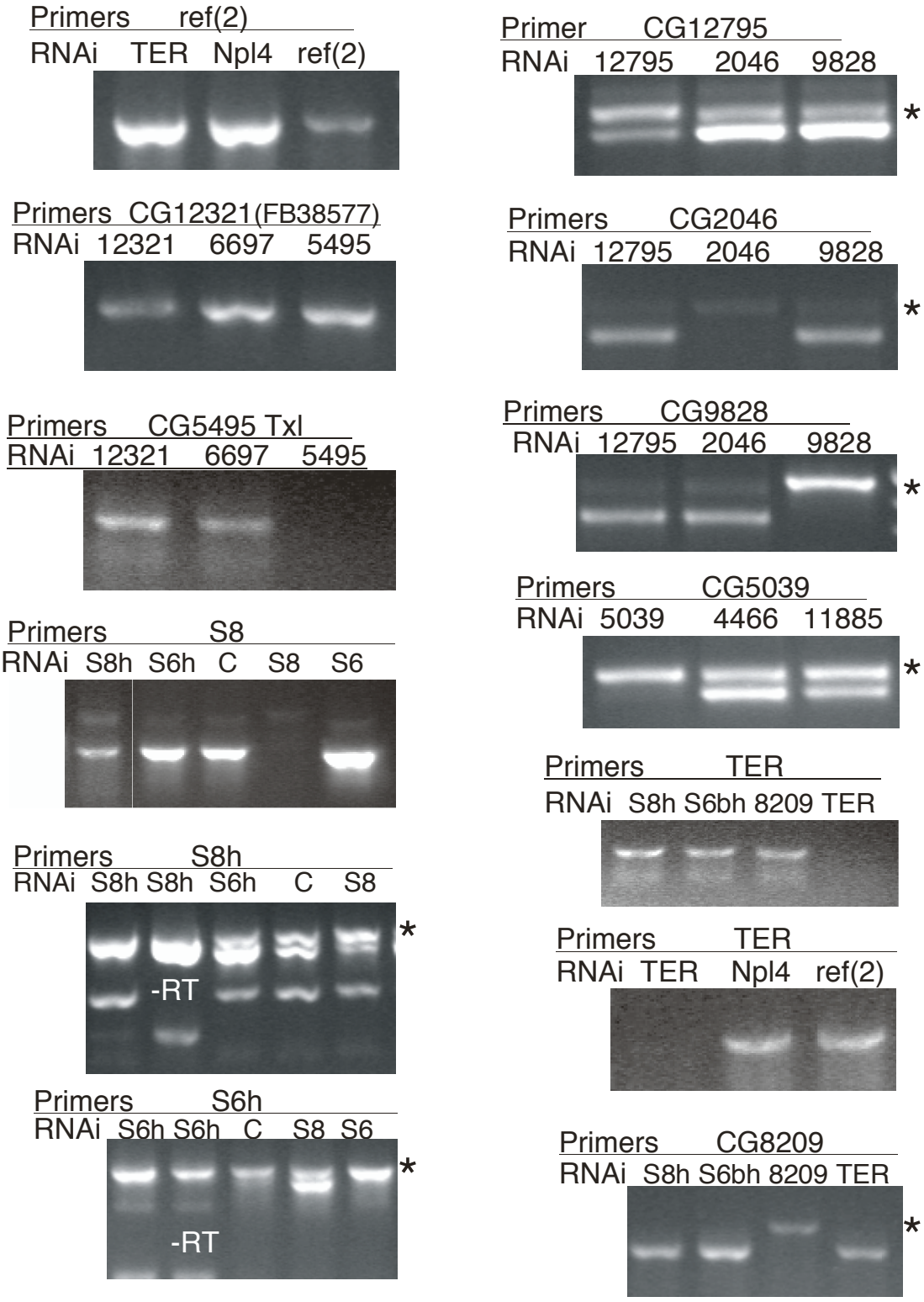

Supplementary Figure S1. Semi-quantitative RT-PCR to analyze mRNA levels after RNAi-mediated knock-down of candidate genes. Three to four days after addition of dsRNA the cells were collected and total RNA isolated. Specific primers for each gene were used to amplify the mRNA with the Promega Access RT-PCR system. -RT indicate that no reverse transcriptase was added to that reaction. * Indicates amplification from genomic DNA. To confirm that RNAi treatment was specific for reducing the target mRNA, RT-PCR reactions were carried out on the specific RNAi knockdown, RNAi knockdowns of other candidate genes and on untreated cells, C.

Table III. Downregulated mRNAs*

CG Number	Name (function)	RNAi Depletion of S5a subunit Treatment Fold decrease	MG132 Fold decrease
CG17970	cytochrome P450, Cyp4ac2	-1.81	increased+1.91
CG7619	S5a proteasome subunit (pros54)	-1.80	increased+3.75
CG9505	neutral endopeptidase, neprilysin Similar to common acute lymphocytic leukemia antigen, human X07166	-1.51	-1.64
CG6815	belphegor "far-relative" AAA ATPases	-1.48	-1.50
CG10687	asparaginyl tRNA synthetase	-1.37	-0.59
CG5535	cationic amino-acid transporter	-1.34	-2.45
CG10833	cytochrome P450, Cyp28d1	-1.32	no change
CG18466	(Nmdmc) methylenetetrahydrofolate dehydrogenase and cyclohydrolase	-1.23	-1.51
CG15304	similar to small Usmg5 protein, mouse	-1.23	-2.15
CG9470	MtnA, Cu/Cd binding	-1.14	-3.21
CG3074	cathepsin B-like, endopeptidase	-1.12	increased+20.68
CG8846	Thor initiation-factor-4E binding protein	-0.91	-7.87

* Only genes that decreased in 7 or more of the 9 comparisonsfor the S5a analysis shown.