



Additional file 5: High stringency RNA-seq analysis. Scatter plot of RPKM values of each condition with MapQ value > 1. Values are calculated as RPKM (Reads Per Kilobase of transcript per Million mapped reads) and are averages for a pair of independent sub-clones. Selected developmentally regulated genes are highlighted. Metacyclic (*mVSG*) and bloodstream (*bVSG*) specific *VSGs* are also shown.