

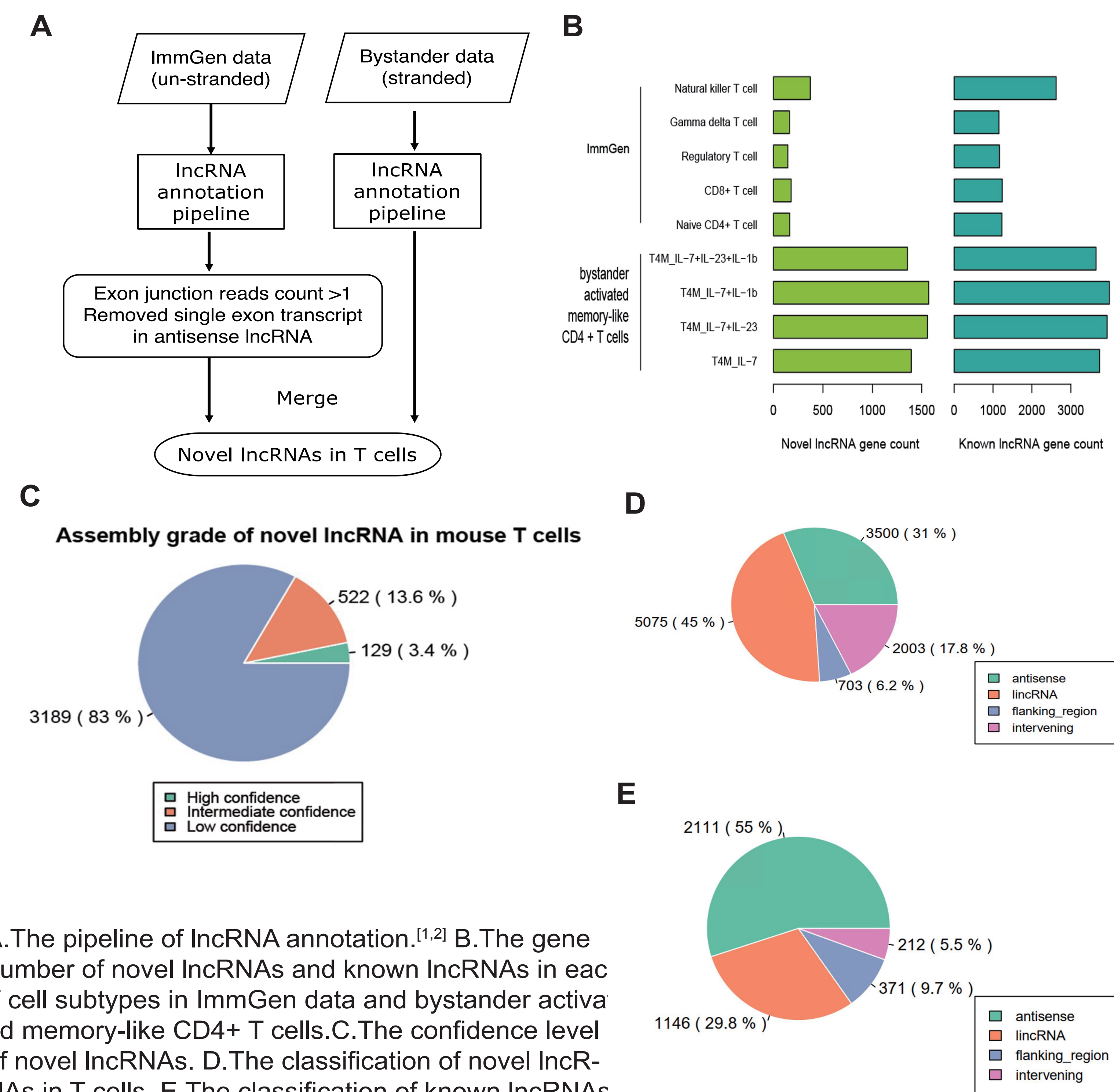
Abstract

With the development of high-throughput sequencing, there is increasing evidence that Long non-coding RNA(lncRNAs) are involved in a large number of cellular functions, including gene regulation, chromosome organization and splicing. T cells play an important role in immune response, and some lncRNAs have been shown to regulate T cell differentiation and function. However, the annotation of lncRNA in T cell is still not complete. We used RNA-seq data from various subtypes of T cells to perform in-depth assembly and annotation of lncRNAs through more appropriate pipelines. Differentially expressed lncRNAs in various types of T cells were identified and functionally annotated. In addition, by comparing human and mouse data, we identified evolutionarily conserved lncRNAs that are more likely to exercise functions in T cells, providing support for functional studies of lncRNAs in T cells.

Keywords: Long non-coding RNA, T cell, RNA-sequencing, Cell type-specific expression, conservation

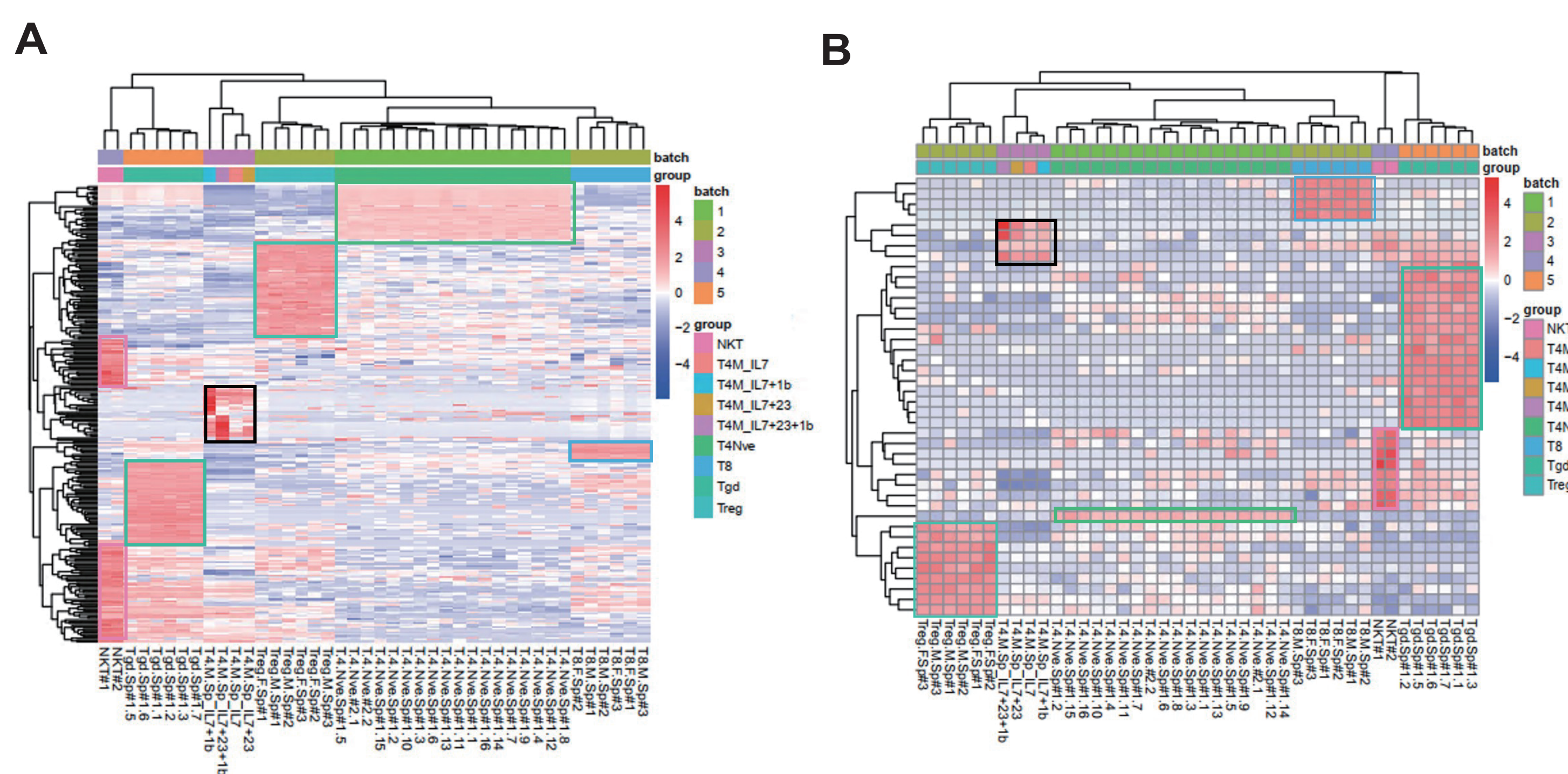
Results

Figure 1. A pipeline for lncRNA profiling in mouse T cells



A. The pipeline of lncRNA annotation.^[1,2] B. The gene number of novel lncRNAs and known lncRNAs in each T cell subtype in ImmGen data and bystander activated memory-like CD4+ T cells. C. The confidence level of novel lncRNAs. D. The classification of novel lncRNAs in T cells. E. The classification of known lncRNAs in T cells.

Figure 2. Differential gene expression between T cell subtypes

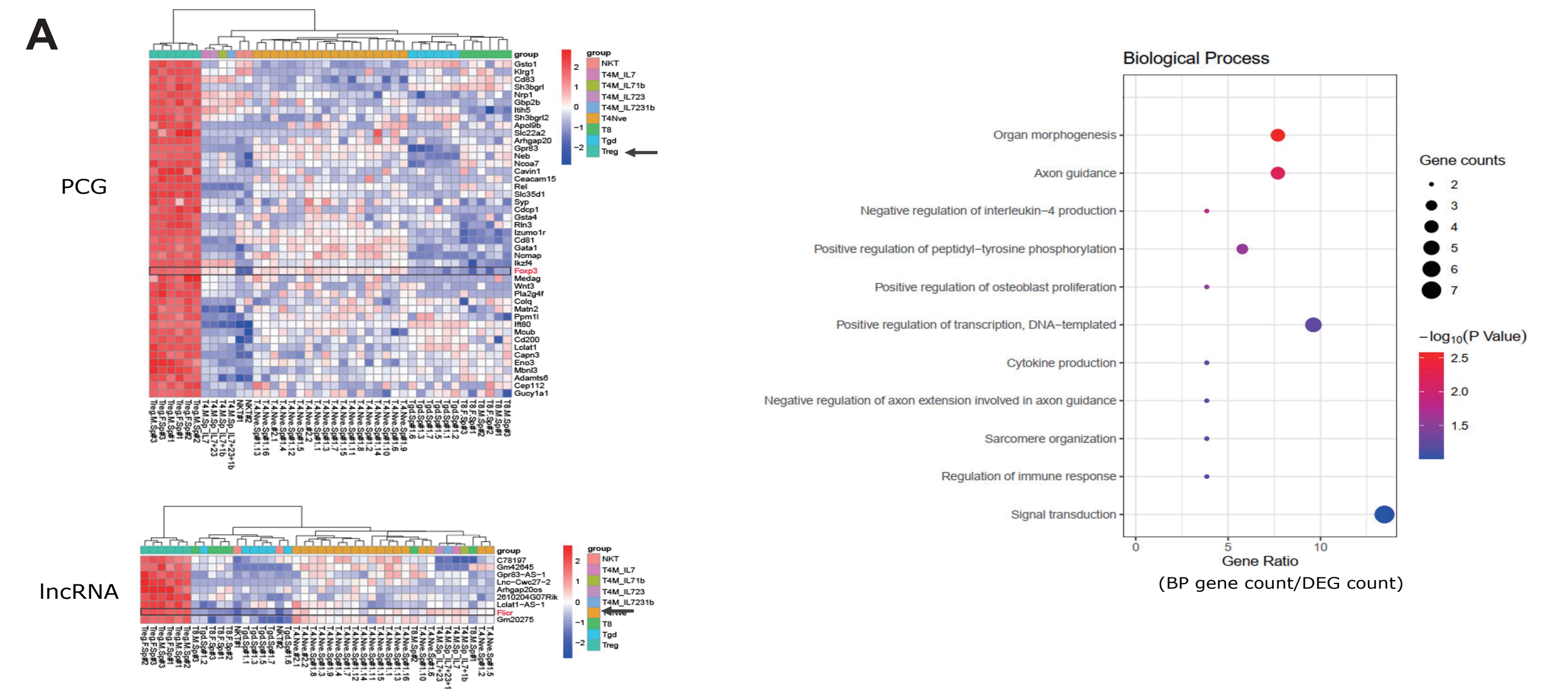


A. Differentially expressed protein coding genes between T cell subtypes. B. Differentially expressed lncRNAs between T cell subtypes.

References

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3. Chen, J., Shishkin, A. A., Zhu, X. et al. Evolutionary analysis across mammals reveals distinct classes of long non-coding RNAs. Genome Biol 17, 19 (2016). <https://doi.org/10.1186/s13059-016-0880-9>

Figure 3. Functional annotation of Treg specific genes



A. The figure on the left shows the specific expression of PCG and lncRNA in Treg, and the figure on the right shows the functional fixation of the specific expression of PCG in Treg. We speculated that the specific expression of PCG and lncRNA in Treg may have similar functions.

Figure 4. The number of lncRNAs in mouse and human T cells.

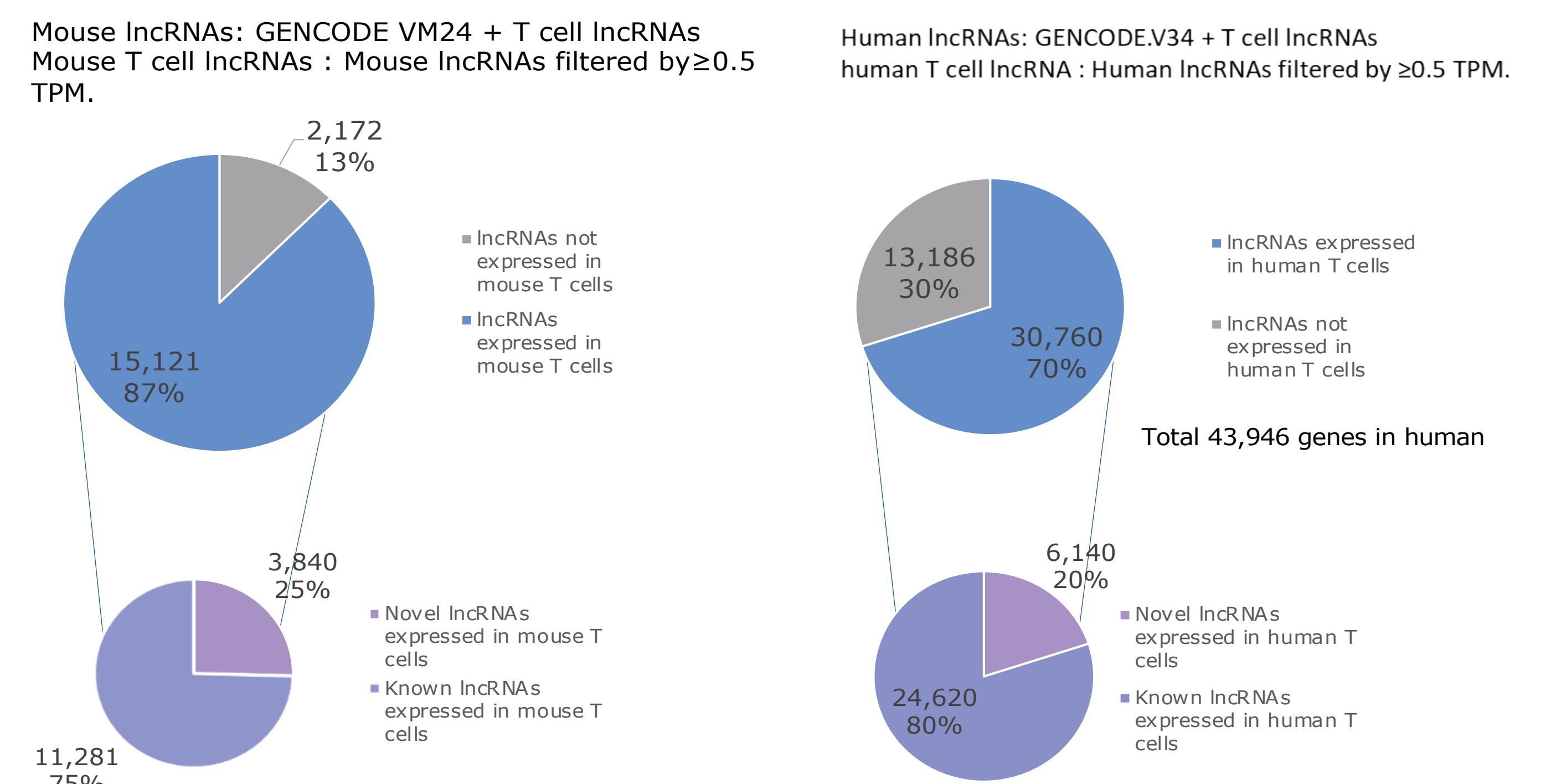
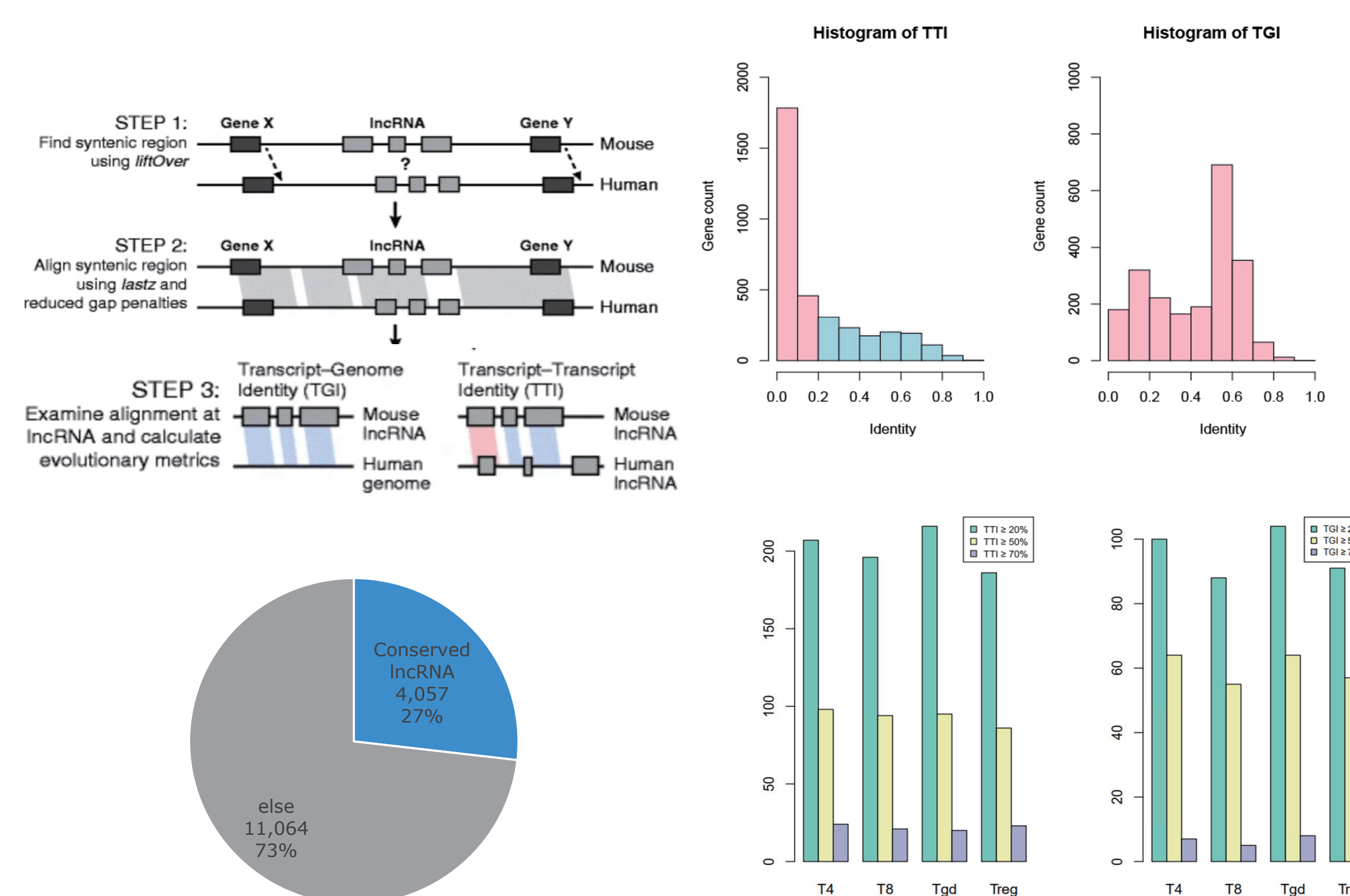


Figure 5. Conserved lncRNAs in mouse and human T cell subtypes



A. Schematic of slinky's orthology pipeline and metrics for measuring sequence and transcript evolution.^[3] B. 4,057 lncRNAs in mouse were conserved with human lncRNAs. C. Histogram of Identify in conserved lncRNAs. TTI: Transcript-Transcript Identity, TGI: Transcript-Genome Identity. D. The number of Conserved lncRNAs at different Identity levels in each T cell subtypes.

Conclusions

- Long non-coding RNAs were cell type-specifically expressed in T cells.
- Functional related lncRNAs were identified by modularization of protein coding genes and lncRNAs and functional annotation of protein gene modules in T cells.
- Functional related lncRNAs were identified by identifying conserved lncRNAs between each T cell subtype in mouse and human T cells.

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