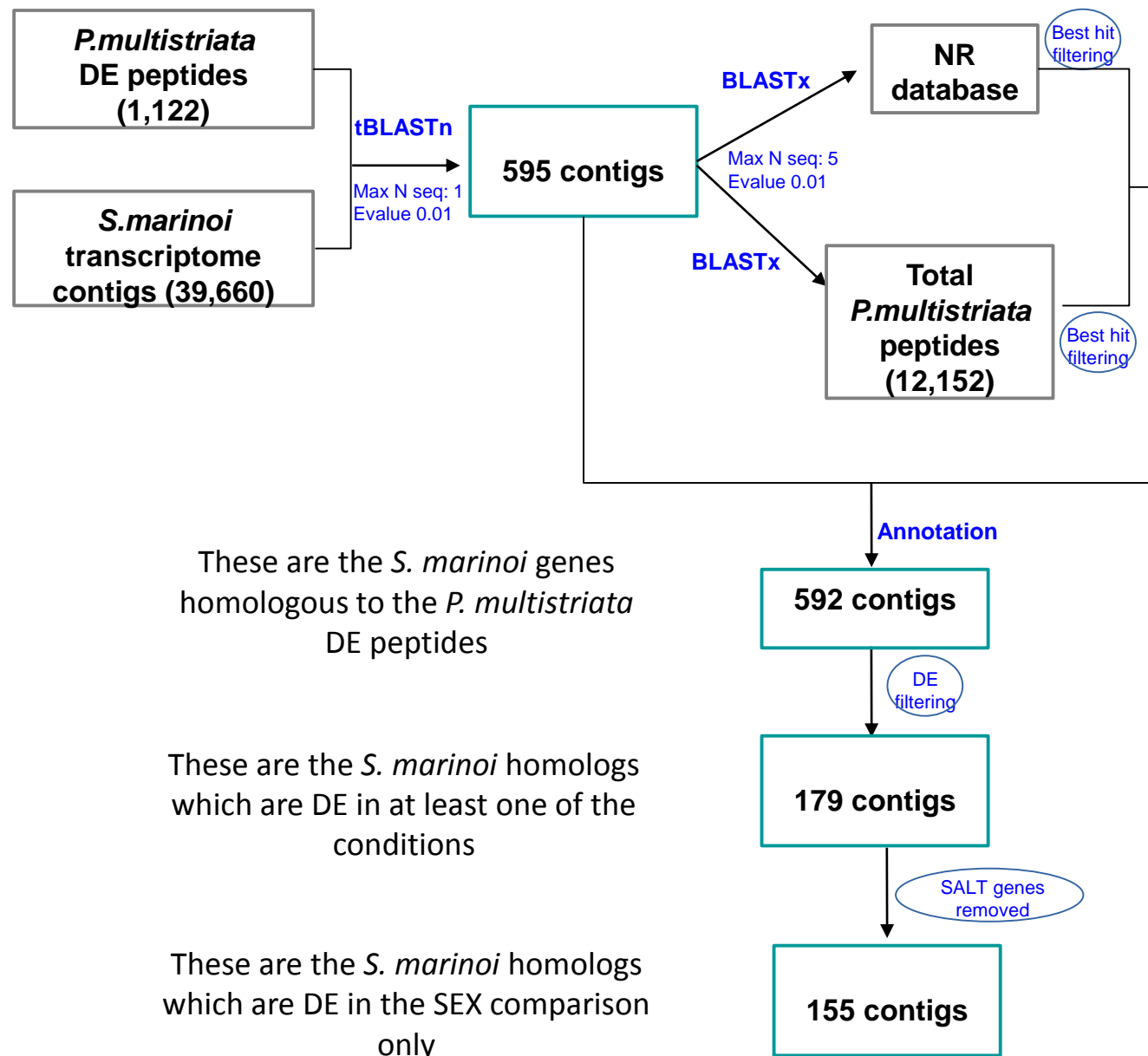
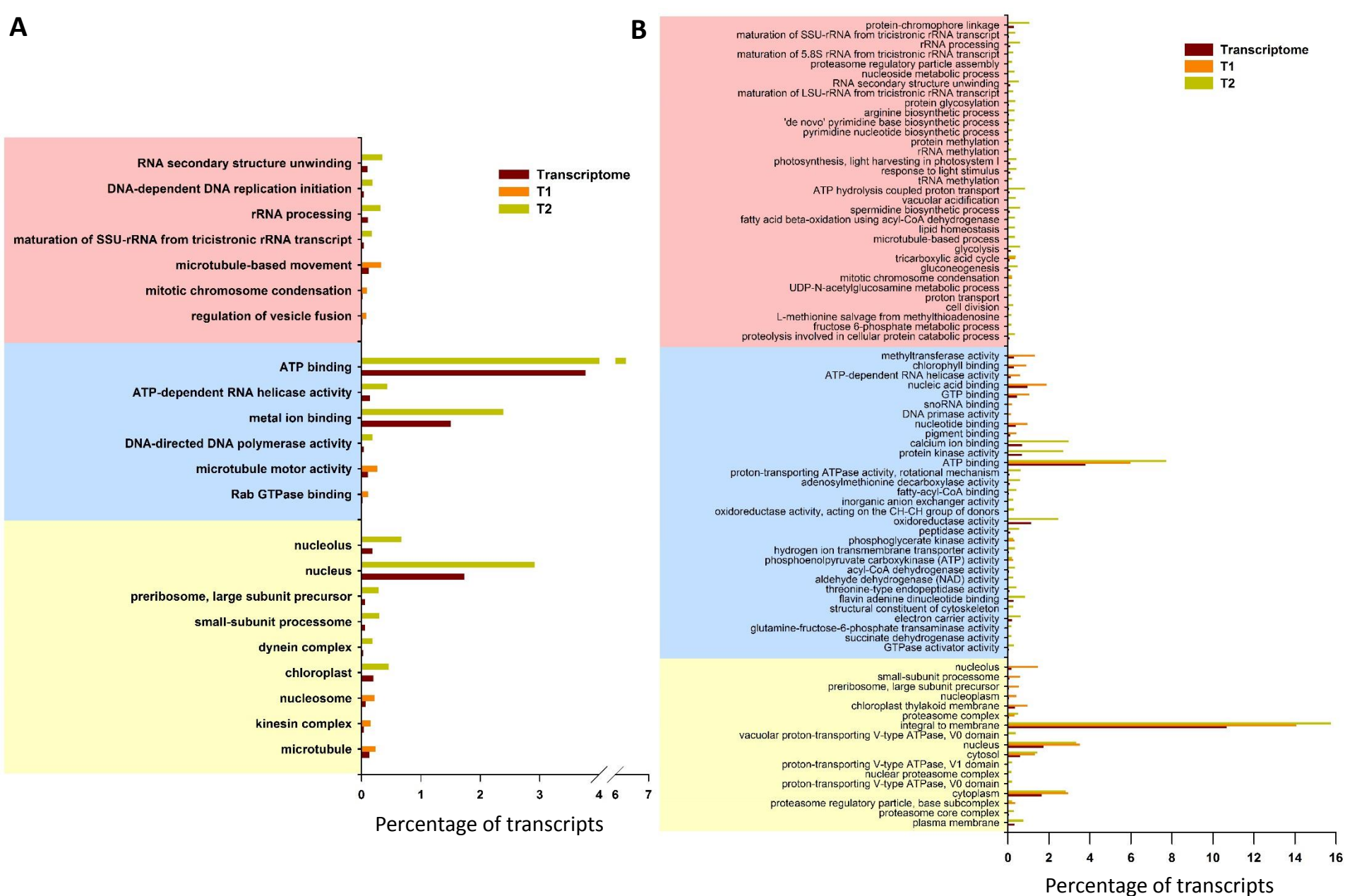


	Cell size	Time	Treatment		
1	Large	T1	Large cells	}	Salt stress (SALT_T1)
2	Large	T1	Large cells		
3	Large	T1	Large cells + salt stress	}	Sex_T1
4	Large	T1	Large cells + salt stress		
5	Small	T1	Small cells + salt stress \Rightarrow sex	}	Sex_T1
6	Small	T1	Small cells + salt stress \Rightarrow sex		
7	Small	T1	Small cells + salt stress \Rightarrow sex		
8	Large	T2	Large cells	}	Salt stress (SALT_T2)
9	Large	T2	Large cells		
10	Large	T2	Large cells + salt stress	}	Sex_T2
11	Large	T2	Large cells + salt stress		
12	Small	T2	Small cells + salt stress \Rightarrow sex	}	Sex_T2
13	Small	T2	Small cells + salt stress \Rightarrow sex		
14	Small	T2	Small cells + salt stress \Rightarrow sex		

Supplementary Figure 1. Schematic representation of the comparisons made between samples in the differential expression analysis.



Supplementary Figure S2. Scheme of the workflow for the identification of *S. marinoi* transcripts homologous to *P. multistriata* sex-related genes (Basu et al., 2017) which are differentially expressed in the SEX condition. See Methods for details.



Supplementary Figure S3. Enriched GO terms for *S. marinoi* SEX (A) and SALT (B) differentially expressed genes. The pink shade highlights the Biological Process, the blue shade the Molecular Function and the yellow shade the Cellular Component categories.