Supplementary

Table S1 The final cutoff of high expression levels for each biomarker. When we calculated the effect of a biomarker, we analyzed the effects of different high-expression cutoff points (>0, >1, >2, and >3). When the effects of the biomarker expression levels were most significant, the cutoff of the expression level was determined to be the final cutoff point.

| Biomarker | Number of patients per score | Standard of high expression levels | Estimated effects (High vs. low, mm/year ± SE) | P-value |
|-----------|------------------------------|-----------------------------------|-----------------------------------------------|---------|
| ATRX      | 9 9 3 1 3                    | >0                                | -2.5±0.4                                      | 0.16×10⁻⁶ |
|           |                              | >1                                | -2.3±0.4                                      | 0.68×10⁻⁷ |
|           |                              | >2                                | -1.2±1.2                                      | 0.34    |
|           |                              | >3                                | -1.9±1.3                                      | 0.16    |
| EGFR      | 0 0 4 3 9                    | >0                                | -                                          |         |
|           |                              | >1                                | -                                          |         |
|           |                              | >2                                | 1.0±0.9                                      | 0.27    |
|           |                              | >3                                | 1.8±0.6                                      | 0.003*  |
| Mutant p53| 9 7 6 3 5                    | >0                                | -0.7±0.7                                     | 0.28    |
|           |                              | >1                                | 2.4±0.4                                      | 0.14×10⁻⁴ |
|           |                              | >2                                | 3.0±0.4                                      | 0.12×10⁻¹⁰ |
|           |                              | >3                                | 2.6±0.5                                      | 0.4×10⁻⁵ |
| Ki-67     | 0 18 15 1 2                  | >0                                | -                                          |         |
|           |                              | >1                                | -0.7±0.4                                     | 0.05*   |
|           |                              | >2                                | 1.7±0.9                                     | 0.07    |
|           |                              | >3                                | 1.6±1.0                                     | 0.10    |

*, A P-value ≤0.05 was considered statistically significant. SE, standard error.

Table S2 Comparing the VDE between 2 subgroups (complete or missing molecular data) to assess potential bias from missing data

| Molecular biomarker | Number of patients in subgroup | eVDE (mm/year) | Estimated effects (mm/year ± SE) | P-value |
|---------------------|--------------------------------|----------------|----------------------------------|---------|
| Ki-67               | Complete                       | 36             | 2.2                              | 0.2±0.3 | 0.40    |
|                     | Missing data                   | 20             | 1.9                              |         |         |
| Mutant p53          | Complete                       | 30             | 2.4                              | 0.5±0.3 | 0.10    |
|                     | Missing data                   | 26             | 2.2                              |         |         |
| TERT promoter       | Complete                       | 45             | 2.3                              | 0.8±0.3 | 0.02*   |
|                     | Missing data                   | 11             | 1.5                              |         |         |
| 1p/19q              | Complete                       | 40             | 3.4                              | -0.14±0.4 | 0.68  |
|                     | Missing data                   | 16             | 2.2                              |         |         |
| EGFR                | Complete                       | 16             | 3.2                              | 1.4±0.3 | <0.01*  |
|                     | Missing data                   | 40             | 1.8                              |         |         |
| ATRX                | Complete                       | 25             | 2.3                              | 0.3±0.3 | 0.26    |
|                     | Missing data                   | 31             | 1.9                              |         |         |
| MGMT promoter       | Complete                       | 39             | 2.1                              | 0.5±0.3 | 0.10    |
|                     | Missing data                   | 17             | 1.7                              |         |         |

*, A P-value ≤0.05 was considered statistically significant. VDE, velocity of diameter expansion; SE, standard error.
### Table S3 The estimated effect of multiple-factor analysis using the mLMEM in the diffuse astrocytoma, IDH mutant subgroup

| Molecular biomarker                                      | Estimated effects (mm/year ± SE) | P-value |
|----------------------------------------------------------|----------------------------------|---------|
| Age                                                      | -0.09±0.03                       | 0.01*   |
| Mutant p53 (High vs. low expression)                     | 3.6±1.7                          | 0.04*   |
| MGMT promoter (Methylation vs. non-methylation)          | -2.6±0.5                         | < 0.01* |

*, A P-value ≤0.05 was considered statistically significant. mLMEM, multivariate linear mixed-effects model; SE, standard error.

### Table S4 The estimated effect of multiple-factor analysis using the mLMEM in the oligodendroglioma, IDH mutant subgroup

| Molecular biomarkers                                      | Estimated effects (mm/year ± SE) | P-value |
|----------------------------------------------------------|----------------------------------|---------|
| Age                                                      | -0.02±0.006                      | <0.01*  |
| Gender (Female vs. male)                                 | 0.7±0.2                          | <0.01*  |

*, A P-value ≤0.05 was considered statistically significant. mLMEM, multivariate linear mixed-effects model; SE, standard error.