## LUCENCE

# Profiling Brain Tumors to Standard-of-Care

### Supporting WHO Blue Book CNS Tumor Classification <sup>1</sup>

**UNITED™ CNS** is a next-generation sequencing (NGS) panel aiding in the classification of central nervous system (CNS) tumors.

The test runs simultaneous interrogation of molecular alterations essential for the classification of various CNS tumor subtypes and grades — supporting accurate diagnosis and treatment of both adult and pediatric CNS tumors.

## WHO 2021 CNS Tumor Classification - Required Targets on UNITED<sup>™</sup> CNS

ADULT-TYPE DIFFUSE GLIOMA				DIATRIC-TYPE	DIFFUSE GLIOMA	CIRCUMSCRIBED	
			l	ow Grade	High Grade	ASTROCYTIC GLIOMA	
<i>IDH</i> -Mut		IDH-WT				<i>ATRX</i> Mut <b>BRAF Mut</b>	
<b>1p/19q Co-del</b> <i>TERT</i> Promoter Mut	omoter Mut 7753 Mut		MA	<b>AF Mut</b> IPK Pathway eration B Mut	EGFR CN Gain/Mut H3-3A/B Mut H3C2 Mut MYCN CN Gain PDGFRA Mut	<i>CDKN22A/B</i> Del <i>CDK4</i> CN Gain <b>MAPK Pathway</b> Alteration <i>MN1</i> Mut <i>TSC1/2</i> Mut	
Oligodendroglioma Astrocytoma CDKN2A/B WT CDKN2A/B Del		EGFR CN Gain		AF Fusion FR2/3 Fusion	ALK Fusion MET Fusion NTRK1/2/3 Fusion	BRAF Fusion	
GLIONEURONAL &	MENINGIOMA	MEDULLOB		FDF	NDYMAI TUMORS	Other Relevant	
EURONAL TUMORS	MENINGIOMA	MEDULLOB		EPE	NDYMAL TUMORS	Biomarkers	
	MENINGIOMA 1p, 6, 14q Del	MEDULLOB WNT-Activated	SHH-Activated	EPE	NDYMAL TUMORS 1q Gain 6 Del	Biomarkers BCOR ITD DICER1 Mut	
EURONAL TUMORS 1p Del 14q Del BRAF Mut			SHH-Activated	EPE	1q Gain	Biomarkers BCOR ITD DICER1 Mut DROSHA Mut GNA11 Mut	
<b>EURONAL TUMORS</b> 1 <b>p Del</b> 14q Del	1p, 6, 14q Del AKTI Mut BAPI Mut KLF4 Mut NF2 LOF	WNT-Activated	SHH-Activated	EPE	1q Gain 6 Del	Biomarkers BCOR ITD DICERT Mut DROSHA Mut GNA71 Mut GNAQ Mut MYC Mut PRKAR1A Mut	
EURONAL TUMORS	1p, 6, 14q Del <i>AKT1</i> Mut <i>BAP1</i> Mut <i>KLF4</i> Mut	WNT-Activated	SHH-Activated	EPE	1q Gain 6 Del MYCN CN Gain	Biomarkers BCOR ITD DICERI Mut DROSHA Mut GNAP Mut GNAQ Mut MYC Mut PRKARIA Mut RBI Mut SMARCA4 Mut	
EURONAL TUMORS 1p Del 14q Del BRAF Mut MAPK Pathway Alteration PDGFRA Mut PIK3CA Mut PTEN Mut	1p, 6, 14q Del AKTI Mut BAPI Mut KLF4 Mut NF2 LOF PIK3CA Mut SMARCEI Mut	WNT-Activated 6 Del CTNNB1 Mut DDX3X Mut	SHH-Activated MYCN CN Gain PTCH1 Mut SM0 Mut SUFU Mut TP53 Mut	d: Essential for cla	1q Gain 6 Del MYCN CN Gain YAP1 Fusion	Biomarkers BCOR ITD DICERT Mut DROSHA Mut GNAQ Mut MYC Mut PRKARIA Mut RB1 Mut SMARCA4 Mut SMARCA4 Mut	
EURONAL TUMORS  1p Del 14q Del BRAF Mut MAPK Pathway Alteration PDGFRA Mut PI/SZCA Mut	1p, 6, 14q Del AKT1 Mut BAP1 Mut KLF4 Mut NF2 LOF PIK3CA Mut SMARCE1 Mut SMARCE1 Mut	WNT-Activated	SHH-Activated MYCN CN Gain PTCH1 Mut SMO Mut SUFU Mut TP53 Mut teration In bo MAPI	ld: Essential for cla	1q Gain 6 Del MYCN CN Gain YAP1 Fusion	Biomarkers BCOR ITD DICERI Mut DROSHA Mut GNAP Mut GNAQ Mut MYC Mut PRKARIA Mut RBI Mut SMARCA4 Mut	
EURONAL TUMORS  1p Del 14q Del BRAF Mut MAPK Pathway Alteration PDGFRA Mut PIK3CA Mut PTEN Mut BRAF Fusion	1p, 6, 14q Del AKT1 Mut BAP1 Mut KLF4 Mut NF2 LOF PIK3CA Mut SMARCE1 Mut SMARCE1 Mut	WNT-Activated 6 Del CTNNB1 Mut DDX3X Mut LOF: Loss-Of-Function alt CN: Copy Number Gene-level mutatio	SHH-Activated MYCN CN Gain PTCHT Mut SMO Mut SUFU Mut TP53 Mut teration In bo MAPI	ld: Essential for cla K Pathway Alteratio MeT Mut, NF1 LOF, Mut/Fusion, ROST Fi	1q Gain 6 Del MYCN CN Gain YAP1 Fusion ssification m: FGFRI Mut/Fusion, KRAS MTRKI/2/3 Fusion, RAFI Mut,	Biomarkers BCOR ITD DICERT Mut DROSHA Mut GNAQ Mut MYC Mut PRKARIA Mut RB1 Mut SMARCA4 Mut SMARCA4 Mut	

# Test Specifications<sup>2</sup>

Methodology	Ultra-deep next-generation sequencing					
Biomarkers analyzed	<ul> <li>SNVs, Indels, Fusions</li> <li>Gene copy number variations, chromosomal copy number alterations</li> <li>Microsatellite Instability (MSI) and Tumor Mutational Burden (TMB)</li> </ul>					
Sample type	FFPE tumor tissue					
Turnaround time	2 weeks					
	Sensitivity Specificity					
SNVs/Indels	98%	100%				
Fusions	91.25%	100%				
MSI-High	100%	100%				
	R <sup>2</sup> Correlation to Wl	nole Exome Sequencing				
ТМВ	98.6%					

Results tested at the stated mutant allele frequencies using reference standards, FFPE cell line samples, and FFPE clinical samples.

Sensitivity and specificity reported for SNVs and Indels are at 5% VAF.
The limit of detection for chromosomal copy number alterations is 30% tumor fraction.

References [1] Gritsch, S. et al. Cancer 2022 128(1):47–58. [2] Ng, CC-Y. et al. Front. Mol. Biosci. 2022. 9:963243.

## Gene List

#### The subset of genes relevant to CNS, targeted by UNITED<sup>™</sup> CNS. Full gene list in UNITED<sup>™</sup> brochure.

#### SNVs, Indels & CNVs

AKT1	CDKN2A	FGFR1	H3C2	МҮВ	NTRK3	RB1	SSX1
ALK	CDKN2B	FGFR2	IDH1	MYC	PDGFRA	RET	SUFU
ATRX	CTNNB1	FGFR3	IDH2	MYCN	PIK3CA	ROS1	TERT
BAP1	DDX3X	GNA11	KLF4	NF1	PRKAR1A	SMARCA4	<b>TP53</b>
BCOR	DICER1	GNAQ	KRAS	NF2	PTCH1	SMARCB1	TRAF7
BRAF	DROSHA	H3-3A	MET	NTRK1	PTEN	SMARCE1	TSC1
CDK4	EGFR	H3-3B	MN1	NTRK2	RAF1	SMO	TSC2

Genes in **bold** are essential for standard-of-care CNS classification.

#### **RNA Fusions**

ALK	FGFR1	MET	NTRK2	PDGFRA	RAF1	ROS1	SSX2*
BRAF	FGFR2	NTRK1	NTRK3	PRKACA*	RET	SSX1	YAP1*
EGFR	FGFR3						

Genes in **bold** are essential for standard-of-care CNS classification. \*Genes tested in RNA panel only.

#### Chromosomal Copy Number Alterations

1p	1q	6	7	10	14q	19p	19q
	1						

Chromosome/chromosome arms in **bold** are essential for standard-of-care CNS classification.

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