Supplementary Table S1. List of genes, copy number variations (CNV) and *KIAA1549-BRAF* fusions tested

DNA-based panels						RNA-based panel	
Gene	RefSeq	Research panel (30-gene panel)[1]		Clinical panel (16-gene panel)[2]			
		Target	Overall Coverage (%)	Target	CNV targeted	Fusion	COSMIC
ACVR1	NM_001105	-	-	Hotspots in exons 6, 7, 8, 9	-	*KIAA1549(19) - BRAF(9)*	COSF511
ATRX	NM_000489	Whole coding sequence, exons 1-35	95,9	Whole coding sequence, exons 1-35	-	*KIAA1549(18) - BRAF(10)*	COSF509
BRAF	NM_004333	Whole coding sequence, exons 1-18	94,6	Hotspots in exons 7, 10, 11, 15	-	*KIAA1549(17) - BRAF(10)*	COSF509
CDKN2A	NM_000077	Whole coding sequence, exons 1-3	50,9	Whole coding sequence, exons 1-3	Homozygous deletion	*KIAA1549(16) - BRAF(10)*	COSF1283
CDKN2B	NM_004936	Whole coding sequence, exons 1-2	64,7	-	-	*KIAA1549(16) - BRAF(11)*	COSF485
CIC	NM_015125	Whole coding sequence, exons 1-20	90,4	-	-	*KIAA1549(16) - BRAF(9)*	COSF481
DAXX	NM_001141970	Whole coding sequence, exons 1-8	90,1	-	-	*KIAA1549(17) - BRAF(10)*	COSF1284
EGFR	NM_005228	Whole coding sequence, exons 1-28	99,9	Whole coding sequence, exons 1-28	Amplification	*KIAA1549(15) - BRAF(11)*	COSF1226
FOXR2	NM_198451	Whole coding sequence, exon 1	100,0	-	-	*KIAA1549(15) - BRAF(9)*	COSF483
FUBP1	NM_003902	Whole coding sequence, exons 1-20	98,8	-	-	*KIAA1549(13) - BRAF(9)*	COSF1474
H3F3A	NM_002107	Whole coding sequence, exons 2-3	63,7	Hotspot in exon 2	-		
HIST1H3B	NM_003537	Whole coding sequence, exon 1	95,2	Hotspot in exon 1	-		
HIST1H3C	NM_003531	Whole coding sequence, exon 1	-	Hotspot in exon 1	-		
IDH1	NM_005896	Whole coding sequence, exons 3-10	97,7	Hotspot in exon 4	-		
IDH2	NM_002168.2	Whole coding sequence, exons 2-11	90,8	Hotspot in exon 4	-		
KEL	NM_000420	Whole coding sequence, exons 1-19	99,3	-	-		
KRAS	NM_033360	Whole coding sequence, exons 2-6	90,3	-	-		
LZTR1	NM_006767	Whole coding sequence, exons 1-21	96,2	-	-		
MET	NM_001127500	Whole coding sequence, exons 2-21	98,9	-	-		
MSH6	NM_000179	Whole coding sequence, exons 1-10	94,8	-	-		
NF1	NM_001042492	Whole coding sequence, exons 1-58	98,5	-	-		
NOP53	NM_015710	Whole coding sequence, exons 1-13	72,0	-	-		
PDGFRA	NM_006206	Whole coding sequence, exons 2-23	100,0	Exons 5-12, 14-15, 18, 21-23	Amplification		
PIK3CA	NM_006218	Whole coding sequence, exons 2-21	96,9	-	-		
PIK3R1	NM_181523	Whole coding sequence, exons 2-16	98,4	-	-		
PTEN	NM_000314	Whole coding sequence, exons 1-9	95,7	Whole coding sequence, exons 1-9	-		
QKI	NM_006775	Whole coding sequence, exons 1-8	98,6	-	-		
RB1	NM_000321	Whole coding sequence, exons 1-27	93,1	-	-		
TERT	NM_001193376	-	-	Hotspot in promoter region	-		
TP53	NM_000546	Whole coding sequence, exons 2-11	100,0	Whole coding sequence, exons 2-11	-		
TP73	NM_005427	Whole coding sequence, exons 2-14	86,0	-	-		
TSC1	NM_000368	Whole coding sequence, exons 3-23	94,8	-	-		
TSC2	NM_000548	Whole coding sequence, exons 2-42	96,8	-	-		
Chr 1p	-	-	-	-	Codeletion		
Chr19q	-	-	-	-	Codeletion		

[1] Cantero D, Rodríguez de Lope Á, Moreno de la Presa R, Sepúlveda JM, Borrás JM, Castresana JS, D'Haene N, García JF, Salmon I, Mollejo M, Rey JA, Hernández-Laín A, Meléndez B (2018) Molecular Study of Long-Term Survivors of Glioblastoma by Gene-Targeted Next-Generation Sequencing. J Neuropathol Exp Neurol 77:710–716. doi: 10.1093/jnen/nly048

[2] D'Haene N, Meléndez B, Blanchard O, De Nève N, Lebrun L, Van Campenhout C, Salmon I (2019) Design and Validation of a Gene-Targeted, Next-Generation Sequencing Panel for Routine Diagnosis in Gliomas. Cancers (Basel) 11. doi: 10.3390/cancers11060773