

FORUM

INTRODUCTION

- Genomics-guided precision medicine has revolutionized human oncology. Simultaneously, in canine cancer, the knowledge of genomics, cutting-edge diagnostics, and therapeutics is constantly growing. (Fig.1)
- Further effort is needed, however, to comprehend the mutation landscape in canine cancers and to effectively leverage the resulting mutation-based biomarkers in clinical management.
- Here, we have utilized SearchLight DNA®, a canine cancer gene sequencing panel, to identify the mutation profiles in 813 canine cases across 53 cancer types, and assess the clinical relevance of mutation-based biomarkers in the treatment of canine cancer patients. (Fig. 2)

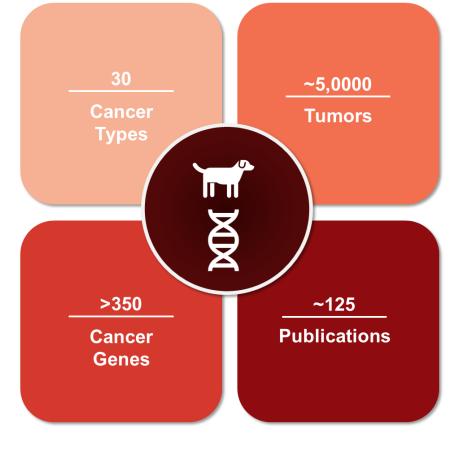
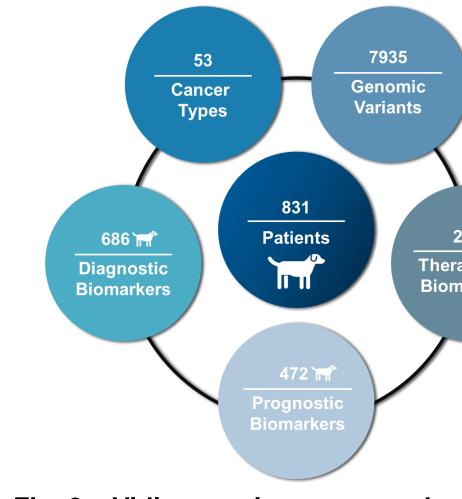


Fig. 1 – Current mutation landscape in canine cancers



METHODS

- We apply a novel workflow using SearchLight DNA, a rigorously validated nextgeneration sequencing-based 120-gene panel, designed to detect key cancerdriving mutation types, such as single nucleotide and indel variants (SNVs and Indels), copy number variants (CNVs), and internal tandem duplications (ITDs). Next, we annotate candidate pathogenic and clinically significant mutations using Vidium Insight[™], a canine precision oncology biomarker knowledgebase,
- comprising over 4,000 mutational biomarkers associated with diagnostic, prognostic, and therapeutic implications.

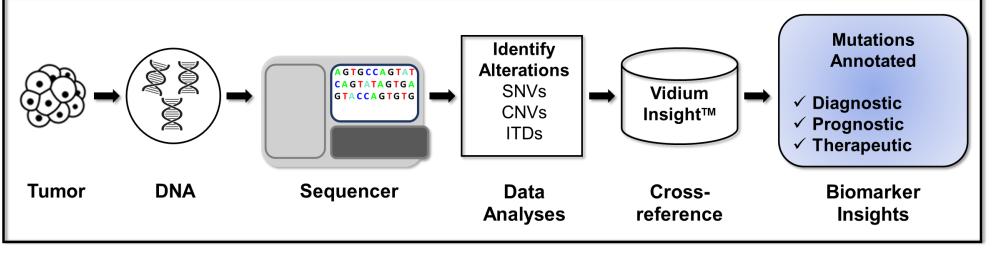


Figure 3 – SearchLight DNA workflow

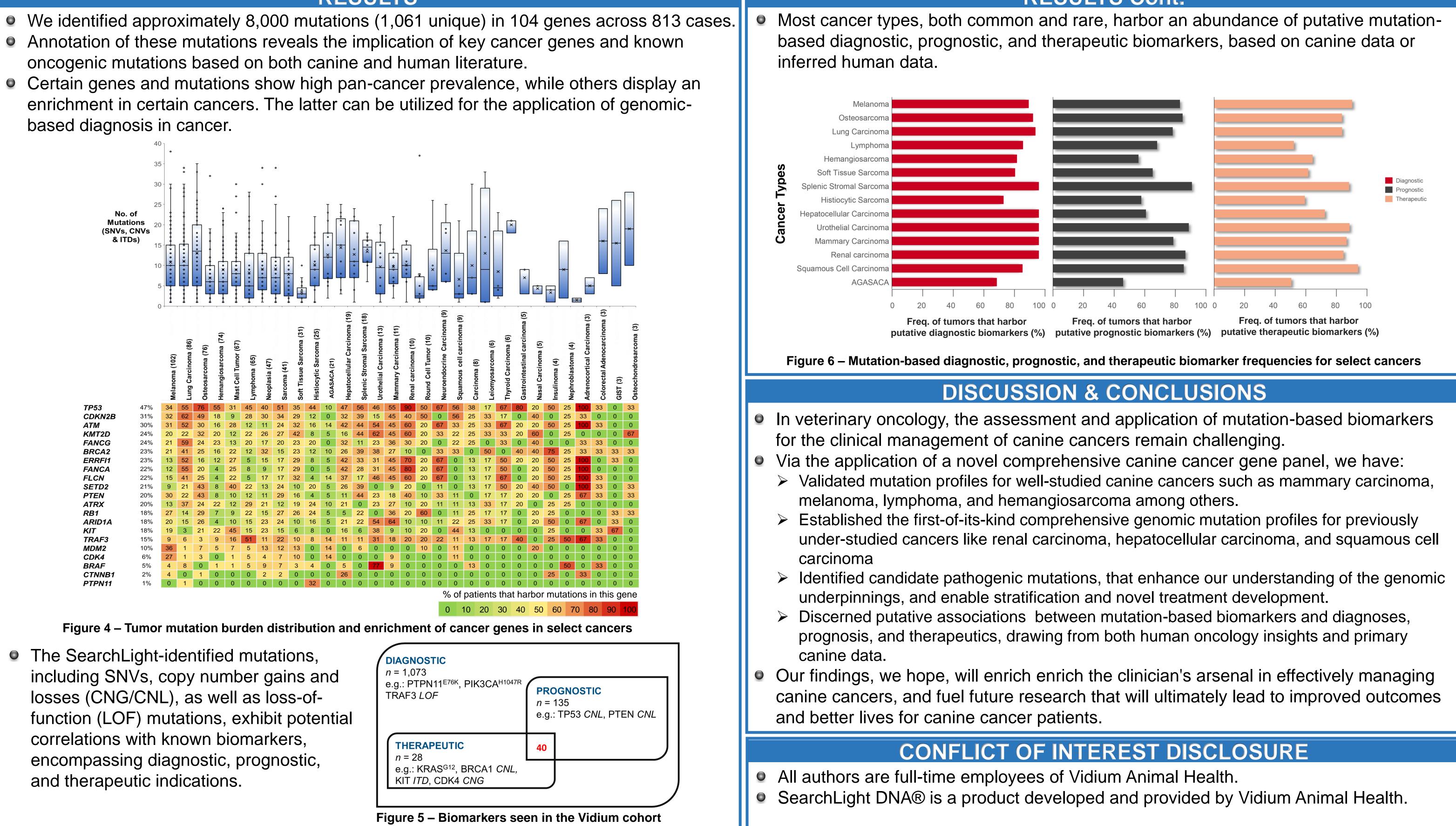
Genomic analysis across 50 canine cancer types reveals novel mutations and putative high clinical actionability

Sharadha Sakthikumar¹, Derick Whitley¹, Manisha Warrier¹, Salvatore Facista¹, Esther Chon¹, Jonathan Adkins¹, Natalie Duran¹, Sara Aman¹, Darwin Tsinajinnie¹, Nidhi Patel¹, David Haworth¹, William PD Hendricks¹, Guannan Wang¹

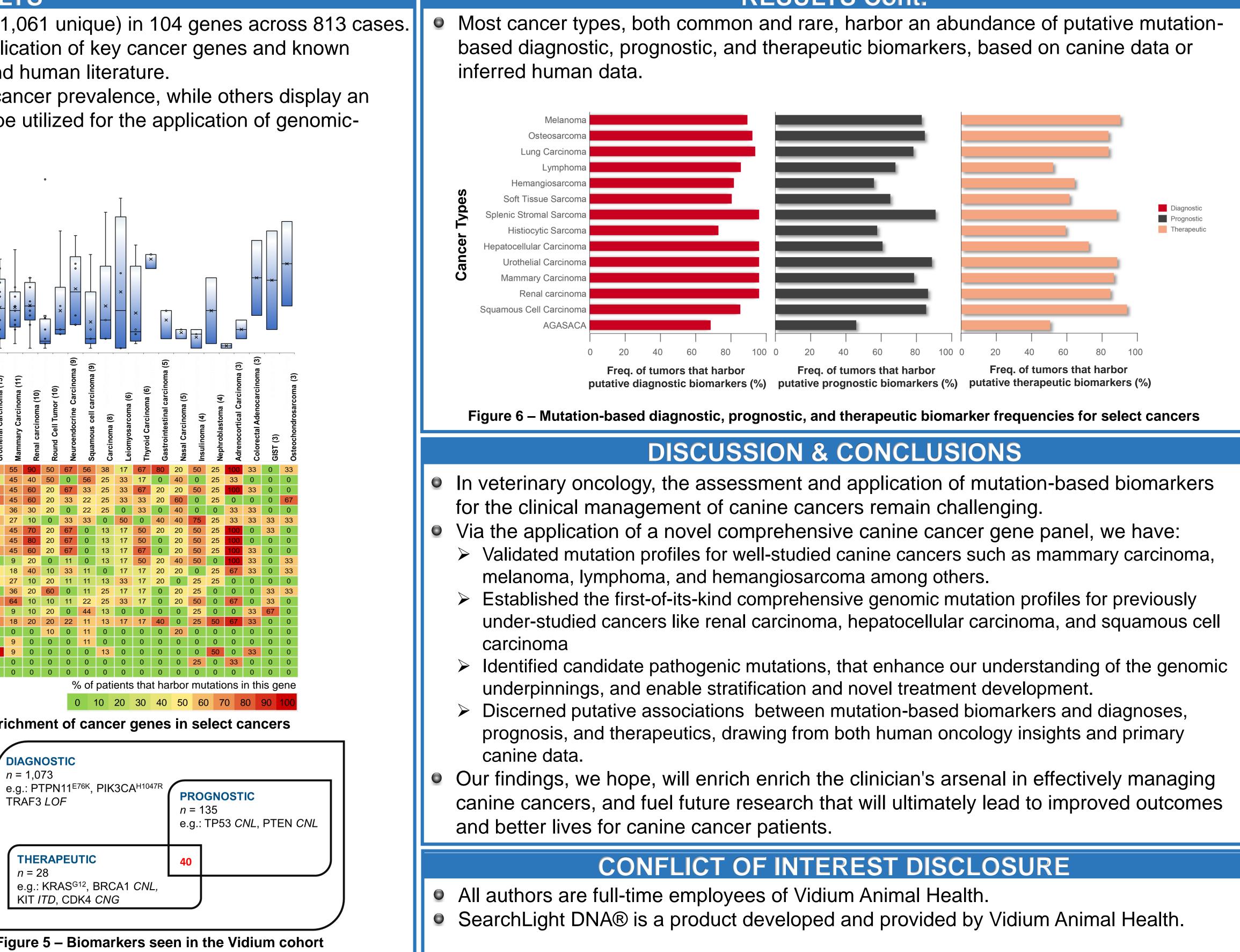
¹Vidium Animal Health, Scottsdale, AZ

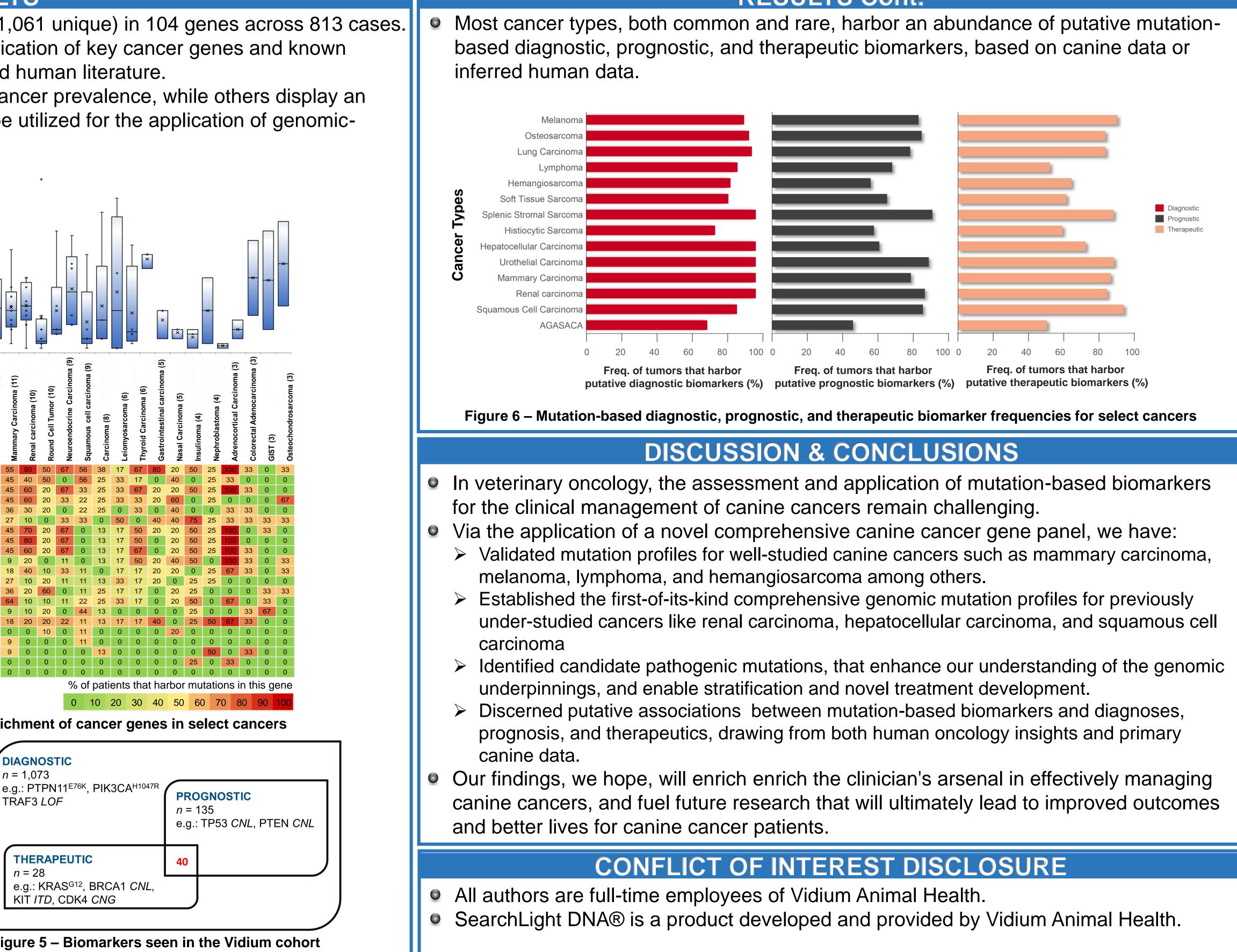
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- Fig. 2 Vidium canine cancer cohort overview



The SearchLight-identified mutations, including SNVs, copy number gains and losses (CNG/CNL), as well as loss-offunction (LOF) mutations, exhibit potential correlations with known biomarkers, encompassing diagnostic, prognostic, and therapeutic indications.





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RESULTS Cont.