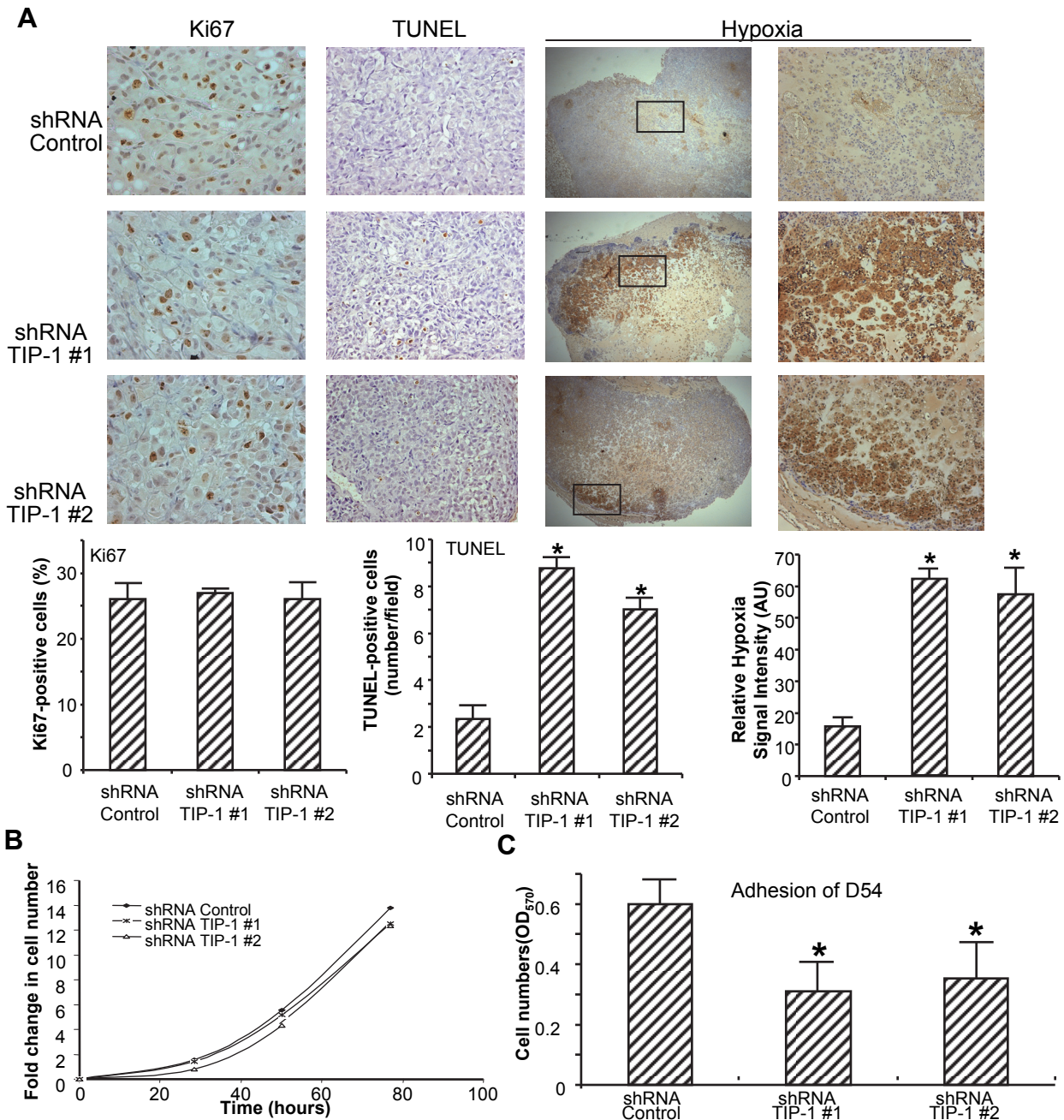
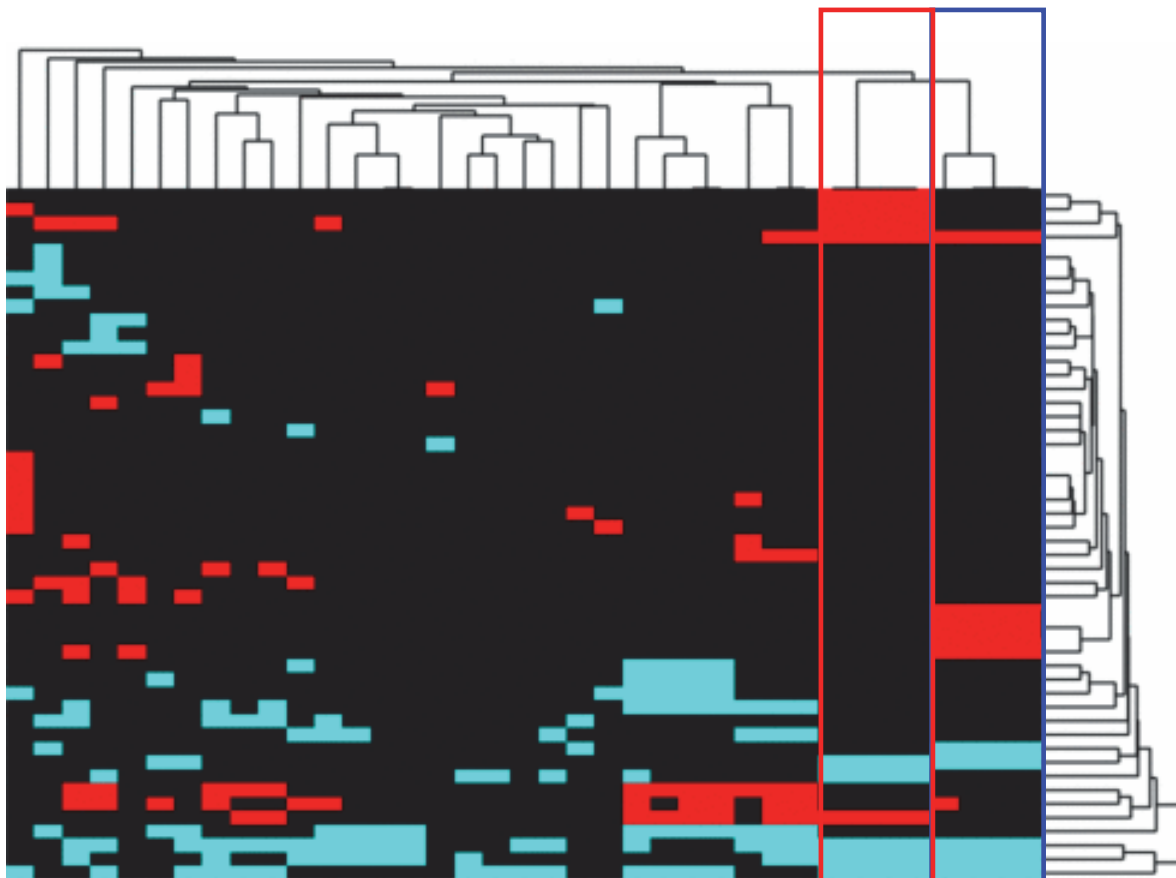


Supplementary Fig. s1. (A) TIP-1 expression level is independent of age of glioblastoma (WHO grade IV) patients at the time of diagnosis. The analysis was based upon dataset GDS1962 (GEO database from NCBI, NIH), in which patients are ranked upon TIP-1 expression levels. Those with upper 35% TIP-1 expression levels are grouped as “TIP-1 High”, and those with lower 35% of TIP-1 expression levels as “TIP-1 Low”. 20 patients were included in each group for statistic analysis. (B) TIP-1 expression level is independent of gender of glioblastoma (WHO grade IV) patients at the time of diagnosis. Same dataset was used as in A. 55 patients were included in the statistic analysis. (C) Survival probability analysis of glioblastoma (WHO grade IV) patients. The analysis was based upon dataset GDS1975 (GEO database from NCBI, NIH). Same standard was applied to identify the “TIP-1 High” and “TIP-1 Low” patients. $p = 0.0116$, 22 cases for each group. Log-rank test.



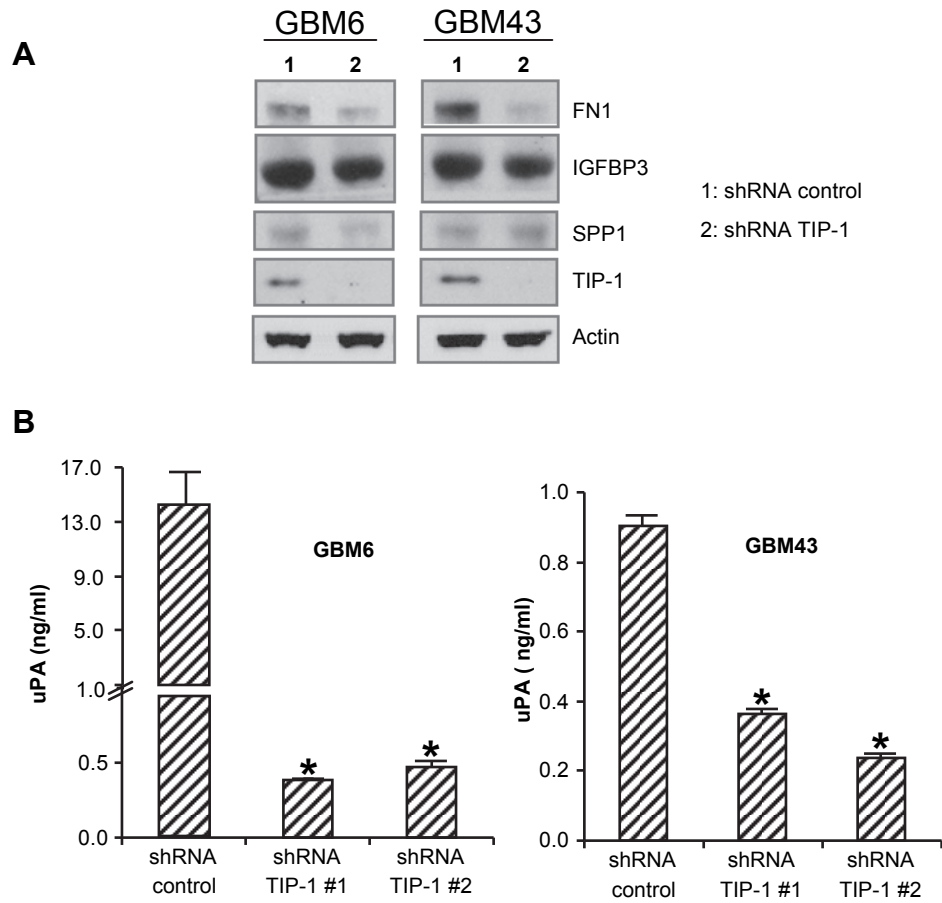
Supplementary Fig. s2. (A) immunohistochemical detection of cell proliferation (Ki67), apoptosis (TUNEL) and hypoxia within D54 xenografts. The hypoxic regions were defined by positive staining with Hypoxyprobe-1. Shown are representative images and quantification (ImageJ) upon more than 12 microscopic fields. (B) *In vitro* cell proliferation was determined with direct cell counting. 4×10^4 D54 cells were seeded in multi-well plates with DMEM culture medium, cells were disaggregated for quantification with hemocytometer at multiple time points. (C) Cell adhesion assays. 4×10^4 D54 cells within 100 μ l of medium were seeded in multi-well plates. After 3 hours incubation at 37 degree, the non-attached cells were washed off with cold phosphate buffered saline. The attached cells were stained with methylene blue, dissolved with 2% SDS solution and quantified upon the colorimetric density (570 nm). Shown are the representative data from three independent triplicated experiments. * $p < 0.05$, $n = 3$, the Student's *t*-test.

50: UNC5C
 49: ICAM1
 48: F28
 47: JAG1
 46: PTX3
 45: CD180
 44: OLR1
 43: S1PR3
 42: PCDH8
 41: CD274
 40: ADAMTS1
 39: PDCD1LG2
 38: PDE5A
 37: PCSK1
 36: TIMP3
 35: KLF4
 34: HSD11B1
 33: PKIA
 32: ZNF354A
 31: CLDN1
 30: AMIGO2
 29: PCDH7
 28: CDH11
 27: DSP
 26: PCDH8
 25: PTN
 24: LRRC17
 23: SPRY2
 22: TNFSF4
 21: CD24
 20: PLXDC1
 19: COL8A1
 18: PTPRB
 17: IL18
 16: IL1RAPL1
 15: C5ORF13
 14: NLGN1
 13: PBX1
 12: TGM2
 11: ENPP1
 10: FN1
 9: ANXA3
 8: IGFBP3
 7: NOG
 6: LIF
 5: SEMA3A
 4: SPP1
 3: SFRP1
 2: ITGB3
 1: SLIT2



GO:0016337_cell-cell_adhesion
 GO:0006954_inflammatory_response
 GO:0008284_positive_regulation_of_cell_proliferation
 GO:0008285_negative_regulation_of_cell_proliferation
 GO:0042098_T_cell_proliferation
 GO:0031099_regeneration
 GO:0048545_response_to_steroid_hormone_stimulus
 GO:0035295_tube_development
 GO:0022612_gland_morphogenesis
 GO:0001763_morphogenesis_of_a_branching_structure
 GO:0051051_negative_regulation_of_transport
 GO:0048771_tissue_remodeling
 GO:0046849_bone_remodeling
 GO:0034103_regulation_of_tissue_remodeling
 GO:0046850_regulation_of_bone_remodeling
 GO:0051593_response_to_folic_acid
 GO:0014909_smooth_muscle_cell_migration
 GO:0014912_negative_regulation_of_smooth_muscle_cell_migration
 GO:0071503_response_to_heparin
 GO:0001933_negative_regulation_of_protein_phosphorylation
 GO:0018149_peptide_cross_linking
 GO:0016339_calcium_dependent_cell-cell_adhesion
 GO:0060284_regulation_of_cell_development
 GO:0045664_regulation_of_neuron_differentiation
 GO:0051960_regulation_of_nervous_system_development
 GO:0050767_regulation_of_neurogenesis
 GO:0001503_ossification
 GO:0045596_negative_regulation_of_cell_differentiation
 GO:0051093_negative_regulation_of_developmental_process
 GO:0040012_regulation_of_locomotion
 GO:0030334_regulation_of_cell_migration
 GO:2000145_regulation_of_cell_motility
 GO:0051270_regulation_of_cellular_component_movement
 GO:0001944_vasculature_development
 GO:0001525_angiogenesis
 GO:0001568_blood_vessel_development
 GO:0048514_blood_vessel_morphogenesis

Supplementary Fig. s3. Functional clustering analyses of genes affected by the TIP-1 knockdown within D54 cells. Microarray data were analyzed with GoMiner software (NCI, NIH). The blue box highlights genes which are involved in angiogenesis-related classification. The red box highlights the genes associated with cell motility. The up-regulated genes are marked as red, while down-regulated ones as green.



Supplementary Fig. s4. TIP-1 regulated FN1 expression and uPA secretion in two xenograft cell lines of human glioblastoma. GBM6 and GBM 43 were maintained as xenograft cell lines of primary human glioblastoma. TIP-1 knockdown with recombinant lentivirus encoding a control or TIP-1-targeted shRNA was conducted as described in the materials and methods. Protein expression in the whole cell lysates was analyzed with western blot (A), and uPA secretion in the pre-conditioned medium was determined with ELISA (B). * $p < 0.05$, $n = 3$, the Student's t -test.