

Table S1. Transcripts of the Notch pathway deregulated in the first relapse.

Symbol	Entrez Gene Name	TPM normal	TPM tumor	Exp Fold Change	Expected	Location	Type(s)
<i>CNTN1</i>	contactin 1	199	1	-199	Up	Plasma Membrane	enzyme
<i>DLL1</i>	delta like canonical Notch ligand 1	5	238	48	Up	Plasma Membrane	enzyme
<i>DLL3</i>	delta like canonical Notch ligand 3	5	105	21	Up	Extracellular Space	other
<i>DTX4</i>	deltex E3 ubiquitin ligase 4	31	2	-15		Cytoplasm	enzyme
<i>HES1</i>	hes family bHLH transcription factor 1	11	160	14		Nucleus	transcription regulator
<i>HES7</i>	hes family bHLH transcription factor 7	1	58	58		Nucleus	transcription regulator
<i>JAG1</i>	jagged 1	9	95	11	Up	Extracellular Space	growth factor
<i>LFNG</i>	LFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	10	741	74	Down	Cytoplasm	enzyme
<i>MAG</i>	myelin associated glycoprotein			-440.212		Plasma Membrane	other
<i>NOTCH1</i>	notch 1	7	183	26	Up	Plasma Membrane	transcription regulator
<i>NUMBL</i>	NUMB like, endocytic adaptor protein	50	4	-12	Down	Cytoplasm	other

The Exp fold change indicates the ratio between the TPMs of the first relapse (TPM tumor) and of the normal brain (TPM normal, sample 111). If known, the expected status (up regulated or down regulated) if the pathway is activate is indicated. The location and function (Type) of the corresponding proteins are also indicated.

Table S2. Transcripts of the BBC pathway deregulated in the first relapse. See supplementary Table 1 for legend.

Symbol	Entrez Gene Name	TPM normal	TPM tumor	Exp Fold Change	Expected	Location	Type(s)
<i>APC2</i>	APC2, WNT signaling pathway regulator	33	1	-33		Cytoplasm	enzyme
<i>BMP4</i>	bone morphogenetic protein 4	2	26	13	Up	Extracellular Space	growth factor
<i>BMP8B</i>	bone morphogenetic protein 8b	2	96	48	Up	Extracellular Space	growth factor
<i>FZD10</i>	frizzled class receptor 10	1	31	31	Up	Plasma Membrane	G-protein coupled receptor
<i>FZD2</i>	frizzled class receptor 2	1	23	23	Up	Plasma Membrane	G-protein coupled receptor
<i>GLI2</i>	GLI family zinc finger 2	1	25	25	Up	Nucleus	transcription regulator
<i>GLIS1</i>	GLIS family zinc finger 1	1	30	30	Up	Nucleus	transcription regulator
<i>HHIP</i>	hedgehog interacting protein	13	1	-13	Up	Plasma Membrane	other
<i>KIF7</i>	kinesin family member 7	2	20	10	Up	Extracellular Space	other
<i>PTCH2</i>	patched 2	3	44	15		Plasma Membrane	transmembrane receptor
<i>WNT10B</i>	Wnt family member 10B	28	1	-28	Up	Extracellular Space	other
<i>WNT3A</i>	Wnt family member 3A	1	44	44	Up	Extracellular Space	cytokine
<i>WNT5A</i>	Wnt family member 5A	3	56	19	Up	Extracellular Space	cytokine
<i>WNT7A</i>	Wnt family member 7A	10	1	-10	Up	Extracellular Space	cytokine

Table S3. Expression of IGF2, IGF1R and INSR in first relapse compared to normal brain.

Symbol	Entrez Gene Name	TPM normal	TPM tumor	Exp Fold Change
<i>IGF2</i>	insulin like growth factor 2	6	1442	240
<i>IGF1</i>	insulin like growth factor 1	4	2	-2
<i>IGF1R</i>	insulin-like growth factor 1 receptor	11	3	-4
<i>INSR</i>	insulin like growth factor 2	13	34	3