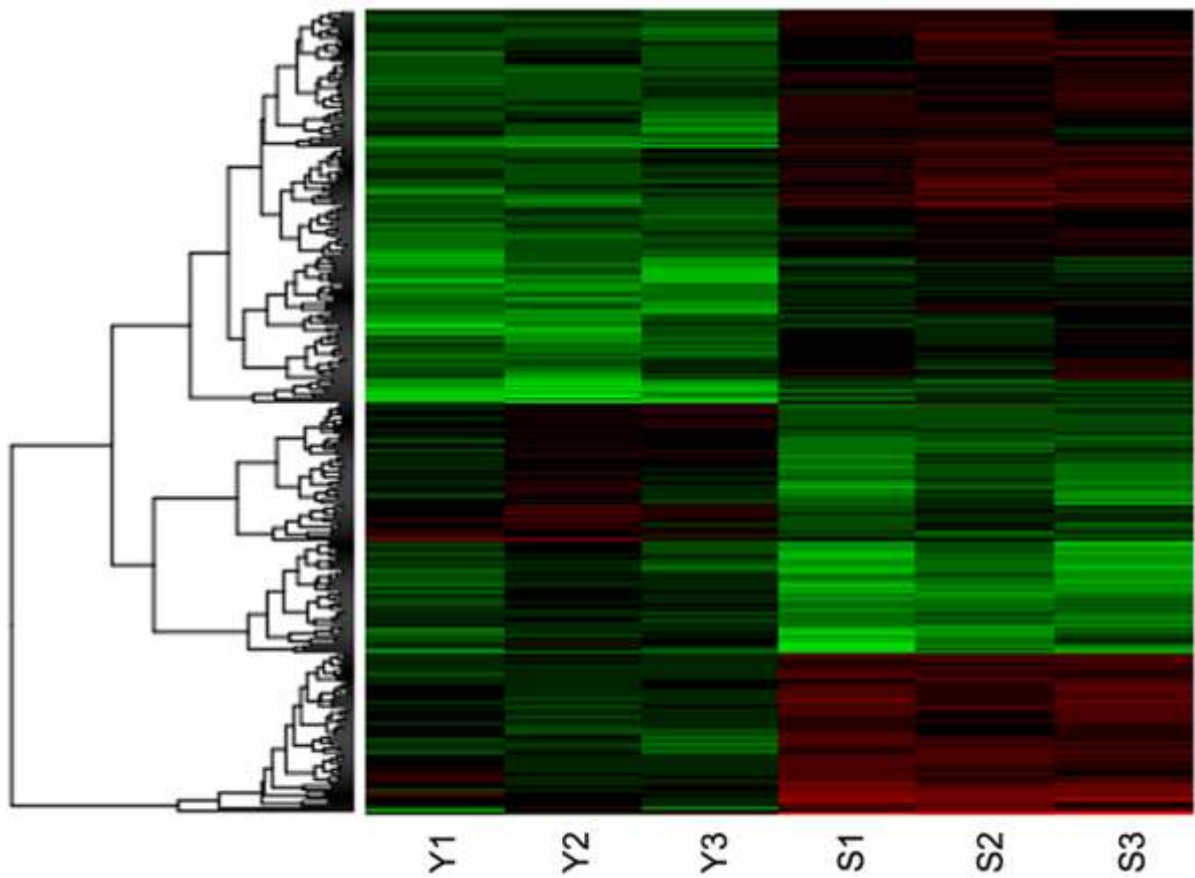


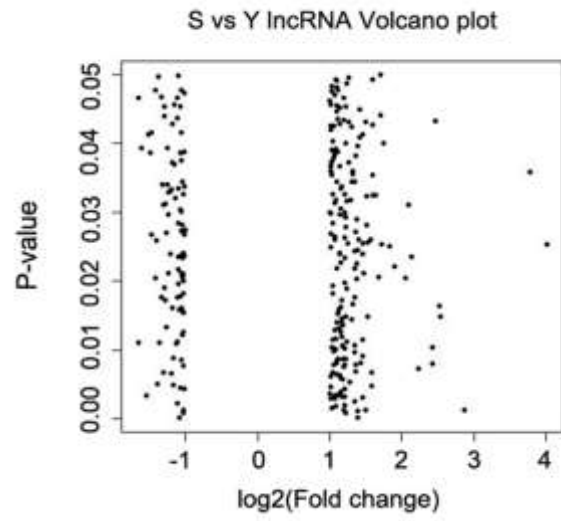
Identification of the lncRNA, AK156230, as a novel regulator of cellular senescence in mouse embryonic fibroblasts

Supplementary Material

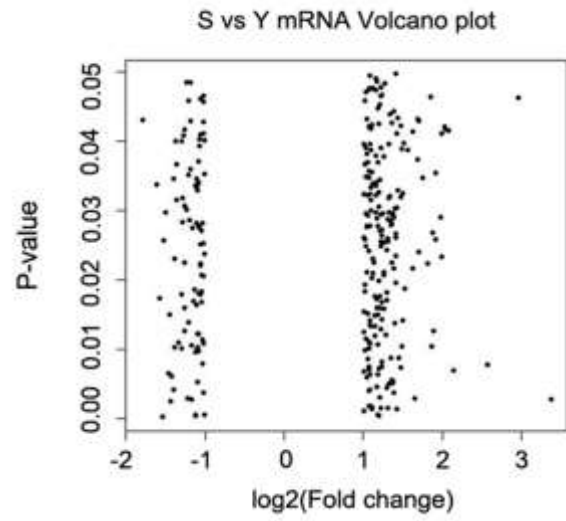


Supplementary Figure S1: mRNA expression profiles in senescent and young MEFs

(A)

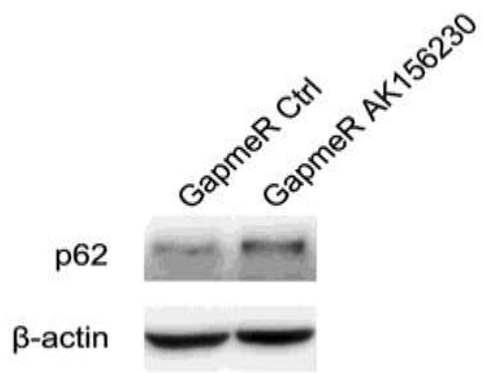


(B)



Supplementary Figure S2: Volcano plot of differentially expressed lncRNAs and mRNAs in senescent and young MEFs.

(A)



(B)

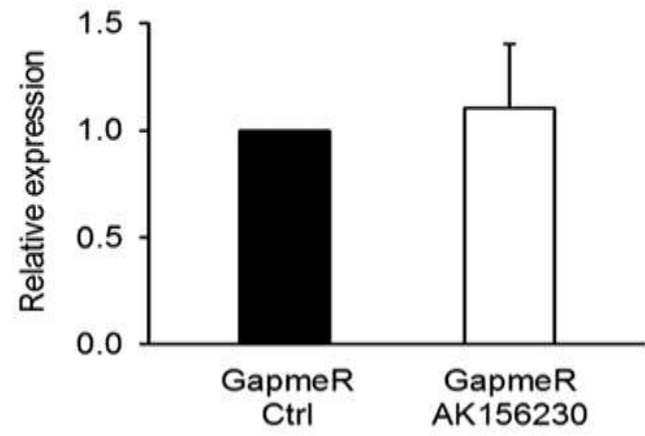


Figure S3: p62 expression after silencing of AK156230 in MEFs.

Table S6: Numbers of expressed differentially lncRNAs and mRNAs in senescent and young MEFs

	Fold change 2-3	Fold change 3-4	Fold change >4	total
lncRNA				
Up-regulation	168	12	12	192
Down-regulation	94	3	0	97
mRNA				
Up-regulation	182	18	7	207
Down-regulation	92	2	0	94

Table S7: Primers used for RT-qPCR analysis to validate lncRNAs expression

Primer	Sequence (sense)	Sequence (antisense)
AK137091	GGGTCGTTGGTTGGTTTC	TCATTAGGCGATTGGTTCA C
AK029004	TTGGGTACTTCCTCTGTGCCT	CAACGAAGCTAAGAGCTG GC
AK048098	TTCTCTGATGACTGCCGAGC	GGAACCCATACCCAACCCT
AK042519	CCTTAGGGCTGCCTGATTC	TTGGTTATAGCTGGTATGG TGC
AK041802	ACGGCATCGCATCGTATGT	TCCAGCATCCTCAGGGTCT G
AK085841	CAAGGTCCGTGGTTTGTC	CACTTACCCATTTCTTCTGT TCC
AK135413	GCCCACTGACACCTCCTATT	ATCAGACCCTTTCTCCAGT TG
AK156230	GAGGCTTTGAAAGTATGCTG C	AAGTGGGGTGTTGAATTGG T
β -actin	AGATGACCCAGATCATGTTT GAG	AGAGCATAGCCCTCGTAGA T

Table S8: Sequences for LNA longRNA GapmeR

LNA GapmeR	Sequence
GapmeR AK156230	GGAATAAAGATGGAC T
GapmeR AK135413	AACTAACAGTAATGG A
GapmeR AK048098	TTTAGCATGCTTGGTT
GapmeR Ctrl	AACACGTCTATACGC

Table S9: Numbers of differentially expressed mRNAs for AK156230 knockdown

mRNA	Fold change 2-4	Fold change 4-8	Fold change >8	total
Up-regulation	412	45	19	476
Down-regulation	900	197	60	1157

Table S10: GO term (Biological process) for the differentially expressed transcripts after AK156230 knockdown

GO.ID	Term	Count	p-Value	q-Value
GO:0007050	cell cycle arrest	16	4.493E-10	3.019E-08
GO:0008285	negative regulation of cell proliferation	31	6.512E-10	4.213E-08
GO:0016242	negative regulation of macroautophagy	6	1.204E-09	6.789E-08
GO:0000046	autophagic vacuole fusion	4	3.145E-07	9.082E-06
GO:0045786	negative regulation of progression through cell cycle	11	0.000151	0.001576
GO:0001302	replicative cell aging	2	0.010895	0.040715
GO:0048147	negative regulation of fibroblast proliferation	2	0.014300	0.050116
GO:0030308	negative regulation of cell growth	5	0.015794	0.054104
GO:0000086	G2/M transition of mitotic cell cycle	2	0.022272	0.063341
GO:0006914	autophagy	3	0.072929	0.131688

Table S11: KEGG pathway terms for the differentially expressed transcripts after AK156230 knockdown

KEGG Pathway	Count	<i>p</i>-Value	<i>q</i>-Value
p53 signaling pathway	7	1.43906E-06	5.58286E-06
Cell cycle	6	0.000366409	0.000746731
mTOR signaling pathway	5	4.7086E-05	0.000135372
Regulation of autophagy	2	0.028836139	0.029016365
Focal adhesion	27	6.5182E-26	1.04943E-23
Axon guidance	23	9.31464E-25	7.49828E-23
ECM-receptor interaction	19	3.433E-23	1.84238E-21
Cytokine-cytokine receptor interaction	26	9.76253E-22	3.92942E-20
Biosynthesis of steroids	11	5.16602E-18	1.66346E-16
Starch and sucrose metabolism	12	4.78614E-17	1.28428E-15

Table S12: Primers used for RT-qPCR analysis to validate mRNAs expression

Primer	Sequence (sense)	Sequence (antisense)
ULK2	TGGGAATGACCCTCGTGAG	AGCTACATCCATTGGTCGT TCT
ATG7	CGCCAAGATCTCCTACTCCA AT	GGCATTCACTCCGGGAAAT A
ATG16L2	CGAATCAGCAATATCCGACA G	CACCAAGCCACGGCATT
CDKN1A	AGGCACCATGTCCAATCC	AAGTCAAAGTTCCACCGTT CT
Rprm	GGTCAACAGTAGCGAGGCG	CAGCCAAGGAAGAAGATG CC
Inhba	CCAAAGTCACCATCCGTCTA	GGTACTCTTCCGAGCATCA AC
Cgref1	GGACCCTGAGGTACAACAGC	GTCATGAAGAGCAAAGAG CG
P62	TCTCTACAGATGCCAGAATC G	CTGTAGGAGCCTGGTGAGC
β -actin	AGATGACCCAGATCATGTTT GAG	AGAGCATAGCCCTCGTAGA T