

A Meta-Analytical Approach to Bridge Fundamental and Applied Research: Finding the Intersection Between Genes Regulating Primary Cilia Development and Cancer.



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Abstract

The primary cilium is a subcellular structure that protrudes from most cell types. The dysfunction of the primary cilium contributes to a variety of diseases termed ciliopathies. Recent studies suggest that alterations in the structure, function, and formation of the primary cilium play a role in cancer progression. However, a comprehensive understanding of the interactions between the primary cilium and cancer development, including the role of specific genes, remains elusive. This literature review sought to examine the genes regulating the primary cilium and assess their contributions to cancer progression. We identified, the three most well-studied gene families involved in regulating cancer progression and the primary cilium: the IFT gene family, the HDAC gene family, and the NPHP gene family. We then itemized individual genes from these families (Primary genes) and further searched the literature for additional genes that interacted closely with these genes in cells (Secondary genes). We used an R-based search to identify the total number of articles for three categories: (Genes AND Cancer), (Genes AND Cilia) and (Gene AND Cilia AND Cancer). The interaction between the genes and the effect of the genes on cancer and cilia respectively were analyzed and weighted based on the number of articles representing each relationship. These weightings can be used to analyze the strongest as well as the weaker and unexplored relationships between these fields. This approach is likely to be of broad interest to researchers as it is a simple yet useful way of identifying specific gaps in knowledge, particularly when trying to bridge fundamental and clinical or applied research. The methodology utilized in this literature review exhibits a unique approach that merges the scope of a meta-analysis by aggregating a vast array of literature with the breadth of an interdisciplinary study by bridging disciplines that have remained relatively distinct. This combination not only enhances the depth of the analysis but also describes a novel approach for integrating complementary but siloed fields of study.

Results

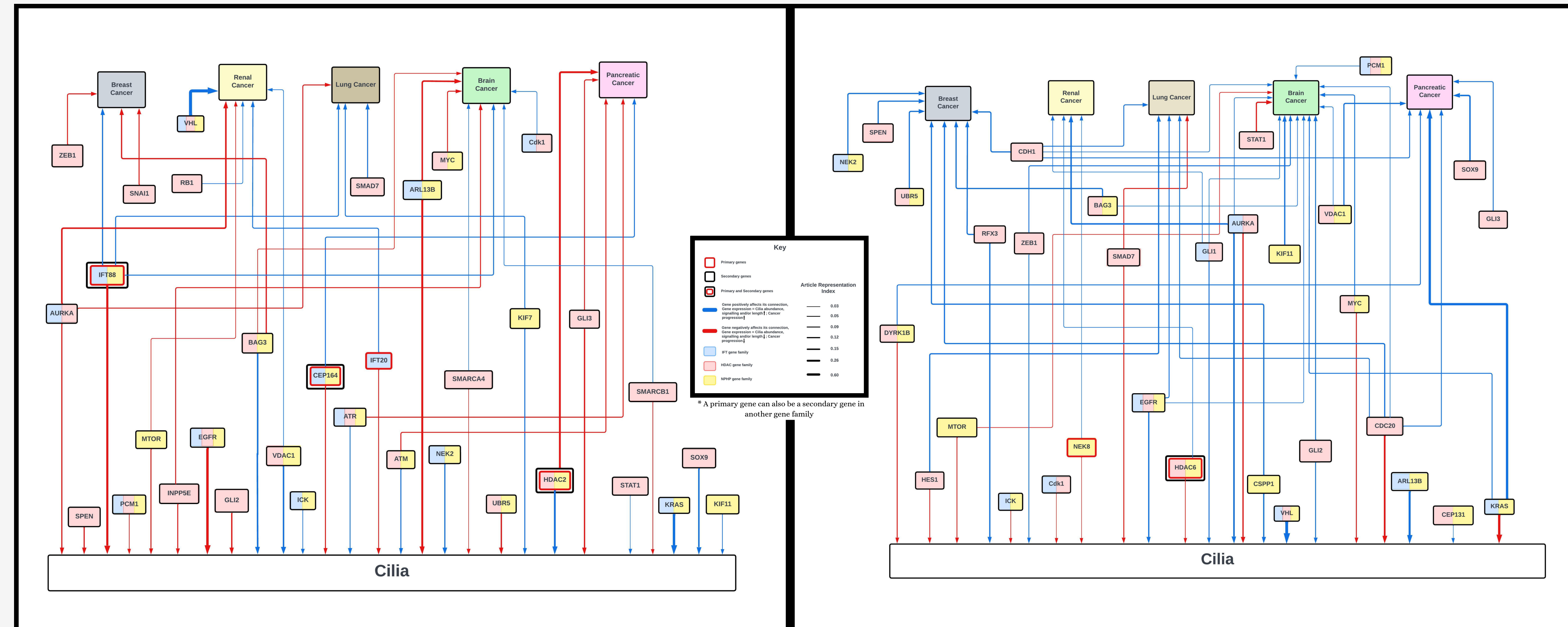


Figure 8. Relationship between underexpression of the genes and their effects on Cilia and Cancer. Genes identified for further research are ICK, RB1, SNAI1, KRAS and EGFR.

Figure 9. Relationship between overexpression of the genes and their effects on Cilia and Cancer. Genes identified for further research are CEP131, VHL and CDK1.

Table 1. Common genes in Figures 8 and 9

Cilia	Cancer
ICK	MYC
ARL13B	SMAD7
EGFR	GLI3
AURKA	BAG3
GLI2	
KRAS	
MTOR	

Methods

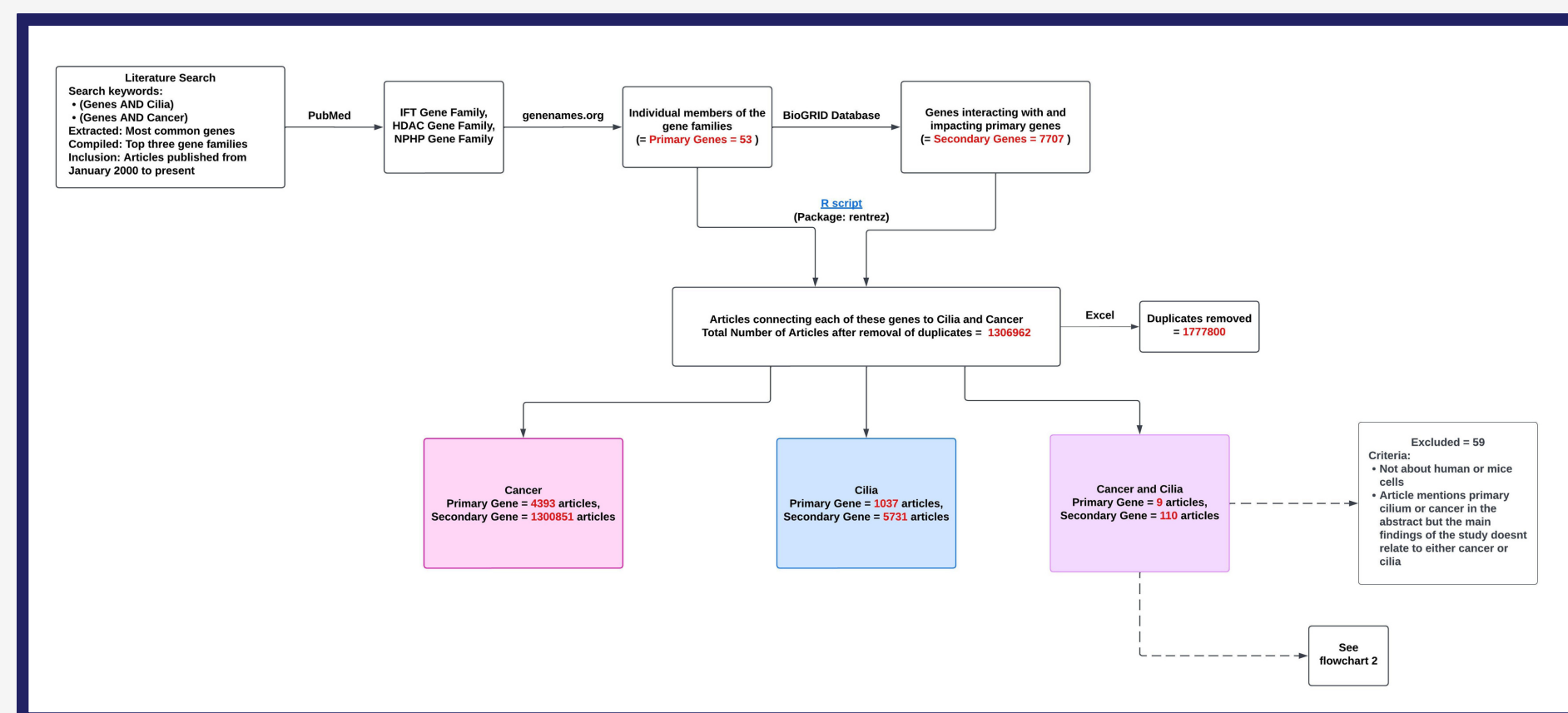


Figure 1. Methodology for identifying and analysing articles related to Cancer and Cilia

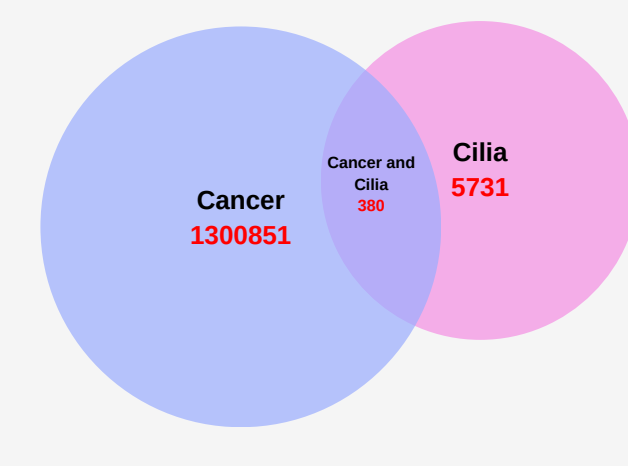


Figure 2. Overlap of the number of articles between Cancer and Cilia search categories

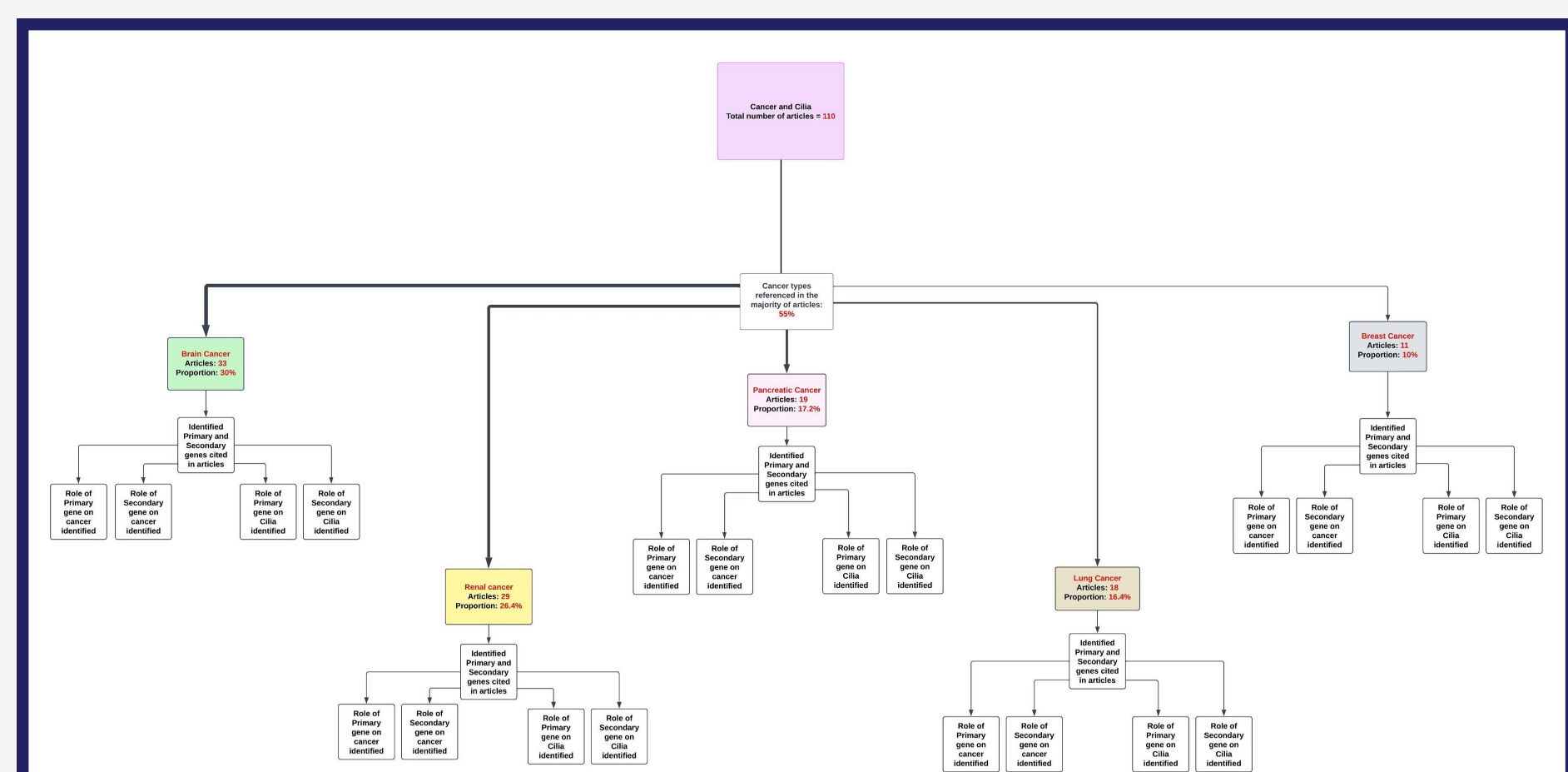


Figure 3. Methodology used to identify the types of relationships between the genes, cilia and cancer for the five primary types of cancer

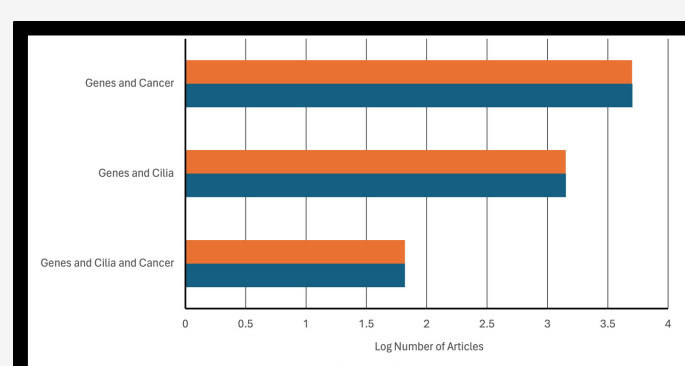


Figure 4. Comparison between R script and Manual search techniques for all search categories. Comparison shows a 99.59% similarity.

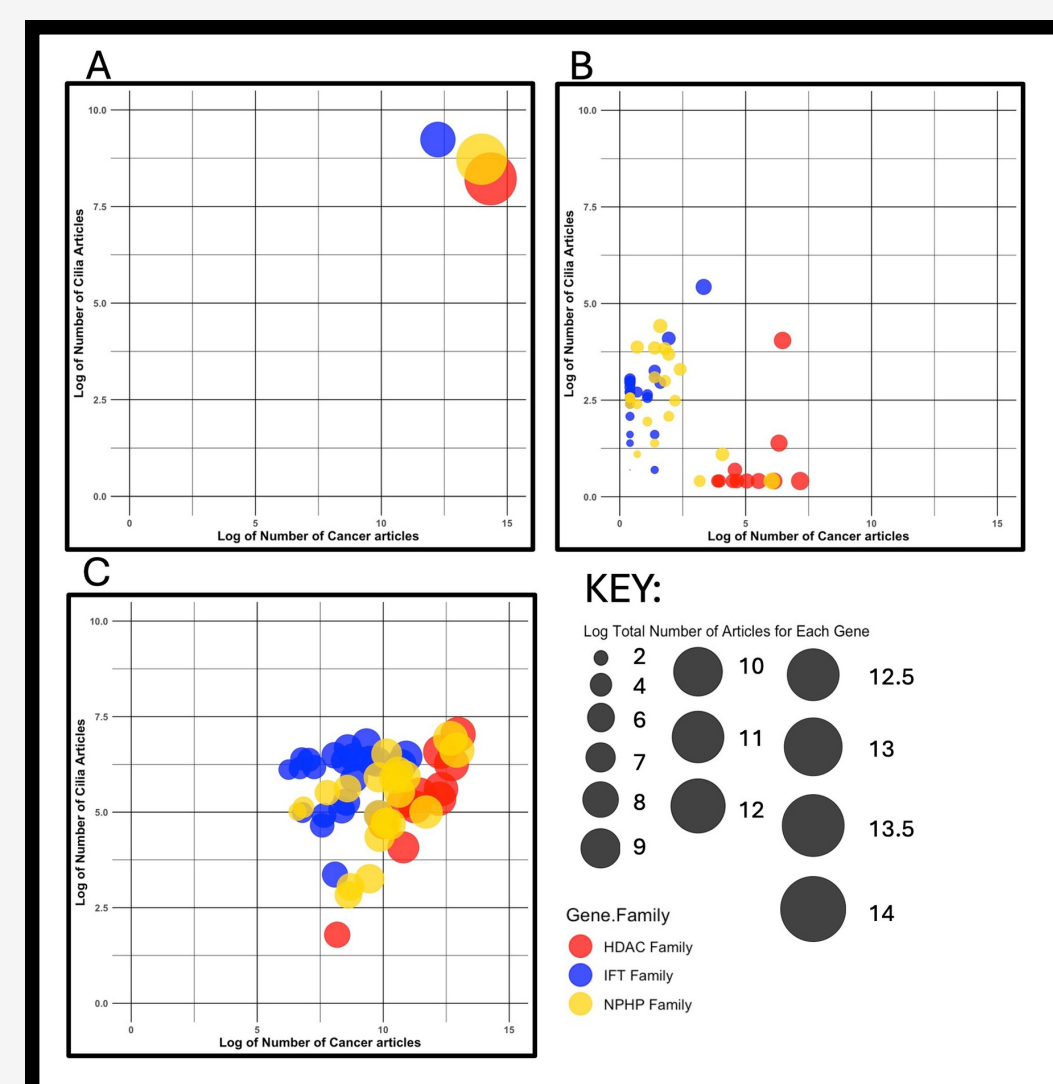


Figure 5. Number of articles citing involvement of the 3 gene families of interest (A), primary genes in each family (B) and secondary genes in each family (C) in cilia development/function and cancer progression.

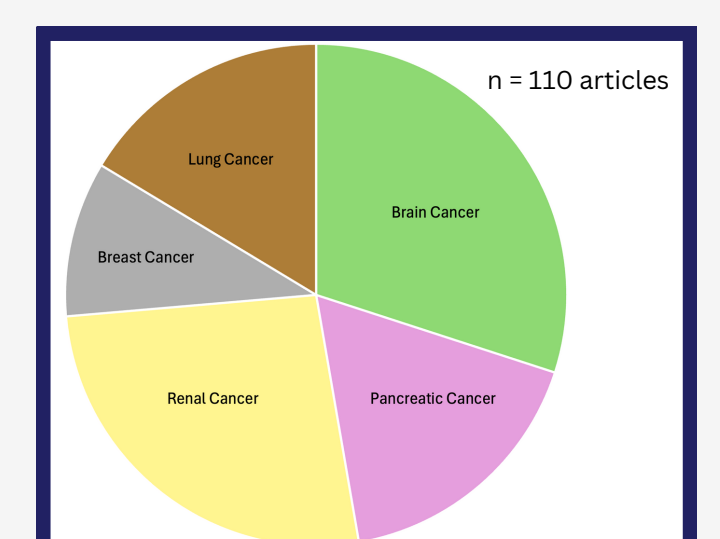


Figure 6. Proportion of the top five cancers from the articles under the search category (Genes AND Cilia AND Cancer)

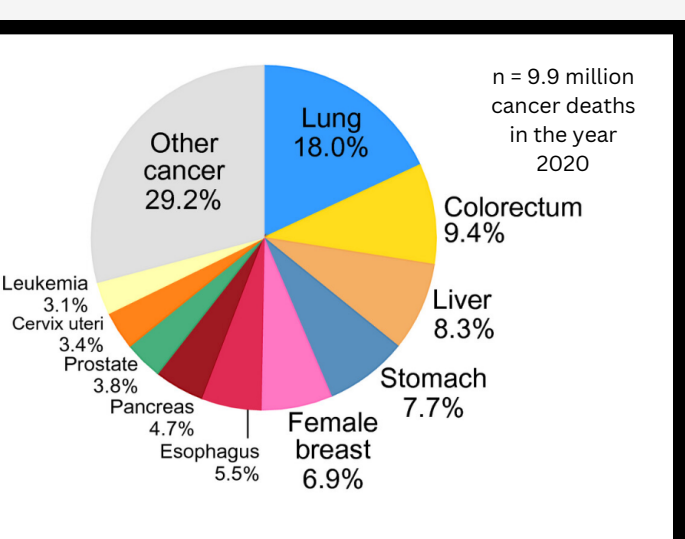


Figure 7. Global incidence of cancer mortality in the year 2020.

Discussion

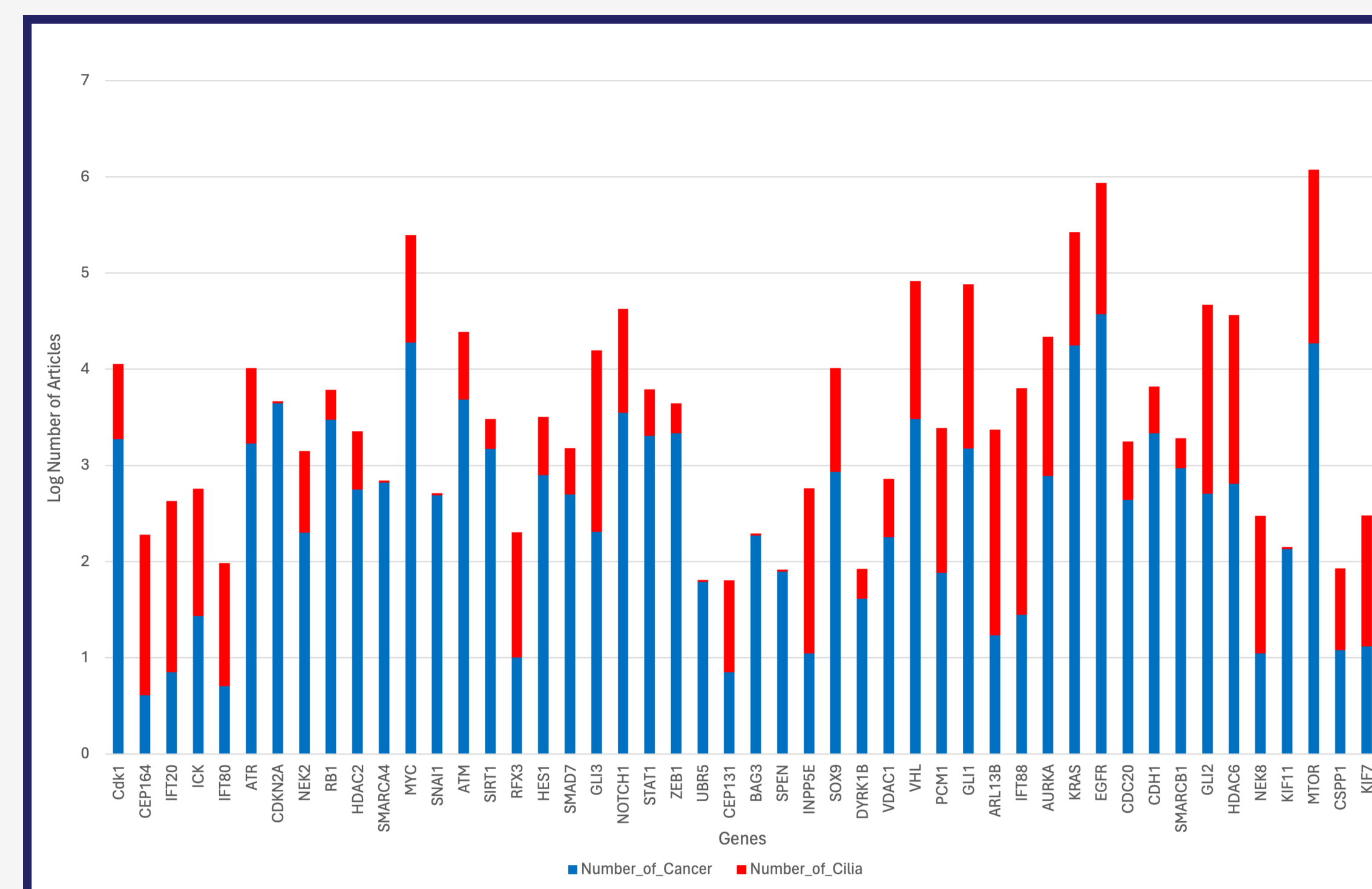


Figure 10. Total number of articles related to Cilia and Cancer represented as a log number for all the genes analysed in Figures 8 and 9.

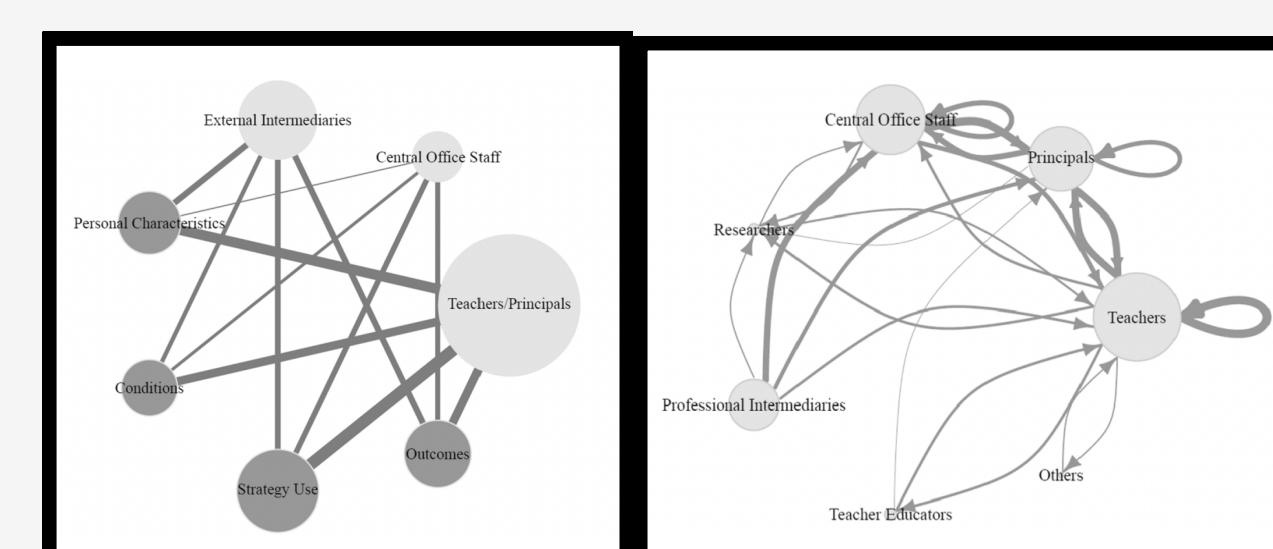


Figure 11. Examples from the literature that use similar methodologies to examine relationships between siloed aspects of other disciplines.

This study integrates concepts from social network analysis and brokerage theory, highlighting how brokers like teachers and principals facilitate knowledge transfer and collaboration across different parts of the educational system. The study identified a convergence between theoretical insights on brokering in educational settings and practical implications from empirical research, revealing how brokers play pivotal roles in bridging gaps between theory, practice, policy, and research in education. This study solely investigates the influence that different brokers have on other stakeholders. It does not consider how alterations in one that might cause changes in the other.

Conclusion

- The approach taken in this study provides a unique method of merging the depth of a meta-analysis along with the scope of an interdisciplinary study.
- The proof of principle example lays the foundation for a comprehensive understanding of the relationships between Genes, Cilia and Cancer.
- Our approach identified genes whose contributions to cilia and cancer were un(der)-explored. A few examples of these genes were, Cep131, SNAI1, ICK, KRAS, VHL and EGFR.
- We hope that our novel approach to bridge typically siloed areas of study in order to postulate new hypotheses (especially connecting applied and fundamental research topics in biology), is of broad interest to the scholarly community

References



Feedback