

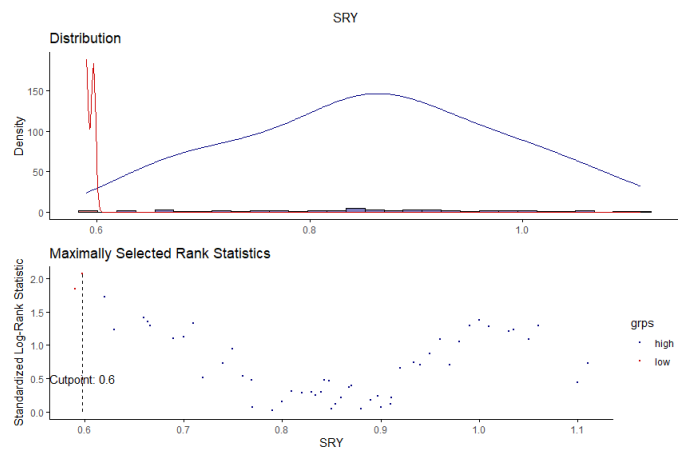
Supplementary Table S1. Clinicopathological data of male GBM patients from TCGA.

		Number of patients	Percentage
Age, years	≤60	107	48%
	>60	118	52%
Treatment type	Alkylating/ TMZ chemo	6	2.7%
	TMZ chemoradiation + TMZ chemo	91	41.6%
	Standard radiation + alkylating/ TMZ chemo	52	23.7%
	Standard radiation	17	7.8%
	Nonstandard/ unspecified radiation	32	14.6%
	Nonstandard/ unspecified radiation + chemo (alkylating/ TMZ)	14	6.4%
	Unspecified therapy	7	3.2%

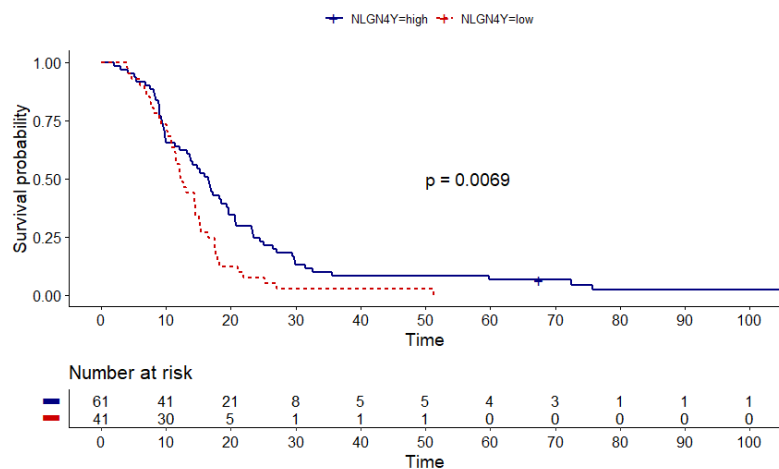
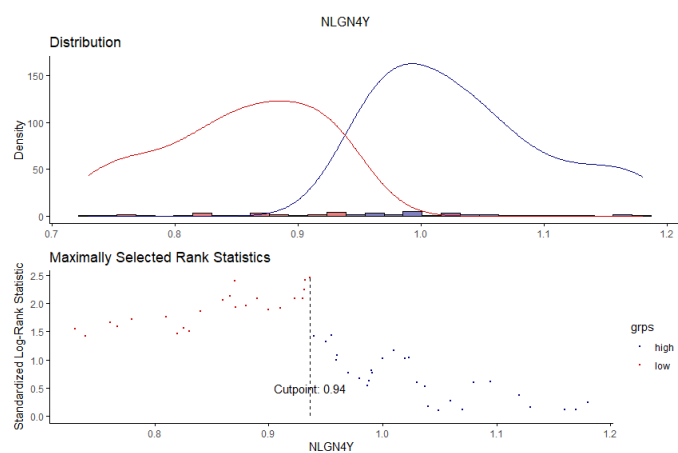
Supplementary Table S2. Probes used in the ddPCR for estimation of CN of the genes on chromosome Y.

Name of the gene	Location on chromosome Y	Name of the assay	Length [nucleotides]	Provider	Reference gene	Annealing temperature [°C]
SRY	2,786,855-2,787,699	dHsaCP250 0472	69	BioRad	AP3B1	60
ZFY	2,935,281-2,982,506	Hs0570806 6_cn	89	Applied Biosystems	AP3B1	60
AMELY	6,865,918-6,911,774	dHsaCNS6 70716622	77	BioRad	AP3B1	57
ARSEP1	12,339,813-12,347,495	dHsaCNS6 83350032	80	BioRad	AP3B1	57
USP9Y	12,537,650-12,860,839	dHsaCP250 6328	69	BioRad	AP3B1	60
UTY	13,248,379-13,480,673	Hs0126180 _cn	84	Applied Biosystems	AP3B1	55
TMSB4Y	13,703,899-13,706,024	dHsaCNS1 86618179	65	BioRad	AP3B1	57
NLGN4Y	14,522,573-14,845,650	Hs0570479 8_cn	85	Applied Biosystems	AP3B1	60
KDM5D	19,703,865-19,744,939	Hs0255539 2_cn	72	Applied Biosystems	AP3B1	55
EIF1AY	20,575,776-20,593,154	Hs0107914 3_cn	77	Applied Biosystems	AP3B1	55

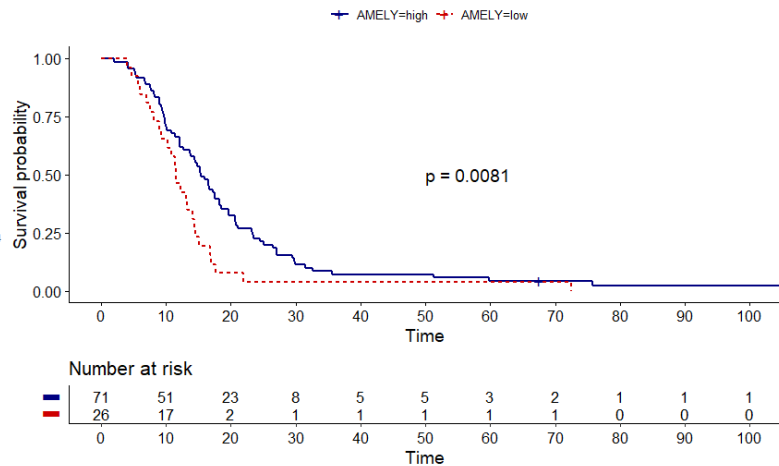
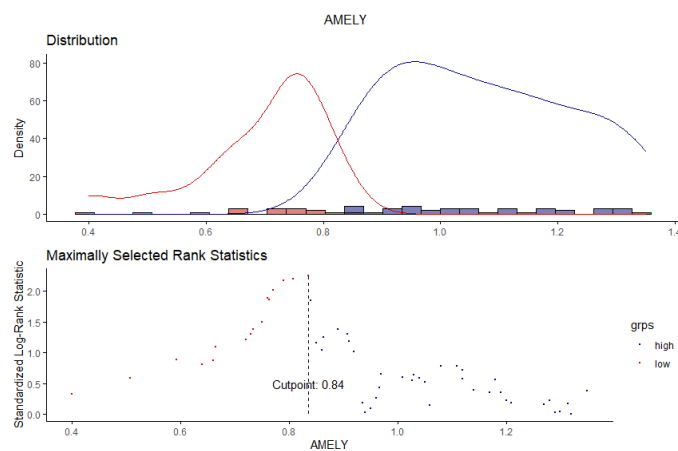
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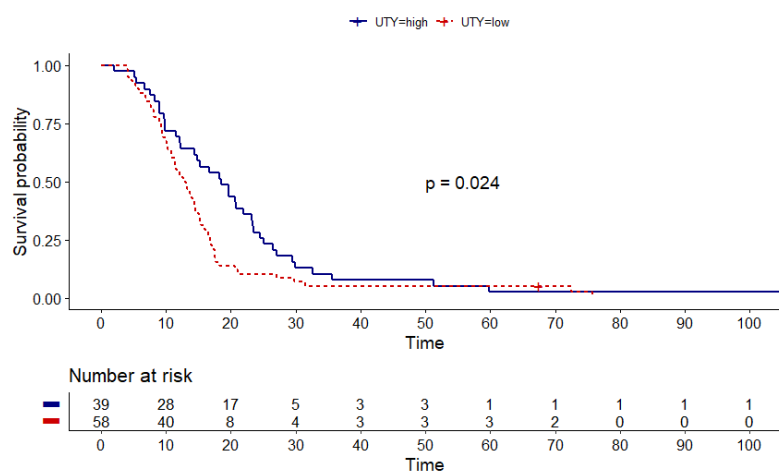
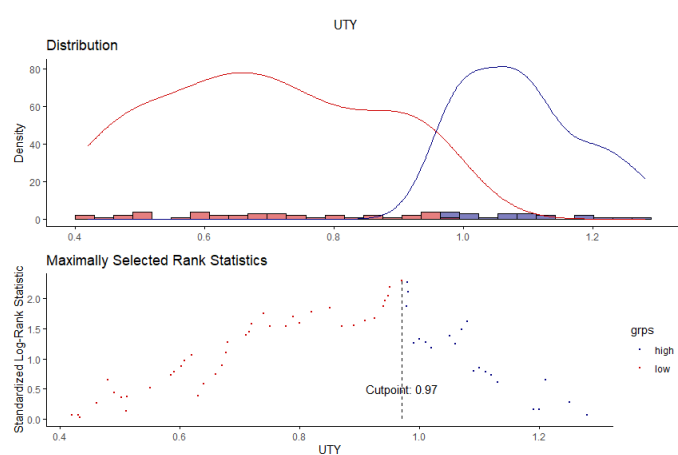
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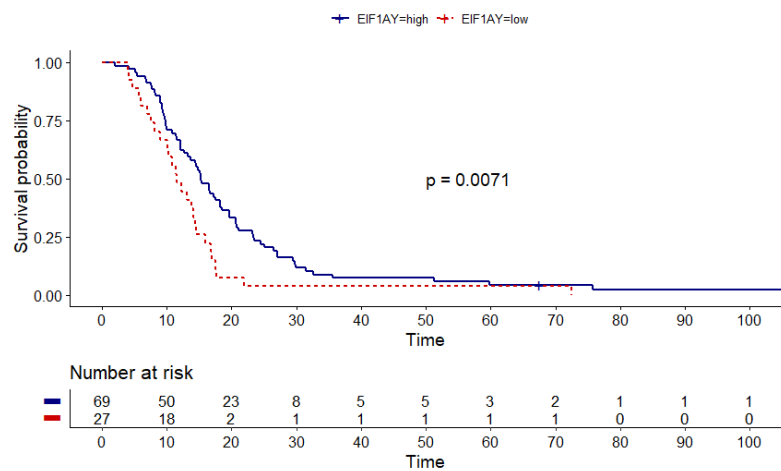
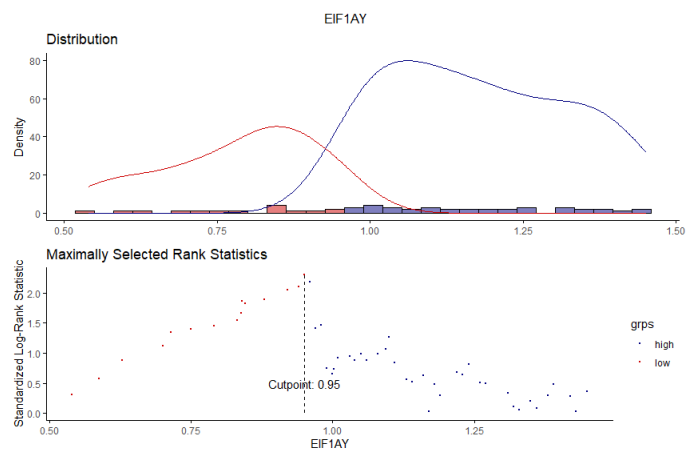
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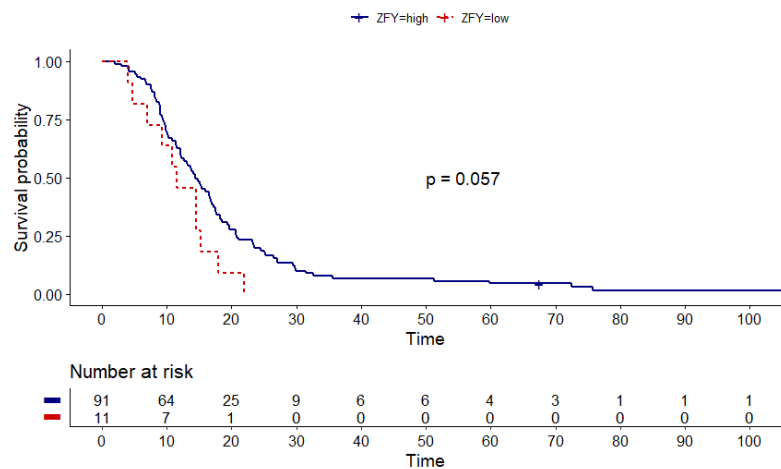
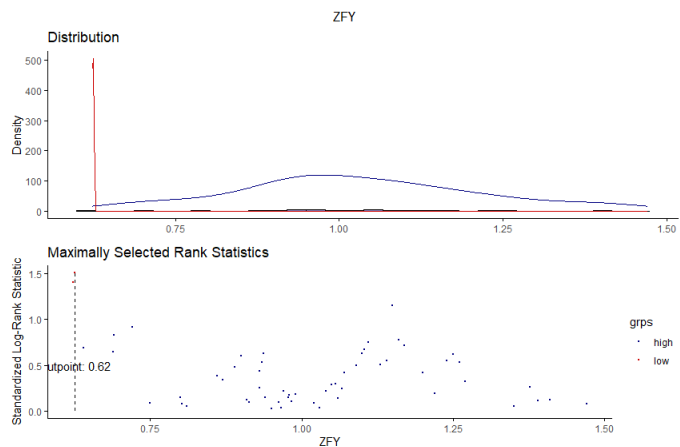
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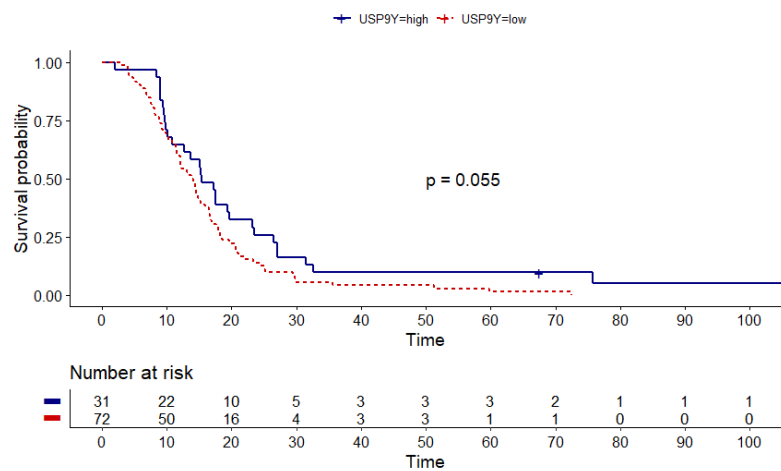
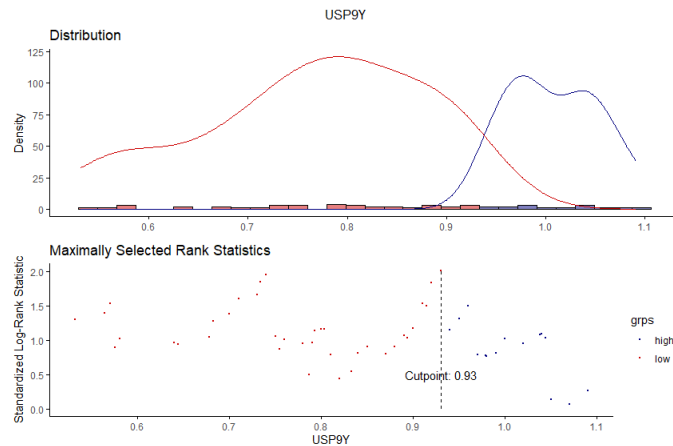
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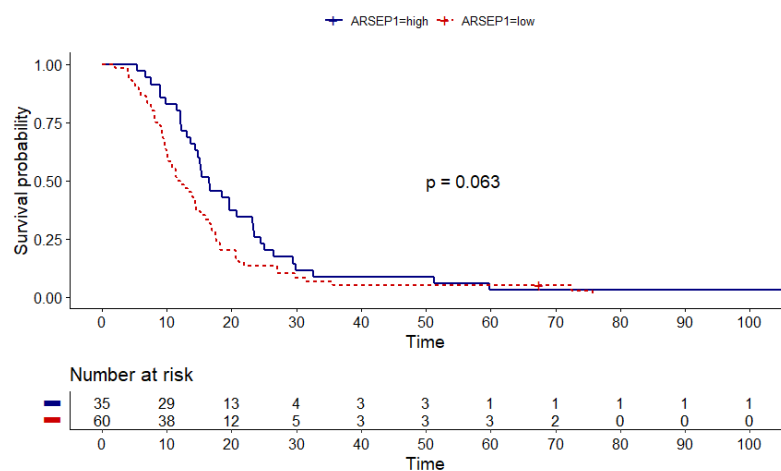
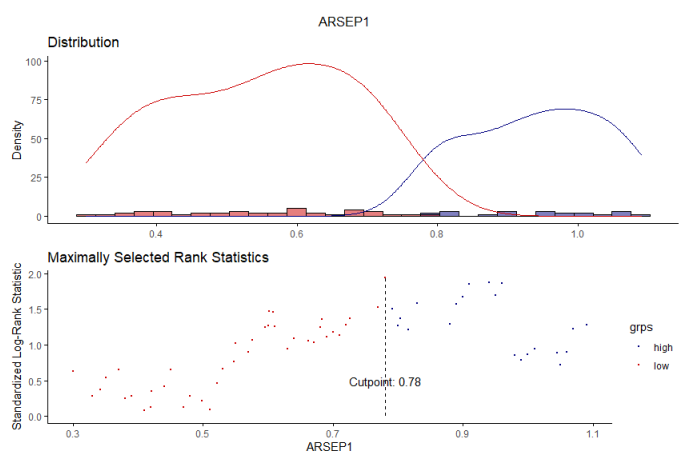
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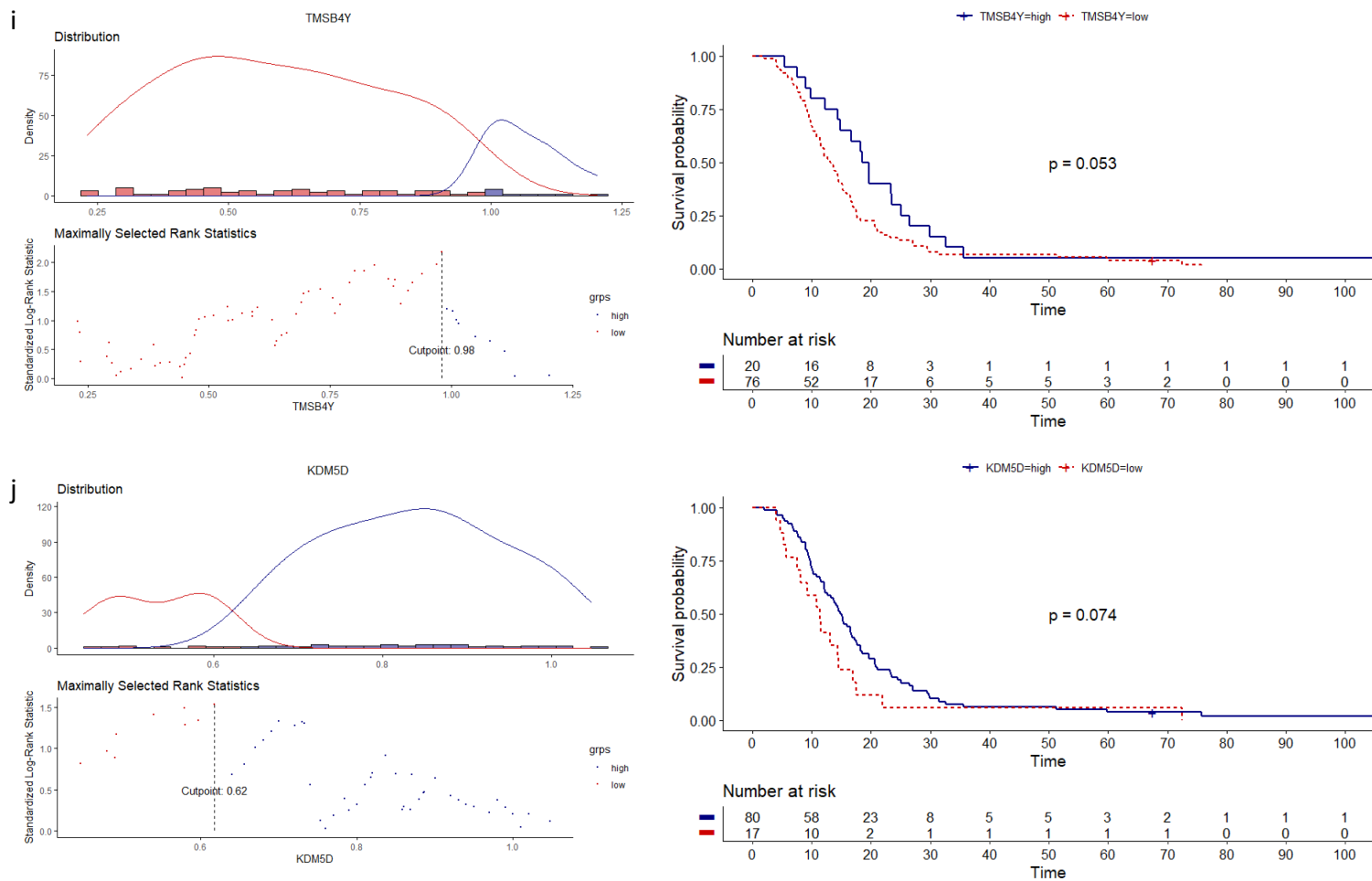


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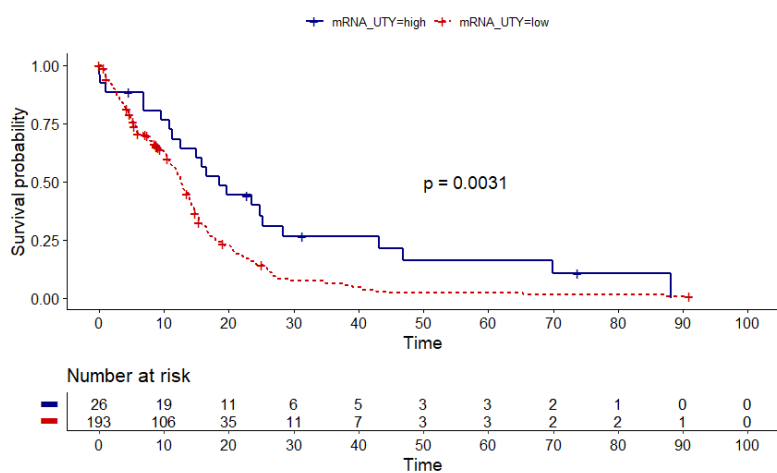
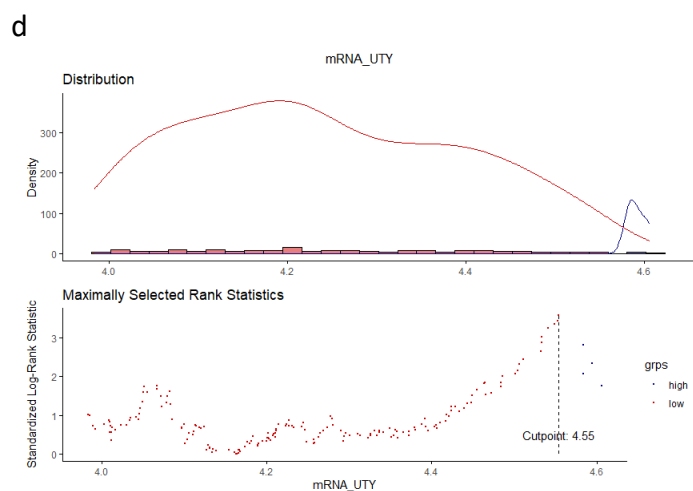
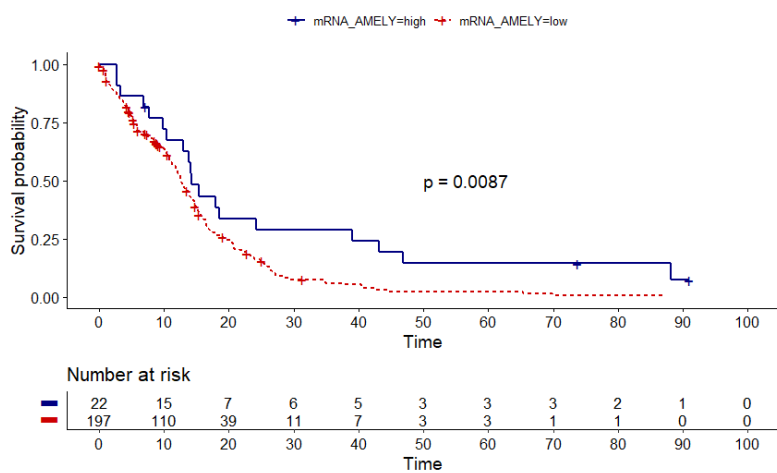
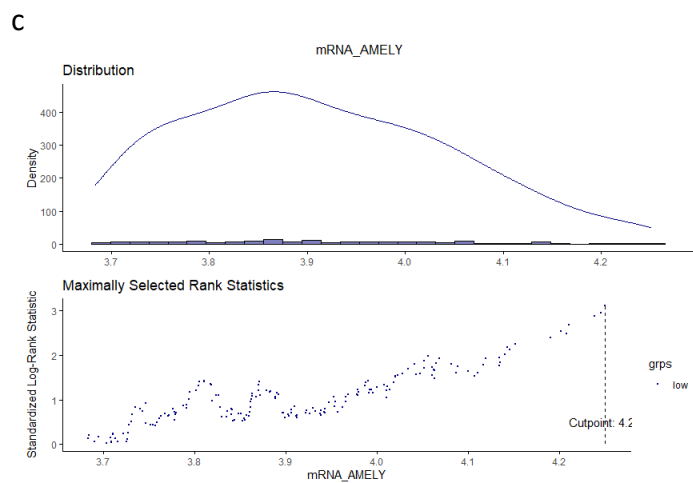
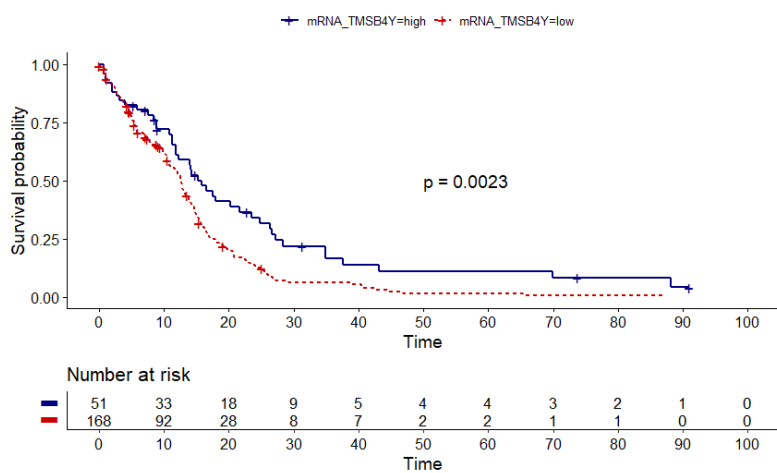
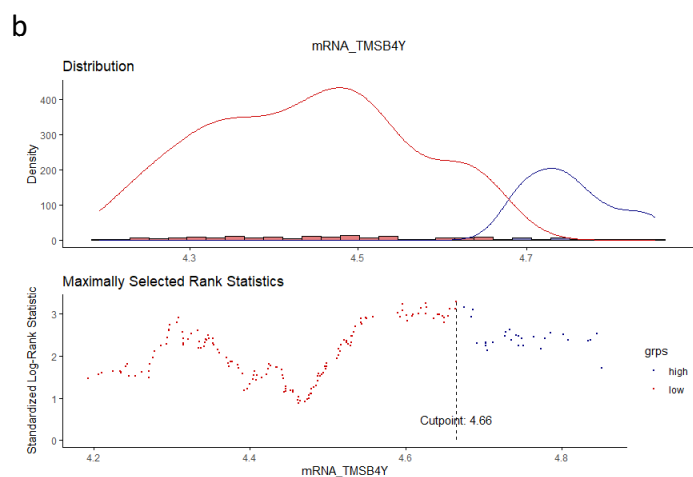
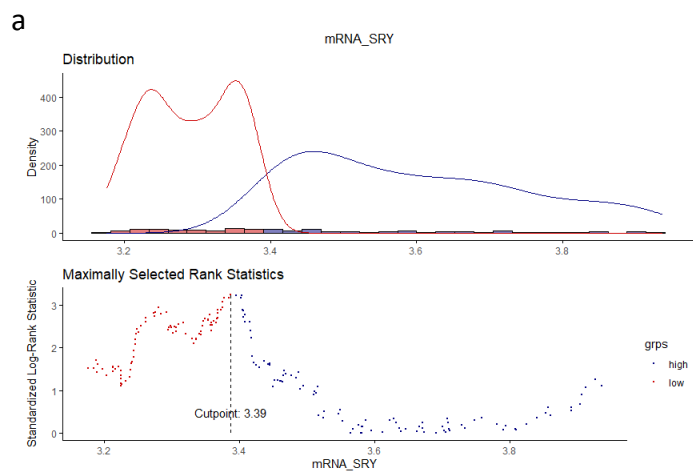


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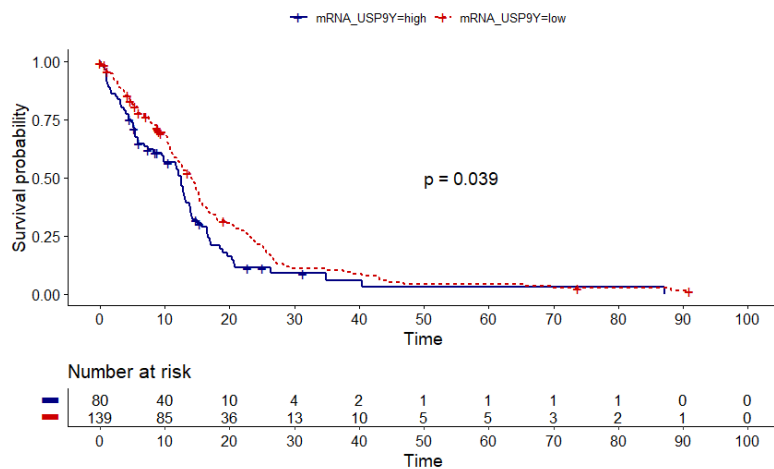
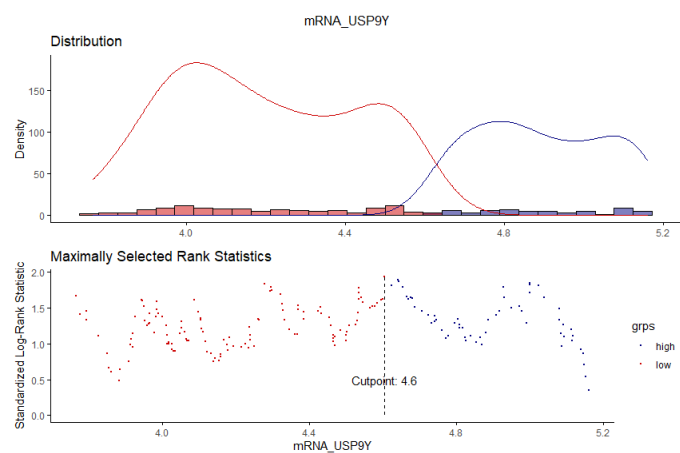




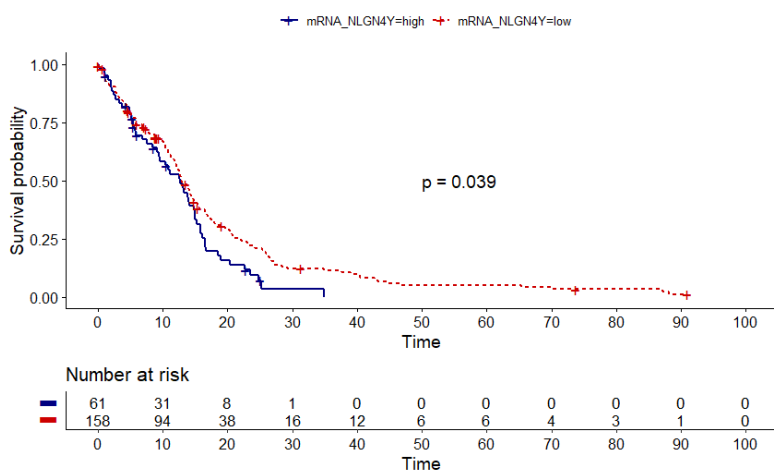
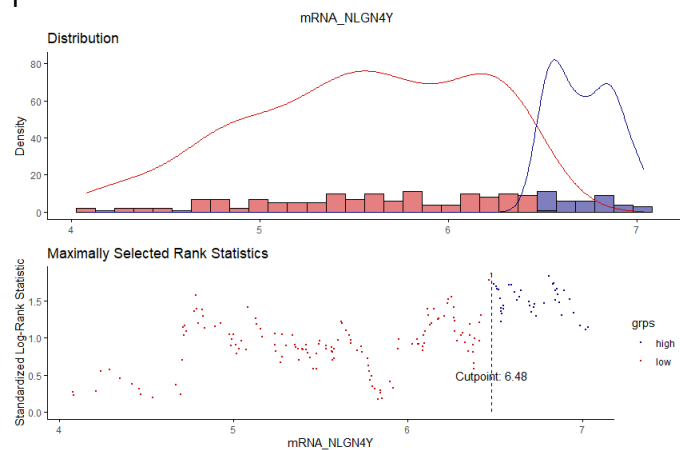
Supplementary Figure S1. Results of the survival analysis based on the CN values with Kaplan-Meier log rank method after cut-off determination via maximally selected rank statistics ($p < 0.05$). On the left, graphs for selection of the best cut-off point, on the right, survival curves ((a) *SRY*; (b) *NLGN4Y*; (c) *AMELY*; (d) *UTY*; (e) *EIF1AY*; (f) *ZFY*; (g) *USP9Y*; (h) *ARSEPI1*; (i) *TMSB4Y*; (j) *KDM5D*).



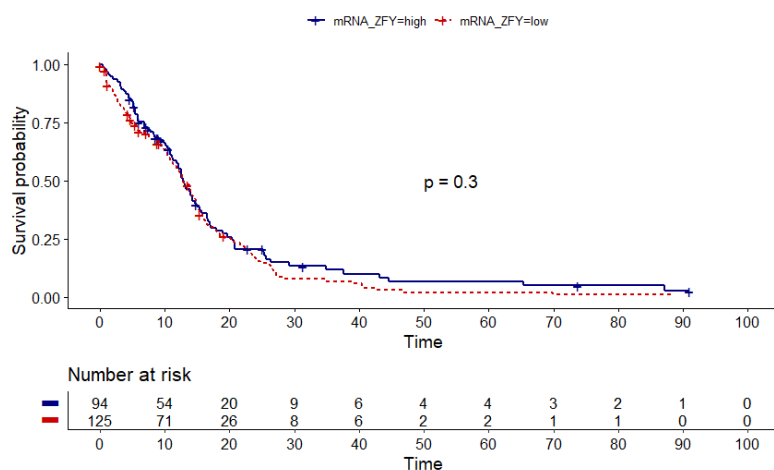
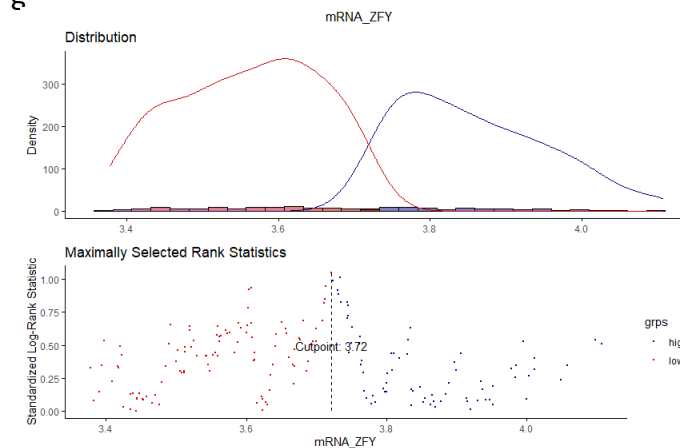
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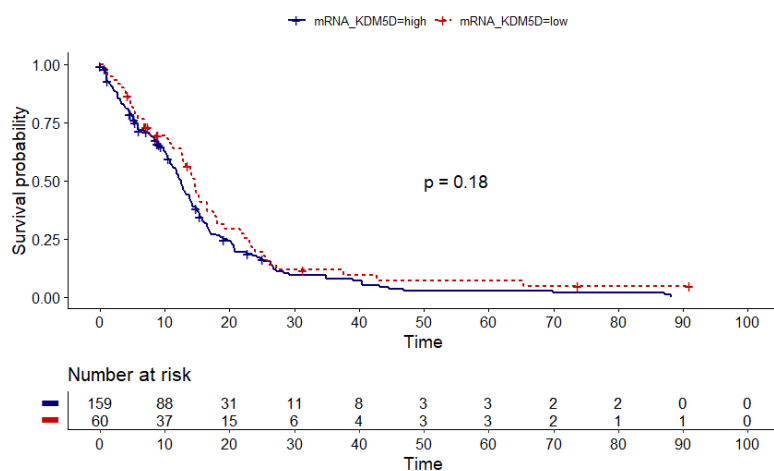
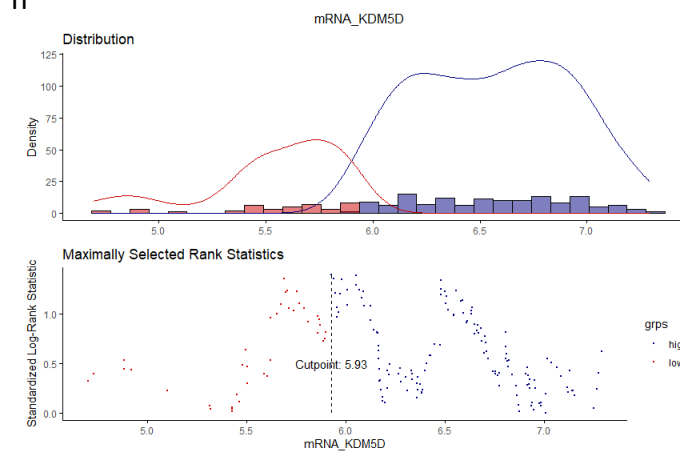
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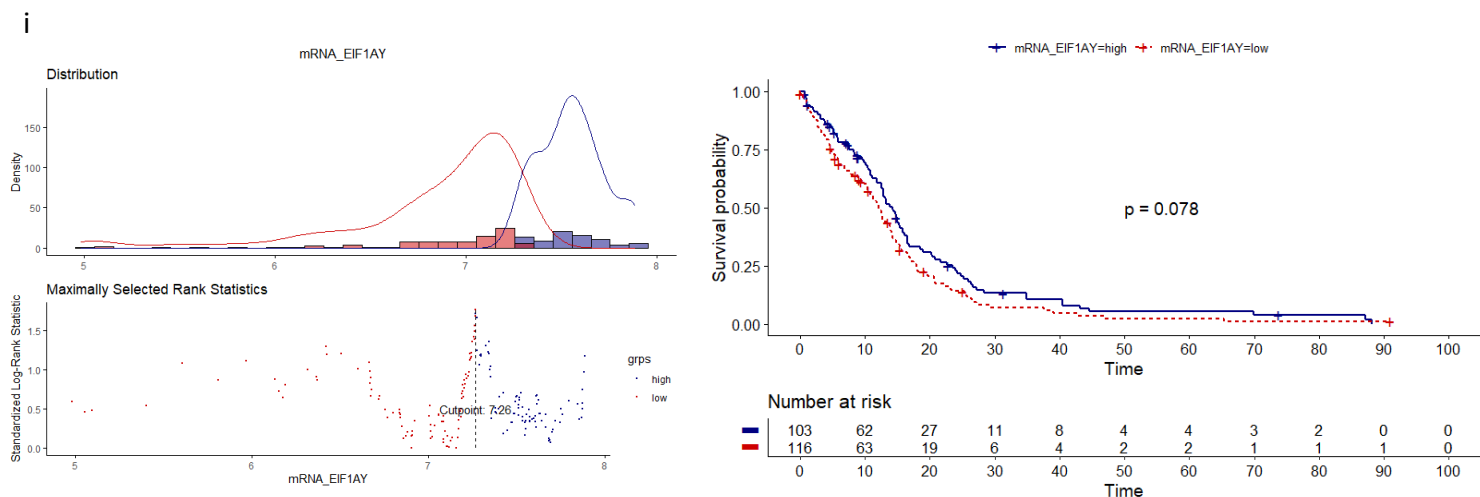


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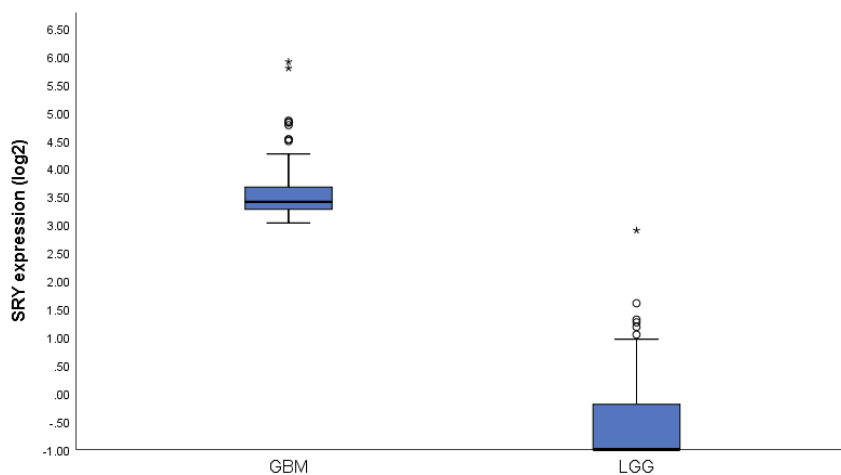


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Supplementary Figure S2. Comparison of relative *SRY* expression between males with GBM and LGG from TCGA. LGG have very low *SRY* expression, nearly undetectable, whereas GBM can be characterized as high *SRY*-expressing tumor. The difference was tested with the non-parametric Mann-Whitney U test and is statistically significant ($p=1.6 \times 10^{-41}$).



Supplementary Figure S3. Results of the survival analysis based on the mRNA gene expression from TCGA with Kaplan-Meier log rank method after cut-off determination via maximally selected rank statistic. On the left, graphs for selection of the best cut-off point, on the right, Kaplan-Meier survival curves. (a) cut-off determination for the most significant gene *SRY*; (b-f) genes with significant influence on the OS of GBM male patients; (e, f) statistically significant results where lower expression of genes correlated with shorter OS; (g-i) genes without significant influence on the OS.