

P30





**Figure W1.** Replicative senescence in late-passage fibroblast. (A) After 30 times of passage, the cells were subjected to SA-β-gal staining. (B) RT-PCR analysis of six candidate mRNAs in U373MG cells at indicated times after infection with Ad-p53 or Ad-LacZ. β2-*Microglobulin* was used for the normalization of expression levels. p21<sup>WAF1</sup> served as a positive control. (C) RT-PCR analysis of C6orf138 and CLCA2 mRNAs in NHDF cells at indicated passage levels. β2-Microglobulin was used for the normalization of expression levels. p21<sup>WAF1</sup> served as a positive control.

Table W1. List of 85 Senescence-Associated Genes.

Table W1. (continued).

Gene	P26/P3	p53 Induction	Gene	P26/P3	p53 Induction
MAST4	>50	++	RNLS	>50	
RGS4	>50		MAST4	41.74	
PPP4R4	>50		SFRP4	41.67	
ZNF367	>50		RGS2	40.24	
SORT1	>50		DTL	39.38	
SYPL2	>50		NPTX1	30.78	
LCE2A	>50	++	INA	29.34	
MOSC1	>50		NAT8L	28.66	+
TOMM40L	>50		MMP1	28.28	
CDNA FLJ32320 fis	>50		DBNDD1	24.25	
SDPR	>50		CCND1	22.55	
PPFIA2	>50		ATP8B4	22.11	
KIAA1147	>50		GLTPD1	22.02	
C6orf138	>50	++	MET	21.58	
DSCC1	>50		CCND1	20.73	
POLR3G	>50		MFAP1	20.20	
ETV4	>50		CCND2	18.71	
PARG	>50		C9orf57	18.21	
SIGLEC15	>50		FNDC5	16.78	
Clone IMAGE:35527	>50		PHLDA1	15.91	
LEPR	>50		CIT	15.55	
RBM24	>50		SLC1A2	15.32	
BRI3BP	>50		KLHDC9	14.87	
ANXA1	>50		TOR1AIP1	14.55	
HSFE-1	>50		IFIT2	14.42	
Clone 23555	>50		ENY2	14.26	
CCIN	>50		RNF219	13.97	
CACNA1H	>50		CDNA: FLJ21245 fis	13.40	++
SLC7A14	>50		PRKG2	12.32	
KLRF1	>50	+	TNIK	12.06	
PANK1	>50	++	APBA1	11.76	
ENPP5	>50		TMEM158	11.58	+
CPEB2	>50		E2F7	11.33	+
C11orf41	>50		CNTN3	10.96	
cDNA DKFZ\$6860 1044	>50		CYYR1	10.93	
TFDP1	>50		SLC35A3	10.77	
RASD1	>50		GPR68	10.76	
NAP1L2	>50		SYNM	10.63	
DHRS12	>50		ITGA6	10.56	
EIF2C1	>50		VWF	10.54	
SLC7A14	>50		PLCB1	10.38	
CLCA2	>50	++	CENPO	10.19	
CYP3A5	>50				
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"+" indicates more than 5-fold induction at 24 or 48 hours after infection with Ad-p53; "++," more than 10-fold induction at 24 or 48 hours after infection with Ad-p53.



**Figure W2.** Ectopic expression of p53 induced CLCA2 protein. (A) Western blot analysis of CLCA2 protein in U373MG cells at 48 hours after infection with Ad-p53 or Ad-LacZ at indicated doze. CBB staining was used for the normalization protein loading. siCLCA2\_1, siCLCA2\_2, or siEGFP was transfected at 7 hours before adenovirus infection at 20 MOI. Black arrowhead indicates CLCA2 protein; open arrowhead, nonspecific band. (B) Quantitative RT-PCR analysis of CLCA2 in U373MG cells 48 hours after infection with Ad-LacZ or Ad-p53 at 20 MOI. siCLCA2\_1, siCLCA2\_2, or siEGFP was transfected 7 hours before adenovirus infection.

A mouse p53BS G a A C T T G T A G A G a C A G G T C C human p53BS G g A C T T G T A G A G g C A G G T C C



**Figure W3.** Comparison of mouse *Clca5* and human CLCA2. (A) Alignment of mouse p53BS and human p53BS. Nucleotides conserved between human and mouse are written in capital letters. (B) Genomic structures of the mouse *Clca5* and human *CLCA2* genes. Gray boxes indicate the locations and relative sizes of the two exons. Arrows indicate the locations of potential p53-binding sites. (C) Results of luciferase assay of p53BR are shown. Luciferase activity is indicated relative to the activity of mock vector with SDs (n = 2).



**Figure W4.** Suppression of *CLCA2* expression in colorectal cancer tissues. (A) Relative *CLCA2* expressions in colorectal cancer tissues compared with normal tissues were examined by quantitative real-time PCR analysis.  $\beta$ -*Actin* was used for the normalization of expression levels. (B) Seven colorectal cancer cell lines were treated with 1 or 5  $\mu$ M of 5-Aza. *CLCA2* expressions were examined by quantitative real-time PCR analysis.  $\beta$ -*Microglobulin* was used for the normalization of expression levels. (C) *CLCA2* expressions were examined by quantitative real-time PCR analysis.  $\beta$ 2-*Microglobulin* was used for the normalization of expression levels. (C) *CLCA2* expressions were examined by quantitative real-time PCR analysis.  $\beta$ 2-*Microglobulin* was used for the normalization of expression levels. (D) *CLCA2* expressions were examined by quantitative real-time PCR analysis in 21 colorectal cancer cell lines.  $\beta$ 2-*Microglobulin* was used for the normalization of expression levels. Student's *t* test was applied for comparing the *CLCA2* expressions in p53 mutant cell lines with those in p53 wild-type cell lines.

Table W2. List of Cancer Cell Lines.

No.	Colorectal Cancer Cell Lines
1	DLD-1
2	HCT-15
3	HT-29
4	KM12C
5	KM12SM
6	NCI-H508
7	NCI-H684
8	NCI-H716
9	SNU-C2A
10	SNU C5
11	SW480
12	SW620
13	SW948
14	WiDr
15	HCT 116
16	LoVo
17	LS 174T
18	NCI-H498
19	RKO
20	SNU C4
21	SW48

Table W3. Sequences of Primers and RNA Nucleotides.

	Sense	Antisense
siRNA oligonucleotides		
siCLCA2_1	GGAAUUUACUCGAGGUAUUTT	AAUACCUCGAGUAAAUUCCTT
siCLCA2_2	GAUGAAUGCUCCAAGGAAATT	UUUCCUUGGAGCAUUCAUCTT
sip53	GACUCCAGUGGUAAUCUACTT	GUAGAUUACCACUGGAGUCTT
siEGFP	GCAGCACGACUUCUUCAAGTT	CUUGAAGAAGUCGUGCUGCTT
	Forward	Reverse
Quantitative real-time PCR (SYBR Green I Master	)	
CLCA2	ATACCTGCCACATGGAAAGC	CCTCTTTTCCACACCCTCTG
p21 <sup>WAF1</sup>	AAGATCAGCCGGCGTTTG	GACCTGTCACTGTCTTGTACCC
β2-Microglobulin	TCTCTCTTTCTGGCCTGGAG	AATGTCGGATGGATGAAACC
Clca5 (mouse)	CCGAGTGGTCTGCTTAGTGA	TACAGTTCGGCTGCTTGTTG
β-Actin (mouse)	CTAAGGCCAACCGTGAAAAG	ACCAGAGGCATACAGGGACA
p16	AGCATGGAGCCTTCGGCTGA	CCATCATCATGACCTGGATCG
Quantitative real-time PCR (Probe Master)		
CLCA2 no. 21	AGAAGAGGTCAGCAGGGAGA	CTCTTGATGGAGAAAGGATTAAAGA
β-Actin no. 55	TAGGAGGGCTGGCAACTTAG	CCAAGATGTTGATGTTGGATAAGA
Site-directed mutagenesis		
mClca5_mtp53BS1	AGATAGTTCCCAGATAGATCCACCCCA	CTAAAAATTCCTCTCCAAGGCAACGC
mClca5_mtp53BS2	GAATGTTCTCAAGAGGTGTGACTTAA	AGGACTATGCCTTTTAAAAACATTATT
mClca5_mtp53BS3	TAATATTTAATCAGTGTGCTAAAATCT	GGGATTACGCTCATGATCTCCCCAAGT
Semiquantitative RT-PCR		
CLCA2	CAGATGTGCAGCCTCAGAAG	TGCTGAGCACAGTGGGTAAG
p21 <sup>WAF1</sup>	GTTCCTTGTGGAGCCGGAGC	GGTACAAGACAGTGACAGGTC
β2-Microglobulin	CACCCCCACTGAAAAAGATGA	TACCTGTGGAGCAACCTGC