Differential Expression of ID4 and Its Association with TP53 Mutation, SOX2, SOX4 and OCT-4 Expression Levels

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Abstract

Inhibitor of DNA Binding 4 (ID4) is a member of the helix-loop-helix ID family of transcription factors, mostly present in the central nervous system during embryonic development, that has been associated with TP53 mutation and activation of SOX2. Along with other transcription factors, ID4 has been implicated in the tumorigenic process of astrocytomas, contributing to cell dedifferentiation, proliferation and chemoresistance. In this study, we aimed to characterize the ID4 expression pattern in human diffusely infiltrative astrocytomas of World Health Organization (WHO) grades II to IV of malignancy (AGII-AGIV); to correlate its expression level to that of SOX2, SOX4, OCT-4 and NANO-G, along with TP53 mutational status; and to correlate the results with the clinical end-point of overall survival among glioblastoma patients. Quantitative real time PCR (qRT-PCR) was performed in 130 samples of astrocytomas for relative expression, showing up-regulation of all transcription factors in tumor cases. Positive correlation was found when comparing ID4 relative expression of infiltrative astrocytomas with SOX2 (r = 0.50; \( p < 0.005 \)), SOX4 (r = 0.43; \( p < 0.005 \)) and OCT-4 (r = 0.39; \( p < 0.05 \)). The results from TP53 coding exon analysis allowed comparisons between wild-type and mutated status only in AGII cases, demonstrating significantly higher levels of ID4, SOX2 and SOX4 in mutated cases (\( p < 0.05 \)). This pattern was maintained in secondary GBM and further confirmed by immunohistochemistry, suggesting a role for ID4, SOX2 and SOX4 in early astrocytoma tumorigenesis. Combined hyperexpression of ID4, SOX4 and OCT-4 conferred a much lower (6 months) median survival than did hypoexpression (18 months). Because both ID4 alone and a complex of SOX4 and OCT-4 activate SOX2 transcription, it is possible that multiple activation of SOX2 impair the prognosis of GBM patients. These observational results of associated expression of ID4 with SOX4 and OCT-4 may be used as a predictive factor of prognosis upon further confirmation in a larger GBM series.

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Introduction

Inhibitor of DNA Binding (ID) proteins (ID1–4) belong to the helix-loop-helix (HLH) superfamily of transcription factors and exert their functions through the highly conserved HLH dimerization domain. Due to the lack of a DNA binding domain, IDs sequester and inhibit the activity of their specific target proteins, playing important roles in cell cycle control, growth, differentiation, angiogenesis and tumorigenesis [1–4]. In healthy organisms, ID expression is up-regulated in stem and progenitor cells, maintaining self-renewal capacity, pluripotency and an undifferentiated state. However, ID expression declines to basal values when cells differentiate towards the destined specific lineage [5], [6]. The expression of ID1–3 proteins is widespread, while the ID4 expression pattern is restricted to the developing brain, particularly in neural progenitor cells [7]. The overexpression of IDs in tumor cells has been suggested to induce reversion to an embryonic-like state, with high rates of proliferation, migration and neo-angiogenesis facilitating tumor formation [4].

Astrocytomas are the most common primary brain tumors. World Health Organization (WHO) classifies the astrocytomas into four grades: grade I or pilocytic astrocytoma, grade II, or low-grade astrocytoma (AGII), grade III, or anaplastic astrocytoma (AGIII) and grade IV astrocytoma or glioblastoma (AGIV or GBM) [8]. Diffusely infiltrative astrocytomas (AGII-GBM) invade the surrounding normal brain tissue, hampering tumor resection. GBM is the most malignant and frequent brain tumor in adults and they can be divided into two subgroups: primary GBM, which arise de novo, and secondary GBM, which results from the progression of a lower grade astrocytoma [9], [10]. The malignant transformation of astrocytomas, is associated with augmented ID expression [3], particularly ID4 [11], [12]. Interestingly, the up-regulation of ID4 has been associated with TP53 mutation status [13], [14], which is an early event in astrocytoma progression; additionally, TP53 mutation is more related to secondary GBM [9]. Moreover, hyperexpression of ID4 was found to be a key regulator of malignant transformation of Ink4a/Arf\(^{-/-}\) (cyclin-dependent kinase inhibitor 2A, isoform 4) murine astrocytes in in
vivo experiments, resulting in formation of high grade gliomas according to clinical and histological analysis [15]. These results may be consistent with astrocyte dedifferentiation to an immature progenitor-like state. It has also been demonstrated that ID4 protein activates SRY (sex determining region Y)-box 2 (SOX2) transcription in GBM and glioma stem cells [16]. Similarly, SOX4 and POU class 5 homebox 1 (OCT-4) proteins were also shown to activate SOX2 transcription in glioma initiating cells [17], [18].

Along with Nanog homeobox (NANOG), these transcription factors are highly expressed in embryonic, progenitor, and tumor stem cells, in contrast to the low levels of expression that are found in differentiated cells [19–21].

This study aimed to characterize the ID4 expression pattern in human astrocytomas of grades II to IV of malignancy; to correlate its expression level to that of SOX2, SOX4, OCT-4 and NANOG, along with TP53 mutational status; and to correlate the results with the clinical end-point of overall survival among GBM patients. In parallel, expression of the neural and brain tumor stem cell marker CD133 was assessed to better evaluate the progenitor cell condition [22–23].

Materials and Methods

Tissue Samples and Ethical Statement

One hundred and thirty diffusely infiltrative astrocytomas (grades II to IV) were obtained during therapeutic surgery of patients treated by the Neurosurgery Group of the Department of Neurology at Hospital das Clinicas at the School of Medicine of the University of Sao Paulo, in the period of 2000 to 2007. The cases were categorized according to the WHO grading system [8] by neuropathologists from the Division of Pathological Anatomy of the same institution. The studied series consisted of 26 AGII, 18 AGIII, 86 GBM, and 22 non-neoplastic (NN) brain anonymized cases from epilepsy patients subjected to temporal lobectomy. Demographic data of the studied cases is presented in Table 1, and the clinical findings are presented in Table S1. Samples were macrodissected and immediately snap-frozen in liquid nitrogen upon surgical removal. A 4-μm-thick cryosection of each sample was analyzed under a light microscope after hematoxylin-eosin staining for assessment of necrotic, cellular debris and non-neoplastic areas (in tumor samples), followed by removal from the frozen block by microdissection prior to DNA and RNA extractions [24], [25]. Eighty-one GBM patients (94.2%) presented with onset of clinical symptoms within 3 months prior to diagnostic surgical intervention and were classified as presenting primary GBM. Five GBM patients (5.8%) presented a tumor which was resected over one year after a lower grade astrocytoma (grade II or III), and were designated as secondary GBM cases. Written informed consent was obtained from all patients according to the ethical guidelines approved by the Department of Neurology, School of Medicine, University of Sao Paulo (0599/10).

Sample Preparation

Total RNA was extracted from frozen tissues (tumor and non-neoplastic) using an RNAeasy Mini Kit (Qiagen, Hilden, Germany). Evaluation of RNA concentration and purity were carried out by measuring absorbance at 260 and 280 nm. Ratios of 260/280 measures ranging from 1.8 to 2.0 were considered satisfactory for purity standards. Denaturing agarose gel electrophoresis was used to assess the quality of the samples. A conventional reverse transcription reaction was performed to yield single-stranded cDNA. The first strand of cDNA was synthesized from 1 μg of total RNA previously treated with 1 unit of DNase I (FPLC-pure, GE Healthcare, Uppsala, Sweden) using random and oligo (dT) primers, RNase inhibitor, and SuperScript III reverse transcriptase according to the manufacturer’s recommendations (Life Technologies, Carlsbad, USA). The resulting cDNA was subsequently treated with 1 unit of RNase H (GE Healthcare, Uppsala, Sweden), diluted with TE buffer, and stored at −20°C until later use.

Quantitative Real Time PCR (qRT-PCR)

The relative expression level of ID4, SOX2, SOX4, OCT-4, NANOG and CD133 were analyzed by qRT-PCR, using the SYBR Green approach. Quantitative data were normalized in relation to the geometric mean of three housekeeping genes, suitable for the analysis: hypoxanthine phosphoribosyltransferase (HPRT), glucuronidase beta (GUSB) and TATA box binding protein (TBP), as previously demonstrated by our group [26]. The primers were designed to amplify 80–120 bp amplicons, with a melting temperature of 60°C and were synthesized by IDT (Integrated DNA Technologies, Coralville, USA) as follows (5′ to 3′): ID4 F: TGAACAACGGAGGGGACAG, ID4 R: CCCCCCTCTATGCTCCTGCTGG; SOX2 F: AAGAGAACCATATCCATCCA, SOX2 R: AGTCCCCCAAAAAAGGTCCA; SOX4 F: CAGAGGAGGGGGAAAACATCA, SOX4 R: GAATCCGGACATAAGGATTGTG; NANOG F: GCAGAGACTCTCACAATCTCGTA, NANOG R: CATTGCGTATTCTCTTGCCAGGT; OCT-4 F: CGTGAAGCTGGAAGGAGA, OCT-4 R: CCTGCGAATTTGCTGGATTGT; CD133 F: TCGGAAAACTGCGAGATAGCA, CD133 R: GTGAAAGCCCTTGCTTCCT; HPRT F: TTAGAATTTTGGAAGGGGTGT, HPRT R: GACGCACAGAGGTTGCTACA; GUSB F: GAAAATACCTGTTGGAGGAGGATCTTT, GUSB R: CCGAGTGGAAGATCCCTTGTTTATA; TBP F: AGGATAAGAGGCGCAGACCA, TBP R: CTTGCGCGACTGTCGACTG.

The minimum primer concentrations necessary were determined to give the lowest threshold cycle (Ct) and maximum amplification efficiency, while minimizing non-specific amplification. Primer concentrations used were 150 nM for ID4, 200 nM for HPRT, 200 nM for TBP, 500 nM for OCT-4, and 400 nM for GUSB, NANOG and CD133. Standard curve was established to ensure amplification efficiency and analysis of melting curves demonstrated a single peak for all PCR products. Additionally, agarose gel electrophoresis was employed to check the size of the PCR product amplified. SYBR Green I amplification mixtures (2 μl) contained 3 μl of cDNA, 6 μl of 2X Power SYBR Green I Master Mix (Life Technologies, Carlsbad, USA) and forward and reverse primers. PCR reactions were run on an ABI Prism 7500 sequence detector (Life Technologies, Carlsbad, USA) as follows: 2 min at

### Table 1. Demographic data from patients analyzed in this study.

| Total of cases | Morphology* | Mean age at diagnosis (years) | Gender* |
|----------------|-------------|------------------------------|---------|
| 22             | NN          | 38±7.6                       | 12 F, 10 M |
| 26             | AGII        | 34±8.1                       | 11 F, 15 M |
| 18             | AGIII       | 35±12.3                      | 7 F, 11 M |
| 86             | GBM         | 54±13.9                      | 28 F, 58 M |

*NANOG, non-neoplastic; AGII, low-grade astrocytoma; AGIII, anaplastic astrocytoma; GBM, glioblastoma.

*Age at diagnosis was calculated from date of birth to date of surgery.

* M, male; F, female.

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50°C, 10 min of polymerase activation at 95°C, and 40 cycles of 15 s at 95°C and 1 min at 60°C. All the reactions were performed in duplicate. The following equations were applied to calculate gene relative expression according to primer efficiency (E) in tumor samples versus the mean of non-neoplastic tissues: $2^{-\Delta\Delta Ct}$ [27] for SOX2, SOX4, OCT-4 and CD133; and $1+E^{-\Delta\Delta Ct}$ [28] for ID4 and NANOG, where $\Delta Ct = Ct_{\text{specific gene}} - \text{mean Ct of housekeeping genes}$ and $\Delta\Delta Ct = \Delta Ct_{\text{tumor}} - \text{mean } \Delta Ct_{\text{non-neoplastic}}$. Red dots represent the secondary GBM cases. Horizontal bars show the median of each group and the values are presented in Table 2. 

The difference of relative gene expressions among the groups were statistically significant ($p<0.0005$ for ID4, SOX2, SOX4, OCT-4 and NANOG; and $p<0.05$ for CD133, Kruskal-Wallis test). A pair-based comparison was assessed using Dunn test. The $p$ value results are shown, where **$p<0.0005$, *$p<0.005$ and *$p<0.05$. 

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50°C, 10 min of polymerase activation at 95°C, and 40 cycles of 15 s at 95°C and 1 min at 60°C. All the reactions were performed in duplicate. The following equations were applied to calculate gene relative expression according to primer efficiency (E) in tumor samples versus the mean of non-neoplastic tissues: $2^{-\Delta\Delta Ct}$ [27] for SOX2, SOX4, OCT-4 and CD133; and $1+E^{-\Delta\Delta Ct}$ [28] for ID4 and NANOG, where $\Delta Ct = Ct_{\text{specific gene}} - \text{mean Ct of housekeeping genes}$ and $\Delta\Delta Ct = \Delta Ct_{\text{tumor}} - \text{mean } \Delta Ct_{\text{non-neoplastic}}$. Red dots represent the secondary GBM cases. Horizontal bars show the median of each group and the values are presented in Table 2. The difference of relative gene expressions among the groups were statistically significant ($p<0.0005$ for ID4, SOX2, SOX4, OCT-4 and NANOG; and $p<0.05$ for CD133, Kruskal-Wallis test). A pair-based comparison was assessed using Dunn test. The $p$ value results are shown, where **$p<0.0005$, *$p<0.005$ and *$p<0.05$. 

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DNA Extraction and TP53 Mutational Analyses
DNA extraction was performed from frozen tumor tissues using All Prep DNA/RNA Mini Kit (Qiagen, Hilden, Germany), and peripheral leukocyte DNA was extracted by a salting-out procedure [29]. Whole coding TP53 exons (2 to 11) analysis was performed using the polymerase chain reaction single-strand conformation polymorphism (PCR-SSCP) assay and DNA sequencing, as previously reported [30,31].

Immunohistochemistry
For immunohistochemical detection, tissue sections were routinely processed and subjected to antigen retrieval. Briefly, slides were immersed in 10 mM citrate buffer, pH 6.0 and incubated at 122°C for 3 min using an electric pressure cooker (BioCare Medical, Walnut Creek, USA). Specimens were then blocked and further incubated with the following antibodies raised against human ID4 (rabbit polyclonal, ab20988, Abcam, Cambridge, UK, 1:100), SOX2 (mouse clone 6, S1451, Sigma Aldrich, St. Louis, USA, 1:100), SOX4 (rabbit polyclonal, S7318, Sigma Aldrich, St. Louis, USA, 1:800) at 16–20°C for 16 hours. The development of the reaction was performed with a commercial kit (Novolink; Novocastra, Newcastle-upon-Tyne, UK) at room temperature, using diaminobenzidine and Harris hematoxylin for nuclear staining. Optimization using positive controls suggested by the manufacturer of each antibody (breast carcinoma for ID4 and SOX4 antibodies, and normal esophagus for SOX2), was performed in order to obtain optimal dilution. Staining intensity of tissue sections was evaluated independently by two observers (SKNM and TFAG). A semi-quantitative score system considering both intensity of staining and percentage of cells was applied as follows: for intensity of staining, 0 = negative, 1 = weak, 2 = moderate and 3 = strong; for cell percentage, 0 = no cells stained, 1 = 10–25%, 2 = 26–50%, 3 = 51–75% and 4 = 76–100%. Only cases with positive cell staining with scores $\geq 2$ were considered as positive. Digital photomicrographs of representative fields were captured and processed using PICASA 3 (Google, Mountain View, USA).

Statistical Analysis
The statistical analysis of relative gene expression in different grades of astrocytoma was assessed using the Kolmogorov-Smirnov normality test, and the non-parametric Kruskal-Wallis
and Dunn tests. Correlation between relative gene expression values was assessed using the non-parametric Spearman-rho correlation test and the parametric Pearson’s correlation test. The Mann-Whitney test was used to compare TP53 mutational status and relative gene expression. The Kaplan-Meier survival curve was analyzed using the log-rank (Mantel Cox) test and multivariate analysis using the Cox proportional hazards model. The logistic regression model included the following parameters: age at diagnosis, gender (female vs male), degree of tumor surgical resection (gross total resection (GTR) vs partial resection (PR) and gene expression status (hyper or hypexpression). Differences were considered statistically significant when $p<0.05$. Calculations were performed using SPSS, version 15.0 (IBM, Armonk, USA).

**Results**

**Relative Expression Levels in Diffusely Infiltrative Astrocytomas**

Gene expression analysis by qRT-PCR for *ID4* showed higher median expression levels in all diffusely infiltrative astrocytoma cases (AGII to GBM) relative to the NN cases, and comparison among the groups was statistically significant (Figure 1A, $p<0.0005$, Kruskall-Wallis test). Although the *ID4* median expression level in GBM cases was lower than in AGII and AGIII, there was a variability of these expression values, with cases presenting both higher and lower values than the other grades. Similar variability of *ID4* expression was also observed in AGII and AGIII (Figure 1A). A multivariate Cox regression model (which considered age at diagnosis, gender, degree of tumor surgical resection, and *ID4* expression status) showed that *ID4* expression (hyper or hypexpression) alone had no impact on patient’s prognosis. Only age at diagnosis was an independent prognostic factor (hazard ratio $=1.02$, $p=0.02$), *SOX2*, *SOX4*, *OCT-4*, *NANOG*, and *CD133* also showed higher mRNA levels in AGII-GBM cases in comparison to NN, as shown in Figure 1B–F. *SOX2* expression levels were compared to *ID4* levels to verify the degree of their co-expression in human diffusively infiltrative astrocytomas. Interestingly, the correlation analysis of *SOX2* showed mRNA levels similar to *ID4*, with positive correlation found in AGII ($r=0.731$; $p=0.00002$), AGIII ($r=0.671$; $p=0.006$) and GBM ($r=0.334$; $p=0.006$). Next, *SOX4*, *OCT-4*, *NANOG* and *CD133* expression levels were also evaluated. *SOX4* expression levels were similar to those of *ID4*, although positive correlation was only found in AGII ($r=0.568$; $p=0.002$) and GBM ($r=0.414$; $p=0.00009$). *OCT-4* relative expression correlated positively with *ID4* in AGII ($r=0.551$; $p=0.02$) and GBM ($r=0.364$; $p=0.01$). In contrast to the other analyzed genes, several GBM cases exhibited very low expression levels of *NANOG*, and no correlation was found between *ID4* and *CD133* expression levels. *ID4* and *CD133* expressions did not correlate. An overview of the results of analyzed correlations is shown in Figure 2.

It is interesting to note that secondary GBM cases (red dots on Figure 1) exhibited a higher median expression level for *ID4* (2.78) than did primary GBM cases (1.84). Similar results were obtained for *SOX2* (3.96 for secondary and 2.26 for primary GBM) and *SOX4* (48.99 for secondary and 6.74 for primary). In contrast, the median of *OCT-4* expression was 0.47 in secondary GBM and 2.03 in primary GBM; the median of *NANOG* expression level in secondary GBM was 0.13 while 0.35 in primary GBM, and the median of *CD133* expression level was 1.28 for secondary GBM and 2.26 for primary GBM. To further investigate the factors contributing to these differences, the expression values were analyzed according to TP53 mutation status.

**Association between *ID4*, *SOX2*, *SOX4*, and *NANOG* mRNA Expressions and TP53 Mutation Status**

The frequency of TP53 mutation was 11.6% in GBM (10 out of 86), 16.6% in AGIII (3 out of 18) and 50% in AGII (13 out of 26), as described in our previous studies [30,31] (Table S1). Our GBM series is composed mainly by primary GBMs, which explains the low frequency of TP53 mutation and corroborates the classification based on clinical presentation. The low frequency of TP53 mutations in GBM and AGIII cases did not permit statistical analyses of the proposed parameters; however, this analysis was feasible among AGII cases. Interestingly, TP53-mutated AGII cases showed higher relative expression of *ID4* when compared to AGII cases with wild-type TP53 (*p=0.048*) (Figure 3A). Also, *SOX2* (*p=0.044*), *SOX4* (*p=0.004*) and *NANOG* (*p=0.025*) relative expressions were higher in mutated than in wild-type TP53 in AGII cases (Figure 3B, 3C and 3E respectively). No difference was found for *OCT-4* relative expression between wild-type and mutated TP53 cases (Figure 3D). Despite the fact that TP53-mutated AGII cases displayed slightly higher relative expression of *CD133*, the difference was not statistically significant (Figure 3F). No difference in expression was found regarding the different types of TP53 mutations (whether missense, nonsense or in splicing sites). Mann-Whitney test was applied for all the above statistical analysis. Moreover, no significant impact was observed in the overall survival time or in the progression free survival time in AGII cases, concerning either relative expression levels of *ID4*, *SOX2*, *SOX4*, *OCT-4*, *NANOG*, and *CD133* or TP53 mutational status (results presented Table S2). Although TP53 mutated AGII cases presented a median of 40 months of overall survival time compared to a median of 51 months of wild-type TP53 AGII cases, it did not reach statistical significance because of the small number of cases in each group (Figure 3, white lozenges for deceased AGII patients). Associated expression of *ID4*, *SOX2* and *SOX4* with TP53 mutational status was further confirmed at the protein level by immunohistochemistry. The wild type TP53 AGII cases

**Table 2.** Median of relative expression levels of the analyzed genes in astrocytomas, according to morphology.

| Morphology | *ID4* | *SOX2* | *SOX4* | *OCT-4* | *NANOG* | *CD133* |
|------------|-------|--------|--------|---------|---------|---------|
| NN         | 1.15  | 1.06   | 1.09   | 0.51    | 0       | 0.87    |
| AGII       | 8.12  | 3.32   | 9.12   | 2.92    | 1.77    | 1       |
| AGIII      | 11.1  | 4.9    | 8.86   | 4       | 3.84    | 2.43    |
| GBM        | 1.89  | 2.32   | 7.63   | 1.79    | 0.25    | 2.26    |

*NN, non-neoplastic; AGII, low-grade astrocytoma; AGIII, anaplastic astrocytoma; GBM, glioblastoma.*

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(Figure 4A–4C) showed weak or no staining for the three targets in comparison to the TP53-mutated cases (Figure 4D–4F), as did the primary GBM cases (Figure 4G–4I) when compared to the secondary GBM (Figure 4J–4L) cases.

The overview of TP53 mutation status, relative gene expression for AGII, and expression differences among AGII, AGIII, primary and secondary GBM are displayed as heatmap in Figure 5.

Impact of ID4, SOX4 and OCT-4 Expression Levels on Clinical Outcome for GBM Patients

Considering the variability of the relative expression values found in GBM cases, we evaluated the impact of up-regulation of the analyzed genes on overall patient survival. For the evaluation, conditions were determined for high and low gene expression.

Secondary GBM cases were excluded from this analysis due to the small number of cases. None of the genes had an impact on overall survival, either on their own or when grouped in pairs for the determined conditions (Figure S1). However, there was a significant difference when comparing GBM cases with high ID4, SOX4 and OCT-4 expressions (median survival of 6 months) with cases with low expressions for the three genes (median survival of 18 months) (log rank \( p = 0.014 \)), as shown on the Kaplan-Meier survival curve in Figure 6.

Discussion

We have demonstrated a differential expression of ID4 in human diffusely infiltrative astrocytoma cases demonstrating...
association with TP53 mutation status, as well as to SOX2, SOX4 and OCT-4 mRNA expression levels.

**ID4 mRNA Levels are Elevated in Astrocytomas in Comparison to Non-neoplastic Brain Tissue**

Our study demonstrated significantly higher mRNA expression levels of *ID4* in astrocytomas when compared to non-neoplastic brain tissue. Similar results have also been described for ID1–3 proteins in astrocytomas, with higher expression levels in tumors than in non-neoplastic white-matter [32]. A previous immunohistochemical report has shown stronger ID4 expression in GBM compared to AGII, AGIII and normal brain tissue [12]. Such association was not significant in our study, most probably due to a larger number of cases analyzed herein, and also to the number of positive cells. The reaction was performed in paraffin embedded tissue sections with a commercial polymer kit (Novolink; Novocastra, UK), using diaminobenzidine as developer and Harris hematoxylin for nuclear counterstaining. 200× magnification for all images.

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**Figure 4. ID4, SOX2 and SOX4 immunohistochemistry.** Representative cases of wild-type TP53 AGII (A-C), mutated TP53 AGII (D-F), primary GBM (G-I) and secondary GBM (J-L) stained for ID4, SOX2 and SOX4 are demonstrated. Both mutated AGII and secondary GBM cases showed stronger and larger number of nuclear stained cells (score 3 for intensity and ≥75% of positive cells) for ID4, SOX2 and SOX4. Comparatively, wild-type TP53 AGII and primary GBM presented score 1 for intensity and <25% of positive cells. The reaction was performed in paraffin embedded tissue sections with a commercial polymer kit (Novolink; Novocastra, UK), using diaminobenzidine as developer and Harris hematoxylin for nuclear counterstaining. 200× magnification for all images.

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heterogeneity inherent to GBM, here corroborated by the widespread ID4 mRNA expression among the studied GBM cases. Nevertheless, the increased ID4 expression level in diffusely infiltrative astrocytoma is in accord with the tumor re-expression model of IDs [4], postulating ID4 as an additional marker of astrocytoma progression in malignancy.

A recent report [34] has shown that ID4 promoter methylation was an independent factor on patient’s prognosis, and that association of ID4 promoter methylation and MGMT methylation status conferred significantly longer overall survival to GBM patients. We assessed the correlation between ID4 hypoexpression and the MGMT methylation status in GBM, previously reported by our group [33]. The Cox regression model showed only MGMT status as an independent factor for prognosis (hazard ratio = 4.684, p = 0.014), differing from the previous report. Further studies on ID4 promoter methylation are needed in the present GBM series.

Figure 5. Heatmap displaying the relative gene expressions in low-grade astrocytoma (AGII), anaplastic astrocytoma (AGIII) and GBM cases according to TP53 mutation status. The TP53 mutated cases are represented by side dashes. The mutated TP53 AGII cases showed more elevated expression levels of ID4, SOX2, SOX4 and NANOG. CD133 expressions were more heterogeneous among the cases. SOX2 and SOX4 showed similar expression levels to ID4. Similarly, secondary GBM cases also presented higher ID4, SOX2, SOX4 expression levels. OCT-4, NANOG and CD133 expression levels were heterogeneous among secondary GBM cases, and OCT-4 presented higher mRNA levels in primary GBM.

Figure 6. Survival curve of GBM patients. Twenty-five GBM cases out of 86 GBM cases presented concomitant high or low ID4, SOX4 and OCT-4 relative expression levels (12 GBM cases presenting high expressions and 13 low expressions for the three genes). The survival time difference between the two groups was statistically significant (log rank p-value = 0.014), presenting median survival time of 6 months for GBM cases presenting concomitant high expressions for the three genes compared to 18 months for GBM cases with low expressions. 

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**ID4 Hyperexpression is Driven by Mutated TP53 in AGII**

Here we demonstrate a significant difference in *ID4* expression between AGII cases harboring *TP53* mutation versus wild-type, mutated cases showing significant increase in *ID4* expression. Other studies in breast cancer models have demonstrated *in vitro* *ID4* up-regulation driven by the mutated p53 protein [13], [14]. *TP53* mutations, present in 50% of AGII cases, are considered one of the earliest events in astrocytoma formation [9]. The significant association shown here between *TP53* mutation and *ID4* expression could possibly classify *ID4* hyperexpression as an early event in astrocytoma formation. The analysis of AGII patients OS time in *TP53* mutated and wild-type cases showed that the mutated cases had a shorter survival by eleven months in comparison to the wild-type group. Considering the low number of cases, further studies are necessary to confirm statistically this result. The great majority of *TP53* mutations are missense, localized in specific gene domains (“hot spots”) that do not inactivate protein function. On the contrary, these alterations stabilize the mutated protein and enhance its oncogenic activity by increasing the transcription of target genes, recruiting other transcription factors and co-factors (recently reviewed in [35]). However, no difference of the analyzed gene expressions were found compared to the different types of *TP53* mutation in the current AGII series, and it remains to be elucidated if the cases harboring inactivating nonsense mutations present alternative activation for *ID4*, *SOX2* and *SOX4*.

**Associated Expression of *ID4* with *SOX2* and *SOX4* and with Mutated *TP53***

*SOX2* also proved to be significantly augmented and correlated to *ID4* in *TP53* mutated AGII cases. *SOX2* overexpression driven by inactivation of p53 in mouse embryonic fibroblasts has been demonstrated [36], although the mechanism remains unknown. One possible explanation is that *ID4* up-regulation activates *SOX2* through inhibition of a microRNA, mir-9*, which is a direct negative regulator of *SOX2*, as shown in glioma cell lines [16]. Our findings of *ID4* up-regulation associated to *TP53* mutated status and to *SOX2* hyperexpression in human astrocytoma specimens corroborate these previous observations in cell lines. Taken together, these data suggest that *ID4* and *SOX2* act jointly post-*TP53* mutation in promoting astrocytoma tumorigenesis.

The association between *SOX4* and p53 has also been reported [37], [38], with *SOX4* stabilizing p53 protein and inhibiting its induction of the apoptotic pathway. In our study, *SOX4* expression was increased in *TP53* mutated cases, in a similar pattern to *ID4*. It remains to be elucidated what role the observed association between *SOX4* and mutated *TP53* plays in the process of astrocytic tumor formation.

Our results showed a significant increase in *NANOG* expression in *TP53* mutated AGII cases. It is known that p53 is a direct negative regulator of *NANOG* [39] and that the absence of a functional p53 protein augments *NANOG* expression. *NANOG* levels did not correlate to any of the other analyzed targets, and its expression pattern in GBM cases was random, enabling us to speculate that *NANOG* works differently to contribute to astrocytoma formation. *CD133* levels were not significantly different when *TP53* mutated and wild-type AGII cases were compared, and GBM cases also displayed a random pattern, suggesting that *CD133* also works differently in the tumorigenic process of astrocytomas.

*OCT-4* relative expression was not influenced by *TP53* mutational status and did not correlate with *ID4* expression in AGII cases. However, the expression pattern of GBM cases was strikingly different: secondary GBM exhibited very low *OCT-4* mRNA levels in comparison to primary GBM. Together with the positive correlation between *OCT-4* and *ID4* found in both AGII and GBM cases, these data indicate a role for this target in the most malignant grades of astrocytoma. These results prompted us to further investigate the combined expression of *ID4*, *SOX4* and *OCT-4*.

**Impact of *ID4*, *SOX4* and *OCT-4* Mutual Hyperexpression on Primary GBM Patients’ Overall Survival**

The expression level variability among GBM cases was present for all analyzed genes (Figure 1), with some cases exhibiting very high mRNA levels in contrast to low levels found in others. Again, this phenomenon may be due to the extensive heterogeneity found in GBM at both the cellular and molecular levels [40], contributing to difficulties in eradicating these tumors. Thus, we believed it was necessary to ascertain whether patients bearing tumors with higher mRNA levels of the analyzed genes showed worse overall survival. When we grouped *ID4*, *SOX4* and *OCT-4* together, patients hyperexpressing these genes exhibited much lower survival time. In bladder cancers, both *ID4* and *SOX4* were amplified and overexpressed heterogeneously [41], similar to astrocytomas, and contributed to the variable biological and clinical behavior of the tumors. As previously mentioned, *OCT-4* and *SOX4* proteins form a transcription complex and induce *SOX2* expression, increasing the tumorigenicity of glioma cells. Although decreased survival was demonstrated in mice inoculated with GBM cells hyperexpressing *OCT-4*, we observed that *OCT-4* alone had no impact on our patients’ overall survival (Figure S1D). Because *ID4* alone, as well as the *SOX4* and *OCT-4* complex, activates *SOX2*, and because chemoresistance is associated with both *SOX2* and *ID4* augmented expression, it is possible to speculate that multiple *SOX2* activation events in GBM may impair patient prognosis. *SOX2* and *OCT-4*, are considered masters of pluripotency in embryonic stem cells [42]. This role is maintained in cancer stem cells (CSC), a subset of tumor cells regarded as possessing traits such as therapeutic resistance, tumor angiogenesis and recurrence [43]. *ID4* has also shown to play an important role in CSC biology, its expression being imperative to the formation and maintenance of CSC population [44]. In GBM stem cells [45–48], *ID4* has been postulated as an important target in the dedifferentiation process, as shown in the *in vitro* reports [15], [16]. Moreover, the re-expression of embryonic stem cells genes in tumors, including gliomas, has been associated with a more aggressive phenotype [22], [49], [50]. It is possible that this is the cause for the worse clinical end-point of overall survival among GBM patients found in our study. However, because of the low number of GBM cases (n = 25) in which this finding was demonstrated, the present result should be validated in an independent study sample containing a higher number of GBM patients.

In this scenario, *ID4* seems to be a promising target for further studies in order to better understand its role in tumorigenesis and its potential use in therapeutics.

**Supporting Information**

**Figure S1** Kaplan-Meier curves of GBM patients according to relative expression levels of *ID4*, *SOX2*, *SOX4*, *OCT-4*, *ID4*x*SOX2*, *ID4*x*SOX4*, *ID4*x*OCT-4*, *SOX4*x*OCT-4* (TIF).

**Table S1** Clinical data of patients in the study (Excel).

**Table S2** Low-grade astrocytoma patients’ survival time analysis (Word).
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Author Contributions

Conceived and designed the experiments: TFdAG SMOS SKNM. Performed the experiments: TFdAG MU. Analyzed the data: TFdAG SMOS SKNM. Contributed reagents/materials/analysis tools: ANA MJT SR SKNM. Wrote the paper: TFdAG SMOS SKNM.

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