

Lower Checkpoint Gene Expression is Associated with Primary Resistance to Nivolumab-Ipilimumab Combination in Advanced Renal Cell Carcinoma

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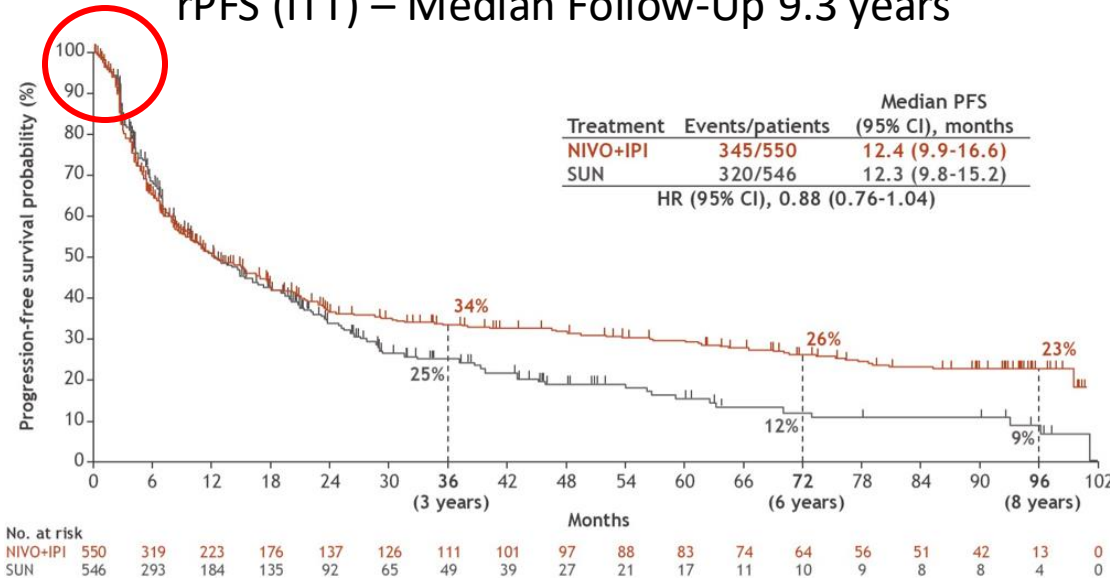
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Background

- Immunotherapy combinations have emerged as the standard of care for patients with advanced RCC
- Nivolumab-ipilimumab is associated with long-term durability, though a subset of patients do not derive any benefit from treatment

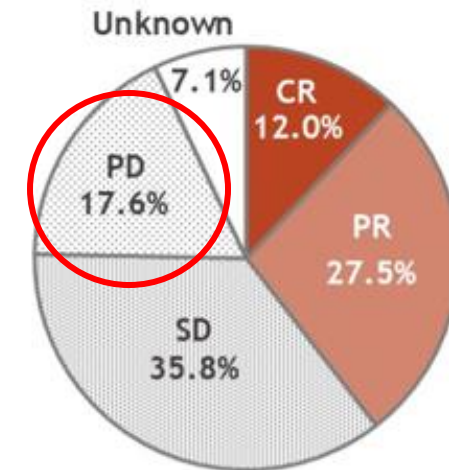
CheckMate 214

rPFS (ITT) – Median Follow-Up 9.3 years



CheckMate 214

Best Objective Response – ITT



Rationale and Hypothesis

Rationale: Urgent need to identify negative selection markers for treatment with nivolumab-ipilimumab

Hypothesis: Molecular differences exist among tumors with and without primary progression to nivolumab-ipilimumab

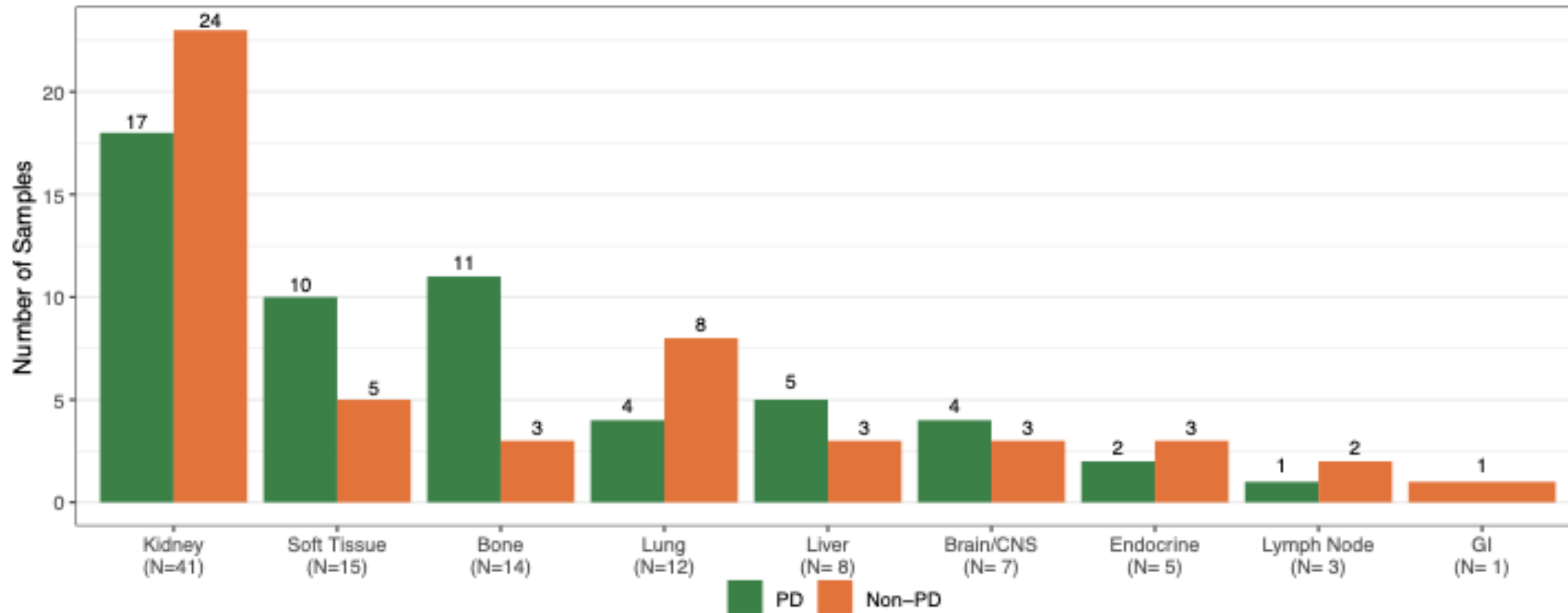
Methods

- Tempus Lens was used to select records for 106 patients with RCC who received 1L nivolumab-ipilimumab
- Eligible patients:
 - Tumor samples collected within one year of treatment initiation
 - Processed using xT (DNA-seq) and xR (RNA-seq) assays
- Treatment response:
 - Investigator-assessed within 90 days of therapy start
 - Categorized as PD versus non-PD
- RNA-seq data were normalized, log2-transformed, and batch-corrected
 - Measured checkpoint and angiogenic gene expression (TPM)
- Immunologic phenotype:
 - TMB (mt/Mb)
 - MSI status
 - PD-L1 (IHC, 22c3)
 - Immune infiltration estimated by quanTlseq (RNA)

Baseline Characteristics

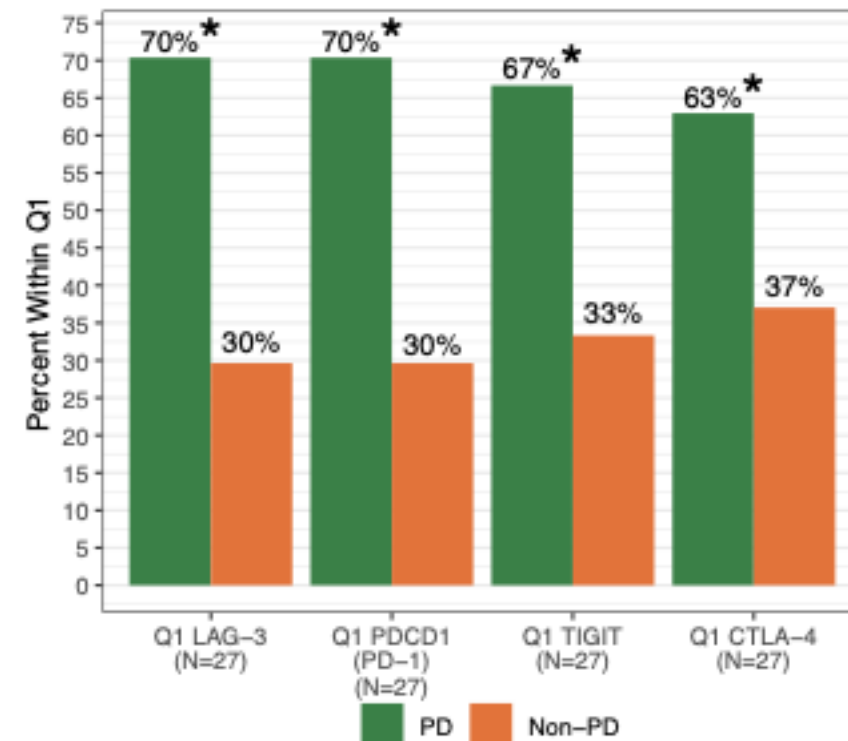
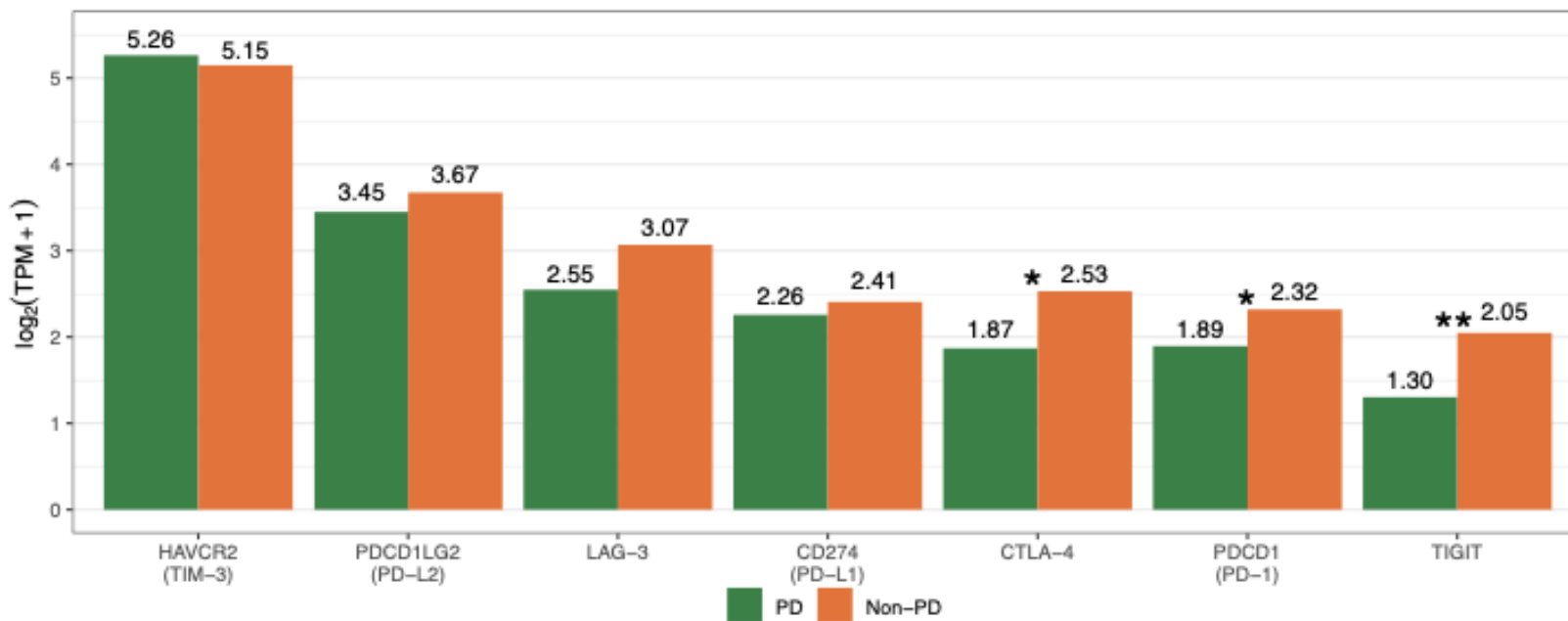
	PD (n=55) Median or N (%)	Non-PD (n=51) Median or N (%)	P-value
Age at Diagnosis, years	59	58	0.962
Male	37 (67%)	40 (78%)	0.198
White	38 (83%)	37 (90%)	0.337
Hispanic/Latino	5 (15%)	7 (25%)	0.307
Current/Former Smoker	20 (36%)	21 (41%)	0.611
Prior nephrectomy	29 (53%)	24 (47%)	0.560
Clear cell RCC	42 (76%)	42 (82%)	0.480
Metastases at Collection	47 (94%)	45 (96%)	>0.999
Bone Metastases at Collection	10 (18%)	7 (14%)	0.532
Liver Metastases at Collection	11 (20%)	3 (5.9%)	0.032

Specimen Source (N=106)

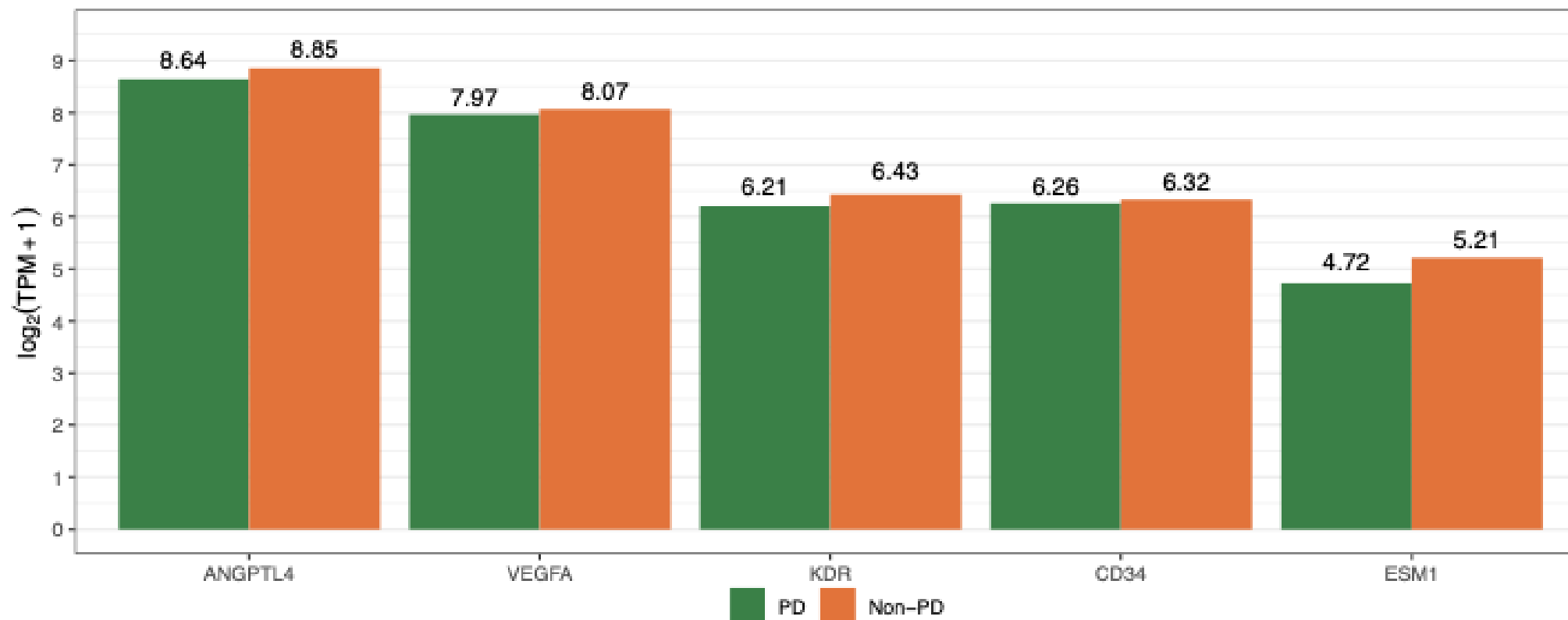


54% with
matched
normal
DNA

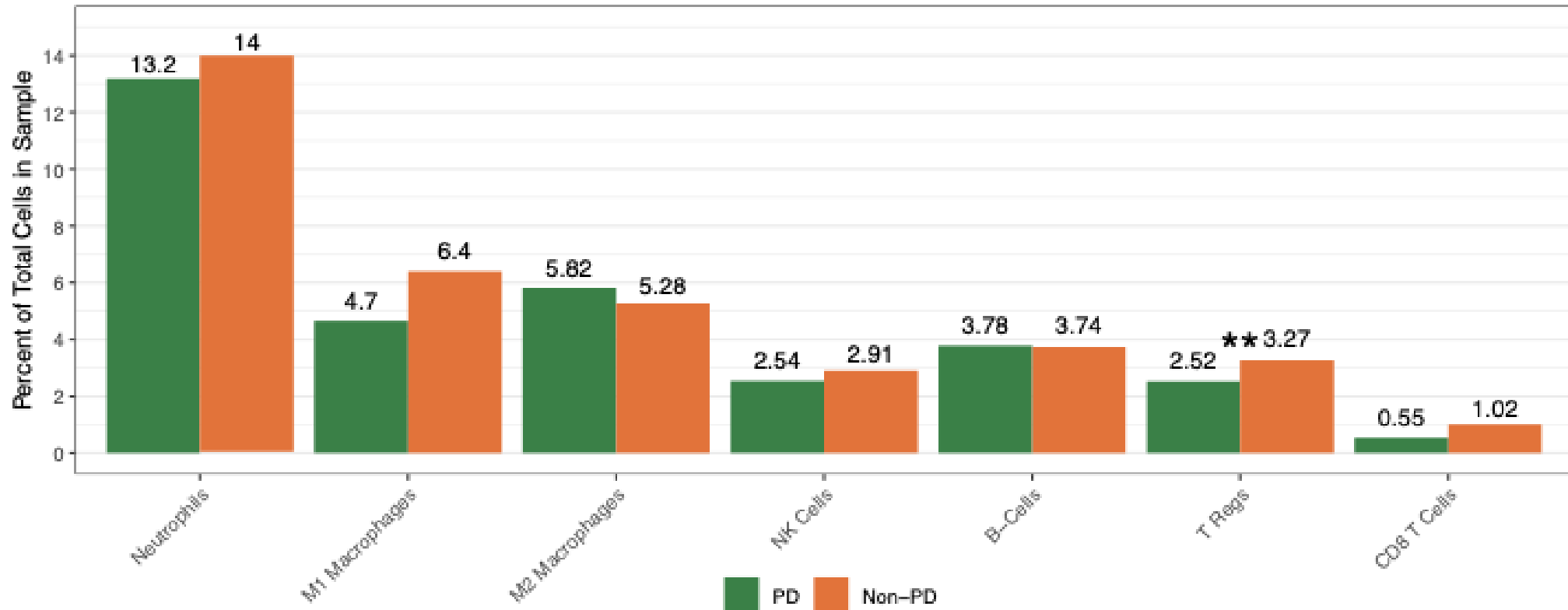
Checkpoint RNA Expression



Angiogenic Gene RNA Expression



Immune Cell Infiltrates



Somatic Alterations

	PD (n=55)	Non-PD (n=51)	P-value	Q-value
VHL, N (%)	34 (67%)	32 (58%)	0.368	0.9
PBRM1, N (%)	15 (29%)	16 (29%)	0.971	>0.9
SETD2, N (%)	8 (16%)	15 (27%)	0.148	0.9
TP53, N (%)	8 (16%)	14 (25%)	0.215	0.9
CDKN2A, N (%)	7 (14%)	11 (20%)	0.390	0.9
BAP1, N (%)	7 (14%)	6 (11%)	0.659	0.9
CDKN2B, N (%)	6 (12%)	8 (15%)	0.673	0.9
TERT, N (%)	7 (14%)	5 (9.1%)	0.452	0.9
KDM5C, N (%)	5 (9.8%)	6 (11%)	0.852	>0.9
PTEN, N (%)	4 (7.8%)	6 (11%)	0.743	0.9
MTAP, N (%)	5 (9.8%)	3 (5.5%)	0.477	0.9
TSC1, N (%)	4 (7.8%)	2 (3.6%)	0.425	0.9
ARID1A, N (%)	3 (5.9%)	2 (3.6%)	0.670	0.9
NF2, N (%)	2 (3.9%)	4 (7.3%)	0.680	0.9

Conclusions

Primary resistant to nivolumab-ipilimumab characterized by lower RNA expression of immune checkpoints

This possibly reflects an immune-cold microenvironment with limited T-cell infiltration and activation

Future prospective studies, including IHC validation, is warranted to confirm these findings

Acknowledgements

- Patients and their families
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