



**Supplemental Figure 5: A.** Transcripts per million (TPM) values for single-cell RNA-seq libraries, mapped to our new asexual *S. mediterranea* annotation, for specific cell types were averaged and top 1000 genes were extracted. Cell types were classified previously by (Wurtzel et al. 2015) and are labelled accordingly. X1 and X2 single cells from (Molinaro and Pearson 2016) are from the head region and labelled ‘head X1’

and head X2'. Each row represents a cell type and the intensity colour represents the density of genes at the position on the proportional expression spectra. **B.** Ternary plots for each cell type were made and dots represent individual loci and their wild-type X1/X2/Xins proportional expression.