Table S1. Copy number abberations (CNA) detected by array comparative genomic hybridization.

Case	Chromosomal location	Loc. Start*	Loc. Stop*	CNA**
Case 1	**3p26.3 - q29 (whole chromosome)**	**93949**	**197845254**	**Gain (0.320935)**
	4q13.2	69223075	69462438	Homozygous deletion (-1.51678)
	6p22.1	29854870	29896710	Gain (2.735431)
	7p22.3 - q36.3 (whole chromosome)	**42976**	**159118566**	**Gain (0.565555)**
	9p24.3 - p13.1 (whole arm)	**204193**	**38768291**	**Gain (0.308436)**
	9p21.3	21944037	22176231	Homozygous deletion (-1.382063)
	9q21.11 - q34.3 (whole arm)	**71151735**	**141018984**	**Gain (0.367163)**
	10p15.3 - q26.3 (whole chromosome)	136361	135089504	Heterozygous deletion (-0.350396)
	13q12.11 - q34 (whole arm)	**19526064**	**115089535**	**Gain (0.313476)**
	18q11.2 - q12.3	19004109	40832816	Heterozygous deletion (-0.327937)
	18q12.3 - q23	**41143464**	**78010032**	**Gain (0.317707)**
	20p13 - q13.33 (whole chromosome)	121521	62880583	Gain (0.330833)
	21q11.2 - q22.3 (whole arm)	15372467	48090317	Gain (0.558608)
Case 2	**1p36.33 - p36.23**	**759762**	**8749497**	**Heterozygous deletion (-0.402625)**
	1p35.3	**28266522**	**29653134**	**Heterozygous deletion (-0.302864)**
	1p34.2 - p22.2	**40288246**	**91311655**	**Heterozygous deletion (-0.279675)**
	1q32.2 - q42.2	**209342761**	**230753927**	**Heterozygous deletion (-0.371906)**
	2p25.3 - p11.2 (whole arm)	**42444**	**89538874**	**Gain (0.345952)**
	2q11.1 - q22.2	**95529039**	**142709232**	**Gain (0.347157)**
	3q24 - q26.2	**145644746**	**169235435**	**Gain (0.362882)**
	4q31.21 - q35.2	**142663747**	**190790881**	**Heterozygous deletion (-0.380461)**
	6p25.3 - p11.2	**389423**	**58435710**	**Heterozygou deletion (-0.317938)**
	6q11.1 - q22.33	**61982931**	**127407686**	**Heterozygous deletion (-0.377149)**
	6q23.3 - q24.1	**138476510**	**142468952**	**Heterozygous deletion (-0.371592)**
	7q33 - q36.3	**135250552**	**159118566**	**Gain (0.593265)**
	8p23.3 - p11.1 (whole arm)	**219683**	**43396776**	**Heterozygous deletion (-0.365243)**
	8q11.21 - q12.3	**49091300**	**62336764**	**Heterozygous deletion (-0.404825)**
	8q13.3	**71238938**	**72406658**	**Heterozygous deletion (-0.42469)**
	8q13.3 - q24.3	**73125197**	**146085532**	**Heterozygous deletion (-0.372239)**
	9p22.1 - p21.2	19564273	26162174	Heterozygous deletion (-0.750144)
	9p21.3	21036673	22733971	Homozygous deletion (-1.333769)
	9q21.13 - q31.3	79086651	112617941	Gain (0.548115)
	11q14.1 - q14.3	**81732787**	**90039085**	**Gain (0.335935)**
	13q11 - q34 (whole arm)	**19296544**	**115096466**	**Heterozygous deletion (-0.374167)**
	16q22.2 - q23.1	**71913790**	**75360302**	**Heterozygous deletion (-0.283991)**
	16q23.2 - q24.3	**79225966**	**89977030**	**Heterozygous deletion (-0.389361)**
	17p13.3 - p11.2 (whole arm)	**76263**	**22154574**	**Heterozygous deletion (-0.349955)**
	17q11.1 - q11.2	**25435421**	**30348467**	**Heterozygous deletion (-0.324576)**
	17q21.2 - q21.31	**40318960**	**42940605**	**Heterozygous deletion (-0.311494)**
	17q21.31 - q25.1	**42962663**	**72659034**	**Gain (0.828081)**
	18p11.32 - q23 (whole chromosome)	**162510**	**78010032**	**Heterozygous deletion (-0.354022)**
	22q12.1 - q13.33	**27099649**	**51219009**	**Gain (0.396596)**
Case 3	**6q11.1 - q27**	**62305272**	**166262838**	**Heterozygous deletion (-0.268362)**
	7p22.3 - q36.3 (whole chromosome)	**65558**	**159118566**	**Gain (0.547574)**
	8p11.22	39237438	39374789	Homozygous deletion (-1.165137)
	9p22.3	**15086757**	**15920360**	**Heterozygous deletion (-0.300928)**
	9p21.3	**21454717**	**22212612**	**Homozygous deletion (-1.268826)**
	21q11.2 - q22.3 (whole arm)	**14420615**	**48090317**	**Gain (0.29937)**
	22q11.23	24347959	24390254	Homozygous deletion (-1.52085)
Case 4	5p15.33 - q35.3 (whole chromosome)	26142	180684501	Gain (0.429411)
	6p22.1	29854870	29896710	Gain (2.672552)
	7p22.3 - q36.3 (whole chromosome)	42976	159118566	Gain (0.439458)
	8p11.22	39237438	39374789	Homozygous deletion (-1.238193)
	9p21.3	21957735	22017397	Homozygous deletion (-1.342227)
	10p15.3 - p11.1(whole arm)	148206	39076591	Heterozygous deletion (-0.549255)
	10q11.21 - q26.3 (whole arm)	**42864620**	**133956779**	**Heterozygous deletion (-0.536525)**
	13q12.11 - q34 (whole arm)	19526064	115089535	Gain (0.775586)
	17p13.3 - p11.2 (whole arm)	**96559**	**22154574**	**Gain (0.339977)**
	17q11.1 - q25.3 (whole arm)	25403446	81062925	Gain (0.420042)
	19q13.12 - q13.13	**37349894**	**38698864**	**Heterozygous deletion (-0.308813)**
	20p13 - q13.33 (whole chromosome)	151549	62904501	Gain (0.356953)
Case 5	**2q22.1**	**141928411**	**142036954**	**Heterozygous deletion (-0.815427)**
	3q13.31	**115593958**	**115644733**	**Homozygous deletion (-1.991462)**
	3q26.1	162514534	162619141	Homozygous deletion (-1.849218)
	4q13.2	69392545	69462438	Homozygous deletion (-1.831354)
	4q34.3 - q35.1	**182902844**	**183568174**	**Heterozygous deletion (-0.61287)**
	6p22.1	29854870	29896710	Homozygous deletion (-1.236831)
	8p11.22	39237438	39345479	Gain (0.671442)
	9p21.3	21944037	22176231	Homozygous deletion (-1.62978)
	15q11.1-q11.2	20575646	21933378	Gain (0.937772)
	20p12.1	14903016	15015311	Heterozygous deletion (-0.880196)
	22q11.23	24347959	24390254	Homozygous deletion (-1.449985)

CNA detected only in the epithelioid glioblastoma area are shown in **bold**.
CNA detected both in the epithelioid glioblastoma and lower-grade glioma areas are not in bold.
Loc., location on chromosome.
*Genome mapping based on genome build hg19.
**The numbers in parentheses are the average log2 ratio of each aberration.