Molecular classification of diffuse cerebral WHO grade II/III gliomas using genome- and transcriptome-wide profiling improves stratification of prognostically distinct patient groups

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SUPPLEMENTARY TABLES

Supplementary Table 1. *Individual patient characteristics: diagnosis, molecular markers, first-line treatment, and outcome.*

Patient	**Age**	**Gender**	**Diagnosis**	***IDH1/2* mutation**	**1p/19q co-deletion**	***MGMT* promoter methylation**	***TERT* promoter mutation**	**First-line therapy**	**PD**	**PFS [years]**	**OS [years]**
P1	37	M	AII	mut	del	strong	mut	no therapy	yes	7.9	9.6
P2	54	F	AII	mut	del	strong	mut	no therapy	yes	5.4	6.1
P3	47	M	AII	mut	del	strong	mut	no therapy	no	-	3.9
P4	54	F	AII	mut	del	strong	mut	CT	no	-	2.7
P5	39	M	AII	mut	no del	strong	wt	no therapy	yes	11.7	17.7
P6	33	M	AII	mut	no del	strong	wt	no therapy	yes	12.6	14.1
P7	24	M	AII	mut	no del	strong	n.d.	no therapy	yes	6.2	12.1
P8	25	F	AII	mut	no del	strong	wt	no therapy	yes	9.1	12.0
P9	35	M	AII	mut	no del	strong	wt	no therapy	yes	5.9	11.4 +
P10	47	M	AII	mut	no del	strong	wt	no therapy	yes	8.4	9.0 +
P11	37	F	AII	mut	no del	strong	wt	no therapy	yes	6.1	8.1
P12	40	F	AII	mut	no del	strong	wt	no therapy	yes	3.4	6.7
P13	31	M	AII	mut	no del	strong	wt	no therapy	yes	5.6	6.6 +
P14	44	M	AII	mut	no del	strong	wt	no therapy	yes	2.2	5.9
P15	36	M	AII	mut	no del	strong	wt	no therapy	yes	5.6	5.6
P16	36	F	AII	mut	no del	strong	wt	no therapy	yes	1.0	5.3
P17	30	M	AII	mut	no del	strong	wt	no therapy	yes	3.0	4.5
P18	43	M	AII	mut	no del	strong	wt	no therapy	yes	1.9	4.2 +
P19	43	M	AII	mut	no del	strong	wt	no therapy	no	-	3.6
P20	35	M	AII	mut	no del	strong	wt	no therapy	yes	3.2	3.6
P21	44	M	AII	mut	no del	strong	wt	no therapy	yes	2.3	3.5
P22	41	F	AII	mut	no del	strong	wt	no therapy	yes	2.4	3.4 +
P23	42	M	AII	mut	no del	strong	n.d.	no therapy	yes	2.2	3.3 +
P24	40	M	AII	mut	no del	strong	wt	no therapy	no	-	3.1

P25	31	M	AII	mut	no del	strong	wt	RT	yes	1.0	2.9 +
P26	47	M	AII	mut	no del	strong	wt	no therapy	yes	2.0	2.2 +
P27	41	M	AII	mut	no del	strong	wt	no therapy	no	-	1.7
P28	50	M	AII	mut	no del	strong	wt	no therapy	yes	0.5	1.0 +
P29	38	F	AII	mut	no del	weak	wt	no therapy	yes	1.2	6.6
P30	21	F	AII	mut	no del	weak	wt	no therapy	yes	1.0	5.7
P31	30	M	AII	mut	no del	weak	wt	no therapy	yes	2.2	4.8
P32	26	M	AII	mut	no del	weak	wt	no therapy	yes	2.9	3.7
P33	29	M	AII	mut	no del	weak	wt	no therapy	yes	1.2	1.2 +
P34	50	M	AII	mut	no del	no	wt	RT plus CT	yes	10.2	12.6 +
P35	28	F	AII	mut	no del	no	wt	no therapy	yes	5.8	6.3
P36	36	M	AII	mut	no del	no	wt	no therapy	yes	0.2	3.9
P37	23	M	AII	mut	no del	no	wt	no therapy	no	-	3.1
P38	35	F	AII	mut	no del	no	wt	no therapy	no	-	2.9
P39	38	M	AII	mut	no del	no	wt	no therapy	no	-	0.6
P40	67	F	AII	wt	no del	strong	mut	no therapy	yes	2.3	3.0 +
P41	41	F	AII	wt	no del	no	wt	no therapy	yes	3.3	9.1 +
P42	54	F	AII	wt	no del	no	wt	no therapy	yes	2.2	3.4 +
P43	47	M	AII	wt	no del	no	wt	no therapy	yes	1.4	2.2 +
P44	28	F	AII	mut	no del	no	wt	no therapy	yes	0.4	3.7 +
P45	35	F	AII	mut	no del	n.d.	wt	other	yes	1.7	1.7
P46	47	M	OAII	mut	del	strong	mut	no therapy	no	-	7.4
P47	41	M	OAII	mut	del	strong	mut	no therapy	yes	2.5	6.2
P48	43	F	OAII	mut	del	strong	mut	no therapy	yes	3.6	5.1
P49	40	F	OAII	mut	del	strong	mut	no therapy	no	-	3.9
P50	33	M	OAII	mut	del	strong	mut	no therapy	no	-	1.0
P51	59	M	OAII	mut	del	no	mut	no therapy	no	-	7.5
P52	56	M	OAII	mut	no del	strong	wt	no therapy	yes	7.5	7.5
P53	30	F	OAII	mut	no del	strong	wt	no therapy	yes	2.6	7.1
P54	24	M	OAII	mut	no del	strong	wt	no therapy	no	-	6.6
P55	44	F	OAII	mut	no del	strong	wt	no therapy	yes	5.5	6.1 +

P56	59	M	OAII	mut	no del	strong	wt	no therapy	no	-	4.4
P57	30	M	OAII	mut	no del	strong	wt	no therapy	yes	2.0	3.2 +
P58	39	F	OAII	wt	no del	strong	wt	CT	yes	7.3	8.1
P59	36	M	OII	mut	del	strong	mut	no therapy	yes	0.9	9.1
P60	39	F	OII	mut	del	strong	mut	no therapy	yes	1.8	5.8
P61	49	M	OII	mut	del	weak	mut	no therapy	no	-	3.1
P62	40	F	AAIII	mut	del	strong	mut	RT plus CT	yes	1.2	8.3
P63	74	M	AAIII	mut	del	strong	mut	RT plus CT	yes	2.4	5.0
P64	52	M	AAIII	mut	no del	strong	wt	RT plus CT	yes	1.3	8.8 +
P65	49	F	AAIII	mut	no del	strong	wt	RT	no	-	8.0
P66	33	F	AAIII	mut	no del	strong	wt	RT plus CT	no	-	7.4
P67	39	M	AAIII	mut	no del	strong	wt	RT plus CT	yes	7.3	7.3
P68	29	F	AAIII	mut	no del	strong	wt	RT	yes	4.9	7.3 +
P69	32	M	AAIII	mut	no del	strong	wt	RT plus CT	yes	0.7	6.4
P70	48	M	AAIII	mut	no del	strong	wt	no therapy	no	-	5.7
P71	27	F	AAIII	mut	no del	strong	wt	RT plus CT	no	-	5.4
P72	50	F	AAIII	mut	no del	strong	wt	RT plus CT	no	-	5.1
P73	30	F	AAIII	mut	no del	strong	wt	no therapy	yes	2.8	4.9
P74	34	M	AAIII	mut	no del	strong	wt	no therapy	yes	0.2	4.9
P75	23	F	AAIII	mut	no del	strong	wt	RT	no	-	4.1
P76	30	M	AAIII	mut	no del	strong	wt	RT	yes	2.6	4.1 +
P77	39	M	AAIII	mut	no del	strong	wt	RT plus CT	yes	0.4	4.0 +
P78	51	M	AAIII	mut	no del	strong	wt	RT plus CT	yes	2.5	3.9 +
P79	24	M	AAIII	mut	no del	strong	wt	CT	yes	0.2	3.3
P80	23	F	AAIII	mut	no del	strong	wt	CT	yes	0.7	3.3
P81	29	M	AAIII	mut	no del	strong	wt	CT	no	-	3.0
P82	25	F	AAIII	mut	no del	strong	wt	RT	yes	1.3	2.4 +
P83	64	M	AAIII	mut	no del	strong	wt	RT plus CT	yes	0.6	2.2 +
P84	66	M	AAIII	mut	no del	strong	wt	RT	no	-	2.0
P85	61	M	AAIII	mut	no del	strong	wt	RT	yes	0.7	1.5 +
P86	37	M	AAIII	mut	no del	weak	wt	RT plus CT	no	-	5.4

P87	28	M	AAIII	mut	no del	weak	mut	RT plus CT	no	-	3.4
P88	21	M	AAIII	mut	no del	no	wt	no therapy	yes	1.7	7.2
P89	55	F	AAIII	wt	no del	strong	mut	RT plus CT	yes	1.5	2.4 +
P90	66	F	AAIII	wt	no del	strong	n.d.	RT	yes	0.5	1.4 +
P91	55	F	AAIII	wt	no del	strong	mut	RT plus CT	yes	0.5	1.2
P92	49	M	AAIII	wt	no del	strong	wt	RT	no	-	0.1 +
P93	29	M	AAIII	wt	no del	weak	wt	RT	yes	4.1	5.8
P94	50	M	AAIII	wt	no del	weak	wt	RT plus CT	yes	1.9	2.7 +
P95	46	M	AAIII	wt	no del	no	wt	no therapy	yes	5.9	11.0
P96	44	M	AAIII	wt	no del	no	mut	RT plus CT	yes	8.0	9.7
P97	61	M	AAIII	wt	no del	no	mut	RT plus CT	yes	1.6	2.4 +
P98	72	F	AAIII	wt	no del	no	wt	RT plus CT	yes	1.1	1.8 +
P99	45	M	AAIII	wt	no del	no	mut	RT plus CT	yes	0.6	1.6 +
P100	65	F	AAIII	wt	no del	no	mut	RT	yes	0.8	1.2 +
P101	64	F	AAIII	wt	no del	no	mut	RT plus CT	yes	0.8	1.0 +
P102	55	M	AAIII	wt	no del	no	mut	RT	yes	0.8	0.8 +
P103	47	F	AAIII	wt	no del	no	wt	no therapy	no	-	0.0 +
P104	63	F	AOAIII	mut	del	strong	mut	RT	no	2.3	4.6
P105	33	M	AOAIII	mut	del	strong	wt	RT plus CT	no	-	6.9
P106	41	M	AOAIII	mut	del	strong	mut	RT	no	4.4-	6.7
P107	57	M	AOAIII	mut	del	strong	mut	RT plus CT	yes	4.7	6.5 +
P108	46	M	AOAIII	mut	del	strong	mut	RT plus CT	no	-	6.4
P109	45	F	AOAIII	mut	del	strong	n.d.	RT plus CT	no	-	6.4
P110	45	F	AOAIII	mut	del	strong	mut	RT	yes	5.9	5.9
P111	60	F	AOAIII	mut	del	strong	mut	RT	yes	5.9	5.9
P112	38	M	AOAIII	mut	del	strong	mut	CT	yes	5.1	5.1
P113	65	M	AOAIII	mut	del	strong	mut	RT plus CT	yes	1.4	4.9
P114	35	M	AOAIII	mut	del	strong	mut	CT	yes	2.7	4.5
P115	51	F	AOAIII	mut	del	strong	mut	RT	yes	2.8	4.4 +
P116	49	F	AOAIII	mut	del	strong	mut	CT	no	-	4.4
P117	32	M	AOAIII	mut	del	strong	wt	CT	no	-	3.9

P118	68	M	AOAIII	mut	del	strong	mut	RT	no	-	2.3 +
P119	68	M	AOAIII	mut	del	strong	mut	RT	yes	1.3	1.3 +
P120	37	M	AOAIII	mut	del	strong	mut	RT plus CT	no	-	0.6
P121	54	M	AOAIII	mut	del	strong	mut	no therapy	yes	0.1	0.1 +
P122	40	F	AOAIII	mut	del	weak	mut	RT plus CT	no	-	9.6
P123	27	M	AOAIII	mut	del	weak	mut	RT plus CT	no	-	6.8
P124	35	M	AOAIII	mut	no del	strong	wt	RT plus CT	yes	7.0	7.0
P125	50	M	AOAIII	mut	no del	strong	wt	CT	yes	5.0	6.6
P126	68	F	AOAIII	mut	no del	strong	wt	no therapy	yes	4.2	4.4 +
P127	34	M	AOAIII	mut	no del	strong	wt	RT plus CT	yes	0.7	3.6 +
P128	52	M	AOAIII	mut	no del	strong	wt	no therapy	no	-	3.6
P129	80	M	AOAIII	mut	no del	strong	wt	CT	no	-	2.8 +
P130	41	F	AOAIII	mut	no del	strong	wt	RT plus CT	no	-	1.2
P131	51	M	AOAIII	mut	no del	weak	mut	RT plus CT	yes	3.6	4.0 +
P132	60	M	AOAIII	mut	no del	no	wt	RT plus CT	yes	3.7	3.7 +
P133	26	F	AOAIII	mut	no del	no	wt	no therapy	no	-	1.7
P134	40	F	AOAIII	wt	no del	no	wt	RT	no	-	8.4
P135	47	F	AOIII	mut	del	strong	mut	RT plus CT	no	-	7.2
P136	64	F	AOIII	mut	del	strong	wt	RT	no	-	4.7
P137	45	F	AOIII	wt	no del	no	mut	CT	yes	1.5	6.3

n.d., no data; no del, no deletion; M, male; F, female; mut, mutant; wt, wild-type; RT, radiotherapy; CT, chemotherapy; PD, progressive disease; PFS, progression-free survival; OS, overall survival; + indicates patients who are deceased. 41 of 47 deceased patients were confirmed to have died of tumor progression. For the other 6 patients, diagnoses and survival times were as follows: AII (n=2, P25, 2.9 and P28, 1 year), AAIII (n=2, P98, 1.8 and P103, 8 days), AOAIII (n=2, P118, 2.3 and P126, 4.4 years). Five patients were reported to have died from tumor progression, but no timepoint of tumor progression was documented: AII (n=1, P33, 1.2 years), AAIII (n=1, P102, 0.8 years), AOAIII (n=3, P119, 1.3, P121, 0.1 and P132, 3.7 years). Histological diagnoses correspond to: AII, diffuse astrocytoma WHO grade II; OAII, oligoastrocytoma WHO grade II; OII, oligodendroglioma WHO grade II; AAIII, anaplastic astrocytoma WHO grade III, AOAIII, anaplastic oligoastrocytoma WHO grade III; AOIII, anaplastic oligodendroglioma WHO grade III.

Supplementary Table 2. *Clinical characteristics, molecular markers, treatment and outcome by histology.*

	AII (n=45)	**OAII (n=13)**	**OII (n=3)**	**AAIII (n=42)**	**AOAIII (n=31)**	**AOIII (n=3)**	**Total (n=137)**
Age (years)							
Median	38	41	39	46	46	47	41
Range	21-67	24-59	36-49	21-74	26-80	45-64	21-80
Gender							
Male	29 (64.4%)	8 (61.5%)	2 (66.7%)	25 (59.5%)	20 (64.5%)	-	84 (61.3%)
Female	16 (35.6%)	5 (38.5%)	1 (33.3%)	17 (40.5%)	11 (35.5%)	3 (100%)	53 (38.7%)
IDH1/2							
Mutant	41 (91.1%)	12 (92.3%)	3 (100%)	27 (64.3%)	30 (96.8%)	2 (66.7%)	115 (83.9%)
Wild-type	4 (8.9%)	1 (7.7%)	-	15 (35.7%)	1 (3.2%)	1 (33.3%)	22 (16.1%)
1p/19q							
Co-deleted	4 (8.9%)	6 (46.2%)	3 (100%)	2 (4.8%)	20 (64.5%)	2 (66.7%)	37 (27.0%)
Not co-deleted	41 (91.1%)	7 (53.8%)	-	40 (95.2%)	11 (35.5%)	1 (33.3%)	100 (73.0%)
***MGMT* promoter**							
Unmethylated	10 (22.7%)	1 (7.7%)	-	10 (23.8%)	3 (9.7%)	1 (33.3%)	25 (18.4%)
Weakly methylated	5 (11.4%)	-	1 (33.3%)	4 (9.5%)	3 (9.7%)	-	13 (9.6%)
Strongly methylated	29 (65.9%)	12 (92.3%)	2 (66.7%)	28 (66.7%)	25 (80.6%)	2 (66.7%)	98 (72.1%)
Unknown	1						1
***TERT* promoter**							
Mutant	5 (11.6%)	6 (46.2%)	3 (100%)	11 (26.8%)	18 (60.0%)	2 (66.7%)	45 (33.8%)
Wild-type	38 (88.4%)	7 (53.8%)	-	30 (73.2%)	12 (40.0%)	1 (33.3%)	88 (66.2%)
Unknown	2			1	1		4
Surgery							
Gross total resection	8 (21.6%)	7 (58.3%)	2 (66.7%)	16 (43.2%)	11 (40.7%)	-	44 (37.0%)
Subtotal resection (50-99%)	16 (43.2%)	4 (33.3%)	1 (33.3%)	9 (24.3%)	11 (40.7%)	2 (66.7%)	43 (36.1%)
Partial resection (<50%)	11 (29.7%)	1 (8.3%)	-	12 (32.4%)	5 (18.5%)	1 (33.3%)	30 (25.2%)
Biopsy	2 (5.4%)	-	-	-	-	-	2 (1.7%)
Unknown	8	1		5	4		18
Initial postsurgical management							
Observation	41 (91.1%)	12 (92.3%)	3 (100%)	6 (14.3%)	4 (12.9%)	-	66 (48.2%)
Radiotherapy	1 (2.2%)	-	-	12 (28.6%)	8 (25.8%)	1 (33.3%)	22 (16.1%)
Chemotherapy	1 (2.2%)	1 (7.7%)	-	3 (7.1%)	6 (19.4%)	1 (33.3%)	12 (8.8%)
Radiotherapy plus chemotherapy	1 (2.2%)	-	-	21 (50.0%)	13 (41.9%)	1 (33.3%)	36 (26.3%)
Other	1 (2.2%)	-	-	-	-	-	1 (0.7%)

Treatment at first progression							
No treatment	2 (5.6%)	1 (14.3%)	-	6 (20.7%)	2 (16.7%)	-	11 (12.6%)
Surgery only	8 (22.2%)	2 (28.6%)	1	2 (6.9%)	4 (33.3%)	-	17 (19.5%)
Surgery plus radiotherapy	3 (8.3%)	-	-	1 (3.4%)	1 (8.3%)	1	6 (6.9%)
Surgery plus chemotherapy	4 (11.1%)	1 (14.3%)	-	3 (10.3%)	2 (16.7%)	-	10 (11.5%)
Surgery plus radiotherapy plus Chemoth.	11 (30.6%)	1 (14.3%)	-	4 (13.8%)	1 (8.3%)	-	17 (19.5%)
Radiotherapy only	5 (13.9%)	1 (14.3%)	-	2 (6.9%)	-	-	8 (9.2%)
Chemotherapy only	3 (8.3%)	1 (14.3%)	1	10 (34.5%)	1 (8.3%)	-	16 (18.4%)
Radiotherapy plus chemotherapy	-	-	-	1 (3.4%)	1 (8.3%)	-	2 (2.3%)
Outcome data							
Follow-up (median, range), years	5.7 (0.6-17.7)	6.6 (1-8.1)	5.8 (3.1-9.1)	5.7 (1.2-11)	5.9 (0.6-9.6)	6.3 (4.7-7.2)	5.9 (0.6-17.7)
PFS (events)	37/45	7/13	2/3	30/42	15/31	1/3	92/137
PFS (median, 95% CI), years	3.2 (2.1-4.3)	7.3 (3.1-11.4)	-	1.7 (0.2-3.1)	5.1 (3.5-6.7)	-	3.7 (2.1-5.3)
OS (events)	16/45	2/13	0/3	19/42	10/31	0/3	47/137
OS (median, 95% CI), years	11.4 (7.8-15.1)	-	-	7.3 (3.5-11.1)	-	-	9.1 (6.7-11.6)
1-year survival rate (%)	97.7 (93.3-100)	-	-	92.9 (85.1-100)	96.8 (90.6-100)	-	96.3 (93.2-99.5)
2-year survival rate (%)	95.5 (89.3-100)	-	-	78.3 (65.8-90.9)	93.3 (84.4-100)	-	90.3 (85.2-95.3)
3-year survival rate (%)	85.7 (75.1-96.3)	-	-	65.7 (51.1-80.3)	86.1 (73.5-98.8)	-	81.6 (74.9-88.3)

Supplementary Table 3. *Clinical characteristics, molecular markers, treatment and outcome by molecular marker status.*

	IDH1/2 **mutant (n=115)**	***IDH1/2*** **Wild-type (n=22)**	***1p/19q*** **co-deleted (n=37)**	***1p/19q*** **not co-deleted (n=100)**	***MGMT*** **promoter methylated (n=111)**	***MGMT*** **promoter not methylated (n=25)**	***TERT*** **promoter mutant (n=45)**	***TERT*** **promoter wild-type (n=88)**	**Total (n=137)**
Age (years)									
Median	40	50	46	40	41	45	47	38	41
Range	21-80	29-72	27-74	21-80	21-80	21-72	27-74	21-80	21-80
Gender									
Male	75 (65.2%)	9 (40.9%)	22 (59.5%)	62 (62.0%)	71 (64.0%)	13 (52.0%)	26 (57.8%)	56 (63.6%)	84 (61.3%)
Female	40 (34.8%)	13 (59.1%)	15 (40.5%)	38 (38.0%)	40 (36.0%)	12 (48.0%)	19 (42.2%)	32 (36.4%)	53 (38.7%)
Histological diagnosis									
AII	41 (35.7%)	4 (18.2%)	4 (10.8%)	41 (41.0%)	34 (30.6%)	10 (40.0%)	5 (11.1%)	38 (43.2%)	45 (32.8%)
OAII	12 (10.4%)	1 (4.5%)	6 (16.2%)	7 (7.0%)	12 (10.8%)	1 (4.0%)	6 (13.3%)	7 (8.0%)	13 (9.5%)
OII	3 (2.6%)	-	3 (8.1%)	-	3 (2.7%)	-	3 (6.7%)	-	3 (2.2%)
AAIII	27 (23.5%)	15 (68.2%)	2 (5.4%)	40 (40.0%)	32 (28.8%)	10 (40.0%)	11 (24.4%)	30 (34.1%)	42 (30.7%)
AOAIII	30 (26.1%)	1 (4.5%)	20 (54.1%)	11 (11.0%)	28 (25.2%)	3 (12.0%)	18 (40.0%)	12 (13.6%)	31 (22.6%)
AOIII	2 (1.7%)	1 (4.5%)	2 (5.4%)	1 (1.0%)	2 (1.8%)	1 (4.0%)	2 (4.4%)	1 (1.1%)	3 (2.2%)
Surgery									
Gross total resection	36 (36.4%)	8 (40.0%)	12 (36.4%)	32 (37.2%)	34 (35.4%)	10 (45.5%)	15 (38.5%)	27 (35.1%)	44 (37.0%)
Subtotal resection (50-99%)	36 (36.4%)	7 (35.0%)	15 (45.5%)	28 (32.6%)	34 (35.4%)	8 (36.4%)	16 (41.0%)	27 (35.1%)	43 (36.1%)
Partial resection (<50%)	25 (25.3%)	5 (25.0%)	6 (18.2%)	24 (27.9%)	26 (27.1%)	4 (18.2%)	8 (20.5%)	21 (27.3%)	30 (25.2%)
Biopsy	2 (2.0%)	-	-	2 (2.3%)	2 (2.1%)	-	-	2 (2.6%)	2 (1.7%)
Unknown	16	2	4	14	15	3	6	11	18
Initial postsurgical management									
Observation	60 (52.2%)	6 (27.3%)	13 (35.1%)	53 (53.0%)	52 (46.8%)	14 (56.0%)	14 (31.1%)	50 (56.8%)	66 (48.2%)
Radiotherapy	16 (13.9%)	6 (27.3%)	8 (21.6%)	14 (14.0%)	19 (17.1%)	3 (12.0%)	9 (20.0%)	12 (13.6%)	22 (16.1%)
Chemotherapy	10 (8.7%)	2 (9.1%)	5 (13.5%)	7 (7.0%)	11 (9.9%)	1 (4.0%)	5 (11.1%)	7 (8.0%)	12 (8.8%)
Radiotherapy plus chemoth.	28 (24.3%)	8 (36.4%)	11 (29.7%)	25 (25.0%)	29 (26.1%)	7 (28.0%)	17 (37.8%)	18 (20.5%)	36 (26.3%)
Other	1 (0.9%)	-	-	1 (1.0%)			-	1 (1.1%)	1 (0.7%)
Treatment at first progression									
No treatment									
Surgery only	8 (11.6%)	3 (16.7%)	2 (13.3%)	9 (12.5%)	9 (12.9%)	1 (6.2%)	6 (24.0%)	5 (8.5%)	11 (12.6%)
Surgery plus radiotherapy	16 (23.2%)	1 (5.6%)	4 (26.7%)	13 (18.1%)	15 (21.4%)	2 (12.5%)	5 (20.0%)	12 (20.3%)	17 (19.5%)
Surgery plus chemotherapy	4 (5.8%)	2 (11.1%)	1 (6.7%)	5 (6.9%)	4 (5.7%)	2 (12.5%)	2 (8.0%)	4 (6.8%)	6 (6.9%)

Surgery plus radiotherapy plus chemotherapy	7 (10.1%)	3 (16.7%)	3 (20.0%)	7 (9.7%)	9 (12.9%)	1 (6.2%)	4 (16.0%)	5 (8.5%)	10 (11.5%)
Radiotherapy only	14 (20.3%)	3 (16.7%)	1 (6.7%)	16 (22.2%)	13 (18.6%)	4 (25.0%)	2 (8.0%)	14 (23.7%)	17 (19.5%)
Chemotherapy only	7 (10.1%)	1 (5.6%)	1 (6.7%)	7 (9.7%)	6 (8.6%)	2 (12.5%)	1 (4.0%)	6 (10.2%)	8 (9.2%)
Radiotherapy plus chemoth.	11 (15.9%)	5 (27.8%)	3 (20.0%)	13 (18.1%)	12 (17.1%)	4 (25.0%)	5 (20.0%)	11 (18.6%)	16 (18.4%)
	2 (2.9%)	-	-	2 (2.8%)	2 (2.9%)	-	-	2 (3.4%)	2 (2.3%)
Outcome data									
Follow-up (median, range), years	5.8 (0.6-17.7)	8.4 (1.2-11.0)	5.9 (0.6-9.6)	6.3 (0.6-17.7)	5.8 (0.6-17.7)	7.2 (0.6-11.0)	5.9 (0.6-9.7)	5.8 (0.6-17.7)	5.9 (0.6-17.7)
PFS (events)	73/115	19/22	17/37	75/100	73/111	18/25	28/45	61/88	92/137
PFS (median, 95% CI), years	5.0 (3.2-6.7)	1.5 (1.2-1.8)	5.9 (4.7-7.1)	3.0 (2.0-4.0)	4.7 (3.1-6.3)	2.2 (0-4.4)	3.6 (0.9-6.2)	3.7 (1.7-5.7)	3.7 (2.1-5.3)
OS (events)	32/115	15/22	5/37	42/100	34/111	13/25	13/45	32/88	47/137
OS (median, 95% CI), years	11.4 (7.6-15.3)	2.4 (1.8-3.1)	-	8.8 (6.0-11.6)	11.5 (7.7-15.2)	9.1 (1.0-17.2)	-	9.0 (7.3-10.8)	9.1 (6.7-11.6)
1-year survival rate (%)	98.2 (95.8-100)	86.4 (72.0-100)	97.3 (92.1-100)	96.0 (92.1-99.8)	97.3 (94.3-100)	91.8 (81.0-100)	95.5 (89.4-100)	96.6 (92.8-100)	96.3 (93.2-99.5)
2-year survival rate (%)	95.5 (91.8-99.2)	62.8 (42.3-83.3)	94.4 (86.9-100)	88.8 (82.5-95.0)	93.5 (88.9-98.2)	74.9 (57.5-92.3)	86.1 (75.8-96.4)	93.0 (87.7-98.4)	90.3 (85.2-95.3)
3-year survival rate (%)	89.9 (84.2-95.6)	38.6 (17.8-59.5)	91.6 (82.4-100)	77.9 (69.6-86.3)	84.9 (78.1-91.7)	66.1 (46.9-85.3)	76.5 (63.7-89.3)	84.5 (76.7-92.2)	81.6 (74.9-88.3)

Supplementary Table 4. *Clinical characteristics, molecular markers, treatment and outcome by genomic group according to IDH1/2 mutation status and array-CGH findings.*

Array-CGH class	**Group I** ***IDH1/2* mutant** **-1p/-19q** **(n=37)**	**Group II** ***IDH1/2* mutant** **+7q** **(n=31)**	**Group III** ***IDH1/2* mutant** **(n=47)**	**Group IV** ***IDH1/2* wild-type** **(n=9)**	**Group V** ***IDH1/2* wild-type** **+7q/-10q** **(n=13)**	**Total** **(n=137)**
Age (years)						
Median	46	38	36	45	55	41
Range	27-74	21-80	21-68	29-72	44-67	21-80
Gender						
Male	22 (59.5%)	19 (61.3%)	34 (72.3%)	4 (44.4%)	5 (38.5%)	84 (61.3%)
Female	15 (40.5%)	12 (38.7%)	13 (27.7%)	5 (55.6%)	8 (61.5%)	53 (38.7%)
Histological diagnosis						
AII	4 (10.8%)	18 (58.1%)	19 (40.4%)	1 (11.1%)	3 (23.1%)	45 (32.8%)
OAII	6 (16.2%)	2 (6.5%)	4 (8.5%)	1 (11.1%)	-	13 (9.5%)
OII	3 (8.1%)	-	-	-	-	3 (2.2%)
AAIII	2 (5.4%)	8 (25.8%)	17 (36.2%)	6 (66.7%)	9 (69.2%)	42 (30.7%)
AOAIII	20 (54.1%)	3 (9.7%)	7 (14.9%)	1 (11.1%)	-	31 (22.6%)
AOIII	2 (5.4%)	-	-	-	1 (7.7%)	3 (2.2%)
IDH1/2						
Mutant	37 (100%)	31 (100%)	47 (100%)	-	-	115 (83.9%)
Wild-type	-	-	-	9 (100%)	13 (100%)	22 (16.1%)
1p/19q						
Co-deleted	37 (100%)	-	-	-	-	37 (27.0%)
Not co-deleted	-	31 (100%)	47 (100%)	9 (100%)	13 (100%)	100 (73.0%)
***MGMT* promoter**						
Unmethylated	1 (2.7%)	5 (16.1%)	5 (10.9%)	6 (66.7%)	8 (61.5%)	25 (18.4%)
Weakly methylated	3 (8.1%)	4 (12.9%)	4 (8.7%)	1 (11.1%)	1 (7.7%)	13 (9.6%)
Strongly methylated	33 (89.2%)	22 (71.0%)	37 (80.4%)	2 (22.2%)	4 (30.8%)	98 (72.1%)
Unknown	-	-	1	-	-	1
***TERT* promoter**						
Mutant	33 (91.7%)	1 (3.3%)	1 (2.2%)	1 (11.1%)	9 (75.0%)	45 (33.8%)
Wild-type	3 (8.3%)	29 (96.7%)	45 (97.8%)	8 (88.9%)	3 (25.0%)	88 (66.2%)
Unknown	1	1	1		1	4
Surgery						
Gross total resection	12 (36.4%)	7 (26.9%)	17 (42.5%)	4 (50.0%)	4 (33.3%)	44 (37.0%)

Subtotal resection (50-99%)	15 (45.5%)	11 (42.3%)	10 (25.0%)	3 (37.5%)	4 (33.3%)	43 (36.1%)
Partial resection (<50%)	6 (18.2%)	7 (26.9%)	12 (30.0%)	1 (12.5%)	4 (33.3%)	30 (25.2%)
Biopsy	-	1 (3.8%)	1 (2.5%)	-	-	2 (1.7%)
Unknown	4	5	7	1	1	18
Initial postsurgical management						
Observation	13 (35.1%)	22 (71.0%)	25 (53.2%)	3 (33.3%)	3 (23.1%)	66 (48.2%)
Radiotherapy	8 (21.6%)	2 (6.5%)	6 (12.8%)	3 (33.3%)	3 (23.1%)	22 (16.1%)
Chemotherapy	5 (13.5%)	1 (3.2%)	4 (8.5%)	1 (11.1%)	1 (7.7%)	12 (8.8%)
Radiotherapy plus chemotherapy	11 (29.7%)	6 (19.4%)	11 (23.4%)	2 (22.2%)	6 (46.2%)	36 (26.3%)
Other	-	-	1 (2.1%)	-	-	1 (0.7%)
Treatment at first progression						
No treatment	2 (13.3%)	2 (11.1%)	4 (11.1%)	-	3 (25.0%)	11 (12.6%)
Surgery only	4 (26.7%)	6 (33.3%)	6 (16.7%)	1 (16.7%)	-	17 (19.5%)
Surgery plus radiotherapy	1 (6.7%)	-	3 (8.3%)	-	2 (16.7%)	6 (6.9%)
Surgery plus chemotherapy	3 (20.0%)	1 (5.6%)	3 (8.3%)	1 (16.7%)	2 (16.7%)	10 (11.5%)
Surgery plus radiotherapy plus chemotherapy	1 (6.7%)	5 (27.8%)	8 (22.2%)	1 (16.7%)	2 (16.7%)	17 (19.5%)
Radiotherapy only	1 (6.7%)	3 (16.7%)	3 (8.3%)	1 (16.7%)	-	8 (9.2%)
Chemotherapy only	3 (20.0%)	1 (5.6%)	7 (19.4%)	2 (33.3%)	3 (25.0%)	16 (18.4%)
Radiotherapy plus chemotherapy	-	-	2 (5.6%)	-	-	2 (2.3%)
Outcome data						
Follow-up (median, range), years	5.9 (0.6-9.6)	5.6 (1.7-7.5)	6.4 (0.6-17.7)	8.4 (5.8-11.0)	6.3 (1.2-9.7)	5.9 (0.6-17.7)
PFS (events)	17/37	20/31	36/47	6/9	13/13	92/137
PFS (median, 95% CI), years	5.9 (4.7-7.1)	3.7 (1.1-6.4)	3.0 (0.8-5.1)	4.1 (2.0-6.2)	1.5 (0.7-2.3)	3.7 (2.1-5.3)
OS (events)	5/37	11/31	16/47	5/9	10/13	47/137
OS (median, 95% CI), years	-	8.9 (4.9-12.7)	12.6 (3.4-21.9)	9.1 (0-20.2)	2.4 (2.0-2.9)	9.1 (6.7-11.6)
1-year survival rate (%)	97.3 (92.1-100)	100	97.8 (93.6-100)	-	92.3 (77.8-100)	96.3 (93.2-99.5)
2-year survival rate (%)	94.4 (86.9-100)	96.8 (90.6-100)	95.6 (89.6-100)	-	68.4 (42.6-94.1)	90.3 (85.2-95.3)
3-year survival rate (%)	91.6 (82.4-100)	89.6 (78.4-100)	88.8 (79.5-98.1)	-	25.6 (0.8-50.5)	81.6 (74.9-88.3)

Supplementary Table 5. *Frequency of high-level amplifications affecting EGFR, PDGFRA, CDK4, MDM2, MDM4 and other loci by genomic group according to array-CGH findings.*

Chromosomal sites with high-level amplification	**Known cancer gene amplified**	**Genomic group I (n=37)**	**Genomic group II (n=31)**	**Genomic group III (n=47)**	**Genomic group IV (n=9)**	**Genomic group V (n=13)**	***IDH1/2* wt primary glioblastoma (n=54)***
1q32.1	*MDM4*	-	-	1 (2%)	-	3 (23%)	6 (11%)
4q12	*PDGFRA*	-	-	-	-	-	4 (7%)
7p11.2	*EGFR*	-	1 (3%)	1 (2%)	-	8 (62%)	26 (48%)
12q14.1	*CDK4*	-	-	1 (2%)	1 (11%)	2 (15%)	9 (17%)
12q15	*MDM2*	-	-	-	1 (11%)	1 (8%)	5 (9%)
Other chromosomal sites (can be >1 per tumor)		1	22	9	10	12	65
Total number of high-level amplifications (can be >1 per tumor)		1	23	12	12	26	115
Average number of high-level amplifications per tumor		0.03	0.74	0.26	1.33	2	2.13
Number of tumors with at least 1 high-level amplification		1 (3%)	10 (32%)	6 (13%)	4 (44%)	11 (85%)	39 (72%)

*Data from reference [1]

Supplementary Table 6. *Clinical characteristics, molecular markers, treatment and outcome by gene expression groups.*

Expression group	**Group 1 (n=11)**	**Group 2 (n=6)**	**Group 3 (n=5)**	**Group 4 (n=22)**	**Group 5 (n=25)**	**Group 6 (n=15)**	**Group 7 (n=26)**	**Group 8 (n=27)**	**Total (n=137)**
Age (years)									
Median	55	48	41	45	30	39	48	37	41
Range	44-67	40-72	29-47	24-80	21-51	25-54	27-74	23-59	21-80
Gender									
Male	4 (36.4%)	2 (33.3%)	3 (60.0%)	15 (68.2%)	15 (60.0%)	10 (66.7%)	13 (50.0%)	22 (81.5%)	84 (61.3%)
Female	7 (63.6%)	4 (66.7%)	2 (40.0%)	7 (31.8%)	10 (40.0%)	5 (33.3%)	13 (50.0%)	5 (18.5%)	53 (38.7%)
Histological diagnosis									
AII	2 (18.2%)	-	2 (40.0%)	1 (4.5%)	13 (52.0%)	13 (86.7%)	1 (3.8%)	13 (48.1%)	45 (32.8%)
AOII	-	-	1 (20.0%)	2 (9.1%)	1 (4.0%)	-	3 (11.5%)	6 (22.2%)	13 (9.5%)
OII	-	-	-	-	-	-	3 (11.5%)	-	3 (2.2%)
AAIII	9 (81.8%)	4 (66.7%)	2 (40.0%)	10 (45.5%)	10 (40.0%)	1 (6.7%)	2 (7.7%)	4 (14.8%)	42 (30.7%)
AOAIII	-	1 (16.7%)	-	9 (40.9%)	1 (4.0%)	1 (6.7%)	15 (57.7%)	4 (14.8%)	31 (22.6%)
AOIII	-	1 (16.7%)	-	-	-	-	2 (7.7%)	-	3 (2.2%)
IDH1/2									
Mutant	-	-	-	22 (100%)	25 (100%)	15 (100%)	26 (100%)	27 (100%)	115 (83.9%)
Wild-type	11 (100%)	6 (100%)	5 (100%)	-	-	-	-	-	22 (16.1%)
1p/19q									
Co-deleted	-	-	-	2 (9.1%)	-	3 (20.0%)	26 (100%)	6 (22.2%)	37 (27.0%)
Not co-deleted	11 (100%)	6 (100%)	5 (100%)	20 (90.9%)	25 (100%)	12 (80.0%)	-	21 (77.8%)	100 (73.0%)
***MGMT* promoter**									
Unmethylated	6 (54.5%)	5 (83.3%)	3 (60.0%)	2 (9.1%)	4 (16.0%)	-	1 (3.8%)	4 (14.8%)	25 (18.4%)
Weakly methylated	1 (9.1%)	-	1 (20.0%)	-	5 (20.0%)	1 (7.1%)	3 (11.5%)	2 (7.4%)	13 (9.6%)
Strongly methylated	4 (36.4%)	1 (16.7%)	1 (20.0%)	20 (90.9%)	16 (64.0%)	13 (92.9%)	22 (84.6%)	21 (77.8%)	98 (72.1%)
Unknown						1			1
***TERT* promoter**									
Mutant	8 (80.0%)	2 (33.3%)	-	-	2 (8.0%)	3 (21.4%)	25 (96.2%)	5 (18.5%)	45 (33.8%)
Wild-type	2 (20.0%)	4 (66.7%)	5 (100%)	20 (100%)	23 (92.0%)	11 (78.6%)	1 (3.8%)	22 (81.5%)	88 (66.2%)
Unknown	1			2		1			4
Surgery									
Gross total resection	3 (30.0%)	2 (40.0%)	3 (60.0%)	8 (40.0%)	8 (33.3%)	2 (20.0%)	10 (43.5%)	8 (36.4%)	44 (37.0%)
Subtotal resection (50-99%)	3 (30.0%)	3 (60.0%)	1 (20.0%)	5 (25.0%)	9 (37.5%)	3 (30.0%)	11 (47.8%)	8 (36.4%)	43 (36.1%)
Partial resection (<50%)	4 (40.0%)	-	1 (20.0%)	7 (35.0%)	7 (29.2%)	3 (30.0%)	2 (8.7%)	6 (27.3%)	30 (25.2%)
Biopsy	-	-	-	-	-	2 (20.0%)	-	-	2 (1.7%)

Unknown	1	1		2	1	5	3	5	18
Initial postsurgical management									
Observation	2 (18.2%)	1 (16.7%)	3 (60.0%)	6 (27.3%)	17 (68.0%)	11 (73.3%)	7 (26.9%)	19 (70.4%)	66 (48.2%)
Radiotherapy	3 (27.3%)	2 (33.3%)	1 (20.0%)	3 (13.6%)	3 (12.0%)	1 (6.7%)	8 (30.8%)	1 (3.7%)	22 (16.1%)
Chemotherapy	-	1 (16.7%)	1 (20.0%)	4 (18.2%)	1 (4.0%)	1 (6.7%)	3 (11.5%)	1 (3.7%)	12 (8.8%)
Radiotherapy plus chemotherapy	6 (54.5%)	2 (33.3%)	-	9 (40.9%)	4 (16.0%)	1 (6.7%)	8 (30.8%)	6 (22.2%)	36 (26.3%)
Other	-	-	-	-	-	1 (6.7%)	-	-	1 (0.7%)
Treatment at first progression									
No treatment	3 (30.0%)	-	-	2 (16.7%)	1 (5.9%)	2 (13.3%)	1 (10.0%)	2 (13.3%)	11 (12.6%)
Surgery only	1 (10.0%)	-	-	2 (16.7%)	3 (17.6%)	4 (26.7%)	3 (30.0%)	4 (26.7%)	17 (19.5%)
Surgery plus radiotherapy	-	1 (33.3%)	1 (20.0%)	-	1 (5.9%)	2 (13.3%)	1 (10.0%)	-	6 (6.9%)
Surgery plus chemotherapy	2 (20.0%)	-	1 (20.0%)	2 (16.7%)	1 (5.9%)	2 (13.3%)	2 (20.0%)	-	10 (11.5%)
Surgery plus radiotherapy plus chemotherapy	2 (20.0%)	-	1 (20.0%)	1 (8.3%)	6 (35.3%)	4 (26.7%)	-	3 (20.0%)	17 (19.5%)
Radiotherapy only	-	-	1 (20.0%)	1 (8.3%)	2 (11.8%)	-	-	4 (26.7%)	8 (9.2%)
Chemotherapy only	2 (20.0%)	2 (66.7%)	1 (20.0%)	3 (25.0%)	2 (11.8%)	1 (6.7%)	3 (30.0%)	2 (13.3%)	16 (18.4%)
Radiotherapy plus chemotherapy	-	-	-	1 (8.3%)	1 (5.9%)	-	-	-	2 (2.3%)
Outcome data									
Follow-up (median, range), years	9.7 (1.2-9.7)	6.3 -	8.1 -	6.4 (1.2-12.1)	4.8 (0.6-7.2)	9.6 (1.7-17.7)	5.8 (0.6-9.6)	6.3 (1.0-8.1)	5.9 (0.6-17.7)
PFS (events)	11/11	3/6	5/5	13/22	17/25	15/15	12/26	16/27	92/137
PFS (median, 95% CI), years	0.8 (0.1-1.6)	1.5 (1.0-2.0)	4.1 (2.3-5.8)	4.2 (1.6-6.8)	2.9 (2.1-3.8)	3.4 (0-7.4)	5.9 (2.6-9.2)	5.9 (5.4-6.3)	3.7 (2.1-5.3)
OS (events)	9/11	4/6	2/5	10/22	5/25	6/15	4/26	7/27	47/137
OS (median, 95% CI), years	2.4 (0.9-3.9)	1.8 (0-4.5)	9.1 (0-19.2)	6.1 (2.8-9.5)	- -	-	-	11.5 (4.5-18.4)	9.1 (6.7-11.6)
1-year survival rate (%)	90.9 (73.9-100)	-	-	100	100	93.3 (80.7-100)	96.2 (88.8-100)	100	96.3 (93.2-99.5)
2-year survival rate (%)	51.9 (21.2-82.7)	-	-	95.2 (86.1-100)	100	93.3 (80.7-100)	92.1 (81.7-100)	96.2 (88.8-100)	90.3 (85.2-95.3)
3-year survival rate (%)	20.8 (0-46.3)	-	-	84.7 (68.6-100)	91.3 (79.8-100)	86.2 (68.3-100)	88.1 (75.5-100)	96.2 (88.8-100)	81.6 (74.9-88.3)

Supplementary Table 7. *Relationships between array-CGH-based genomic and mRNA expression profiling-based groups.*

	Expression group 1	**Expression group 2**	**Expression group 3**	**Expression group 4**	**Expression group 5**	**Expression group 6**	**Expression group 7**	**Expression group 8**	**Total**
Genomic group I				2		3	**26***	6	37
Genomic group II				7	12	4		8	31
Genomic group III				13	13	8		13	47
Genomic group IV	1	4	4						9
Genomic group V	**10****	2	1						13
Total	11	6	5	22	25	15	26	27	137

*Corresponding to "integrated molecular group A" as defined by integration of genomic and transcriptomic classification.**Corresponding to "integrated molecular group C" as defined by integration of genomic and transcriptomic classification. All other tumors were assigned to "integrated molecular group B" (see Supplementary Table 8 and Supplementary Fig. 3)

Supplementary Table 8. *Clinical characteristics, molecular markers, treatment and outcome by the three-tiered molecular classification based on array-CGH findings ("genomic groups") or array-CGH findings combined with mRNA expression data ("integrated molecular groups"). For further information see also Fig. 4 and Supplementary Fig. 3).*

Array-CGH class	**Genomic group I (n=37)**	**Genomic groups II-IV (n=87)**	**Genomic group V (n=13)**	**Integrated molecular group A (n=26)**	**Integrated molecular group B (n=101)**	**Integrated molecular group C (n=10)**	**Total (n=137)**
Age (years)							
Median	46	38	55	48	39	55	41
Range	27-74	21-80	44-67	27-74	21-80	44-67	21-80
Gender							
Male	22 (59.5%)	57 (65.5%)	5 (38.5%)	13 (50.0%)	68 (67.3%)	3 (30.0%)	84 (61.3%)
Female	15 (40.5%)	30 (34.5%)	8 (61.5%)	13 (50.0%)	33 (32.7%)	7 (70.0%)	53 (38.7%)
Histological diagnosis							
AII	4 (10.8%)	38 (43.7%)	3 (23.1%)	1 (3.8%)	42 (41.6%)	2 (20.0%)	45 (32.8%)
OAII	6 (16.2%)	7 (8.0%)	-	3 (11.5%)	10 (9.9%)	-	13 (9.5%)
OII	3 (8.1%)	-	-	3 (11.5%)	-	-	3 (2.2%)
AAIII	2 (5.4%)	31 (35.6%)	9 (69.2%)	2 (7.7%)	32 (31.7%)	8 (80.0%)	42 (30.7%)
AOAIII	20 (54.1%)	11 (12.6%)		15 (57.7%)	16 (15.8%)	-	31 (22.6%)
AOIII	2 (5.4%)	-	1 (7.7%)	2 (7.7%)	1 (1.0%)	-	3 (2.2%)
IDH1/2							
Mutant	37 (100%)	78 (89.7%)	-	26 (100%)	89 (88.1%)	-	115 (83.9%)
Wild-type	-	9 (10.3%)	13 (100%)	-	12 (11.9%)	10 (100%)	22 (16.1%)
1p/19q							
Co-deleted	37 (100%)	-	-	26 (100%)	11 (10.9%)	-	37 (27.0%)
Not co-deleted	-	87 (100%)	13 (100%)	-	90 (89.1%)	10 (100%)	100 (73.0%)
***MGMT* promoter**							
Unmethylated	1 (2.7%)	16 (18.6%)	8 (61.5%)	1 (3.8%)	19 (19.0%)	5 (50.0%)	25 (18.4%)
Weakly methylated	3 (8.1%)	9 (10.5%)	1 (7.7%)	3 (11.5%)	9 (9.0%)	1 (10.0%)	13 (9.6%)
Strongly methylated	33 (89.2%)	61 (70.9%)	4 (30.8%)	22 (84.6%)	72 (72.0%)	4 (40.0%)	98 (72.1%)
Unknown					1		1
***TERT* promoter**							
Mutant	33 (91.7%)	3 (3.5%)	9 (75.0%)	25 (96.2%)	13 (13.3%)	7 (77.8%)	45 (33.8%)
Wild-type	3 (8.3%)	82 (96.5%)	3 (25.0%)	1 (3.8%)	85 (86.7%)	2 (22.2%)	88 (66.2%)
Unknown	1	2	1		3	1	4

Surgery							
Gross total resection	12 (36.4%)	28 (37.8%)	4 (33.3%)	10 (43.5%)	31 (35.6%)	3 (33.3%)	44 (37.0%)
Subtotal resection (50-99%)	15 (45.5%)	24 (32.4%)	4 (33.3%)	11 (47.8%)	30 (34.5%)	2 (22.2%)	43 (36.1%)
Partial resection (<50%)	6 (18.2%)	20 (27.0%)	4 (33.3%)	2 (8.7%)	24 (27.6%)	4 (44.4%)	30 (25.2%)
Biopsy	-	2 (2.7%)	-	-	2 (2.3%)	-	2 (1.7%)
Unknown	4	13	1	3	14	1	18
Initial postsurgical management							
Observation	13 (35.1%)	50 (57.5%)	3 (23.1%)	7 (26.9%)	57 (56.4%)	2 (20.0%)	66 (48.2%)
Radiotherapy	8 (21.6%)	11 (12.6%)	3 (23.1%)	8 (30.8%)	11 (10.9%)	3 (30.0%)	22 (16.1%)
Chemotherapy	5 (13.5%)	6 (6.9%)	1 (7.7%)	3 (11.5%)	9 (8.9%)	-	12 (8.8%)
Radiotherapy plus chemotherapy	11 (29.7%)	19 (21.8%)	6 (46.2%)	8 (30.8%)	23 (22.8%)	5 (50.0%)	36 (26.3%)
Other	-	1 (1.1%)	-	-	1 (1.0%)	-	1 (0.7%)
Treatment at first progression							
No treatment	2 (13.3%)	6 (10.0%)	3 (25.0%)	1 (10.0%)	7 (10.3%)	3 (33.3%)	11 (12.6%)
Surgery only	4 (26.7%)	13 (21.7%)	-	3 (30.0%)	14 (20.6%)	-	17 (19.5%)
Surgery plus radiotherapy	1 (6.7%)	3 (5.0%)	2 (16.7%)	1 (10.0%)	5 (7.4%)	-	6 (6.9%)
Surgery plus chemotherapy	3 (20.0%)	5 (8.3%)	2 (16.7%)	2 (20.0%)	6 (8.8%)	2 (22.2%)	10 (11.5%)
Surgery plus radiotherapy plus chemotherapy	1 (6.7%)	14 (23.3%)	2 (16.7%)	-	15 (22.1%)	2 (22.2%)	17 (19.5%)
Radiotherapy only	1 (6.7%)	7 (11.7%)	-	-	8 (11.8%)	-	8 (9.2%)
Chemotherapy only	3 (20.0%)	10 (16.7%)	3 (25.0%)	3 (30.0%)	11 (16.2%)	2 (22.2%)	16 (18.4%)
Radiotherapy plus chemotherapy	-	2 (3.3%)	-	-	2 (2.9%)	-	2 (2.3%)
Outcome data							
Follow-up (median, range), years	5.9 (0.6-9.6)	5.9 (0.6-17.7)	6.3 (1.2-9.7)	5.8 (0.6-9.6)	6.2 (0.6-17.7)	9.7 (1.2-9.7)	5.9 (0.6-17.7)
PFS (events)	17/37	62/87	13/13	12/26	70/101	10/10	92/137
PFS (median, 95% CI), years	5.9 (4.7-7.1)	3.7 (2.0-5.5)	1.5 (0.7-2.3)	5.9 (2.6-9.2)	4.2 (2.5-5.8)	0.8 (0-1.8)	3.7 (2.1-5.3)
OS (events)	5/37	32/87	10/13	4/26	35/101	8/10	47/137
OS (median, 95% CI), years	-	9.0 (7.2-10.9)	2.4 (2.0-2.9)	-	9.0 (8.6-9.5)	2.4 (0.7-4.1)	9.1 (6.7-11.6)
1-year survival rate (%)	97.3 (92.1-100)	96.5 (92.7-100)	92.3 (77.8-100)	96.2 (88.8-100)	97.0 (93.7-100)	90.0 (71.4-100)	96.3 (93.2-99.5)
2-year survival rate (%)	94.4 (86.9-100)	91.8 (85.9-97.6)	68.4 (42.6-94.1)	92.1 (81.7-100)	92.9 (87.8-98.0)	58.3 (26.8-89.9)	90.3 (85.2-95.3)
3-year survival rate (%)	91.6 (82.4-100)	85.6 (78.0-93.1)	25.6 (0.8-50.5)	88.1 (75.5-100)	85.4 (78.4-92.5)	23.3 (0-51.4)	81.6 (74.9-88.3)

Supplementary Table 9. *List of genes differentially expressed between IDH1/2 mutant astrocytic and oligodendroglial/oligoastrocytic gliomas.*

Top 100 genes significantly upregulated in astrocytic (AII+AAIII) versus oligodendroglial/oligoastrocytic (OII/OAII+AOIII/AOAIII) tumors.

Affymetrix probeset ID	Gene location	Gene symbol	Gene description	Expression fold change	P-value	Local FDR
226192_at	X q12	AR	androgen receptor [Source:HGNC Symbol;Acc:644]	10.10	2.22E-16	2.26E-12
243952_at	22 q11	TPTEP1	transmembrane phosphatase with tensin homology pseudogene 1 [Source:HGNC Symbol;Acc:43648]	17.12	8.88E-16	1.58E-10
205856_at	18 q12	SLC14A1	solute carrier family 14 (urea transporter), member 1 (Kidd blood group) [Source:HGNC Symbol;Acc:10918]	6.81	4.73E-11	3.16E-07
203085_s_at	19 q13	TGFB1	transforming growth factor, beta 1 [Source:HGNC Symbol;Acc:11766]	5.25	1.36E-10	1.03E-06
213506_at	5 q13	F2RL1	coagulation factor II (thrombin) receptor-like 1 [Source:HGNC Symbol;Acc:3538]	5.59	4.29E-10	5.64E-06
227300_at	12 q23	TMEM119	transmembrane protein 119 [Source:HGNC Symbol;Acc:27884]	4.72	2.63E-09	1.25E-05
1553202_at	10 q21	STOX1	storkhead box 1 [Source:HGNC Symbol;Acc:23508]	4.79	7.35E-09	4.02E-05
205786_s_at	16 p11	ITGAM	integrin, alpha M (complement component 3 receptor 3 subunit) [Source:HGNC Symbol;Acc:6149]	3.87	1.21E-08	7.57E-05
243337_at	4 q31	FREM3	FRAS1 related extracellular matrix 3 [Source:HGNC Symbol;Acc:25172]	6.08	1.30E-08	7.57E-05
228442_at	20 q13	NFATC2	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 [Source:HGNC Symbol;Acc:7776]	4.52	1.75E-08	7.57E-05
209879_at	12 q24	SELPLG	selectin P ligand [Source:HGNC Symbol;Acc:10722]	3.83	2.36E-08	7.57E-05
207107_at	1 p31	RPE65	retinal pigment epithelium-specific protein 65kDa [Source:HGNC Symbol;Acc:10294]	4.97	3.60E-08	0.0001
235783_at	1 p36	MRTO4	mRNA turnover 4 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:18477]	3.89	3.82E-08	0.0001
204990_s_at	17 q25	ITGB4	integrin, beta 4 [Source:HGNC Symbol;Acc:6158]	3.92	4.33E-08	0.0001
202295_s_at	15 q25	CTSH	cathepsin H [Source:HGNC Symbol;Acc:2535]	3.86	4.69E-08	0.0002
213160_at	5 q35	DOCK2	dedicator of cytokinesis 2 [Source:HGNC Symbol;Acc:2988]	3.83	5.65E-08	0.0002
211105_s_at	18 q23	NFATC1	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1 [Source:HGNC Symbol;Acc:7775]	3.74	8.39E-08	0.0002
208253_at	19 q13	SIGLEC8	sialic acid binding Ig-like lectin 8 [Source:HGNC Symbol;Acc:10877]	3.73	9.97E-08	0.0002
203868_s_at	1 p21	VCAM1	vascular cell adhesion molecule 1 [Source:HGNC Symbol;Acc:12663]	4.27	1.04E-07	0.0002
226909_at	4 p16	ZNF518B	zinc finger protein 518B [Source:HGNC Symbol;Acc:29365]	3.92	1.22E-07	0.0002

206171_at	1 p13	ADORA3	adenosine A3 receptor [Source:HGNC Symbol;Acc:268]	3.96	1.29E-07	0.0002
230781_at	4 q21	LINC01088	long intergenic non-protein coding RNA 1088 [Source:HGNC Symbol;Acc:49148]	3.95	1.33E-07	0.0002
226068_at	9 q22	SYK	spleen tyrosine kinase [Source:HGNC Symbol;Acc:11491]	3.83	1.49E-07	0.0002
231044_at	1 p13	C1orf194	chromosome 1 open reading frame 194 [Source:HGNC Symbol;Acc:32331]	4.31	1.64E-07	0.0002
204983_s_at	X q26	GPC4	glypican 4 [Source:HGNC Symbol;Acc:4452]	3.95	1.92E-07	0.0003
219256_s_at	4 p16	SH3TC1	SH3 domain and tetratricopeptide repeats 1 [Source:HGNC Symbol;Acc:26009]	4.12	2.39E-07	0.0004
220005_at	3 q25	P2RY13	purinergic receptor P2Y, G-protein coupled, 13 [Source:HGNC Symbol;Acc:4537]	3.67	2.40E-07	0.0004
206811_at	8 q24	ADCY8	adenylate cyclase 8 (brain) [Source:HGNC Symbol;Acc:239]	4.34	2.75E-07	0.0004
205067_at	2 q13	IL1B	interleukin 1, beta [Source:HGNC Symbol;Acc:5992]	4.30	2.78E-07	0.0004
204320_at	1 p21	COL11A1	collagen, type XI, alpha 1 [Source:HGNC Symbol;Acc:2186]	5.06	2.80E-07	0.0004
219994_at	10 p12	APBB1IP	amyloid beta (A4) precursor protein-binding, family B, member 1 interacting protein [Source:HGNC Symbol;Acc:17379]	3.74	2.88E-07	0.0004
227346_at	7 p12	IKZF1	IKAROS family zinc finger 1 (Ikaros) [Source:HGNC Symbol;Acc:13176]	3.62	3.31E-07	0.0004
232231_at	6 p21	RUNX2	runt-related transcription factor 2 [Source:HGNC Symbol;Acc:10472]	4.11	3.39E-07	0.0004
239229_at	X p22	PHEX	phosphate regulating endopeptidase homolog, X-linked [Source:HGNC Symbol;Acc:8918]	3.55	4.09E-07	0.0004
219235_s_at	1 p35	PHACTR4	phosphatase and actin regulator 4 [Source:HGNC Symbol;Acc:25793]	3.02	4.38E-07	0.0006
222236_s_at	1 p36	ASAP3	ArfGAP with SH3 domain, ankyrin repeat and PH domain 3 [Source:HGNC Symbol;Acc:14987]	2.86	4.98E-07	0.0006
232861_at	16 q22	PDP2	pyruvate dehyrogenase phosphatase catalytic subunit 2 [Source:HGNC Symbol;Acc:30263]	3.12	5.06E-07	0.0006
212873_at	19 p13	HMHA1	histocompatibility (minor) HA-1 [Source:HGNC Symbol;Acc:17102]	3.58	5.06E-07	0.0006
204192_at	19 q13	CD37	CD37 molecule [Source:HGNC Symbol;Acc:1666]	3.64	6.66E-07	0.0008
207075_at	1 q44	NLRP3	NLR family, pyrin domain containing 3 [Source:HGNC Symbol;Acc:16400]	3.35	6.76E-07	0.0008
221900_at	1 p34	COL8A2	collagen, type VIII, alpha 2 [Source:HGNC Symbol;Acc:2216]	3.36	6.92E-07	0.0008
229435_at	9 p24	GLIS3	GLIS family zinc finger 3 [Source:HGNC Symbol;Acc:28510]	3.25	6.98E-07	0.0008
229816_at	1 p31	WDR78	WD repeat domain 78 [Source:HGNC Symbol;Acc:26252]	3.82	9.94E-07	0.0008
215046_at	2 q34	KANSL1L	KAT8 regulatory NSL complex subunit 1-like [Source:HGNC Symbol;Acc:26310]	3.59	1.04E-06	0.0009

204446_s_at	10 q11	ALOX5	arachidonate 5-lipoxygenase [Source:HGNC Symbol;Acc:435]	3.28	1.08E-06	0.0009
205168_at	1 q23	DDR2	discoidin domain receptor tyrosine kinase 2 [Source:HGNC Symbol;Acc:2731]	3.41	1.11E-06	0.0009
218786_at	12 q23	NT5DC3	5'-nucleotidase domain containing 3 [Source:HGNC Symbol;Acc:30826]	3.71	1.16E-06	0.0009
208130_s_at	7 q34	TBXAS1	thromboxane A synthase 1 (platelet) [Source:HGNC Symbol;Acc:11609]	3.36	1.20E-06	0.0009
215813_s_at	9 q33	PTGS1	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase) [Source:HGNC Symbol;Acc:9604]	3.72	1.22E-06	0.001
228338_at	11 q23	COLCA2	colorectal cancer associated 2 [Source:HGNC Symbol;Acc:26978]	3.71	1.28E-06	0.001
204174_at	13 q12	ALOX5AP	arachidonate 5-lipoxygenase-activating protein [Source:HGNC Symbol;Acc:436]	3.51	1.58E-06	0.001
202934_at	2 p12	HK2	hexokinase 2 [Source:HGNC Symbol;Acc:4923]	3.02	1.70E-06	0.001
221860_at	19 q13	HNRNPL	heterogeneous nuclear ribonucleoprotein L [Source:HGNC Symbol;Acc:5045]	2.64	1.71E-06	0.001
219202_at	17 q25	RHBDF2	rhomboid 5 homolog 2 (Drosophila) [Source:HGNC Symbol;Acc:20788]	3.42	1.71E-06	0.001
205466_s_at	4 p15	HS3ST1	heparan sulfate (glucosamine) 3-O-sulfotransferase 1 [Source:HGNC Symbol;Acc:5194]	3.75	1.72E-06	0.001
204439_at	1 p31	IFI44L	interferon-induced protein 44-like [Source:HGNC Symbol;Acc:17817]	3.09	1.74E-06	0.001
1558101_at	1 p31	NFIA	nuclear factor I/A [Source:HGNC Symbol;Acc:7784]	3.58	1.75E-06	0.002
201693_s_at	5 q31	EGR1	early growth response 1 [Source:HGNC Symbol;Acc:3238]	3.32	2.47E-06	0.002
238135_at	1 p36	AGTRAP	angiotensin II receptor-associated protein [Source:HGNC Symbol;Acc:13539]	3.25	2.51E-06	0.002
205485_at	19 q13	RYR1	ryanodine receptor 1 (skeletal) [Source:HGNC Symbol;Acc:10483]	3.23	2.67E-06	0.002
242525_at	1 p36	SLC2A5	solute carrier family 2 (facilitated glucose/fructose transporter), member 5 [Source:HGNC Symbol;Acc:11010]	3.21	2.78E-06	0.002
207695_s_at	X q26	IGSF1	immunoglobulin superfamily, member 1 [Source:HGNC Symbol;Acc:5948]	4.11	2.79E-06	0.003
210560_at	2 q37	GBX2	gastrulation brain homeobox 2 [Source:HGNC Symbol;Acc:4186]	3.07	3.71E-06	0.003
230252_at	12 p13	LPAR5	lysophosphatidic acid receptor 5 [Source:HGNC Symbol;Acc:13307]	3.02	3.73E-06	0.003
210764_s_at	1 p22	CYR61	cysteine-rich, angiogenic inducer, 61 [Source:HGNC Symbol;Acc:2654]	3.37	3.77E-06	0.003
206283_s_at	1 p33	TAL1	T-cell acute lymphocytic leukemia 1 [Source:HGNC Symbol;Acc:11556]	2.80	3.93E-06	0.004
203332_s_at	2 q37	INPP5D	inositol polyphosphate-5-phosphatase, 145kDa [Source:HGNC Symbol;Acc:6079]	2.82	4.23E-06	0.004
219747_at	4 q27	NDNF	neuron-derived neurotrophic factor [Source:HGNC Symbol;Acc:26256]	3.84	4.53E-06	0.004
201404_x_at	1 p34	PSMB2	proteasome (prosome, macropain) subunit, beta type, 2 [Source:HGNC	2.78	4.95E-06	0.004

			Symbol;Acc:9539]			
202957_at	3 q13	HCLS1	hematopoietic cell-specific Lyn substrate 1 [Source:HGNC Symbol;Acc:4844]	2.84	5.27E-06	0.004
1552365_at	7 p21	SCIN	scinderin [Source:HGNC Symbol;Acc:21695]	3.48	5.77E-06	0.005
203104_at	5 q32	CSF1R	colony stimulating factor 1 receptor [Source:HGNC Symbol;Acc:2433]	2.37	6.08E-06	0.005
206170_at	5 q32	ADRB2	adrenoceptor beta 2, surface [Source:HGNC Symbol;Acc:286]	3.09	6.90E-06	0.005
235892_at	11 q23	COLCA1	colorectal cancer associated 1 [Source:HGNC Symbol;Acc:33789]	3.56	6.91E-06	0.005
207085_x_at	X p22	CSF2RA	colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage) [Source:HGNC Symbol;Acc:2435]	3.32	7.77E-06	0.005
202833_s_at	14 q32	SERPINA1	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 [Source:HGNC Symbol;Acc:8941]	3.87	8.16E-06	0.005
220927_s_at	10 q24	HPSE2	heparanase 2 [Source:HGNC Symbol;Acc:18374]	3.57	8.36E-06	0.005
201124_at	3 q21	ITGB5	integrin, beta 5 [Source:HGNC Symbol;Acc:6160]	3.14	8.78E-06	0.005
204731_at	1 p22	TGFBR3	transforming growth factor, beta receptor III [Source:HGNC Symbol;Acc:11774]	2.45	9.26E-06	0.008
1557433_at	1 p13	CLCC1	chloride channel CLIC-like 1 [Source:HGNC Symbol;Acc:29675]	2.65	1.01E-05	0.008
223958_s_at	14 q24	DNAL1	dynein, axonemal, light chain 1 [Source:HGNC Symbol;Acc:23247]	2.87	1.04E-05	0.008
218035_s_at	4 p14	RBM47	RNA binding motif protein 47 [Source:HGNC Symbol;Acc:30358]	3.41	1.08E-05	0.008
236666_s_at	11 q12	LRRC10B	leucine rich repeat containing 10B [Source:HGNC Symbol;Acc:37215]	3.01	1.11E-05	0.008
223737_x_at	18 q11	CHST9	carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9 [Source:HGNC Symbol;Acc:19898]	3.49	1.13E-05	0.008
204787_at	X q12	VSIG4	V-set and immunoglobulin domain containing 4 [Source:HGNC Symbol;Acc:17032]	2.86	1.37E-05	0.008
213566_at	14 q11	RNASE6	ribonuclease, RNase A family, k6 [Source:HGNC Symbol;Acc:10048]	3.08	1.39E-05	0.008
218551_at	1 p36	MIIP	migration and invasion inhibitory protein [Source:HGNC Symbol;Acc:25715]	2.52	1.41E-05	0.008
225328_at	8 q24	FBXO32	F-box protein 32 [Source:HGNC Symbol;Acc:16731]	2.70	1.49E-05	0.008
209521_s_at	X q23	AMOT	angiomotin [Source:HGNC Symbol;Acc:17810]	2.89	1.53E-05	0.008
202581_at	6 p21	HSPA1B	heat shock 70kDa protein 1B [Source:HGNC Symbol;Acc:5233]	2.73	1.54E-05	0.008
212103_at	1 p35	KPNA6	karyopherin alpha 6 (importin alpha 7) [Source:HGNC Symbol;Acc:6399]	2.20	1.57E-05	0.008
210166_at	1 q41	TLR5	toll-like receptor 5 [Source:HGNC Symbol;Acc:11851]	2.90	1.64E-05	0.01
227376_at	7 p14	GLI3	GLI family zinc finger 3 [Source:HGNC Symbol;Acc:4319]	2.71	1.67E-05	0.01
206726_at	4 q22	HPGDS	hematopoietic prostaglandin D synthase [Source:HGNC	3.31	1.75E-05	0.01

			Symbol;Acc:17890]			
227645_at	17 p13	PIK3R5	phosphoinositide-3-kinase, regulatory subunit 5 [Source:HGNC Symbol;Acc:30035]	2.96	1.77E-05	0.01
211742_s_at	17 q11	EVI2B	ecotropic viral integration site 2B [Source:HGNC Symbol;Acc:3500]	2.65	1.77E-05	0.01
202545_at	3 p21	PRKCD	protein kinase C, delta [Source:HGNC Symbol;Acc:9399]	3.21	1.78E-05	0.01
242086_at	1 p33	SPATA6	spermatogenesis associated 6 [Source:HGNC Symbol;Acc:18309]	3.40	2.13E-05	0.01
220146_at	X p22	TLR7	toll-like receptor 7 [Source:HGNC Symbol;Acc:15631]	3.33	2.14E-05	0.01
244352_at	1 q23	CD84	CD84 molecule [Source:HGNC Symbol;Acc:1704]	2.73	2.25E-05	0.01

Top 100 genes significantly downregulated in astrocytic (AII+AAIII) versus oligodendroglial/oligoastrocytic (OII/OAII+AOIII/AOAIII) tumors

Affymetrix probeset ID	Gene location	Gene symbol	Gene description	Expression fold change	P-value	Local FDR
242774_at	14 q23	SYNE2	spectrin repeat containing, nuclear envelope 2 [Source:HGNC Symbol;Acc:17084]	0.09	2.22E-16	2.26E-12
211022_s_at	X q21	ATRX	alpha thalassemia/mental retardation syndrome X-linked [Source:HGNC Symbol;Acc:886]	0.11	2.22E-16	2.26E-12
209591_s_at	20 q13	BMP7	bone morphogenetic protein 7 [Source:HGNC Symbol;Acc:1074]	0.13	3.77E-14	1.96E-08
223940_x_at	11 q13	MALAT1	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding) [Source:HGNC Symbol;Acc:29665]	0.19	1.11E-12	1.96E-08
206984_s_at	18 q12	RIT2	Ras-like without CAAX 2 [Source:HGNC Symbol;Acc:10017]	0.13	5.28E-12	1.49E-07
230112_at	2 q35	MARCH4	membrane-associated ring finger (C3HC4) 4, E3 ubiquitin protein ligase [Source:HGNC Symbol;Acc:29269]	0.12	1.00E-11	1.49E-07
235009_at	4 p15	BOD1L1	biorientation of chromosomes in cell division 1-like 1 [Source:HGNC Symbol;Acc:31792]	0.18	1.11E-11	1.52E-07
209966_x_at	1 q41	ESRRG	estrogen-related receptor gamma [Source:HGNC Symbol;Acc:3474]	0.16	1.71E-11	3.16E-07
1555609_a_at	3 q26	ZMAT3	zinc finger, matrin-type 3 [Source:HGNC Symbol;Acc:29983]	0.18	3.74E-11	3.16E-07
214464_at	1 q42	CDC42BPA	CDC42 binding protein kinase alpha (DMPK-like) [Source:HGNC Symbol;Acc:1737]	0.21	4.07E-11	3.16E-07
235388_at	16 q12	CHD9	chromodomain helicase DNA binding protein 9 [Source:HGNC Symbol;Acc:25701]	0.22	4.55E-11	3.16E-07
208065_at	18 q21	ST8SIA3	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 3 [Source:HGNC Symbol;Acc:14269]	0.17	8.63E-11	5.58E-07

210693_at	19 p13	SPPL2B	signal peptide peptidase like 2B [Source:HGNC Symbol;Acc:30627]	0.19	1.32E-10	5.58E-07
1553415_at	12 q23	SLC17A8	solute carrier family 17 (vesicular glutamate transporter), member 8 [Source:HGNC Symbol;Acc:20151]	0.17	1.80E-10	1.69E-06
229399_at	10 q25	C10orf118	chromosome 10 open reading frame 118 [Source:HGNC Symbol;Acc:24349]	0.20	2.13E-10	3.18E-06
221683_s_at	12 q21	CEP290	centrosomal protein 290kDa [Source:HGNC Symbol;Acc:29021]	0.22	2.75E-10	5.64E-06
242665_at	2 q23	FMNL2	formin-like 2 [Source:HGNC Symbol;Acc:18267]	0.24	6.10E-10	1.21E-05
204840_s_at	12 q22	EEA1	early endosome antigen 1 [Source:HGNC Symbol;Acc:3185]	0.21	1.19E-09	1.21E-05
206013_s_at	7 q22	ACTL6B	actin-like 6B [Source:HGNC Symbol;Acc:160]	0.18	1.33E-09	1.21E-05
236620_at	2 q23	RIF1	RAP1 interacting factor homolog (yeast) [Source:HGNC Symbol;Acc:23207]	0.25	1.35E-09	1.21E-05
216375_s_at	3 q27	ETV5	ets variant 5 [Source:HGNC Symbol;Acc:3494]	0.19	1.56E-09	1.25E-05
219387_at	2 p16	CCDC88A	coiled-coil domain containing 88A [Source:HGNC Symbol;Acc:25523]	0.22	2.21E-09	1.25E-05
233064_at	19 p13	ZFR2	zinc finger RNA binding protein 2 [Source:HGNC Symbol;Acc:29189]	0.17	2.89E-09	1.25E-05
227608_at	11 q12	HNRNPUL2	heterogeneous nuclear ribonucleoprotein U-like 2 [Source:HGNC Symbol;Acc:25451]	0.29	3.16E-09	1.25E-05
204035_at	2 q36	SCG2	secretogranin II [Source:HGNC Symbol;Acc:10575]	0.27	3.29E-09	1.86E-05
234919_s_at	8 q11	SNTG1	syntrophin, gamma 1 [Source:HGNC Symbol;Acc:13740]	0.21	3.66E-09	4.02E-05
209891_at	2 q31	SPC25	SPC25, NDC80 kinetochore complex component [Source:HGNC Symbol;Acc:24031]	0.22	6.08E-09	4.02E-05
204584_at	X q28	L1CAM	L1 cell adhesion molecule [Source:HGNC Symbol;Acc:6470]	0.22	7.47E-09	4.02E-05
206381_at	2 q24	SCN2A	sodium channel, voltage-gated, type II, alpha subunit [Source:HGNC Symbol;Acc:10588]	0.22	1.07E-08	7.57E-05
220821_at	18 q23	GALR1	galanin receptor 1 [Source:HGNC Symbol;Acc:4132]	0.20	1.46E-08	7.57E-05
226471_at	20 q11	GGT7	gamma-glutamyltransferase 7 [Source:HGNC Symbol;Acc:4259]	0.27	2.20E-08	7.57E-05
233357_at	1 q42	TRIM67	tripartite motif containing 67 [Source:HGNC Symbol;Acc:31859]	0.23	2.31E-08	7.57E-05
1554287_at	7 q22	TRIM4	tripartite motif containing 4 [Source:HGNC Symbol;Acc:16275]	0.25	2.48E-08	9.50E-05
235343_at	1 q32	VASH2	vasohibin 2 [Source:HGNC Symbol;Acc:25723]	0.24	3.04E-08	9.50E-05
204737_s_at	14 q11	MYH6	myosin, heavy chain 6, cardiac muscle, alpha [Source:HGNC Symbol;Acc:7576]	0.22	3.25E-08	9.50E-05
220112_at	5 q11	ANKRD55	ankyrin repeat domain 55 [Source:HGNC Symbol;Acc:25681]	0.24	4.29E-08	0.0001
234701_at	16 q24	ANKRD11	ankyrin repeat domain 11 [Source:HGNC Symbol;Acc:21316]	0.24	4.47E-08	0.0001
1569302_at	11 q21	KIAA1731	KIAA1731 [Source:HGNC Symbol;Acc:29366]	0.28	6.83E-08	0.0002

237828_at	12 q24	SRRM4	serine/arginine repetitive matrix 4 [Source:HGNC Symbol;Acc:29389]	0.21	7.86E-08	0.0002
241585_at	11 p12	LRRC4C	leucine rich repeat containing 4C [Source:HGNC Symbol;Acc:29317]	0.23	7.94E-08	0.0002
242319_at	3 q27	DGKG	diacylglycerol kinase, gamma 90kDa [Source:HGNC Symbol;Acc:2853]	0.23	8.44E-08	0.0002
205184_at	1 q42	GNG4	guanine nucleotide binding protein (G protein), gamma 4 [Source:HGNC Symbol;Acc:4407]	0.30	9.55E-08	0.0002
236390_at	20 p12	SLX4IP	SLX4 interacting protein [Source:HGNC Symbol;Acc:16225]	0.24	1.00E-07	0.0002
206137_at	8 q22	RIMS2	regulating synaptic membrane exocytosis 2 [Source:HGNC Symbol;Acc:17283]	0.25	1.06E-07	0.0002
206849_at	5 q34	GABRG2	gamma-aminobutyric acid (GABA) A receptor, gamma 2 [Source:HGNC Symbol;Acc:4087]	0.19	1.37E-07	0.0002
208427_s_at	9 p21	ELAVL2	ELAV like neuron-specific RNA binding protein 2 [Source:HGNC Symbol;Acc:3313]	0.27	1.44E-07	0.0002
240841_at	14 q13	INSM2	insulinoma-associated 2 [Source:HGNC Symbol;Acc:17539]	0.24	1.48E-07	0.0002
238661_at	8 q12	LINC00966	long intergenic non-protein coding RNA 966 [Source:HGNC Symbol;Acc:48723]	0.25	1.49E-07	0.0002
230475_at	15 q24	C15orf59	chromosome 15 open reading frame 59 [Source:HGNC Symbol;Acc:33753]	0.28	1.56E-07	0.0002
244170_at	5 q11	RAB3C	RAB3C, member RAS oncogene family [Source:HGNC Symbol;Acc:30269]	0.21	1.59E-07	0.0002
1558747_at	18 p11	SMCHD1	structural maintenance of chromosomes flexible hinge domain containing 1 [Source:HGNC Symbol;Acc:29090]	0.28	1.78E-07	0.0002
235880_at	7 q11	SRRM3	serine/arginine repetitive matrix 3 [Source:HGNC Symbol;Acc:26729]	0.27	1.82E-07	0.0002
1552694_at	12 q12	SLC2A13	solute carrier family 2 (facilitated glucose transporter), member 13 [Source:HGNC Symbol;Acc:15956]	0.28	2.01E-07	0.0004
230180_at	22 q13	DDX17	DEAD (Asp-Glu-Ala-Asp) box helicase 17 [Source:HGNC Symbol;Acc:2740]	0.31	2.41E-07	0.0004
205952_at	2 p23	KCNK3	potassium channel, subfamily K, member 3 [Source:HGNC Symbol;Acc:6278]	0.26	2.58E-07	0.0004
206343_s_at	8 p12	NRG1	neuregulin 1 [Source:HGNC Symbol;Acc:7997]	0.23	2.92E-07	0.0004
205481_at	1 q32	ADORA1	adenosine A1 receptor [Source:HGNC Symbol;Acc:262]	0.25	3.20E-07	0.0004
230217_at	8 q12	CLVS1	clavesin 1 [Source:HGNC Symbol;Acc:23139]	0.26	3.43E-07	0.0004
1570395_a_at	12 p13	FAM66C	family with sequence similarity 66, member C [Source:HGNC Symbol;Acc:21644]	0.29	3.54E-07	0.0004
1558411_at	3 q26	EGFEM1P	EGF-like and EMI domain containing 1, pseudogene [Source:HGNC Symbol;Acc:25149]	0.27	3.59E-07	0.0004

1555058_a_at	1 q32	LPGAT1	lysophosphatidylglycerol acyltransferase 1 [Source:HGNC Symbol;Acc:28985]	0.28	3.64E-07	0.0004
229032_at	12 q23	WSCD2	WSC domain containing 2 [Source:HGNC Symbol;Acc:29117]	0.20	4.06E-07	0.0004
203699_s_at	14 q31	DIO2	deiodinase, iodothyronine, type II [Source:HGNC Symbol;Acc:2884]	0.20	4.09E-07	0.0004
1556057_s_at	2 q31	NEUROD1	neuronal differentiation 1 [Source:HGNC Symbol;Acc:7762]	0.27	4.17E-07	0.0006
233084_s_at	10 q26	SYCE1	synaptonemal complex central element protein 1 [Source:HGNC Symbol;Acc:28852]	0.27	4.82E-07	0.0006
207210_at	X q28	GABRA3	gamma-aminobutyric acid (GABA) A receptor, alpha 3 [Source:HGNC Symbol;Acc:4077]	0.30	4.96E-07	0.0006
210814_at	4 q27	TRPC3	transient receptor potential cation channel, subfamily C, member 3 [Source:HGNC Symbol;Acc:12335]	0.30	6.12E-07	0.0008
1553654_at	1 q32	SYT14	synaptotagmin XIV [Source:HGNC Symbol;Acc:23143]	0.29	6.26E-07	0.0008
201291_s_at	17 q21	TOP2A	topoisomerase (DNA) II alpha 170kDa [Source:HGNC Symbol;Acc:11989]	0.24	6.37E-07	0.0008
1555355_a_at	11 q24	ETS1	v-ets avian erythroblastosis virus E26 oncogene homolog 1 [Source:HGNC Symbol;Acc:3488]	0.28	6.40E-07	0.0008
213957_s_at	1 q25	CEP350	centrosomal protein 350kDa [Source:HGNC Symbol;Acc:24238]	0.31	7.47E-07	0.0008
229978_at	16 p13	SHISA9	shisa family member 9 [Source:HGNC Symbol;Acc:37231]	0.24	7.64E-07	0.0008
220675_s_at	22 q13	PNPLA3	patatin-like phospholipase domain containing 3 [Source:HGNC Symbol;Acc:18590]	0.27	7.86E-07	0.0008
1554633_a_at	2 p25	MYT1L	myelin transcription factor 1-like [Source:HGNC Symbol;Acc:7623]	0.25	8.35E-07	0.0008
228986_at	12 q21	OSBPL8	oxysterol binding protein-like 8 [Source:HGNC Symbol;Acc:16396]	0.30	8.61E-07	0.0008
232904_at	3 q26	SLC7A14	solute carrier family 7, member 14 [Source:HGNC Symbol;Acc:29326]	0.29	9.16E-07	0.0008
235957_at	12 q14	GRIP1	glutamate receptor interacting protein 1 [Source:HGNC Symbol;Acc:18708]	0.29	9.29E-07	0.0008
238784_at	12 q14	DPY19L2	dpy-19-like 2 (C. elegans) [Source:HGNC Symbol;Acc:19414]	0.28	9.51E-07	0.0008
1555935_s_at	21 q22	HUNK	hormonally up-regulated Neu-associated kinase [Source:HGNC Symbol;Acc:13326]	0.28	9.58E-07	0.0008
205347_s_at	X q22	TMSB15A	thymosin beta 15a [Source:HGNC Symbol;Acc:30744]	0.26	1.07E-06	0.0009
210479_s_at	15 q22	RORA	RAR-related orphan receptor A [Source:HGNC Symbol;Acc:10258]	0.26	1.11E-06	0.0009
210807_s_at	12 q14	SLC16A7	solute carrier family 16 (monocarboxylate transporter), member 7 [Source:HGNC Symbol;Acc:10928]	0.31	1.20E-06	0.0009
218994_s_at	7 q11	STAG3L4	stromal antigen 3-like 4 (pseudogene) [Source:HGNC Symbol;Acc:33887]	0.30	1.29E-06	0.001
203849_s_at	2 q37	KIF1A	kinesin family member 1A [Source:HGNC Symbol;Acc:888]	0.29	1.32E-06	0.001

1559163_at	7 p14	INHBA-AS1	INHBA antisense RNA 1 [Source:HGNC Symbol;Acc:40303]	0.28	1.33E-06	0.001
239415_at	4 q32	MAP9	microtubule-associated protein 9 [Source:HGNC Symbol;Acc:26118]	0.31	1.40E-06	0.001
227860_at	20 p13	CPXM1	carboxypeptidase X (M14 family), member 1 [Source:HGNC Symbol;Acc:15771]	0.25	1.56E-06	0.001
210319_x_at	5 q35	MSX2	msh homeobox 2 [Source:HGNC Symbol;Acc:7392]	0.26	1.62E-06	0.001
211094_s_at	17 q11	NF1	neurofibromin 1 [Source:HGNC Symbol;Acc:7765]	0.31	1.72E-06	0.001
205967_at	6 p22	HIST1H4C	histone cluster 1, H4c [Source:HGNC Symbol;Acc:4787]	0.35	2.13E-06	0.002
236638_at	2 q21	AMER3	APC membrane recruitment protein 3 [Source:HGNC Symbol;Acc:26771]	0.29	2.19E-06	0.002
235461_at	4 q24	TET2	tet methylcytosine dioxygenase 2 [Source:HGNC Symbol;Acc:25941]	0.29	2.35E-06	0.002
220345_at	2 p12	LRRTM4	leucine rich repeat transmembrane neuronal 4 [Source:HGNC Symbol;Acc:19411]	0.30	2.50E-06	0.002
213067_at	17 p13	MYH10	myosin, heavy chain 10, non-muscle [Source:HGNC Symbol;Acc:7568]	0.34	2.53E-06	0.002
205165_at	3 p21	CELSR3	cadherin, EGF LAG seven-pass G-type receptor 3 [Source:HGNC Symbol;Acc:3230]	0.29	2.61E-06	0.002
223254_s_at	14 q12	G2E3	G2/M-phase specific E3 ubiquitin protein ligase [Source:HGNC Symbol;Acc:20338]	0.34	2.77E-06	0.002
221226_s_at	2 q35	ASIC4	acid-sensing (proton-gated) ion channel family member 4 [Source:HGNC Symbol;Acc:21263]	0.30	2.78E-06	0.002
241801_at	2 q33	PGAP1	post-GPI attachment to proteins 1 [Source:HGNC Symbol;Acc:25712]	0.32	2.87E-06	0.003

Supplementary Table 10. *List of genes differentially expressed between IDH1/2 mutant 1p/19q co-deleted versus 1p/19q intact gliomas.*

Top 100 genes significantly upregulated in 1p/19q co-deleted versus 1p/19q intact tumors.

Affymetrix probeset ID	Gene location	Gene symbol	Gene description	Expression fold change	P-value	Local FDR
230112_at	2 q35	MARCH4	membrane-associated ring finger (C3HC4) 4, E3 ubiquitin protein ligase [Source:HGNC Symbol;Acc:29269]	21,90	2.22E-16	8.34E-14
233064_at	19 p13	ZFR2	zinc finger RNA binding protein 2 [Source:HGNC Symbol;Acc:29189]	18.51	2.22E-16	8.34E-14
206984_s_at	18 q12	RIT2	Ras-like without CAAX 2 [Source:HGNC Symbol;Acc:10017]	12.36	2.22E-16	8.34E-14
241585_at	11 p12	LRRC4C	leucine rich repeat containing 4C [Source:HGNC Symbol;Acc:29317]	12.24	2.22E-16	8.34E-14
216375_s_at	3 q27	ETV5	ets variant 5 [Source:HGNC Symbol;Acc:3494]	10.87	2.22E-16	8.34E-14
1555230_a_at	10 q24	KCNIP2	Kv channel interacting protein 2 [Source:HGNC Symbol;Acc:15522]	10.77	2.22E-16	8.34E-14
210319_x_at	5 q35	MSX2	msh homeobox 2 [Source:HGNC Symbol;Acc:7392]	10.24	2.22E-16	8.34E-14
233357_at	1 q42	TRIM67	tripartite motif containing 67 [Source:HGNC Symbol;Acc:31859]	10.24	2.22E-16	8.34E-14
203699_s_at	14 q31	DIO2	deiodinase, iodothyronine, type II [Source:HGNC Symbol;Acc:2884]	9.90	2.22E-16	8.34E-14
229978_at	16 p13	SHISA9	shisa family member 9 [Source:HGNC Symbol;Acc:37231]	9.86	2.22E-16	8.34E-14
204737_s_at	14 q11	MYH6	myosin, heavy chain 6, cardiac muscle, alpha [Source:HGNC Symbol;Acc:7576]	9.78	2.22E-16	8.34E-14
206849_at	5 q34	GABRG2	gamma-aminobutyric acid (GABA) A receptor, gamma 2 [Source:HGNC Symbol;Acc:4087]	9.60	2.22E-16	8.34E-14
1553415_at	12 q23	SLC17A8	solute carrier family 17 (vesicular glutamate transporter), member 8 [Source:HGNC Symbol;Acc:20151]	9.35	2.22E-16	8.34E-14
227614_at	10 q22	HKDC1	hexokinase domain containing 1 [Source:HGNC Symbol;Acc:23302]	9.28	2.22E-16	8.34E-14
204014_at	8 p12	DUSP4	dual specificity phosphatase 4 [Source:HGNC Symbol;Acc:3070]	8.88	2.22E-16	8.34E-14
229032_at	12 q23	WSCD2	WSC domain containing 2 [Source:HGNC Symbol;Acc:29117]	8.71	2.22E-16	8.34E-14
206013_s_at	7 q22	ACTL6B	actin-like 6B [Source:HGNC Symbol;Acc:160]	8.56	2.22E-16	8.34E-14
205952_at	2 p23	KCNK3	potassium channel, subfamily K, member 3 [Source:HGNC Symbol;Acc:6278]	8.41	2.22E-16	8.34E-14
235343_at	1 q32	VASH2	vasohibin 2 [Source:HGNC Symbol;Acc:25723]	8.41	2.22E-16	8.34E-14
204584_at	X q28	L1CAM	L1 cell adhesion molecule [Source:HGNC Symbol;Acc:6470]	8.34	2.22E-16	8.34E-14
233220_at	9 q31	GRIN3A	glutamate receptor, ionotropic, N-methyl-D-aspartate 3A [Source:HGNC Symbol;Acc:16767]	8.26	2.22E-16	8.34E-14

209591_s_at	20 q13	BMP7	bone morphogenetic protein 7 [Source:HGNC Symbol;Acc:1074]	8.13	2.22E-16	8.34E-14
210735_s_at	15 q22	CA12	carbonic anhydrase XII [Source:HGNC Symbol;Acc:1371]	8.07	2.22E-16	8.34E-14
211022_s_at	X q21	ATRX	alpha thalassemia/mental retardation syndrome X-linked [Source:HGNC Symbol;Acc:886]	8.04	2.22E-16	8.34E-14
209966_x_at	1 q41	ESRRG	estrogen-related receptor gamma [Source:HGNC Symbol;Acc:3474]	7.90	2.22E-16	8.34E-14
208065_at	18 q21	ST8SIA3	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 3 [Source:HGNC Symbol;Acc:14269]	7.78	2.22E-16	8.34E-14
230217_at	8 q12	CLVS1	clavesin 1 [Source:HGNC Symbol;Acc:23139]	7.48	2.22E-16	8.34E-14
227860_at	20 p13	CPXM1	carboxypeptidase X (M14 family), member 1 [Source:HGNC Symbol;Acc:15771]	7.29	2.22E-16	8.34E-14
220112_at	5 q11	ANKRD55	ankyrin repeat domain 55 [Source:HGNC Symbol;Acc:25681]	7.27	2.22E-16	8.34E-14
1554633_a_at	2 p25	MYT1L	myelin transcription factor 1-like [Source:HGNC Symbol;Acc:7623]	7.17	2.22E-16	8.34E-14
229818_at	12 q24	SVOP	SV2 related protein homolog (rat) [Source:HGNC Symbol;Acc:25417]	7.14	2.22E-16	8.34E-14
1555609_a_at	3 q26	ZMAT3	zinc finger, matrin-type 3 [Source:HGNC Symbol;Acc:29983]	7.08	2.22E-16	8.34E-14
206330_s_at	9 q22	SHC3	SHC (Src homology 2 domain containing) transforming protein 3 [Source:HGNC Symbol;Acc:18181]	7.06	2.22E-16	8.34E-14
207873_x_at	22 q12	SEZ6L	seizure related 6 homolog (mouse)-like [Source:HGNC Symbol;Acc:10763]	7.01	2.22E-16	8.34E-14
240841_at	14 q13	INSM2	insulinoma-associated 2 [Source:HGNC Symbol;Acc:17539]	6.66	2.22E-16	8.34E-14
224580_at	12 q13	SLC38A1	solute carrier family 38, member 1 [Source:HGNC Symbol;Acc:13447]	6.50	2.22E-16	8.34E-14
226907_at	6 q25	PPP1R14C	protein phosphatase 1, regulatory (inhibitor) subunit 14C [Source:HGNC Symbol;Acc:14952]	6.42	2.22E-16	8.34E-14
233337_s_at	16 p11	SEZ6L2	seizure related 6 homolog (mouse)-like 2 [Source:HGNC Symbol;Acc:30844]	6.37	2.22E-16	8.34E-14
206137_at	8 q22	RIMS2	regulating synaptic membrane exocytosis 2 [Source:HGNC Symbol;Acc:17283]	6.29	2.22E-16	8.34E-14
221489_s_at	5 q31	SPRY4	sprouty homolog 4 (Drosophila) [Source:HGNC Symbol;Acc:15533]	6.22	2.22E-16	8.34E-14
230788_at	6 p24	GCNT2	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme (I blood group) [Source:HGNC Symbol;Acc:4204]	6.20	2.22E-16	8.34E-14
214954_at	3 p22	SUSD5	sushi domain containing 5 [Source:HGNC Symbol;Acc:29061]	6.10	2.22E-16	8.34E-14
214495_at	22 q12	CACNG2	calcium channel, voltage-dependent, gamma subunit 2 [Source:HGNC Symbol;Acc:1406]	6.09	2.22E-16	8.34E-14
236638_at	2 q21	AMER3	APC membrane recruitment protein 3 [Source:HGNC Symbol;Acc:26771]	5.96	2.22E-16	8.34E-14
223529_at	18 q12	SYT4	synaptotagmin IV [Source:HGNC Symbol;Acc:11512]	5.95	2.22E-16	8.34E-14
230826_at	7 p22	MMD2	monocyte to macrophage differentiation-associated 2 [Source:HGNC Symbol;Acc:30133]	5.83	2.22E-16	8.34E-14

203267_s_at	17 p11	DRG2	developmentally regulated GTP binding protein 2 [Source:HGNC Symbol;Acc:3030]	5.64	2.22E-16	8.34E-14
1558706_a_at	2 p11	ATOH8	atonal homolog 8 (Drosophila) [Source:HGNC Symbol;Acc:24126]	5.61	2.22E-16	8.34E-14
1556641_at	3 q26	SLC7A14	solute carrier family 7, member 14 [Source:HGNC Symbol;Acc:29326]	5.40	2.22E-16	8.34E-14
229550_at	14 q32	UNC79	unc-79 homolog (C. elegans) [Source:HGNC Symbol;Acc:19966]	4.92	2.22E-16	8.34E-14
229313_at	11 p14	ANO5	anoctamin 5 [Source:HGNC Symbol;Acc:27337]	4.83	2.22E-16	8.34E-14
204035_at	2 q36	SCG2	secretogranin II [Source:HGNC Symbol;Acc:10575]	4.74	2.22E-16	8.34E-14
228060_at	6 q22	SLC35F1	solute carrier family 35, member F1 [Source:HGNC Symbol;Acc:21483]	3.97	2.22E-16	8.34E-14
244435_at	10 q26	FAM196A	family with sequence similarity 196, member A [Source:HGNC Symbol;Acc:33859]	5.82	4.44E-16	1.32E-12
210246_s_at	11 p15	ABCC8	ATP-binding cassette, sub-family C (CFTR/MRP), member 8 [Source:HGNC Symbol;Acc:59]	5.10	4.44E-16	1.32E-12
227550_at	10 q25	GFRA1	GDNF family receptor alpha 1 [Source:HGNC Symbol;Acc:4243]	4.35	4.44E-16	1.32E-12
229029_at	5 q22	CAMK4	calcium/calmodulin-dependent protein kinase IV [Source:HGNC Symbol;Acc:1464]	6.53	1.33E-15	5.65E-12
1553997_a_at	16 p11	ASPHD1	aspartate beta-hydroxylase domain containing 1 [Source:HGNC Symbol;Acc:27380]	4.67	1.78E-15	5.65E-12
213676_at	6 p21	TMEM151B	transmembrane protein 151B [Source:HGNC Symbol;Acc:21315]	5.52	2.44E-15	5.65E-12
205165_at	3 p21	CELSR3	cadherin, EGF LAG seven-pass G-type receptor 3 [Source:HGNC Symbol;Acc:3230]	5.56	2.89E-15	5.65E-12
220727_at	14 q31	KCNK10	potassium channel, subfamily K, member 10 [Source:HGNC Symbol;Acc:6273]	4.79	2.89E-15	5.65E-12
213201_s_at	19 q13	TNNT1	troponin T type 1 (skeletal, slow) [Source:HGNC Symbol;Acc:11948]	5.68	3.11E-15	1.24E-11
1554576_a_at	17 q21	ETV4	ets variant 4 [Source:HGNC Symbol;Acc:3493]	6.24	3.55E-15	1.24E-11
213059_at	11 p11	CREB3L1	cAMP responsive element binding protein 3-like 1 [Source:HGNC Symbol;Acc:18856]	5.23	4.00E-15	1.24E-11
239580_at	4 q32	GUCY1A3	guanylate cyclase 1, soluble, alpha 3 [Source:HGNC Symbol;Acc:4685]	5.79	5.33E-15	1.46E-11
225541_at	3 q26	RPL22L1	ribosomal protein L22-like 1 [Source:HGNC Symbol;Acc:27610]	4.41	1.58E-14	5.09E-11
218994_s_at	7 q11	STAG3L4	stromal antigen 3-like 4 (pseudogene) [Source:HGNC Symbol;Acc:33887]	5.18	2.38E-14	5.30E-11
204260_at	20 p12	CHGB	chromogranin B (secretogranin 1) [Source:HGNC Symbol;Acc:1930]	3.93	3.06E-14	5.30E-11
238617_at	1 q44	KIF26B	kinesin family member 26B [Source:HGNC Symbol;Acc:25484]	4.88	5.28E-14	1.21E-10
204713_s_at	1 q24	F5	coagulation factor V (proaccelerin, labile factor) [Source:HGNC Symbol;Acc:3542]	8.43	6.82E-14	1.66E-10
233025_at	5 p13	PDZD2	PDZ domain containing 2 [Source:HGNC Symbol;Acc:18486]	5.23	8.26E-14	1.66E-10

219361_s_at	15 q26	AEN	apoptosis enhancing nuclease [Source:HGNC Symbol;Acc:25722]	4.79	9.04E-14	1.66E-10
227522_at	5 p15	CMBL	carboxymethylenebutenolidase homolog (Pseudomonas) [Source:HGNC Symbol;Acc:25090]	3.32	9.26E-14	1.66E-10
237828_at	12 q24	SRRM4	serine/arginine repetitive matrix 4 [Source:HGNC Symbol;Acc:29389]	6.10	1.74E-13	3.59E-10
208211_s_at	2 p23	ALK	anaplastic lymphoma receptor tyrosine kinase [Source:HGNC Symbol;Acc:427]	5.12	1.98E-13	4.24E-10
229651_at	17 q11	SEZ6	seizure related 6 homolog (mouse) [Source:HGNC Symbol;Acc:15955]	4.15	2.08E-13	4.24E-10
220821_at	18 q23	GALR1	galanin receptor 1 [Source:HGNC Symbol;Acc:4132]	6.24	2.31E-13	4.24E-10
228490_at	15 q26	ABHD2	abhydrolase domain containing 2 [Source:HGNC Symbol;Acc:18717]	4.60	3.00E-13	4.24E-10
235880_at	7 q11	SRRM3	serine/arginine repetitive matrix 3 [Source:HGNC Symbol;Acc:26729]	5.21	3.05E-13	6.28E-10
205733_at	15 q26	BLM	Bloom syndrome, RecQ helicase-like [Source:HGNC Symbol;Acc:1058]	5.80	3.36E-13	6.28E-10
210814_at	4 q27	TRPC3	transient receptor potential cation channel, subfamily C, member 3 [Source:HGNC Symbol;Acc:12335]	4.55	3.46E-13	6.28E-10
1555958_at	10 q24	CRTAC1	cartilage acidic protein 1 [Source:HGNC Symbol;Acc:14882]	3.93	4.16E-13	6.28E-10
212279_at	17 q11	TMEM97	transmembrane protein 97 [Source:HGNC Symbol;Acc:28106]	3.02	4.39E-13	6.28E-10
220345_at	2 p12	LRRTM4	leucine rich repeat transmembrane neuronal 4 [Source:HGNC Symbol;Acc:19411]	4.57	4.52E-13	6.28E-10
205230_at	12 q24	RPH3A	rabphilin 3A homolog (mouse) [Source:HGNC Symbol;Acc:17056]	4.87	4.80E-13	6.28E-10
206395_at	3 q27	DGKG	diacylglycerol kinase, gamma 90kDa [Source:HGNC Symbol;Acc:2853]	4.23	5.29E-13	1.68E-09
204465_s_at	10 q24	INA	internexin neuronal intermediate filament protein, alpha [Source:HGNC Symbol;Acc:6057]	3.75	7.47E-13	1.68E-09
219668_at	20 q13	GDAP1L1	ganglioside induced differentiation associated protein 1-like 1 [Source:HGNC Symbol;Acc:4213]	4.22	7.64E-13	1.68E-09
232027_at	6 q25	SYNE1	spectrin repeat containing, nuclear envelope 1 [Source:HGNC Symbol;Acc:17089]	5.38	8.56E-13	1.68E-09
220675_s_at	22 q13	PNPLA3	patatin-like phospholipase domain containing 3 [Source:HGNC Symbol;Acc:18590]	5.35	9.62E-13	1.68E-09
1553654_at	1 q32	SYT14	synaptotagmin XIV [Source:HGNC Symbol;Acc:23143]	4.76	1.00E-12	1.68E-09
230475_at	15 q24	C15orf59	chromosome 15 open reading frame 59 [Source:HGNC Symbol;Acc:33753]	4.38	1.14E-12	1.68E-09
209891_at	2 q31	SPC25	SPC25, NDC80 kinetochore complex component [Source:HGNC Symbol;Acc:24031]	5.46	1.16E-12	1.68E-09
205390_s_at	8 p11	ANK1	ankyrin 1, erythrocytic [Source:HGNC Symbol;Acc:492]	4.88	1.16E-12	1.68E-09
225777_at	9 q34	SAPCD2	suppressor APC domain containing 2 [Source:HGNC Symbol;Acc:28055]	3.96	1.28E-12	1.68E-09
204870_s_at	20 p12	PCSK2	proprotein convertase subtilisin/kexin type 2 [Source:HGNC Symbol;Acc:8744]	4.81	1.60E-12	1.68E-09

221585_at	17 q24	CACNG4	calcium channel, voltage-dependent. gamma subunit 4 [Source:HGNC Symbol;Acc:1408]	4.50	1.90E-12	2.24E-09
233084_s_at	10 q26	SYCE1	synaptonemal complex central element protein 1 [Source:HGNC Symbol;Acc:28852]	5.28	1.97E-12	2.24E-09
212768_s_at	13 q14	OLFM4	olfactomedin 4 [Source:HGNC Symbol;Acc:17190]	5.60	2.20E-12	2.24E-09
1559163_at	7 p14	INHBA-AS1	INHBA antisense RNA 1 [Source:HGNC Symbol;Acc:40303]	5.25	2.45E-12	2.82E-09

Top 100 genes significantly downregulated in 1p/19q co-deleted versus 1p/19q intact tumors

Affymetrix probeset ID	**Gene location**	**Gene symbol**	**Gene description**	**Expression fold change**	**P-value**	**Local FDR**
243952_at	22 q11	TPTEP1	transmembrane phosphatase with tensin homology pseudogene 1 [Source:HGNC Symbol;Acc:43648]	0.01	2.22E-16	8.34E-14
204320_at	1 p21	COL11A1	collagen, type XI, alpha 1 [Source:HGNC Symbol;Acc:2186]	0.04	2.22E-16	8.34E-14
226192_at	X q12	AR	androgen receptor [Source:HGNC Symbol;Acc:644]	0.05	2.22E-16	8.34E-14
243337_at	4 q31	FREM3	FRAS1 related extracellular matrix 3 [Source:HGNC Symbol;Acc:25172]	0.05	2.22E-16	8.34E-14
207107_at	1 p31	RPE65	retinal pigment epithelium-specific protein 65kDa [Source:HGNC Symbol;Acc:10294]	0.06	2.22E-16	8.34E-14
203868_s_at	1 p21	VCAM1	vascular cell adhesion molecule 1 [Source:HGNC Symbol;Acc:12663]	0.08	2.22E-16	8.34E-14
205466_s_at	4 p15	HS3ST1	heparan sulfate (glucosamine) 3-O-sulfotransferase 1 [Source:HGNC Symbol;Acc:5194]	0.08	2.22E-16	8.34E-14
230561_s_at	2 q34	KANSL1L	KAT8 regulatory NSL complex subunit 1-like [Source:HGNC Symbol;Acc:26310]	0.09	2.22E-16	8.34E-14
229816_at	1 p31	WDR78	WD repeat domain 78 [Source:HGNC Symbol;Acc:26252]	0.09	2.22E-16	8.34E-14
228504_at	2 q24	SCN7A	sodium channel, voltage-gated, type VII, alpha subunit [Source:HGNC Symbol;Acc:10594]	0.09	2.22E-16	8.34E-14
235201_at	7 q31	FOXP2	forkhead box P2 [Source:HGNC Symbol;Acc:13875]	0.10	2.22E-16	8.34E-14
213506_at	5 q13	F2RL1	coagulation factor II (thrombin) receptor-like 1 [Source:HGNC Symbol;Acc:3538]	0.10	2.22E-16	8.34E-14
223737_x_at	18 q11	CHST9	carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9 [Source:HGNC Symbol;Acc:19898]	0.10	2.22E-16	8.34E-14
202833_s_at	14 q32	SERPINA1	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 [Source:HGNC Symbol;Acc:8941]	0.11	2.22E-16	8.34E-14
235275_at	1 p34	BMP8B	bone morphogenetic protein 8b [Source:HGNC Symbol;Acc:1075]	0.11	2.22E-16	8.34E-14
219747_at	4 q27	NDNF	neuron-derived neurotrophic factor [Source:HGNC Symbol;Acc:26256]	0.12	2.22E-16	8.34E-14

227300_at	12 q23	TMEM119	transmembrane protein 119 [Source:HGNC Symbol;Acc:27884]	0.12	2.22E-16	8.34E-14
231044_at	1 p13	C1orf194	chromosome 1 open reading frame 194 [Source:HGNC Symbol;Acc:32331]	0.13	2.22E-16	8.34E-14
242086_at	1 p33	SPATA6	spermatogenesis associated 6 [Source:HGNC Symbol;Acc:18309]	0.13	2.22E-16	8.34E-14
203085_s_at	19 q13	TGFB1	transforming growth factor, beta 1 [Source:HGNC Symbol;Acc:11766]	0.13	2.22E-16	8.34E-14
1553202_at	10 q21	STOX1	storkhead box 1 [Source:HGNC Symbol;Acc:23508]	0.13	2.22E-16	8.34E-14
204472_at	8 q22	GEM	GTP binding protein overexpressed in skeletal muscle [Source:HGNC Symbol;Acc:4234]	0.13	2.22E-16	8.34E-14
1552931_a_at	15 q25	PDE8A	phosphodiesterase 8A [Source:HGNC Symbol;Acc:8793]	0.14	2.22E-16	8.34E-14
228442_at	20 q13	NFATC2	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 [Source:HGNC Symbol;Acc:7776]	0.14	2.22E-16	8.34E-14
226068_at	9 q22	SYK	spleen tyrosine kinase [Source:HGNC Symbol;Acc:11491]	0.14	2.22E-16	8.34E-14
202295_s_at	15 q25	CTSH	cathepsin H [Source:HGNC Symbol;Acc:2535]	0.15	2.22E-16	8.34E-14
206012_at	1 q42	LEFTY2	left-right determination factor 2 [Source:HGNC Symbol;Acc:3122]	0.15	2.22E-16	8.34E-14
238135_at	1 p36	AGTRAP	angiotensin II receptor-associated protein [Source:HGNC Symbol;Acc:13539]	0.16	2.22E-16	8.34E-14
211105_s_at	18 q23	NFATC1	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1 [Source:HGNC Symbol;Acc:7775]	0.16	2.22E-16	8.34E-14
220991_s_at	7 q36	RNF32	ring finger protein 32 [Source:HGNC Symbol;Acc:17118]	0.17	2.22E-16	8.34E-14
223660_at	1 p13	ADORA3	adenosine A3 receptor [Source:HGNC Symbol;Acc:268]	0.12	4.44E-16	1.32E-12
1558101_at	1 p31	NFIA	nuclear factor I/A [Source:HGNC Symbol;Acc:7784]	0.15	4.44E-16	1.32E-12
226909_at	4 p16	ZNF518B	zinc finger protein 518B [Source:HGNC Symbol;Acc:29365]	0.16	4.44E-16	1.32E-12
211286_x_at	X p22	CSF2RA	colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage) [Source:HGNC Symbol;Acc:2435]	0.16	4.44E-16	1.32E-12
227091_at	7 q11	CCDC146	coiled-coil domain containing 146 [Source:HGNC Symbol;Acc:29296]	0.19	4.44E-16	1.32E-12
222236_s_at	1 p36	ASAP3	ArfGAP with SH3 domain, ankyrin repeat and PH domain 3 [Source:HGNC Symbol;Acc:14987]	0.23	4.44E-16	1.32E-12
215813_s_at	9 q33	PTGS1	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase) [Source:HGNC Symbol;Acc:9604]	0.15	6.66E-16	5.30E-12
206432_at	8 q24	HAS2	hyaluronan synthase 2 [Source:HGNC Symbol;Acc:4819]	0.15	6.66E-16	5.30E-12
220005_at	3 q25	P2RY13	purinergic receptor P2Y, G-protein coupled, 13 [Source:HGNC Symbol;Acc:4537]	0.16	6.66E-16	5.30E-12
227346_at	7 p12	IKZF1	IKAROS family zinc finger 1 (Ikaros) [Source:HGNC Symbol;Acc:13176]	0.16	6.66E-16	5.30E-12
207826_s_at	1 p36	ID3	inhibitor of DNA binding 3, dominant negative helix-loop-helix protein [Source:HGNC Symbol;Acc:5362]	0.27	6.66E-16	5.30E-12

206811_at	8 q24	ADCY8	adenylate cyclase 8 (brain) [Source:HGNC Symbol;Acc:239]	0.13	1.11E-15	5.30E-12
219202_at	17 q25	RHBDF2	rhomboid 5 homolog 2 (Drosophila) [Source:HGNC Symbol;Acc:20788]	0.17	1.33E-15	5.65E-12
212873_at	19 p13	HMHA1	histocompatibility (minor) HA-1 [Source:HGNC Symbol;Acc:17102]	0.17	1.78E-15	5.65E-12
204439_at	1 p31	IFI44L	interferon-induced protein 44-like [Source:HGNC Symbol;Acc:17817]	0.19	2.00E-15	5.65E-12
219235_s_at	1 p35	PHACTR4	phosphatase and actin regulator 4 [Source:HGNC Symbol;Acc:25793]	0.22	2.22E-15	5.65E-12
232231_at	6 p21	RUNX2	runt-related transcription factor 2 [Source:HGNC Symbol;Acc:10472]	0.14	2.44E-15	5.65E-12
213992_at	X q22	COL4A6	collagen, type IV, alpha 6 [Source:HGNC Symbol;Acc:2208]	0.16	2.44E-15	5.65E-12
220146_at	X p22	TLR7	toll-like receptor 7 [Source:HGNC Symbol;Acc:15631]	0.14	2.66E-15	5.65E-12
1552367_a_at	7 p21	SCIN	scinderin [Source:HGNC Symbol;Acc:21695]	0.14	3.11E-15	1.24E-11
219994_at	10 p12	APBB1IP	amyloid beta (A4) precursor protein-binding, family B, member 1 interacting protein [Source:HGNC Symbol;Acc:17379]	0.17	3.11E-15	1.24E-11
219256_s_at	4 p16	SH3TC1	SH3 domain and tetratricopeptide repeats 1 [Source:HGNC Symbol;Acc:26009]	0.15	4.44E-15	1.24E-11
202096_s_at	22 q13	TSPO	translocator protein (18kDa) [Source:HGNC Symbol;Acc:1158]	0.20	4.44E-15	1.24E-11
204174_at	13 q12	ALOX5AP	arachidonate 5-lipoxygenase-activating protein [Source:HGNC Symbol;Acc:436]	0.16	6.00E-15	1.46E-11
210895_s_at	3 q13	CD86	CD86 molecule [Source:HGNC Symbol;Acc:1705]	0.16	6.44E-15	1.46E-11
1553411_s_at	18 q23	SALL3	spalt-like transcription factor 3 [Source:HGNC Symbol;Acc:10527]	0.15	6.66E-15	1.46E-11
229435_at	9 p24	GLIS3	GLIS family zinc finger 3 [Source:HGNC Symbol;Acc:28510]	0.19	7.11E-15	4.24E-11
205786_s_at	16 p11	ITGAM	integrin, alpha M (complement component 3 receptor 3 subunit) [Source:HGNC Symbol;Acc:6149]	0.19	1.18E-14	4.77E-11
220061_at	16 p12	ACSM5	acyl-CoA synthetase medium-chain family member 5 [Source:HGNC Symbol;Acc:26060]	0.17	1.20E-14	5.09E-11
209879_at	12 q24	SELPLG	selectin P ligand [Source:HGNC Symbol;Acc:10722]	0.19	1.73E-14	5.30E-11
213160_at	5 q35	DOCK2	dedicator of cytokinesis 2 [Source:HGNC Symbol;Acc:2988]	0.18	1.89E-14	5.30E-11
226789_at	5 q11	EMB	embigin [Source:HGNC Symbol;Acc:30465]	0.16	2.35E-14	5.30E-11
235783_at	1 p36	MRTO4	mRNA turnover 4 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:18477]	0.20	3.13E-14	5.30E-11
213258_at	2 q32	TFPI	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor) [Source:HGNC Symbol;Acc:11760]	0.15	3.40E-14	5.83E-11
206726_at	4 q22	HPGDS	hematopoietic prostaglandin D synthase [Source:HGNC Symbol;Acc:17890]	0.16	3.42E-14	1.21E-10
230252_at	12 p13	LPAR5	lysophosphatidic acid receptor 5 [Source:HGNC Symbol;Acc:13307]	0.20	4.20E-14	1.21E-10
48659_at	1 p36	MIIP	migration and invasion inhibitory protein [Source:HGNC Symbol;Acc:25715]	0.21	4.33E-14	1.21E-10
204912_at	11 q23	IL10RA	interleukin 10 receptor, alpha [Source:HGNC Symbol;Acc:5964]	0.16	4.42E-14	1.21E-10

204192_at	19 q13	CD37	CD37 molecule [Source:HGNC Symbol;Acc:1666]	0.18	5.55E-14	1.21E-10
226219_at	1 q23	ARHGAP30	Rho GTPase activating protein 30 [Source:HGNC Symbol;Acc:27414]	0.17	5.71E-14	1.21E-10
1555349_a_at	21 q22	ITGB2	integrin, beta 2 (complement component 3 receptor 3 and 4 subunit) [Source:HGNC Symbol;Acc:6155]	0.16	6.02E-14	1.21E-10
1558256_at	19 q11	LINC00662	long intergenic non-protein coding RNA 662 [Source:HGNC Symbol;Acc:27122]	0.22	6.22E-14	1.66E-10
215017_s_at	1 p22	FNBP1L	formin binding protein 1-like [Source:HGNC Symbol;Acc:20851]	0.23	7.59E-14	1.66E-10
205098_at	3 p21	CCR1	chemokine (C-C motif) receptor 1 [Source:HGNC Symbol;Acc:1602]	0.17	8.02E-14	1.66E-10
213125_at	1 q23	OLFML2B	olfactomedin-like 2B [Source:HGNC Symbol;Acc:24558]	0.17	9.84E-14	1.66E-10
209716_at	1 p13	CSF1	colony stimulating factor 1 (macrophage) [Source:HGNC Symbol;Acc:2432]	0.25	1.30E-13	3.59E-10
228462_at	5 p15	IRX2	iroquois homeobox 2 [Source:HGNC Symbol;Acc:14359]	0.14	1.76E-13	3.60E-10
206011_at	11 q22	CASP1	caspase 1, apoptosis-related cysteine peptidase [Source:HGNC Symbol;Acc:1499]	0.18	2.30E-13	4.24E-10
218035_s_at	4 p14	RBM47	RNA binding motif protein 47 [Source:HGNC Symbol;Acc:30358]	0.17	2.66E-13	4.24E-10
230781_at	4 q21	LINC01088	long intergenic non-protein coding RNA 1088 [Source:HGNC Symbol;Acc:49148]	0.17	2.76E-13	4.24E-10
207145_at	2 q32	MSTN	myostatin [Source:HGNC Symbol;Acc:4223]	0.16	2.80E-13	4.24E-10
236646_at	12 p13	TMEM52B	transmembrane protein 52B [Source:HGNC Symbol;Acc:26438]	0.20	2.88E-13	4.24E-10
204429_s_at	1 p36	SLC2A5	solute carrier family 2 (facilitated glucose/fructose transporter), member 5 [Source:HGNC Symbol;Acc:11010]	0.20	3.19E-13	6.28E-10
235802_at	14 q32	PLD4	phospholipase D family, member 4 [Source:HGNC Symbol;Acc:23792]	0.20	4.37E-13	6.28E-10
204787_at	X q12	VSIG4	V-set and immunoglobulin domain containing 4 [Source:HGNC Symbol;Acc:17032]	0.21	4.75E-13	6.28E-10
213566_at	14 q11	RNASE6	ribonuclease, RNase A family, k6 [Source:HGNC Symbol;Acc:10048]	0.18	4.89E-13	6.28E-10
212353_at	8 q13	SULF1	sulfatase 1 [Source:HGNC Symbol;Acc:20391]	0.17	5.10E-13	6.28E-10
203665_at	22 q12	HMOX1	heme oxygenase (decycling) 1 [Source:HGNC Symbol;Acc:5013]	0.15	5.16E-13	6.28E-10
202545_at	3 p21	PRKCD	protein kinase C, delta [Source:HGNC Symbol;Acc:9399]	0.18	7.16E-13	1.68E-09
204446_s_at	10 q11	ALOX5	arachidonate 5-lipoxygenase [Source:HGNC Symbol;Acc:435]	0.21	1.03E-12	1.68E-09
1560751_at	18 q11	AQP4-AS1	AQP4 antisense RNA 1 [Source:HGNC Symbol;Acc:26399]	0.20	1.04E-12	1.68E-09
203591_s_at	1 p34	CSF3R	colony stimulating factor 3 receptor (granulocyte) [Source:HGNC Symbol;Acc:2439]	0.22	1.11E-12	1.68E-09
225384_at	1 p31	DOCK7	dedicator of cytokinesis 7 [Source:HGNC Symbol;Acc:19190]	0.33	1.25E-12	1.68E-09
203104_at	5 q32	CSF1R	colony stimulating factor 1 receptor [Source:HGNC Symbol;Acc:2433]	0.31	1.27E-12	1.68E-09

210644_s_at	19 q13	LAIR1	leukocyte-associated immunoglobulin-like receptor 1 [Source:HGNC Symbol;Acc:6477]	0.19	1.31E-12	1.68E-09
202445_s_at	1 p11	NOTCH2	notch 2 [Source:HGNC Symbol;Acc:7882]	0.23	1.45E-12	1.68E-09
213425_at	3 p14	WNT5A	wingless-type MMTV integration site family, member 5A [Source:HGNC Symbol;Acc:12784]	0.24	1.53E-12	1.68E-09
204924_at	4 q31	TLR2	toll-like receptor 2 [Source:HGNC Symbol;Acc:11848]	0.17	1.62E-12	2.24E-09
228885_at	9 q21	MAMDC2	MAM domain containing 2 [Source:HGNC Symbol;Acc:23673]	0.20	1.78E-12	2.24E-09
203561_at	1 q23	FCGR2A	Fc fragment of IgG, low affinity IIa, receptor (CD32) [Source:HGNC Symbol;Acc:3616]	0.18	1.82E-12	2.24E-09

Supplementary Table 11. *Overview of the major gene ontology terms associated with the gene sets showing differential expression between (i) astrocytic versus oligodendroglial/oligoastrocytic gliomas, (ii) 1p/19q co-deleted versus 1p/19q intact gliomas, and (iii) WHO grade II versus WHO grade III gliomas.* Association strenghts with gene sets were estimated using the gene set enrichment Z-score (GSZ) of the differential log-expression between the respective condition for all genes studied [2, 4]. The p-values obtained are given in parentheses.

Regulation	**Astrocytic (AII+AAIII) versus oligodendroglial/oligoastrocytic (OII/OAII+AOIII/AOAIII) tumors**	**1p/19q co-deleted versus 1p/19q intact tumors**	**WHO grade II versus WHO grade III tumors**
Up	1. chromosome 1 ($<10^{-6}$) 2. chromosome 19 ($<10^{-6}$) 3. inflammatory response ($8\ 10^{-5}$) 4. immune response (2×10^{-4}) 5. innate immune response (2×10^{-4})	1. normal brain ($<10^{-6}$) 2. synaptic transmission ($<10^{-6}$) 3. chromosome 5 (5×10^{-5}) 4. chromosome 2 (3×10^{-4}) 5. nervous system development (3×10^{-4})	1. normal brain ($<10^{-6}$) 2. synaptic transmission ($<10^{-6}$) 3. plasma membrane (9×10^{-5}) 4. postsynaptic membrane (1×10^{-4}) 5. chromosome 19 (3×10^{-4})
Down	1. normal brain ($<10^{-6}$) 2. mitotic cell cycle (2×10^{-4}) 3. chromosome 2 (2×10^{-4}) 4. chromosome 5 (3×10^{-4}) 5. mitochondrion (7×10^{-4})	1. chromosome 1 ($<10^{-6}$) 2. chromosome 19 ($<10^{-6}$) 3. inflammatory response ($<10^{-6}$) 4. immune response ($<10^{-6}$) 5. innate immune response (5×10^{-5})	1. mitotic cell cycle (5×10^{-5}) 2. nucleic acid binding 1×10^{-4}) 3. nucleus (1×10^{-4}) 4. DNA repair (2×10^{-4}) 5. DNA replication (5×10^{-4})

Supplementary Table 12. *List of genes differentially expressed between IDH1/2 mutant gliomas of WHO grade II and III.*

Top 100 genes significantly upregulated in WHO grade II versus WHO grade III tumors.

Affymetrix probeset ID	Chromosomal location	Gene symbol	Gene description	Expression fold change	P-value	Local FDR
206899_at	2 p25	NTSR2	neurotensin receptor 2 [Source:HGNC Symbol;Acc:8040]	5.05	6.70E-10	8.76E-05
214745_at	3 q25	PLCH1	phospholipase C, eta 1 [Source:HGNC Symbol;Acc:29185]	4.01	4.50E-09	8.76E-05
219734_at	3 q13	SIDT1	SID1 transmembrane family, member 1 [Source:HGNC Symbol;Acc:25967]	3.61	1.53E-08	0.0002
208320_at	12 q24	CABP1	calcium binding protein 1 [Source:HGNC Symbol;Acc:1384]	4.55	3.06E-08	0.0002
206384_at	16 p12	CACNG3	calcium channel, voltage-dependent, gamma subunit 3 [Source:HGNC Symbol;Acc:1407]	5.04	3.67E-08	0.0002
231771_at	13 q12	GJB6	gap junction protein, beta 6, 30kDa [Source:HGNC Symbol;Acc:4288]	4.63	3.79E-08	0.0002
232010_at	4 q32	FSTL5	follistatin-like 5 [Source:HGNC Symbol;Acc:21386]	4.12	3.94E-08	0.0002
239275_at	10 q11	FRMPD2	FERM and PDZ domain containing 2 [Source:HGNC Symbol;Acc:28572]	4.04	4.05E-08	0.0002
233059_at	2 q24	KCNJ3	potassium inwardly-rectifying channel, subfamily J, member 3 [Source:HGNC Symbol;Acc:6264]	3.95	4.31E-08	0.0008
214788_x_at	12 q13	DDN	dendrin [Source:HGNC Symbol;Acc:24458]	3.63	5.80E-08	0.001
238697_at	X q26	LINC00086	long intergenic non-protein coding RNA 86 [Source:HGNC Symbol;Acc:34499]	3.31	8.60E-08	0.001
210347_s_at	2 p16	BCL11A	B-cell CLL/lymphoma 11A (zinc finger protein) [Source:HGNC Symbol;Acc:13221]	4.61	1.15E-07	0.001
221950_at	10 q26	EMX2	empty spiracles homeobox 2 [Source:HGNC Symbol;Acc:3341]	3.88	1.19E-07	0.001
210227_at	8 p23	DLGAP2	discs, large (Drosophila) homolog-associated protein 2 [Source:HGNC Symbol;Acc:2906]	3.84	1.48E-07	0.001
223122_s_at	4 q31	SFRP2	secreted frizzled-related protein 2 [Source:HGNC Symbol;Acc:10777]	3.97	1.71E-07	0.001
210381_s_at	11 p15	CCKBR	cholecystokinin B receptor [Source:HGNC Symbol;Acc:1571]	4.12	1.95E-07	0.002
220927_s_at	10 q24	HPSE2	heparanase 2 [Source:HGNC Symbol;Acc:18374]	3.71	2.59E-07	0.002
232003_at	19 q13	PNMAL2	paraneoplastic Ma antigen family-like 2 [Source:HGNC Symbol;Acc:29206]	2.91	4.05E-07	0.002
216452_at	9 q21	TRPM3	transient receptor potential cation channel, subfamily M, member 3 [Source:HGNC Symbol;Acc:17992]	3.25	4.23E-07	0.002

227217_at	9 q22	WNK2	WNK lysine deficient protein kinase 2 [Source:HGNC Symbol;Acc:14542]	3.37	4.62E-07	0.002
213636_at	9 p13	KIAA1045	KIAA1045 [Source:HGNC Symbol;Acc:29180]	4.12	5.61E-07	0.003
235468_at	NA	RBFOX3	RNA binding protein, fox-1 homolog (C. elegans) 3 [Source:HGNC Symbol;Acc:27097]	4.00	8.20E-07	0.005
205485_at	19 q13	RYR1	ryanodine receptor 1 (skeletal) [Source:HGNC Symbol;Acc:10483]	2.97	8.24E-07	0.005
229406_at	NA	RBFOX3	RNA binding protein, fox-1 homolog (C. elegans) 3 [Source:HGNC Symbol;Acc:27097]	3.47	1.02E-06	0.005
210408_s_at	14 q11	CPNE6	copine VI (neuronal) [Source:HGNC Symbol;Acc:2319]	3.77	1.24E-06	0.005
220429_at	4 q26	NDST3	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 3 [Source:HGNC Symbol;Acc:7682]	3.57	1.32E-06	0.005
215972_at	5 q12	PART1	prostate androgen-regulated transcript 1 (non-protein coding) [Source:HGNC Symbol;Acc:17263]	3.35	1.36E-06	0.005
239291_at	9 q21	TRPM3	transient receptor potential cation channel, subfamily M, member 3 [Source:HGNC Symbol;Acc:17992]	3.38	1.80E-06	0.005
230255_at	1 p36	GABRD	gamma-aminobutyric acid (GABA) A receptor, delta [Source:HGNC Symbol;Acc:4084]	3.40	1.95E-06	0.005
207695_s_at	X q26	IGSF1	immunoglobulin superfamily, member 1 [Source:HGNC Symbol;Acc:5948]	3.62	2.17E-06	0.005
204229_at	19 q13	SLC17A7	solute carrier family 17 (vesicular glutamate transporter), member 7 [Source:HGNC Symbol;Acc:16704]	3.56	2.29E-06	0.005
205626_s_at	8 q21	CALB1	calbindin 1, 28kDa [Source:HGNC Symbol;Acc:1434]	3.48	2.49E-06	0.005
206191_at	3 p22	ENTPD3	ectonucleoside triphosphate diphosphohydrolase 3 [Source:HGNC Symbol;Acc:3365]	3.59	3.06E-06	0.007
228194_s_at	10 q25	SORCS1	sortilin-related VPS10 domain containing receptor 1 [Source:HGNC Symbol;Acc:16697]	3.09	3.41E-06	0.007
208359_s_at	22 q13	KCNJ4	potassium inwardly-rectifying channel, subfamily J, member 4 [Source:HGNC Symbol;Acc:6265]	3.24	3.73E-06	0.007
219671_at	1 p34	HPCAL4	hippocalcin like 4 [Source:HGNC Symbol;Acc:18212]	3.38	4.06E-06	0.007
207404_s_at	6 q14	HTR1E	5-hydroxytryptamine (serotonin) receptor 1E, G protein-coupled [Source:HGNC Symbol;Acc:5291]	2.80	4.09E-06	0.007
222920_s_at	12 q13	TESPA1	thymocyte expressed, positive selection associated 1 [Source:HGNC Symbol;Acc:29109]	3.79	4.49E-06	0.007
215267_s_at	19 q13	SLC8A2	solute carrier family 8 (sodium/calcium exchanger), member 2 [Source:HGNC Symbol;Acc:11069]	3.20	4.74E-06	0.007
1557107_at	7 q22	SLC26A4-AS1	SLC26A4 antisense RNA 1 [Source:HGNC Symbol;Acc:22385]	3.14	4.87E-06	0.007

236532_at	11 q22	C11orf87	chromosome 11 open reading frame 87 [Source:HGNC Symbol;Acc:33788]	3.43	4.96E-06	0.007
230238_at	5 q31	SOWAHA	sosondowah ankyrin repeat domain family member A [Source:HGNC Symbol;Acc:27033]	3.32	5.09E-06	0.007
204081_at	11 q24	NRGN	neurogranin (protein kinase C substrate, RC3) [Source:HGNC Symbol;Acc:8000]	3.32	5.26E-06	0.007
205856_at	18 q12	SLC14A1	solute carrier family 14 (urea transporter), member 1 (Kidd blood group) [Source:HGNC Symbol;Acc:10918]	3.24	5.45E-06	0.007
213965_s_at	1 p36	CHD5	chromodomain helicase DNA binding protein 5 [Source:HGNC Symbol;Acc:16816]	3.20	5.82E-06	0.007
219140_s_at	10 q23	RBP4	retinol binding protein 4, plasma [Source:HGNC Symbol;Acc:9922]	3.16	5.86E-06	0.007
204718_at	7 q34	EPHB6	EPH receptor B6 [Source:HGNC Symbol;Acc:3396]	3.22	6.22E-06	0.007
233002_at	14 q32	PPP4R4	protein phosphatase 4, regulatory subunit 4 [Source:HGNC Symbol;Acc:23788]	3.15	6.33E-06	0.007
210400_at	17 q25	GRIN2C	glutamate receptor, ionotropic, N-methyl D-aspartate 2C [Source:HGNC Symbol;Acc:4587]	2.85	6.41E-06	0.007
227053_at	6 p21	PACSIN1	protein kinase C and casein kinase substrate in neurons 1 [Source:HGNC Symbol;Acc:8570]	3.71	6.82E-06	0.007
238426_at	7 q22	TMEM130	transmembrane protein 130 [Source:HGNC Symbol;Acc:25429]	3.72	6.83E-06	0.007
219572_at	7 q31	CADPS2	Ca++-dependent secretion activator 2 [Source:HGNC Symbol;Acc:16018]	2.59	6.86E-06	0.007
232735_at	1 q21	ANKRD34A	ankyrin repeat domain 34A [Source:HGNC Symbol;Acc:27639]	3.14	7.29E-06	0.008
204230_s_at	19 q13	SLC17A7	solute carrier family 17 (vesicular glutamate transporter), member 7 [Source:HGNC Symbol;Acc:16704]	3.48	8.03E-06	0.008
205625_s_at	8 q21	CALB1	calbindin 1, 28kDa [Source:HGNC Symbol;Acc:1434]	3.49	8.23E-06	0.008
235128_at	5 q33	SYNPO	synaptopodin [Source:HGNC Symbol;Acc:30672]	2.89	8.26E-06	0.008
227996_at	13 q32	FARP1	FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived) [Source:HGNC Symbol;Acc:3591]	2.46	8.56E-06	0.008
202768_at	19 q13	FOSB	FBJ murine osteosarcoma viral oncogene homolog B [Source:HGNC Symbol;Acc:3797]	2.92	8.60E-06	0.008
204339_s_at	1 q23	RGS4	regulator of G-protein signaling 4 [Source:HGNC Symbol;Acc:10000]	3.64	8.77E-06	0.008
208457_at	1 p36	GABRD	gamma-aminobutyric acid (GABA) A receptor, delta [Source:HGNC Symbol;Acc:4084]	3.14	9.80E-06	0.01
223121_s_at	4 q31	SFRP2	secreted frizzled-related protein 2 [Source:HGNC Symbol;Acc:10777]	2.97	1.12E-05	0.01
238600_at	4 p16	JAKMIP1	janus kinase and microtubule interacting protein 1 [Source:HGNC	2.72	1.17E-05	0.01

			Symbol;Acc:26460]			
218546_at	1 q41	C1orf115	chromosome 1 open reading frame 115 [Source:HGNC Symbol;Acc:25873]	2.92	1.19E-05	0.01
219308_s_at	1 p31	AK5	adenylate kinase 5 [Source:HGNC Symbol;Acc:365]	3.20	1.43E-05	0.01
214596_at	1 q43	CHRM3	cholinergic receptor, muscarinic 3 [Source:HGNC Symbol;Acc:1952]	3.53	1.48E-05	0.01
230973_at	1 p36	SH2D5	SH2 domain containing 5 [Source:HGNC Symbol;Acc:28819]	2.94	1.49E-05	0.01
241398_at	22 q13	MPPED1	metallophosphoesterase domain containing 1 [Source:HGNC Symbol;Acc:1306]	2.81	1.53E-05	0.01
241717_at	3 p22	MOBP	myelin-associated oligodendrocyte basic protein [Source:HGNC Symbol;Acc:7189]	3.32	1.53E-05	0.01
206084_at	12 q15	PTPRR	protein tyrosine phosphatase, receptor type, R [Source:HGNC Symbol;Acc:9680]	3.38	1.56E-05	0.01
205551_at	15 q26	SV2B	synaptic vesicle glycoprotein 2B [Source:HGNC Symbol;Acc:16874]	3.47	1.59E-05	0.01
228132_at	4 p16	ABLIM2	actin binding LIM protein family, member 2 [Source:HGNC Symbol;Acc:19195]	2.54	1.59E-05	0.01
241805_at	4 p12	GABRG1	gamma-aminobutyric acid (GABA) A receptor, gamma 1 [Source:HGNC Symbol;Acc:4086]	2.80	1.59E-05	0.01
236195_x_at	19 q13	PRKCG	protein kinase C, gamma [Source:HGNC Symbol;Acc:9402]	2.73	1.60E-05	0.01
205113_at	8 p21	NEFM	neurofilament, medium polypeptide [Source:HGNC Symbol;Acc:7734]	3.73	1.62E-05	0.01
210181_s_at	12 q24	CABP1	calcium binding protein 1 [Source:HGNC Symbol;Acc:1384]	3.03	1.70E-05	0.01
207014_at	4 p12	GABRA2	gamma-aminobutyric acid (GABA) A receptor, alpha 2 [Source:HGNC Symbol;Acc:4076]	3.39	1.70E-05	0.01
212664_at	19 p13	TUBB4A	tubulin, beta 4A class IVa [Source:HGNC Symbol;Acc:20774]	2.42	1.71E-05	0.01
1552953_a_at	17 q12	NEUROD2	neuronal differentiation 2 [Source:HGNC Symbol;Acc:7763]	2.79	1.74E-05	0.01
228436_at	1 p13	KCNC4	potassium voltage-gated channel, Shaw-related subfamily, member 4 [Source:HGNC Symbol;Acc:6236]	2.56	1.74E-05	0.01
208321_s_at	12 q24	CABP1	calcium binding protein 1 [Source:HGNC Symbol;Acc:1384]	3.14	1.78E-05	0.01
214735_at	6 q25	IPCEF1	interaction protein for cytohesin exchange factors 1 [Source:HGNC Symbol;Acc:21204]	2.54	1.79E-05	0.01
230972_at	14 q32	ANKRD9	ankyrin repeat domain 9 [Source:HGNC Symbol;Acc:20096]	2.26	1.89E-05	0.02
207316_at	19 q13	HAS1	hyaluronan synthase 1 [Source:HGNC Symbol;Acc:4818]	2.66	1.90E-05	0.02
202071_at	20 q13	SDC4	syndecan 4 [Source:HGNC Symbol;Acc:10661]	2.79	2.05E-05	0.02

203407_at	16 p13	PPL	periplakin [Source:HGNC Symbol;Acc:9273]	3.01	2.12E-05	0.02
235488_at	17 q12	RASL10B	RAS-like, family 10, member B [Source:HGNC Symbol;Acc:30295]	2.70	2.15E-05	0.02
229770_at	12 q24	GLT1D1	glycosyltransferase 1 domain containing 1 [Source:HGNC Symbol;Acc:26483]	2.81	2.20E-05	0.02
204337_at	1 q23	RGS4	regulator of G-protein signaling 4 [Source:HGNC Symbol;Acc:10000]	3.20	2.21E-05	0.02
204505_s_at	8 p21	DMTN	dematin actin binding protein [Source:HGNC Symbol;Acc:3382]	2.62	2.22E-05	0.02
232426_at	15 q26	SV2B	synaptic vesicle glycoprotein 2B [Source:HGNC Symbol;Acc:16874]	3.37	2.43E-05	0.02
206267_s_at	19 p13	MATK	megakaryocyte-associated tyrosine kinase [Source:HGNC Symbol;Acc:6906]	2.41	2.45E-05	0.02
229778_at	12 p12	C12orf39	chromosome 12 open reading frame 39 [Source:HGNC Symbol;Acc:28139]	2.71	2.47E-05	0.02
220331_at	14 q32	CYP46A1	cytochrome P450, family 46, subfamily A, polypeptide 1 [Source:HGNC Symbol;Acc:2641]	2.26	2.47E-05	0.02
213276_at	7 p13	CAMK2B	calcium/calmodulin-dependent protein kinase II beta [Source:HGNC Symbol;Acc:1461]	2.94	2.53E-05	0.02
229039_at	3 p25	SYN2	synapsin II [Source:HGNC Symbol;Acc:11495]	2.92	2.59E-05	0.02
1556096_s_at	15 q21	UNC13C	unc-13 homolog C (C. elegans) [Source:HGNC Symbol;Acc:23149]	3.29	2.62E-05	0.02
205635_at	3 q21	KALRN	kalirin, RhoGEF kinase [Source:HGNC Symbol;Acc:4814]	2.91	2.63E-05	0.02
207557_s_at	1 q43	RYR2	ryanodine receptor 2 (cardiac) [Source:HGNC Symbol;Acc:10484]	2.91	2.75E-05	0.02
228262_at	X p22	MAP7D2	MAP7 domain containing 2 [Source:HGNC Symbol;Acc:25899]	3.29	2.84E-05	0.02
235781_at	9 q34	CACNA1B	calcium channel, voltage-dependent, N type, alpha 1B subunit [Source:HGNC Symbol;Acc:1389]	2.92	2.92E-05	0.02

Top 100 genes significantly downregulated in WHO grade II versus WHO grade III tumors.

Affymetrix probeset ID	Chromosomal location	Gene symbol	Gene description	Expression fold change	P-value	Local FDR
203474_at	5 q13	IQGAP2	IQ motif containing GTPase activating protein 2 [Source:HGNC Symbol;Acc:6111]	0.20	1.27E-10	2.83E-05
218883_s_at	4 q35	CENPU	centromere protein U [Source:HGNC Symbol;Acc:21348]	0.22	2.99E-09	8.76E-05
1555564_a_at	4 q25	CFI	complement factor I [Source:HGNC Symbol;Acc:5394]	0.21	5.72E-09	0.0002
201852_x_at	2 q32	COL3A1	collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]	0.19	1.32E-08	0.0002

205572_at	8 p23	ANGPT2	angiopoietin 2 [Source:HGNC Symbol;Acc:485]	0.29	4.63E-07	0.003
211161_s_at	2 q32	COL3A1	collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]	0.28	5.62E-07	0.003
202291_s_at	12 p12	MGP	matrix Gla protein [Source:HGNC Symbol;Acc:7060]	0.27	6.12E-07	0.005
204162_at	18 p11	NDC80	NDC80 kinetochore complex component [Source:HGNC Symbol;Acc:16909]	0.33	1.04E-06	0.005
206584_at	8 q21	LY96	lymphocyte antigen 96 [Source:HGNC Symbol;Acc:17156]	0.31	1.23E-06	0.005
211966_at	13 q34	COL4A2	collagen, type IV, alpha 2 [Source:HGNC Symbol;Acc:2203]	0.29	1.74E-06	0.005
204146_at	12 p13	RAD51AP1	RAD51 associated protein 1 [Source:HGNC Symbol;Acc:16956]	0.34	1.92E-06	0.005
214467_at	14 q31	GPR65	G protein-coupled receptor 65 [Source:HGNC Symbol;Acc:4517]	0.29	1.96E-06	0.005
210559_s_at	10 q21	CDK1	cyclin-dependent kinase 1 [Source:HGNC Symbol;Acc:1722]	0.32	2.13E-06	0.005
242774_at	14 q23	SYNE2	spectrin repeat containing, nuclear envelope 2 [Source:HGNC Symbol;Acc:17084]	0.29	2.35E-06	0.005
202503_s_at	15 q22	KIAA0101	KIAA0101 [Source:HGNC Symbol;Acc:28961]	0.32	2.62E-06	0.005
201141_at	7 p15	GPNMB	glycoprotein (transmembrane) nmb [Source:HGNC Symbol;Acc:4462]	0.30	2.79E-06	0.005
211981_at	13 q34	COL4A1	collagen, type IV, alpha 1 [Source:HGNC Symbol;Acc:2202]	0.32	2.82E-06	0.005
230550_at	11 q12	MS4A6A	membrane-spanning 4-domains, subfamily A, member 6A [Source:HGNC Symbol;Acc:13375]	0.31	2.86E-06	0.005
215076_s_at	2 q32	COL3A1	collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]	0.29	3.05E-06	0.005
210052_s_at	20 q11	TPX2	TPX2. microtubule-associated [Source:HGNC Symbol;Acc:1249]	0.33	3.19E-06	0.007
222680_s_at	1 q32	DTL	denticleless E3 ubiquitin protein ligase homolog (Drosophila) [Source:HGNC Symbol;Acc:30288]	0.33	4.84E-06	0.007
204822_at	6 q14	TTK	TTK protein kinase [Source:HGNC Symbol;Acc:12401]	0.35	5.88E-06	0.007
219666_at	11 q12	MS4A6A	membrane-spanning 4-domains, subfamily A, member 6A [Source:HGNC Symbol;Acc:13375]	0.32	5.89E-06	0.007
204006_s_at	1 q23	FCGR3A	Fc fragment of IgG, low affinity IIIa, receptor (CD16a) [Source:HGNC Symbol;Acc:3619]	0.27	5.94E-06	0.007
201664_at	3 q25	SMC4	structural maintenance of chromosomes 4 [Source:HGNC Symbol;Acc:14013]	0.37	6.88E-06	0.008
219918_s_at	1 q31	ASPM	asp (abnormal spindle) homolog, microcephaly associated (Drosophila) [Source:HGNC Symbol;Acc:19048]	0.34	7.99E-06	0.008
209773_s_at	2 p25	RRM2	ribonucleotide reductase M2 [Source:HGNC Symbol;Acc:10452]	0.33	8.01E-06	0.008
1552862_at	1 q22	RUSC1-AS1	RUSC1 antisense RNA 1 [Source:HGNC Symbol;Acc:26680]	0.37	8.89E-06	0.008

209138_x_at	22 q11	IGLC2	immunoglobulin lambda constant 2 (Kern-Oz- marker) [Source:HGNC Symbol;Acc:5856]	0.27	8.94E-06	0.008
203214_x_at	10 q21	CDK1	cyclin-dependent kinase 1 [Source:HGNC Symbol;Acc:1722]	0.35	9.15E-06	0.01
205394_at	11 q24	CHEK1	checkpoint kinase 1 [Source:HGNC Symbol;Acc:1925]	0.38	1.07E-05	0.01
219148_at	8 p21	PBK	PDZ binding kinase [Source:HGNC Symbol;Acc:18282]	0.33	1.35E-05	0.01
201291_s_at	17 q21	TOP2A	topoisomerase (DNA) II alpha 170kDa [Source:HGNC Symbol;Acc:11989]	0.31	1.40E-05	0.01
1558411_at	3 q26	EGFEM1P	EGF-like and EMI domain containing 1, pseudogene [Source:HGNC Symbol;Acc:25149]	0.35	1.54E-05	0.01
232724_at	11 q12	MS4A6A	membrane-spanning 4-domains, subfamily A, member 6A [Source:HGNC Symbol;Acc:13375]	0.36	1.55E-05	0.01
209561_at	1 q22	THBS3	thrombospondin 3 [Source:HGNC Symbol;Acc:11787]	0.40	1.68E-05	0.01
208368_s_at	13 q13	BRCA2	breast cancer 2, early onset [Source:HGNC Symbol;Acc:1101]	0.41	1.82E-05	0.02
218542_at	10 q23	CEP55	centrosomal protein 55kDa [Source:HGNC Symbol;Acc:1161]	0.39	1.96E-05	0.02
201744_s_at	12 q21	LUM	lumican [Source:HGNC Symbol;Acc:6724]	0.34	1.99E-05	0.02
227055_at	12 q13	METTL7B	methyltransferase like 7B [Source:HGNC Symbol;Acc:28276]	0.32	2.09E-05	0.02
218663_at	4 p15	NCAPG	non-SMC condensin I complex, subunit G [Source:HGNC Symbol;Acc:24304]	0.37	2.19E-05	0.02
220132_s_at	12 p13	CLEC2D	C-type lectin domain family 2, member D [Source:HGNC Symbol;Acc:14351]	0.38	2.22E-05	0.02
207165_at	5 q34	HMMR	hyaluronan-mediated motility receptor (RHAMM) [Source:HGNC Symbol;Acc:5012]	0.39	2.58E-05	0.02
220821_at	18 q23	GALR1	galanin receptor 1 [Source:HGNC Symbol;Acc:4132]	0.34	2.59E-05	0.02
201292_at	17 q21	TOP2A	topoisomerase (DNA) II alpha 170kDa [Source:HGNC Symbol;Acc:11989]	0.36	2.79E-05	0.02
215170_s_at	15 q21	CEP152	centrosomal protein 152kDa [Source:HGNC Symbol;Acc:29298]	0.41	2.85E-05	0.02
203645_s_at	12 p13	CD163	CD163 molecule [Source:HGNC Symbol;Acc:1631]	0.30	3.31E-05	0.02
210510_s_at	10 p11	NRP1	neuropilin 1 [Source:HGNC Symbol;Acc:8004]	0.40	3.50E-05	0.02
223280_x_at	11 q12	MS4A6A	membrane-spanning 4-domains, subfamily A, member 6A [Source:HGNC Symbol;Acc:13375]	0.35	3.63E-05	0.02
202954_at	20 q13	UBE2C	ubiquitin-conjugating enzyme E2C [Source:HGNC Symbol;Acc:15937]	0.37	3.83E-05	0.02
209040_s_at	6 p21	PSMB8	proteasome (prosome, macropain) subunit, beta type, 8 [Source:HGNC Symbol;Acc:9545]	0.38	3.96E-05	0.02
210260_s_at	5 q23	TNFAIP8	tumor necrosis factor, alpha-induced protein 8 [Source:HGNC	0.40	4.10E-05	0.02

			Symbol;Acc:17260]			
203213_at	10 q21	CDK1	cyclin-dependent kinase 1 [Source:HGNC Symbol;Acc:1722]	0.38	4.37E-05	0.02
214677_x_at	22 q11	IGLL5	immunoglobulin lambda-like polypeptide 5 [Source:HGNC Symbol;Acc:38476]	0.30	4.47E-05	0.02
211864_s_at	10 q23	MYOF	myoferlin [Source:HGNC Symbol;Acc:3656]	0.38	4.61E-05	0.03
227860_at	20 p13	CPXM1	carboxypeptidase X (M14 family), member 1 [Source:HGNC Symbol;Acc:15771]	0.35	5.25E-05	0.03
219978_s_at	15 q15	NUSAP1	nucleolar and spindle associated protein 1 [Source:HGNC Symbol;Acc:18538]	0.37	5.26E-05	0.03
203854_at	4 q25	CFI	complement factor I [Source:HGNC Symbol;Acc:5394]	0.36	5.35E-05	0.03
207714_s_at	11 q13	SERPINH1	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1) [Source:HGNC Symbol;Acc:1546]	0.40	5.69E-05	0.03
209642_at	2 q13	BUB1	BUB1 mitotic checkpoint serine/threonine kinase [Source:HGNC Symbol;Acc:1148]	0.41	6.57E-05	0.05
231725_at	5 q31	PCDHB2	protocadherin beta 2 [Source:HGNC Symbol;Acc:8687]	0.33	7.61E-05	0.05
218755_at	5 q31	KIF20A	kinesin family member 20A [Source:HGNC Symbol;Acc:9787]	0.42	8.06E-05	0.05
226936_at	6 q22	CENPW	centromere protein W [Source:HGNC Symbol;Acc:21488]	0.43	8.22E-05	0.05
208309_s_at	18 q21	MALT1	mucosa associated lymphoid tissue lymphoma translocation gene 1 [Source:HGNC Symbol;Acc:6819]	0.41	8.28E-05	0.05
204846_at	3 q25	CP	ceruloplasmin (ferroxidase) [Source:HGNC Symbol;Acc:2295]	0.34	8.69E-05	0.05
202589_at	18 p11	TYMS	thymidylate synthetase [Source:HGNC Symbol;Acc:12441]	0.42	8.79E-05	0.05
241981_at	17 q24	FAM20A	family with sequence similarity 20, member A [Source:HGNC Symbol;Acc:23015]	0.42	8.93E-05	0.05
230205_at	19 p13	ZNF561	zinc finger protein 561 [Source:HGNC Symbol;Acc:28684]	0.44	9.17E-05	0.05
225646_at	11 q14	CTSC	cathepsin C [Source:HGNC Symbol;Acc:2528]	0.39	9.19E-05	0.05
223922_x_at	11 q12	MS4A6A	membrane-spanning 4-domains, subfamily A, member 6A [Source:HGNC Symbol;Acc:13375]	0.39	9.76E-05	0.05
224356_x_at	11 q12	MS4A6A	membrane-spanning 4-domains, subfamily A, member 6A [Source:HGNC Symbol;Acc:13375]	0.37	9.93E-05	0.05
218710_at	2 p22	TTC27	tetratricopeptide repeat domain 27 [Source:HGNC Symbol;Acc:25986]	0.42	0.00010762	0.05
244434_at	X p11	GPR82	G protein-coupled receptor 82 [Source:HGNC Symbol;Acc:4533]	0.40	0.0001131	0.05
1563629_a_at	16 p13	ERVK13-1	endogenous retrovirus group K13, member 1 [Source:HGNC Symbol;Acc:27548]	0.44	0.00011507	0.05

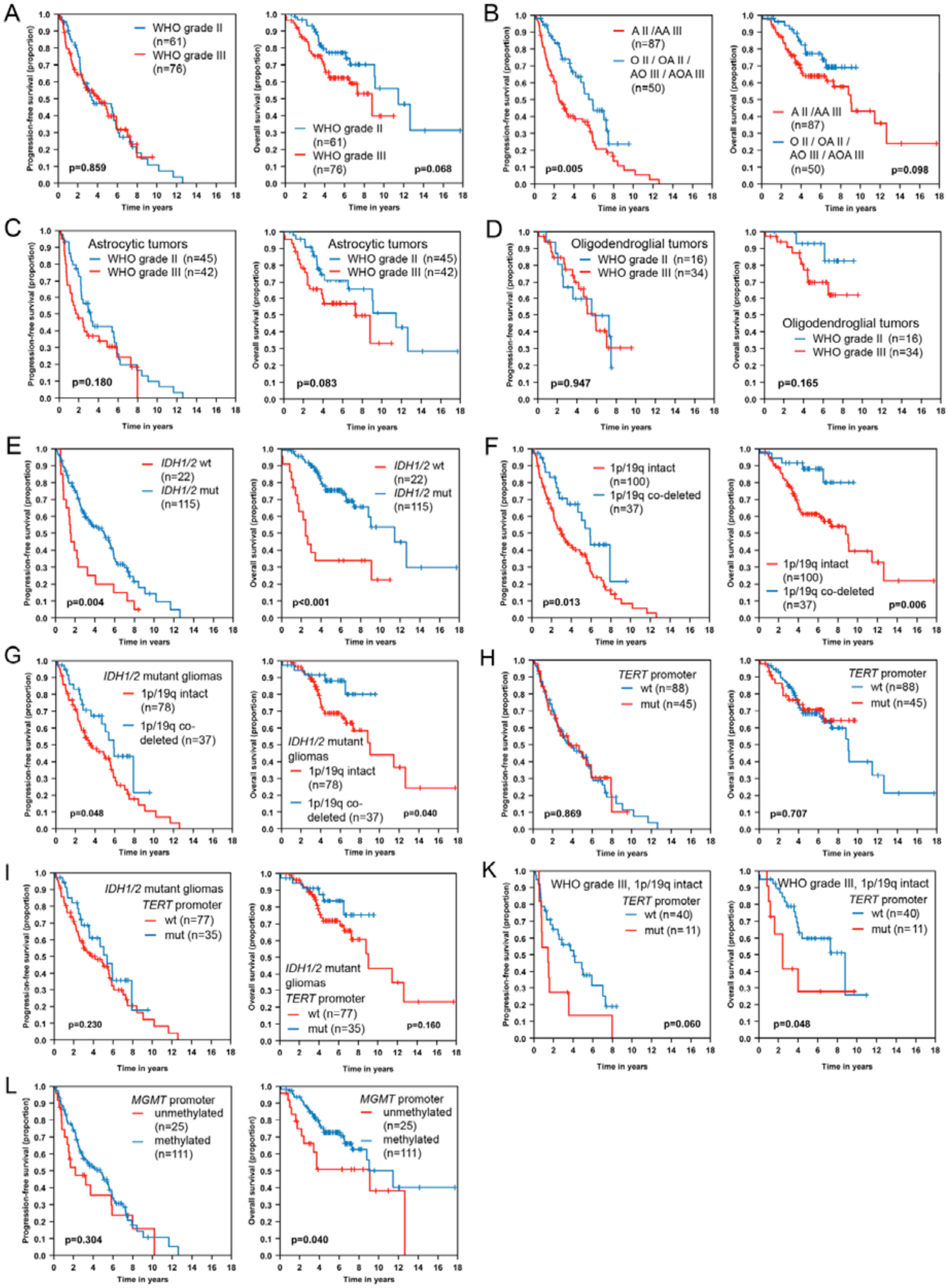
241726_at	21 q22	SIM2	single-minded family bHLH transcription factor 2 [Source:HGNC Symbol;Acc:10883]	0.33	0.00012188	0.05
212865_s_at	8 q24	COL14A1	collagen, type XIV. alpha 1 [Source:HGNC Symbol;Acc:2191]	0.40	0.00012353	0.05
222848_at	5 q12	CENPK	centromere protein K [Source:HGNC Symbol;Acc:29479]	0.42	0.00012921	0.05
229551_x_at	9 q22	ZNF367	zinc finger protein 367 [Source:HGNC Symbol;Acc:18320]	0.44	0.00013057	0.05
215044_s_at	2 q23	STAM2	signal transducing adaptor molecule (SH3 domain and ITAM motif) 2 [Source:HGNC Symbol;Acc:11358]	0.44	0.00013589	0.05
215121_x_at	22 q11	IGLC2	immunoglobulin lambda constant 2 (Kern-Oz- marker) [Source:HGNC Symbol;Acc:5856]	0.34	0.00013899	0.05
213975_s_at	12 q15	LYZ	lysozyme [Source:HGNC Symbol;Acc:6740]	0.36	0.00014084	0.05
213415_at	X q28	CLIC2	chloride intracellular channel 2 [Source:HGNC Symbol;Acc:2063]	0.43	0.00014336	0.05
1555247_a_at	5 q31	RAPGEF6	Rap guanine nucleotide exchange factor (GEF) 6 [Source:HGNC Symbol;Acc:20655]	0.43	0.00014361	0.05
236034_at	8 p23	ANGPT2	angiopoietin 2 [Source:HGNC Symbol;Acc:485]	0.41	0.0001472	0.05
239413_at	15 q21	CEP152	centrosomal protein 152kDa [Source:HGNC Symbol;Acc:29298]	0.45	0.00014832	0.05
1554696_s_at	18 p11	TYMS	thymidylate synthetase [Source:HGNC Symbol;Acc:12441]	0.43	0.00015068	0.05
237261_at	8 p23	ANGPT2	angiopoietin 2 [Source:HGNC Symbol;Acc:485]	0.42	0.00015342	0.05
225303_at	1 q23	KIRREL	kin of IRRE like (Drosophila) [Source:HGNC Symbol;Acc:15734]	0.44	0.00015439	0.05
204962_s_at	2 p23	CENPA	centromere protein A [Source:HGNC Symbol;Acc:1851]	0.45	0.00015741	0.05
225107_at	7 p15	HNRNPA2B1	heterogeneous nuclear ribonucleoprotein A2/B1 [Source:HGNC Symbol;Acc:5033]	0.47	0.00016264	0.05
201890_at	2 p25	RRM2	ribonucleotide reductase M2 [Source:HGNC Symbol;Acc:10452]	0.38	0.00016272	0.05
201508_at	17 q21	IGFBP4	insulin-like growth factor binding protein 4 [Source:HGNC Symbol;Acc:5473]	0.40	0.00016281	0.05
232898_at	5 p13	DAB2	Dab, mitogen-responsive phosphoprotein, homolog 2 (Drosophila) [Source:HGNC Symbol;Acc:2662]	0.44	0.00016298	0.05
201663_s_at	3 q25	SMC4	structural maintenance of chromosomes 4 [Source:HGNC Symbol;Acc:14013]	0.44	0.0001695	0.05
214770_at	8 p22	MSR1	macrophage scavenger receptor 1 [Source:HGNC Symbol;Acc:7376]	0.38	0.00017371	0.05
228144_at	5 q33	ZNF300	zinc finger protein 300 [Source:HGNC Symbol;Acc:13091]	0.47	0.00017614	0.07
223381_at	1 q23	NUF2	NUF2, NDC80 kinetochore complex component [Source:HGNC Symbol;Acc:14621]	0.44	0.00017663	0.08
225681_at	8 q22	CTHRC1	collagen triple helix repeat containing 1 [Source:HGNC Symbol;Acc:18831]	0.42	0.00018948	0.09

210609_s_at	2 p23	TP53I3	tumor protein p53 inducible protein 3 [Source:HGNC Symbol;Acc:19373]	0.43	0.00019882	0.09
218802_at	4 q25	CCDC109B	coiled-coil domain containing 109B [Source:HGNC Symbol;Acc:26076]	0.43	0.00020151	0.09

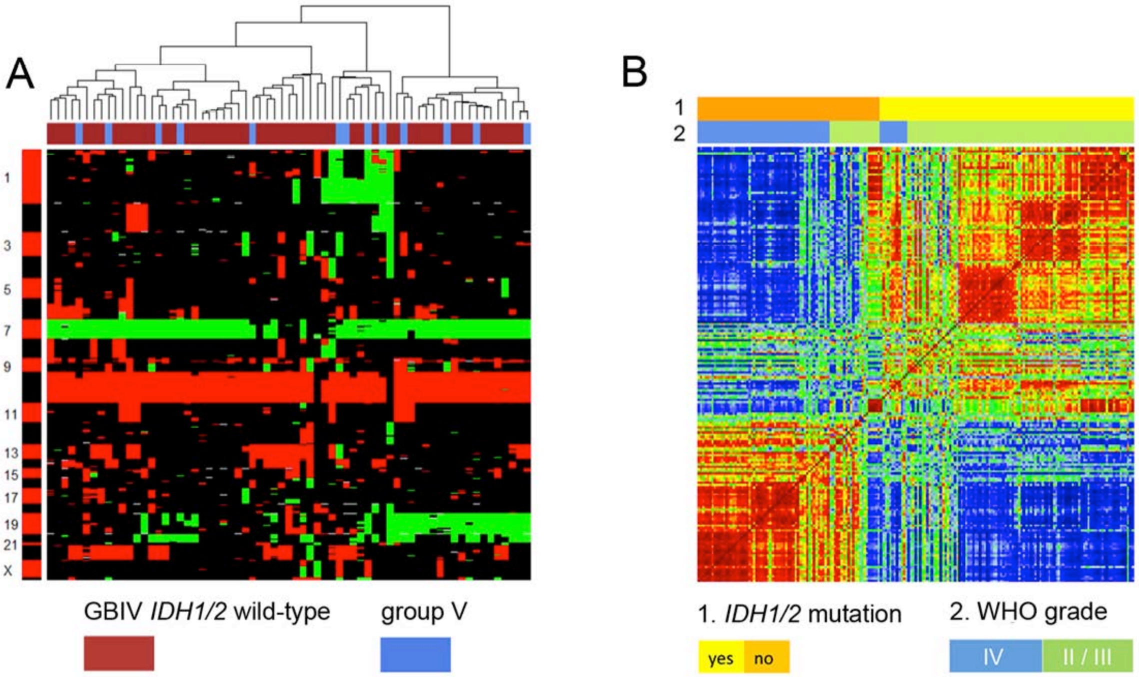
Supplementary Table 13. *Multivariate analyses based on clinical and histological parameters as well as array-CGH analysis with consideration of mRNA expression profiling (integrated molecular groups A-C), or based on IDH1/2 and 1p/19q status alone.*

	Modeling with mRNA expression profiling					
Model	**Factor**	**HR**	**95% CI**	**P value**	**Model fit deviance**	**Improvement**
1	Astrocytic vs. oligodendroglial (ref)	2.59	1.30 - 5.15	0.007	374.02	Model 1 to null model: p<0.001
	WHO grade III vs. WHO grade II (ref)	1.71	0.92 - 3.20	0.090		
	Age > 40 vs. ≤ 40 (ref)	4.40	2.21 - 8.79	<0.001		
2	Age > 40 vs. ≤ 40 (ref)	3.79	1.87 - 7.68	<0.001	371.45	Model 2 to null model: p<0.001
	Group B vs. group A (ref)	2.92	1.03 - 8.31	0.045		
	Group C vs. group A (ref)	8.08	2.38 - 27.49	0.001		
3	Age >40 vs. ≤ 40 (ref)	3.96	1.93 - 8.10	<0.001	367.78	Model 3 to 2: p=0.167
	Group B vs.group A (ref)	2.59	0.83 - 8.05	0.100		
	Group C vs. group A (ref)	5.43	1.36 - 21.64	0.016		
	Astrocytic vs. oligodendroglial (ref)	1.60	0.74 - 3.46	0.230		
	WHO grade III vs. WHO grade II (ref)	1.66	0.88 - 3.14	0.118		
	Modeling based on *IDH1/2* and *1p/19q* status alone					
Model	**Factor**	**HR**	**95% CI**	**P value**	**Model fit deviance**	**Improvement**
1	Astrocytic vs. oligodendroglial (ref)	2.59	1.30 - 5.15	0.007	374.02	Model 1 to null model: p<0.001
	WHO grade III vs. WHO grade II (ref)	1.71	0.92 - 3.20	0.090		
	Age > 40 vs. ≤ 40 (ref)	4.40	2.21 - 8.79	<0.001		
2	Age > 40 vs. ≤ 40 (ref)	4.06	2.00 - 8.25	<0.001	366.87	Model 2 to null model: p<0.001
	IDH mut/1p/19q non- co-deleted vs. 1p/19q co-deleted (ref)	3.67	1.34 - 9.71	0.009		
	IDH wt vs. 1p/19q-co-deleted (ref)	6.82	2.44 - 19.08	<0.001		
3	Age >40 vs. ≤ 40 (ref)	4.05	1.97 - 8.30	<0.001	364.57	Model 3 to 2: p=0.316
	IDH mut/1p/19q non-co-deleted vs. 1p/19q co-deleted (ref)	3.38	1.17 - 9.80	0.025		
	IDH wt vs. 1p/19q co-deleted (ref)	5.52	1.74 - 17.46	0.004		
	Astrocytic vs. oligodendroglial (ref)	1.34	0.62 - 2.87	0.456		
	WHO grade III vs. WHO grade II (ref)	1.56	0.83 - 2.95	0.167		

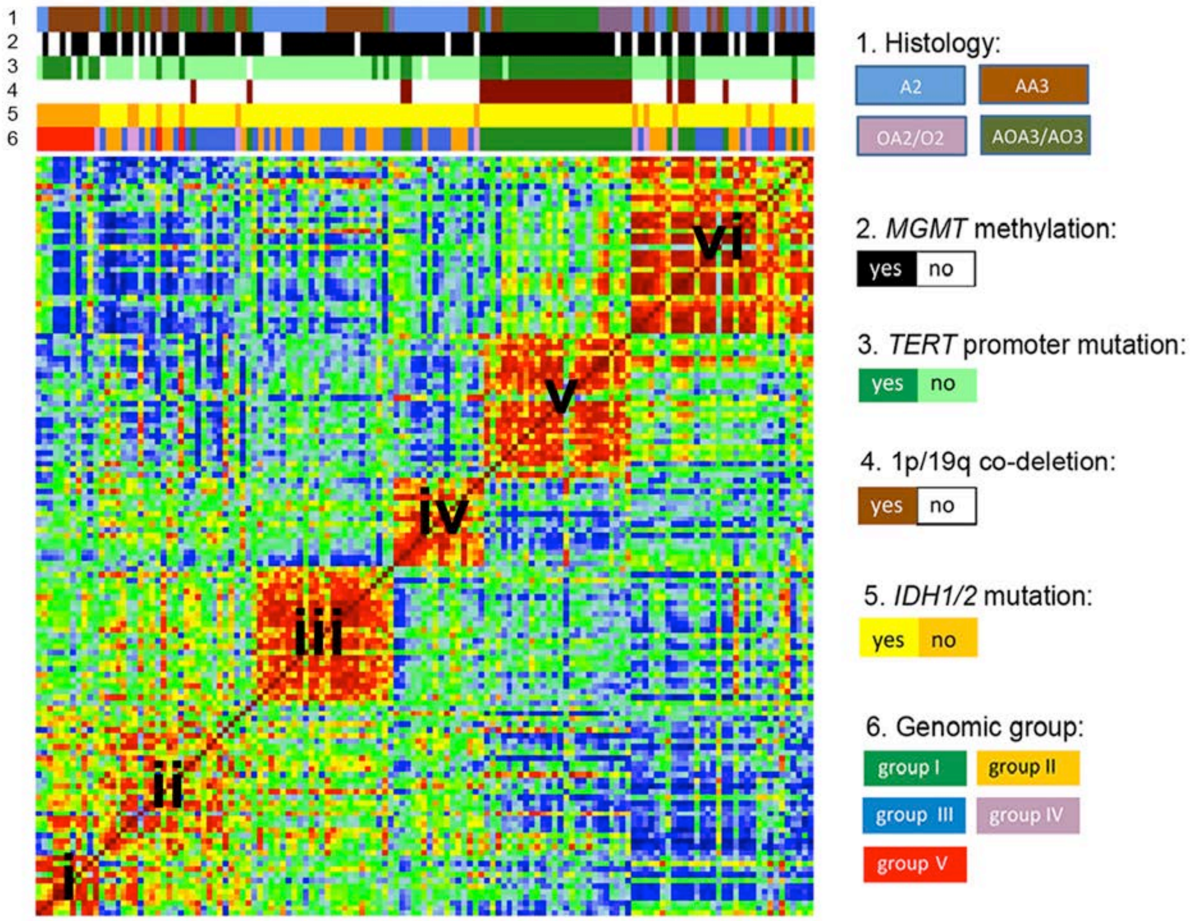
SUPPLEMENTARY FIGURES



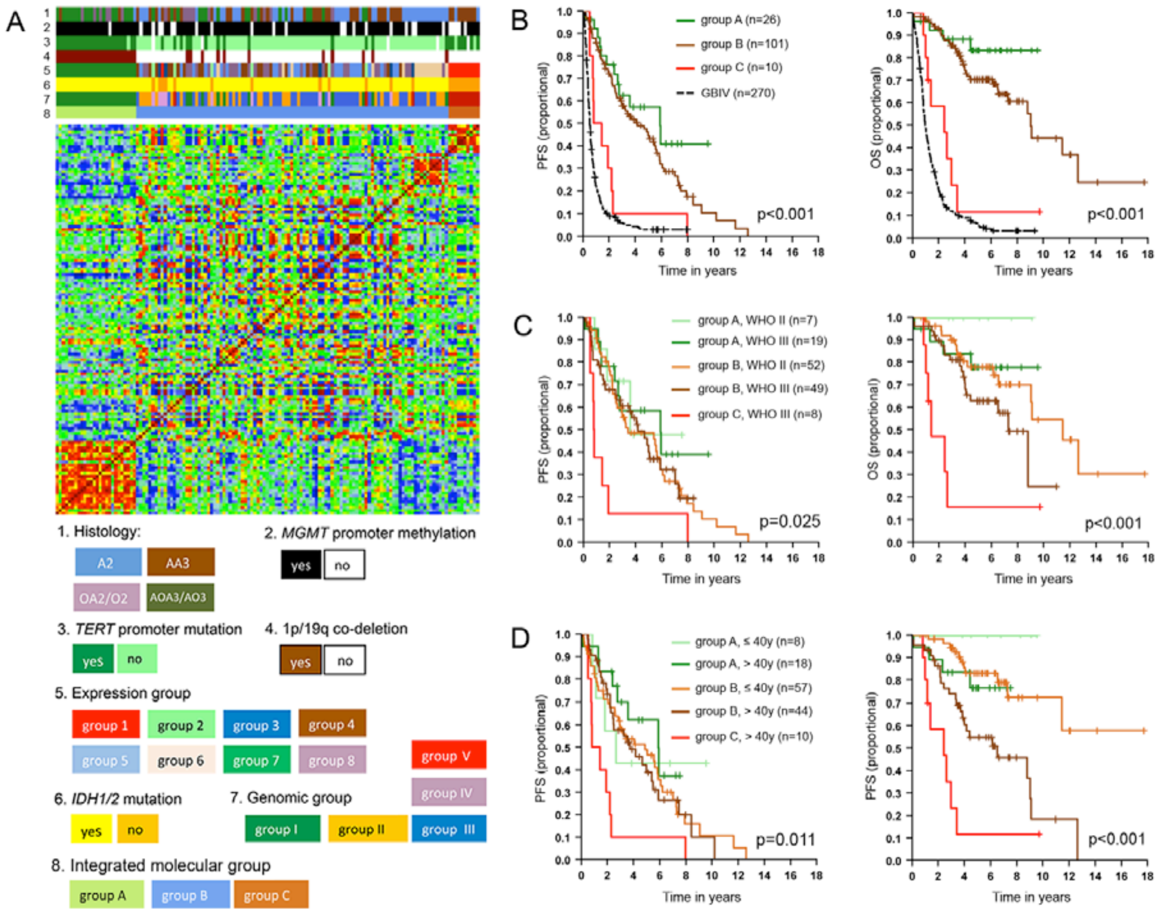
Supplementary Figure 1. *Prognostic associations of WHO grade, tumor type and established molecular markers in the study cohort of 137 glioma patients.* **A.** WHO grade II versus WHO grade III. **B.** Astrocytic histology (AII / AAIII) versus oligodendroglial or oligoastrocytic histology (O II / AO III / OA II / AOA III). **C.** WHO grade II *versus* WHO grade III for astrocytic tumors. **D.** WHO grade II versus WHO grade III for oligodendroglial tumors. **E.** *IDH1/2* mutant versus *IDH1/2* wild-type. **F.** 1p/19q co-deleted versus 1p/19q intact. **G.** 1p/19q co-deleted versus 1p/19q intact in the subgroup of patients with *IDH1/2* mutant tumors. **H.** *TERT* promoter mutant versus wild-type in the entire patient cohort. **I.** *TERT* promoter mutant versus wild-type in the subgroup of patients with *IDH1/2* mutant tumors. **K.** *TERT* promoter mutant versus wild-type in the subgroup of patients with 1p/19q intact anaplastic gliomas of WHO grade III. **L.** *MGMT* promoter methylated versus unmethylated. For each marker, associations with PFS (left) and OS (right) are depicted.



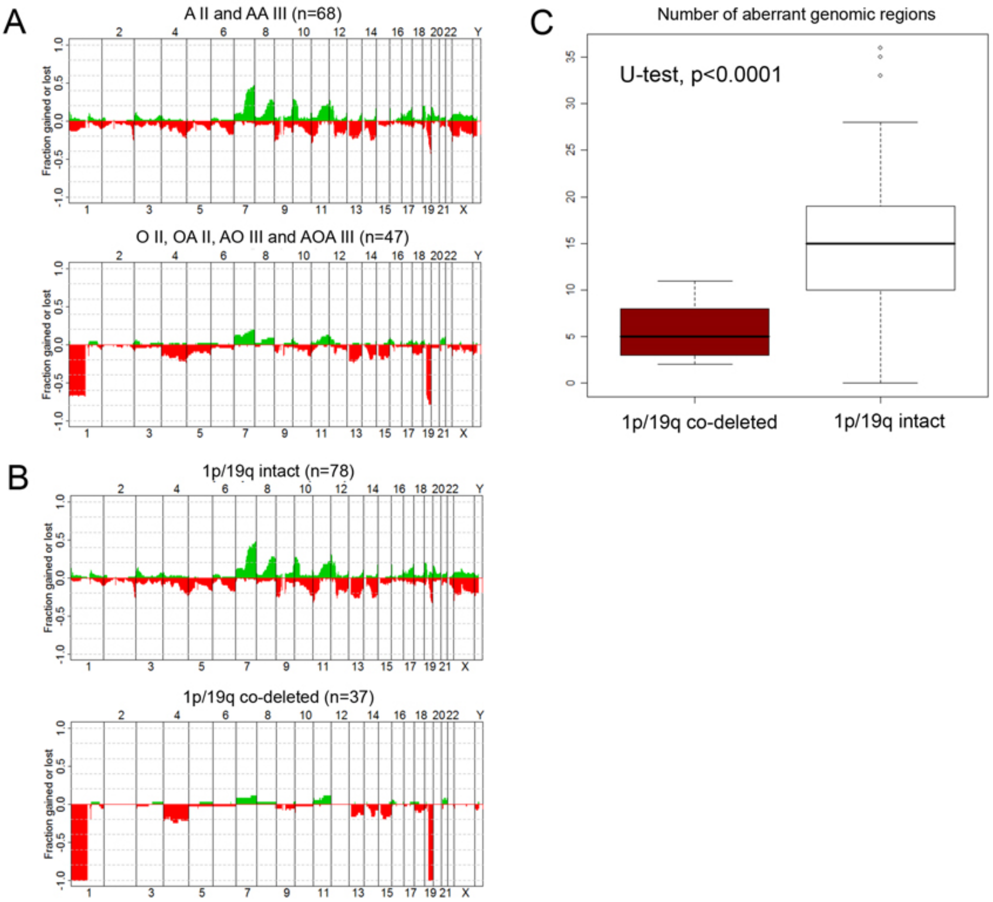
Supplementary Figure 2. A. *Comparison of genomic aberrations in group V gliomas with those in primary IDH1/2 wild-type glioblastomas.* Unsupervised analysis of the 13 group V gliomas together with 54 primary glioblastomas investigated before on the same array-CGH platform [1] revealed that the group V gliomas are loosely distributed among the primary glioblastomas without forming a separate cluster. This indicates that group V tumors share a primary glioblastoma-associated genomic aberration profile. The depicted heatmap shows genomic losses in red and genomic gains in green. The individual chromosomes are indicated on the left hand side of the heat map. **B.** *Comparison of expression profiles in the 137 WHO grade II and III gliomas of the present patient cohort with expression profiles previously obtained in 70 glioblastomas [1].* The supervised pairwise correlation matrix is based on SOM analysis and stratified according to the *IDH1/2* mutation status. Note that *IDH1/2* wild-type gliomas of WHO grade II or III share similar expression profiles with *IDH1/2* wild-type glioblastomas while *IDH1/2* mutant gliomas of WHO grade II or III share similar expression profiles with *IDH1/2* mutant glioblastomas.



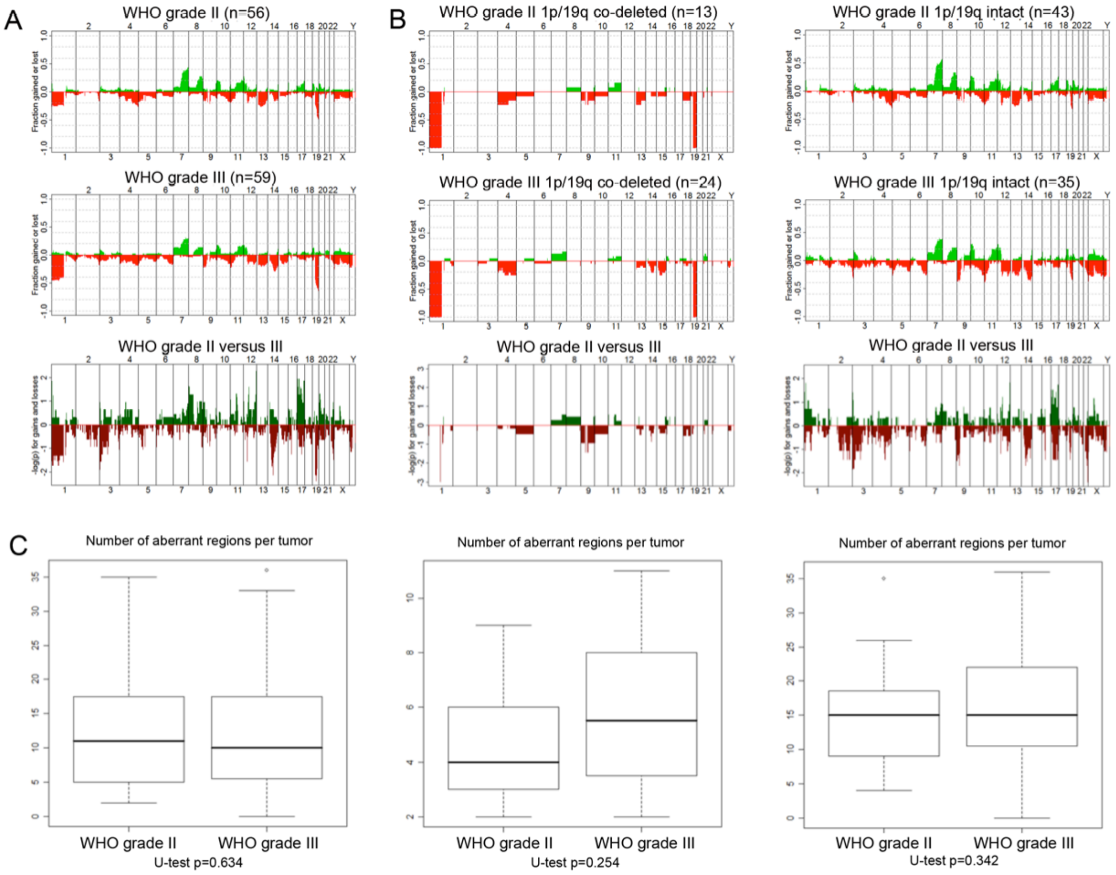
Supplementary Figure 3. *Pairwise correlation matrix based on SOM analysis of mRNA expression data of the 137 investigated gliomas.* Samples were clustered by means of maximum spanning graph partitioning. In total, 6 major transcriptional subgroups of gliomas (i - vi) become evident. The color bars on top of each correlation matrix refer to the histological classification (1), as well as the status of *MGMT* promoter methylation (2), *TERT* promoter mutation (3), 1p/19q co-deletion (4), *IDH1/2* mutation (5), and the genomic group defined by array-CGH analysis for each tumor (6).



Supplementary Figure 4. *Molecular subgroups defined by integrating mRNA and genomic profiling data of WHO grade II and III gliomas.* **A.** Supervised pairwise correlation matrix of metagene expression data obtained by SOM analysis stratified according to three groups of tumors defined by combining genomic and transcriptomic classification ("intergrated molecular goups" A, B and C). The color bars on top refer to the histological classification (1), *MGMT* promoter methylation status (2), *TERT* promoter mutation status (3), 1p/19q co-deletion (4), expression group (5) *IDH1/2* mutation (6), genomic group defined by array-CGH analysis (7), and "integrated molecular group" (8). Group A consists only of genomic group I (*IDH1/2* mutant, 1p/19q co-deleted) tumors with an expression group 7 profile, while group C consists only of group V (*IDH1/2* wild-type, +7q/-10q) tumors with expression group 1 profile. All the remaining tumors with were compiled in group B. **B.** Progression-free (PFS) and overall survival (OS) according to these three "integrated molecular groups A, B and C". An *IDH1/2* wild-type glioblastoma cohort published previously [3] is included for comparison. **C,** PFS and OS in groups A and B stratified by WHO grade (grade II versus III). **D.** PFS and OS in groups A and B stratified by patient age (≤ 40 years versus >40 years). Patients in group C were all > 40 years old and except for two patients had WHO grade III tumors. Thus, group C was not further stratified according to WHO grade and age.



Supplementary Figure 5. *Genomic changes detected by array-CGH in* ***(A)*** *IDH1/2 mutant astrocytic (A II and AA III) versus oligodendroglial/oligoastrocytic (O II, OA II, AO III, AOA III) and (****B****) 1p/19q intact versus 1p/19q co-deleted gliomas.* Shown are frequency plots of genomic imbalances detected in each tumor group. Gains of genomic material are indicated by green bars while losses are indicated by red bars. The bar length indicates the percentage of tumors in each group showing gains or losses at the respective chromosomal location. The individual chromosomes are indicated on the bottom and top of each frequency plot, with markers on each chromosomes being sorted from pter on the left to qter on the right. Most commonly detectable imbalances in oligodendroglial tumors are losses on 1p and 19q, followed by losses on chromosomes 4, 13, 14 and 15. Most common changes in astrocytic gliomas are gains on 7 or 7q, followed by gains on 8q, 10p and 11q as well as losses on 9p, 10q, 11p, 12, 13, 14 and 19q (**A**). These patterns of genomic aberrations become even more clear when tumors are stratified according to 1p/19q co-deletion status (**B**). Overall, 1p/19q co-deleted (oligodendroglial) gliomas show significantly fewer genomic aberrations per tumor (average number of aberrant genomic regions/tumor: 5) as 1p/19q intact (astrocytic) gliomas (average number of aberrant genomic regions/tumor: 15), indicating a lower degree of genomic instability in 1p/19q co-deleted tumors (**C**).



Supplementary Figure 6. *Genomic changes associated with WHO grade in IDH1/2 mutant gliomas.* Shown are frequency plots of genomic imbalances detected in WHO grade II or III gliomas as well as plots illustrating genomic differences between the WHO grades. Gains of genomic material are indicated by green bars while losses are indicated by red bars. The bar length indicates the percentage of tumors in each group showing gains or losses at the respective chromosomal location. The individual chromosomes are indicated on the bottom and top of each frequency plot, with markers on each chromosomes being sorted from pter on the left to qter on the right. To compare the incidence of copy number aberrations between subgroups, we performed a clone-wise comparison of copy number gains and losses using Fisher's exact test. For visualization, the p-values were transformed to the negative log10 scale in which 2 corresponds to a nominal p-value of 0.01 and 1.3 to a p-value of 0.05 (third row). **(A)** WHO grade II versus III in all 115 *IDH1/2* mutant gliomas. **(B)** WHO grade II versus III in the 1p/19q co-deleted gliomas (left) and the 1p/19q intact gliomas (right). There is no dominant aberration that may drive progression in the majority of cases. In 1p/19q co-deleted tumors, gain of chromosome 7 occurs little more frequently in WHO grade III tumors, while losses on 9p, 11p, 14q and the sex chromosomes are little more common in WHO grade III tumors with the 1p/19q intact genotype. **(C)** Box plots indicating the number of aberrant genomic regions per tumor in WHO grade II versus III tumors in all 115 *IDH1/2* mutant gliomas (left), the subgroup of 1p/19q co-deleted gliomas (middle) and the subgroup of 1p/19q intact gliomas (right). In general, WHO grade III gliomas do not appear to carry significantly more genomic aberrations per tumor as WHO grade II gliomas. In 1p/19q co-deleted tumors (middle) the number of aberrations per tumor is generally lower and tends to increase with WHO grade.

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