

Immune infiltration in p53abn endometrial carcinomas

Authors

Abstract

TODO: Nice abstract

Keywords: Endometrial cancer, p53, Immune

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0.1. Introduction

Endometrial cancer is the second most common type of gynecologic malignancy worldwide and the most common gynecologic malignancy in North America [1]. Molecular classification has separated endometrial cancers into 4 prognostically distinct subtypes: POLE (polymerase epsilon-mutated), MMRd (mismatch repair-deficient), p53abn (p53 abnormal) and NSMP (no specific molecular profile, [2, 3, 4, 5]). p53abn cancers, the worst prognostic subtype, comprise only 15% of all endometrial cancers but account for 50-70% of mortalities [3, 6, 7, 8], with extrauterine involvement in over 50% of cases [5, 9]. Most patients recur within five years on standard-of-care carboplatin-paclitaxel chemotherapy with or without radiotherapy, highlighting the need for alternative therapeutic options [6, 10, 7].

Increased CD8+ cytotoxic T and CD4+ helper T tumor-infiltrating lymphocytes (TILs) are associated with longer overall and recurrence-free survival in endometrial cancer [11], while immunosuppressive regulatory T cells are associated with shorter survival [12]. TILs are known to respond to and track tumor-associated antigens [13] to eradicate cancer cells. In response, cancer cells activate immunosuppressive pathways, including the immune checkpoint molecule programmed death-ligand 1 (PD-L1), to evade immune surveillance [14]. Treatment with immune checkpoint inhibitors reactivates exhausted T cells and is particularly effective in tumors with many neoantigens due to high mutational burden [14]. In endometrial cancer, POLE and MMRd tumors have over 10 times as many mutations as p53abn and NSMP tumors [2] and correspondingly higher TIL densities [15]. While systemic therapy is typically unnecessary

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in POLE cancers due to exceptionally favorable outcomes with hysterectomy alone, anti-PD1 immune-checkpoint inhibitors have demonstrated promising efficacy in advanced, recurrent, or persistent MMRd endometrial cancers after multiple lines of therapy [16, 17].

More recently, [18] showed that the anti-PD1 antibody dostarlimab was associated with significantly improved outcomes not only in MMRd but also MMRp (MMR proficient, non-POLE) endometrial cancer when added to standard-of-care chemotherapy. While the benefit of dostarlimab in MMRp cancers was less than in MMRd cancers, subgroup analysis showed that the benefit in MMRp was driven by p53abn cases [19]. These findings contrast to those observed in high-grade serous ovarian cancer (HGSC), a p53-mutated gynecologic cancer with similar histologic and genomic characteristics to p53abn endometrial cancer [2], where despite well-documented correlations between TIL and prolonged survival [20, 21, 22] immune checkpoint inhibition has shown limited efficacy [23, 24, 25]. The factors underlying this promising response to immune checkpoint inhibitors in p53abn endometrial cancer remain poorly understood.

PARP inhibitors are another class of targeted therapies under investigation in p53abn endometrial cancer [26]. Spurred by remarkable clinical responses in HGSC [27], PARP inhibitors have become standard-of-care in *BRCA1/BRCA2*-mutated or homologous recombination deficient (HRD) cancers across multiple cancer types [28]. Compared to HGSC, HRD is less common in p53abn endometrial cancer, with approximately 25% of cases showing evidence of HRD and fewer than 5% with *BRCA* mutations [29]. In HGSC, HRD tumors have higher immunogenicity than non-HRD tumors, and markers of adaptive immunity are associated with longer overall survival in HRD but not non-HRD tumors [30]. Understanding the relationship between HRD and the immune microenvironment in p53abn endometrial cancers may help inform combination PARP inhibitor and immunotherapy clinical trials [31].

To understand the clinical relevance of TILs in p53abn endometrial cancer, we systematically profiled the immune microenvironment of 256 clinically annotated p53abn endometrial cancers with multiplex immunofluorescence. We evaluated the expression patterns of PD1, PDL1 and IDO1, three pharmacologically actionable immunosuppressive molecules with translational relevance to current clinical trials in endometrial cancer. Finally, we investigated the relationship between TILs, homologous recombination deficiency, and HER2 in p53abn endometrial cancer.

0.2. Methods

0.2.1. Data acquisition

0.2.1.1. Sample acquisition.

Ethics approval for this study was obtained from the University of British Columbia (UBC) Research Ethics Board (REB NUMBERS). The cohort consisted of 256 treatment-naive p53-abnormal endometrial carcinomas collected

between XXXX and XXXX in Vancouver and in the Cross Canada endometrial cancer cohort. CONSENT? Clinicopathologic and outcome data were collected by chart review.

0.2.2. Experimental methods

0.2.2.1. Tissue microarray construction.

Representative samples of endometrial carcinomas from our Vancouver cohort were cored (0.6 mm) in duplicate and arrayed as described previously ([3]). CROSS CANADA COHORT? TMAs were cut at WHAT thickness for immunofluorescence.

0.2.2.2. Multiplex immunofluorescence.

TODO.

0.2.3. Computational analysis

0.2.3.1. Cell and region counting.

Two multiplex immunofluorescence panels to classify TIL types (CD3, CD8, FOXP3, CD20, CD79a) and quantify immunosuppressive markers (PD1, PDL1, IDO1, CD8, CD68) were performed on each tissue microarray. For each immunofluorescence panel, 3 tissue segmentation and cell phenotyping algorithms were trained in HALO using 10 representative images for each algorithm. Regions were classified as epithelial, stromal, glass, or other (including necrosis) for tissue segmentation. The mean and standard deviation across all algorithms was calculated for each core, and any cores with a standard deviation of >5 were flagged for manual review by a pathology resident (SM). Final epithelial and stromal areas were calculated by subtracting glass and other areas from tissue area.

Phenotypes were defined according to combinations of positive and negative markers in each cell. Cytotoxic T cells were defined by positivity for both CD3 and CD8, helper T cells by positivity for CD3 and negativity for CD8 and FOXP3, regulatory T cells by CD3 and FOXP3 positivity with CD8 negativity, B cells by positivity for both CD20 and CD79a, and plasma cells by CD79a positivity in the absence of CD20. Cells were classified according to cytoplasmic and/or nuclear positivity for each marker. Each phenotype was scored independently by 3 algorithms, and averages across all algorithms were calculated separately for epithelial and stromal regions. Standard deviations across algorithms of >5 were flagged for manual review by a technologist and pathology resident (SM). All immune cells touching tumor cells were considered epithelial.

0.2.3.2. Mixture modeling of cell counts.

TIL count $y_{i,c,r}$ for a given core i , cell type t , and region (tumour/stroma) r were described as follows:

$$y_{i,t,r} \sim \mathcal{NB}(\mu_{i,t,r}, \alpha_{i,t,r})$$

where the mean $\mu_{i,t,r}$ follows:

$$\begin{aligned}\mu_{i,t,r} &= A_{i,r} z_{c_i,t,r} \\ z_{c_i,t,r} &\sim \text{Gamma}(\bar{\mu}_{t,r}, 100)\end{aligned}$$

where c_i is the inferred cluster of core i , $A_{i,r}$ is the area of region r in core i , and $\bar{\mu}_{t,r}$ is the mean density (count divided by area) value across all cores i . The Gamma distribution was parametrized in terms of a mean and scale parameter, with the scale parameter set to 100 to allow for a fairly uninformed prior.

To reduce the dimensionality of the parameter space, the dispersion parameter $\alpha_{i,t,r}$ was formulated semi-parametrically in terms of a set of Gaussian radial-basis kernels with parameters a_k and b_k , for a specified number of centers \bar{y}_k uniformly distributed between 0 and the maximum number of counts [32, 33], with the default number of centers set equal to 20:

$$\begin{aligned}\alpha_{i,t,r} &= \sum_k a_k \exp(-b_k(z_{c_i,t,r} - \bar{y}_k)^2) \\ a_k &\sim \text{Lognormal}(0, 1) \\ b_k &\sim \text{Lognormal}(0, 1)\end{aligned}$$

where a_k and b_k follow relatively agnostic lognormal priors as above.

Inference was performed in pymc v5.9.1 [34]. To determine the optimal number of clusters $|C|$, a Dirichlet process prior was first fitted to a version of the model marginalized over cluster membership z . At a minimum threshold of 0.05 for cluster proportion, two clusters with proportions of at least 0.05 were inferred (first cluster with mean proportion 0.588, 95% CI 0.512-0.656; second cluster with mean proportion 0.347, 95% CI 0.289-0.407). The lower bound of the 95% CI for the third most prevalent cluster was 0.004 (equivalent to 1 out of the 256 input samples), supporting the presence of only 2 clusters. Thus, the model was fitted with 2 clusters ($|C| = 2$) to sample cluster membership z .

0.2.3.3. Shallow whole-genome copy number analysis.

TODO. In short, sWGS signatures taken from CITE paper, and copy number results for HER2 derived from ...

0.2.3.4. Statistical analysis.

All statistical analysis was performed in R (v4.3.2). The Mann-Whitney U test was used to evaluate significance in two-way comparisons. Comparisons for categorical count data were evaluated for significance with Fisher's exact test. Multiple testing correction was performed with the Holm method. Statistically significant results were considered those with $P < 0.05$.

P values for Kaplan-Meier analyses were computed with log-rank tests. Cox proportional hazards analysis was performed in R with the survival package (v3.5-7). Proportional hazards assumptions were evaluated with weighted Schoenfeld residuals [35]. Posterior distribution samples were used to calculate confidence intervals and P values.

0.2.3.5. Code availability.

Code associated with this project is publicly available at https://github.com/Irrationone/tfri_halo.

0.3. Results

0.3.1. Cohort

We assembled a cohort of 256 treatment-naive p53abn endometrial carcinomas diagnosed between XXXX and XXXX (Table 1, OTHER REF) [15]. All cancers were classified according to ProMisE [3] by p53 and MMR immunohistochemistry in addition to next-generation sequencing for POLE and p53 mutations. Histotypes included were serous (n=136), endometrioid (n=52), carcinosarcoma (n=31), clear cell (n=15), mixed (n=17), undifferentiated/dedifferentiated (n=2) and other (n=3). All patients received treatment in accordance with standard-of-care at the time of diagnosis, with most patients receiving adjuvant chemotherapy and a smaller proportion receiving adjuvant brachytherapy or radiotherapy (Table 1). No patients received immunotherapy.

Source: [Cohort-level analysis](#)

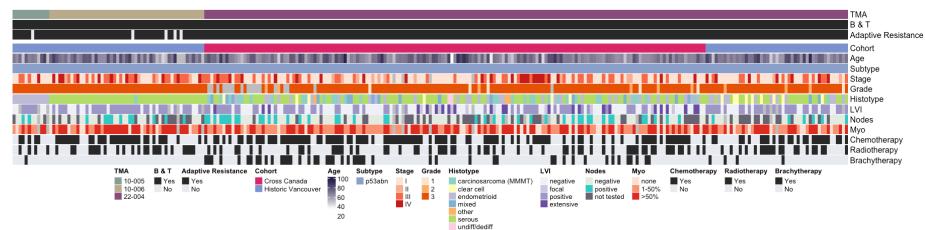


Figure 1: Cohort overview

Source: [Cohort-level analysis](#)

We performed multiplex immunofluorescence and automated image analysis to segment tumors into epithelial (intratumoral) and stromal regions and quantify CD8+ T cells (CD3+CD8+), CD4+ T cells (CD3+CD8-FOXP3-), T regulatory cells (CD3+CD8-FOXP3+), B cells (CD20+CD79a+) and plasma cells (CD20-CD79a+) (Section 0.2). Cells within epithelial and stromal regions were counted separately, and automated counts were manually verified. At least two

Table 1: Cohort statistics

		(a)	Statistic (N=256)
Histotype	carcinosarcoma (MMMT)	31 (12.1%)	
	clear cell	15 (5.9%)	
	endometrioid	52 (20.3%)	
	mixed	17 (6.6%)	
	other	3 (1.2%)	
	serous	136 (53.1%)	
	undiff/dediff	2 (0.8%)	
Age	Mean (SD)	69.8 (9.6)	
	Median (IQR)	69.1 (12.7)	
	Range	35.0 - 94.2	
	Missing	8 (3.1%)	
Stage	I	128 (50.0%)	
	II	15 (5.9%)	
	III	72 (28.1%)	
	IV	37 (14.5%)	
	Missing	4 (1.6%)	
Myoinvasion	none	39 (15.2%)	
	1-50%	90 (35.2%)	
	>50%	117 (45.7%)	
	Missing	10 (3.9%)	
Lymph node status	negative	120 (46.9%)	
	positive	56 (21.9%)	
	not tested	67 (26.2%)	
	Missing	13 (5.1%)	
Lymphovascular invasion	negative	108 (42.2%)	
	positive	102 (39.8%)	
	focal	9 (3.5%)	
	extensive	23 (9.0%)	
	Missing	14 (5.5%)	
Chemotherapy	Yes	150 (58.6%)	
	No	106 (41.4%)	
Radiotherapy	Yes	102 (39.8%)	
	No	154 (60.2%)	
Brachytherapy	Yes	51 (19.9%)	
	No	205 (80.1%)	
	6		

TMA cores were sampled from each tumor to account for spatial heterogeneity. Sarcomatoid areas in carcinosarcomas were considered epithelial. Densities for all cell types in epithelial and stromal regions were highly correlated (Figure S1). Representative H&E and immunofluorescence images with corresponding epithelial-stromal region segmentation and cell type identification results are shown in Figure 2.

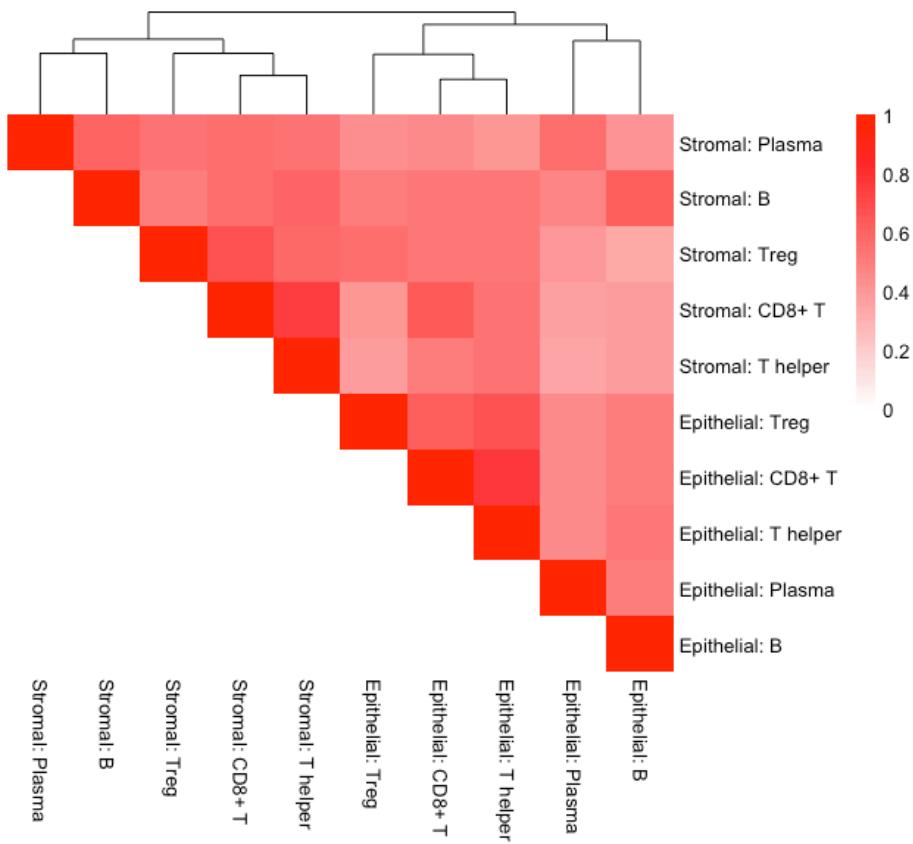


Figure S1

Source: [Clustering results](#)

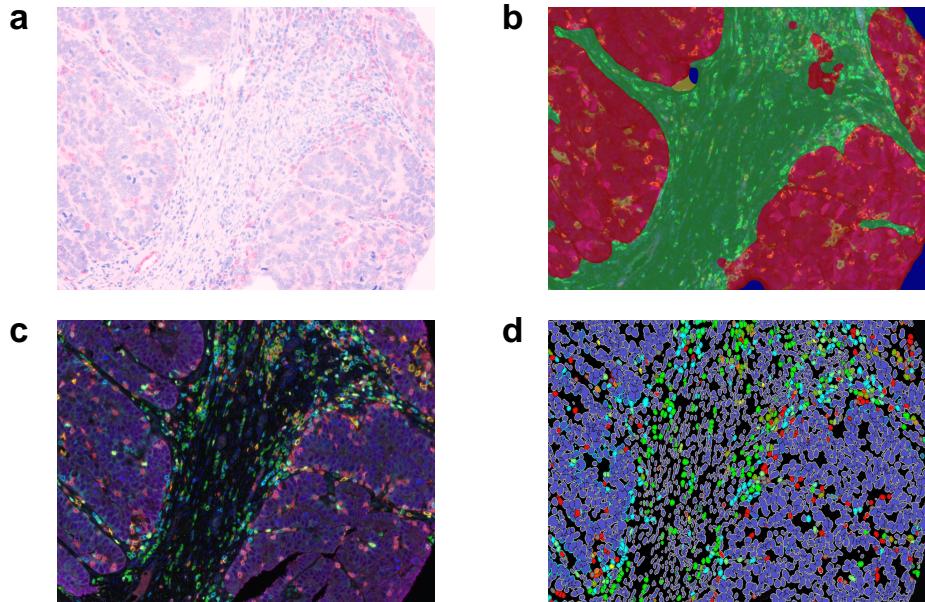


Figure 2

Source: [Article Notebook](#)

0.3.2. TIL-rich tumors are associated with longer survival

Next, we clustered tumors based on epithelial and stromal counts normalized by region area with a negative binomial mixture model. The optimal number of clusters, as determined by a Dirichlet process prior, was two: a TIL-rich and a TIL-poor cluster (Section 0.2). TIL-rich tumors were highly infiltrated by both epithelial and stromal T and B cells, including CD3+CD8+ cytotoxic T cells, CD3+CD8-FOXP3- T helper cells, CD3+CD8-FOXP3+ T regulatory cells, CD79a+CD20+ B cells, and CD79a+CD20- plasma cells. TIL-rich tumors had more stroma than TIL-poor tumors ($P = 1.98e-03$). Vascular density was similar in TIL-rich and TIL-poor tumors ($P = 0.224$). Contrary to observations in high-grade serous ovarian carcinoma, where tumors with both epithelial and stromal TIL are an immunologically and genetically distinct subgroup from those with stroma-restricted TIL [30], we were not able to identify a distinct subgroup of p53abn endometrial cancers with stroma-restricted TIL. However, TIL-rich tumors had significantly higher epithelial but not stromal CD8/Treg ratios, suggestive of tumor-specific T cell activation (Figure 3) [11, 36].

We next assessed whether TIL subgroup was associated with survival. In univariate Kaplan-Meier analyses, there was no significant association between TIL cluster and overall, progression-free, or disease-specific survival (all $P > 0.175$). However, TIL cluster was significantly associated with prolonged overall and disease-specific survival in multivariate Cox proportional-hazards analysis

accounting for age at diagnosis, FIGO stage [37], and adjuvant treatment (Table 2). TIL cluster was also associated with longer progression-free survival, but this was not statistically significant ($P = 0.15$). Age was associated with shorter overall survival. None of the adjuvant treatment modalities tested were significantly associated with longer survival. The discordance in the effect of TIL between univariate and multivariate analyses was at least partially explained by differences between limited and advanced stage disease. Univariate Kaplan-Meier analyses stratified by stage highlighted that the association between TIL cluster and survival was most pronounced in patients with stage III disease (Figure S2). The median 5-year overall survival was 24.9% (95% CI, 9.6%-64.7%) for TIL-poor stage III cancers and 55.2% (95% CI, 38.3%-79.6%) for TIL-rich stage III cancers ($n = 71$). Comparatively, the median 5-year overall survival was 74.9% (95% CI, 61.9%-90.6%) for TIL-poor stage I cancers and 79.1% (95% CI, 67%-93.4%) for TIL-rich stage I cancers ($n = 118$). Neither TIL subgroup nor individual TIL densities were correlated with HER2 status by immunohistochemistry or shallow whole-genome sequencing. Thus, TILs are associated with longer survival in p53abn endometrial carcinoma.

As p53abn endometrial carcinomas represent a mixture of different histotypes, we investigated whether histotype modifies the association between TIL and survival. TIL subgroup was significantly associated with histotype ($P = 6.51e-03$), with most carcinosarcomas falling in the TIL-poor group (23/31), compared to 97/224 of non-carcinosarcoma histotypes (adjusted $P = 0.011$). Other non-serous histotypes were not significantly associated with histotype. To account for the differences in immune composition between carcinosarcomas and other p53abn endometrial cancer histotypes, we included carcinosarcoma as an explanatory variable in our multivariate analysis. The association between TIL subgroup and overall survival remained significant (HR 0.65, 95% CI 0.426-0.989, $P = 0.044$), suggesting that TIL subgroup is prognostic independently of histotype. Carcinosarcomas were associated with shorter overall, progression-free and disease-specific survival, consistent with prior findings [38, 39, 40], but this was not statistically significant (all $P > 0.067$).

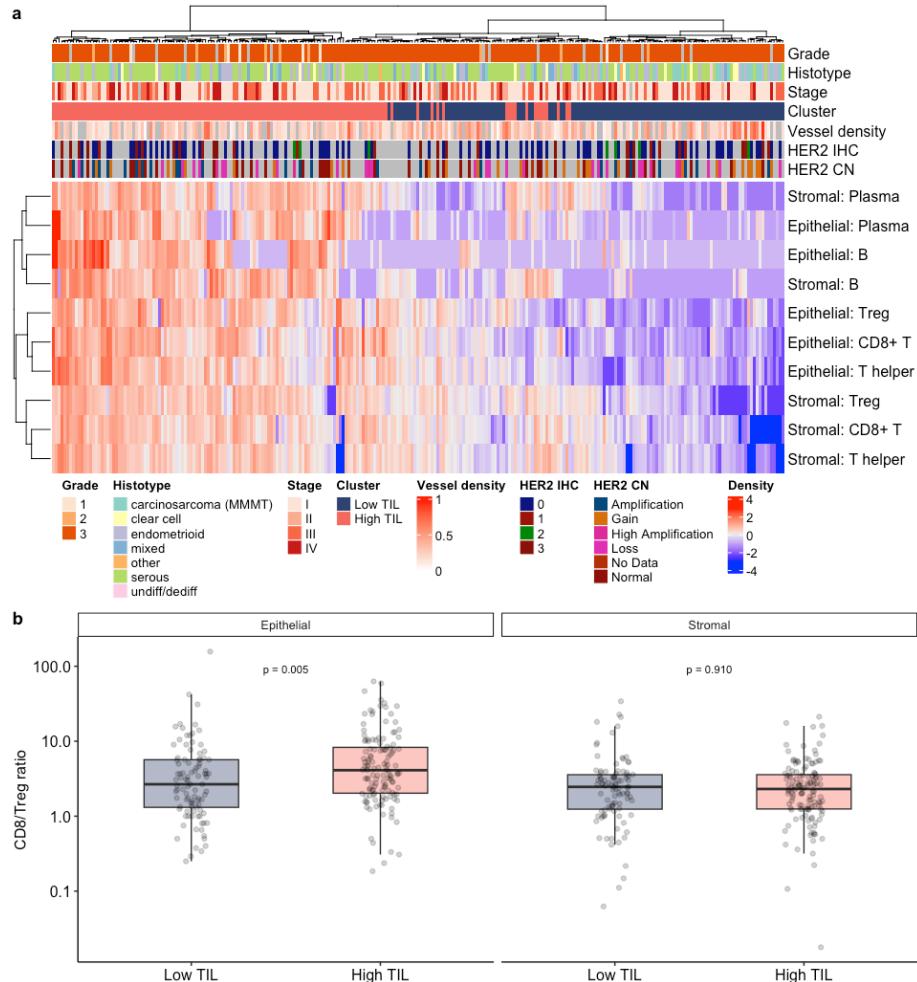


Figure 3: Clusters and association with survival

Source: Clustering results

Source: Clustering results

Source: Clustering results

0.3.3. Overexpression of immune checkpoint molecules in TIL-rich samples

Next, we profiled immune checkpoint expression to determine the extent of exhaustion within the tumor microenvironment. Consistent with our previous findings [15], TIL-rich tumors contained more CD8+PD1+ and CD8+PD1- T cells (Figure 4). Additionally, there was relative enrichment of PD1+ cytotoxic T cells, suggestive of T cell exhaustion (Figure 4).

Table 2: Cox hazards table

Characteristic	(a)								
	Overall survival			Progression-free survival			Disease-specific survival		
	HR ¹	95% CI ¹	p-value	HR ¹	95% CI ¹	p-value	HR ¹	95% CI ¹	p-value
Age	1.02	0.99, 1.04	0.14	1.00	0.98, 1.03	0.7	1.01	0.98, 1.03	0.6
TIL	0.63	0.42, 0.96	0.031	0.74	0.49, 1.12	0.2	0.58	0.35, 0.97	0.037
Chemotherapy	0.58	0.34, 0.98	0.041	0.98	0.57, 1.68	>0.9	0.69	0.36, 1.34	0.3
Radiotherapy	0.82	0.48, 1.43	0.5	0.83	0.50, 1.38	0.5	0.95	0.49, 1.85	0.9
Brachytherapy	1.10	0.54, 2.23	0.8	1.08	0.61, 1.93	0.8	1.16	0.52, 2.58	0.7
Stage									
I	—	—		—	—		—	—	
II	2.58	0.73, 9.06	0.14	1.05	0.24, 4.58	>0.9	1.68	0.21, 13.6	0.6
III	3.39	1.94, 5.94	<0.001	4.19	2.48, 7.08	<0.001	5.27	2.54, 10.9	<0.001
IV	11.0	5.84, 20.7	<0.001	9.10	4.86, 17.1	<0.001	16.6	7.54, 36.5	<0.001

¹HR = Hazard Ratio, CI = Confidence Interval

PDL1 is expressed by both tumor and immune cells, particularly macrophages, and binds to PD1 on T cells to suppress the immune response [41]. Mirroring the pattern seen with PD1 in cytotoxic T cells, PDL1-positive macrophages were enriched in TIL-rich tumors (Figure 4). In contrast, there was no significant difference in PDL1-negative macrophages between TIL-rich and TIL-poor tumors, irrespective of IDO1 status. However, tumor cell expression of PDL1 and IDO1, both individually and in combination, was significantly higher in TIL-rich tumors compared to TIL-poor tumors (Figure 4). Neither PDL1 nor IDO1 expression in tumor cells or macrophages was significantly associated with longer survival on multivariate analysis (all $P > 0.3$). Our results highlight upregulation of immunosuppressive molecules in TIL-rich p53-abnormal endometrial carcinomas which may be therapeutically exploitable with immunotherapy.

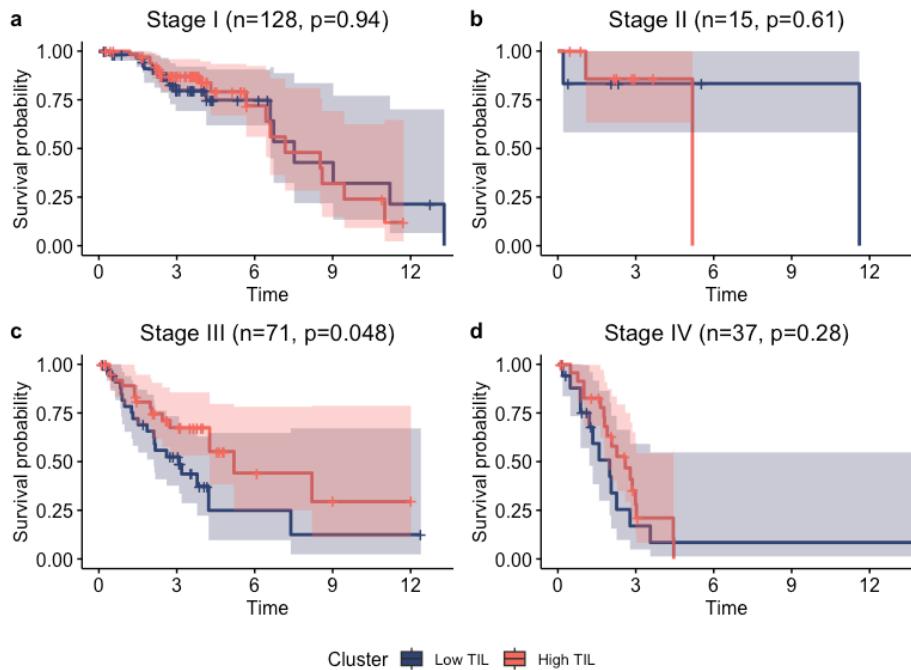
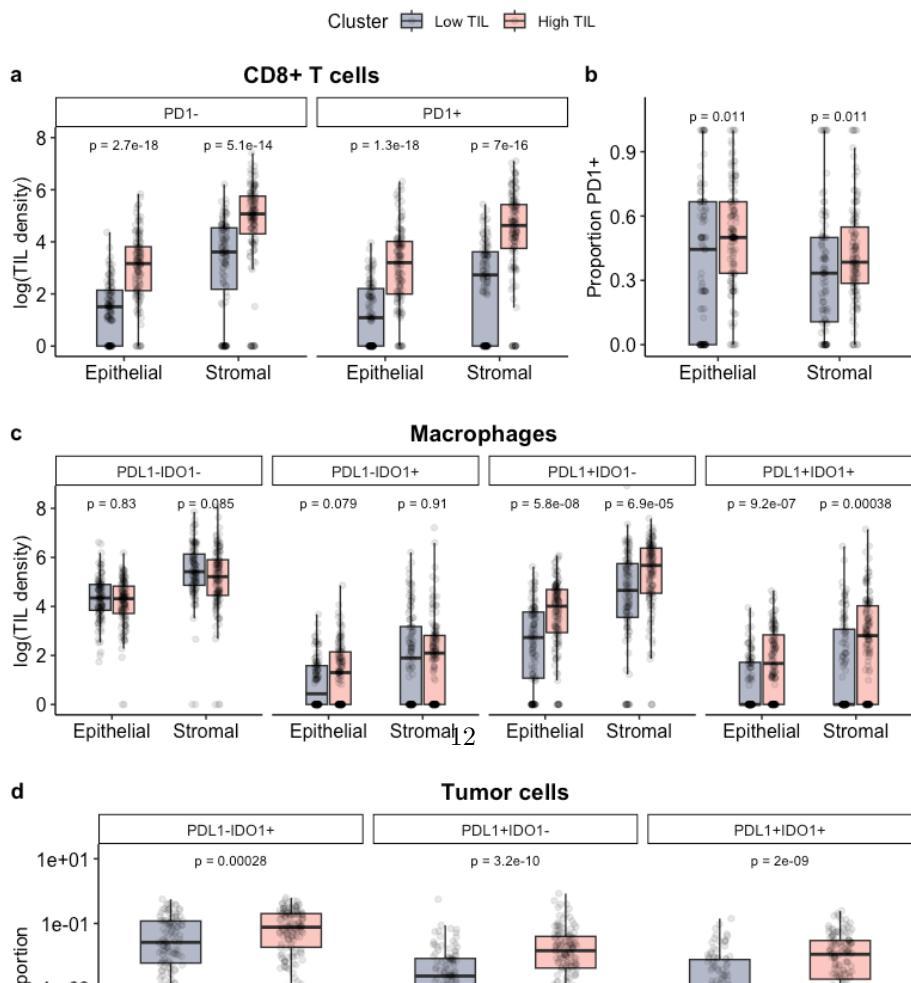


Figure S2



Source: Adaptive response

0.3.4. Mutational signatures and TILs in endometrial cancer

Finally, we evaluated the relationship between TIL subgroups and mutational processes. Using shallow whole genome sequencing data-derived copy number signatures that we previously described in endometrial cancer [CITE], we correlated signature exposures to TIL subgroup for n=126 p53abn endometrial carcinomas. None of the copy number signatures, including the HRD signature VS3 (CHECK WITH DAWN), were significantly associated with TIL subgroup in p53abn endometrial carcinoma. Densities for individual TIL types in epithelial and stromal regions were not significantly correlated with any mutational signature, and none of the mutational signature exposures were significantly associated with survival in multivariate Cox analyses including TIL cluster. Thus, mutational signatures show different patterns of co-segregation with TILs and prognostic significance in p53abn endometrial carcinoma compared to HGSC [30].

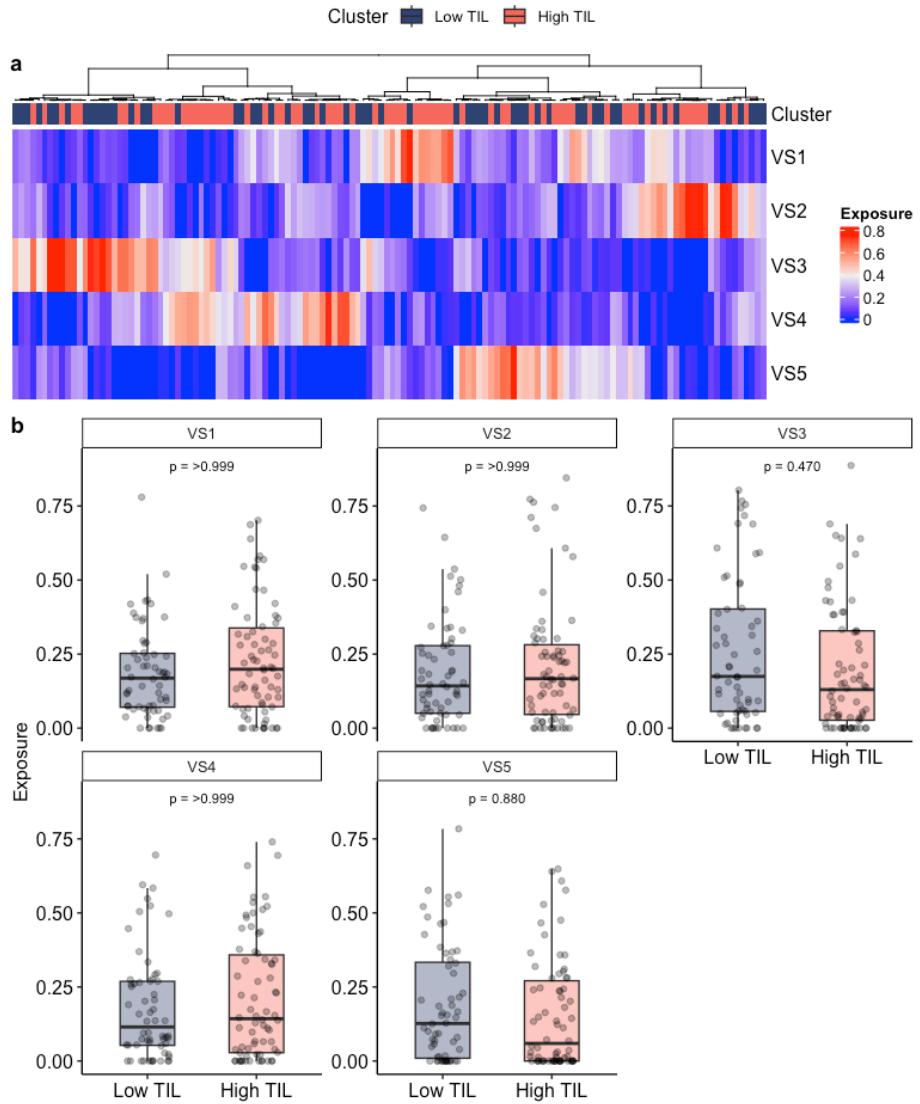


Figure 5: Mutational signatures

Source: [Mutational signatures](#)

0.4. Discussion

Historically considered one of the less immunogenic subtypes of endometrial cancer, p53abn tumors have received minimal attention in immunotherapy research. Initial trials showed only modest response rates to pembrolizumab in

advanced and recurrent MMRp endometrial cancer [10], mirroring similar results in epithelial ovarian cancer [25]. More recently, dostarlimab in addition to standard-of-care chemotherapy demonstrated benefit in both MMRd and MMRp cancers [18], with p53abn cases responding substantially better than NSMP cases [19]. We systemically profiled the immune microenvironment in one of the largest cohorts of p53abn endometrial cancers to date, revealing 2 immunologically distinct subgroups defined by extensive and limited infiltration of T cells, B cells, and macrophages. Over half of p53abn cancers are highly infiltrated by TIL, challenging the belief that p53abn cancers are immune depleted [42]. Cytotoxic T cells, but not immunosuppressive T regulatory cells, co-localized with tumor cells in TIL-rich tumors. TIL-rich tumors expressed high levels of PD1 and PDL1, providing mechanistic rationale for the effectiveness of anti-PD1 inhibitors. TIL-rich tumors were also associated with longer overall and disease-specific survival, in contrast to prior findings in smaller cohorts [15]. Notably, TILs were more strongly associated with survival in patients with advanced disease, who have the most presing treatment requirements. These findings may inform clinical trials of immunotherapies in early-stage endometrial cancer (NCT04634877, NCT04214067), where TILs were not significantly associated with longer survival.

The pervasiveness of TIL-rich p53abn endometrial cancers underscores potential shortcomings of molecular subtype-based strategies for selecting patients for immunotherapy [10, 43]. While TIL-rich tumors are more frequent in MMRd (78% [15]) than other subtypes, 53% of p53abn tumors in our study were also TIL-rich. Histotype likely has limited importance, as apart from carcinosarcomas, which were mostly TIL-poor, histotype was not associated with TIL status. NSMP, the most TIL-poor molecular subtype [15, 44], derived correspondingly limited benefit from dostarlimab in the RUBY trial [19]. Thus, TIL response, not molecular subtype alone, may be more informative for stratifying endometrial cancer patients for immunotherapy.

In our study, IDO1 expression was not associated with TIL-rich tumors, contrasting with PD1 and PDL1 expression patterns. This may indicate a different mechanism for IDO1 induction in the tumor microenvironment. While IDO1+ macrophages were less prevalent than PDL1+ macrophages, their presence irrespective of overall TIL infiltration may make IDO1 a suitable target for immunotherapy in a subset of TIL-poor tumors.

Our data show for the first time the relationship between immune response and mutational processes in p53abn endometrial cancer. Despite genomic similarities between HGSC and p53abn endometrial cancer [2, 30], TILs were not correlated with mutational signatures, including HRD, in p53abn endometrial cancer. In contrast to HGSC, p53abn endometrial cancer may elicit TIL responses through mechanisms independent of HRD. Other mutational processes generating widespread genomic instability in endometrial cancer [CITE DAWN] may elicit TIL responses through common cGAS-STING pathway activation [45, 46]. Additionally, TILs were not correlated with HER2 status by immunohistochem-

istry or whole-genome sequencing. Immunotherapies, anti-HER2 therapies, and PARP inhibitors targeting HRD tumors may represent orthogonal approaches effective in different groups of p53abn endometrial cancers, with some tumors susceptible to multiple agents.

As the use of immunotherapies extends to MMRp endometrial cancers, the immune microenvironment must be considered in addition to molecular subtype as a relevant factor. Our findings highlight properties of the immune microenvironment that may portend susceptibility to immune checkpoint susceptibility in p53abn endometrial cancers, and how these relate to other clinically actionable targets being explored in clinical trials.

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