

SUPPLEMENTARY DATA FOR:

P14ARF inhibits human glioblastoma-induced angiogenesis by regulating the expression of TIMP3

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TABLE OF CONTENTS:

Suppl. Table1: Angiogenesis related genes modulated by P14ARF in A5 cells.

Suppl. Figure 1: Regulation of *TIMP1*, *TIMP2* and *TIMP3* mRNA expression by P14ARF.

Suppl. Figure 2: Regulation of *TIMP3*, *MMP2*, *MMP9* and *VEGF* by P14ARF.

Suppl. Figure 3: Role of P53 in the effect of P14ARF on TIMP3 and TSP1 expression.

Suppl. Figure 4: *P14ARF* Silencing in HFF-1 downregulates TIMP3 expression.

Suppl. Figure 5: Expression of *Timp3* in a different batch of MEFs (passage 10)

Authors' contributions

S Table 1: List of angiogenesis –related genes modulated by P14ARF in A5 cells.

A5 human glioma cells were grown in duplicate plates to 80% confluence; then, the *P14ARF* gene was induced in one plate by exposing the cells to doxycycline (2ug/ml) for 48hrs after which the cells were lysed and total RNA prepared from two independent experiments using Trizol (Invitrogen, Carlsbad, CA). The integrity of the RNA was first monitored by agarose gel electrophoresis and then reverse transcribed to DNA, followed by *in vitro* transcription using BioArray High Yield RNA transcript labelling kit (Enzo, Farmingdale, NY). Biotin labelled cRNA was then fragmented according to the Affymetrix standard protocols. cRNA probes were hybridized overnight at 45°C to the Human Genome U133A arrays (Affymetrix, Santa Clara, CA), washed in a Fluidics Workstation, and scanned according to the manufacturer’s protocols. The Affymetrix CEL files were normalized using the robust multi-chip_analysis (RMA) method. After data normalization a list of genes up- and down-regulated upon *P14ARF* induction (dox) was generated by comparing gene expression profiles of A5 (+dox vs ctrl) using Gen Traffic software. **Microarray gene expression data were deposited at EMBL-EBI Array Express under accession E-MEXP-3476.** Angiogenesis-related genes with hybridization detection signal above 100 (background) and significantly modulated by P14ARF in A5 cells (dox vs ctrl) are highlighted. Changes in gene expression levels are considered significant when p -value < 0.05.

Probe set ID	Gene Symbol	A5 Ctrl	A5+dox	Fold induction	p-value	Entrez Gene Name
208042_at	AGGF1	99.75	74.45	0.75	0.289	angiogenic factor with G patch and FHA domains 1
218534_s_at	AGGF1	185.6	171.7	0.93	0.524	angiogenic factor with G patch and FHA domains 1
210710_at	AGGF1	41.9	51.8	1.24	0.577	angiogenic factor with G patch and FHA domains 1
205609_at	ANGPT1	27.2	21.95	0.81	0.469	angiopoietin 1
205609_at	ANGPT1	27.2	21.95	0.81	0.469	angiopoietin 1
205608_s_at	ANGPT1	112.7	98.55	0.87	0.705	angiopoietin 1
205608_s_at	ANGPT1	112.7	98.55	0.87	0.705	angiopoietin 1
221009_s_at	ANGPTL4	26.45	76.55	2.89	0.027	angiopoietin-like 4
205290_s_at	BMP2	57.5	105.2	1.83	0.014	bone morphogenetic protein 2
205289_at	BMP2	51.9	79	1.52	0.290	bone morphogenetic protein 2

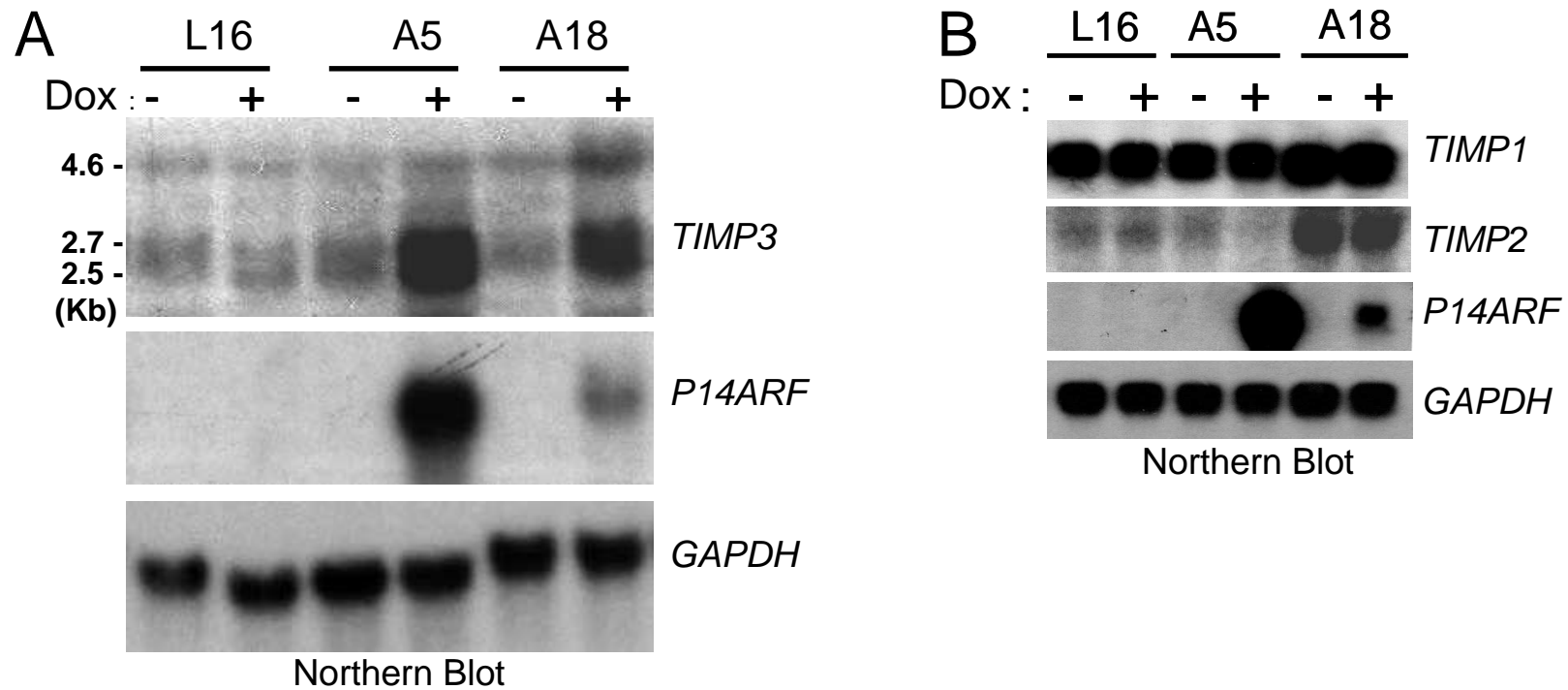
200920_s_at	BTG1	733.2	1335.35	1.82	0.064	B-cell translocation gene 1, anti-proliferative
200921_s_at	BTG1	395.7	624.4	1.58	0.372	B-cell translocation gene 1, anti-proliferative
216598_s_at	CCL2	2715	2118.85	0.78	0.777	chemokine (C-C motif) ligand 2
201926_s_at	CD55	297.8	543.1	1.82	0.010	CD55 molecule, decay accelerating factor for complement (Cromer blood group)
201925_s_at	CD55	125.15	168.95	1.35	0.384	CD55 molecule, decay accelerating factor for complement (Cromer blood group)
200984_s_at	CD59	2249.3	2918.6	1.30	0.029	CD59 molecule, complement regulatory protein
212463_at	CD59	436.8	497.75	1.14	0.006	CD59 molecule, complement regulatory protein
200983_x_at	CD59	3847	5416.85	1.41	0.055	CD59 molecule, complement regulatory protein
200985_s_at	CD59	1777.6	2266.1	1.27	0.213	CD59 molecule, complement regulatory protein
209082_s_at	COL18A1	146.85	82.95	0.56	0.117	collagen, type XVIII, alpha 1
209081_s_at	COL18A1	135.4	70.95	0.52	0.297	collagen, type XVIII, alpha 1
216898_s_at	COL4A3	17.4	13	0.75	0.131	collagen, type IV, alpha 3 (Goodpasture antigen)
216896_at	COL4A3	2.85	11.85	4.16	0.424	collagen, type IV, alpha 3 (Goodpasture antigen)
216368_s_at	COL4A3	46.95	32	0.68	0.479	collagen, type IV, alpha 3 (Goodpasture antigen)
214641_at	COL4A3	17.1	10.65	0.62	0.583	collagen, type IV, alpha 3 (Goodpasture antigen)
216367_at	COL4A3	23.2	12.65	0.55	0.591	collagen, type IV, alpha 3 (Goodpasture antigen)
216893_s_at	COL4A3	11.05	12.5	1.13	0.879	collagen, type IV, alpha 3 (Goodpasture antigen)
222073_at	COL4A3	16.15	16.5	1.02	0.973	collagen, type IV, alpha 3 (Goodpasture antigen)
204470_at	CXCL1	354.7	860.1	2.42	0.524	chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha)
204533_at	CXCL10	71.5	67.95	0.95	0.447	chemokine (C-X-C motif) ligand 10
209687_at	CXCL12	6.75	16.5	2.44	0.128	chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1)
203666_at	CXCL12	78	54.45	0.70	0.137	chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1)
207379_at	EDIL3	155.6	102.75	0.66	0.266	EGF-like repeats and discoidin I-like domains 3
202669_s_at	EFNB2	51.85	121.75	2.35	0.302	ephrin-B2
202668_at	EFNB2	100.15	107.45	1.07	0.863	ephrin-B2
206254_at	EGF	23.4	20.5	0.88	0.530	epidermal growth factor (beta-urogastrone)
216680_s_at	EPHB4	87.2	66.65	0.76	0.616	EPH receptor B4
202894_at	EPHB4	86.3	79.45	0.92	0.865	EPH receptor B4
205767_at	EREG	7.75	39.35	5.08	0.224	epiregulin
205110_s_at	FGF13	166.25	147.25	0.89	0.560	fibroblast growth factor 13
204421_s_at	FGF2	68.2	97	1.42	0.145	fibroblast growth factor 2 (basic)

204422_s_at	FGF2	43	23.55	0.55	0.360	fibroblast growth factor 2 (basic)
211719_x_at	FN1	2198.8	1891	0.86	0.569	fibronectin 1
216442_x_at	FN1	2569.05	2236.85	0.87	0.640	fibronectin 1
214701_s_at	FN1	265.7	249.95	0.94	0.662	fibronectin 1
210495_x_at	FN1	2758.95	2581.55	0.94	0.683	fibronectin 1
212464_s_at	FN1	2091.4	2050.9	0.98	0.840	fibronectin 1
214702_at	FN1	22.85	20.55	0.90	0.881	fibronectin 1
204948_s_at	FST	530.7	1008.3	1.90	0.444	follistatin
207345_at	FST	76.25	100.8	1.32	0.494	follistatin
200678_x_at	GRN	680.15	985.35	1.45	0.013	granulin
211284_s_at	GRN	231.8	376	1.62	0.093	granulin
216041_x_at	GRN	637.6	857.85	1.35	0.210	granulin
210755_at	HGF	15.5	9.45	0.61	0.354	hepatocyte growth factor (hepapoietin A; scatter factor)
209960_at	HGF	1.25	6.65	5.32	0.441	hepatocyte growth factor (hepapoietin A; scatter factor)
210998_s_at	HGF	2.3	3	1.30	0.645	hepatocyte growth factor (hepapoietin A; scatter factor)
210997_at	HGF	2.1	2	0.95	0.698	hepatocyte growth factor (hepapoietin A; scatter factor)
209961_s_at	HGF	84.3	85	1.01	0.980	hepatocyte growth factor (hepapoietin A; scatter factor)
200989_at	HIF1A	1893.75	2348.3	1.24	0.608	hypoxia inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)
219403_s_at	HPSE	120.55	179.55	1.49	0.369	heparanase
208937_s_at	ID1	320.9	297.35	0.93	0.869	inhibitor of DNA binding 1, dominant negative helix-loop-helix protein
207160_at	IL12A	16.2	21.05	1.30	0.201	interleukin 12A (natural killer cell stimulatory factor 1, cytotoxic lymphocyte maturation factor 1, p35)
207901_at	IL12B	11.4	13.75	1.21	0.561	interleukin 12B (natural killer cell stimulatory factor 2, cytotoxic lymphocyte maturation factor 2, p40)
39402_at	IL1B	61	375.8	6.16	0.332	interleukin 1, beta
205067_at	IL1B	80.45	593.45	7.38	0.352	interleukin 1, beta
205207_at	IL6	42.05	48.05	1.14	0.778	interleukin 6 (interferon, beta 2)
211506_s_at	IL8	46.15	446.45	9.67	0.394	interleukin 8
202859_x_at	IL8	114.15	639.65	5.60	0.423	interleukin 8
202351_at	ITGAV	475.9	324.1	0.68	0.239	integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51)
204628_s_at	ITGB3	169.5	178.35	1.05	0.034	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)

215240_at	ITGB3	54.95	46	0.84	0.421	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)
204627_s_at	ITGB3	338.45	284.3	0.84	0.480	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)
204625_s_at	ITGB3	192.55	211.15	1.10	0.792	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)
211579_at	ITGB3	17.45	19.95	1.14	0.819	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)
216261_at	ITGB3	73.45	80.15	1.09	0.855	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)
204626_s_at	ITGB3	136.35	134.1	0.98	0.927	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)
209098_s_at	JAG1	34.3	66.95	1.95	0.039	jagged 1 (Alagille syndrome)
216268_s_at	JAG1	75.95	175.75	2.31	0.072	jagged 1 (Alagille syndrome)
209099_x_at	JAG1	67.35	210	3.12	0.098	jagged 1 (Alagille syndrome)
209097_s_at	JAG1	3.35	6.25	1.87	0.467	jagged 1 (Alagille syndrome)
211124_s_at	KITLG	10.55	34.7	3.29	0.098	KIT ligand
207029_at	KITLG	29.25	54.25	1.85	0.326	KIT ligand
209035_at	MDK	179.1	183.95	1.03	0.873	midkine (neurite growth-promoting factor 2)
201069_at	MMP2	4083.8	3300.8	0.81	0.056	matrix metalloproteinase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase)
203936_s_at	MMP9	120.25	101.35	0.84	0.508	matrix metalloproteinase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV collagenase)
205247_at	NOTCH4	46.7	38.35	0.82	0.712	Notch homolog 4 (Drosophila)
212298_at	NRP1	95.35	166.9	1.75	0.035	neuropilin 1
210615_at	NRP1	20.45	13.25	0.65	0.643	neuropilin 1
210841_s_at	NRP2	92.75	131.25	1.42	0.025	neuropilin 2
214632_at	NRP2	60.05	126.6	2.11	0.217	neuropilin 2
210842_at	NRP2	6.65	13	1.95	0.356	neuropilin 2
211844_s_at	NRP2	3.8	24.55	6.46	0.425	neuropilin 2
219367_s_at	NRP2	87.95	90	1.02	0.928	neuropilin 2
205463_s_at	PDGFA	639.95	499.2	0.78	0.601	platelet-derived growth factor alpha polypeptide
216867_s_at	PDGFA	147.7	181.3	1.23	0.798	platelet-derived growth factor alpha polypeptide
219304_s_at	PDGFD	66.7	47	0.70	0.137	platelet derived growth factor D
209652_s_at	PGF	20.5	14.7	0.72	0.415	placental growth factor
215179_x_at	PGF	378.95	323.25	0.85	0.487	placental growth factor
205479_s_at	PLAU	39.8	60.7	1.53	0.252	plasminogen activator, urokinase
211668_s_at	PLAU	54.1	42.55	0.79	0.357	plasminogen activator, urokinase
209977_at	PLG	8.05	3.8	0.47	0.333	plasminogen
219700_at	PLXDC1	26.45	31.8	1.20	0.603	plexin domain containing 1

214081_at	PLXDC1	30.25	28.65	0.95	0.882	plexin domain containing 1
205445_at	PRL	50.05	35.05	0.70	0.322	prolactin
205127_at	PTGS1	8.7	11.75	1.35	0.051	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)
215813_s_at	PTGS1	101.95	66.75	0.65	0.004	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)
205128_x_at	PTGS1	64.65	84.2	1.30	0.213	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)
212099_at	RHOB	327.9	418.45	1.28	0.461	ras homolog gene family, member B
206050_s_at	RNH1	754.45	782.35	1.04	0.261	ribonuclease/angiogenin inhibitor 1
216798_at	RNH1	40.85	32.4	0.79	0.285	ribonuclease/angiogenin inhibitor 1
209359_x_at	RUNX1	22.8	103.35	4.53	0.120	runt-related transcription factor 1
211180_x_at	RUNX1	36.2	104.9	2.90	0.189	runt-related transcription factor 1
210805_x_at	RUNX1	3.4	5.35	1.57	0.294	runt-related transcription factor 1
211182_x_at	RUNX1	9.8	25.85	2.64	0.325	runt-related transcription factor 1
211620_x_at	RUNX1	9.7	30.2	3.11	0.331	runt-related transcription factor 1
209360_s_at	RUNX1	141.85	165.7	1.17	0.474	runt-related transcription factor 1
208129_x_at	RUNX1	36.95	41.35	1.12	0.550	runt-related transcription factor 1
210365_at	RUNX1	43.1	57.1	1.32	0.594	runt-related transcription factor 1
217263_x_at	RUNX1	26.1	20.3	0.78	0.719	runt-related transcription factor 1
211181_x_at	RUNX1	39.6	52.2	1.32	0.770	runt-related transcription factor 1
211179_at	RUNX1	2.15	2.3	1.07	0.827	runt-related transcription factor 1
219257_s_at	SPHK1	227	252.95	1.11	0.860	sphingosine kinase 1
205015_s_at	TGFA	152.2	263.7	1.73	0.041	transforming growth factor, alpha
205016_at	TGFA	711.65	1027.9	1.44	0.101	transforming growth factor, alpha
211258_s_at	TGFA	168.2	261.85	1.56	0.136	transforming growth factor, alpha
203085_s_at	TGFB1	253.3	442.25	1.75	0.027	transforming growth factor, beta 1
203084_at	TGFB1	6.9	5.7	0.83	0.633	transforming growth factor, beta 1
201109_s_at	THBS1	197	473.4	2.40	0.153	thrombospondin 1
201108_s_at	THBS1	305.85	528.5	1.73	0.218	thrombospondin 1
201110_s_at	THBS1	80	135.2	1.69	0.223	thrombospondin 1
215775_at	THBS1	76	81.25	1.07	0.690	thrombospondin 1
203083_at	THBS2	622.45	678.85	1.09	0.536	thrombospondin 2
201666_at	TIMP1	2268.7	3163.8	1.39	0.063	TIMP metalloproteinase inhibitor 1

203167_at	TIMP2	495.45	391.95	0.79	0.467	TIMP metalloproteinase inhibitor 2
201149_s_at	TIMP3	674.9	2403.15	3.56	0.021	TIMP metalloproteinase inhibitor 3
201147_s_at	TIMP3	474.5	1532.25	3.23	0.005	TIMP metalloproteinase inhibitor 3
201148_s_at	TIMP3	433.1	1160	2.68	0.027	TIMP metalloproteinase inhibitor 3
204858_s_at	TYMP	100	134.55	1.35	0.142	thymidine phosphorylase
217497_at	TYMP	17.2	7.8	0.45	0.218	thymidine phosphorylase
211527_x_at	VEGFA	23.9	69.85	2.92	0.134	vascular endothelial growth factor A
210513_s_at	VEGFA	124.85	154.2	1.24	0.154	vascular endothelial growth factor A
210512_s_at	VEGFA	42.45	75.2	1.77	0.387	vascular endothelial growth factor A
212171_x_at	VEGFA	151.75	171.95	1.13	0.391	vascular endothelial growth factor A
209946_at	VEGFC	72.4	57.65	0.80	0.061	vascular endothelial growth factor C

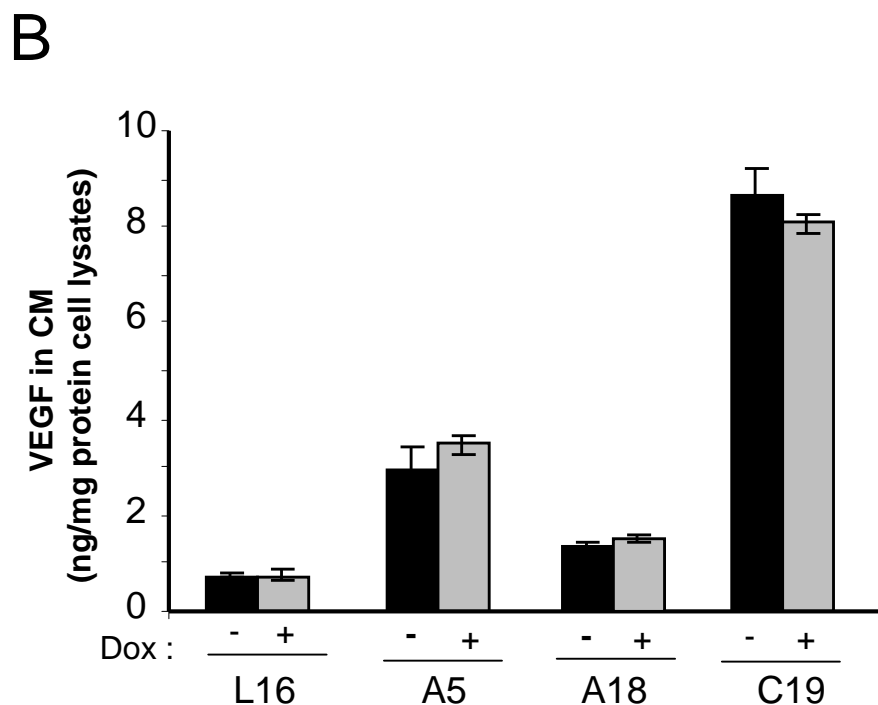
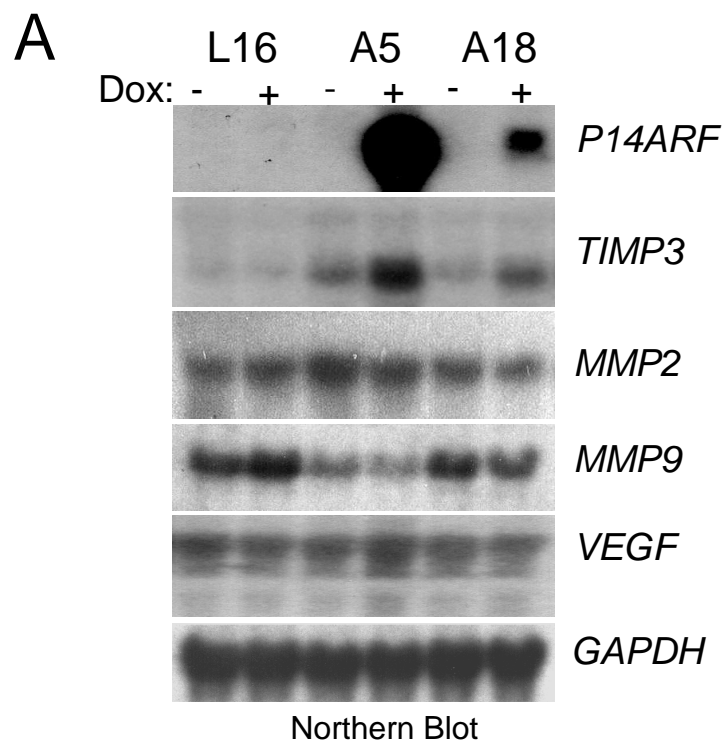


Supplementary Figure 1:

Regulation of *TIMP1*, *TIMP2* and *TIMP3* mRNA expression by *P14ARF*.

A. Independent repeat of the experiment in Figure 2A. Northern Blot showing the induction of *TIMP3* mRNA expression with doxycycline (2µg/ml for 48hrs) in *P14ARF*-expressing A5 and A18 cells. Note that dox treatment of LN229-L16 parental cells does not affect the basal expression level of all three *TIMP3* mRNA isoforms (estimated sizes in Kb are indicated).

B. Effect of *P14ARF* on the mRNA expression of *TIMP1* and *TIMP2* genes in A5 and A18 cells by Northern blot. Please note that neither *TIMP1* nor *TIMP2* mRNA levels were affected by *ARF* induction with dox (2µg/ml for 48hrs). *TIMP4* (not shown) was not detectable in these cells.

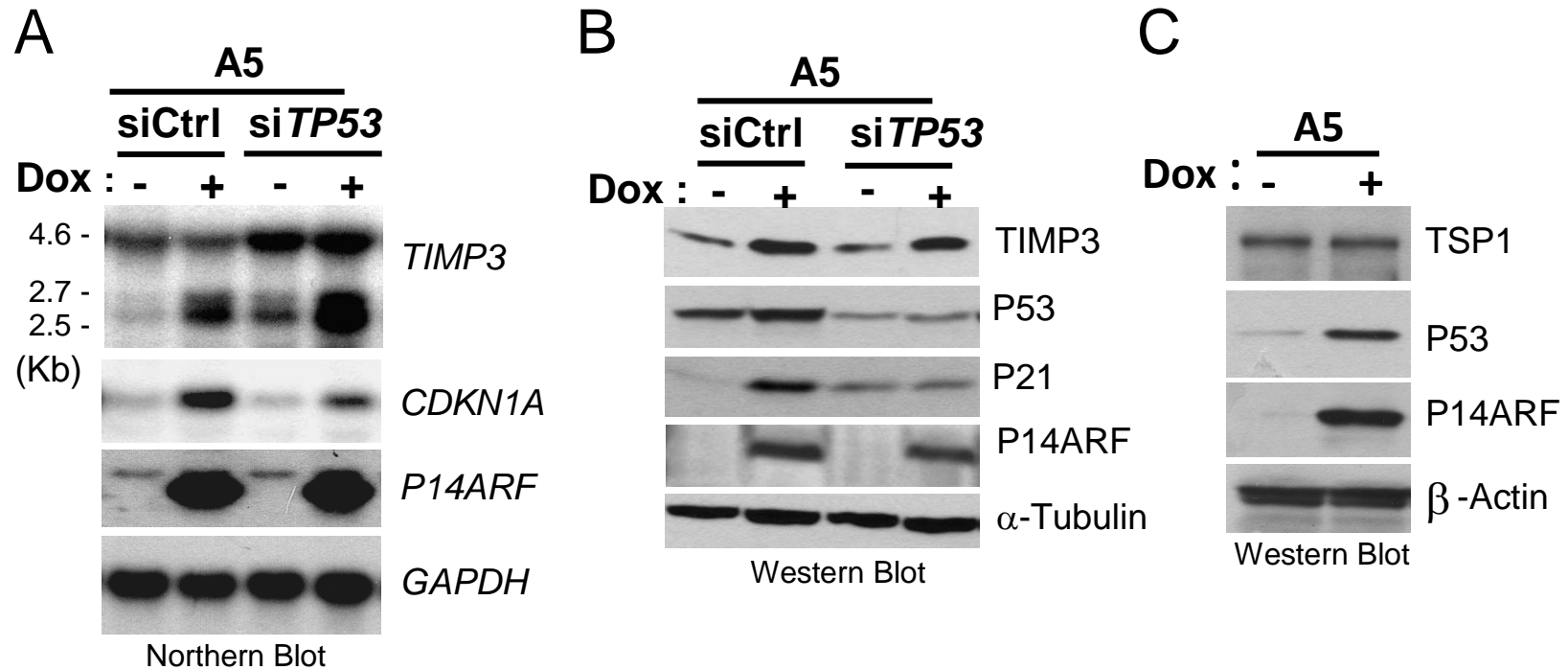


Supplementary Figure 2:

Regulation of *TIMP3*, *MMP2*, *MMP9* and *VEGF* by *P14ARF*.

A- Northern blot showing the effect of *P14ARF* expression on the transcription of *TIMP3*, *MMP2*, *MMP9* and *VEGF* genes. L16, A5 and A18 cells were treated with 2 μ g/ml dox for 48hrs. Note that the induction of *P14ARF* in A5 and A18 cells increases *TIMP3* mRNA levels while it does not affect the steady state of *MMP2*, *MMP9* and *VEGF* mRNAs. L16 are parental cells which do not express the *P14ARF* gene.

B- Effect of *P14ARF* expression on the levels of secreted VEGF by L16, A5, A18 and C19 cells in the culture media. Cells were plated in 12 well plate, cultured in 1 ml of serum free medium in the absence or presence of dox (2 μ g/ml) during 48hrs. CM was collected and VEGF was quantified using the Quantikine ELISA kit (R&D Systems, MN). No significant changes (using Student's t-test) in the levels of VEGF in culture media following the induction of *P14ARF* by dox versus controls (-dox).



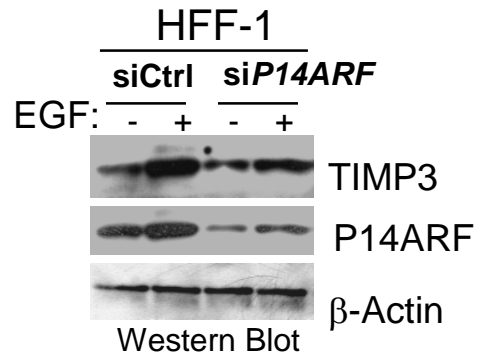
Supplementary SFigure 3:

Role of P53 in the effect of P14ARF on TIMP3 and TSP1 expression.

A- Northern blot showing that the silencing of *TP53* has no effect on p14ARF's ability to induce *TIMP3* gene expression in LN229-L16 derived A5 cells. In fact, *TP53* silencing even increased the basal expression levels of the three major *TIMP3* mRNA isoforms expressed in these cells (size in Kb estimated after Byrne JA et al, Molecular Medicine, 1:418. 1995). *P14ARF* activation with dox (2 μ g/ml dox for 48hrs) and *TP53* silencing (si*TP53*) synergistically activated the expression levels of the 2.5 and 2.7 Kb *TIMP3* mRNA isoforms. The expression level of *CDKN1A/P21*, a P53 transcriptional target, was used as a control to monitor that si*TP53* indeed decreased P53 levels and consequently the transcriptional activity of P53 as previously shown in **Figure 3A**.

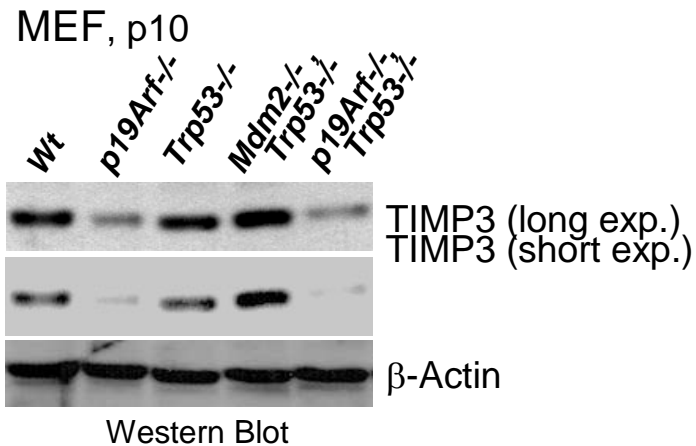
B- Western Blot showing that siRNA mediated silencing of *TP53* dramatically decreases P53 protein levels, yet does not inhibit the induction of *TIMP3* gene expression by P14ARF in LN229 L16-derived A5 cells (2 μ g/ml dox for 48hrs). *TP53* silencing even slightly increased the basal expression levels of TIMP3 protein as observed in panel A at the mRNA levels. The expression of *CDKN1A/P21* is used as a control to monitor the transcriptional activity of P53.

C-Western Blot showing that while P14ARF increases P53 protein levels, it failed to induce Thrombospondin (TSP1) expression in A5 cells, suggesting that the *THBS1* gene is not induced by P14ARF nor by P53 in glioma cells, confirming our previous findings with a *TP53*-inducible glioma cell line (Tenan, M. et al, J Exp Med, 191:1789-98, 2000)



Supplementary Figure 4: *P14ARF* silencing downregulates TIMP3 expression in HFF-1 cells

HFF-1 immortalised human fibroblasts were transfected with either siCtrl or si*P14ARF* using Lipofectamine 2000, starved for 12 hrs and then treated or not with EGF (100ng/ml) for 24 hrs. Expression of TIMP3 and P14ARF was analyzed by western blot. Note that silencing of *P14ARF* decreases EGF-induced TIMP3 levels.



Supplementary Figure 5: Expression of *Timp3* in a different batch of MEFs (passage 10).

Expression of *Timp3* in different mouse embryonic fibroblasts knocked out for genes as indicated in long and short exposures of the blot. *Timp3* is decreased in *p19Arf*-null MEFs vs *Trp53*-null or *Trp53* and *Mdm2* double null (*p19Arf* positive). The absence of *p19Arf* (lane 2) or the presence of *Mdm2* (lane 5) decreases TIMP3 expression.

Authors' contributions:

AZ and EGVM conceived the project and designed experiments, AZ performed and coordinated experiments in collaboration with BP for northern, western and microarray analyses (Figure 3A-C, Suppl. Table 1), MF for cornea assays (Figure 1C and 4A), DJB for pathology (Figure 1D), and AZ and EGVM interpreted the data and wrote the manuscript.