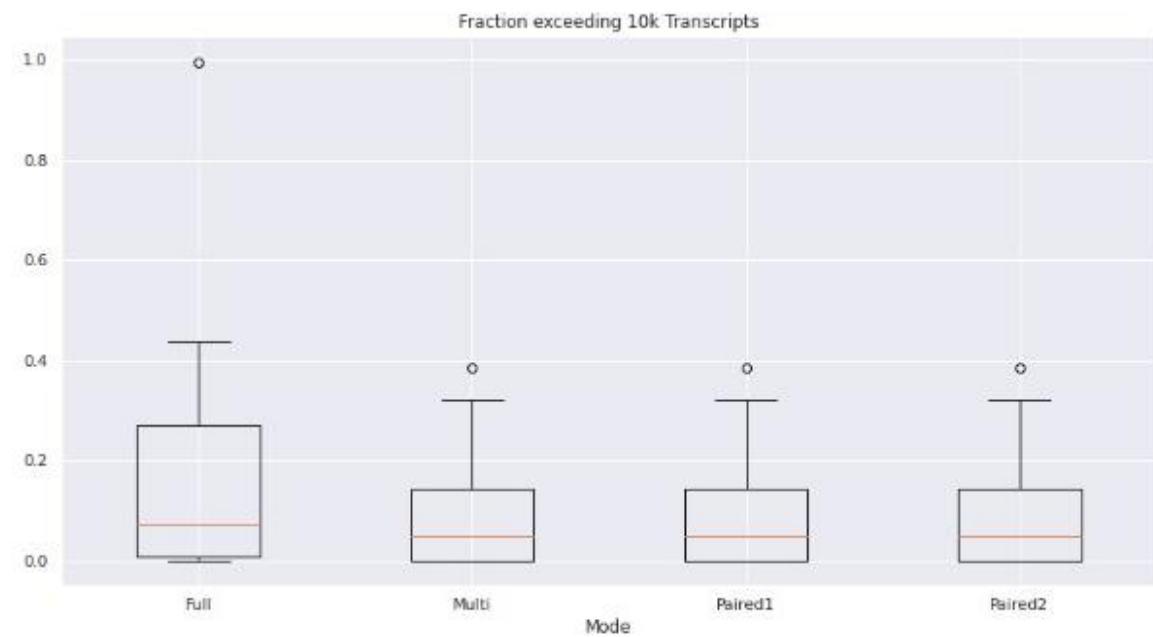
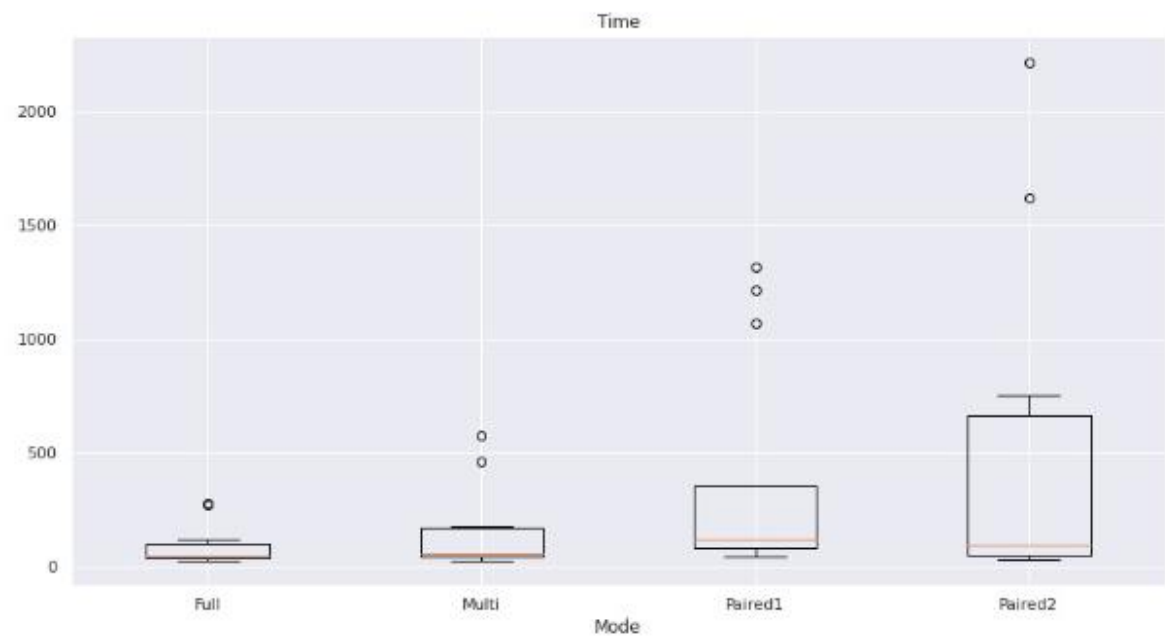


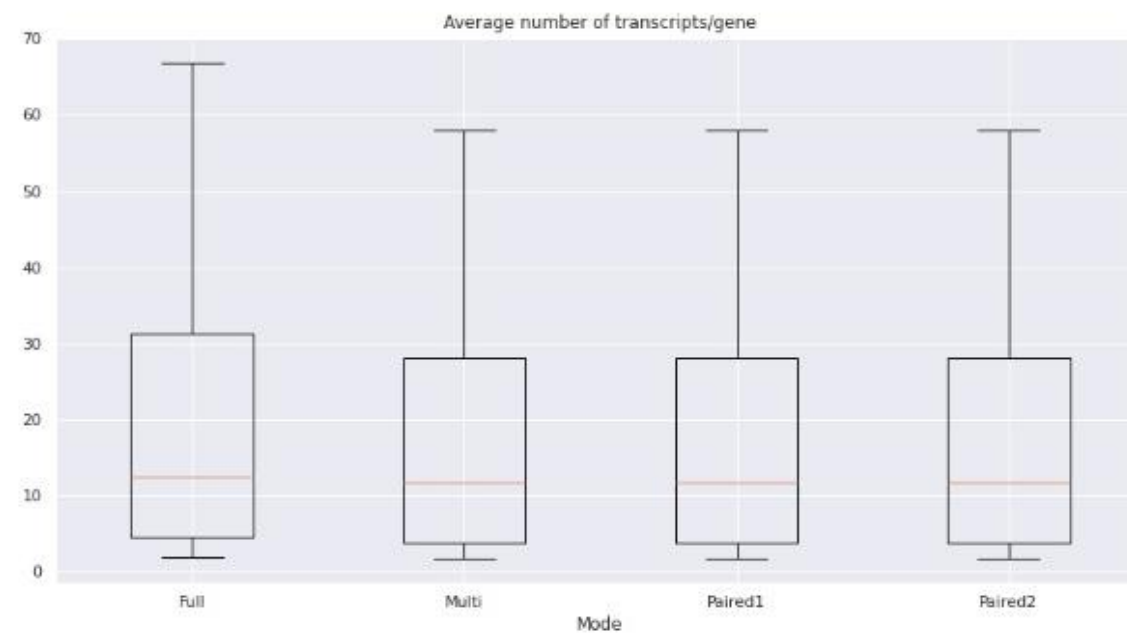
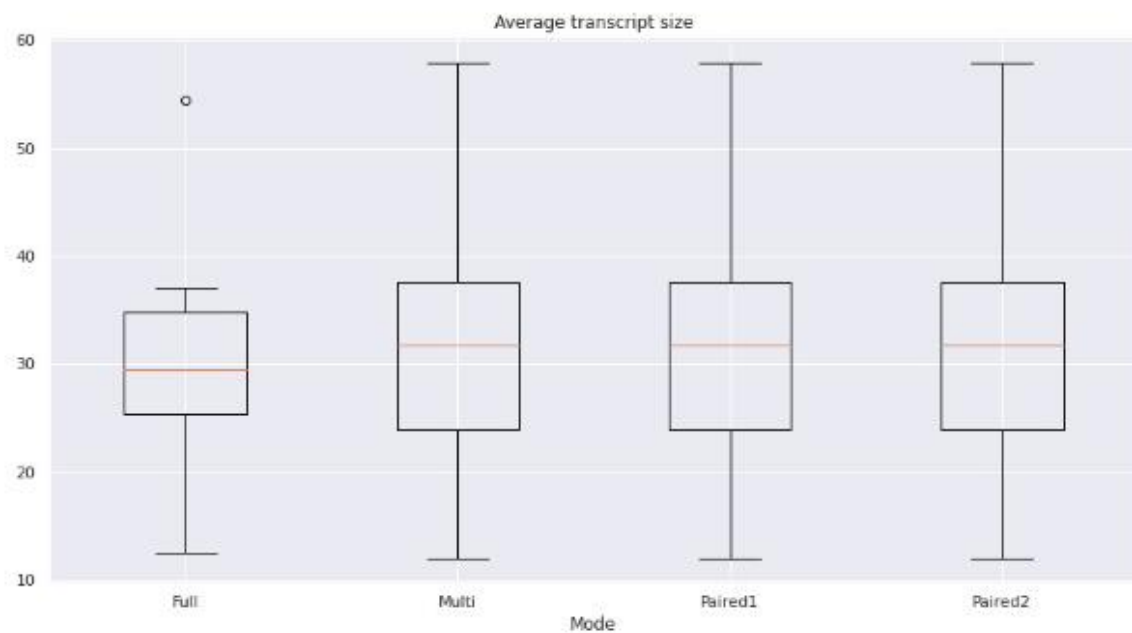
WP1

Path Enumeration

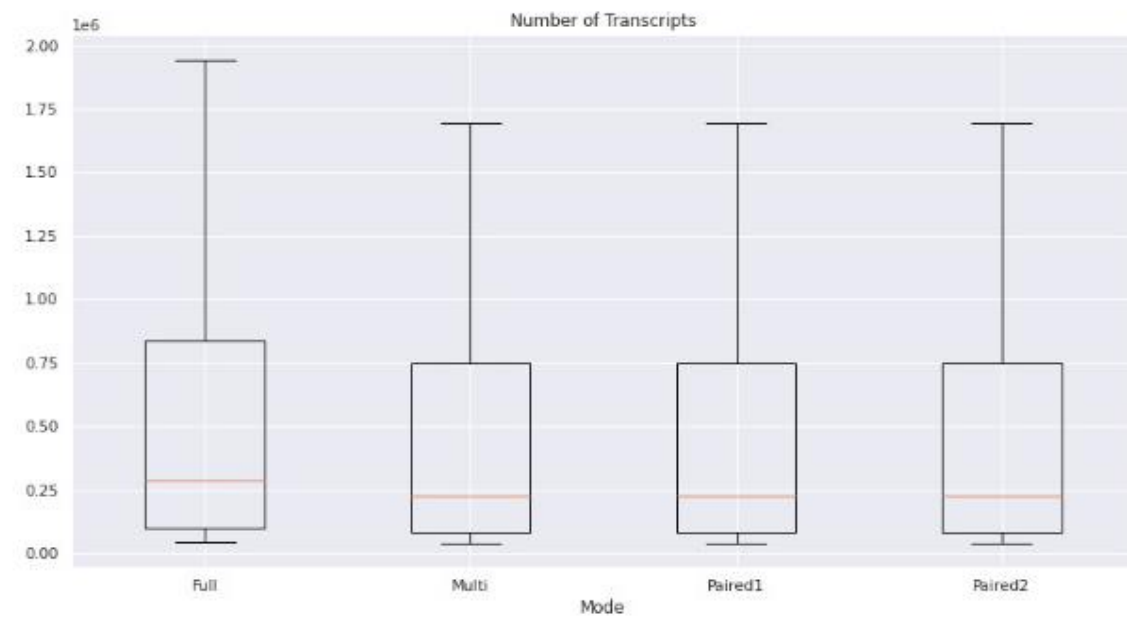
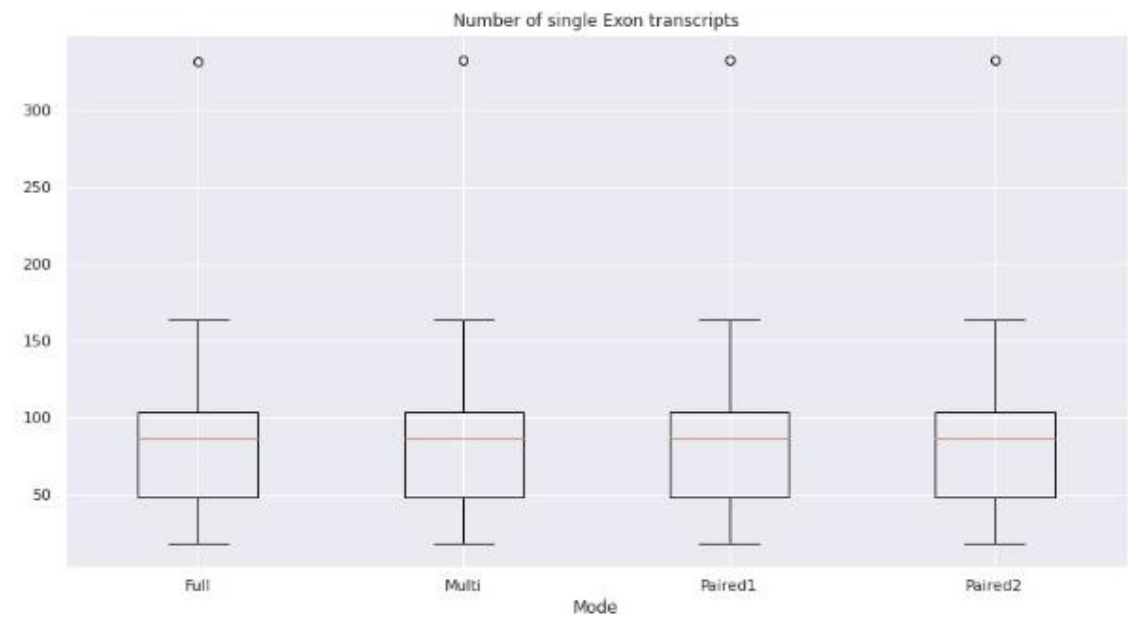
Runtime and Fraction exceeding 10k Transcripts



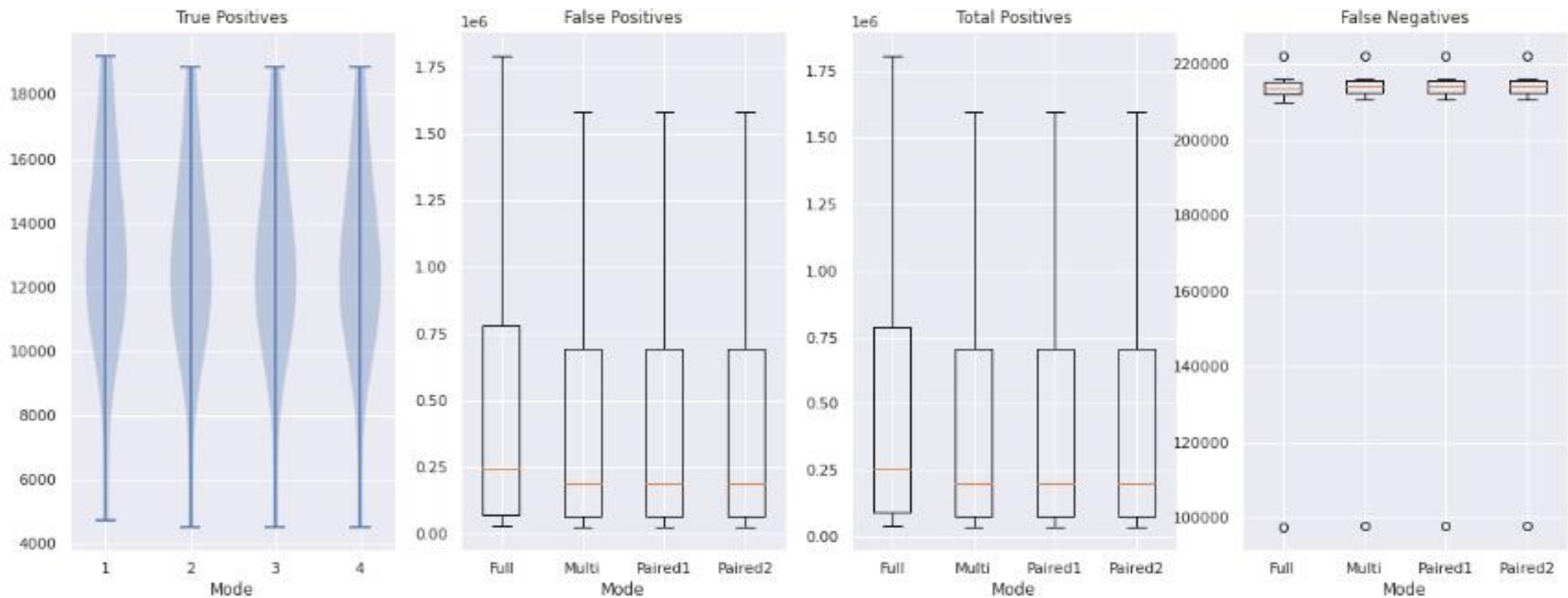
Transcript size and Transcripts per gene



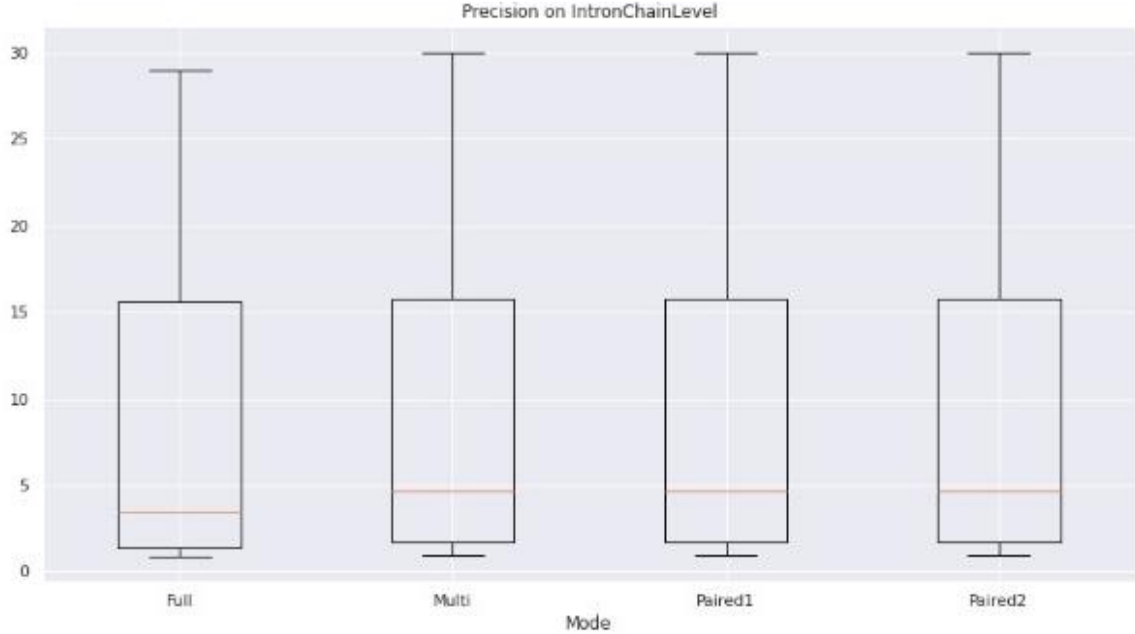
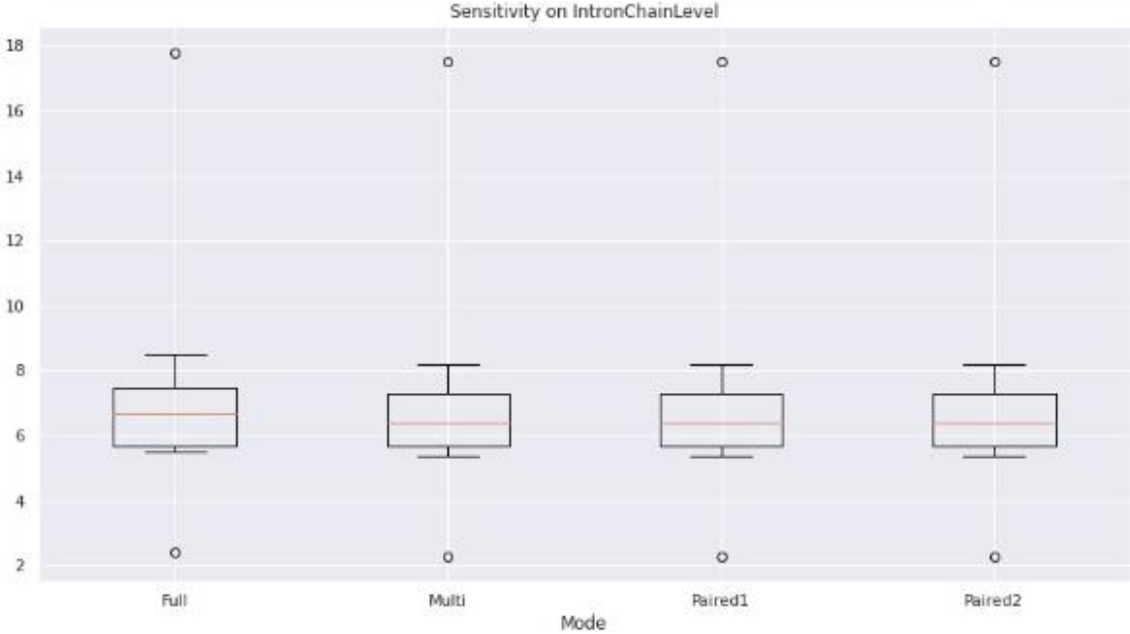
Single Exon Transcripts and Number of Transcripts



Single Exon Transcripts and Number of Transcripts



Sensitivity and Precision



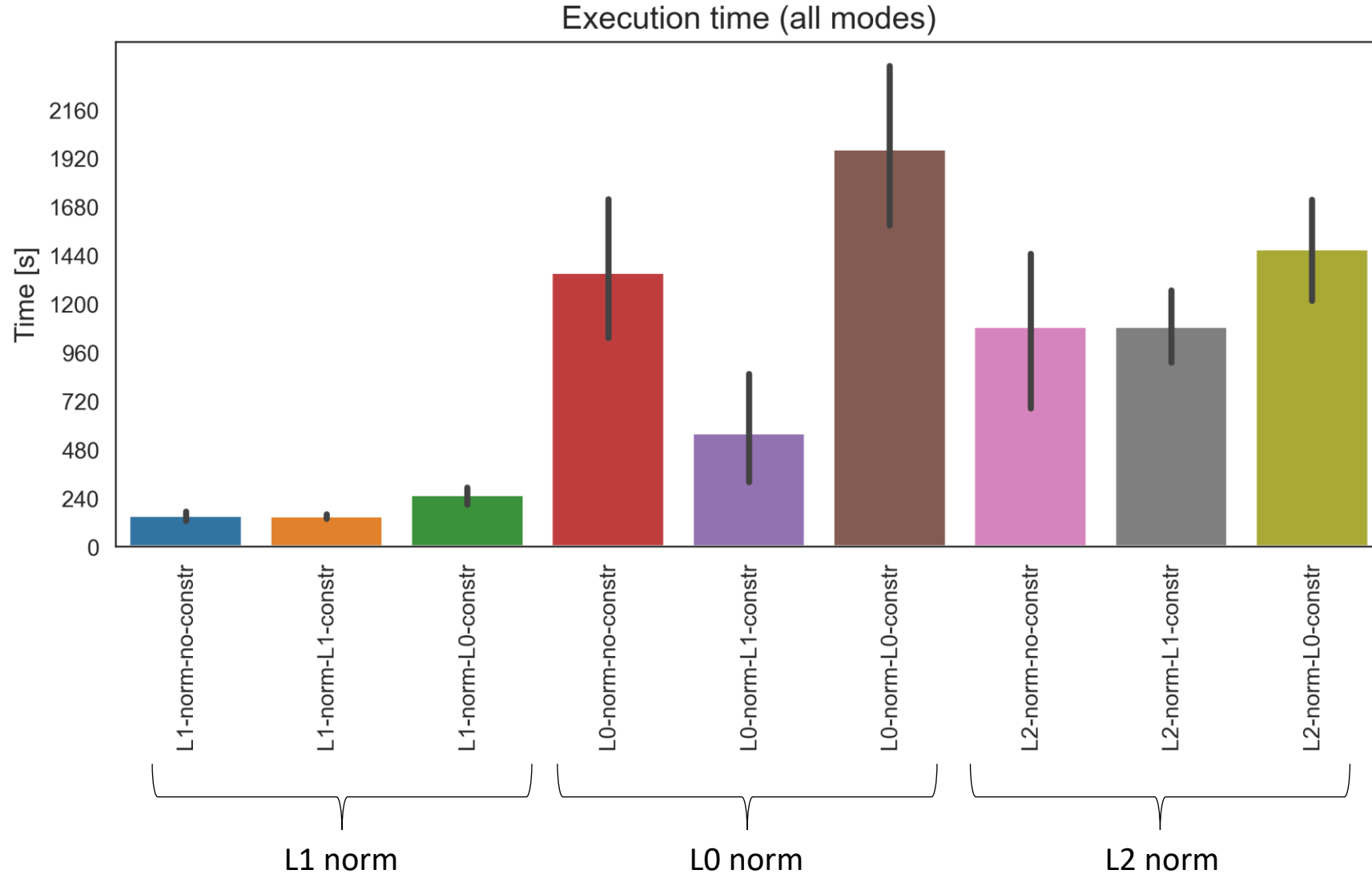
Datasets:

- Human_simulated
- Human_leukemia
- Human Diverse:
 - SRR307903
 - SRR307911
 - SRR315323
 - SRR315334
 - SRR387661
 - SRR534291
 - SRR534307
 - SRR534319
 - SRR545695

WP2

Optimization with Gurobi

- Execution time for one graph file

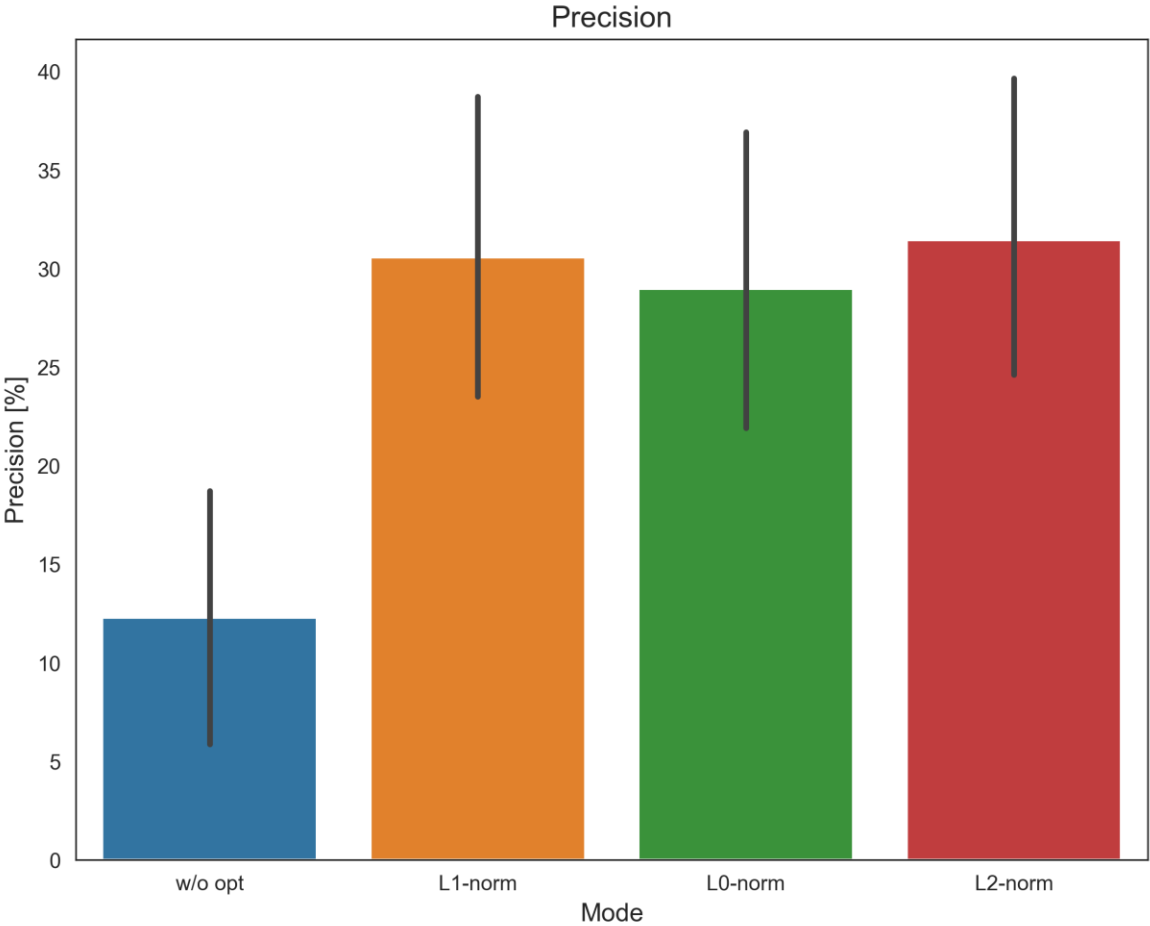
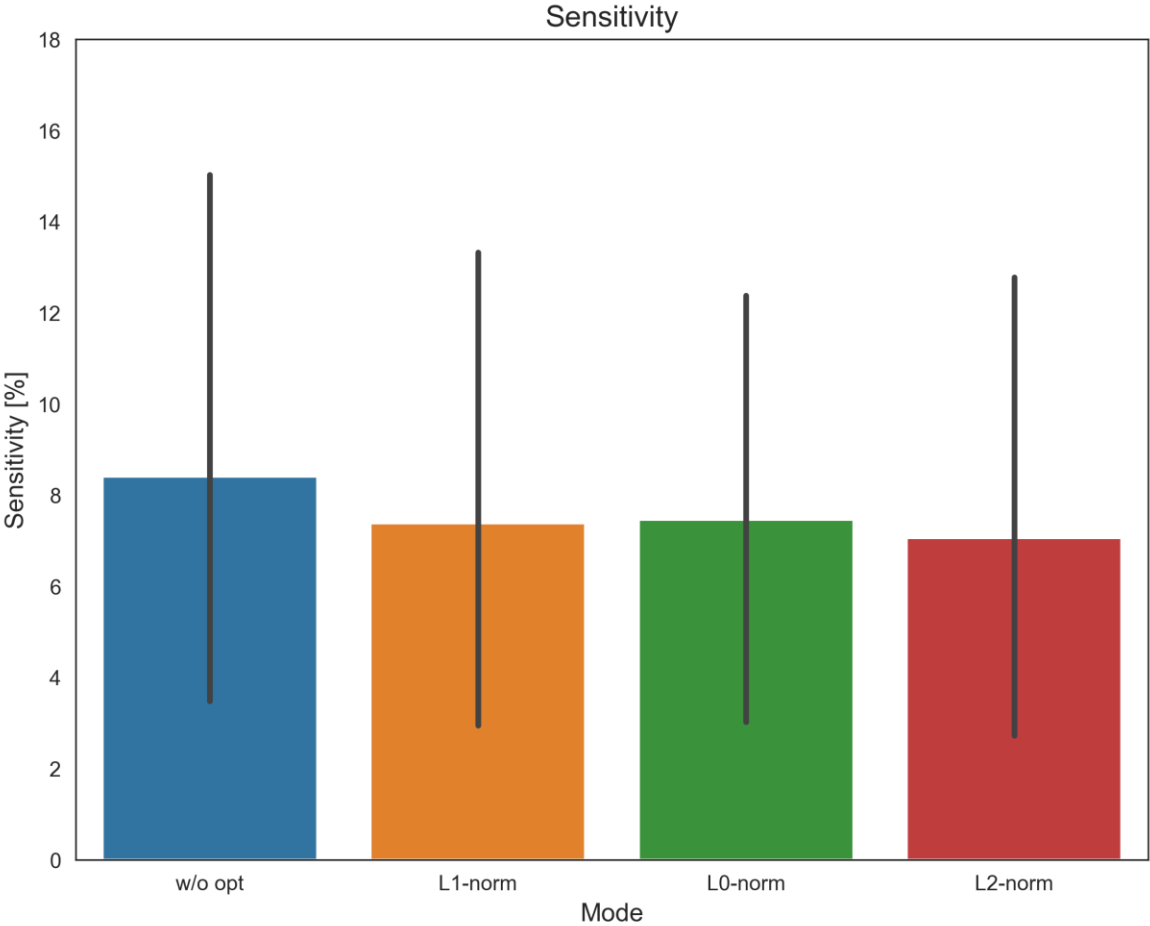


- Full Path Enumeration

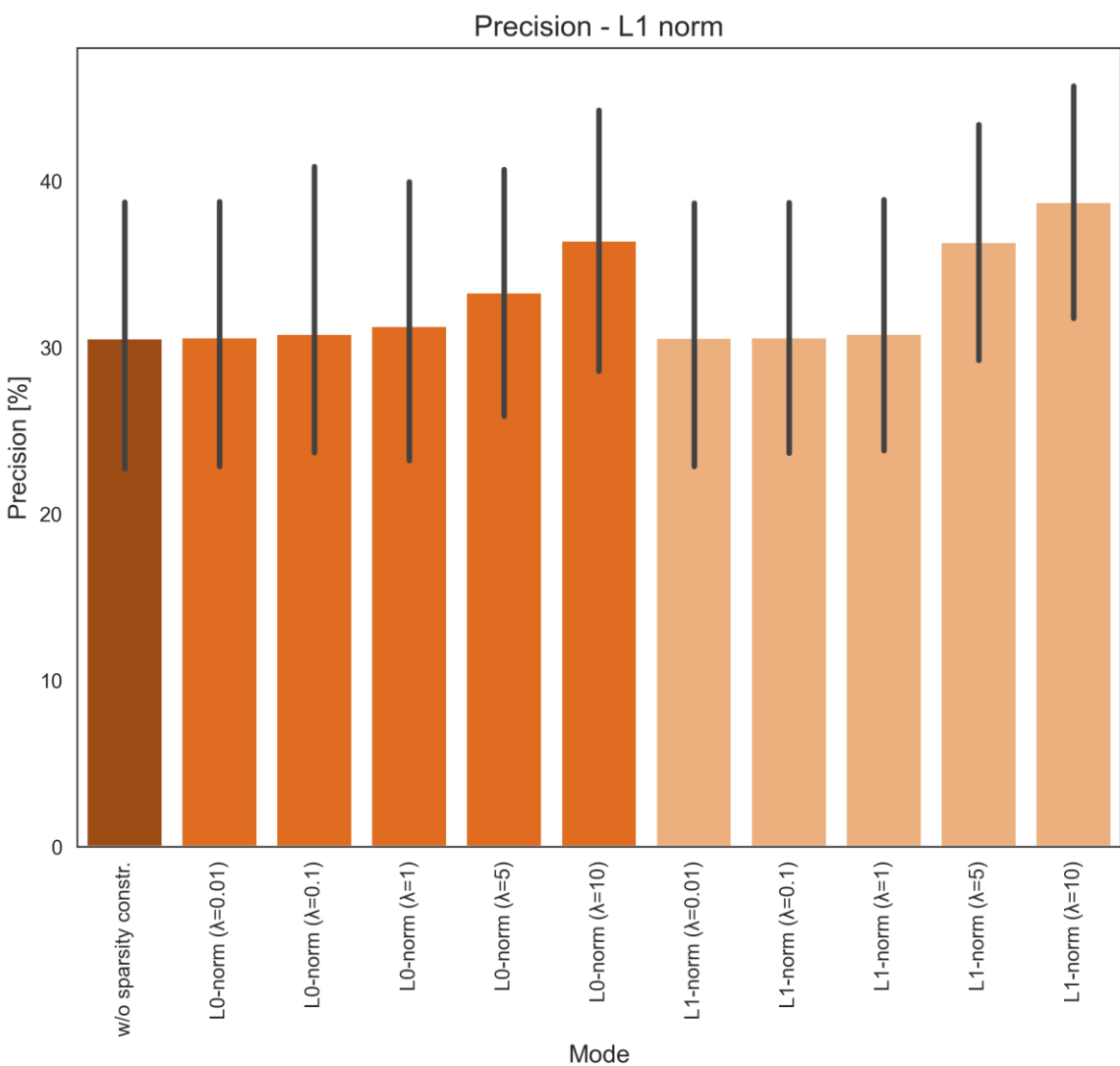
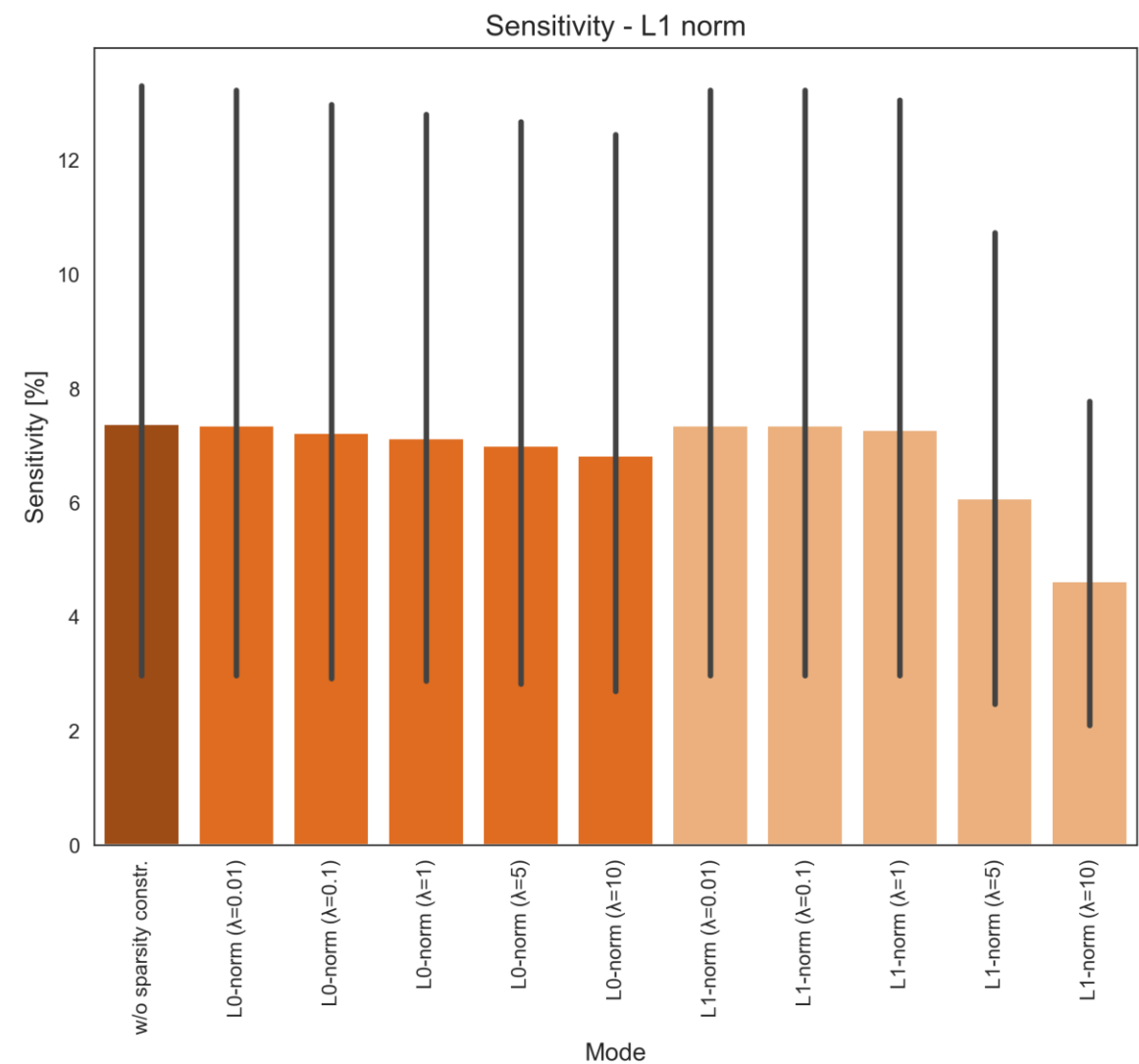
Datasets

- Human geuvadis simulated
- Human leukemia real
- Human diverse
 - SRR307903 (Fibroblasts)
 - SRR307911 (Embryonic stem cells)

- Sensitivity and Precision
- Without sparsity constraints



- Sensitivity and Precision
- With sparsity constraints

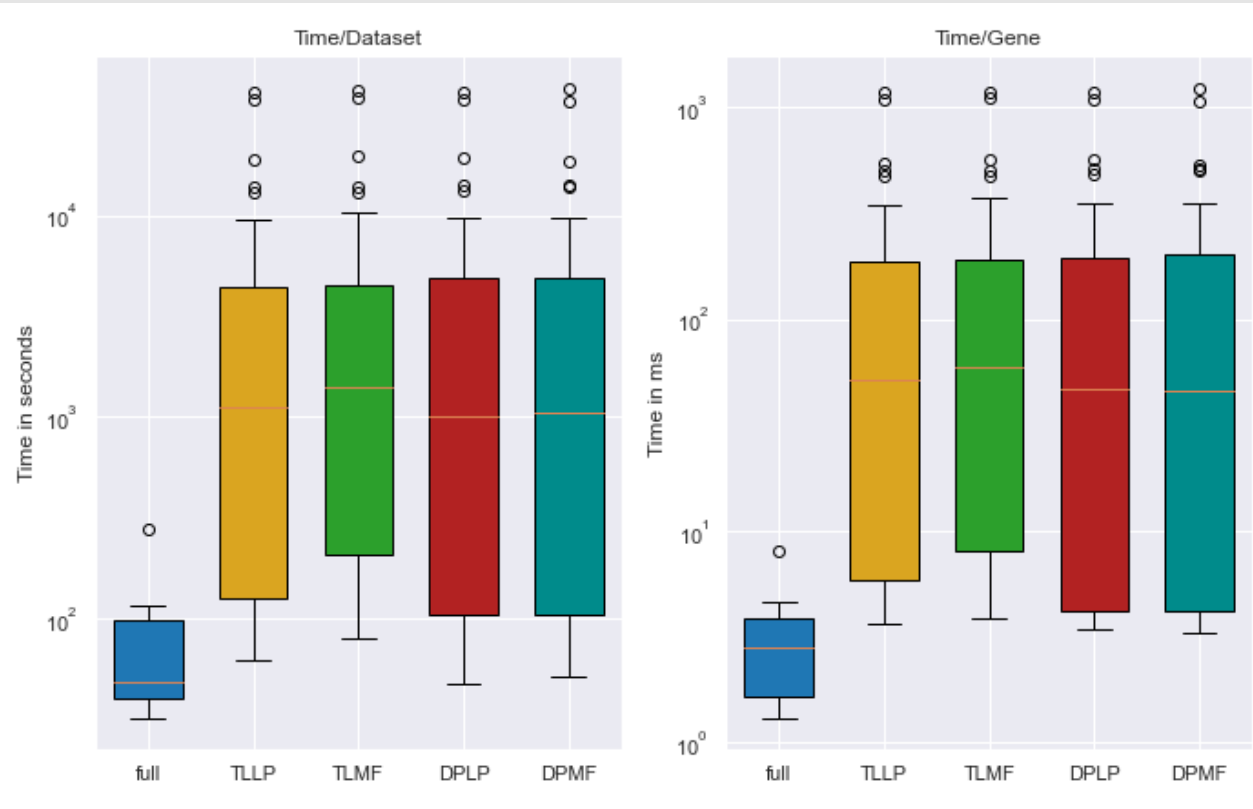


WP3

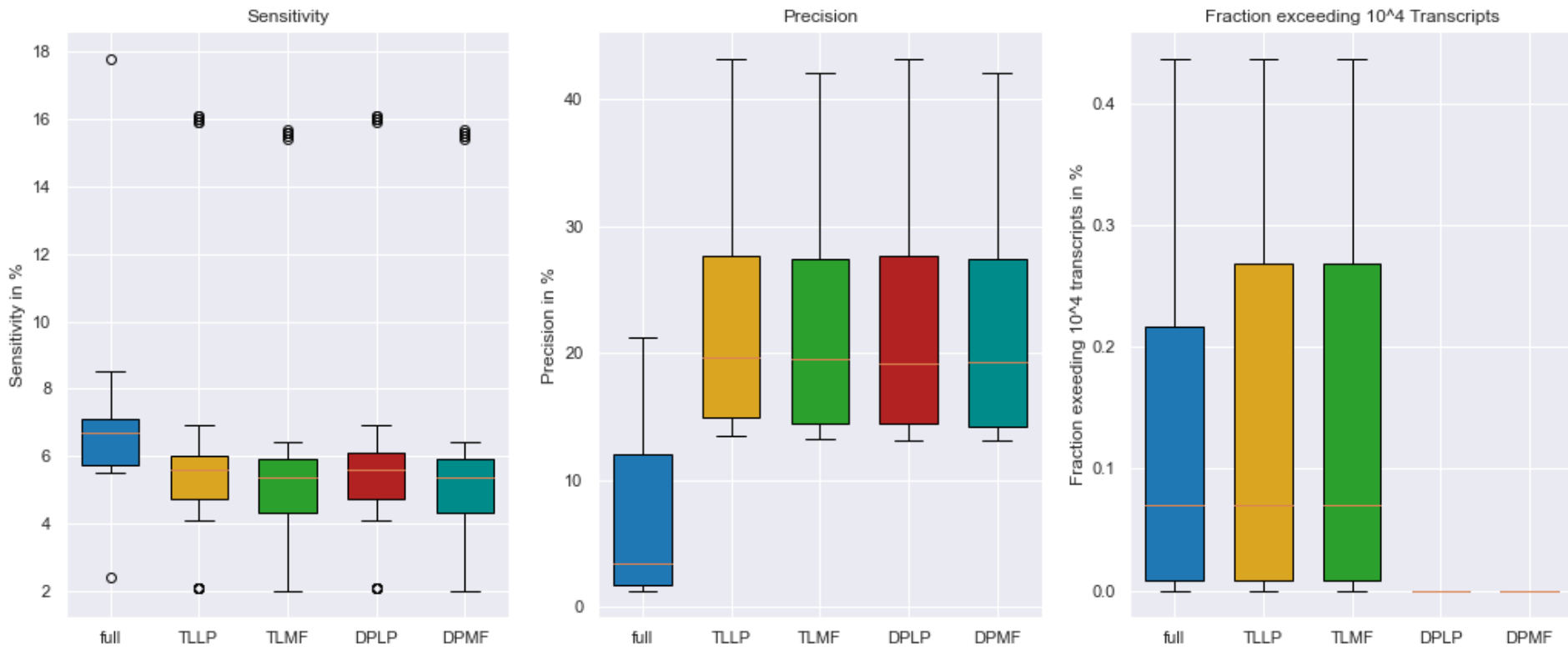
Flow-based Optimization

Time Analysis for flow-based Optimization

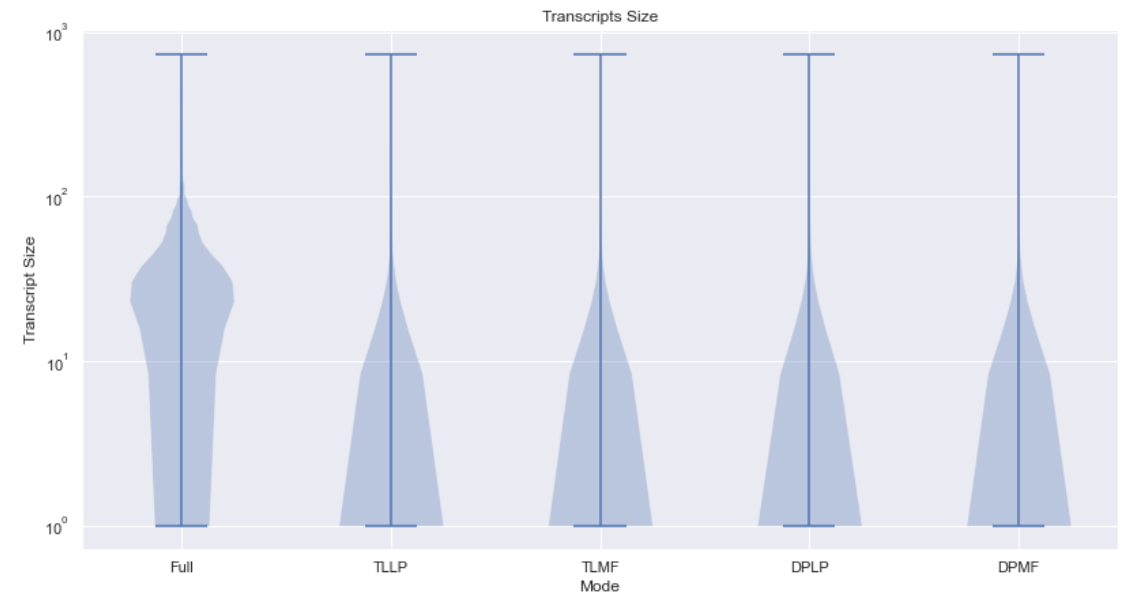
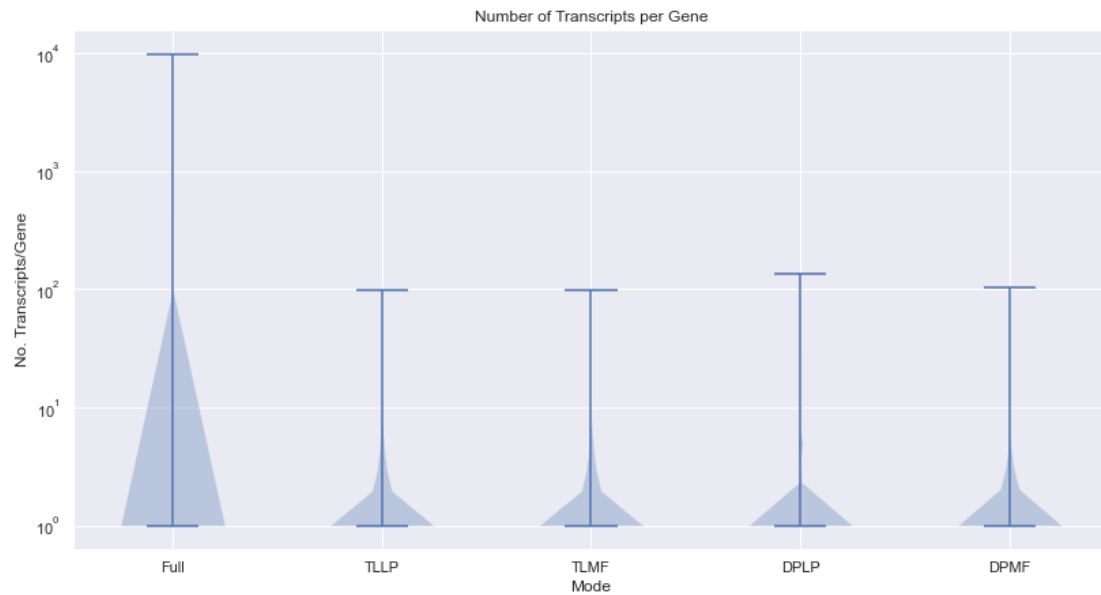
- 11 datasets:
 - Human_simulated
 - Human_leukemia
 - Human Diverse
 - SRR307903
 - SRR307911
 - SRR315323
 - SRR315334
 - SRR387661
 - SRR534291
 - SRR534307
 - SRR534319
 - SRR545695
- 6 cost-functions per mode
 - 3 linear
 - 3 quadratic



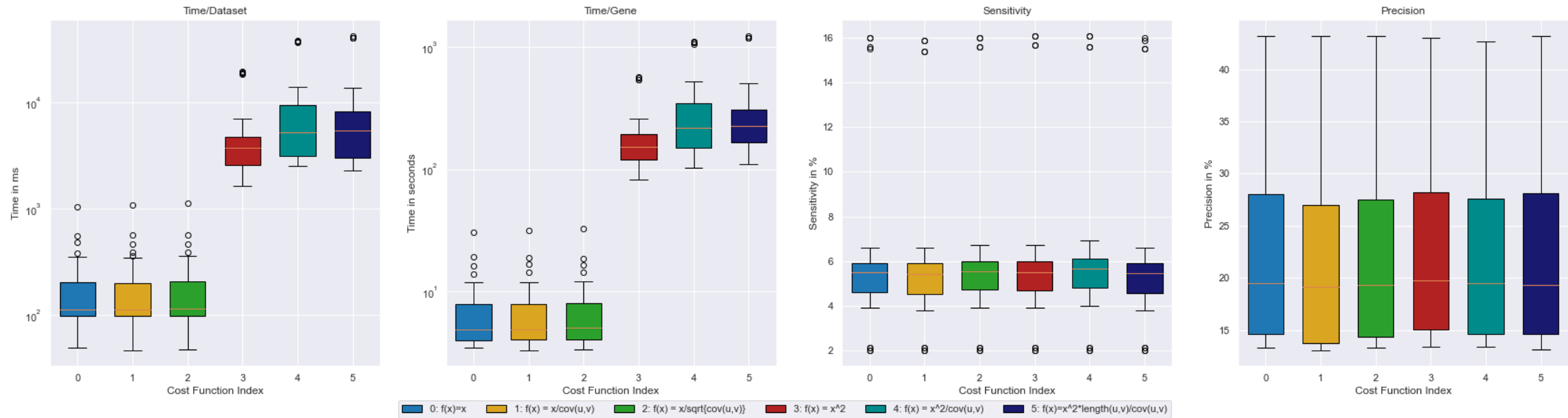
Precision and Sensitivity for flow-based Optimization



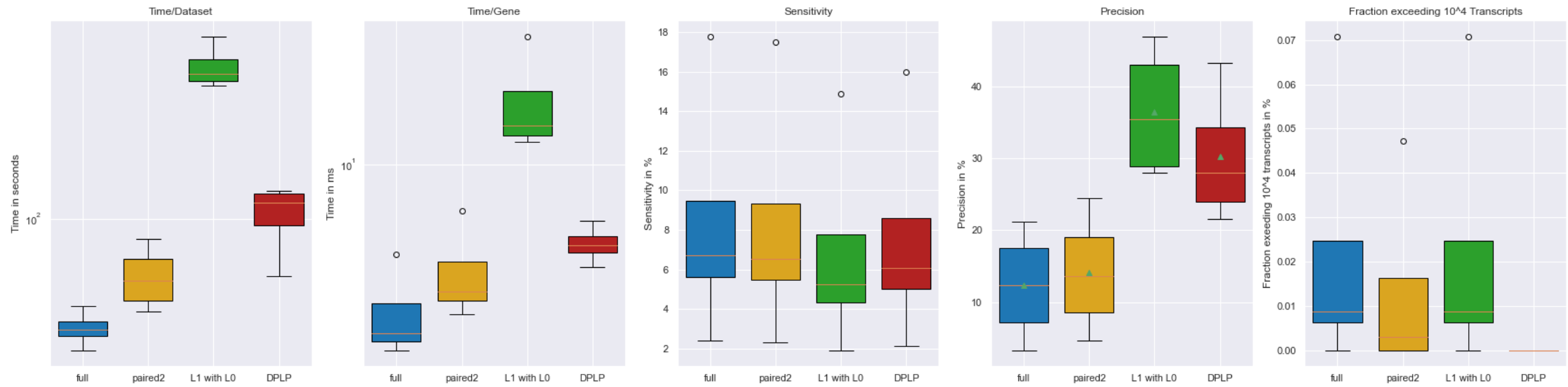
Number of Transcripts and Transcript Size for flow-based Optimization



Cost-function dependent results for flow-based Optimization



Overall results

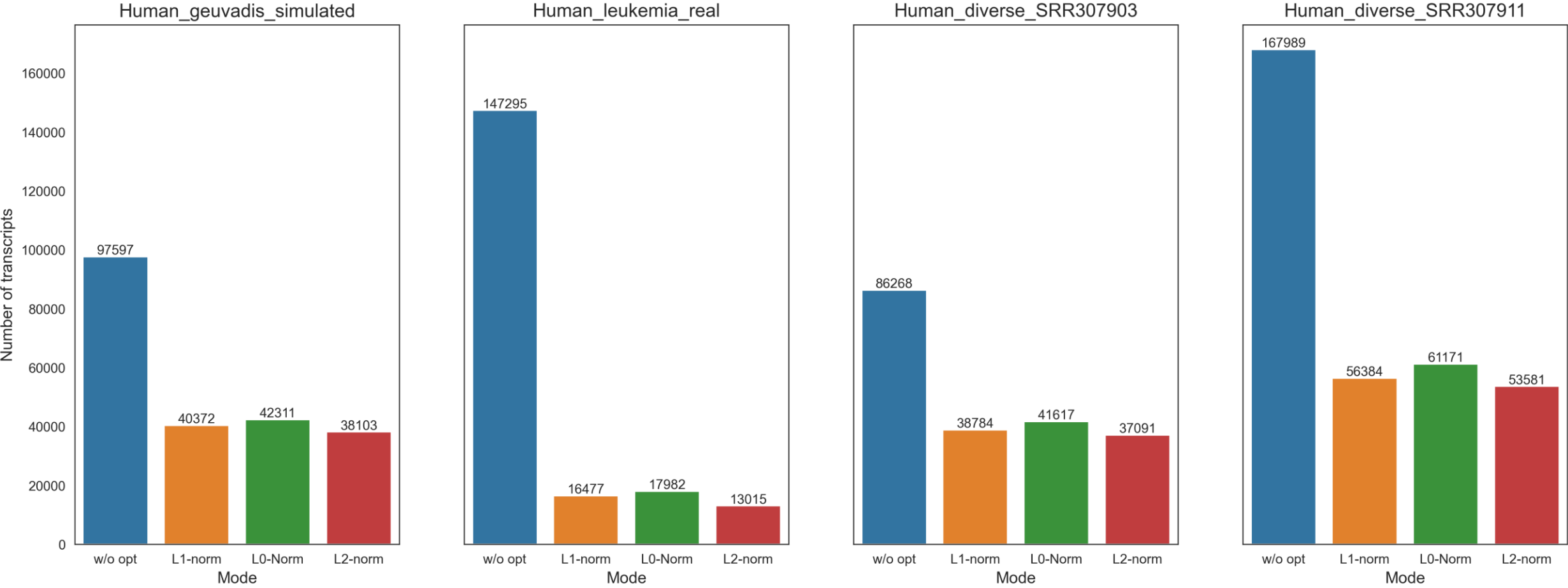


Vielen Dank.

Anhang

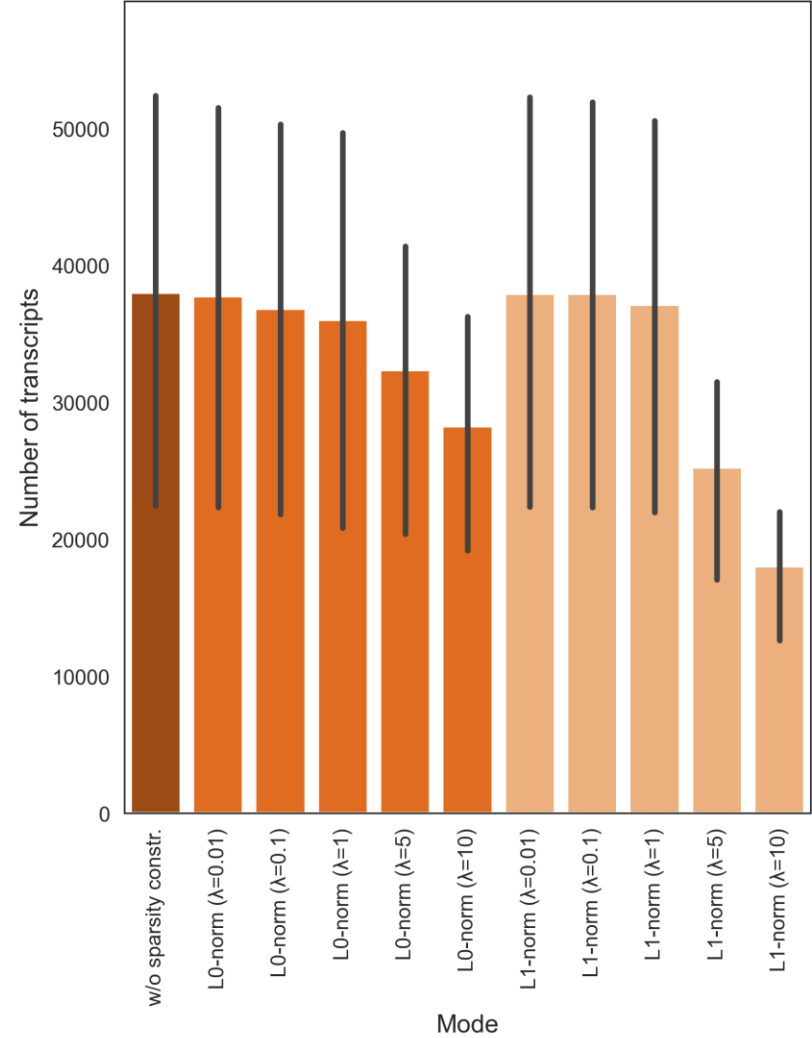
WP2 - Anhang

- Total number of transcripts
- Without sparsity constraints

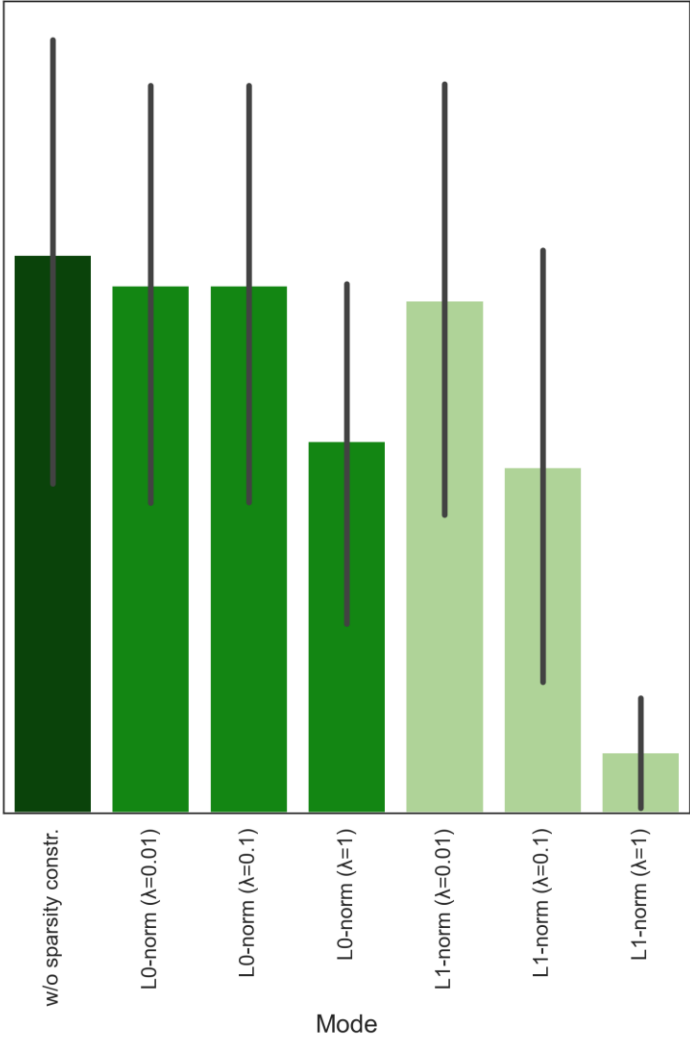


- Total number of transcripts
- With sparsity constraints

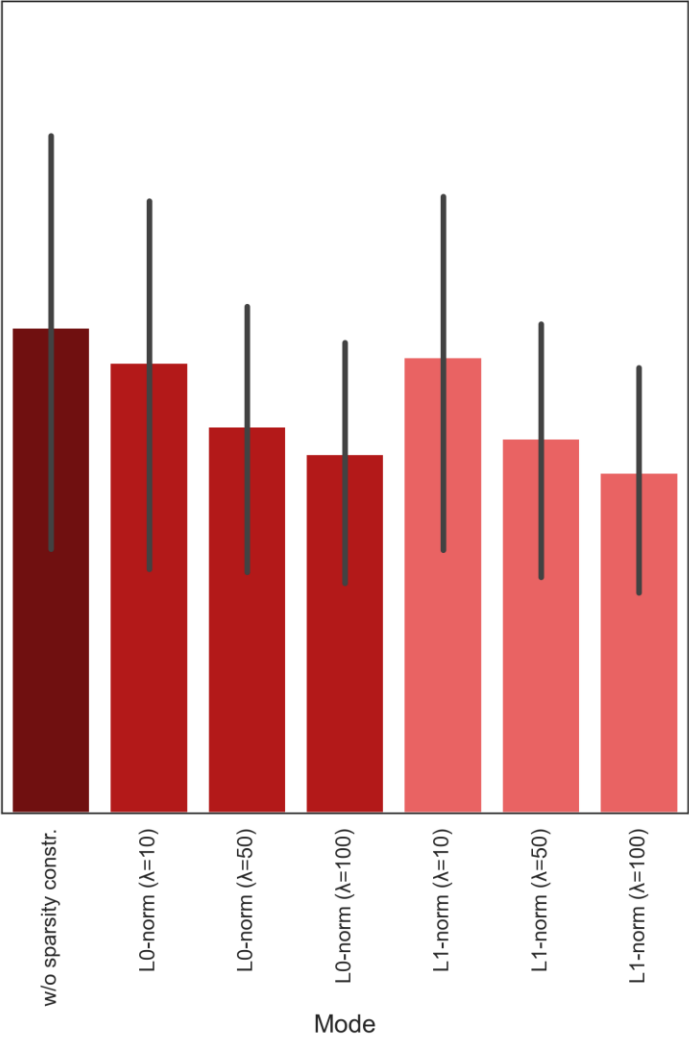
All datasets - L1-norm



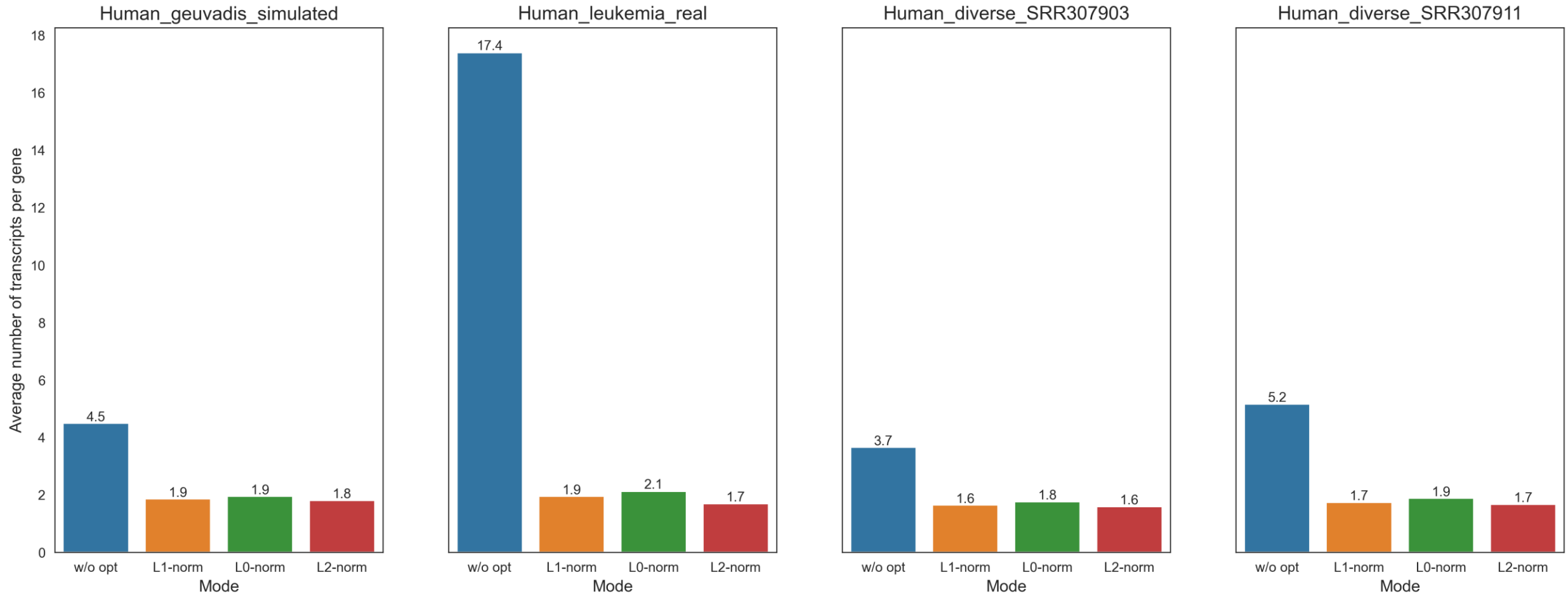
All datasets - L0 norm



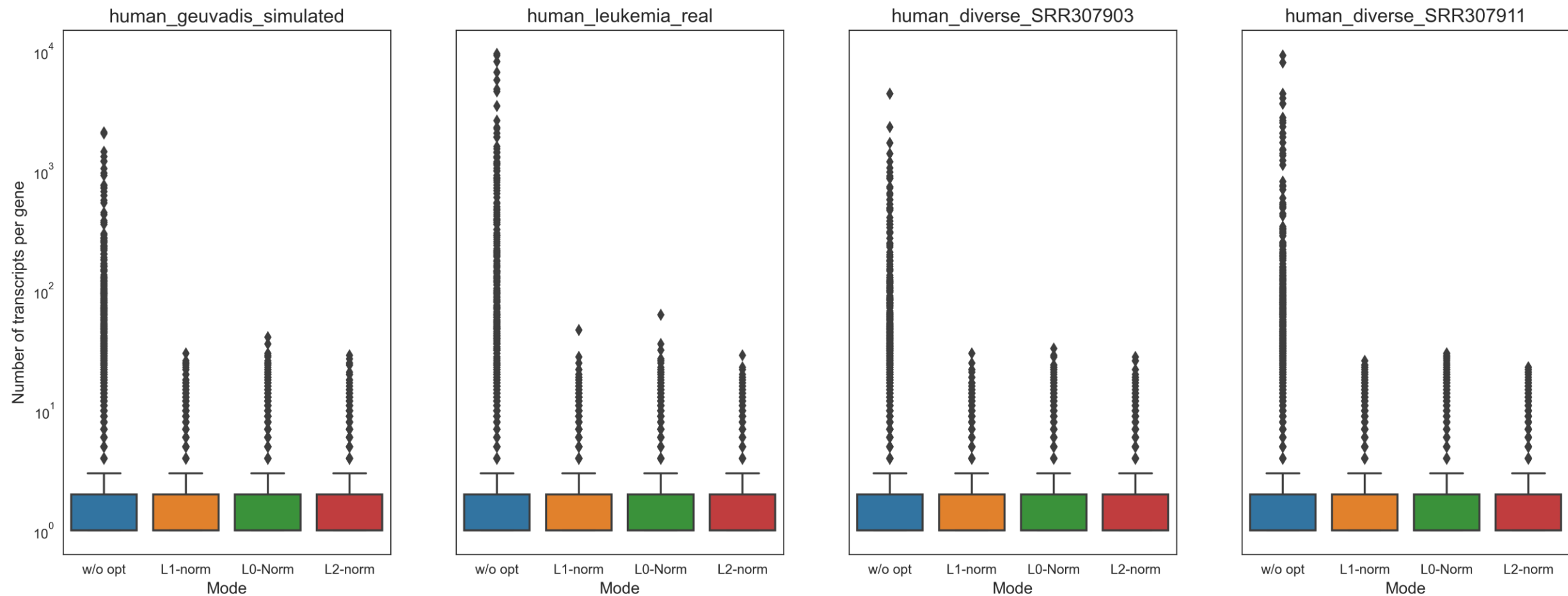
All datasets - L2 norm



- Number of transcripts per gene
- Without sparsity constraints

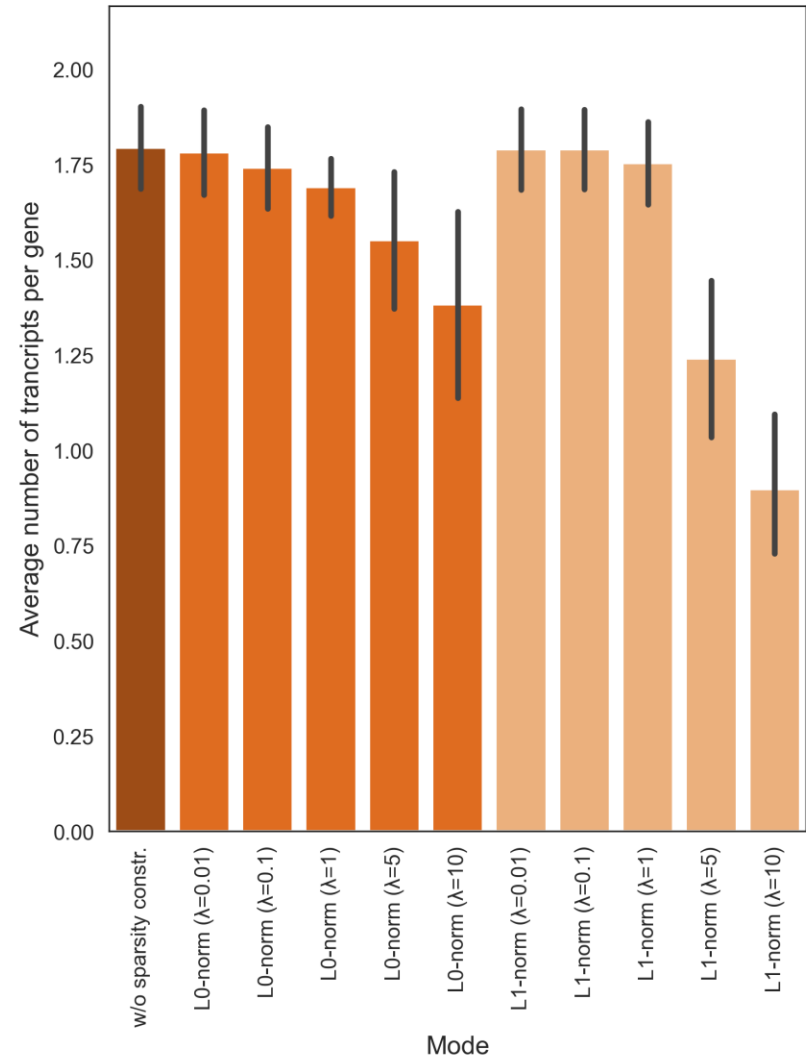


- Number of transcripts per gene
- Without sparsity constraints

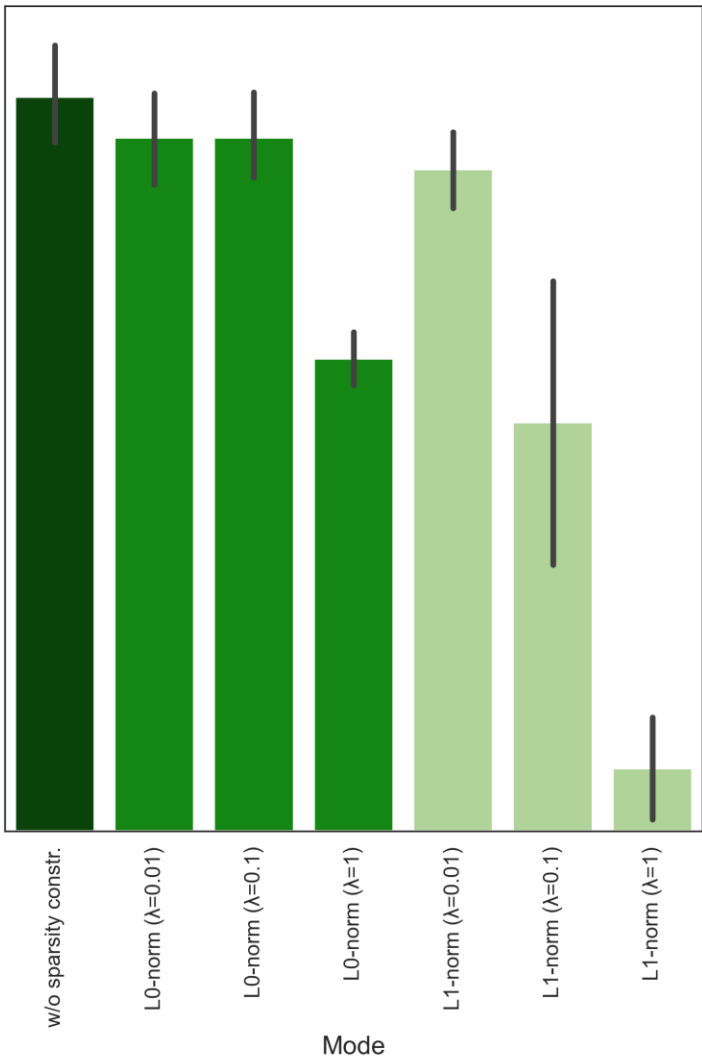


- Number of transcripts per gene
- With sparsity constraints

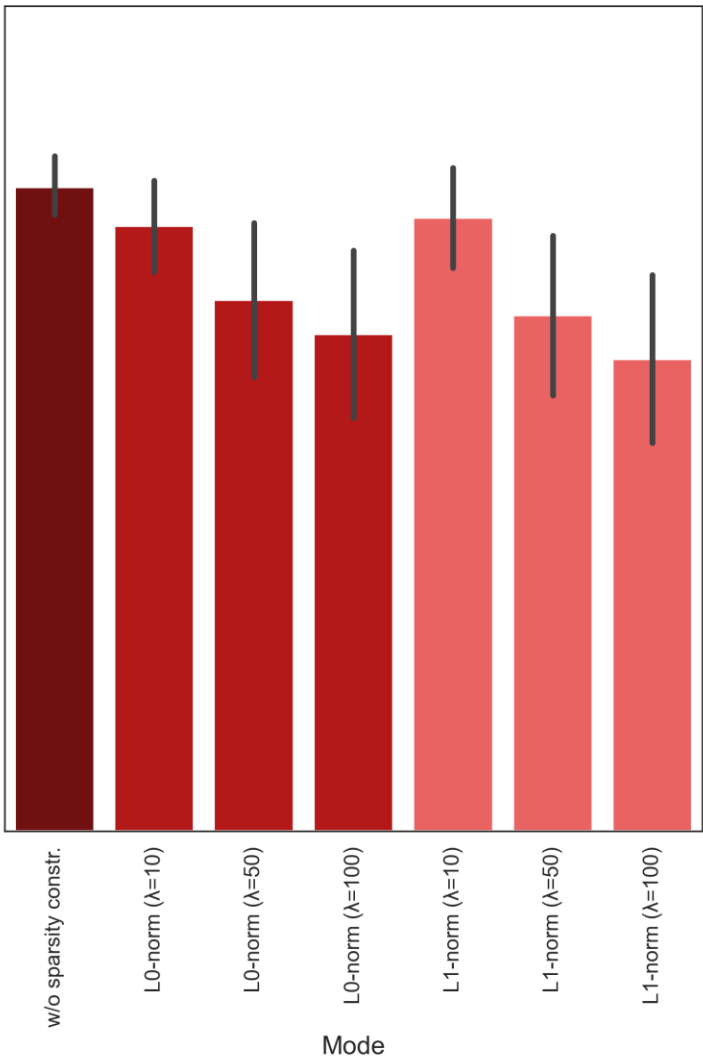
All datasets - L1-norm



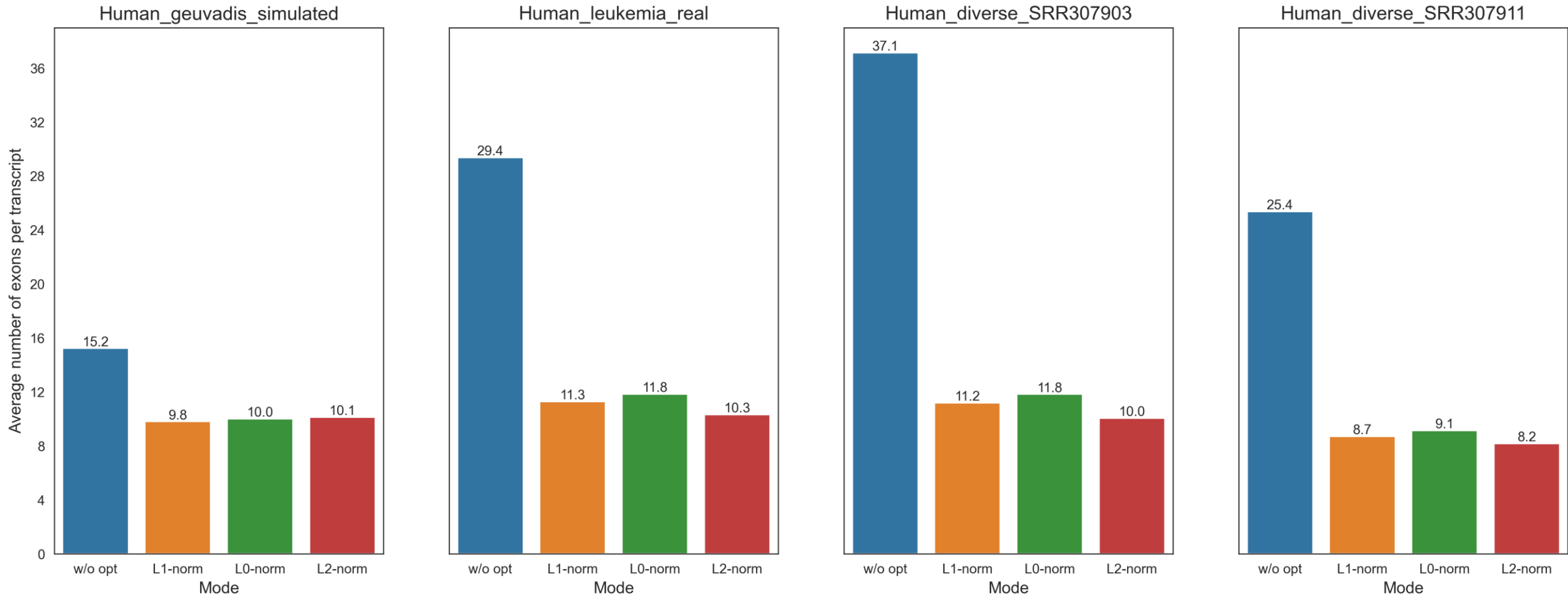
All datasets - L0 norm



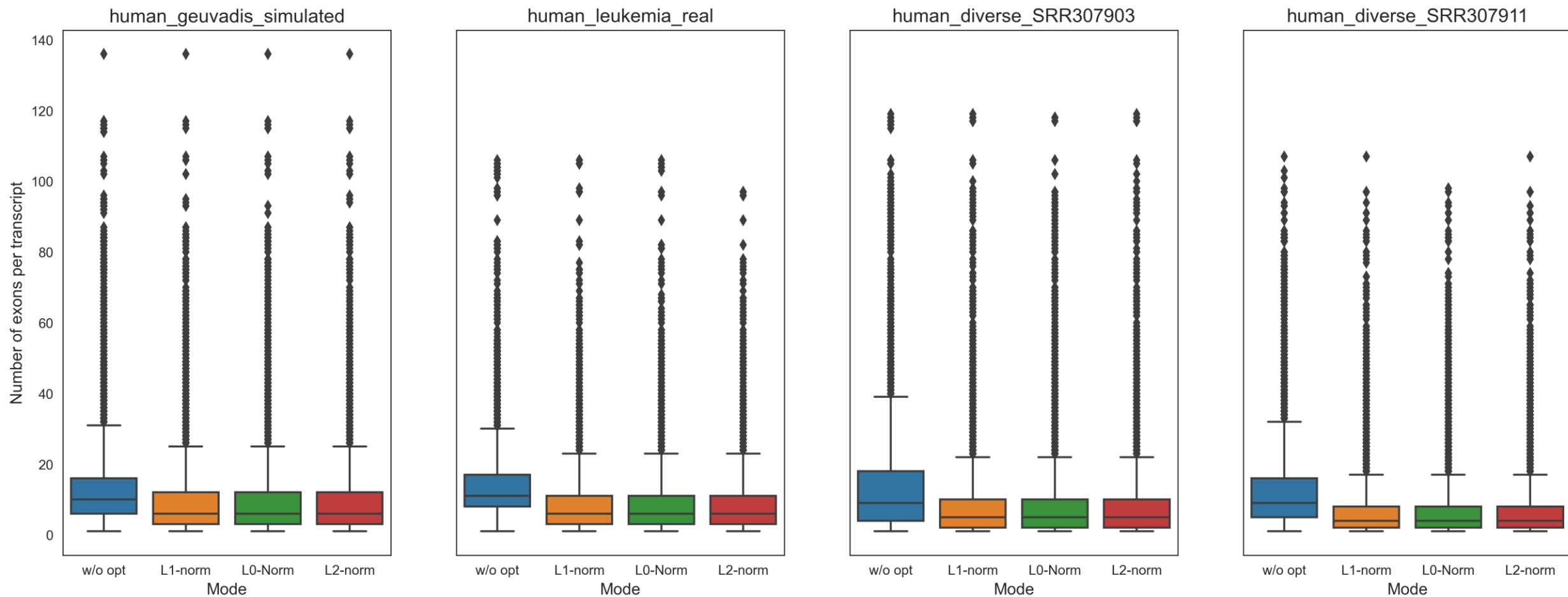
All datasets - L2 norm



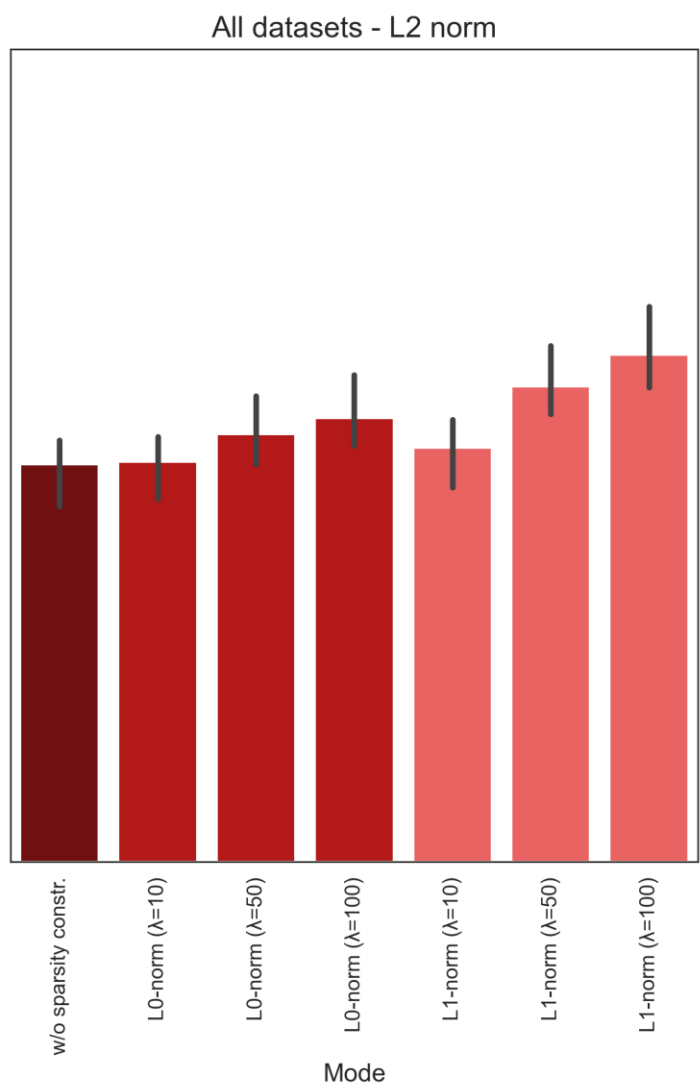
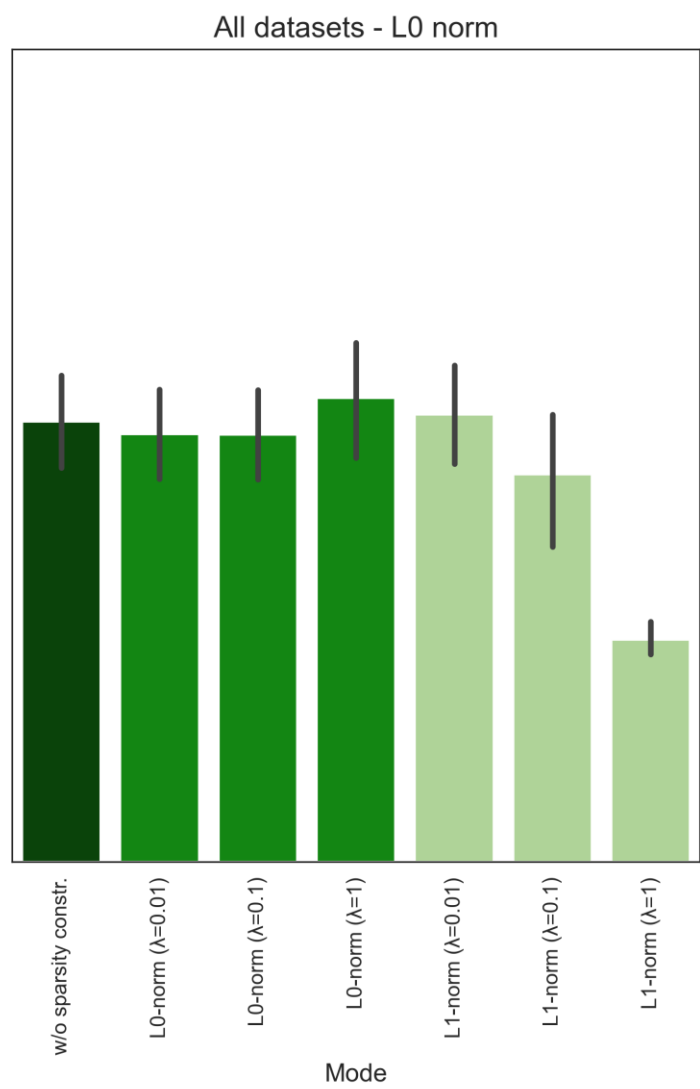
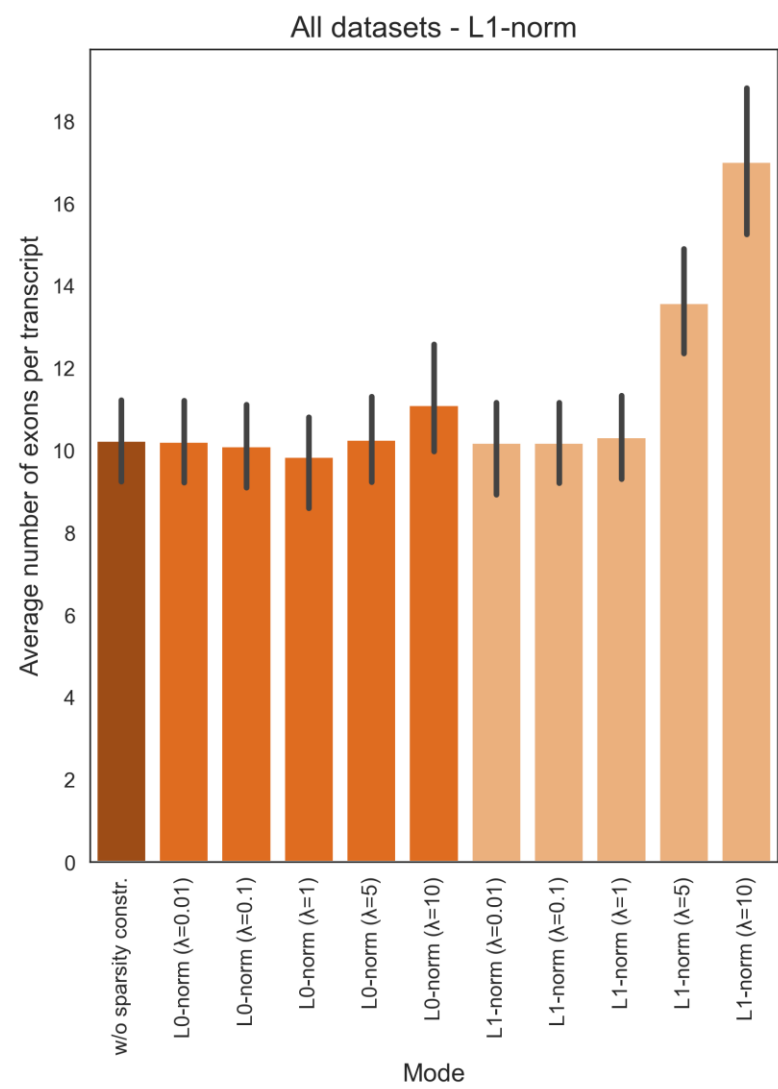
- Number of exons per transcript
- Without sparsity constraints



- Number of exons per transcript
- Without sparsity constraints

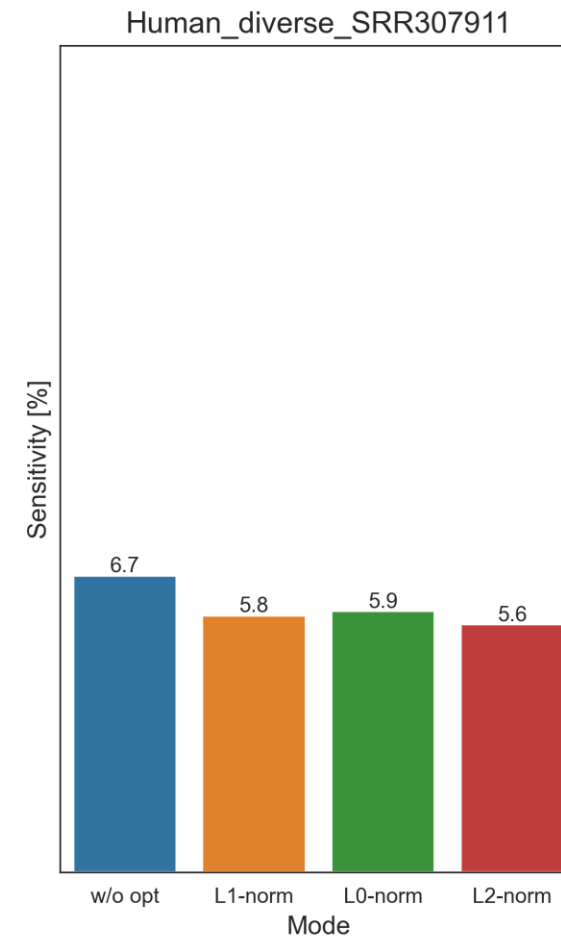
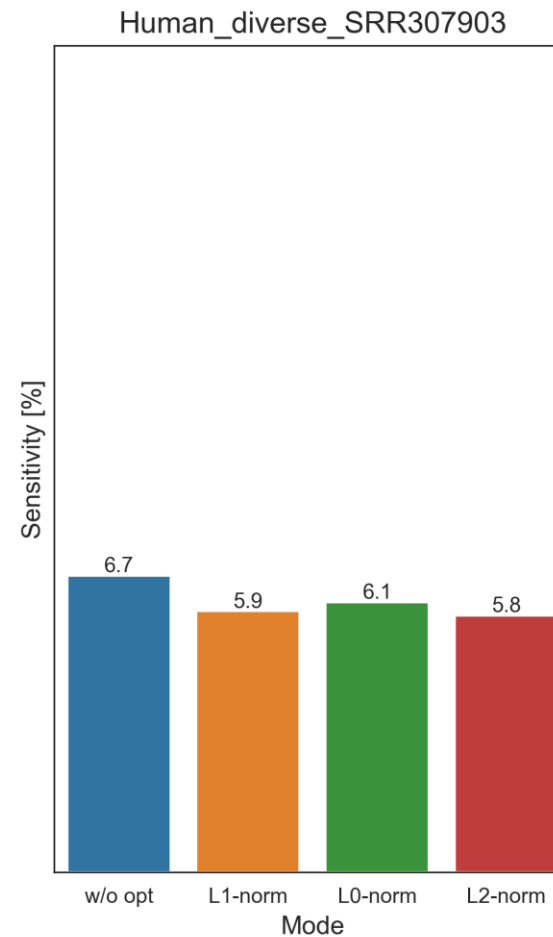
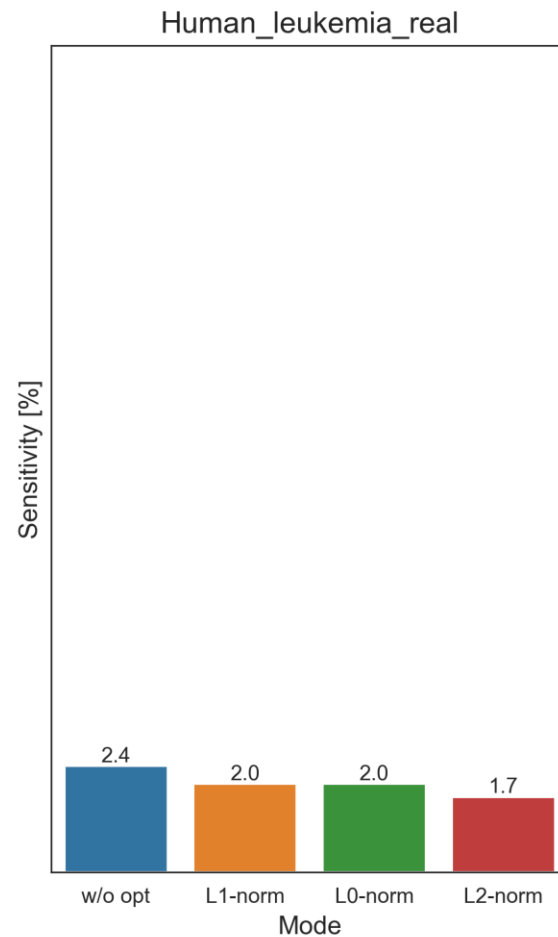
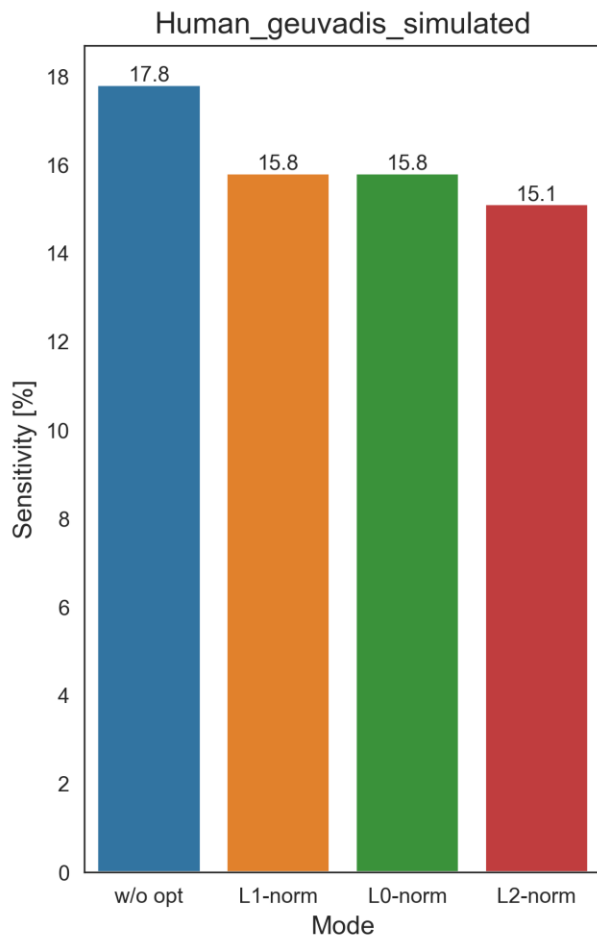


- Number of exons per transcript
- With sparsity constraints



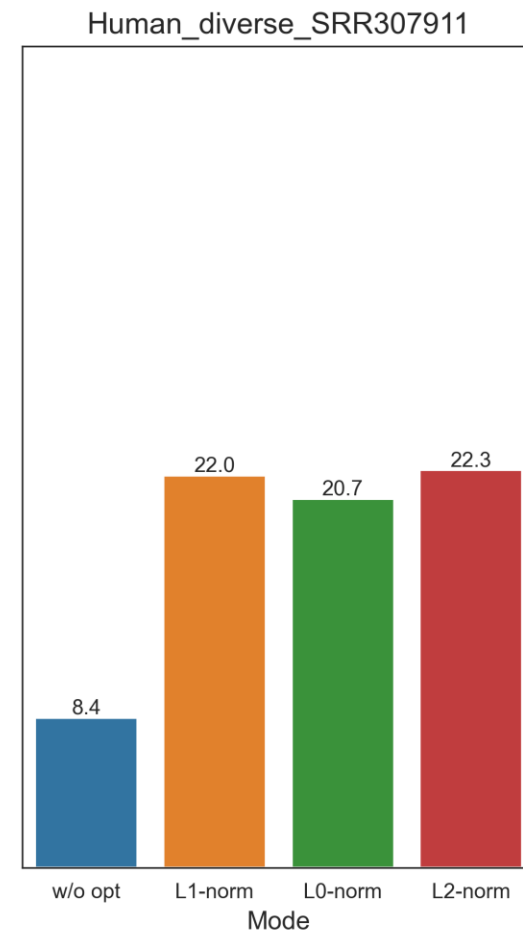
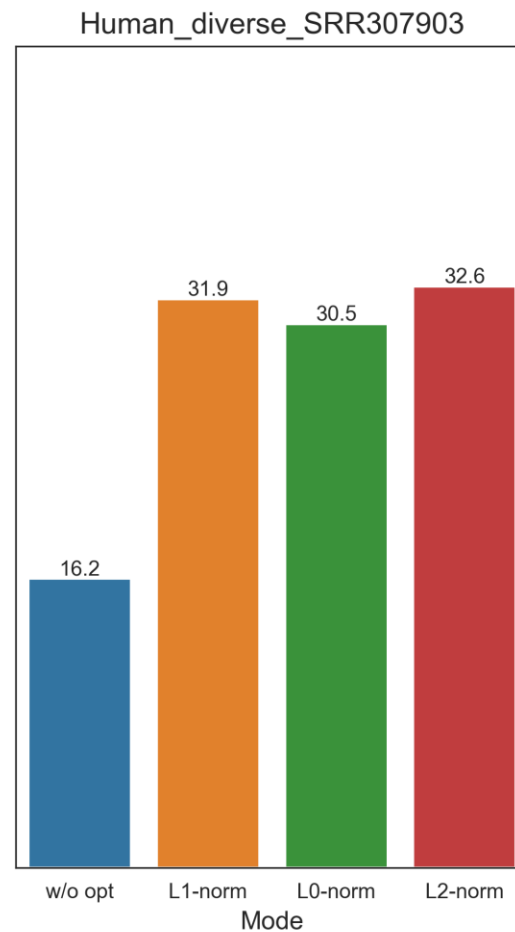
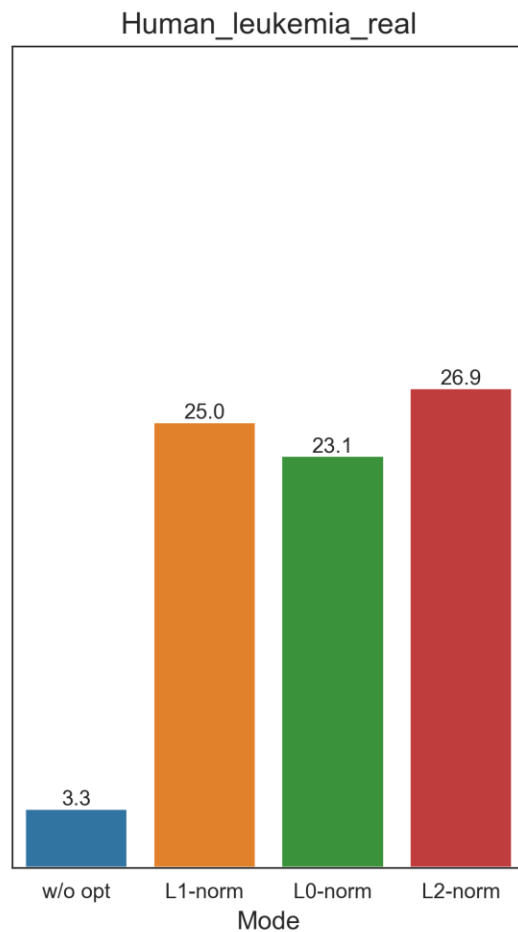
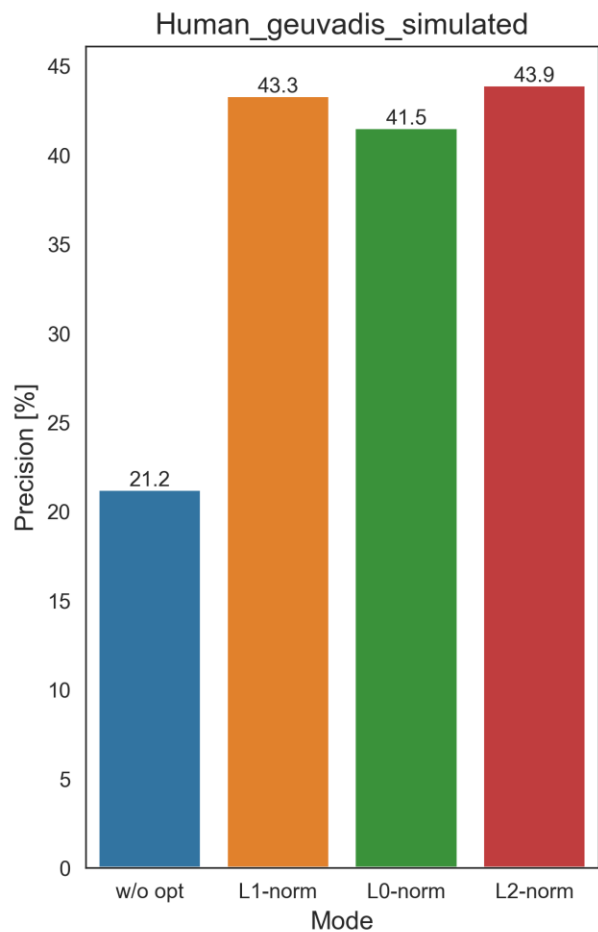
- Sensitivity
- Without sparsity constraints

$$\text{Sensitivity} = \frac{\text{TP}}{\text{TP} + \text{FN}}$$

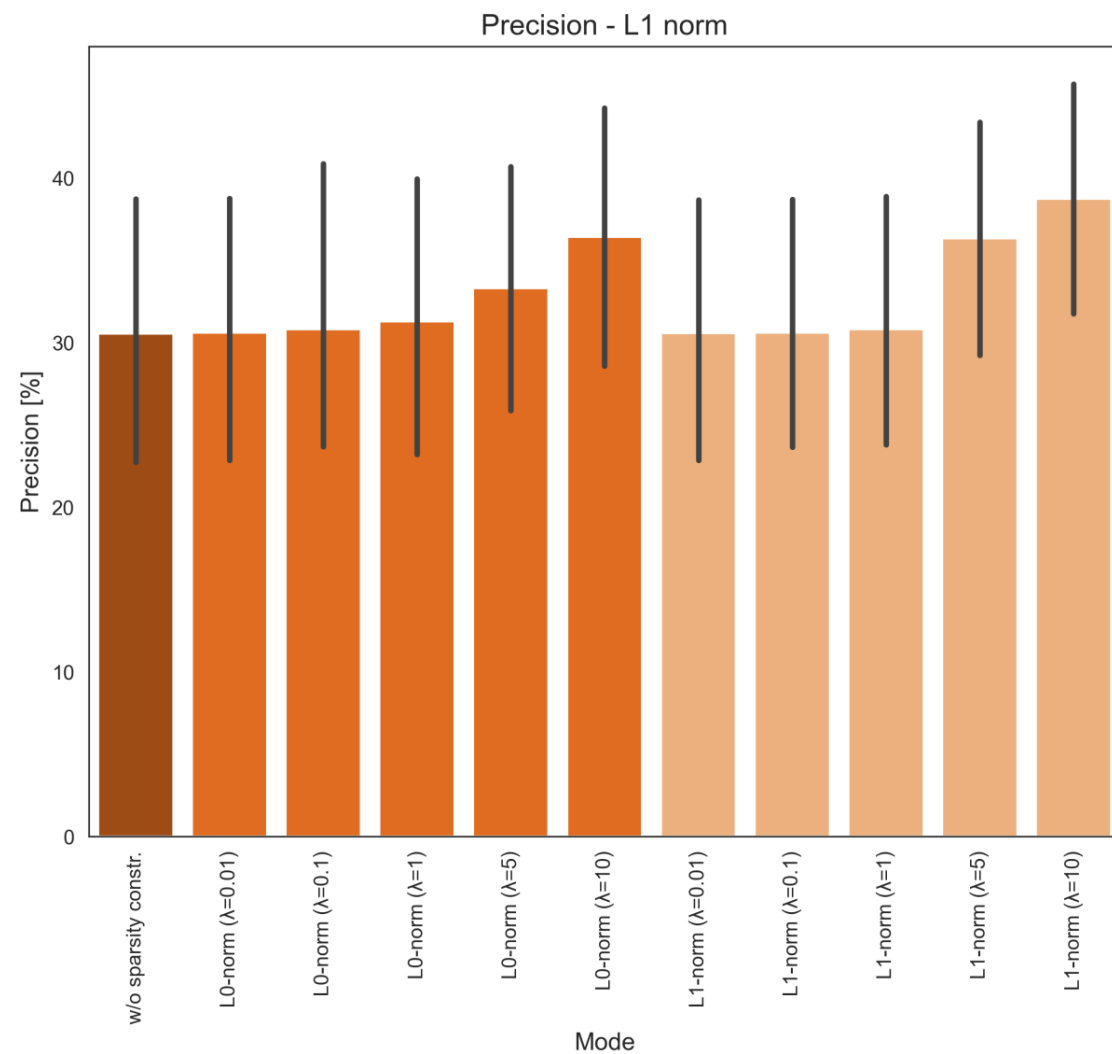
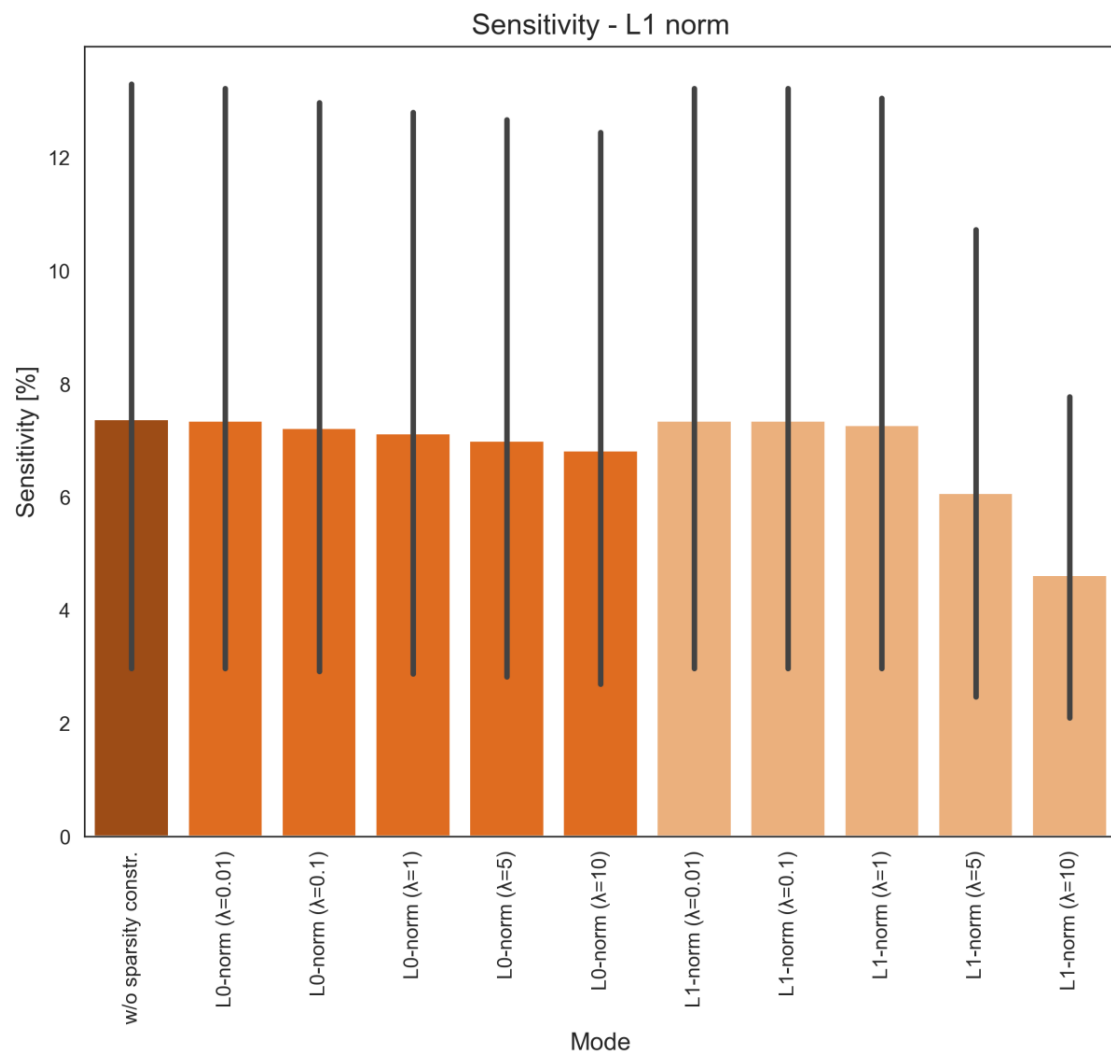


- Precision
- Without sparsity constraints

$$\text{Precision} = \frac{\text{TP}}{\text{P}}$$

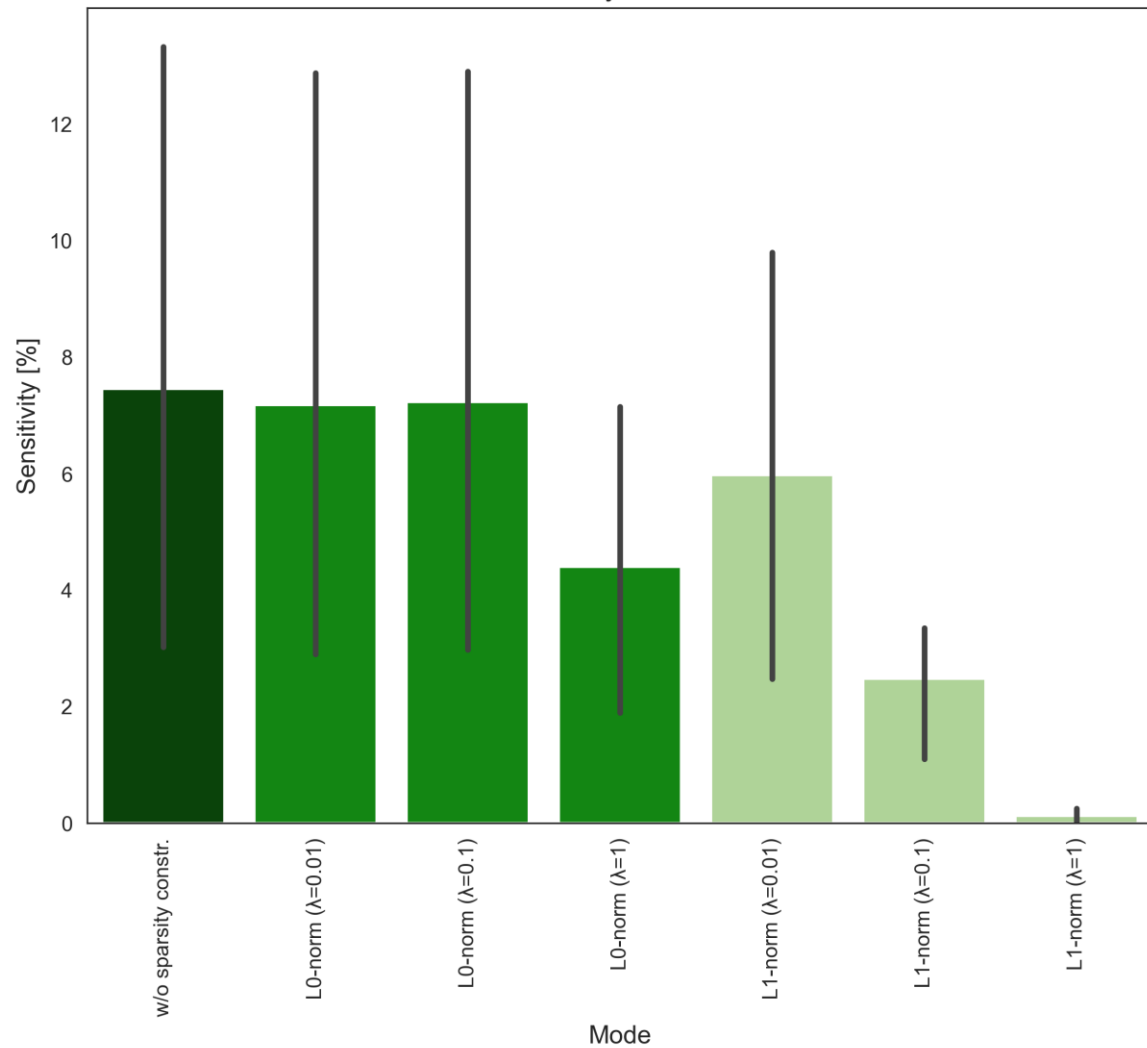


- Sensitivity and Precision
- L1 norm
- With sparsity constraints

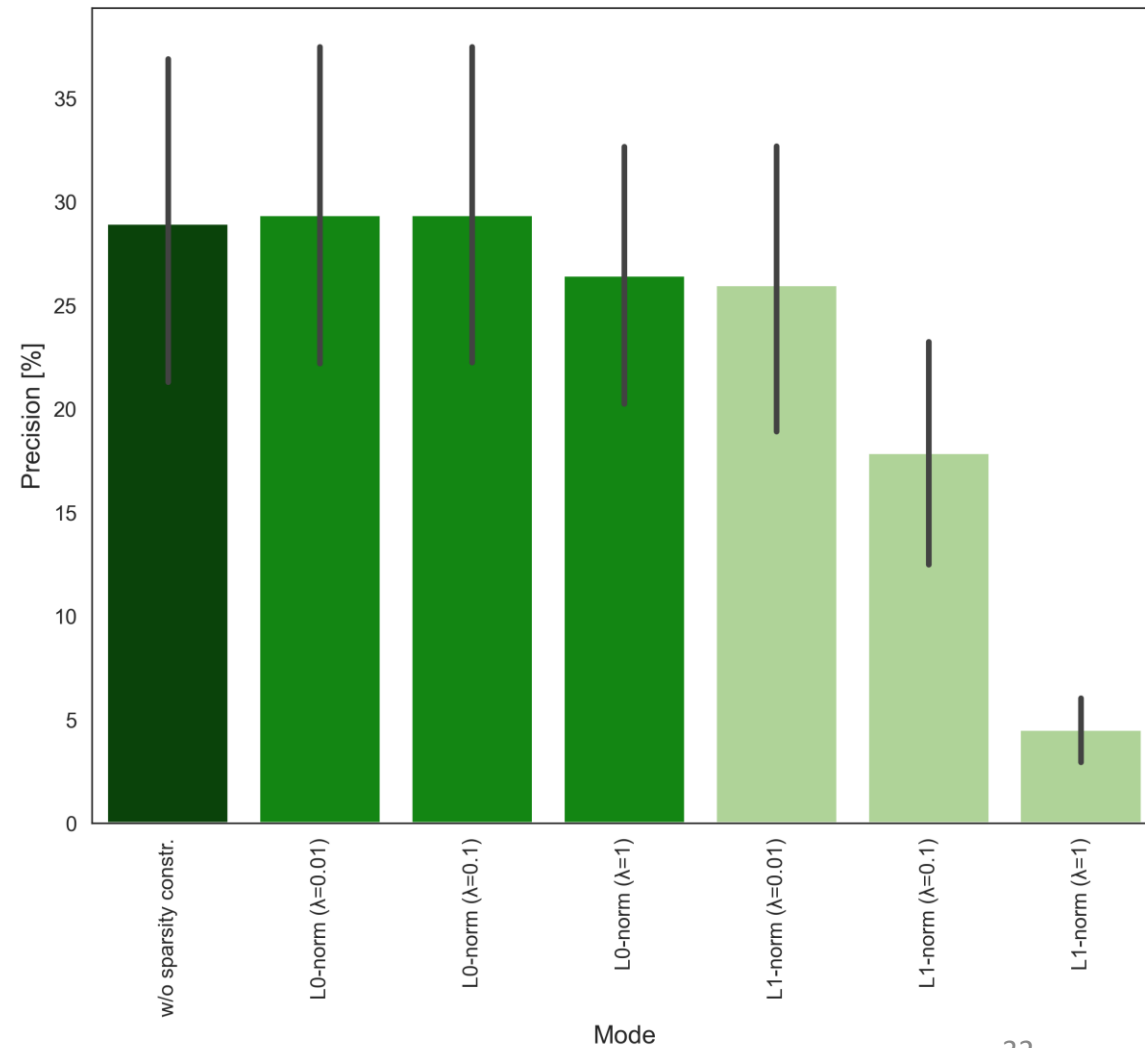


- Sensitivity and Precision
- L0 norm
- With sparsity constraints

Sensitivity - L0 norm

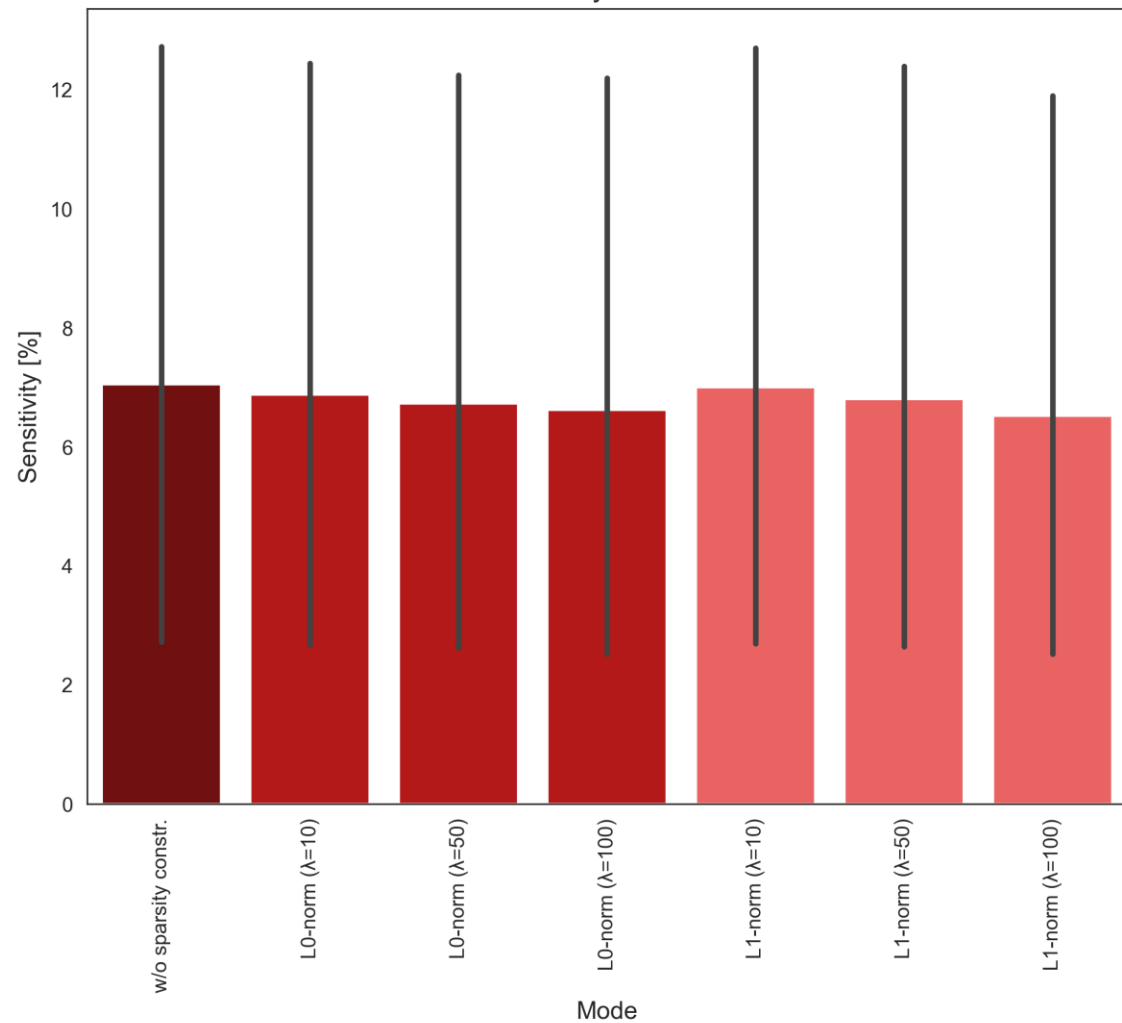


Precision - L0 norm

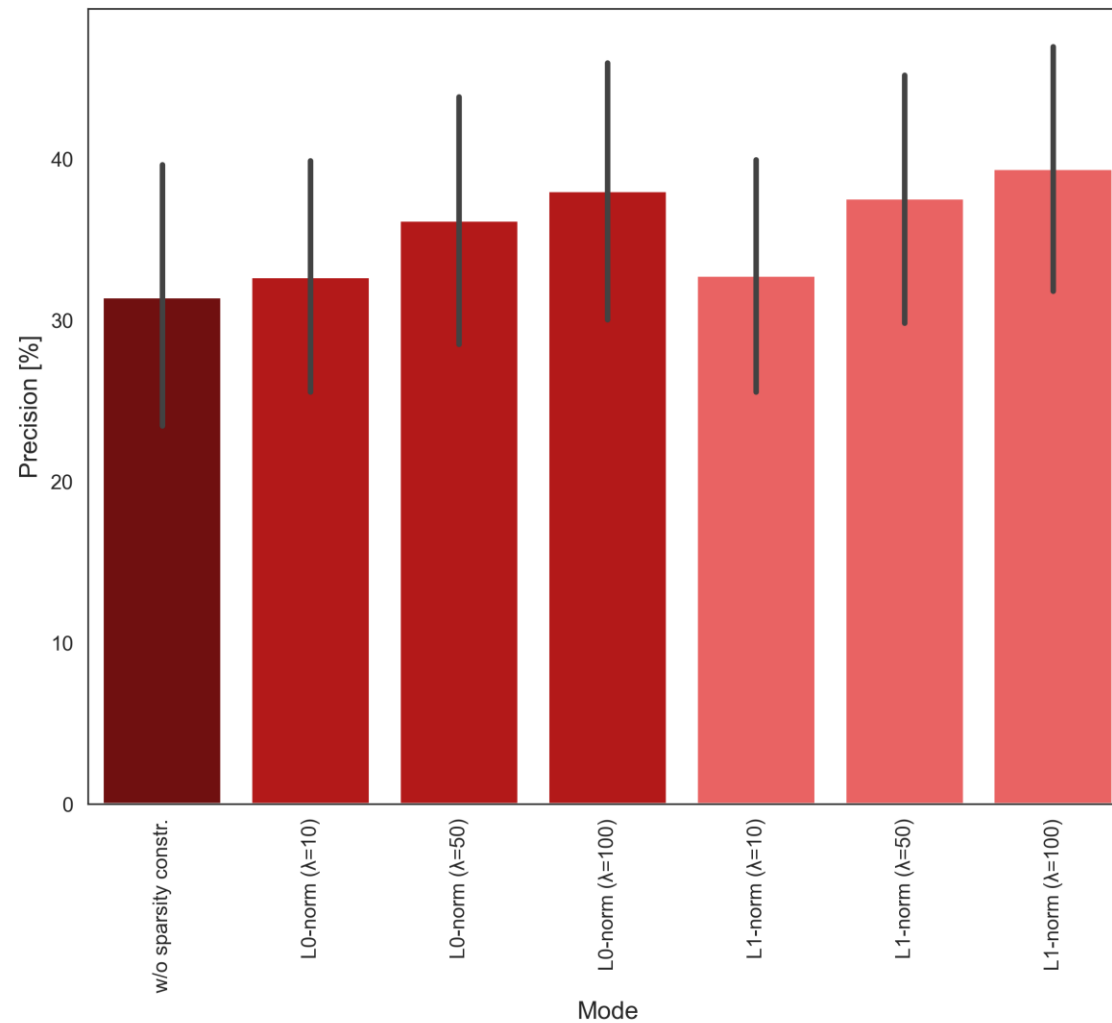


- Sensitivity and Precision
- L2 norm
- With sparsity constraints

Sensitivity - L2 norm

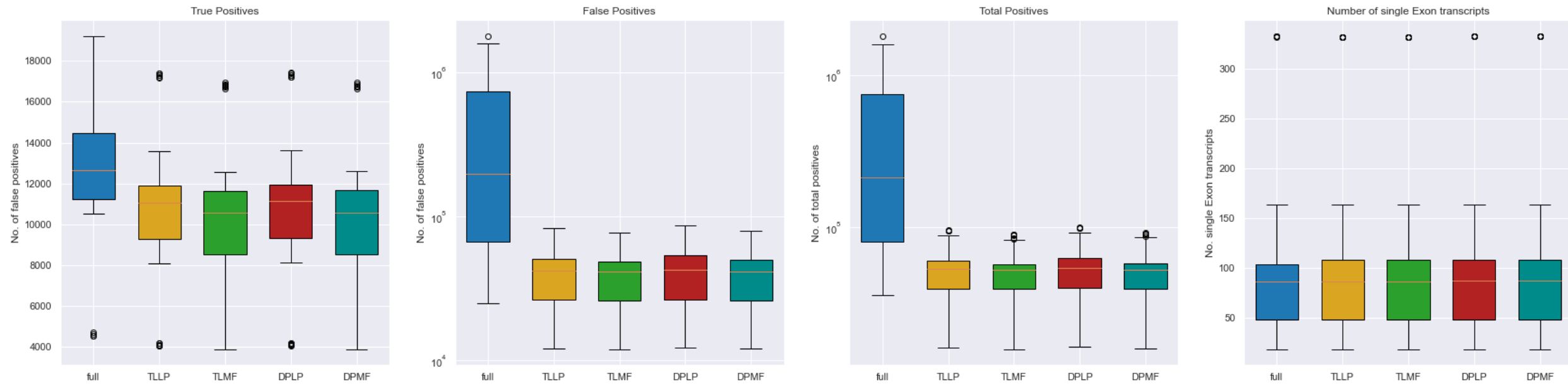


Precision - L2 norm

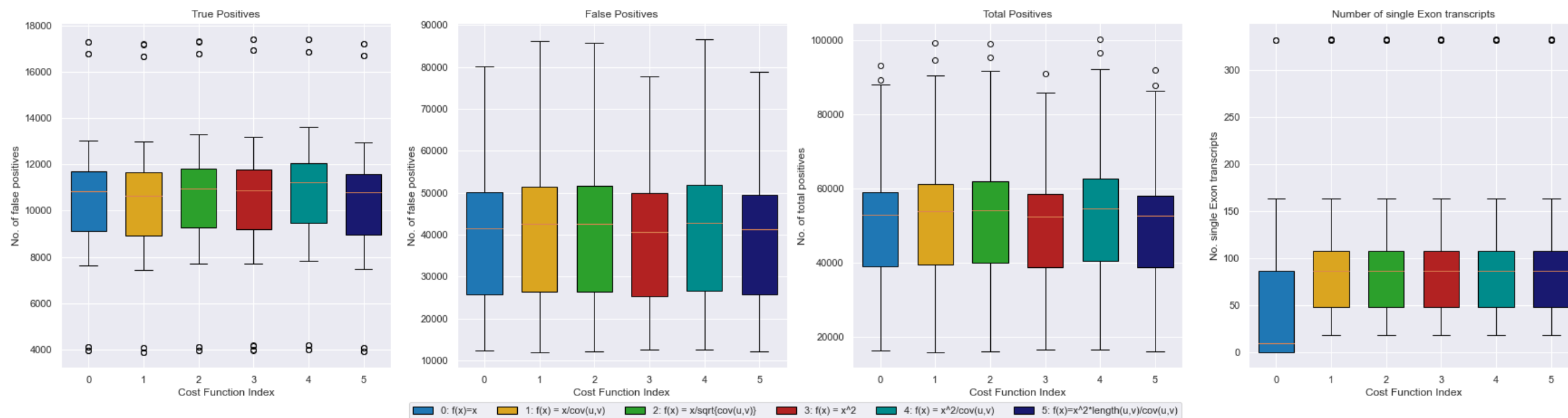


Anhang WP3

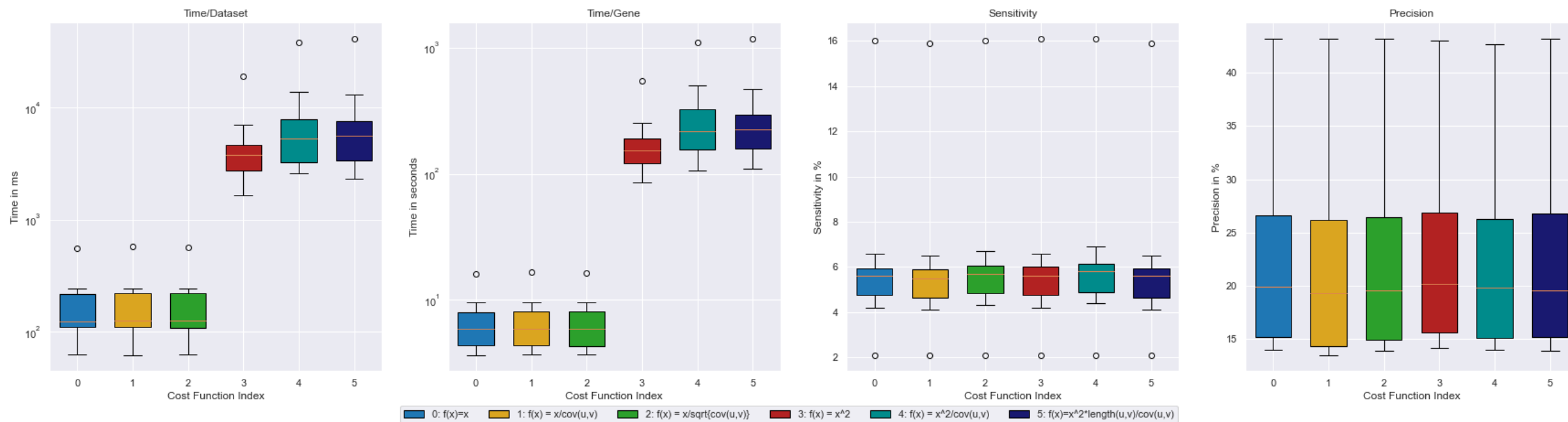
Further Analysis for flow-based Optimization



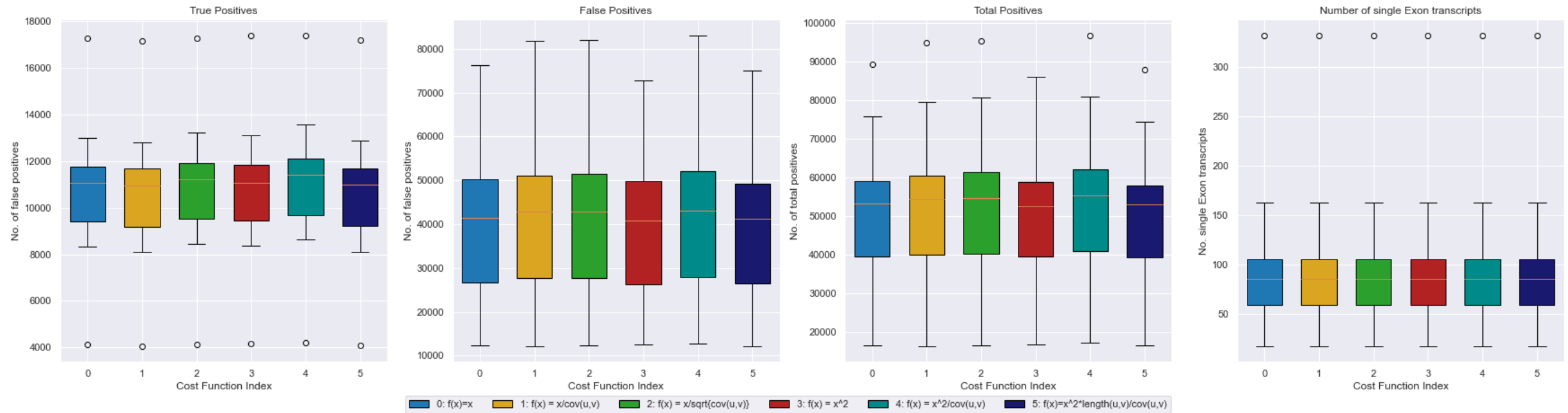
Further Analysis for flow-based Optimization



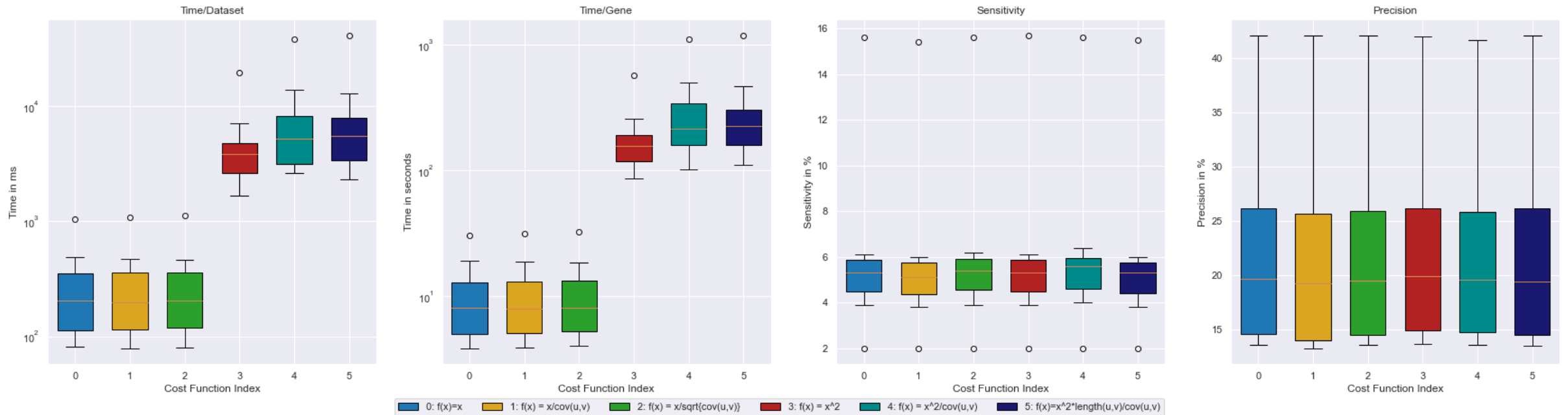
Analysis for flow-based Optimization (TLLP)



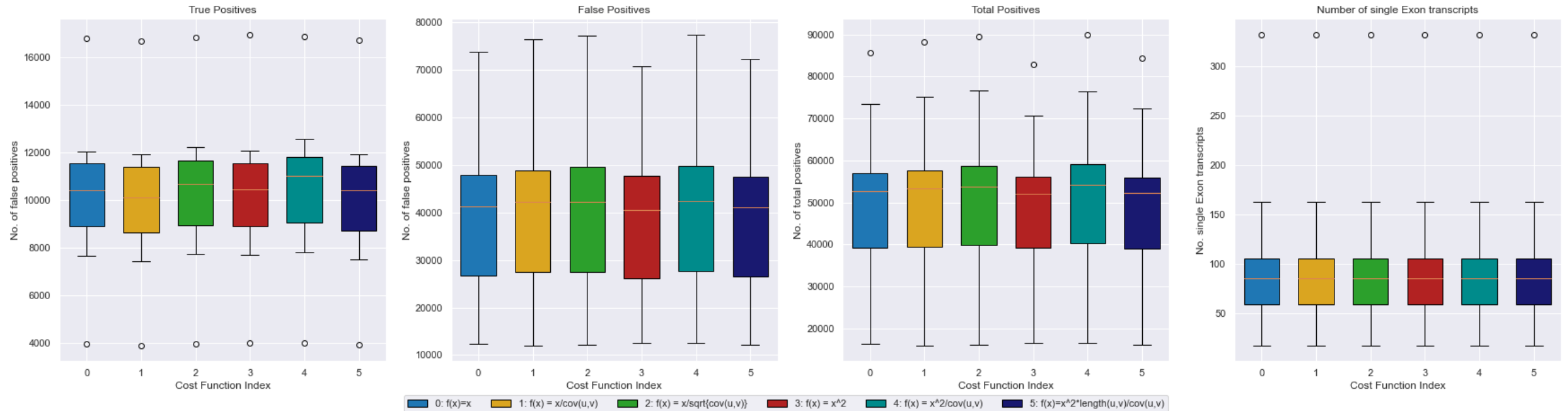
Analysis for flow-based Optimization (TLLP)



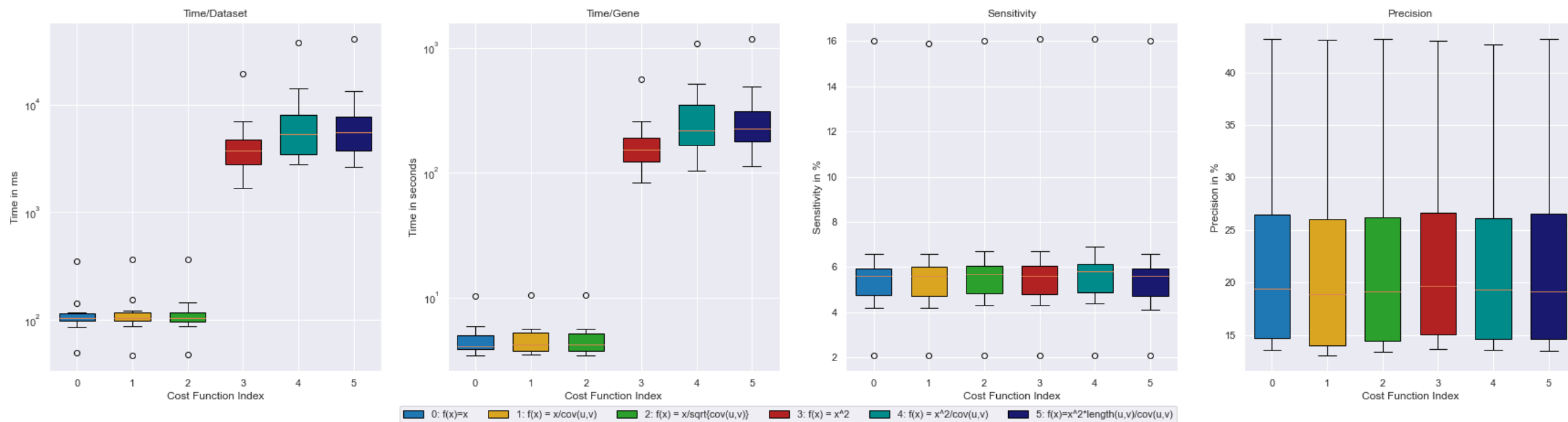
Analysis for flow-based Optimization (TLMF)



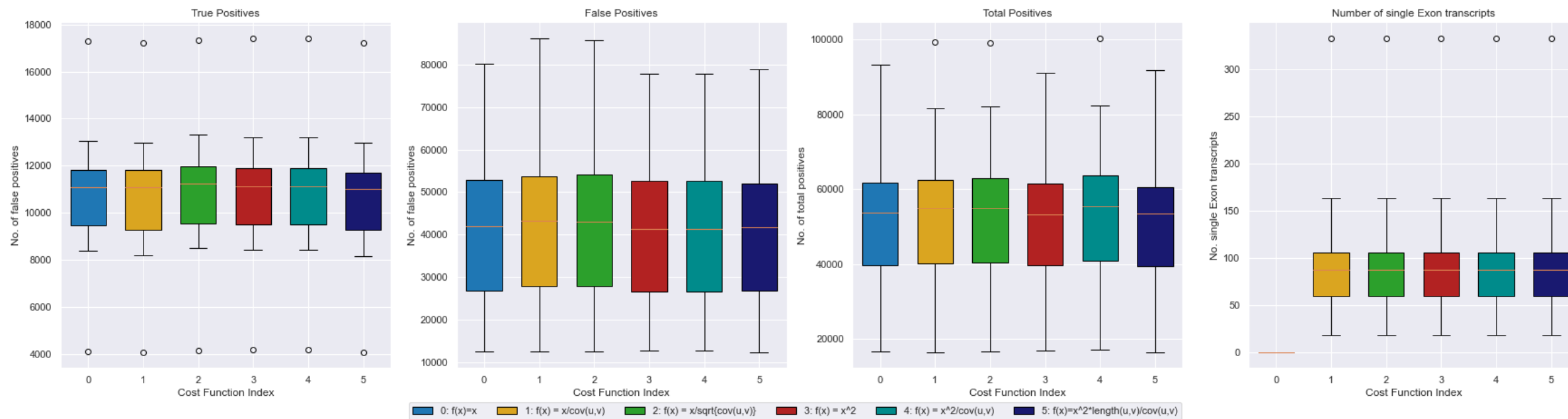
Analysis for flow-based Optimization (TLMF)



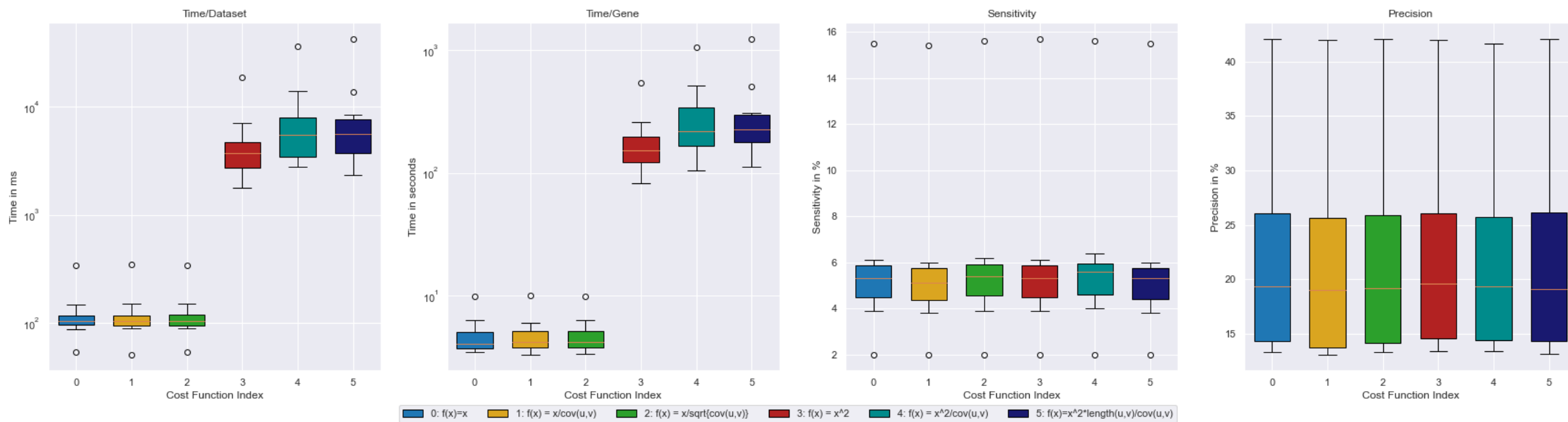
Analysis for flow-based Optimization (DPLP)



Analysis for flow-based Optimization (DPLP)



Analysis for flow-based Optimization (DPMF)



Analysis for flow-based Optimization (DPMF)

