SUPPLEMENTAL MATERIAL

Supplemental Table 1: RT-qPCR and RT-PCR primers

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

SARS1	Forward: GGAACAGGCTCTCATCCAGTA
(RT-PCR)	Reverse: AGGAGACCAACTCACGGAAG

Supplemental Table 2: Yeast strains used in this study.

Name	Genotype	Source
Y23962	MATa/MATa; ura $3\Delta 0$ /ura $3\Delta 0$; leu $2\Delta 0$ /leu $2\Delta 0$; his $3\Delta 1$ /his $3\Delta 1$;	EUROSARF
	met15\D/MET15; LYS2/lys2\D; YDR023w/YDR023w::kanMX4	
hSARS	MATa; ura3∆0; leu2∆0; his3∆1;YDR023w::kanMX4	This study
shuffle	+ pRS316-hSARS	
WT	MATa; ura3∆0; leu2∆0; his3∆1;YDR023w::kanMX4	This study
	+ pRS316-ySARS + pRS315	
hSARS	MATa; ura3∆0; leu2∆0; his3∆1;YDR023w::kanMX4	This study
	+ pRS316-hSARS + pRS315	
hSARS	MATa; ura3∆0; leu2∆0; his3∆1;YDR023w::kanMX4	This study
+	+ pRS316-hSARS + pRS315-hSARSm	
hSARSm		

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-CR 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	
		× _	<pre>% IDENTITY</pre>
Н.	sapiens	IFRVHOFEKIEOFVYS 330	
Ρ.	troglodytes	IFRVHQFEKIEQFVYS 330	99,81
м.	musculus	IFRVHQFEKIEQFVYS 330	95,90
G.	gallus	IFRVHQFEKIEQFVYA 330	85,80
х.	tropicalis	IFRVHQFEKIEQFIYA 329	81,57
D.	renio	IFRVHQFEKIEQFVYA 330	81,52
D.	melanogaster	IFRVHQFEKVEQFVLT 331	68,95
c.	elegans	IFRVHQFEKIEQFVLC 330	66,26
s.	cerevisiae	VFRVHAFEKIEQFVIT 305	49,89
Ε.	coli	LIRMHOFDKVEMVQIV 296	32,94

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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.

