Supplementary



Figure S1. Graph clusters from BioGRID. enriched gene expression data on (**A**) general glioma, (**B**) glioblastoma multiforme, and (**C**) low-grade astrocytoma, filtered by gene ontology term "proliferation" related genes: Cytoscape visualization of enrichment using BioGRID database, rendered with Prefuse Force Directed Layout, clustered by ClusterOne (grey: outlier, yellow: overlap, red: cluster, blue: unassigned/default).



Figure S2. Graph clusters from StringDB. enriched gene expression data on (**A**) general glioma, (**B**) glioblastoma multiforme, and (**C**) low-grade astrocytoma, filtered by gene ontology term "proliferation" related genes: Cytoscape visualization of enrichment using NetworkAnalyst via StringDB, clustered by ClusterOne (grey: outlier, yellow: overlap, red: cluster).



Figure S3. PPI graph on anaplastic glioma with or without the mutated IDH1/2. enriched gene expression data, filtered by gene ontology term "proliferation" related genes: Cytoscape visualization of enrichment using (**A**) via BioGRID database, (**B**) via NetworkAnalyst with StringDB, both clustered by ClusterOne (grey: outlier, yellow: overlap, red: cluster).

Table S1. Exemplary significant GO-terms within PPI networks of glioblastoma multiforme, general glioma and low-grade astrocytoma: based on elevated expression levels of genes associated with GO-term "proliferation"; significance expressed as p-value, calculated by BinGO.

Cancer Type	GO Biological Process	<i>p</i> -value
	regulation of cell cycle	$1.05 * 10 E^{-44}$
Glioblastoma multiforme	post-translational protein modification	$5.82 * 10E^{-44}$
	regulation of phosphorylation	$1.03 * 10E^{-29}$
General glioma po	regulation of cell cycle	$3.49 * 10E^{-33}$
	st-translational protein modification	$5.03 * 10E^{-46}$
	regulation of phosphorylation	$4.35 * 10E^{-30}$
Low-grade astrocytoma	regulation of cell cycle	$1.37 * 10E^{-29}$
	post-translational protein modification	$3.82 * 10E^{-45}$
	regulation of phosphorylation	$1.68 * 10E^{-31}$

Table S2. High degree nodes within general glioma: comparison of top ten hubs in BioGRID and StringDB constructed networks, with degree as number of interactions, gene identifiers, component of cluster.

BioGrid			StringDB		
Degree	Gene	Cluster No.	Degree	Node	Cluster No.
289	ERBB2/HER2	1	66	ERBB2/HER2	1
117	ERBB4/HER4	1	39	ERBB4/HER4	na
115	CCND3	2	30	TEK	na
36	INCA1	10	27	CCND3	na
31	P8/NUPR1	7	12	TGFB3	na
29	TIE-2	na	4	TGFA	na
16	CDK4	na	3	KRAS	1
15	TGFA	na	3	HRAS	1
12	CDKN1A/CIP1	na	3	GRB2	na
11	CDK6	na	3	NRAS	1

Table S3. High degree nodes within glioblastoma multiforme: comparison of top ten hubs in BioGRID and StringDB constructed networks, with degree as number of interactions, gene identifiers, component of cluster.

	BioGrid			StringDB	
Degree	Gene	Cluster No.	Degree	Node	Cluster No.
1178	p33/CDK2	1	165	CDK2	na
314	CCNA2/CCN1	4,3	89	CCNB1	na
290	CCNB1/CCNB	4,3	66	ERBB2/HER2	na
289	CD340/ERBB2/HER2	1	42	CCNA2	na
228	CCNE1	1	40	CCNE1	na
115	CCND3	4,3	38	CCNB2	na
107	LPC1/ANXA1	27,13	27	CCND3	na
100	CDKN1A/CIP1	1	23	VEGFA	na
66	HIF1A	1	16	TGFB2	na
83	P34CDC2/CDK1	1	12	TGFB3	na

	BioGrid			StringDB	
Degree	Gene	Cluster No.	Degree	Node	Cluster No.
117	ERBB4/HER4	2	39	ERBB4/HER4	na
107	LPC1/ANXA1	12	23	VEGFA/VEGF	na
62	MVCD1/VEGF	3	17	CCNE2	na
36	CYCE2/CCNE2	1	16	TGFB2	na
20	IL-6R-1/IL6R	11	7	IL6R	na
13	p33/CDK2	1	4	ANXA1	na
9	CCNI2	na	4	CD86	na
9	NRP1/NP1	3	3	STAT3	na
8	TGFB2	na	3	UBC	na
8	CD86	10	2	DCN	na

Table S4. High degree nodes within astrocytoma: comparison of top ten hubs in BioGRID and StringDB constructed networks, with degree as number of interactions, gene identifiers, and component of cluster.