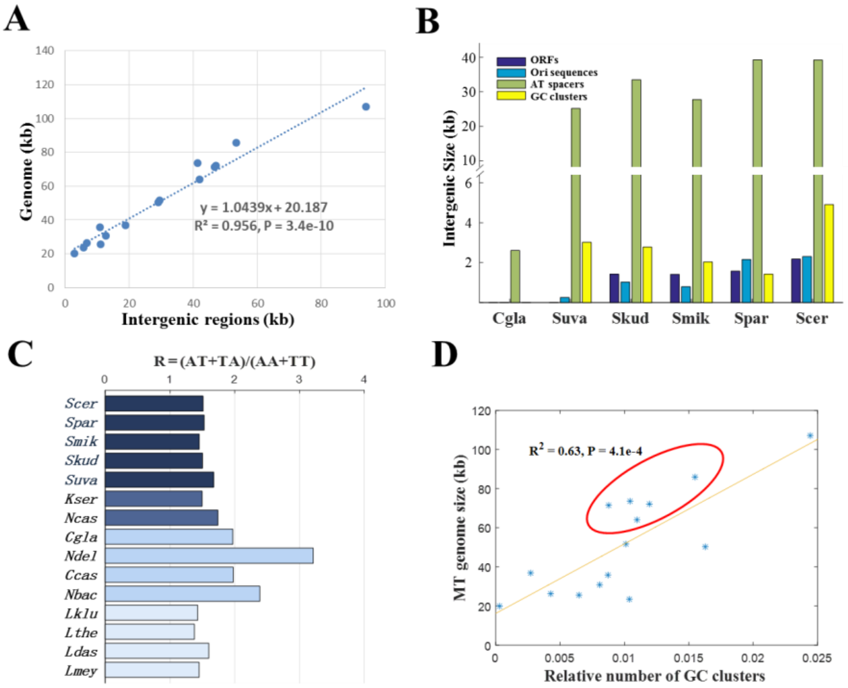

S1 Fig. (A) Scatter plot and line regression of the relationship between the size of MT genome and intergenic regions. (**B) The expansion of intergenic region of mtDNA.** The intergenic sequences were divided into four types: ORF sequences, *ori* sequences, AT spacers and GC clusters. The Y axis represented the size of four types of intergenic regions, for detailed data, see the S3 Table. **(C) The (AT+TA)/(AA+TT) ratio in the AT spacers of fifteen yeasts.** (**D) Scatter plot and line regression of the relationship between the MT genome size and the relative number of GC clusters.** The scatter plots in red ellipse represented five *SSS* yeasts.