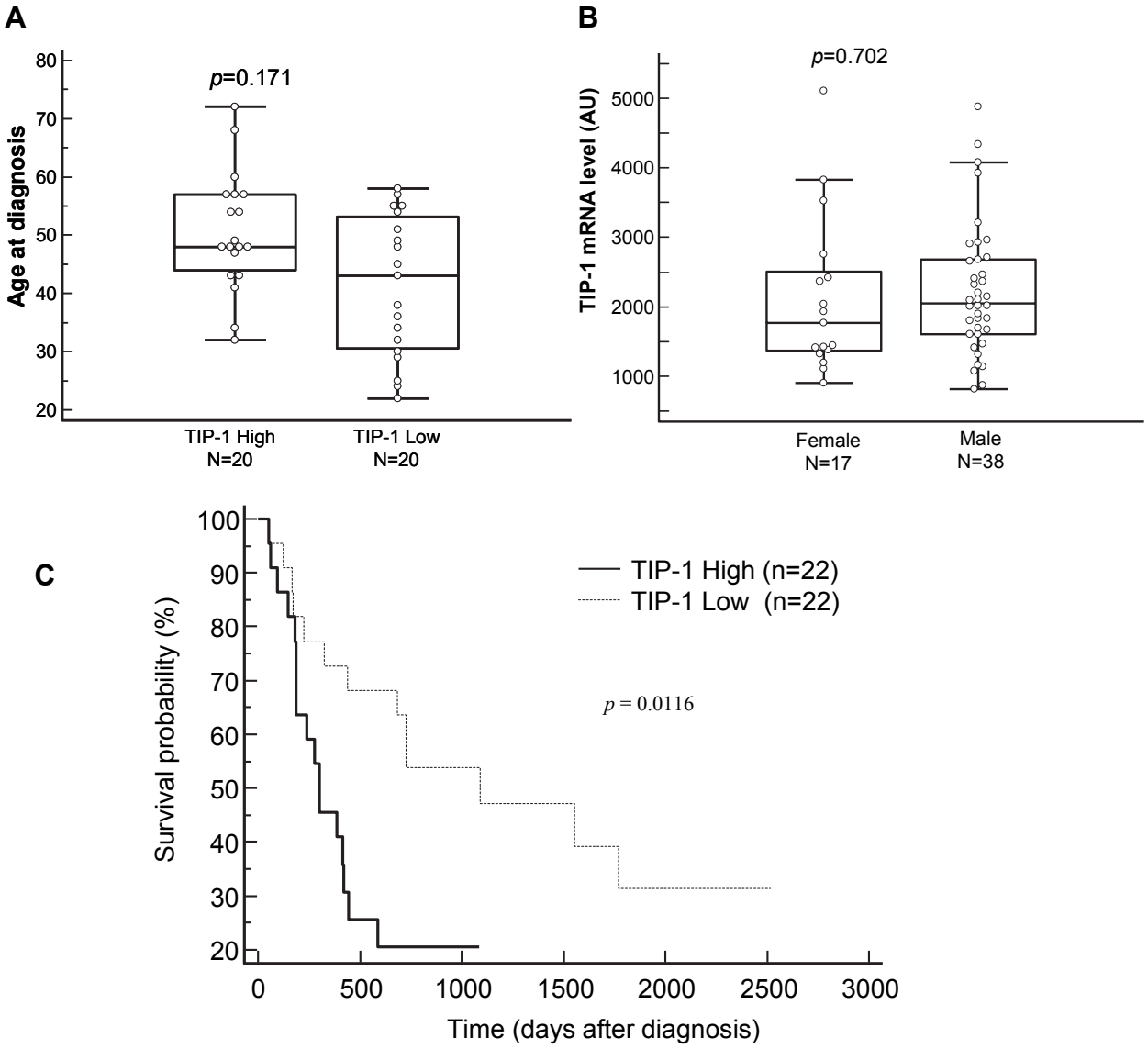
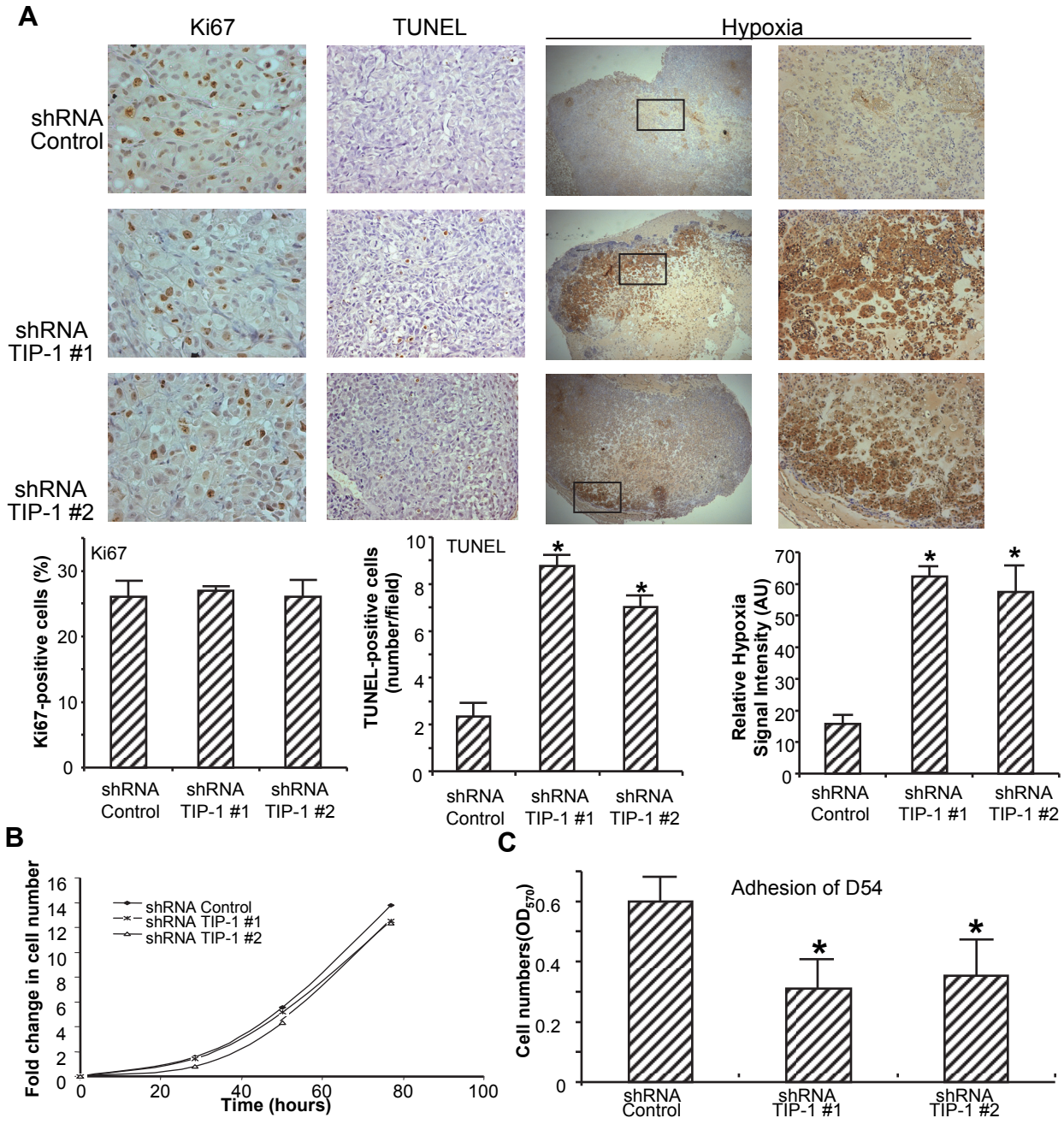
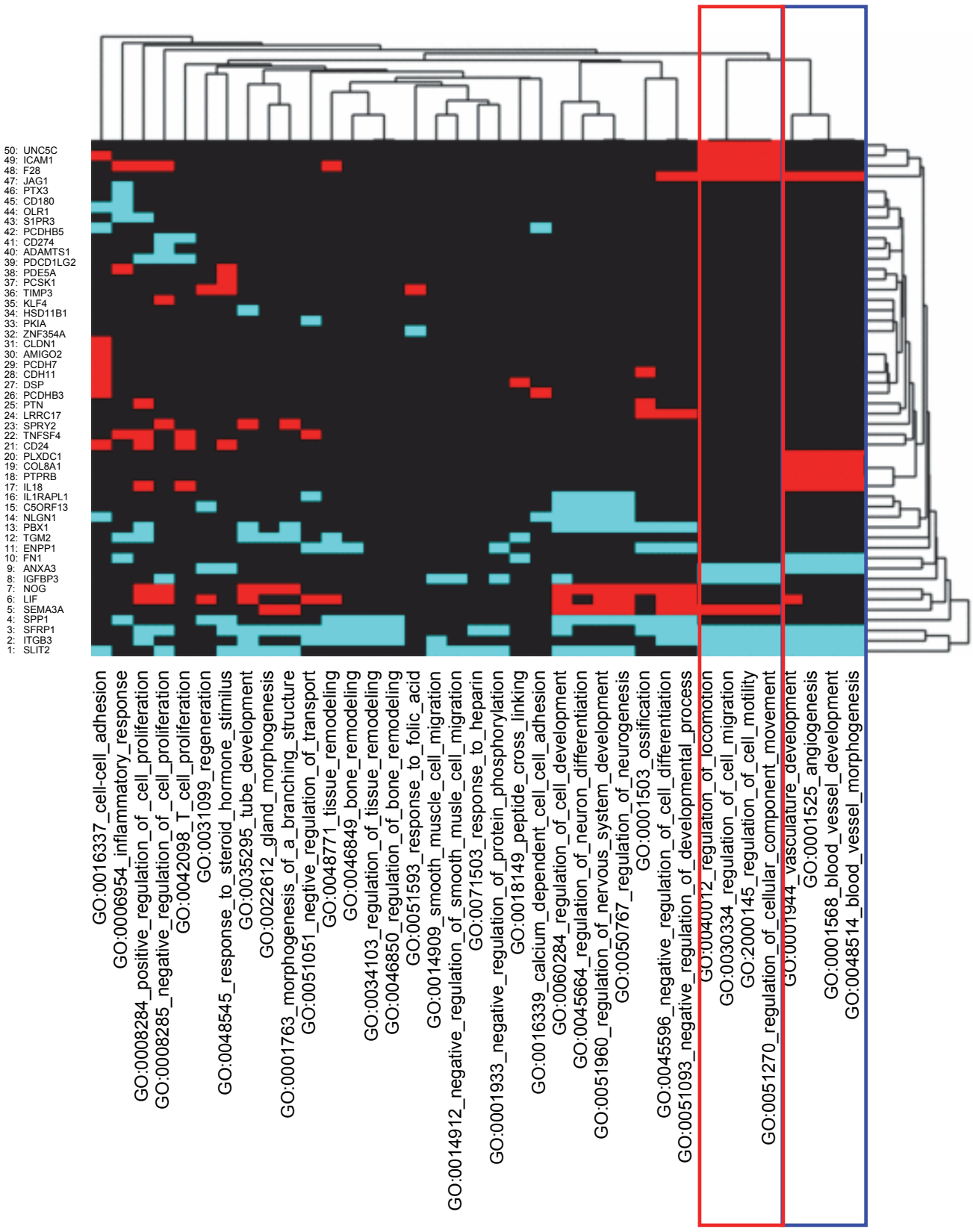


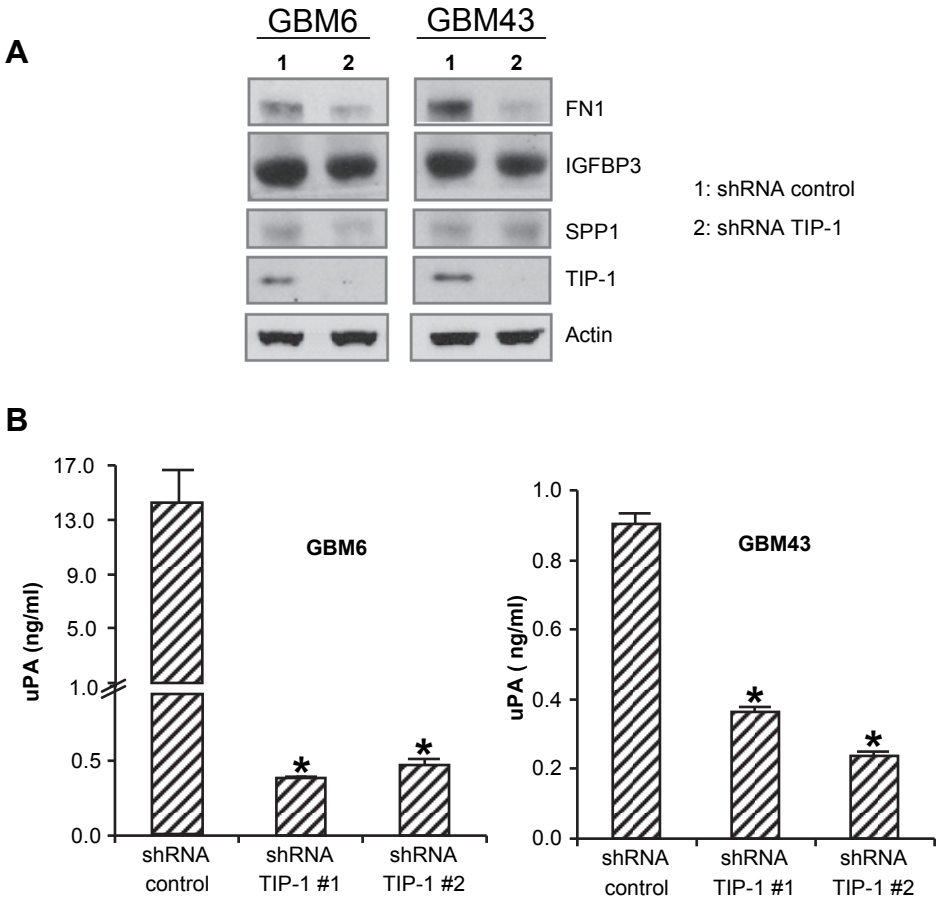
Supplementary Fig. s1. (A) TIP-1 expression level is independent of age of glioblastoma (WHO grade IV) patients at the time of diagnosis. The analysis was based upon dataset GDS1962 (GEO database from NCBI, NIH), in which patients are ranked upon TIP-1 expression levels. Those with upper 35% TIP-1 expression 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 x 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 x 10^4 D54 cells within 100 µl 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.



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.