**SUPPLEMENTAL FILE LEGENDS:**

**Supplemental File 1:** 164 RNA-seq SRA IDs used for independent transcriptome assembly in the annotation of the *S. mediterranea* asexual genome.

**Supplemental File 2:** IPython notebook describing re-annotation process of the *S. mediterranea* asexual genome.

**Supplemental File 3:** IPython notebook describing calculation of FACS categorisation of annotated genomic loci.

**Supplemental File 4:** IPython notebook documenting code for production of ChIP-seq profiles for Figures.

**Supplemental File 5:** Table documenting 278 out of 285 downregulated genes (>2fold, p-value<= 0.05) after *mex3-1* RNAi that also have FACS category proportions. BLAST hits are given where applicable, and annotated manually for planarian specific genes.

**Supplemental File 6:** Transcript sequence and Dresden IDs (dd\_smed\_v6) (Brandl et al. 2016) of plotted X1 and Xins enriched genes and bivalent loci.

**Supplemental File 7**: X1, X2, Xins proportional expression values for annotated loci

**Supplemental File 8:** GTF annotation file to be used with *S. meditteranea* asexual genome (SmedGD Asexual v1.1 genome)