Supplemental Tables and Figures

Supplemental Table 1a-k. Baseline clinical data and genetic aberrancies by histology

- **Supplemental Table 1a.** Clinical data
- **Supplemental Table 1b.** PTCL-NOS mutations
- **Supplemental Table 1c.** PTCL-NOS CNA
- **Supplemental Table 1d.** AITL mutations
- **Supplemental Table 1e.** AITL CNA
- **Supplemental Table 1f.** PTCL-TFH mutations
- **Supplemental Table 1g.** PTCL-TFH CNA
- **Supplemental Table 1h.** ALCL mutations
- **Supplemental Table 1i.** ALCL CNA
- **Supplemental Table 1j.** MEITL mutations
- **Supplemental Table 1k.** MEITL CNA

[Data in spreadsheet]

PTCL, peripheral T-cell lymphomas; NOS, not otherwise specified; CNA, copy number alteration; AITL, angioimmunoblastic T-cell lymphoma; TFH, follicular T-helper cell phenotype; ALK, anaplastic lymphoma kinase; ALCL, anaplastic large cell lymphoma; MEITL, monomorphic epitheliotropic T-cell lymphoma; M, male; F, female; Y, yes; N, no; BMB, bone marrow biopsy; LDH, lactate dehydrogenase; ECOG, Eastern Cooperative Oncology Group Performance Status; ASCT, autologous stem-cell transplant; PFS, progression-free survival; MSK-IMPACT, Memorial Sloan Kettering Cancer Center Integrated Mutation Profiling of Actionable Cancer Targets; LN, lymph node; BM, bone marrow; Pos, position; Ref, reference; Var, variant; HGVSg, Human Genome Variation Society gene; AA, dominant allele; DEL, deletion; INS, insertion; SNP, single nucleotide polymorphism; DeepDel, deep deletion; AMP, amplification; Freq, frequency; OncoKB, Oncology Knowledge Base

Supplemental Table 2. Responses and survival among the 3 cohorts

	Entire cohort (N=132)	CCD cohort (n=87)	Prospective cohort (n=72)	*P*
Response at EOT, n (%)				.59
Complete response	82 (62)	58 (67)	53 (74)	
Partial response	9 (7)	5 (6)	4 (6)	
Progressive disease	41 (31)	24 (28)	15 (21)	
Median follow-up among survivors in months (range)	26 (2-118)	23 (2-118)	24 (6-118)	.92
1-year PFS (%) (95% CI)	45.0 (37.0-54.0)	49.0 (39.0-61.0)	59.0 (48.0-72.0)	.06
2-year PFS (%) (95% CI)	28.0 (21.0-38.0)	34.0 (25.0-47.0)	43.0 (32.0-58.0)	Entire vs CCD cohort (*P*=.27)
Median PFS, months (95% CI)	9.4 (7.3-13.9)	10.8 (7.8-20.1)	19.1 (10.8-40.7)	Entire vs prospective (***P*=.02**)
				CCD vs prospective (*P*=.19)
1-year OS (%) (95% CI)	88.0 (83.0-94.0)	89.0 (82.0-96.0)	88.0 (80.0-96.0)	
2-year OS (%) (95% CI)	74.0 (66.0-82.0)	73.0 (63.0-84.0)	77.0 (66.0-88.0)	
Median OS, months (95% CI)	53.2 (42.5-70.7)	56.7 (44.6-NR)	NR (45.9-NR)	.57

EOT; end of curative-intent treatment; PFS, progression-free survival; OS, overall survival; NR, not reached

Supplemental Table 3. Survival of entire cohort stratified by *TP53* mutation and *CDKN2A* copy number status

ENTIRE COHORT (N=132)	*TP53*-mutated (n=21)	*TP53*-unmutated (n=111)	*P*	*CDKN2A*-deleted (n=9)	*CDKN2A*-not deleted (n=123)	*P*
Median follow-up among survivors in months (range)	20.0 (3.0-89.0)	27.0 (6.0-118.0)	.36	26.0 (3.0-118.0)	26.0 (6.0-38.0)	.56
1-year PFS (%) (95% CI)	29.0 (15.0-56.0)	48.0 (39.0-58.0)		11.0 (2.0-71.0)	47.0 (39.0-57.0)	
2-year PFS (%) (95% CI)	10.0 (3.0-36.0)	32.0 (24.0-43.0)		11.0 (2.0-71.0)	30.0 (22.0-40.0)	
Median PFS, months (95% CI)	4.5 (3.8-13.9)	10.5 (7.8-18.1)	**<.001**	5.0 (2.6-NR)	9.8 (7.5-16.4)	.06
Cox regression						
HR (95% CI)	2.3 (1.4-3.8)	1	**.001**	2.0 (1.0-4.1)	1	.06
1-year OS (%) (95% CI)	84.0 (70.0-100.0)	89.0 (83.0-95.0)		76.0 (52.0-100.0)	89.0 (84.0-95.0)	
2-year OS (%) (95% CI)	77.0 (60.0-100.0)	73.0 (64.0-83.0)		38.0 (16.0-92.0)	76.0 (68.0-85.0)	
Median OS, months (95% CI)	48.2 (29.2-NR)	53.2 (42.3-71.0)	.98	17.6 (12.8-NR)	56.7 (44.6-101.0)	**.004**
Cox regression						
HR (95% CI)	1.0 (0.5-2.1)	1	0.98	3.3 (1.4-8.0)	1	**.007**

PFS, progression-free survival; OS, overall survival; NR, not reached

Supplemental Table 4. Survival of prospective cohort stratified by *TP53* mutation and *CDKN2A* copy number status

Prospective cohort (n=72)	*TP53*-mutated (n=7)	*TP53*-unmutated (n=65)	*P*	*CDKN2A*-deleted (n=4)	*CDKN2A*-not deleted (n=68)	*P*
Median follow-up among survivors in months (range)	31.0 (12.0-67.0)	24.0 (6.0-118.0)	.50	22.0 (6.0-38.0)	24.0 (6.0-118.0)	.>.99
1-year PFS (%) (95% CI)	43.0 (18.0-100.0)	61.0 (49.0-74.0)		25.0 (5.0-100.0)	61.0 (50.0-74.0)	
2-year PFS (%) (95% CI)	0.0	47.0 (35.0-6.03)		25.0 (5.0-100.0)	44.0 (32.0-60.0)	
Median PFS, months (95% CI)	4.1 (2.8-NR)	19.7 (10.8-72.3)	**.02**	2.2 (1.3-NR)	19.1 (12.2-40.7)	.09
Cox regression						
HR (95% CI)	2.8 (1.2-6.7)	1.0	**.02**	2.7 (0.8-8.9)	1	.10
1-year OS (%) (95% CI)	86.0 (63.0-100.0)	88.0 (80-97)		75.0 (43.0-100.0)	88.0 (81.0-97.0)	
2-year OS (%) (95% CI)	86.0 (63.0-100.0)	76 (65-88)		38.0 (8.0-100.0)	79.0 (68.0-90.0)	
Median OS, months (95% CI)	NR (NA-NA)	58.7 (45.9-NR)	.37	12.8 (5.3-NR)	NR (56.7-NR)	.07
Cox regression						
HR (95% CI)	0.4 (0.1-3.1)	1.0	.39	3.6 (0.8-15.9)	1.0	.09

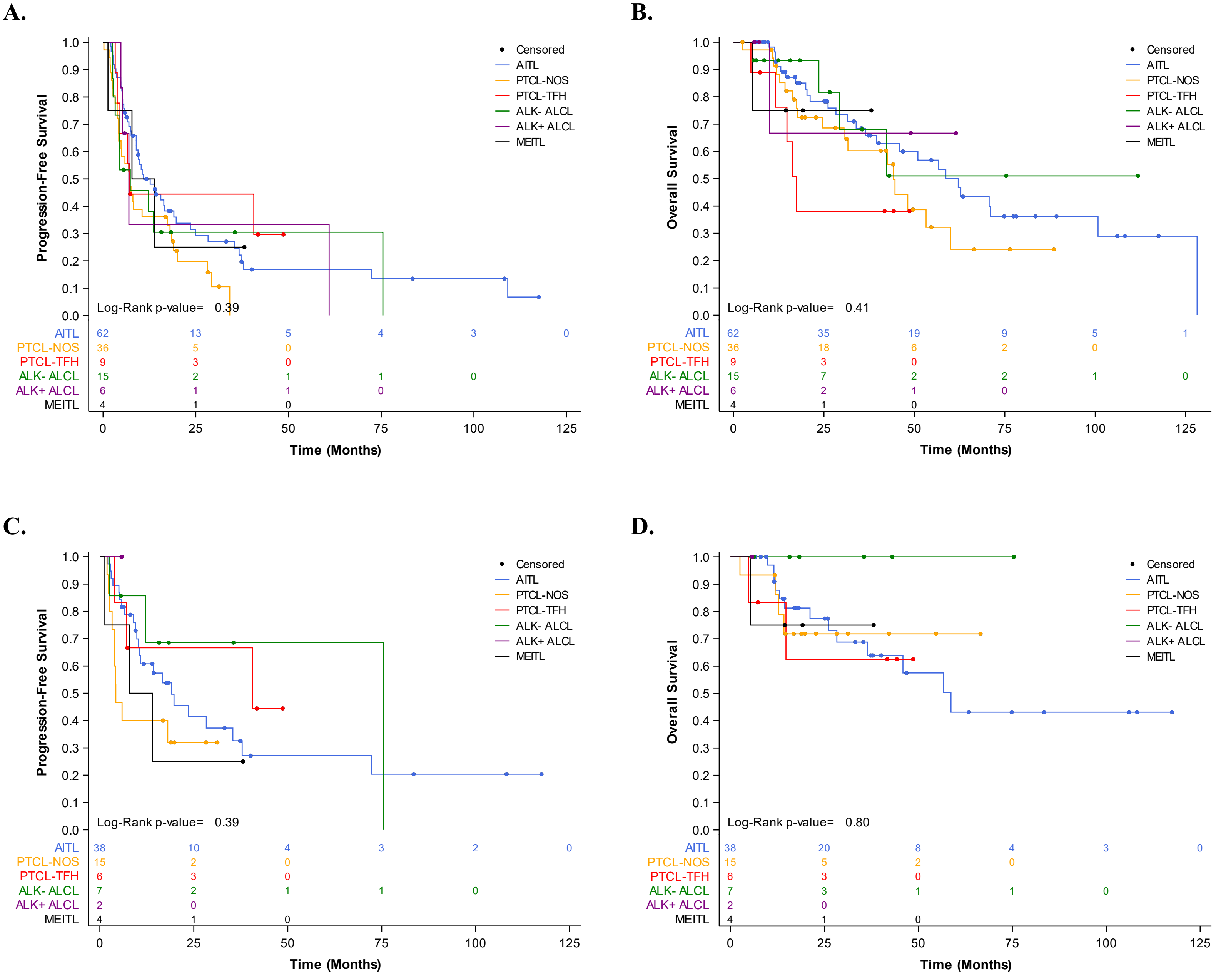
PFS, progression-free survival; OS, overall survival; NR, not reached; NA, not applicable

Supplemental Table 5. Survival of patients with non-AITL-PTCL in entire cohort stratified by *TP53* mutation and *CDKN2A* copy number status

Entire cohort excluding AITL (n=70)	*TP53*-mutated (n=19)	*TP53*-unmutated (n=51)	*P*	*CDKN2A*-deleted (n=8)	*CDKN2A* not deleted (n=62)	*P*
Median follow-up among survivors in months (range)	14.5 (2.5-88.5)	29.8 (5.6-112.0)	.34	22.2 (6.3-38.1)	26.6 (2.5-112.0)	.97
1-year PFS (%) (95% CI)	32.0 (16.0-61.0)	42.0 (30.0-59.0)		13.0 (2.0-78.0)	43.0 (32.0-58.0)	
2-year PFS (%) (95% CI)	11.0 (3.0-39.0)	32.0 (21.0-49.0)		13.0 (2.0-78.0)	27.0 (17.0-42.0)	
Median PFS, months (95% CI)	4.5 (4.1-17.4)	7.8 (7.1-20.1)	**.02**	3.8 (2.6-NR)	7.5 (6.8-18.1)	.11
Cox regression						
HR (95% CI)	2.0 (1.1-3.6)	1.0	**.02**	1.9 (0.8-4.2)	1.0	.12
1-year OS (%) (95% CI)	83.0 (66.0-100.0)	87.0 (78.0-97.0)		73.0 (47.0-100.0)	88.0 (79.0-97.0)	
2-year OS (%) (95% CI)	74.0 (55.0-100.0)	68.0 (55.0-84.0)		29.0 (9.0-93.0)	75.0 (64.0-88.0)	
Median OS, months (95% CI)	44.6 (24.7-NR)	44.2 (31.6-NR)	.86	17.4 (11.1-NR)	48.2 (42.5-NR)	**.004**
Cox regression						
HR (95% CI)	1.1 (0.5-2.4)	1.0	.86	3.6 (1.4-9.2)	1.0	**.007**

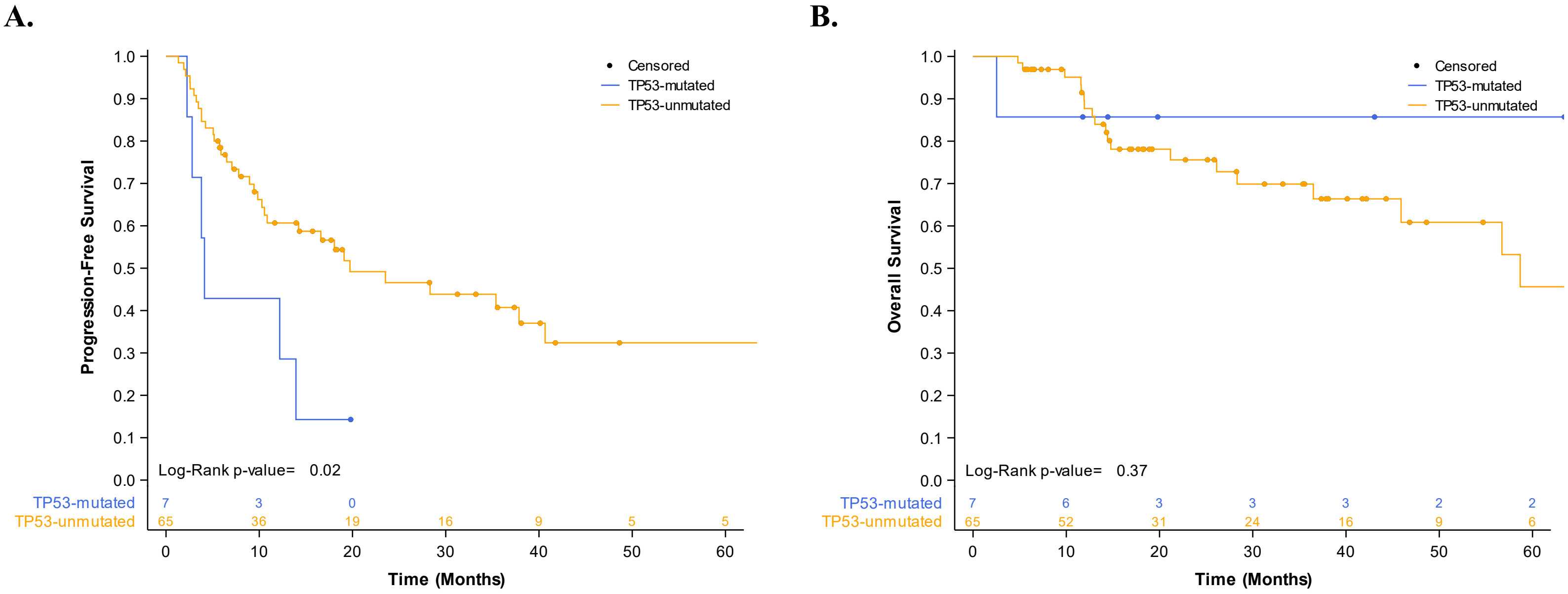
PFS, progression-free survival; OS, overall survival; NR, not reached

Supplemental Figure 1



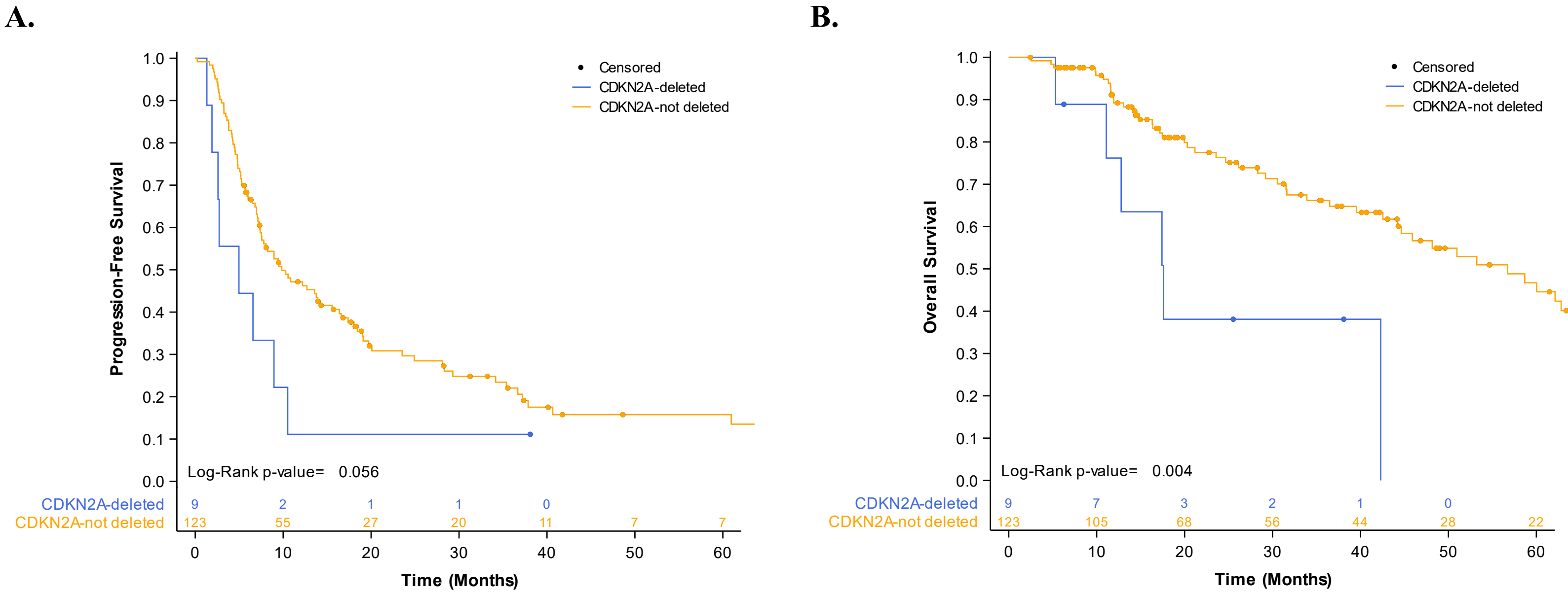
Kaplan-Meier survival curves by histology. (A) Progression-free survival (PFS) and **(B)** overall survival (OS) of entire cohort. **(C)** PFS and **(D)** OS of the prospective cohort. Living patients were censored at time of last follow-up (filled circles). The number of patients at risk at each time point is noted.

Supplemental Figure 2



Kaplan-Meier survival curves of the prospective cohort (n=72) stratified by *TP53* mutation status. **(A)** Progression-free survival and **(B)** overall survival. Living patients were censored at the time of last follow-up (filled circles). The number of patients at risk at each time point is noted.

Supplemental Figure 3:



Kaplan-Meier survival curves for entire cohort (N=132) stratified by *CDKN2A* copy number status. (A) Progression-free survival and **(B)** overall survival. Living patients were censored at time of last follow-up (filled circles). The number of patients at risk at each time point is noted.

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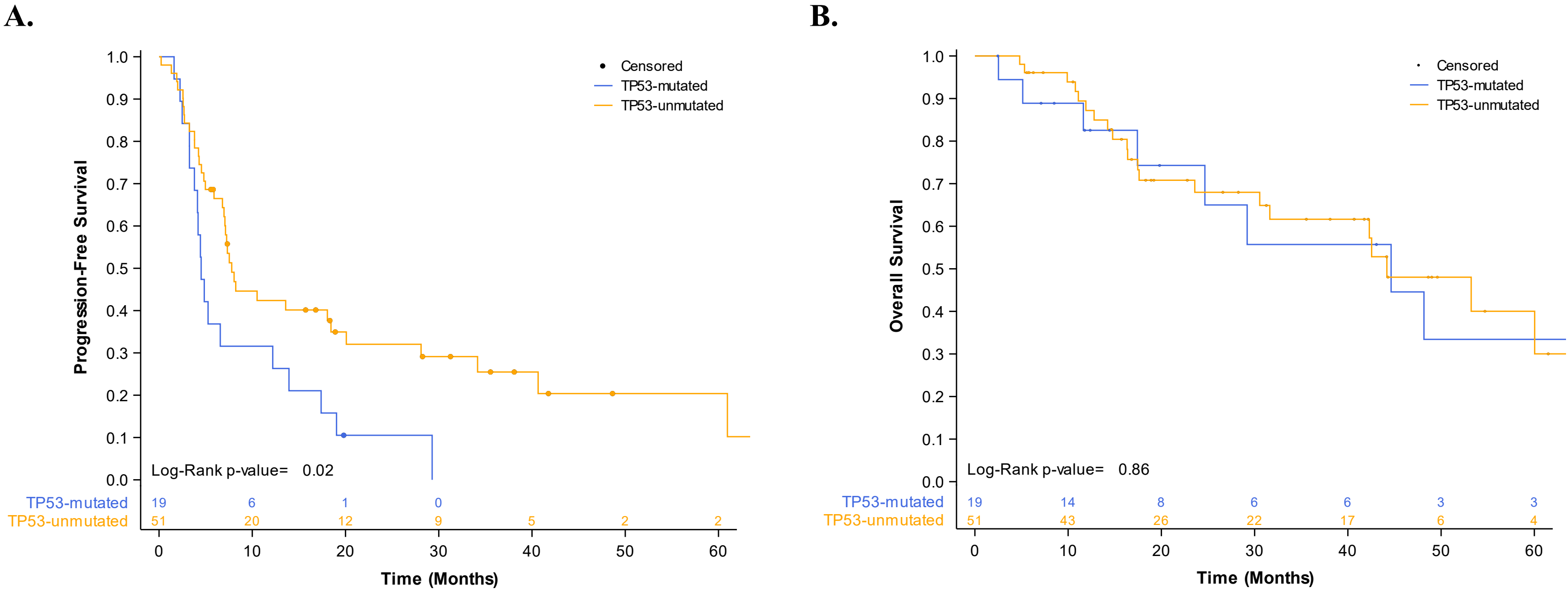
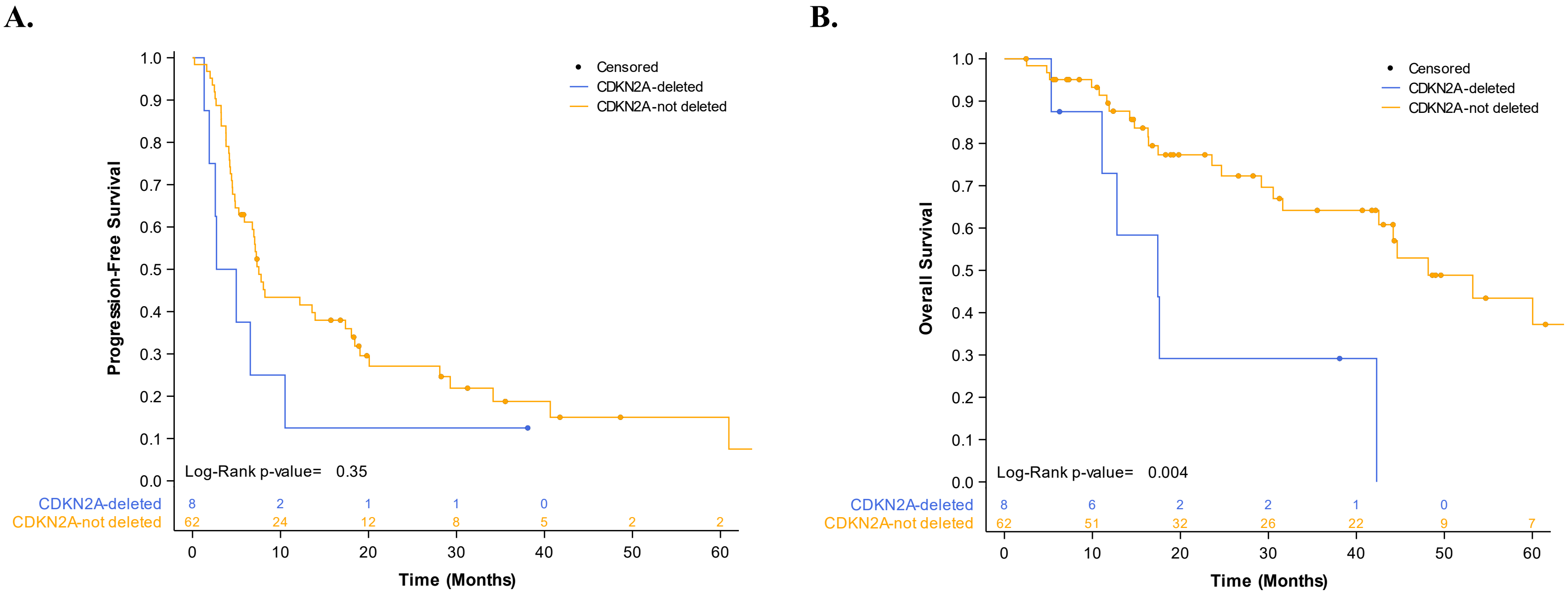
Supplemental Figure 4



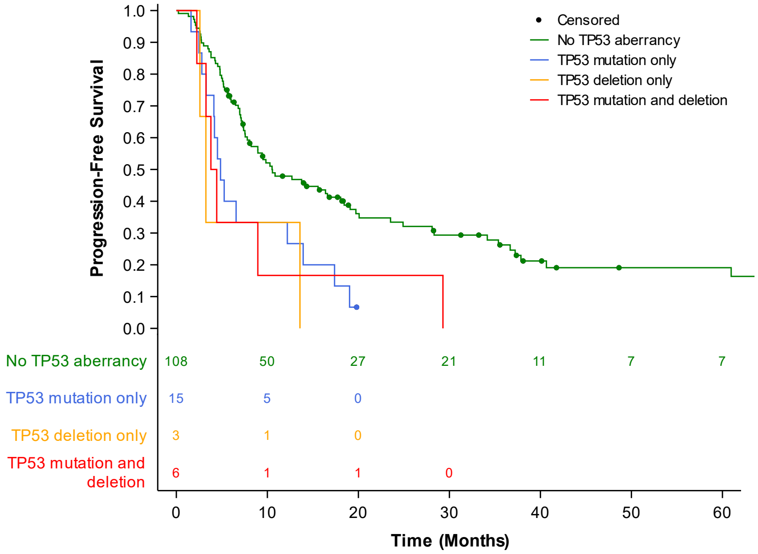
Kaplan-Meier survival curves for patients with non-angioimmunoblastic T-cell lymphoma (AITL)-peripheral T-cell lymphoma (PTCL; n=70) stratified by *TP53* mutation status. (A) Progression-free survival and **(B)** overall survival. Living patients were censored at time of last follow-up (filled circles). The number of patients at risk at each time point is noted.

Supplemental Figure 5



Kaplan-Meier survival curves for patients with non-AITL-PTCL (n=70) stratified by *CDKN2A* copy number status. (A) Progression-free survival and **(B)** overall survival. Living patients were censored at time of last follow-up (filled circles). The number of patients at risk at each time point is noted.

Supplemental Figure 6



Kaplan-Meier survival curve of progression-free survival for entire cohort (N=132) stratified by *TP53* mutation and copy number status. Living patients were censored at time of last follow-up (filled circles). The number of patients at risk at each time point is noted.