## **Supplementary Information**

Figure S1: Conservation of the DSL motif in fibulin-3 and canonical Notch ligands. A) Representation and alignment of canonical Notch ligands of the Delta and Jagged families together with fibulin-3 (*Fib-3*). B) Alignment (using ClustalW software) of the N-terminal sequences containing the Delta-Serrate-Lag (*DSL*) motif involved in Notch activation. Fibulin-3 contains 8 of the 11 aminoacids that form the DSL consensus. This sequence is highly conserved in fibulin-3 across species. <u>b</u>: basic aminoacid; <u>a</u>: acidic aminoacid. Aminoacids in red indicate conservation of the DSL residues between fibulin-3 and the Notch ligands while those in green show divergence from the consensus in fibulin-3 or in the Notch ligands themselves. *VWFC:* vonWillebrand Factor consensus sequence; *EGF:* epidermal growth factor; *aa:* aminoacid.

Figure S2: Specificity and efficacy of siRNAs against fibulin-3 and Notch-1. SiRNA sequences against human and rat fibulin-3 have been previously described (Hu et. al., 2009). Notch-1 (*N1*) validated siRNAs were purchased from Qiagen. A-B) Targeting siRNAs (two per target gene) were tested alone or combined. Knockdown of each target gene was quantified by qRT-PCR (A) and Western blotting (B) in rat (*CNS1*) and human (*G8*) cells. The non-targeting sequence *AllStars* siRNA (Qiagen) was used as negative control.

<u>Figure S3</u>: *Conditional knockdown of fibulin-3*. A) Lentiviral design used to induce fibulin-3 shRNA. The chimeric repressor TetR-KRAB targets the hybrid promoter TetOp-U6 and causes epigenetic silencing of a 2-3 kilobase region, preventing expression of shRNA and eGFP. This repressor is inactivated by Doxycycline (Dox). B) U251MG cells stably transduced with a control lentivirus were exposed to 20  $\mu$ g/ml Dox (or vehicle) for 48h, fixed and stained with propidium iodide (red). Results show the efficient induction of the system. Bar: 100  $\mu$ m. C)

Glioma cells stably transduced with control or fibulin-3-targeted lentiviruses were cultured in presence or absence of Dox during 48 h. Results from qRT-PCR demonstrate efficient knockdown of fibulin-3 mRNA (mean  $\pm$  SD: \*\*\* p<0.001, two-way ANOVA for each cell type). D) Western blotting of serum-free conditioned medium from U251MG and CNS1 cells show efficient reduction of secreted fibulin-3 after shRNA induction. *BSA*: bovine serum albumin was added as loading control in the conditioned medium.

<u>Figure S4</u>: *Fibulin-3 is not a Notch target in glioma cells*. Glioma cells (U251 and CNS1) transfected with Notch-1 intracellular domain (NICD), Notch-1 siRNA, or their respective controls were processed for qRT-PCR. Results show that genes typically regulated by Notch (Hes1 and Hes5) responded to upregulation or downregulation of Notch signaling. However, fibulin-3 was not affected by these treatments (mean  $\pm$  SD: \*\* p<0.01, \*\*\* p< 0.01, one-way ANOVA for each gene).

<u>Figure S5</u>: *Fibulin-3 knockdown slows cell growth and increases cell death*. A) CNS1 cells transfected with fibulin-3 or control siRNAs were serum-starved for 24 h, fixed, stained with propidium iodide and analyzed by flow cytometry. Results from a representative experiment (repeated in triplicate) show that fibulin-3 knockdown increased cell death (sub-G1 fraction) in serum-starved glioma cells. B-C) U251MG glioma cells were stably transfected with fibulin-3 or control shRNAs and subjected to antibiotic selection for two weeks. Once selection was completed, cells with stable fibulin-3 knockdown showed reduced viability (B) and clumped morphology over time (C), which prevented the use of these cells for long-term experiments (mean  $\pm$  SD: \*\* p<0.01, two-way ANOVA).

Figure S6: Knockdown of fibulin-3 in the tumor downregulates Notch-dependent genes and increases apoptosis. A) Representative images of a G8-derived tumor transduced with control lentivirus. Nuclei were stained with DAPI and false-colored in red. Notice the invasive tumor cells (arrows) past the bulk of the tumor (dashed line) and the efficient activation of the lentiviral system (eGFP expression). Bar: 50  $\mu$ m. B) Control and fibulin-3-targeted G8 tumors (N=3/condition) were microdissected and processed for qRT-PCR. Results show significant knockdown of fibulin-3 mRNA in the tumor tissue as well as downregulation of the Notch-dependent genes Hes1 and Hes5 (mean  $\pm$  SD: \* p<0.05; \*\* p<0.01 by two-tailed Student's t-test for each gene). C) Cell proliferation (Ki67-positive cells) quantified in CNS1- and G8-derived tumors did not show significant changes after fibulin-3 knockdown. Bar: 100  $\mu$ m. D) In contrast, TUNEL staining in the same tumors showed a 3- to 4-fold increase in the number of apoptotic figures (arrowheads) after induction of fibulin-3 shRNA. Bar: 50  $\mu$ m (\*\*\*p<0.001, two-tailed t-test).

Figure S7: Fibulin-3 is highly upregulated in high-grade gliomas and associates with the mesenchymal phenotype. A) Normalized microarray results showing expression of fibulin-3 in glioblastoma, collected from the databases The Cancer Genome Atlas (TCGA) and Repository for Molecular Brain Neoplasia Data (REMBRANDT). Frequency analysis shows that fibulin-3 was upregulated 2-fold or higher over control levels in more than 80% of the samples from both databases. B) Normalized microarray results showing expression of fibulin-3 (probeset 201842\_s\_at) and fibulin-4 (206580\_s\_at) in grade III and grade IV gliomas, collected from the Gene Expression Omnibus dataset GSE4271 (49). Tumor groups are 1: WHO grade III primary; 2: WHO grade III recurrent; 3: WHO grade IV primary without necrosis; 4: WHO grade IV primary with necrosis; 5: WHO grade IV recurrent. The center of the bubbles shows the average

expression value in each group; the size of the bubbles represents the number of samples in each group. The results show that, for all tumor groups, fibulin-3 levels were higher in samples matching the mesenchymal signature compared with samples matching the proneural signature. Results were almost identical for fibulin-4.







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DSL motif	c	- ¥ c	:c		C G W - G C
Homo sapiens DLL1 (177-221)	FVCDE	HYYGEGC	SVFCRPRDI	DA-FGHFTCGERGE	KVCNPGWKGPYC
Homo sapiens DLL3 (176-214)	ARCEP	PAVGTAC	TRLCRPRS	A P S R C G P - G L	RPCAPLEDEC
Homo sapiens DLL4 (173-217)	VICSD	NYYGDNC	SRLCKKRNI	DH-FGHYVCOPDGN	LSCLPGWTGEYC
Homo sapiens JAG1 (185-229)	VTCDD	YYYGFGC	NKFCRPRDI	DF-FGHYACDQNGN	KTCMEGWMGPEC
Homo sapiens JAG2 (196-240)	VRCDE	NYYSATC	NKFCRPRN	DF-FGHYTCDQYGN	KACMDGWMGKEC
Homo sapiens FIB-3 (27-70)	TQCTD	GYEWDPV	RQQCKDIDE	ECDIVPDACK GG	MKCVNHYGGYLC
Rattus norvegicus FIB-3 (27-70)	TQCTD	GYEWDPV	RQQCKDIDE	ECDIVPDACKGG	MKCVNHYGGYLC
Mus musculus FIB-3 (27-70)	TQCTD	GYEWDPI	RQQCKDIDE	ECDIVPDACKGG	MKCVNHYGGYLC
Bos Taurus FIB-3 (27-70)	TQCTD	GYEWDPV	ROOCKDIDE	ECDIVPDACKGG	MKCVNHYGGYLC
Canis familiaris FIB-3 (27-20)	TQCTD	GYEWDPV	RQQCKDIDE	ECDIVPDACKGG	MKCVNHYGGYLC
consensus	c	- Y C	:c <u>b</u> <u>a</u>	<u>a</u> C G -	C g w - G C





brightfield

eGFP

## Hu et al., Figure S4









## Supplemental Table I:

Antibodies used for Western blotting and immunohistochemistry

Antigen	Source	Catalog number
EGF Receptor	Cell Signaling Technology	2232
pTyr <sup>1173</sup> EGFR	Cell Signaling Technology	4407
P42/P44 MAPK (Erk 1/2)	Santa Cruz Biotechnology	SC-94
pThr <sup>202</sup> /pTyr <sup>204</sup> Erk 1/2	Cell Signaling Technology	4377
Akt	Cell Signaling Technology	9272
pSer <sup>473</sup> Akt	Cell Signaling Technology	4058
Notch-1 (human)	Cell Signaling Technology, #D6F11	4380
Notch-1 (rat)	Santa Cruz Biotechnology, #8G10	SC-32756
neoepitope Val <sup>1744</sup> -Notch-1 (NICD)	Cell Signaling Technology	2421 and 4147
Hes1	Santa Cruz Biotechnology	SC-25392
caspase-3	Cell Signaling Technology	9662
Ki67	Thermo Scientific	RM-9106
Fibulin-3 (human)	Santa Cruz Technology, #mab3-5	SC-33722
Fibulin-3 (rat)	Santa Cruz Technology, N-16	SC-46100
alpha/beta tubulin	Cell Signaling Technology	2148