

Supplementary Table B. GO categories of genes that were up-regulated in all infected cells compared to their basal level in the uninfected control

GO CATEGORY	NUMBER
protein metabolism	6
nucleobase, nucleoside, nucleotide and nucleic acid metabolism	5
catabolism	4
biosynthesis	3
cell growth and/or maintenance	3
lipid metabolism	3
unclassified	5

Supplementary Table C. GO categories of genes that were down-regulated in all infected cells compared to their basal level in the uninfected control

GO CATEGORY	NUMBER
cell growth and/or maintenance	19
nucleobase, nucleoside, nucleotide and nucleic acid metabolism	17
response to external stimulus	13
cell adhesion	10
signal transduction	10
protein metabolism	9
immune response	8
organogenesis	6
regulation of cell proliferation	6
response to stress	6
catabolism	4
cell death	4
regulation of cell growth	4
cell motility	3
cell-cell signaling	3
neurophysiological process	3
organismal movement	3
phosphorus metabolism	3
response to endogenous stimulus	3
unclassified	23

Supplementary Table E. MAS5 vs RMA

		(I) C_0a vs C_0b	(II) C_0a vs C_4a	(III) <C_0> vs <C_4>
MAS5	Up	278	342	148
	Down	202	318	251
RMA	Up	11	74	95
	Down	7	58	68

Comparison of expression levels computed by MAS5 and RMA. Number of genes whose expression level was increased (Up) or decreased (Down) 1.5-fold (I) when two replicates of control cells are compared at time 0, (II) in a single chip prior to and 4 hrs after NCS treatment, and (III) in triplicate averaged chips of samples prior to and after NCS treatment. Expression levels below 30 were set to 30. Note the 25-fold decrease in the noise between two control replicates measured by the two methods (see also Supplementary Fig 3).

Supplementary Table F. Primers used in quantitative real-time RT-PCR assays.

Gene name	Locuslink ID	Forward primer (5'→3')	Reverse primer (5'→3')
CD83 (450-602)	9308	GTCTCCTGGGTCAAGTTATTGGA	AGTGTTTCGGATCTTCAGGGAATAG
IER3 (211-339)	8870	GCAGCCGCAGGGTTCTC	CCTCTTCAGCCATCAGGATCTG
NFκB1a (389-469)	4792	GGAGACCTGGCTTTCCTCAACT	TTCTGGCTGGTTGGTGATCAC
RelB (1299-1349)	5971	GCCATTGCCTTTCACGTACCT	TCCACGCCGTAGCTGTCAT
TNFAIP3 (2071-2181)	7128	GGAAGCACCATGTTTGAAGGATAC	TCTGCGCTGGCTCGATCT
TNFRSF9 (659-759)	3604	TGCGAGAGAGCCAGGACACT	AGAAACGGAGCGTGAGGAAG
ATF3 (462-542)	467	GCTGCAAAGTGCCGAAACA	AGCATTCACACTTTCAGCTTCT
DUSP1 (959-1129)	1843	CAACGAGGCCATTGACTTCATAG	ATGCTTCGCCTCTGCTTCA
EGR1 (1459-1531)	1958	GCCTGCGACATCTGTGGAA	GCCGCAAGTGGATCTTGGTA
ETR101 (1778-1890)	9592	CCCTCAGACACACGGACACA	AGCAACTGGTCTCAGCTCAGC
Fos (533-593)	2353	GGGCAAGGTGGAACAGTTATCT	CCTTTCCTTCGGATTCTCCT
GADD45A (669-803)	1647	TGCTGGTGACGAATCCACA	TCAGATGCCATCACCGTTCA
cJun (1270-1320)	3725	TGGAGCGCCTGATAATCCA	TCGGCGTGGTGGTGATG
GAPDH (943-1043)	2597	ACCCACTCCTCCACCTTTGA	CTGTTGCTGTAGCCAAATTCGT

Primers were designed with the PRIMER EXPRESS™ 1.0 software (PE Applied Biosystems, Foster city, CA, USA).

Supplementary Table G. Sequences of shRNAs used in this study.

ATM_I (7218) 5'-gatccccctggttagcagaaacgtgcttcaagagagcacgtttctgctaaccagtttttgaaa-3'.

ATM_II (p480): 5'-gatccccgataccagatccttgagattcaagagatctccaaggatctggtatcttttgaaa-3'.

(ATM level was knocked-down using a combination of two different siRNAs).

Rel_A: 5'-gatccccgaagagtccttcagcggattcaagagatccgctgaaaggactcttcttttgaaa -3'

p53: 5'-gatccccgactccagtggttaattacttcaagagagtagattaccactggagcttttttgaaa-3' (previously described in Brummelkamp et al.(Brummelkamp et al., 2002)).

LacZ: 5'-gatccccaaggccagacgcgaattatttcaagagaataattcgctctggccttttttgaaa-3'

Brummelkamp, T.R., Bernards, R. and Agami, R. (2002) Stable suppression of tumorigenicity by virus-mediated RNA interference. *Cancer Cell*, 2, 243-247.