



**Supplementary Figure 17.** Co-expression network of *IDH1* mutant gliomas. **(a)** Hierarchical clustering of gene co-expression in 62 gliomas. Modules of co-expressed genes are identified and assigned a color and label (*M1* to *M8*). **(b)** Hierarchical clustering of module eigenvalues. **(c)** Functional enrichment analyses of modules associated with cell of origin or progression status. Boxplots compare module eigenvalues of gliomas of different cell of origins or progression status. For cell of origin and progression status comparisons, *P* values are calculated using un-paired or paired two-sided Student's *t* tests, respectively. Results of functional enrichment analyses for each module is represented in the bar plots. Mitotic cell cycle module (*M1*) and angiogenesis module (*M2*) are significantly upregulated during progression, whereas organic acid metabolism module (*M3*) and synaptic transmission module (*M4*) are downregulated. Module upregulated in astrocytic tumors (*M5*) contains genes functioning in immune response, whereas module upregulated in oligodendroglial tumors (*M6*) contains genes important for mRNA processing. BP: gene ontology biological process; CC: cellular component; MF: molecular function; RT: Reactome gene sets.