# Creating a new Human Brain Transcriptome from Iso-Seq data

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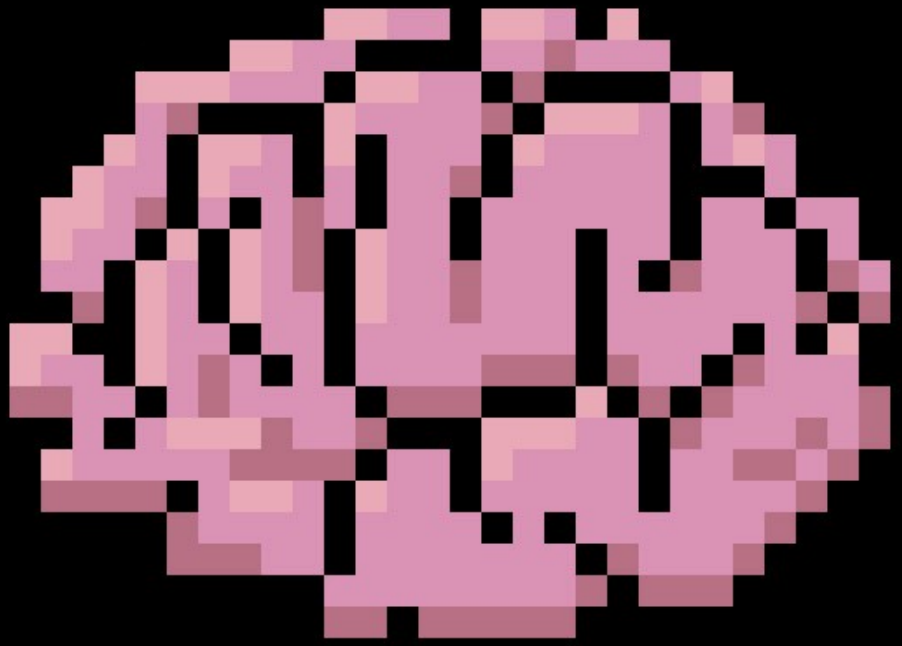
PI: Dr. Chunyu Liu

# Goals

- Create new reference of human brain
- Update with new Isoforms
- Study through RNA-Seq Alignment



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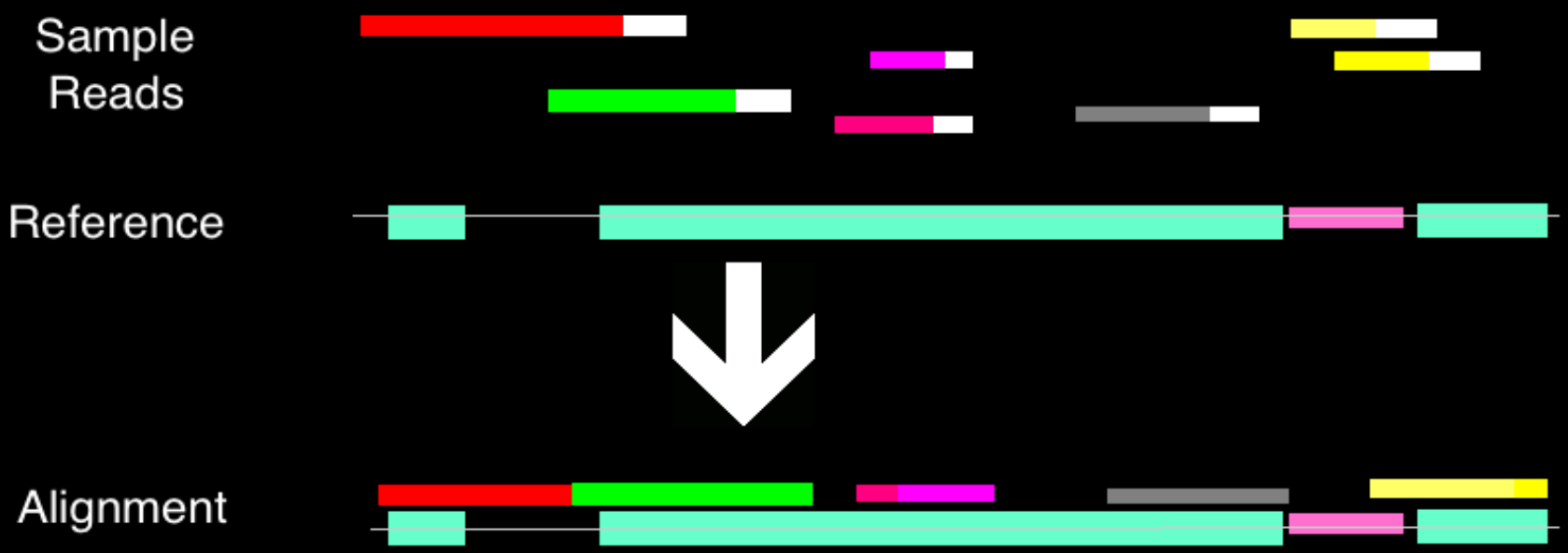
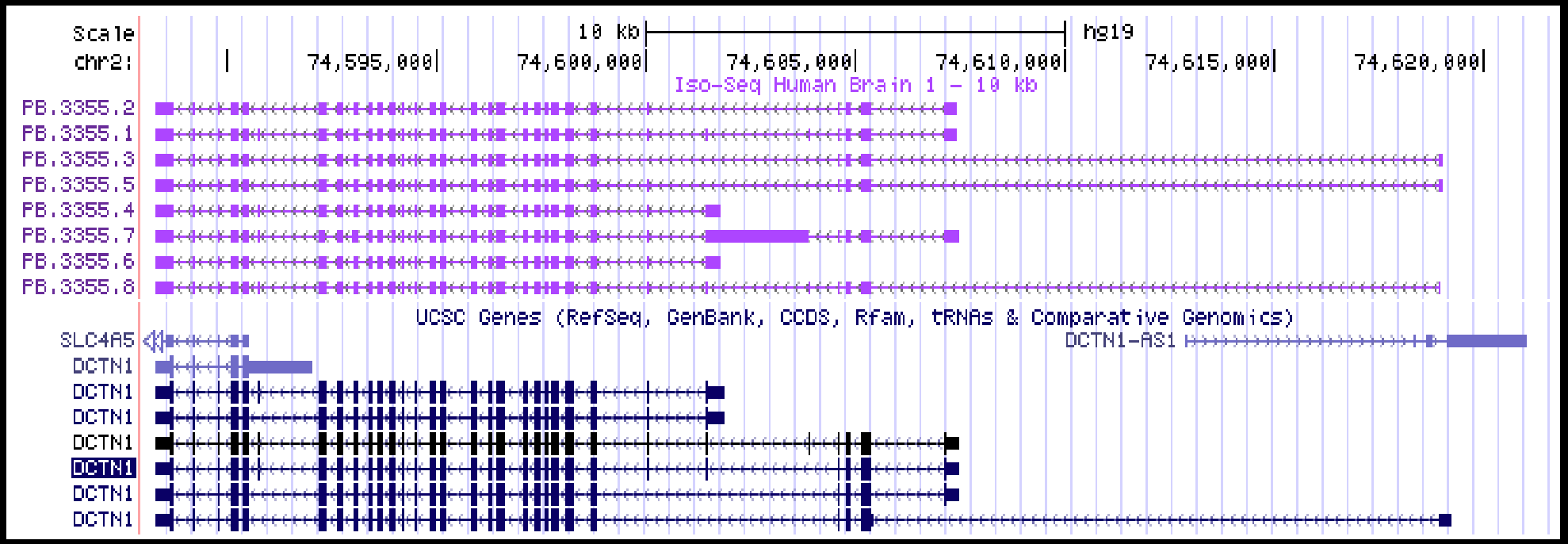


# Pacific Biosciences (PacBio)

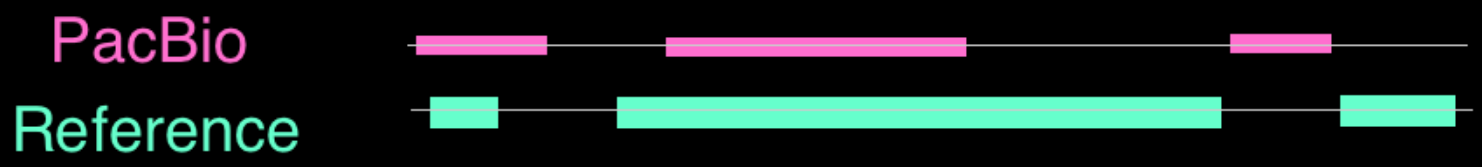


- Iso-Seq data (Very long transcripts)
- DCTN1 gene in UCSC Genome Browser



# Adding Iso-Seq (PacBio) data





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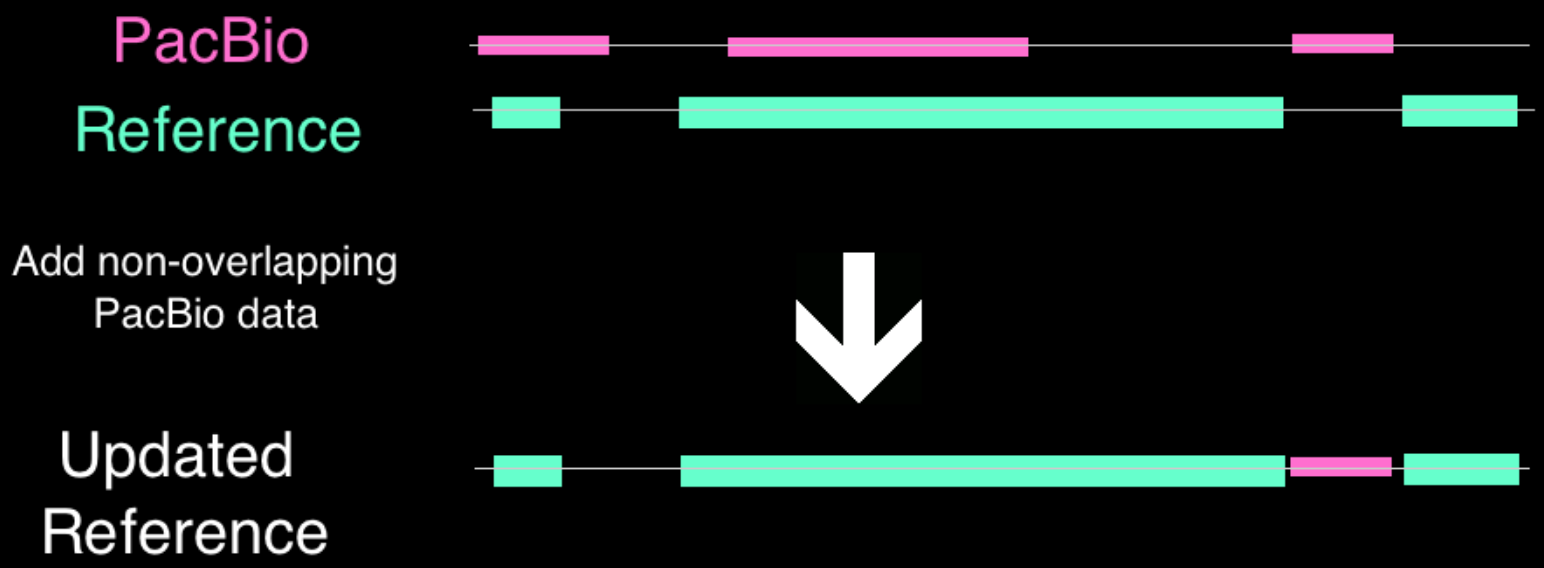

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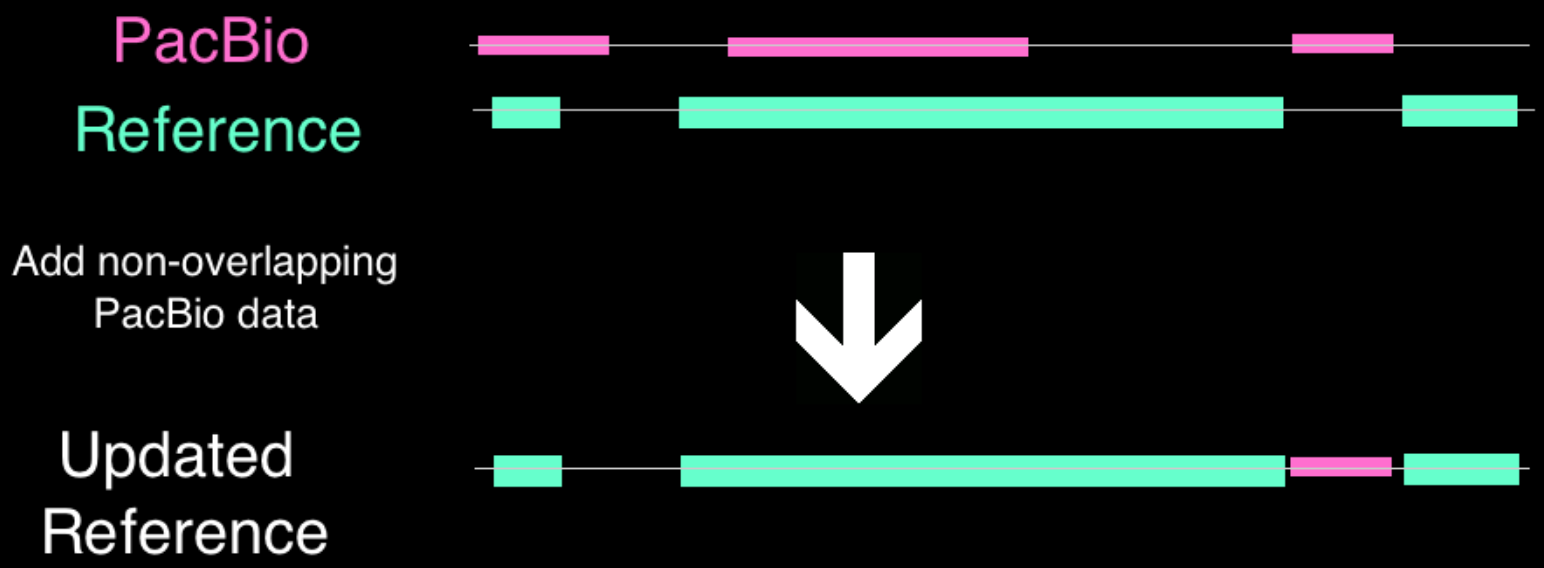


## PacBio transcripts/exons

166 non-overlapping

$4 \times 10^6$ overlapping

# RNA-Seq Alignment

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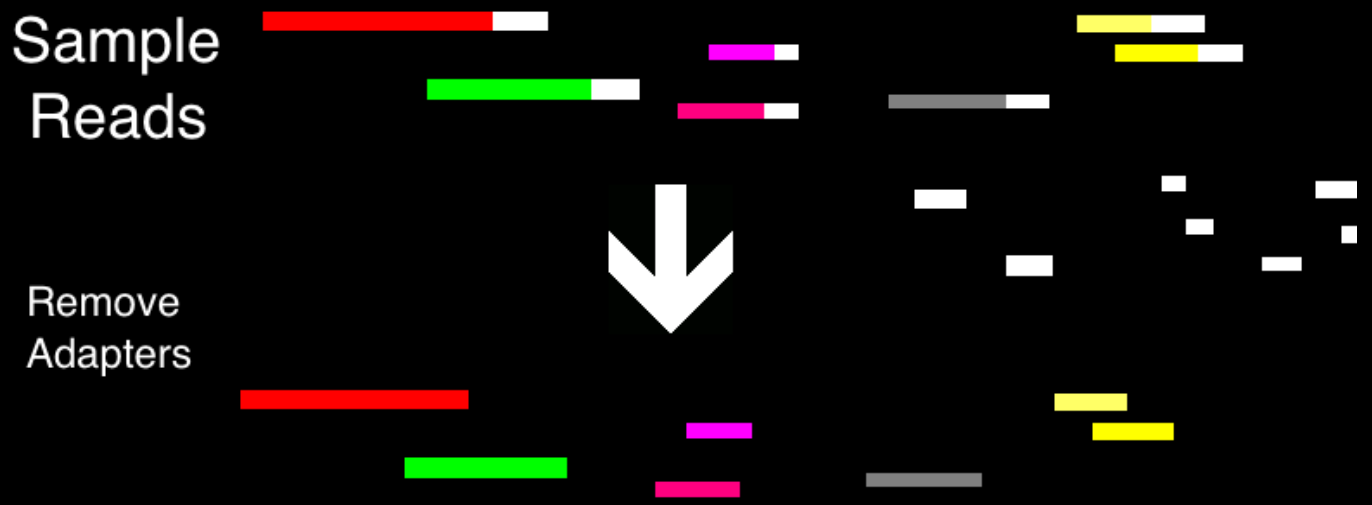

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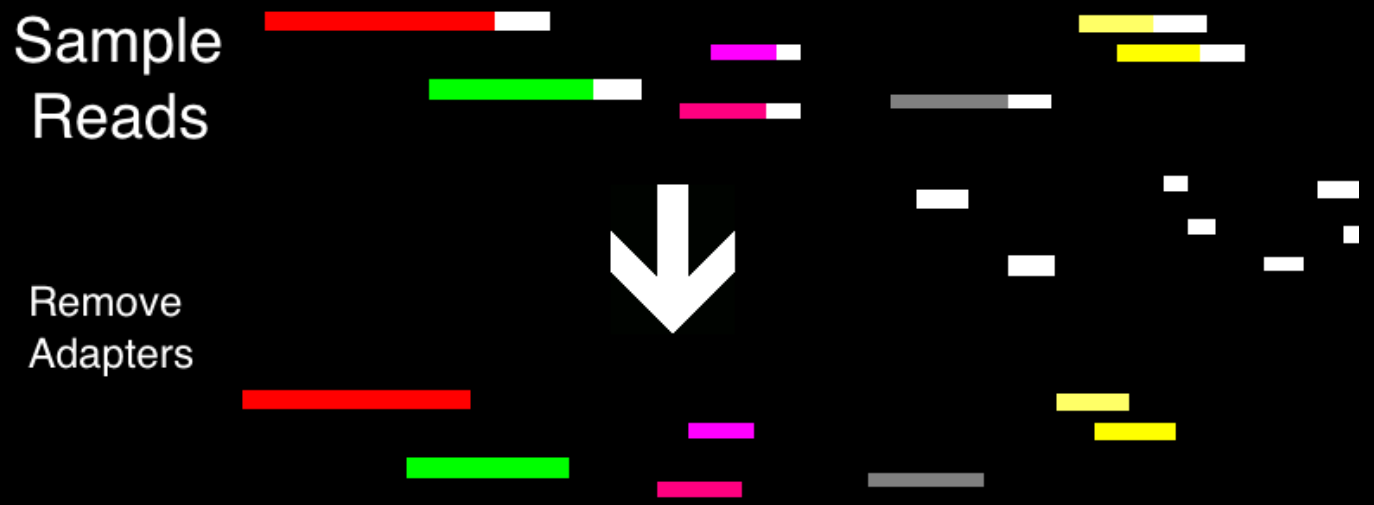


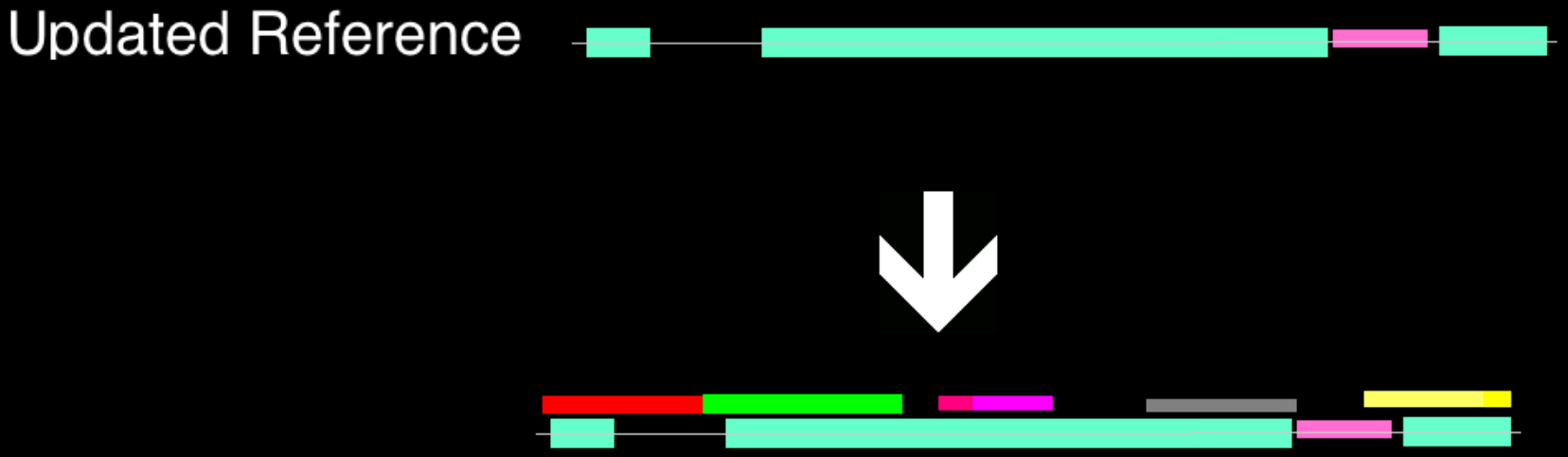

# RNA-Seq Alignment

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Alignment Statistics

Read Count
FPKM (length-normalized expression)

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Read Count

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FPKM

# Sequence Samples

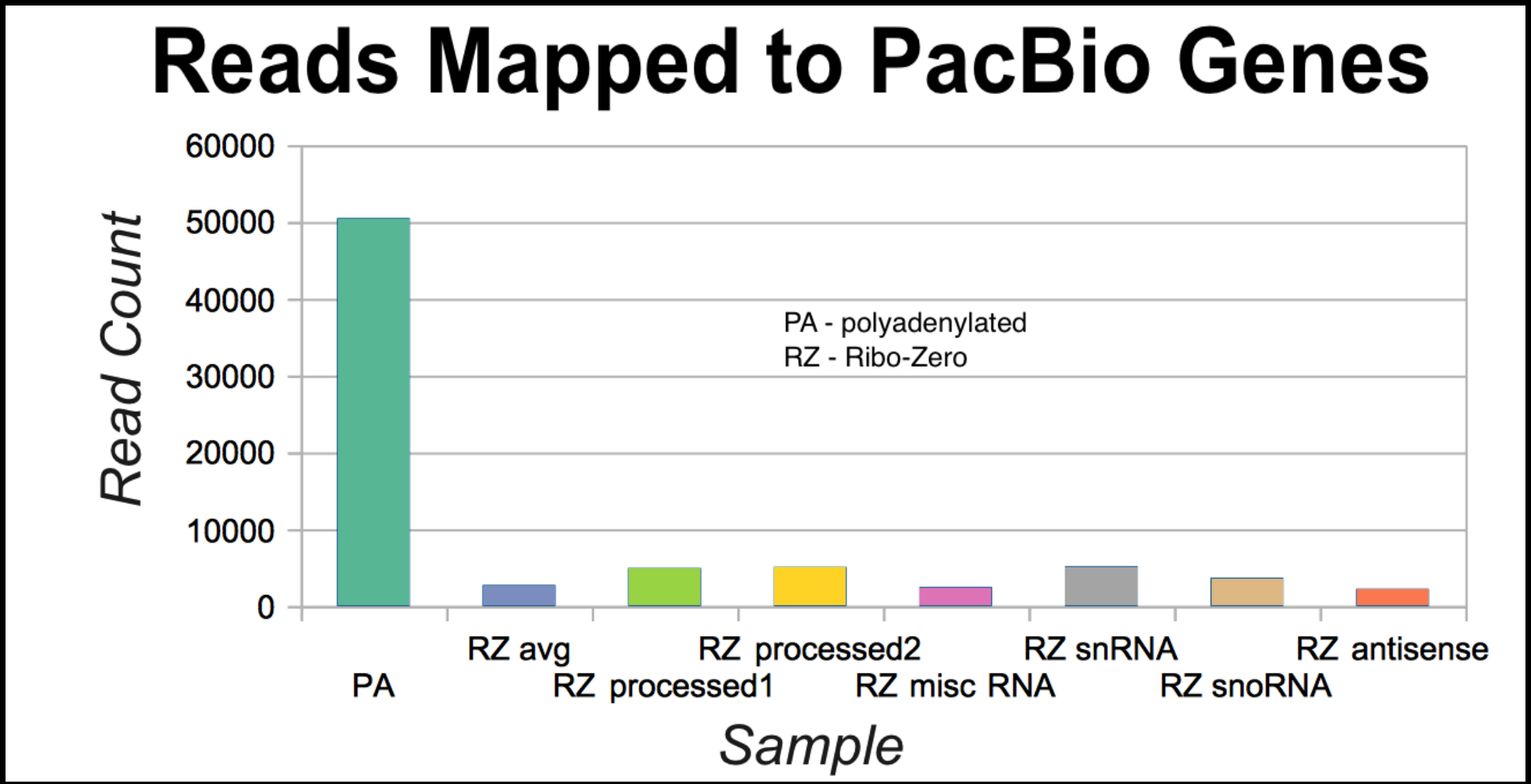
- Polyadenylated (Protein Coding RNA)
- Ribo-Zero (All RNA)
    - Average among all RNA types
    - High in specific type of RNA
        - Antisense
        - Processed Transcripts
        - snRNA
        - snoRNA
        - misc RNA

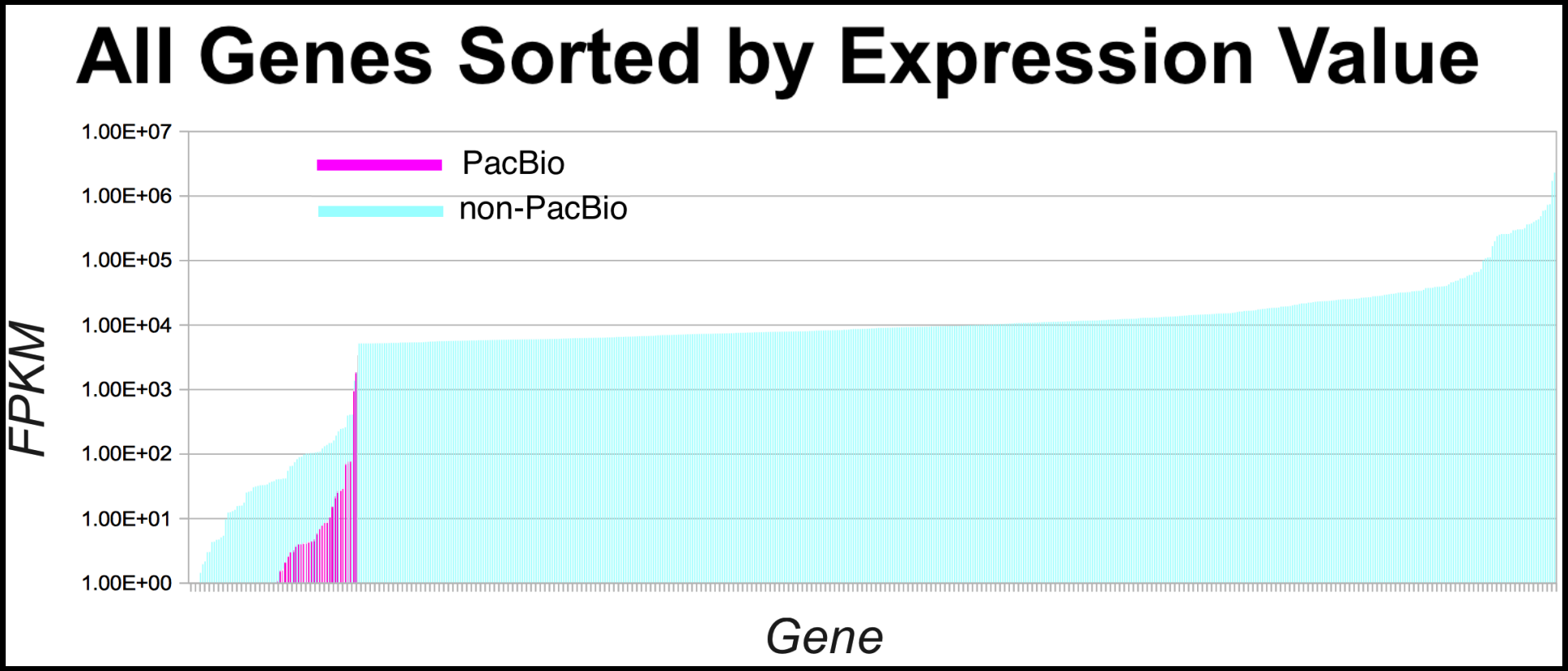
# Results

- Out of 166 non-overlapping (PacBio) transcripts/exons:

96 had aligned reads (from either polyA or Ribo-Zero),

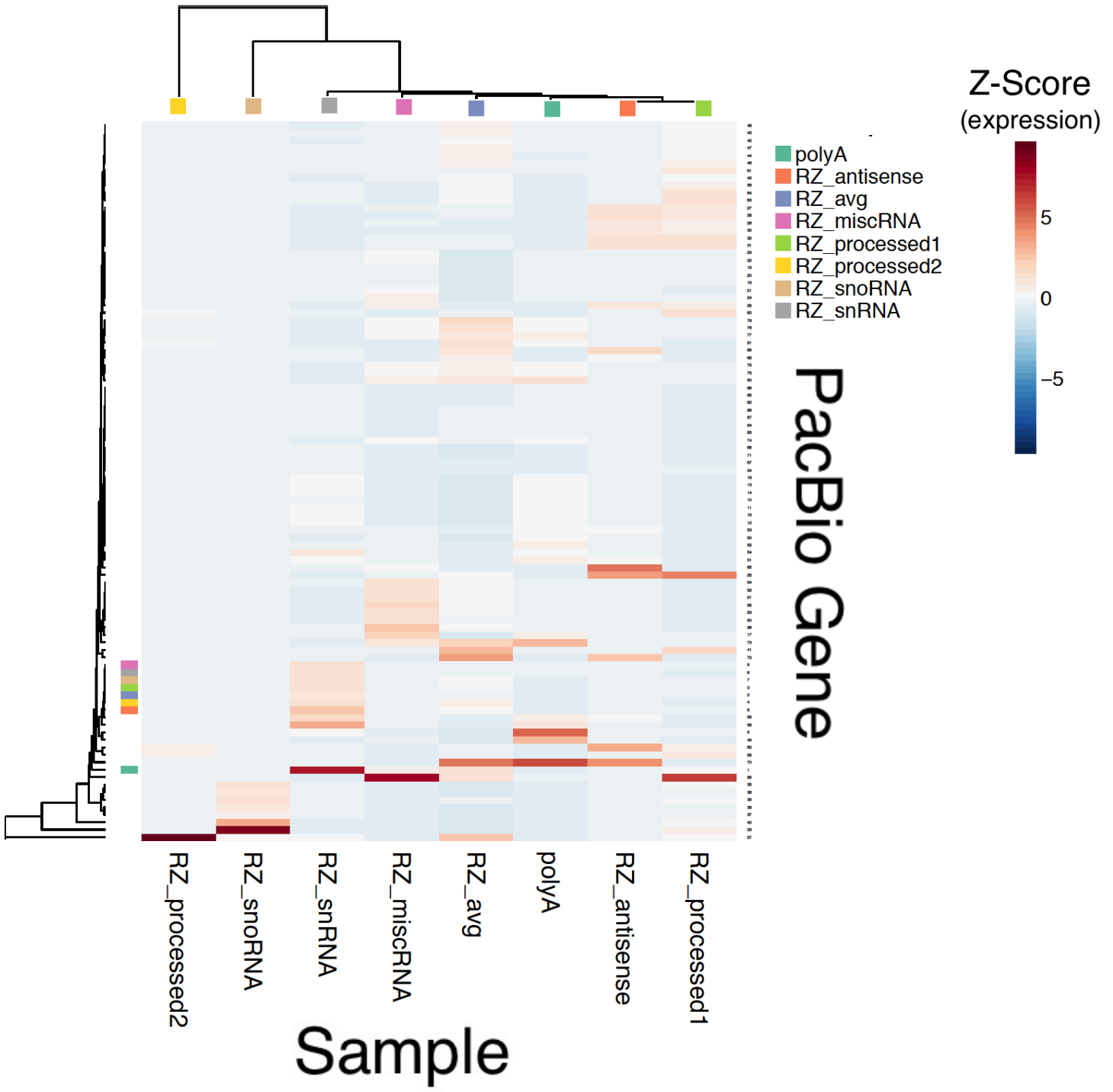
73 of which had FPKM > 0.1


Reads Mapped to PacBio Genes
Read Count
60000
50000
40000
30000
20000
10000
0
PA - polyadenylated
RZ - Ribo-Zero
PA
RZ avg
RZ processed1
RZ processed2
RZ misc RNA
RZ snRNA
RZ snoRNA
RZ antisense
Sample


All Genes Sorted by Expression Value
1.00E+07
1.00E+06
1.00E+05
1.00E+04
1.00E+03
1.00E+02
1.00E+01
1.00E+00
PacBio
non-PacBio
FPKM
Gene

# FPKM Heatmap of PacBio Genes



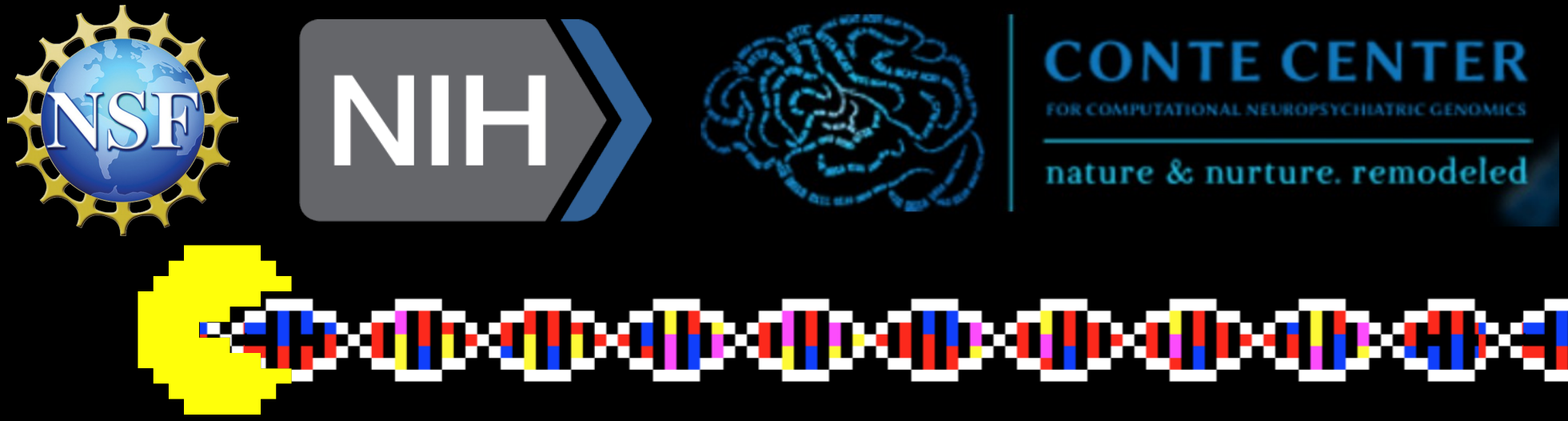
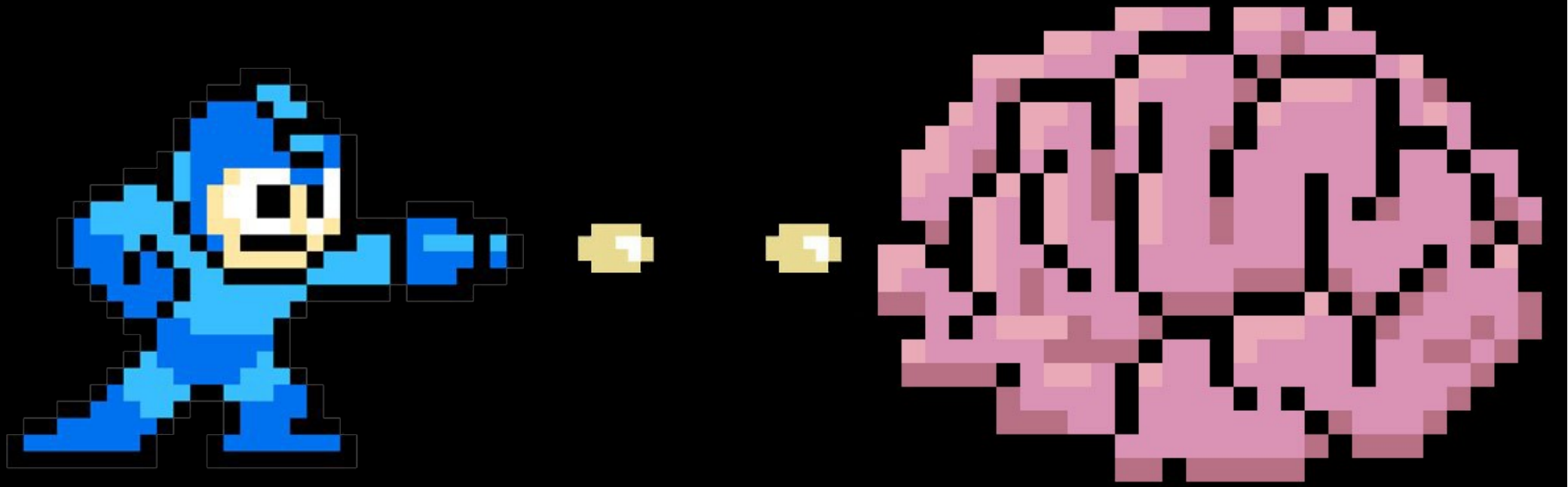


# Conclusion

- New information for reference
- Application of genetic factors to disorders
- Ability to annotate sequencing samples
- Rough estimate
- What next?

# Acknowledgements

Dr. Chunyu Liu
Dr. Elliot Gershon
Miguel Brown
Dr. Barry Aprison



# Questions?