

Supplementary Figure Legends

Supplementary Figure 1. Generation of *Pten* conditional allele.

Schematic of *Pten* targeting vector. LoxP sites were inserted into intronic sites flanking *Pten* exon 5. The conditional allele was generated after crossing the targeted mice with E2a-Fp1 mice.

Supplementary Figure 2. *hGFAP-Cre* recombinase is activated during early CNS development as well as gliomagenesis.

a, β -gal staining of E14.5 embryos with the genotype of *hGFAP-Cre*, *Rosa26-LSL-LacZ*.

b, β -gal staining of sections of mouse forebrain with the genotype of *hGFAP-Cre*, *Rosa26-LSL-LacZ*.

c, Sections from normal cerebral cortex and two high-grade gliomas were subjected to immunofluorescent labeling with anti-GFAP (green), anti-Cre (red) and DAPI (blue). Scale bar, 50 μ m.

Supplementary Figure 3. *hGFAP-Cre*; *P53*^{lox/lox}; *Pten*^{lox/+} mice develop high-grade malignant gliomas.

a, Histological features of glioblastomas observed in *hGFAP-Cre*; *P53*^{lox/lox}; *Pten*^{lox/+} mouse brains. “N” designates areas of the palisading with regional necrosis in the tumors; “V” regions suggestive of microvascular proliferation; “S” subpial spread; arrows in (h) point to perineuronal satellitosis and arrowheads in (i) point to perivascular satellitosis. Note (a) and (d), (b) and (e), (c) and (f) represent the same tumor regions with different magnification. Scale bar, 50 μ m.

b, Small emerging tumors in asymptomatic mice show highly malignant histological features. Note arrow points to multinucleated giant cell; and arrowheads indicate mitotic figures amid the tumor cells. Scale bar, 50 μ m.

Supplementary Figure 4. EGFR and PDGFR α are co-activated within the murine malignant glioma cells.

a, PDGFR α is specifically overexpressed in the tumor cells as compared to normal brain cells. “N” designates the normal brain region. Note the infiltration of PDGFR α -positive glioma cells into the adjacent normal brain.

b, EGFR is activated in the malignant glioma cells. Adjacent sections from control normal brain and two independent high-grade gliomas were subjected to H&E (a-c), immunohistochemical staining for EGFR (d-f), and phospho-EGFR (pEGFR; g-i). Note the robust staining of the pEGFR in the tumor cells as compared to the normal cells. Scale bar, 50 μ m.

c, EGFR and PDGFR α are co-activated within the murine malignant glioma cells. Adjacent sections from a control normal brain and two high-grade gliomas were stained with H&E and co-immunohistochemically stained with antibodies against-PDGFR α (brown) and pEGFR (pink). Scale bar, 50 μ m.

d, Activated PDGFR α and EGFR are co-localized in the murine glioma tumor sphere (TNS) cells. Two freshly isolated TNS lines and *p53/Pten* double-null NSCs in EGF/bFGF-free medium were subjected to immunofluorescent staining with antibodies against pEGFR (green), pPDGFR α (red) and DAPI (blue). Scale bar, 10 μ m.

Supplementary Figure 5. *hGFAP-Cre;P53^{lox/lox};Pten^{lox/+}* murine malignant gliomas present high inter- and intra-tumoral histological heterogeneity.

Images a-c, d-f and g-i represent three different regions of tumor #1, #2 and #3, respectively. Note the mixed conspicuously fibrillated matrix of astrocytoma and “fried egg” appearance of oligodendroglioma features in tumor #3 (g-i); arrows designate astrocytoma cells and arrowheads oligodendroglioma cells.

Supplementary Figure 6. Malignant glioma cells express progenitor but not terminally differentiated CNS cell lineage markers.

a, Sections from control normal brain and two independent high-grade gliomas were subjected to H&E and immunohistochemical staining with antibodies against Nestin, GFAP, Olig-2 and Tuj-1. Scale bar, 50 μ m.

b, Malignant glioma cells do not express terminally differentiated CNS cell lineage markers. Adjacent sections of normal brain and two independent malignant gliomas were stained with H&E (a-c), and antibodies against mature oligodendrocyte marker MBP as well as neuronal marker NeuN. Note “N” designates the normal brain region adjacent to the tumor mass region. Scale bar, 50 μ m.

Supplementary Figure 7. Secondary tumors generated from orthotopic injection of tumor-spheres recapitulate the pathological features of primary tumors.

Adjacent sections of two independent primary malignant gliomas and their derived secondary tumors were stained with H&E and antibodies against GFAP. Scale bar, 50 μ m.

Supplementary Figure 8. Wild-type and mutant NSCs present different proliferation rate but similar stem/progenitor features when cultured in NSC medium.

a, The proliferation of *p53/Pten* double-null NSCs is enhanced as compared with wild-type and singly null NSCs. NSCs were cultured in NSC medium and proliferation was measured at indicated time points (n=3). Values represent mean \pm s.d. from three experiments.

b, Upper panel, wild-type and indicated mutant NSCs cultured in NSC medium with EGF and bFGF were subjected to immunofluorescent staining with antibodies against NSC/progenitor marker Nestin (red), astrocyte lineage marker GFAP (green), neuronal lineage marker Tuj1 (red) and DAPI (blue). Lower panel, quantification histograms indicate percentages of different lineage markers staining positive cells in wild-type and mutant NSCs as shown in b. Values represent mean from three independent experiments.

Supplementary Figure 9. Both embryonic and adult p53/Pten double-null NSCs are defective in their self-renewal and differentiation.

a, Quantification histograms indicate the 1% FBS-induced multi-lineage differentiation of E13.5 double-null NSCs was markedly abrogated as compared with wild-type and

singly null NSCs as shown in Figure **3b** (* $P < 0.005$; ** $P < 0.05$; $n = 3$). Values represent mean \pm s.d. from three experiments.

b, The number of multipotent neurospheres formed by adult *p53/Pten* double-null NSCs in culture was significantly increased as compared with that of wild-type or singly null NSCs (* $P < 0.001$; $n = 3$). Indicated NSCs were seeded 1,000 cells per well and incubated in the NSC medium with EGF and bFGF for 14 days before counting. Values represent mean \pm s.d. from three experiments.

c, The multi-lineage differentiation induced by 1% FBS was markedly abrogated in adult double-null NSCs as compared with wild-type and singly null NSCs. Left panel – adult NSCs were cultured in differentiation medium with 1% FBS for 7 days before being subjected to immuno-staining with antibodies against Nestin, GFAP, and Tuj1. Note “Nes” designates for Nestin (red); “G” for GFAP (green); “Tuj” for Tuj1 (red) and “D” for DAPI (blue). Right panel - quantification of left panel (* $P < 0.005$; $n = 3$). For all graphs, values represent mean \pm s.d. from at least three experiments.

Supplementary Figure 10. Inhibition of PI-3K/AKT pathway sensitizes *p53/Pten* double-null NSCs to differentiation.

a, E13.5 *p53/Pten* double-null NSCs cultured in 1% FBS in the absence or presence of AKT inhibitor (triciribine, 5 μ M) for 7 days were subjected to immunofluorescent staining with antibodies against nestin (red), GFAP(green) and DAPI (blue).

b, Quantification of figure A (** $P < 0.05$; * $P < 0.001$; $n = 3$). Error bars (s.d.) are derived from three experiments.

Supplementary Figure 11. c-Myc level is crucial for regulating NSC differentiation.

a, Histograms show percentages of cells immuno-positive for different lineage markers after knockdown of c-Myc in *p53/Pten* double-null NSCs as shown in Figure **3d** (* $P < 0.005$; ** $P < 0.05$; $n = 3$). Values represent mean \pm s.d. from three experiments.

b, Ectopical c-Myc expression in *p53*-null NSCs represses their differentiation potential. *p53* singly null NSCs infected with c-Myc or vector control were incubated in 1% FBS differentiation medium for 7 days before being subjected to immunofluorescent staining

with antibodies against NSC/progenitor markers nestin (red) or Sox2 (red), astrocytic marker GFAP(green), and DAPI (blue).

Supplementary Figure 12. Reduction of c-Myc expression inhibits murine malignant glioma TNS cell self-renewal and proliferation, while enhances their differentiation.

a, Inhibition of AKT pathway with triciribine induces TNS cell differentiation. Histogram graph indicates the percentage of TNS cells immuno-positive for different lineage markers as shown in Figure 4a (n=3).

b, Knockdown of c-Myc expression reduces the TNS cell growth. TNS cells infected with indicated lenti-shRNA virus were cultured in NSC medium and cell proliferation measured 6 days after seeding (** $P < 0.01$; * $P < 0.001$; n=3).

c, Reduction of c-Myc expression reduces the sphere size of the TNS cells. TNS cells infected with indicated lenti-shRNA were cultured in NSC medium with soft-agar.

d, Quantification histograms of Figure 4d indicate reduction of c-Myc expression in murine TNS cells by shRNA sensitizes cells to differentiation (* $P < 0.005$; ** $P < 0.05$; n=3).

For all graphs values represent mean \pm s.d. from at least three experiments.

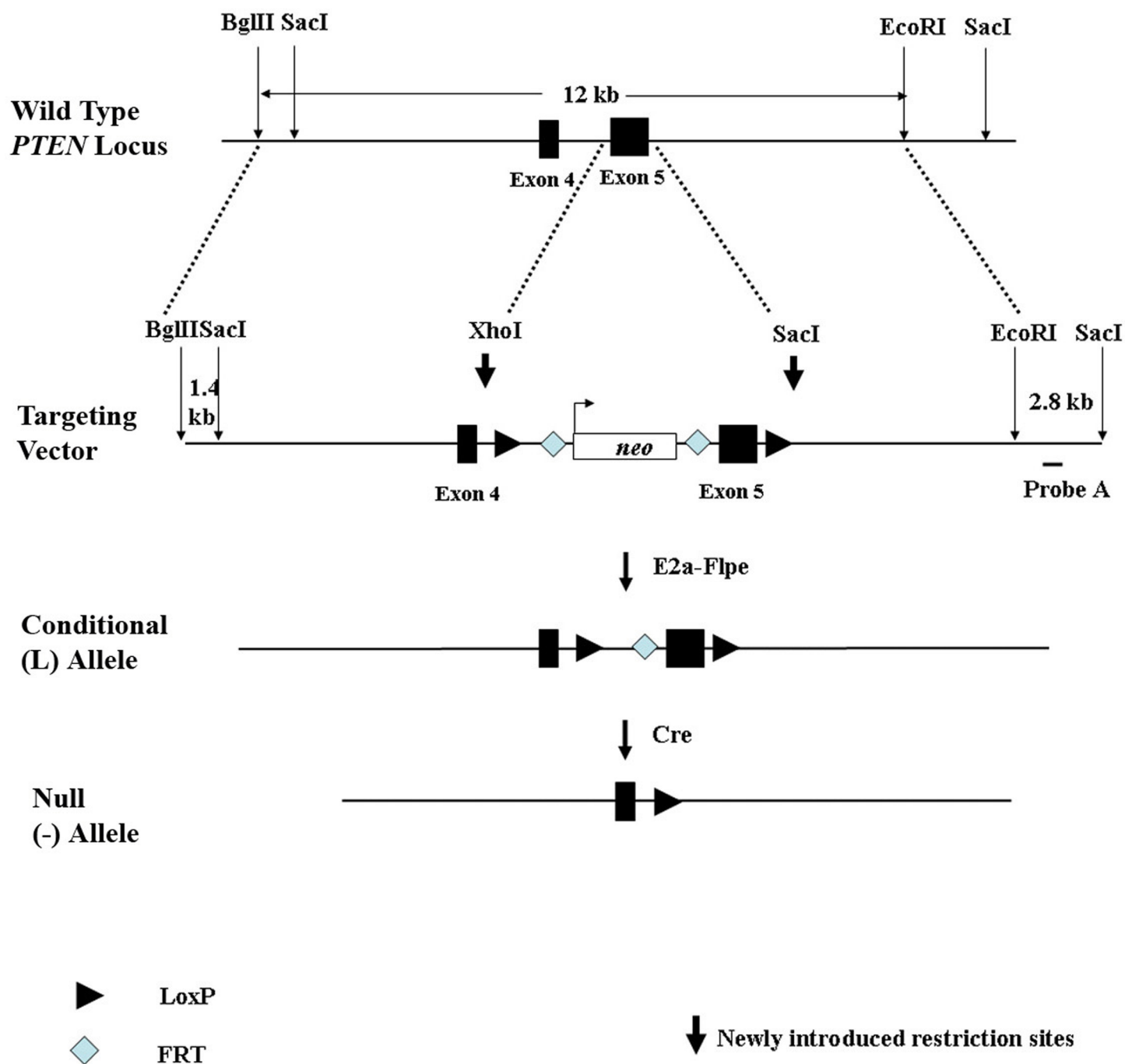
Supplementary Figure 13. p53 and Pten converge on c-Myc to regulate normal and malignant stem/progenitor self-renewal and differentiation.

Combinatorial inactivation of both *p53* and *Pten* tumor suppressors collectively elevate c-MYC and E2F activity to enhance NSC self-renewal and impede their differentiation capacity.

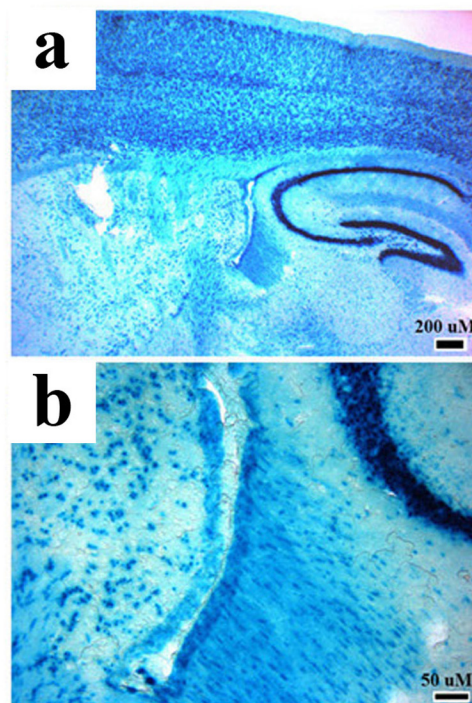
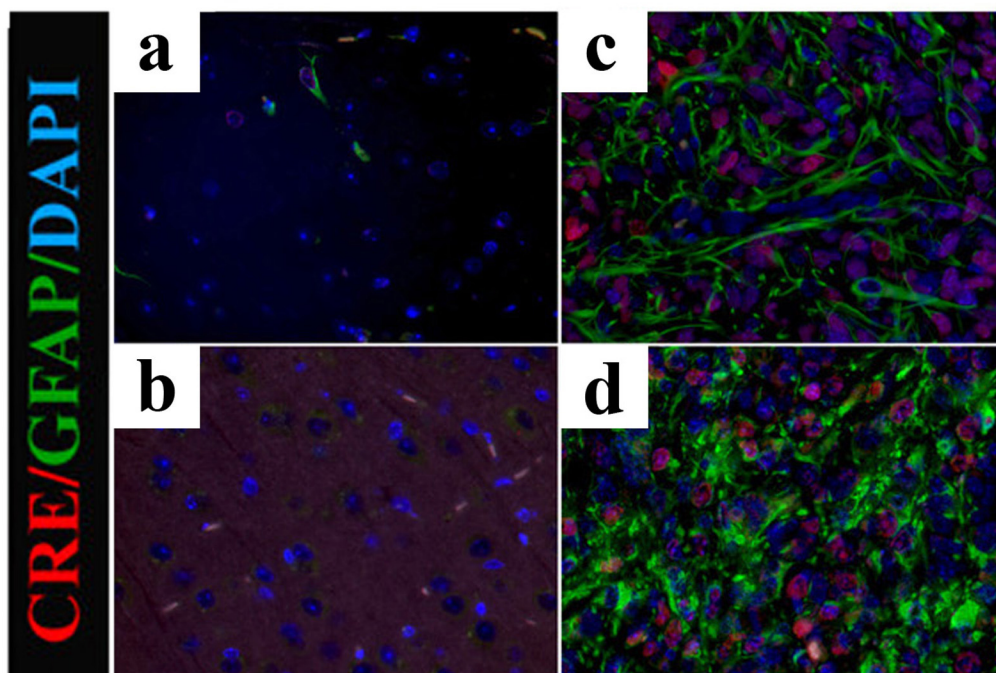
Supplementary Table 1. P53 and PTEN status in 35 human primary glioblastoma samples.

Supplementary Table 2. List of Top 410 Differentially Expressed Genes.

The list of genes differentially expressed in p53/Pten double-null and p53-null NSCs 1 day post differentiation induction was generated using the SAM statistic, with a cutoff of ± 2.0 .

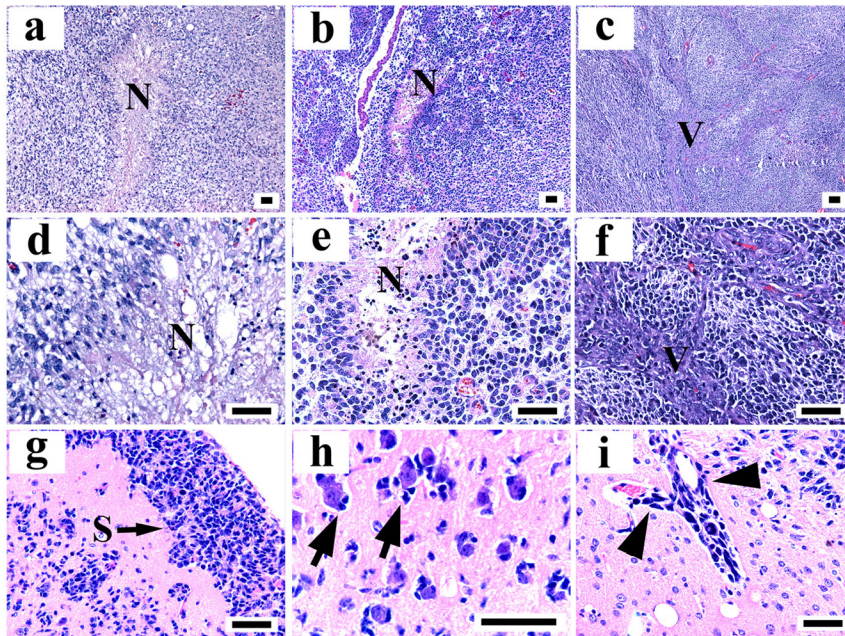


Supplementary Figure S1

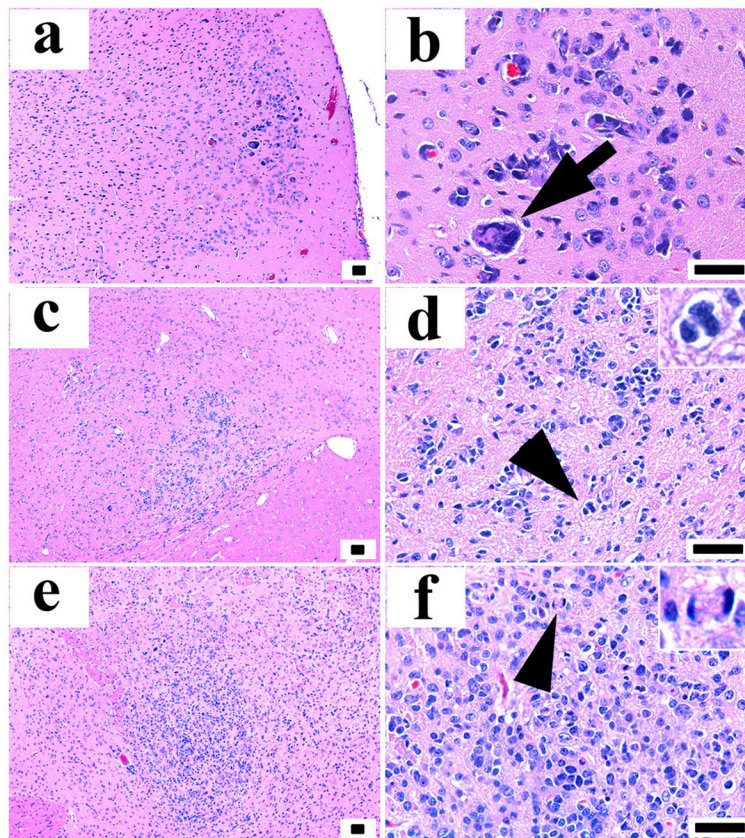
a**b****c****Control****Tumor**

Supplementary Figure S2

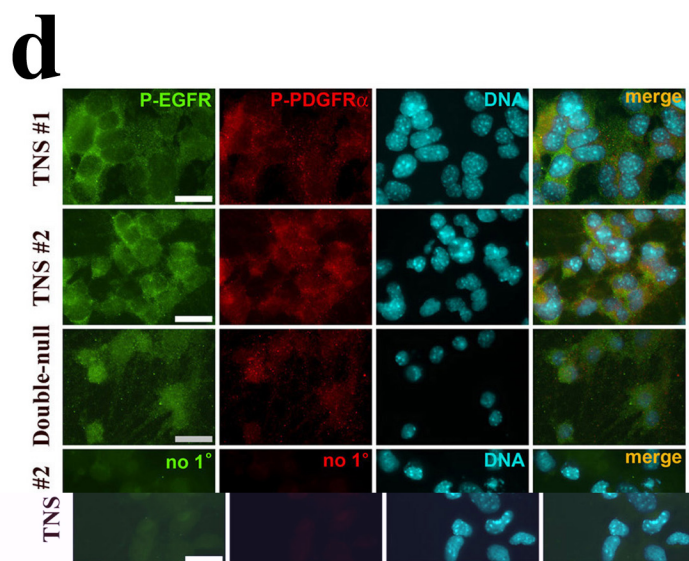
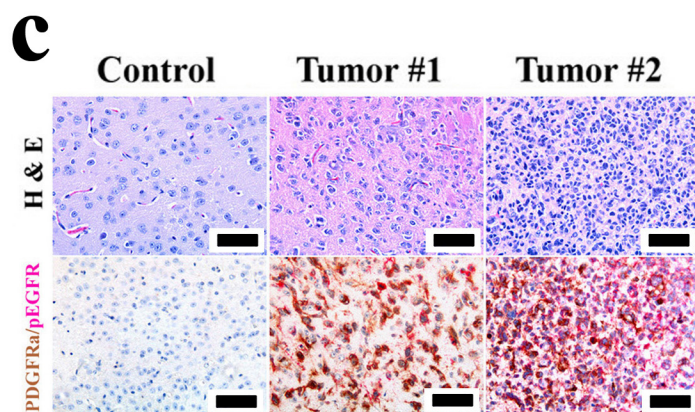
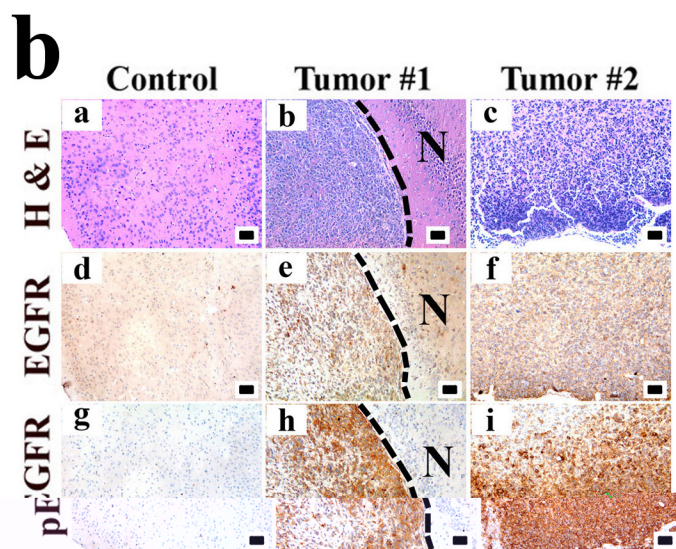
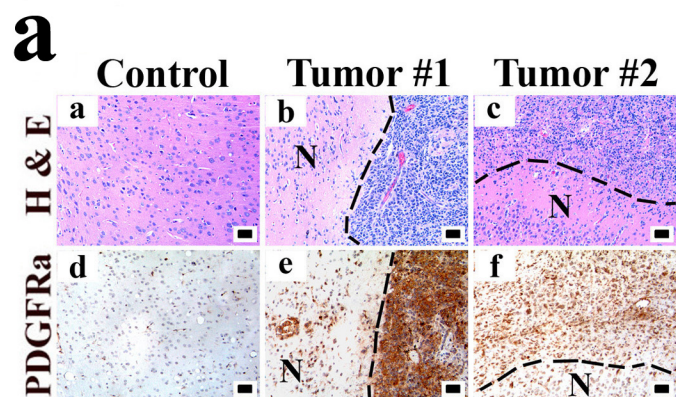
a



b

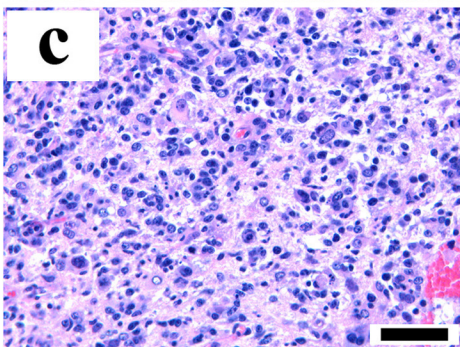
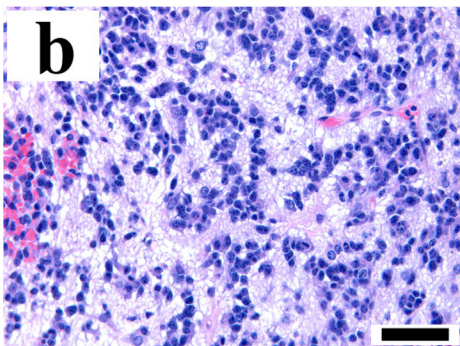
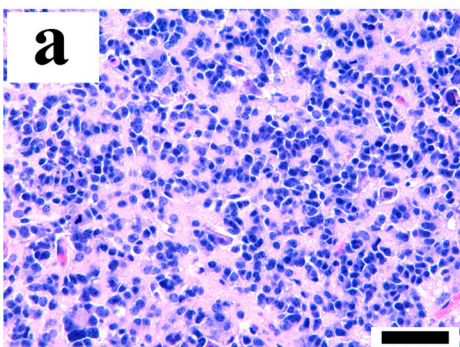


Supplementary Figure S3

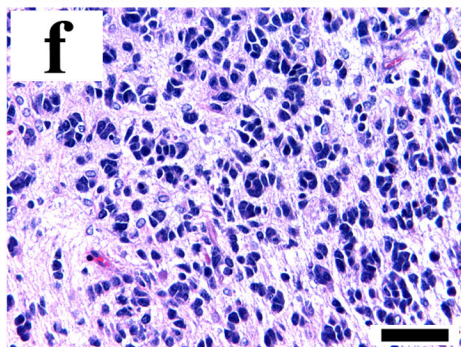
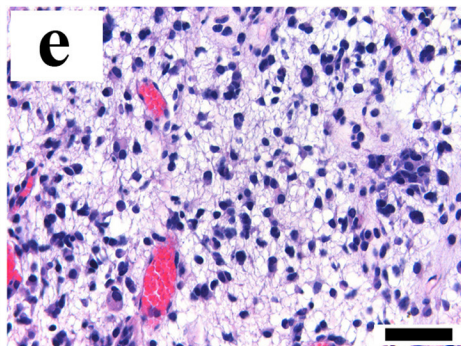
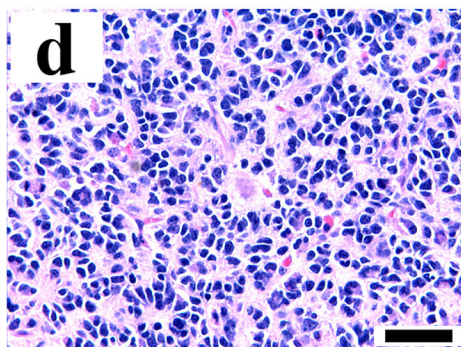


Supplementary Figure S4

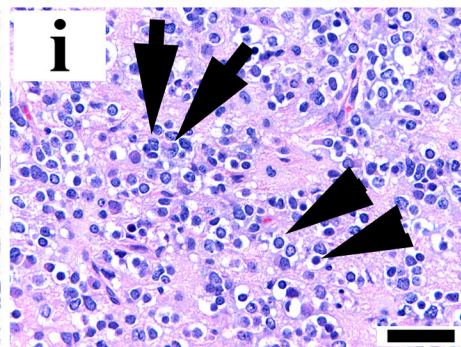
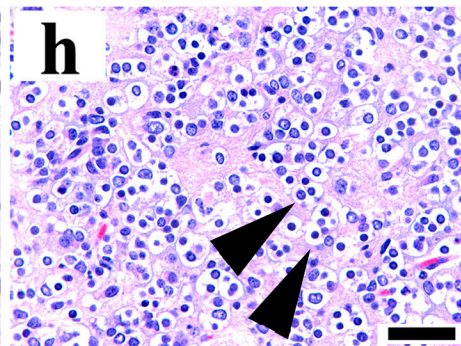
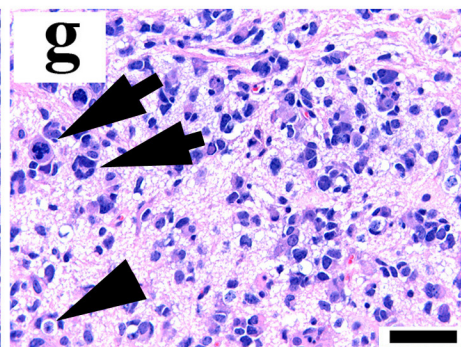
Tumor #1

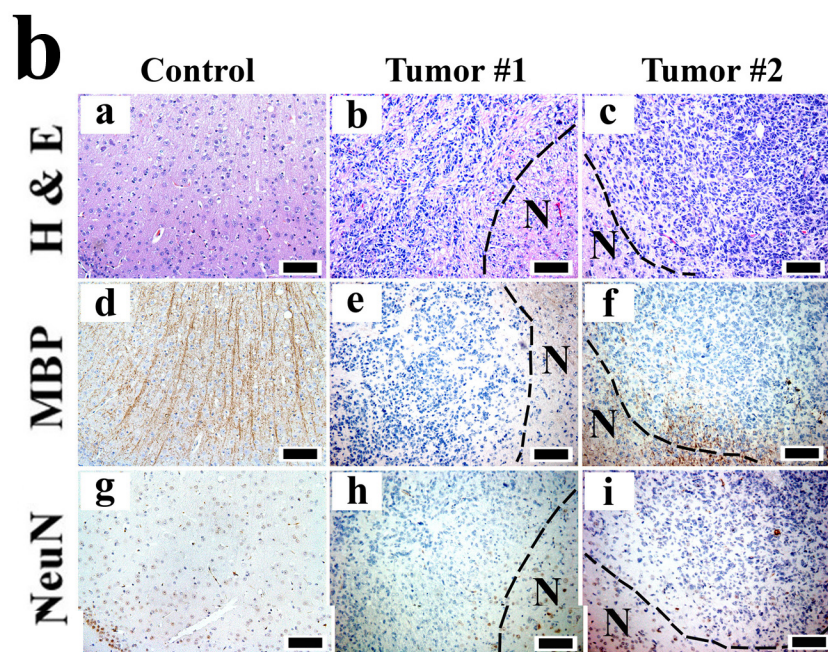
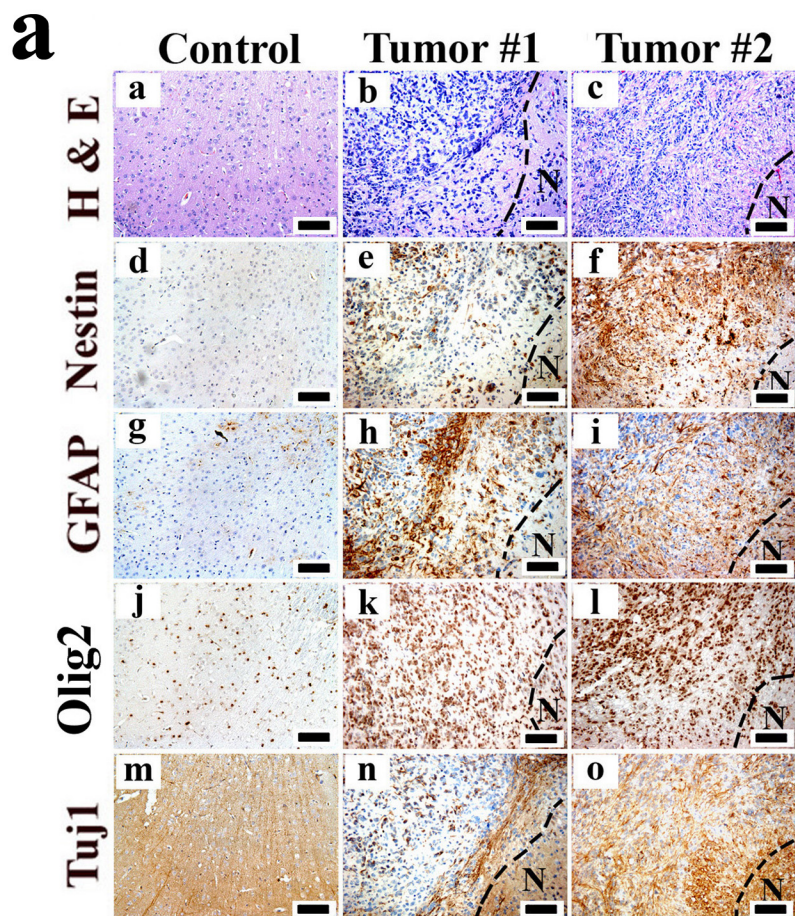


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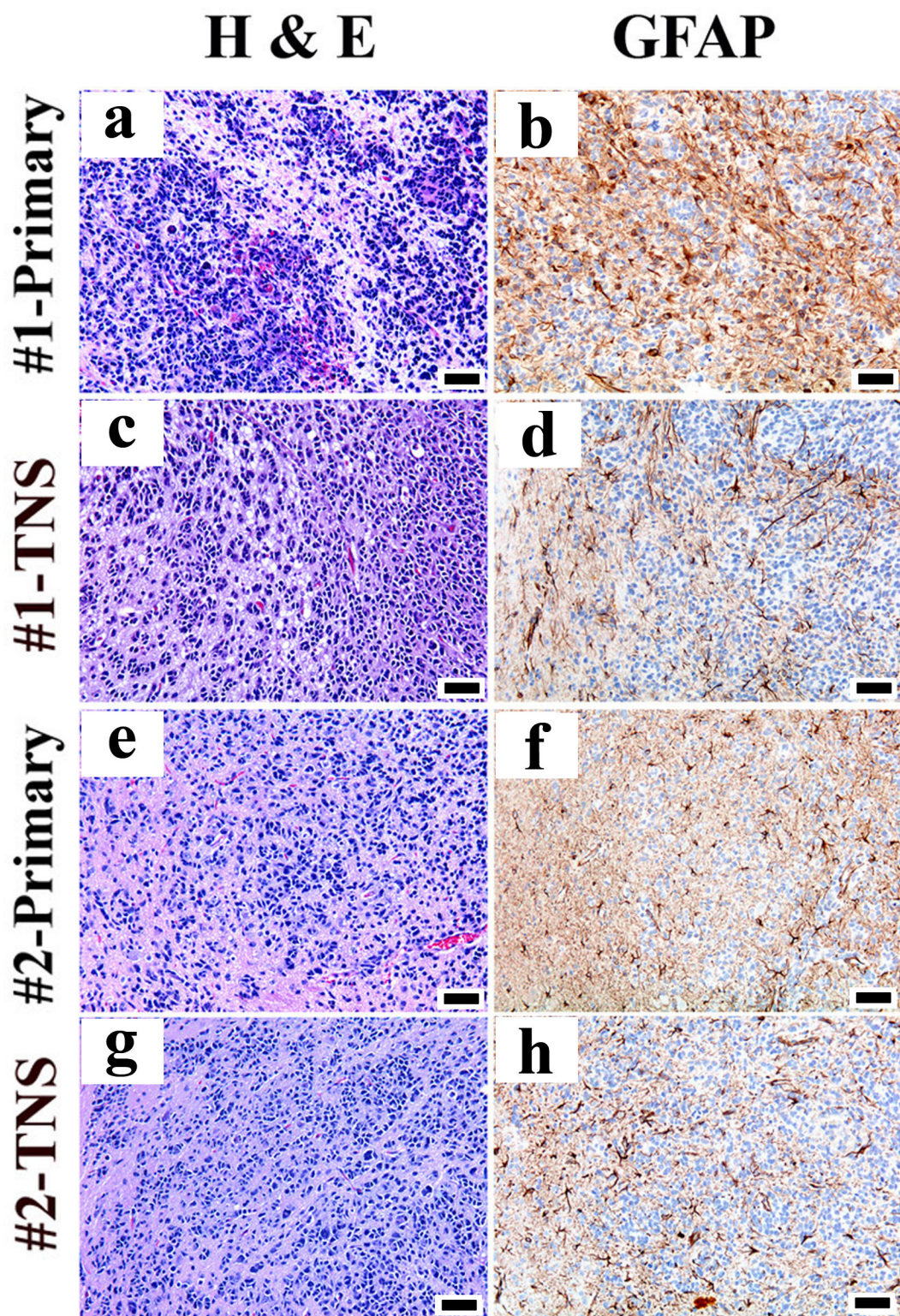


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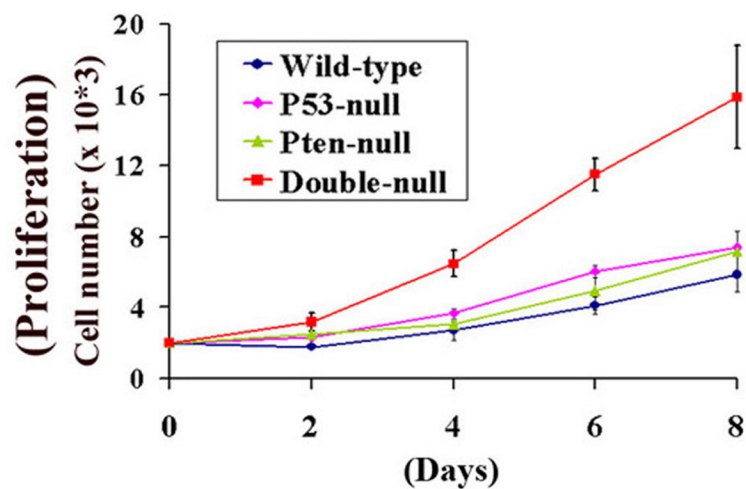
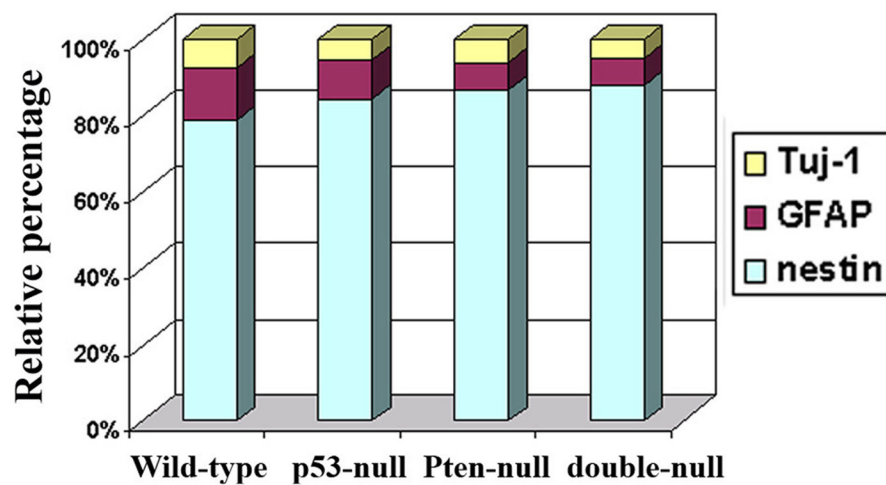
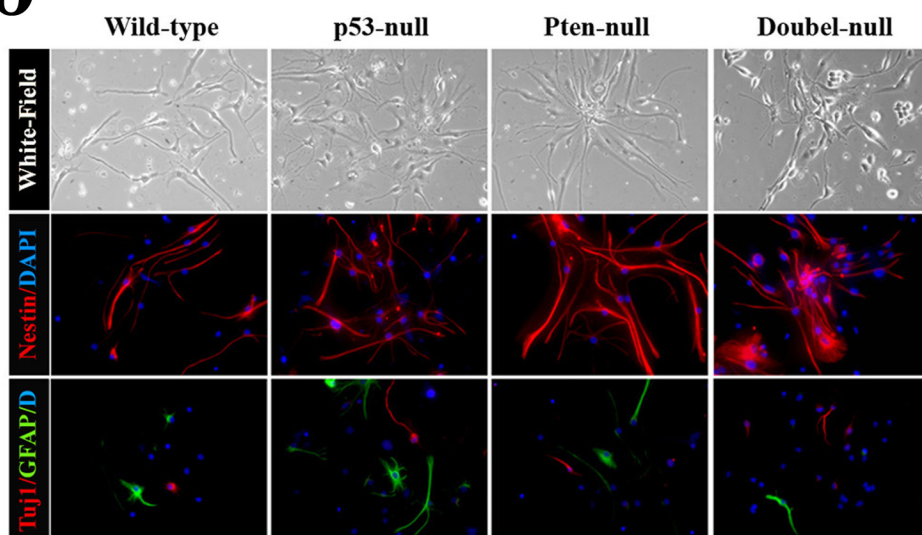


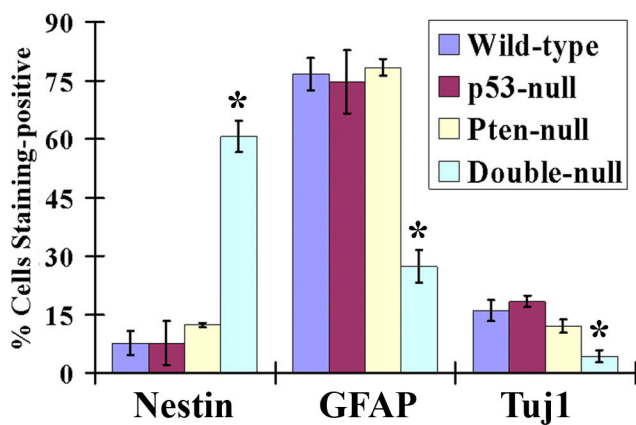
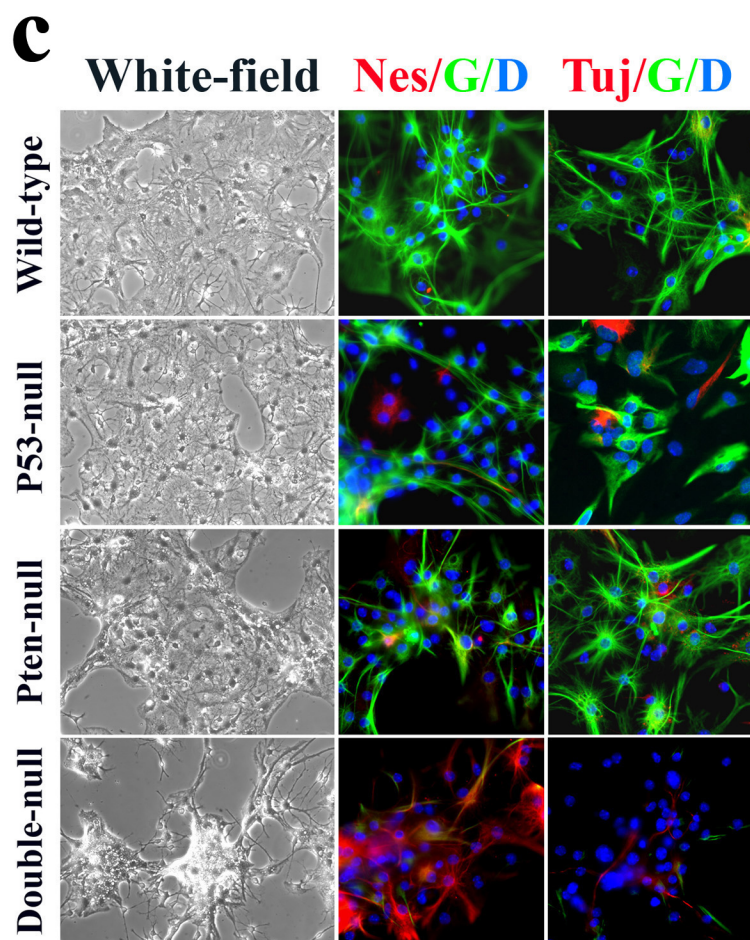
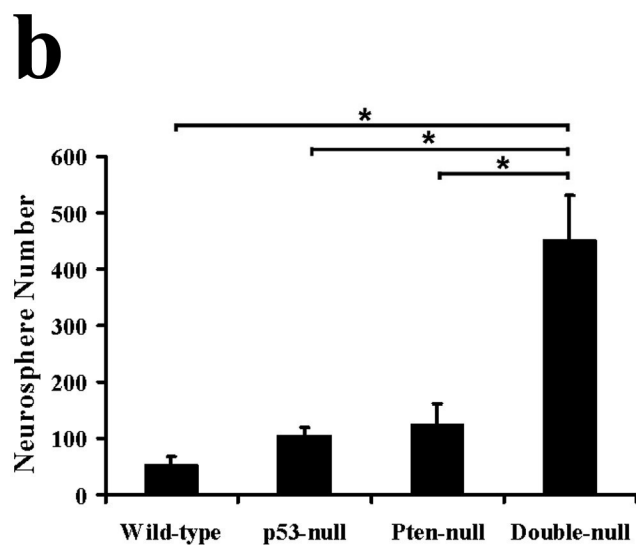
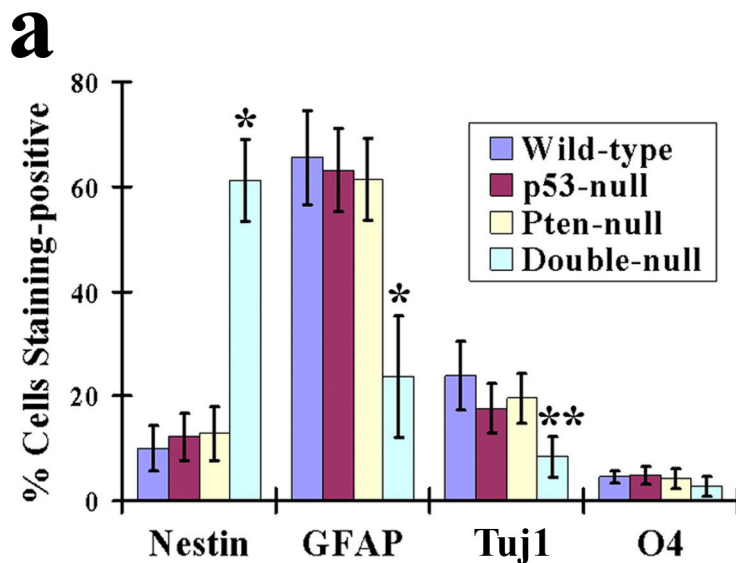


Supplementary Figure S6

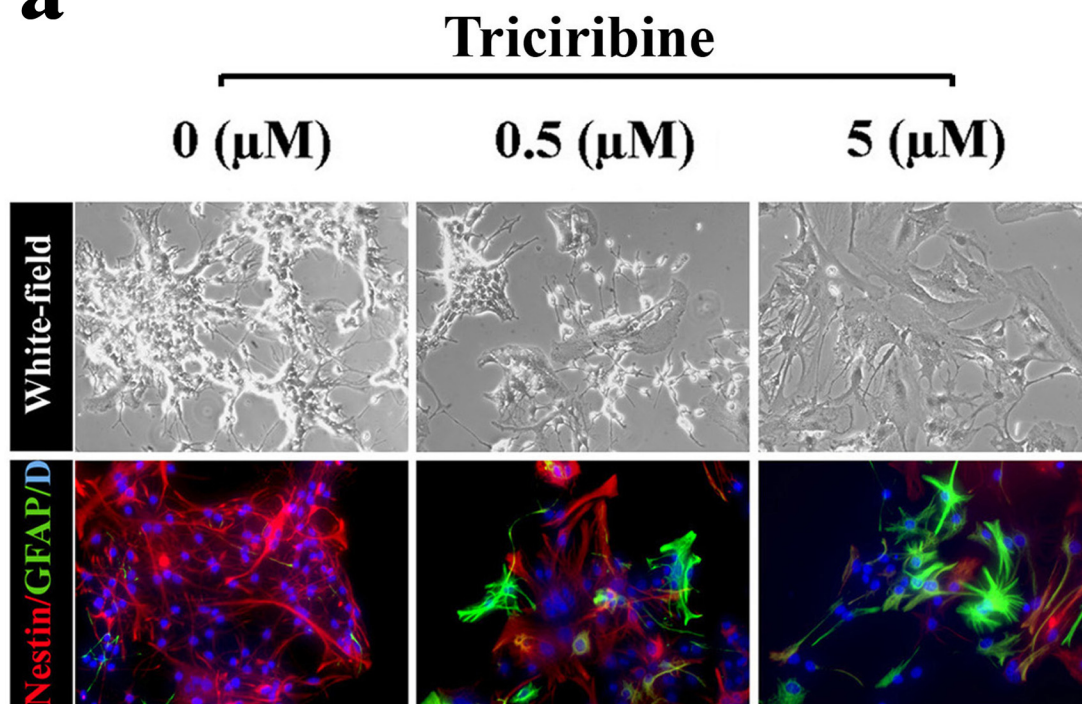
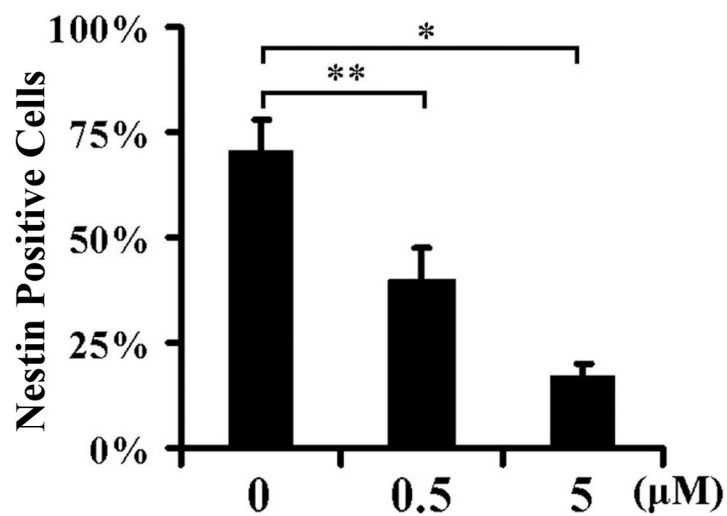


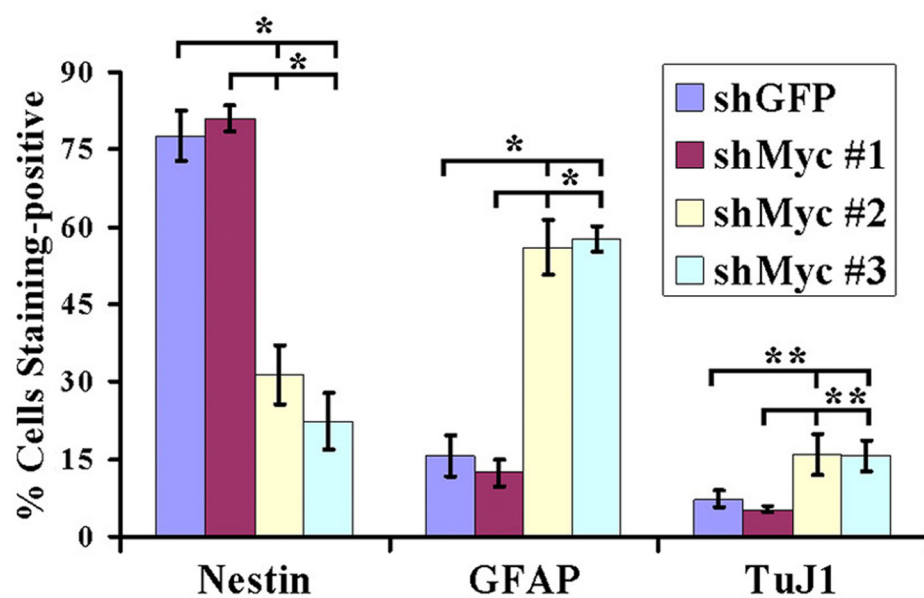
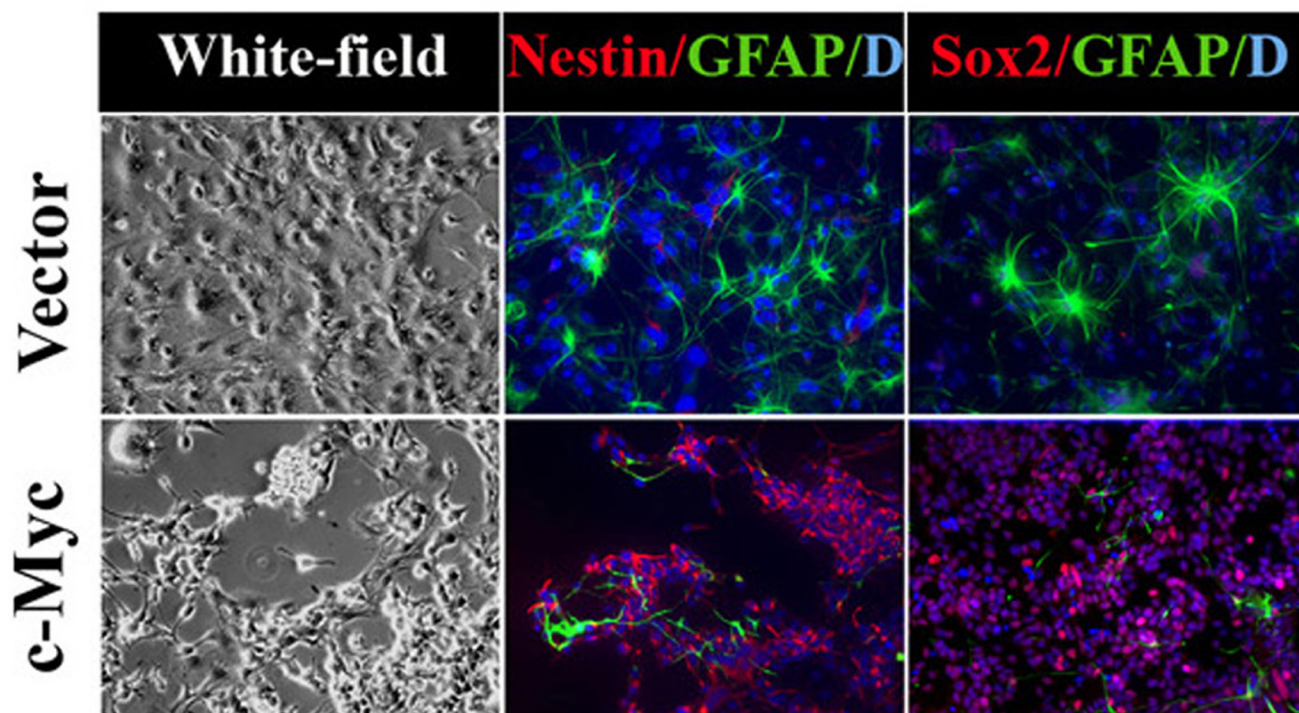
Supplementary Figure S7

a**b****Supplementary Figure S8**

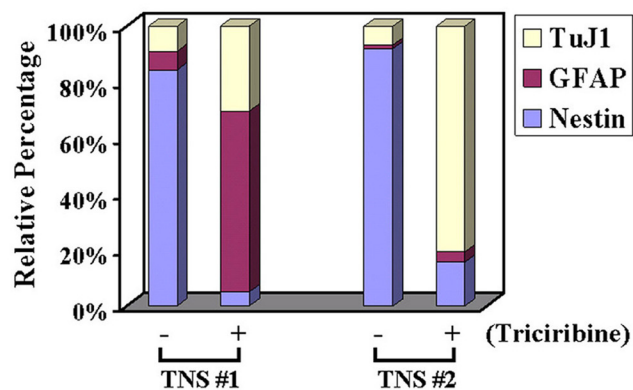
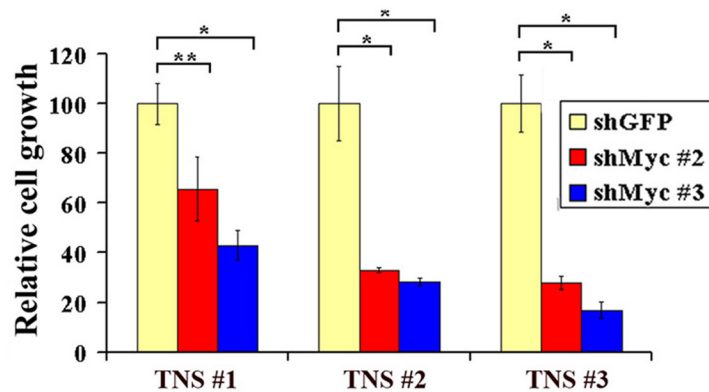
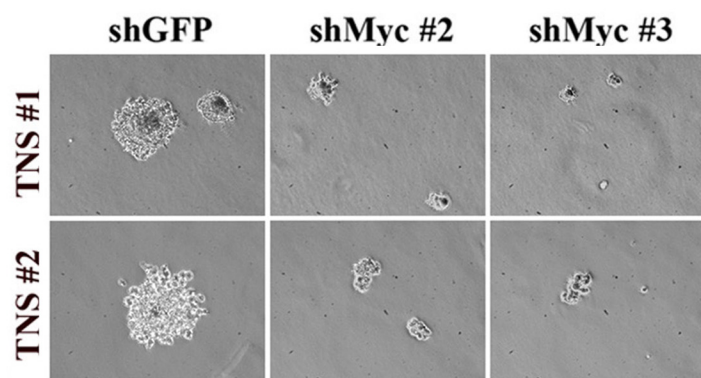
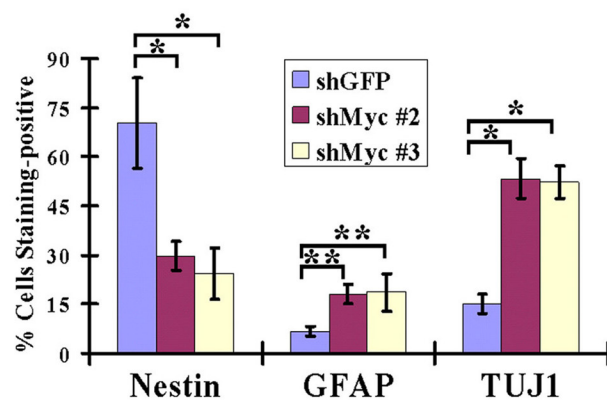


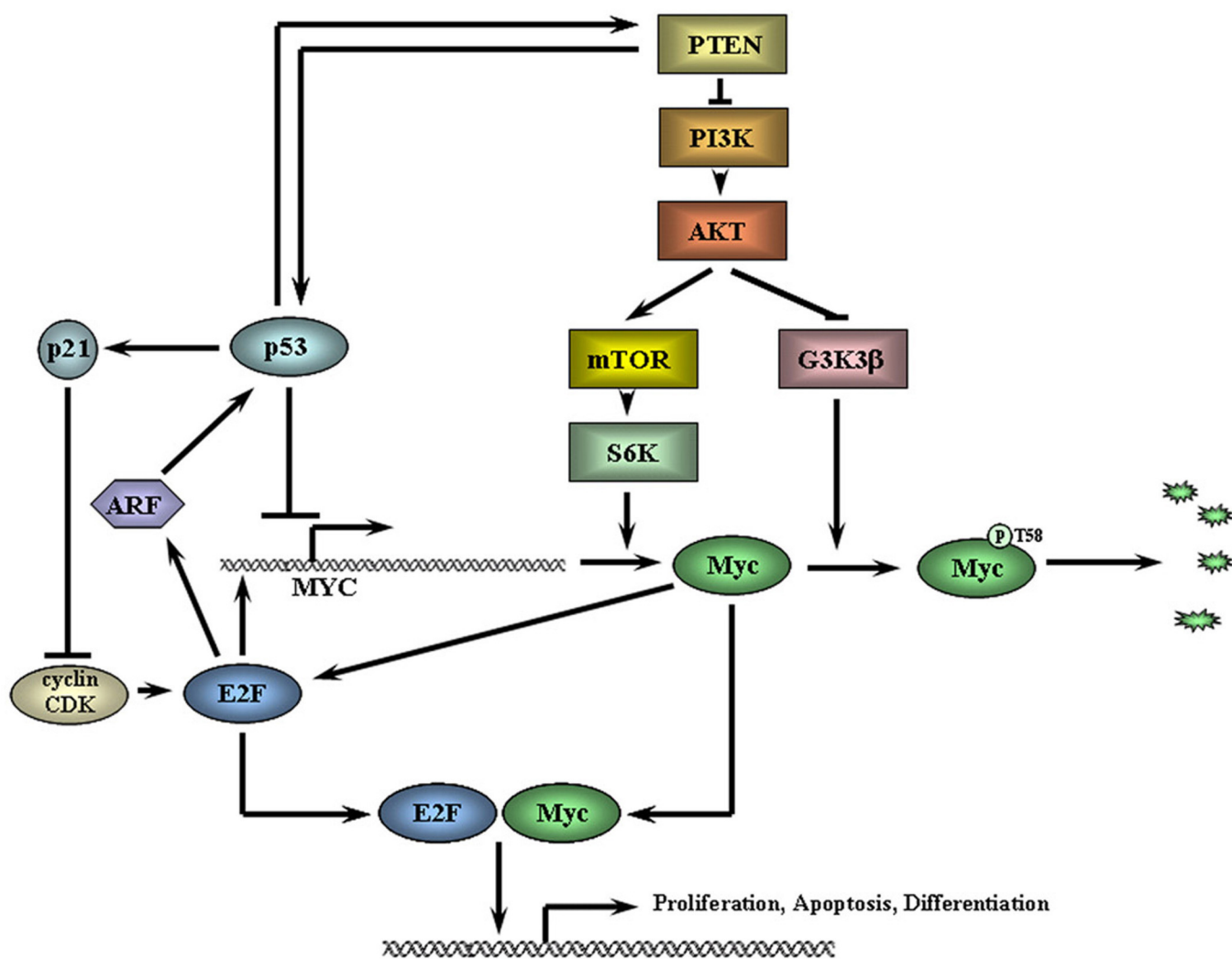
Supplementary Figure S9

a**b**

a**b**

Supplementary Figure S11

a**b****c****d**



Supplementary Figure S13

Supplementary Table 1: *P53* and *PTEN* status in 35 human primary glioblastoma samples

Sample ID	<i>P53</i> mutation status	<i>PTEN</i> mutation status	<i>PTEN</i> copy loss ^a
#1	WT	493G>A (G165R)	HET
#2	818G>C (R273L)	210+2_3ins (splice donor)	WT
#3	WT	499_502dup (168fs)	HET
#4	WT	764T>C (V255A)	HET
#5	WT	WT	HET
#6	WT	801+1G>T (splice donor)	HET
#7	821T>C (V274A)	477G>T (R159S)	HET
#8	753-763del (252-254del)	WT	HET
#9	821T>C (V274A)	477G>T (R159S)	HET
#10	WT	WT	WT
#11	WT	WT	WT
#12	WT	WT	HET
#13	WT	164+1G>A (splice donor)	HET
#14	WT	WT	HET
#15	711G>A (M237I)	WT	HET
#16	WT	WT	WT
#17	WT	WT	WT
#18	WT	WT	HET
#19	WT	594_597del (199fs)	HET
#20	WT	WT	HET
#21	WT	1040del (347fs)	HET
#22	WT	697C>T (R233X)	WT
#23	796G>A (G266R)	WT	HOM
#24	WT	WT	WT
#25	WT	WT	HET
#26	WT	388C>T (R129X)	HET
#27	WT	WT	n.a.
#28	WT	WT	n.a.
#29	WT	WT	n.a.
#30	403T>C (C135R)	1026+1G>C (splice donor)	n.a.
#31	586C>T (R196X)	WT	n.a.
#32	403T>C (C135R)	1027+1G>A (splice donor)	n.a.
#33	817C>A (R273S)	WT	n.a.
#34	WT	WT	n.a.
#35	WT	WT	n.a.

All mutations are relative to the +1 adenine nucleotide of the ATG start codon, with the amino acid change given in parentheses. WT, wild type; HET, loss of one copy; HOM, homozygous deletion; n.a., not available.
^a *PTEN* copy number status is taken from ⁵.

Identifier	EntrezGene	Name	SAM Statistic	Lower Bound Fold Change
NM_009970	12982	factor 2 receptor, alpha, low-affinity (granu	8.47	15.36
NM_007904	13618	endothelin receptor type B	8.3	62.37
NM_007606	12350	carbonic anhydrase 3	7.13	54.63
NM_007598	12331	adenylate cyclase-associated protein 1 (6.79	10.37
NM_146067	223978	RIKEN cDNA C530044N13 gene	6.74	16.73
NM_024263	74761	RIKEN cDNA 1200013A08 gene	6.63	7.36
NM_007992	14115	fibulin 2	6.54	19.52
NM_080639	110595	tissue inhibitor of metalloproteinase 4	6.45	18.64
NM_010329	14726	glycoprotein 38	6.43	14.97
NM_008028	14252	flotillin 2	6.42	14.59
NM_030704	80888	heat shock 27kDa protein 8	6.09	38.57
NM_178684	218975	RIKEN cDNA C130032J12 gene	5.98	11.54
NM_138758	192289	trimethyllysine hydroxylase, epsilon	5.94	15.33
NM_010790	17279	maternal embryonic leucine zipper kinase	5.76	11.77
NM_019754	56370	transgelin 3	5.67	7.57
NM_021344	57816	tescalcin	5.48	6.47
NM_030704	80888	heat shock 27kDa protein 8	5.36	10.4
NM_010516	16007	cysteine rich protein 61	-5.32	-9.46
NM_009829	12444	cyclin D2	5.32	7.48
NM_138758	192289	trimethyllysine hydroxylase, epsilon	5.3	9.03
NM_133990	16164	interleukin 13 receptor, alpha 1	5.3	5.52
NM_026515	68026	RIKEN cDNA 2810417H13 gene	5.29	5.02
NM_009829	12444	cyclin D2	5.25	8.77
NM_008017	14211	ctural maintenance of chromosomes 2-lik	5.24	6.36
NM_009829	12444	cyclin D2	5.1	6.58
NM_027406	107747	formyltetrahydrofolate dehydrogenase	5.04	9.93
NM_176073	54381	plasma glutamate carboxypeptidase	5.02	11.56
NM_018827	12931	cytokine receptor-like factor 1	5	6.99
NM_023465	67087	catenin beta interacting protein 1	4.9	6.23
NM_009263	20750	secreted phosphoprotein 1	4.88	16.54
NM_009538	22634	pleiomorphic adenoma gene-like 1	-4.87	-7.92
NM_007697	12661	adhesion molecule with homology to L1C	4.84	22.68
NM_010747	17096	uchi sarcoma viral (v-yes-1) oncogene h	4.8	6.16
NM_147776	246228	RIKEN cDNA 4932416A11 gene	4.65	6.99
NM_010516	16007	cysteine rich protein 61	-4.63	-9.11
NM_144841	18424	orthodenticle homolog 2 (Drosophila)	4.62	3.95
NM_007904	13618	endothelin receptor type B	4.61	5.39
NM_028101	72106	RIKEN cDNA 2610003J06 gene	4.55	4.53
NM_026268	67603	dual specificity phosphatase 6	4.54	5.35
NM_175013	226041	phosphoglucomutase 5	-4.54	-4.73
NM_007494	11898	argininosuccinate synthetase 1	4.53	6.86
NM_008815	18612	ant gene 4 (E1A enhancer binding proteir	4.5	6.2
NM_009829	12444	cyclin D2	4.48	6.94
NM_007630	12442	cyclin B2	4.45	7.28
NM_009931	12826	procollagen, type IV, alpha 1	-4.45	-5.75
NM_133662	15937	immediate early response 3	4.44	5.73
NM_011058	18595	derived growth factor receptor, alpha pol	4.34	6.44
NM_010517	16010	nsulin-like growth factor binding protein 4	4.3	6.81
NM_007709	12705	g transactivator with Glu/Asp-rich carbox	4.29	5.12
NM_010517	16010	nsulin-like growth factor binding protein 4	4.24	5.93

NM_027307	105348	golgi phosphoprotein 2	4.23	5.77
NM_011228	19337	AB33A, member of RAS oncogene famil	4.23	4.35
NM_013568	16494	age-gated channel, shaker-related, subfa	-4.21	-5.25
NM_021883	21916	tropomodulin 1	4.2	5.49
NM_011674	22239	UDP-glucuronosyltransferase 8	4.16	7.4
NM_023879	77945	igmentosa GTPase regulator interacting	4.15	5.11
NM_010274	14571	rol phosphate dehydrogenase 2, mitocho	4.11	4.4
NM_009829	12444	cyclin D2	4.09	5.28
NM_010271	14555	erol-3-phosphate dehydrogenase 1 (solu	4.09	6.18
NM_010517	16010	nsulin-like growth factor binding protein 4	4.06	5.54
NM_012025	26934	Rac GTPase-activating protein 1	4.05	6.26
NM_007467	11803	amyloid beta (A4) precursor-like protein 1	4.04	5.64
NM_011369	20419	Shc SH2-domain binding protein 1	4.04	6.81
NM_010517	16010	nsulin-like growth factor binding protein 4	4.04	6.05
NM_009846	12484	CD24a antigen	4.03	5.12
NM_009931	12826	procollagen, type IV, alpha 1	-4.03	-5.41
NM_007706	216233	suppressor of cytokine signaling 2	3.97	3.89
NM_178739	245404	WD repeat domain 40B	-3.95	-4.06
NM_008564	17216	some maintenance deficient 2 mitotin (S.	3.94	4.31
NM_023794	104156	ets variant gene 5	3.93	4.49
NM_007708	12704	citron	3.93	4.86
NM_009846	12484	CD24a antigen	3.92	5.93
NM_009946	12890	Complexin 2	3.85	5.07
NM_009964	12955	crystallin, alpha B	-3.83	-5.01
NM_007678	12606	, Similar to CCAATenhancer binding prot	3.81	4.54
NM_178609	52679	E2F transcription factor 7	3.79	2.94
NM_177033	319922	RIKEN cDNA A930041G11 gene	3.79	4.28
NM_178399	76982	RIKEN cDNA 3110035E14 gene	3.78	3.67
NM_080639	110595	tissue inhibitor of metalloproteinase 4	3.78	4.62
NM_172800	237979	sidekick homolog 2 (chicken)	3.77	4.13
NM_008017	14211	ctural maintenance of chromosomes 2-lik	3.77	3.16
NM_011271	19752	onuclease, RNase A family, 1 (pancreat	-3.75	-4.4
NM_028472	73230	BMP-binding endothelial regulator	3.74	4.81
NM_007724	12789	cyclic nucleotide gated channel alpha 2	-3.72	-8.91
NM_007904	13618	endothelin receptor type B	3.68	6.31
NM_026560	52276	cell division cycle associated 8	3.67	7.57
NM_177287	320895	RIKEN cDNA C030025P15 gene	3.67	4.93
NM_007646	12494	CD38 antigen	3.64	4.06
NM_008564	17216	some maintenance deficient 2 mitotin (S.	3.61	3.17
NM_176930	319504	RIKEN cDNA C130076O07 gene	3.6	4.07
NM_009387	21877	thymidine kinase 1	3.6	3.06
NM_008638	17768	ydrogenase (NAD+ dependent), metheny	3.59	3.16
NM_009846	12484	CD24a antigen	3.58	5.08
NM_016894	51801	eptor (calcitonin) activity modifying prote	-3.56	-5.41
NM_011898	24066	sprouty homolog 4 (Drosophila)	3.55	4.61
NM_025582	66469	RIKEN cDNA 2810405K02 gene	3.55	3.94
NM_176845	114874	DDHD domain containing 1	-3.54	-4.14
NM_023465	67087	catenin beta interacting protein 1	3.53	3.6
NM_010128	13730	epithelial membrane protein 1	-3.52	-4.74
NM_010142	13844	Eph receptor B2	3.51	3.92
NM_007631	12443	cyclin D1	3.51	4.08
NM_008036	14282	FBJ osteosarcoma oncogene B	-3.51	-4.11

NM_009964	12955	crystallin, alpha B	-3.49	-4.2
NM_028829	74229	RIKEN cDNA 1700019B16 gene	3.48	3.6
NM_010171	14066	coagulation factor III	3.45	3.66
NM_008751	18231	neurexophilin 1	3.44	4.44
NM_008563	17215	chromosome maintenance deficient 3 (S. cerevisiae)	3.44	4.53
NM_022656	64652	nischarin	-3.42	-3.88
NM_009013	19362	RAD51 associated protein 1	3.42	3.17
NM_007631	12443	cyclin D1	3.4	3.77
NM_033075	110956	DNA segment, Chr 17, human D6S56E5	3.37	4.65
NM_009366	21807	transforming growth factor beta 1 induced transcript 1 (cysteine) proteinase inhibitor, clade H, member 1	-3.37	-3.74
NM_009825	12406	proteinase inhibitor, clade H, member 1	-3.37	-3.92
NM_028375	72865	RIKEN cDNA 2900027G03 gene	3.36	4.23
NM_010777	17196	myelin basic protein	3.35	4.8
NM_015731	11981	ATPase, class II, type 9A	3.35	2.88
NM_008566	17218	chromosome maintenance deficient 5, cell division cycle 45 homolog (S. cerevisiae)	3.34	3.93
NM_019703	56421	phosphofructokinase, platelet	3.33	3.08
NM_009946	12890	Complexin 2	3.32	3.46
NM_022656	64652	nischarin	-3.32	-3.66
NM_008892	18968	polymerase (DNA directed), alpha 1	3.31	3.18
NM_053185	94216	procollagen, type IV, alpha 6	3.3	3.2
NM_017407	54141	sperm associated antigen 5	3.28	3.14
NM_133348	70025	brain acyl-CoA hydrolase	3.28	2.8
NM_009472	22253	unc-5 homolog C (C. elegans)	3.27	2.96
NM_011322	20266	channel, voltage-gated, type I, beta polypeptide	3.27	2.71
NM_011898	24066	sprouty homolog 4 (Drosophila)	3.26	2.91
NM_009829	12444	cyclin D2	3.26	4.08
NM_030706	80890	tripartite motif protein 2	3.25	3.64
NM_008587	17289	c-met proto-oncogene tyrosine kinase	-3.24	-3.81
NM_010181	14119	fibrillin 2	3.24	3.05
NM_007631	12443	cyclin D1	3.24	3.77
NM_008563	17215	chromosome maintenance deficient 3 (S. cerevisiae)	3.23	3.6
NM_009862	12544	division cycle 45 homolog (S. cerevisiae)	3.22	3.12
NM_009946	12890	complexin 2	3.2	3.55
NM_013737	27226	group VII (platelet-activating factor acetyltransferase) protein kinase regulatory subunit	3.19	3.22
NM_025415	66197	CDK28 protein kinase regulatory subunit	3.18	4.14
NM_008567	17219	chromosome maintenance deficient 6 (MIS5 homolog, S. cerevisiae)	3.17	3.72
NM_175655	319161	histone 1, H4b histone 1, H4m histone 1	3.17	3.66
NM_009099	20128	tripartite motif protein 30	-3.17	-3.76
NM_031258	83453	chordin-like 1	3.16	3.29
NM_008567	17219	chromosome maintenance deficient 6 (MIS5 homolog, S. cerevisiae)	3.16	3.63
NM_009527	22421	viral integrase-related MMTV integration site 7	3.16	3
NM_011234	19361	RAD51 homolog (S. cerevisiae)	3.15	3.08
NM_00100758	333564	Gene model 784, (NCBI)	-3.15	-6.48
NM_178110	67525	RIKEN cDNA 6330414G21 gene	3.15	3.49
NM_007598	12331	adenylate cyclase-associated protein 1 (CAP1)	3.14	3.86
NM_010097	13602	SPARC-like 1 (mast9, hevin)	3.13	5.53
NM_009382	21838	thymus cell antigen 1, theta	-3.13	-3.33
NM_009320	21366	family 6 (neurotransmitter transporter, taurine)	3.1	3.47
NM_024245	71819	kinesin family member 23	3.1	3.83
NM_139303	228421	kinesin family member 18A	3.09	3.07
NM_007752	12870	ceruloplasmin	3.08	4.52
NM_013645	19293	parvalbumin	-3.08	-3.46

NM_024283	78896	RIKEN cDNA 1500015O10 gene	3.07	4.23
NM_009052	19716	reduced expression 3	3.05	3.61
NM_007643	12491	CD36 antigen	3.04	3.85
NM_025994	27984	EF hand domain containing 2	3.03	3.9
NM_172301	268697	cyclin B1	3.03	3.98
NM_008563	17215	chromosome maintenance deficient 3 (S. cerevisiae)	3.03	3.34
NM_020599	19771	retinaldehyde binding protein 1	3.03	2.46
NM_007643	12491	CD36 antigen	3.02	3.4
NM_178075	18761	protein kinase C, theta	-3.02	-2.74
NM_010931	18140	phosphatase-like, containing PHD and RING finger domains	2.99	3.14
NM_028829	74229	RIKEN cDNA 1700019B16 gene	2.98	3.31
NM_013864	29811	N-myc downstream regulated gene 2	-2.98	-3.67
NM_010274	14571	mitochondrial phosphate dehydrogenase 2, mitochondrial	2.98	3.36
NM_010777	17196	myelin basic protein	2.97	4.02
NM_00100226	215798	G protein-coupled receptor 126	2.96	2.73
NM_028707	74002	pleckstrin and Sec7 domain containing 2	-2.95	-3.12
NM_133878	100088	chromosome condensation 1	2.95	3.02
NM_007467	11803	amyloid beta (A4) precursor-like protein 1	2.95	2.85
NM_133955	69581	ras homolog gene family, member U	-2.94	-3.04
NM_011254	19659	retinol binding protein 1, cellular	2.94	2.69
NM_009437	22117	adenosine sulfatase, mitochondrial	-2.94	-2.96
NM_153594	245867	RIKEN cDNA 5330414D10 gene	-2.93	-3.21
NM_009825	12406	(cysteine) proteinase inhibitor, clade H, member 1	-2.92	-3.46
NM_008630	17750	metallothionein 2	2.92	2.87
NM_009104	20135	ribonucleotide reductase M2	2.92	3.38
NM_153581	234267	glycoprotein m6a	2.92	3.23
NM_011595	21859	tissue inhibitor of metalloproteinase 3	-2.91	-2.97
NM_019738	56312	nuclear protein 1	2.91	3.47
NM_025994	27984	EF hand domain containing 2	2.9	3.49
NM_010516	16007	cysteine rich protein 61	-2.89	-3.04
NM_026560	52276	cell division cycle associated 8	2.89	4.27
NM_025943	66573	RIKEN cDNA 2810422M04 gene	-2.89	-3.11
NM_021560	59058	basic helix-loop-helix domain containing, class 1	2.89	4.94
NM_173447	270190	Eph receptor B1	-2.88	-2.86
NM_175606	74318	homeobox only domain	2.88	3.1
NM_026172	67460	3-oxo-4-dienoyl CoA reductase 1, mitochondrial	2.87	2.79
NM_016748	51797	cytidine 5'-triphosphate synthase	2.87	2.53
NM_008923	19085	kinase, cAMP dependent regulatory, type 1	2.87	2.91
NM_029620	76477	procollagen C-endopeptidase enhancer 2	-2.86	-2.97
NM_011756	22695	zinc finger protein 36	-2.86	-2.96
NM_175494	238673	zinc finger protein 367	2.85	2.91
NM_023223	107995	cell division cycle 20 homolog (S. cerevisiae)	2.84	3.7
NM_023270	66889	ring finger protein 128	2.83	2.68
NM_175628	232345	alpha-2-macroglobulin	2.83	2.79
NM_021436	230157	secretory protein with EGF-like and two follistatin repeats	2.82	2.66
NM_199007	68549	shugoshin-like 2 (S. pombe)	2.82	3.46
NM_009130	20255	secretogranin III	2.82	2.77
NM_011993	26757	dihydropyrimidinase-like 4	2.82	2.55
NM_019738	56312	nuclear protein 1	2.81	3.55
NM_009254	20719	(cysteine) proteinase inhibitor, clade B, member 1	2.8	2.95
NM_010517	16010	insulin-like growth factor binding protein 4	2.8	3.2
NM_008566	17218	chromosome maintenance deficient 5, cell division cycle	2.8	3.94

NM_033075	110956	DNA segment, Chr 17, human D6S56E 5	2.8	2.04
NM_011896	24063	sprouty homolog 1 (Drosophila)	2.78	2.62
NM_030704	80888	heat shock 27kDa protein 8	2.78	2.23
NM_175267	77868	RIKEN cDNA E130112H22 gene	-2.77	-2.6
NM_026385	67801	transmembrane 4 superfamily member 1	2.75	2.44
NM_008609	17388	matrix metalloproteinase 15	2.75	2.59
NM_017407	54141	sperm associated antigen 5	2.75	2.61
NM_024283	78896	RIKEN cDNA 1500015O10 gene	2.72	3.36
NM_010777	17196	myelin basic protein	2.71	4.08
NM_010112	13644	embryonal Fyn-associated substrate	-2.71	-3.49
NM_173016	270097	expressed sequence A1427515	2.71	2.82
NM_007999	14156	flap structure specific endonuclease 1	2.71	2.56
NM_146001	215114	huntingtin interacting protein 1	2.69	2.52
NM_023595	110074	deoxyuridine triphosphatase	2.68	2.78
NM_026014	67177	retroviral integration site 2	2.68	2.79
NM_011211	19266	protein tyrosine phosphatase, receptor type	2.68	3.06
NM_031863	83815	RIKEN cDNA 2610528M18 gene	2.68	2.58
NM_176933	319520	dual specificity phosphatase 4	2.68	2.17
NM_009104	20135	ribonucleotide reductase M2	2.68	3.1
NM_016692	16319	inner centromere protein	2.67	3.05
NM_025415	66197	CD28 protein kinase regulatory subunit	2.66	3.44
NM_175606	74318	homeobox only domain	2.66	2.73
NM_178606	28193	cent, Chr 10, University of California at Los Angeles	2.66	2.34
NM_025815	66871	copine VIII	2.65	2.46
NM_008565	17217	home maintenance deficient 4 homolog (5	2.65	2.55
NM_008037	14284	fos-like antigen 2	-2.64	-2.76
NM_138956	192678	association (RalGDS/AF-6) domain family	2.64	2.21
NM_153594	245867	RIKEN cDNA 5330414D10 gene	-2.64	-3
NM_009920	12794	cornichon-like (Drosophila)	2.64	2.73
NM_008056	14368	frizzled homolog 6 (Drosophila)	2.64	1.97
NM_011595	21859	tissue inhibitor of metalloproteinase 3	-2.63	-2.62
NM_011599	21885	like enhancer of split 1, homolog of Drosophila	2.62	2.9
NM_146007	12834	procollagen, type VI, alpha 2	-2.62	-2.8
NM_145473	105859	expressed sequence A1481750	2.62	2.2
NM_028817	74205	-CoA synthetase long-chain family member	2.62	2.59
NM_133719	70083	meteorin	2.62	3.03
NM_013492	12759	clusterin	-2.61	-2.27
NM_146007	12834	procollagen, type VI, alpha 2	-2.6	-2.83
NM_012012	26909	exonuclease 1	2.59	2.12
NM_153098	235505	CD109 antigen	-2.59	-2.72
NM_146001	215114	huntingtin interacting protein 1	2.59	2.6
NM_010863	17912	myosin IB	2.58	2.54
NM_013492	12759	clusterin	-2.58	-2.36
NM_025565	66442	RIKEN cDNA 2600017H08 gene	2.57	3.13
NM_028829	74229	RIKEN cDNA 1700019B16 gene	2.57	2.6
NM_009772	12235	inhibited by benzimidazoles 1 homolog (S	2.57	2.89
NM_010777	17196	myelin basic protein	2.57	3.16
NM_010577	16402	integrin alpha 5 (fibronectin receptor alpha 5	-2.56	-2.58
NM_172947	268490	RIKEN cDNA 2600001B17 gene	2.56	2.68
NM_023813	108058	calcium/calmodulin-dependent protein kinase II	2.56	1.9
NM_172890	243616	gamma-aminobutyric acid (GABA-A) transporter	2.54	3.01
NM_134006	19682	retinol dehydrogenase 5	-2.54	-2.56

NM_021891	60530	fidgetin-like 1	2.54	2.4
NM_133851	108907	nucleolar and spindle associated protein	2.53	2.54
NM_026346	67731	F-box only protein 32	-2.52	-2.46
NM_023066	65973	aspartate-beta-hydroxylase	2.52	2.89
NM_133816	98402	SH3-domain binding protein 4	-2.52	-2.93
NM_145473	105859	expressed sequence AI481750	2.52	2.26
NM_013492	12759	clusterin	-2.52	-2.3
NM_177960	319554	isopentenyl-diphosphate delta isomerase	2.51	2.62
NM_022316	64075	PARC related modular calcium binding	-2.51	-3.15
NM_030706	80890	tripartite motif protein 2	2.51	2.74
NM_00101227	11799	baculoviral IAP repeat-containing 5	2.5	3.21
NM_030706	80890	tripartite motif protein 2	2.5	2.34
NM_028390	68743	actin binding protein (scraps homolog, Drc	2.5	2.61
NM_026346	67731	F-box only protein 32	-2.49	-2.74
NM_145480	106344	replication factor C (activator 1) 4	2.49	2.52
NM_146228	235633	ALS2 C-terminal like	-2.48	-2.57
NM_019790	56363	a protein with EGF-like and two follistatin	2.48	2.56
NM_008446	16571	kinesin family member 4	2.48	2.58
NM_010863	17912	myosin IB	2.48	2.86
NM_028810	74194	ras homolog gene family, member E	-2.48	-2.79
NM_010715	16881	ligase I, DNA, ATP-dependent	2.47	2.55
NM_023794	104156	ets variant gene 5	2.47	3.24
NM_019562	56207	ubiquitin carboxyl-terminal esterase L5	2.46	2.54
NM_172301	268697	cyclin B1	2.45	3.42
NM_008594	17304	milk fat globule-EGF factor 8 protein	-2.45	-2.62
NM_026515	68026	RIKEN cDNA 2810417H13 gene	2.43	2.69
NM_009308	20983	synaptotagmin 4	-2.42	-3.21
NM_030706	80890	tripartite motif protein 2	2.42	2.44
NM_009477	22271	uridine phosphorylase 1	2.42	2.37
NM_175554	269582	claspin homolog (Xenopus laevis)	2.41	2.28
NM_173169	20873	polo-like kinase 4 (Drosophila)	2.41	2.34
NM_009640	11600	angiopoietin 1	-2.41	-2.26
NM_010274	14571	pyruvate dehydrogenase 2, mitochondrial	2.41	2.87
NM_009381	21835	hormone responsive SPOT14 homolog (2.41	2.98
NM_010516	16007	cysteine rich protein 61	-2.4	-2.49
NM_181585	18710	inositol 3 kinase, regulatory subunit, polyp	2.4	2.31
NM_175149	69551	RIKEN cDNA 2310022B05 gene	-2.4	-2.55
NM_009152	20346	immunoglobulin domain (Ig), short basic domain, s	2.39	2.47
NM_009015	19366	RAD54 like (S. cerevisiae)	2.39	2.56
NM_172589	218454	lipoma HMGIC fusion partner-like 2	2.38	2.21
NM_008017	14211	structural maintenance of chromosomes 2-like	2.38	2.56
NM_008770	18417	claudin 11	2.38	1.52
NM_011249	19650	retinoblastoma-like 1 (p107)	2.37	2.1
NM_007560	12167	neurotrophin morphogenetic protein receptor, type	-2.37	-2.39
NM_008234	15201	helicase, lymphoid specific	2.36	2.26
NM_009381	21835	hormone responsive SPOT14 homolog (2.36	2.83
NM_009877	12578	cyclin-dependent kinase inhibitor 2A	2.36	2.61
NM_023284	66977	cell division cycle associated 1	2.36	3.13
NM_009447	22145	tubulin, alpha 4	2.36	2.61
NM_020269	16513	inwardly-rectifying channel, subfamily J,	2.36	2.38
NM_013492	12759	clusterin	-2.36	-2.11
NM_010308	14681	uridine nucleotide binding protein, alpha	2.35	1.91

NM_013726	27214	expressed sequence AA545217	2.34	2.29
NM_028131	72155	RIKEN cDNA 2610510J17 gene	2.34	2.02
NM_080555	67916	phosphatidic acid phosphatase type 2B	2.33	2.35
NM_023160	66116	camello-like 1	2.32	2.51
NM_016777	50927	ir autoantigenic sperm protein (histone-bi	2.3	2.33
NM_008905	19024	phatase, receptor-type, F interacting pro	-2.3	-2.3
NM_008565	17217	ome maintenance deficient 4 homolog (S	2.29	2.39
NM_008069	14400	ninobutyric acid (GABA-A) receptor, sub	2.29	2.3
NM_011132	18973	polymerase (DNA directed), epsilon	2.28	1.71
NM_028817	74205	small nucleolar ribonucleoprotein, homol	2.28	2.54
NM_011497	20878	serine/threonine kinase 6	2.28	2.65
NM_010931	18140	-like, containing PHD and RING finger dc	2.28	2.42
NM_030706	80890	tripartite motif protein 2	2.27	2.24
NM_025422	66205	RIKEN cDNA 1110055L24 gene	2.26	2.31
NM_010777	17196	myelin basic protein	2.26	2.4
NM_031999	83924	transmembrane 7 superfamily member 1	2.26	2.27
NM_146073	224454	zinc finger, DHHC domain containing 14	-2.26	-2.12
NM_011623	21973	topoisomerase (DNA) II alpha	2.23	2.48
NM_008963	19215	prostaglandin D2 synthase (brain)	-2.23	-2.31
NM_019409	18377	oligodendrocyte myelin glycoprotein	2.22	1.91
NM_008812	18600	peptidyl arginine deiminase, type II	-2.21	-2.17
NM_011436	20660	elated receptor, LDLR class A repeats-cc	-2.21	-2.34
NM_144875	226422	AB7, member RAS oncogene family-like	2.2	1.94
NM_175549	268902	roundabout homolog 2 (Drosophila)	2.2	2.35
NM_027426	70433	RIKEN cDNA 2610109H07 gene	-2.2	-2.32
NM_145588	110033	kinesin family member 22	2.19	2.28
NM_145134	211949	SPRY domain-containing SOCS box 4	2.19	2.17
NM_011131	18971	erase (DNA directed), delta 1, catalytic s	2.19	2.02
NM_011496	20877	aurora kinase B	2.19	2.4
NM_133918	100952	elastin microfibril interfacer 1	-2.19	-2.13
NM_013538	14793	cell division cycle associated 3	2.18	2.49
NM_172578	217653	expressed sequence C79407	2.18	2.03
NM_197982	68278	EAD (Asp-Glu-Ala-Asp) box polypeptide :	2.18	2.14
NM_011595	21859	tissue inhibitor of metalloproteinase 3	-2.18	-2.39
NM_007616	12389	caveolin, caveolae protein 1	-2.17	-2.04
NM_010753	17122	Max dimerization protein 4	-2.16	-2.49
NM_146144	230484	ubiquitin specific protease 1	2.16	2.17
NM_175548	268890	nbic system-associated membrane prote	-2.16	-2.26
NM_177118	320262	RIKEN cDNA A830073O21 gene	-2.16	-2.16
NM_197982	68278	EAD (Asp-Glu-Ala-Asp) box polypeptide :	2.16	2.27
NM_008398	16404	integrin alpha 7	-2.15	-2.48
NM_016904	54124	CDC28 protein kinase 1b	2.15	2.17
NM_007900	13605	ect2 oncogene	2.15	2.58
NM_016701	18008	nestin	2.15	2.26
NM_011595	21859	tissue inhibitor of metalloproteinase 3	-2.14	-2.56
NM_011986	26562	neurochondrin	2.14	2.16
NM_009727	11980	iospholipid transporter (APLT), class I, ty	-2.14	-2.34
NM_011121	18817	polo-like kinase 1 (Drosophila)	2.14	2.46
NM_019499	56150	(mitotic arrest deficient, homolog)-like 1	2.14	2.29
NM_145134	211949	SPRY domain-containing SOCS box 4	2.13	2.14
NM_144551	217410	tribbles homolog 2 (Drosophila)	2.13	2.17
NM_007885	13521	carrier family 26 (sulfate transporter), me	-2.13	-2.26

NM_130796	170625	sorting nexin associated golgi protein 1	2.13	2.16
NM_011131	18971	erase (DNA directed), delta 1, catalytic s	2.13	1.92
NM_139001	121021	chondroitin sulfate proteoglycan 4	-2.12	-2.02
NM_010838	17762	microtubule-associated protein tau	-2.11	-2.26
NM_008515	16978	cine rich repeat (in FLII) interacting prote	2.11	2.17
NM_009104	20135	ribonucleotide reductase M2	2.1	2.46
NM_007634	12449	cyclin F	2.1	1.72
NM_009791	12316	calmodulin binding protein 1	2.1	2.47
NM_028392	72930	e 2 (formerly 2A), regulatory subunit B (F	2.1	2.17
NM_146142	100121	tudor domain containing 7	2.09	2.15
NM_009936	12841	procollagen, type IX, alpha 3	-2.09	-2.33
NM_028109	72119	microtubule-associated protein homolog (Xen	2.09	2.31
NM_008963	19215	prostaglandin D2 synthase (brain)	-2.09	-2.05
NM_011521	20971	syndecan 4	2.08	2.18
NM_178721	239857	immunoglobulin superfamily, member 4	2.08	2.07
NM_023279	22152	tubulin, beta 3	2.08	2.12
NM_013681	20965	synapsin II	-2.08	-2.51
NM_013822	16449	jagged 1	2.07	2.24
NM_172829	240119	beta galactoside alpha 2,6 sialyltransferase	2.07	2.13
NM_176930	319504	RIKEN cDNA C130076O07 gene	2.07	2.12
NM_010721	16906	lamin B1	2.07	2.25
NM_028109	72119	microtubule-associated protein homolog (Xen	2.06	2.06
NM_033474	11877	repeat gene deleted in velo-cardio-facial	-2.06	-2.06
NM_010336	14745	phosphatidylcholine, lysophosphatidic acid G-protein-c	-2.06	-1.97
NM_009780	12268	complement component 4 (within H-2S)	2.06	1.77
NM_009103	20133	ribonucleotide reductase M1	2.06	2.15
NM_009936	12841	procollagen, type IX, alpha 3	-2.06	-2.08
NM_134010	103468	nucleoporin 107	2.05	1.75
NM_009984	13039	cathepsin L	2.05	2.11
NM_010424	15216	hemochromatosis	2.05	1.74
NM_009320	21366	family 6 (neurotransmitter transporter, taur	2.05	2.32
NM_009791	12316	calmodulin binding protein 1	2.05	2.34
NM_175247	22690	zinc finger protein 28	2.05	2.03
NM_010838	17762	microtubule-associated protein tau	-2.04	-2.09
NM_013847	26912	transferase (2-amino-3-ketobutyrate-coe	2.03	2.02
NM_019417	30794	PDZ and LIM domain 4	-2.03	-1.83
NM_009754	12125	BCL2-like 11 (apoptosis facilitator)	-2.02	-2.03
NM_011436	20660	related receptor, LDLR class A repeats-cc	-2.02	-2.18
NM_012061	27062	Ca ²⁺ -dependent activator protein for secre	-2.02	-1.73
NM_176845	114874	DDHD domain containing 1	-2.01	-2.16
NM_026024	67196	RIKEN cDNA 2700084L22 gene	2.01	2
NM_028627	73728	RIKEN cDNA 1110007H17 gene	2.01	2.12
NM_029815	76960	breast carcinoma amplified sequence 1	2.01	2.04
NM_023294	67052	kinetochore associated 2	2.01	1.74
NM_145150	233406	protein regulator of cytokinesis 1	2.01	1.98
NM_031999	83924	transmembrane 7 superfamily member 1	2	2.01
NM_018761	54366	catenin alpha-like 1	2	1.95
NM_009791	12316	calmodulin binding protein 1	2	1.97