

## Supplementary Materials

**Table S1.** Studies reviewed in Table 1 grouped by input data category

| Input data category         | Total Number |
|-----------------------------|--------------|
| Somatic mutation            | 12           |
| Copy number change profiles | 13           |
| Gene expression             | 20           |
| miRNA expression            | 6            |
| DNA methylation             | 9            |
| Protein expression          | 6            |
| Metabolomic profiling       | 1            |
| Histopathological images    | 1            |
| mRNA expression             | 1            |
| MRI                         | 1            |
| Clinical                    | 1            |
| WES                         | 1            |

Abbreviations: MRI, magnetic resonance imaging; WES, whole exome sequencing.

**Table S2.** Studies reviewed in Table 1 grouped by input dataset

| Dataset          | Total number |
|------------------|--------------|
| TCGA             | 17           |
| GEO              | 4            |
| cell line        | 3            |
| CGGA             | 2            |
| POLA             | 1            |
| TCIA             | 1            |
| MUHC             | 1            |
| CGGA             | 1            |
| Private dataset  | 2            |
| GTE <sub>x</sub> | 1            |
| Ivy GAP          | 1            |

Abbreviations: TCGA, The Cancer Genome Atlas; TCIA, The Cancer Imaging Archive; GEO, Gene Expression Omnibus; GTE<sub>x</sub>, Genotype-Tissue Expression; CGGA, Chinese Glioma Genome Atlas; POLA, Prise en charge des OLigodendrogliomes Anaplasiques; MUHC, McGill University Health Centre; Ivy GAP, Ivy Glioblastoma Atlas Project.