

ANNEX

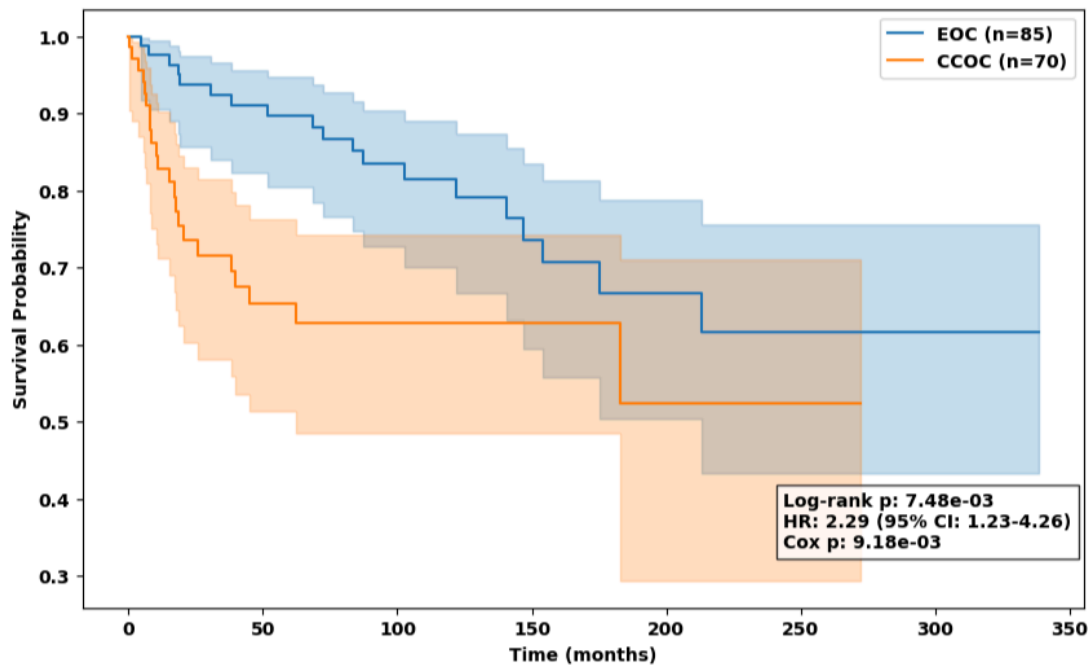
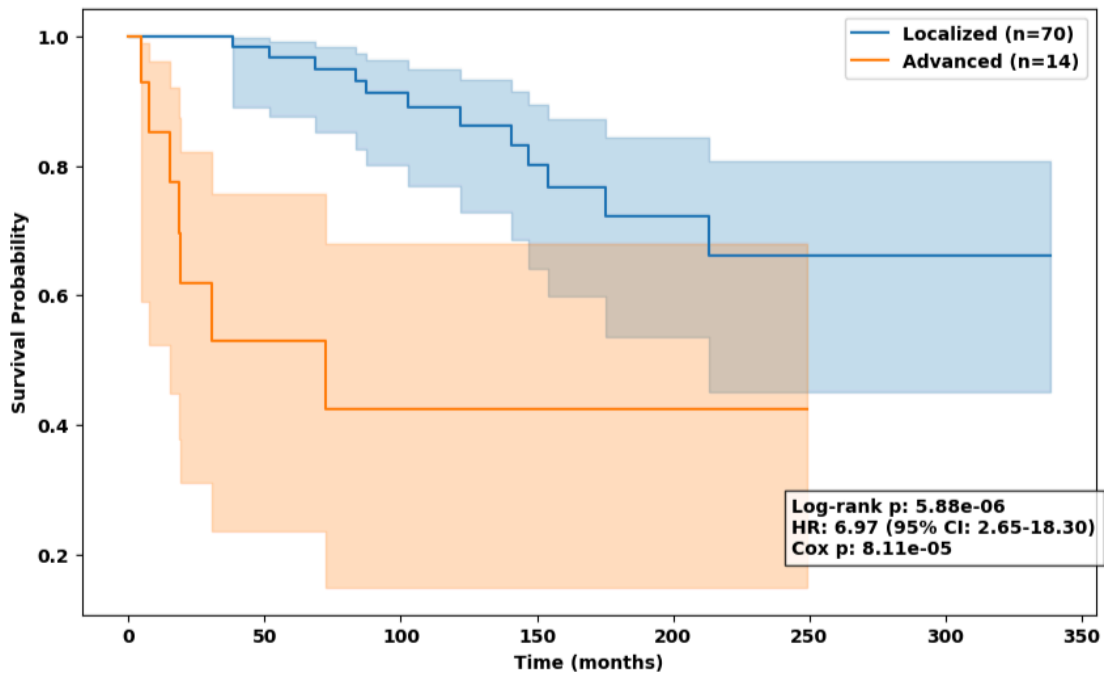


Figure 1. Survival analysis of EOC and CCOC histotypes. Number of samples in each histology is indicated in the top legend. P-values of the log-rank test and the results of the univariate analysis using the Cox proportional-hazards model adjusted for the histology variable including the hazard ratio (HR), its 95% confidence interval and p-value are indicated.

A)



B)

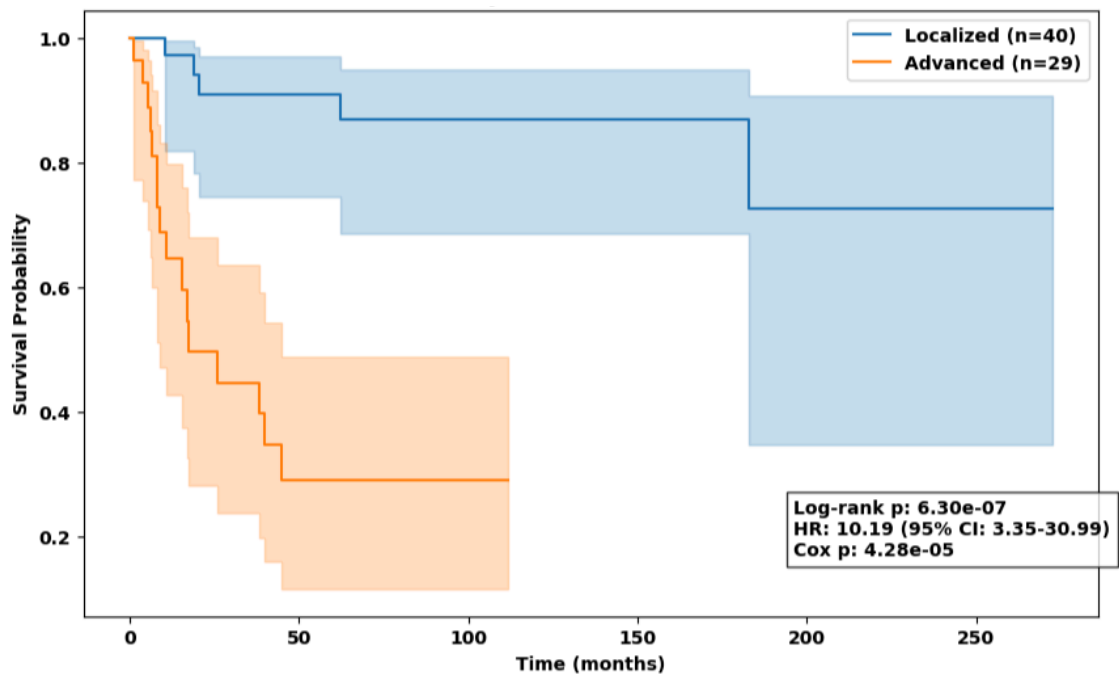


Figure 2. Survival analysis to compare survival in EOC (A) and CCOC (B) between FIGO stage categories. Number of samples in each group is indicated in the top legend. P-values of the log-rank test and the results of the univariate analysis using the Cox proportional-hazards model adjusted for the FIGO stage variable including the hazard ratio (HR), its 95% confidence interval and p-values are indicated.

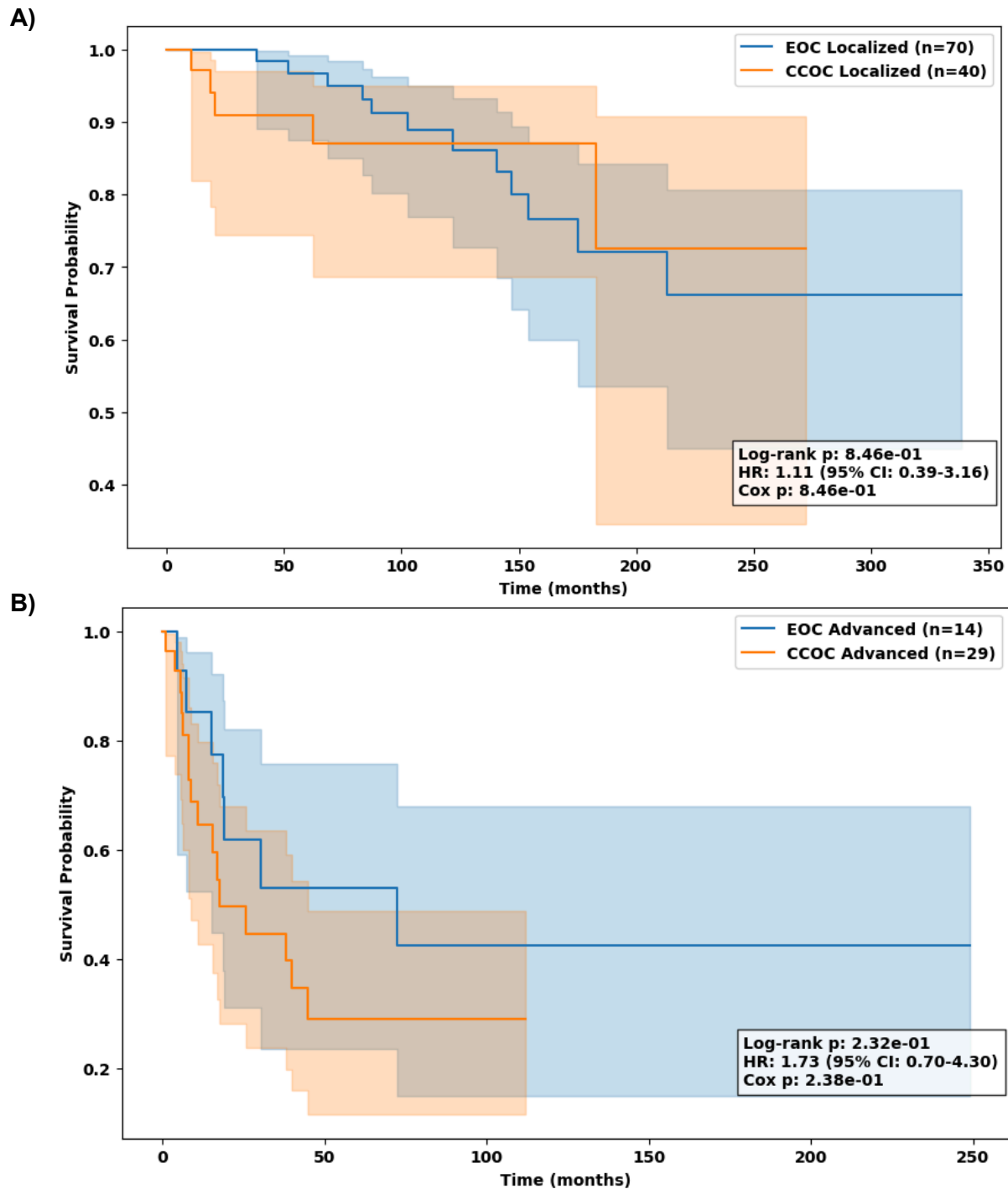


Figure 3. Survival analysis to compare survival between EOC and CCOC in every category of FIGO stage: localized stage tumors (A) and advanced-stage tumors (B). Number of samples in each group is indicated in the top legend. P-values of the log-rank test and the results of the univariate analysis using the Cox proportional-hazards model adjusted for the FIGO stage variable including the hazard ratio (HR), its 95% confidence interval and p-values are indicated.

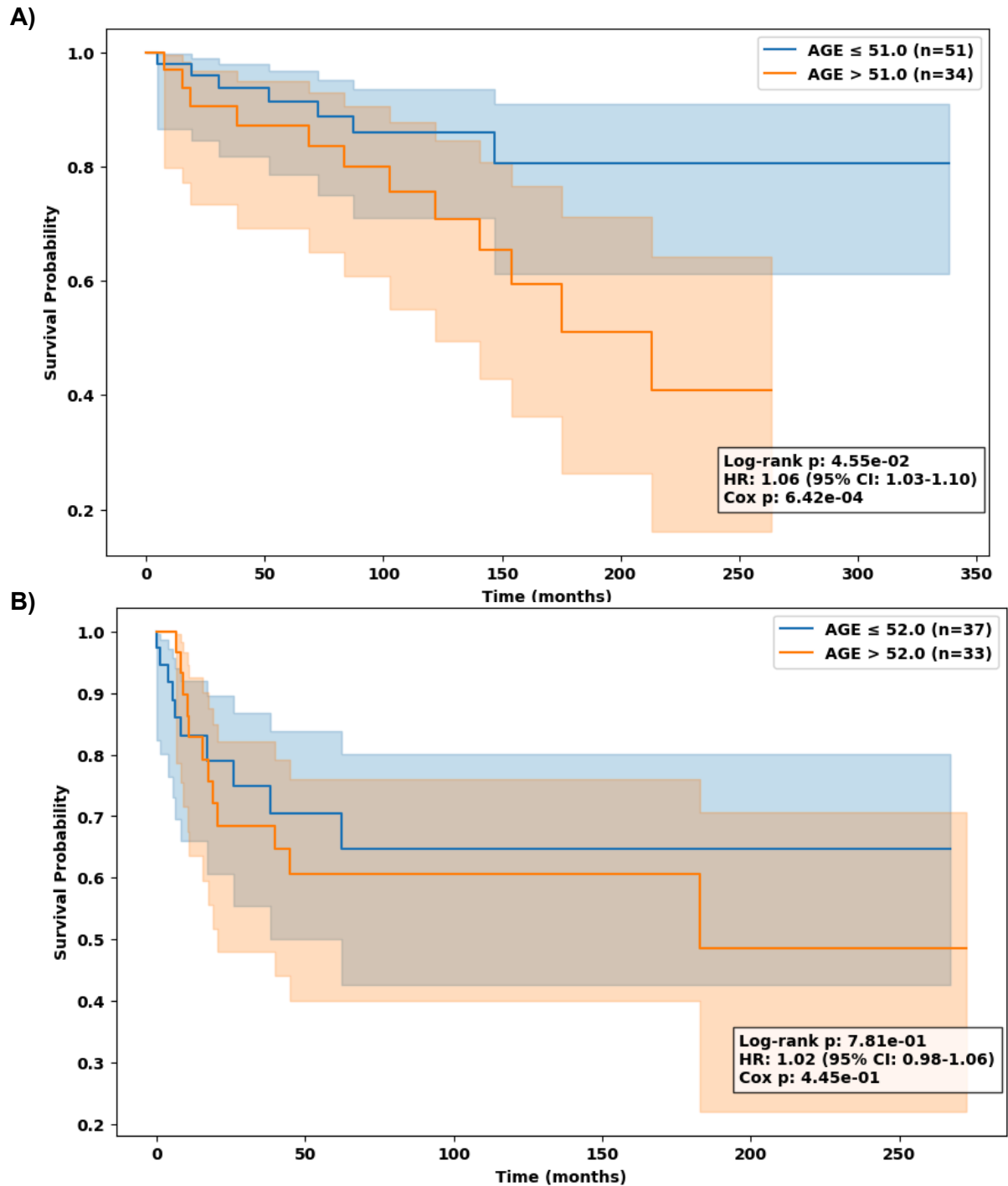
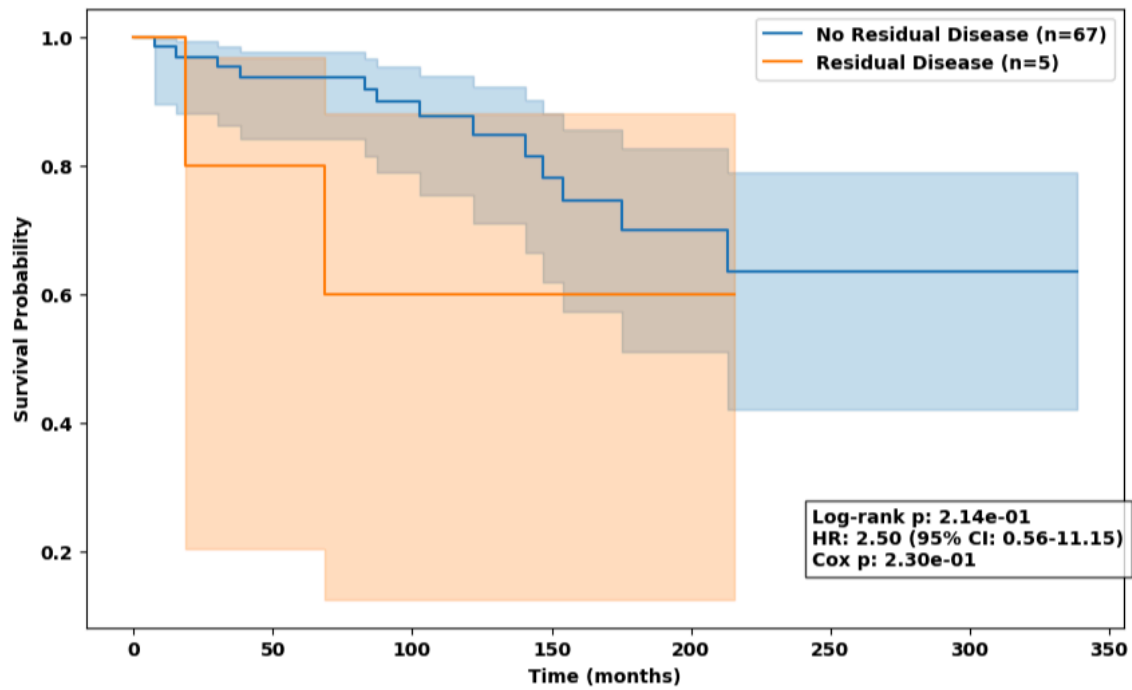


Figure 4. Survival analysis of the 'Age at diagnosis' groups in EOC (A) and CCOC (B). Median values of 'Age at diagnosis' in the EOC series (A) and CCOC series (B) were used as a cut-off to divide in two groups indicated in the top legend of every graphic. P-values of the log-rank test and the results of the univariate analysis using the Cox proportional-hazards model adjusted for the age variable including the hazard ratio (HR), its 95% confidence interval and p-values are indicated.

A)



B)

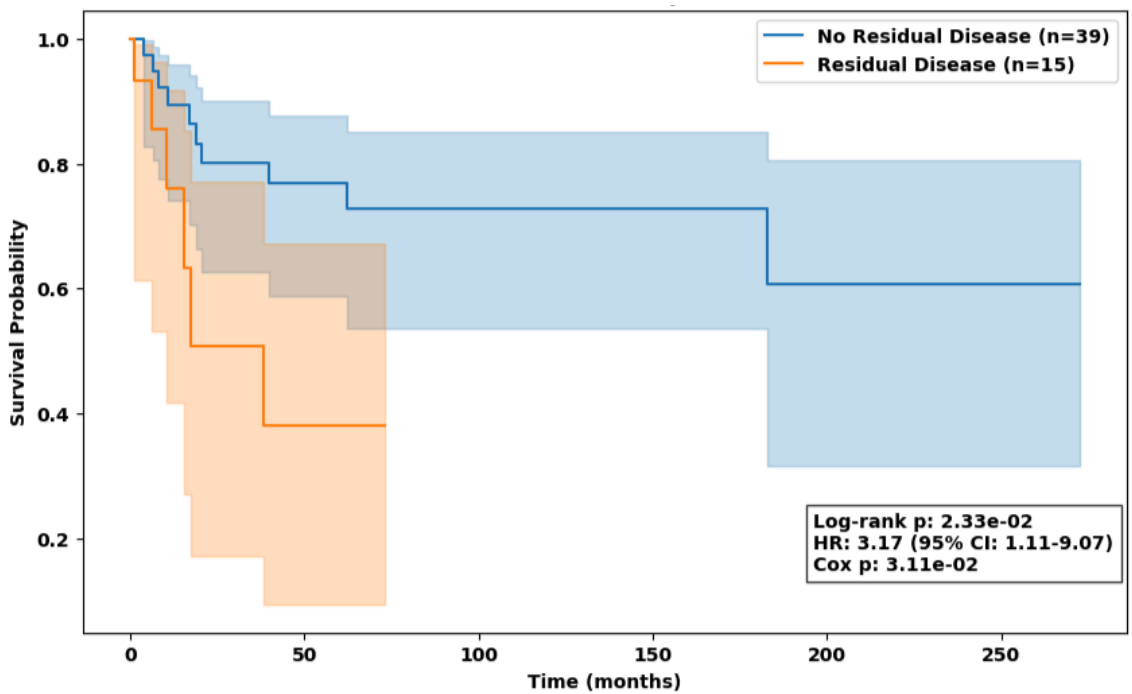
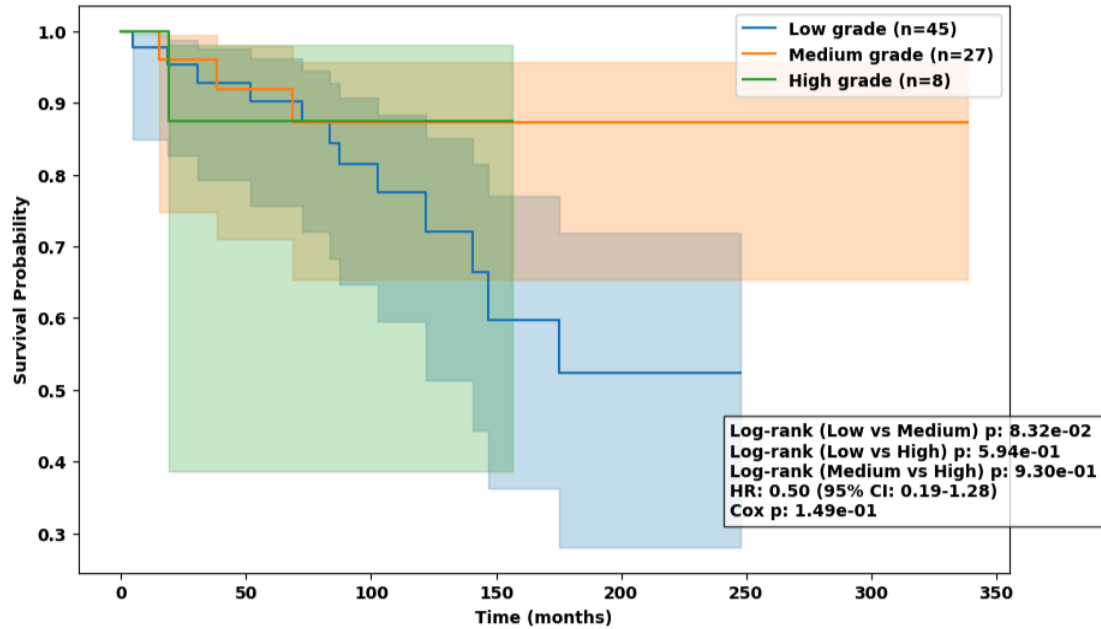


Figure 5. Survival analysis to compare survival in EOC (A) and CCOC (B) between residual disease categories. Number of samples in each group is indicated in the top legend. P-values of the log-rank test and the results of the univariate analysis using the Cox proportional-hazards model adjusted for the residual disease variable including the hazard ratio (HR), its 95% confidence interval and p-values are indicated.

A)



B)

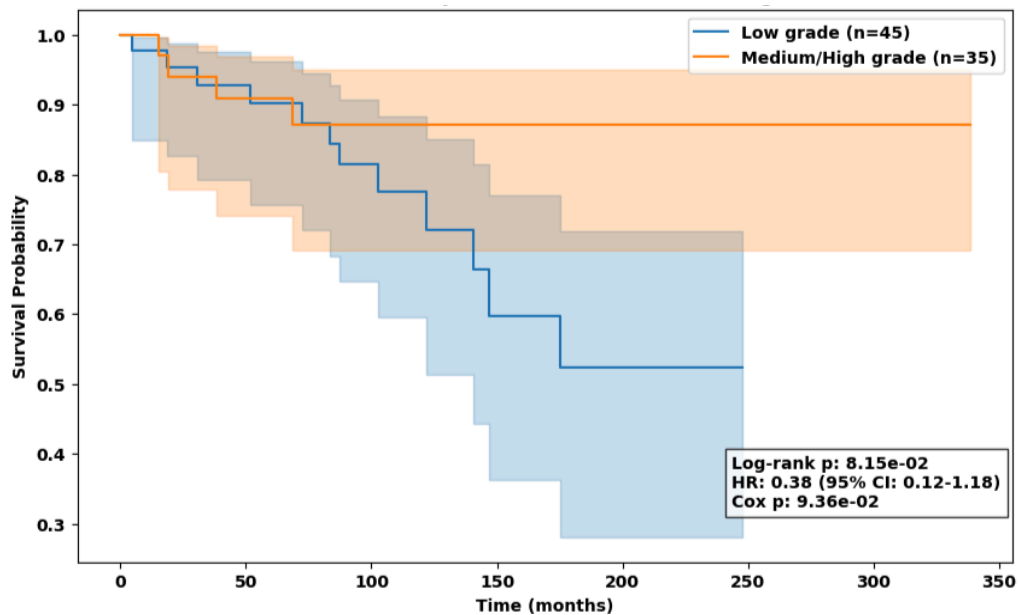
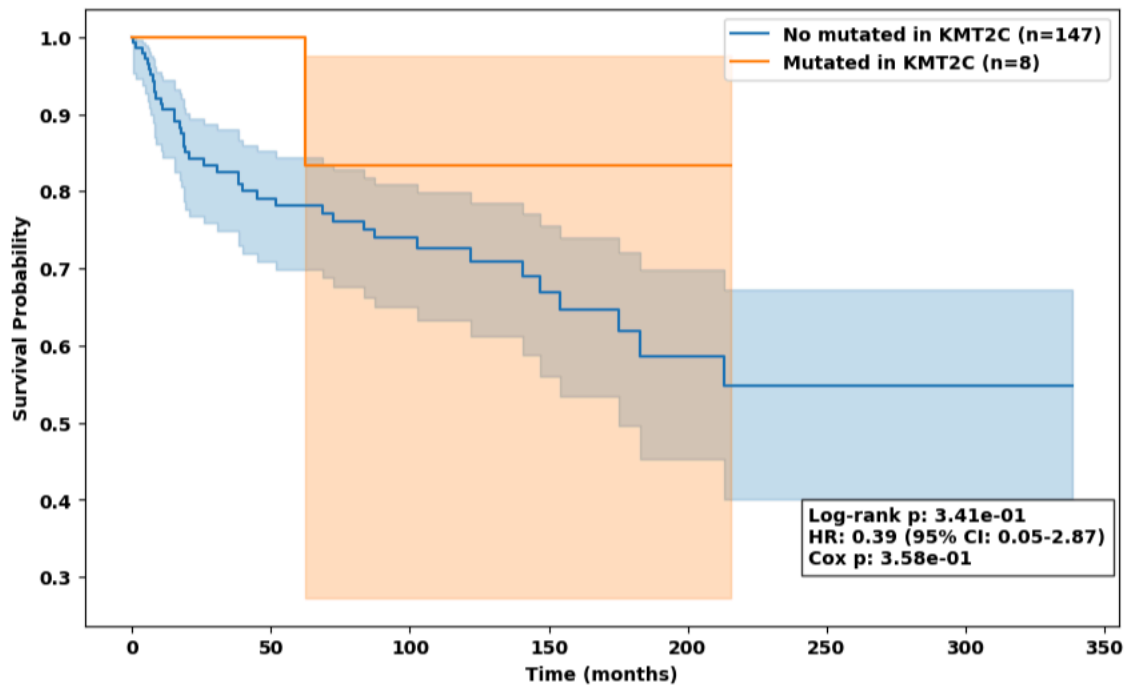


Figure 6. Survival analysis to compare survival in EOC among the three different categories (A) or between the categories low and medium/high grade (B) of the variable ‘differentiation grade of the tumor’. In A) the analysis includes all the 3 grades separated. In B) we observed the same analysis but after grouping medium (grade 2) and high grade tumors (grade 3) in an unique category. Number of samples in each group is indicated in the top legend. P-values of the log-rank test and the results of the univariate analysis using the Cox proportional-hazards model adjusted for this variable including the hazard ratio (HR), its 95% confidence interval and p-values are indicated.. No significant differences were observed after grouping low and medium grade categories (data not shown).

A)



B)

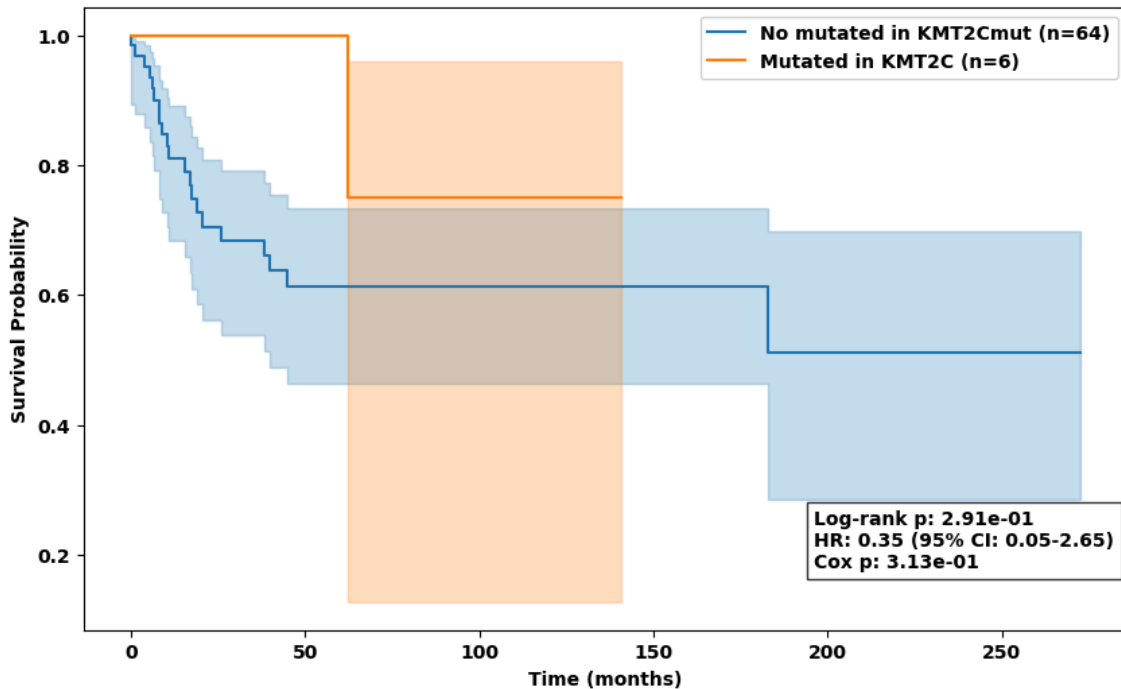


Figure 7. Survival analysis comparing samples with and without mutations in the *KMT2C* gene in the entire cohort (A) and the CCOC series (B). The *KMT2C* mutation status was used to divide the cohort into two groups: samples with the *KMT2C* mutation and those without it. The plots include the p-values from the log-rank test comparing the survival distributions of the two groups. Additionally, results from the univariate Cox proportional-hazards model, which quantify the association between *KMT2C* mutation and survival are indicated (include HR and its confidence interval and the p-value of Cox).

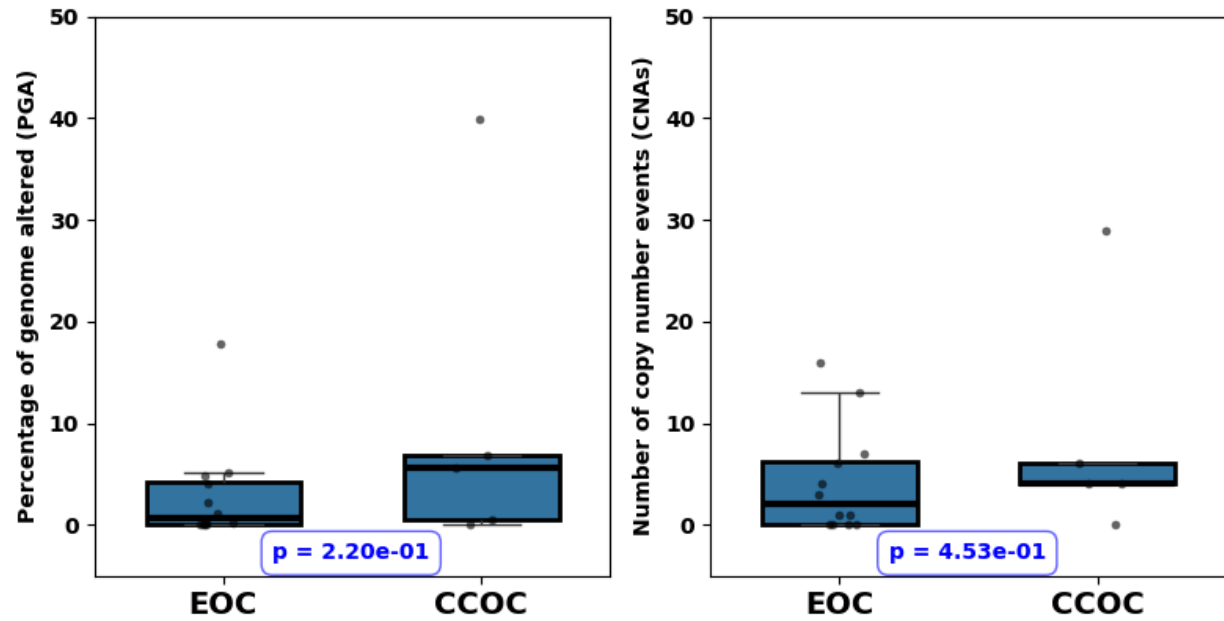
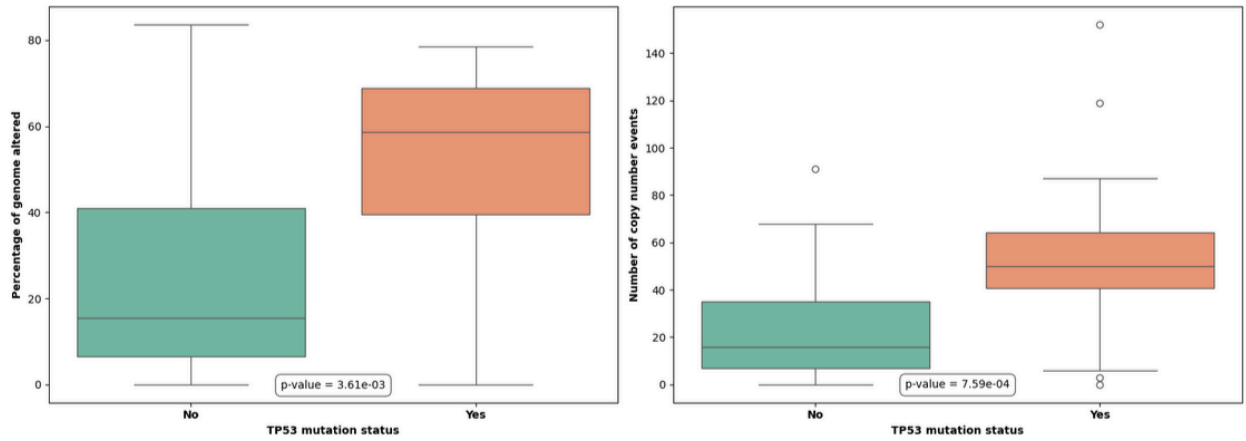


Figure 8. Boxplots showing the comparative distribution of PGA (left) and copy number events (right) between EOC and CCOC series in the MMRd group. The p-value indicating statistical significance of the comparison between EOC and CCOC in MMRd groups is indicated in the blue box.

A)



B)

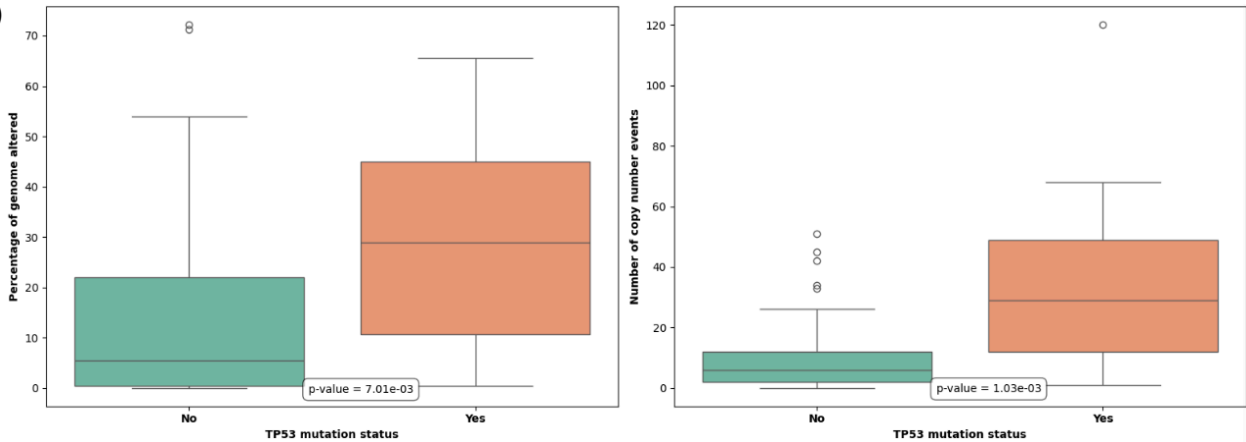


Figure 9. Boxplots showing the distribution of percentage of genome altered (left) and number of copy number events (right) in CCOC (A) and EOC (B) depending on TP53 mutation status. P-values results of Mann-Whitney U Test are indicated. 'Yes' category indicates that *TP53* is mutated and 'No' category indicates that *TP53* is not mutated.

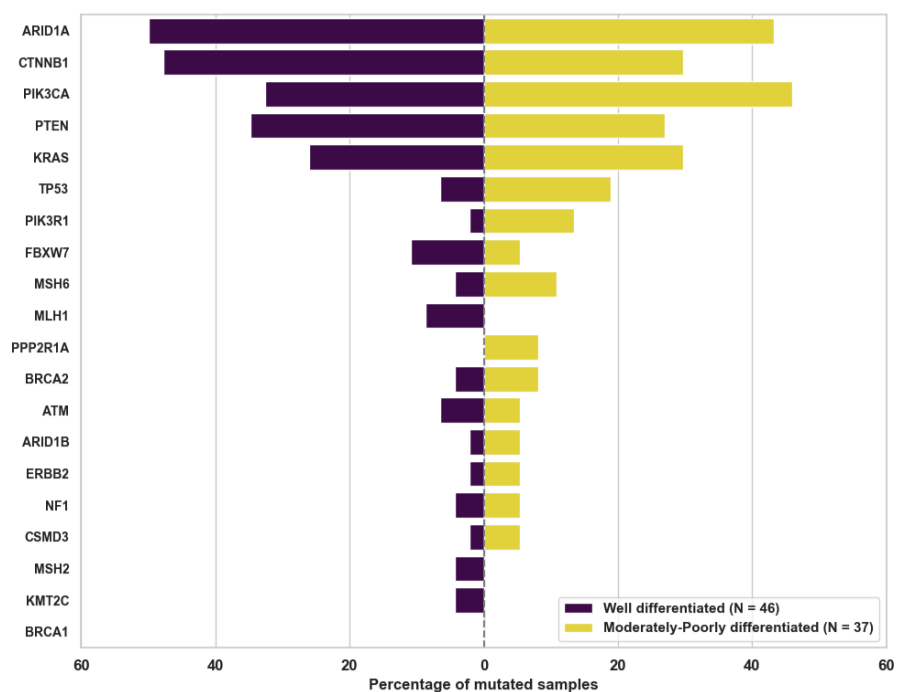


Figure 10. Horizontal histograms displaying the percentages of samples mutated in the top 20 most mutated genes (ranked by their frequency in the entire combined cohort) across each grouped category of the 'Differentiation grade' clinical feature in EOC.

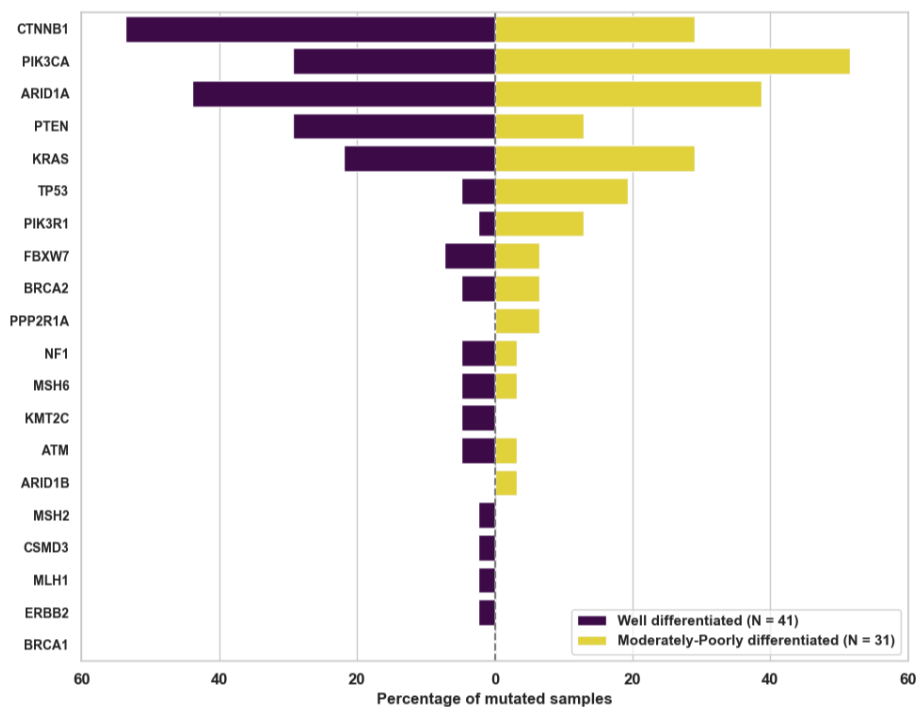


Figure 11. Horizontal histograms displaying the percentages of samples mutated in the top 20 most mutated genes (ranked by their frequency in the entire combined cohort) across each grouped category of the 'Differentiation grade' clinical feature in EOC MMRp.

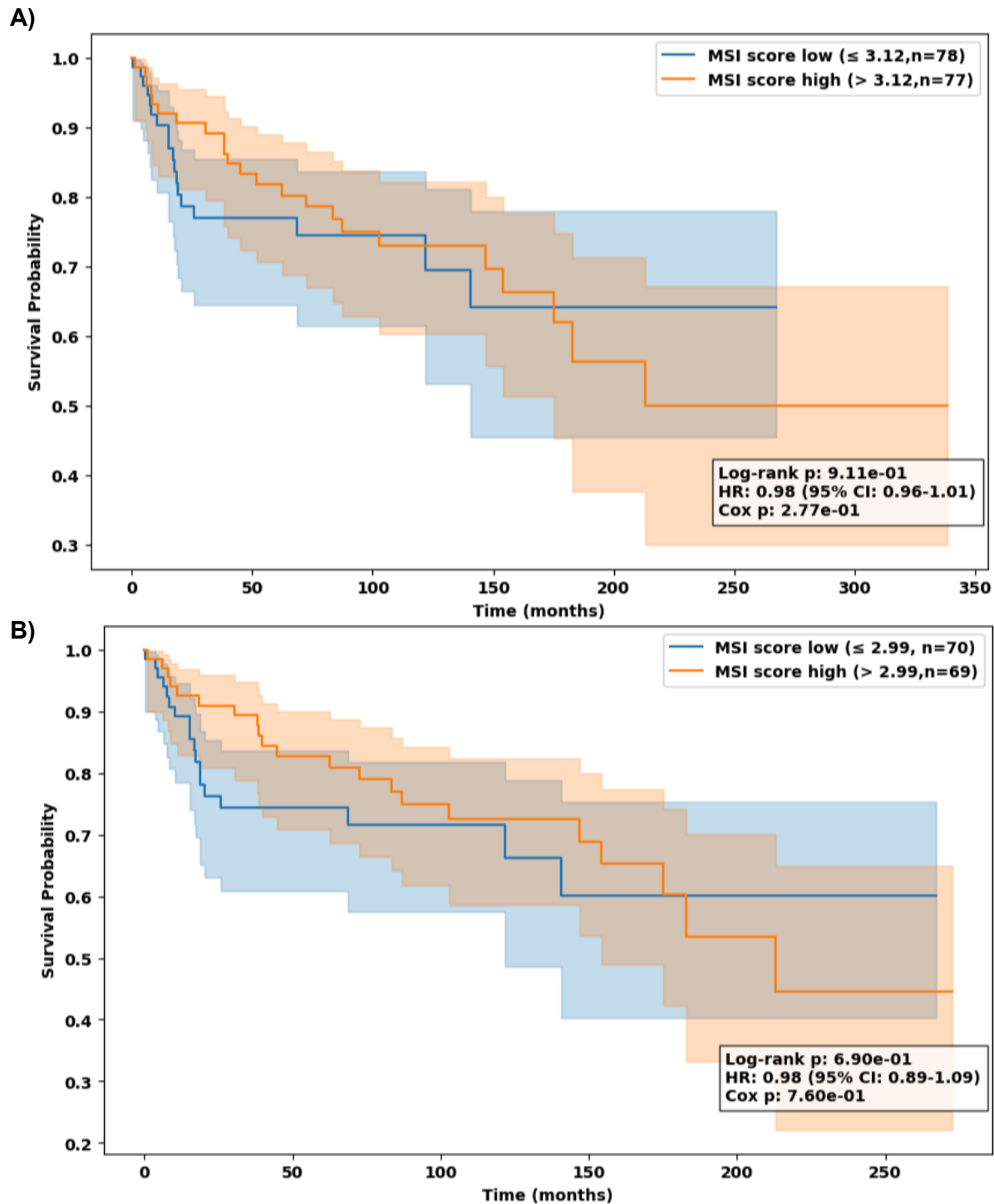


Figure 12. Survival analysis comparing MSI score high and MSI score low samples in the entire cohort (A) and the MMRp group (B). The median MSI score within each group was used as the cut-off to classify samples into MSI score high and MSI score low, as indicated in the top legend of each panel.

The plots include the p-values from the log-rank test comparing the survival distributions of the two groups. Additionally, results from the univariate Cox proportional-hazards model adjusted for the MSI score variable are displayed, including the hazard ratio (HR), its 95% confidence interval and p-values.

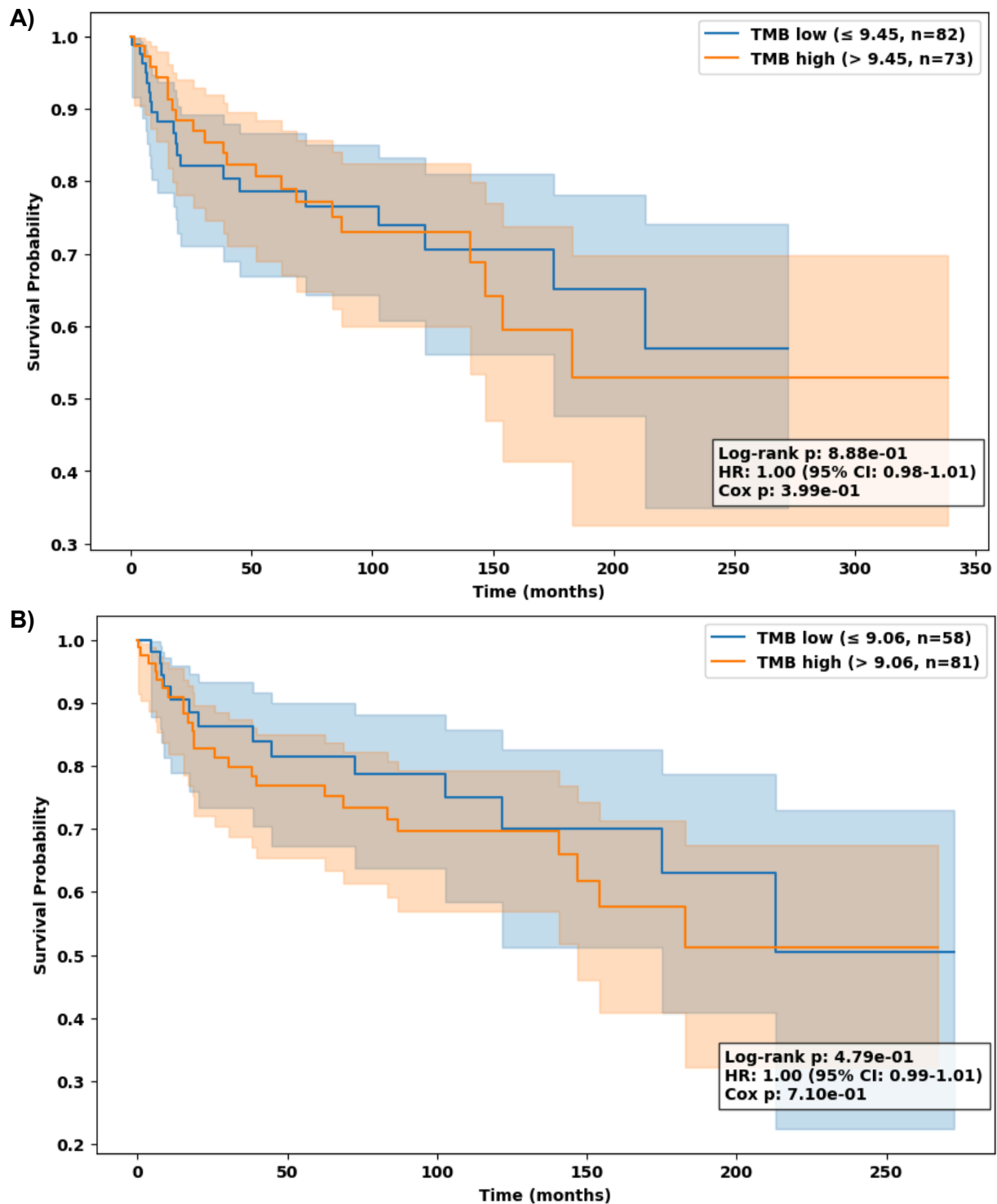


Figure 13. Survival analysis comparing TMB high and TMB low samples in the entire cohort (A) and the MMRp group (B). The median TMB score within each group was used as the cut-off to classify samples into TMB high and TMB low, as indicated in the top legend of each panel. The plots include the p-values from the log-rank test comparing the survival distributions of the two groups. Additionally, results from the univariate Cox proportional-hazards model adjusted for the TMB variable are displayed, including the hazard ratio (HR), its 95% confidence interval and p-values.

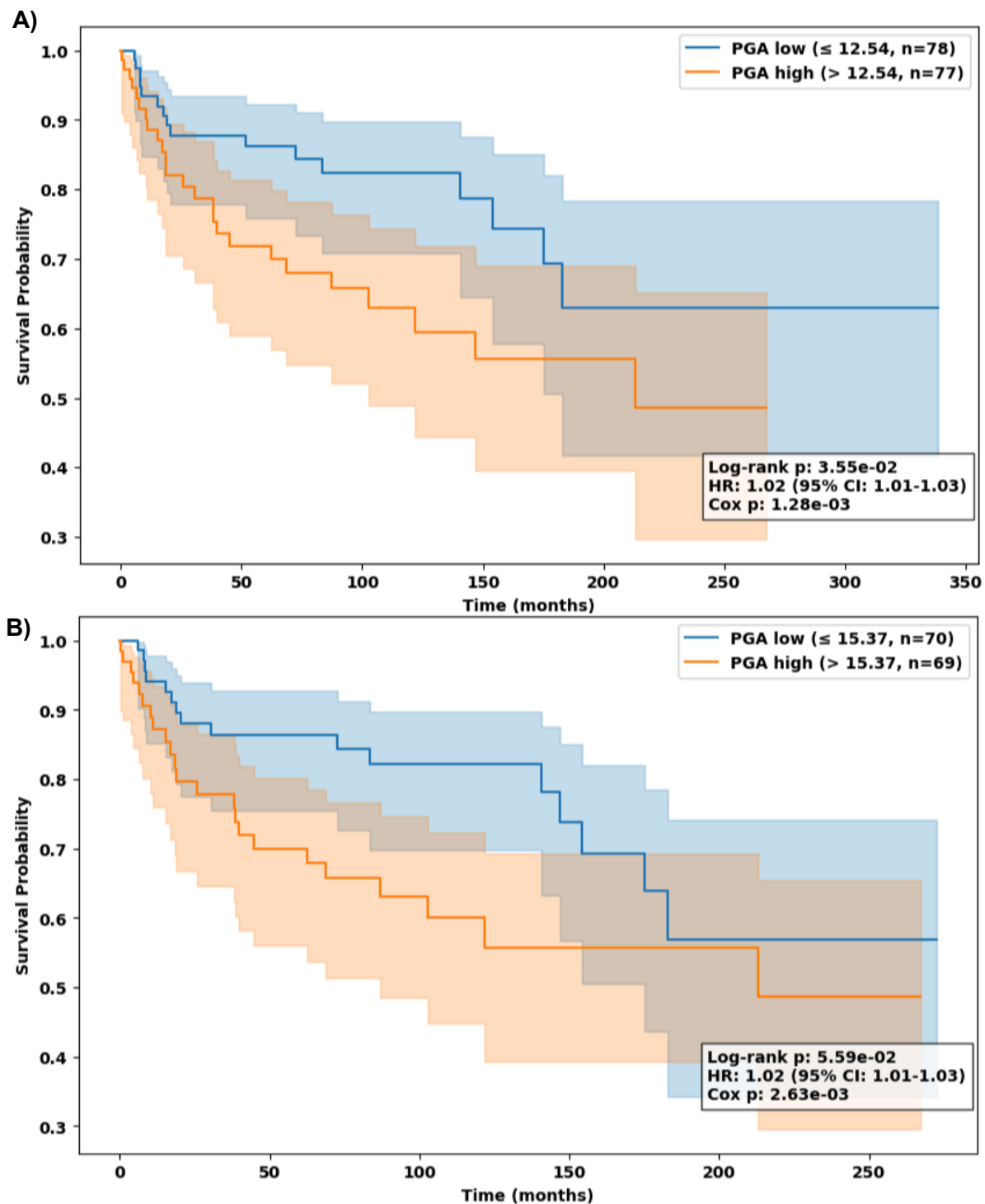


Figure 14. Survival analysis comparing PGA high and PGA low samples in the entire cohort (A) and the MMRp group (B). The median PGA value within each group was used as the cut-off to classify samples into PGA high and PGA low, as indicated in the top legend of each panel. The plots include the p-values from the log-rank test comparing the survival distributions of the two groups. Additionally, results from the univariate Cox proportional-hazards model adjusted for the PGA variable are displayed, including the hazard ratio (HR), its 95% confidence interval and p-values.

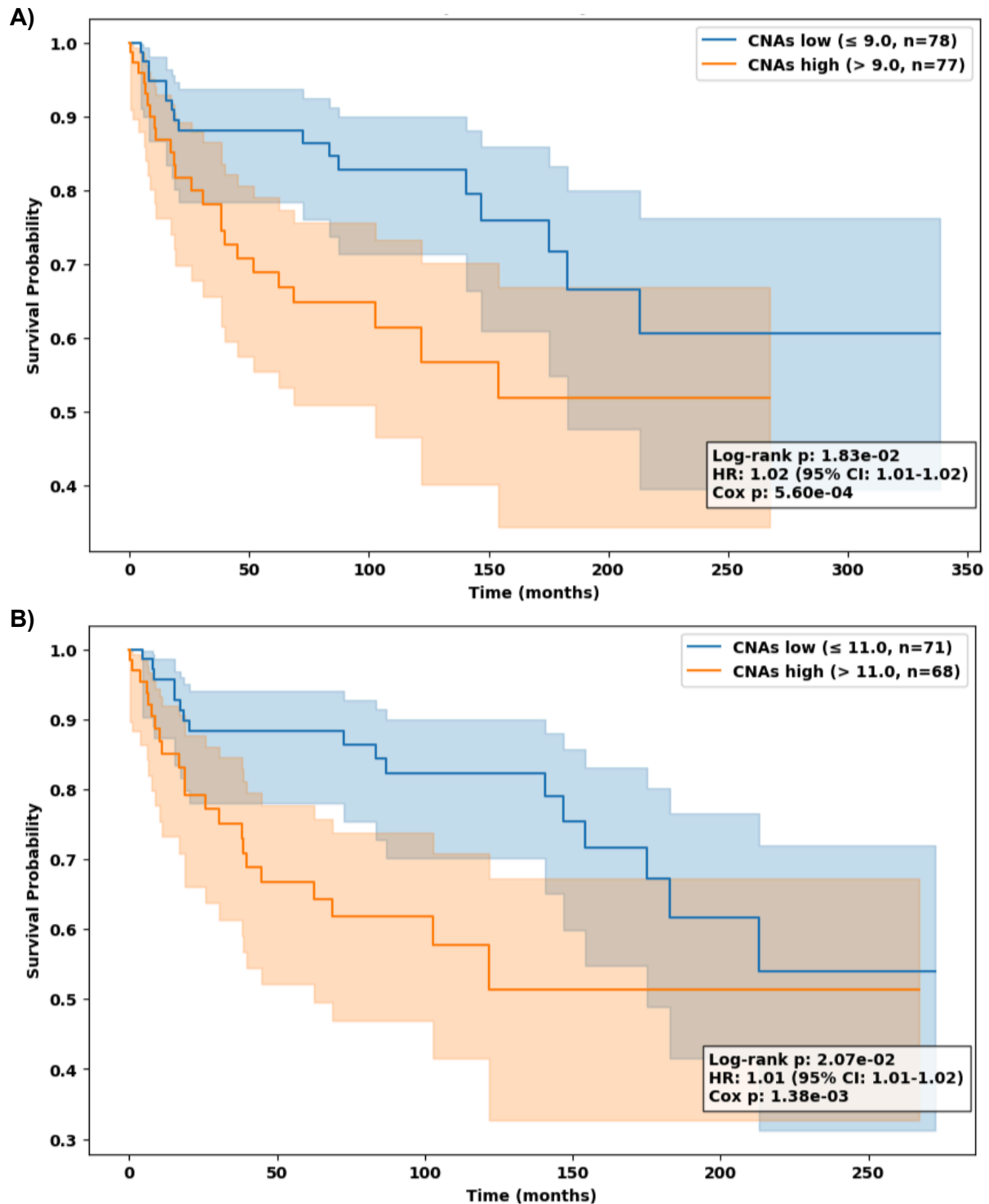


Figure 15. Survival analysis comparing CNAs high and CNAs low samples in the entire cohort (A) and the MMRp group (B). The median of copy number aberrations within each group was used as the cut-off to classify samples into CNAs high and CNAs low, as indicated in the top legend of each panel.

The plots include the p-values from the log-rank test comparing the survival distributions of the two groups. Additionally, results from the univariate Cox proportional-hazards model adjusted for the CNAs variable are displayed, including the hazard ratio (HR), its 95% confidence interval and p-values.

MLH1	RBBP8	BARD1	NTRK3	CDKN2A	SMARCA4	NTHL1	GABRA6
MSH2	BLM	CHEK2	KIT	FGFR1	ARID1B	CHEK1	RB1
MSH6	ATM	MRE11	EGFR	FGFR2	KEAP1	ERCC4	SMAD4
MLH3	ACVR2A	RAD51B	ALK	KDM6A	STAT3	ERCC5	BMPR1A
MSH3	TGFBR2	XRCC2	TSC1	NF1	FBXW7	CUL3	TRIM25
PMS1	RPL22	SLX4	TSC2	SMARCB1	KDM5C	ERCC3	EPCAM
PIK3CA	RNF43	NBN	MET	NTRK1	PIK3R1	ATRAX	AXIN2
ARID1A	KMT2C	FANCM	PDGFRA	CASP8	PTPRD	BABAM1	GREM1
PTEN	PRDM2	RECQL	AKT1	B2M	SOX9	MDC1	FAN1
KRAS	JAK1	CDH1	ARAF	JAK2	PBRM1	POLQ	DPYD
PPP2R1A	ALPK2	STK11	ERBB2	TAP1	TET1	REV3L	EIF1AX
CTNNB1	DPYSL2	FANCA	ERCC2	TAP2	SMARCE1	FANCD2	NF2
BRAF	TCF7L2	FANCC	ESR1	TAPBP	SMARCA2	CENPE	RBM10
TP53	BRCA1	RAD51	HRAS	HLA-A	BRD7	CDK12	CDKN2B
POLD1	BRCA2	TP53BP1	MAP2K1	CANX	ARID2	IDH1	DICER1
POLE	PMS2	RAD52	PTCH1	CALR	GTF2H5	ABRAXAS1	
PRKDC	RAD51D	PPP4R2	RET	PSMB5	SHPRH	FAT4	
APC	BRIP1	RAD54L	FGFR3	PSMB8	PARP1	LRP1B	
RAD50	RAD51C	RECQL4	MTOR	TERT	ELOC	CSMD3	
ATR	PALB2	RTEL1	NRAS	SPOP	MUTYH	FAT3	

Figure 16. Genes included in the OVAseq gene targeted sequencing panel. In black, the genes included in OVAseq.1 and OVAseq.2. In red, the genes included only in OVAseq.2.