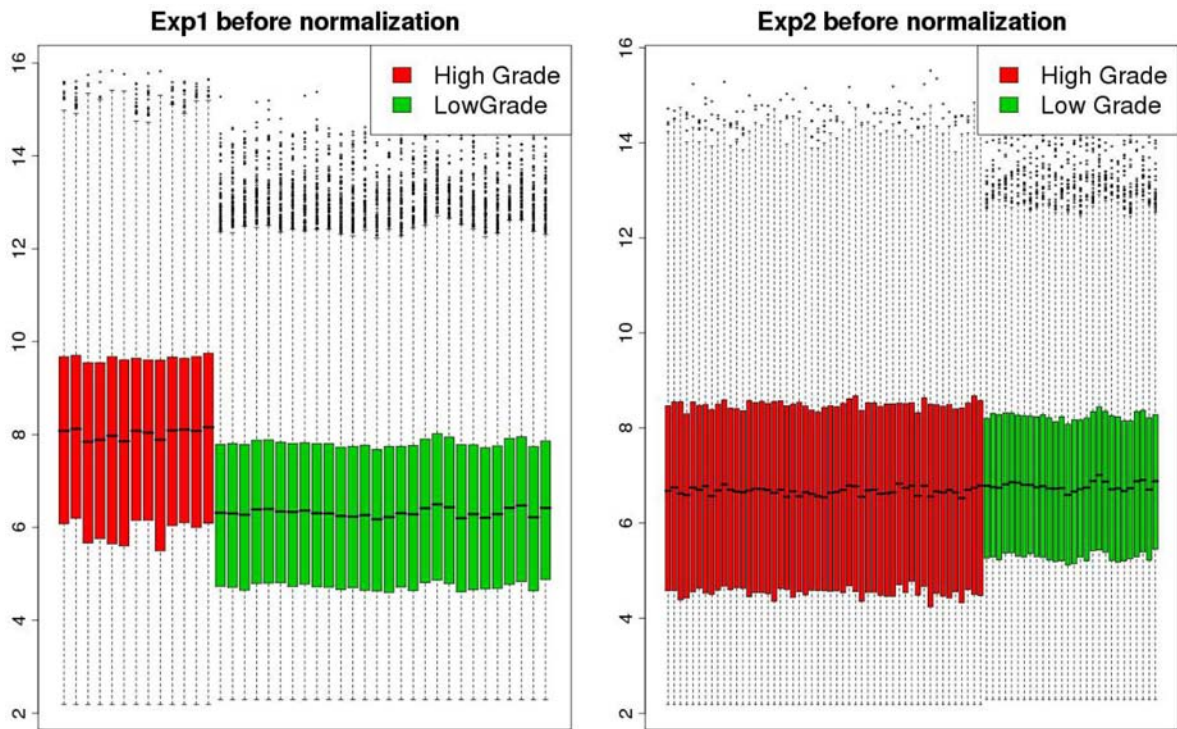
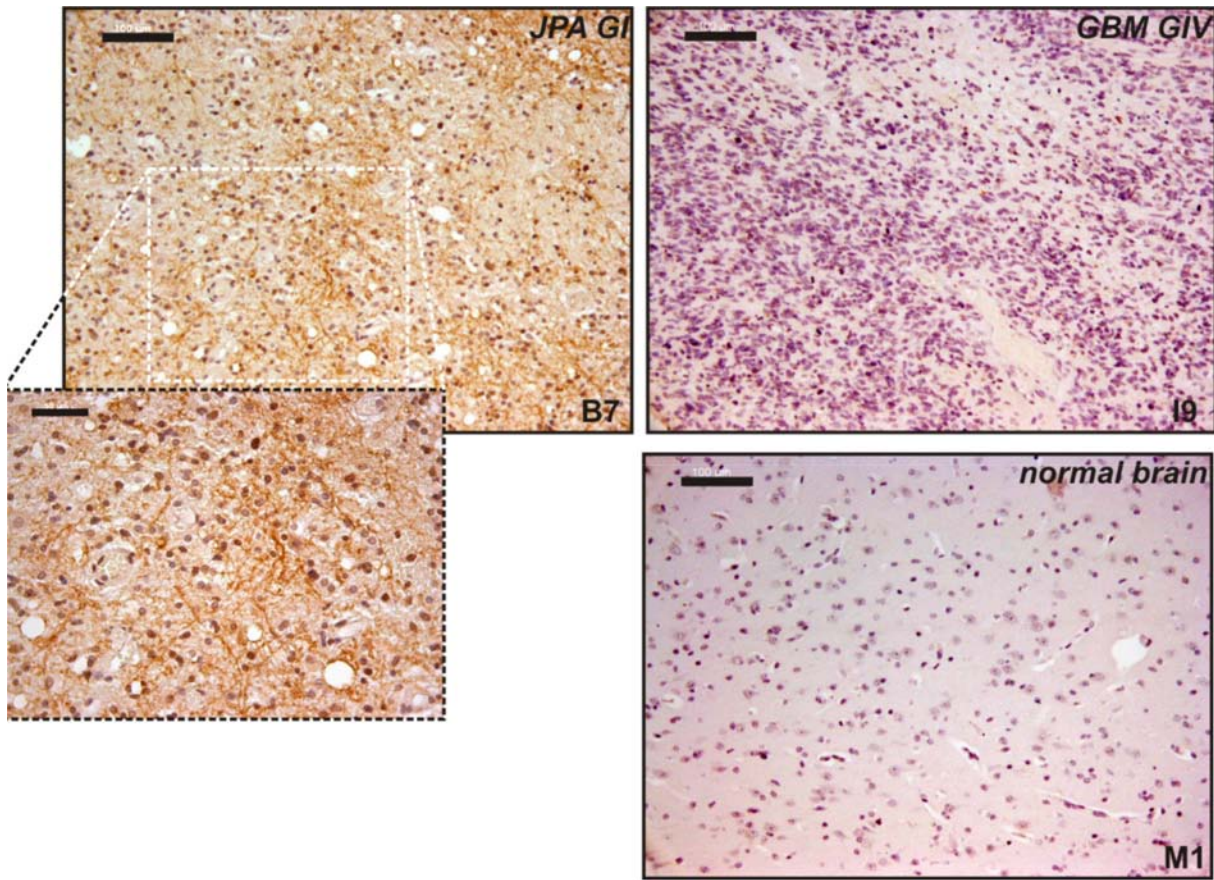


SUPPLEMENTARY FIGURES AND TABLES



Supplementary Figure S1: Quantile normalization. The boxplots present overall gene expression distributions in all samples. The association between original data sets (before merging) is clearly visible.



Supplementary Figure S2: Representative images of immunohistochemistry for IKK β (brown) in JPA, GBM and normal brain.

Supplementary Table S1: Histopathological classification of tumors enclosed in the merged dataset and used for a meta-analysis

Data set name	Gene profile repository	Gene profiles of low grade gliomas	Gene profiles of high grade gliomas	Reference
GSE5675	NCBI GEO	41 juvenile pilocytic astrocytoma WHO grade I		31
GSE2817	NCBI GEO	4 oligodendroglioma WHO grade II, 6 oligoastrocytoma WHO grade II and 6 astrocytoma WHO grade II	6 anaplastic oligoastrocytoma WHO grade III, 4 anaplastic astrocytoma WHO grade III	32
GSE8692	NCBI GEO	2 mixed gliomas WHO grade II, 1 oligodendroglioma WHO grade II	6 GBM WHO grade IV, 3 gliosarcomas WHO grade IV	33
GSE4271	NCBI GEO		100 GBM WHO grade IV	34
E-MEXP-1507	ArrayExpress		8 oligodendroglioma WHO grade III and 5 GBM grade IV	35

Supplementary Table S2: Gene names and expression scores in GBM and JPA

	GBM.score	JPA.score
<i>PTPN11</i>	-0,1641	0,3609
<i>HFE</i>	0,1414	-0,3111
<i>IL6ST</i>	-0,1408	0,3097
<i>C7</i>	-0,1393	0,3065
<i>PTPRC</i>	-0,1372	0,3018
<i>TCF7</i>	0,1271	-0,2796
<i>AZGP1</i>	-0,1231	0,2709
<i>DUSP10</i>	0,1161	-0,2555
<i>ITCH</i>	0,1147	-0,2523
<i>CXCL10</i>	0,1078	-0,2372
<i>CDK1</i>	0,1059	-0,233
<i>P2RY14</i>	-0,1012	0,2226
<i>NCAM1</i>	-0,0975	0,2146
<i>CX3CL1</i>	0,0923	-0,203
<i>TLR7</i>	-0,0911	0,2004
<i>TLR1</i>	-0,0748	0,1646
<i>IL27RA</i>	-0,06	0,132
<i>IGF1R</i>	-0,0581	0,1279
<i>KCNJ10</i>	-0,0579	0,1275
<i>ST6GAL1</i>	-0,0565	0,1242
<i>PRDX2</i>	0,0523	-0,1152
<i>ADORA1</i>	0,0508	-0,1118
<i>POLR3F</i>	-0,047	0,1035
<i>MR1</i>	0,0467	-0,1028
<i>CD86</i>	-0,0415	0,0913
<i>MEF2A</i>	-0,041	0,0901
<i>PLCG1</i>	0,0383	-0,0842
<i>SMAD6</i>	-0,0365	0,0803
<i>TLR4</i>	-0,0336	0,0738
<i>IRAK4</i>	0,0331	-0,0727
<i>VCAM1</i>	0,0326	-0,0718
<i>MAPKAPK3</i>	0,0309	-0,068
<i>RPS6KA3</i>	-0,0302	0,0664
<i>ADORA3</i>	-0,0286	0,0629
<i>IL1B</i>	-0,0282	0,0621
<i>MGLL</i>	-0,0274	0,0602

(Continued)

	GBM.score	JPA.score
<i>NT5E</i>	-0,0245	0,0539
<i>FADD</i>	0,0227	-0,0499
<i>GNL1</i>	0,0223	-0,049
<i>RGS1</i>	-0,0212	0,0467
<i>IL1R1</i>	-0,0209	0,046
<i>FCGR3B</i>	-0,0204	0,0449
<i>MAPK9</i>	-0,019	0,0419
<i>IL1RAPL1</i>	-0,0186	0,041
<i>LAT2</i>	0,0183	-0,0403
<i>PLEKHA1</i>	-0,0181	0,0397
<i>JAK2</i>	-0,0179	0,0395
<i>OLR1</i>	-0,0178	0,0392
<i>IL16</i>	-0,0169	0,0372
<i>SPN</i>	0,0168	-0,037
<i>CYLD</i>	-0,0155	0,0341
<i>PSTPIP1</i>	-0,0144	0,0316
<i>MEF2C</i>	-0,0139	0,0305
<i>APP</i>	-0,0129	0,0283
<i>SWAP70</i>	-0,0125	0,0276
<i>ECSIT</i>	0,0124	-0,0273
<i>CD37</i>	-0,0123	0,0271
<i>LIG4</i>	-0,0116	0,0256
<i>COLEC12</i>	-0,0114	0,0251
<i>SEMA4D</i>	-0,0099	0,0218
<i>SOCS3</i>	-0,0077	0,017
<i>MAP3K7</i>	-0,0076	0,0167
<i>ICAM2</i>	-0,0061	0,0134
<i>FAS</i>	-0,0054	0,0118
<i>IKBKB</i>	-0,0036	0,0079
<i>CD55</i>	-0,0019	0,0041
<i>TGFBI</i>	-4e-04	0,001
<i>PIK3CB</i>	-3e-04	8e-04

Supplementary Table S3: Primer sequences for qPCR

Gene name	Forward primer	Reverse primer
<i>TLR1</i>	5'TTTTGTGGCCAGGGTCTTCAT 3'	5' TCCTTTTTGTAGGGGTGCCCA 3'
<i>TLR4</i>	5'CCAAGAACCTGGACTGAGC 3'	5' TGTCTGGATTTACACCTGGAT 3'
<i>TLR7</i>	5' TCAAGAAAGTTGATGCTATTGGGC 3'	5' ACCATCTAGCCCCAAGGAGT 3'
<i>IRF7</i>	5'GCGGTGCAAGAGCCCAGCCC3'	5'CGTGCAGCTCGGGTGTCCCA3'
<i>NOS2</i>	5'GCAGGACTCACAGCCTTTGGACC3'	5'GGCACGGCTGGATGTCGGACT3'
<i>ARG1</i>	5'TCTCAAAGGGACAGCCACGAGGA 3'	5'TCAGCAAAGGGCAGGTCCCCATA3'
<i>MT1-MMP</i>	5'CTCGGCCCAAAGCAGCAGCT 3'	5'GCGATGGCCGCTGAGAGTGA 3'