

**Table S5.** Summary of expression differences between genes-pair classifiers.

Node #	Node phenotype classes	Sample number	Gene <i>i</i>		Gene <i>j</i>		<i>k</i>	Mean	St. dev.	Max.	Min.	Median
			Gene symbol	Affymetrix Probe ID	Gene symbol	Affymetrix Probe ID						
2	EPN GBM MDL MNG OLG PA	718	<i>PRPF40A</i>	218053_at	<i>PURA</i>	204021_s_at	1	4,314.7	1,685.5	10,889.0	-2,593.0	4,370.5
3	normal	203	<i>PURA</i>	204021_s_at	<i>PRPF40A</i>	218053_at	1	1,793.5	1,122.2	9,249.0	176.0	1,591.0
4	EPN GBM MDL OLG PA	557	<i>NRCAM</i>	204105_s_at	<i>ISLR</i>	207191_s_at	1	10,376.0	2,475.5	13,271.0	-7,491.0	11,283.0
			<i>IDH2</i>	210046_s_at	<i>GMDS</i>	214106_s_at		5,153.1	1,647.1	9,264.0	-6,662.0	5,238.0
5	MNG	161	<i>ISLR</i>	207191_s_at	<i>NRCAM</i>	204105_s_at	1	8,568.9	2,449.9	11,884.0	-11,674.0	8,977.0
6	EPN GBM OLG PA	456	<i>SALL1</i>	206893_at	<i>PAFAH1B3</i>	203228_at	2	8,239.6	2,767.1	12,574.0	-9,364.0	8,728.0
			<i>SRI</i>	208920_at	<i>NBEA</i>	221207_s_at		4,513.8	2,001.8	10,692.0	-401.0	4,536.5
			<i>DDR1</i>	210749_x_at	<i>TIA1</i>	201447_at		4,227.7	1,528.7	9,580.0	-3,227.0	4,536.0
			<i>DDR1</i>	208779_x_at	<i>MAB21L1</i>	206163_at		9,514.9	2,223.0	13,251.0	-1,759.0	10,267.0
			<i>ITPKB</i>	203723_at	<i>PDS5B</i>	204742_s_at		7,051.7	2,551.4	11,373.0	-1,524.0	7,478.5
7	MDL	101	<i>PAFAH1B3</i>	203228_at	<i>SALL1</i>	206893_at	4	8,729.6	2,776.6	12,096.0	9.0	9,341.0
			<i>NBEA</i>	221207_s_at	<i>SRI</i>	208920_at		3,858.3	2,074.7	8,440.0	-28.0	3,715.0
			<i>TIA1</i>	201447_at	<i>DDR1</i>	210749_x_at		3,476.4	1,618.5	8,709.0	27.0	3,481.0
			<i>MAB21L1</i>	206163_at	<i>DDR1</i>	208779_x_at		4,510.6	1,845.9	8,771.0	-5,415.0	4,562.0
8	EPN	102	<i>PDS5B</i>	204742_s_at	<i>ITPKB</i>	203723_at	2	5,495.4	2,515.1	11,625.0	-2,026.0	5,538.0
			<i>NUP62CL</i>	220520_s_at	<i>ZNF280A</i>	216034_at		5,676.0	3,444.6	11,512.0	-830.0	6,079.5
			<i>GALNS</i>	206335_at	<i>WAS</i>	38964_r_at		3,952.7	2,095.5	7,831.0	-1,216.0	4,098.5
			<i>CELSR1</i>	41660_at	<i>OR10H3</i>	208520_at		4,959.8	2,798.6	11,365.0	-1,367.0	5,058.5
			<i>TLE4</i>	216997_x_at	<i>OLIG2</i>	213824_at		3,423.4	2,401.5	9,765.0	-3,239.0	3,386.5

**Node #:** Corresponds to numerical labels shown in the brain phenotype diagnostic hierarchy (Fig. 1). **Brain phenotype abbreviation (name):** EPN (Ependymoma), GBM (Glioblastoma multiforme), MDL (Medulloblastoma), MNG (Meningioma), normal (Normal brain), OLG (Oligodendroglioma), and PA (Pilocytic astrocytoma). **Sample number:** Number of total samples in classes of respective Node #. **Gene *i* / Gene *j*:** the gene expressed higher and lower in the gene-pair, respectively, within each corresponding phenotype. **Gene name / Chromosome locus:** according to Entrez Gene. **Affymetrix Probe ID:** For both Affymetrix Human Genome U133A and U133Plus2.0 Arrays. ***k*:** The minimum number of gene-pair classifiers whose decision rule outcomes for a test sample are required to be 'true (= 1)' for the sample to be classified as the phenotype(s) of the corresponding node. Ranked expression differences of each gene pair (i.e. Rank\_gene\_*i* – Rank\_gene\_*j*) were calculated for each sample, and **Mean, St. dev., Max., Min., and Median** were found across all samples within classes of respective Node #.

**Table S5.** (Continued) Summary of expression differences between genes-pair classifiers.

Node #	Node phenotype classes	Sample number	Gene <i>i</i>		Gene <i>j</i>		<i>k</i>	Mean	St. dev.	Max.	Min.	Median
			Gene symbol	Affymetrix Probe ID	Gene symbol	Affymetrix Probe ID						
9	GBM OLG PA	354	ZNF280A	216034_at	NUP62CL	220520_s_at	1	1,392.5	673.9	3,211.0	-4,279.0	1,354.0
10	GBM OLG	292	DDX27	215693_x_at	KCNMA1	221584_s_at	1	2,144.8	1,366.3	6,451.0	-1,681.0	2,124.5
			COX7A2	217249_x_at	GNPTAB	212959_s_at		1,777.2	1,106.8	5,125.0	-2,040.0	1,664.0
11	PA	62	KCNMA1	221584_s_at	DDX27	215693_x_at	3	1,832.2	942.5	3,558.0	105.0	1,853.0
			GNPTAB	212959_s_at	NDUFS2	201966_at		1,149.7	737.3	3,061.0	-825.0	1,112.5
			APOD	201525_at	PPIA	211378_x_at		121.4	117.3	494.0	-426.0	104.5
			CD59	212463_at	SNRNP2	202505_at		1,169.1	1,038.0	3,989.0	-2,247.0	1,059.0
			SEMA3E	206941_x_at	ADAMTS3	214913_at		4,376.3	3,026.1	8,551.0	-8,061.0	5,194.5
			CD59	200985_s_at	HINT1	208826_x_at		388.5	422.5	1,586.0	-270.0	214.5
12	GBM	231	BAMBI	203304_at	CIAPIN1	208968_s_at	1	1,976.4	975.1	3,802.0	-594.0	1,984.0
			FLNA	214752_x_at	TNKS2	218228_s_at		3,238.8	2,804.3	9,691.0	-4,133.0	3,557.0
13	OLG	61	ITGB3BP	205176_s_at	RB1CC1	202034_x_at	1	1,793.7	2,357.9	8,665.0	-4,597.0	1,560.0
			DDX27	215693_x_at	TRIM8	221012_s_at		1,819.1	1,492.6	6,083.0	-1,099.0	1,636.0
13	OLG	61	LARP5	208953_at	ANXA1	201012_at	1	2,843.4	3,463.0	9,055.0	-5,831.0	2,788.0

**Node #:** Corresponds to numerical labels shown in the brain phenotype diagnostic hierarchy (Fig. 1). **Brain phenotype abbreviation (name):** EPN (Ependymoma), GBM (Glioblastoma multiforme), MDL (Medulloblastoma), MNG (Meningioma), normal (Normal brain), OLG (Oligodendroglioma), and PA (Pilocytic astrocytoma). **Sample number:** Number of total samples in classes of respective Node #. **Gene *i* / Gene *j*:** the gene expressed higher and lower in the gene-pair, respectively, within each corresponding phenotype. **Gene name / Chromosome locus:** according to Entrez Gene. **Affymetrix Probe ID:** For both Affymetrix Human Genome U133A and U133Plus2.0 Arrays. ***k*:** The minimum number of gene-pair classifiers whose decision rule outcomes for a test sample are required to be 'true (= 1)' for the sample to be classified as the phenotype(s) of the corresponding node. Ranked expression differences of each gene pair (i.e. Rank\_gene\_*i* – Rank\_gene\_*j*) were calculated for each sample, and **Mean, St. dev., Max., Min., and Median** were found across all samples within classes of respective Node #.