Supplementary figure legends

**Figure S1. MGMT-expression in GIC** A. *MGMT* mRNA (upper row) and protein (lower row) levels in GIC cells were assessed by PCR and immunoblot. Parental, *MGMT*-transfected LNT-229 cells and LN-18 cells were used as negative and positive controls. B. GS-2, GS-5, GS-7 or GS-9 were pre-treated with 50 µM of O6-BG or vehicle for 2 h and then exposed to TMZ in increasing concentrations for 24 h. Cell density was assessed by MTT assay after 2 weeks (white square, control; black diamond, O6-BG). Data are expressed as mean ± SEM (n=3) (**p<0.01, ***p<0.001).

**Figure S2. Affymetrix gene expression** A. Gene regulation as assessed by Affymetrix gene expression profiling was determined for exclusive and overlapping gene regulation for all 3 investigated cell lines at 6 h (left diagram) and 24 h (right diagram).

**Figure S3. Gene cluster analysis** A. Functional interactions were analyzed for IFN-β-responsive genes induced by IFN-β as assessed in Affymetrix micro-array based gene expression profiling by STRING analysis. Interactions with confidence score of 0.9 or higher were integrated to the interactome. (left). B. Identical analysis was performed for apoptotic genes specifically induced by IFN-β in Affymetrix gene expression analysis. C. Functional interactions were analyzed for negative regulators of proliferation and cell growth induced by IFN-β in GIC. Interactions with confidence score of 0.7 or higher were integrated to the interactome. Clusters were determined by MCL algorithm and presented with different node colors. Inter-cluster edges are represented by dashed-lines.

**Figure S4. IFN-β–induced sensitization of LTL glioma cells to TMZ and irradiation.** A. LTL characterized by different genetic status and expression pattern of MGMT and TP53 were exposed to vehicle (white squares) or IFN-β at 150 IU/ml (black diamonds) for 24 h, then to TMZ at increasing concentrations in IFN-β-free-medium for further 24 h, and, after removal of TMZ, allowed to grow for 2 weeks in FCS-enriched medium. Data are expressed
as mean ± SEM (n=3) (*p<0.05, **p<0.01, ***p<0.001). Selected synergy data are displayed for LNT-229 and LN-18 calculated according to the fractional product method (right). B. LNT-229, LN-18 or LN-308 cells were exposed to vehicle (white bar) or 150 IU/ml IFN-β (black bar) for 24 h and then irradiated with a single dose of 1, 3 or 5 Gy. Clonogenic survival was assessed by crystal violet staining after 2 weeks. Data are expressed as mean ± SEM (n=3) (***p<0.001). C. LNT-229 and LN-18 cell lysates were assessed for TP53 or MGMT protein levels after exposure to IFN-β at 150 or 450 IU/ml. GAPDH was used as a reference. D. LN-18 or LNT-229 cells with or without IFN-β exposure (24 h, 150 IU/ml) were transiently transfected with pGL2-Luc MGMT or TP53 Luc and pRL-CMV. Reporter activity is presented in RLU units normalized to the respective control. LNT-229 was used as a negative control for the MGMT reporter; LNT-229 cells exposed to 8 Gy were used as a positive control for the TP53 reporter assay (*p<0.05, **p<0.01).

Table S1. Altered gene expression of IFN-β response genes and apoptosis-related genes induced by IFN-β; detected by Affymetrix microarray-based gene expression profiling (absolute fold-change; cut-off: 2.0, cell line specific analyses). Affymetrix total mRNA expression analysis was performed in LNT-229 cells, GS-2 cells and GS-9 cells with or without exposure to IFN-β at 6 h or 24 h of exposure. Genes annotated to IFN regulation or apoptosis by gene ontology and the respective fold changes are listed hierarchically.

Table S2. Altered gene expression of growth-related genes in LTL and GIC induced by IFN-β; detected by Affymetrix microarray-based gene expression profiling (absolute fold-change; cut-off: 2.0, exclusive analyses). Affymetrix total mRNA expression analysis was performed in LNT-229 cells, GS-2 cells and GS-9 cells with or without exposure to IFN-β at 6 h or 24 h of exposure for differential regulation of genes annotated to cell growth and proliferation by gene ontology. Analysis was performed for each cell line exclusively (FC > 2).
Gene symbols listed in more than one cell line originate from different Affymetrix probe sets.

Genes and corresponding fold changes are listed hierarchically.