

Supplementary Material: A Comprehensive Analysis of Baseline Clinical Characteristics and Biomarkers Associated with Outcome in Advanced Melanoma Patients Treated with Pembrolizumab

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Table S1. Scores in the NanoString PanCancer IO360 gene expression profiling panel.

TIS: tumor inflammation score	IFN Gamma: interferon	PD-L2: programmed cell death
APM: antigen-presenting	gamma	ligand 2
machinery	IL10: interleukin-10	Proliferation
Apoptosis	Immunoproteasome	Stroma
ARG1: arginase 1	Inflammatory Chemokines	T Cells
B7-H3: B7 homolog 3	Lymphoid	TGF-Beta: transforming
CD45	Macrophages	growth factor beta
CD8 T Cells	MAGEs: melanoma-associated	TH1 Cells: T helper 1 cells
CTLA4: cytotoxic T-	antigens	TIGIT: T cell immunoreceptor
lymphocyte associated	Mast Cells	with Ig and ITIM domains
antigen-4	MHC2: major	Treg: regulatory T cells
Cytotoxic Cells	histocompatibility complex 2	MMR Loss: mismatch repair
Cytotoxicity	Myeloid	loss
DC: dendritic cells	Myeloid Inflammation	Hypermutation
Endothelial Cells	Neutrophils	MSI Predictor: microsatellite
Exhausted CD8	NK CD56dim	instability predictor
Glycolytic activity	NK Cells: natural killer cells	APM Loss: antigen-presenting
Hypoxia	NOS2: Nitric oxide synthase 2	machinery loss
IDO1: indoleamine 2,3-	PD-1: programmed cell death	JAKSTAT Loss
dioxygenase 1	1	
IFN Downstream: interferon	PD-L1: programmed cell death	
downstream signaling	ligand 1	

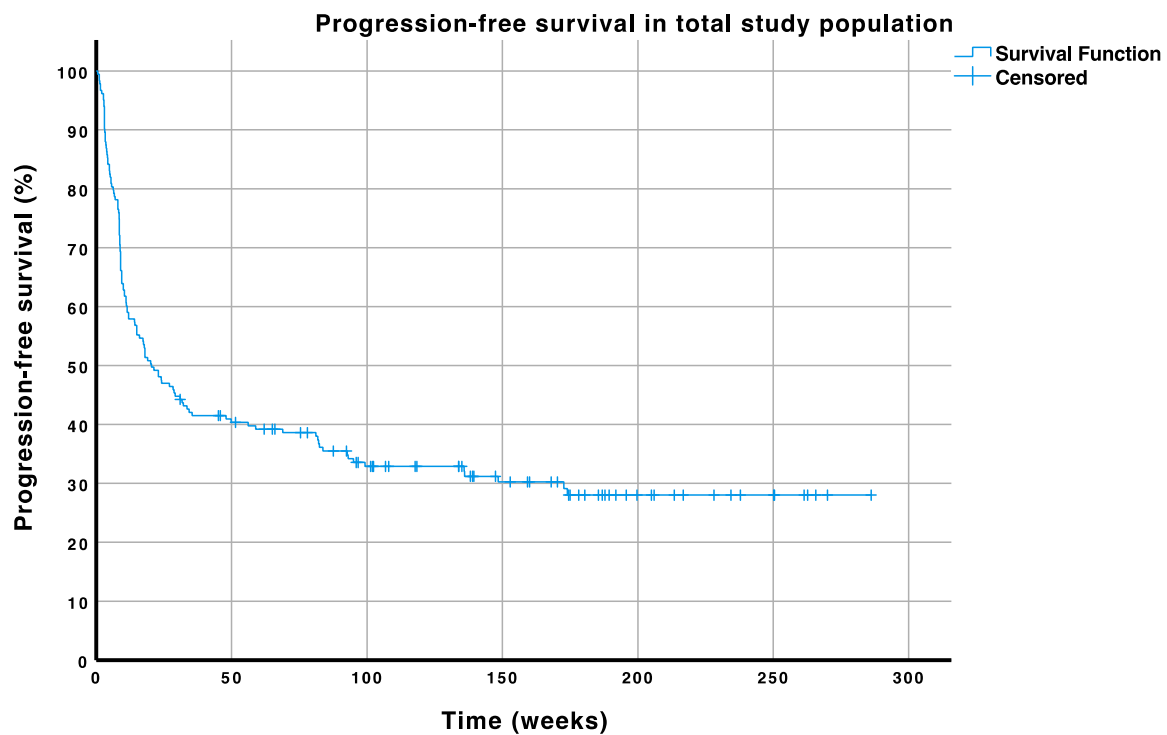


Figure S1. Progression-free survival in the total study population ($n = 183$).

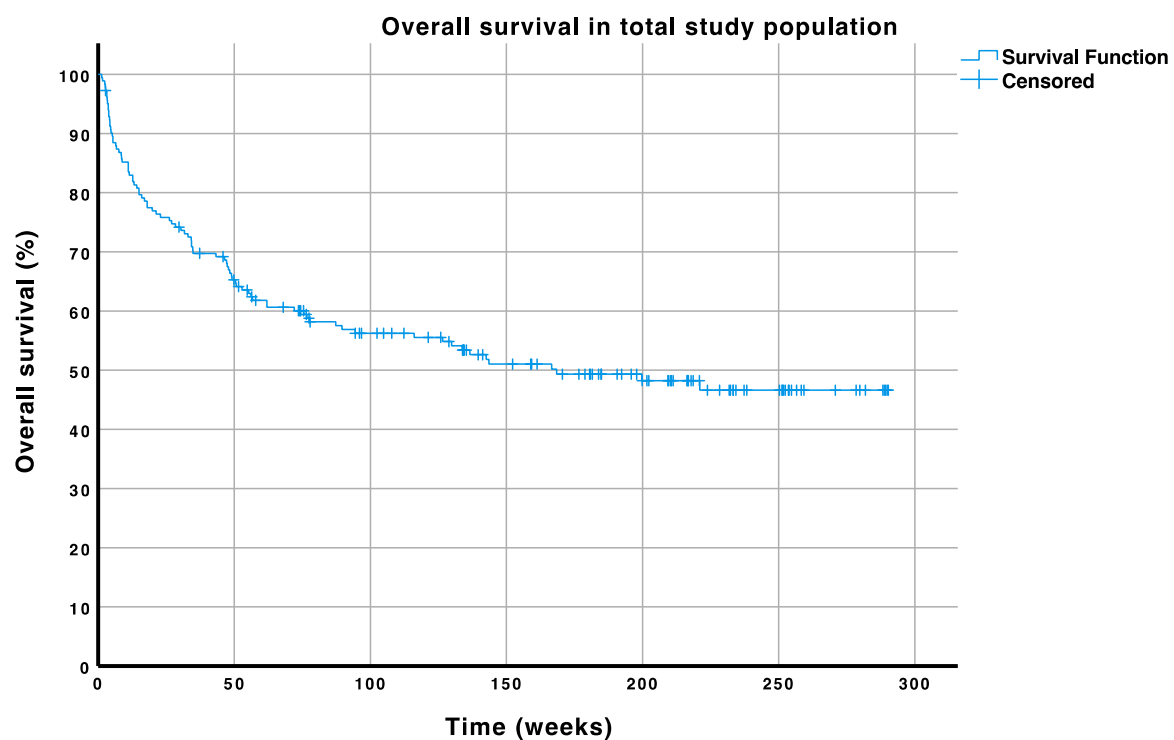


Figure S2. Overall survival in the total study population ($n = 183$).

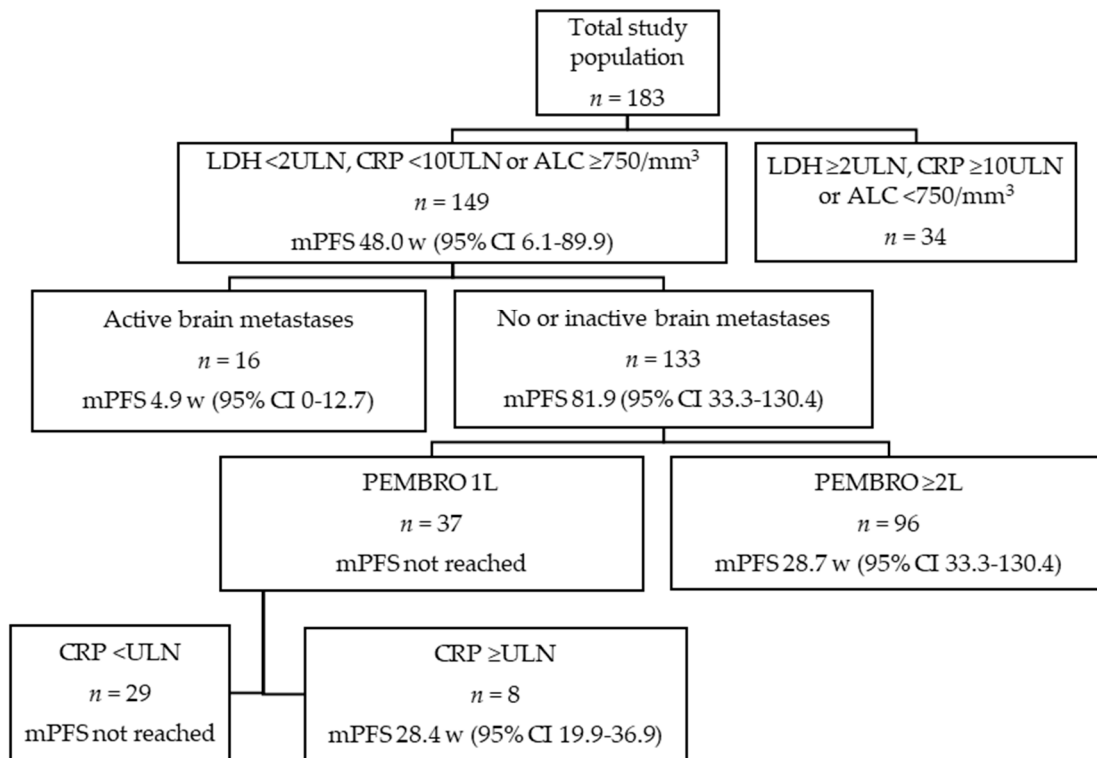


Figure S3. Recursive partitioning analysis in the population of patients with CRP <10ULN, LDH <2ULN or ALC ≥750/mm³ (*n* = 149) with regards to progression-free survival. Abbreviations: 95% CI: 95% confidence interval; ALC: absolute lymphocyte count; CRP: C-reactive protein; LDH: lactate dehydrogenase; mPFS: median progression-free survival; PEMBRO 1L: pembrolizumab as first-line treatment; PEMBRO ≥2L: pembrolizumab as second line or later treatment; ULN: upper limit of normal; w: weeks.

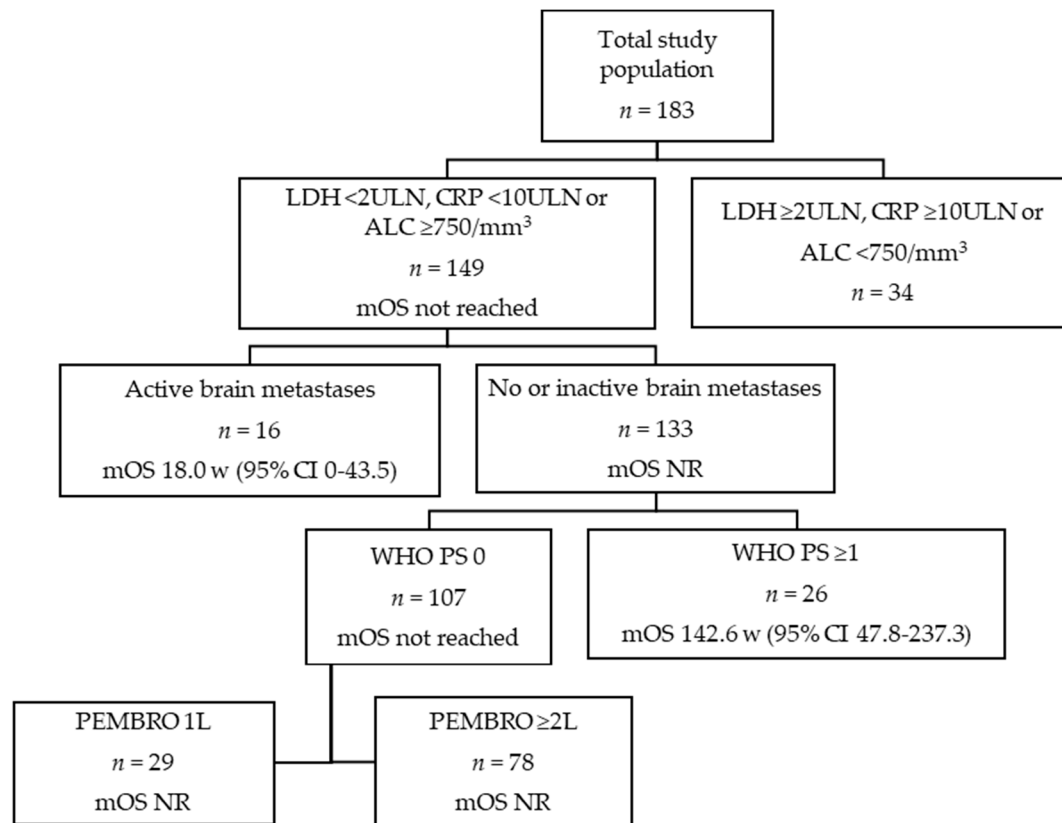


Figure S4. Recursive partitioning analysis in the population of patients with CRP <10ULN, LDH <2ULN or ALC ≥750/mm³ (n = 149) with regards to overall survival. Abbreviations: 95% CI: 95% confidence interval; ALC: absolute lymphocyte count; CRP: C-reactive protein; LDH: lactate dehydrogenase; mOS: median overall survival; PEMBRO 1L: pembrolizumab as first-line treatment; PEMBRO ≥2L: pembrolizumab as second line or later treatment; ULN: upper limit of normal; w: weeks; WHO PS: World Health Organization Performance Status.

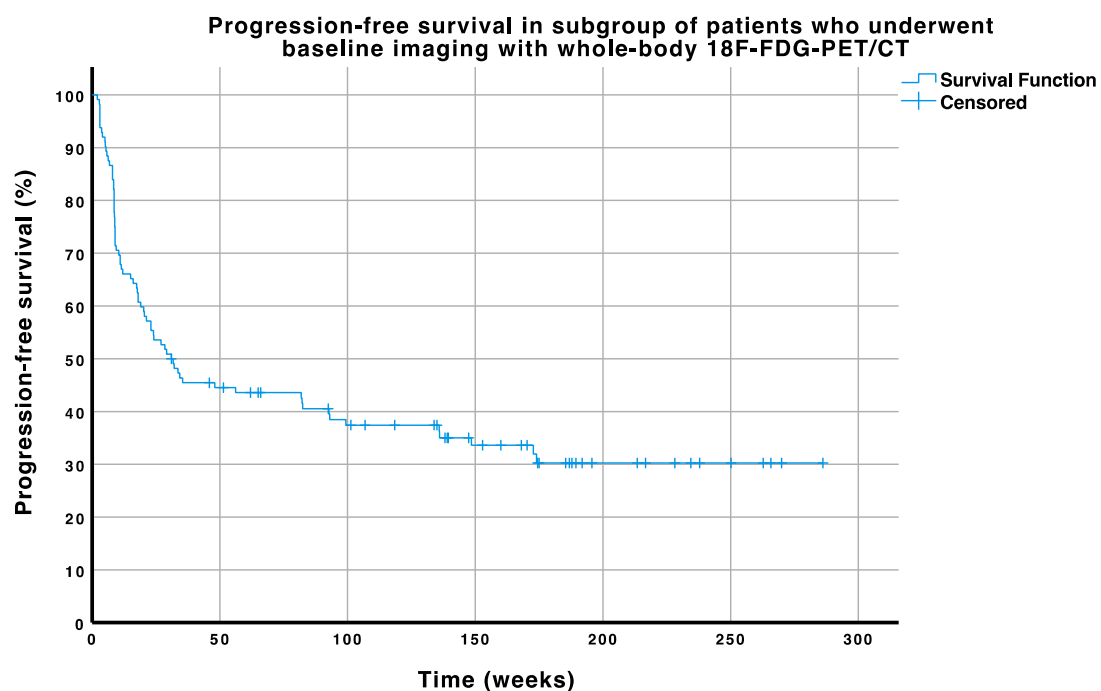


Figure S5. Progression-free survival in the subgroup of patients who underwent baseline imaging with whole-body ^{18}F -FDG-PET/CT ($n = 112$). Abbreviations: ^{18}F -FDG-PET/CT: 18-fluorodeoxyglucose positron emission tomography/computed tomography.

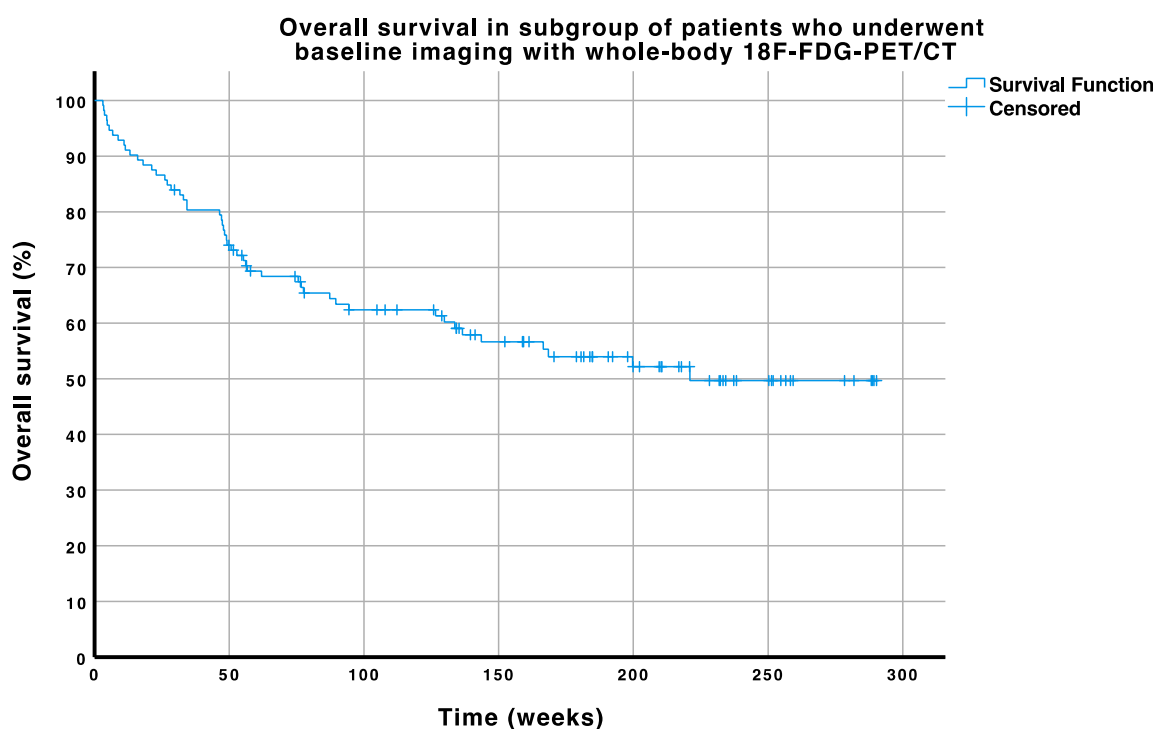


Figure S6. Overall survival in the subgroup of patients who underwent baseline imaging with whole-body ^{18}F -FDG-PET/CT ($n = 112$). Abbreviations: ^{18}F -FDG-PET/CT: 18-fluorodeoxyglucose positron emission tomography/computed tomography.

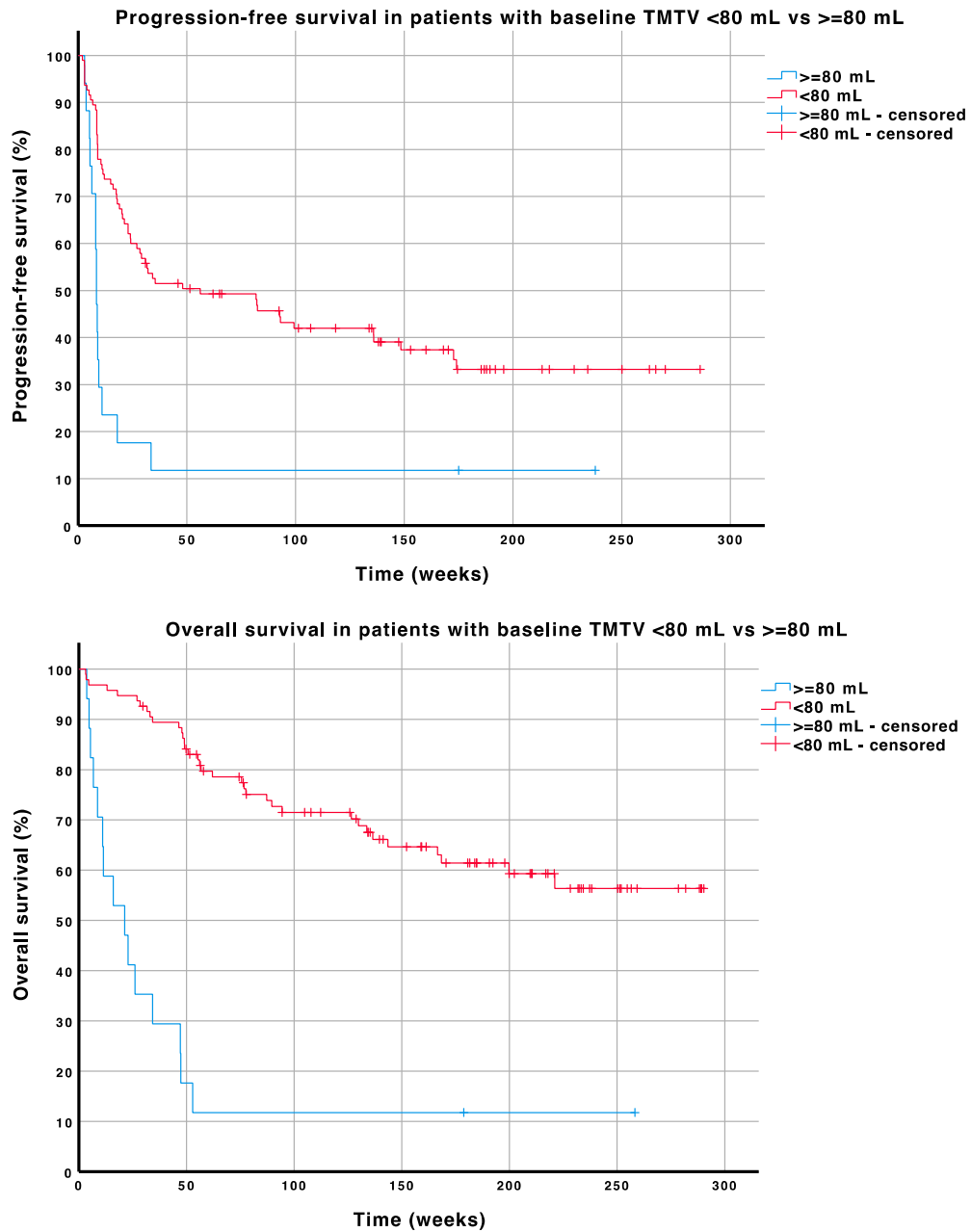


Figure S7. Progression-free and overall survival in the subgroup of patients who underwent baseline imaging with whole-body ^{18}F -FDG-PET/CT with baseline TMTV of <80 mL ($n = 95$) versus ≥ 80 mL ($n = 17$). Abbreviations: ^{18}F -FDG-PET/CT: 18-fluorodeoxyglucose positron emission tomography/computed tomography; TMTV: total metabolic tumor volume.

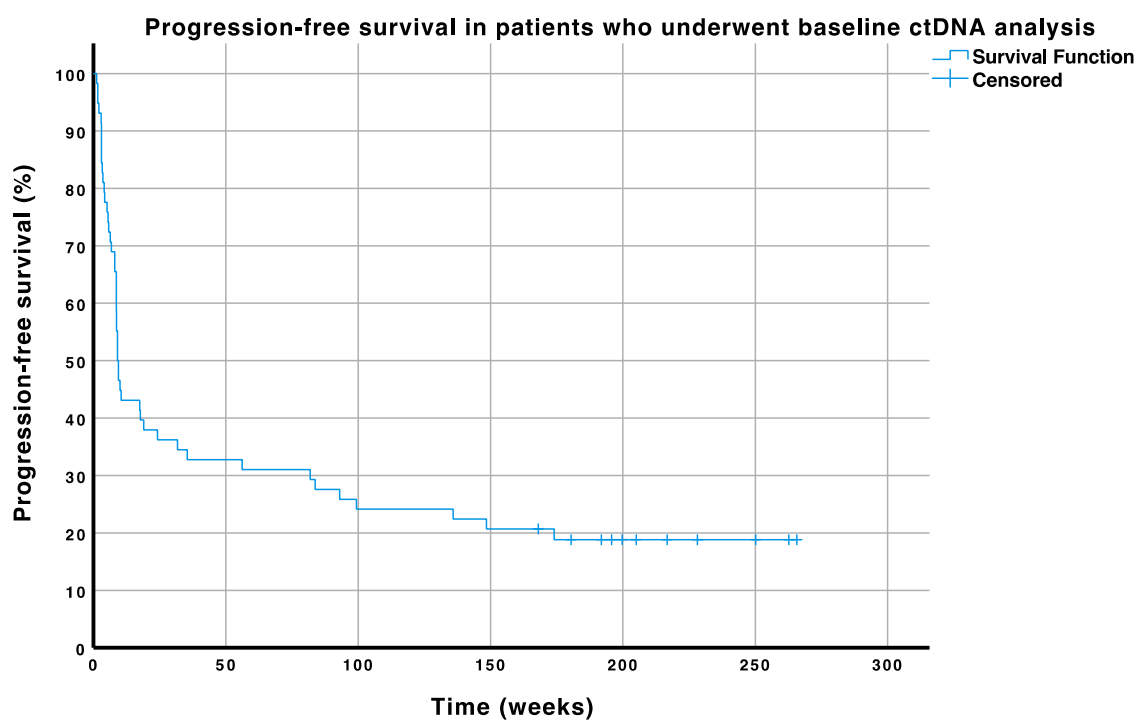


Figure S8. Progression-free survival curve in the subgroup of patients who underwent baseline ctDNA analysis ($n = 58$). Abbreviations: ctDNA: circulating tumor DNA.

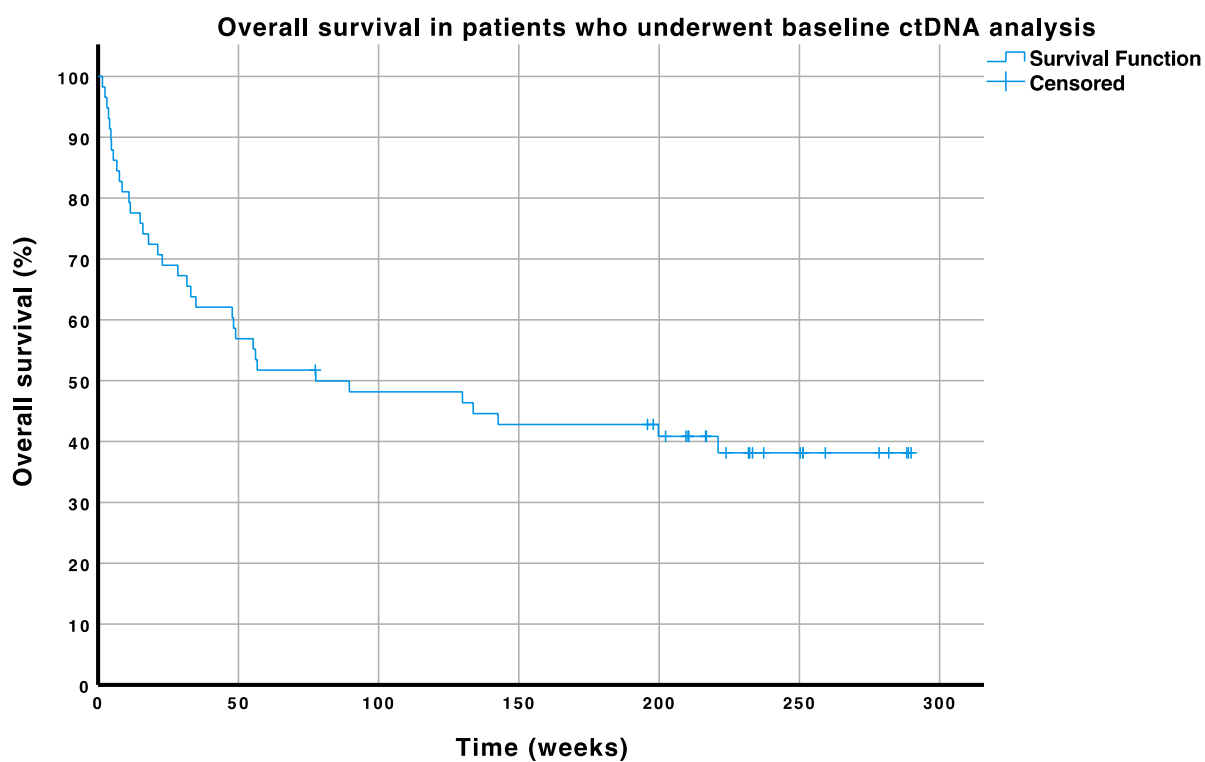


Figure S9. Overall survival curve in the subgroup of patients who underwent baseline ctDNA analysis ($n = 58$). Abbreviations: ctDNA: circulating tumor DNA.



Figure S10. Progression-free survival curve in the subgroup of patients who underwent baseline gene expression profiling on tumor tissue ($n = 27$).

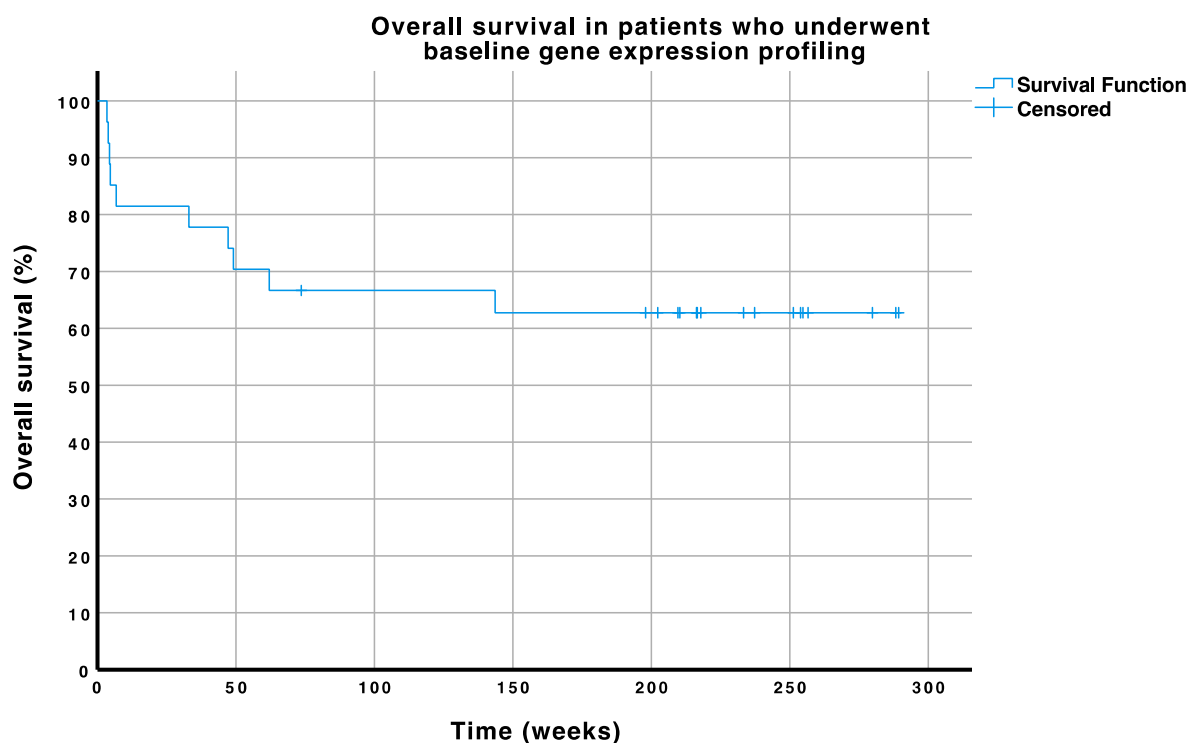


Figure S11. Overall survival curve in the subgroup of patients who underwent baseline gene expression profiling on tumor tissue ($n = 27$).