

【解析結果一覧機能】

解析結果の一覧 | 登録 | 解析結果一覧

解析結果一覧

+ 登録日 2006 / 03 / 06 ~ 2007 / 03 / 06

解析結果名 部分一致

解析結果ラベル 部分一致

クリア 検索

実行	登録日	更新日	解析結果名	解析結果ラベル	結果タイプ	解析コメント
	2007/03/06		Human Chromosomes - GDB#1741	CV連携の仕様書と対応のテストデータ	ChromosomeView	
<input type="checkbox"/>	2007/03/07		dummy01	dummy01 label	ChromosomeView	dummy01 comment
<input type="checkbox"/>	2007/03/07		サンプルデータ	サンプルデータ ラベル	ChromosomeView	サンプルデータ + ダミーのCSVファイルです。
<input type="checkbox"/>	2007/03/07		test	test label	ChromosomeView	test comment
<input type="checkbox"/>	2007/02/23		dummy01	a dummy01 ラベル	ChromosomeView	dummy01のコメント
<input type="checkbox"/>	2007/02/22	2007/03/01	dummy02	b dummy02 ラベル	ChromosomeView	dummy02のコメント
<input type="checkbox"/>	2007/02/21	2007/03/07	dummy01	c dummy01 ラベル	test	dummy01のコメント

追加解析結果を一括実行

ページ表示枚数: 1/1

多様な解析結果を管理するために、本システムでは登録された解析結果について名称やコメントを一覧で表示できる。また、簡易な検索機能が付属するため、解析結果の管理を容易にする。

【解析結果検索機能】

解析結果の一覧 | 解析結果検索

解析結果検索

+ 登録日 2006 / 03 / 06 ~ 2007 / 03 / 06

解析結果名 部分一致 前方一致 完全一致

解析結果ラベル 部分一致 前方一致 完全一致

解析結果タイプ 部分一致 前方一致 完全一致

結果グループ

一括実行 対象外

解析結果ラベル 部分一致 前方一致 完全一致

解析結果コメント 部分一致 前方一致 完全一致

クリア 検索

ページ表示枚数: 1/1

登録した解析結果を登録日時や解析結果のファイル名から検索できる。

【CV 連携機能】

退院サマリーに登録した MRI 画像およびコメント情報を患者匿名化 ID に関連づけて CV 画面上で表示する。

232535_at - Human Chromosomes - GBM survival 12months - Mozilla Firefox

http://127.0.0.1:8000/gbm_survival_12months/chr7/gf1.23/232535_at.html

GeneID	222194
ProbeID	232535_at
Symbol	R.SBN1L
Description	round spermid basic protein 1-like [Source RefSeq_peptide,Acc.NP_940869]
Start Pos.	77163696 (bp)
End Pos.	77246932 (bp)
Strand	+
Chromosome	chr7
Band	q11.23
P-value	0.00430288988613

case [232535_at] (4.630)

AS05801 Rank.1(5.277)

GEM AS05801

AS05201 Rank.2(5.170)

GEM AS05201

control [232535_at] (3.942)

AS00201 Rank.28(2.773)

GEM AS00201

AS03901 Rank.27(3.212)

GEM AS03901

7

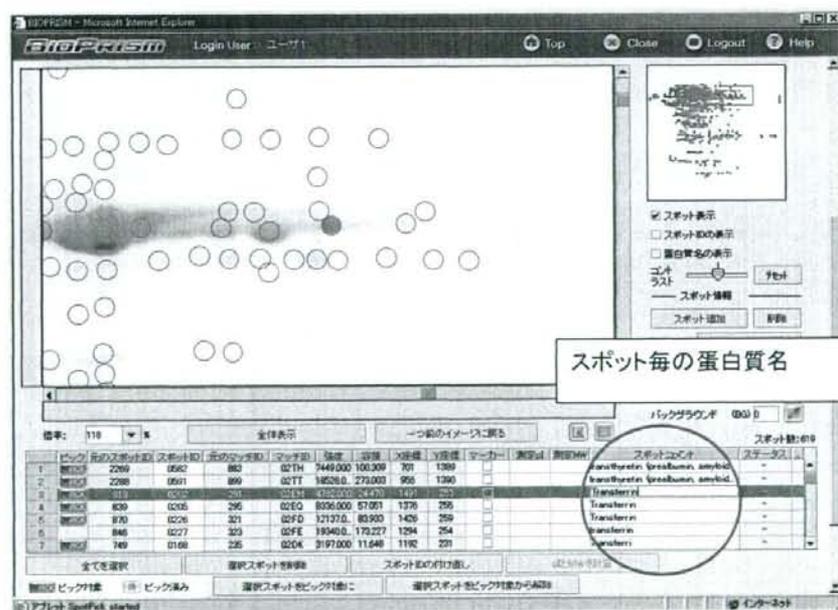
5-4. プロテオーム解析結果閲覧機能

【ゲル一覧】



プロテオーム解析結果をゲル情報として登録して、各実験ごとにゲル画像を一覧表示する。

【ゲル画像詳細情報】



脳脊髄液や脳腫瘍に関するプロテオーム実験データを登録、閲覧できる。この画面では、ゲル画像に関連付けられたスポット情報を一覧表示し、NEC プロテオミクス研究センターにて検出した主要な蛋白質について併せて表示する。ゲル画像は自由に縮小拡大が可能であり、登録されたスポットの位置情報やスポットの容積、強度を表示する。

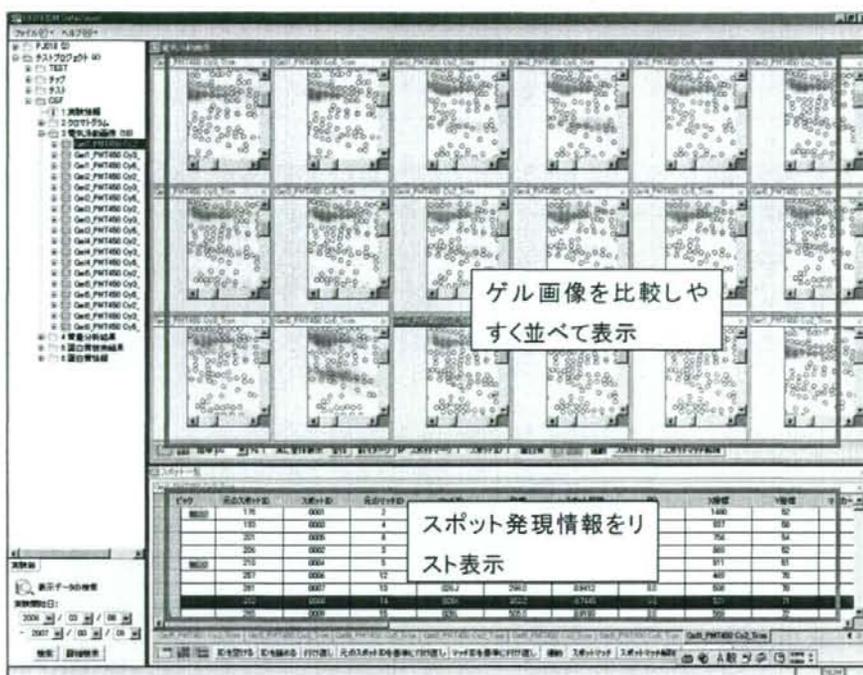
【スポット詳細情報】

マッチング情報やマッチしたスポットの発現量を参照する場合は、ゲル画像詳細画面においてスポットを選択し、「選択スポットの詳細データ表示」ボタンよりスポット詳細情報を表示する。

スポットID	ゲル画像名	スポットX	スポットY	容積	強度
291	Gell_PMT450_Cy2_Trim	0202	037	0.777	
291	Gell_PMT450_Cy2_Trim	0202	0432	0.714	
291	Gell_PMT450_Cy2_Trim	0197	1.090	1.203	
291	Gell_PMT450_Cy2_Trim	0197	2.989	2.811	
291	Gell_PMT450_Cy2_Trim	0197	0.725	0.96	
291	Gell_PMT450_Cy2_Trim	0199	1.347	1.956	
291	Gell_PMT450_Cy2_Trim	0199	0.790	1.369	
291	Gell_PMT450_Cy2_Trim	0199	1.643	2.282	
291	Gell_PMT450_Cy2_Trim	0191	0.654	1.869	
291	Gell_PMT450_Cy2_Trim	0191	1.971	2.854	
291	Gell_PMT450_Cy2_Trim	0191	0.822	1.71	
291	Gell_PMT450_Cy2_Trim	0200	0.818	0.764	
291	Gell_PMT450_Cy2_Trim	0200	0.495	0.636	
291	Gell_PMT450_Cy2_Trim	0200	2.709	2.720	
291	Gell_PMT450_Cy2_Trim	0270	1.494	1.221	
291	Gell_PMT450_Cy2_Trim	0270	1.086	1.274	
291	Gell_PMT450_Cy2_Trim	0270	0.694	0.807	

【統合表示機能】

プロテオーム実験結果で得られたゲル画像について複数枚同時に同じ画面上で表示することが出来る。その際に、関連するスポットの情報および蛋白質の情報を表示して、スポットの発現量を複数サンプル間で比較可能である。



【Excel への Export 機能】



プロテオーム解析で得られたスポット発言情報と蛋白質情報を併せて Microsoft Excel 上に出力できる。これによって、他の Excel ファイルとの融合や、Excel のフィル機能などを活用して、データ整理を容易に行うことができる。

資料2

Chromosome Viewer (Microarray data解析ソフトウェア) の概要

国立がんセンター
日本電気株式会社 (NEC)
バイオIT事業推進センター

成田善孝
滝中徹 秋葉幸範

Affymetrix社のHG-U133 plusなどから得られた遺伝子発現プロファイルデータ (Microarray data) の解析は、統計的な手法により、ある群と対照群との有意な遺伝子発現の差をもとに、両群間で異なる遺伝子を同定する。しかし、膨大な数の解析結果が得られ、抽出された遺伝子の臨床的意味を考えることが困難なことが多い。

ここ10年間でCGH(Comparative Genomic Hybridization)法やFISH法などにより染色体のLOHなどが明らかになり、どの染色体に神経膠腫の重要な遺伝子が存在するかはおおよそ明らかになってきた。たとえば、乏突起膠腫系の腫瘍 (Oligodendroglioma/Oligoastrocytoma) は、染色体1pのLOHが化学療法の感受性と関係があることが判明している。

そこで、染色体情報も参考にしながらMicroarray dataからより重要な遺伝子を探索するツールとしてChromosome viewerを開発することとなった。

Chromosome viewerでは以下のことが可能である。

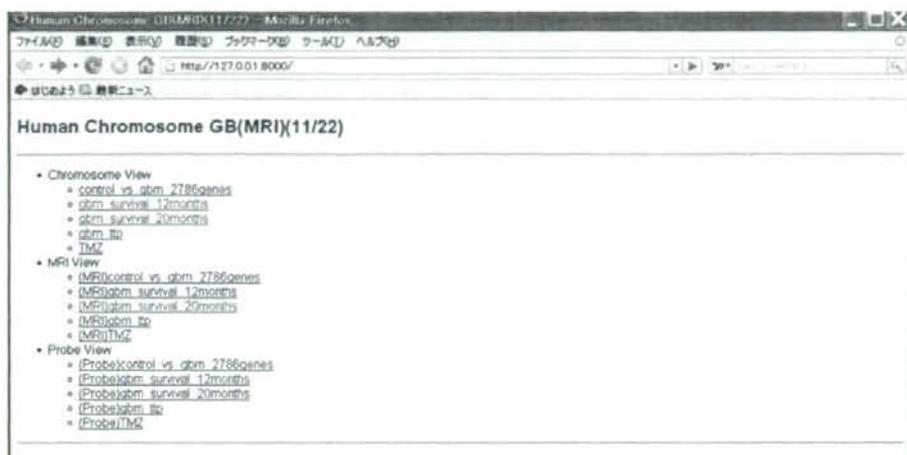
- ・ Microarray dataから得られた遺伝子発現情報を統計的に解析して有意な遺伝子を、染色体上に表示。
- ・ 有意な遺伝子はp値により表示可能 (より有意な遺伝子を視覚的に表示)
- ・ 遺伝子の存在する部位に加え、二群間の遺伝子の発現を表示
- ・ 染色体を拡大することにより、遺伝子の詳細な部位を塩基単位で表示
- ・ 2群間の症例を、MRI画像・病理画像とともに表示可能。

Microarray dataからは膨大な情報が得られるが、この手法により発現の差や有意差だけでなく、過去に行われた神経膠腫のDNA/RNA解析結果を利用した遺伝子探索が可能となった。

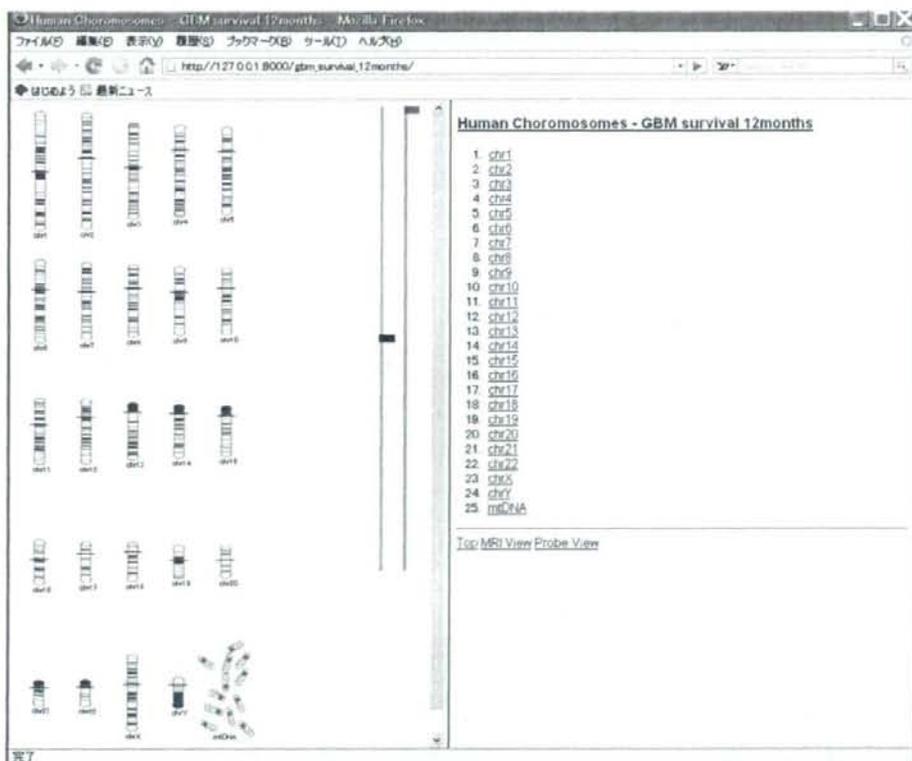
また、症例を見ながら抽出された遺伝子情報の重要性を検討することが可能となる。

(1) メインメニュー

例：GBM(膠芽腫)の生存率12ヶ月以上・以下で比較



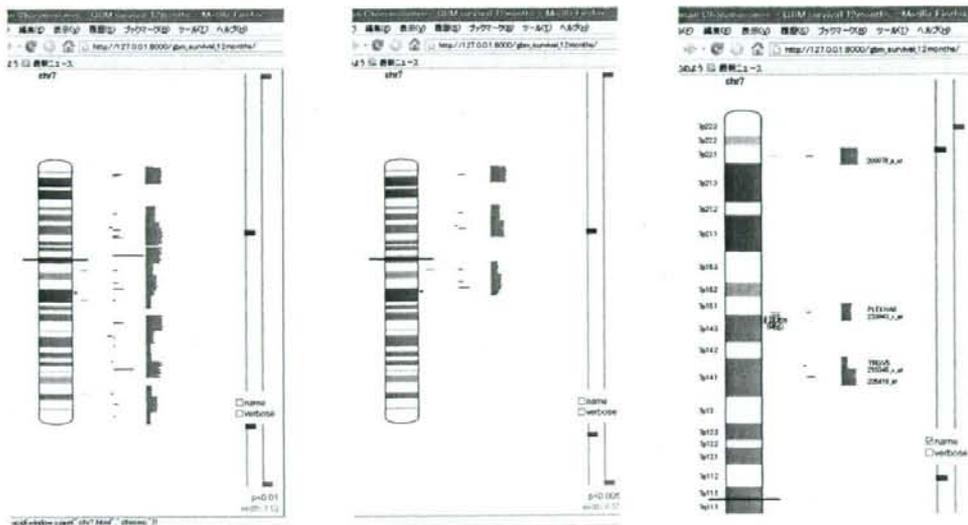
(3) 染色体選択画面



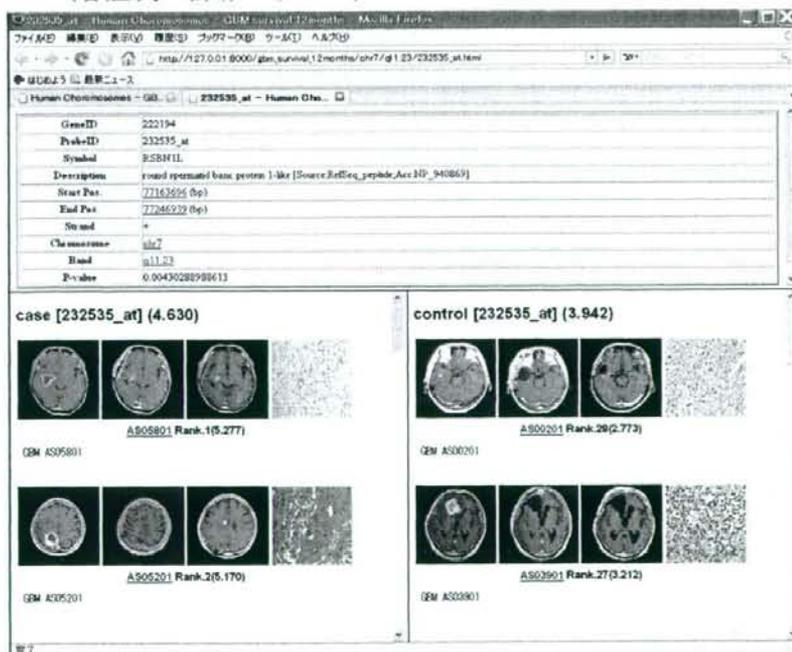
(3) Microarray 解析結果を表示

例：7番染色体上の遺伝子を表示。p値を変更することにより、より有意な遺伝子を絞ることができる

(a) $p < 0.01$ の遺伝子 (b) $p < 0.001$ に絞る (c) 染色体を拡大し、遺伝子表示



(4) 比較群 (生存期間>12ヶ月) と対照群 (生存期間<12ヶ月) 症例を呈示 (各症例の詳細ヘルリンク)



資料3

1. Oligodendroglial tumorで発現が亢進している遺伝子 OD+AO VS NB+A2+A3

No.	Gene Title	Gene Symbol	Chromosome	wilcox p v	diff
1	Atonal homolog 8 (Drosophila)	ATOH8	2p11.2	3.42E-07	2.612215
2	myosin, heavy polypeptide 6, cardiac muscle, alpha	MYH6 /// MYH6	14q12	3.54E-08	2.110458
3	guanine nucleotide binding protein (G protein), gamma 4	GNG4	1q42.3	1.15E-07	1.649755
4	BH3 interacting domain death agonist	BID	22q11.1	1.74E-07	1.349824
5	embryonal Fyn-associated substrate	EFS	14q11.2-q	2.00E-07	1.326052
6	solute carrier family 7 (cationic amino acid transporters), member 14	SLC7A14	3q26.2	4.43E-07	1.317748
7	guanine nucleotide binding protein (G protein), gamma 4	GNG4	1q42.3	2.62E-07	1.278075
8	---	---	---	2.29E-07	1.250321
9	TEA domain family member 1 (SV40 transcription factor)	TEAD1	11p15.2	2.29E-07	1.223731
10	Transcribed locus	---	---	8.63E-08	1.179829
11	BH3 interacting domain death agonist	BID	22q11.1	5.73E-07	1.111584
12	chromosome 9 open reading frame 126	C9orf126	9q33.3	8.35E-07	1.050964
13	Chromosome 20 open reading frame 160	C20orf160	20q11.2	5.97E-09	1.032766
14	BH3 interacting domain death agonist /// BH3 interacting domain death agonist	BID	22q11.1	2.62E-07	1.028568
15	myristoylated alanine-rich protein kinase C substrate 1	MARCKS	6q22.2	7.37E-07	0.964858
16	sialic acid acetyltransferase	SIAE	11q24	1.32E-07	0.959213
17	stromal antigen 3-like	FLJ13195	7p11.2-q1	1.32E-07	0.954318
18	similar to tripartite motif-containing 16	LOC653524	17p11.2	6.45E-08	0.948486
19	---	---	---	2.60E-08	0.940172
20	G protein-coupled receptor 19	GPR19	12p12.3	3.54E-08	0.92674
21	hypothetical protein LOC645469 /// hypothetical protein LOC645469	LOC645469 /// LOC645469	1q21.3	2.29E-07	0.902505
22	suppression of tumorigenicity 13 (colon carcinoma)	ST13	22q13.2	5.57E-08	0.872321
23	DnaJ (Hsp40) homolog, subfamily C, member 12	DNAJC12	10q22.1	8.35E-07	0.871503
24	myosin, heavy polypeptide 7, cardiac muscle, beta	MYH7	14q12	2.00E-07	0.845109
25	Chromosome 20 open reading frame 44	C20orf44	20q11.22	2.00E-07	0.844625
26	---	---	---	9.44E-07	0.842365
27	transcription termination factor, RNA polymerase II	TTF1	9q34.13	8.35E-07	0.796712
28	mitochondrial ribosomal protein S25	MRPS25	3p25	5.57E-08	0.758015
29	heat shock protein 90kDa alpha (cytosolic), class B	HSP90AB1	6p12	1.52E-07	0.748261
30	ribonuclease H2, subunit C	RNASEH2C	11q13.1	3.42E-07	0.736244
31	hypothetical protein TI-227H /// taurine upregulation 1	TI-227H /// TAU227H	22q12.2	5.25E-10	0.713516
32	sorting and assembly machinery component 50 homolog	SAMM50	22q13.31	9.96E-08	0.705053
33	sepiapterin reductase (7,8-dihydrobiopterin:NADPH oxidoreductase)	SPR	2p14-p12	4.80E-08	0.704638
34	matrix metalloproteinase 24 (membrane-inserted)	MMP24	20q11.2	8.63E-08	0.678169
35	GS homeobox 1	GSH1	13q12.2	7.47E-08	0.669826
36	bromodomain and PHD finger containing, 3	BRPF3	6p21	6.45E-08	0.635994
37	mediator of RNA polymerase II transcription, subunit 19	MED19	11q12.1	3.04E-08	0.610299
38	thioredoxin domain containing 14	TXNDC14	11cen-q22	5.97E-09	0.60891
39	hexamethylene bis-acetamide inducible 2	HEXIM2	17q21.31	6.50E-07	0.60566
40	limb region 1 homolog (mouse)	LMBR1	7q36	9.44E-07	0.605582
41	F-box protein 38	FBXO38	5q33.1	8.35E-07	0.603925
42	family with sequence similarity 36, member A	FAM36A	1q44	8.63E-08	0.602606
43	hypothetical LOC25845	LOC25845	5p15.33	6.45E-08	0.600468
44	suppression of tumorigenicity 13 (colon carcinoma)	ST13	22q13.2	5.04E-07	0.588726
45	Keratin associated protein 4-7	KRTAP4-7	17q12-q21	3.42E-07	0.581717
46	NEFA-interacting nuclear protein NIP30	NIP30	16q13	4.80E-08	0.57157
47	zinc finger protein 41 homolog (mouse)	ZFP41	8q24.3	5.04E-07	0.568474
48	remodeling and spacing factor 1	RSF1	11q14.1	3.89E-07	0.557641
49	RRN3 RNA polymerase I transcription factor homolog	RRN3	16p12	7.37E-07	0.555737
50	---	---	---	3.42E-07	0.552208

2. Oligodendroglial tumorで発現が抑制されている遺伝子 OD+AO VS NB+A2+A3

No.	Gene Title	Gene Symbol	Chromosome	Wilcoxon p value	diff
1	KIAA1729 protein	KIAA1729	4p16.1	1.90E-08	-1.91056
2	solute carrier family 2 (facilitated glucose transporter)	SLC2A10	20q13.1	5.73E-07	-1.90618
3	Hypothetical protein FLJ23861	FLJ23861	2q34	1.32E-07	-1.48643
4	amylase, alpha 1A; salivary /// amylase, alpha 1B	AMY1A /// AMY1B	1p21	9.55E-10	-1.34798
5	dehydrogenase/reductase (SDR family) member	DHRS3	1p36.1	2.99E-07	-1.34551
6	KIAA0485 protein	KIAA0485	---	5.73E-07	-1.30526
7	chitinase, di-N-acetyl-	CTBS	1p22	8.63E-08	-1.19943
8	phosphopantothencysteine synthetase	PPCS	1p34.2	5.73E-07	-1.07291
9	---	---	---	3.89E-07	-1.03686
10	WD repeat domain 78	WDR78	1p31.3	8.35E-07	-1.03199
11	protein tyrosine phosphatase, receptor type, F	PTPRF	1p34	7.85E-10	-1.01944
12	histone deacetylase 1	HDAC1	1p34	9.44E-07	-1.00972
13	RAP1A, member of RAS oncogene family	RAP1A	1p13.3	1.52E-07	-0.99167
14	Ubiquitin specific peptidase 53	USP53	4q26	7.37E-07	-0.92195
15	myb-like, SWIRM and MPN domains 1	MYSM1	1p32.1	1.52E-07	-0.89928
16	---	---	---	7.08E-09	-0.86931
17	solute carrier family 35 (UDP-glucuronic acid/UDP-glucose)	SLC35D1	1p32-p31	1.90E-08	-0.86408
18	syntaxin binding protein 3	STXBP3	1p13.3	7.47E-08	-0.84298
19	serine/threonine kinase 40	STK40	1p34.3	2.29E-07	-0.83686
20	CDNA FLJ12742 fis, clone NT2RP2000644	---	---	4.13E-08	-0.82879
21	capping protein (actin filament) muscle Z-line, beta	CAPZB	1p36.1	1.52E-07	-0.8283
22	oxysterol binding protein-like 9	OSBPL9	1p32.3	2.62E-07	-0.82743
23	WAS protein family, member 2	WASF2	1p36.11-p36.1	3.42E-07	-0.82056
24	Suppression of tumorigenicity 7 like	ST7L	1p13.2	4.13E-08	-0.81446
25	mesoderm induction early response 1 homolog (Xenopus laevis)	MIER1	1p31.3	1.41E-09	-0.80387
26	microtubule-actin crosslinking factor 1	MACF1	1p32-p31	8.39E-09	-0.78841
27	TM2 domain containing 1 /// TM2 domain containing 1	TM2D1	1p31.3	9.91E-09	-0.78212
28	microtubule-actin crosslinking factor 1	MACF1	1p32-p31	3.54E-08	-0.77934
29	peroxiredoxin 1	PRDX1	1p34.1	7.37E-07	-0.77117
30	protein tyrosine phosphatase, receptor type, F	PTPRF	1p34	2.23E-08	-0.76146
31	vacuolar protein sorting 13 homolog D (S. cerevisiae)	VPS13D /// VPS13D	1p36.22	5.73E-07	-0.75912
32	zinc finger, CCHC domain containing 11	ZCCHC11	1p32.3	2.26E-10	-0.74646
33	---	---	---	6.50E-07	-0.73697
34	CDNA clone IMAGE:3030163	---	---	9.44E-07	-0.73655
35	stromal membrane-associated protein 1-like	SMAP1L	1p35.3-p35.3	5.57E-08	-0.72907
36	exostosin (multiple)-like 2	EXTL2	1p21	3.42E-07	-0.72179
37	capping protein (actin filament) muscle Z-line, beta	CAPZB	1p36.1	7.08E-09	-0.72078
38	CDNA FLJ33255 fis, clone ASTRO2005553	---	---	2.60E-08	-0.71231
39	karyopherin alpha 6 (importin alpha 7)	KPNA6	1p35.1-p35.1	5.57E-08	-0.71165
40	protein kinase N2	PKN2	1p22.2	1.62E-08	-0.71104
41	Transcribed locus, strongly similar to XP_513313	---	---	2.29E-07	-0.70985
42	cyclin L2 /// similar to Aurora kinase A-interacting protein 1	CCNL2 /// CCNL2	1p36.33	5.04E-07	-0.69438
43	chromosome 1 open reading frame 108	C1orf108	1p34.3	1.38E-08	-0.69191
44	mago-nashi homolog, proliferation-associated (Drosophila melanogaster)	MAGOH	1p34-p33	1.74E-07	-0.68672
45	LSM14 homolog A (SCD6, S. cerevisiae)	LSM14A	19q13.11	1.38E-08	-0.67958
46	serine/arginine repetitive matrix 1	SRRM1	1p36.11	6.43E-10	-0.67636
47	Nardilysin (N-arginine dibasic convertase)	NRD1	1p32.2-p32.2	6.50E-07	-0.67623
48	hippocampus abundant transcript 1	HIAT1	1p21.2	9.44E-07	-0.66423
49	TM2 domain containing 1	TM2D1	1p31.3	6.43E-10	-0.65443
50	chromosome 1 open reading frame 119 /// similar to C1orf119	C1orf119 /// C1orf119	1p13.3	8.35E-07	-0.65382

3.GBMで発現が亢進している遺伝子

GBM vs DA,AA,AO,AOA

No.	Gene Title	Gene Symbol	Chromosome	wilcox p v	diff
1	chitinase 3-like 1 (cartilage glycoprotein-39)	CHI3L1	1q32.1	5.92E-10	4.251603
2	chitinase 3-like 1 (cartilage glycoprotein-39)	CHI3L1	1q32.1	3.60E-10	4.022079
3	nicotinamide N-methyltransferase	NNMT	11q23.1	1.35E-11	3.773668
4	Integrin-binding sialoprotein (bone sialoprotein, b	IBSP	4q21-q25	5.19E-10	3.018054
5	podoplanin	PDPN	1p36.21	3.51E-11	2.844567
6	pentraxin-related gene, rapidly induced by IL-1 b	PTX3	3q25	9.96E-11	2.840536
7	nicotinamide N-methyltransferase	NNMT	11q23.1	4.89E-12	2.828797
8	lysyl oxidase	LOX	5q23.2	1.00E-09	2.794021
9	TIMP metalloproteinase inhibitor 1	TIMP1	Xp11.3-p1	2.33E-10	2.648243
10	insulin-like growth factor 2 mRNA binding protein	IGF2BP3	7p11	2.58E-10	2.615635
11	collagen, type V, alpha 2	COL5A2	2q14-q32	4.98E-11	2.543785
12	transmembrane protein 49	TMEM49	17q23.1	3.27E-11	2.522978
13	glycoprotein (transmembrane) nmb	GNPMB	7p15	5.36E-10	2.419624
14	insulin-like growth factor binding protein 2, 36kD	IGFBP2	2q33-q34	2.33E-10	2.36644
15	transforming growth factor, beta-induced, 68kDa	TGFBI	5q31	4.40E-10	2.240801
16	Growth arrest-specific 2 like 3	GAS2L3	12q23.1	2.56E-11	2.204922
17	tumor necrosis factor, alpha-induced protein 6	TNFAIP6	2q23.3	1.03E-10	2.16241
18	serpin peptidase inhibitor, clade E (nexin, plasmin	SERPINE1	7q21.3-q2	3.98E-10	2.116157
19	collagen, type V, alpha 2	COL5A2	2q14-q32	1.27E-10	2.103091
20	adrenomedullin	ADM	11p15.4	7.21E-10	2.086751
21	branched chain aminotransferase 1, cytosolic	BCAT1	12pter-q1	8.50E-10	2.079675
22	microRNA 21	MIRN21	---	3.77E-11	2.062771
23	adipose differentiation-related protein	ADFP	9p22.1	3.39E-12	2.044614
24	annexin A2	ANXA2	15q21-q22	4.65E-11	2.038594
25	annexin A2	ANXA2	15q21-q22	5.53E-11	2.021704
26	coiled-coil domain containing 109B	CCDC109B	4q25	2.38E-11	2.019792
27	annexin A2	ANXA2	15q21-q22	4.65E-11	2.015908
28	lysyl oxidase	LOX	5q23.2	4.71E-12	1.996011
29	plasminogen activator, urokinase	PLAU	10q24	9.37E-10	1.965683
30	branched chain aminotransferase 1, cytosolic	BCAT1	12pter-q1	1.40E-10	1.938162
31	tumor necrosis factor, alpha-induced protein 6	TNFAIP6	2q23.3	6.12E-10	1.92668
32	chromosome 1 open reading frame 24	C1orf24	1q25	5.92E-10	1.910518
33	vimentin	VIM	10p13	2.33E-10	1.902564
34	epithelial membrane protein 3	EMP3	19q13.3	3.33E-11	1.893657
35	C-type lectin domain family 5, member A	CLEC5A	7q33	6.98E-10	1.892696
36	CD44 molecule (Indian blood group)	CD44	11p13	3.85E-10	1.866842
37	vascular endothelial growth factor	VEGF	6p12	8.98E-11	1.861378
38	vascular endothelial growth factor	VEGF	6p12	2.85E-10	1.842776
39	interferon, gamma-inducible protein 30	IFI30	19p13.1	1.93E-11	1.826143
40	S100 calcium binding protein A4 (calcium protein	S100A4	1q21	2.11E-10	1.824117
41	pre-B-cell colony enhancing factor 1 /// pre-B	PBEF1 /// RP	7q22.2 ///	5.36E-10	1.812179
42	CD58 molecule	CD58	1p13	1.17E-11	1.808085
43	procollagen-lysine, 2-oxoglutarate 5-dioxygenase	PLOD2	3q23-q24	2.95E-10	1.807575
44	heme oxygenase (decycling) 1	HMOX1	22q12.22q	1.55E-10	1.797278
45	vascular endothelial growth factor	VEGF	6p12	1.50E-10	1.796775
46	glycoprotein (transmembrane) nmb	GNPMB	7p15	4.25E-10	1.79574
47	transgelin 2	TAGLN2	1q21-q25	2.84E-11	1.794159
48	capping protein (actin filament), gelsolin-like	CAPG	2p11.2	1.35E-11	1.790226
49	runt-related transcription factor 1 (acute myeloid	RUNX1	21q22.3	1.84E-10	1.782013
50	chromosome 15 open reading frame 48	C15orf48	15q21.1	3.26E-12	1.770702

4. GBMで発現が抑制されている遺伝子

GBM vs DA,AA,AO,AOA

No.	Gene Title	Gene Symbol	Chromosome	wilcox p v	diff
1	secretogranin III	SCG3	15q21	6.98E-10	-2.18084
2	Full length insert cDNA clone ZE05A03	----	----	1.31E-10	-2.05868
3	hypothetical protein FLJ37659	RP1-32F7.2	Xq21.32	2.75E-11	-1.99477
4	Metallophosphoesterase 1	MPPE1	18p11.21	5.54E-10	-1.97242
5	CD226 molecule	CD226	18q22.3	6.33E-10	-1.95006
6	family with sequence similarity 19 (chemokine (C	FAM19A2	12q14.1	2.00E-11	-1.93398
7	hypothetical protein LOC284214	LOC284214	18p11.31	5.92E-10	-1.93363
8	potassium voltage-gated channel, Shab-related s	KCNB1	20q13.2	2.84E-11	-1.86266
9	unc-5 homolog A (C. elegans)	UNC5A	5q35.2	4.86E-10	-1.81451
10	hepatic leukemia factor	HLF	17q22	7.33E-10	-1.75517
11	tubby homolog (mouse)	TUB	11p15.5	8.10E-11	-1.68312
12	CDNA FLJ42259 fis, clone TKIDN2011289	----	----	7.21E-10	-1.67104
13	docking protein 6	DOK6	18q22.2	6.54E-10	-1.66254
14	Metallophosphoesterase 1	MPPE1	18p11.21	1.61E-10	-1.6334
15	UDP-N-acetyl-alpha-D-galactosamine:polypepti	GALNT13	2q23.3-q2	2.75E-11	-1.59255
16	Neuregulin 3	NRG3	10q22-q23	8.38E-11	-1.56674
17	hypothetical protein FLJ37659	RP1-32F7.2	Xq21.32	2.84E-11	-1.50688
18	melanoma antigen family E, 1	MAGEE1	Xq13.3	2.18E-10	-1.45699
19	septin 8	39333	5q31	3.72E-10	-1.43967
20	(clone CTG-A4) mRNA sequence	----	----	5.19E-10	-1.41712
21	nucleosome assembly protein 1-like 3	NAP1L3	Xq21.3-q2	4.70E-10	-1.409
22	CDNA clone IMAGE:5263177	----	----	7.96E-10	-1.39769
23	chromosome 13 open reading frame 21	C13orf21	13q14.11	2.43E-12	-1.39007
24	histone deacetylase 4	HDAC4	2q37.2	1.34E-12	-1.34614
25	furry homolog (Drosophila)	FRY	13q13.1	5.73E-11	-1.29193
26	phospholipase C, beta 1 (phosphoinositide-specif	PLCB1	20p12	6.76E-10	-1.28713
27	solute carrier family 25, member 27	SLC25A27	6p11.2-q1	3.90E-11	-1.27575
28	Splicing factor 3a, subunit 3, 60kDa	SF3A3	1p34.3	1.30E-11	-1.23389
29	butyrophilin-like 9	BTNL9	5q35.3	4.33E-11	-1.16831
30	Ribosomal protein L13	RPL13	16q24.31	3.27E-11	-1.14896
31	solute carrier family 22 (organic cation transport	SLC22A17	14q11.2	1.61E-11	-1.1243
32	CDNA clone IMAGE:5263177	----	----	1.18E-10	-1.10263
33	neurotrophic tyrosine kinase, receptor, type 3	NTRK3	15q25	5.73E-10	-1.10103
34	ubiquinol-cytochrome c reductase binding protei	UQCRCB	8q22	1.24E-12	-1.09603
35	----	----	----	2.25E-12	-1.09257
36	hypothetical protein LOC646405 /// hypothetical	LOC646405 //	13q12.12-	4.33E-11	-1.09189
37	Ribosomal protein L37	RPL37	5p13	3.72E-10	-1.0763
38	protocadherin 21	PCDH21	10q22.1-q	7.45E-10	-1.01918
39	similar to CG9643-PA	LOC399818	10q26.13	2.30E-11	-0.96487
40	----	----	----	7.21E-10	-0.94885
41	FCH and double SH3 domains 2	FCHSD2	11q13.4	5.02E-10	-0.93354
42	ATP synthase, H+ transporting, mitochondrial FO	ATP5S	14q22.1	6.14E-11	-0.93057
43	histone deacetylase 4	HDAC4	2q37.2	3.16E-11	-0.93027
44	Ribosomal protein L15	RPL15	3p24.2	1.50E-11	-0.92934
45	Transcribed locus	----	----	1.66E-10	-0.90662
46	thyrotrophic embryonic factor	TEF	22q13 22q	3.37E-10	-0.90455
47	Chromosome 13 open reading frame 21	C13orf21	13q14.11	2.41E-10	-0.90344
48	zinc finger protein 651	ZNF651	3p22.1	3.15E-10	-0.89298
49	hypothetical protein FLJ10159	FLJ10159	6q21	4.86E-10	-0.88996
50	LAS1-like (S. cerevisiae)	LAS1L	Xq12-q13	6.81E-11	-0.88973

5. Progression (AA→GBM)で発現が亢進している遺伝子

No.	Gene Title	Gene Symbol	Chromosome	wilcox p v	diff
1	topoisomerase (DNA) II alpha 170kDa	TOP2A	17q21-q22	2.10E-05	2.660138
2	ribonucleotide reductase M2 polypeptide	RRM2	2p25-p24	6.19E-06	2.581518
3	PDZ binding kinase	PBK	8p21.2	9.75E-05	2.441424
4	asp (abnormal spindle)-like, microcephaly associ	ASPM	1q31	3.77E-05	2.398938
5	ribonucleotide reductase M2 polypeptide	RRM2	2p25-p24	8.25E-06	2.371371
6	insulin-like growth factor 2 mRNA binding protein	IGF2BP3	7p11	2.20E-05	2.356241
7	topoisomerase (DNA) II alpha 170kDa	TOP2A	17q21-q22	6.10E-05	2.311182
8	monooxygenase, DBH-like 1	MOXD1	6q23.1-23	1.61E-04	2.236116
9	cyclin B1	CCNB1	5q12	5.62E-06	2.212356
10	discs, large homolog 7 (Drosophila)	DLG7	14q22.3	3.60E-05	2.190074
11	interleukin 8	IL8	4q13-q21	7.93E-04	2.173022
12	maternal embryonic leucine zipper kinase	MELK	9p13.2	2.75E-05	2.166626
13	baculoviral IAP repeat-containing 5 (survivin)	BIRC5	17q25	1.26E-05	2.087457
14	insulin-like growth factor 2 mRNA binding protein	IGF2BP3	7p11	6.36E-05	2.08217
15	centromere protein F, 350/400ka (mitosin)	CENPF	1q32-q41	2.00E-05	2.080228
16	CDC20 cell division cycle 20 homolog (S. cerevis)	CDC20	1p34.1	1.45E-05	2.058915
17	E2F transcription factor 7	E2F7	12q21.2	2.88E-05	2.055456
18	MLF1 interacting protein	MLF1IP	4q35.1	2.20E-05	2.025427
19	KIAA0101	KIAA0101	15q22.31	1.15E-05	2.01993
20	kinetochore associated 2	KNTC2	18p11.32	5.90E-06	2.006971
21	cyclin B2	CCNB2	15q22.2	3.94E-05	1.999548
22	Growth arrest-specific 2 like 3	GAS2L3	12q23.1	5.16E-07	1.992963
23	kinesin family member 20A	KIF20A	5q31	1.15E-05	1.964715
24	denticleless homolog (Drosophila)	DTL	---	1.15E-04	1.963094
25	collagen, type V, alpha 2	COL5A2	2q14-q32	7.09E-04	1.961991
26	BUB1 budding uninhibited by benzimidazoles 1 he	BUB1	2q14	2.75E-05	1.945385
27	nucleolar and spindle associated protein 1	NUSAP1	15q15.1	6.10E-05	1.920673
28	chromosome condensation protein G	HCAP-G	4p15.33	7.24E-05	1.905516
29	centromere protein F, 350/400ka (mitosin) /// c	CENPF	1q32-q41	2.00E-05	1.892871
30	BUB1 budding uninhibited by benzimidazoles 1 he	BUB1B	15q15	6.36E-05	1.873816
31	kinesin family member 23	KIF23	15q23	3.28E-06	1.860659
32	family with sequence similarity 83, member D	FAM83D	20q11.22-	3.77E-05	1.848072
33	cell division cycle associated 1	CDCA1	1q23.3	7.89E-05	1.843665
34	cyclin B1	CCNB1	5q12	2.63E-05	1.841352
35	hyaluronan-mediated motility receptor (RHAMM)	HMMR	5q33.2-q34	4.30E-05	1.816226
36	insulin-like growth factor binding protein 2, 36kD	IGFBP2	2q33-q34	3.57E-04	1.811386
37	aurora kinase A	AURKA	20q13.2-q	1.59E-05	1.793754
38	protein regulator of cytokinesis 1	PRC1	15q26.1	1.15E-05	1.783855
39	epithelial cell transforming sequence 2 oncogene	ECT2	3q26.1-q2	7.87E-06	1.774762
40	kinesin family member 4A	KIF4A	Xq13.1	7.89E-05	1.748039
41	centromere protein A	CENPA	2p24-p21	3.15E-05	1.744194
42	cyclin-dependent kinase inhibitor 3 (CDK2-asso	CDKN3	14q22	8.25E-06	1.736108
43	TTK protein kinase	TTK	6q13-q21	2.88E-05	1.735167
44	tumor necrosis factor, alpha-induced protein 6	TNFAIP6	2q23.3	3.71E-04	1.7262
45	cancer susceptibility candidate 5	CASC5	15q14	9.35E-05	1.69802
46	asp (abnormal spindle)-like, microcephaly associ	ASPM	1q31	3.60E-05	1.689005
47	cell division cycle 2, G1 to S and G2 to M	CDC2	10q21.1	1.61E-04	1.670811
48	homeobox A3	HOXA3	7p15-p14	7.24E-05	1.658151
49	MAD2 mitotic arrest deficient-like 1 (yeast)	MAD2L1	4q27	4.49E-05	1.654962
50	nucleolar and spindle associated protein 1	NUSAP1	15q15.1	1.10E-05	1.652582

6. Progression (AA→GBM)で発現が抑制されている遺伝子

No.	Gene Title	Gene Symbol	Chromosome	wilcox p	v diff
1	purinergic receptor P2Y, G-protein coupled, 12	P2RY12	3q24-q25	2.10E-05	-2.26499
2	phosphatase and actin regulator 3	PHACTR3	20q13.32	4.51E-04	-1.76282
3	purinergic receptor P2Y, G-protein coupled, 12	P2RY12	3q24-q25	7.89E-05	-1.75502
4	chemokine (C-X3-C motif) receptor 1	CX3CR1	3p21.3p21	1.20E-04	-1.68422
5	Neuregulin 3	NRG3	10q22-q23	1.54E-06	-1.63855
6	phosphatidic acid phosphatase type 2 domain co	PPAPDC1A	10q26.12	1.71E-06	-1.60678
7	Full length insert cDNA clone ZE05A03	---	---	2.05E-04	-1.59544
8	purinergic receptor P2Y, G-protein coupled, 13 /	P2RY13	3q24	5.35E-05	-1.48671
9	deleted in bladder cancer 1	DBC1	9q32-q33	6.58E-04	-1.47411
10	MRNA full length insert cDNA clone EUROIMAGE	---	---	3.71E-04	-1.47128
11	potassium voltage-gated channel, Shab-related s	KCNB1	20q13.2	6.36E-05	-1.47116
12	voltage gated channel like 1	VGCNL1	13q32.3	5.66E-04	-1.47042
13	hypothetical protein FLJ37659	RP1-32F7.2	Xq21.32	3.29E-05	-1.4648
14	CDNA FLJ37610 fis, clone BRCOC2011398	---	---	2.13E-04	-1.44988
15	Glycoprotein, alpha-galactosyltransferase 1	GGTA1	9q34.11	3.15E-05	-1.40807
16	Metallophosphoesterase 1	MPPE1	18p11.21	1.36E-04	-1.3902
17	netrin 4	NTN4	12q22-q23	3.86E-04	-1.39004
18	low density lipoprotein-related protein 1B (delete	LRP1B	2q21.2	2.94E-04	-1.38779
19	neural cell adhesion molecule 1	NCAM1	11q23.1	9.18E-04	-1.3675
20	chromosome 10 open reading frame 85	C10orf85	10q26.12	2.56E-06	-1.35499
21	neuregulin 3	NRG3	10q22-q23	5.59E-05	-1.31704
22	sarcoglycan, delta (35kDa dystrophin-associated	SGCD	5q33-q34	2.71E-04	-1.31152
23	meningioma (disrupted in balanced translocation)	MN1	22q11.22q	9.87E-04	-1.25609
24	hepatic leukemia factor	HLF	17q22	4.01E-04	-1.24835
25	butyrophilin-like 9	BTNL9	5q35.3	7.87E-07	-1.21991
26	DEP domain containing 6	DEPDC6	8q24.12	3.18E-04	-1.21911
27	dehydrogenase/reductase (SDR family) member	DHRS9	2q31.1	7.93E-04	-1.19348
28	neuronal growth regulator 1	NEGR1	1p31.1	4.17E-04	-1.18505
29	CDNA FLJ10145 fis, clone HEMBA1003322	---	---	7.36E-04	-1.1774
30	hepatic leukemia factor	HLF	17q22	6.83E-04	-1.16191
31	potassium large conductance calcium-activated	KCNMA1	10q22.3	1.36E-04	-1.16105
32	hypothetical protein FLJ37659	RP1-32F7.2	Xq21.32	3.01E-05	-1.13234
33	ATP-binding cassette, sub-family G (WHITE), me	ABCG2	4q22	5.66E-04	-1.11545
34	neurotrophic tyrosine kinase, receptor, type 3	NTRK3	15q25	6.58E-04	-1.09822
35	UDP-N-acetyl-alpha-D-galactosamine:polypepti	GALNT13	2q23.3-q2	6.36E-05	-1.09816
36	bromodomain and WD repeat domain containing 4	BRWD2	10q26	1.39E-06	-1.09646
37	phospholipase C, beta 1 (phosphoinositide-speci	PLCB1	20p12	1.54E-04	-1.09478
38	Full length insert cDNA YI37C01	---	---	7.09E-04	-1.09389
39	MRNA from chromosome 5q31-33 region	---	---	6.11E-04	-1.06746
40	Ca2+-dependent secretion activator	CADPS	3p14.2	5.05E-04	-1.06175
41	dehydrogenase/reductase (SDR family) member	DHRS9	2q31.1	7.64E-04	-1.04792
42	neurotrophic tyrosine kinase, receptor, type 3	NTRK3	15q25	7.56E-05	-1.0428
43	nucleosome assembly protein 1-like 3	NAP1L3	Xq21.3-q2	3.30E-04	-1.04021
44	adrenergic, beta-2-, receptor, surface	ADRB2	5q31-q32	6.58E-04	-1.03412
45	potassium channel tetramerisation domain conta	KCTD4	13q14.12	8.53E-04	-1.02832
46	CDNA FLJ10145 fis, clone HEMBA1003322	---	---	9.75E-05	-1.0203
47	septin 8	SEPT8	5q31	8.85E-04	-1.01774
48	chromosome 10 open reading frame 56	C10orf56	10q22.3	5.35E-05	-1.01349
49	dehydrogenase/reductase (SDR family) member	DHRS9	2q31.1	8.85E-04	-1.01144
50	family with sequence similarity 19 (chemokine C	FAM19A2	12q14.1	2.75E-05	-1.01038

7. Progression (DA grade 2→AA grade 3)で発現が亢進している遺伝子

No.	Gene Title	Gene Symbol	Chromosome	wilcox p v	diff
1	collagen, type I, alpha 1	COL1A1	17q21.33	6.66E-04	5.634157
2	collagen, type III, alpha 1 (Ehlers-Danlos syndrome)	COL3A1	2q31	6.66E-04	5.498635
3	collagen, type III, alpha 1 (Ehlers-Danlos syndrome)	COL3A1	2q31	6.66E-04	5.078031
4	TIMP metalloproteinase inhibitor 1	TIMP1	Xp11.3-p1	6.66E-04	4.944947
5	CD163 molecule	CD163	12p13.3	6.66E-04	4.807787
6	annexin A1	ANXA1	9q12-q21	6.66E-04	4.787225
7	collagen, type I, alpha 2	COL1A2	7q22.1	6.66E-04	4.751814
8	hypothetical protein LOC643911 /// hypothetical	LOC643911 ///	16q12.2	6.66E-04	4.733911
9	transmembrane protein 49	TMEM49	17q23.1	6.66E-04	4.709935
10	CD163 molecule	CD163	12p13.3	6.66E-04	4.67746
11	periostin, osteoblast specific factor	POSTN	13q13.3	6.66E-04	4.639798
12	collagen, type III, alpha 1 (Ehlers-Danlos syndrome)	COL3A1	2q31	6.66E-04	4.594704
13	tubulin, beta 6	TUBB6	18p11.21	6.66E-04	4.565739
14	collagen, type IV, alpha 1	COL4A1	13q34	6.66E-04	4.073254
15	collagen, type VI, alpha 3	COL6A3	2q37	6.66E-04	3.977168
16	major histocompatibility complex, class II, DQ alpha	HLA-DQA1 ///	6p21.3	6.66E-04	3.951178
17	collagen, type IV, alpha 2	COL4A2	13q34	6.66E-04	3.901004
18	Fc fragment of IgG binding protein	FCGBP	19q13.1	6.66E-04	3.872366
19	CD93 molecule	CD93	20p11.21	6.66E-04	3.845584
20	glycoprotein (transmembrane) nmb	GNPMB	7p15	6.66E-04	3.808801
21	membrane-spanning 4-domains, subfamily A, member 6	MS4A6A	11q12.1	6.66E-04	3.773399
22	complement component 1, s subcomponent	C1S	12p13	6.66E-04	3.686403
23	major histocompatibility complex, class II, DQ beta	HLA-DQB1	6p21.3	6.66E-04	3.667005
24	lysyl oxidase	LOX	5q23.2	6.66E-04	3.612316
25	collagen, type I, alpha 1	COL1A1	17q21.33	6.66E-04	3.57917
26	---	---	---	6.66E-04	3.521668
27	laminin, beta 1	LAMB1	7q22	6.66E-04	3.577764
28	annexin A2	ANXA2	15q21-q22	6.66E-04	3.562935
29	complement component 1, r subcomponent /// s	C1R /// LOC6	12p13 ///	6.66E-04	3.523544
30	vimentin	VIM	10p13	6.66E-04	3.497031
31	collagen, type IV, alpha 1	COL4A1	13q34	6.66E-04	3.483472
32	microRNA 21	MIRN21	---	6.66E-04	3.481886
33	CDNA FLJ31066 fis, clone HSYRA2001153	---	---	6.66E-04	3.430856
34	serpin peptidase inhibitor, clade G (C1 inhibitor), member 1	SERPING1	11q12-q13	6.66E-04	3.460302
35	complement factor I	CFI	4q25	6.66E-04	3.450166
36	major histocompatibility complex, class II, DR alpha	HLA-DRA	6p21.3	6.66E-04	3.439021
37	protease, serine, 23	PRSS23	11q14.1	6.66E-04	3.424038
38	protease, serine, 23	PRSS23	11q14.1	6.66E-04	3.396124
39	annexin A2	ANXA2	15q21-q22	6.66E-04	3.38666
40	membrane-spanning 4-domains, subfamily A, member 6	MS4A6A	11q12.1	6.66E-04	3.37902
41	---	---	---	6.66E-04	3.376174
42	major histocompatibility complex, class II, DP alpha	HLA-DPA1	6p21.3	6.66E-04	3.377836
43	annexin A2	ANXA2	15q21-q22	6.66E-04	3.373996
44	met proto-oncogene (hepatocyte growth factor receptor tyrosine kinase)	MET	7q31	6.66E-04	3.365789
45	macrophage scavenger receptor 1	MSR1	8p22	6.66E-04	3.364157
46	major histocompatibility complex, class II, DR alpha	HLA-DRA	6p21.3	6.66E-04	3.337739
47	collagen, type V, alpha 2	COL5A2	2q14-q32	6.66E-04	3.331375
48	major histocompatibility complex, class II, DR beta	HLA-DRB1	6p21.3	6.66E-04	3.314677
49	IQ motif containing GTPase activating protein 2	IQGAP2	5q13.3	6.66E-04	3.284303
50	major histocompatibility complex, class II, DP alpha	HLA-DPA1	6p21.3	6.66E-04	3.283839

8. Progression (DA grade 2→AA grade 3)で発現が抑制されている遺伝子

No.	Gene Title	Gene Symbol	Chromosome	wilcox p v	diff
1	follistatin-like 5	FSTL5	4q32.3	6.66E-04	-4.34699
2	HMP19 protein	HMP19	5q35.2	6.66E-04	-4.27151
3	RAS-related on chromosome 22	RRP22	22q12.2	6.66E-04	-4.1678
4	Hypothetical protein LOC650392	LOC650392	---	6.66E-04	-4.16011
5	delta-like 3 (Drosophila)	DLL3	19q13	6.66E-04	-4.12979
6	SRY (sex determining region Y)-box 8	SOX8	16p13.3	6.66E-04	-4.03937
7	zinc finger, MYND domain containing 11	ZMYND11	10p14	6.66E-04	-0.77226
8	CUB and Sushi multiple domains 1	CSMD1	8p23.2	6.66E-04	-3.81639
9	zinc finger, FYVE domain containing 20	ZFYVE20	3p24.3	6.66E-04	-0.89336
10	zinc finger protein 2 homolog (mouse)	ZFP2	5q35.3	6.66E-04	-0.7008
11	Full-length cDNA clone CS0DF015YK23 of Fetal	LOC650392	---	6.66E-04	-3.72698
12	CUB and Sushi multiple domains 3	CSMD3	8q23.3	6.66E-04	-3.7007
13	glutamate receptor, ionotropic, AMPA 2	GRIA2	4q32-q33	6.66E-04	-3.69904
14	YTH domain containing 1	YTHDC1	4q13.2	6.66E-04	-0.56738
15	yippee-like 1 (Drosophila)	YPEL1	22q11.2	6.66E-04	-0.78839
16	WW domain containing oxidoreductase	WFOX	16q23.3-q	6.66E-04	-0.9584
17	WIRE protein	WIRE	17q21.2	6.66E-04	-0.96267
18	WD repeat domain 71	WDR71	11q13.4	6.66E-04	-0.89461
19	WD repeat domain 48	WDR48	3p21.33	6.66E-04	-0.4365
20	glutamate receptor, ionotropic, AMPA 2	GRIA2	4q32-q33	6.66E-04	-3.65857
21	WD repeat and FYVE domain containing 3	WDFY3	4q21.23	6.66E-04	-0.8256
22	WW domain binding protein 4 (formin binding prot	WBP4	13q14.11	6.66E-04	-0.58254
23	WW domain containing adaptor with coiled-coil	WAC	---	6.66E-04	-0.78361
24	G protein-coupled receptor 98	GPR98	5q13	6.66E-04	-3.65683
25	ventricular zone expressed PH domain homolog	VEPH1	3q24-q25	6.66E-04	-0.73778
26	hypothetical protein LOC285878	LOC285878	7p11.2	6.66E-04	-3.64198
27	bruno-like 5, RNA binding protein (Drosophila)	BRUNOL5	19p13	6.66E-04	-3.63326
28	Ubiquitin specific peptidase 49	USP49	6p21	6.66E-04	-0.27421
29	gamma-aminobutyric acid (GABA) A receptor, be	GABRB3	15q11.2-q	6.66E-04	-3.62567
30	Ubiquitin specific peptidase 27, X-linked	USP27X	Xp11.23	6.66E-04	-0.82271
31	ELAV (embryonic lethal, abnormal vision, Drosop	ELAVL2	9p21	6.66E-04	-3.52787
32	similar to RIKEN cDNA D630023F18	LOC389073	2q33.3	6.66E-04	-3.52674
33	Family with sequence similarity 77, member D	FAM77D	8q12.3	6.66E-04	-3.47572
34	ubiquitin-like 3	UBL3	13q12-q13	6.66E-04	-0.99881
35	hypothetical protein DKFZp761N09121	DKFZP761N09	---	6.66E-04	-3.46678
36	gamma-aminobutyric acid (GABA) A receptor, be	GABRB3	15q11.2-q	6.66E-04	-3.44079
37	tetratricopeptide repeat domain 3	TTC3	21q22.2	6.66E-04	-0.99385
38	tetratricopeptide repeat domain 3	TTC3	21q22.2	6.66E-04	-0.95766
39	tetratricopeptide repeat domain 3	TTC3	21q22.2	6.66E-04	-0.87211
40	Tau tubulin kinase 2	TTBK2	15q15.2	6.66E-04	-0.95699
41	chondroitin sulfate proteoglycan 5 (neuroglycan	CSPG5	3p21.3	6.66E-04	-3.43972
42	SH3 and multiple ankyrin repeat domains 2	SHANK2	11q13.3	6.66E-04	-3.42607
43	T-SNARE domain containing 1	TSNARE1	8q24.3	6.66E-04	-0.43315
44	transient receptor potential cation channel, subfa	TRPV1	17p13.3	6.66E-04	-0.43737
45	chromosome 20 open reading frame 42	C20orf42	20p12.3	6.66E-04	-3.41918
46	seizure related 6 homolog (mouse)-like	SEZ6L	22q12.1	6.66E-04	-3.41509
47	target of myb1-like 2 (chicken)	TOM1L2	17p11.2	6.66E-04	-0.97331
48	trinucleotide repeat containing 6B	TNRC6B	22q13.1	6.66E-04	-0.83262
49	trinucleotide repeat containing 4	TNRC4	1q21	6.66E-04	-0.86299
50	Homo sapiens, clone IMAGE:4915189, mRNA	---	---	6.66E-04	-3.4024

9. 生存期間(20ヶ月)が短いGBMで亢進している遺伝子

No.	Gene Title	Gene Symbol	Chromosome	wilcox p v	diff
1	hypothetical protein LOC643911 /// hypothetical	LOC643911 ///	16q12.2	6.38E-03	2.409594
2	metastasis associated lung adenocarcinoma tran	MALAT1	11q13.1	4.60E-03	2.130363
3	phosphoserine phosphatase	PSPH	7p15.2-p1	7.04E-03	1.888289
4	v-jun sarcoma virus 17 oncogene homolog (avian	JUN	1p32-p31	7.77E-04	1.829345
5	serpin peptidase inhibitor, clade A (alpha-1 anti	SERPINA3	14q32.1	5.24E-03	1.783477
6	hypothetical protein LOC643911 /// hypothetical	LOC643911 ///	16q12.2	1.72E-03	1.761823
7	S100 calcium binding protein A10 (annexin II ligar	S100A10	1q21	1.61E-03	1.608952
8	podoplanin	PDPN	1p36.21	4.05E-03	1.545221
9	S100 calcium binding protein A10 (annexin II ligar	S100A10	1q21	6.61E-03	1.467719
10	spen homolog, transcriptional regulator (Drosoph	SPEN	1p36.33-p	4.16E-03	1.27326
11	cysteine and glycine-rich protein 2	CSRP2	12q21.1	4.74E-03	1.265945
12	carbonic anhydrase XII	CA12	15q22	8.90E-03	1.24388
13	filamin C, gamma (actin binding protein 280)	FLNC	7q32-q35	9.44E-03	1.24313
14	nestin	NES	1q23.1	4.51E-03	1.23246
15	cysteine and glycine-rich protein 2	CSRP2	12q21.1	2.88E-03	1.192913
16	neuromedin B	NMB	15q22-qte	4.54E-03	1.185047
17	ATPase type 13A3	ATP13A3	3q29	9.59E-03	1.136739
18	POU domain, class 3, transcription factor 2	POU3F2	6q16	2.64E-03	1.136572
19	villin 2 (ezrin)	VIL2	6q25.2-q2	7.91E-03	1.124742
20	WAS protein family, member 2	WASF2	1p36.11-p	3.44E-03	1.103929
21	Transcribed locus	---	---	2.33E-03	1.097479
22	villin 2 (ezrin)	VIL2	6q25.2-q2	5.71E-03	1.079397
23	EF-hand domain family, member B	EFHB	3p24.3	3.35E-03	1.061082
24	Similar to peptidylglycine alpha-amidating monoo	LOC644943	11p15.2	7.40E-03	1.059073
25	nucleolar protein 3 (apoptosis repressor with CA	NOL3	16q21-q23	1.34E-03	1.043765
26	---	---	---	9.15E-03	1.037663
27	leucyl-tRNA synthetase	LARS	5q32	1.18E-03	1.036676
28	glucosaminyl (N-acetyl) transferase 2, I-branchin	GCNT2	6p24	1.18E-03	1.022585
29	zinc finger protein 395	ZNF395	8p21.1	2.01E-03	1.019353
30	palladin, cytoskeletal associated protein	PALLD	4q32.3	6.55E-03	1.007006
31	translocated promoter region (to activated MET	TPR	1q25	1.69E-03	0.996985
32	TAF9B RNA polymerase II, TATA box binding pro	TAF9B	Xq13.1-q2	8.77E-03	0.995809
33	histone 1, H1c	HIST1H1C	6p21.3	7.35E-03	0.987186
34	retinoblastoma-like 2 (p130)	RBL2	16q12.2	5.60E-03	0.982723
35	insulin-like growth factor 2 receptor	IGF2R	6q26	3.10E-03	0.974315
36	zinc finger protein 395 /// F-box protein 16	ZNF395 /// F	8p21.1	1.96E-03	0.941097
37	restin (Reed-Steinberg cell-expressed intermed	RSN	12q24.3	5.55E-03	0.935
38	translocated promoter region (to activated MET	TPR	1q25	1.20E-03	0.932091
39	MRNA; cDNA DKFZp586K1922 (from clone DKF2	---	---	7.79E-03	0.920258
40	nucleolar protein 3 (apoptosis repressor with CA	NOL3	16q21-q23	7.16E-04	0.914218
41	peroxiredoxin 4	PRDX4	Xp22.11	7.17E-03	0.912667
42	---	---	---	1.08E-03	0.910568
43	contactin associated protein-like 3B /// similar	CNTNAP3B ///	9p11.2 ///	4.25E-03	0.908434
44	---	---	---	5.50E-03	0.898087
45	nudix (nucleoside diphosphate linked moiety X)-t	NUDT4 /// NU	12q21 ///	2.64E-04	0.895218
46	apolipoprotein C-I	APOC1	19q13.2	8.36E-03	0.890502
47	HIV-1 Tat specific factor 1	HTATSF1	Xq26.1-q2	8.59E-03	0.881304
48	nucleolar protein 3 (apoptosis repressor with CA	NOL3	16q21-q23	1.98E-03	0.856496
49	TBC1 domain family, member 22A	TBC1D22A	22q13.3	7.90E-04	0.855316
50	zinc finger protein 395 /// F-box protein 16	ZNF395 /// F	8p21.1	3.78E-03	0.839738

10. 生存期間(20ヶ月)が短いGBMで抑制されている遺伝子

No.	Gene Title	Gene Symbol	Chromosome	wilcox p value	diff
1	coiled-coil domain containing 67	CCDC67	11q21	2.48E-03	-0.09897
2	Low density lipoprotein receptor-related protein	LRP5L	22q11.23	7.22E-03	-0.10363
3	----	----	----	9.56E-03	-0.11193
4	tousled-like kinase 2	TLK2	17q23	9.19E-03	-0.11379
5	Homo sapiens, clone IMAGE:4106638	----	----	5.47E-03	-0.11437
6	sperm adhesion molecule 1 (PH-20 hyaluronidas	SPAM1	7q31.3	8.46E-03	-0.11755
7	RNA binding motif protein, Y-linked, family 2, me	RBMV2FP	Yq11.223	3.25E-03	-0.11896
8	hypothetical LOC203413	RP3-452H17.2	Xq23	8.97E-03	-0.12135
9	leucine rich repeat containing 38	LRRC38	1p36.21	3.00E-03	-0.12217
10	----	----	----	3.40E-04	-0.12279
11	similar to IQ motif containing F1	LOC389124	3p21.1	7.23E-03	-0.12295
12	Fraser syndrome 1	FRAS1	4q21.21	4.79E-04	-0.12343
13	CDNA clone IMAGE:4819376	----	----	1.82E-03	-0.12605
14	Growth arrest and DNA-damage-inducible, gamma	GADD45GIP1	19p13.13	8.39E-03	-0.12692
15	chloride channel, calcium activated, family memb	CLCA2	1p31-p22	2.83E-03	-0.12737
16	Chromosome 9 open reading frame 5	C9orf5	9q31	8.40E-03	-0.1279
17	LY6/PLAUR domain containing 4	LYPD4	19q13.2	8.11E-03	-0.13037
18	CDNA clone IMAGE:5267328	----	----	8.83E-03	-0.13536
19	Transcribed locus	----	----	9.77E-03	-0.13742
20	chromosome 20 open reading frame 186	C20orf186	20q11.21	5.60E-03	-0.13811
21	phosphodiesterase 1A, calmodulin-dependent	PDE1A	2q32.1	5.91E-03	-0.14093
22	CDNA clone IMAGE:5297258	----	----	7.28E-04	-0.14197
23	cytochrome P450, family 1, subfamily A, polypept	CYP1A1	15q22-q24	9.84E-03	-0.14445
24	olfactory receptor, family 2, subfamily A, member	OR2A20P ///	7q35	7.86E-03	-0.14667
25	----	----	----	1.17E-03	-0.14757
26	5-hydroxytryptamine (serotonin) receptor 3A	HTR3A	11q23.1	3.90E-03	-0.14843
27	cutaneous T-cell lymphoma-associated antigen	CTAGE1	18p11.2	4.26E-03	-0.14843
28	solute carrier family 6 (neurotransmitter transpor	SLC6A2	16q12.2	2.41E-04	-0.15185
29	CD8b molecule	CD8B	2p12	6.60E-03	-0.15338
30	Hepsin (transmembrane protease, serine 1)	HPN	19q11-q13	8.18E-03	-0.15341
31	replication initiator 1	REPIN1	7q36.1	5.03E-04	-0.154
32	chromosome 3 open reading frame 49	C3orf49	3p14.1	1.99E-03	-0.15464
33	snail homolog 3 (Drosophila)	SNAI3	16q24.3	9.00E-03	-0.15514
34	pleckstrin homology-like domain, family B, memb	PHLDB1	11q23.3	9.63E-03	-0.15521
35	glycoprotein hormone beta 5	GPHB5	14q23.2	9.36E-03	-0.15528
36	----	----	----	7.72E-03	-0.1571
37	integrin, alpha 2b (platelet glycoprotein IIb of IIb/	ITGA2B	17q21.32	4.99E-03	-0.15795
38	plakophilin 1 (ectodermal dysplasia/skin fragility	PKP1	1q32	7.78E-03	-0.16219
39	sperm associated antigen 11	SPAG11	8p23-p22	8.01E-03	-0.16323
40	Microtubule-actin crosslinking factor 1	MACF1	1p32-p31	6.64E-03	-0.16433
41	CDNA clone IMAGE:4838157	----	----	6.16E-03	-0.16586
42	phospholipase C-like 2	PLCL2	3p24.3	2.06E-03	-0.1674
43	WD repeat domain 62	WDR62	19q13.12	9.48E-03	-0.16914
44	hypothetical LOC440731	LOC440731	1q42.2	9.14E-03	-0.17203
45	cyclin N-terminal domain containing 2	CNTD2	19q13.2	4.56E-03	-0.17223
46	CD300 molecule-like family member g	CD300LG	17q21.31	9.59E-03	-0.17293
47	chromosome 20 open reading frame 62	C20orf62	20q13.12	3.17E-04	-0.17302
48	Cell division cycle and apoptosis regulator 1	CCAR1	10q21.3	6.37E-03	-0.17358
49	Transcribed locus	----	----	3.87E-03	-0.17452
50	TAF1 RNA polymerase II, TATA box binding prot	TAF1	Xq13.1	2.95E-03	-0.17462

12. 再発までの期間(6ヶ月)が短いGBMで抑制されている遺伝子

No.	Gene Title	Gene Symbol	Chromosome	wilcox p v	diff
1	GALK2	galactose meta	15q21.1	7.33E-03	-0.08076
2	----	----	----	1.49E-03	-0.08671
3	RNF43	ubiquitin cycle	17q22	5.65E-03	-0.08683
4	FCRL1	----	1q21-q22	9.42E-03	-0.08888
5	RAB3IP	protein transp	12q14.3	8.79E-03	-0.10089
6	----	----	----	4.01E-03	-0.10578
7	SCGB2A2	----	11q13	4.26E-04	-0.10708
8	----	----	----	5.62E-03	-0.11058
9	GRHL2	----	8q22.3	9.81E-03	-0.11333
10	TRA@	cellular defens	14q11.2	7.39E-03	-0.11337
11	KRTAP4-4	----	17q12-q21	8.01E-03	-0.11431
12	MUSK	protein amino	9q31.3-q3	8.74E-03	-0.11803
13	ABCA1	lipid metabolis	9q31.1	2.88E-03	-0.11849
14	RP11-647M7.1	----	Xq22.3	9.24E-03	-0.11853
15	NSUN3	----	3q11.2	5.28E-03	-0.1219
16	AGTR2	apoptosis ///	Xq22-q23	3.00E-03	-0.12292
17	NHSL1	----	6q23.3	2.81E-03	-0.12492
18	HTR2C	signal transduc	Xq24	3.51E-03	-0.1287
19	C6orf78	----	6q22.1	5.57E-03	-0.12874
20	RNH1 /// FLJ23519	RNA catabolis	11p15.5	1.05E-03	-0.13316
21	----	----	----	2.30E-03	-0.14423
22	UBE2U	ubiquitin cycle	1p31.3	9.96E-03	-0.145
23	C9orf5	----	9q31	2.41E-03	-0.14999
24	MGC32805	----	5q23.2	3.26E-03	-0.15159
25	C11orf54	----	11q21	9.98E-03	-0.15256
26	ARMCX4	----	Xq22.1	8.36E-03	-0.15582
27	LCE1E	----	1q21.3	1.57E-03	-0.15624
28	----	----	----	3.62E-05	-0.15824
29	OR2A20P /// OR2A9P	signal transduc	7q35	1.56E-03	-0.15977
30	CTSE	proteolysis ///	1q31	1.68E-03	-0.16033
31	PLGLB2 /// PLGLB1 /// PLGLA1	----	2p11-q11	4.28E-03	-0.16091
32	MFSD1	transport	3q25.33	2.91E-03	-0.16444
33	DDX51	----	12q24.33	6.53E-03	-0.16574
34	----	----	----	6.90E-03	-0.16803
35	TRIM3	nervous system	11p15.5	5.78E-03	-0.17578
36	----	----	----	6.40E-03	-0.1789
37	----	----	----	8.52E-04	-0.18105
38	TBC1D5	----	3p24.3	6.79E-03	-0.18522
39	CSNK2A1	protein amino	20p13	7.70E-03	-0.19038
40	ZBTB10	transcription /	8q13-q21	6.83E-03	-0.19253
41	UBE2O	ubiquitin cycle	17q25.1	3.60E-03	-0.19276
42	C10orf93	----	10q26.3	5.16E-03	-0.19586
43	SSH2	protein amino	17q11.2	3.76E-03	-0.19726
44	C12orf47	----	12q24.12	5.19E-03	-0.20144
45	SLC4A5	anion transport	2p13	7.51E-03	-0.20714
46	----	----	----	3.39E-03	-0.22033
47	KIAA1303	----	17q25.3	4.62E-03	-0.22628
48	MAS1	signal transduc	6q25.3-q2	4.90E-03	-0.23196
49	KTN1	microtubule-ba	14q22.1	6.69E-03	-0.23278
50	PAIP2 /// LOC153095	regulation of tr	5q31.2 ///	5.23E-04	-0.23534