900, Pf3D7 0808600, Pf3D7 0420700, Pf3D7 0712000, Pf3D7 0412900, Pf3D7 0420900, Pf3D7 0421300, Pf3D7 0412400, Pf3D7 0712600, Pf3D7 0711700, Pf3D7 1240600, Pf3D7 0412700, Pf3D7 0617400; upsD-type: Pf3D7 0533100; upsE-type: Pf3D7 1200600.

1. Lavstsen T, Salanti A, Jensen AT, Arnot DE, Theander TG (2003) Sub-grouping of Plasmodium falciparum 3D7 var genes based on sequence analysis of coding and non-coding regions. Malaria Journal 2: 27.