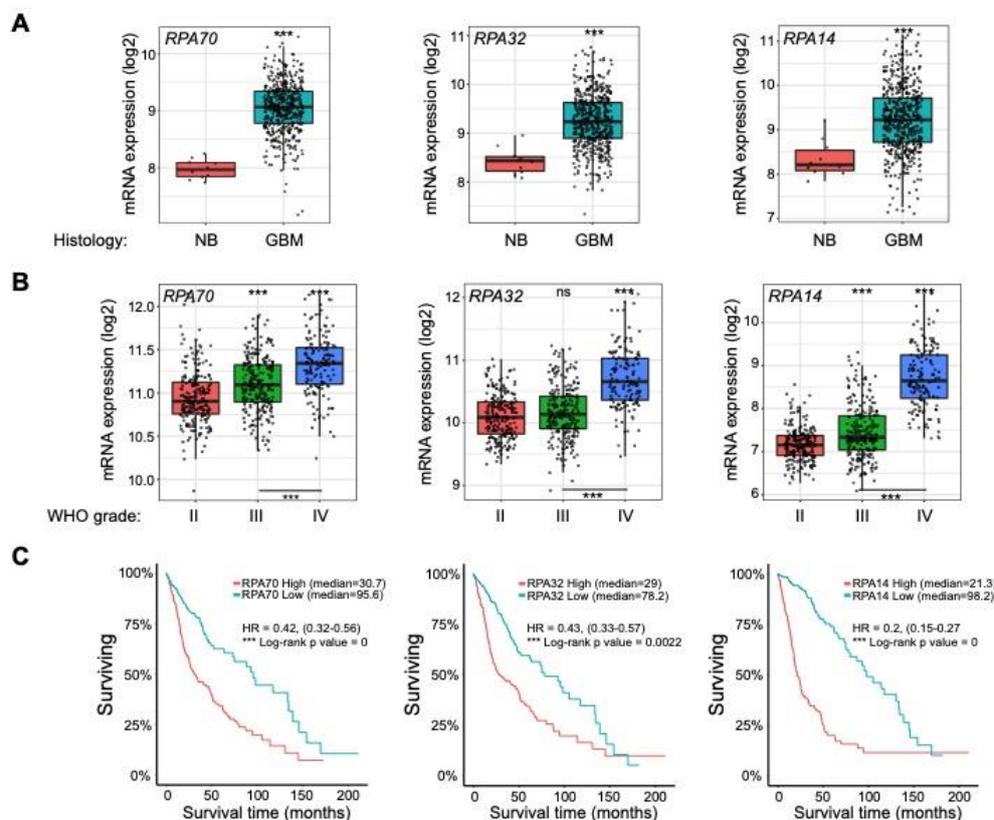




## 1 SUPPLEMENTARY FIGURES AND FIGURE LEGENDS

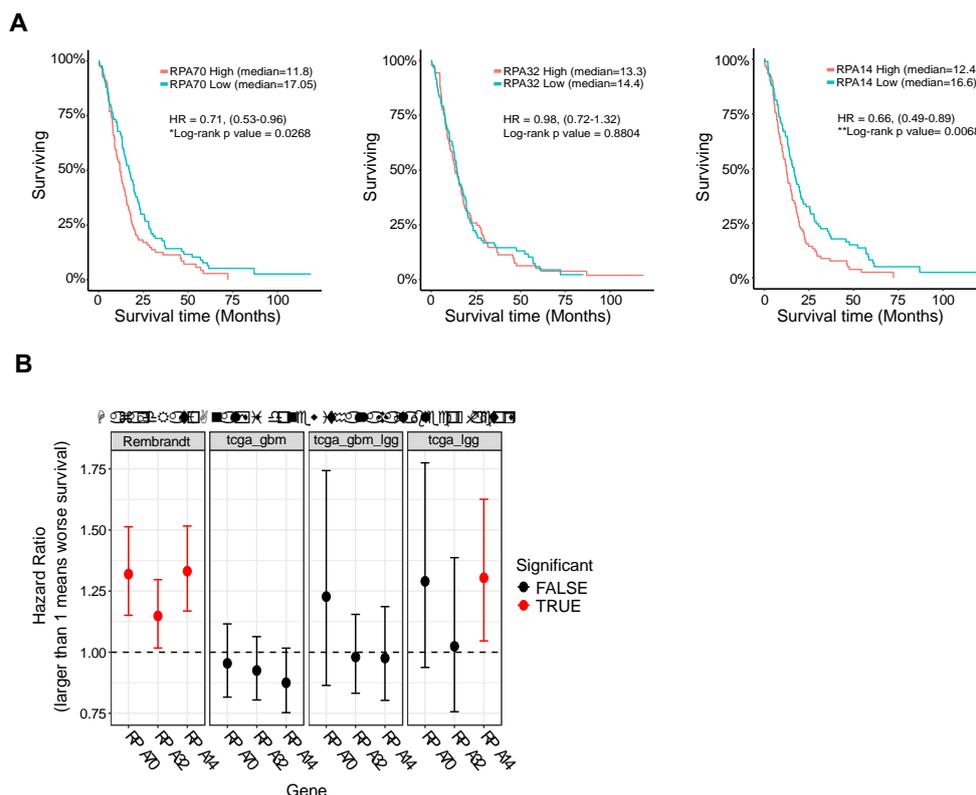


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3 **Supplementary Figure S1. Figure providing supplementary information to main Figure 1.**

4 (A) *RPA70*, *RPA32*, *RPA14* expression analysis of TCGA data (The Cancer Genome Atlas GBMLGG cohort) in  
5 GBM and normal brain (NB) controls. (B) *RPA70*, *RPA32*, *RPA14* expression analysis of TCGA glioma data set  
6 comparing WHO grade II, III and IV gliomas. Data are presented as mean ± SD. Statistical significance was  
7 tested using Tukey's Honestly Significant Difference test, HSD. ns: not significant; \*p<0.05; \*\*p<0.01. (C) Kaplan-  
8 Meier survival analysis of TCGA glioma data set shows that high RPA expression (all subunits) informs poor  
9 patient prognosis.

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**Supplementary Figure S2. Figure providing supplementary information to main Figure 1.**

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(A) Kaplan-Meier survival analysis of REMBRANDT GBM data set shows that high RPA expression (RPA70 and

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RPA14 subunits) informs poor patient prognosis. (B) An overview of available co-variates and their correlation

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with RPA subunits in regards to informing patients' survival in REMBRANT and TCGA data sets.

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36 **Supplementary Table S1.** A multi-variate Cox proportional hazard analysis – REMBRANDT data set.

<b>Data</b>	<b>Clinical cofactor</b>	<b>Hazard ratio</b>	<b>Hazard ratio 95% confidence interval</b>	<b>p_value</b>
Rembrandt	Grade_IV_GBM	2,761	1.794 - 4.25	3,87541E-06
Rembrandt	RPA3_expression	1,247	1.059 - 1.47	0,007947761
Rembrandt	RPA1_expression	1,214	1.029 - 1.43	0,021534727
Rembrandt	ATRX_expression	1,086	0.963 - 1.22	0,180268743
Rembrandt	Grade_III_Oligodendroglioma	1,464	0.803 - 2.67	0,213156129
Rembrandt	Grade_III_Astrocytoma	1,360	0.822 - 2.25	0,231625911
Rembrandt	RPA2_expression	0,950	0.819 - 1.10	0,493812318
Rembrandt	Grade_II_Oligodendroglioma	1,174	0.606 - 2.27	0,634352115
Rembrandt	gender_male	NA	NA	NA
Rembrandt	IDH1_status_Wild_type	NA	NA	NA
Rembrandt	MGMT_status_Unmethylated	NA	NA	NA
Rembrandt	Age	NA	NA	NA

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55 **Supplementary Table S2.** A multi-variate Cox proportional hazard analysis – TCGA data sets.

Data	Clinical cofactor	Hazard ratio	Hazard ratio 95% confidence interval	p_value
tcga_gbm	Age	1,028	1.015 - 1.04	1,4538E-05
tcga_gbm	gender_male	1,660	1.228 - 2.24	0,000984265
tcga_gbm	IDH1_status_Wild_type	2,455	1.132 - 5.32	0,022900353
tcga_gbm	MGMT_status_Unmethylated	1,256	0.948 - 1.66	0,11285813
tcga_gbm	RPA3_expression	0,883	0.739 - 1.05	0,170738562
tcga_gbm	ATRX_expression	1,091	0.919 - 1.30	0,319268788
tcga_gbm	RPA2_expression	0,987	0.824 - 1.18	0,883562296
tcga_gbm	RPA1_expression	0,993	0.835 - 1.18	0,94060235
tcga_gbm_lgg	IDH1_status_Wild_type	3,943	2.492 - 6.24	4,55379E-09
tcga_gbm_lgg	Grade_IV_GBM	20,489	3.504 -119.80	0,000803303
tcga_gbm_lgg	gender_male	1,524	1.185 - 1.96	0,001007619
tcga_gbm_lgg	Grade_III_Astrocytoma	3,974	0.937 - 16.86	0,061339739
tcga_gbm_lgg	ATRX_expression	1,340	0.902 - 1.99	0,146856271
tcga_gbm_lgg	Grade_III_Oligoastrocytoma	2,922	0.634 - 13.48	0,169186315
tcga_gbm_lgg	RPA1_expression	1,306	0.890 - 1.92	0,173071362
tcga_gbm_lgg	Grade_III_Oligodendroglioma	1,594	0.349 - 7.29	0,547461188
tcga_gbm_lgg	RPA2_expression	0,941	0.770 - 1.15	0,549288399
tcga_gbm_lgg	Grade_II_Oligoastrocytoma	1,442	0.295 - 7.05	0,651138341
tcga_gbm_lgg	Grade_II_Oligodendroglioma	0,761	0.161 - 3.59	0,730545829
tcga_gbm_lgg	RPA3_expression	0,976	0.780 - 1.22	0,833431443
tcga_gbm_lgg	MGMT_status_Unmethylated	NA	NA	NA
tcga_gbm_lgg	Age	NA	NA	NA
tcga_lgg	IDH1_status_Wild_type	3,749	2.007 - 7.00	3,40239E-05
tcga_lgg	RPA3_expression	1,389	1.071 - 1.80	0,013380746
tcga_lgg	Grade_III_Astrocytoma	3,638	0.835 - 15.85	0,085434123
tcga_lgg	RPA2_expression	0,761	0.535 - 1.08	0,129149523
tcga_lgg	Grade_III_Oligoastrocytoma	3,056	0.621 - 15.04	0,169456674
tcga_lgg	RPA1_expression	1,281	0.899 - 1.82	0,169943065
tcga_lgg	Grade_III_Oligodendroglioma	1,785	0.362 - 8.81	0,476475099
tcga_lgg	gender_male	0,867	0.520 - 1.45	0,584857639
tcga_lgg	Grade_II_Oligoastrocytoma	1,476	0.292 - 7.45	0,637657112
tcga_lgg	Grade_II_Oligodendroglioma	0,707	0.142 - 3.52	0,671995752
tcga_lgg	ATRX_expression	0,978	0.692 - 1.38	0,900530695
tcga_lgg	MGMT_status_Unmethylated	NA	NA	NA
tcga_lgg	Age	NA	NA	NA

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60 **Supplementary Table S3.** Primary GBM cell lines characteristics.

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Primary GBM cell line	Passage	Diagnosis	Age at diagnosis	Gender	Survival (Months)	Primary /Recurrent	MGMT	IDH1	ATRX
<b>4121</b>	N.A.	WHO gr. IV glioma/GBM	N.A.	N.A.	N.A.	N.A.	N.A.	N.A.	N.A.
<b>G01</b>	xp8	WHO gr. IV glioma/GBM	41	M	†11	Primary	N.A.	N.A.	N.A.
<b>G06</b>	xp4	WHO gr. IV glioma/GBM	80	M	†0	Primary	Non-methylated	WT	N.A.
<b>G40</b>	xp2	WHO gr. IV glioma/GBM	62	M	†11	Recurrent	N.A.	WT	WT
<b>G07</b>	xp3	WHO gr. IV glioma/GBM	54	M	†17	Recurrent	N.A.	N.A.	N.A.
<b>G16</b>	xp2	WHO gr. IV glioma/GBM	76	M	†45	Primary	Methylated	WT	N.A.
<b>G20</b>	xp1	WHO gr. IV glioma/GBM	40	M	†16	Primary	Non-methylated	WT	WT

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