Abstract 2543: Analysis of immune checkpoint blockade biomarkers in elderly patients using large-scale cancer genomics data

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Background:

- The majority of cancer patients are older individuals
- Older individuals tend to have less effective immune responses to most diseases
- Existing clinical trial data suggests older patients receive no reduced benefit from ICB compared to their younger counterparts
- Use high-throughput multi-omics data to better understand this counterintuitive observation

Methods:

- Large-scale analysis of genomics, transcriptomics, and clinical data
- TCGA, Caris Life Sciences, GENIE, METABRIC
  - Totaling 64,859 patients across 31 cancer types
- Multivariate linear models are applied to model the relationship of ICB biomarkers to patient age
- TMB, TCR diversity, immune checkpoint gene expression, immune pathway enrichment, and immune infiltration are assessed
- Analysis results made available as the Cancer Associations with Molecular Aging (CAMA) Atlas
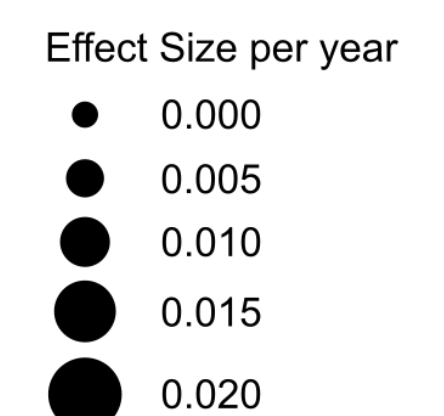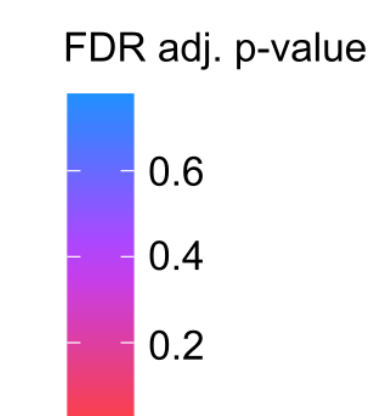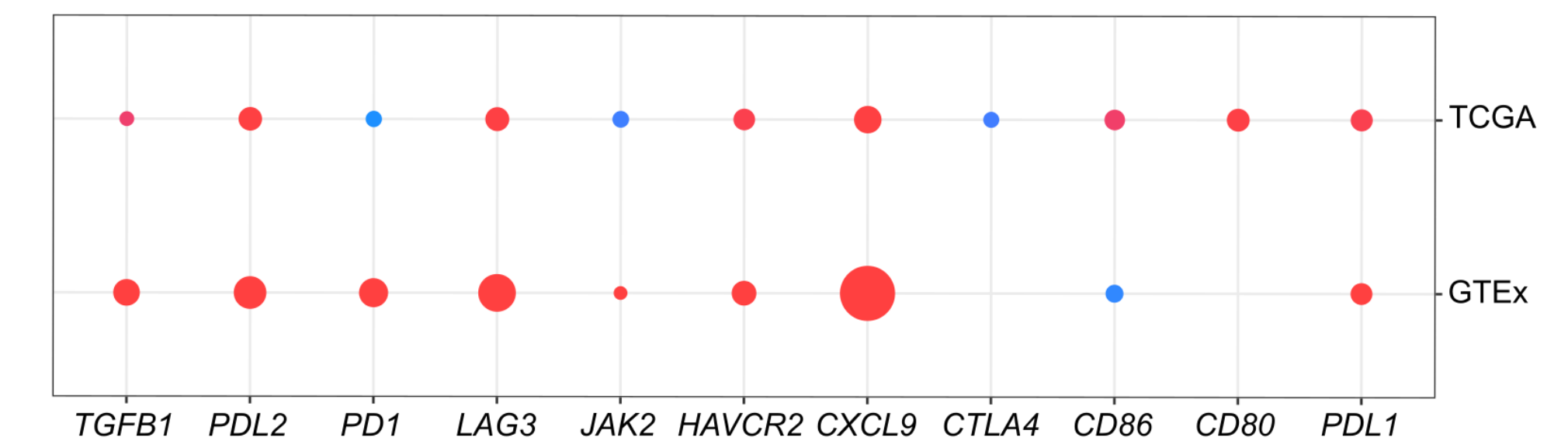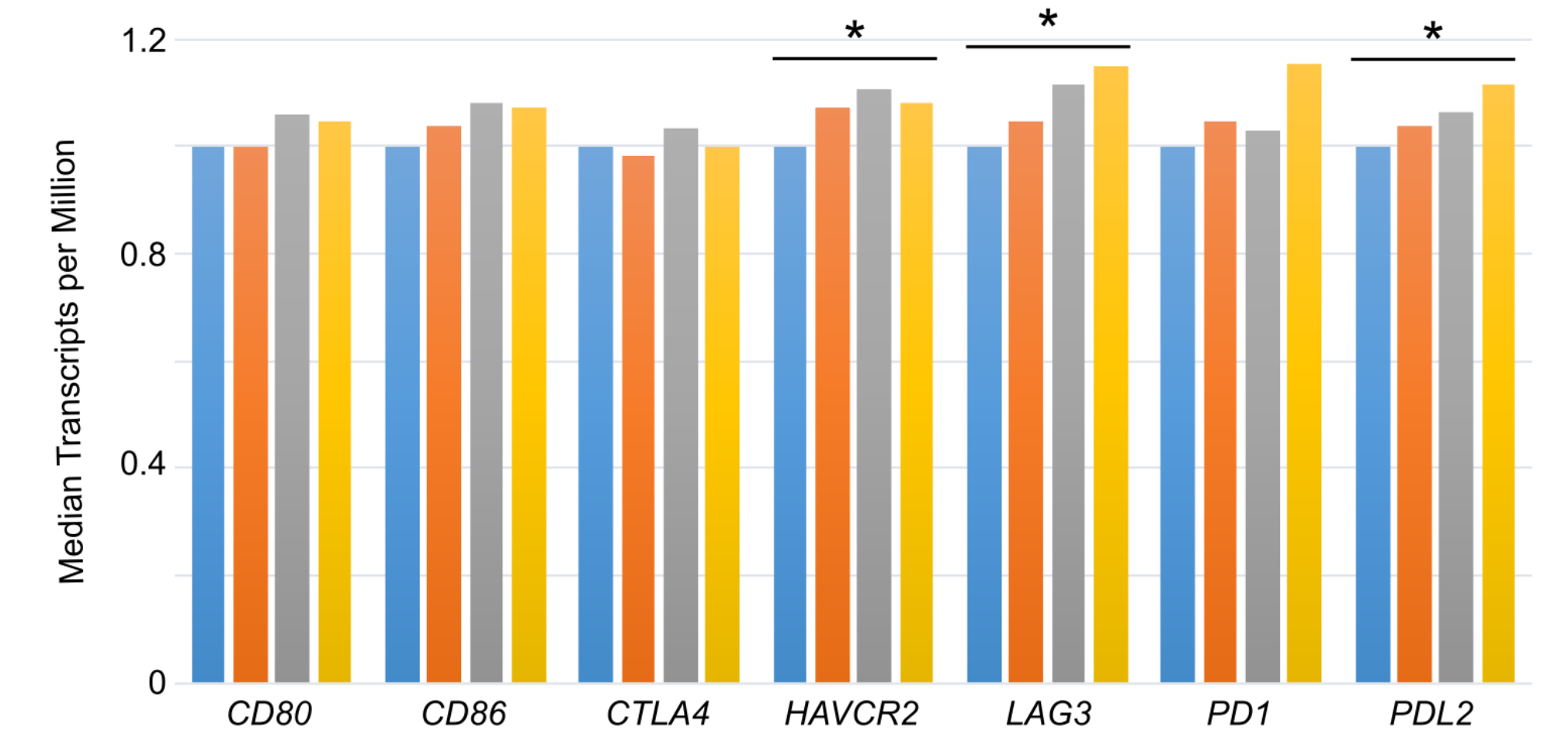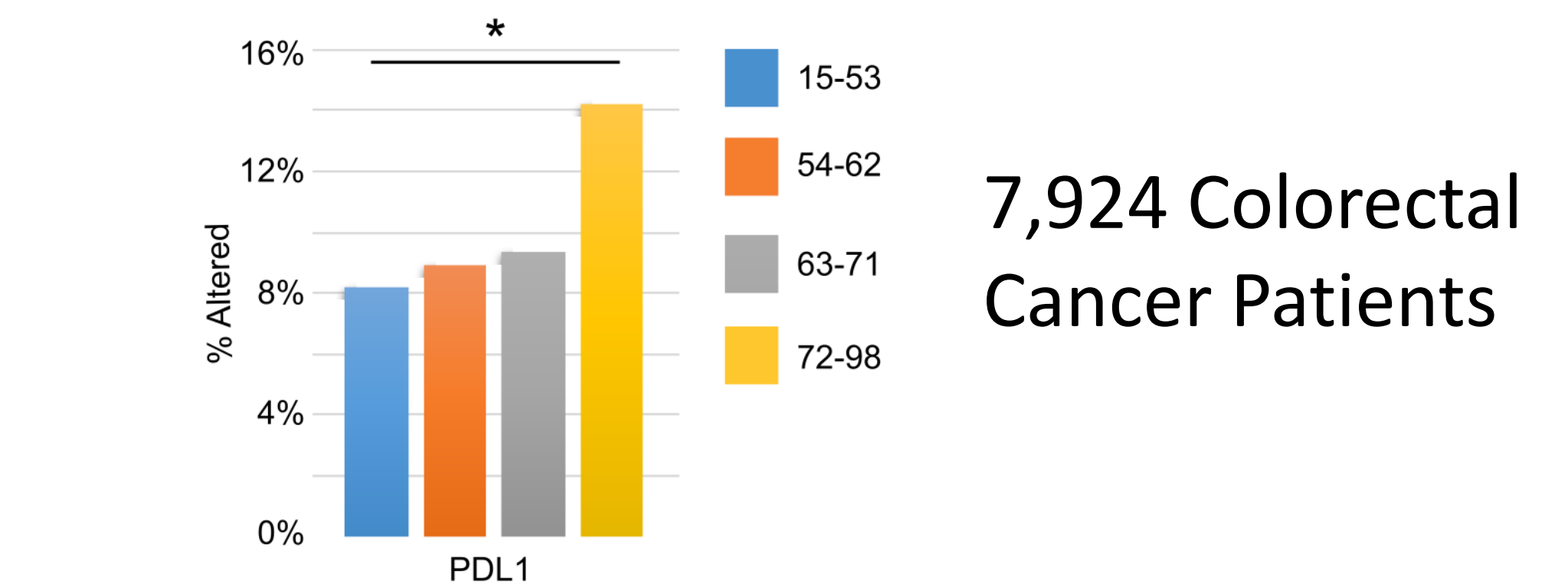 - http://www.lab-apps.onc.jhmi.edu/CAMAAtlas

Patient age correlates with an adapting ITME that displays mechanistic biomarkers associated with ICB response

http://www.lab-apps.onc.jhmi.edu/CAMAAtlas
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PRECISION ONCOLOGY ALLIANCE

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MEDICINE

Cancer Type	Estimated change in logTMB per year of age	Adjusted p-value	n
Breast	0.00550	9.17×10^{-28}	9485
Melanoma	0.0152	4.16×10^{-26}	3120
Esophagogastric	0.0120	8.23×10^{-20}	2133
Renal Cell Carcinoma	0.00942	5.91×10^{-15}	1329
Head and Neck	0.0125	5.90×10^{-12}	1255
Bladder	0.0107	3.14×10^{-10}	1762
Non-Small Cell Lung	0.00260	6.13×10^{-4}	10620
Colorectal	0.00230	1.34×10^{-3}	8257

Results:

7,924 Colorectal Cancer Patients

Pan-cancer