Gliomas are brain tumors arising from neuroglia. In most cases astrocytic or oligodendroglial component is the main element of the tumor. Non-random chromosomal abberations are found in tumor cells as was revealed previously. The aim of this study was a fluorescence in-situ hybridisation analysis (FISH) of tissue samples obtained during neurosurgical procedures, determine the frequence of selected chromosomal abberations, further correlation with morphological and clinical data and statistical analysis of the results. During six years 264 tissue samples were gained in which FISH with defined probes was performed. The acquired results were compared with histological analysis and selected clinical data (age, Karnofsky score, extent of resection, overall survival). The whole series was divided into 7 groups by tumor type for further statistical analysis. In every group median and mean survival time was calculated, Kaplan-Meier analysis was focused on influence of selected parameters to overall survival. In some categories Cox regression model was created to achieve a hazard ratio of selected parameters. In WHO Grade II and III tumors the risk of malignant progression and tumor upgrading is significantly higher in comparison with samples where specific abberations were not found (EGFR amplification, CDKN2A and RB1 deletion, monosomy of chromosome 10 and trisomy of chromosome 7). In glioblastoma polyploidy is good prognostic marker, monosomy of chromosome 10 is linked to worse clinical course and shorter overall survival.