

MULTI-OMIC ANALYSIS OF THE PROGNOSTIC AND PREDICTIVE VALUE OF LAG3 EXPRESSION IN UROTHELIAL CARCINOMA

Adanma Ayanambakkam¹, Anh Lam¹, Kieran Sweeney², Andrew Elliott², Chadi Nabhan², Rana R. McKay³, Abhishek Tripathi⁴, Sumati Gupta⁵, Xu Chao¹, Jad Chahoud⁶, Debasish Sundi⁷, Paul Skelton⁸, Laura Graham⁹, Lyudmyla Berim¹⁰, Bodour Salhia¹¹, Sean Kern¹², Yousef Zakharia¹³, Stephen Edge¹⁴, Abdul Rafah Naqash¹

¹Stephenson Cancer Center, OK; ²Caris Life Sciences; ³University of California San Diego, CA; ⁴City of Hope Cancer Center, CA; ⁵Huntsman Cancer Institute, UT; ⁶Moffitt Cancer Center, FL; ⁷Ohio State University, OH; ⁸UVA Health Emory Couric Cancer Center; ⁹University of Colorado Cancer Center; ¹⁰Rutgers Cancer Institute of New Jersey, NJ; ¹¹USC Norris Cancer Center, ¹²Murtha Cancer Center, MD; ¹³Holden Cancer Center, IA; ¹⁴Roswell Park Cancer Center, NY

INTRODUCTION

- LAG3 is an immune checkpoint receptor protein expressed on immune cells, and LAG3 negatively regulates T-cell function and can promote tumor cell immune escape
- Co-blockade of PD1 and LAG3 enhanced anti-tumor responses in preclinical mouse models (ovarian cancer and colon adenocarcinoma)
- Nivolumab (anti-PD1) and Relatlimab (anti-LAG3) combination therapy has been approved to treat metastatic melanoma
- Despite its established prognostic significance in other malignancies, the role of *LAG3* as a prognostic or predictive biomarker in urothelial carcinoma (UC) remains inadequately studied

METHODS

- DNA (592-gene or whole exome) and RNA (whole transcriptome) sequencing were performed for 3343 patient tumors submitted to *Caris Life Sciences*
- Clinical and molecular data from patients enrolled in the *Oncology Research Information Exchange Network (ORIEN)*, including tumor RNA-seq sequencing, were used as a validation cohort for analysis
- In this study, we investigate the correlation between LAG3 expression levels in tumor tissues of patients diagnosed with urothelial carcinoma and a range of clinicopathological parameters. We also assessed the impact on overall survival and response to standard therapies, aiming to elucidate potential mechanisms of resistance.
- PD-L1+ status (22c3, combined positive score ≥ 10) was determined by IHC and TMB-High (TMB-H) was defined as ≥ 10 mutations/Mb
- LAG3* high (*LAG3-H*) and low (*LAG3-L*) cohorts were defined by the top and bottom quartiles of *LAG3* RNA transcripts per million (TPM), respectively
- Tumor microenvironment (TME) cell fractions were estimated by RNA deconvolution using quantIseq
- Significance was tested using Mann-Whitney U and χ^2 tests with multiple testing correction as appropriate
- Real-world overall survival (OS) was obtained from insurance claims data and calculated from start of Atezolimumab, Avelumab, Nivolumab or Pembrolizumab to last contact.
- Pembrolizumab time on treatment (ToT) was calculated from start of Pembrolizumab to last of Pembrolizumab
- Hazard ratios (HR) and associated p-values were calculated using the Cox proportional hazards model
- Multivariate analysis (MVA) was performed using a Cox Proportional-Hazards model

RESULTS

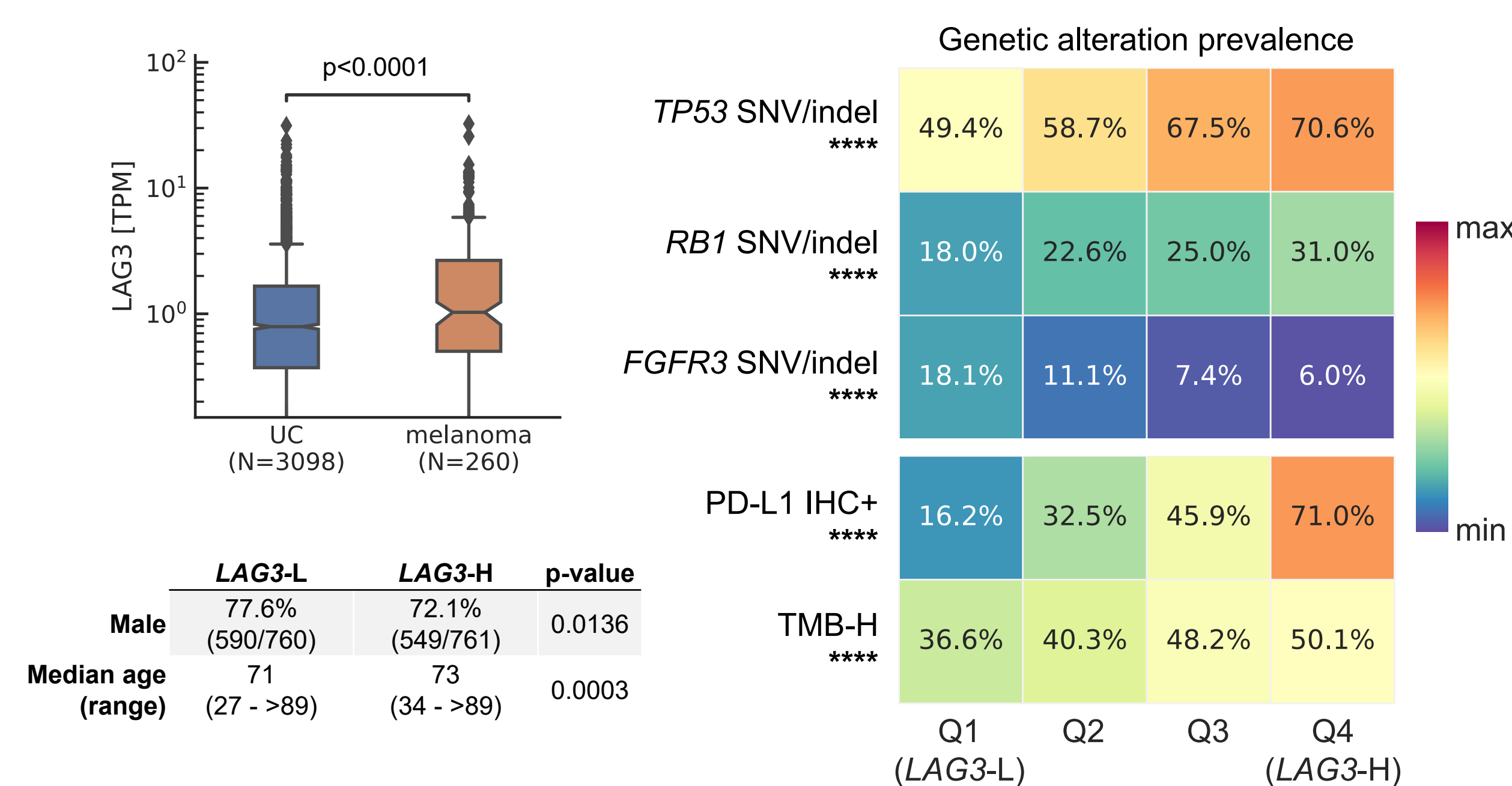


Figure 1. LAG3 expression in UC and association with increased TP53 mutations and PD-L1+ and TMB-H status

- (Top left) *LAG3* expression in UC vs metastatic melanoma patients treated with Nivolumab + Relatlimab combination therapy
- (Bottom left) Demographics of *LAG3-H* and *LAG3-L* cohorts
- (Right) Prevalence of genetic alterations vs *LAG3* expression quartile. Q-values for *LAG3-H* vs *LAG3-L* comparisons

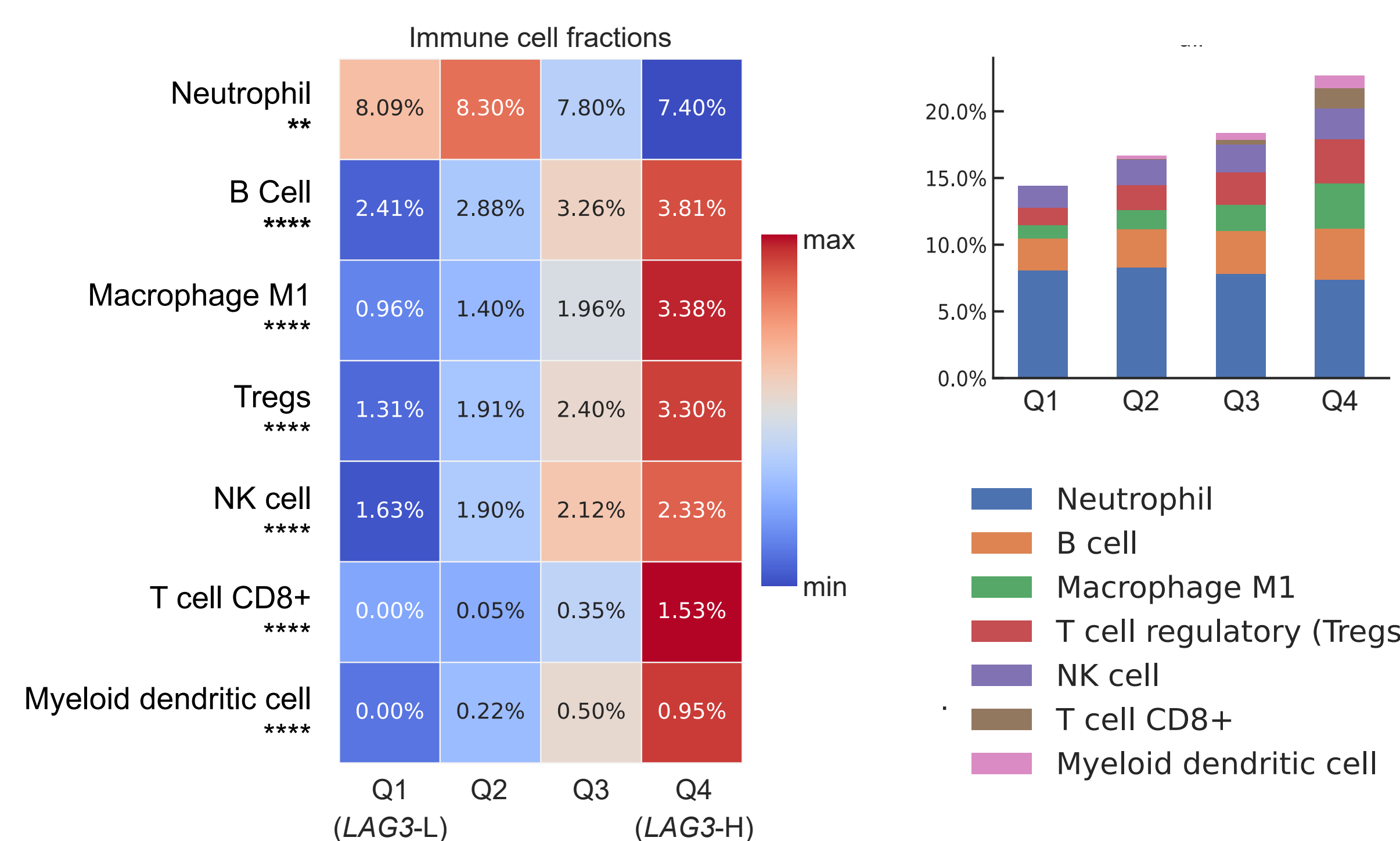


Figure 2. LAG3-H cohort had increased immune cell infiltration and increased Tregs

- (Left) Immune cell fractions vs *LAG3* expression quartile
- (Right) Total immune cell fractions by *LAG3* expression quartile. Stars represent q-values for *LAG3-H* vs *LAG3-L* comparisons

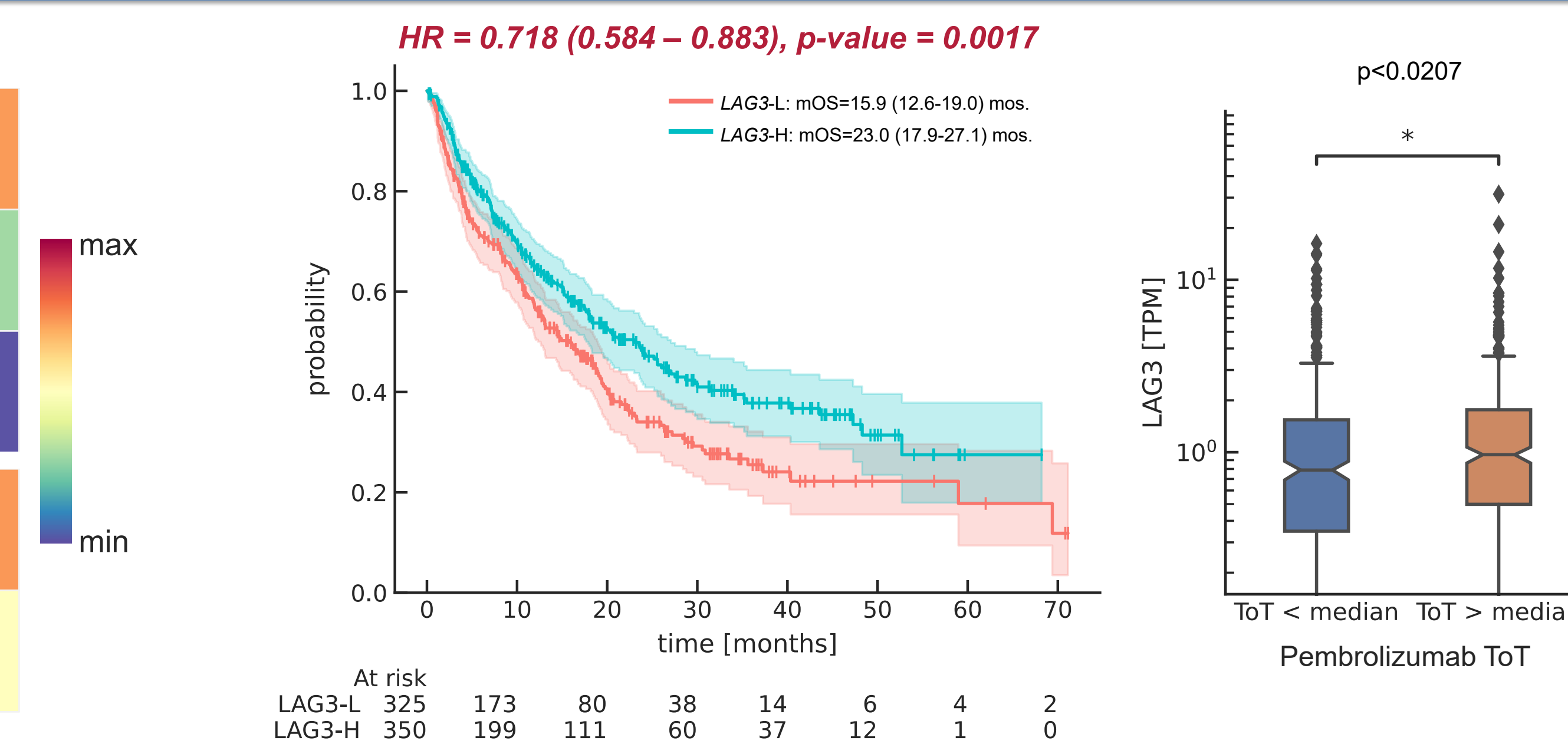


Figure 3. High LAG3 expression associated with longer OS and Pembrolizumab ToT

- (Left) Post-ICI OS for *LAG3-H* vs *LAG3-L* cohorts
- (Right) *LAG3* expression in cohorts stratified by Pembrolizumab ToT

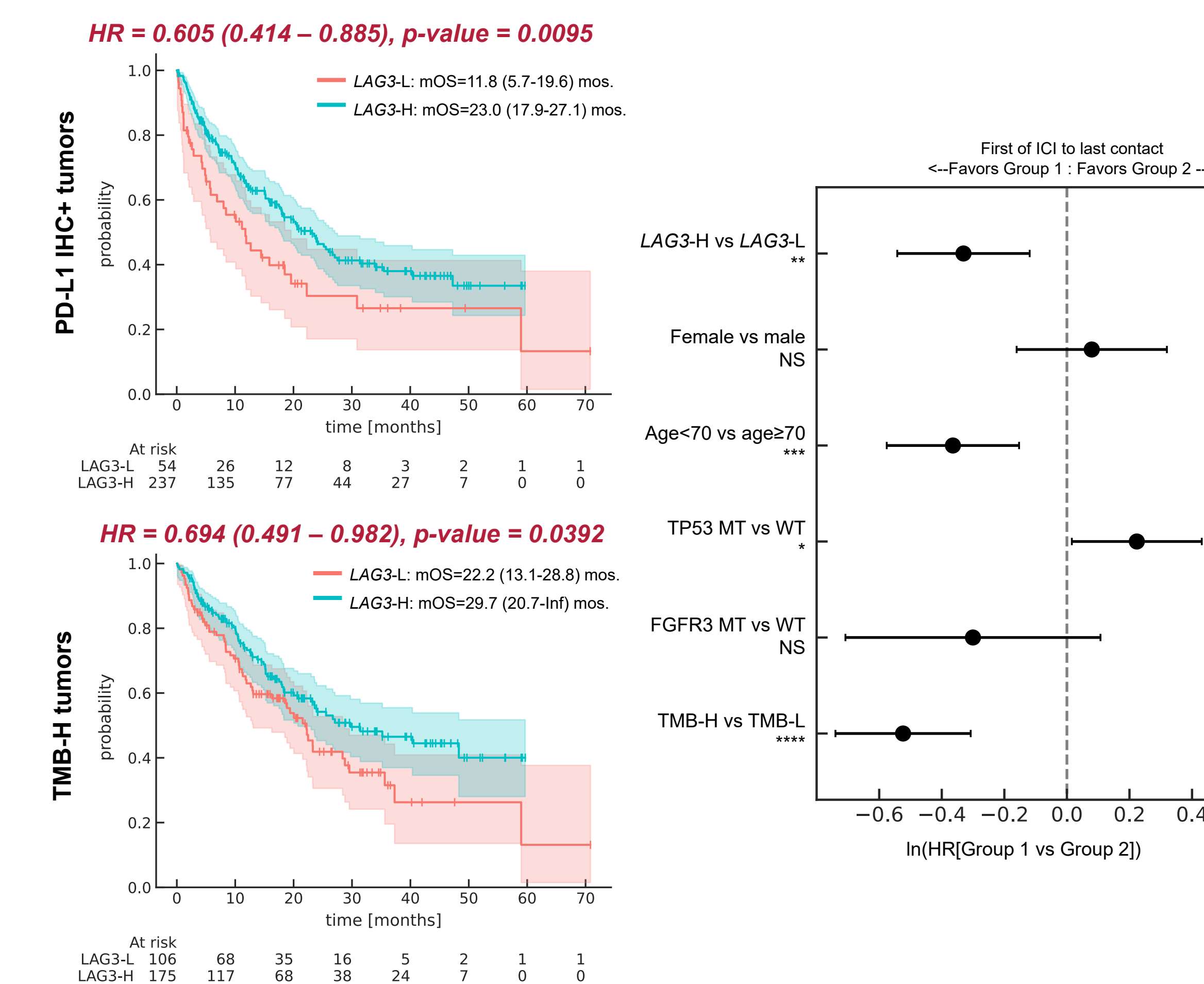


Figure 4. Longer OS for LAG3-H cohort persisted in PD-L1+ and TMB-H tumors

- Post-ICI OS for *LAG3-H* vs *LAG3-L* cohorts among PD-L1 IHC+ tumors (top left) and TMB-H tumors (bottom left)
- (Right) HRs and 95% CI from Multivariate analysis

VALIDATION COHORT

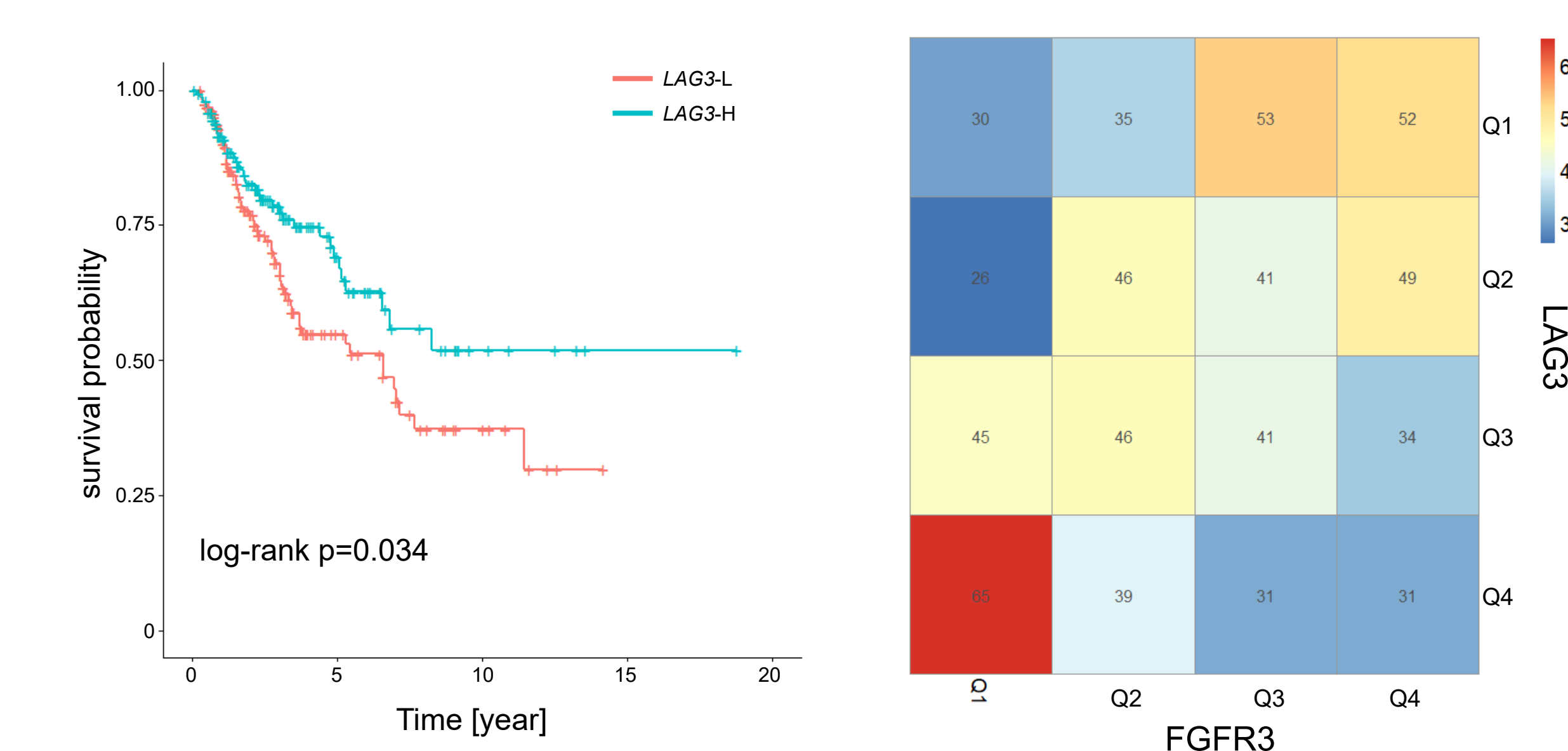


Figure 5. Validation cohort utilizing the ORIEN database

- (Left) OS for *LAG3-H* vs *LAG3-L* cohorts in ORIEN database
- (Right) *LAG3* expression vs prevalence of *FGFR3* mutations (spearman correlation coefficient = -0.205, p < 0.0001)

CONCLUSIONS

- In UC, high *LAG3* expression is associated with improved survival and a hot tumor micro-environment
- Among patients with TMB-H, who received immune checkpoint inhibitors (ICI), *LAG3-H* had improved OS vs *LAG3-L* (HR=0.69, p=0.039).
- High *LAG3* is associated with increased *TP53* and *RB1* mutations, decreased *FGFR3* mutations, and increased PD-L1 IHC+ and TMB-H status
- UC patients may benefit from combination ICI because high *LAG3* expression is associated with increased immune cell infiltration, but also higher levels of inhibitory Tregs



Adanma Ayanambakkam, MD

adanma-ayanambakkam@ouhsc.edu
800 NE 10th street, Oklahoma City, OK 73104
Stephenson Cancer Center, University of Oklahoma