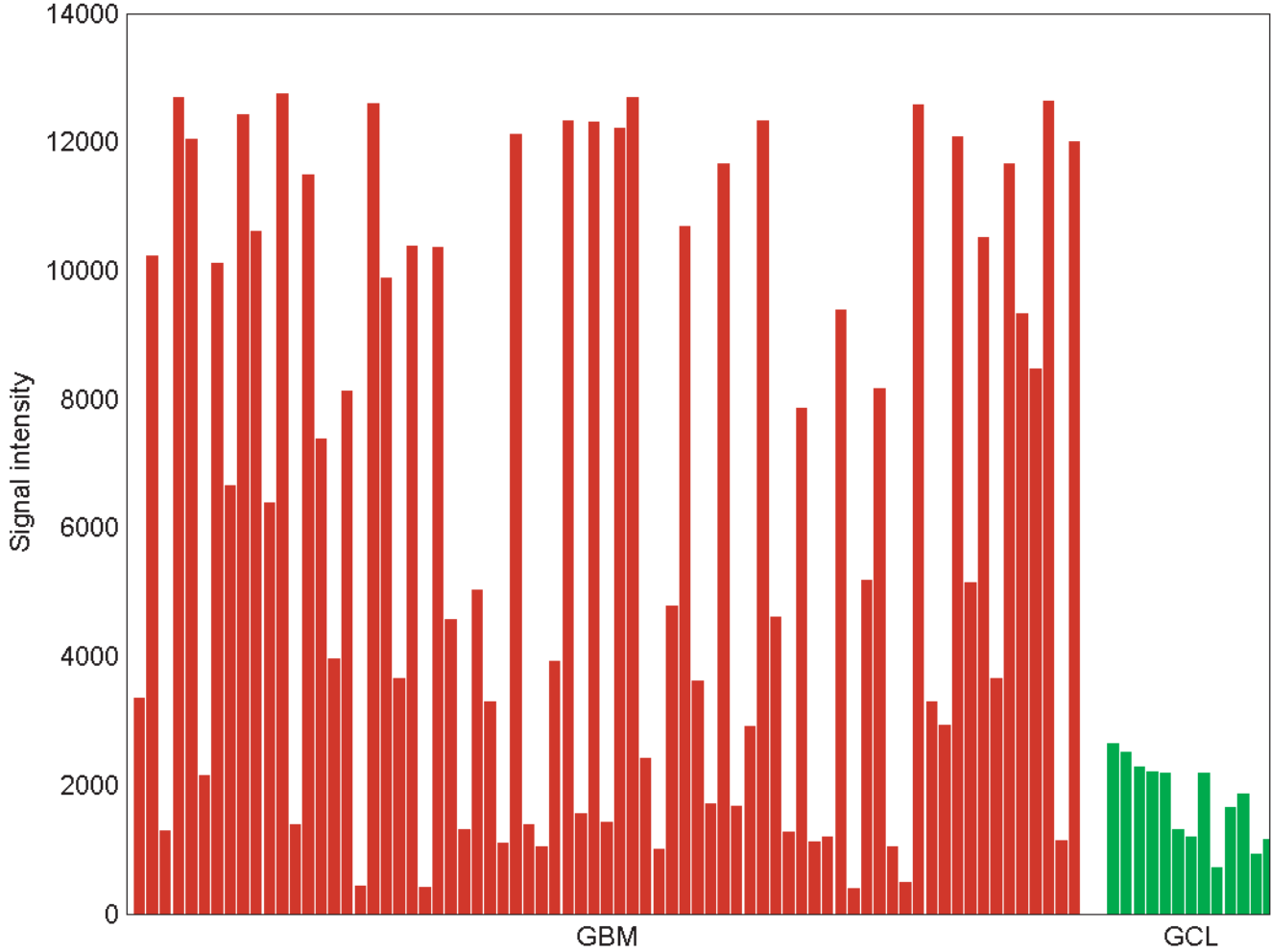


Supplemental Figure 1
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Supplementary Table S1: Summary of chromosome copy number aberrations (both base pairs and in cytobands) found in A172, Hs683, T98g, U251 and U87 cell lines

Chr No.	A172	Hs683	T98g	U251	U87
1	Deletion: 3122295- 93776703 (p36.32- p22.1); Amplification: 143877844- 243754339 (q21.1-q44)		Amplification: 40211994- 223649081 (p34.2- q42.13)	Amplification: 118603976- 119786066 (p12-p12)	Amplification: 94262576- 108974013 (p22.1-p13.3)
2		Deletion: 157739- 86239841 (p25.3-p11.2); Amplification: 100923789- 239912287 (q11.2-q37.3)	Deletion: 157739- 34454801 (p25.3-p22.3); Amplification: 209789135- 239912287 (q34-q37.3)		
3	Deletion: 39440781- 74019454 (p22.2-p13)	Deletion: 540961- 64258539 (p26.3-p14.1); Amplification: 64298514- 86911082 (p14.1-p12.1); Amplification: 136181475- 199368514 (q22.2-q29)		Amplification: 30092404- 46119188 (p24.1- p21.31); Amplification: 184643446- 195868916 (q27.1-q29)	
4	Deletion: 65445374- 82634835 (q13.1- q21.21)			Amplification: 64130376- 77457078 (q13.1-q21.1)	

5	Amplification: 1677351- 178472006 (p15.33- q35.3)	Amplification: 1677351- 178472006 (p15.33- q35.3)	Amplification: 1677351- 178472006 (p15.33- q35.3)	Amplification: 1677351- 178472006 (p15.33- q35.3)	
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6	Deletion: 150447380- 168107667 (q25.1-q27)	Amplification: 86689038- 87506207 (q14.3-q14.3)	Deletion: 54554337- 165791762 (p12.1-q27)	Amplification: 1478115- 147252370 (p25.3-q24.3)	Deletion: 150610- 44421400 (p25.3-p21.1); Amplification: 44442628- 58574774 (p21.1-p11.2); Amplification: 85815921- 132944108 (q14.3-q23.2)
7	Amplification: 1591238- 82356950 (p22.3- q21.11)	Amplification: 1591238- 158466134 (p22.3-q36.3)	Amplification: 1591238- 158466134 (p22.3-q36.3)	Amplification: 1591238- 158466134 (p22.3-q36.3)	Amplification: 1591238- 158466134 (p22.3-q36.3)
8	Amplification: 1130901- 40204591 (p23.3- p11.21)		Amplification: 54206225- 142072079 (q11.23- q24.3)	Deletion: 2761850- 115097126 (p23.2-q23.3)	
9	Deletion: 21413049- 22449115 (p21.3-p21.3); Amplification: 70808020- 133708634 (q21.11- q34.2)	Deletion: 21204877- 25099106 (p21.3-p21.3)		Deletion: 21701815- 22089568 (p21.3-p21.3)	Deletion: 6136121- 28027082 (p24.1-p21.2)
10	Deletion: 123131120- 132636938 (q26.13- q26.3)	Deletion: 135698- 132636938 (p15.3-q26.3)	Deletion: 135698- 132636938 (p15.3-q26.3)	Deletion: 135698- 36889598 (p15.3- p11.21)	
11	Deletion: 85969331- 105716737 (q14.2- q32.33)			Deletion: 4096805- 22349700 (p15.4-p14.3)	Deletion: 59769249- 105716737 (q12.1- q32.33)

14	Deletion: 19490525- 106312036 (q11.2- q32.33)		Deletion: 19490525- 106312036 (q11.2- q32.33)	Deletion: 19490525- 106312036 (q11.2- q32.33)	Deletion: 19490525- 106312036 (q11.2- q32.33)
16				Amplification: 47539499- 64852827 (q12.1-q22.1)	
18	Deletion: 39071934- 74983838 (q12.3-q23)			Deletion: 19749481- 74983838 (q11.2-q23)	
19	Amplification: 58908108- 62189739 (q13.42- q13.43)				Deletion: 3542590- 62189739 (p13.3- q13.43)
20			Amplification: 95685- 61366354 (p13-q13.33)		Deletion: 117701- 25127155 (p13-p11.21); Amplification: 31982015- 61366354 (q11.22- q13.33)
21	Amplification: 17395964- 45028663 (q21.1-q22.3)				
22	Deletion: 16604328- 48880960 (q11.21- q13.33)				
X	Amplification: 4065309- 38129187 (p22.33-q12)				Deletion: 4065309- 151099450 (p22.33-q28)

Supplementary Table 2. Summary of loss of heterozygosity encountered in A172, Hs683, T98g, U251 and U87 glioma cell lines.

Chro No.	A172	Hs683	T98g	U251	U87
1	3122295 - 48920638 (p36.32 - p33)		20144358 - 28993467 (p36.13 - p35.3); 40211994 - 55492954 (p34.2 - p32.3)	71790605 - 80842481 (p31.1 - p31.1)	20144358 - 28993467 (p36.13 - p35.3); 40211994 - 55492954 (p34.2 - p32.3); 172303160 - 183826861 (q31.1 - q32.1); 5517727 - 35102773 (p26.1 - p22.3); 58615101 - 71010828 (p14.2 - p13); 120037119 - 135991269 (q13.32 - q22.2)
2			172303160 - 183826861 (q31.1 - q32.1)	157739 - 11957213 (p25.3 - p25.1); 48760717 - 56269233 (p16.3 - p16.1); 80303867 - 113638507 (p12 - q13); 134353100 - 181039717 (q21.2 - q31.3); 211087017 - 231228396 (q34 - q37.1)	
3	60555772 - 72627547 (p14.2 - p13)		5517727 - 35102773 (p26.1 - p22.3); 58615101 - 71010828 (p14.2 - p13); 120037119 - 135991269 (q13.32 - q22.2)	82849478 - 100813854 (p12.2 - q12.1); 141267572 - 149081896 (q23 - q24); 186224958 - 199368514 (q27.2 - q29)	

4			398952 - 102340089 (p16.3 - q24); 106509246 - 121050651 (q24 - q26); 135647990 - 150060747 (q28.3 - q31.23); 154390932 - 161722748 (q31.3 - q32.1); 163047964 - 172026711 (q32.2 - q33)	53716143 - 78008076 (q12 - q21.1)	
5			101363154 - 108426241 (q21.1 - q21.3)	125467952 - 132915437 (q23.2 - q31.1)	
6	82587633 - 91450041 (q14.1 - q15); 160251585 - 165635264 (q25.3 - q27)		54509248 - 170506286 (p12.1 - q27)	150610 - 170445163 (p25.3 - q27)	150610 - 41551593 (p25.3 - p21.1) 57471407 - 82587967 (p11.2 - q14.1)
7	90034297 - 111153998 (q21.13 - q31.1); 123738950 - 158466437 (q31.33 - q36.3)				
8	63859197 - 76351897 (q12.3 - q21.13)				
9	239391 - 68275512 (p24.3 - q21.11)	239391 - 24816156 (p24.3 - p21.3)	239391 - 72892558 (p24.3 - q21.12)	239391 - 135054595 (p24.3 - q34.3)	5719377 - 32033426 (p24.1 - p21.1)
10	135698 - 133792769 (p15.3 - q26.3)	135698 - 133792769 (p15.3 - q26.3)	135698 - 133792769 (p15.3 - q26.3)	135698 - 133792769 (p15.3 - q26.3)	42852037 - 53244158 (q11.21 - q21.1); 54174055 - 133792769 (q21.1 - q26.3)
11	46093998 - 56906803 (p11.2 - q12.1); 84316412 - 134402514 (q14.1 - q25)		45687359 - 58368570 (p11.2 - q12.1); 98558777 - 102721462 (q22.1 - q22.3); 105875694 - 112801829 (q22.3 - q23.2)	2573106 - 134402514 (p15.5 - q25)	60971628 - 1376941 (q12.2 - p13.33)
12	93683 - 16986322 (p13.33 - p12.3)				74670090 - 100431481 (q21.2 - q23.2)

13	91870277 - 114040116 (q31.3 - q34)				18478972 - 32641347 (q12.11 - q13.1); 47129992 - 60629369 (q14.2 - q21.2); 62909664 - 71199633 (q21.31 - q21.33)
14	19490525 - 106312036 (q11.2 - q32.33)		19490525 - 1063120369 (q11.2 - q32.33)	19490525 - 106312036 (q11.2 - q32.33)	19490525 - 106312036 (q11.2 - q32.33)
15			19842052 - 100181650 (q11.2 - q26.3)	72130383 - 80178342 (q24.1 - q25.2)	
16				25554613 - 53933860 (p12.1 - q12.2)	
17			895321 - 17350285 (p13.3 - p11.2)	895321 - 76399520 (p13.3 - q25.3)	
18	242559 - 39071934 (p11.32 - q12.3)			30686115 - 75267441 (q12.1 - q23)	
19			3542590 - 34206067 (p13.3 - q12); 34339297 - 62431059 (q12 - q13.43)	34722418 - 62431059 (q12 - q13.43)	
20					4327086 - 40318090 (p13 - q12)
21				13520510 - 46782195 (q11.2 - q22.3)	
22				14886561 - 48881270 (q11.1 - q13.33)	

Supplementary Table 3: Up-regulated gene sets in Glioblastomas when compared to established glioma cell lines.

Gene Set	Enrichment Score	Nominal p-value
cell_adhesion	0.385	0.009
par1Pathway	0.620	0.011
fatty_acid_metabolism	0.568	0.013
GPCRs_Class_B_Secretin-like	0.480	0.016
ST_ADRENERGIC	0.458	0.034
badPathway	0.458	0.035
HEMO_TF_LIST_JP	0.350	0.069
il7Pathway	0.493	0.086
dcPathway	0.474	0.095
hdacPathway	0.459	0.120
MAP00562_Inositol_phosphate_metabolism	0.525	0.123
MAP00361_gamma_Hexachlorocyclohexane_degradation	0.443	0.125
S1P_Signaling	0.404	0.129
SIG_PIP3_signaling_in_B_lymphocytes	0.428	0.137
cell_adhesion_receptor_activity	0.391	0.139
nfatPathway	0.358	0.144
calcineurinPathway	0.493	0.145
rasPathway	0.428	0.147
SIG_BCR_Signaling_Pathway	0.397	0.159
RAR_UP	0.434	0.181
MAP00910_Nitrogen_metabolism	0.443	0.183
CBF_LEUKEMIA_DOWNING_AML	0.345	0.186
biopeptidesPathway	0.385	0.189
BRCA_UP	0.343	0.203
NFKB_REDUCED	0.437	0.211
FRASOR_ER_DOWN	0.344	0.213
ST_MONOCYTE_AD_PATHWAY	0.418	0.216
INS	0.403	0.225
amiPathway	0.376	0.226
cskPathway	0.376	0.226
no1Pathway	0.395	0.229
rac1Pathway	0.383	0.231
ctla4Pathway	0.424	0.233
ccr5Pathway	0.499	0.233
pparaPathway	0.339	0.234
ST_G_alpha_i_Pathway_	0.354	0.247
MAP00590_Prostaglandin_and_leukotriene_metabolism	0.465	0.249
MAPK_Cascade	0.382	0.250
cell_adhesion_molecule_activity	0.291	0.250
AR_MOUSE_PLUS_TESTO_FROM_NETAFFX	0.298	0.261
crebPathway	0.379	0.266
gata3Pathway	0.418	0.270
ST GRANULE_CELL_SURVIVAL_PATHWAY	0.376	0.285
fcgr1Pathway	0.381	0.286
CR_IMMUNE_FUNCTION	0.372	0.289
alkPathway	0.326	0.298
edg1Pathway	0.379	0.301
P53_UP	0.357	0.308
th1th2Pathway	0.426	0.322

cell_surface_receptor_linked_signal_transduction	0.269	0.326
ptdinsPathway	0.340	0.334
ST_Differentiation_Pathway_in_PC12_Cells	0.323	0.337
nos1Pathway	0.441	0.339
aktPathway	0.375	0.341
nkcellsPathway	0.379	0.343
EMT_DOWN	0.360	0.343
INSULIN_2F_DOWN	0.318	0.348
tidPathway	0.395	0.348
ghPathway	0.343	0.352
p53hypoxiaPathway	0.373	0.358
SIG_CD40PATHWAYMAP	0.348	0.358
il2rbPathway	0.322	0.363
MAP00280_Valine_leucine_and_ileucine_degradation	0.351	0.388
arapPathway	0.348	0.389
ANTI_CD44_UP	0.353	0.397
rarrxrPathway	0.382	0.397
lairPathway	0.416	0.401
cxcr4Pathway	0.343	0.402
MAP00260_Glycine_serine_and_threonine_metabolism	0.355	0.402
G13_Signaling_Pathway	0.321	0.404
ccr3Pathway	0.349	0.404
cardiacegfPathway	0.371	0.406
vipPathway	0.360	0.407
gleevecPathway	0.360	0.419
nktPathway	0.353	0.424
pgc1aPathway	0.395	0.426
GPCRs_Class_A_Rhodopsin-like	0.269	0.427
CR_TRANSPORT_OF_VESICLES	0.350	0.430
MAP00380_Tryptophan_metabolism	0.295	0.443
MAP00350_Tyrosine_metabolism	0.323	0.445
ST_T_Cell_Signal_Transduction	0.293	0.446
erk5Pathway	0.359	0.459
CR_SIGNALLING	0.247	0.460
fmlppathway	0.303	0.465
Glycogen_Metabolism	0.297	0.477
MAP00640_Propanoate_metabolism	0.340	0.478
MAP00340_Histidine_metabolism	0.339	0.484
ck1Pathway	0.340	0.485
RAP_UP	0.232	0.489
SA_B_CELL_RECEPTOR_COMPLEXES	0.323	0.491
il3Pathway	0.349	0.493
EIF4Pathway	0.323	0.505
ST_JNK_MAPK_Pathway	0.279	0.507
tollPathway	0.295	0.510
mtorPathway	0.313	0.512
mef2dPathway	0.326	0.513
ST_Phosphoinositide_3_Kinase_Pathway	0.275	0.529
gcrPathway	0.333	0.534
ST_Wnt_Ca2_cyclic_GMP_Pathway	0.337	0.538
gpcrPathway	0.297	0.543
MAP00071_Fatty_acid_metabolism	0.264	0.543
CR_TRANSCRIPTION_FACTORS	0.255	0.545
hcmvPathway	0.351	0.546

FETAL_LIVER_HS_ENRICHED_TF_JP	0.241	0.547
intrinsicPathway	0.325	0.568
ptenPathway	0.328	0.568
gsk3Pathway	0.273	0.584
ST_Fas_Signaling_Pathway	0.245	0.585
GLUT_UP	0.228	0.585
SIG_IL4RECEPTOR_IN_B_LYPHOCYTES	0.295	0.588
ucalpainPathway	0.310	0.596
GO_ROS	0.298	0.598
ANDROGEN_GENES_FROM_NETAFFX	0.240	0.599
electron_transport	0.227	0.600
arfPathway	0.321	0.602
tpoPathway	0.293	0.606
HUMAN_CD34_ENRICHED_TF_JP	0.221	0.611
at1rPathway	0.273	0.612
CR_PROTEIN_MOD	0.209	0.626
KRAS_TOP100_KNOCKDOWN	0.258	0.626
shhPathway	0.308	0.627
Matrix_Metalloproteinases	0.280	0.637
AR_ORTHOS_MAPPED_TO_U133_VIA_NETAFFX	0.247	0.643
AR_MOUSE	0.247	0.643
GATA1_WEISS	0.278	0.659
ndkDynaminPathway	0.297	0.660
MAP00193_ATP_synthesis	0.318	0.663
MAP03070_Type_III_secretion_system	0.318	0.663
TESTIS_GENES_FROM_XHX_AND_NETAFFX	0.229	0.670
ST_Wnt_beta_catenin_Pathway	0.254	0.671
ST_Ga12_Pathway	0.270	0.673
MAP00561_Glycerolipid_metabolism	0.239	0.675
etsPathway	0.283	0.681
ST_B_Cell_Antigen_Receptor	0.261	0.686
tob1Pathway	0.297	0.692
bcl2family_and_reg_network	0.267	0.694
bcrPathway	0.263	0.699
igf1rPathway	0.310	0.700
cell_growth_and_or_maintenance	0.222	0.702
ca_nf_at_signalling	0.208	0.704
egfPathway	0.264	0.707
CR_CAM	0.220	0.715
raccycdPathway	0.274	0.717
keratinocytePathway	0.238	0.723
cell_motility	0.209	0.734
GLUCOSE_UP	0.247	0.737
HOXA9_DOWN	0.247	0.740
sppaPathway	0.270	0.752
il1rPathway	0.249	0.754
SIG_InsulinReceptorPathwayInCardiacMyocytes	0.216	0.756
MAP00195_Photosynthesis	0.287	0.766
spryPathway	0.265	0.770
cdmacPathway	0.283	0.772
SIG_CHEMOTAXIS	0.209	0.785
insulin_signalling	0.202	0.785
ST_Ga13_Pathway	0.226	0.791
cytokinePathway	0.263	0.803

nthiPathway	0.251	0.812
MAP00120_Bile_acid_biosynthesis	0.238	0.823
Wnt_Signaling	0.203	0.823
SIG_PIP3SIGINCARDIACMYOCTES	0.201	0.826
epoPathway	0.240	0.833
telPathway	0.261	0.833
shh_lisa	0.252	0.840
wntPathway	0.231	0.840
pdgfPathway	0.238	0.844
MAP00500_Starch_and_sucrose_metabolism	0.242	0.845
MAP00150_Androgen_and_estrogen_metabolism	0.245	0.850
GNF_FEMALE_GENES	0.189	0.853
ST_Dictyostelium_discoideum_cAMP_Chemotaxis_Pathway	0.212	0.865
mcalpainPathway	0.224	0.866
MAP00480_Glutathione_metabolism	0.232	0.891
XINACT_MERGED	0.211	0.902
tcrPathway	0.195	0.903
SIG_Regulation_of_the_actin_cytoskeleton_by_Rho_GTPases	0.177	0.908
inflamPathway	0.211	0.914
ST_Integrin_Signaling_Pathway	0.179	0.920
p53_signalling	0.183	0.920
metPathway	0.193	0.924
41bbPathway	0.213	0.948
DOWNREG_BY_HOXA9	0.199	0.950
PROLIF_GENES	0.162	0.950
ST_p38_MAPK_Pathway	0.176	0.957
igf1Pathway	0.182	0.968
Il12Pathway	0.159	0.995

Supplementary Table 4: Up-regulated gene sets in Glioblastomas when compared to established non-glioma tumor cell lines.

Gene Set	Enrichment Score	Nominal p-value
cell_adhesion	0.436	0.002
fatty_acid_metabolism	0.586	0.008
badPathway	0.496	0.019
GPCRs_Class_B_Secretin-like	0.467	0.026
dcPathway	0.525	0.028
SIG_PIP3_signaling_in_B_lymphocytes	0.491	0.037
calcineurinPathway	0.539	0.048
nfatPathway	0.397	0.048
ANTI_CD44_UP	0.483	0.049
cell_adhesion_molecule_activity	0.361	0.056
pparaPathway	0.416	0.063
ST_ADRENERGIC	0.447	0.068
HEMO_TF_LIST_JP	0.336	0.072
ST_GRANULE_CELL_SURVIVAL_PATHWAY	0.505	0.073
gata3Pathway	0.498	0.078
ccr5Pathway	0.579	0.086
crebPathway	0.458	0.089
il7Pathway	0.507	0.101
MAP00910_Nitrogen_metabolism	0.485	0.104
S1P_Signaling	0.440	0.105
par1Pathway	0.530	0.106
gsk3Pathway	0.409	0.122
MAP00562_Inositol_phosphate_metabolism	0.512	0.124
amiPathway	0.405	0.128
cskPathway	0.405	0.128
ST_Differentiation_Pathway_in_PC12_Cells	0.384	0.131
cardiacegfPathway	0.498	0.137
ST_MONOCYTE_AD_PATHWAY	0.460	0.143
erk5Pathway	0.476	0.149
CBF_LEUKEMIA_DOWNING_AML	0.353	0.151
cell_adhesion_receptor_activity	0.385	0.153
fcer1Pathway	0.427	0.164
hdacPathway	0.436	0.164
RAR_UP	0.453	0.167
MAP00361_gamma_Hexachlorocyclohexane_degradation	0.411	0.173
GPCRs_Class_A_Rhodopsin-like	0.312	0.177
ST_Wnt_Ca2_cyclic_GMP_Pathway	0.456	0.185
CR_IMMUNE_FUNCTION	0.417	0.205
gpcrPathway	0.408	0.208
SIG_BCR_Signaling_Pathway	0.372	0.212
G13_Signaling_Pathway	0.401	0.216
cell_surface_receptor_linked_signal_transduction	0.296	0.216
AR_MOUSE_PLUS_TESTO_FROM_NETAFFX	0.301	0.220
biopeptidesPathway	0.400	0.222
tpoPathway	0.437	0.223
ST_G_alpha_i_Pathway_	0.370	0.230
cxcr4Pathway	0.415	0.232
hcmvPathway	0.456	0.243

BRCA_UP	0.348	0.251
alkPathway	0.345	0.263
FETAL_LIVER_HS_ENRICHED_TF_JP	0.279	0.271
ck1Pathway	0.391	0.272
INSULIN_2F_DOWN	0.338	0.272
nktPathway	0.387	0.275
tollPathway	0.366	0.277
P53_UP	0.377	0.280
nkcellsPathway	0.428	0.281
pgc1aPathway	0.455	0.287
edg1Pathway	0.381	0.290
MAP00590_Prostaglandin_and_leukotriene_metabolism	0.427	0.294
th1th2Pathway	0.421	0.297
no1Pathway	0.382	0.299
MAP00500_Starch_and_sucrose_metabolism	0.375	0.301
shhPathway	0.400	0.305
CR_TRANSPORT_OF_VESICLES	0.388	0.313
CR_TRANSCRIPTION_FACTORS	0.303	0.316
MAP00280_Valine_leucine_and_ileucine_degradation	0.364	0.317
FRASOR_ER_DOWN	0.314	0.319
ST_Phosphoinositide_3_Kinase_Pathway	0.319	0.326
SIG_IL4RECEPTOR_IN_B_LYMPHOCYTES	0.348	0.329
CR_SIGNALLING	0.270	0.330
SIG_CD40PATHWAYMAP	0.337	0.330
MAP00260_Glycine_serine_and_threonine_metabolism	0.371	0.335
ptdinsPathway	0.367	0.337
bcrPathway	0.361	0.339
nos1Pathway	0.440	0.344
rasPathway	0.377	0.347
MAPK_Cascade	0.363	0.353
gleevecPathway	0.388	0.356
Glycogen_Metabolism	0.329	0.357
egfPathway	0.377	0.360
KRAS_TOP100_KNOCKDOWN	0.350	0.364
lairPathway	0.430	0.369
pdgfPathway	0.380	0.369
ST_JNK_MAPK_Pathway	0.310	0.372
cell_growth_and_or_maintenance	0.263	0.373
SA_B_CELL_RECEPTOR_COMPLEXES	0.381	0.374
ctla4Pathway	0.359	0.376
rac1Pathway	0.348	0.383
ANDROGEN_GENES_FROM_NETAFFX	0.270	0.388
rarrxrPathway	0.374	0.391
MAP00561_Glycerolipid_metabolism	0.276	0.394
HUMAN_CD34_ENRICHED_TF_JP	0.246	0.408
tob1Pathway	0.355	0.416
CR_CAM	0.267	0.418
SIG_InsulinReceptorPathwayInCardiacMyocytes	0.284	0.427
ucalpainPathway	0.369	0.432
tcrPathway	0.293	0.440
inflamPathway	0.322	0.453
vipPathway	0.331	0.456
Matrix_Metalloproteinases	0.326	0.459
at1rPathway	0.323	0.462

MAP00380_Tryptophan_metabolism	0.277	0.465
ccr3Pathway	0.328	0.466
MAP00640_Propanoate_metabolism	0.326	0.466
il3Pathway	0.361	0.470
MAP00350_Tyrosine_metabolism	0.304	0.472
ndkDynaminPathway	0.401	0.475
etsPathway	0.348	0.479
ptenPathway	0.370	0.481
ANDROGEN_UP_GENES	0.263	0.484
ghPathway	0.305	0.489
ST_Fas_Signaling_Pathway	0.257	0.489
igf1rPathway	0.365	0.504
CR_PROTEIN_MOD	0.218	0.505
arfPathway	0.331	0.515
il2rbPathway	0.287	0.518
intrinsicPathway	0.324	0.521
gcrPathway	0.342	0.529
INS	0.302	0.534
GNF_FEMALE_GENES	0.252	0.535
cdmacPathway	0.350	0.541
GLUT_UP	0.235	0.541
mcalpainPathway	0.300	0.541
epoPathway	0.310	0.543
GATA1_WEISS	0.303	0.551
mef2dPathway	0.322	0.557
fmlppathway	0.279	0.561
aktPathway	0.312	0.565
ecmPathway	0.320	0.568
HOXA9_DOWN	0.268	0.575
ST_Ga12_Pathway	0.286	0.580
MAP00071_Fatty_acid_metabolism	0.257	0.583
cytokinePathway	0.304	0.586
arapPathway	0.300	0.596
ST_T_Cell_Signal_Transduction	0.251	0.607
RAP_UP	0.206	0.615
spryPathway	0.317	0.633
DOWNREG_BY_HOXA9	0.255	0.652
ST_Dictyostelium_discoideum_cAMP_Chemotaxis_Pathway	0.257	0.661
keratinocytePathway	0.251	0.674
breast_cancer_estrogen_signalling	0.214	0.677
ST_Integrin_Signaling_Pathway	0.215	0.680
ST_Wnt_beta_catenin_Pathway	0.263	0.681
AR_ORTHOS_MAPPED_TO_U133_VIA_NETAFFX	0.242	0.689
AR_MOUSE	0.242	0.689
MAP00193_ATP_synthesis	0.299	0.698
MAP03070_Type_III_secretion_system	0.299	0.698
ca_nf_at_signalling	0.207	0.701
metPathway	0.249	0.716
nthiPathway	0.283	0.716
igf1Pathway	0.279	0.720
SIG_CHEMOTAXIS	0.229	0.722
Wnt_Signaling	0.218	0.726
p53hypoxiaPathway	0.276	0.733
il2Pathway	0.253	0.735

tidPathway	0.273	0.740
raccycdPathway	0.270	0.741
p53Pathway	0.290	0.743
pyk2Pathway	0.248	0.755
insulinPathway	0.262	0.768
cell_motility	0.202	0.768
electron_transport	0.198	0.784
GO_ROS	0.242	0.797
il6Pathway	0.265	0.799
MAP00195_Photosynthesis	0.261	0.806
ST_B_Cell_Antigen_Receptor	0.220	0.814
TESTIS_GENES_FROM_XHX_AND_NETAFFX	0.204	0.815
SIG_Regulation_of_the_actin_cytoskeleton_by_Rho_GTPases	0.215	0.827
wntPathway	0.230	0.830
GLUCOSE_UP	0.224	0.831
EMT_DOWN	0.234	0.838
PROLIF_GENES	0.172	0.844
MAP00120_Bile_acid_biosynthesis	0.220	0.871
insulin_signalling	0.186	0.872
sppaPathway	0.234	0.873
il1rPathway	0.215	0.875
ngfPathway	0.232	0.880
MAP00150_Androgen_and_estrogen_metabolism	0.233	0.884
ST_p38_MAPK_Pathway	0.211	0.886
shh_lisa	0.234	0.899
TGF_Beta_Signaling_Pathway	0.199	0.904
SIG_PIP3SIGINCARDIACMYOCTES	0.177	0.912
SA_PTEN_PATHWAY	0.229	0.919
mapkPathway	0.179	0.931
CR_CYTOSKELETON	0.204	0.954
bcl2family_and_reg_network	0.192	0.956
Il12Pathway	0.190	0.966
EMT_UP	0.174	0.969
Inflammatory_Response_Pathway	0.171	0.972
XINACT_MERGED	0.170	0.980
ST_Ga13_Pathway	0.155	0.984
NFKB_REDUCED	0.151	0.991

Supplementary Table 5: Up-regulated gene sets in established glioma cell lines when compared to Glioblastomas.

Gene Set	Enrichment Score	Nominal p-value
Proteasome_Degradation	0.786	0.000
proteasomePathway	0.863	0.002
MAP00230_Purine_metabolism	0.414	0.029
HTERT_UP	0.558	0.036
RAP_DOWN	0.570	0.051
CR_CELL_CYCLE	0.510	0.051
PGC	0.413	0.052
MAP00970_Aminoacyl_tRNA_biosynthesis	0.739	0.063
deathPathway	0.471	0.064
GLUT_DOWN	0.542	0.078
MAP00510_N_Glycans_biosynthesis	0.667	0.087
Cell_Cycle	0.533	0.091
tRNA_Synthetases	0.698	0.098
LEU_DOWN	0.532	0.105
ST_Tumor_Necrosis_Factor_Pathway	0.493	0.106
cell_cycle_checkpoint	0.554	0.107
CR_DEATH	0.368	0.108
atrbrcaPathway	0.526	0.113
ceramidePathway	0.520	0.116
GLUCOSE_DOWN	0.355	0.126
caspasePathway	0.492	0.127
mitochondr	0.402	0.142
SA_TRKA_RECEPTOR	0.516	0.146
MAP00330_Arginine_and_proline_metabolism	0.339	0.146
human_mitoDB_6_2002	0.399	0.147
MAP00251_Glutamate_metabolism	0.527	0.177
mRNA_splicing	0.537	0.184
electron_transporter_activity	0.302	0.185
MAP00030_Pentose_phosphate_pathway	0.437	0.185
cell_cycle_regulator	0.464	0.186
g1Pathway	0.440	0.195
GLYCOL	0.518	0.196
MAP00710_Carbon_fixation	0.502	0.200
MAP00860_Porphyrin_and_chlorophyll_metabolism	0.434	0.204
Krebs-TCA_Cycle	0.477	0.217
MAP00252_Alanine_and_aspartate_metabolism	0.447	0.221
VOXPPOS	0.510	0.225
carm-erPathway	0.427	0.229
SA_CASPASE_CASCADE	0.446	0.234
MAP00650_Butanoate_metabolism	0.415	0.238
GLUCO	0.431	0.247
mitochondriaPathway	0.419	0.254
mRNA_processing	0.501	0.261
erkPathway	0.386	0.261
relaPathway	0.459	0.265
DNA_DAMAGE_SIGNALLING	0.317	0.266
CR_REPAIR	0.433	0.266
drug_resistance_and_metabolism	0.260	0.269
cellcyclePathway	0.413	0.283

MAP00240_Pyrimidine_metabolism	0.414	0.285
INSULIN_2F_UP	0.315	0.289
actinYPathway	0.431	0.298
tnfr1Pathway	0.357	0.299
HOX_LIST_JP	0.332	0.299
MAP00020_Citrate_cycle_TCA_cycle	0.514	0.317
vegfPathway	0.356	0.320
TCA	0.522	0.322
pitx2Pathway	0.387	0.324
MAP00620_Pyruvate_metabolism	0.410	0.326
GO_0005739	0.311	0.341
Electron_Transport_Chain	0.410	0.350
MAP00220_Urea_cycle_and_metabolism_of_amino_groups	0.379	0.352
MAP00010_Glycolysis_Gluconeogenesis	0.316	0.356
nfkbPathway	0.366	0.375
GLYCOGEN	0.354	0.378
stressPathway	0.346	0.381
MAP00052_Galactose_metabolism	0.355	0.385
FRASOR_ER_UP	0.304	0.390
MAP00410_beta_Alanine_metabolism	0.360	0.393
mprPathway	0.329	0.397
KRAS_TOP100_CONTROL	0.256	0.400
hivnefPathway	0.295	0.408
rhoPathway	0.302	0.447
MAP00190_Oxidative_phosphorylation	0.338	0.452
MAP00051_Fructose_and_mannose_metabolism	0.343	0.456
radiation_sensitivity	0.327	0.471
P53_DOWN	0.339	0.471
g2Pathway	0.332	0.479
ST_ERK1_ERK2_MAPK_Pathway	0.336	0.479
fasPathway	0.306	0.494
integrinPathway	0.321	0.497
HTERT_DOWN	0.258	0.500
LEU_UP	0.261	0.500
cell_proliferation	0.207	0.541
atmPathway	0.315	0.546
FA	0.359	0.551
ADULT_LIVER_vs_FETAL_LIVER_GNF2	0.235	0.576
tumor_supressor	0.294	0.592
igf1mTORPathway	0.301	0.615
MAP03020_RNA_polymerase	0.354	0.631
tnfr2Pathway	0.319	0.637
ecmPathway	0.280	0.651
chemicalPathway	0.265	0.698
tall1Pathway	0.278	0.708
ANDROGEN_UP_GENES	0.218	0.731
Inflammatory_Response_Pathway	0.248	0.734
p53Pathway	0.292	0.737
ST_Interleukin_4_Pathway	0.239	0.740
cell_cycle_arrest	0.234	0.767
CR_DNA_MET_AND_MOD	0.254	0.773
chrebpPathway	0.256	0.785
ngfPathway	0.247	0.794
CR_CYTOSKELETON	0.234	0.798

TGF_Beta_Signaling_Pathway	0.222	0.801
UPREG_BY_HOXA9	0.223	0.821
mapkPathway	0.201	0.827
EMT_UP	0.215	0.827
p38mapkPathway	0.221	0.836
Fatty_Acid_Synthesis	0.234	0.869
pyk2Pathway	0.219	0.879
breast_cancer_estrogen_signalling	0.170	0.913
tnf_and_fas_network	0.214	0.914
SA_PTEN_PATHWAY	0.219	0.917
il6Pathway	0.211	0.928
NFKB_INDUCED	0.169	0.936
ST_Gaq_Pathway	0.180	0.944
Fatty_Acid_Degradation	0.197	0.970
no2il12Pathway	0.203	0.974
insulinPathway	0.189	0.975
il2Pathway	0.165	0.991

Supplementary Table 6: Up-regulated gene sets in established non-glioma tumor cell lines when compared to Glioblastomas.

Gene Set	Enrichment Score	Nominal p-value
Proteasome_Degradation	0.787	0.000
MAP00230_Purine_metabolism	0.477	0.000
proteasomePathway	0.902	0.000
Cell_Cycle	0.615	0.000
CR_CELL_CYCLE	0.562	0.002
GLUT_DOWN	0.595	0.010
cellcyclePathway	0.560	0.011
RAP_DOWN	0.606	0.015
LEU_DOWN	0.609	0.016
HTERT_UP	0.563	0.017
PGC	0.427	0.037
mitochondr	0.456	0.055
human_mitoDB_6_2002	0.454	0.060
atrbrcaPathway	0.577	0.061
cell_cycle_checkpoint	0.578	0.070
mRNA_splicing	0.585	0.077
CR_REPAIR	0.521	0.080
deathPathway	0.457	0.098
MAP00970_Aminoacyl_tRNA_biosynthesis	0.701	0.099
cell_cycle_regulator	0.482	0.105
MAP00510_N_Glycans_biosynthesis	0.628	0.111
VOXPHOS	0.563	0.112
Krebs-TCA_Cycle	0.542	0.113
g1Pathway	0.462	0.116
vegfPathway	0.414	0.122
caspasePathway	0.488	0.127
MAP00020_Citrate_cycle_TCA_cycle	0.597	0.128
MAP00240_Pyrimidine_metabolism	0.459	0.130
MAP00650_Butanoate_metabolism	0.501	0.137
mitochondriaPathway	0.462	0.146
MAP00252_Alanine_and_aspartate_metabolism	0.475	0.147
DNA_DAMAGE_SIGNALLING	0.351	0.148
mRNA_processing	0.549	0.148
CR_DEATH	0.366	0.165
Electron_Transport_Chain	0.501	0.169
MAP00620_Pyruvate_metabolism	0.479	0.171
drug_resistance_and_metabolism	0.283	0.175
tRNA_Synthetases	0.645	0.177
TCA	0.599	0.180
GO_0005739	0.364	0.188
ST_Tumor_Necrosis_Factor_Pathway	0.460	0.190
GLUCOSE_DOWN	0.326	0.193
electron_transporter_activity	0.313	0.200
MAP00251_Glutamate_metabolism	0.502	0.216
g2Pathway	0.409	0.235
MAP00330_Arginine_and_proline_metabolism	0.326	0.241
MAP00860_Porphyrin_and_chlorophyll_metabolism	0.410	0.248
ceramidePathway	0.449	0.258
MAP00220_Urea_cycle_and_metabolism_of_amino_groups	0.420	0.273

atmPathway	0.410	0.274
carm-erPathway	0.387	0.275
HTERT_DOWN	0.309	0.277
relaPathway	0.449	0.281
INSULIN_2F_UP	0.299	0.287
GLYCOGEN	0.370	0.290
MAP00710_Carbon_fixation	0.452	0.295
igf1mTORPathway	0.379	0.296
KRAS_TOP100_CONTROL	0.285	0.310
SA_TRKA_RECEPTOR	0.419	0.324
FA	0.431	0.327
MAP00410_beta_Alanine_metabolism	0.371	0.331
radiation_sensitivity	0.363	0.341
MAP00340_Histidine_metabolism	0.338	0.365
GLUCO	0.384	0.376
CR_DNA_MET_AND_MOD	0.338	0.386
HOX_LIST_JP	0.302	0.386
stressPathway	0.345	0.386
hivnefPathway	0.303	0.388
SA_CASPASE_CASCADE	0.389	0.388
fasPathway	0.316	0.390
tnfr1Pathway	0.318	0.399
MAP00190_Oxidative_phosphorylation	0.354	0.401
actinYPathway	0.381	0.401
mprPathway	0.314	0.411
P53_DOWN	0.359	0.412
MAP03020_RNA_polymerase	0.420	0.428
mtorPathway	0.325	0.430
ADULT_LIVER_vs_FETAL_LIVER_GNF2	0.250	0.458
cell_cycle_arrest	0.281	0.469
nfkbPathway	0.308	0.534
ST_Interleukin_4_Pathway	0.274	0.537
LEU_UP	0.242	0.548
ST_ERK1_ERK2_MAPK_Pathway	0.293	0.550
erkPathway	0.286	0.562
rhoPathway	0.271	0.564
MAP00051_Fructose_and_mannose_metabolism	0.290	0.569
MAP00010_Glycolysis_Gluconeogenesis	0.257	0.574
MAP00030_Pentose_phosphate_pathway	0.303	0.585
GLYCOL	0.334	0.602
tnfr2Pathway	0.326	0.607
MAP00052_Galactose_metabolism	0.286	0.611
cell_proliferation	0.196	0.621
Fatty_Acid_Synthesis	0.315	0.626
tnf_and_fas_network	0.294	0.632
41bbPathway	0.289	0.667
p53_signalling	0.205	0.693
tumor_suppressor	0.257	0.699
tall1Pathway	0.296	0.699
FRASOR_ER_UP	0.261	0.747
UPREG_BY_HOXA9	0.226	0.797
eif4Pathway	0.238	0.816
integrinPathway	0.227	0.835
telPathway	0.260	0.841

chemicalPathway	0.222	0.872
pitx2Pathway	0.236	0.901
MAP00480_Glutathione_metabolism	0.211	0.930
p38mapkPathway	0.187	0.942
chrebpPathway	0.202	0.944
NFKB_INDUCED	0.161	0.960
Fatty_Acid_Degradation	0.191	0.962
ST_Gaq_Pathway	0.171	0.968
no2il12Pathway	0.174	0.985

Supplementary Table S7: Summary of significantly up-regulated gene sets in glioma cell lines between *in vivo* and *in vitro* condition

	Gene sets	Sources	Genes	ES	Nom p
<i>In vivo</i>	Tissue specific				
	cell_adhesion	GO	162	-0.288	0.042*
	cell_adhesion_molecule_activity	na	100	-0.347	0.009**
	Matrix_Metalloproteinases	BioCarta	25	-0.512	0.004**
	GPCR signaling				
	GPCRs_Class_B_Secretin-like	GO	24	-0.483	0.027*
	G13_Signaling_Pathway	BioCarta	31	-0.410	0.013**
ANTI_CD44_up	Exp. sig.	23	-0.503	0.023*	
<i>In vitro</i>	tRNA synthesis pathway				
	Aminoacyl_tRNA_biosynthesis	GenMapp	17	0.842	0.004**
	tRNA_Synthetases	BioCarta	19	0.796	0.013**
	Interleukin signaling				
	il2Pathway	BioCarta	22	0.423	0.033*
	il3Pathway	BioCarta	15	0.538	0.039*
	ST_Interleukin_4_pathway	STKE	26	0.477	0.023*
	SIG_IL4receptor_in_B_lymphocytes	Sig.Alli.	27	0.517	0.054*
	il6Pathway	BioCarta	21	0.564	0.014**
	Nutrition metabolism				
	Glucose_up	Exp. sig.	33	0.533	0.010**
	Alanine_and_aspartate_metabolism	GenMapp	17	0.533	0.010**
	Glutamate_metabolism	GenMapp	16	0.608	0.023*
	Fatty_Acid_Synthesis	BioCarta	16	0.586	0.051*
	LEU_up	Exp. sig.	99	0.486	0.025*
	IGF signaling				
	igf1Pathway	BioCarta	20	0.549	0.008**
	igf1mtorPathway	BioCarta	20	0.482	0.016*
	insulinPathway	BioCarta	21	0.487	0.053*
	epoPathway	na	18	0.557	0.004**
	cell_cycle_arrest	na	30	0.48	0.027*
Others					
ngfPathway	BioCarta	17	0.477	0.037*	
HTERT_up	Exp. sig	98	0.599	0.006**	
ST_ERK1_ERK2_MAPK_pathway	STKE	35	0.478	0.042*	
ST_Phosphoinositide_3_kinase_pathway	STKE	35	0.390	0.011**	

“*” indicates the levels of statistical significance with “*” “ representing nominal p value < 0.05, “**” representing nominal p value < 0.01 and “***” representing nominal p values < 0.001. “ES” is enrichment score and “Nom p” is nominal p value. “Exp. sig”

refers to expression signatures. “na” refers to that data source information is not available.

Supplementary Table 8: Up-regulated gene sets in glioma cell lines cultured in intracranial conditions (in vivo) when compared to in vitro growth conditions.

Gene Set	Enrichment Score	Nominal p-value
Matrix_Metalloproteinases	0.512	0.004
cell_adhesion_molecule_activity	0.348	0.009
G13_Signaling_Pathway	0.411	0.013
ANTI_CD44_UP	0.503	0.023
GPCRs_Class_B_Secretin-like	0.483	0.027
RAR_UP	0.378	0.043
AR_MOUSE_PLUS_TESTO_FROM_NETAFFX	0.360	0.058
ST_Wnt_Ca2_cyclic_GMP_Pathway	0.528	0.062
KRAS_TOP100_KNOCKDOWN	0.383	0.082
intrinsicPathway	0.460	0.180
lairPathway	0.421	0.129
cell_adhesion	0.288	0.042
cell_growth_and_or_maintenance	0.325	0.112
AR_ORTHOS_MAPPED_TO_U133_VIA_NETAFFX	0.365	0.220
AR_MOUSE	0.365	0.220
TESTIS_GENES_FROM_XHX_AND_NETAFFX	0.343	0.152
ANDROGEN_GENES_FROM_NETAFFX	0.320	0.116
GO_ROS	0.383	0.187
nos1Pathway	0.378	0.159
GPCRs_Class_A_Rhodopsin-like	0.298	0.159
amiPathway	0.330	0.126
cskPathway	0.330	0.126
SA_CASPASE_CASCADE	0.400	0.243
MAP00361_gamma_Hexachlorocyclohexane_degradation	0.317	0.262
MAP00150_Androgen_and_estrogen_metabolism	0.379	0.258
deathPathway	0.296	0.255
ck1Pathway	0.418	0.331
ST_Ga12_Pathway	0.344	0.250
MAP00071_Fatty_acid_metabolism	0.301	0.267
cell_adhesion_receptor_activity	0.323	0.309
rhoPathway	0.316	0.339
ST_GRANULE_CELL_SURVIVAL_PATHWAY	0.352	0.349
caspasePathway	0.348	0.372
CR_IMMUNE_FUNCTION	0.291	0.321
cell_motility	0.228	0.336
P53_UP	0.298	0.370
ccr5Pathway	0.358	0.388
MAPK_Cascade	0.300	0.407
FA	0.375	0.410
no1Pathway	0.326	0.432
gsk3Pathway	0.329	0.413
Fatty_Acid_Degradation	0.358	0.444
S1P_Signaling	0.287	0.425
ST_Dictyostelium_discoideum_cAMP_Chemotaxis_Pathway	0.281	0.426
MAP03020_RNA_polymerase	0.360	0.452
atrbrcaPathway	0.364	0.475
SIG_Regulation_of_the_actin_cytoskeleton_by_Rho_GTPases	0.276	0.472
MAP00051_Fructose_and_mannose_metabolism	0.365	0.465
edg1Pathway	0.284	0.504

ADULT_LIVER_vs_FETAL_LIVER_GNF2	0.245	0.558
tnf_and_fas_network	0.356	0.525
GNF_FEMALE_GENES	0.203	0.582
CR_CAM	0.213	0.627
GLYCOL	0.308	0.582
bcl2family_and_reg_network	0.259	0.636
ST_T_Cell_Signal_Transduction	0.248	0.581
hivnefPathway	0.237	0.582
CBF_LEUKEMIA_DOWNING_AML	0.230	0.613
rac1Pathway	0.265	0.675
Inflammatory_Response_Pathway	0.277	0.611
TGF_Beta_Signaling_Pathway	0.289	0.580
MAP00561_Glycerolipid_metabolism	0.228	0.643
ANDROGEN_UP_GENES	0.236	0.643
CR_SIGNALLING	0.182	0.734
MAP00240_Pyrimidine_metabolism	0.297	0.543
MAP00052_Galactose_metabolism	0.283	0.604
cell_surface_receptor_linked_signal_transduction	0.193	0.756
MAP00562_Inositol_phosphate_metabolism	0.303	0.639
nkcellsPathway	0.275	0.693
HTERT_DOWN	0.239	0.671
shhPathway	0.268	0.694
cell_proliferation	0.191	0.712
cell_cycle_checkpoint	0.282	0.601
mcalpainPathway	0.258	0.693
ctla4Pathway	0.251	0.717
ucalpainPathway	0.274	0.730
CR_CYTOSKELETON	0.278	0.700
ST_Fas_Signaling_Pathway	0.206	0.769
par1Pathway	0.272	0.766
ccr3Pathway	0.226	0.812
NFKB_INDUCED	0.185	0.900
mitochondriaPathway	0.219	0.808
pgc1aPathway	0.231	0.840
ecmPathway	0.237	0.794
MAP00220_Urea_cycle_and_metabolism_of_amino_groups	0.257	0.834
ST_Wnt_beta_catenin_Pathway	0.222	0.865
P53_DOWN	0.239	0.848
sppaPathway	0.235	0.838
crebPathway	0.196	0.914
chrebpPathway	0.205	0.872
MAP00230_Purine_metabolism	0.194	0.862
mprPathway	0.209	0.899
no2il12Pathway	0.220	0.942
Cell_Cycle	0.201	0.835
chemicalPathway	0.184	0.966
HOX_LIST_JP	0.138	0.992
CR_DNA_MET_AND_MOD	0.200	0.976

Supplementary Table 9: Up-regulated gene sets in glioma cell lines cultured in vitro growth conditions when compared to in intracranial conditions (in vivo).

Gene Set	Enrichment Score	Nominal p-value
DOWNREG_BY_HOXA9	0.587	0.000
epoPathway	0.557	0.004
MAP00970_Aminoacyl_tRNA_biosynthesis	0.842	0.004
HTERT_UP	0.599	0.006
HOXA9_DOWN	0.451	0.008
igf1Pathway	0.549	0.008
GLUCOSE_UP	0.533	0.010
ST_Phosphoinositide_3_Kinase_Pathway	0.390	0.011
tRNA_Synthetases	0.796	0.013
il6Pathway	0.564	0.014
igf1mTORPathway	0.482	0.016
ST_Interleukin_4_Pathway	0.477	0.023
UPREG_BY_HOXA9	0.509	0.023
MAP00252_Alanine_and_aspartate_metabolism	0.599	0.023
MAP00251_Glutamate_metabolism	0.608	0.024
LEU_UP	0.486	0.025
cell_cycle_arrest	0.480	0.027
il2Pathway	0.423	0.033
SA_TRKA_RECEPTOR	0.630	0.035
ngfPathway	0.477	0.037
il3Pathway	0.538	0.039
ST_ERK1_ERK2_MAPK_Pathway	0.478	0.042
Fatty_Acid_Synthesis	0.586	0.051
insulinPathway	0.487	0.053
SIG_IL4RECEPTOR_IN_B_LYPHOCYTES	0.517	0.054
RAP_DOWN	0.488	0.056
SIG_PIP3SIGINCARDIACMYOCYTES	0.366	0.058
MAP00620_Pyruvate_metabolism	0.561	0.061
arfPathway	0.430	0.061
MAP00710_Carbon_fixation	0.439	0.065
insulin_signalling	0.315	0.073
egfPathway	0.444	0.074
MAP00260_Glycine_serine_and_threonine_metabolism	0.523	0.075
GLUCO	0.455	0.083
GLUT_UP	0.378	0.088
SIG_BCR_Signaling_Pathway	0.382	0.092
FETAL_LIVER_HS_ENRICHED_TF_JP	0.299	0.096
GO_0005739	0.328	0.102
actinYPathway	0.451	0.112
SIG_InsulinReceptorPathwayInCardiacMyocytes	0.366	0.113
alkPathway	0.406	0.125
MAP00350_Tyrosine_metabolism	0.382	0.131
SIG_PIP3_signaling_in_B_lymphocytes	0.364	0.133
MAP00340_Histidine_metabolism	0.459	0.134
drug_resistance_and_metabolism	0.347	0.135
tollPathway	0.370	0.139
MAP00190_Oxidative_phosphorylation	0.375	0.140
MAP00020_Citrate_cycle_TCA_cycle	0.660	0.146
hcmvPathway	0.452	0.148
mtorPathway	0.447	0.150

SA_B_CELL_RECEPTOR_COMPLEXES	0.510	0.159
Glycogen_Metabolism	0.386	0.161
il2rbPathway	0.373	0.161
telPathway	0.558	0.166
PGC	0.339	0.167
inflamPathway	0.391	0.181
ghPathway	0.347	0.184
etsPathway	0.504	0.184
tpoPathway	0.398	0.185
eif4Pathway	0.429	0.186
bcrPathway	0.360	0.189
tidPathway	0.519	0.193
gleevecPathway	0.449	0.195
ST_Integrin_Signaling_Pathway	0.260	0.203
fcgr1Pathway	0.330	0.204
ca_nf_at_signalling	0.310	0.206
ST_ADRENERGIC	0.360	0.210
pyk2Pathway	0.361	0.214
igf1rPathway	0.436	0.216
INSULIN_2F_UP	0.275	0.231
MAP00193_ATP_synthesis	0.472	0.231
MAP03070_Type_III_secretion_system	0.472	0.231
erkPathway	0.375	0.232
nthiPathway	0.465	0.235
arapPathway	0.353	0.239
TCA	0.626	0.244
EMT_UP	0.347	0.251
Krebs-TCA_Cycle	0.488	0.252
ptdinsPathway	0.340	0.255
MAP00640_Propanoate_metabolism	0.494	0.255
cell_cycle_regulator	0.461	0.257
mef2dPathway	0.343	0.263
MAP00860_Porphyrin_and_chlorophyll_metabolism	0.444	0.264
ST_B_Cell_Antigen_Receptor	0.342	0.267
pdgfPathway	0.356	0.268
ST_JNK_MAPK_Pathway	0.300	0.268
MAP00195_Photosynthesis	0.463	0.276
FRASOR_ER_DOWN	0.316	0.278
electron_transporter_activity	0.309	0.281
HUMAN_CD34_ENRICHED_TF_JP	0.281	0.286
tcgPathway	0.287	0.289
NFKB_REDUCED	0.405	0.293
mapkPathway	0.306	0.294
SIG_CHEMOTAXIS	0.327	0.314
ptenPathway	0.377	0.320
wntPathway	0.355	0.322
cdmacPathway	0.428	0.323
MAP00120_Bile_acid_biosynthesis	0.390	0.325
LEU_DOWN	0.376	0.328
MAP00480_Glutathione_metabolism	0.444	0.333
human_mitoDB_6_2002	0.304	0.333
at1rPathway	0.316	0.334
calcineurinPathway	0.337	0.337
tob1Pathway	0.368	0.338

CR_TRANSPORT_OF_VESICLES	0.413	0.339
KRAS_TOP100_CONTROL	0.275	0.340
HEMO_TF_LIST_JP	0.295	0.353
mitochondr	0.295	0.353
stressPathway	0.316	0.357
GLUT_DOWN	0.357	0.361
p53hypoxiaPathway	0.361	0.376
MAP00030_Pentose_phosphate_pathway	0.329	0.379
SA_PTEN_PATHWAY	0.384	0.382
rasPathway	0.295	0.389
GLUCOSE_DOWN	0.251	0.394
biopeptidesPathway	0.293	0.406
MAP00510_N_Glycans_biosynthesis	0.414	0.409
keratinocytePathway	0.291	0.414
gpcrPathway	0.300	0.415
gata3Pathway	0.390	0.422
CR_PROTEIN_MOD	0.222	0.425
BRCA_UP	0.287	0.428
MAP00330_Arginine_and_proline_metabolism	0.301	0.430
vegfPathway	0.303	0.432
vipPathway	0.324	0.434
CR_DEATH	0.268	0.437
SIG_CD40PATHWAYMAP	0.311	0.459
p38mapkPathway	0.296	0.459
ST_Gaq_Pathway	0.342	0.464
ST_G_alpha_i_Pathway_	0.282	0.477
nfatPathway	0.251	0.490
MAP00380_Tryptophan_metabolism	0.258	0.494
dcPathway	0.337	0.505
ceramidePathway	0.345	0.507
ST_p38_MAPK_Pathway	0.295	0.508
gcrPathway	0.325	0.510
p53Pathway	0.395	0.515
tnfr2Pathway	0.329	0.518
CR_TRANSCRIPTION_FACTORS	0.285	0.521
tumor_supressor	0.289	0.525
nfkbPathway	0.299	0.548
GATA1_WEISS	0.294	0.552
EMT_DOWN	0.287	0.566
CR_REPAIR	0.337	0.566
ST_Ga13_Pathway	0.261	0.573
fmlppathway	0.261	0.581
MAP00280_Valine_leucine_and_ileucine_degradation	0.306	0.593
raccycdPathway	0.332	0.596
il1rPathway	0.271	0.604
ST_MONOCYTE_AD_PATHWAY	0.292	0.616
MAP00910_Nitrogen_metabolism	0.279	0.620
RAP_UP	0.199	0.626
p53_signalling	0.226	0.627
breast_cancer_estrogen_signalling	0.234	0.627
ST_Differentiation_Pathway_in_PC12_Cells	0.232	0.628
radiation_sensitivity	0.309	0.636
mRNA_splicing	0.277	0.646
VOXPPOS	0.308	0.648

mRNA_processing	0.287	0.650
MAP00590_Prostaglandin_and_leukotriene_metabolism	0.269	0.659
ndkDynaminPathway	0.292	0.660
Wnt_Signaling	0.236	0.662
pparaPathway	0.255	0.662
electron_transport	0.213	0.663
PROLIF_GENES	0.192	0.669
CR_CELL_CYCLE	0.264	0.677
nktPathway	0.278	0.678
FRASOR_ER_UP	0.293	0.689
atmPathway	0.286	0.703
metPathway	0.241	0.707
Electron_Transport_Chain	0.253	0.707
rarrxrPathway	0.260	0.709
DNA_DAMAGE_SIGNALLING	0.237	0.711
GLYCOGEN	0.290	0.711
cytokinePathway	0.266	0.723
fatty_acid_metabolism	0.248	0.724
th1th2Pathway	0.276	0.730
celcyclePathway	0.279	0.755
cardiacegfPathway	0.299	0.757
integrinPathway	0.218	0.776
41bbPathway	0.278	0.776
Il12Pathway	0.263	0.787
MAP00410_beta_Alanine_metabolism	0.315	0.796
shh_lisa	0.266	0.800
cxcr4Pathway	0.241	0.807
aktPathway	0.243	0.809
carm-erPathway	0.218	0.816
tall1Pathway	0.270	0.825
MAP00650_Butanoate_metabolism	0.263	0.844
tnfr1Pathway	0.217	0.858
MAP00010_Glycolysis_Gluconeogenesis	0.212	0.862
pitx2Pathway	0.226	0.864
il7Pathway	0.237	0.866
g1Pathway	0.223	0.868
XINACT_MERGED	0.234	0.870
MAP00500_Starch_and_sucrose_metabolism	0.235	0.877
proteasomePathway	0.201	0.896
g2Pathway	0.218	0.900
ST_Tumor_Necrosis_Factor_Pathway	0.205	0.910
fasPathway	0.193	0.923
erk5Pathway	0.219	0.925
hdacPathway	0.177	0.928
badPathway	0.206	0.933
spryPathway	0.216	0.938
relaPathway	0.188	0.949
Proteasome_Degradation	0.160	0.953
INS	0.179	0.968
INSULIN_2F_DOWN	0.197	0.983

Supplementary Table S10: Summary of significantly up-regulated gene sets when compare between glioma cell lines and non-glioma tumor cell lines

	Gene sets	Sources	Genes	ES	Nom p
Glioma cell lines	par1Pathway	BioCarta	18	0.664	0.002**
	vegfPathway	BioCarta	26	0.436	0.023*
	inflamPathway	BioCarta	26	0.504	0.025*
	il7pathway	BioCarta	15	0.554	0.044*
	spry pathway	BioCarta	18	0.547	0.046*
	dcpathway	BioCarta	20	0.517	0.049*
	edg1Pathway	BioCarta	24	0.538	0.010**
	at1r pathway	BioCarta	34	0.504	0.047*
	tpopathway	BioCarta	22	0.568	0.053*
	ST_JNK_MAPK_Pathway	STKE	40	0.479	0.011**
	ST_Differentiation_pathway_in_PC12 cells	STKE	43	0.452	0.029*
	Pentose_phosphate_pathway	GenMapp	17	0.569	0.017*
	cell_adhesion	GO	162	0.377	0.015*
	Kras_top100_knockdown	Exp. sig.	70	0.611	0***
	Anti_CD44_up	Exp. sig.	23	0.574	0.017*
	EMT_UP	Exp. sig.	50	0.457	0.013*
	CR_signalling	Exp. sig.	175	0.339	0.013*
Insulin 2f up	Exp. sig.	188	0.347	0.048*	
ngtcl	CR_REPAIR	Exp. sig.	35	-0.519	0.047*
	atrbrcaPathway	BioCarta	21	-0.527	0.057

“*” indicates the levels of statistical significance with “* “ representing nominal p value < 0.05, “***” representing nominal p value < 0.01 and “****” representing nominal p values < 0.001. “ES” is enrichment score and “Nom p” is nominal p value. “Exp. sig” refers to expression signatures. “na” refers to that data source information is not available. “ngtcl” refers to non-glioma tumor cell lines.