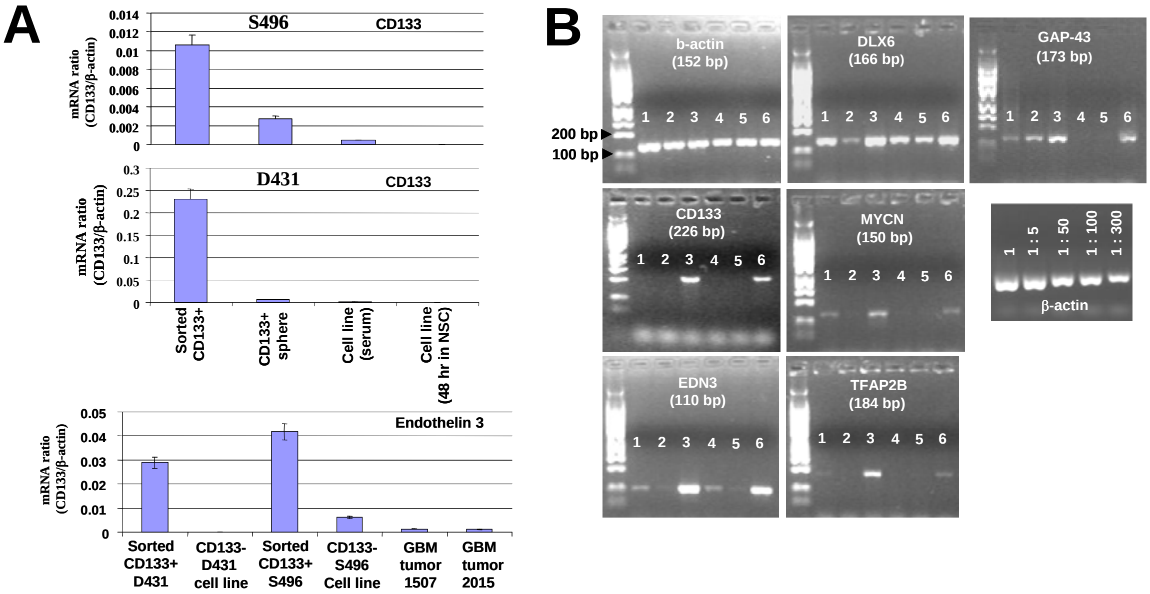
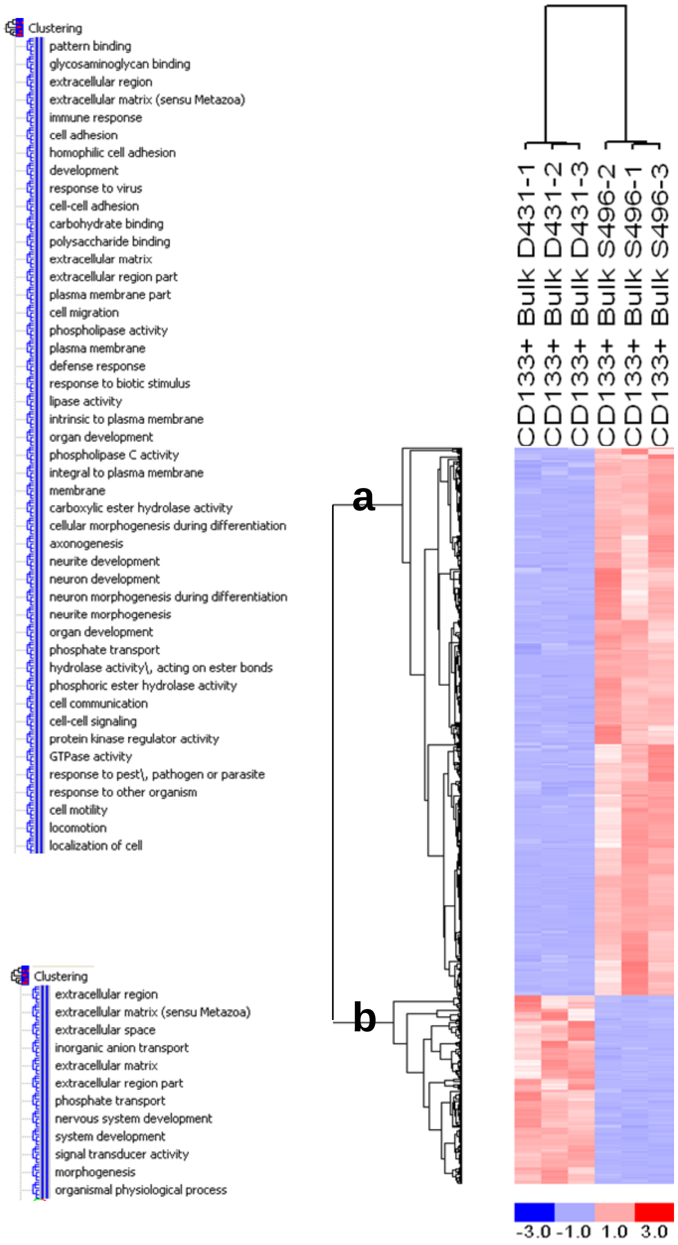
Supplementary Figure 1



Supplementary Figure 1. Verification of molecular markers expressed in CD133+ GBM cells using RT-PCR analysis. A. Real-time quantitative RT-PCR analysis of CD133 and endothelin 3 (EDN3) mRNA expression in the indicated cell cultures. The quantitation of specific transcripts in cells was calculated and expressed by the specific mRNA ratio to β-actin. B. Semi-quantitative analysis of indicated markers expressed in the following cultures: lane 1 (L1): D431 cell line (serum), L2: D431 cell line switched to NSC culture condition for 48 hr, L3: Purified CD133+ D431GBM cells sorted from CD133+ GBM sphere culture, L4: S496 cell line (serum), L5: S496 cell line switched to NSC culture condition for 48 hr, L6: Purified CD133+ S496 GBM cells sorted from the CD133+ GBM sphere culture.

Supplementary Figure 2



Supplementary Figure 2. Two-way unsupervised gene and sample clustering of CD133+ D431 GBM spheres and CD133+ S496 GBM spheres. The analysis was based on a cutoff of 4-fold increase or decrease in relative expression in CD133+ D431 GBM spheres compared to CD133+ S496 GBM spheres (P<0.05). All plots show normalized gene expression values converted into a heat map.

Supplementary Table 1

Gene function categories of gene clusters of 64 common genes determined in both CD133+ D431 and CD133+ S496 cells

```
{Hierarchical clustering
  Read in genes listed in file E:\New Folder\Table 1 common genes for clusting.txt...
    Found 64 genes

  Begin clustering...
    Calculate distance 60
    Find nearest neighbor 60
    Merge node 56
    Calculate distance 20
    Find nearest neighbor 20
    Merge node 16

  Finding significant Gene Ontology clusters...
    Found 21 "signal transducer activity" genes in a 64-cluster (all: 5865/36426, PValue: 0.000741)
    Found 16 "receptor activity" genes in a 64-cluster (all: 3593/36426, PValue: 0.000378)
    Found 11 "transmembrane receptor activity" genes in a 64-cluster (all: 2066/36426, PValue: 0.000875)
    Found 7 "ion channel activity" genes in a 64-cluster (all: 771/36426, PValue: 0.000404)
    Found 4 "extracellular ligand-gated ion channel activity" genes in a 64-cluster (all: 133/36426,
PValue: 0.000091)
    Found 12 "extracellular region" genes in a 64-cluster (all: 2275/36426, PValue: 0.000538)
    Found 24 "development" genes in a 64-cluster (all: 4817/36426, PValue: 0.000001)
    Found 17 "nervous system development" genes in a 64-cluster (all: 1242/36426, PValue: 0.000000)
    Found 7 "channel or pore class transporter activity" genes in a 64-cluster (all: 888/36426, PValue:
0.000928)
    Found 7 "alpha-type channel activity" genes in a 64-cluster (all: 834/36426, PValue: 0.000643)
    Found 5 "ligand-gated ion channel activity" genes in a 64-cluster (all: 214/36426, PValue: 0.000038)
    Found 6 "neurotransmitter receptor activity" genes in a 64-cluster (all: 163/36426, PValue: 0.000000)
    Found 7 "extracellular matrix" genes in a 64-cluster (all: 871/36426, PValue: 0.000830)
    Found 6 "neurotransmitter binding" genes in a 64-cluster (all: 167/36426, PValue: 0.000001)
    Found 5 "synapse part" genes in a 64-cluster (all: 187/36426, PValue: 0.000020)
    Found 5 "synapse" genes in a 64-cluster (all: 291/36426, PValue: 0.000163)
    Found 5 "postsynaptic membrane" genes in a 64-cluster (all: 168/36426, PValue: 0.000012)
    Found 17 "system development" genes in a 64-cluster (all: 1248/36426, PValue: 0.000000)
    Found 5 "extracellular matrix part" genes in a 63-cluster (all: 438/36426, PValue: 0.000974)
    Found 5 "cation channel activity" genes in a 40-cluster (all: 569/36426, PValue: 0.000383)
    Found 23 "membrane" genes in a 40-cluster (all: 11696/36426, PValue: 0.000807)
    Found 20 "integral to membrane" genes in a 40-cluster (all: 8595/36426, PValue: 0.000251)
    Found 20 "intrinsic to membrane" genes in a 40-cluster (all: 8612/36426, PValue: 0.000258)
    Found 21 "membrane part" genes in a 40-cluster (all: 9371/36426, PValue: 0.000267)
```

Supplementary Table 2

Supplementary Table 2. Distinct genes expressed at higher levels in CD133+ D431 GBM cells compared with autologous CD133-GBM cells cultured in serum-containing media *

Gene	Symbol	Gene I.D.	Fold change	P value	Functional involvement
heparan sulfate 6-O-sulfotransferase 2	HS6ST2	90161	175.31	0.002817	biosynthesis of heparan sulfate; FGF-2 signaling
ABI gene family, member 3 (NESH) binding protein	ABI3BP	25890	129.49	0.007108	tumor suppressor
transient receptor potential cation channel	TRPA1	8989	128.20	0.008552	highly expressed in sensory neurons; pain sensation
coagulation factor XIII, A1 polypeptide	F13A1	2162	83.67	0.000529	stabilizes the fibrin clot; tissue regeneration
reticulon 1	RTN1	6252	71.49	0.001792	neuroendocrine secretion
sidekick homolog 2 (chicken)	SDK2	54549	68.99	0.005304	cell adhesion protein that guides axonal terminals
EPH receptor B1	EPHB1	2047	56.20	0.0025	regulates proliferation/migration/polarity of neural progenitors
neuronal growth regulator 1	NEGR1	257194	55.06	0.003549	trans-neural growth-promoting factor
leucine rich repeat containing 7	LRRC7	57554	45.36	0.023261	organization of synaptic cell-cell contacts
MEGF10 protein	MEGF10	84466	45.17	0.014488	engulfment of apoptotic corpses
glutamate decarboxylase 1 (brain, 67kDa)	GAD1	2571	43.24	0.007724	catalyzes the production of gamma-aminobutyric acid
Scm-like with four mbt domains 2	SFMBT2	57713	42.91	0.004102	development of the brain
POU domain, class 3, transcription factor 2	POU3F2	5454	39.87	0.011541	transcription factors in neurogenesis
testis derived transcript (3 LIM domains)	TES	26136	31.88	0.025432	candidate tumor suppressor gene
Ksp37 protein	KSP37	83888	30.19	0.008142	protein produced by CD4 and cytotoxic lymphocytes
v-myc myelocytomatosis viral related oncogene	MYCN	4613	30.06	0.007178	embryonal tumor initiation factor
Calcium/calmodulin-dependent protein kinase IV	CAMK4	814	29.17	0.002284	Ca(2+)-dependent transcriptional regulation
chemokine (C-C motif) ligand 11	CCL11	6356	27.94	0.034323	prevention of acute inflammation
neuroligin 4, X-linked	NLGN4X	57502	26.53	0.001435	neuronal cell surface protein involved in cell-cell-interactions
protein phosphatase 1E (PP2C domain containing)	PPM1E	22843	26.03	0.009441	inactivates multifunctional CaM kinases
orthodenticle homolog 2 (Drosophila)	OTX2	5015	25.97	0.043899	brain and sensory organ development
hairy/enhancer-of-split related with YRPW motif 1	HEY1	23462	25.20	0.001073	mediates notch signaling in maintaining neural precursor cells
Phosphodiesterase 4D, cAMP-specific	PDE4D	5144	24.00	0.002695	degrades the second messenger cAMP
transmembrane protein	TMEFF2	23671	23.33	0.000012	inhibiting cell growth; suppressed by c-Myc expression
dystrophin	DMD	1756	18.39	0.000195	brain development, synapse formation, and plasticity
complement factor H	CFH	3075	14.65	0.014121	inhibition of complement activation
protein tyrosine phosphatase, receptor type, O	PTPRO	5800	14.60	0.006974	inhibition of cell proliferation and inducion of cell apoptosis
cholinergic receptor, nicotinic, alpha polypeptide 3	CHRNA5	1136	14.52	0.004947	ligand-binding subunit of the ganglionic type nicotinic receptor
gastrulation brain homeo box 2	GBX2	2637	12.26	0.022769	early patterning of the vertebrate brain
glutamate receptor, metabotropic 1	GRM1	2911	12.01	0.006675	excitatory neurotransmitter in the central nervous system
amiloride-sensitive cation channel 1, neuronal	ACCN1	40	11.80	0.001059	neurotransmission
ras homolog gene family, member U	RHOU	58480	10.73	0.002902	induce filopodium formation and stress fiber dissolution
potassium voltage-gated channel, KQT-like subfamily	KCNQ2	3785	10.67	0.021453	regulation of neuronal excitability
syntrophin, gamma 1	SNTG1	54212	10.59	0.022576	dystrophin-binding proteins localized in neuronal cells
phosphodiesterase 7B	PDE7B	27115	9.85	0.015903	degrades the phosphodiester bond in cAMP
Protein kinase inhibitor alpha	PKIA	5569	9.24	0.002198	cAMP-dependent protein kinase inhibitor
vasohibin 1	VASH1	22846	9.15	0.007076	inhibitory activity of angiogenesis
MCF.2 cell line derived transforming sequence	MCF2	4168	8.15	0.029575	GDP-GTP exchange factors; directional cell migration
synaptopodin 2	SYNPO2	171024	7.26	0.003422	tumor suppressor gene; limit tumor growth
ribonuclease T2	RNASET2	8635	7.16	0.000609	antitumorigenic and antiangiogenic effects
v-myb myeloblastosis viral oncogene homolog (avian)	MYB	4602	6.24	0.036489	intrinsic factor for neural progenitor cell proliferation
tetraspanin 12	TSPAN12.31	23554	6.20	0.000666	regulation of cell development, growth and motility
inter-alpha (globulin) inhibitor H5	ITIH5	80760	6.03	0.000382	tumour suppressor; growth suppression
dual specificity phosphatase 6	DUSP6	1848	5.59	0.000093	suppress growth and differentiation
Slit homolog 2 (Drosophila)	SLIT2	9353	5.33	0.000142	inhibits neurite outgrowth; hypermethylation in gliomas
frizzled homolog 1 (Drosophila)	FZD1	8321	5.09	0.003911	Wnt/planar cell polarity
Mdm2, transformed 3T3 cell double minute 2,	MDM2	4193	5.08	0.02827	inhibits TP53 mediated cell cycle arrest and apoptosis
LAG1 longevity assurance homolog 6 (S. cerevisiae)	LASS6	253782	4.91	0.008114	ceramide synthesis
Stanniocalcin 1	STC1	6781	4.75	0.027726	a paracrine regulator of growth plate chondrogenesis
interferon induced transmembrane protein 1 (9-27)	IFITM1	8519	4.64	0.005911	immune suppressive molecules

*analysis was based on a cutoff of 3-fold increase in relative expression compared to autologous CD133- GBM cells cultured in serum ($p < 0.05$).

Supplementary Table 3

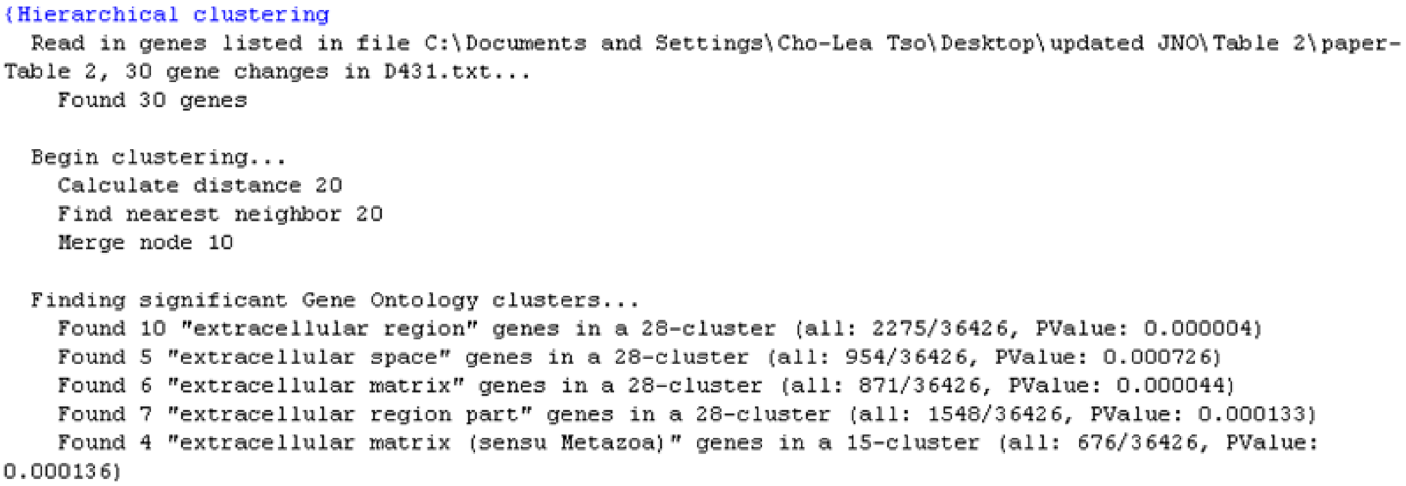
Supplementary Table 3. Distinct genes expressed at higher levels in CD133+ S496 GBM cells compared with autologous CD133-GBM cells cultured in serum-containing media*

Gene	Symbol	Gene I.D.	Fold change	P value	Functional involvement
fatty acid binding protein 7, brain	FABP7	2173	126.26	0.015286	establishes radial glial fiber system; malignant glioblastoma
solute carrier family 17	SLC17A6	57084	79.82	0.047145	transports glutamate in synaptic vesicles
endomucin	EMCN	51705	56.08	0.030959	inhibits interaction between cells and the extracellular matrix
SPARC-like 1 (mast9, hevin)	SPARCL1	8404	45.50	0.01794	radial glial surface antigen; tumor suppressor; antiangiogenesis
FRAS1 related extracellular matrix protein 2	FREM2	341640	45.46	0.001827	maintenance of the integrity of epithelium
NEL-like 2 (chicken) /// NEL-like 2 (chicken)	NELL2	4753	43.48	0.01664	motor and sensory neuron genesis
glypican 3	GPC3	2719	41.15	0.025203	cell polarity and movements; suppress cell proliferation
Adrenergic, alpha-1A-, receptor	ADRA1A	148	34.01	0.043709	suppresses growth and proliferation
zinc finger protein 423	ZNF423	23090	33.71	0.012303	DNA binding-dependent transcriptional repressor
Prostaglandin E receptor 3 (subtype EP3)	PTGER3	5733	28.67	0.012303	decreases intracellular cAMP levels; growth inhibition
MyoD family inhibitor	MDFI	4188	23.85	0.020999	interferes with myogenic factor function
SIAT7E/MGC3184/ST6GalNAcV	ST6GALNAC5	81849	21.56	0.010969	biosynthesis of ganglioside GD1a
Leucine rich repeat neuronal 6C	LINGO2	158038	20.67	0.014161	express in limbic system and neocortex
neurotensin	NTS	4922	19.94	0.014243	regulates the growth of intestinal cells and fat metabolism
inhibitor of DNA binding 4	ID4	3400	19.55	0.027988	tumor suppressor gene
Hyaluronan and proteoglycan link protein 1	HAPLN1	1404	19.05	0.018423	stabilizes cartilage extracellular matrix.
integral membrane protein 2A	ITM2A	9452	18.46	0.032728	marker gene of chondrogenic/osteoblastic cells
gastrin-releasing peptide	GRP	2922	18.24	0.018365	stimulates gastrointestinal hormones
angiotensin II receptor, type 1	AGTR1	185	18.05	0.014783	modulation of nervous system activity, cardiac contractility
DIRAS family, GTP-binding RAS-like 3	DIRAS3	9077	15.68	0.036822	growth suppression; tumor suppressor
leucine rich repeat neuronal 1	LRRN1	57633	14.26	0.047712	cell-cell recognition pathways in neuroepithelial cells.
nuclear factor I/A	NFIA	4774	13.84	0.02239	abrogation of neurogenesis to a generic program of gliogenesis
angiopoietin-like 1	ANGPTL1	9068	13.66	0.047674	antiangiogenesis; antitumor growth
dynamin 3	DNM3	26052	13.27	0.000407	vesicular trafficking processes
chromosome 6 open reading frame 32	C6orf32	9750	13.06	0.000044	cytoskeletal rearrangement and filopodia formation
lipase, endothelial	LIPG1	9388	12.98	0.002796	lipoprotein metabolism and vascular biology
potassium conductance calcium-activated channel	KCNN2	3781	12.78	0.037762	sustained Ca2+ influx in the G0/G1 phase
coagulation factor II (thrombin) receptor-like 2	F2RL2	2151	12.55	0.000002	stimulates phosphoinositide hydrolysis
fibrillin 2 (congenital contractural arachnodactyly)	FBN2	2201	12.29	0.027358	skeletal development
ras homolog gene family, member J	RHOJ	57381	12.29	0.01132	cell proliferation, motility and cell polarity
collagen, type VIII, alpha 2	COL8A2	1296	12.20	0.038404	membrane of corneal endothelial cells (neural crest origin)
sorbin and SH3 domain containing 1	SORBS1	10580	12.06	0.011481	formation actin stress fibers and focal adhesion
protocadherin 20	PCDH20	64881	11.74	0.015779	specific cell-cell connections; tumor suppressor
latrophilin 3	LPHN3	23284	11.18	0.016641	cell adhesion and signal transduction
carbonic anhydrase II	CA2	760	10.95	0.017791	bone resorption and osteoclast differentiation
Protease, serine, 12 (neurotrypsin, motopsin)	PRSS12	8492	9.92	0.017152	normal synaptic function
protein kinase inhibitor beta	PKIB	5570	9.57	0.016691	inhibit cAMP-dependent protein kinase activity
thymosin-like 8	TMSL8	11013	9.54	0.008662	promotes cell migration; neuroblastoma marker
visinin-like 1	VSNL1	7447	9.31	0.00788	neuronal calcium sensor proteins
mab-21-like 2 (C. elegans)	MAB21L2	10586	9.15	0.00496	antagonizes the effects of bone morphogenetic protein 4
solute carrier family 7	SLC7A2	6542	8.85	0.003108	transports the cati onic amino acids
butyrylcholinesterase	BCHE	590	8.81	0.000087	hydrolysis of the neurotransmitter acetylcholine
collagen, type XI, alpha 1	COL11A1	1301	8.73	0.008972	an integral component of the cartilage fibrillar network
zinc finger protein 6 (CMPX1)	ZNF711	7552	8.57	0.020772	highly expressed in brain
potassium voltage-gated channel, subfamily G, member 1	KCNG1	3755	8.44	0.000397	neurotransmitter release, neuronal excitability,
ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 2	ST8SIA2	8128	8.44	0.021621	development and sialic acid synthesis on NCAM
fibroblast growth factor receptor 2	FGFR2	2263	8.39	0.000014	maintaining the neural stem cell pool
E2a-Pbx1-associated protein	ANKS1B	56899	8.22	0.001655	blocks differentiation of myeloid progenitors
chondroitin sulfate synthase 3	CHSY3	337876	8.13	0.007312	neuritogenesis.
dachsous 1 (Drosophila)	DCHS1	8642	8.11	0.006951	controls the establishment of planar cell polarity

*analysis was based on a cutoff of 3-fold increase in relative expression compared to autologous CD133- GBM cells ($p < 0.05$).

Supplementary Table 4

Gene function categories of gene clusters of top 30 modulated genes in CD133- D431 GBM daughter cells when compared to CD133+ GBM daughter cells



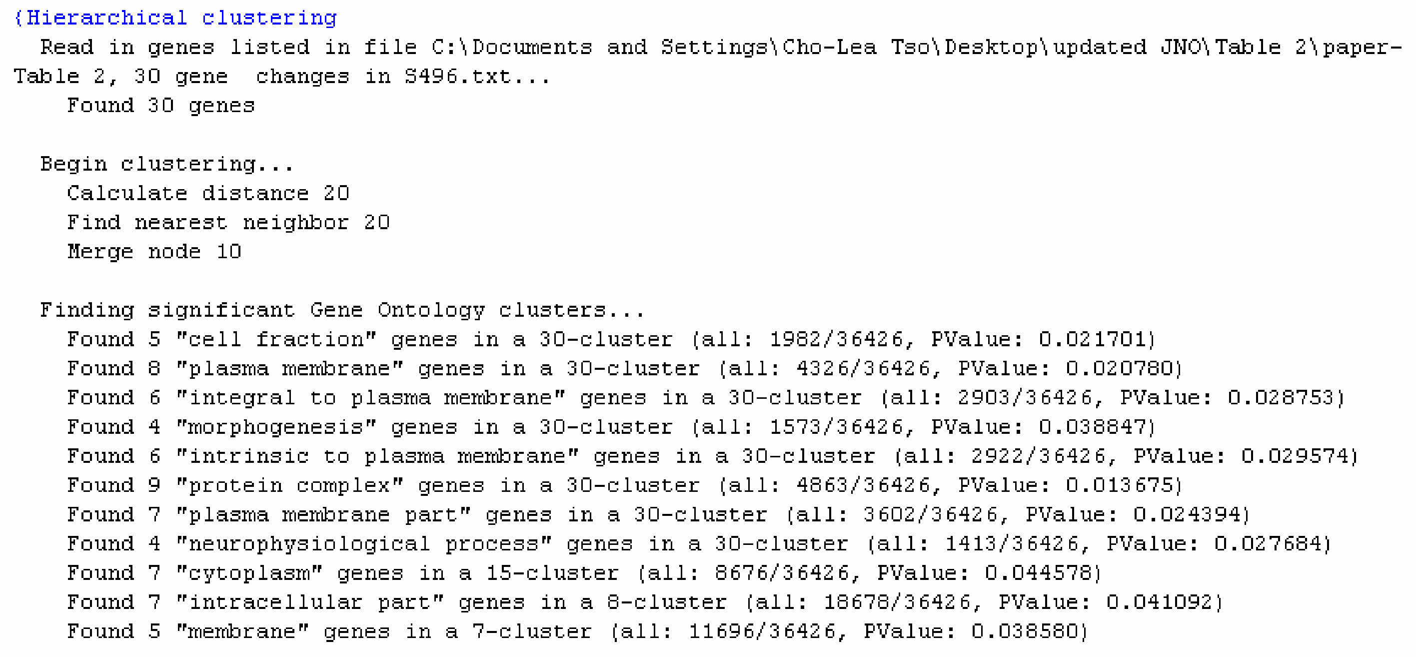
```
{Hierarchical clustering
  Read in genes listed in file C:\Documents and Settings\Cho-Lea Tso\Desktop\updated JNO\Table 2\paper-
Table 2, 30 gene changes in D431.txt...
    Found 30 genes

  Begin clustering...
    Calculate distance 20
    Find nearest neighbor 20
    Merge node 10

  Finding significant Gene Ontology clusters...
    Found 10 "extracellular region" genes in a 28-cluster (all: 2275/36426, PValue: 0.000004)
    Found 5 "extracellular space" genes in a 28-cluster (all: 954/36426, PValue: 0.000726)
    Found 6 "extracellular matrix" genes in a 28-cluster (all: 871/36426, PValue: 0.000044)
    Found 7 "extracellular region part" genes in a 28-cluster (all: 1548/36426, PValue: 0.000133)
    Found 4 "extracellular matrix (sensu Metazoa)" genes in a 15-cluster (all: 676/36426, PValue:
0.000136)
```

Supplementary Table 5

Gene function categories of gene clusters of top 30 modulated genes in CD133- S496 GBM daughter cells when compared to CD133+ S496GBM daughter cells



```
(Hierarchical clustering
  Read in genes listed in file C:\Documents and Settings\Cho-Lea Tso\Desktop\updated JNO\Table 2\paper-
Table 2, 30 gene  changes in S496.txt...
    Found 30 genes

  Begin clustering...
    Calculate distance 20
    Find nearest neighbor 20
    Merge node 10

  Finding significant Gene Ontology clusters...
    Found 5 "cell fraction" genes in a 30-cluster (all: 1982/36426, PValue: 0.021701)
    Found 8 "plasma membrane" genes in a 30-cluster (all: 4326/36426, PValue: 0.020780)
    Found 6 "integral to plasma membrane" genes in a 30-cluster (all: 2903/36426, PValue: 0.028753)
    Found 4 "morphogenesis" genes in a 30-cluster (all: 1573/36426, PValue: 0.038847)
    Found 6 "intrinsic to plasma membrane" genes in a 30-cluster (all: 2922/36426, PValue: 0.029574)
    Found 9 "protein complex" genes in a 30-cluster (all: 4863/36426, PValue: 0.013675)
    Found 7 "plasma membrane part" genes in a 30-cluster (all: 3602/36426, PValue: 0.024394)
    Found 4 "neurophysiological process" genes in a 30-cluster (all: 1413/36426, PValue: 0.027684)
    Found 7 "cytoplasm" genes in a 15-cluster (all: 8676/36426, PValue: 0.044578)
    Found 7 "intracellular part" genes in a 8-cluster (all: 18678/36426, PValue: 0.041092)
    Found 5 "membrane" genes in a 7-cluster (all: 11696/36426, PValue: 0.038580)
```

Supplementary Table 6. Differential gene expression in CD133+ D431 GBM spheres versus CD133+ S496 GBM spheres

gene	CD133+ D431 spheres/CD133+S496 spheres	LocusLink	fold change	P value
Hypothetical protein FLJ36031		168455	100.52	0.009805
chitinase 3-like 1 (cartilage glycoprotein-39)		1116	91.68	0.03526
cytochrome c oxidase subunit VIIa polypeptide 1 (muscle)		1346	67.18	0.002736
hydroxysteroid (11-beta) dehydrogenase 1		3290	64.75	0.043937
coagulation factor XIII, A1 polypeptide		2162	55.9	0.023753
Transcribed locus			55.85	0.028174
RAB3A interacting protein (rabin3)		117177	51.66	0.019807
CDNA clone IMAGE:5261489			45.2	0.03861
Mdm2, transformed 3T3 cell double minute 2, p53 binding protein (m		4193	43.68	0.023129
delta-like 1 (Drosophila)		28514	41.88	0.034983
leucine rich repeat containing 7		57554	34.17	0.033767
family with sequence similarity 20, member A		54757	33.87	0.01041
cytochrome b-245, alpha polypeptide		1535	31.05	0.002295
chemokine (C-C motif) ligand 11		6356	30.93	0.025824
MEGF10 protein		84466	27.62	0.00955
ankylosis, progressive homolog (mouse)		56172	26.47	0.012389
family with sequence similarity 11, member B		79134	22.38	0.039456
mucin 15		143662	21.2	0.013264
G protein-coupled receptor 68		8111	20.05	0.000176
tryptophan 2,3-dioxygenase		6999	19.74	0.049863
ring finger protein 149		284996	18.64	0.00047
chromosome 20 open reading frame 103		24141	18.4	0.027346
gamma-aminobutyric acid (GABA) receptor, rho 1		2569	17.94	0.023181
chromosome 13 open reading frame 18		80183	16.78	0.005736
ATP-binding cassette, sub-family A (ABC1), member 1		19	16.08	0.010759
multiple C2-domains with two transmembrane regions 2		55784	15.65	0.010809
Fibroblast growth factor receptor substrate 2		10818	15.15	0.012426
Transcribed locus			14.15	0.002773
platelet-derived growth factor alpha polypeptide		5154	13.37	0.039304
F-box and leucine-rich repeat protein 16		146330	13.31	0.047391
sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testica		6695	12.78	0.022073
HSPC171 protein		29100	12.61	0.000237
zinc finger protein 415		55786	12.3	0.014314
solute carrier family 26, member 4		5172	12.25	0.049675
hypothetical protein FLJ14213		79899	12.03	0.000012
gb:AI332764 /DB_XREF=gi:4069323 /DB_XREF=qp92h04.x1 /CLONE=IMAGE			11.97	0.032457
hypothetical protein MGC72075		340277	11.87	0.049728
myosin IB		4430	11.83	0.04198
BAI1-associated protein 2-like 1		55971	11.62	0.047216
Fas apoptotic inhibitory molecule 2		23017	11.59	0.014841
transmembrane protein with EGF-like and two follistatin-like domains		23671	11.17	0.012402
CD82 antigen		3732	11	0.031066
collapsin response mediator protein 1		1400	10.81	0.023307
Cleavage and polyadenylation specific factor 6, 68kDa		11052	10.6	0.002071
ribosomal protein L39-like		116832	10.5	0.000438

retinoblastoma 1 (including osteosarcoma)	5925	10.05	0.025829
glutathione S-transferase theta 1	2952	10	0.000766
likely ortholog of mouse limb-bud and heart gene /// likely ortholog o	81606	9.15	0.025396
Transcribed locus		9.15	0.039904
Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-termi	4435	9.11	0.028626
cathepsin B	1508	8.92	0.012927
hypothetical protein MGC5370	84825	8.7	0.000046
Family with sequence similarity 20, member A	54757	8.66	0.010482
protocadherin beta 5	26167	8.61	0.002226
neuronal growth regulator 1	257194	8.44	0.000116
similar to hypothetical protein	221091	8.37	0.040003
tripartite motif-containing 4	89122	8.03	0.002782
chromosome 10 open reading frame 58 /// chromosome 10 open rea	84293	8.02	0.015894
tubulin, beta 6	84617	8.01	0.02216
chromosome 10 open reading frame 58	84293	7.84	0.007907
Sema domain, immunoglobulin domain (Ig), short basic domain, sec	10371	7.75	0.028314
Transcribed locus		7.7	0.040105
interleukin 27 receptor, alpha	9466	7.68	0.015561
transforming growth factor, beta 1 (Camurati-Engelmann disease)	7040	7.58	0.014125
von Willebrand factor A domain containing 1	64856	7.52	0.002005
CDNA FLJ41269 fis, clone BRAMY2036079		7.52	0.046837
MRNA; clone CD 43T7		7.41	0.016015
biglycan	633	7.32	0.046886
biglycan /// serologically defined colon cancer antigen 33	10194 /// 6	7.28	0.006976
carbamoyl-phosphate synthetase 1, mitochondrial	1373	7.26	0.044476
MRNA; clone CD 43T7		7.15	0.014902
CDNA FLJ42287 fis, clone TLIVE2005866		7.13	0.008599
hydrolethalus syndrome 1	219844	7	0.008569
chromosome 6 open reading frame 160	387066	6.99	0.005061
adenylate cyclase 1 (brain)	107	6.92	0.000028
endothelial differentiation, sphingolipid G-protein-coupled receptor,	1903	6.87	0.038541
Glioma amplified sequence 64		6.87	0.04478
CDNA FLJ26796 fis, clone PRS05079		6.78	0.046183
Homo sapiens, clone IMAGE:4398657, mRNA		6.71	0.038834
FLJ20160 protein	54842	6.64	0.000296
dispatched homolog 2 (Drosophila)	85455	6.53	0.048561
ABI gene family, member 3 (NESH) binding protein	25890	6.51	0.041326
programmed cell death 6	10016	6.46	0.005711
likely ortholog of mouse neighbor of Punc E11	57722	6.45	0.009625
chromogranin B (secretogranin 1)	1114	6.4	0.042886
collagen and calcium binding EGF domains 1	147372	6.23	0.010205
KIAA1324	57535	6.22	0.016084
hypothetical protein MGC5370	84825	6.21	0.000198
chromosome 20 open reading frame 22	26090	6.17	0.042111
HMG-box transcription factor 1	26959	6.12	0.032318
adenylate cyclase 1 (brain)	107	5.99	0.001425
prostaglandin E receptor 4 (subtype EP4)	5734	5.96	0.001773
stathmin-like 3	50861	5.88	0.002361
chromosome 6 open reading frame 52	347744	5.84	0.031479
Hypothetical protein LOC283480	283480	5.79	0.006964
zinc finger protein 179	7732	5.73	0.032841

HRAS-like suppressor 3	11145	5.65	0.009871
sema domain, transmembrane domain (TM), and cytoplasmic domai	10501	5.63	0.026898
MRNA; cDNA DKFZp686M0856 (from clone DKFZp686M0856)		5.62	0.00093
CDNA clone IMAGE:5286843		5.6	0.021638
Early B-cell factor	1879	5.55	0.006026
integrin, beta-like 1 (with EGF-like repeat domains)	9358	5.51	0.000503
Phosphorylase kinase, beta	5257	5.47	0.014764
C1q and tumor necrosis factor related protein 6	114904	5.37	0.011962
mitochondrial ribosomal protein L41	64975	5.36	0.002489
fyn-related kinase	2444	5.31	0.000833
lysocardiolipin acyltransferase	253558	5.29	0.00124
chromosome 1 open reading frame 54	79630	5.28	0.007411
phosphodiesterase 9A	5152	5.27	0.024804
hypothetical protein DKFZp566N034	81615	5.22	0.01086
cytochrome P450, family 1, subfamily B, polypeptide 1	1545	5.17	0.021213
hypothetical protein BC008326	89944	5.16	0.045649
MRNA; clone CD 43T7		5.15	0.026519
Furry homolog (Drosophila)	10129	5.13	0.021078
AD031 protein	83935	5.1	0.008614
zinc finger protein ZNF468	90333	5.07	0.003962
BIC transcript	114614	5.05	0.047049
COMM domain containing 10	51397	5.05	0.000132
protein tyrosine phosphatase, receptor type, O /// protein tyrosine ph	5800	5.03	0.045297
ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 5	29906	5.02	0.000852
chaperonin containing TCP1, subunit 2 (beta)	10576	5.01	0.000005
leucine rich repeat transmembrane neuronal 2	26045	4.94	0.024264
lectin, galactoside-binding, soluble, 12 (galectin 12)	85329	4.88	0.048344
loss of heterozygosity, 11, chromosomal region 2, gene A	4013	4.86	0.026138
LOC440203	440203	4.85	0.009443
seizure related 6 homolog (mouse)-like 2	26470	4.84	0.001598
RAS p21 protein activator (GTPase activating protein) 1	5921	4.82	0.048138
thrombospondin 3	7059	4.81	0.014352
mitogen-activated protein kinase kinase kinase kinase 4	9448	4.77	0.017005
testis specific, 14	95681	4.75	0.000653
Notch homolog 3 (Drosophila)	4854	4.74	0.027055
decorin	1634	4.71	0.005605
collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosom	1281	4.7	0.003446
zinc finger-like	400713	4.7	0.000113
cystatin C (amyloid angiopathy and cerebral hemorrhage)	1471	4.66	0.006676
LCHN protein	57189	4.65	0.032791
homeo box A1	3198	4.62	0.003112
F-box and leucine-rich repeat protein 8	55336	4.57	0.000263
insulin-like growth factor binding protein 6	3489	4.53	0.02407
gb:BE504098 /DB_XREF=gi:9706506 /DB_XREF=hv85b02.x1 /CLONE=IMAGE		4.45	0.033715
Full length insert cDNA clone YT94E02		4.44	0.000197
hypothetical protein DKFZp434H1419	150967	4.43	0.022708
neuronal pentraxin receptor	23467	4.42	0.005321
leukemia inhibitory factor receptor	3977	4.41	0.007007
beaded filament structural protein 1, filensin	631	4.4	0.000636
Yip1 domain family, member 4	84272	4.4	0.000026
ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4	7903	4.39	0.007878

spastic paraplegia 20, spartin (Troyer syndrome)	23111	4.38	0.002015
complement component 4A /// complement component 4B /// comple	432395 ///	4.37	0.003653
mitogen-activated protein kinase kinase kinase kinase 4	9448	4.34	0.009301
component of oligomeric golgi complex 5	10466	4.32	0.0022
Homo sapiens, clone IMAGE:5019307, mRNA		4.31	0.026081
yippee-like 5 (Drosophila)	51646	4.3	0.002719
rhomboid, veinlet-like 7 (Drosophila)	57414	4.28	0.001546
clusterin (complement lysis inhibitor, SP-40,40, sulfated glycoprotein	1191	4.27	0.018514
hypothetical protein DKFZp434J1015	54753	4.26	0.002983
propionyl Coenzyme A carboxylase, alpha polypeptide	5095	4.25	0.004692
glutaminase	2744	4.24	0.02668
Transcribed locus, weakly similar to NP_055301.1 neuronal thread protein AD7		4.24	0.00449
protective protein for beta-galactosidase (galactosialidosis)	5476	4.23	0.007893
CDNA FLJ30386 fis, clone BRACE2008216		4.21	0.001268
ubiquitin-conjugating enzyme E2D 4 (putative)	51619	4.19	0.000128
hypothetical protein LOC255458	255458	4.17	0.000271
actin related protein 2/3 complex, subunit 1B, 41kDa	10095	4.12	0.006649
transmembrane protein induced by tumor necrosis factor alpha	83862	4.11	0.009394
chromosome 11 open reading frame 32	442871	4.09	0.004197
churchill domain containing 1	91612	4.09	0.00068
protease, serine, 23	11098	4.04	0.036825
Splicing factor, arginine/serine-rich, 46kD	10929	4.04	0.005346
poly(A) binding protein interacting protein 1	10605	4.03	0.016474
ASAP	79884	-4.05	0.000161
serpin peptidase inhibitor, clade I (neuroserpin), member 1	5274	-4.09	0.024349
apoptosis-inducing factor (AIF)-like mitochondrion-associated induce	84883	-4.1	0.000484
transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila)	7091	-4.13	0.005759
optineurin	10133	-4.15	0.000204
hypothetical protein MGC3040	66000	-4.16	0.003905
transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)	6891	-4.17	0.002875
trichorhinophalangeal syndrome I	7227	-4.18	0.000382
zinc finger protein 367	195828	-4.2	0.012899
transcription factor Dp-1	7027	-4.21	0.001699
mitochondrial ribosomal protein L43	84545	-4.23	0.030031
Kruppel-like factor 4 (gut)	9314	-4.24	0.000928
amphiphysin (Stiff-Man syndrome with breast cancer 128kDa autoar	273	-4.26	0.001762
dihydropyrimidinase-like 5	56896	-4.27	0.0002
RCC1 domain containing 1	91433	-4.27	0.004342
fibulin 1	2192	-4.29	0.000621
UL16 binding protein 3	79465	-4.29	0.004541
Transcribed locus		-4.29	0.019846
Protein tyrosine phosphatase, receptor type, J	5795	-4.3	0.018624
piggyBac transposable element derived 5	79605	-4.31	0.000411
beta 3-glycosyltransferase-like	145173	-4.35	0.001172
MAP/microtubule affinity-regulating kinase 1	4139	-4.36	0.003702
SRY (sex determining region Y)-box 5	6660	-4.38	0.008835
hypothetical protein FLJ20245	54863	-4.38	0.001726
poly (ADP-ribose) polymerase family, member 9	83666	-4.38	0.03286
optineurin	10133	-4.39	0.000226
fibronectin type III domain containing 3B	64778	-4.39	0.000094
hypothetical protein FLJ25006	124923	-4.39	0.020184

outer dense fiber of sperm tails 2-like	57489	-4.41	0.000102
zinc finger protein 85 (HPF4, HTF1)	7639	-4.41	0.000406
protein kinase, cAMP-dependent, catalytic, beta	5567	-4.42	0.006153
zinc finger protein 542	147947	-4.43	0.000444
hypothetical gene supported by AK094796	400764	-4.47	0.014375
proline-serine-threonine phosphatase interacting protein 2	9050	-4.51	0.009868
hypothetical gene supported by AL713796	389831	-4.52	0.000295
hypothetical protein DKFZp762A217	160335	-4.52	0.001819
transcription factor Dp-1	7027	-4.53	0.009887
MRNA (clone ICRFp507I1077)		-4.53	0.008931
transcription factor Dp-1	7027	-4.53	0.00179
gb:BE326808 /DB_XREF=gi:9200584 /DB_XREF=hr65b11.x1 /CLONE=IMAGE		-4.55	0.004141
melanoma antigen family C, 2	51438	-4.56	0.000959
tripartite motif-containing 34 /// tripartite motif-containing 6 and tripart	445372 ///	-4.58	0.002381
ankyrin repeat domain 13C	81573	-4.58	0.005915
microfibrillar-associated protein 2	4237	-4.59	0.015365
Transcribed locus, moderately similar to XP_518244.1 PREDICTED: similar to s		-4.59	0.000508
chromosome 21 open reading frame 7	56911	-4.62	0.028157
CDNA FLJ37216 fis, clone BRALZ2008696		-4.63	0.00302
S100 calcium binding protein A2	6273	-4.64	0.000033
grancalcin, EF-hand calcium binding protein /// grancalcin, EF-hand	25801	-4.66	0.013046
SMAD, mothers against DPP homolog 6 (Drosophila)	4091	-4.66	0.000331
inhibitor of DNA binding 4, dominant negative helix-loop-helix protei	3400	-4.66	0.011998
coagulation factor II (thrombin) receptor-like 2	2151	-4.67	0.031941
mucolipin 3	55283	-4.67	0.009635
protein tyrosine phosphatase, non-receptor type 3	5774	-4.68	0.00302
Tenascin C (hexabrachion)	3371	-4.68	0.011998
neuropilin 2	8828	-4.69	0.036984
Full-length cDNA clone CS0DM012YE14 of Fetal liver of Homo sapi	9760	-4.69	0.027851
synovial sarcoma, X breakpoint 2 interacting protein	117178	-4.7	0.00769
melanoma antigen family E, 1	57692	-4.75	0.000238
UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 6	9331	-4.76	0.029466
glutamate receptor, ionotropic, N-methyl-D-aspartate 3A	116443	-4.76	0.044987
hypothetical gene supported by AL713796	389831	-4.83	0.001176
hypothetical protein	387882	-4.84	0.000679
gb:AI523391 /DB_XREF=gi:4437526 /DB_XREF=ar72c09.x1 /CLONE=IMAGE:		-4.84	0.001432
melanoma antigen family C, 1	9947	-4.86	0.002171
CD99 antigen	4267	-4.86	0.002191
aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenas	1646	-4.87	0.00543
sarcoglycan, delta (35kDa dystrophin-associated glycoprotein)	6444	-4.88	0.000376
chromosome X open reading frame 33	139322	-4.89	0.022506
neurotrimin	50863	-4.92	0.000921
fibroblast growth factor receptor 2 (bacteria-expressed kinase, kerati	2263	-4.94	0.000268
protocadherin 18	54510	-4.95	0.042764
2'-5'-oligoadenylate synthetase-like	8638	-4.97	0.032546
sphingomyelin phosphodiesterase, acid-like 3A	10924	-4.97	0.001339
myosin, light polypeptide kinase	4638	-4.98	0.014771
cadherin 10, type 2 (T2-cadherin)	1008	-4.99	0.009904
glucosaminyl (N-acetyl) transferase 1, core 2 (beta-1,6-N-acetylgluc	2650	-5	0.006004
gb:U08626 /DB_XREF=gi:551473 /FEA=DNA /CNT=1 /TID=Hs.247984.0 /TIER		-5.02	0.019615
membrane protein, palmitoylated 6 (MAGUK p55 subfamily member	51678	-5.06	0.013894

Coxsackie virus and adenovirus receptor	1525	-5.08	0.001847
ankyrin repeat and SOCS box-containing 9	140462	-5.1	0.000138
interferon regulatory factor 7	3665	-5.13	0.012109
Transmembrane and tetratricopeptide repeat containing 2	160335	-5.13	0.00069
special AT-rich sequence binding protein 1 (binds to nuclear matrix/s	6304	-5.14	0.001967
brother of CDO	91653	-5.15	0.005454
Transcription factor AP-2 alpha (activating enhancer binding protein	7020	-5.16	0.008032
hypothetical protein FLJ10094	55068	-5.17	0.002791
FOS-like antigen 1	8061	-5.19	0.029302
CDNA clone IMAGE:5312516		-5.19	0.001673
choline phosphotransferase 1	56994	-5.19	0.000648
CDNA FLJ37216 fis, clone BRALZ2008696		-5.24	0.000669
tropomyosin 2 (beta)	7169	-5.26	0.005132
adrenergic, alpha-2A-, receptor /// adrenergic, alpha-2A-, receptor	150	-5.27	0.001442
hypothetical gene supported by AK123403	389834	-5.27	0.009857
glutamate-ammonia ligase (glutamine synthetase)	2752	-5.28	0.009253
Hermansky-Pudlak syndrome 3	84343	-5.28	0.004688
procollagen C-endopeptidase enhancer 2	26577	-5.3	0.003392
UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosa	114805	-5.3	0.011532
tripartite motif-containing 14	9830	-5.31	0.005441
nuclear factor I/B	4781	-5.33	0.030481
spondin 2, extracellular matrix protein	10417	-5.33	0.001546
gb:AV731490 /DB_XREF=gi:10840911 /DB_XREF=AV731490 /CLONE=HTFA		-5.34	0.0166
neuroligin 1	22871	-5.35	0.001527
Transcribed locus, weakly similar to NP_060312.1 hypothetical protein FLJ2048		-5.36	0.000398
Transcribed locus		-5.37	0.005346
cysteine and glycine-rich protein 1	1465	-5.43	0.001087
CDNA FLJ37216 fis, clone BRALZ2008696		-5.43	0.000291
nuclear factor (erythroid-derived 2)-like 3	9603	-5.46	0.010469
tumor suppressor candidate 1	286319	-5.5	0.00049
XIAP associated factor-1	54739	-5.51	0.04476
fatty acid binding protein 3, muscle and heart (mammary-derived grc	2170	-5.53	0.034997
rhomboid, veinlet-like 2 (Drosophila)	54933	-5.53	0.000649
TCDD-inducible poly(ADP-ribose) polymerase	25976	-5.57	0.007835
v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	4094	-5.6	0.020022
Transmembrane protein 56	148534	-5.6	0.001022
protocadherin 9	5101	-5.62	0.013551
Rho GTPase activating protein 28	79822	-5.62	0.000078
integrin, alpha 9	3680	-5.64	0.015404
cartilage paired-class homeoprotein 1	8092	-5.67	0.000797
regeneration associated muscle protease	25891	-5.67	0.029334
solute carrier family 7 (cationic amino acid transporter, y+ system), n	6542	-5.69	0.026401
family with sequence similarity 26, member B	51063	-5.7	0.000537
phospholipase A2-activating protein	9373	-5.71	0.000424
cadherin 18, type 2	1016	-5.73	0.000537
similar to hypothetical protein MGC27019	389833	-5.76	0.000194
nephroblastoma overexpressed gene	4856	-5.79	0.014753
chromosome 20 open reading frame 45	51012	-5.79	0.005735
Protein kinase, AMP-activated, alpha 2 catalytic subunit	5563	-5.79	0.020989
aldolase C, fructose-bisphosphate	230	-5.81	0.009451
hypothetical protein FLJ10770	55225	-5.83	0.000312

CDNA clone IMAGE:6250506		-5.84	0.026572
carbonic anhydrase XII	771	-5.85	0.00011
ropporin, rhophilin associated protein 1B	152015	-5.85	0.000953
Hypothetical protein MGC21644	153768	-5.85	0.000313
melanoma antigen family A, 1 (directs expression of antigen MZ2-E)	4100	-5.89	0.004944
Transcribed locus		-5.89	0.001483
chromosome 20 open reading frame 45	51012	-5.9	0.021705
angiopoietin-like 1	9068	-5.92	0.020411
insulin-like growth factor binding protein 4	3487	-5.93	0.000093
cystathionase (cystathionine gamma-lyase)	1491	-5.95	0.037043
adenosine A2b receptor	136	-5.96	0.01343
gephyrin	10243	-6.01	0.002552
insulin-like growth factor 1 receptor	3480	-6.02	0.02217
male sterility domain containing 1	55711	-6.03	0.017222
tripartite motif-containing 59	286827	-6.04	0.005338
vascular endothelial growth factor	7422	-6.05	0.003337
ankyrin repeat domain 45	339416	-6.05	0.00756
Transcribed locus		-6.07	0.027685
hexokinase 2	3099	-6.11	0.008709
hypothetical protein LOC129607	129607	-6.12	0.011777
hyaluronan-mediated motility receptor (RHAMM)	3161	-6.14	0.022321
coiled-coil domain containing 2	80173	-6.15	0.008351
aquaporin 1 (channel-forming integral protein, 28kDa)	358	-6.16	0.046638
gb:AF127481.1 /DB_XREF=gi:5199315 /GEN=proto-LBC /FEA=FLmRNA /CNT		-6.16	0.013135
LOC440669	440669	-6.17	0.000248
BTB (POZ) domain containing 11	121551	-6.17	0.018879
catalase	847	-6.18	0.003688
olfactomedin-like 3	56944	-6.2	0.012389
chromosome 10 open reading frame 11	83938	-6.22	0.001014
Poly (ADP-ribose) polymerase family, member 8	79668	-6.22	0.000808
chromosome 9 open reading frame 95	54981	-6.24	0.000153
Holocarboxylase synthetase (biotin-(proprionyl-Coenzyme A-carbox	3141	-6.26	0.024899
interferon-induced protein with tetratricopeptide repeats 1 /// interfer	3434	-6.28	0.01059
DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	23586	-6.3	0.002979
twist homolog 2 (Drosophila)	117581	-6.3	0.012437
mucolipin 2	255231	-6.32	0.008669
catalase /// catalase	847	-6.34	0.004849
cullin-associated and neddylation-dissociated 2 (putative)	23066	-6.34	0.000251
hypothetical protein FLJ10178	55086	-6.34	0.001198
neuro-oncological ventral antigen 1	4857	-6.36	0.034779
pentraxin-related gene, rapidly induced by IL-1 beta	5806	-6.43	0.014418
likely ortholog of mouse schlafen 8/9	91607	-6.44	0.000823
Transcribed locus, strongly similar to NP_002137.3 homeo box B3; homeo box		-6.45	0.001231
collagen, type XXI, alpha 1 /// collagen, type XXI, alpha 1	81578	-6.46	0.013912
similar to Histone H3.3	392533	-6.48	0.003318
tripartite motif-containing 14	9830	-6.49	0.00436
Paired box gene 8	7849	-6.5	0.002629
paired box gene 3 (Waardenburg syndrome 1)	5077	-6.52	0.000652
chromosome 10 open reading frame 48	283078	-6.52	0.003405
phosphodiesterase 1C, calmodulin-dependent 70kDa	5137	-6.54	0.023316
chromosome 21 open reading frame 91	54149	-6.59	0.000334

absent in melanoma 1	202	-6.6	0.003686
trichorhinophalangeal syndrome I	7227	-6.61	0.038526
roundabout, axon guidance receptor, homolog 2 (Drosophila)	6092	-6.61	0.03421
v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)	2114	-6.62	0.02335
tubulin tyrosine ligase-like family, member 7	79739	-6.62	0.005829
Chromosome 9 open reading frame 3	84909	-6.63	0.002053
testis expressed sequence 15	56154	-6.63	0.008609
follistatin	10468	-6.64	0.029848
hypothetical protein FLJ30046	122060	-6.67	0.025733
arylsulfatase J	79642	-6.69	0.038715
Chromosome 20 open reading frame 45	51012	-6.69	0.041078
cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	1030	-6.7	0.00648
tetraspanin 15	23555	-6.75	0.031275
matrix-remodelling associated 5	25878	-6.76	0.000305
similar to Polyadenylate-binding protein 4 (Poly(A)-binding protein 4)	132430	-6.83	0.033473
protocadherin beta 3	56132	-6.83	0.025458
dimethylarginine dimethylaminohydrolase 1	23576	-6.85	0.018508
interleukin 11 receptor, alpha	3590	-6.87	0.007056
Fraser syndrome 1	80144	-6.92	0.036913
tight junction protein 2 (zona occludens 2)	9414	-6.94	0.002043
protocadherin beta 2	56133	-6.95	0.019903
ropporin, rhophilin associated protein 1	54763	-6.97	0.000084
sclerostin domain containing 1	25928	-6.99	0.003942
Connector enhancer of kinase suppressor of Ras 2	22866	-7	0.005218
CDNA FLJ30740 fis, clone FEBRA2000319		-7.05	0.000452
2'-5'-oligoadenylate synthetase 3, 100kDa	4940	-7.08	0.015163
six transmembrane epithelial antigen of the prostate 1	26872	-7.12	0.019233
pleckstrin homology domain containing, family A member 5	54477	-7.17	0.004999
growth factor receptor-bound protein 10	2887	-7.18	0.005262
ring finger protein 182	221687	-7.2	0.028713
growth arrest-specific 1	2619	-7.22	0.011178
28kD interferon responsive protein	64108	-7.22	0.018689
Phosphodiesterase 3B, cGMP-inhibited	5140	-7.23	0.018651
Proline rich Gla (G-carboxyglutamic acid) 4 (transmembrane)	79056	-7.23	0.007804
fasciculation and elongation protein zeta 1 (zygin I)	9638	-7.27	0.002646
Transcribed locus		-7.29	0.018169
mesenchyme homeo box 2 (growth arrest-specific homeo box)	4223	-7.32	0.005313
hypothetical LOC402110	402110	-7.32	0.015994
desmoglein 2	1829	-7.37	0.005834
Male sterility domain containing 1	55711	-7.47	0.009703
gb:AI341053 /DB_XREF=gi:4077980 /DB_XREF=qx89a08.x1 /CLONE=IMAGE:		-7.5	0.00246
Hypothetical protein MGC39606	399668	-7.5	0.000374
midline 1 (Opitz/BBB syndrome)	4281	-7.52	0.012081
G protein-coupled receptor 37 (endothelin receptor type B-like)	2861	-7.53	0.0024
transforming growth factor, beta 2	7042	-7.55	0.001843
Choroideremia (Rab escort protein 1)	1121	-7.55	0.025805
PTPRF interacting protein, binding protein 2 (liprin beta 2)	8495	-7.56	0.000473
laminin, alpha 1	284217	-7.59	0.021162
adenylate kinase 3-like 1 /// adenylate kinase 3-like 2	205 /// 387	-7.61	0.000446
interleukin 15	3600	-7.62	0.000485
leucine rich repeat containing 44	127255	-7.63	0.00997

solute carrier family 16 (monocarboxylic acid transporters), member	9123	-7.69	0.02147
v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog	3815	-7.74	0.042668
chromosome 9 open reading frame 3	84909	-7.74	0.009463
solute carrier family 38, member 4	55089	-7.76	0.001194
placenta-specific 9	219348	-7.8	0.019791
insulin-like growth factor binding protein 3	3486	-7.81	0.001375
CDNA clone IMAGE:5294528		-7.81	0.001466
absent in melanoma 2	9447	-7.9	0.041098
protein kinase, cGMP-dependent, type I	5592	-7.93	0.020644
ST6 beta-galactosamide alpha-2,6-sialyltranferase 2	84620	-7.99	0.046817
KIAA1679 protein	80731	-8.02	0.004678
sorbin and SH3 domain containing 1	10580	-8.1	0.004775
enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrog	1962	-8.11	0.00692
Aldolase A, fructose-bisphosphate pseudogene 2	387718	-8.12	0.035325
L1 cell adhesion molecule	3897	-8.16	0.010297
chromosome 6 open reading frame 32	9750	-8.18	0.0076
pleckstrin homology-like domain, family B, member 2	90102	-8.2	0.009582
guanylate binding protein 2, interferon-inducible	2634	-8.2	0.018273
ropporin, rhophilin associated protein 1	54763	-8.23	0.000798
protocadherin 20	64881	-8.26	0.007614
stimulated by retinoic acid gene 6 homolog (mouse) /// stimulated by	64220	-8.31	0.000369
brain expressed X-linked-like 1	56271	-8.34	0.001202
inter-alpha (globulin) inhibitor H4 (plasma Kallikrein-sensitive glycopr	3700	-8.41	0.001173
Collagen, type VIII, alpha 1	1295	-8.45	0.037481
trinucleotide repeat containing 9	27324	-8.48	0.007399
interferon, alpha-inducible protein (clone IFI-15K)	9636	-8.5	0.000549
cytochrome P450, family 2, subfamily J, polypeptide 2	1573	-8.57	0.00698
Similar to hypothetical protein MGC27019	389833	-8.57	0.029123
toll-like receptor 3	7098	-8.59	0.017449
chromosome 2 open reading frame 32	25927	-8.59	0.000027
potassium channel, subfamily K, member 1	3775	-8.64	0.000516
hypothetical protein LOC283824	283824	-8.64	0.038063
Hypothetical LOC401384	402560	-8.65	0.000084
PDZ and LIM domain 4	8572	-8.68	0.000447
mucolipin 2	255231	-8.73	0.000341
monoglyceride lipase /// monoglyceride lipase	11343	-8.77	0.009086
T-box 3 (ulnar mammary syndrome)	6926	-8.77	0.000373
fibroblast growth factor 2 (basic)	2247	-8.84	0.044607
CDNA clone IMAGE:4820330		-8.85	0.001555
cadherin 13, H-cadherin (heart)	1012	-8.95	0.023185
chromosome 1 open reading frame 24	116496	-8.99	0.023971
chromosome 9 open reading frame 64	84267	-9	0.026548
CDNA clone IMAGE:30343207		-9.06	0.004147
protein phosphatase 1K (PP2C domain containing)	152926	-9.12	0.0341
dynamin 3	26052	-9.17	0.000194
hypothetical gene supported by BC013438	375295	-9.18	0.047115
RAS-like, family 12	51285	-9.19	0.010782
phospholipase C, epsilon 1	51196	-9.24	0.016274
trichorhinophalangeal syndrome I	7227	-9.33	0.024097
cathepsin Z	1522	-9.37	0.039734
tensin 1 /// tensin 1	7145	-9.37	0.023617

interferon induced with helicase C domain 1	64135	-9.38	0.033841
potassium inwardly-rectifying channel, subfamily J, member 15	3772	-9.4	0.007763
P antigen family, member 5 (prostate associated)	90737	-9.43	0.021324
PDZ and LIM domain 4	8572	-9.5	0.004656
four and a half LIM domains 2	2274	-9.52	0.035661
ADAM metallopeptidase with thrombospondin type 1 motif, 3	9508	-9.57	0.045149
neuromedin U	10874	-9.62	0.024909
proteoglycan 1, secretory granule	5552	-9.65	0.02353
Transcribed locus		-9.75	0.001306
ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 2	8128	-9.8	0.003939
adenylate kinase 3-like 1	205	-9.84	0.001034
RAB3B, member RAS oncogene family	5865	-9.85	0.042702
ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu anti	1993	-9.86	0.04847
coagulation factor II (thrombin) receptor-like 2	2151	-9.86	0.003601
KIAA0527 protein	26032	-9.98	0.010459
RNA binding motif protein 24	221662	-10.09	0.007072
plastin 1 (I isoform)	5357	-10.17	0.033822
Glypican 6	10082	-10.25	0.000257
neuronal cell adhesion molecule	4897	-10.29	0.034467
carboxypeptidase X (M14 family), member 2	119587	-10.31	0.028909
Lysyl oxidase-like 1	4016	-10.39	0.010837
chromosome 6 open reading frame 32	9750	-10.42	0.00089
stanniocalcin 1	6781	-10.44	0.015384
cache domain containing 1	57685	-10.44	0.001244
ecotropic viral integration site 1	2122	-10.44	0.005983
2',5'-oligoadenylate synthetase 1, 40/46kDa	4938	-10.46	0.006627
cytochrome b-561	1534	-10.57	0.000152
unc-13 homolog B (C. elegans)	10497	-10.58	0.021855
runt-related transcription factor 1; translocated to, 1 (cyclin D-related	862	-10.7	0.039623
collagen, type XXV, alpha 1	84570	-10.75	0.049495
mab-21-like 2 (C. elegans)	10586	-10.88	0.003764
gb:AI480314 /DB_XREF=gi:4373482 /DB_XREF=tm26h05.x1 /CLONE=IMAGE		-11	0.025602
LOC440669	440669	-11.14	0.000309
phospholipid scramblase 1	5359	-11.15	0.00637
protein tyrosine phosphatase, non-receptor type 20	26095	-11.23	0.020615
RAR-related orphan receptor A	6095	-11.26	0.025275
dipeptidylpeptidase 6	1804	-11.41	0.048752
interferon, alpha-inducible protein (clone IFI-6-16)	2537	-11.53	0.002756
Transcribed locus		-11.56	0.001388
hypothetical protein DKFZp313A2432	258010	-11.63	0.002348
thymus high mobility group box protein TOX	9760	-11.64	0.038529
SRY (sex determining region Y)-box 11	6664	-11.85	0.048079
cytochrome P450, family 39, subfamily A, polypeptide 1	51302	-11.92	0.008453
E2a-Pbx1-associated protein	56899	-12	0.007279
diaphanous homolog 2 (Drosophila)	1730	-12.02	0.025399
Unc-5 homolog D (C. elegans)	137970	-12.09	0.03656
KIAA1729 protein	85460	-12.15	0.000356
growth factor receptor-bound protein 10	2887	-12.37	0.008833
SRY (sex determining region Y)-box 2	6657	-12.45	0.00059
Rho GTPase activating protein 28	79822	-12.46	0.001032
junctophilin 1	56704	-12.48	0.035475

cyclin D1	595	-12.49	0.029428
thioredoxin interacting protein	10628	-12.67	0.022254
Malic enzyme 1, NADP(+)-dependent, cytosolic	4199	-12.68	0.000039
RAR-related orphan receptor A	6095	-12.79	0.023342
WD repeat domain 72	256764	-12.9	0.002879
epithelial stromal interaction 1 (breast)	94240	-12.93	0.0006
solute carrier family 16 (monocarboxylic acid transporters), member	9194	-13.02	0.00297
Proprotein convertase subtilisin/kexin type 5	5125	-13.05	0.002744
transcription factor AP-2 gamma (activating enhancer binding protei	7022	-13.09	0.041195
hypothetical LOC554202	554202	-13.12	0.00007
microsomal glutathione S-transferase 1	4257	-13.21	0.011527
monoamine oxidase A	4128	-13.23	0.031279
collagen, type XIII, alpha 1	1305	-13.23	0.045344
R-spondin 2 homolog (Xenopus laevis)	340419	-13.23	0.012198
cellular retinoic acid binding protein 2	1382	-13.32	0.000075
hect domain and RLD 6	55008	-13.38	0.019233
gb:AU151107 /DB_XREF=gi:11012628 /DB_XREF=AU151107 /CLONE=NT2R		-13.39	0.023717
Leucine rich repeat neuronal 6C	158038	-13.54	0.040253
phosphodiesterase 3B, cGMP-inhibited	5140	-13.78	0.018593
tensin 1 /// tensin 1	7145	-13.86	0.032193
Transcribed locus		-13.87	0.019613
transcription factor AP-2 alpha (activating enhancer binding protein	7020	-13.88	0.011034
secreted and transmembrane 1	6398	-13.96	0.007154
C-type lectin domain family 2, member B	9976	-14.45	0.017595
myxovirus (influenza virus) resistance 2 (mouse)	4600	-14.46	0.011019
gastrin-releasing peptide	2922	-14.7	0.035202
synaptotagmin I	6857	-14.81	0.002493
collagen, type IX, alpha 3	1299	-14.96	0.023833
PDZ and LIM domain 4	8572	-15.08	0.006476
synapse defective 1, Rho GTPase, homolog 2 (C. elegans)	84144	-15.11	0.005939
glutathione peroxidase 7	2882	-15.21	0.010613
ephrin-B2	1948	-15.35	0.00757
Chimerin (chimaerin) 2	1124	-15.38	0.019592
paired-like homeodomain transcription factor 2	5308	-15.42	0.031805
integrin, alpha 6	3655	-15.57	0.000006
endomucin	51705	-15.88	0.000164
hydroxyprostaglandin dehydrogenase 15-(NAD)	3248	-16.07	0.005778
interferon-induced protein 44-like	10964	-16.11	0.033083
CDNA clone IMAGE:5288238 /// CDNA FLJ43039 fis, clone BRTHA3003023		-16.17	0.041388
Hypothetical protein LOC285513	285513	-16.53	0.022928
hypothetical protein FLJ37659	286499	-16.75	0.025158
fibronectin leucine rich transmembrane protein 3	23767	-16.82	0.009865
guanylate binding protein 1, interferon-inducible, 67kDa	2633	-17.26	0.013088
Ca2+-dependent activator protein for secretion 2	93664	-17.45	0.024912
CDNA clone IMAGE:6186815		-17.85	0.001101
ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgal	81849	-17.86	0.009698
hephaestin	9843	-17.87	0.000348
cytochrome P450, family 26, subfamily B, polypeptide 1	56603	-18.01	0.003805
Two transmembrane A	388459	-18.17	0.000245
CDNA FLJ39164 fis, clone OCBBF2002656		-18.18	0.037639
Desmoglein 2	1829	-18.21	0.012145

netrin G1	22854	-18.39	0.011222
calmegin	1047	-18.65	0.007608
doublecortex; lissencephaly, X-linked (doublecortin)	1641	-18.74	0.040701
integrin, alpha 6	3655	-18.83	0.004139
phosphatidic acid phosphatase type 2B	8613	-18.95	0.003288
tumor protein D52	7163	-18.99	0.007582
dynamin 3	26052	-19.07	0.044824
SH3-domain GRB2-like 3	401131	-19.15	0.002507
proprotein convertase subtilisin/kexin type 5	5125	-19.21	0.015318
Homo sapiens, clone IMAGE:3618365, mRNA		-19.22	0.003545
leucine zipper, down-regulated in cancer 1	23641	-19.36	0.002696
T-box 3 (ulnar mammary syndrome)	6926	-19.46	0.002537
CDNA FLJ43039 fis, clone BRTHA3003023		-19.5	0.037812
2'-5'-oligoadenylate synthetase 2, 69/71kDa	4939	-19.53	0.00508
embryonal Fyn-associated substrate	10278	-19.63	0.035002
ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgal	256435	-20.52	0.020815
butyrylcholinesterase	590	-20.98	0.028956
hypothetical gene LOC133874	133874	-20.98	0.019423
bone morphogenetic protein 2	650	-20.99	0.026123
C-type lectin domain family 1, member A	51267	-21.29	0.009787
X (inactive)-specific transcript	7503	-21.45	0.018652
claudin 11 (oligodendrocyte transmembrane protein)	5010	-21.59	0.032076
tropomyosin 2 (beta)	7169	-21.62	0.000861
methylthioadenosine phosphorylase	4507	-21.7	0.014338
myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Dro	4300	-21.73	0.004203
Runt-related transcription factor 1; translocated to, 1 (cyclin D-relate	862	-21.85	0.031851
glutamate receptor, ionotrophic, AMPA 3	2892	-21.88	0.010654
Full-length cDNA clone CS0DI062YC15 of Placenta Cot 25-normalized of Homo		-22.03	0.001556
collectin sub-family member 12 /// collectin sub-family member 12	81035	-22.33	0.011976
hormonally upregulated Neu-associated kinase	30811	-22.53	0.018862
CDNA FLJ39164 fis, clone OCBBF2002656		-22.75	0.012512
cell division cycle associated 7-like	55536	-23.69	0.019179
Sarcoglycan, delta (35kDa dystrophin-associated glycoprotein)	6444	-23.71	0.002428
potassium voltage-gated channel, Isk-related family, member 4	23704	-24.03	0.020773
Hyaluronan and proteoglycan link protein 1	1404	-24.14	0.039639
EPH receptor A2	1969	-24.15	0.034916
glypican 4	2239	-24.17	0.000547
Homo sapiens, clone IMAGE:4246712, mRNA		-24.27	0.019685
G0/G1switch 2	50486	-24.89	0.010458
tripartite motif-containing 59	286827	-24.99	0.01086
layilin	143903	-25.19	0.010431
potassium intermediate/small conductance calcium-activated channe	3781	-25.54	0.018412
latrophilin 2	23266	-25.6	0.036795
blood vessel epicardial substance	11149	-25.94	0.000518
Prostaglandin E receptor 3 (subtype EP3)	5733	-25.98	0.017214
protein phosphatase 1, regulatory (inhibitor) subunit 1C	151242	-26.12	0.021086
thioesterase superfamily member 4	117145	-26.16	0.006879
popeye domain containing 3	64208	-26.8	0.004287
hect domain and RLD 5	51191	-26.99	0.03648
CDNA clone IMAGE:6186815		-27	0.017141
Transcribed locus		-27.62	0.033579

ring finger protein 150	57484	-27.67	0.000041
hypothetical protein LOC283666	283666	-27.81	0.016109
met proto-oncogene (hepatocyte growth factor receptor)	4233	-27.86	0.001626
KIAA1797	54914	-27.91	0.006845
phospholipase C, beta 1 (phosphoinositide-specific)	23236	-29	0.00505
DKFZP434B061 protein	26080	-29.96	0.02162
kelch-like 14 (Drosophila)	57565	-29.99	0.034487
potassium voltage-gated channel, Isk-related family, member 4	23704	-30.16	0.016798
Synapse defective 1, Rho GTPase, homolog 2 (C. elegans)	84144	-30.29	0.01481
PDZ domain containing RING finger 3	23024	-30.58	0.011072
EPH receptor A3	2042	-30.76	0.040292
collagen, type VIII, alpha 2	1296	-31.31	0.010093
CDNA FLJ39164 fis, clone OCBBF2002656		-31.78	0.028527
glutaminyl-peptide cyclotransferase (glutaminyl cyclase)	25797	-32.83	0.01599
X (inactive)-specific transcript	7503	-32.85	0.010491
growth arrest-specific 2	2620	-33.39	0.001093
protein tyrosine phosphatase, receptor type, M	5797	-33.56	0.006529
fibronectin leucine rich transmembrane protein 3	23767	-34.1	0.025056
interferon-induced protein 44	10561	-34.53	0.013864
X (inactive)-specific transcript	7503	-34.65	0.01147
hypothetical protein MGC33365	205428	-35.37	0.031311
CUG triplet repeat, RNA binding protein 2	10659	-35.92	0.035013
Adrenergic, alpha-1A-, receptor	148	-36.09	0.024325
transcription elongation factor A (SII)-like 7	56849	-36.84	0.008165
myxovirus (influenza virus) resistance 1, interferon-inducible protein	4599	-36.91	0.011645
kelch-like 9 (Drosophila)	55958	-36.92	0.001018
chemokine (C-X-C motif) ligand 14	9547	-37.17	0.041468
Potassium voltage-gated channel, Isk-related family, member 4	23704	-37.27	0.003881
fatty acid binding protein 5 (psoriasis-associated)	2171	-38.7	0.002601
protein tyrosine phosphatase, receptor type, M	5797	-38.9	0.009965
X (inactive)-specific transcript	7503	-39.19	0.014671
endomucin	51705	-39.9	0.000809
Mst3 and SOK1-related kinase	51765	-41.23	0.007628
ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylga	81849	-41.34	0.006659
inhibitor of DNA binding 3, dominant negative helix-loop-helix protei	3399	-42.41	0.001231
visinin-like 1	7447	-42.54	0.011797
nuclear factor I/A	4774	-42.93	0.015824
glypican 3	2719	-43.03	0.028887
melanoma antigen family A, 2 /// melanoma antigen family A, 2B	266740 ///	-45.86	0.026463
leucine-rich repeats and calponin homology (CH) domain containing	57631	-51.32	0.003553
inhibitor of DNA binding 4, dominant negative helix-loop-helix protei	3400	-53.06	0.027083
fibronectin leucine rich transmembrane protein 2	23768	-53.51	0.003567
lipase, endothelial	9388	-56.15	0.030105
protein kinase (cAMP-dependent, catalytic) inhibitor beta	5570	-58.91	0.027824
inhibitor of DNA binding 1, dominant negative helix-loop-helix protei	3397	-59.19	0.005202
integral membrane protein 2A	9452	-60.82	0.041634
visinin-like 1	7447	-63.48	0.010113
interferon, alpha-inducible protein 27	3429	-66.52	0.01151
fatty acid binding protein 7, brain	2173	-77.17	0.008192
CD24 antigen (small cell lung carcinoma cluster 4 antigen)	934	-85.26	0.008739
similar to RIKEN cDNA 1200014N16 gene	92092	-86.48	0.007004

cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4	1029	-101.02	0.007481
secreted frizzled-related protein 2	6423	-105.14	0.013556
Down syndrome critical region gene 8	84677	-127.58	0.000638
cysteine-rich secretory protein LCCL domain containing 1	83690	-147.67	0.001707
ZW10 interactor	11130	-156.67	0.002363
transmembrane protein 47	83604	-233.79	0.001764

Supplementary Table 7

Supplementary Table 7. p values of shared genes overexpressed in CD133+ D431 and CD133+ S496 GBM cells shown in Table 1*

Gene	Symbol	Gene I.D.	Chromosome	Fold change D431	P value	Fold change S496	P value
sema, transmembrane, and cytoplasmic domain, 6D	SEMA6D	80031	15q21	117.89	0.004256	4.16	0.004085
growth associated protein 43	GAP43	2596	3q13.1-q13.2	110.32	0.003414	25.56	0.008886
distal-less homeo box 6	DLX6	1750	7q22	78.94	0.000513	40.90	0.023314
BH-protocadherin (brain-heart)	PCDH7	5099	4p15	62.58	0.003992	3.76	0.00506
prominin 1/CD133	PROM1	8842	4p15.32	52.87	0.010701	13.70	0.040133
endothelin 3	EDN3	1908	20q13.2-q13.3	43.96	0.01585	26.35	0.00035
ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4	ST8SIA4	7903	5q21	43.56	0.006025	5.39	0.001432
transcription factor AP-2 beta	TFAP2B	7021	6p12	37.28	0.016388	22.01	0.045574
distal-less homeo box 5	DLX5	1749	7q22	36.64	0.004973	17.18	0.004164
neurexin 3	NRXN3	9369	14q31	27.84	0.003597	5.79	0.000087
cholinergic receptor, nicotinic, alpha polypeptide 9	CHRNA9	55584	4p14	27.24	0.005201	3.99	0.023476
fatty acid binding protein 4, adipocyte	FABP4	2167	8q21	26.43	0.008978	70.07	0.001769
peptidase inhibitor 15	PI15	51050	8q21.11	24.09	0.002221	7.79	0.033561
cholinergic receptor, nicotinic, alpha polypeptide 1 (muscle)	CHRNA1	1134	2q24-q32	23.12	0.000005	6.33	0.005373
glycoprotein M6B	GPM6B	2824	Xp22.2	23.12	0.001827	5.79	0.001799
sortilin-related VPS10 domain containing receptor 1	SORCS1	114815	10q23-q25	19.39	0.02014	45.42	0.011354
protein phosphatase, EF-hand calcium binding domain 1	PPEF1	5475	Xp22.2-p22.1	19.18	0.014379	9.59	0.034167
kinesin family member 5C	KIF5C	3800	2q23.1	19.03	0.003683	17.36	0.002331
Down syndrome critical region gene 1-like 1	RCAN2	10231	6p12.3	18.71	0.011425	10.06	0.033844
leucine-rich repeat-containing G protein-coupled receptor 5	LGR5	8549	12q22-q23	18.56	0.012666	4.59	0.020432
glutamate receptor, ionotropic, AMPA 1	GRIA1	2890	5q31.1	16.48	0.013535	14.20	0.017366
mesenchyme homeo box 2	MEOX2	4223	7p22.1-p21.3	15.64	0.014484	47.53	0.006567
monooxygenase, DBH-like 1	MOXD1	26002	6q23.1-q23.3	15.53	0.006919	23.19	0.000125
cholinergic receptor, muscarinic 3	CHRM3	1131	1q43	14.44	0.01216	7.26	0.004492
sulfatase 1	SULF1	23213	8q13.2-q13.3	13.96	0.007959	30.43	0.001326
regulator of G-protein signalling 5	RGS5	8490	1q23.1	13.19	0.015608	15.10	0.000153
frizzled-related protein	FRZB	2487	2qter	12.98	0.013552	6.01	0.01531
neurocalcin delta	NCALD	83988	8q22.2	11.78	0.006287	3.54	0.01064
gamma-aminobutyric acid (GABA) receptor, rho 1	GABRR1	2569	6q13-q16.3	11.35	0.000006	5.08	0.001133
protocadherin 19	PCDH19	57526	Xq13.3	11.04	0.000595	5.16	0.029916
SRY (sex determining region Y)-box 2	SOX2	6657	3q26.3-q27	10.74	0.014059	7.49	0.000005
TRAF2 and NCK interacting kinase	TNIK	23043	3q26.2-q26.31	9.72	0.006537	3.41	0.017156
mesoderm specific transcript homolog (mouse)	MEST	4232	7q32	8.79	0	45.13	0.031869
phosphorylase kinase, gamma 2 (testis)	PHKG2	5261	16p12.1-p11.2	8.79	0.048872	8.01	0.009605
spondin 1, extracellular matrix protein	SPON1	10418	11p15.2	8.43	0.003573	33.87	0.046194
Rap guanine nucleotide exchange factor (GEF) 5	RAPGEF5	9771	7p15.3See	8.42	0.000574	19.43	0.015611
trinucleotide repeat containing 9	TOX3	27324	16q12.1	8.36	0.025791	56.65	0.030959
insulin-like growth factor binding protein 2, 36kDa	IGFBP2	3485	2q33-q34	7.83	0.00621	3.09	0.021598
death-associated protein kinase 1	DAPK1	1612	9q34.1	7.69	0.001319	15.44	0.014172
formin homology 2 domain containing 3	FHOD3	80206	18q12	7.49	0.0039	3.15	0.006515
scrapie responsive protein 1	SCRG1	11341	4q31-q32	7.09	0.004505	80.65	0.029035
potassium large conductance calcium-activated channel	KCNMB4	27345	12q	7.09	0.0176	6.00	0.01504
retinoic acid receptor, alpha	RARA	5914	17q21	6.67	0.018781	12.21	0.01322
neurofilament, light polypeptide 68kDa	NEFL	4747	8p21	6.6	0.049396	6.28	0.024439
Oxoglutarate (alpha-ketoglutarate) dehydrogenase	OGDH	4967	7p14-p13	6.24	0.046619	4.36	0.04865
ADAM metallopeptidase domain 23	ADAM23	8745	2q33	5.32	0.002473	4.38	0.006696
cadherin 2, type 1, N-cadherin (neuronal)	CDH2	1000	18q11.2	5.06	0.000016	11.21	0.024117
immunoglobulin superfamily, member 4C	IGSF4C	199731	19q13.31	4.75	0.027726	10.07	0.022956
ankyrin 3, node of Ranvier (ankyrin G)	ANK3	288	10q21	4.71	0.000627	4.19	0.000358
alpha-2-macroglobulin	A2M	2	12p13.3-p12.3	4.31	0.005988	11.49	0.040597
inhibin, beta A (activin A, activin AB alpha polypeptide)	INHBA	3624	7p15-p13	4.28	0.00255	7.16	0.045151
neuropilin 2	NRP2	8828	2q33.3	4.26	0.000052	5.96	0.01319
very low density lipoprotein receptor	VLDLR	7436	9p24	4.18	0.000073	5.83	0.000113
sortilin-related VPS10 domain containing receptor 2	SORCS2	57537	4p16.1	3.81	0.000836	8.95	0.015024
GalNAc-T10	GALNT10	55568	5q33.2	3.67	0.001408	4.30	0.010526
FXYD domain containing ion transport regulator 6	FXYD6	53826	11q23.3	3.49	0.000074	22.75	0.012433
leucine rich repeat neuronal 3	LRRN3	54674	7q31.1	3.49	0.004413	3.49	0.003336
Interleukin 17 receptor D	IL17RD	54756	3p14.3	3.44	0.003099	9.59	0.000008
pleiotrophin	PTN	5764	7q33-q34	3.37	0.00091	4.86	0.005846
Muscleblind-like 2 (Drosophila)	MBNL2	10150	13q32.1	3.15	0.024769	3.67	0.005968
Microtubule-associated protein 2	MAP2	4133	2q34-q35	3.09	0.001547	4.36	0.010646
apical protein-like (Xenopus laevis)	SHROOM2	357	Xp22.3	3.06	0.001867	6.24	0.007724
EPH receptor B3	EPHB3	2049	3q21-qter	3.01	0.005485	8.71	0.002983
FK506 binding protein 1B, 12.6 kDa	FKBP1B	2281	2p23.3	3.00	0.003688	4.18	0.032092

***analysis was based on a cutoff of 3-fold increase in relative expression compared to autologous CD133- GBM cells ($p < 0.05$).**

Supplementary Table 8

Sequences of primers for RT-PCR analysis
ACTB: actin, beta
GeneID: 60
LEFT PRIMER ACTCAGGATTTAAAAACTGGAACG
RIGHT PRIMER GACTTCCTGTAACAATGCATCTCAT
PRODUCT SIZE: 152

PROM1: prominin 1 (CD133)
LocusID: 8842 OLIGO
LEFT PRIMER AAACATTAATTGGAGTGCAGCTAAC
RIGHT PRIMER TCTTCATTGCTGATCACTTTTGATA
PRODUCT SIZE: 226

EDN3: endothelin 3
GeneID: 1908
LEFT PRIMER ACAACCTATGCACCAGGTATTTAAC
RIGHT PRIMER AGTAGCATTCCATTTTCTTGAAGTG
PRODUCT SIZE: 110

DLX6: distal-less homeobox 6
GeneID: 1750
LEFT PRIMER GCATTTTGGACTCCTGCATT
RIGHT PRIMER TCCTGGTCATTGCATTTTGA
PRODUCT SIZE: 166

FABP7: fatty acid binding protein 7, brain
GeneID: 2173
LEFT PRIMER TTATGACCCTTACTTTTGGTGATGT
RIGHT PRIMER CAAGTTGCTTGGAGTAACAAGTTTT
PRODUCT SIZE: 216

MYCN: v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian)
GeneID: 4613
LEFT PRIMER TTTCGTATGAAAATGAGTTGTGAAA
RIGHT PRIMER GCACCAAACATGAACAAATACATTA
PRODUCT SIZE: 150

GAP43: growth associated protein 43
GeneID: 2596
LEFT PRIMER AGTCAAACAGTGTGGCTTAAACATT
RIGHT PRIMER TTGGAACAGAGAGAGAGAGAGAGAG
PRODUCT SIZE: 173

TFAP2B: transcription factor AP-2 beta
GeneID: 7021
LEFT PRIMER ATCGGAGAAACGTTGGTGTC
RIGHT PRIMER CCCAGAAGATTCCCGTAACA
PRODUCT SIZE: 184

RAPGEF5: Rap guanine nucleotide exchange factor (GEF) 5
GeneID: 9771
LEFT PRIMER TCAGGGACTACACTTGGTAGTTTTC

RIGHT PRIMER TTATATTGCTTGGCCATTTTTACAT
PRODUCT SIZE: 217

MELK: maternal embryonic leucine zipper kinase
GeneID: 9833
LEFT PRIMER GTTCATTGGAACTACCAACTTGTTT
RIGHT PRIMER TGGAAGTGAATCTAAGAAAGTCAACA
PRODUCT SIZE: 185

PDGFRA platelet-derived growth factor receptor, alpha
GeneID: 5156
LEFT PRIMER CCTATTTTTGTGAAGAGGGACATAA
RIGHT PRIMER CTGTGGGGATTATCACAGTTAAAAA
PRODUCT SIZE: 157

SOX4: SRY (sex determining region Y)-box 4
GeneID: 6659
LEFT PRIMER GCAATATGCCGTGTAGAATATTTGT
RIGHT PRIMER CAGCTGATTTTATTTCCTTCTCAAA
PRODUCT SIZE: 172

MSI1: musashi homolog 1 (Drosophila)
GeneID: 4440
LEFT PRIMER TAATTGTCTGTGTGAGGTGCTTAAC
RIGHT PRIMER GACTCAGCTCAAACGTGTAGAAAAT
PRODUCT SIZE: 180