Supplementary Data

***IDH*-mutation status is associated with a distinct hypoxia/angiogenesis transcriptome signature which is non-invasively predictable with rCBV-imaging in human glioma.**

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Supplementary Figure 1. Gene expression heat-map of key *HIF1A* target genes showing increased expression of key angiogenic regulators such as *VEGFA*, *ANGPT* or *PDGF* in *IDH-1/2* wild-type tumors and on the contrary, increased expression of *EglN 1* and *3* – responsible for degradation of *HIF1A* – in *IDH-1/2* mutant tumors. Columns represent samples of 288 patients with low-grade diffuse or anaplastic gliomas from The Cancer Genome Atlas (TCGA). The statistical track at the bottom shows the logarithmic plot of p-values for each genomic position, with colored bars indicating either significantly increased expression of the genomic location for *IDH-1/2* wild-type (red) or mutant (blue) tumors.

Supplementary Table 1. Detailed information on histology and *IDH* mutation status from both TCGA and local dataset. (Excel file)

Supplementary Table 2. Gene sets evaluated for differential mRNA-expression between *IDH-1/2* mutated and wild-type tumors in the gene set variation analysis (GSVA). (Excel file)

Supplementary Table 3. Ingenuity pathway analysis of upstream regulators and downstream biological functions. (Excel file)

Supplementary Figure 1.