

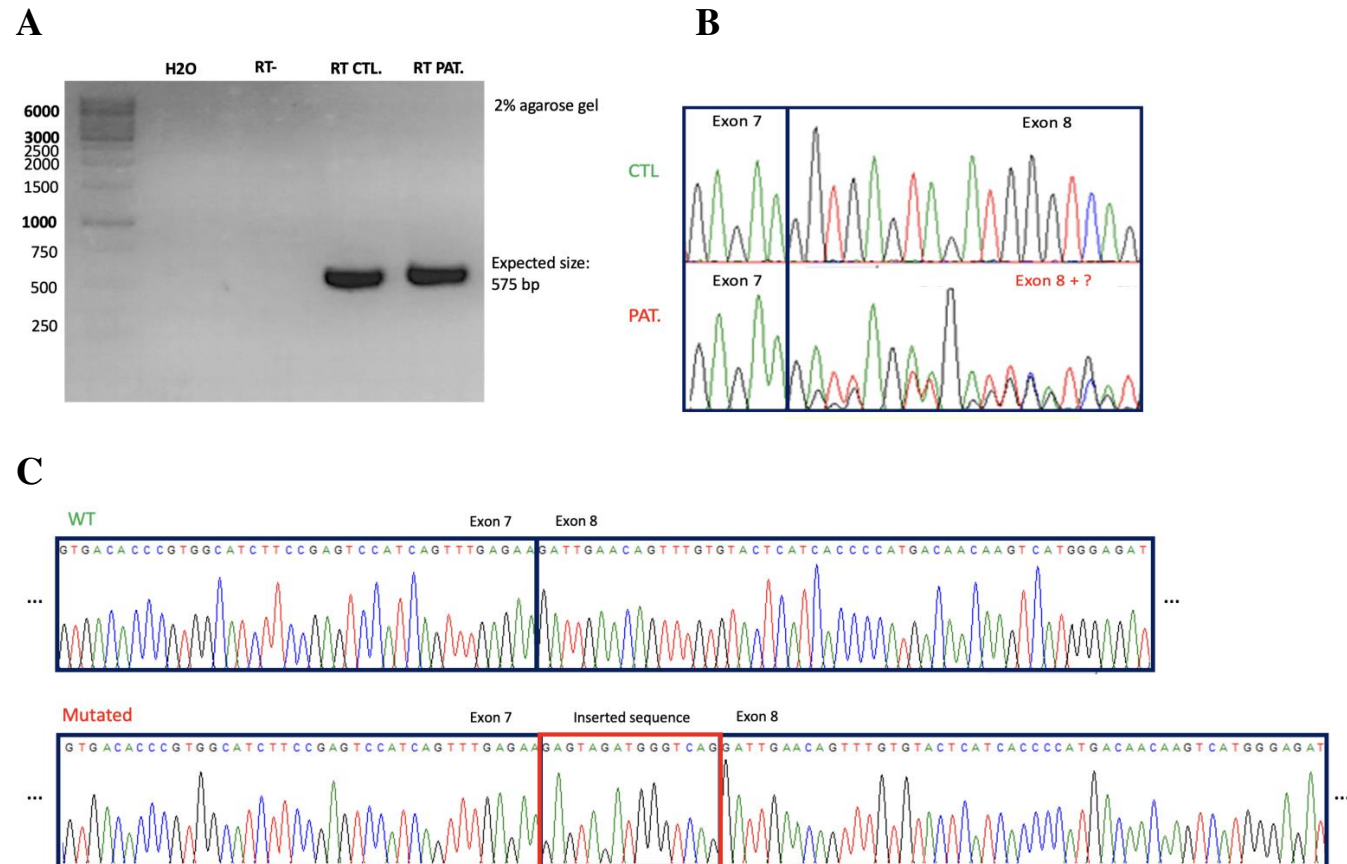
SUPPLEMENTAL MATERIAL**Supplemental Table 1: RT-qPCR and RT-PCR primers**

IL-6 (RT-qPCR)	Forward: AGTCCTGATCCAGTTCCTGC Reverse: CTACATTTGCCGAAGAGCCC
p16 (RT-qPCR)	Forward: CTGAGGAGCTGGGCCATC Reverse: GCAGTTGTGGCCCTGTAG
p21 (RT-qPCR)	Forward: CTGGAGACTCTCAGGGTCGAA Reverse: CCAGGACTGCAGGCTTCCT
p53 (RT-qPCR)	Forward: AAGAAACCACTGGATGGAGAA Reverse: CAGCTCTCGGAACATCTCGSS
LMNB1 (RT-qPCR)	Forward: AAGCAGCTGGAGTGGTTGTT Reverse: TTGGATGCTCTTGGGGTTC
SARS1 (RT-qPCR)	Forward: CCACTACCCGTACCATCTGC Reverse: CTGCCCTCATGTTGCTTCTT
SARS2 (RT-qPCR)	Forward: CCTTCTCATCGCGCTCCT Reverse: TGTGGGTGGGTTCTTAGCTT
H36B4 (RT-qPCR)	Forward: ACGGGTACAAACGAGTCCTG Reverse: GCCTTGACCTTTTCAGCAAG
SARS1 (RT-PCR)	Forward: GGAACAGGCTCTCATCCAGTA Reverse: AGGAGACCAACTCACGGAAG

Supplemental Table 2: Yeast strains used in this study.

Name	Genotype	Source
Y23962	MATa/MAT α ; ura3 Δ 0/ura3 Δ 0; leu2 Δ 0/leu2 Δ 0; his3 Δ 1/his3 Δ 1; met15 Δ 0/MET15; LYS2/lys2 Δ 0; YDR023w/YDR023w::kanMX4	EUROSARF
hSARS shuffle	MATa; ura3 Δ 0; leu2 Δ 0; his3 Δ 1;YDR023w::kanMX4 + pRS316-hSARS	This study
WT	MATa; ura3 Δ 0; leu2 Δ 0; his3 Δ 1;YDR023w::kanMX4 + pRS316-ySARS + pRS315	This study
hSARS	MATa; ura3 Δ 0; leu2 Δ 0; his3 Δ 1;YDR023w::kanMX4 + pRS316-hSARS + pRS315	This study
hSARS + hSARSm	MATa; ura3 Δ 0; leu2 Δ 0; his3 Δ 1;YDR023w::kanMX4 + pRS316-hSARS + pRS315-hSARSm	This study

Supplemental Figure 1: RT-PCR and cDNA sequencing results from fibroblasts for SARS1-mutated patient and a control. A: Agarose gel electrophoresis image showing RT-PCR products. B: Sanger sequencing results of patient and control RT-PCR products. C: Sanger sequencing results of WT/mutated sequences after cloning patient's cDNA PCR products into a pCMV-Tag2 plasmid.



Supplemental Figure 2: Conservation of mutation site in SARS1. p.Lys323_Ile324 insSerArgTrpValArg insertion is located in an evolutionary conserved region of SARS1 protein. Motif 2 (291-329 aa) is colored in yellow, and contains active site residues important for SARS1 aminoacylation (in boxes).

	p.K323_I324insSRWVR		% IDENTITY
<i>H. sapiens</i>	I F R V H Q F E K I E Q F V Y S	330	
<i>P. troglodytes</i>	I F R V H Q F E K I E Q F V Y S	330	99,81
<i>M. musculus</i>	I F R V H Q F E K I E Q F V Y S	330	95,90
<i>G. gallus</i>	I F R V H Q F E K I E Q F V Y A	330	85,80
<i>X. tropicalis</i>	I F R V H Q F E K I E Q F I Y A	329	81,57
<i>D. rerio</i>	I F R V H Q F E K I E Q F V Y A	330	81,52
<i>D. melanogaster</i>	I F R V H Q F E K V E Q F V L T	331	68,95
<i>C. elegans</i>	I F R V H Q F E K I E Q F V L C	330	66,26
<i>S. cerevisiae</i>	V F R V H A F E K I E Q F V I T	305	49,89
<i>E. coli</i>	L I R M H Q F D K V E M V Q I V	296	32,94

Supplemental Figure 3: Diploid *S cerevisiae* yeast strains used for complementation assays. Tetrad analysis of haploid spores showed that haploid strains containing pRS316-hSARSm (carrying the SARS1 mutation) did not grow.

