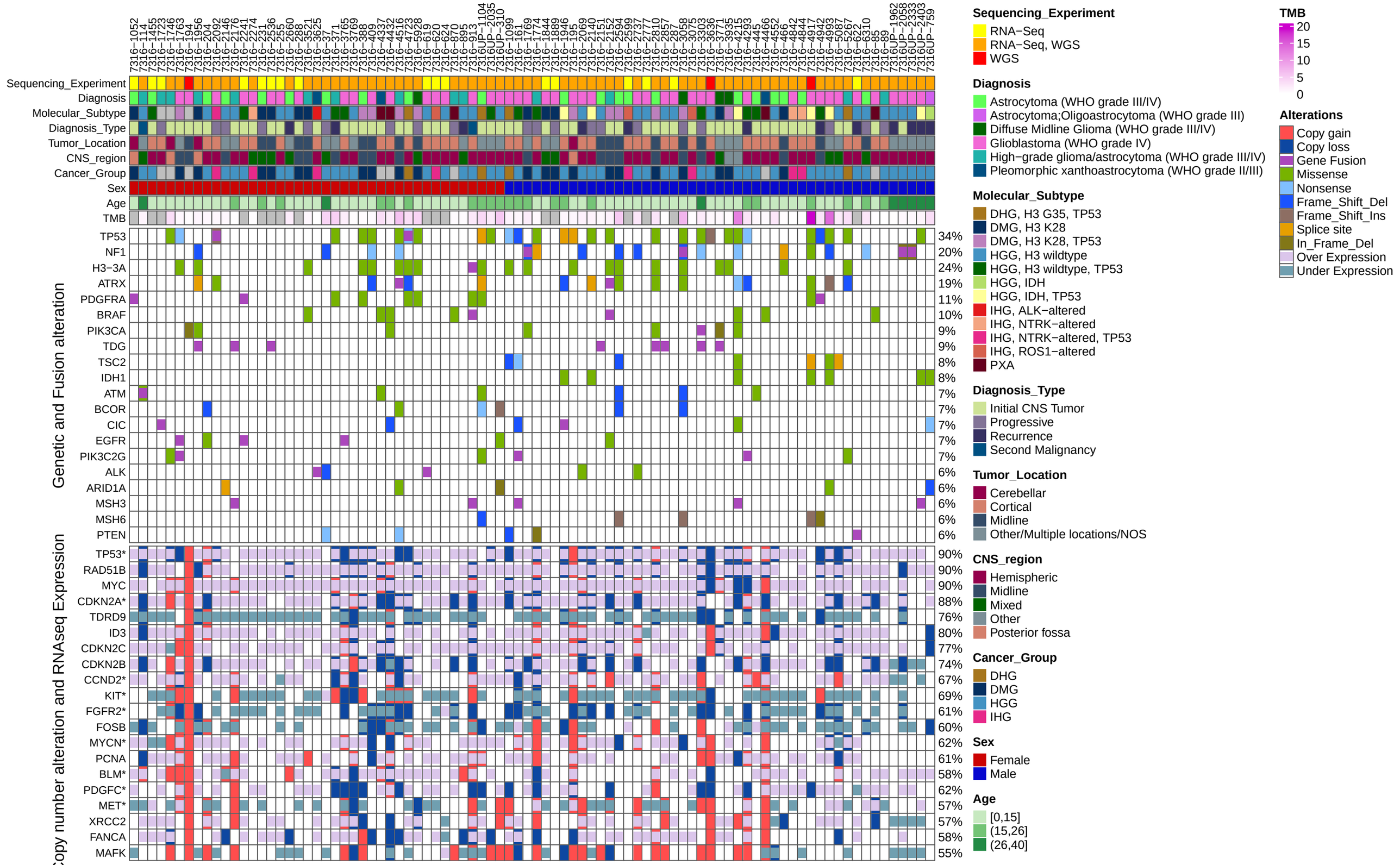
Sequencing_Experiment
Diagnosis
Molecular_Subtype
Diagnosis_Type
Tumor_Location
CNS_region
Cancer_Group
Sex
Age
TMB
Genetic and Fusion alteration
TP53 34%
NF1 20%
H3−3A 24%
ATRX 19%
PDGFRA 11%
BRAF 10%
PIK3CA 9%
TDG 9%
TSC2 8%
IDH1 8%
ATM 7%
BCOR 7%
CIC 7%
EGFR 7%
PIK3C2G 7%
ALK 6%
ARID1A 6%
MSH3 6%
MSH6 6%
PTEN 6%
Copy number alteration and RNAseq Expression
TP53* 90%
RAD51B 90%
MYC 90%
CDKN2A* 88%
TDRD9 76%
ID3 80%
CDKN2C 77%
CDKN2B 74%
CCND2* 67%
KIT* 69%
FGFR2* 61%
FOSB 60%
MYCN* 62%
PCNA 61%
BLM* 58%
PDGFC* 62%
MET* 57%
XRCC2 57%
FANCA 58%
MAFK 55%
Sequencing_Experiment
RNA−Seq
RNA−Seq, WGS
WGS
Diagnosis
Astrocytoma (WHO grade III/IV)
Astrocytoma;Oligoastrocytoma (WHO grade III)
Diffuse Midline Glioma (WHO grade III/IV)
Glioblastoma (WHO grade IV)
High−grade glioma/astrocytoma (WHO grade III/IV)
Pleomorphic xanthoastrocytoma (WHO grade II/III)
Molecular_Subtype
DHG, H3 G35, TP53
DMG, H3 K28
DMG, H3 K28, TP53
HGG, H3 wildtype
HGG, H3 wildtype, TP53
HGG, IDH
HGG, IDH, TP53
IHG, ALK−altered
IHG, NTRK−altered
IHG, NTRK−altered, TP53
IHG, ROS1−altered
PXA
Diagnosis_Type
Initial CNS Tumor
Progressive
Recurrence
Second Malignancy
Tumor_Location
Cerebellar
Cortical
Midline
Other/Multiple locations/NOS
CNS_region
Hemispheric
Midline
Mixed
Other
Posterior fossa
Cancer_Group
DHG
DMG
HGG
IHG
Sex
Female
Male
Age
[0,15]
(15,26]
(26,40]
TMB
20
15
10
5
0
Alterations
Copy gain
Copy loss
Gene Fusion
Missense
Nonsense
Frame_Shift_Del
Frame_Shift_Ins
Splice site
In_Frame_Del
Over Expression
Under Expression