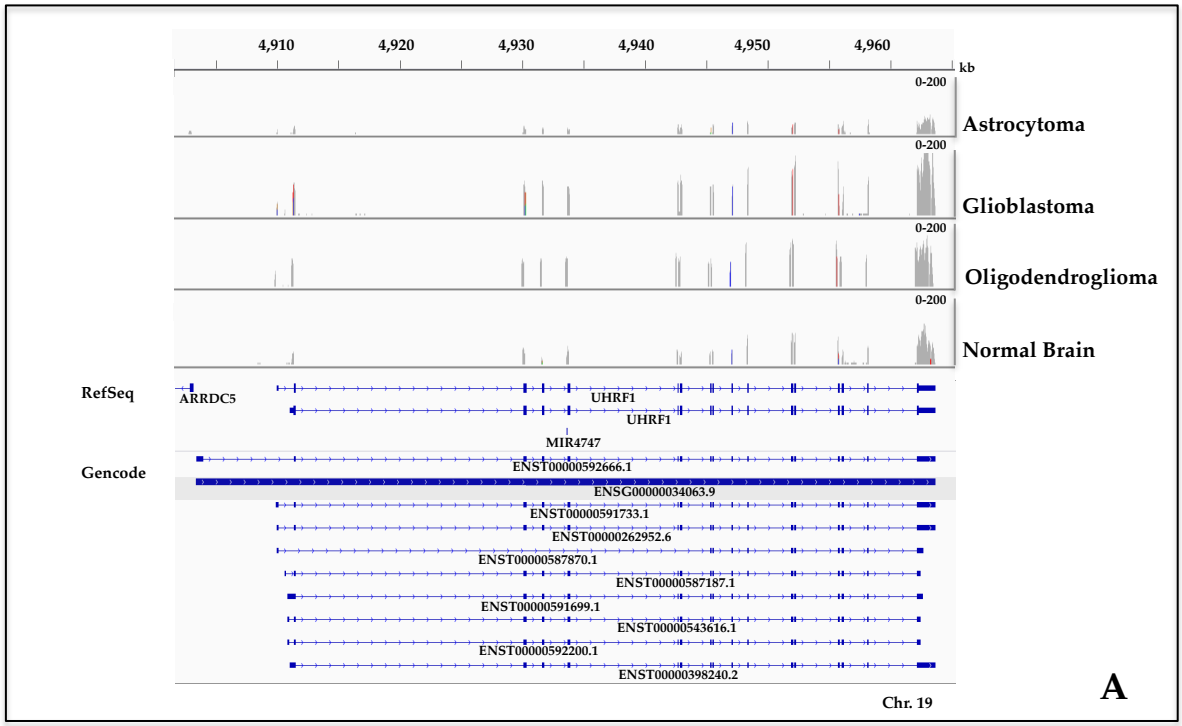
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4,960
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0-200
Glioblastoma
0-200
Oligodendroglioma
0-200
Normal Brain
RefSeq
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UHRF1
MIR4747
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Chr. 19
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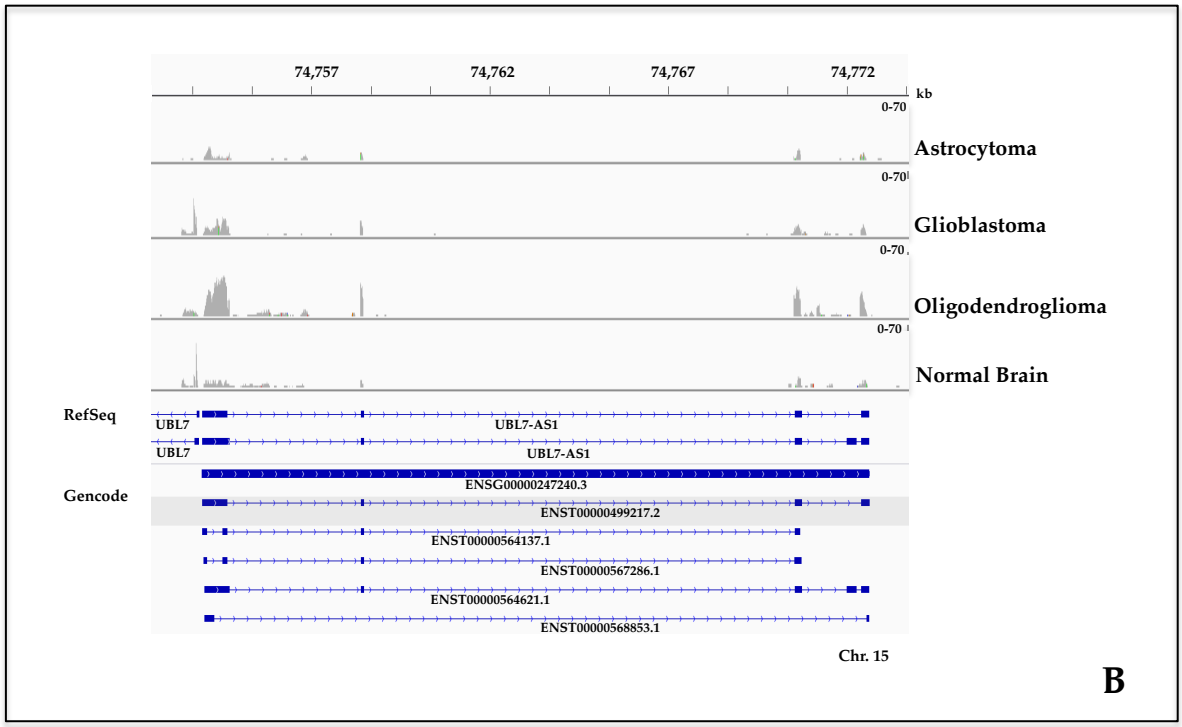
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UBL7-AS1
UBL7
UBL7-AS1
Gencode
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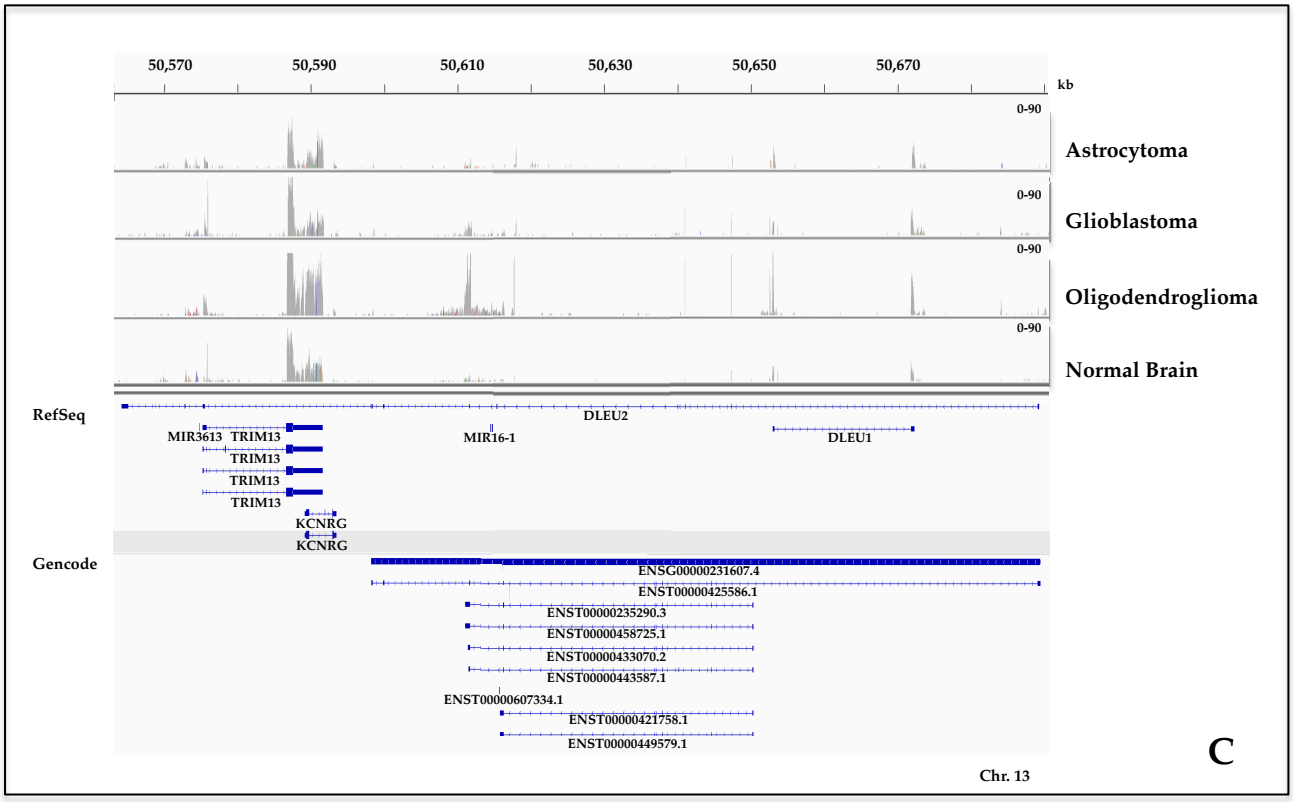
Chr. 15
B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RefSeq
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DLEU1
TRIM13
TRIM13
TRIM13
KCNRG
KCNRG
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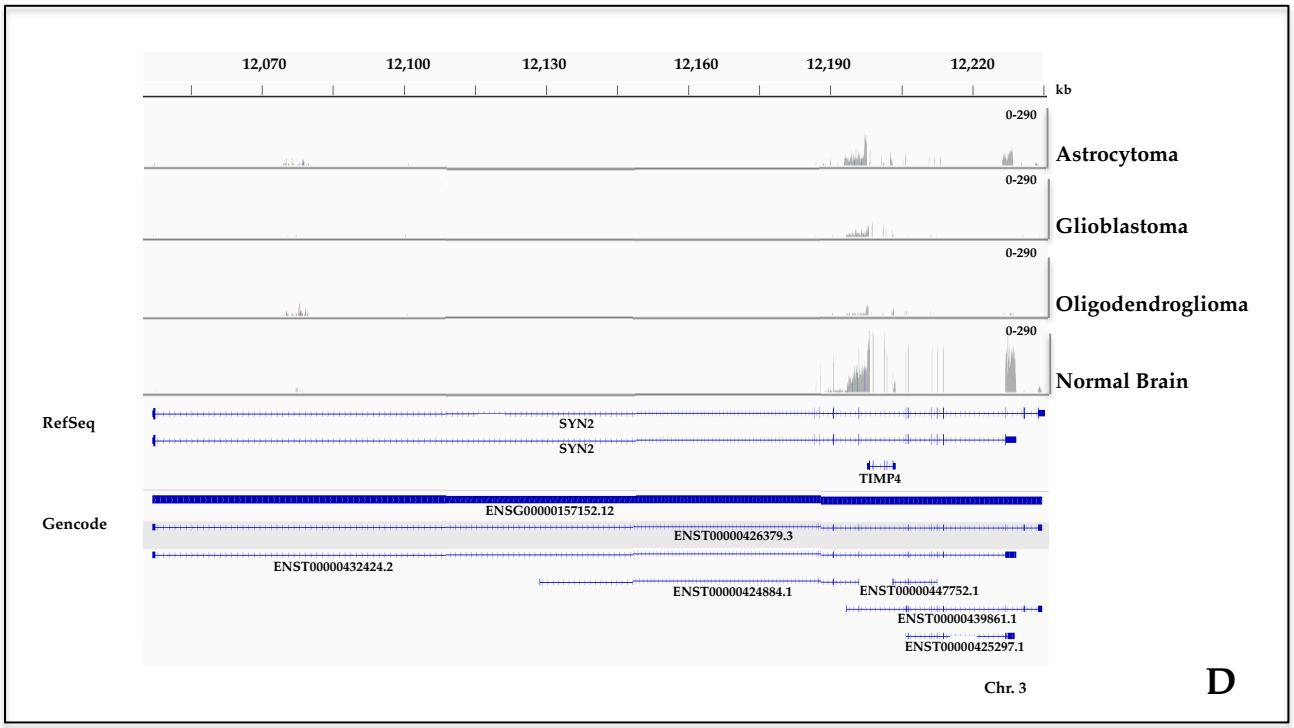
Chr. 13
C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Normal Brain
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SYN2
SYN2
TIMP4
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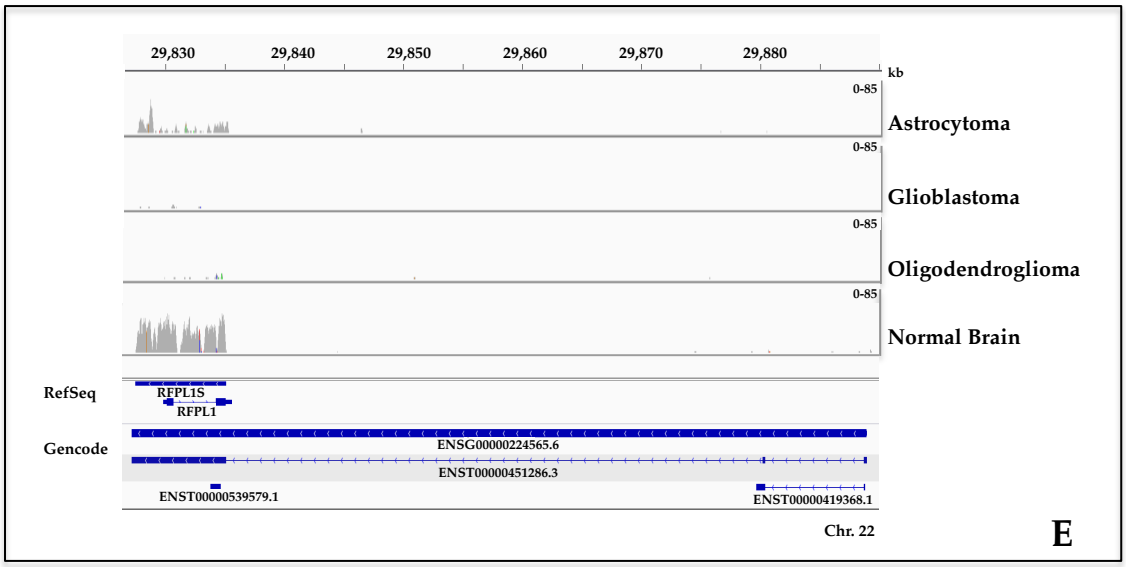
Chr. 3
D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Glioblastoma
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Normal Brain
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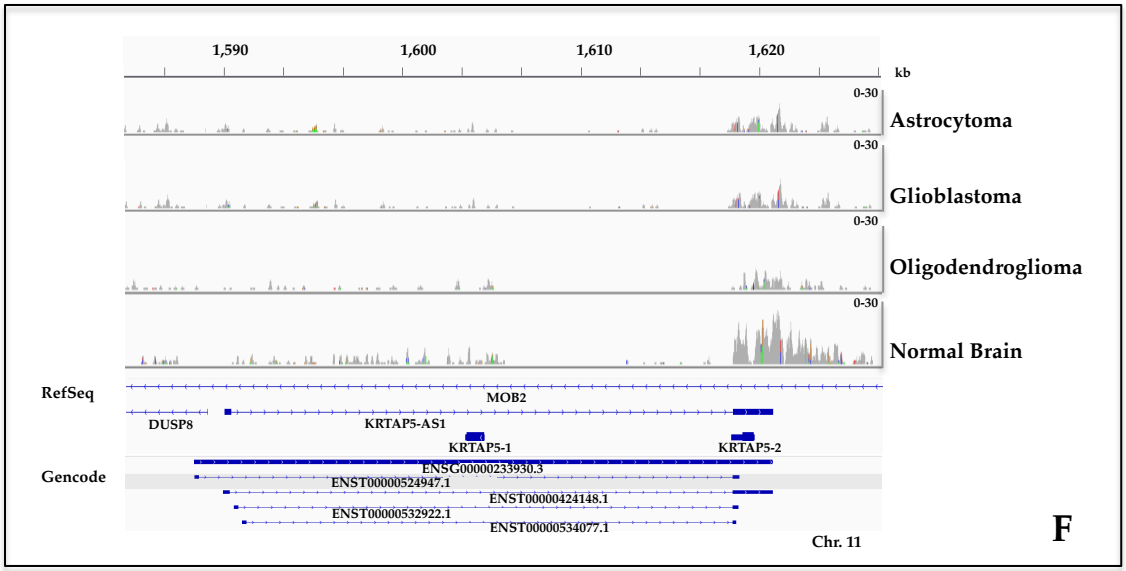
Chr. 22
E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Glioblastoma
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Oligodendroglioma
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Normal Brain
RefSeq
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DUSP8
KRTAP5-AS1
KRTAP5-1
KRTAP5-2
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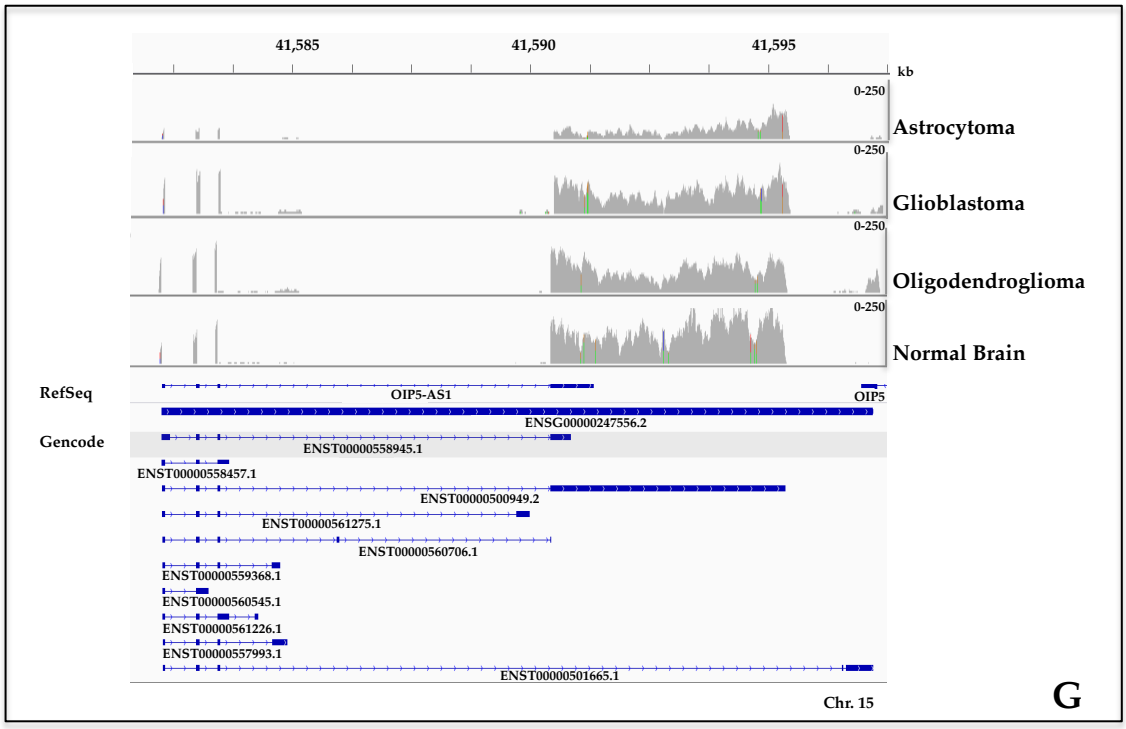
Chr. 11
F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OIP5-AS1
OIP5
ENSG00000247556.2
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ENST00000558945.1
ENST00000558457.1
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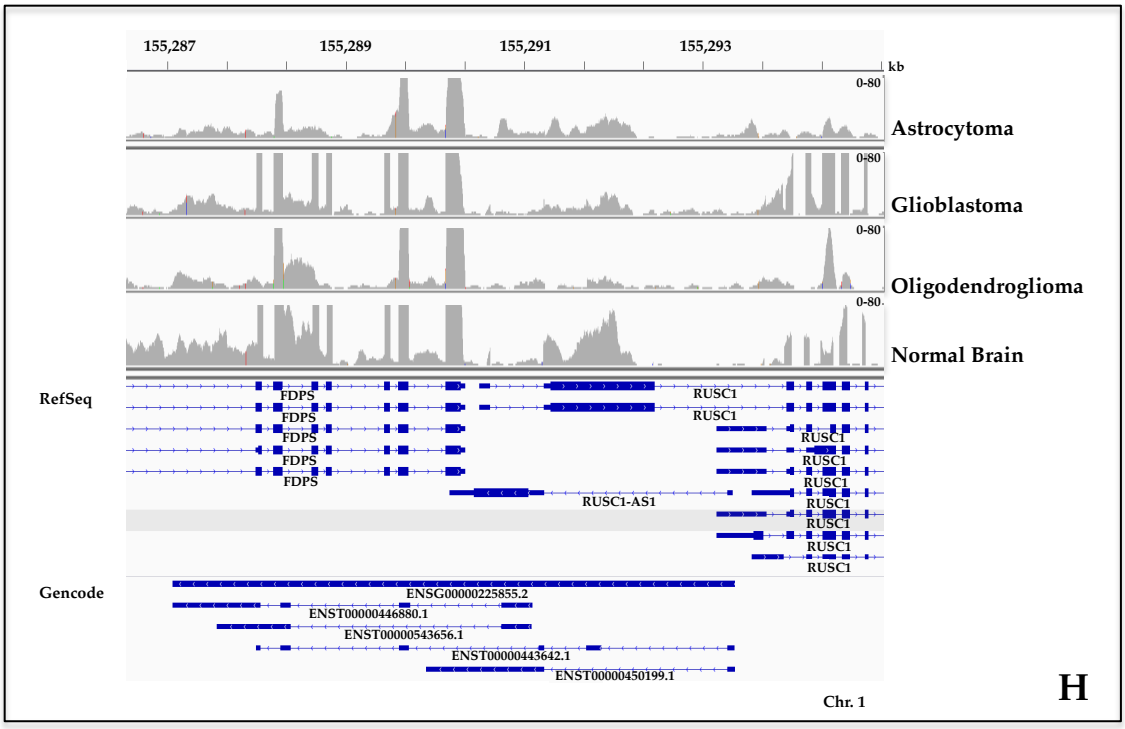
Chr. 15
G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155,291
155,293
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Normal Brain
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FDPS
RUSC1
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Gencode
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ENST00000543656.1
ENST00000443642.1
ENST00000450199.1
Chr. 1
H

Figure S1. Genomic alignments of RNA-seq reads corresponding to the eight remaining lncRNAs in the three brain tumors types: (A) UHRF1, (B) UBL7-AS1, (C) DLEU2, (D) SYN2, (E) RFPL1S, (F) KRTAP5-AS1, (G) OIP5-AS1 and (H) RUSC1-AS1. In each panel the transcript annotations from both RefSeq and Gencode were displayed. The visualization of the alignments was obtained with the IGV software that did not operate any normalization of the read counts. For this reason it appears useful to remember the total number of reads aligned for each sample: 36.615.170 for Astrocytoma, 56.810.365 for Glioblastoma, 45.522.007 for Oligodendroglioma and 43.987.358 for Normal Brain.