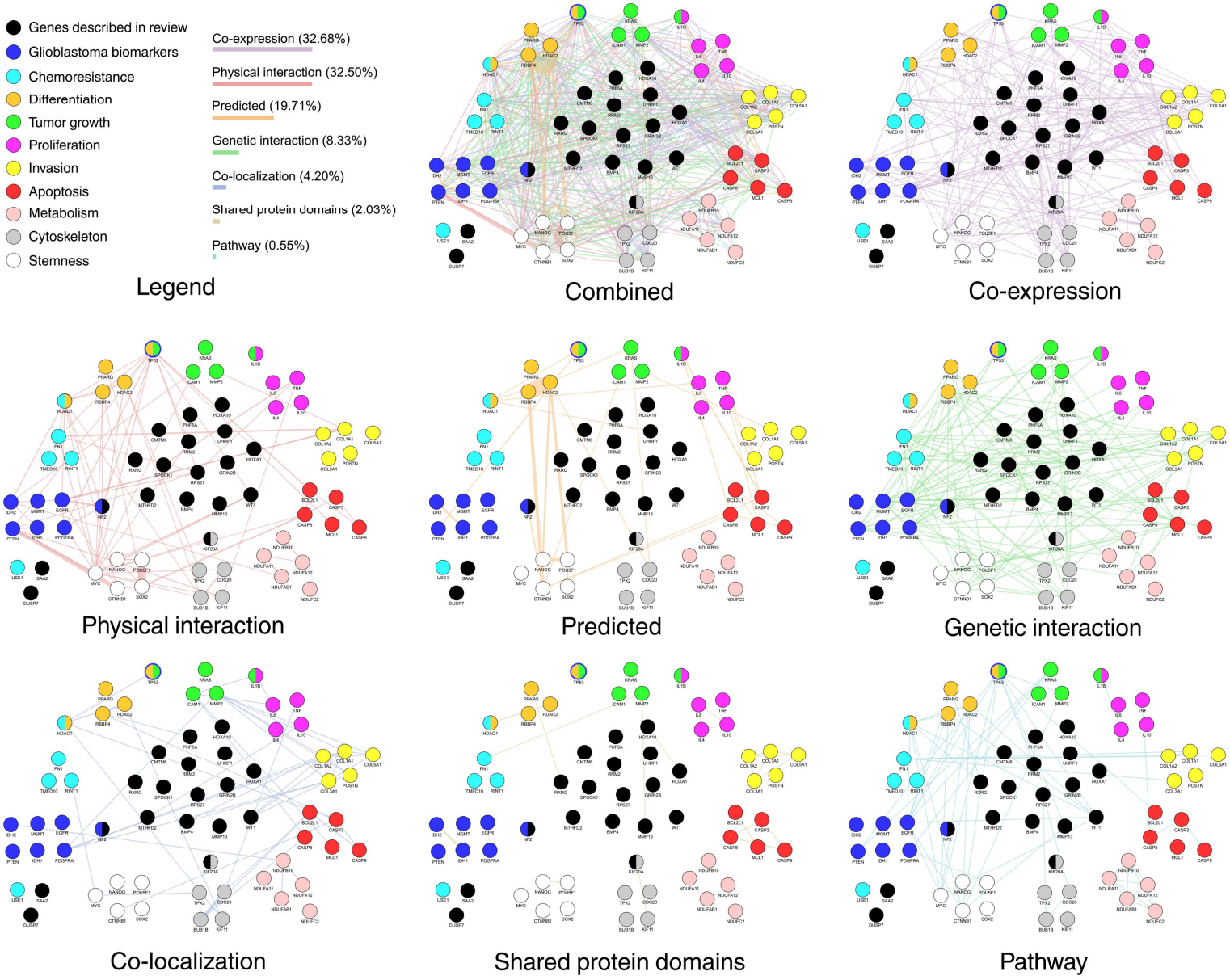
Supplementary Table 1 Summary of the previously identified genes included or excluded from the present review based on its known role in stemness regulation.

Gene	Included in the present review? (*i.e.*, implicated in stemness regulation in any tissue?)	Regulates the cytoskeleton?	Regulates the metabolism?
BMP4	✓ *	✓	×
GRIN2B	✓ *	✓	×
HOXA10	✓ *	✓	×
HOXA1	✓ *	✓	×
MMP13	✓ *	✓	✓
MTHFD2	✓ *	✓	✓
PHF5A	✓ *	×	✓
RPS27	✓ *	✓	×
RRM2	✓ *	✓	✓
SAA2	✓ *	✓	×
WT1	✓ *	✓	×
CMTM6	✓	✓	×
DUSP7	✓	✓	×
KIF20A	✓	✓	×
NF2	✓	✓	×
RXRG	✓	×	✓
SPOCK1	✓	✓	×
UHRF1	✓	✓	×
C15orf48	×	×	×
CCL11	×	✓	×
COL3A1	×	×	×
CUX2	×	✓	×
FAM92B	×	✓	×
GCSH	×	×	✓
GLB1	×	×	×
LBP	×	×	×
PLEK2	×	✓	×
RNF141	×	×	×
TAF10	×	×	×
TTR	×	✓	×

* – the gene is confirmed to regulate stemness specifically in glioblastoma

Supplementary Table 2 The datasets used in the workflow of cross-talk network development.

Biological process	Dataset unique identifier and database
Chemoresistance	M12825 and M12618 (Molecular Signatures Database)
Differentiation	M4547 (Molecular Signatures Database)
Tumor growth	MP_0003447 and MP_0003721 (Mammalian Phenotype Ontology)
Proliferation	M4627 (Molecular Signatures Database)
Invasion	M2572 (Molecular Signatures Database)
Apoptosis	M5902 (Molecular Signatures Database)
Metabolism	R-HSA-1430728 (Reactome)
Cytoskeleton	GO_0005856 (Gene Ontology Resource)
Stemness	M30411 (Molecular Signatures Database)



Supplementary Figure 1 Cross-talk network between described genes, the processes that are frequently regulated by them, as well as glioblastoma biomarkers, cytoskeleton, and metabolism. The list of genes per process (except for the glioblastoma biomarkers and genes included in this review) were acquired from few databases (see Supplementary Table 2) and further narrowed to five representatives using the maximal clique centrality (MCC) method of cytoHubba. Collectively, all representatives were compiled into cross-talk network with the use of GeneMania (no "resultant" genes included). Figure created using Cytoscape and Inkscape.