S8 Table. Seven blocks in mitochondria genome of *SSS*

Blocks	Transcriptional units	Genes
1	1.1	*rnl* *tRNA-Thr2*
	1.2	*tRNA-Cys* *tRNA-His*
	1.3	*tRNA-Leu* *tRNA-Gln* *tRNA-Lys* *tRNA-Arg1* *tRNA-Gly* *tRNA-Asp* *tRNA-Ser1* *tRNA-Arg2*
	1.4	*tRNA-Ala* *tRNA-Ile* *tRNA-Tyr* *tRNA-Asn* *tRNA-Met1*
	1.5	*cox2*
2	2.1	*tRNA-Phe* *tRNA-Val* *cox3*
	2.2	*tRNA-Thr1*
3	3.1	*tRNA-Met2*
	3.2	*RPM1* *tRNA-Pro*
4	4.1	*cox1* *atp8* *atp6*
5	5.1	*tRNA-Glu* *cob*
6	6.1	*rns* *tRNA-Trp*
7	7.1	*atp9*
	7.2	*tRNA-Ser2* *var1*

Note: All 35 genes were divided into seven syntenic orthologs blocks constituted by fourteen transcriptional units known in *S. cerevisiae*. For other *SSS* yeasts, we predicted transcription initiation site based on the motif WTATAAGTA. The predicted transcriptional units were similar to that in *S. cerevisiae* (data not shown).