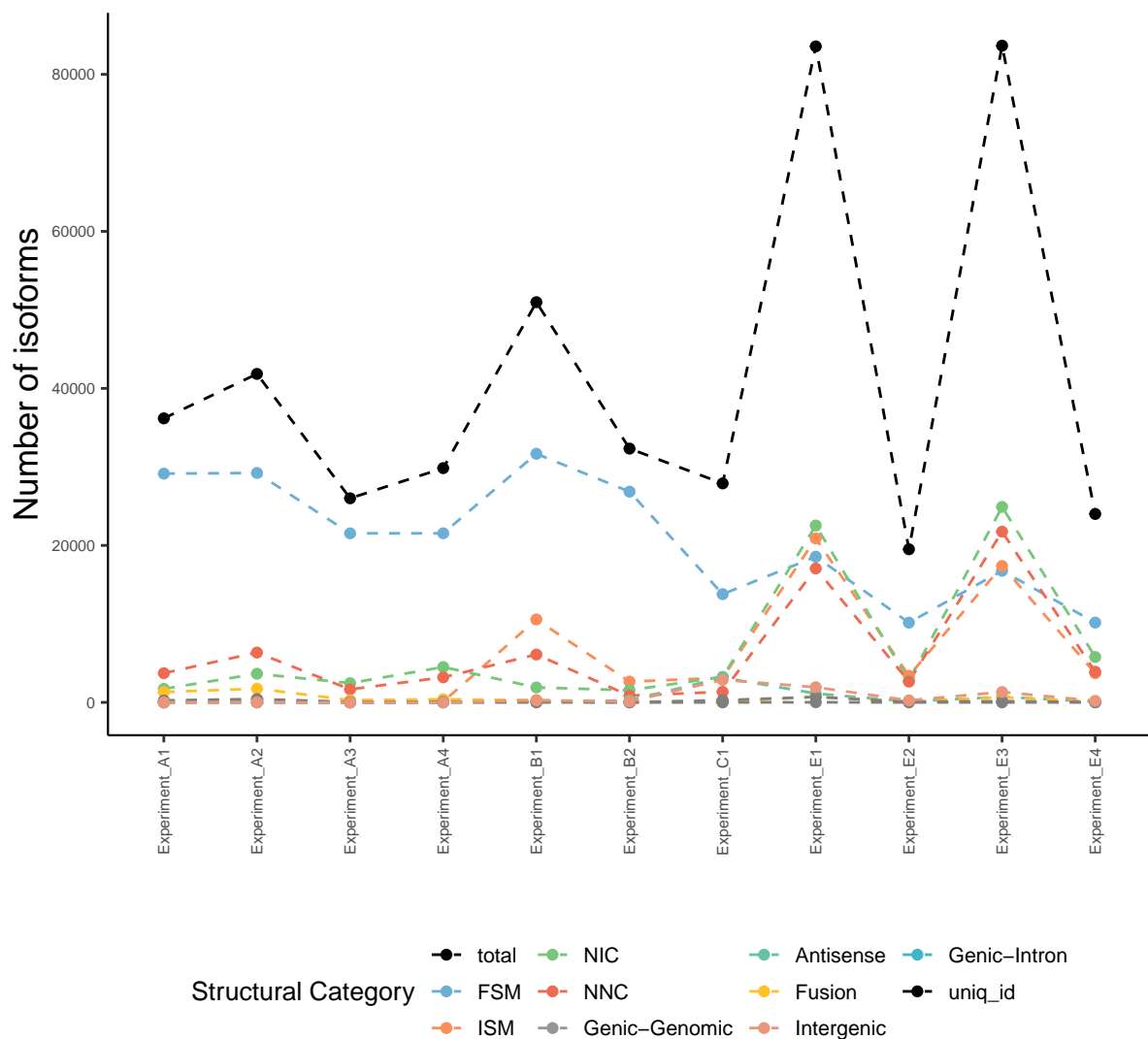


LRGASP Challenge 1

comparison report

Isoforms detected by pipeline



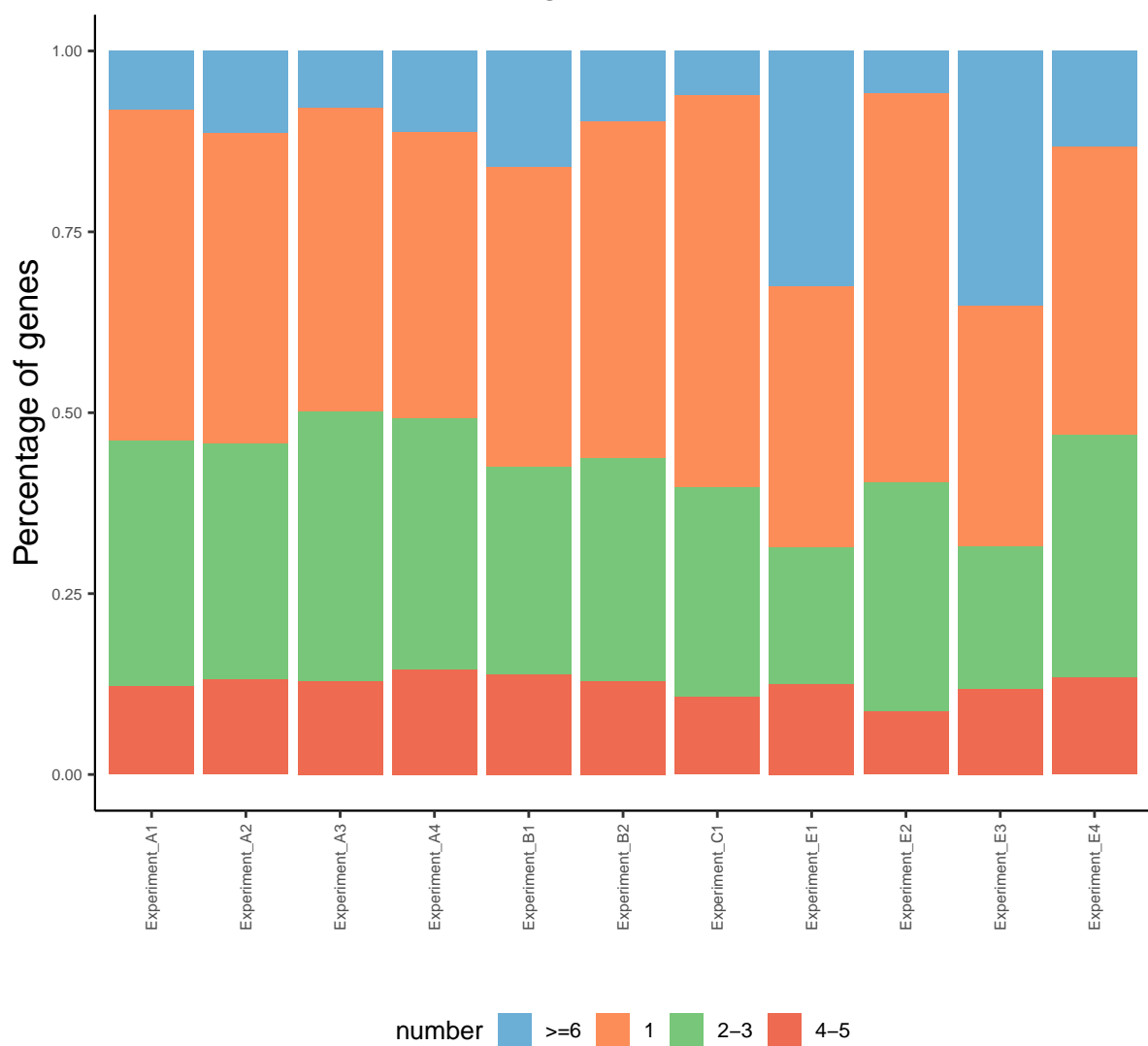
The graph displays the performance of five models across four experiments. The y-axis represents performance, and the x-axis lists the experiments. The models are represented by different colored lines and markers: A1 (black dashed line), A2 (blue dashed line), A3 (green dashed line), A4 (red dashed line), and B1 (orange dashed line). Model A1 consistently shows the highest performance, peaking at Experiment E1 and E3. Model A2 shows moderate performance, peaking at Experiment B1. Model A3 and A4 show low performance, while Model B1 shows a peak at Experiment B1. Model B2 shows the lowest performance across all experiments.

| Experiment | A1 | A2 | A3 | A4 | B1 | B2 |
|---------------|------|------|------|------|------|------|
| Experiment_A1 | 0.85 | 0.65 | 0.15 | 0.10 | 0.12 | 0.05 |
| Experiment_A2 | 0.90 | 0.65 | 0.15 | 0.10 | 0.12 | 0.05 |
| Experiment_A3 | 0.55 | 0.45 | 0.15 | 0.10 | 0.12 | 0.05 |
| Experiment_A4 | 0.60 | 0.45 | 0.15 | 0.10 | 0.12 | 0.05 |
| Experiment_B1 | 0.80 | 0.70 | 0.15 | 0.10 | 0.25 | 0.05 |
| Experiment_B2 | 0.70 | 0.60 | 0.15 | 0.10 | 0.12 | 0.05 |
| Experiment_C1 | 0.55 | 0.35 | 0.15 | 0.10 | 0.12 | 0.05 |
| Experiment_E1 | 1.00 | 0.60 | 0.25 | 0.20 | 0.25 | 0.05 |
| Experiment_E2 | 0.55 | 0.35 | 0.15 | 0.10 | 0.12 | 0.05 |
| Experiment_E3 | 1.00 | 0.60 | 0.25 | 0.20 | 0.25 | 0.05 |
| Experiment_E4 | 0.60 | 0.40 | 0.15 | 0.10 | 0.12 | 0.05 |

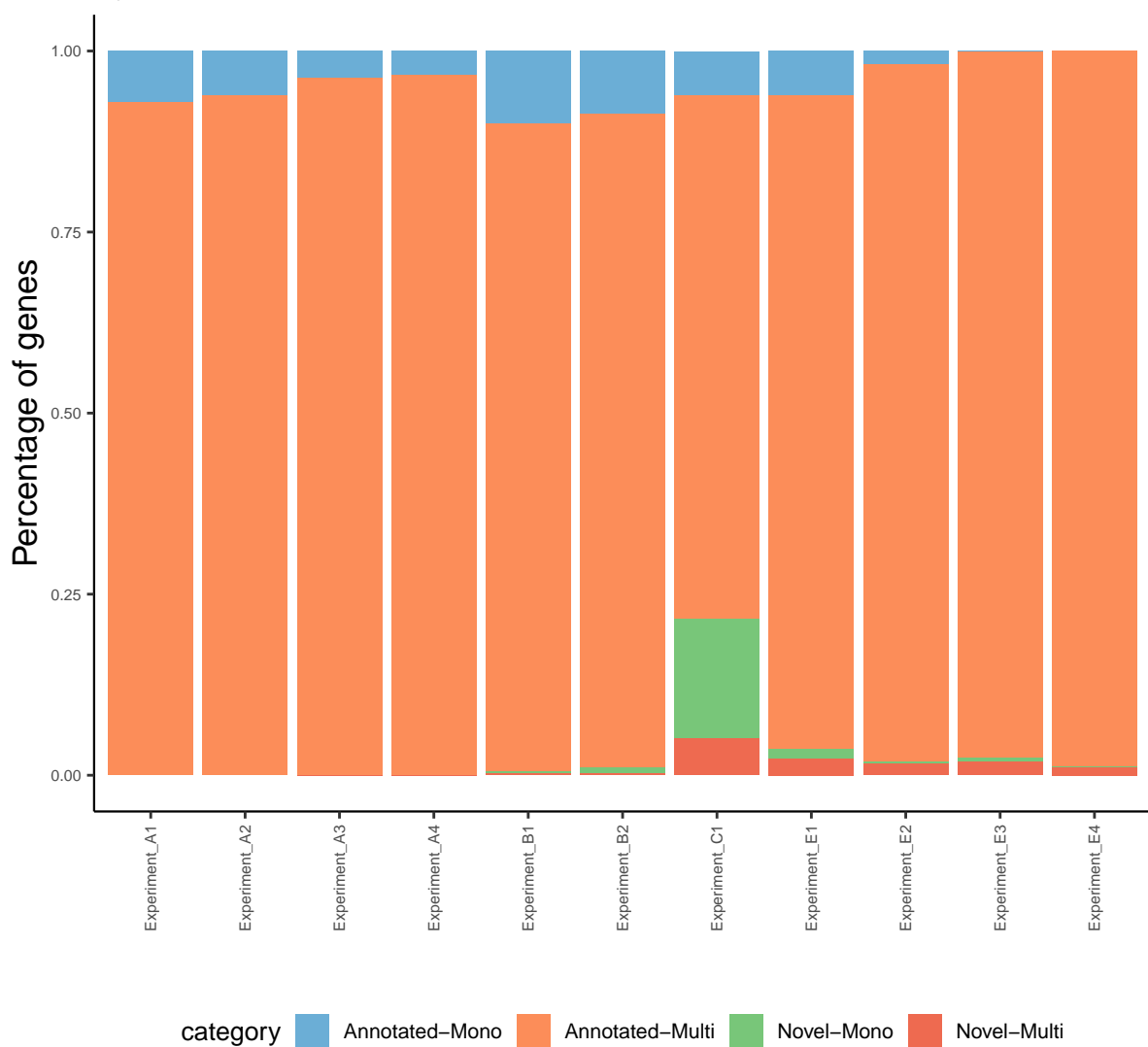
● total ● NIC ● Antisense ● Genic-Intron
 ● FSM ● NNC ● Fusion ● uniq_id
 ● ISM ● Genic-Genomic ● Intergenic

Gene Characterization

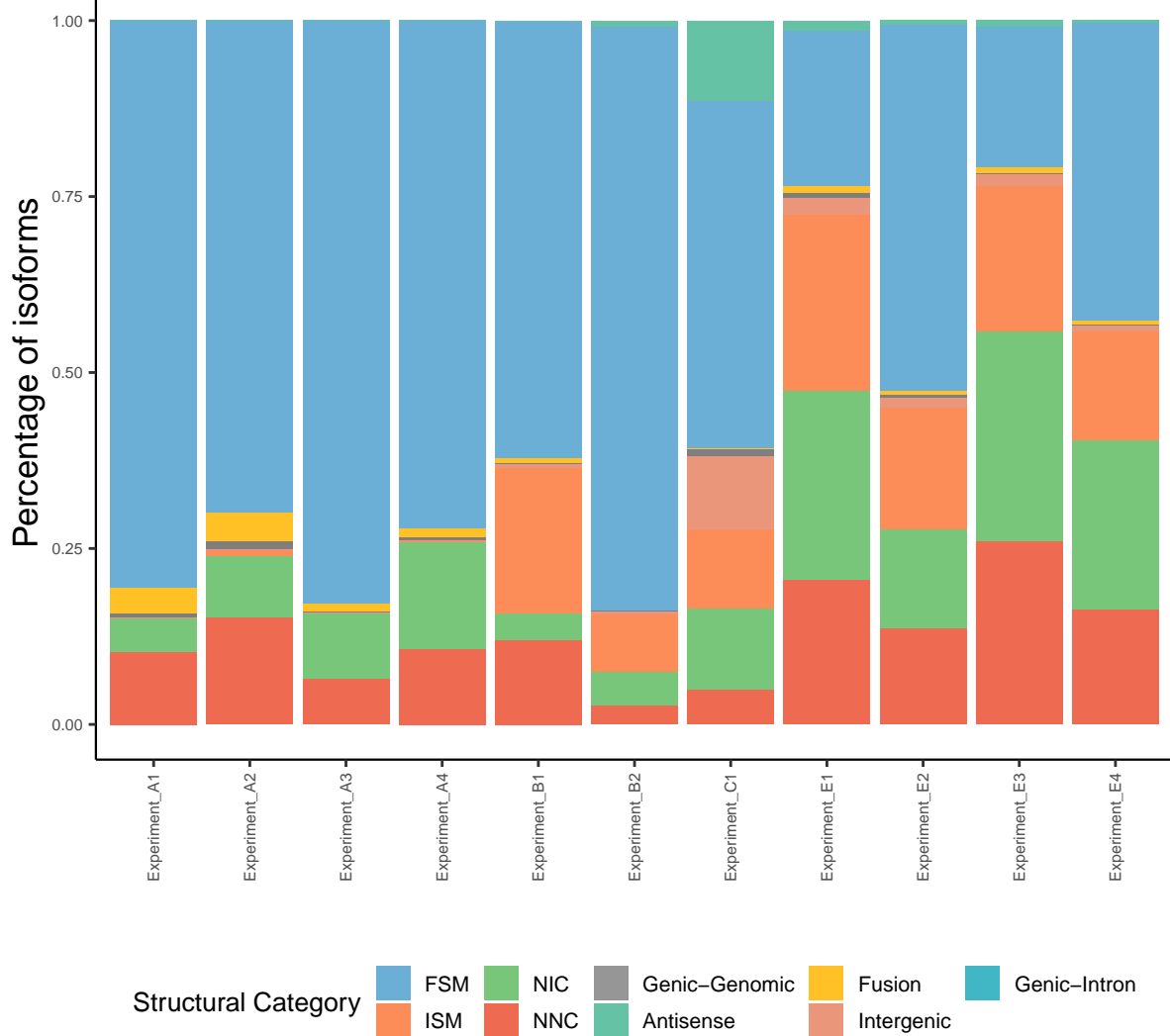
Number of isoforms per gene



Type of isoforms

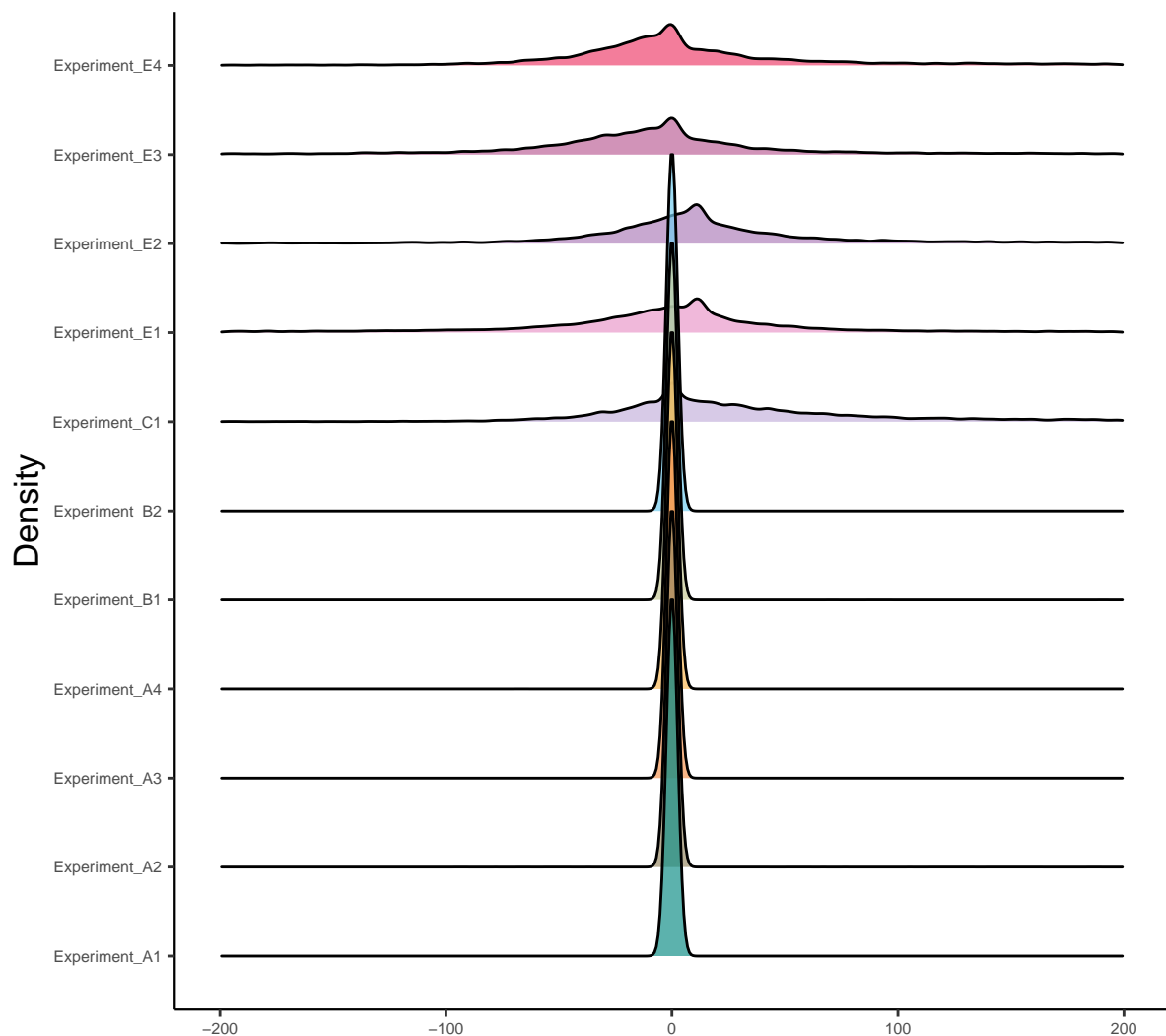


Distribution of Structural Categories

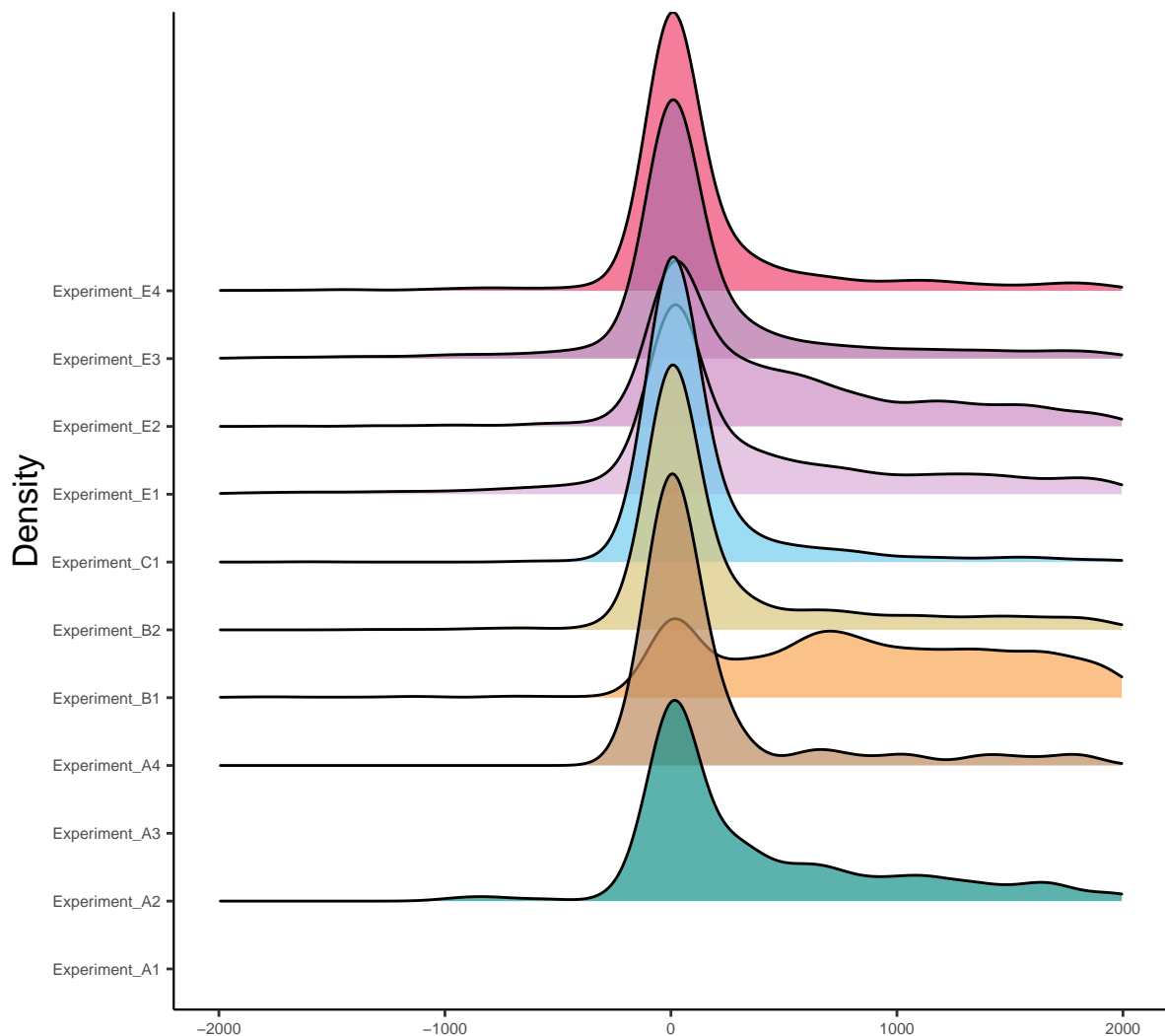


Distance to annotated TSS and TTS

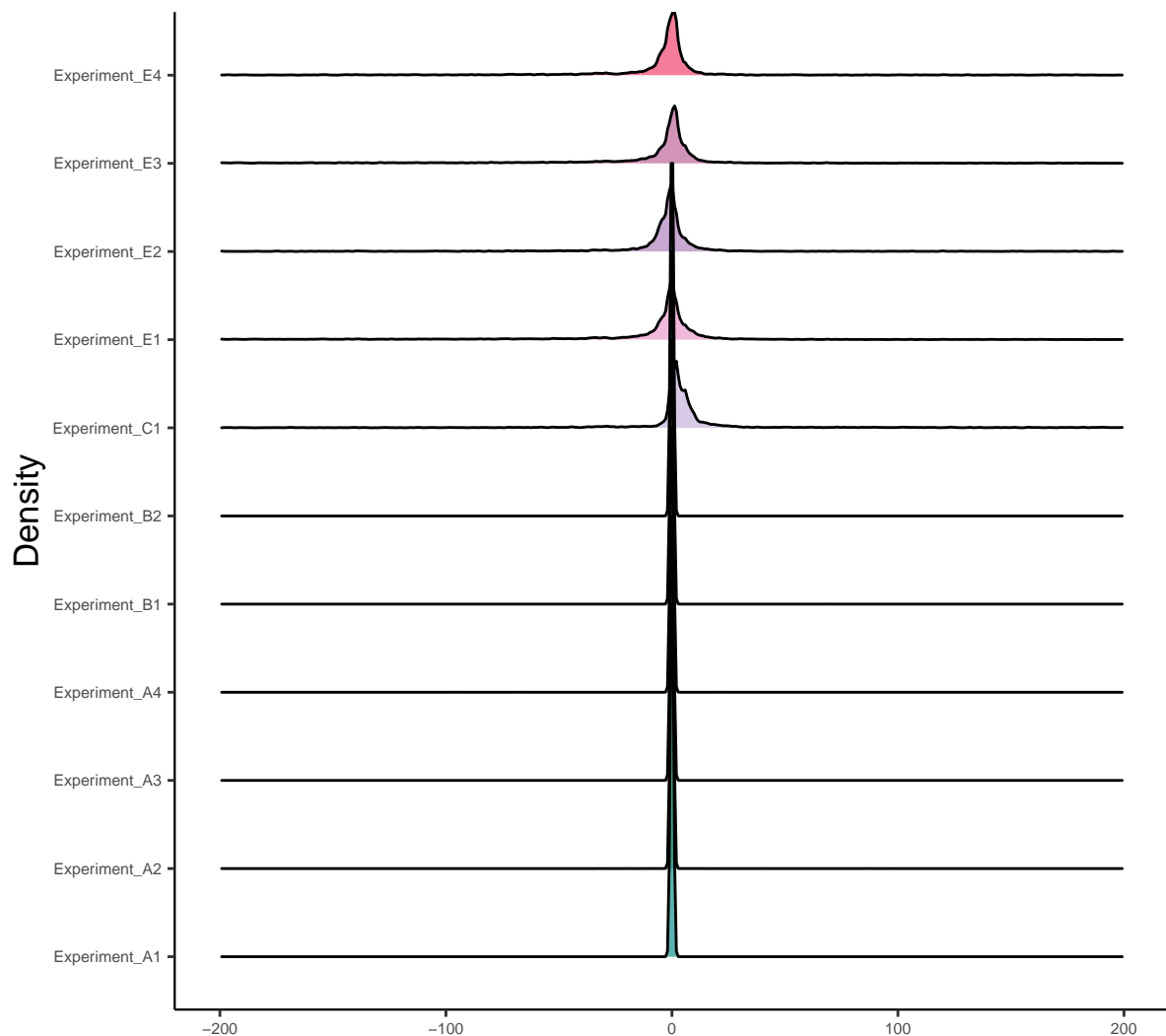
Distance to TSS of FSM isoforms



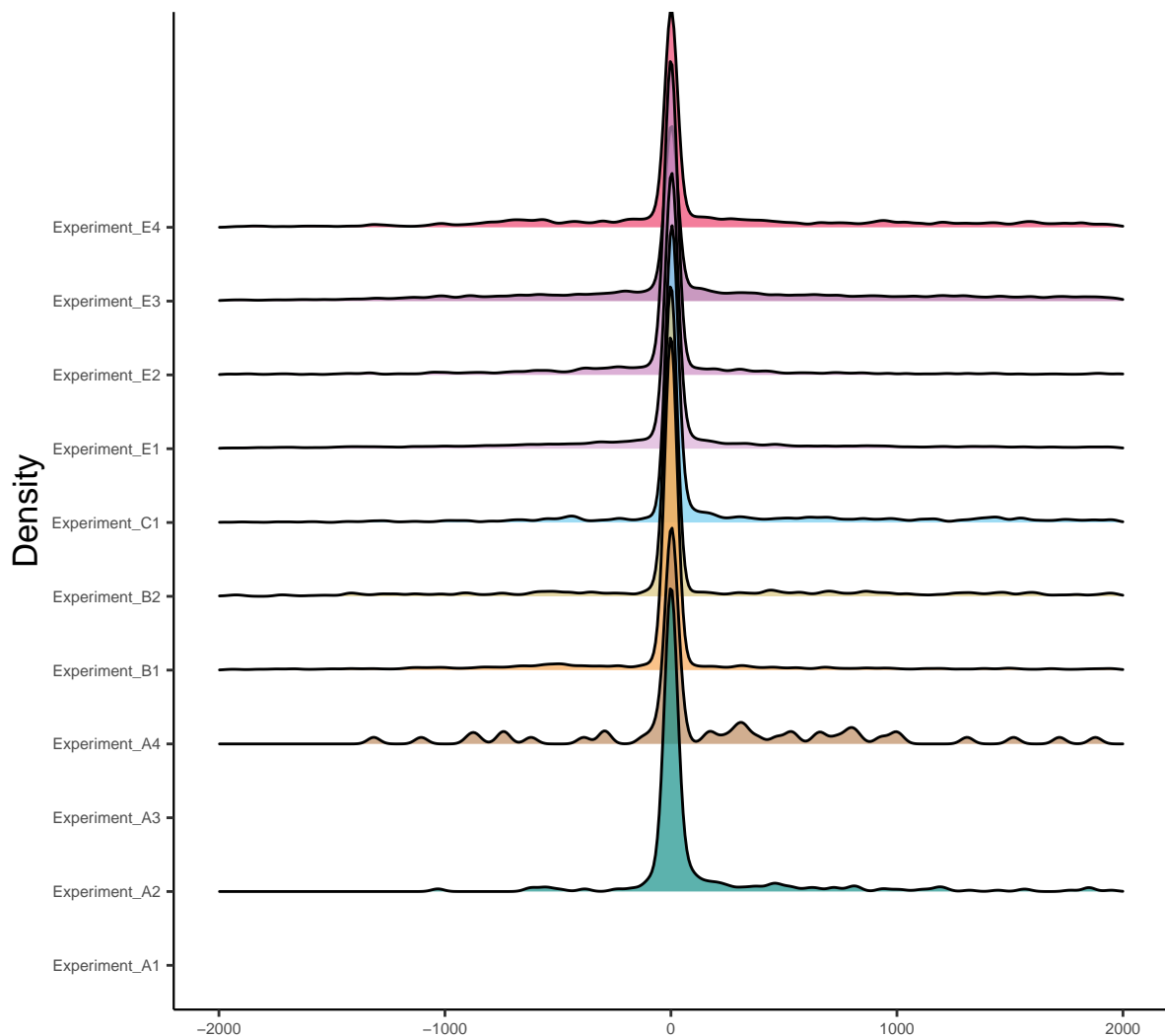
Distance to TSS of ISM isoforms



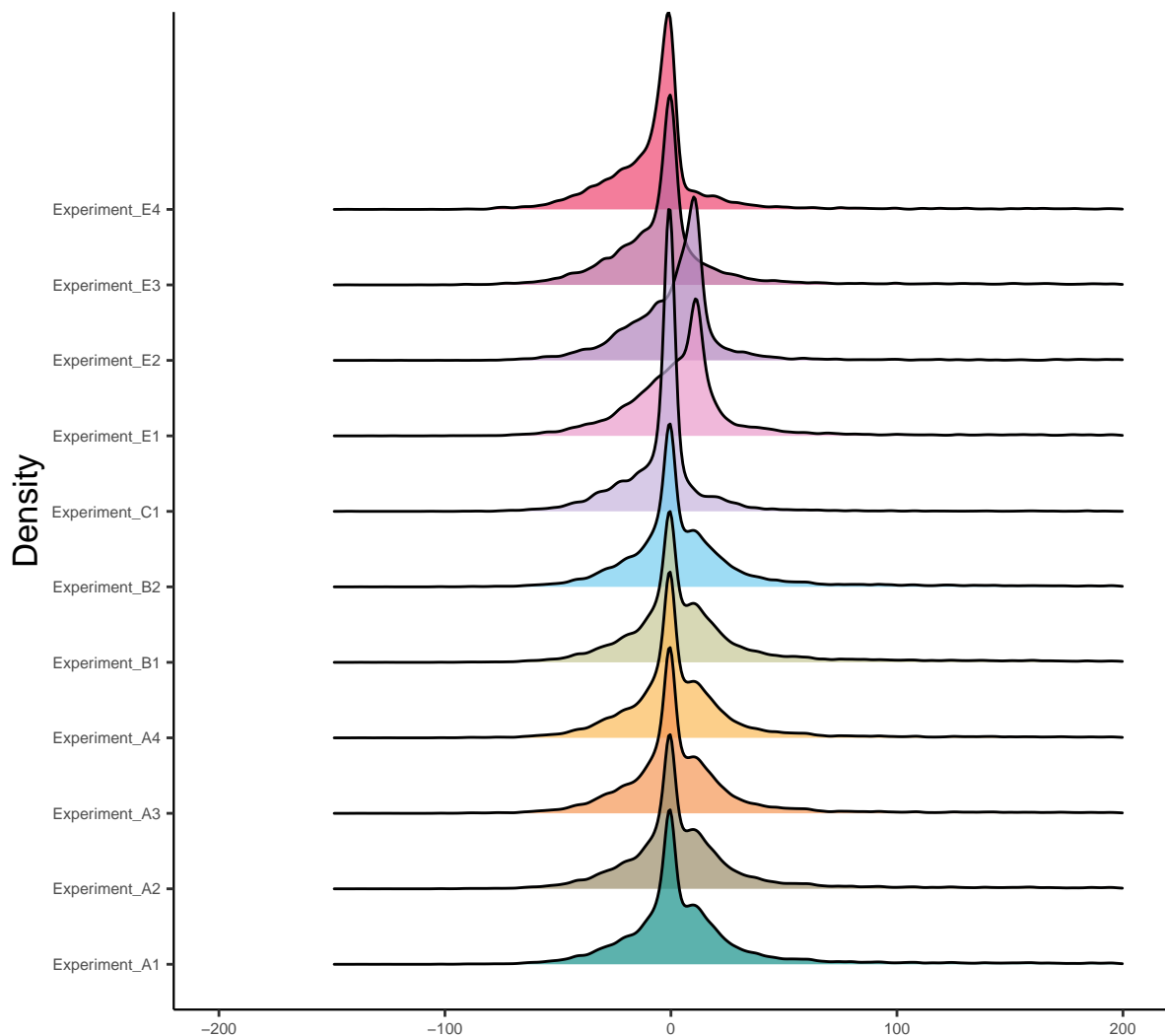
Distance to TTS of FSM isoforms



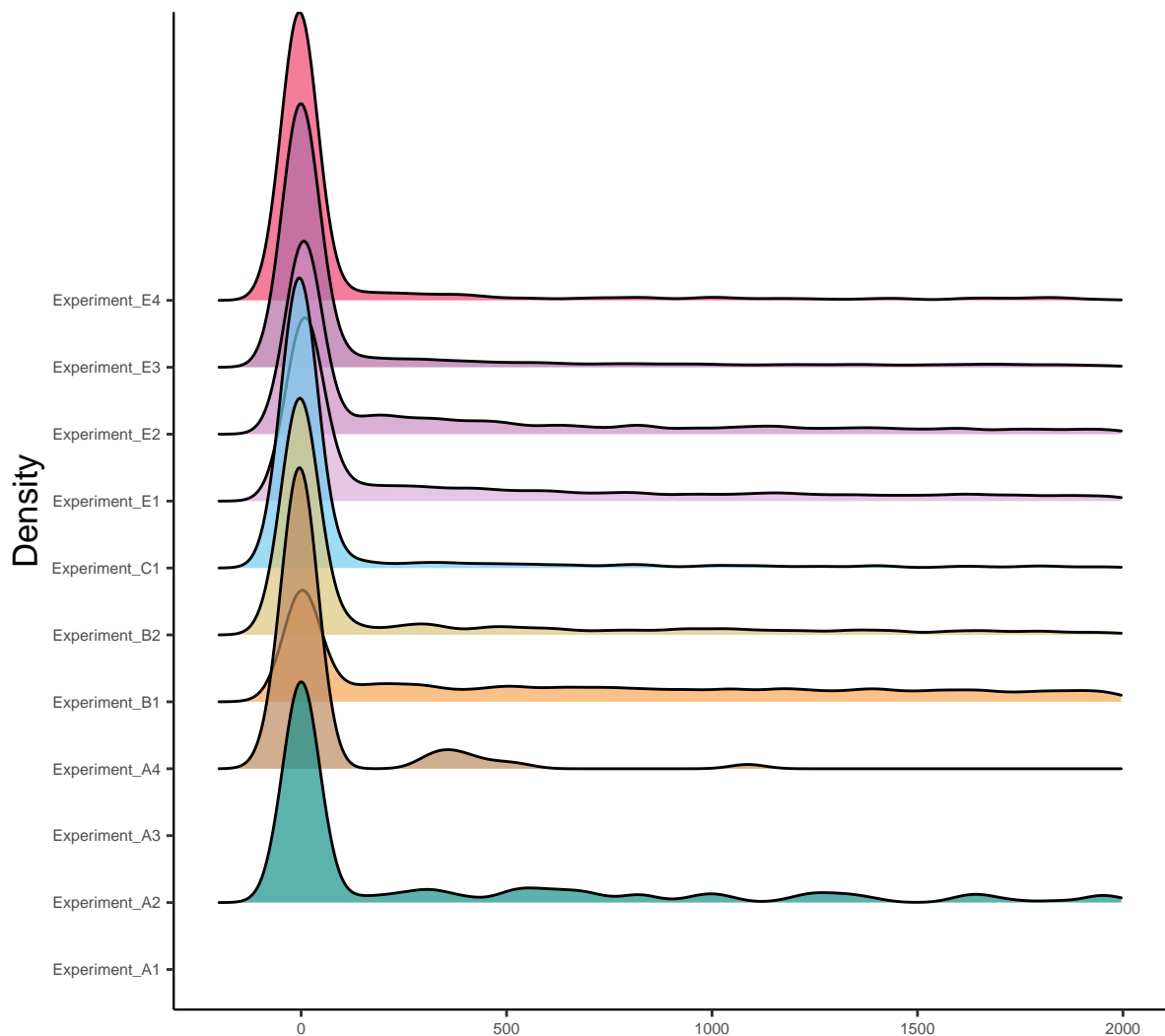
Distance to TTS of ISM isoforms



Distance to closest CAGE peak (FSM only)

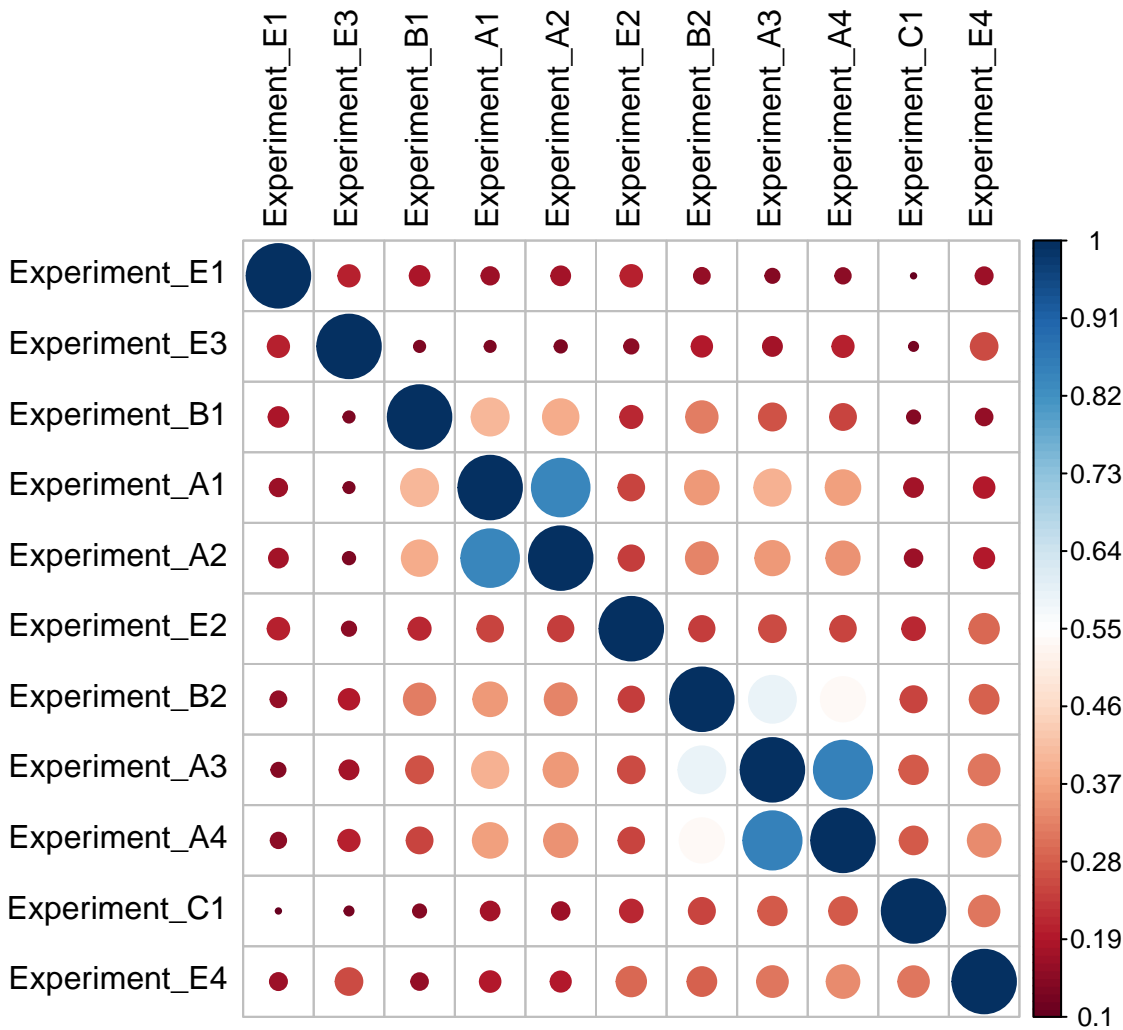


Distance to closest CAGE peak (ISM only)



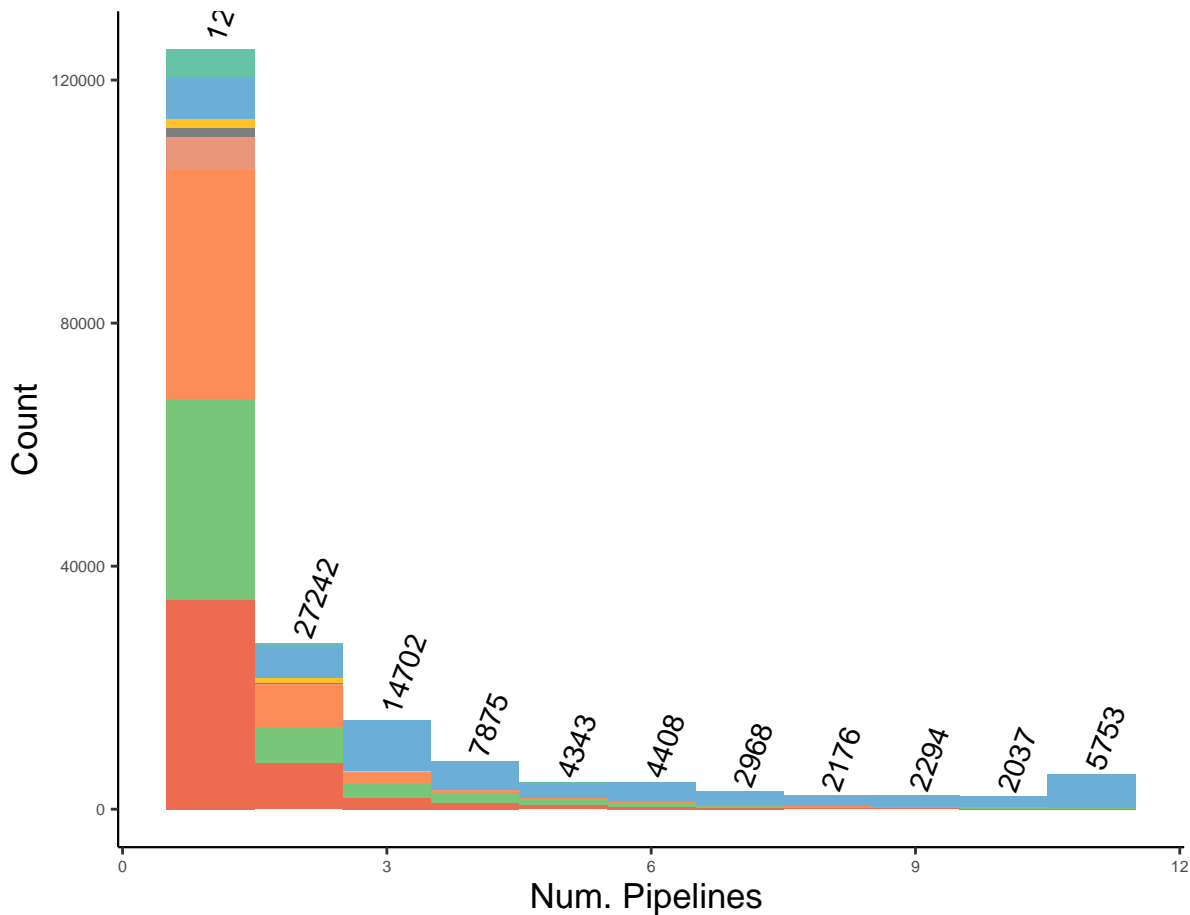
*Presence/absence analysis
of UJC across pipelines*

Pair-wise Jaccard index between submissions



Number of pipelines that found a certain UJC

Coloured by Structural Categories



Structural Category



FSM



ISM



NNC



NIC



Antisense



Genic-Genomic



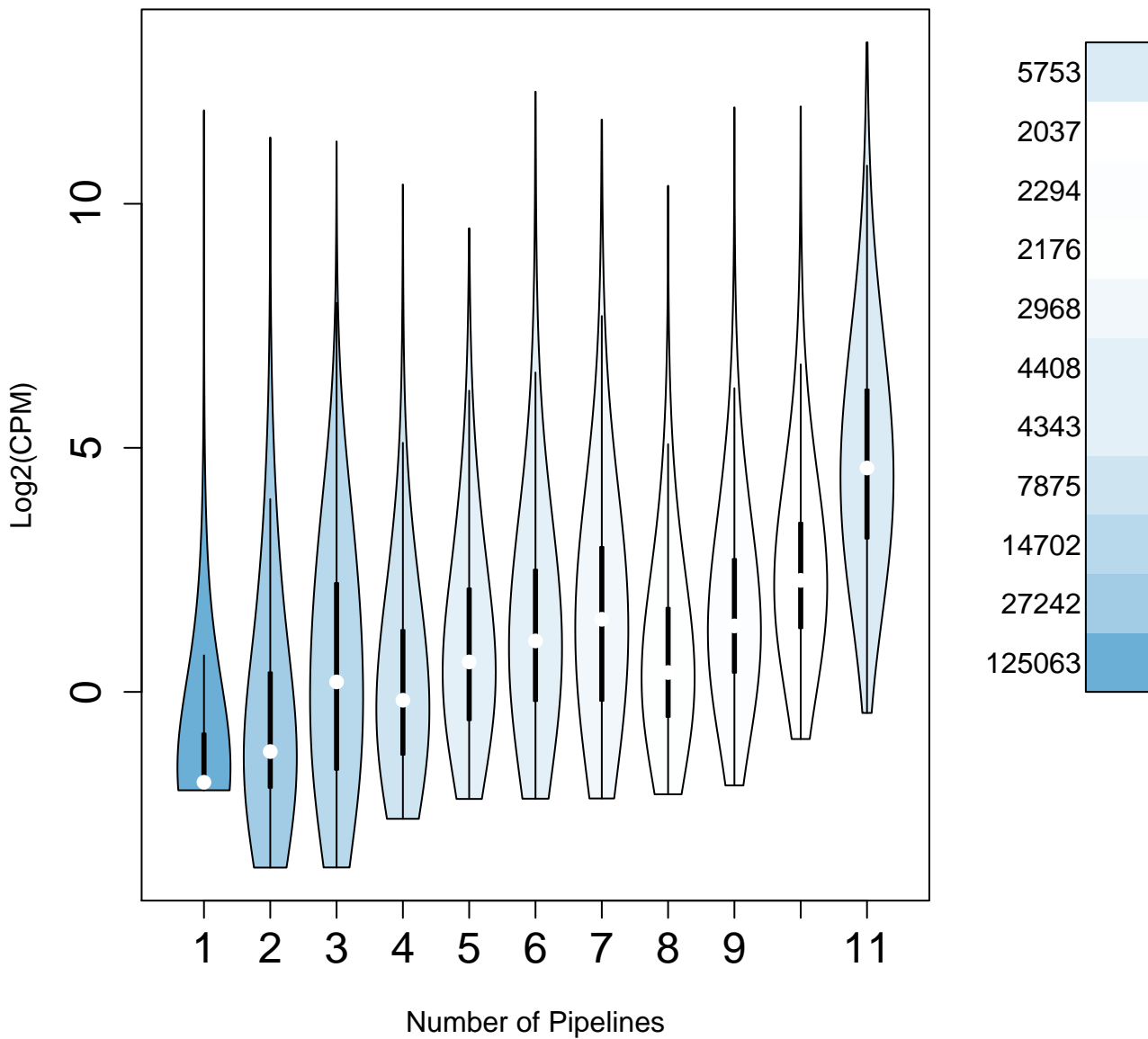
Fusion



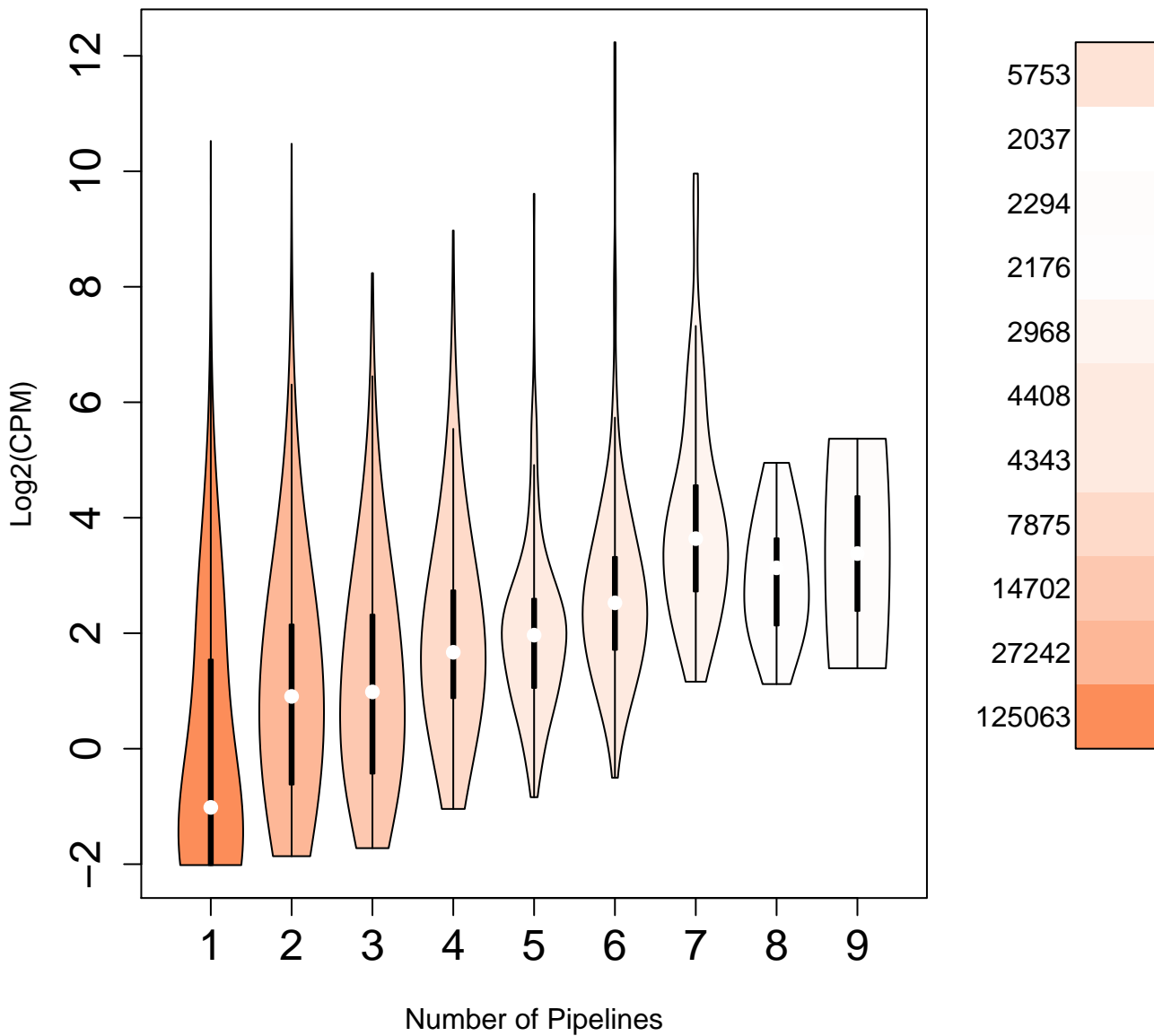
Intergenic

Genic-Intron

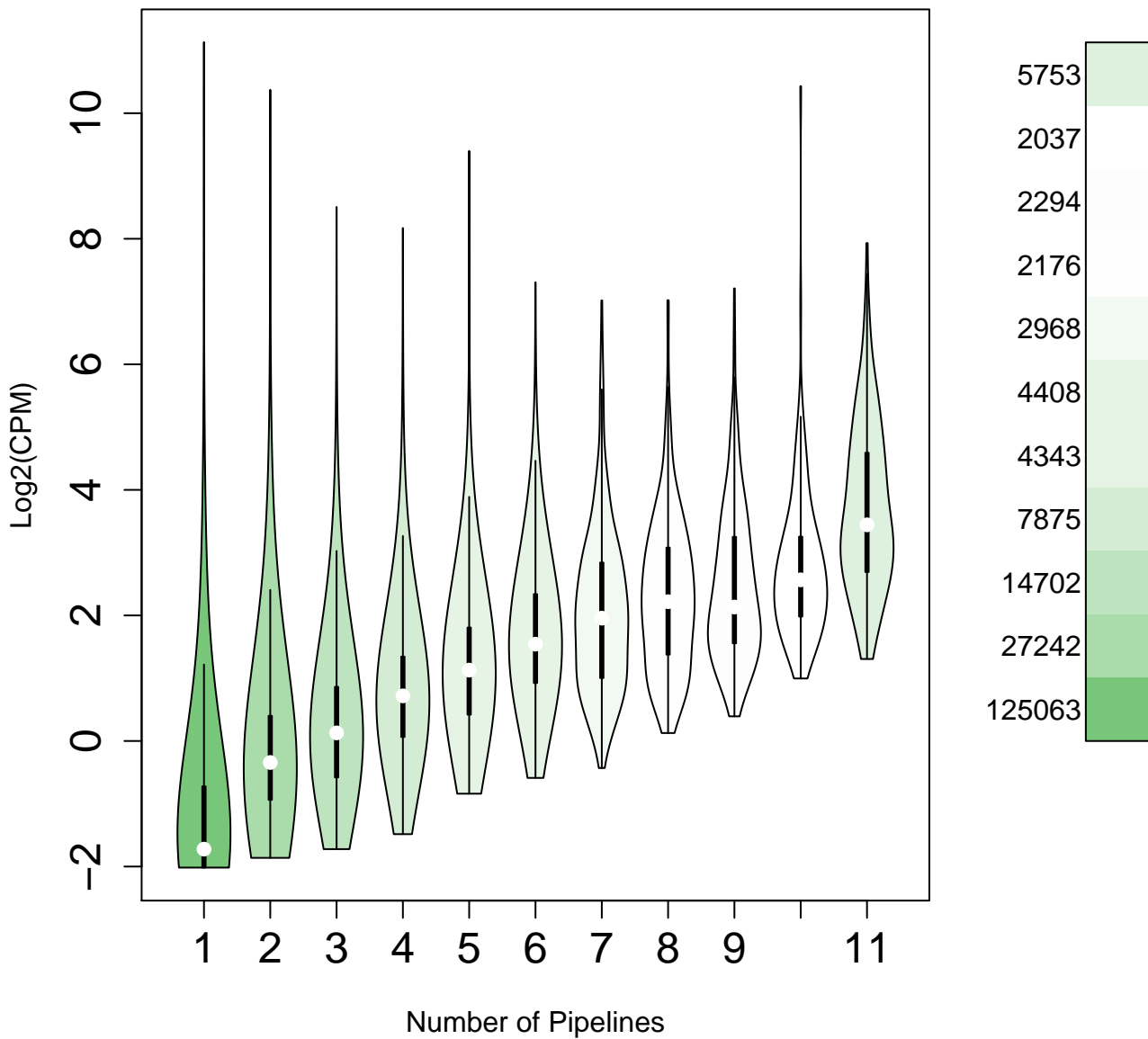
FSM



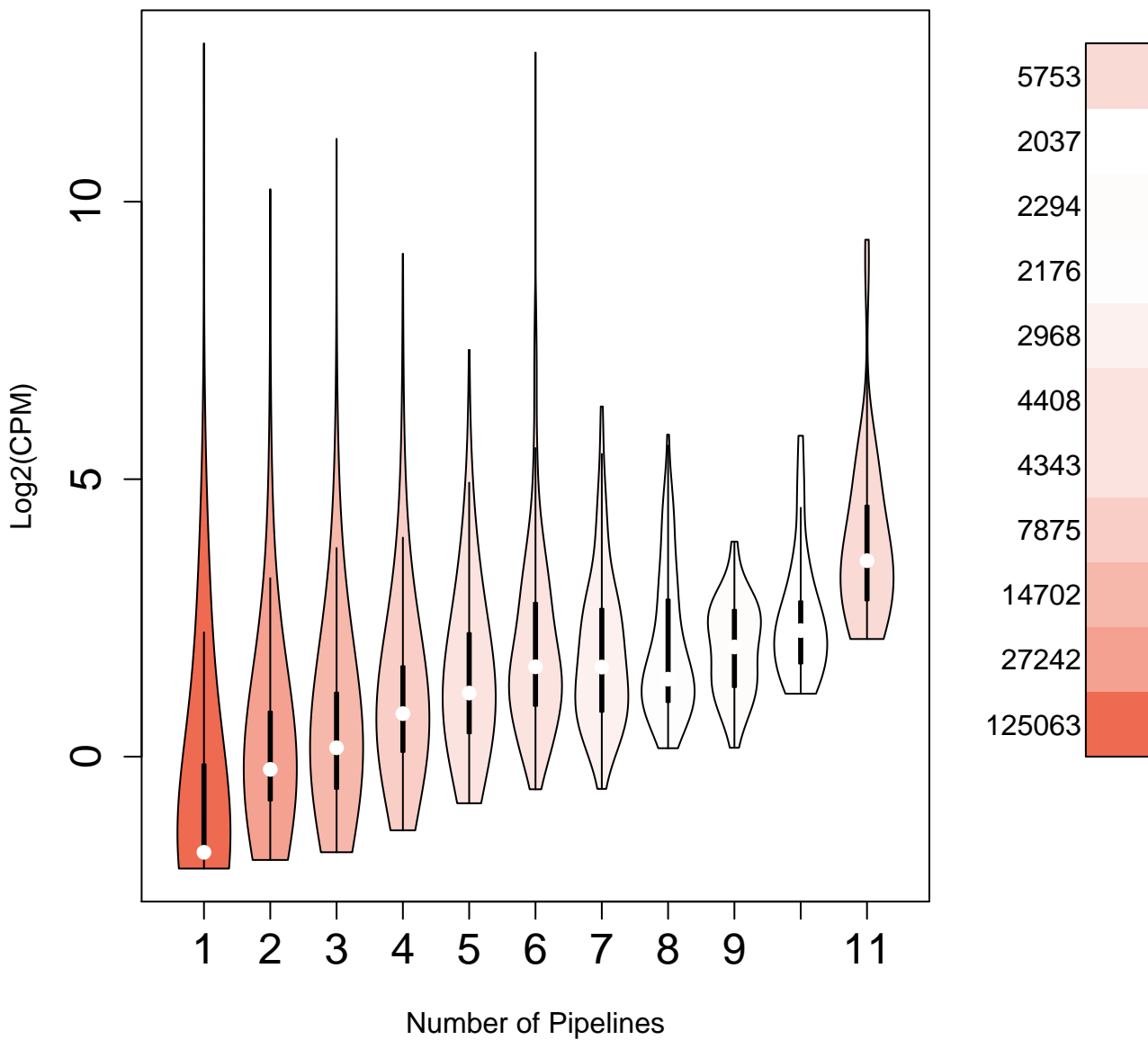
ISM



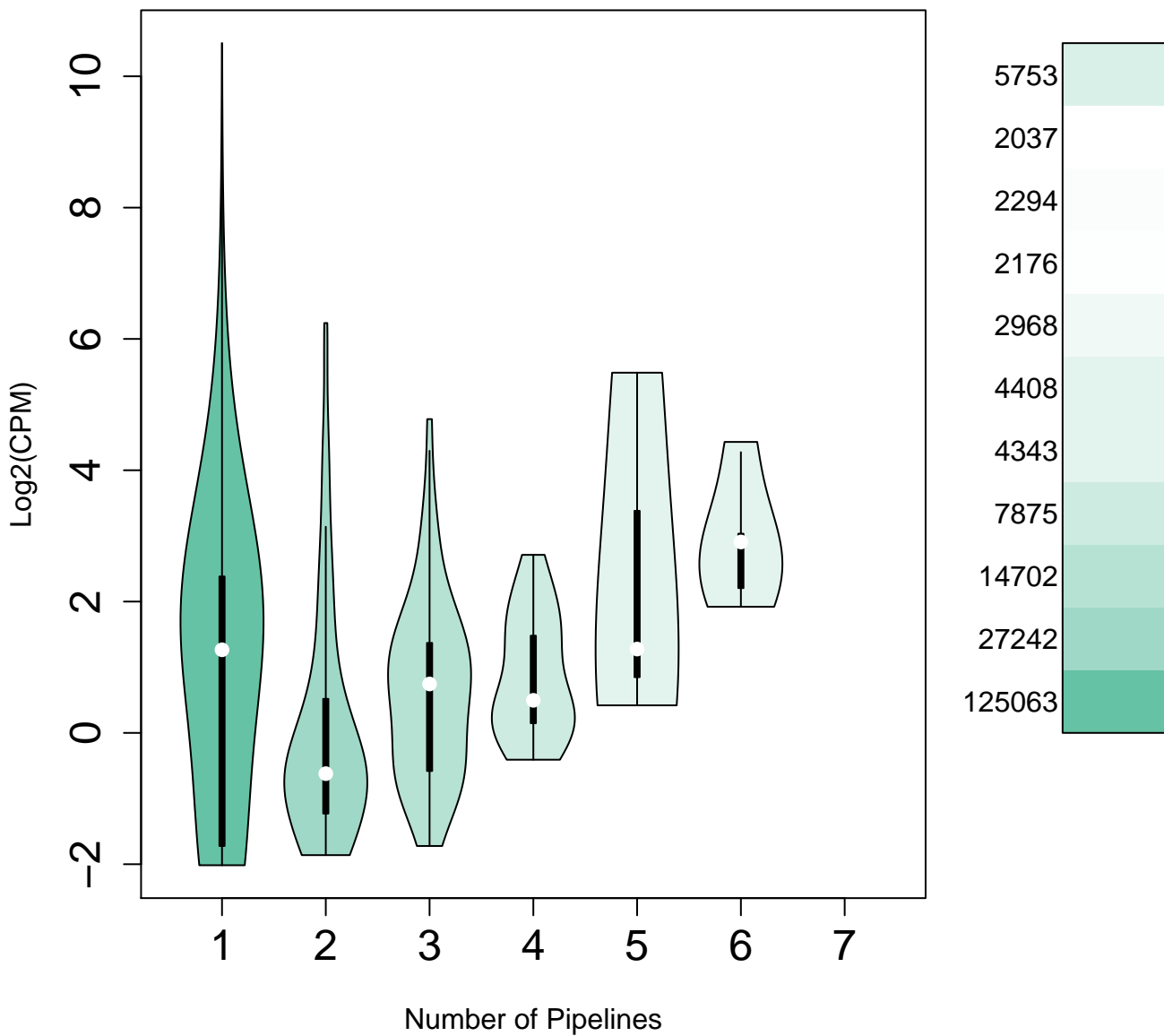
NIC



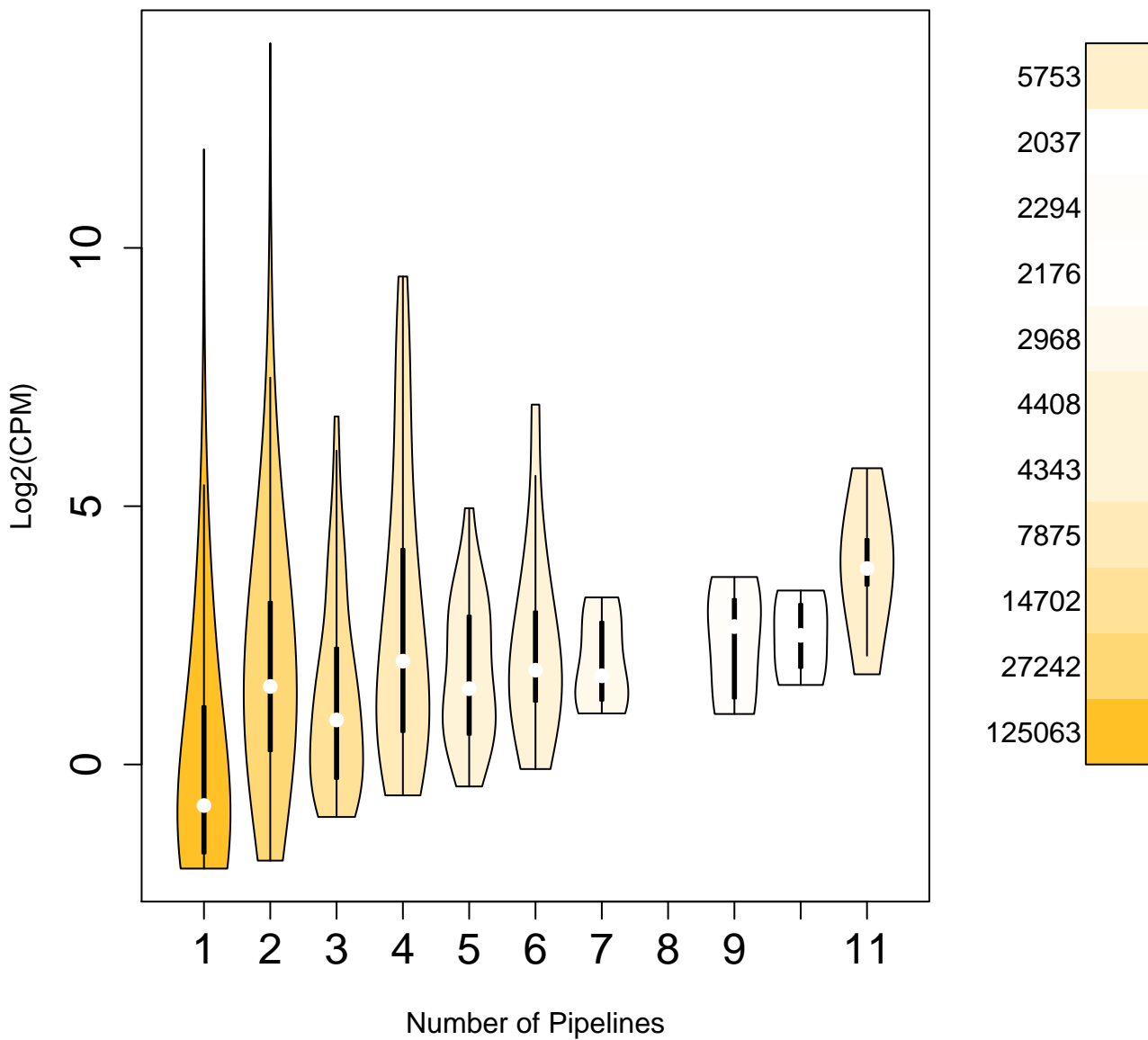
NNC



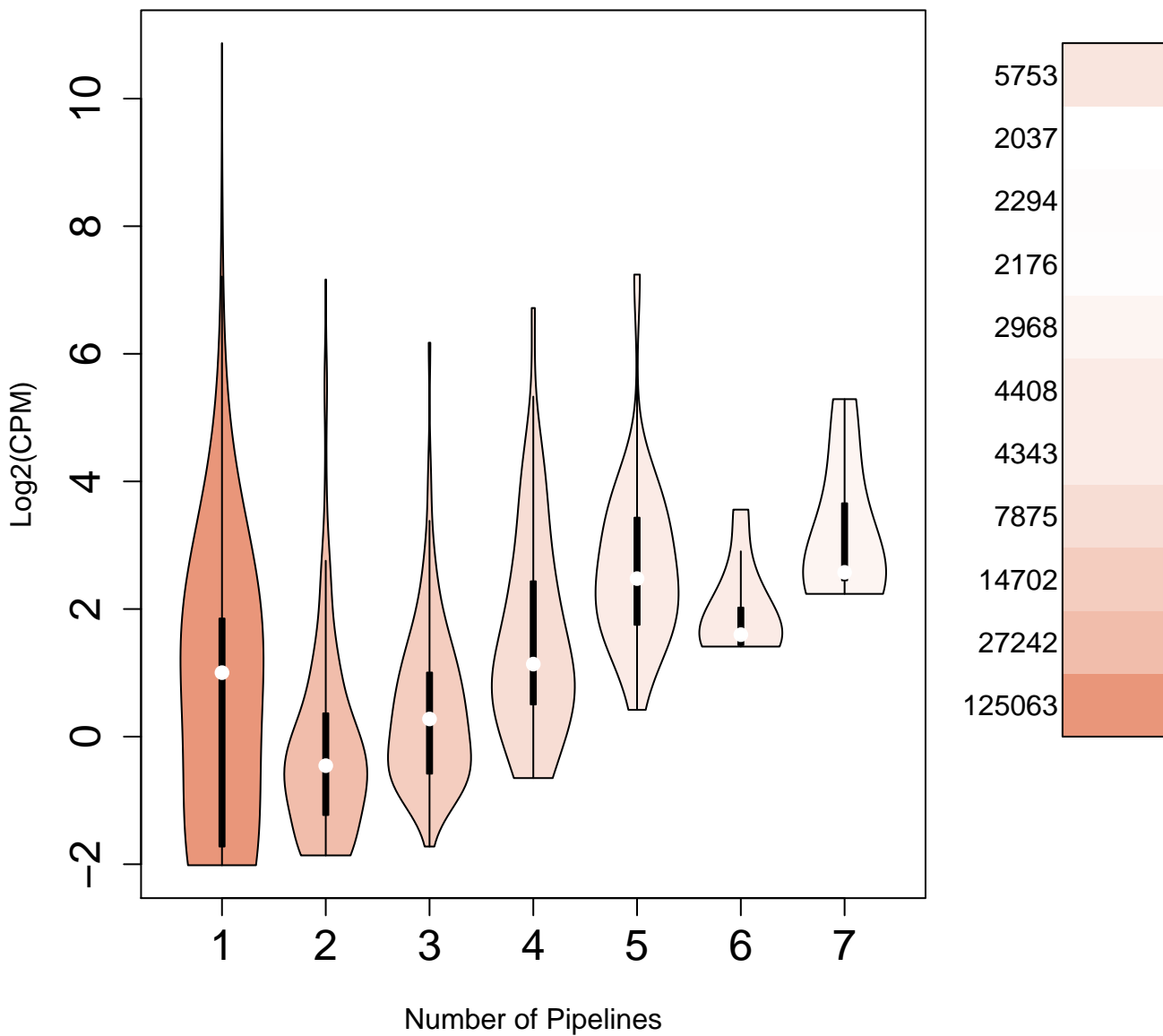
Antisense



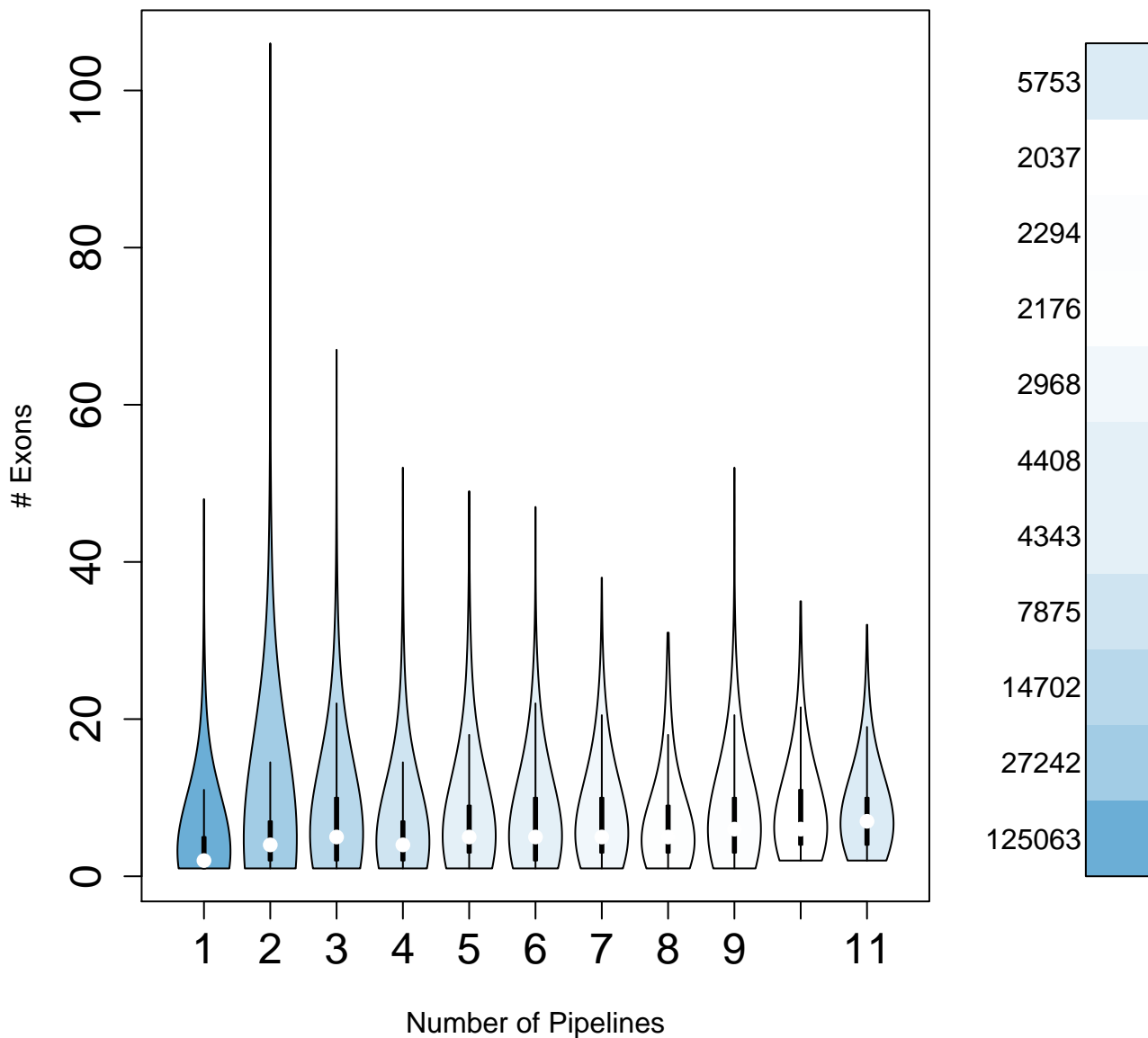
Fusion



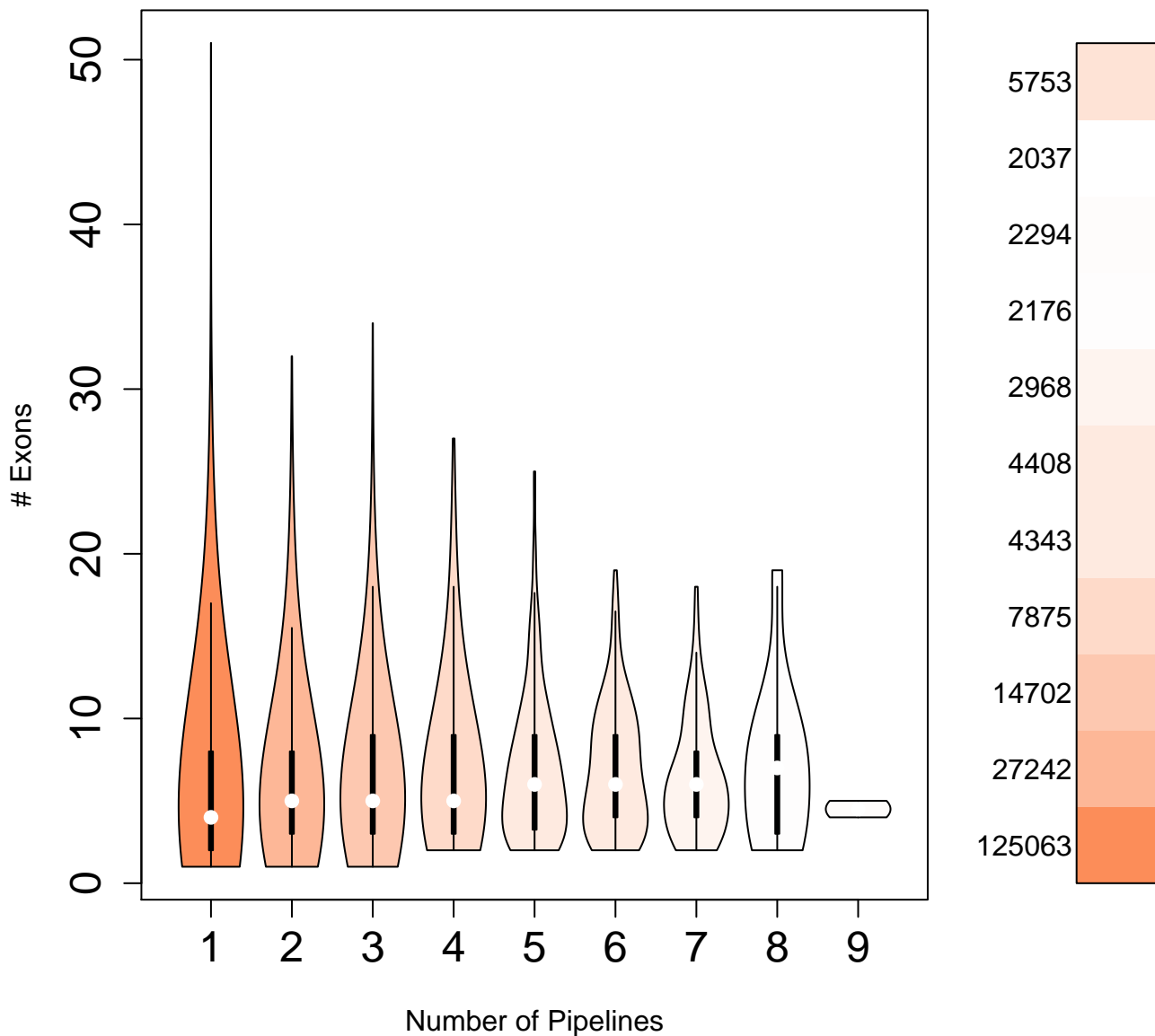
Intergenic



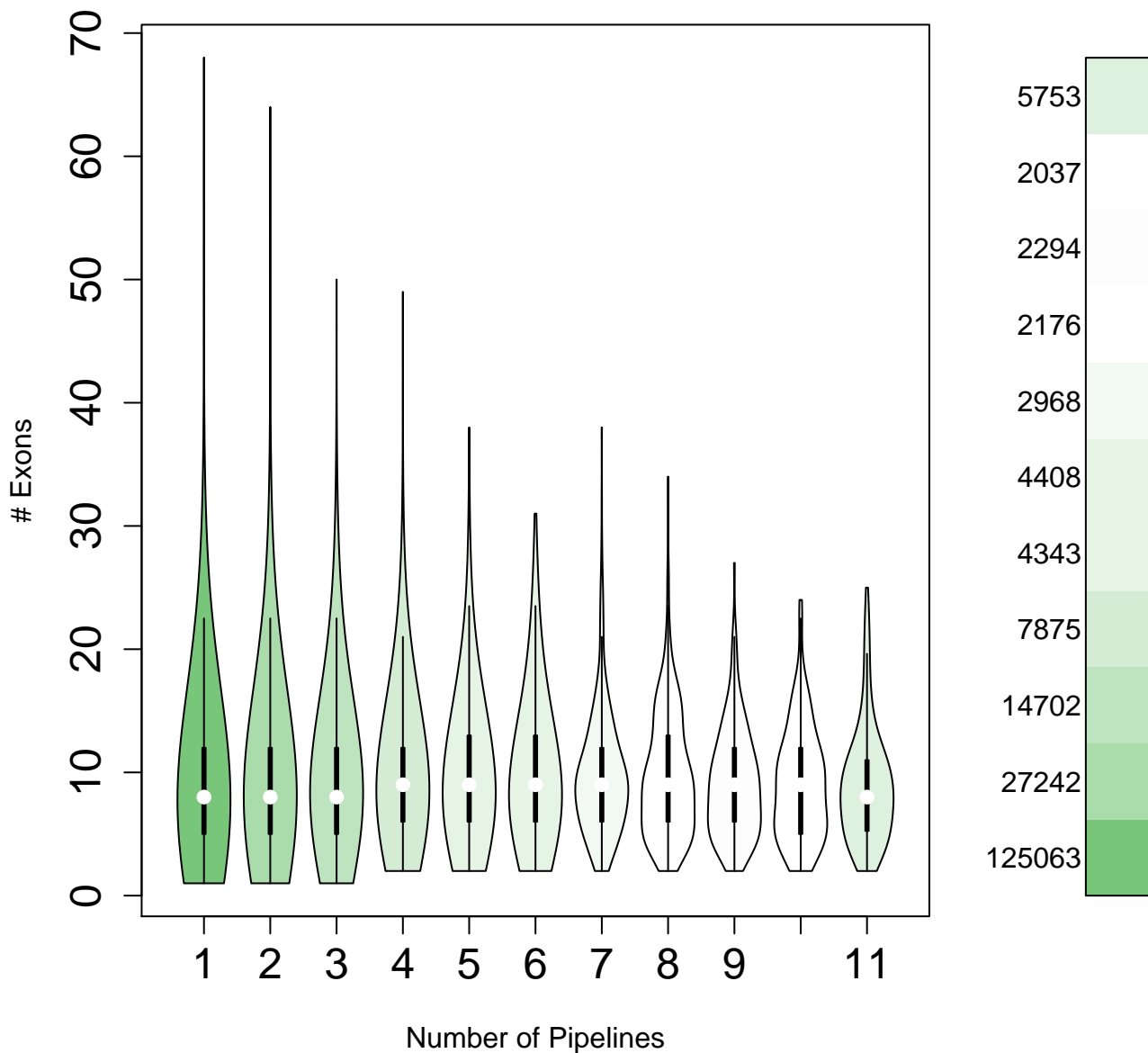
FSM



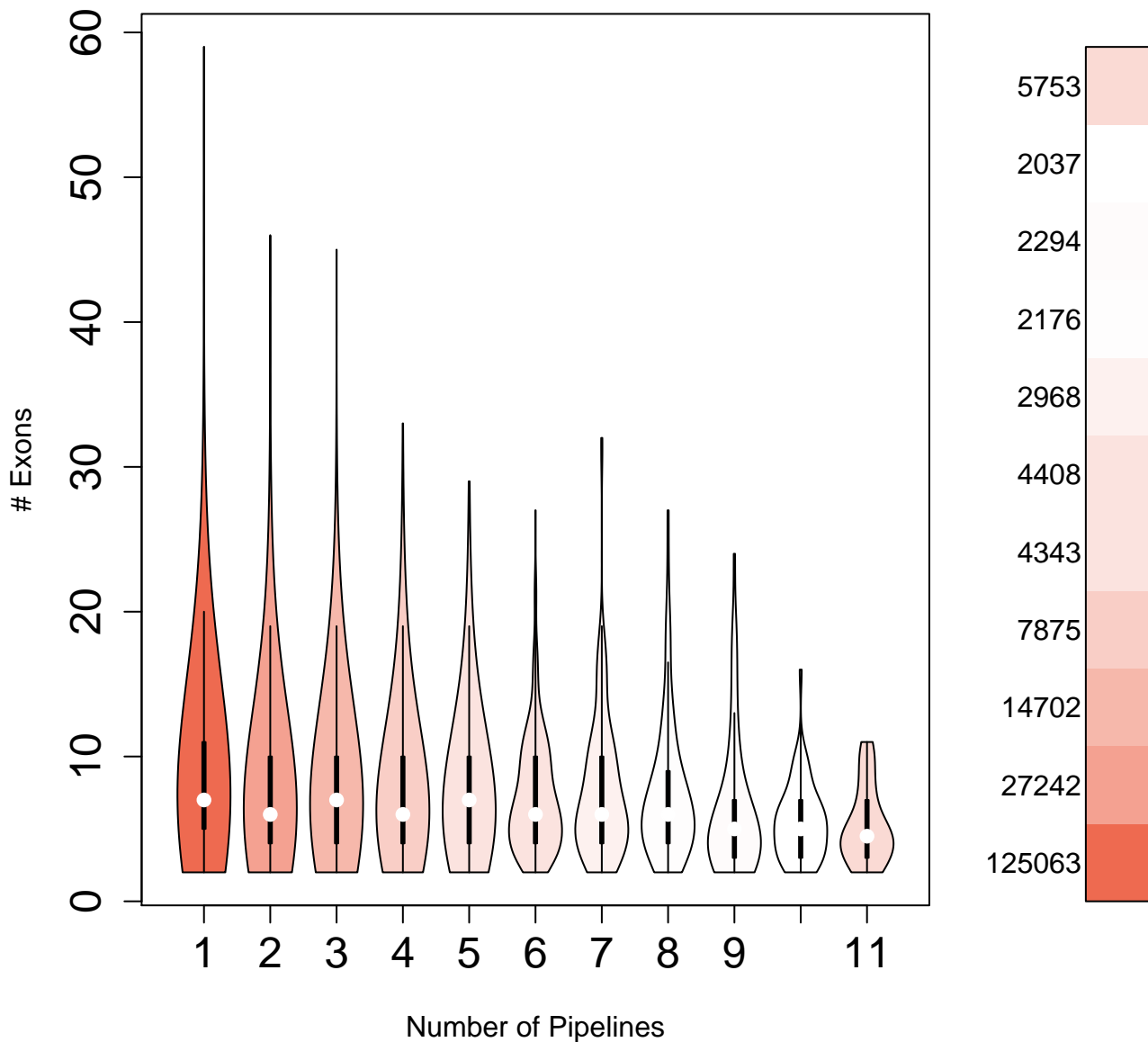
ISM



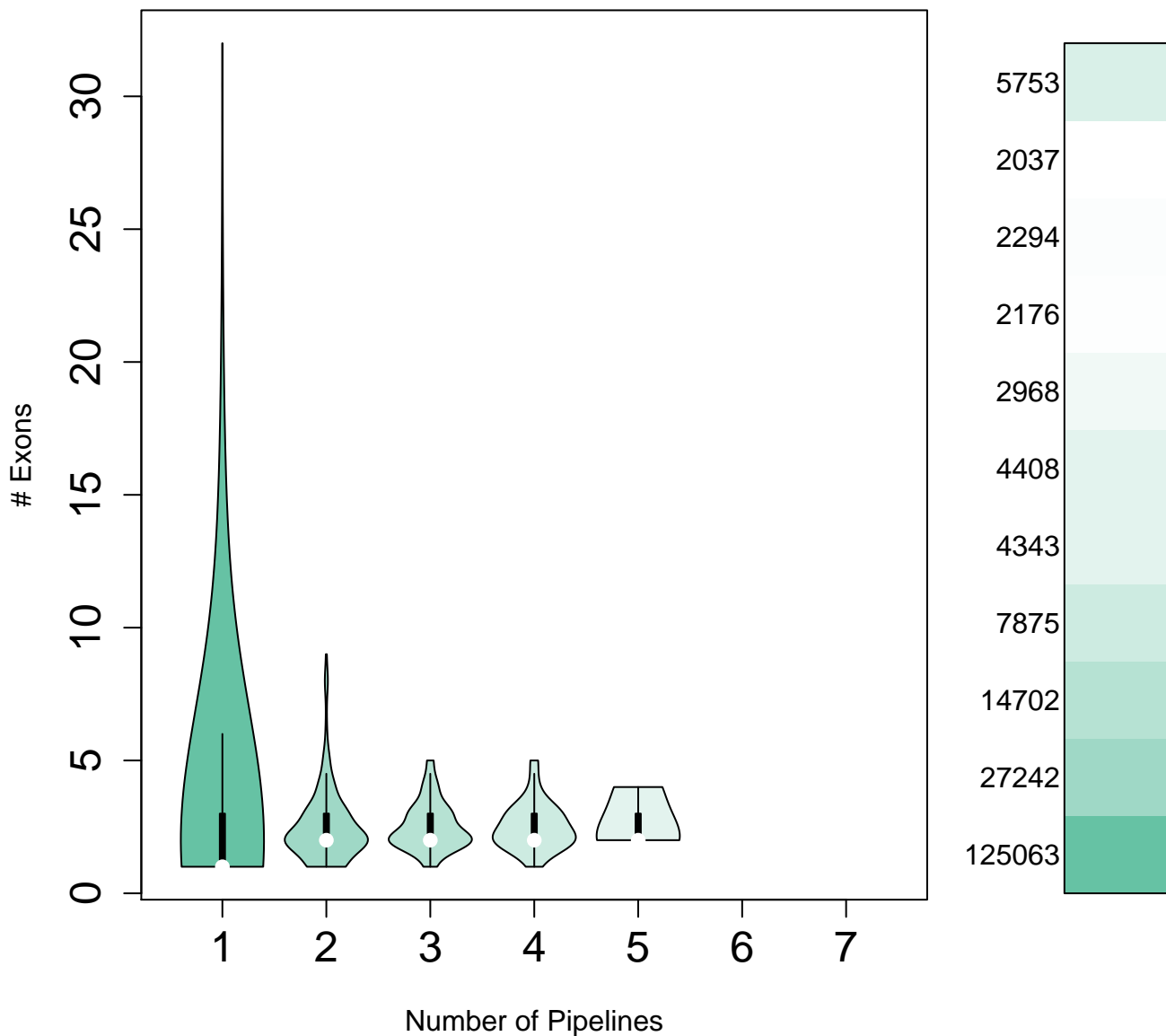
NIC



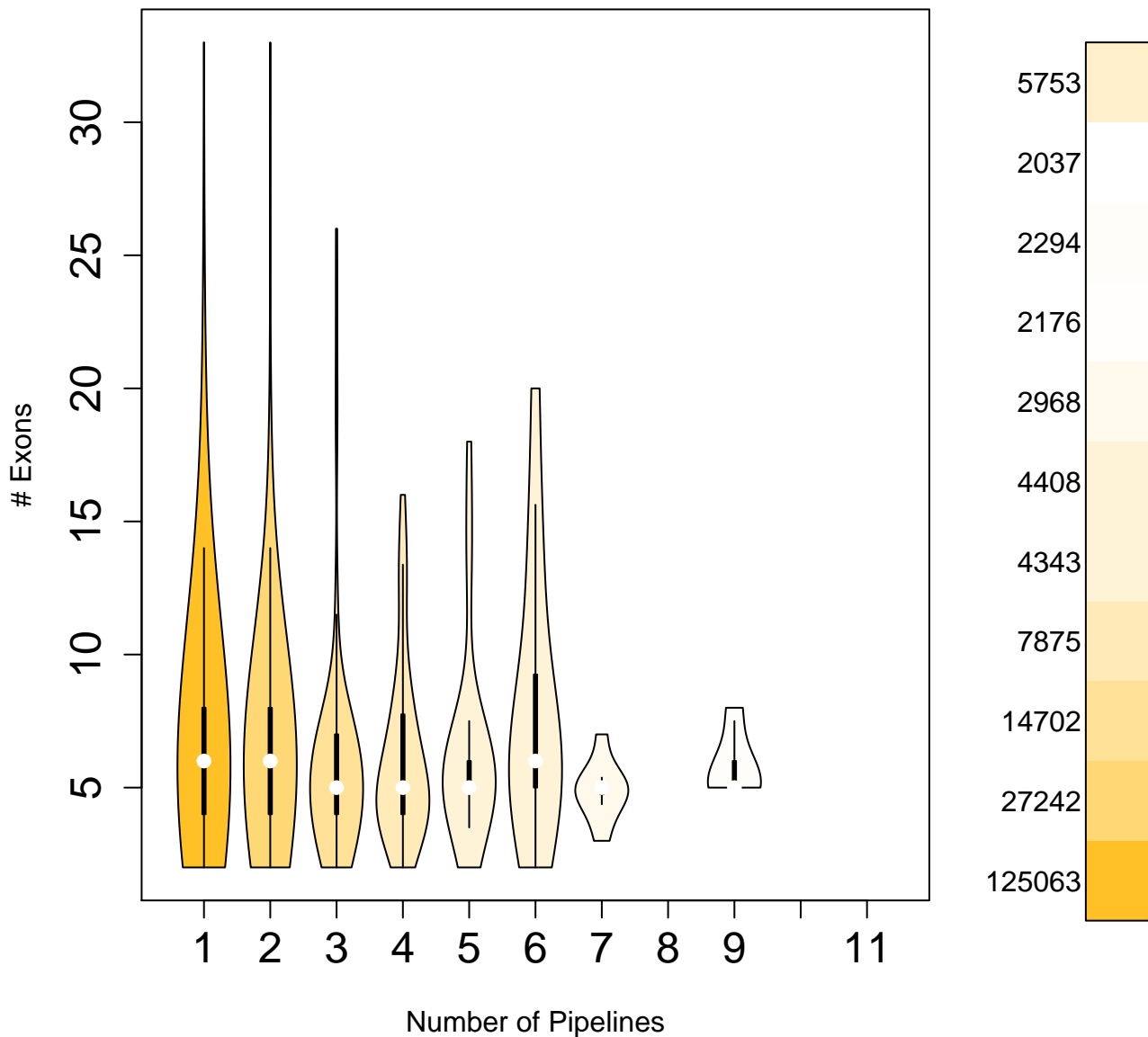
NNC



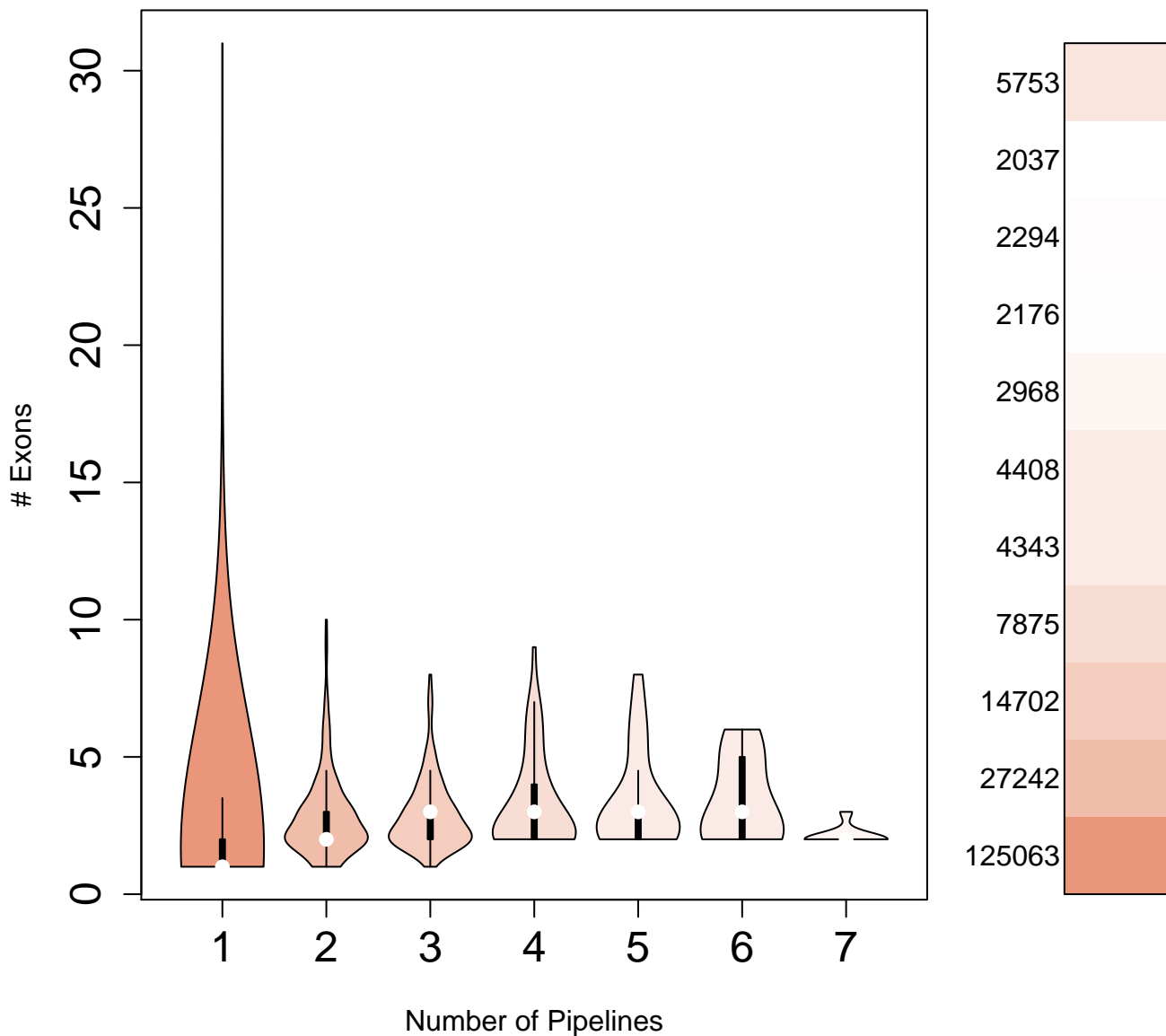
Antisense



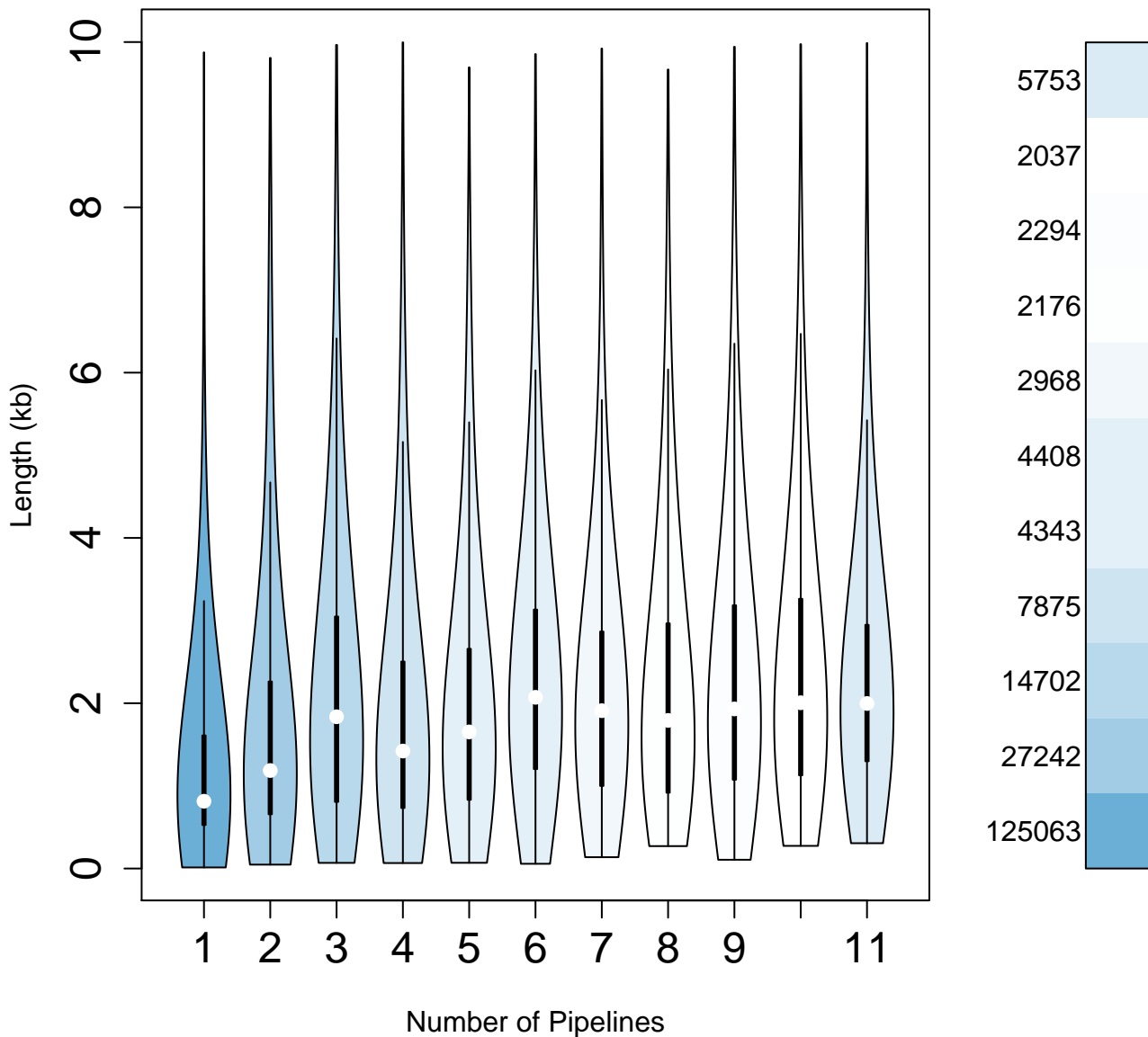
Fusion



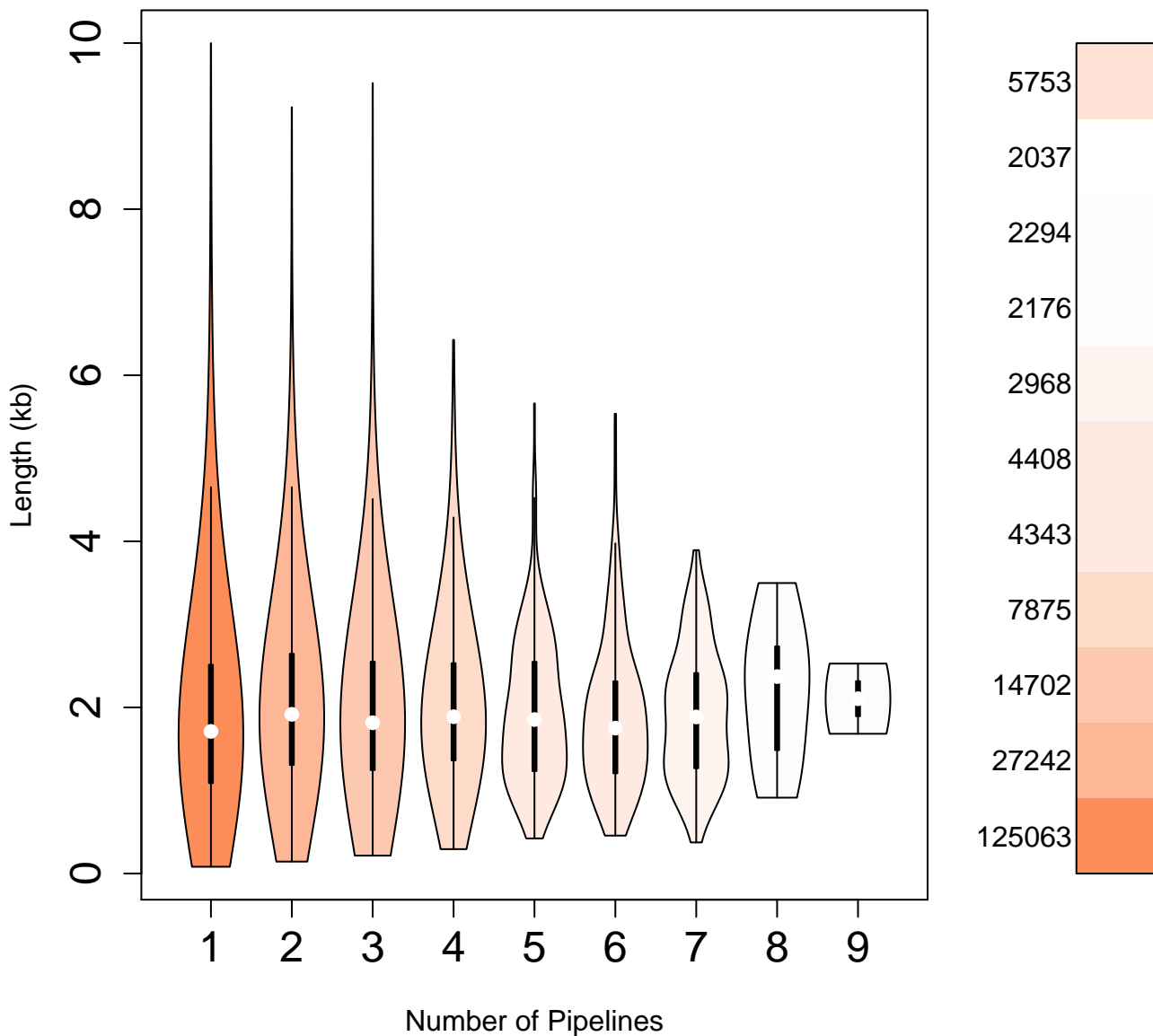
Intergenic



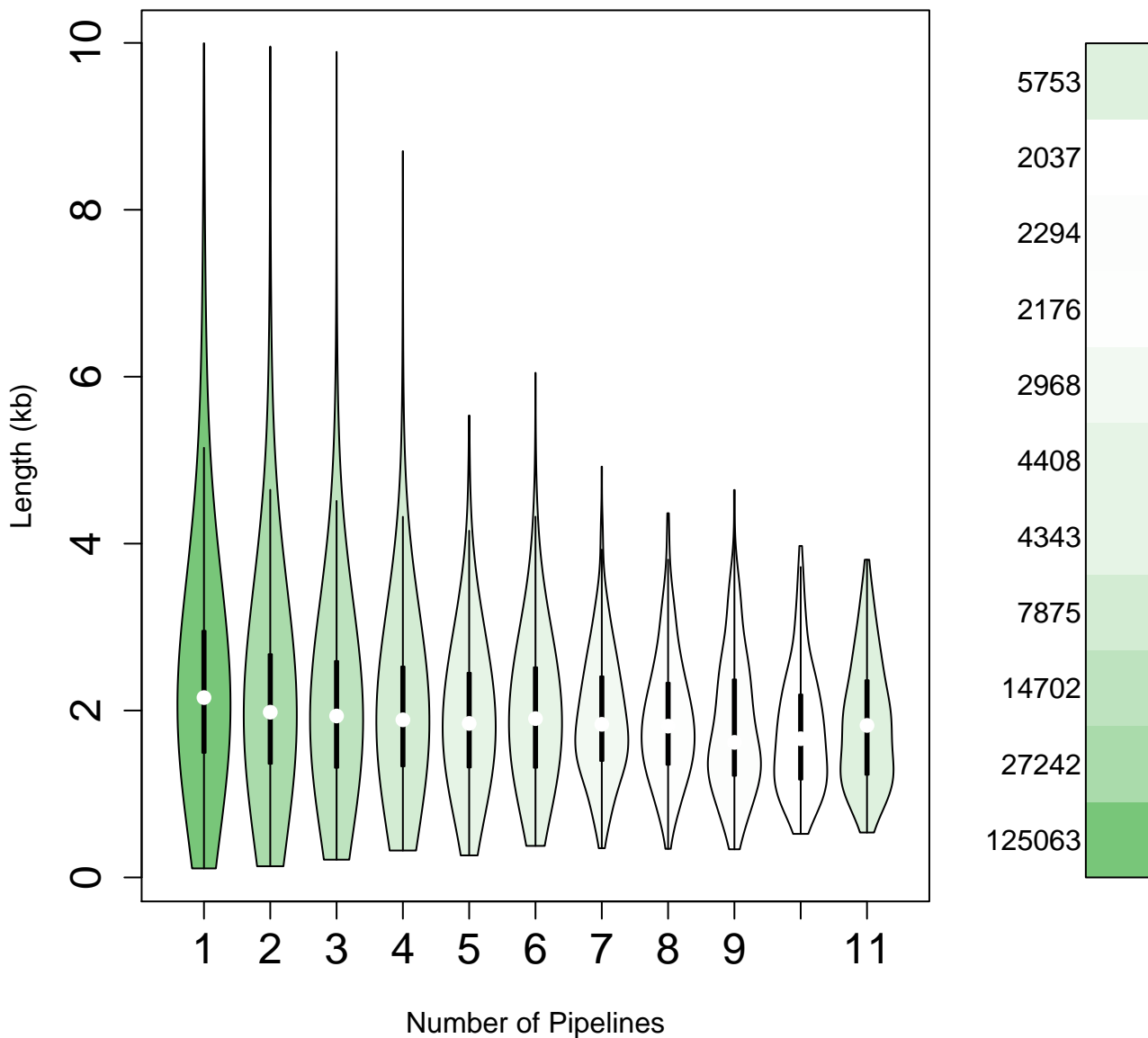
FSM



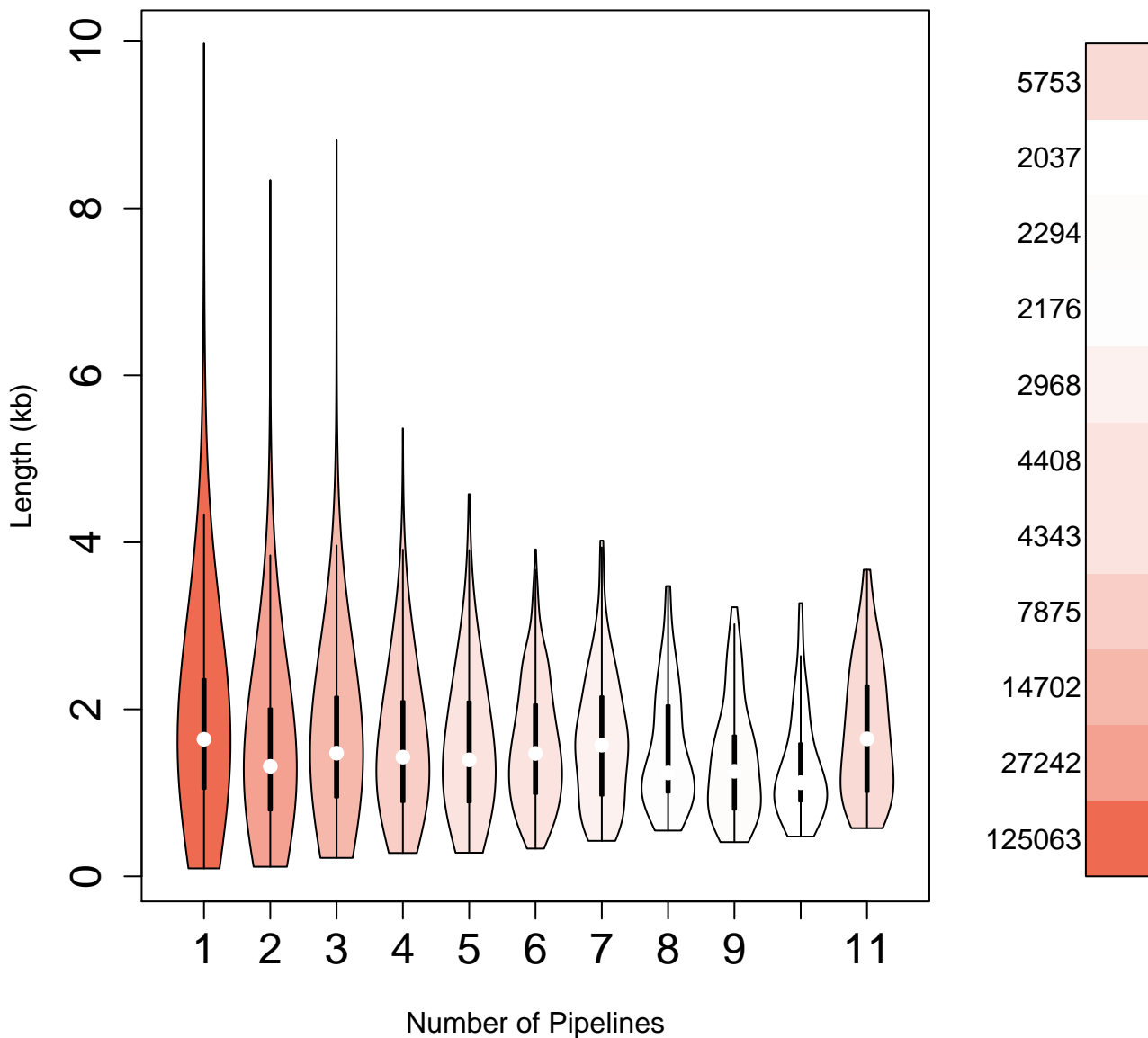
ISM



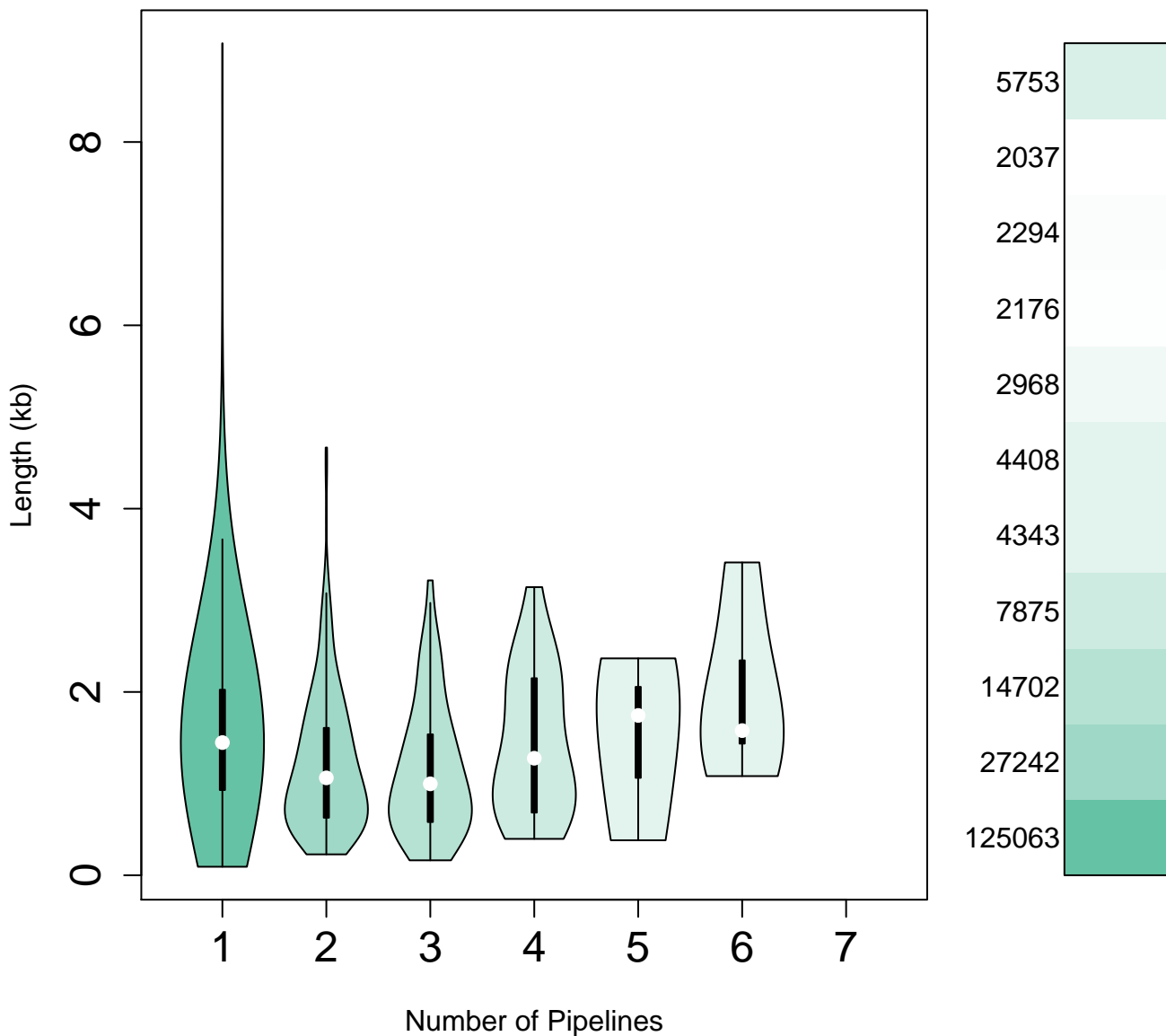
NIC



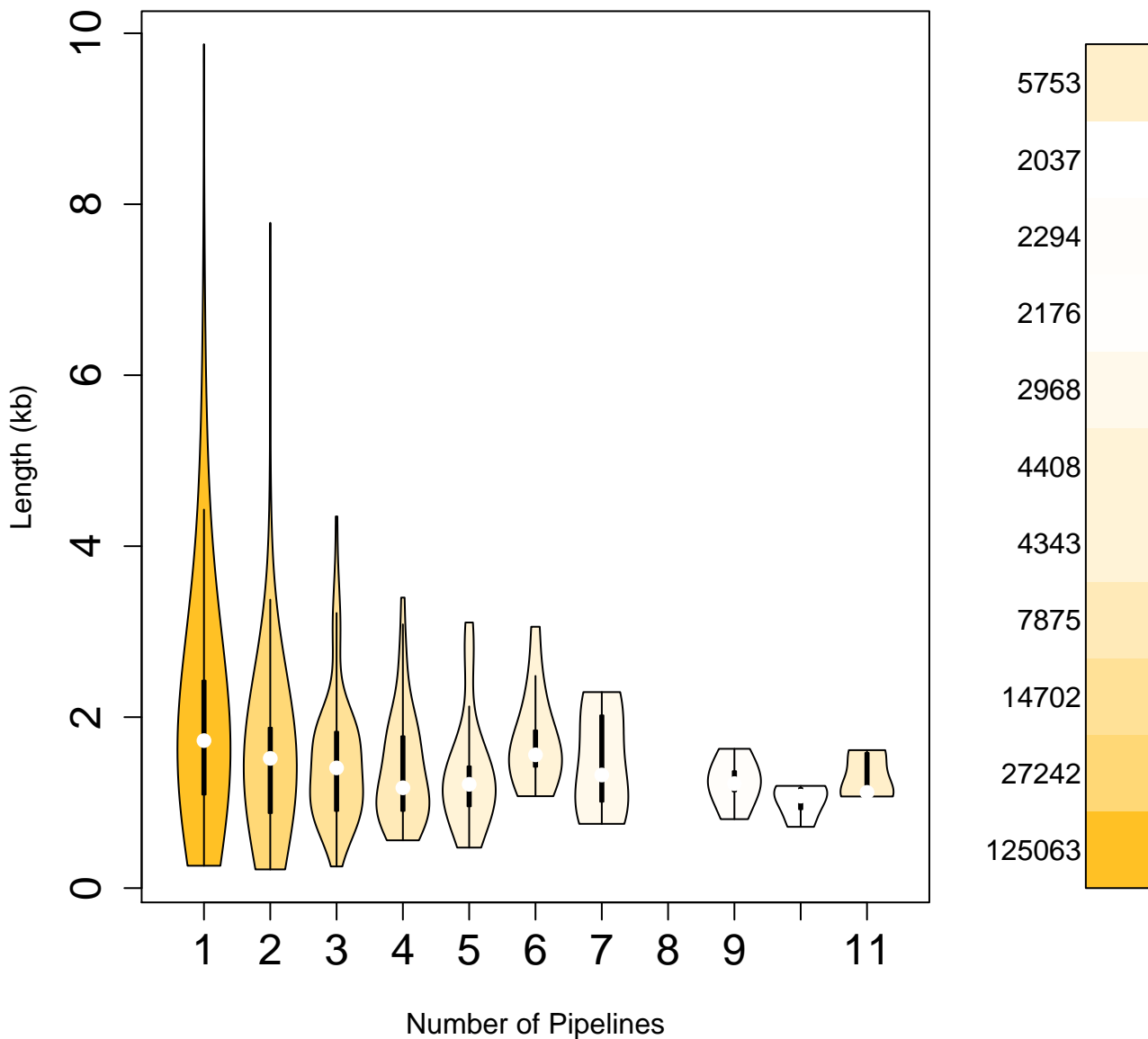
NNC



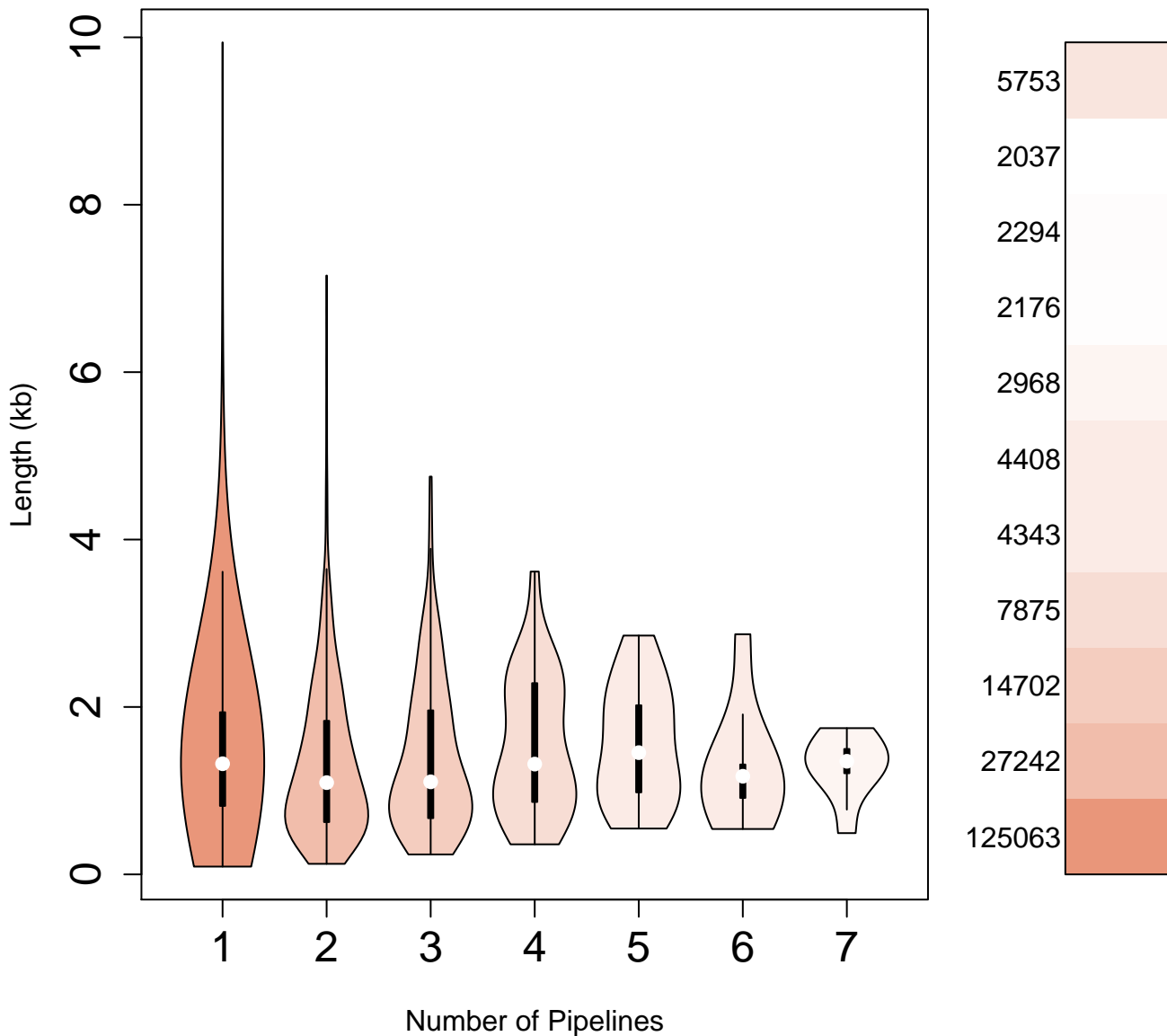
Antisense



Fusion

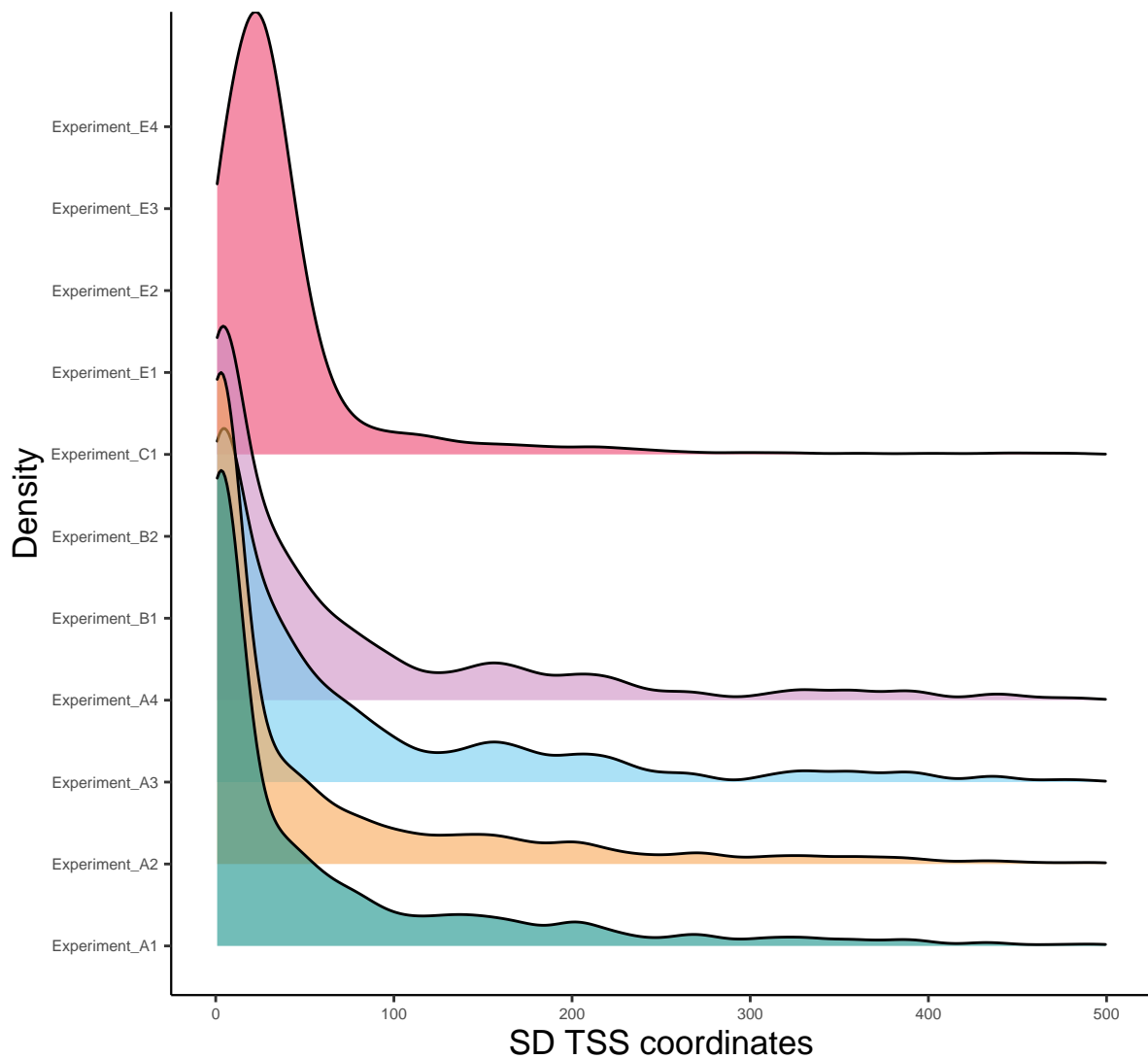


Intergenic

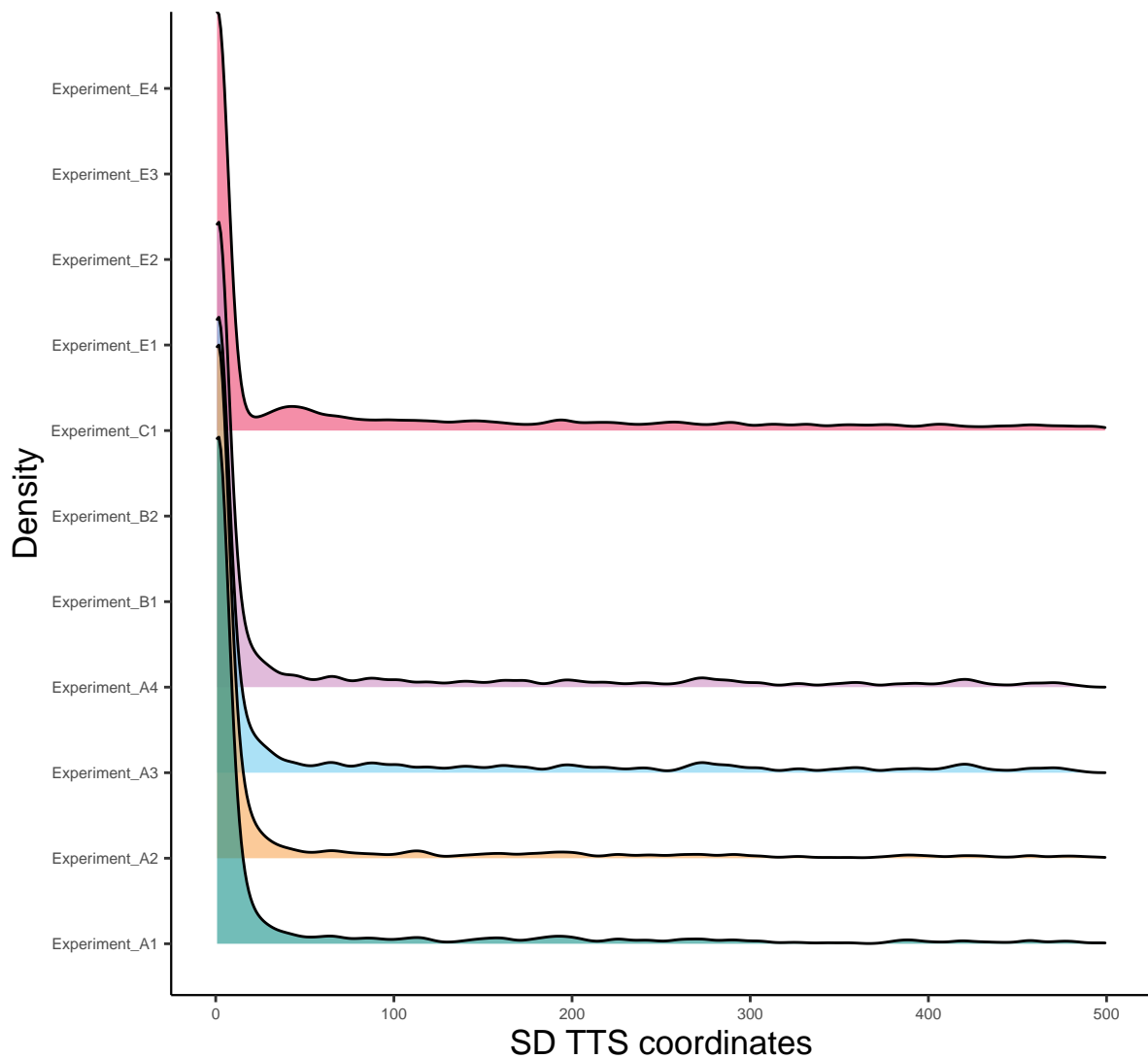


Standard Deviation of TSS and TTS

Standard deviation of genomic TSS coordinates

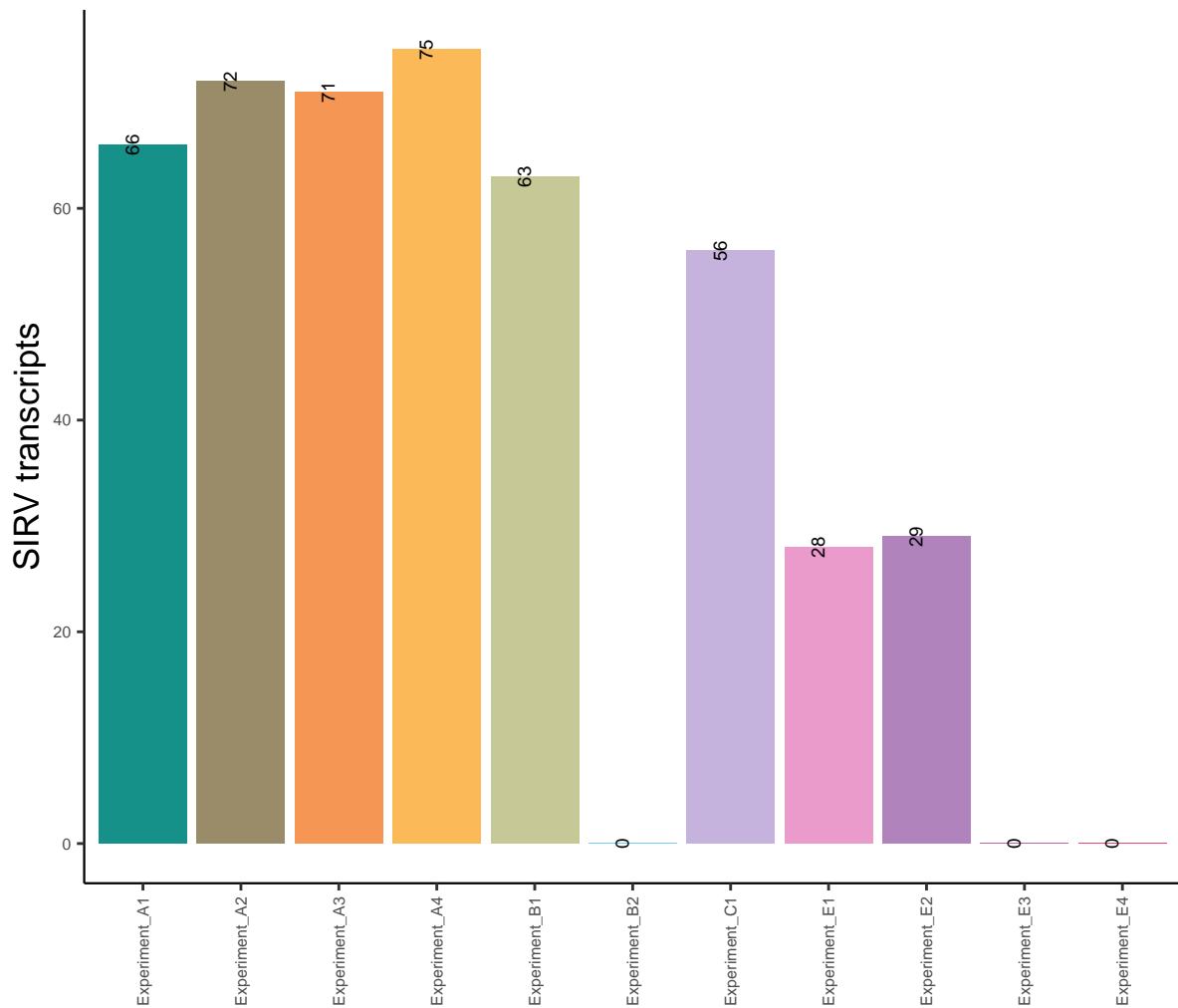


Standard deviation of genomic TTS coordinates

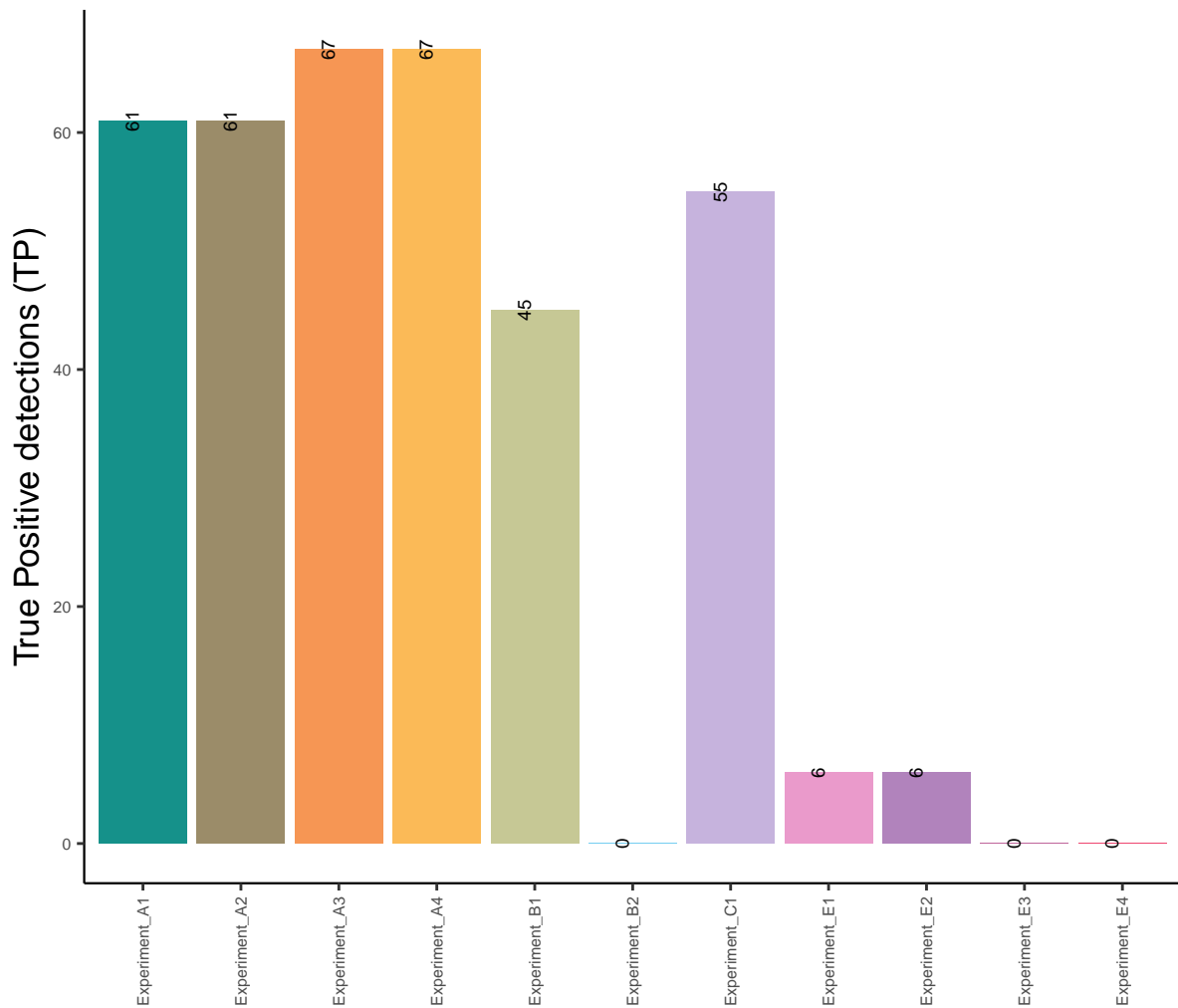


LRGASP metrics Comparison

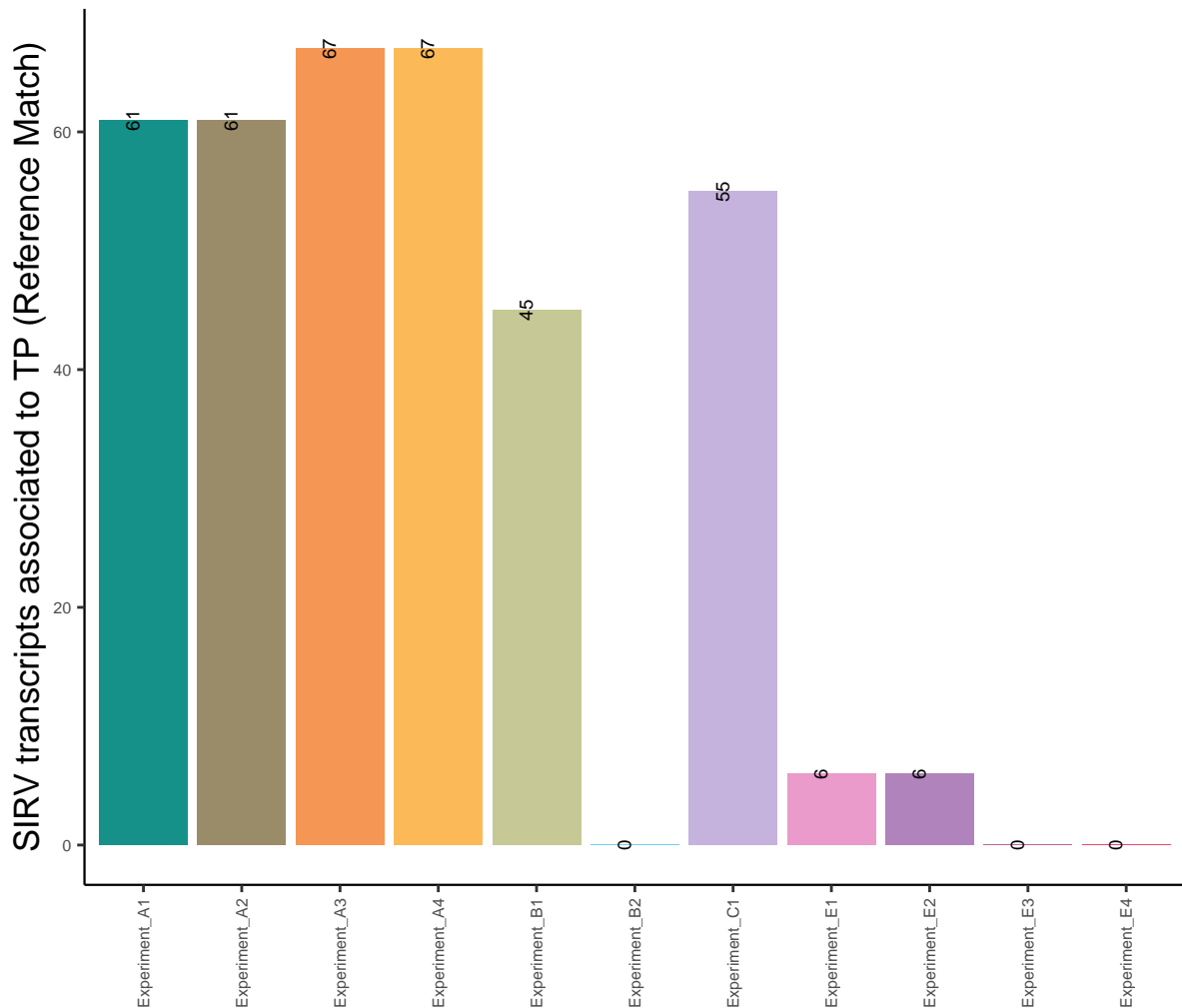
SIRV transcripts Comparison



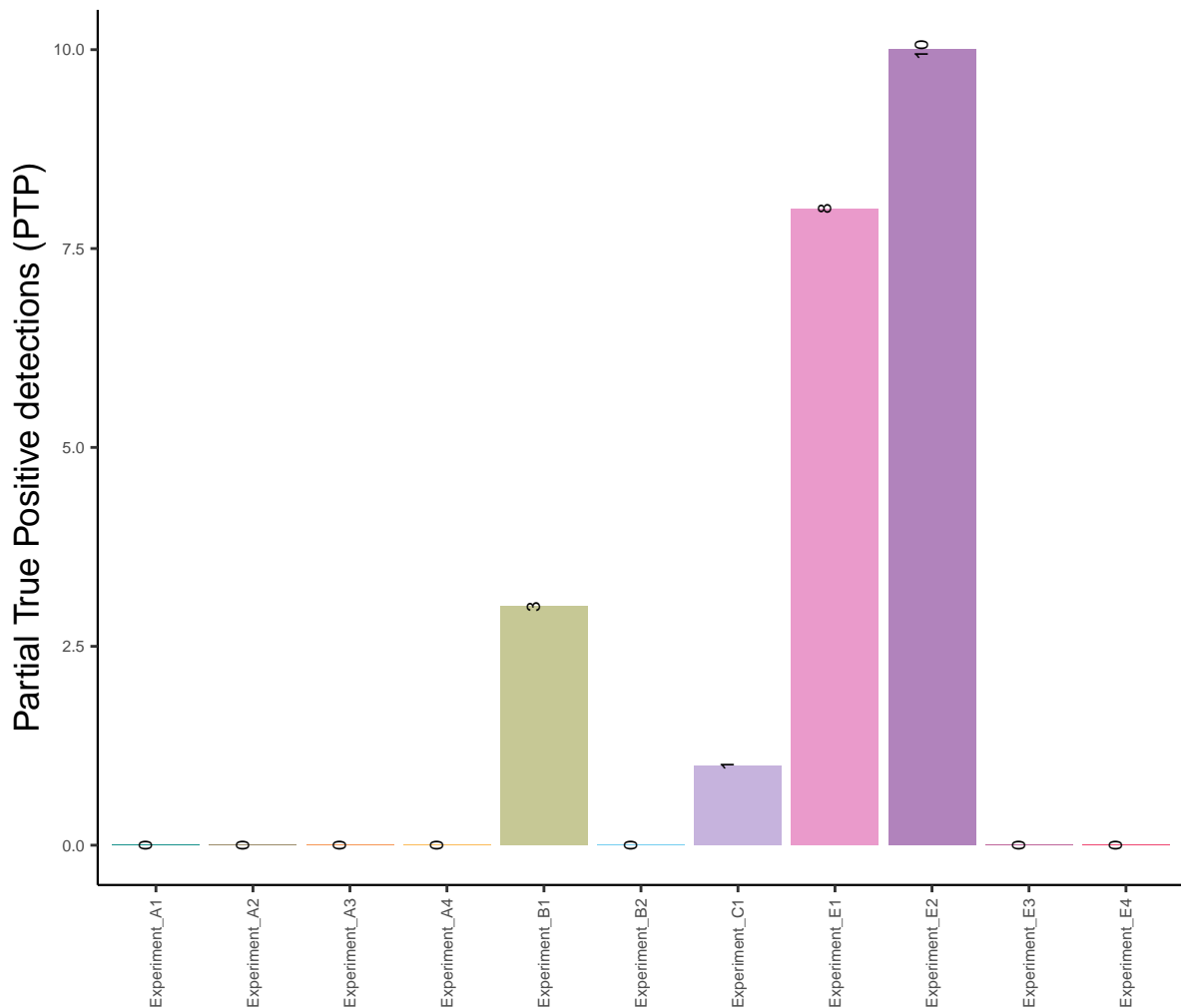
True Positive detections (TP) Comparison



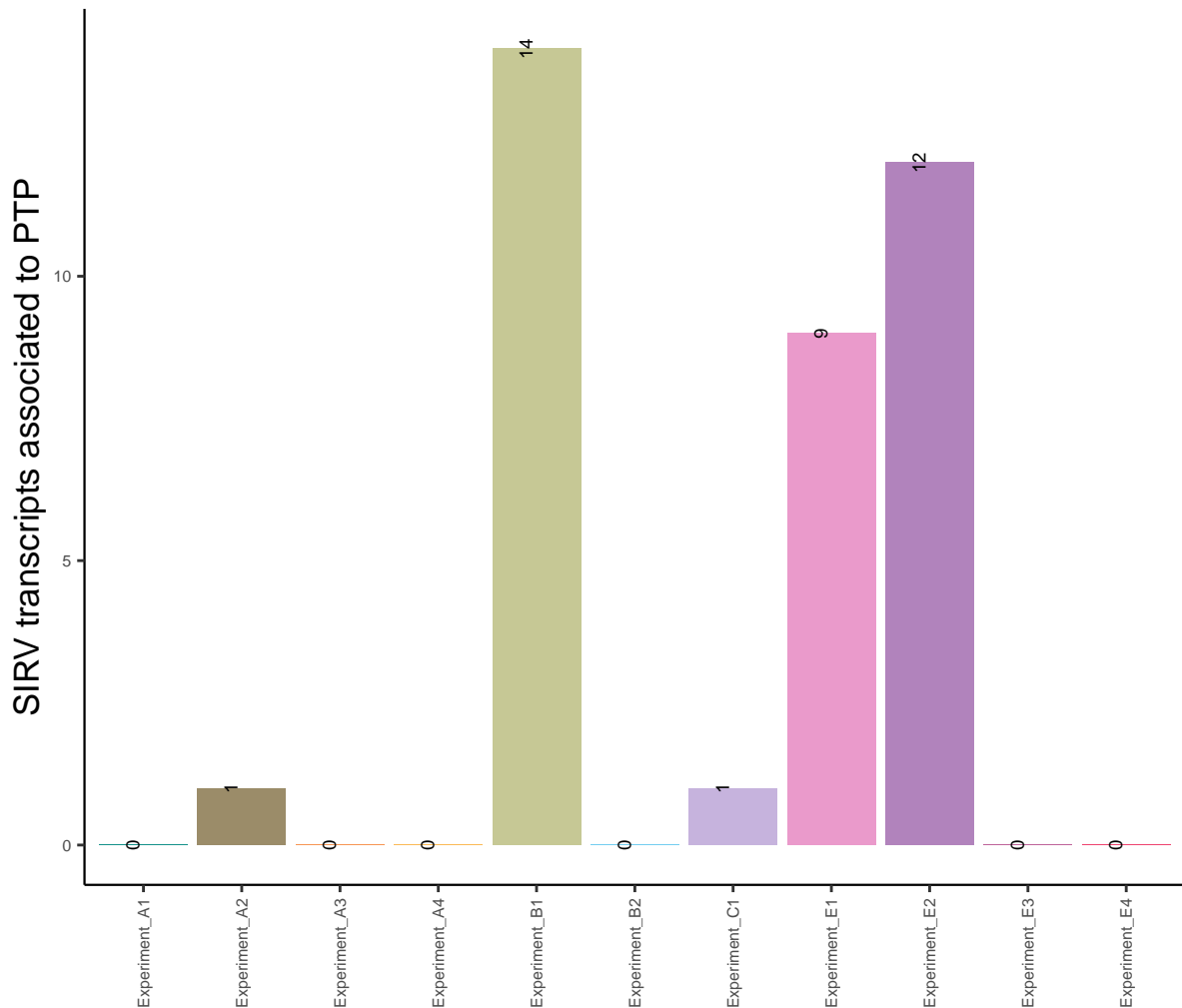
SIRV transcripts associated to TP (Reference Match) Comparison



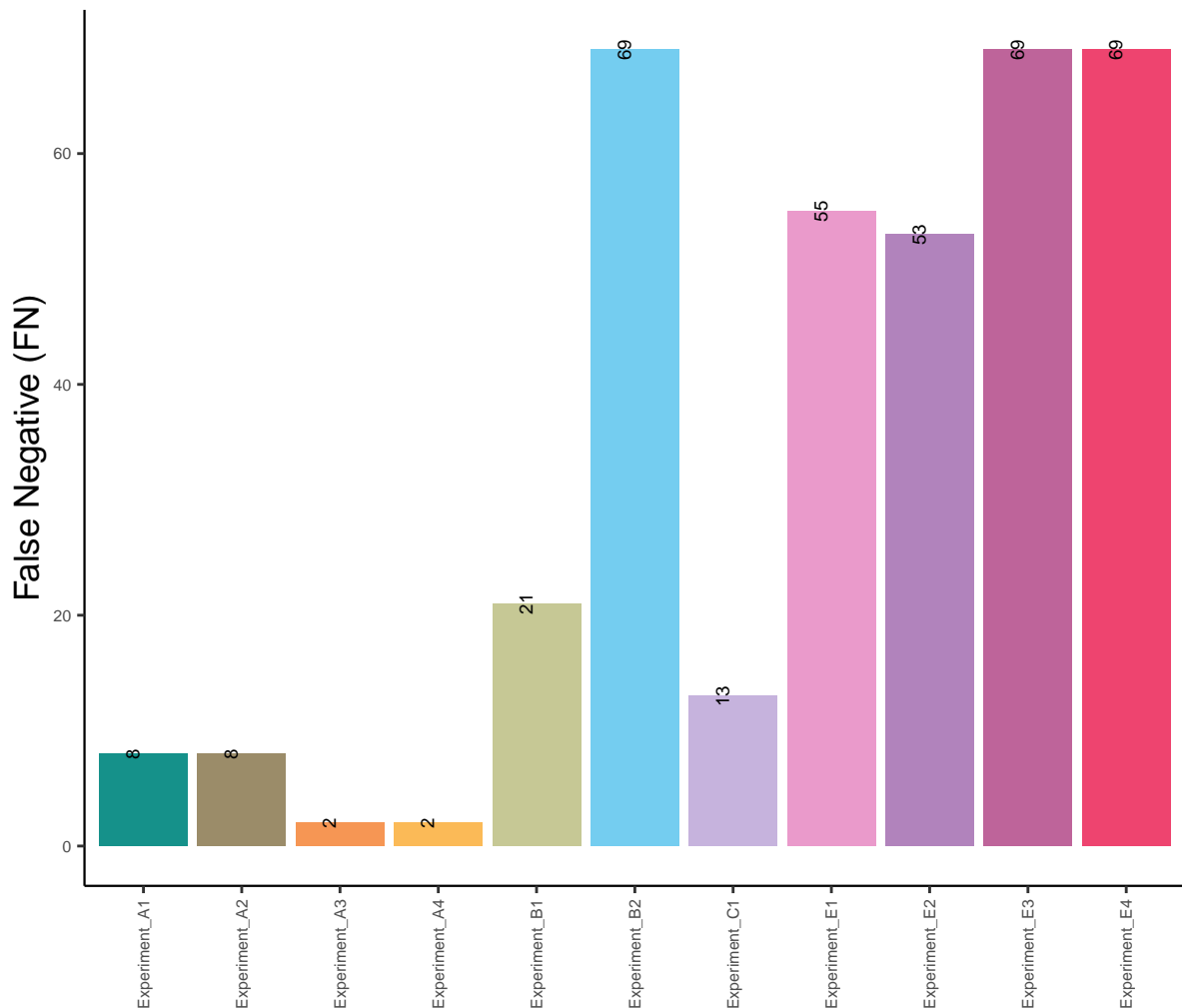
Partial True Positive detections (PTP) Comparison



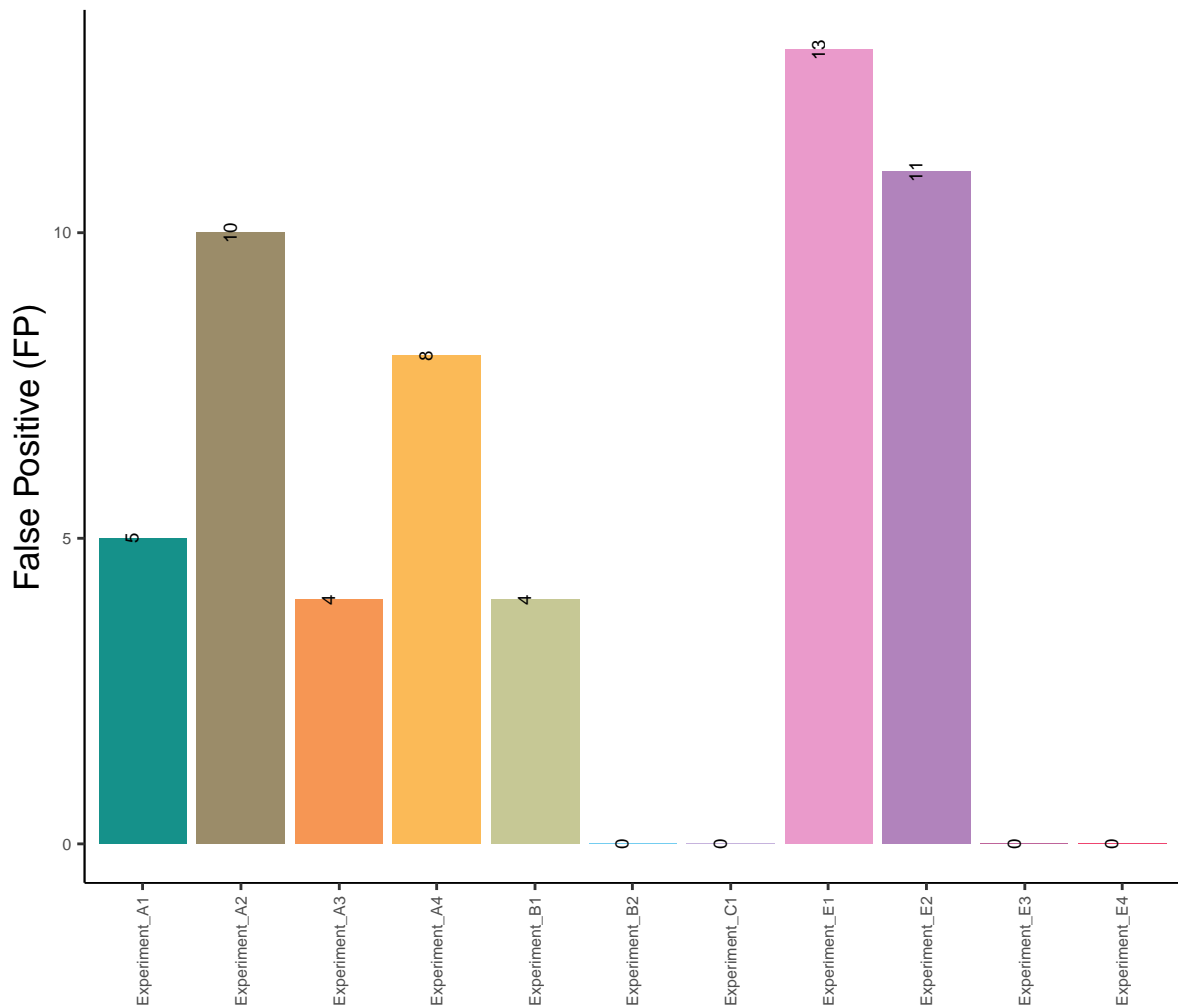
SIRV transcripts associated to PTP Comparison



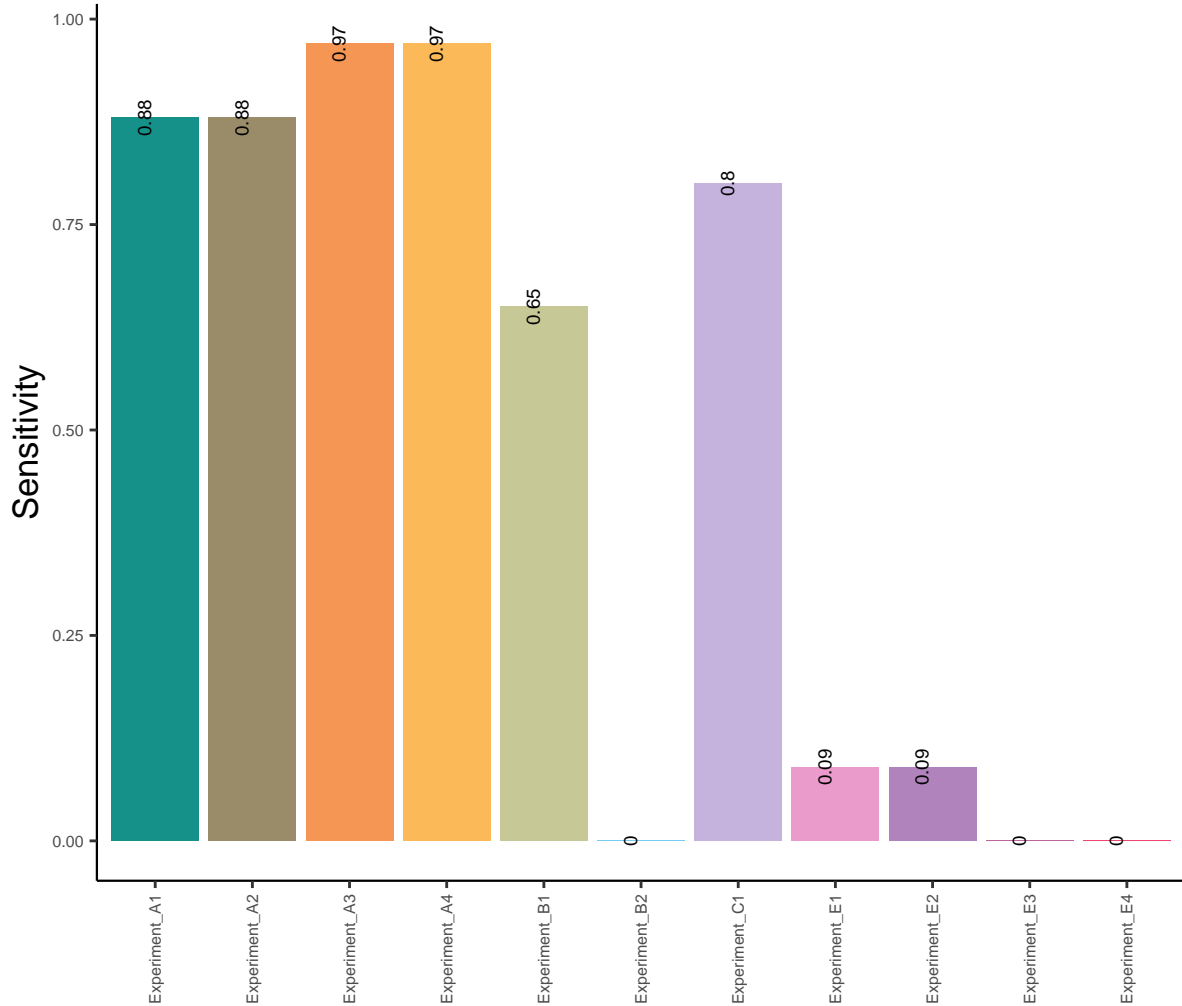
False Negative (FN) Comparison



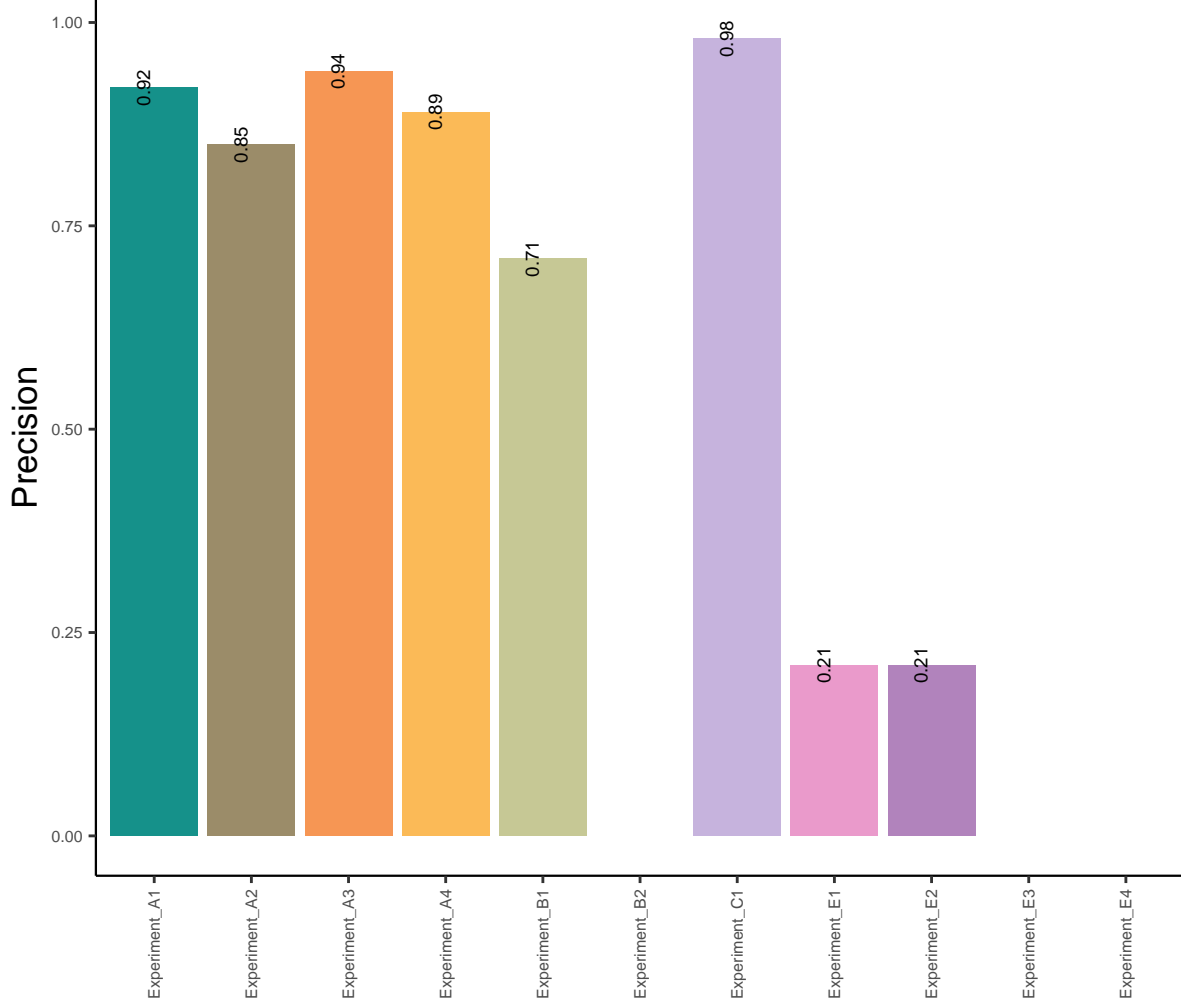
False Positive (FP) Comparison



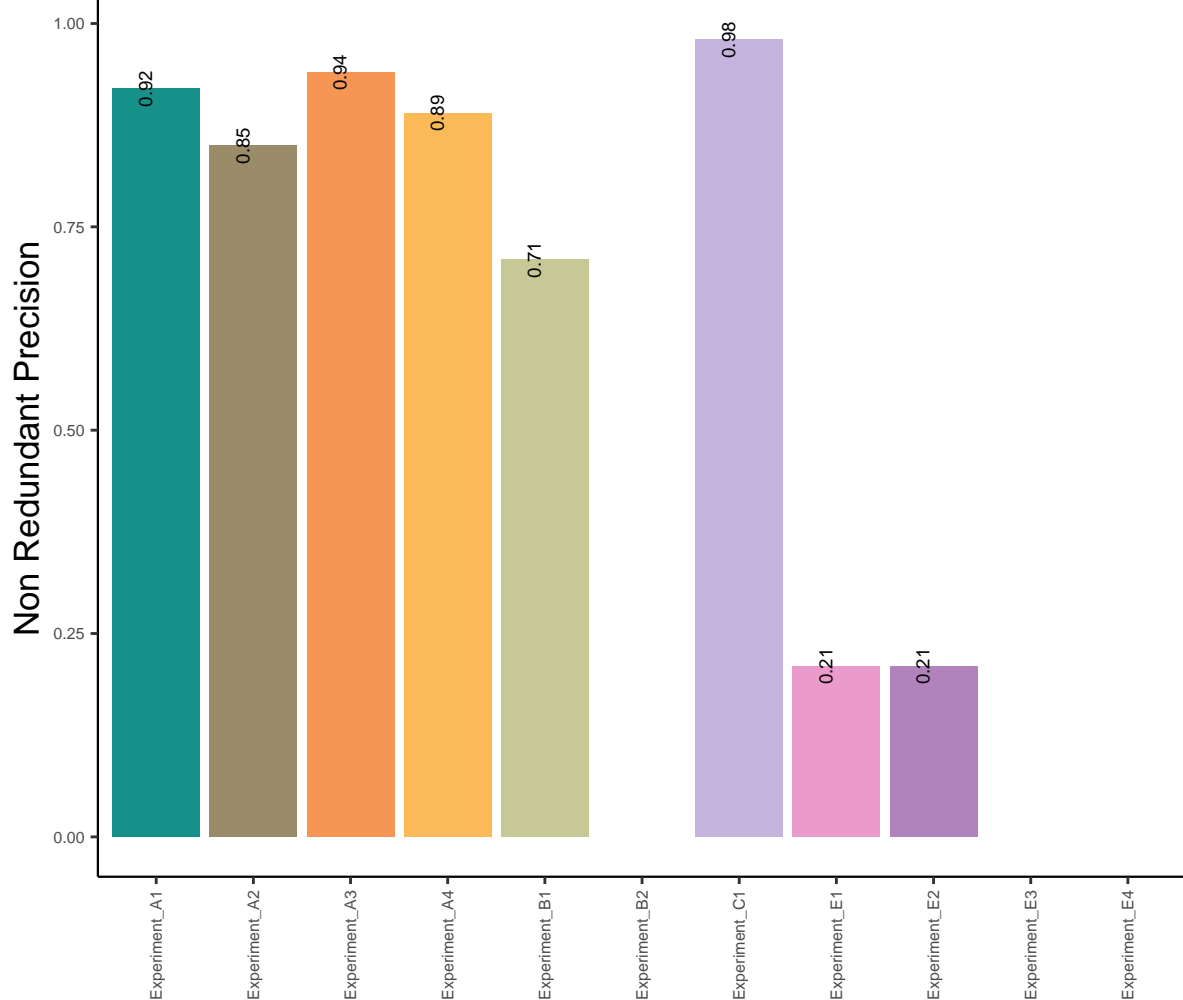
Sensitivity Comparison



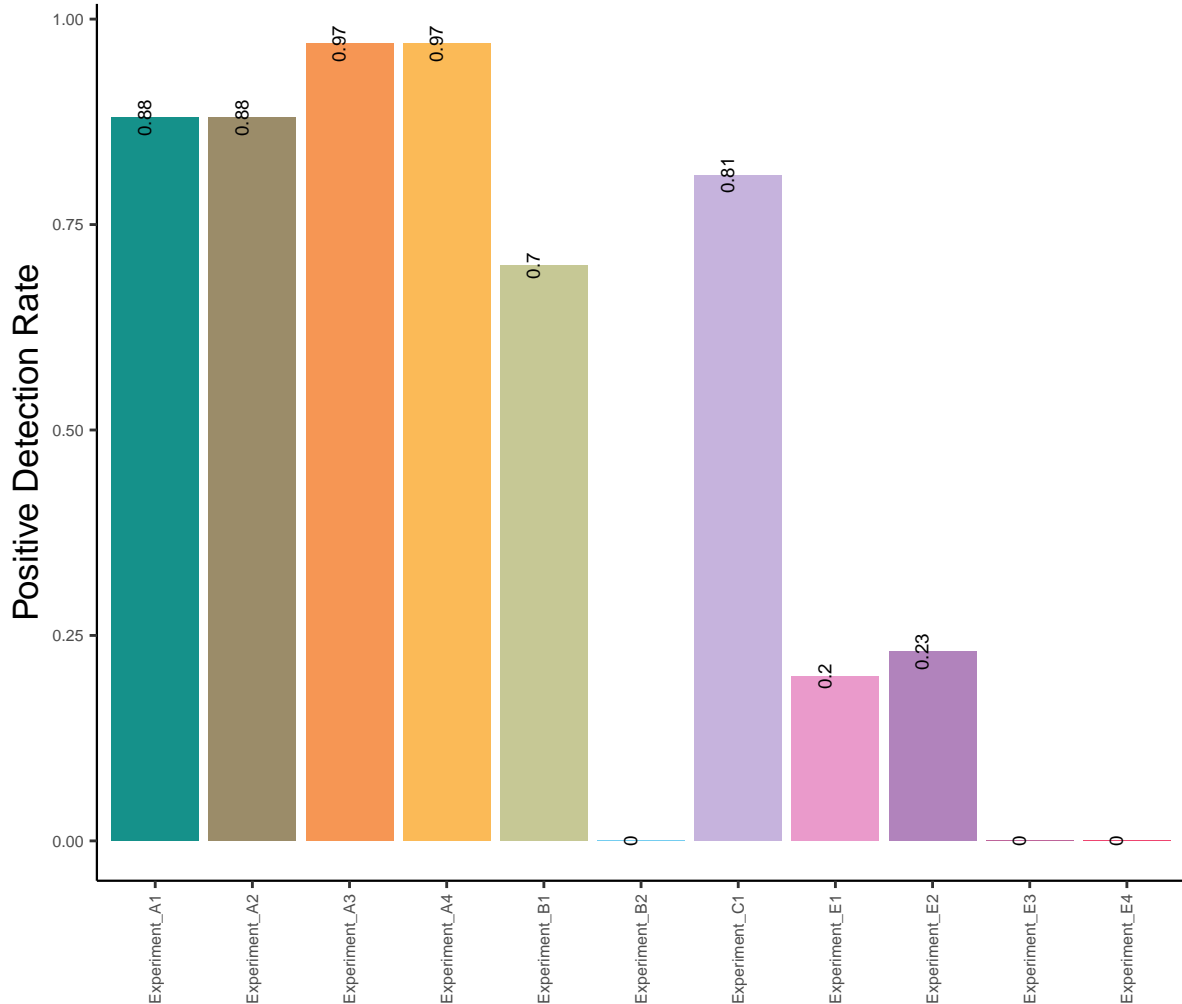
Precision Comparison



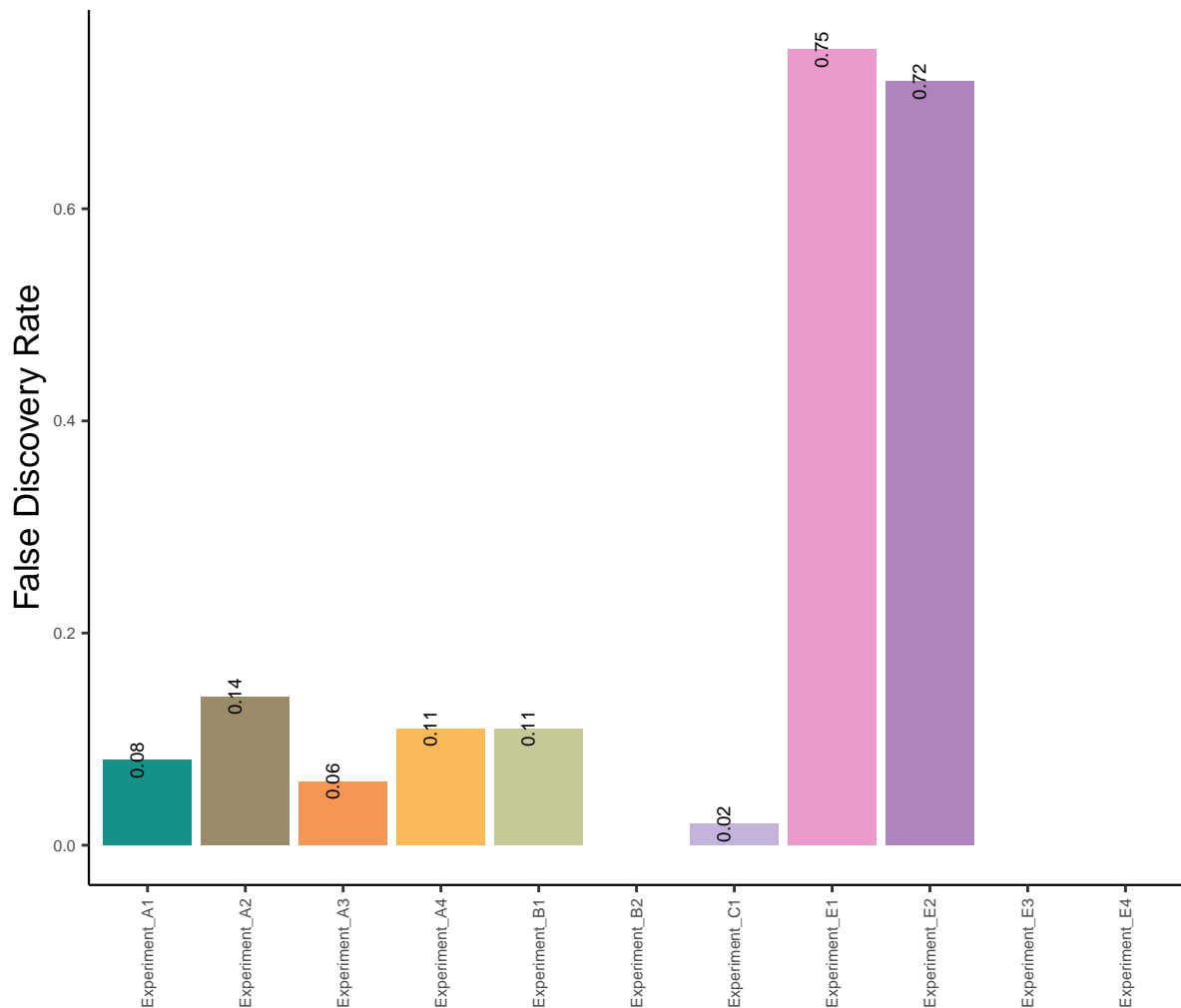
Non Redundant Precision Comparison



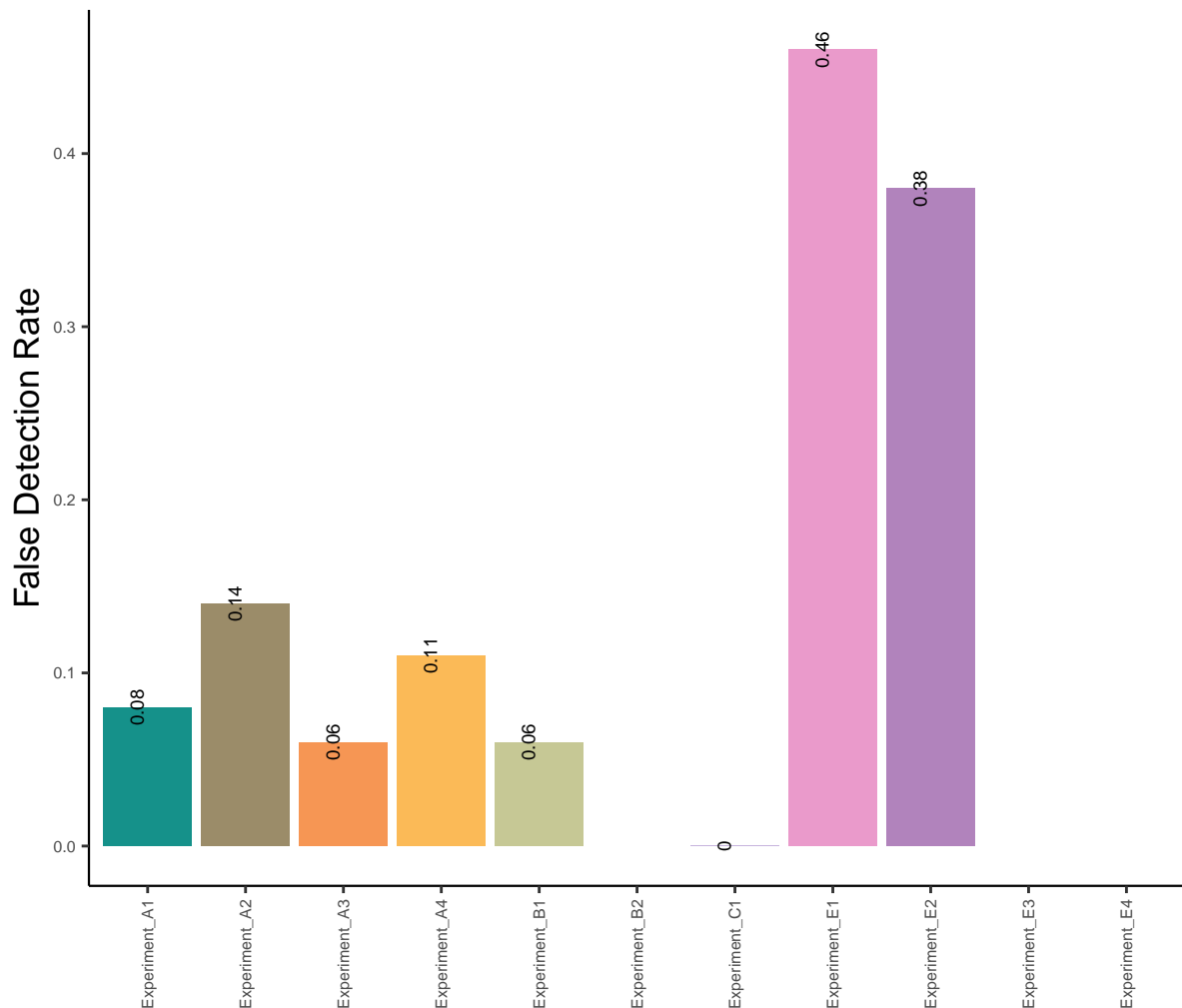
Positive Detection Rate Comparison



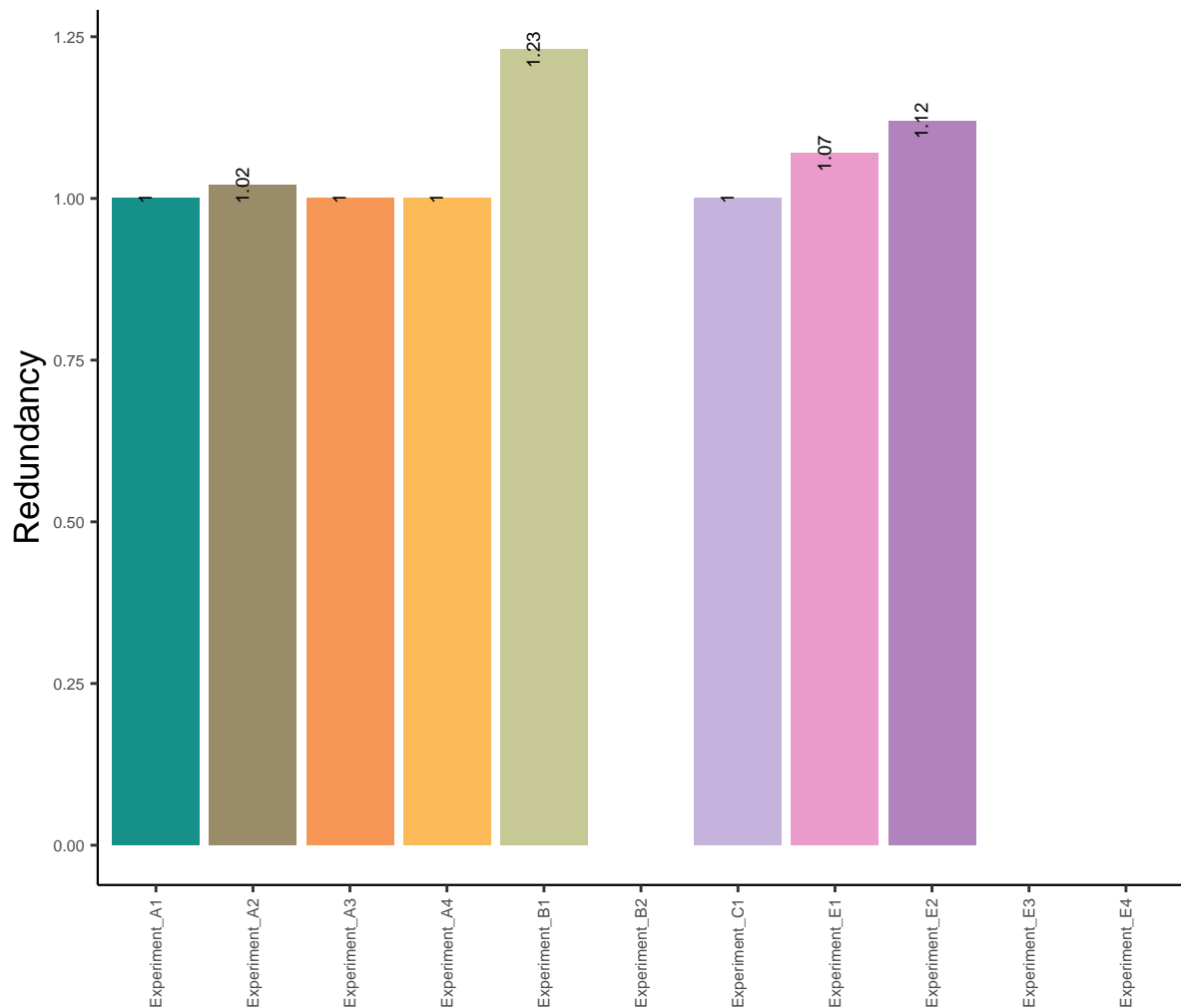
False Discovery Rate Comparison



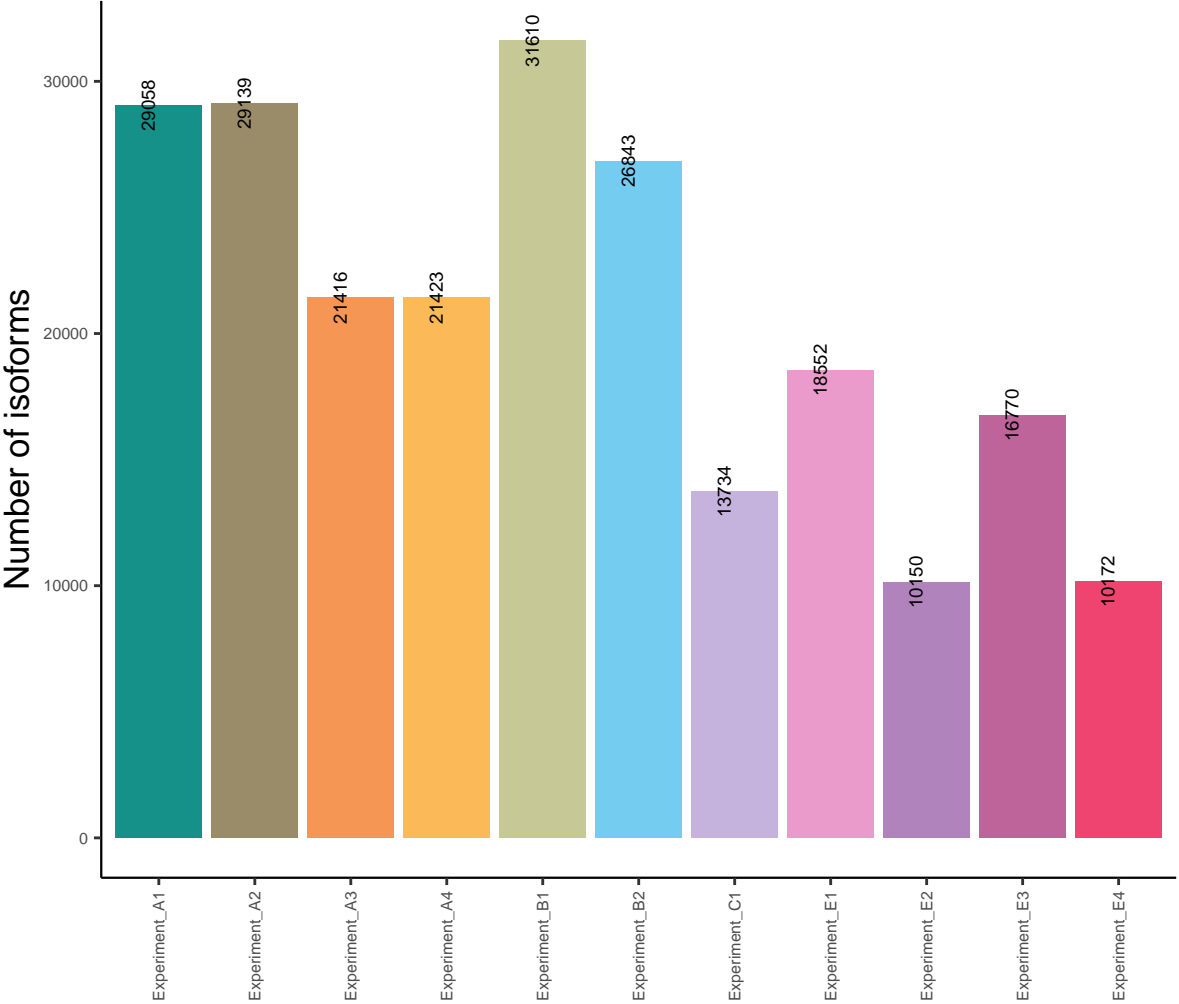
False Detection Rate Comparison



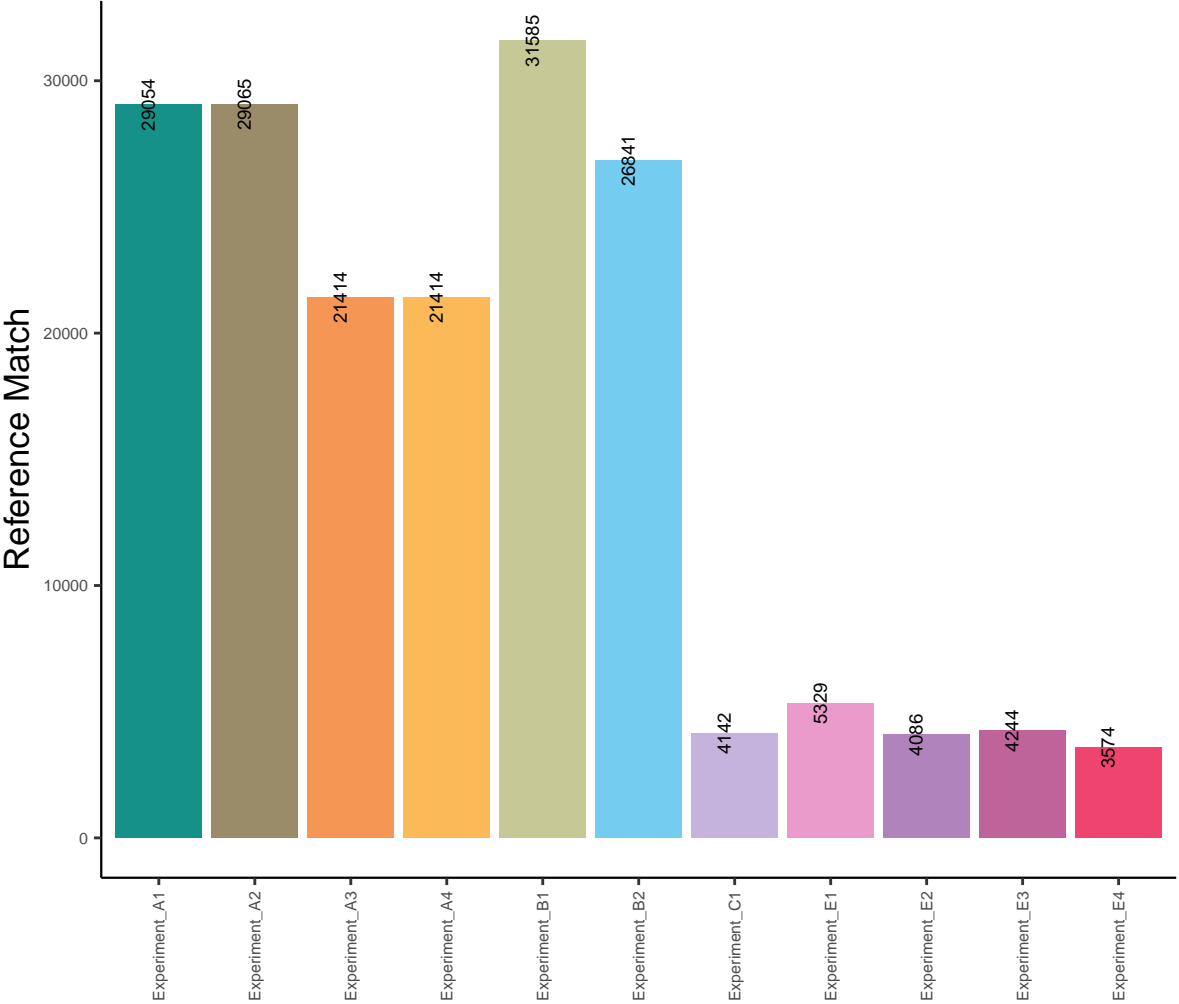
Redundancy Comparison



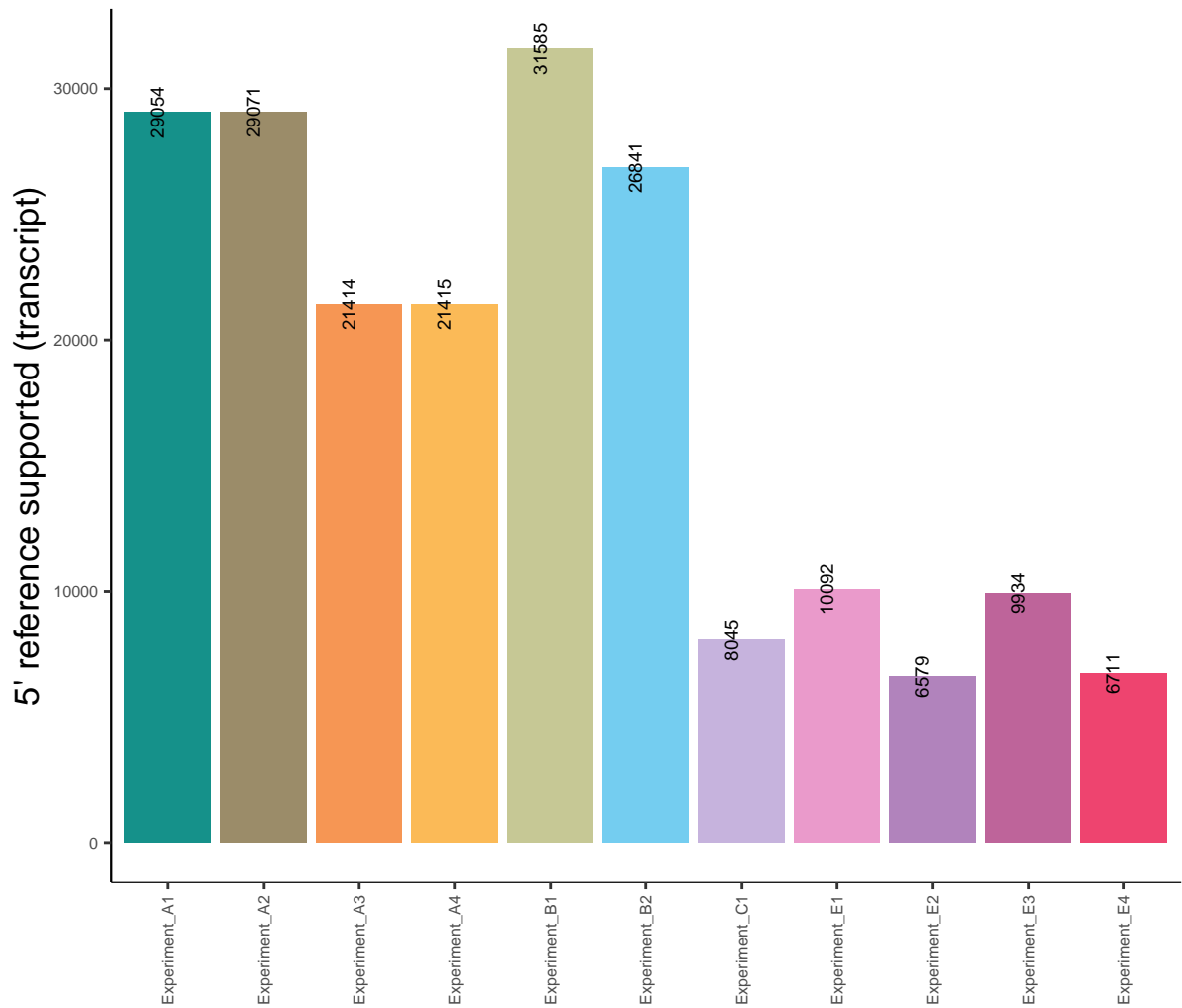
FSM Number of isoforms Comparison



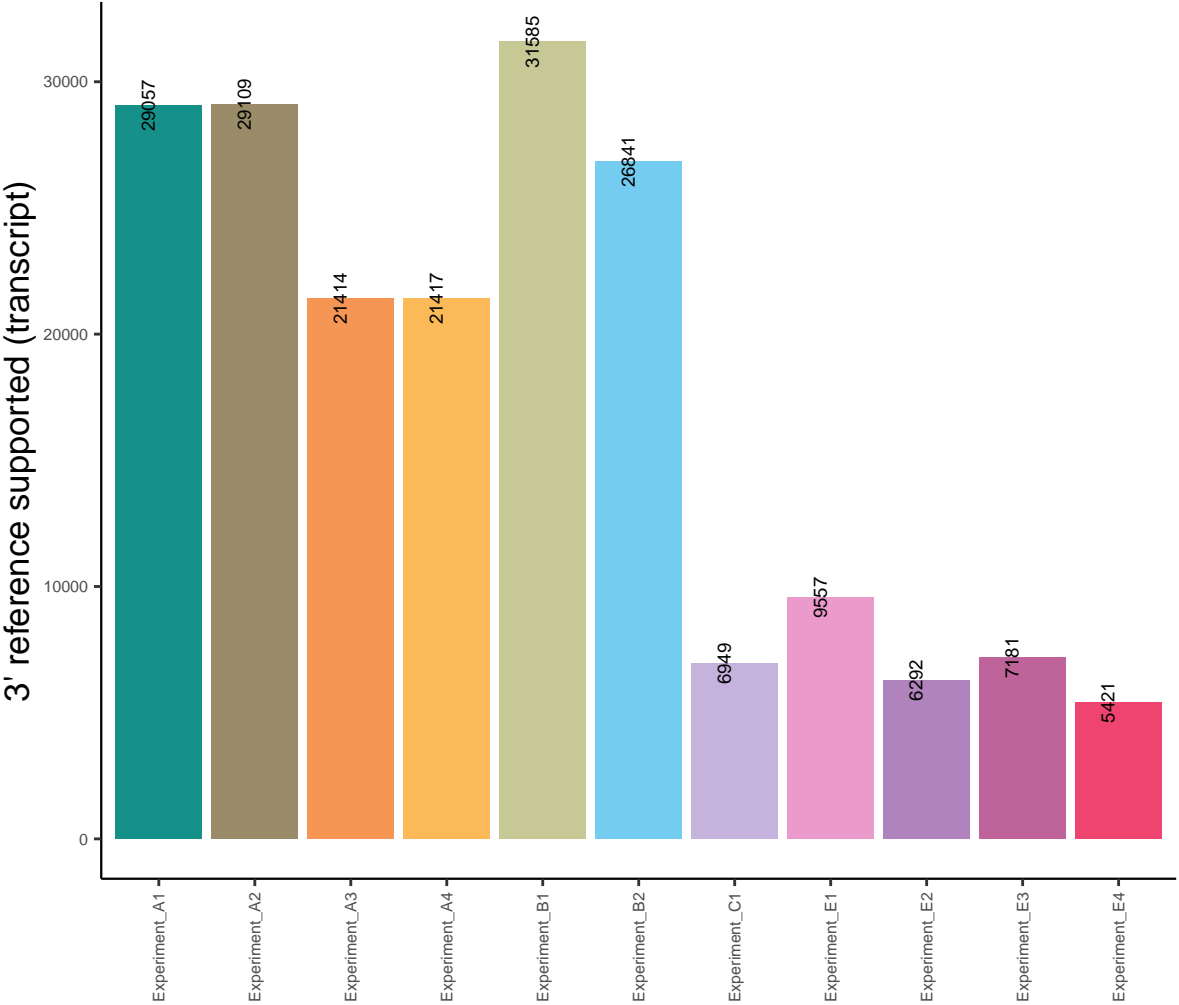
FSM Reference Match Comparison



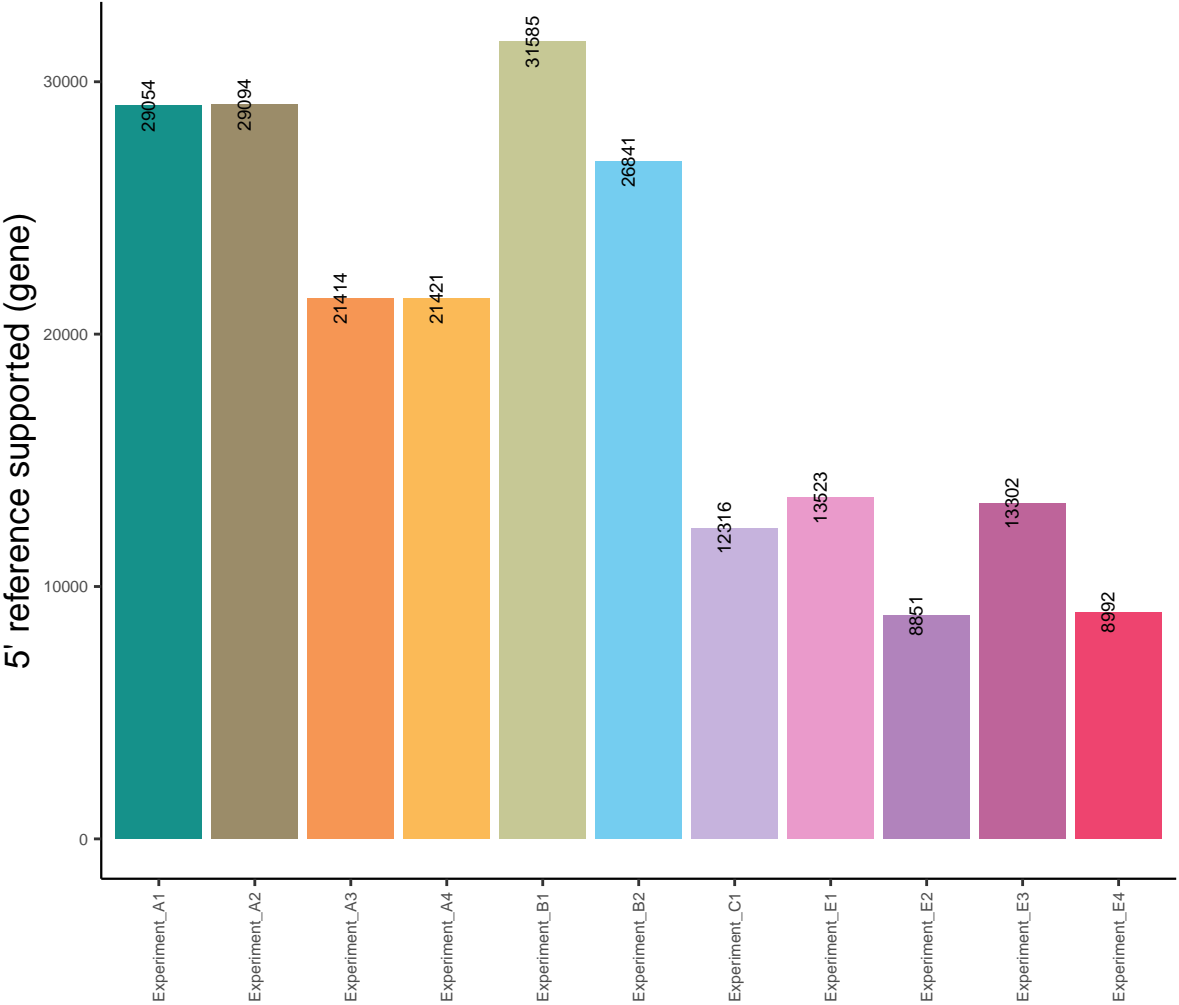
FSM 5' reference supported (transcript) Comparison



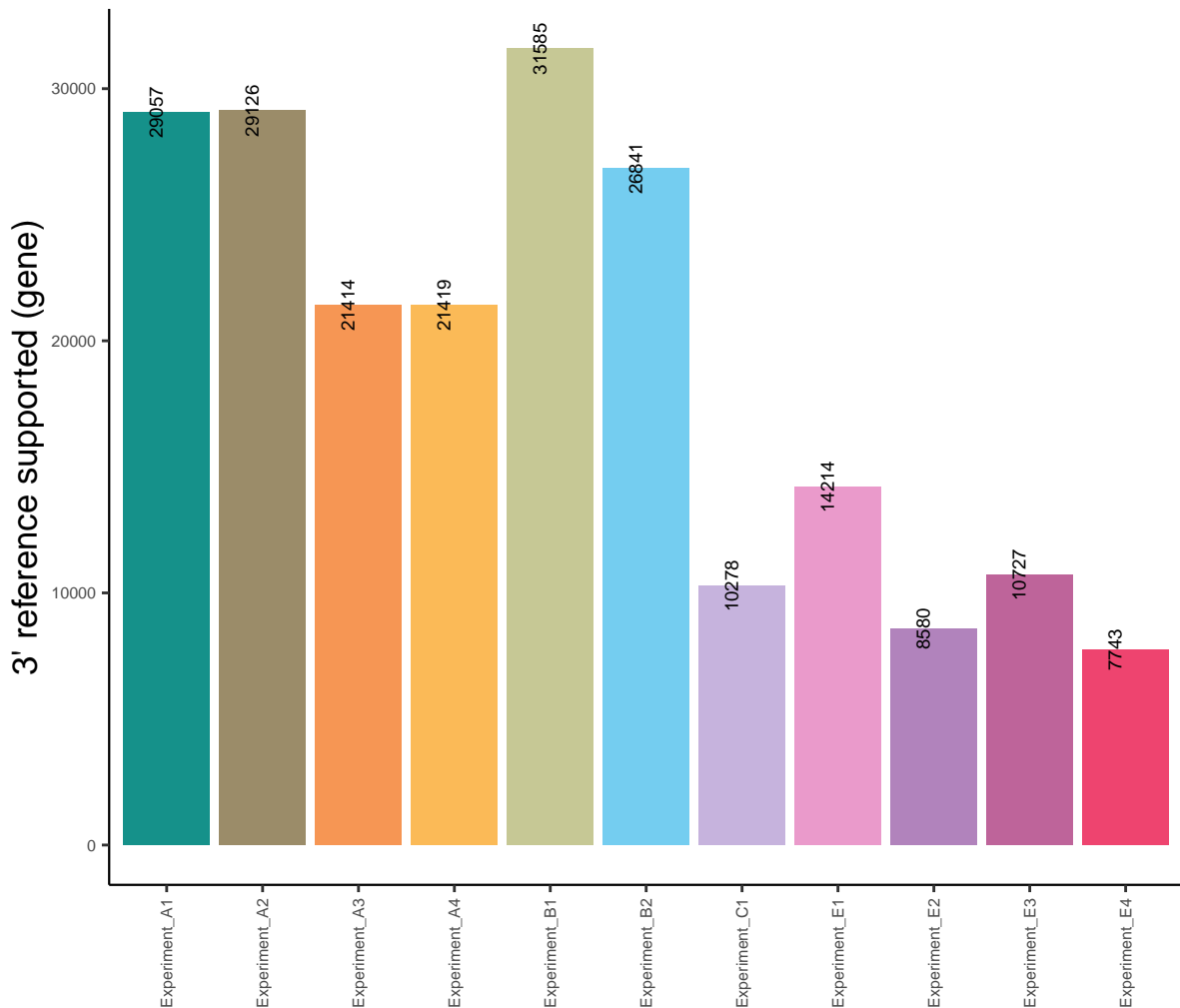
FSM 3' reference supported (transcript) Comparison



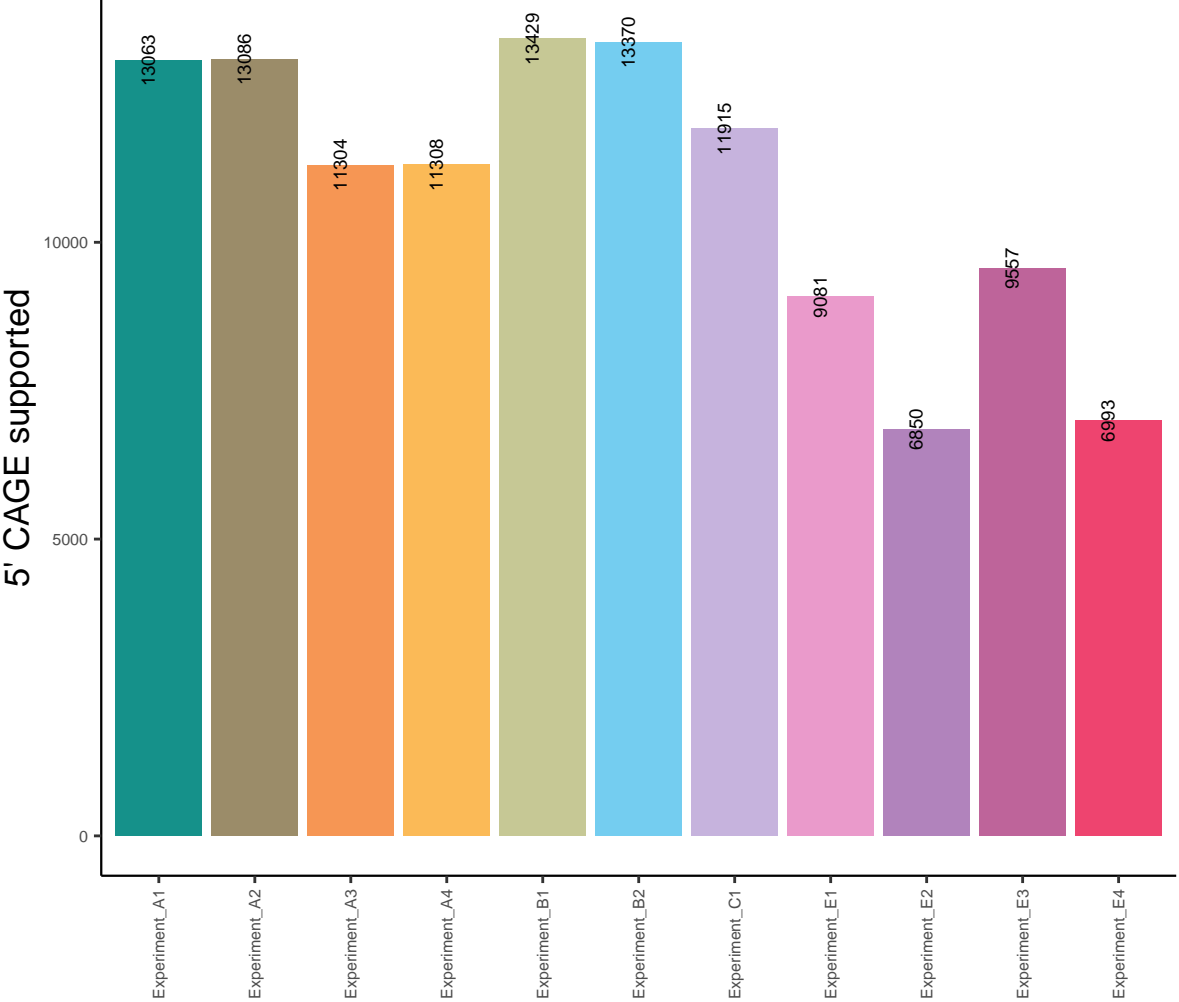
FSM 5' reference supported (gene) Comparison



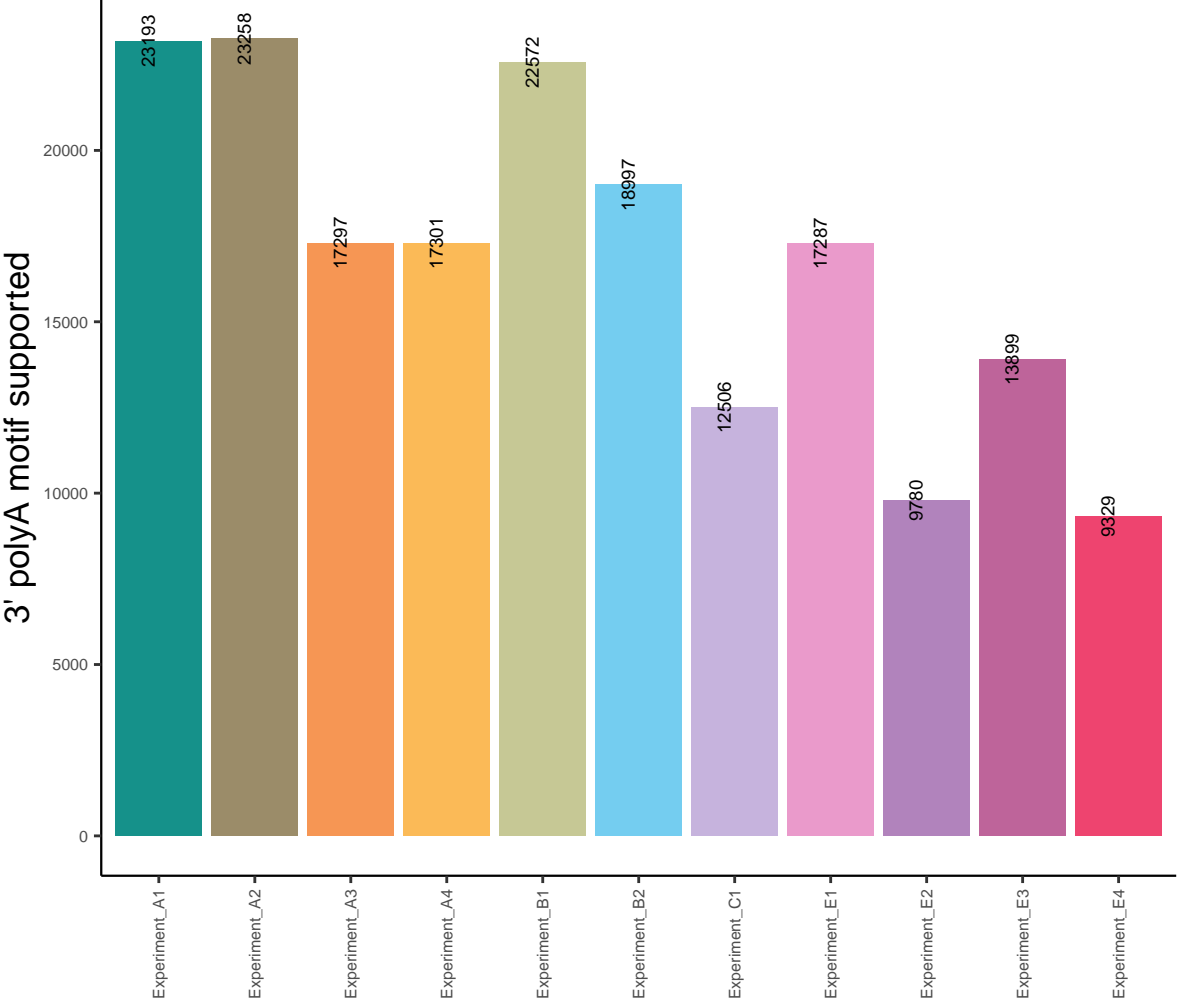
FSM 3' reference supported (gene) Comparison



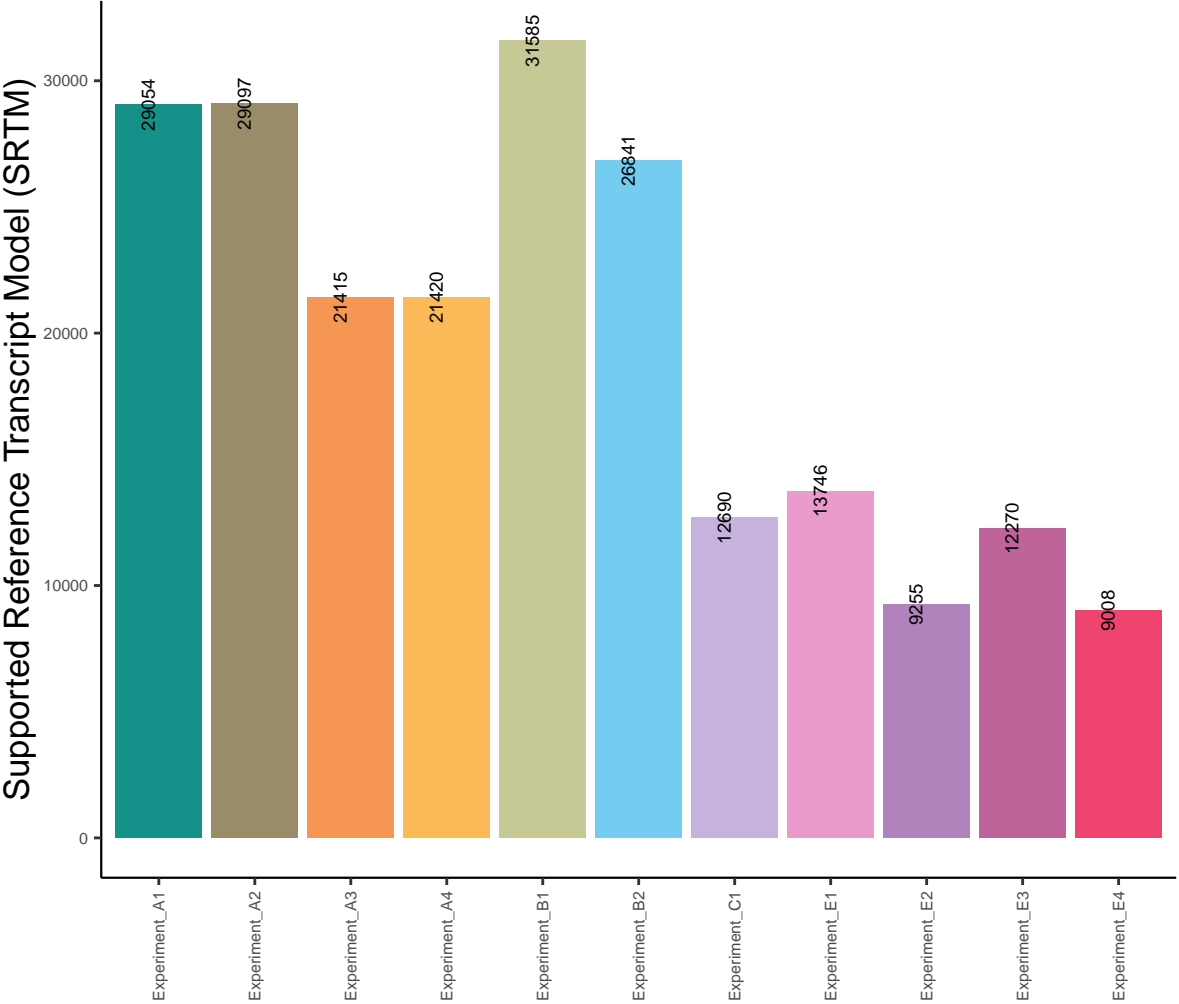
FSM 5' CAGE supported Comparison



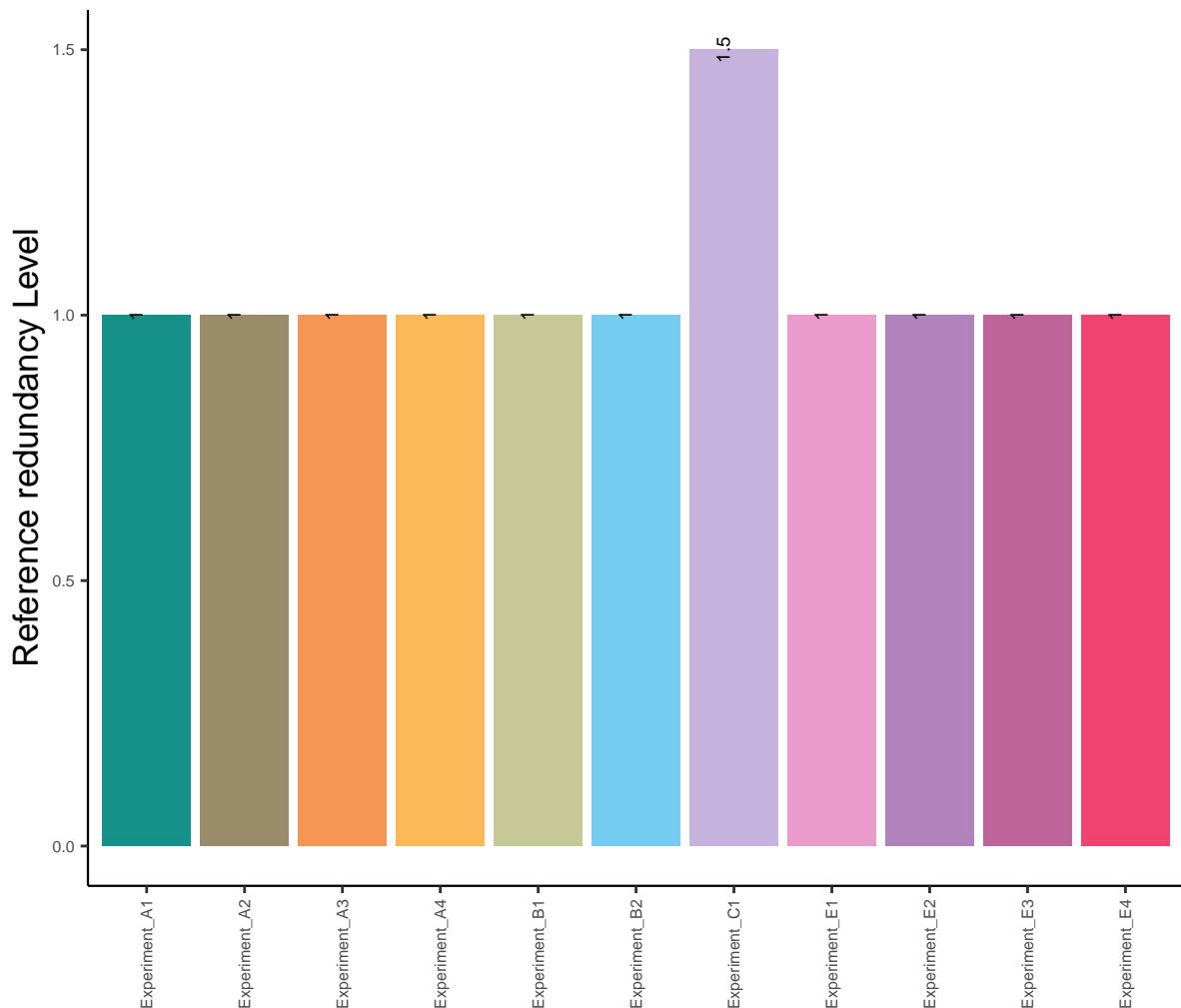
FSM 3' polyA motif supported Comparison



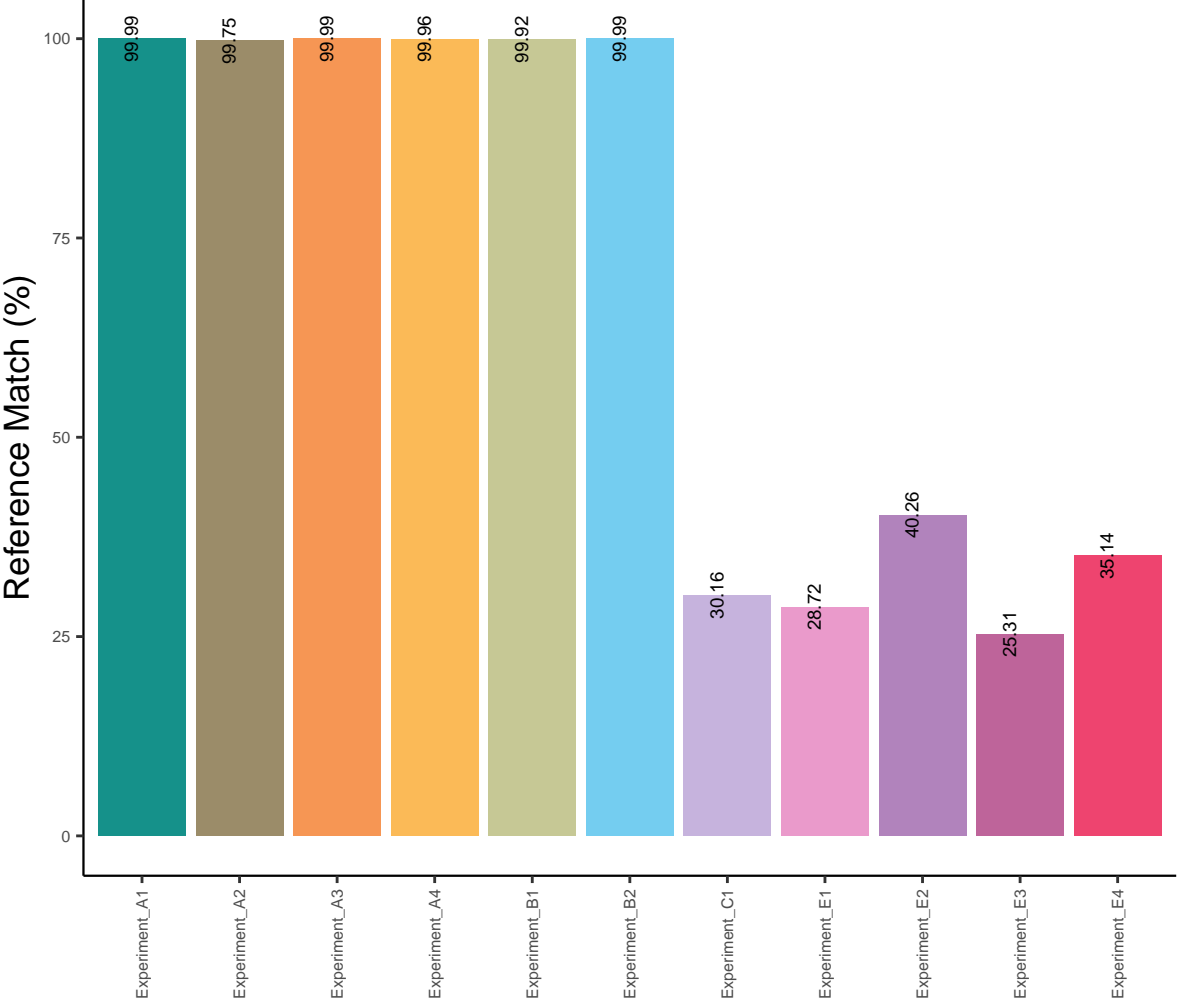
FSM Supported Reference Transcript Model (SRTM) Comparison



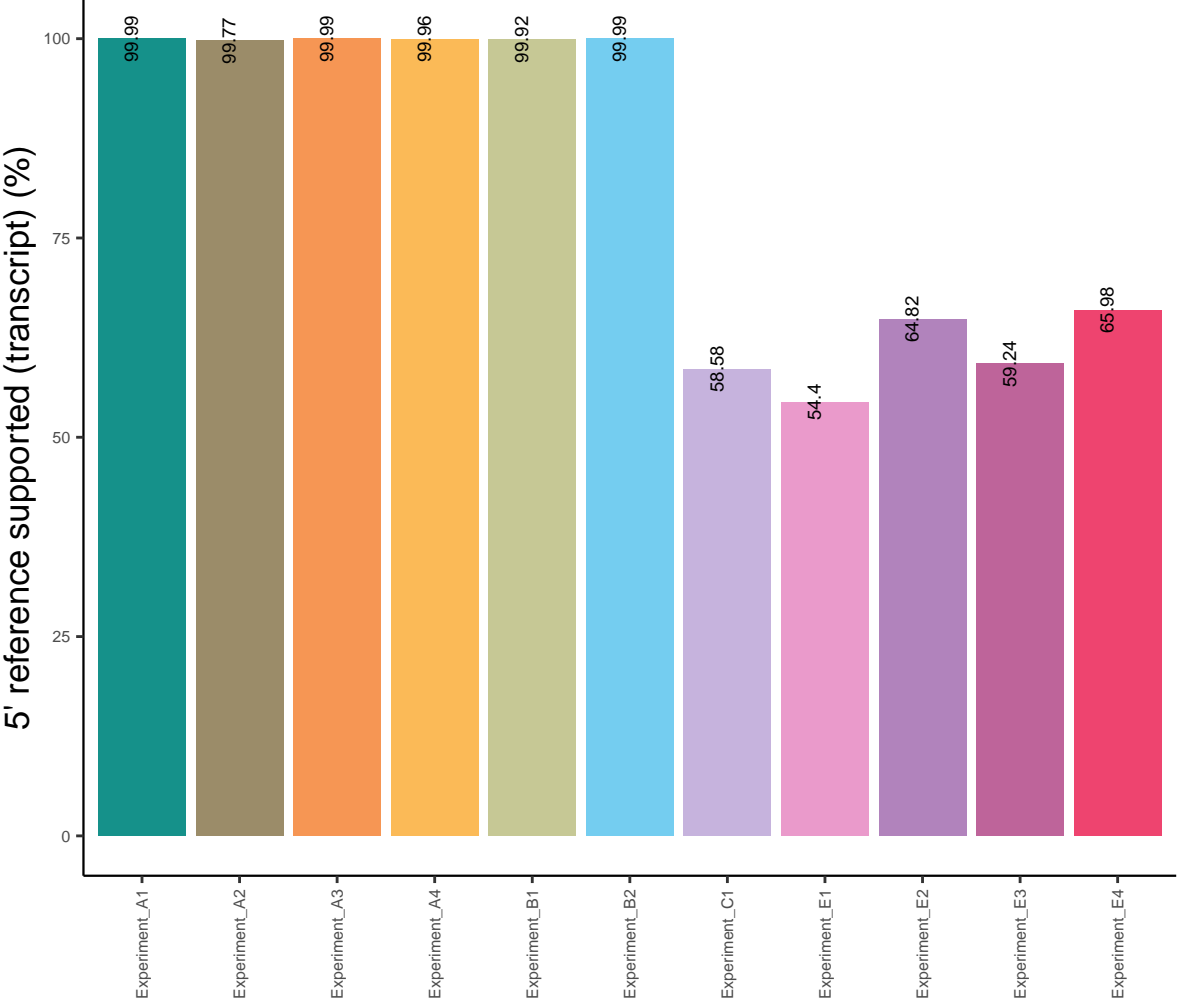
FSM Reference redundancy Level Comparison



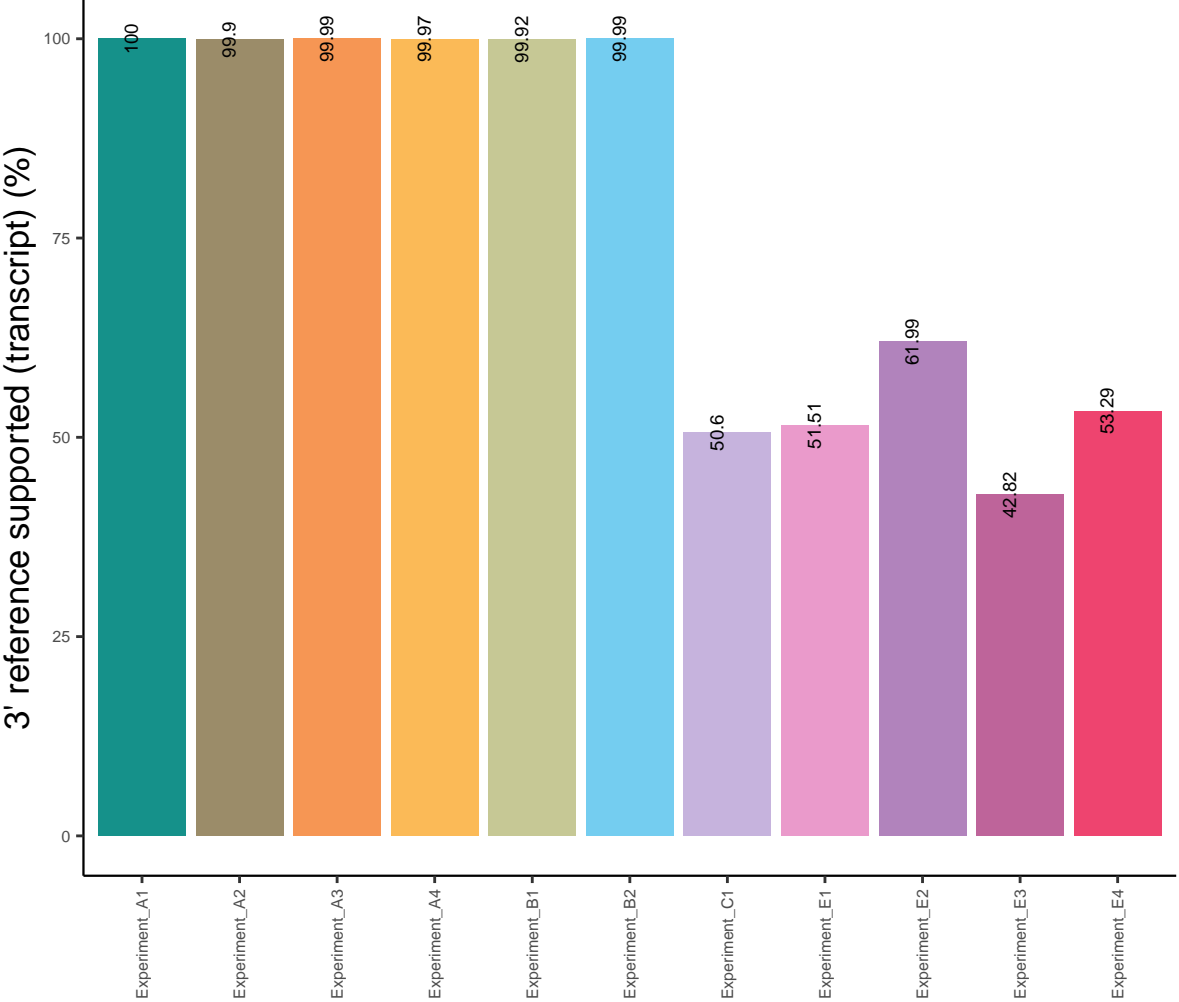
FSM Reference Match Comparison



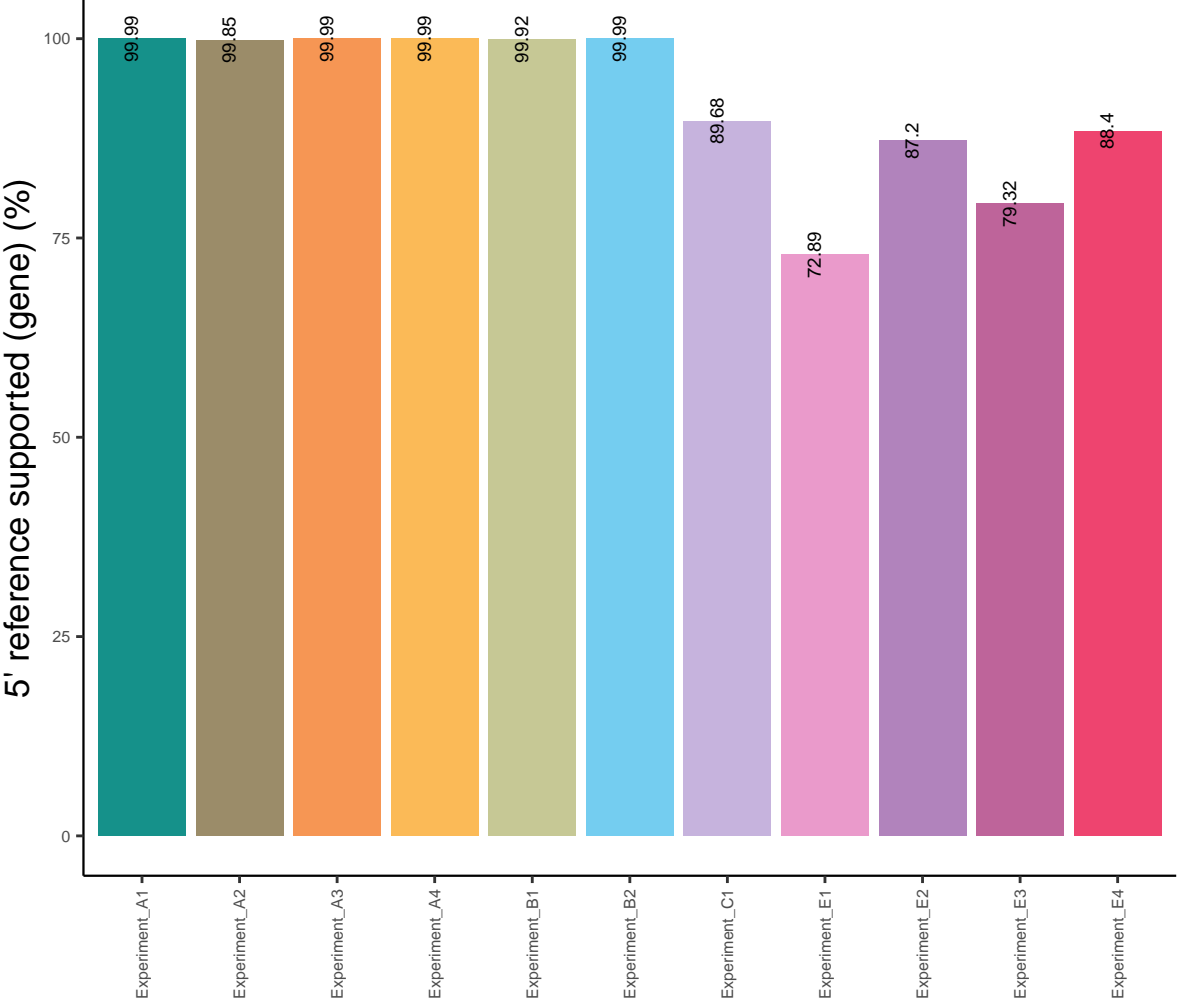
FSM 5' reference supported (transcript) Comparison



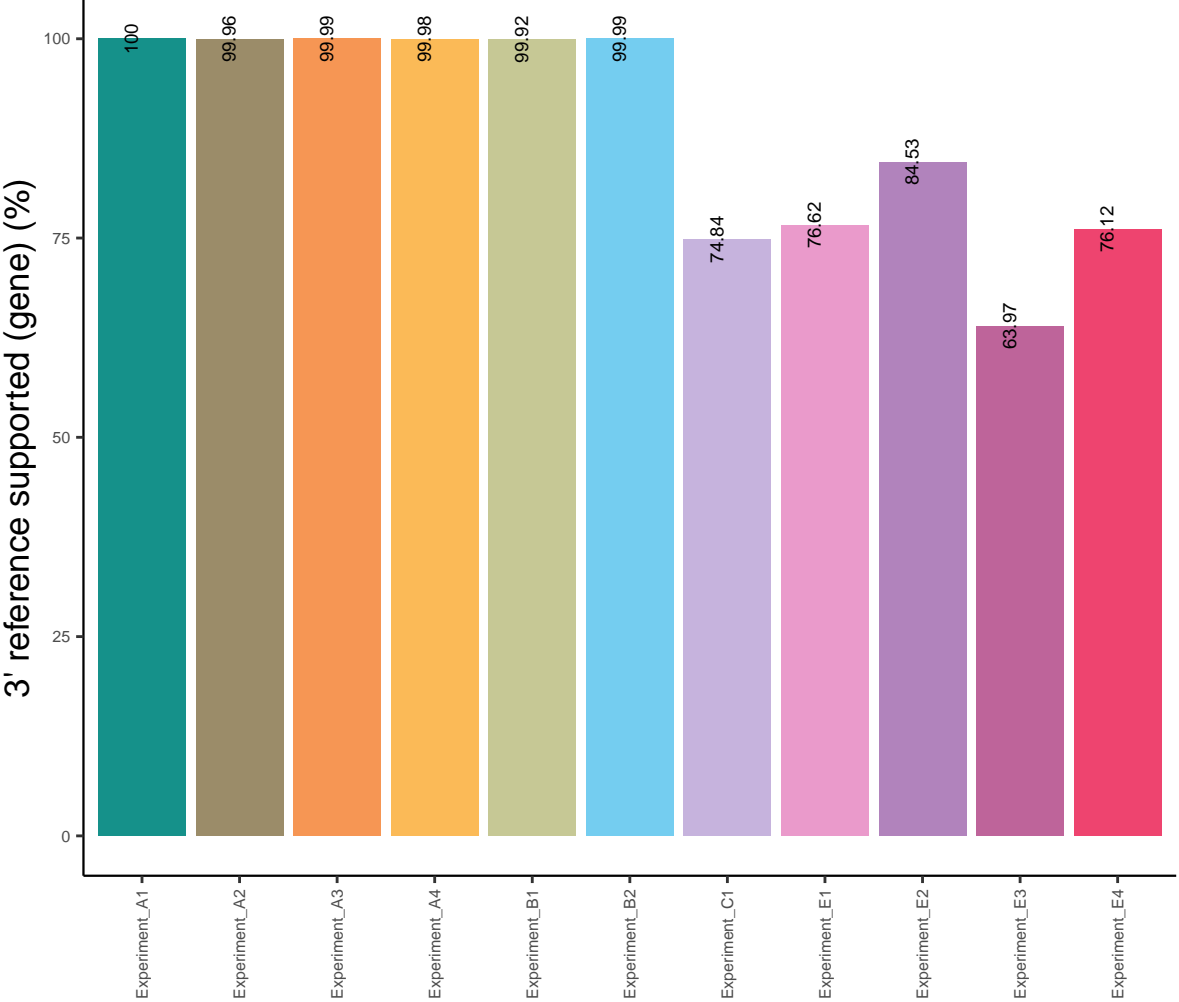
FSM 3' reference supported (transcript) Comparison



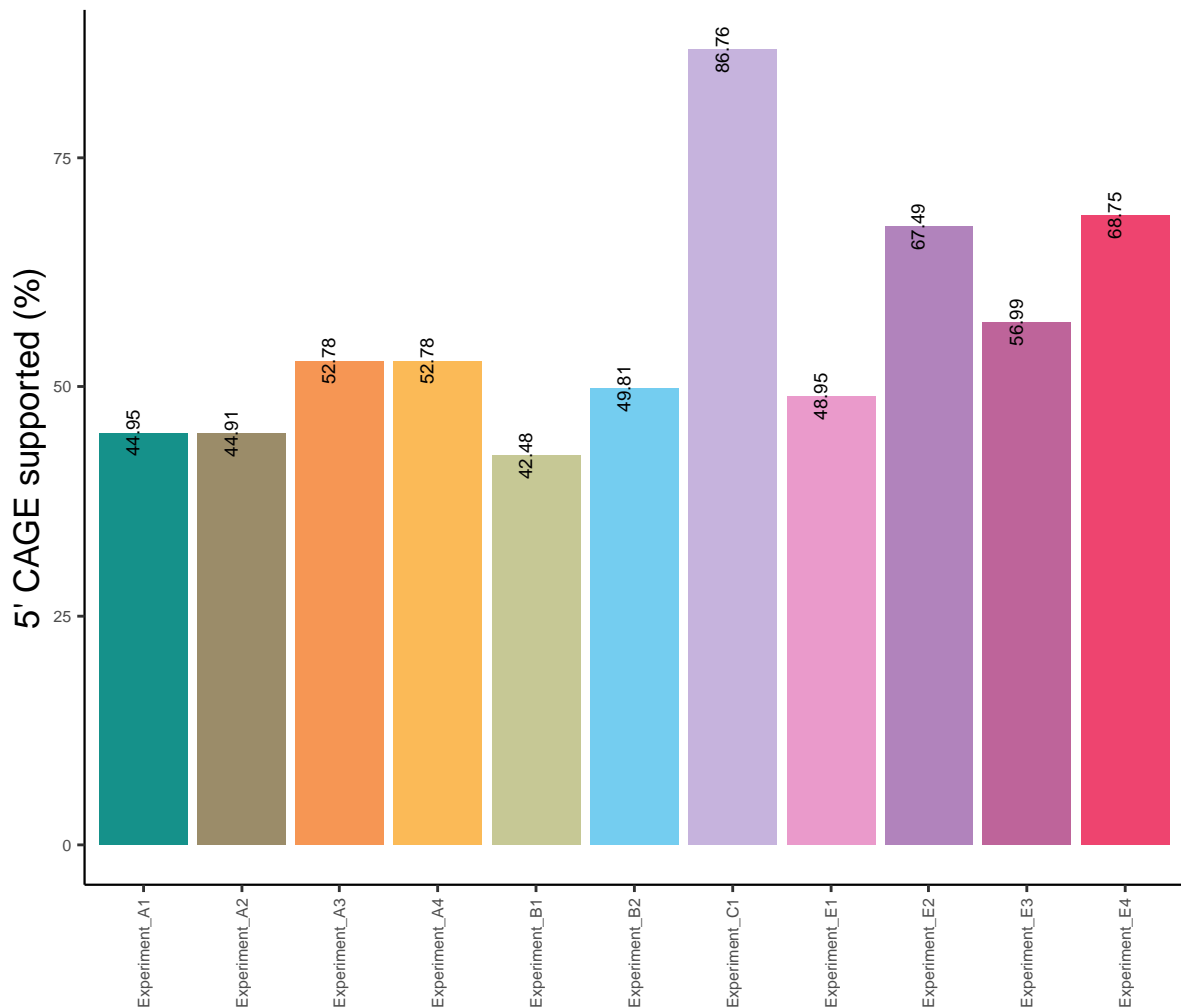
FSM 5' reference supported (gene) Comparison



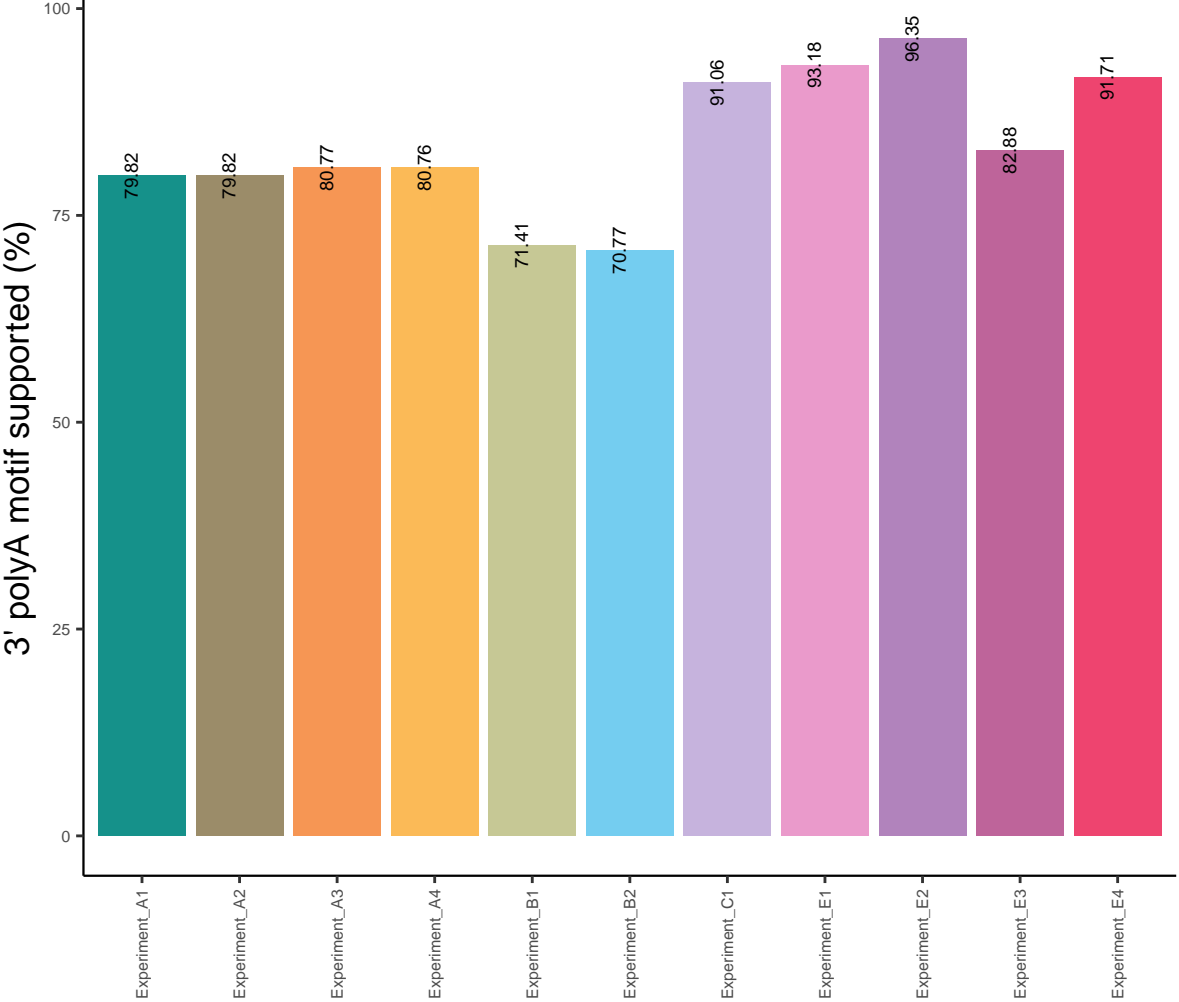
FSM 3' reference supported (gene) Comparison



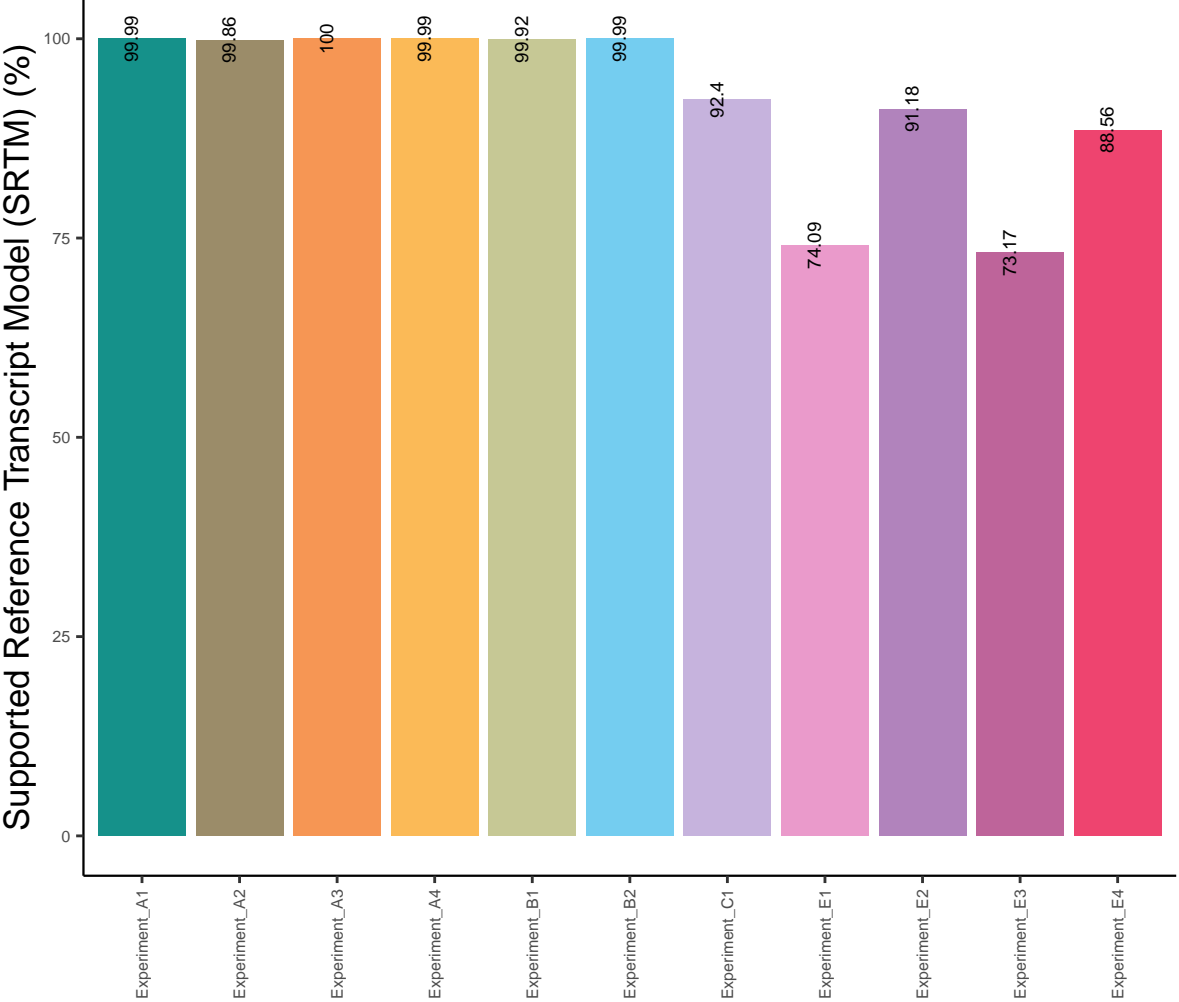
FSM 5' CAGE supported Comparison



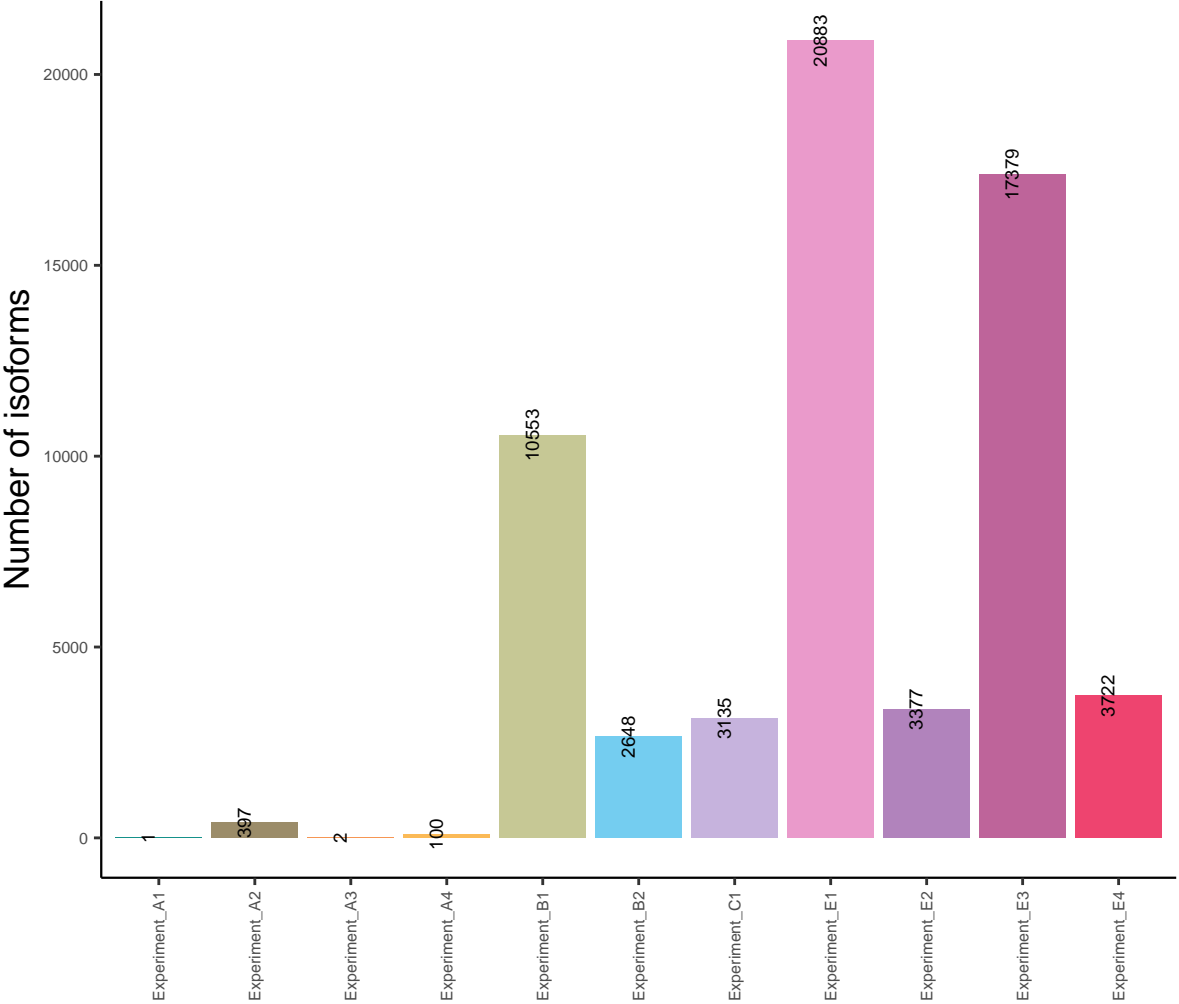
FSM 3' polyA motif supported Comparison



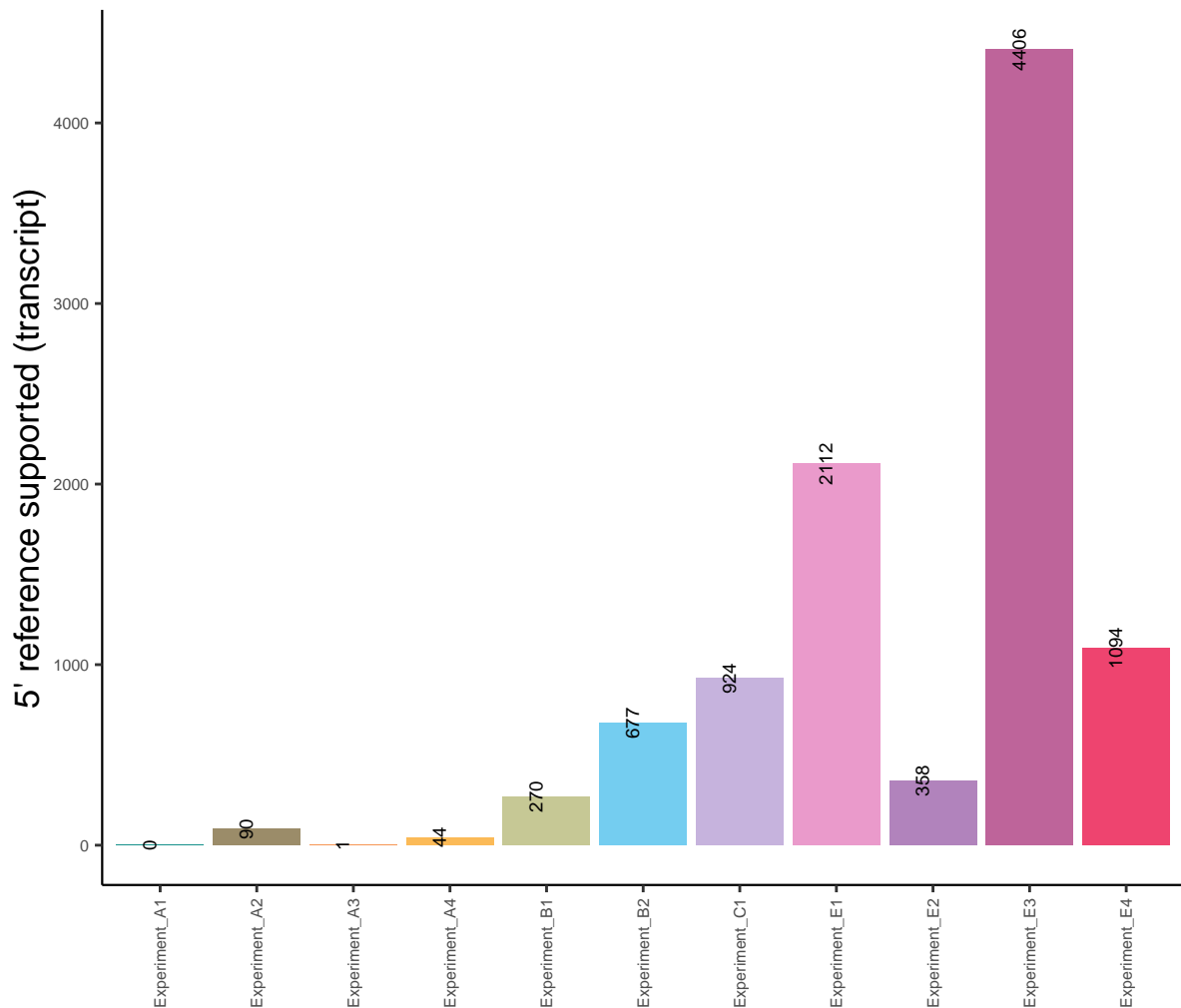
FSM Supported Reference Transcript Model (SRTM) Comparison



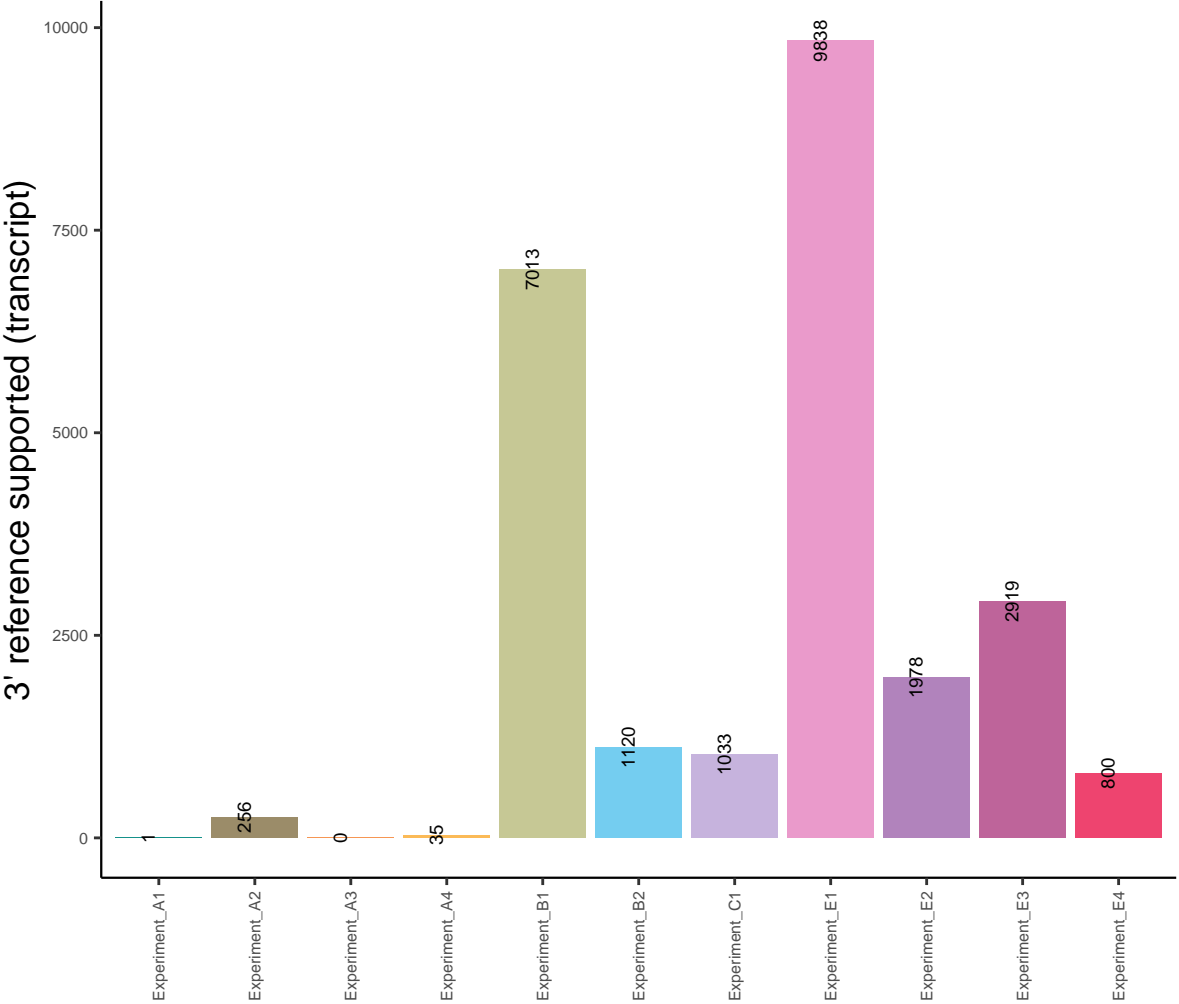
ISM Number of isoforms Comparison



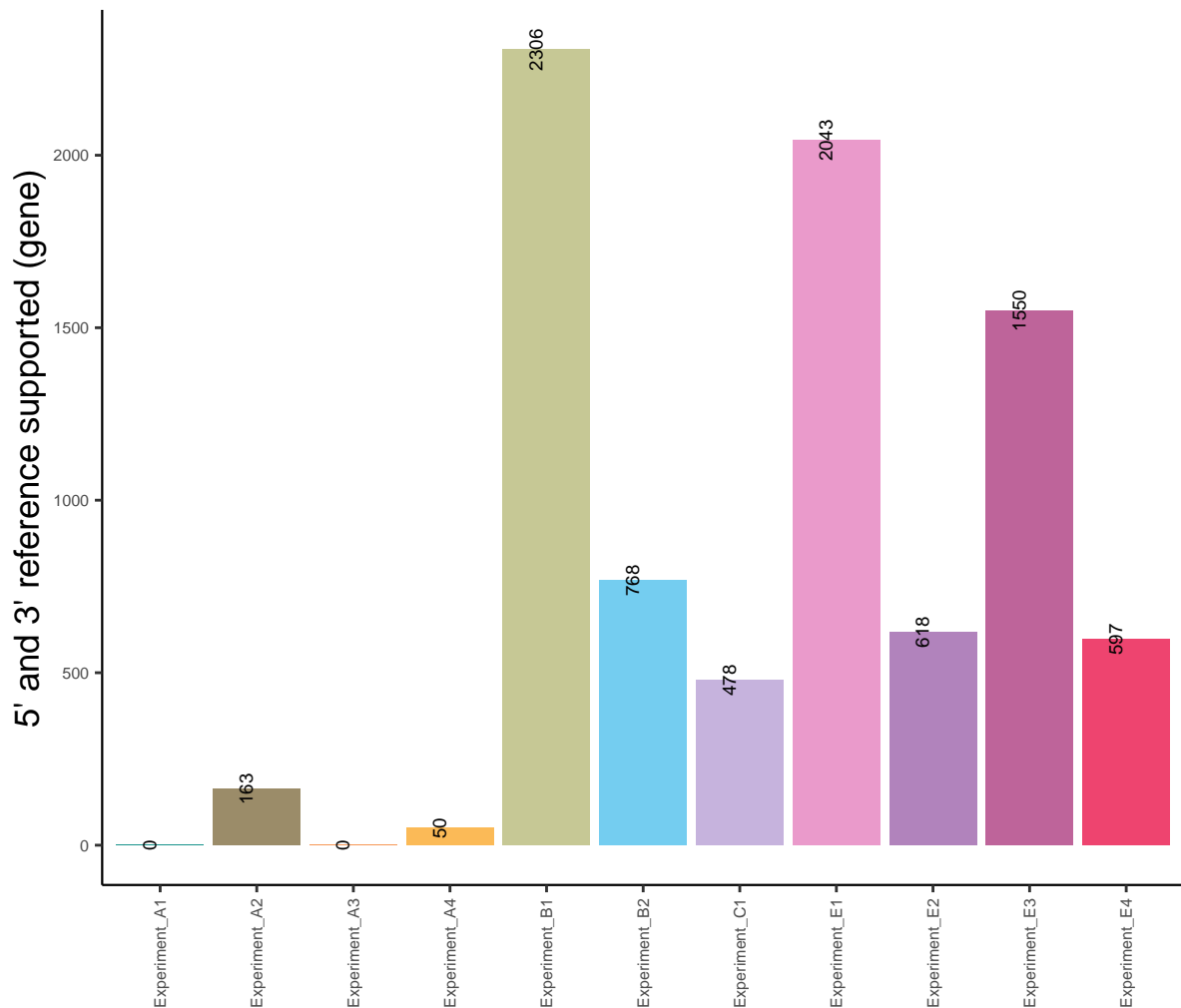
ISM 5' reference supported (transcript) Comparison



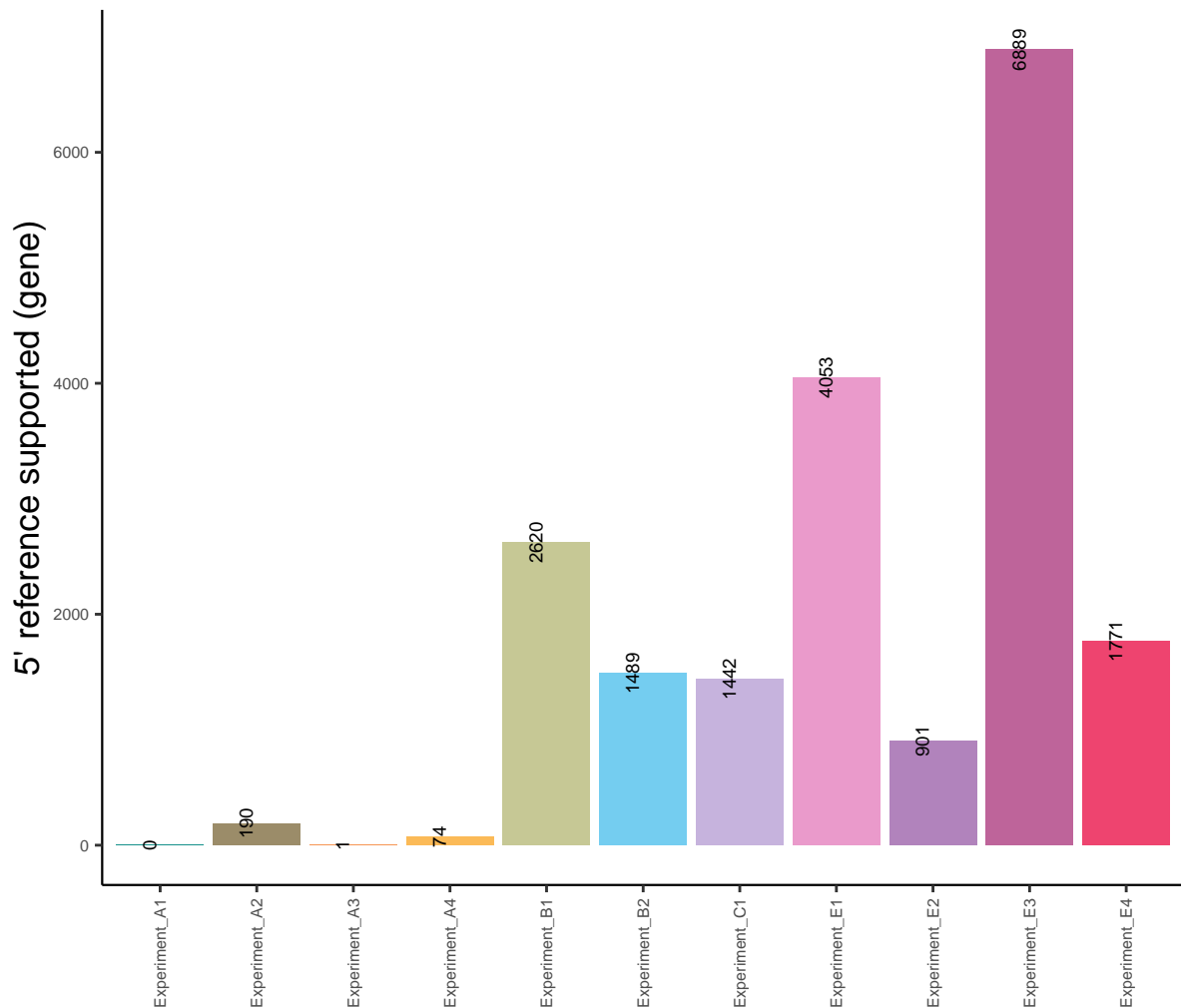
ISM 3' reference supported (transcript) Comparison



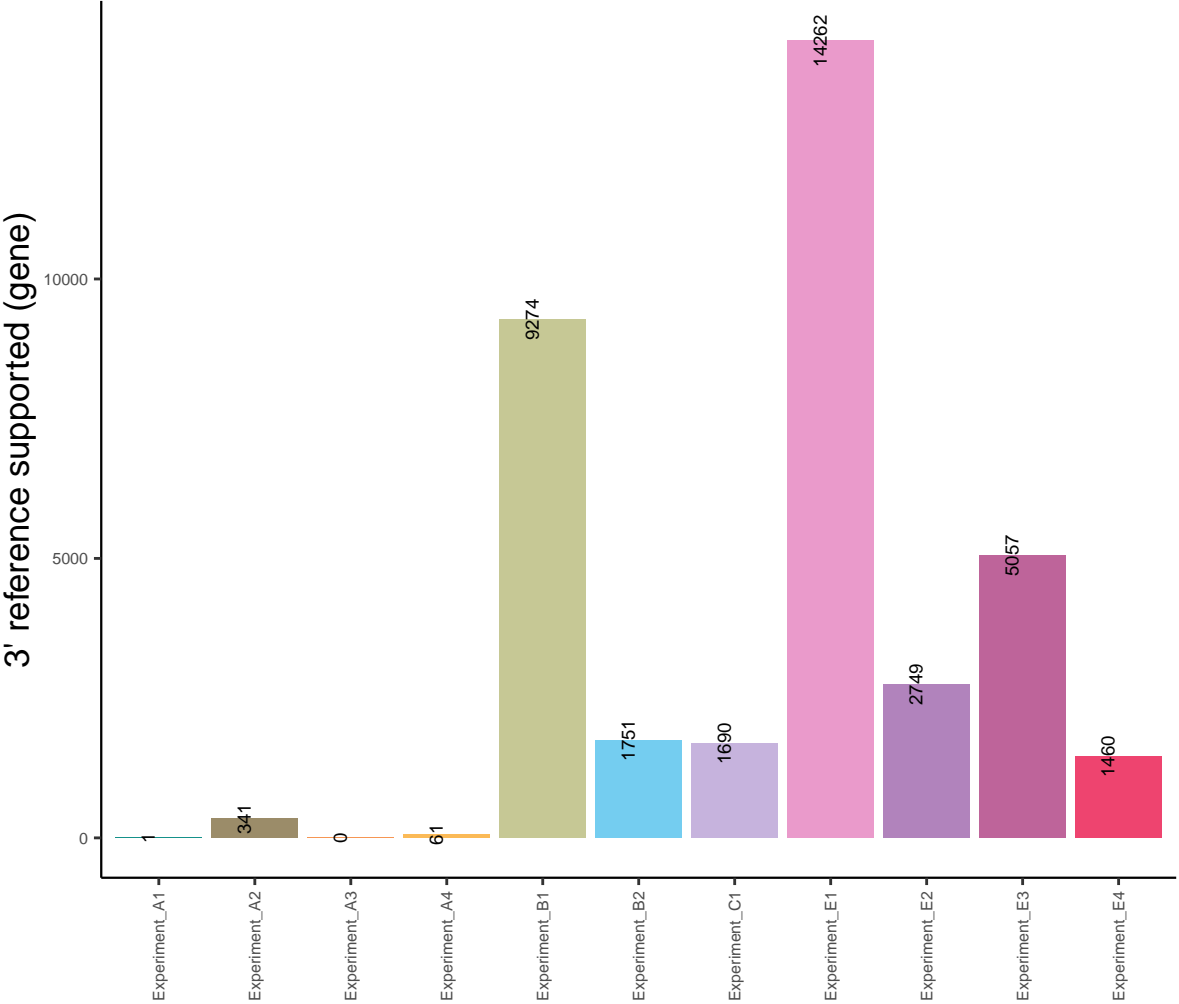
ISM 5' and 3' reference supported (gene) Comparison



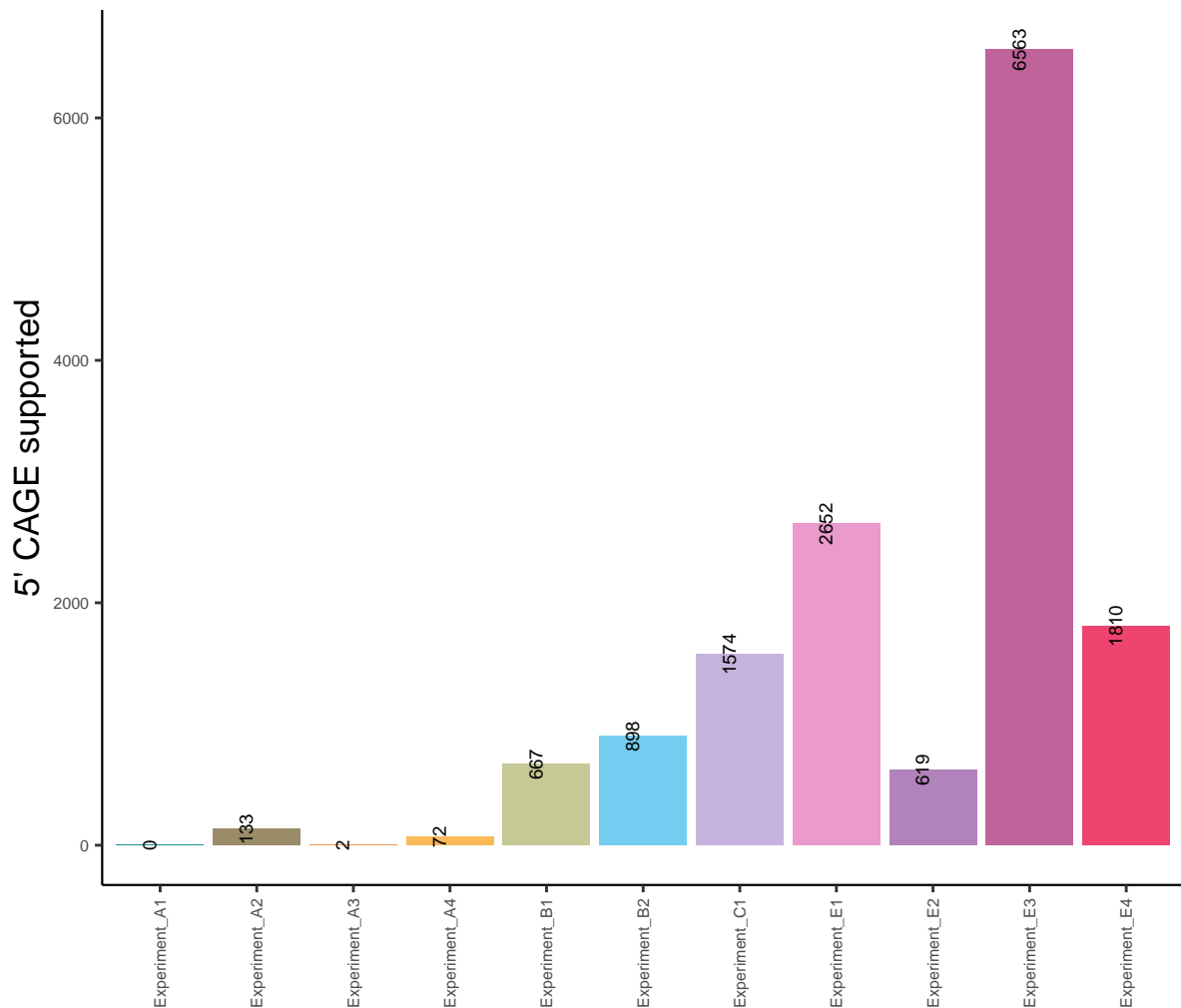
ISM 5' reference supported (gene) Comparison



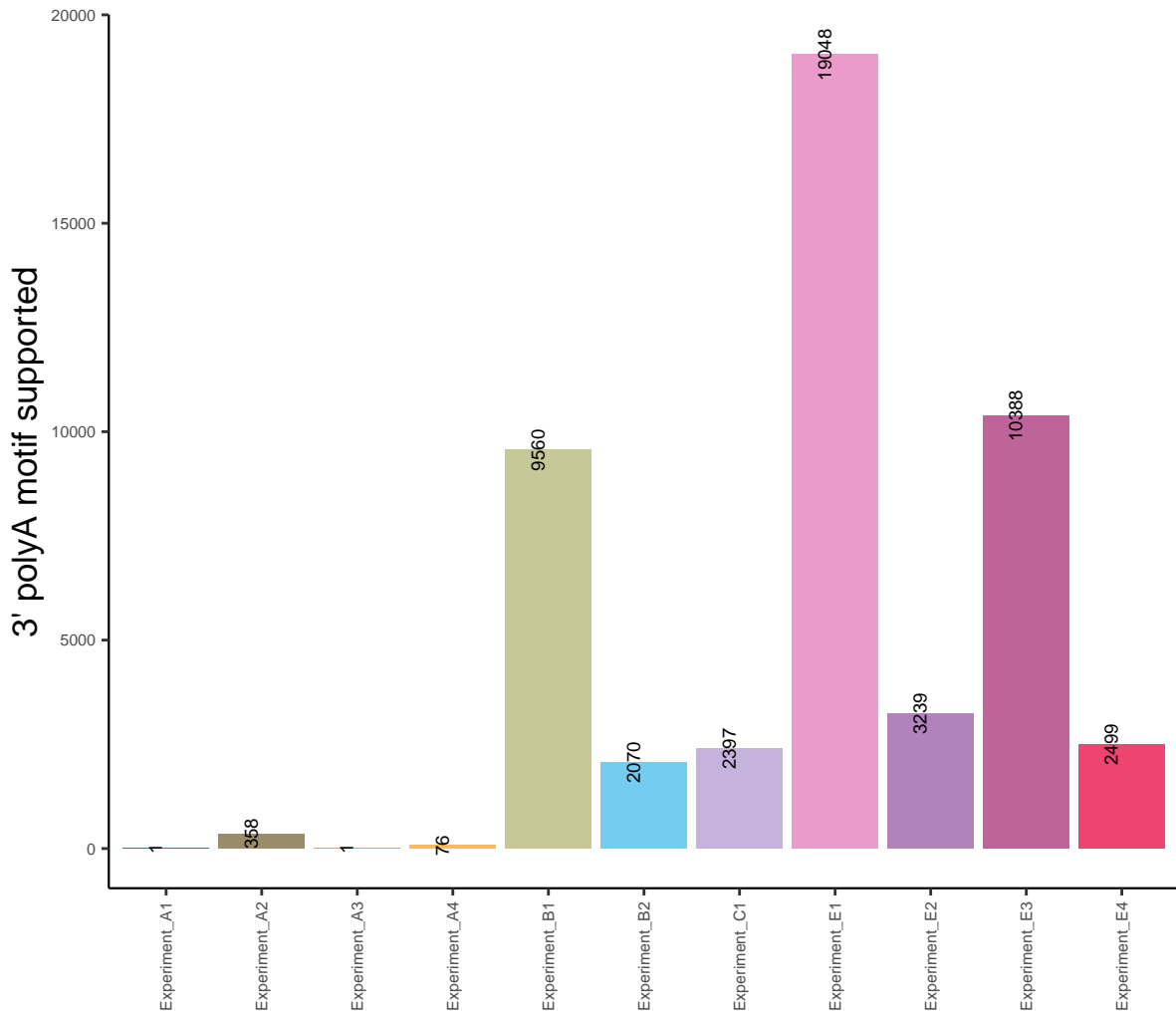
ISM 3' reference supported (gene) Comparison



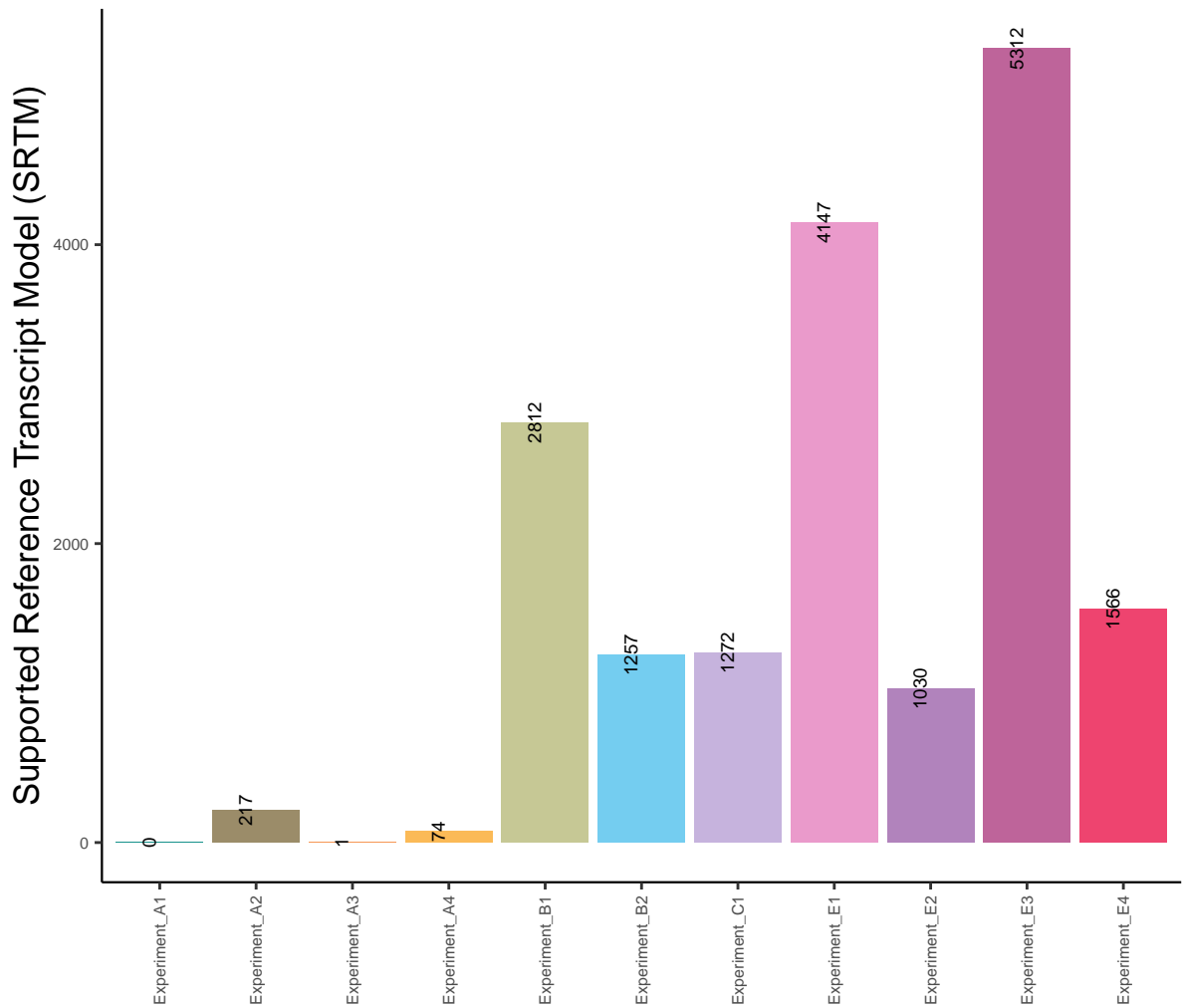
ISM 5' CAGE supported Comparison



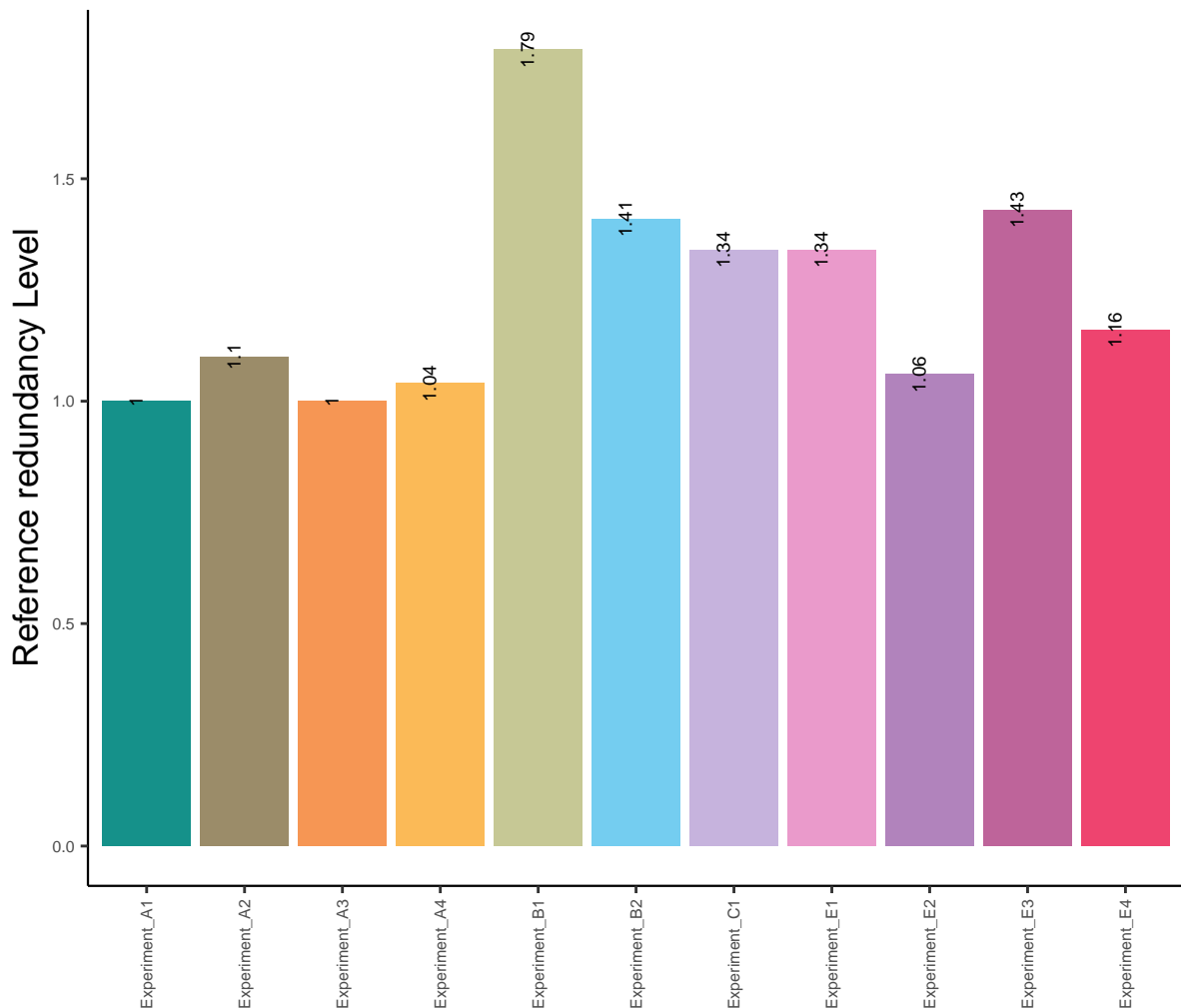
ISM 3' polyA motif supported Comparison



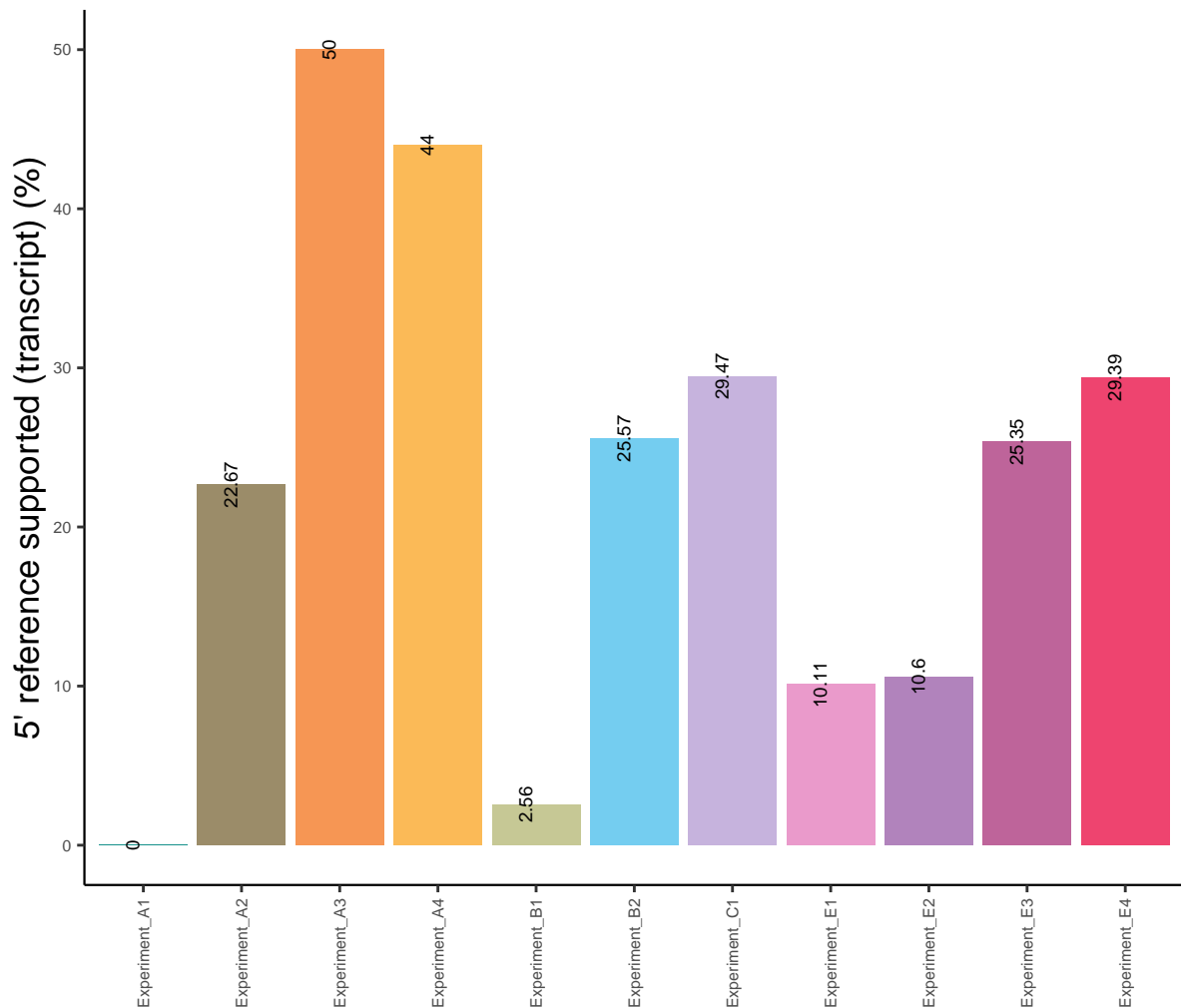
ISM Supported Reference Transcript Model (SRTM) Comparison



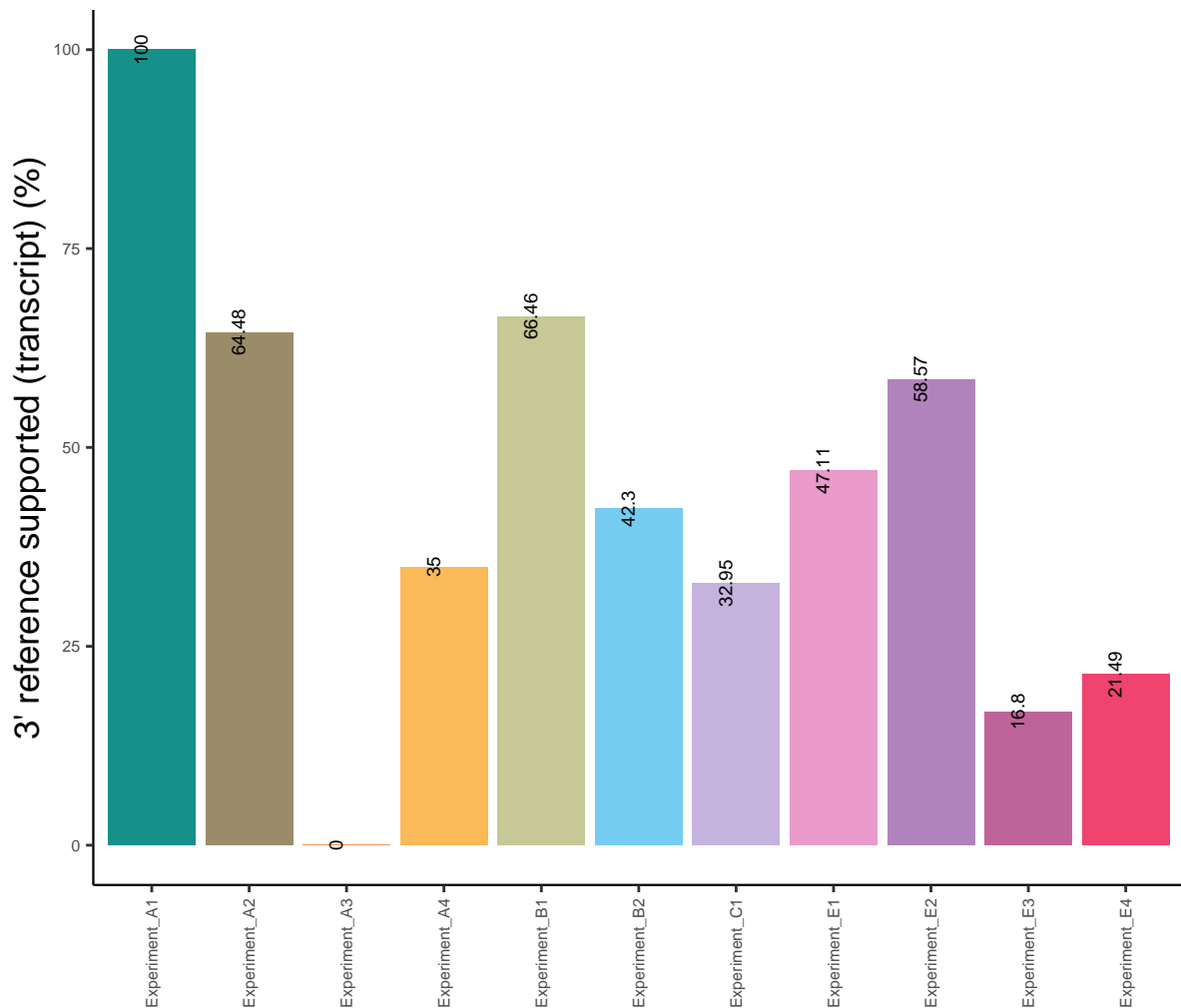
ISM Reference redundancy Level Comparison



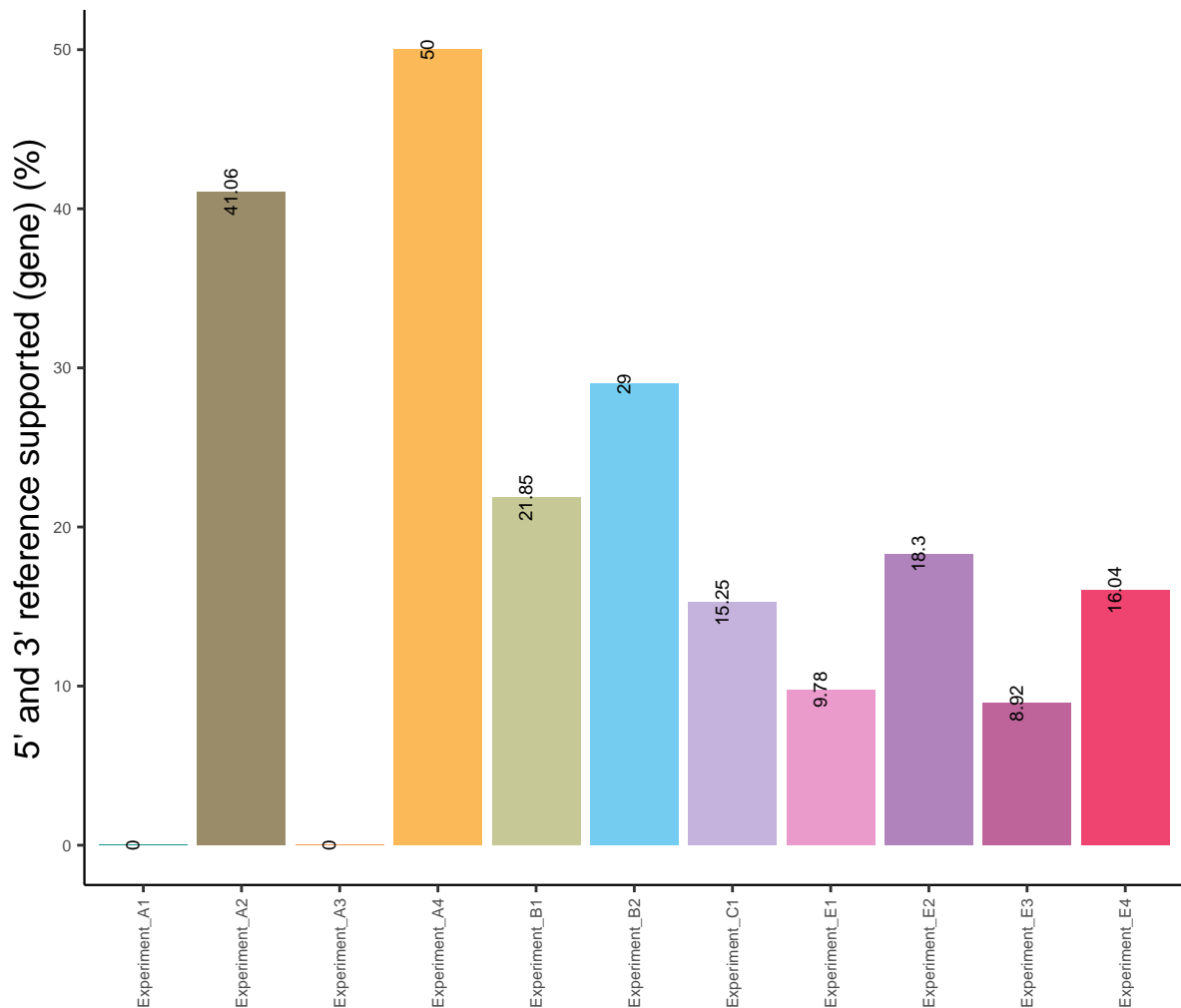
ISM 5' reference supported (transcript) Comparison



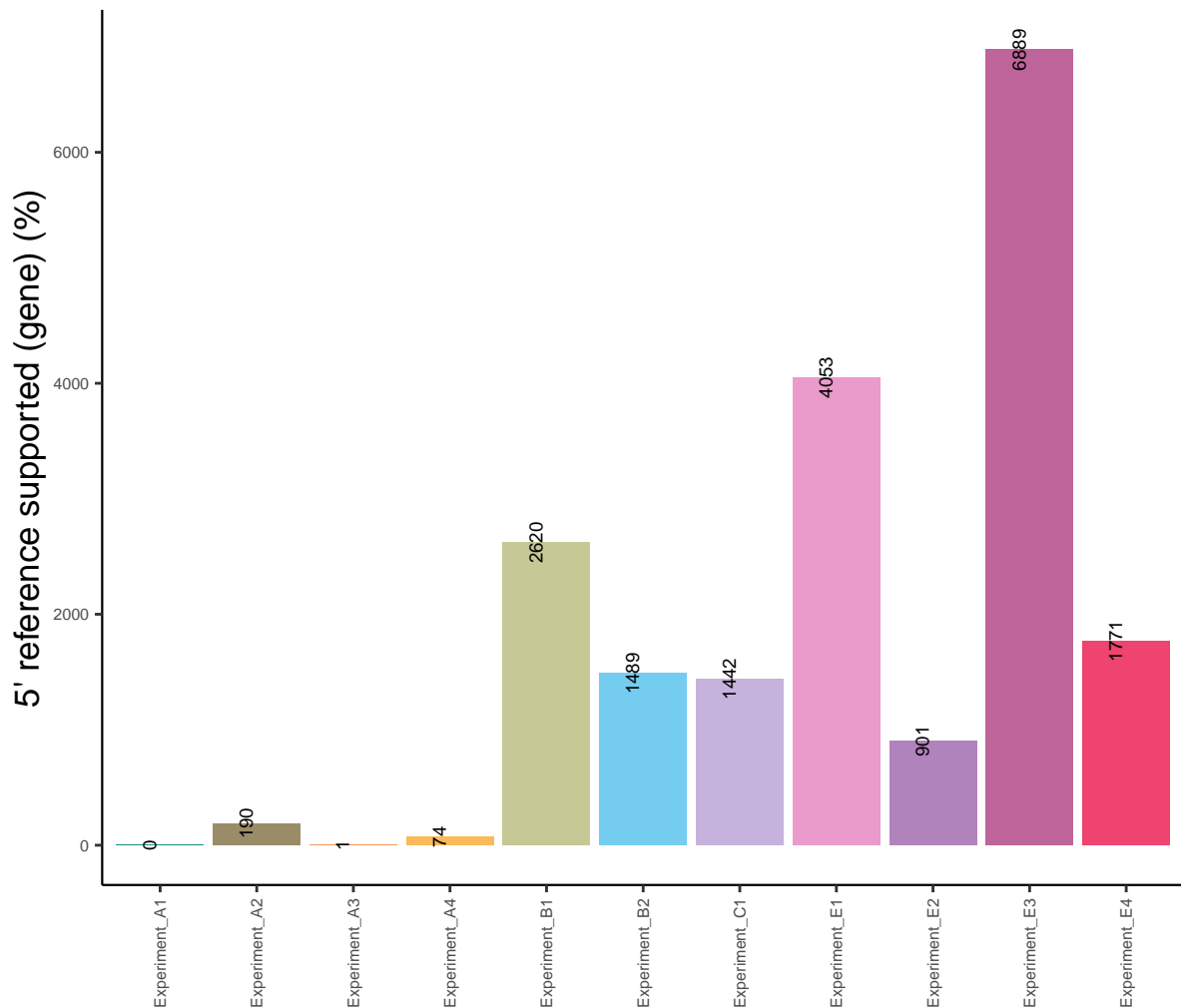
ISM 3' reference supported (transcript) Comparison



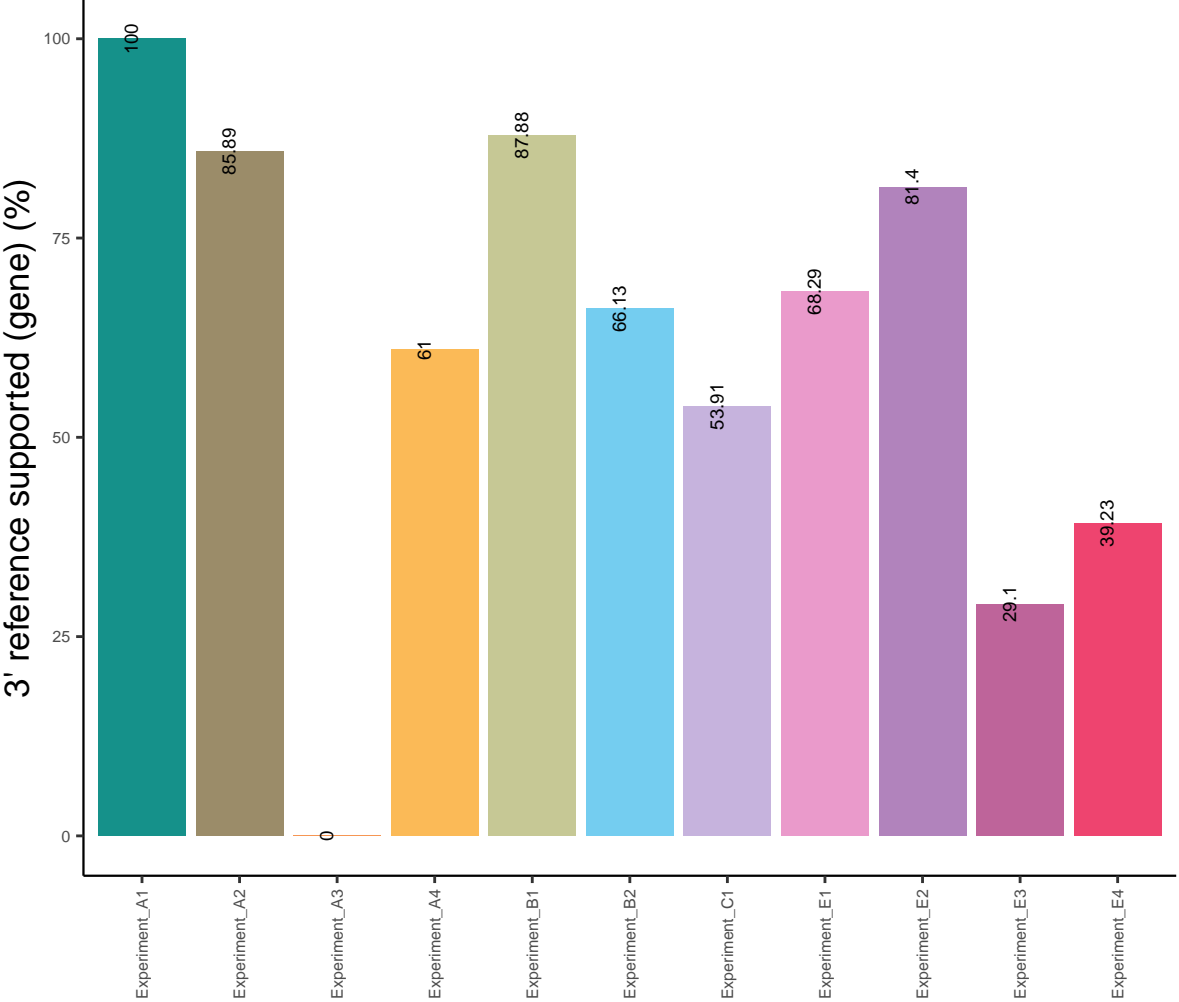
ISM 5' and 3' reference supported (gene) Comparison



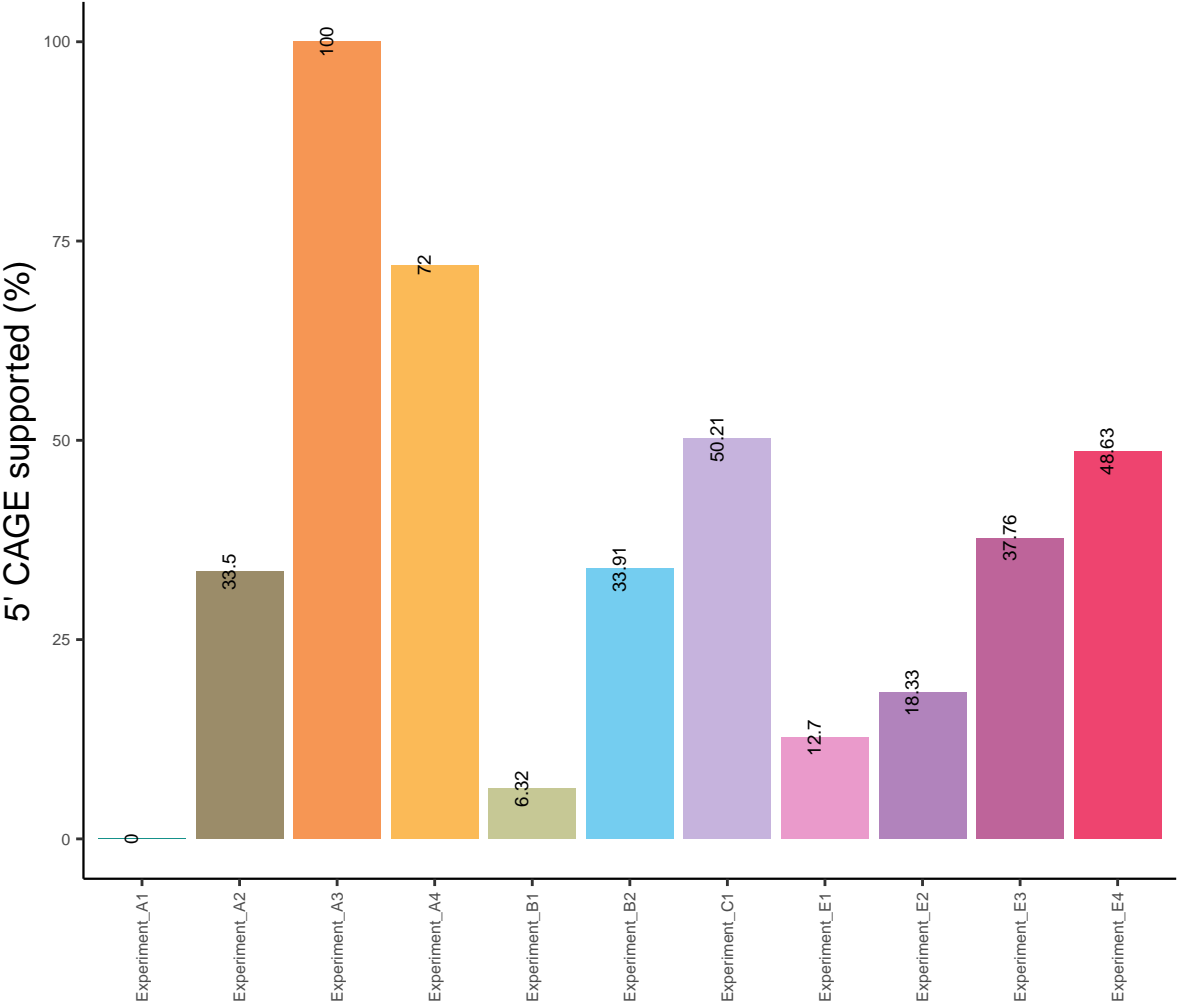
ISM 5' reference supported (gene) Comparison



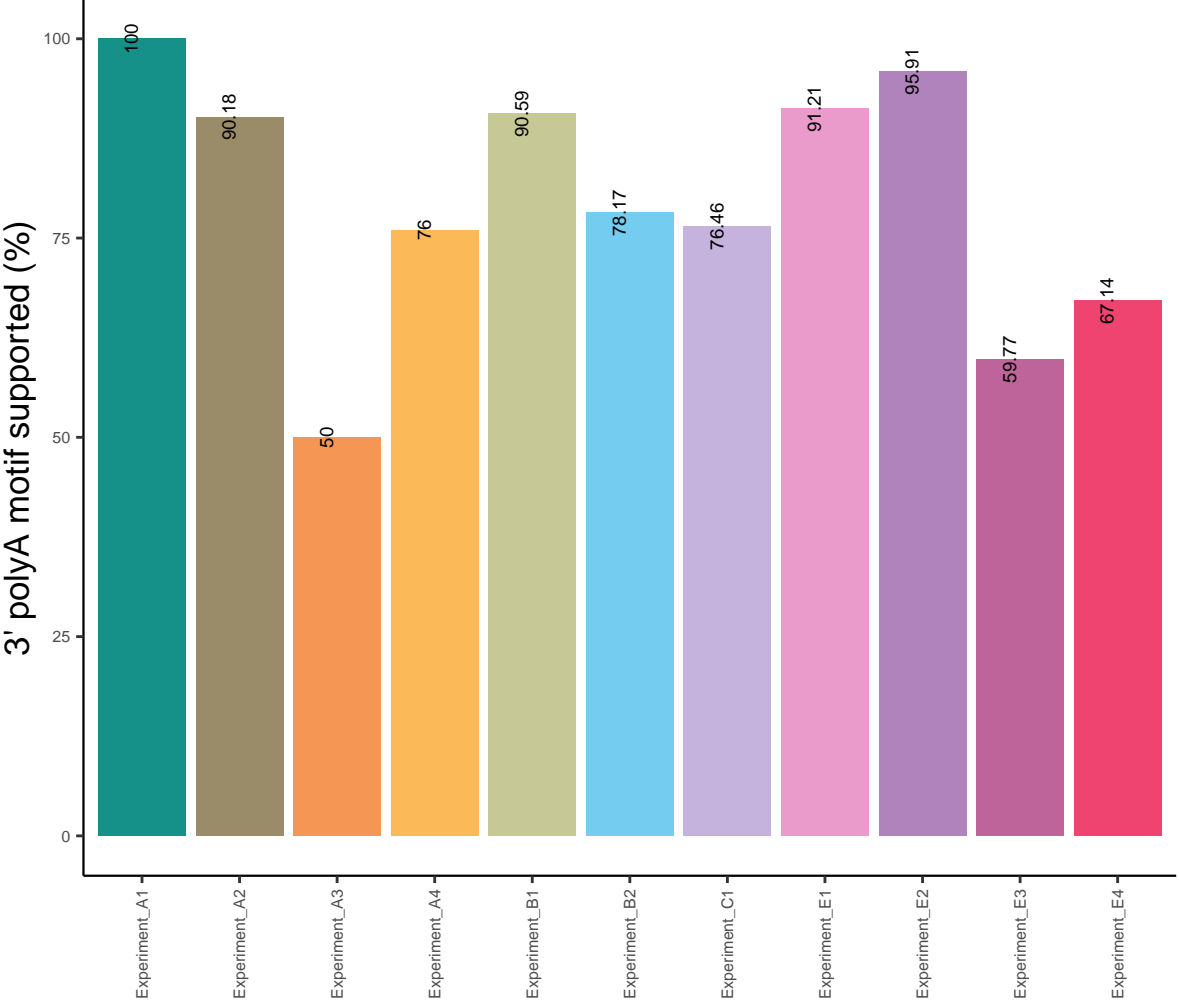
ISM 3' reference supported (gene) Comparison



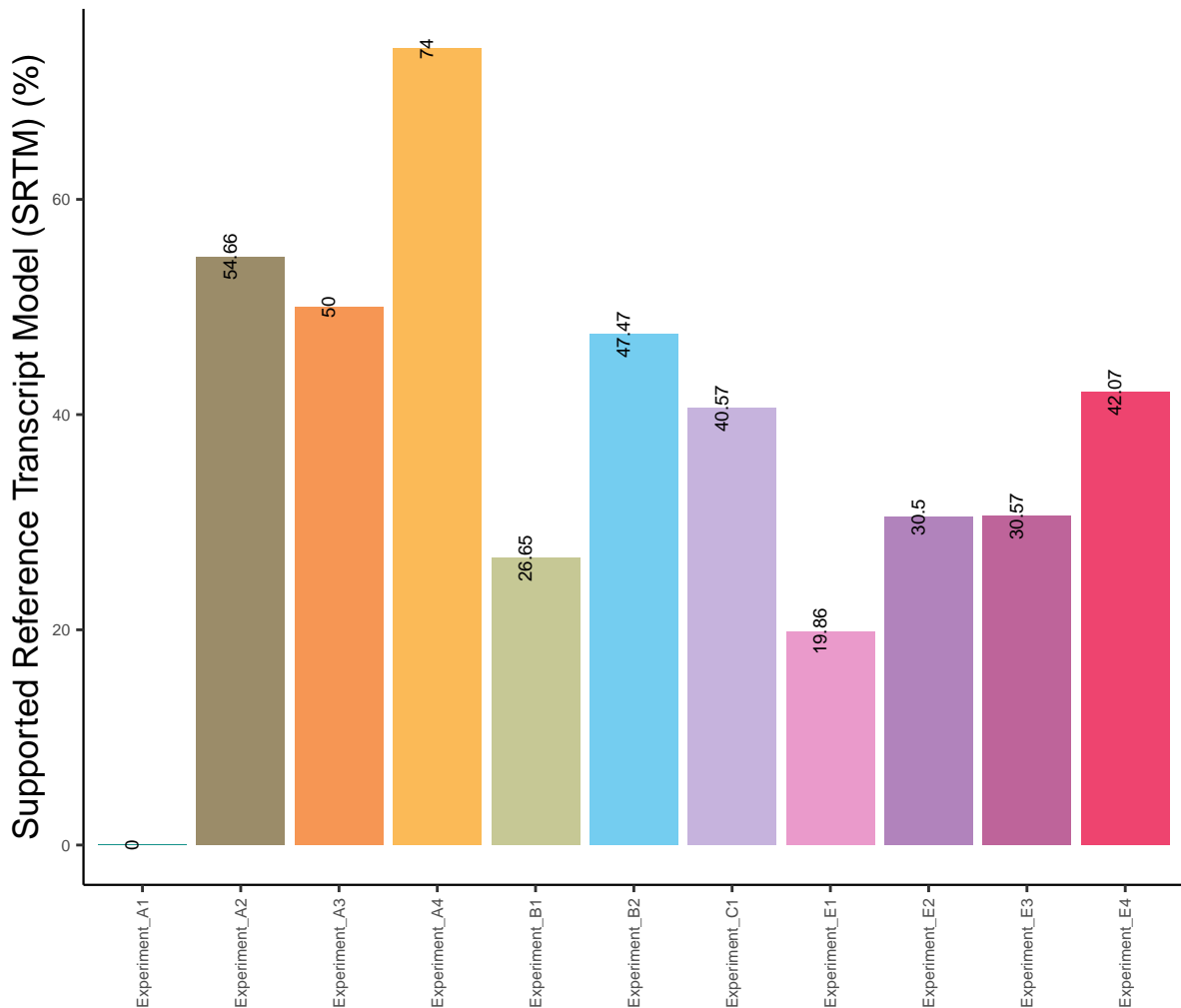
ISM 5' CAGE supported Comparison



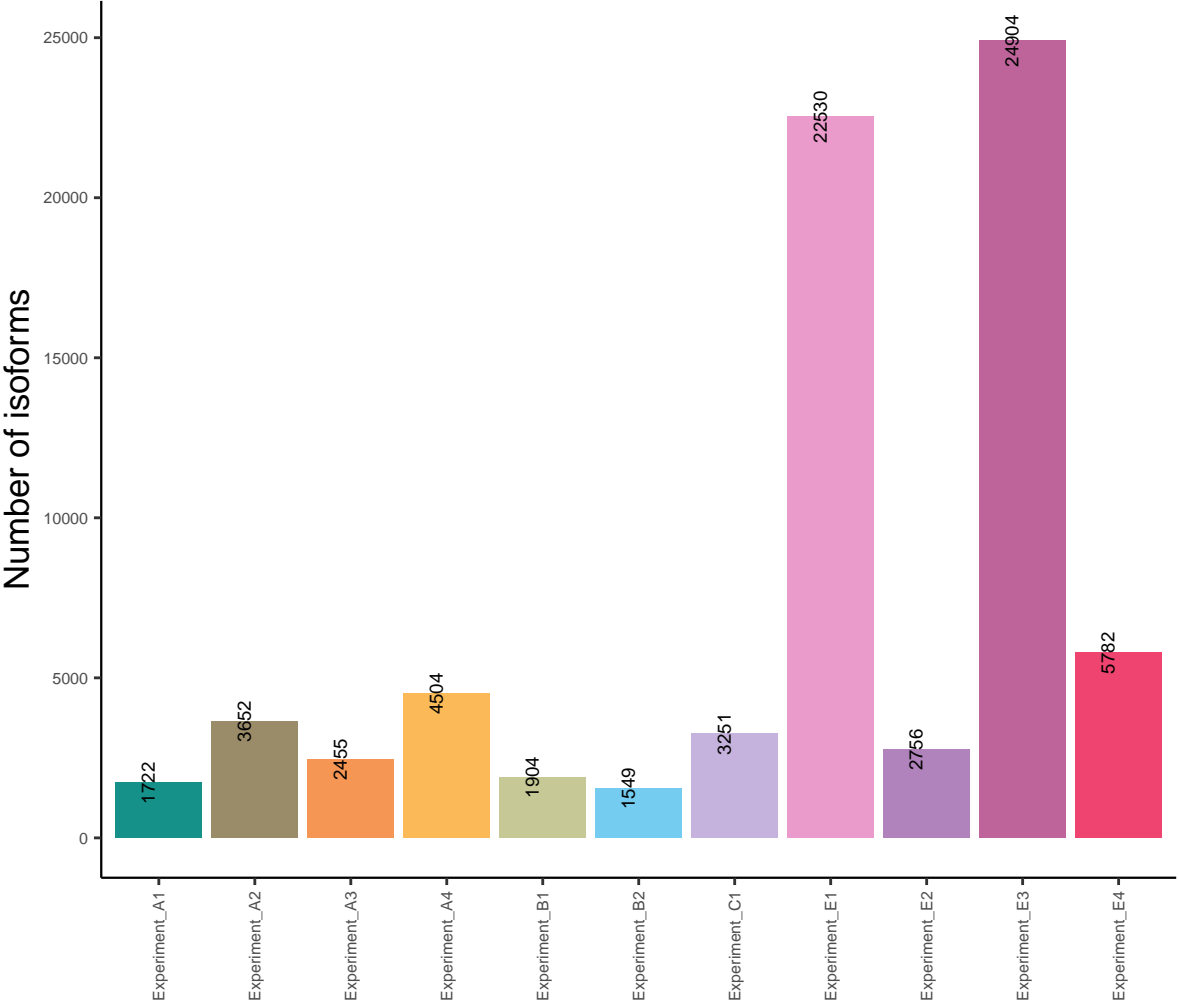
ISM 3' polyA motif supported Comparison



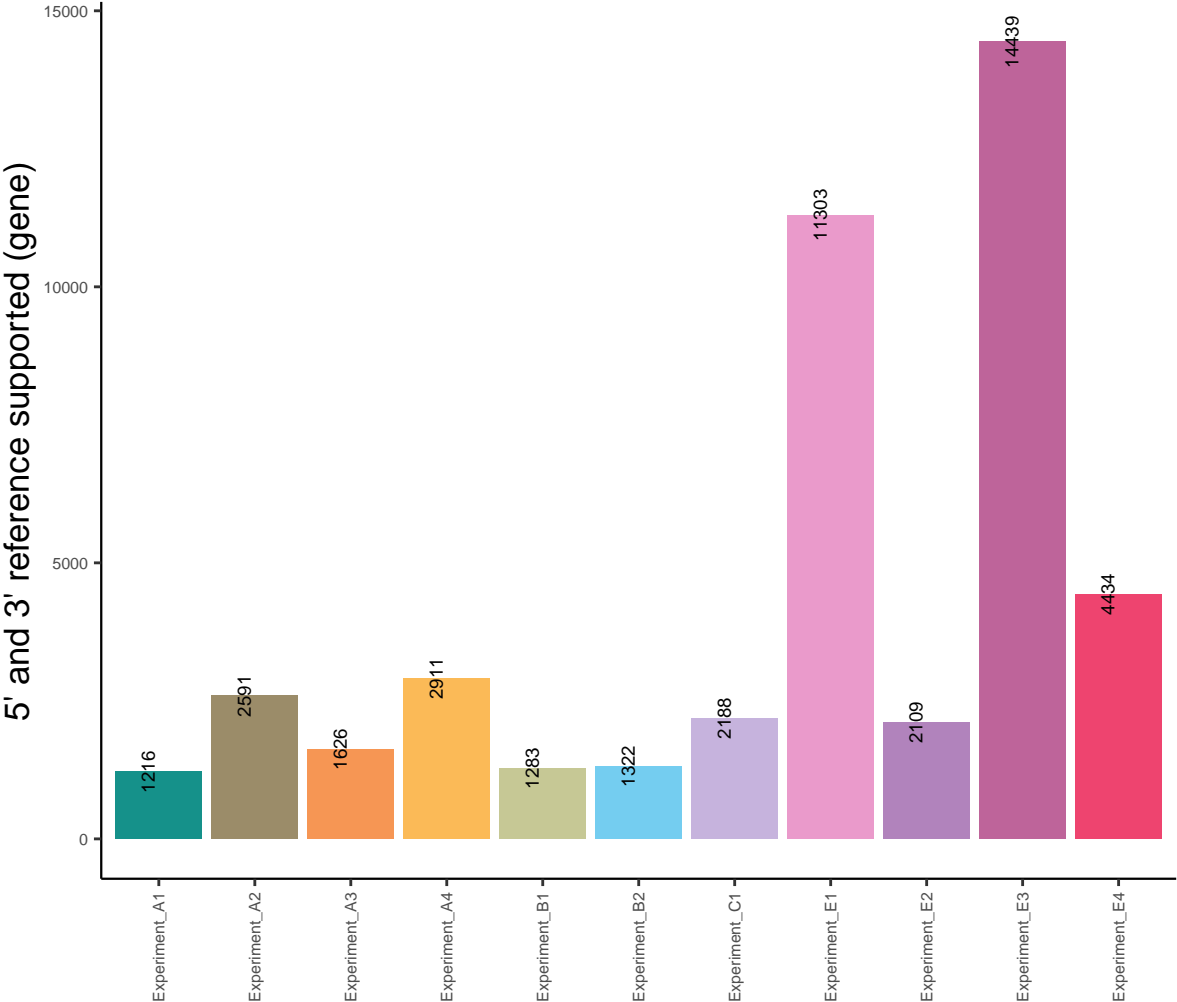
ISM Supported Reference Transcript Model (SRTM) Comparison



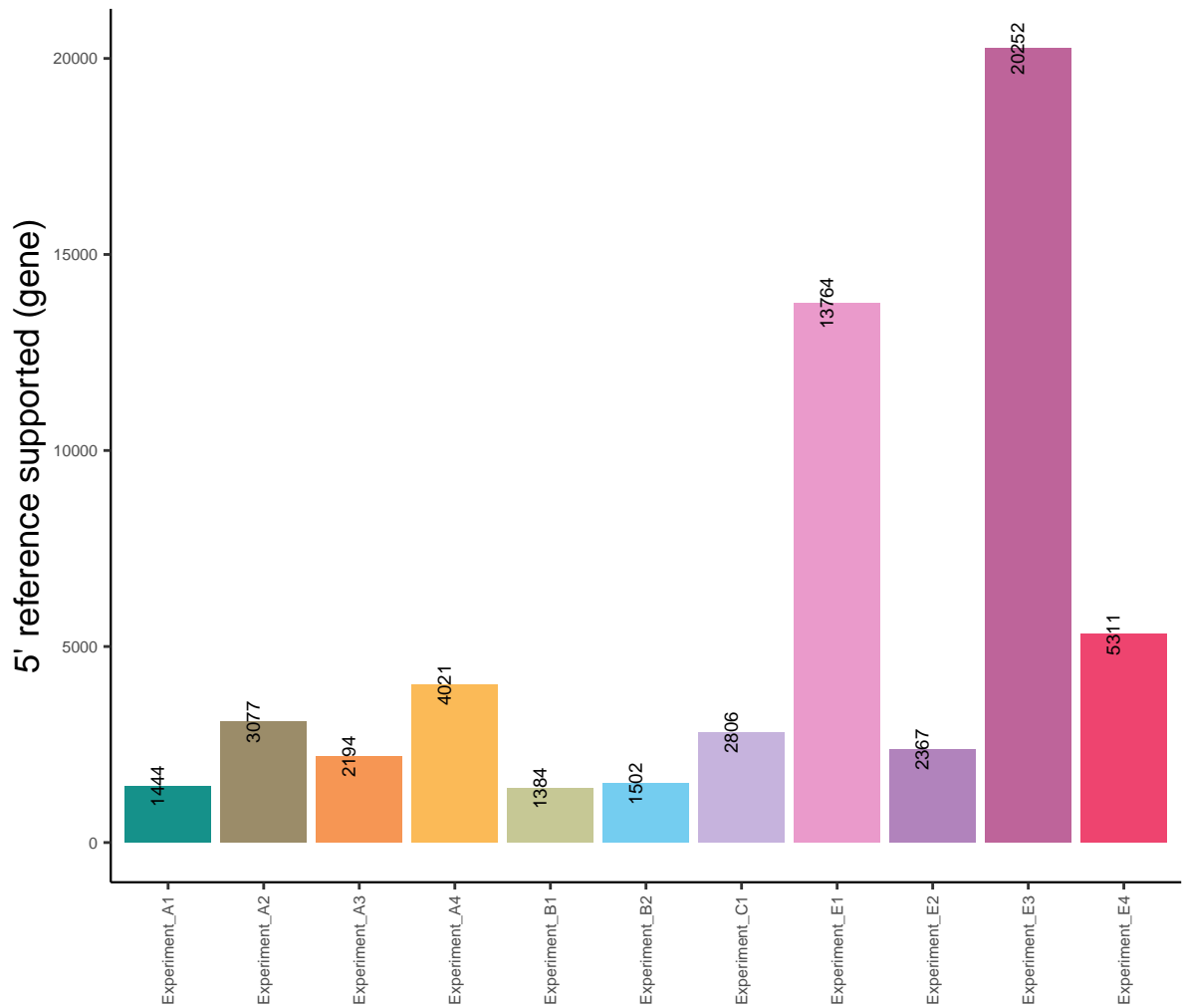
NIC Number of isoforms Comparison



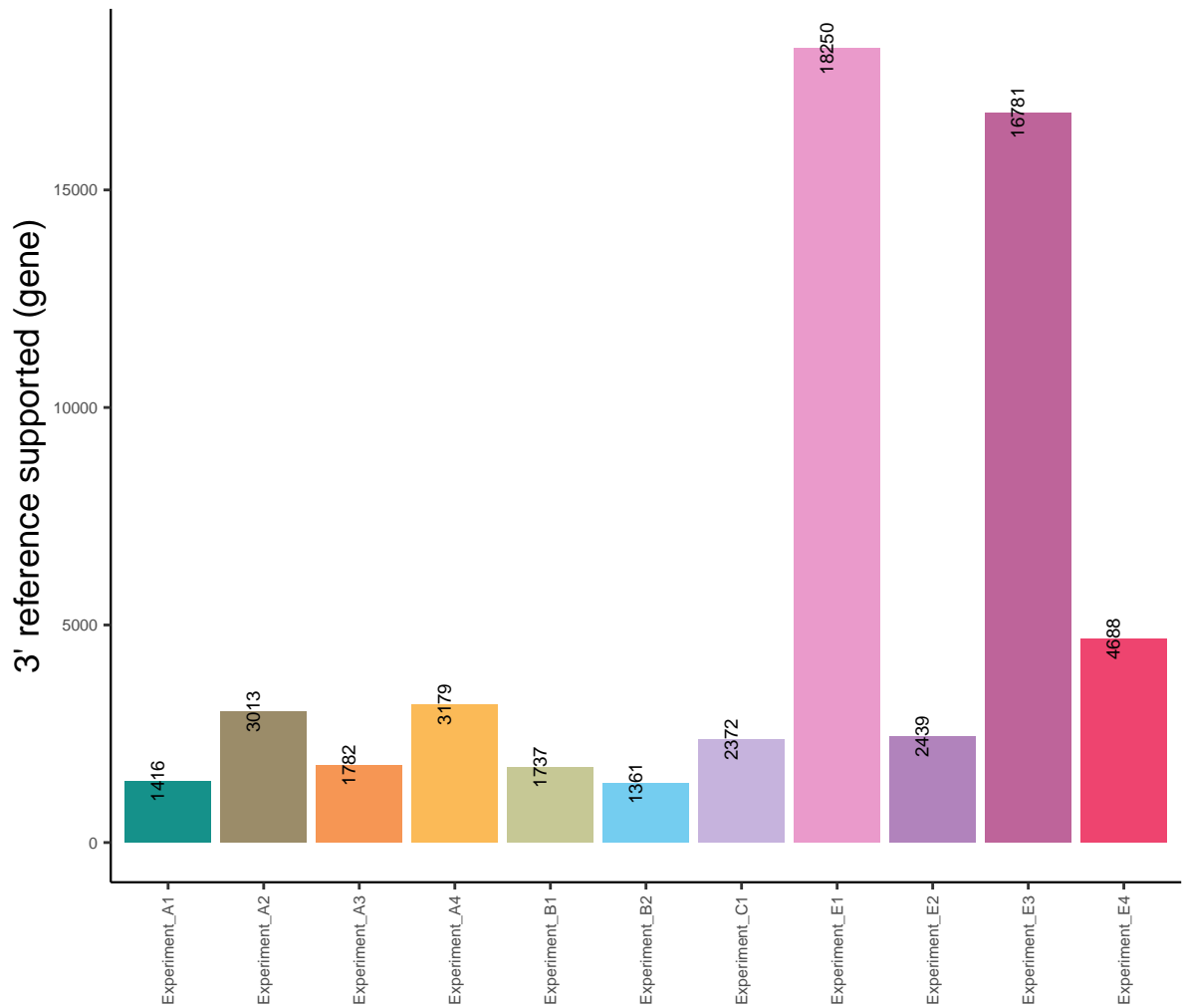
NIC 5' and 3' reference supported (gene) Comparison



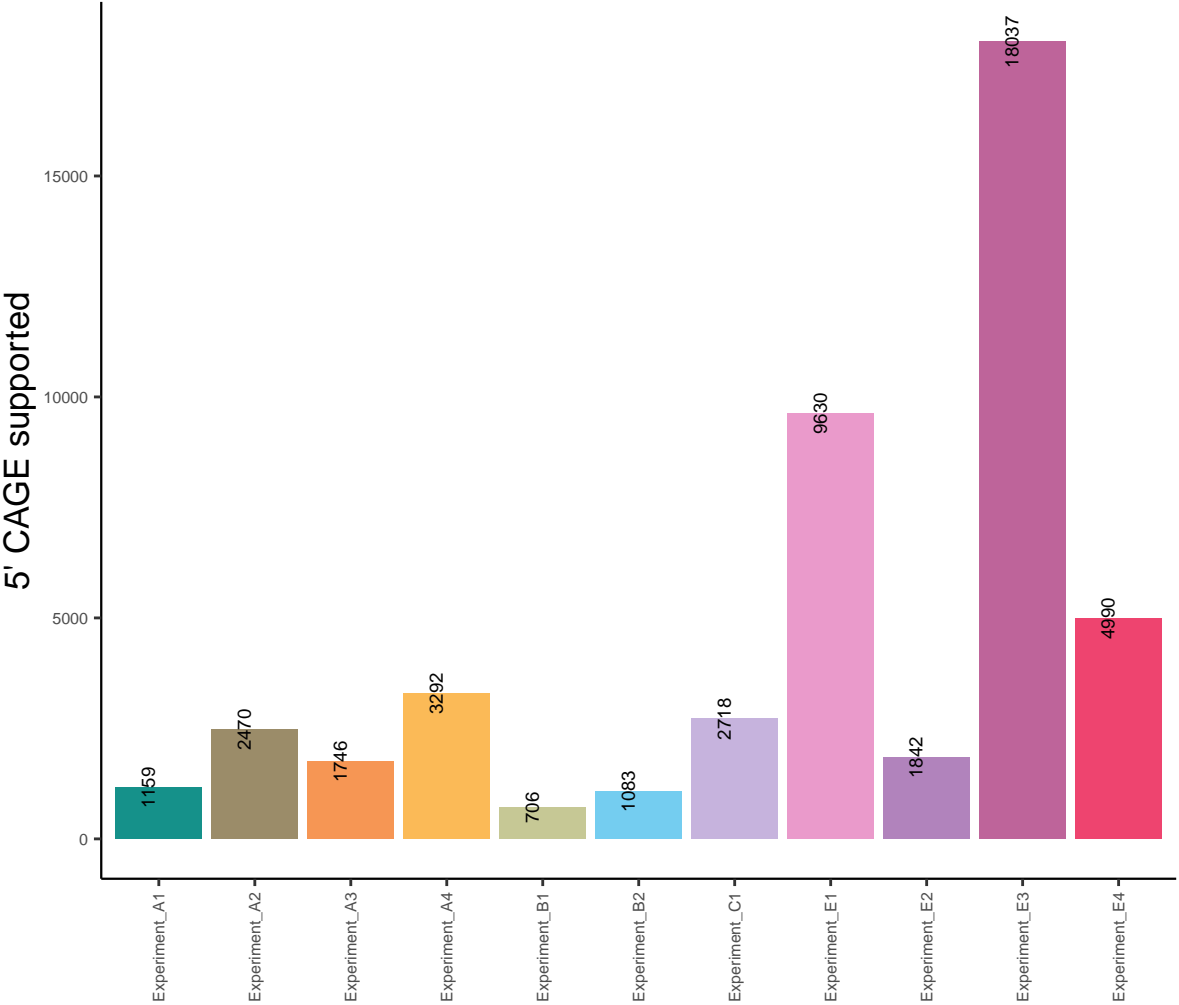
NIC 5' reference supported (gene) Comparison



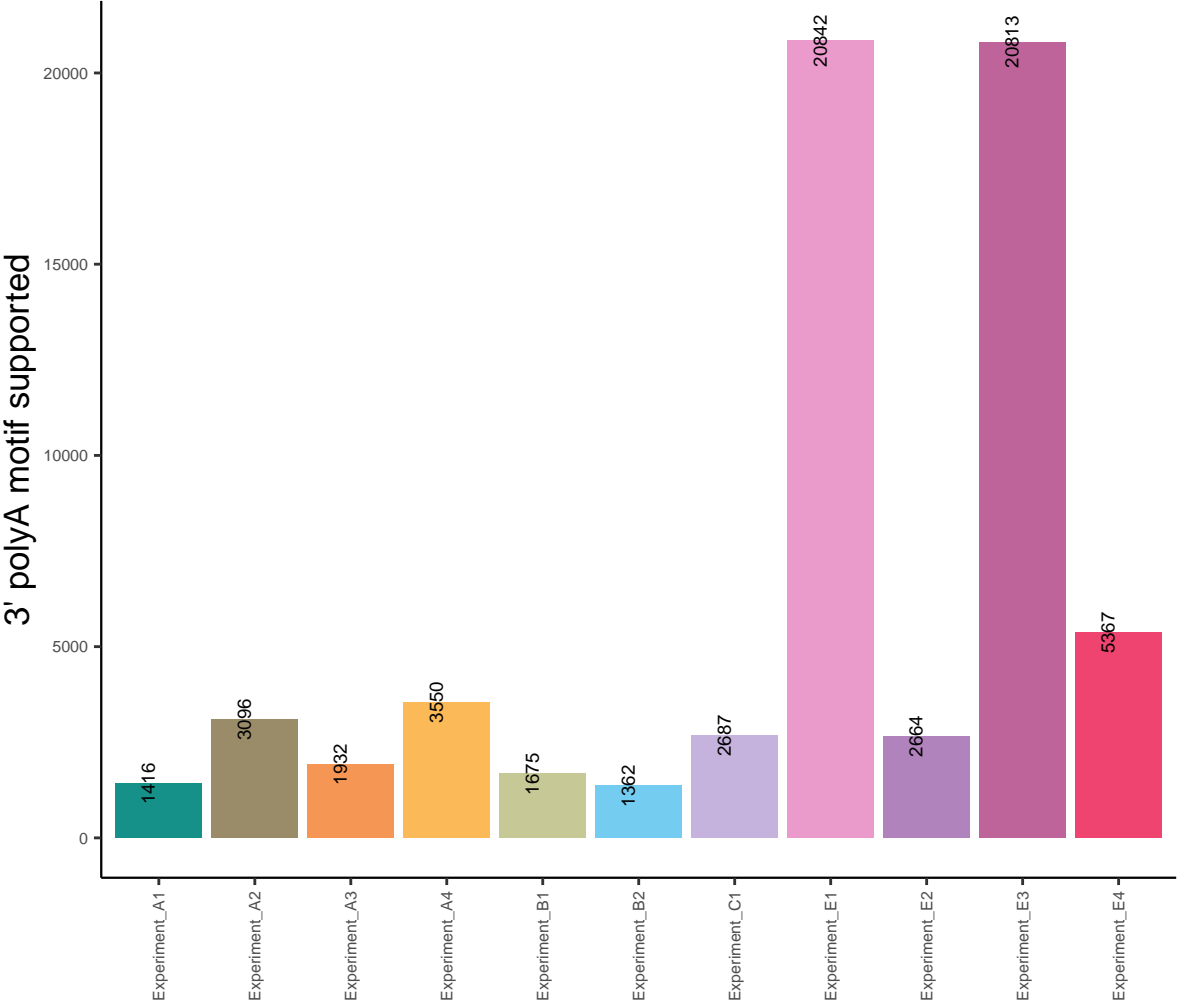
NIC 3' reference supported (gene) Comparison



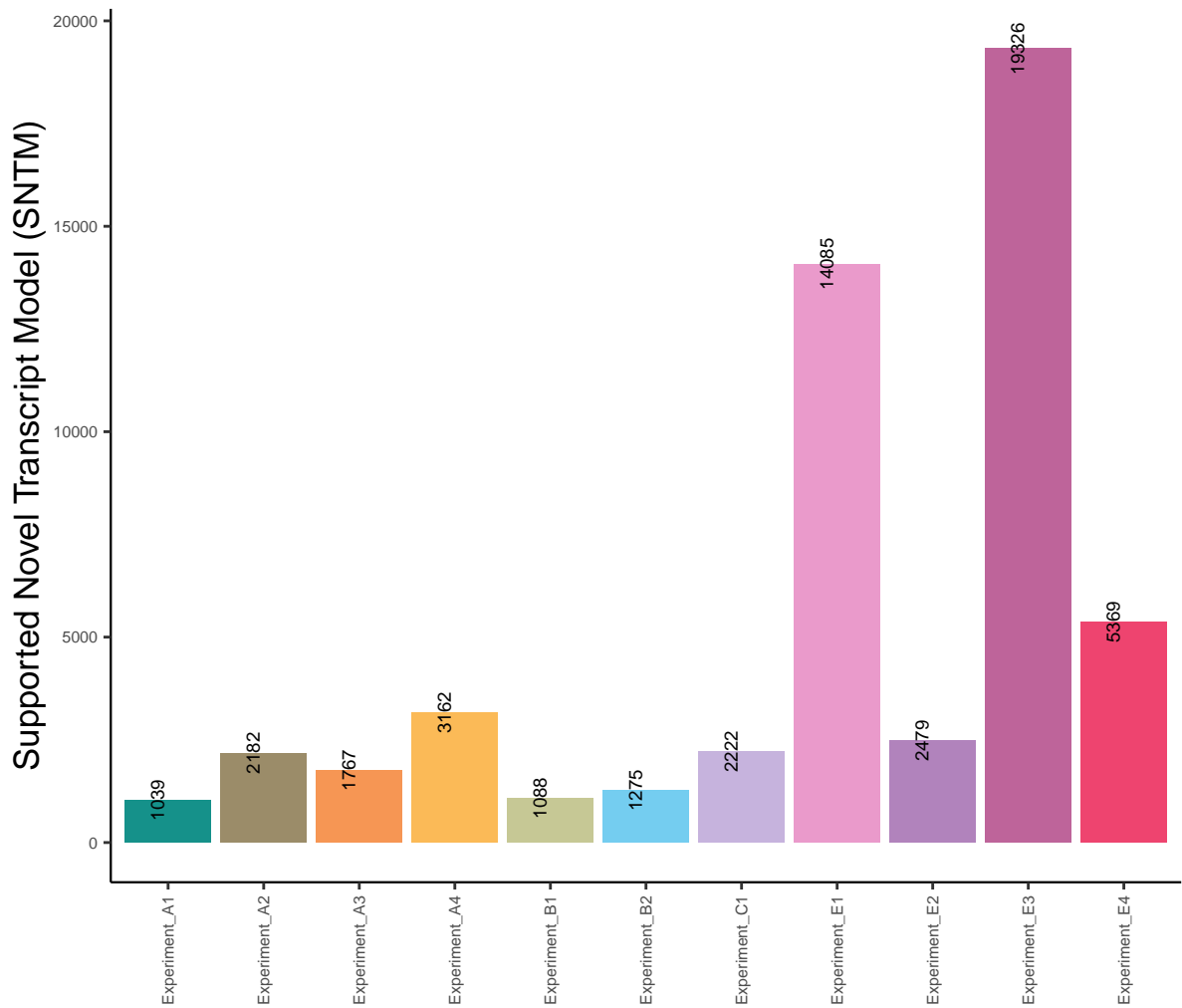
NIC 5' CAGE supported Comparison



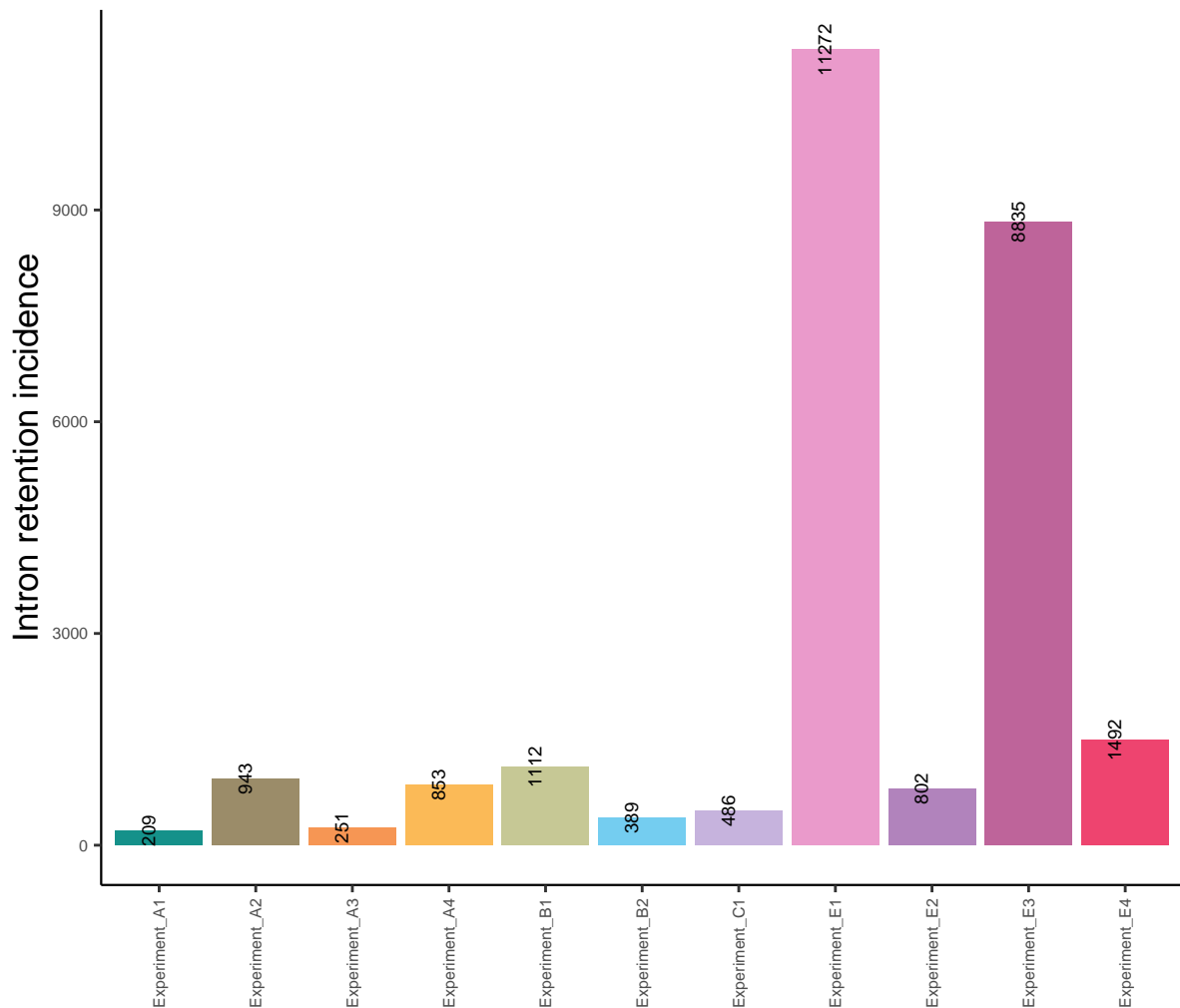
NIC 3' polyA motif supported Comparison



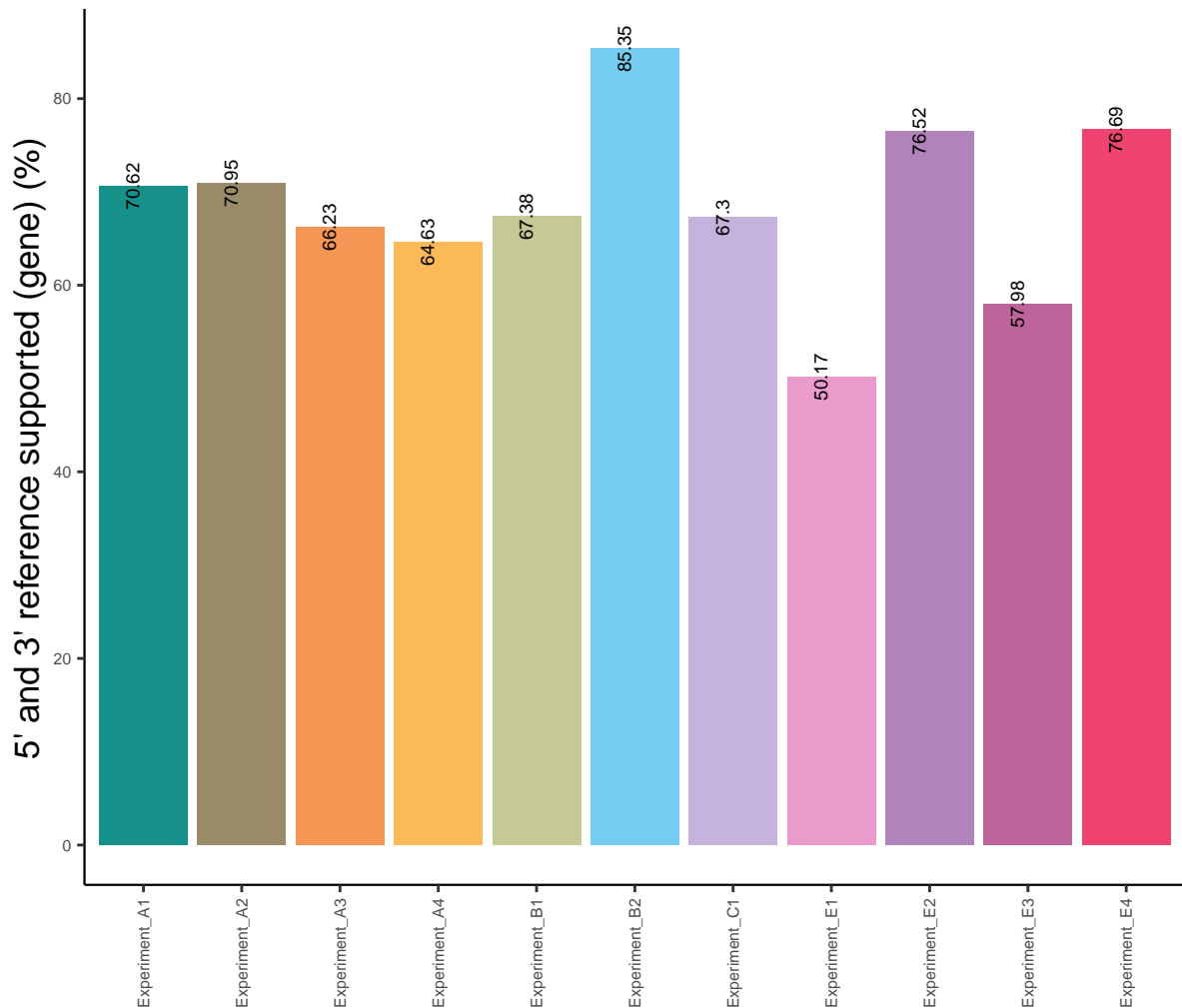
NIC Supported Novel Transcript Model (SNTM) Comparison



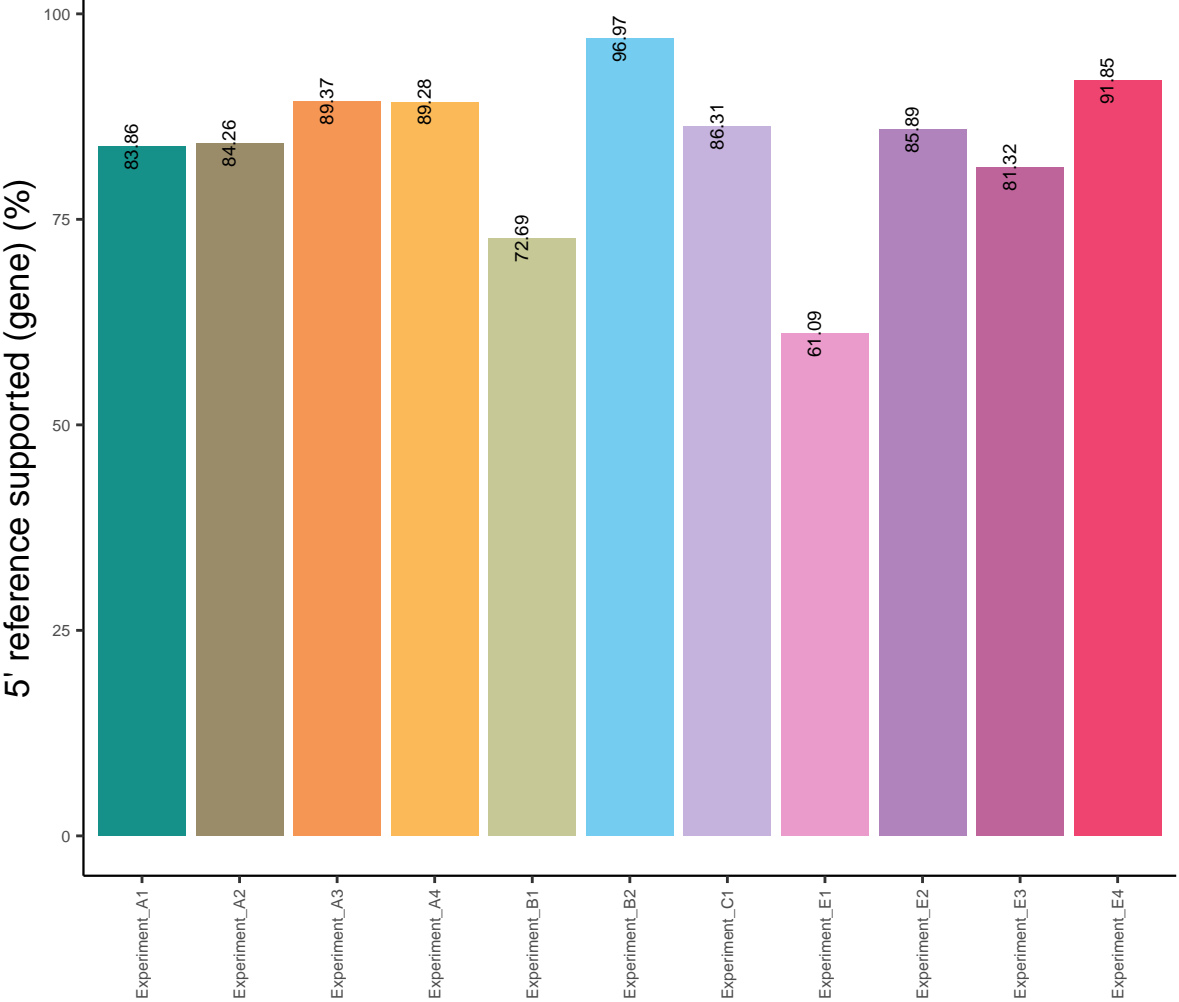
NIC Intron retention incidence Comparison



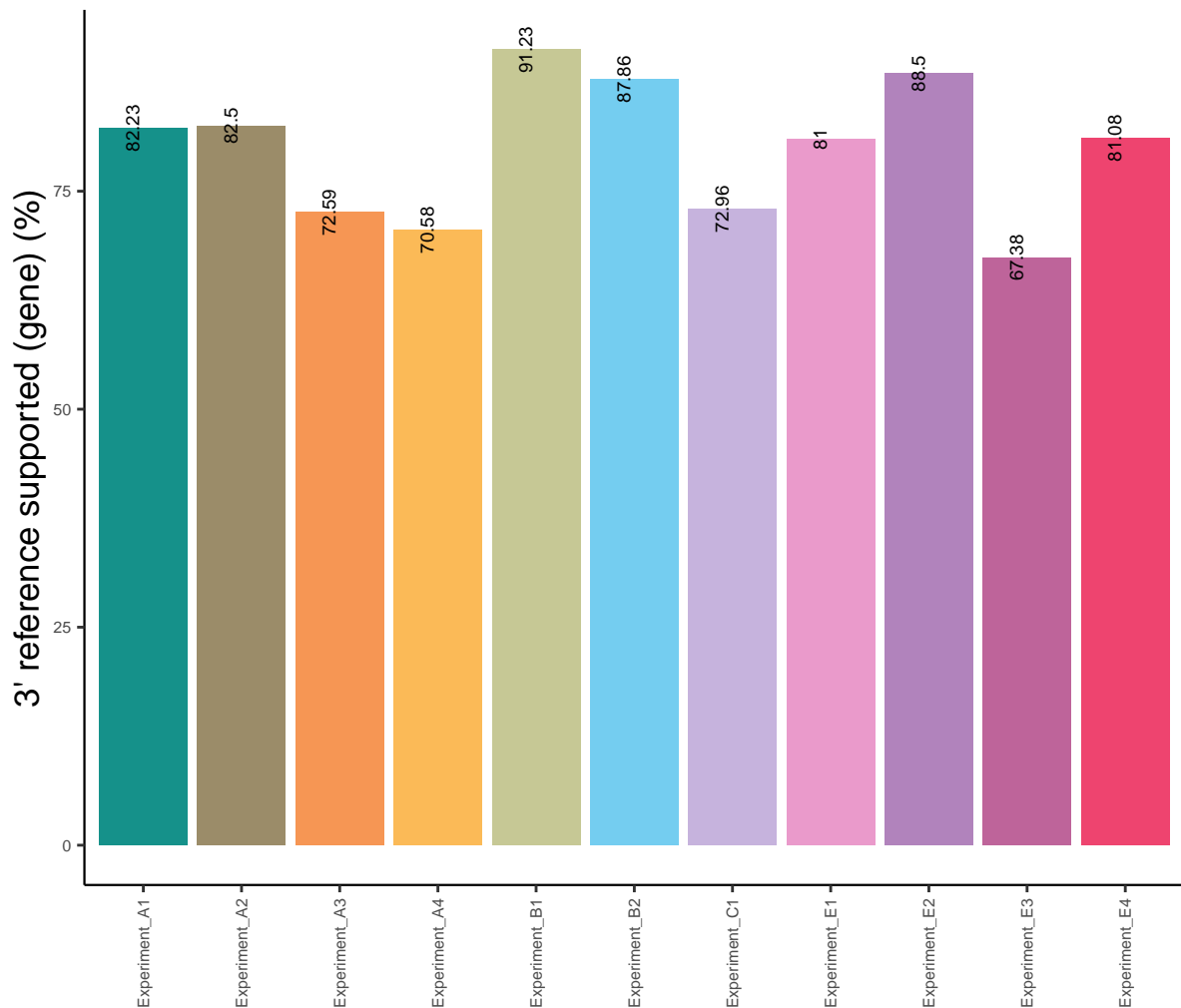
NIC 5' and 3' reference supported (gene) Comparison



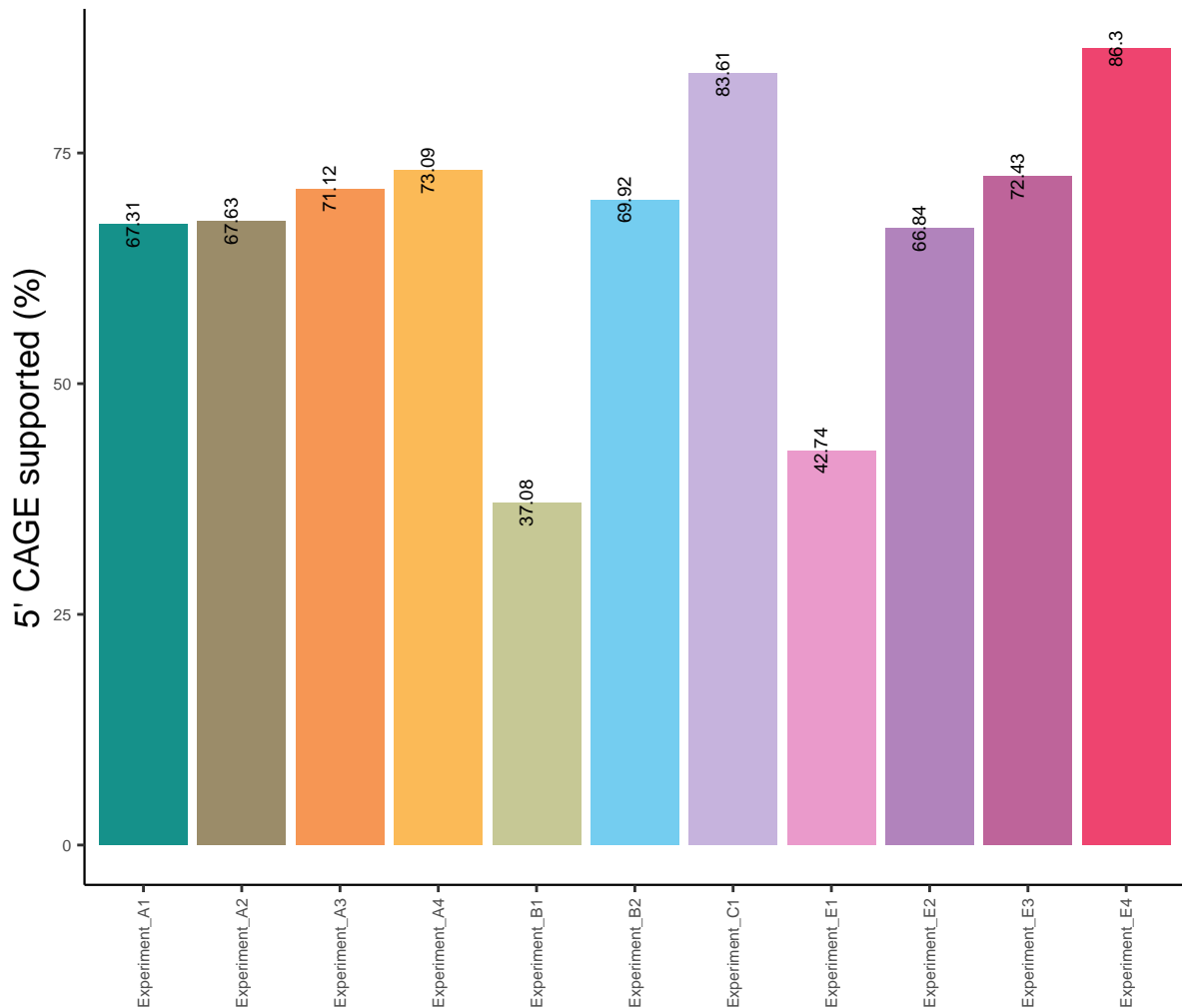
NIC 5' reference supported (gene) Comparison



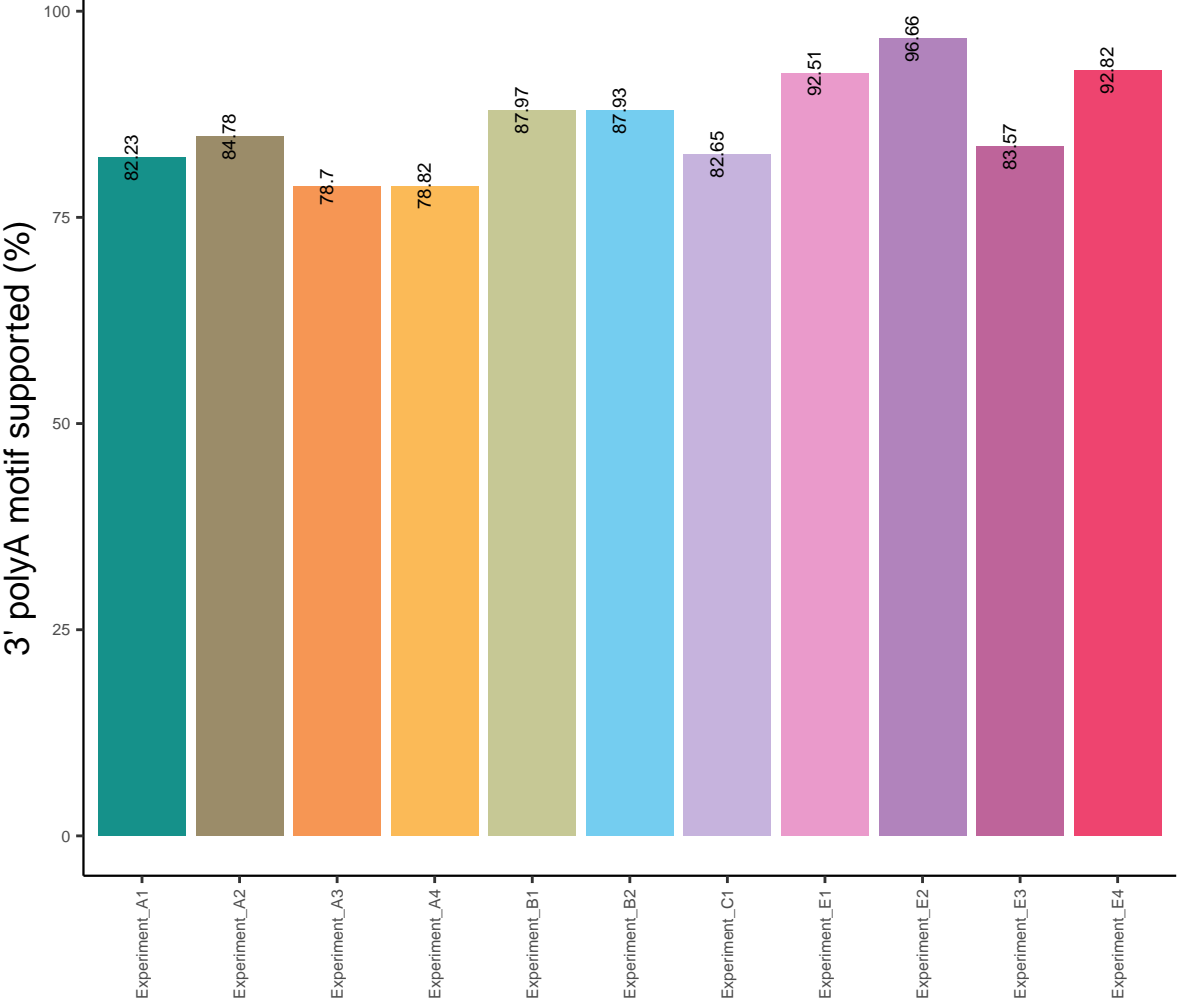
NIC 3' reference supported (gene) Comparison



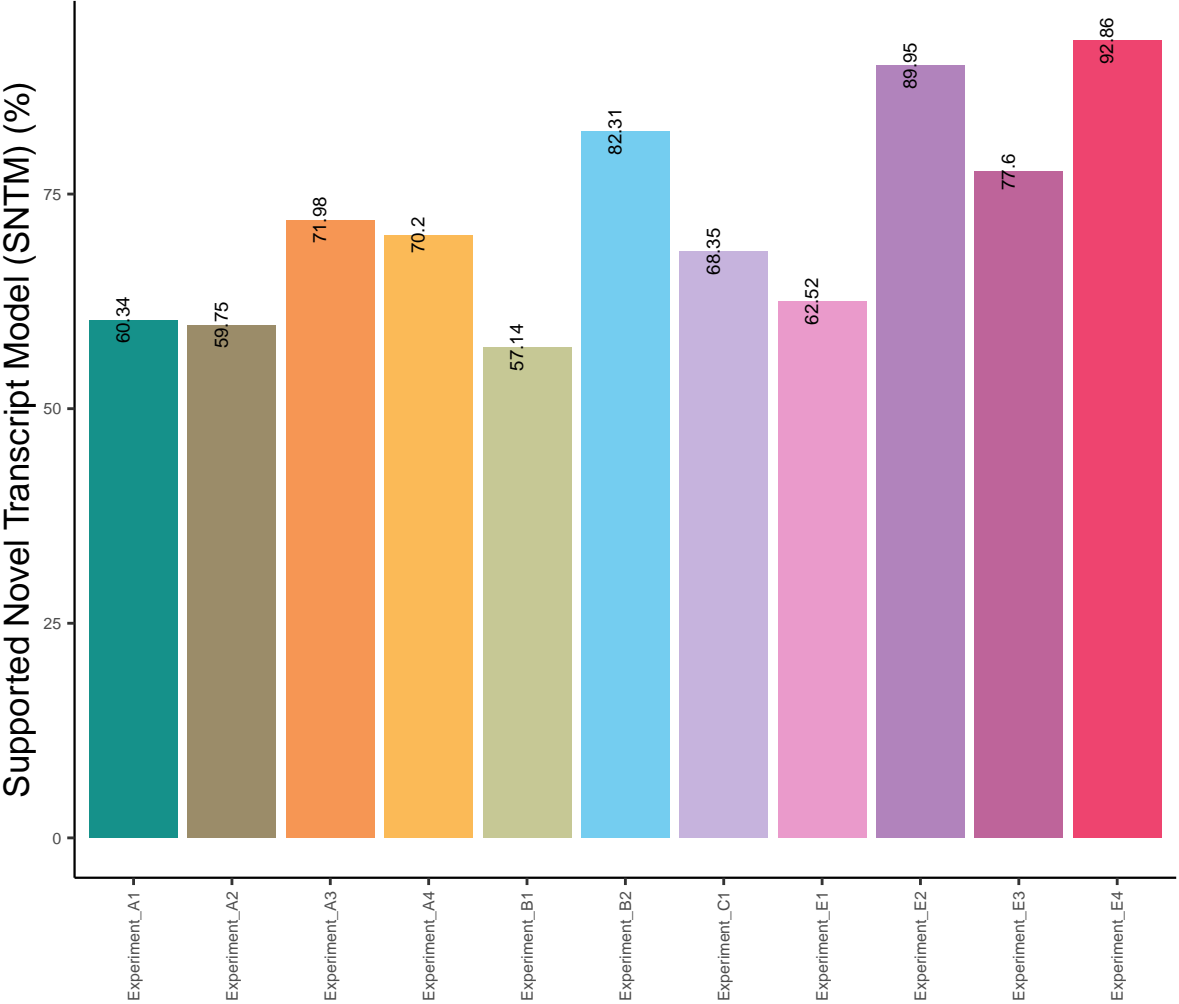
NIC 5' CAGE supported Comparison



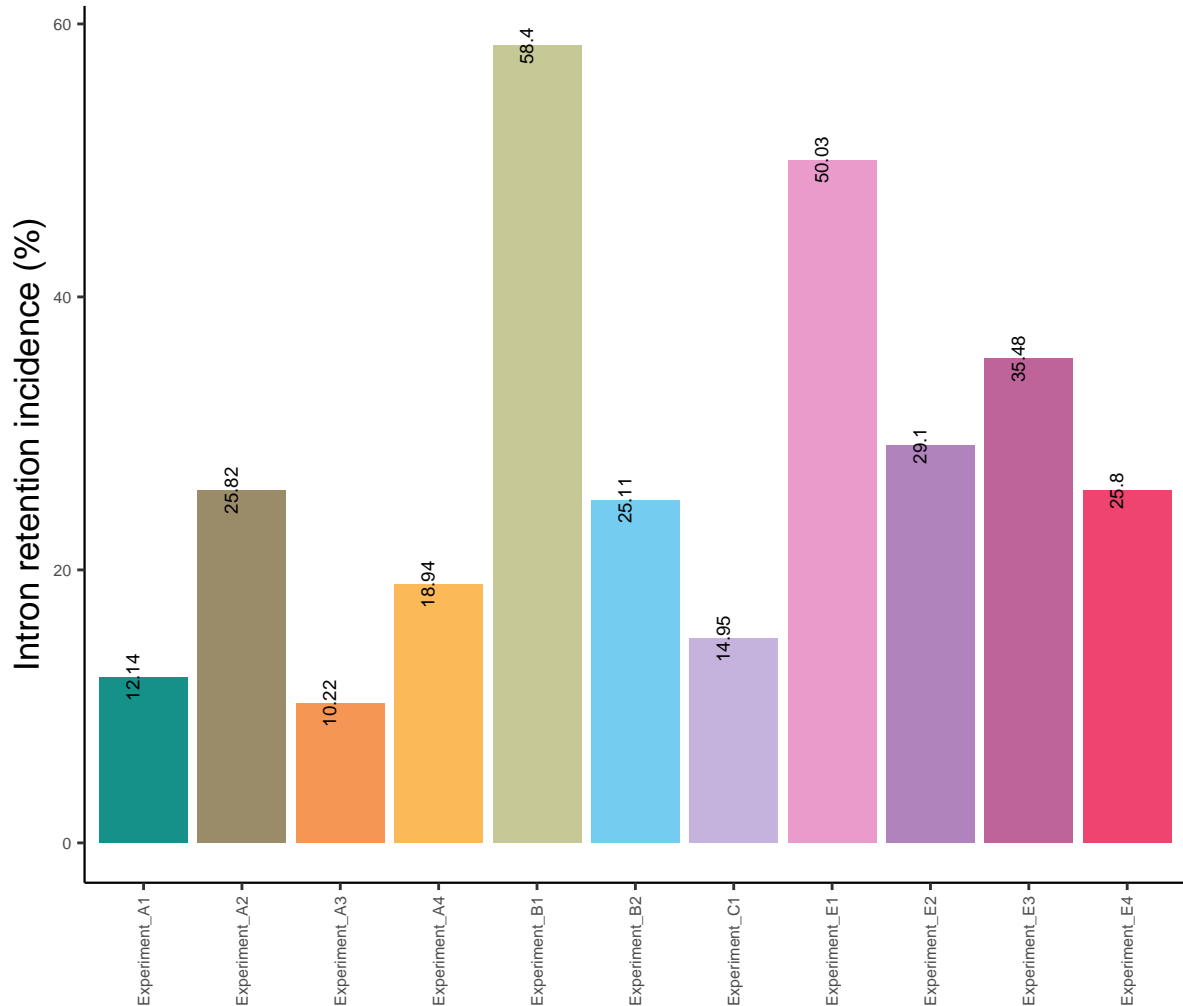
NIC 3' polyA motif supported Comparison



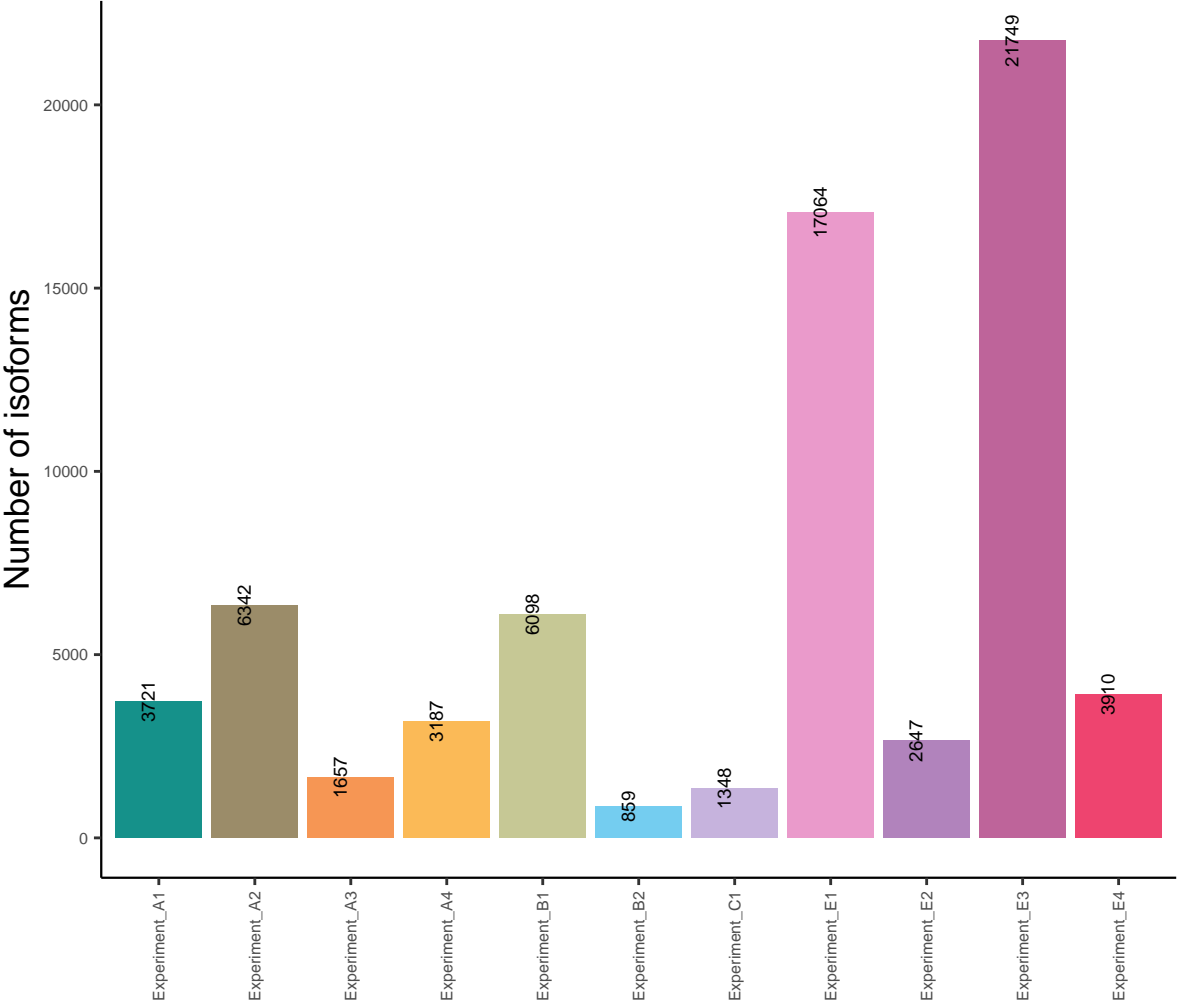
NIC Supported Novel Transcript Model (SNTM) Comparison



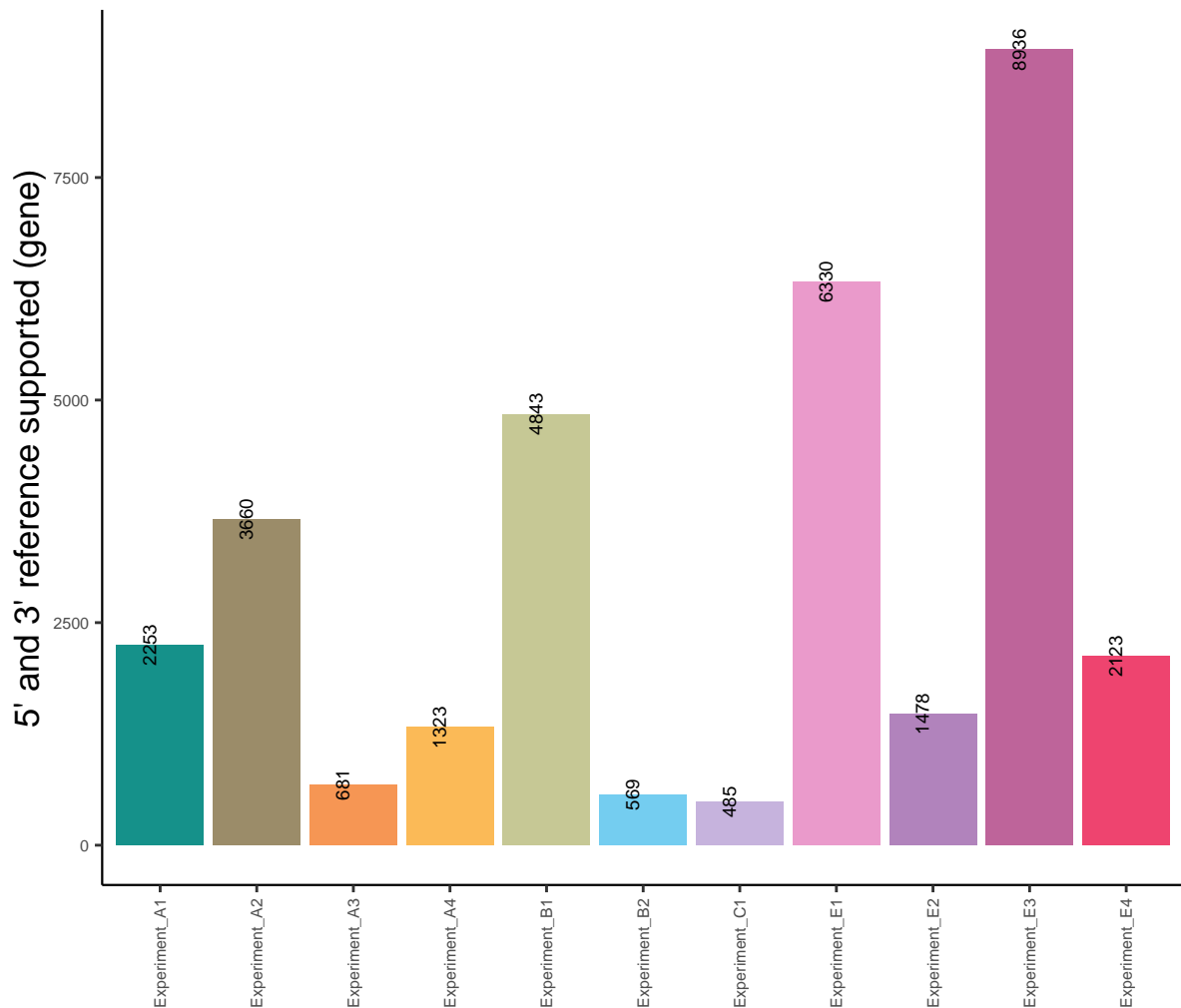
NIC Intron retention incidence Comparison



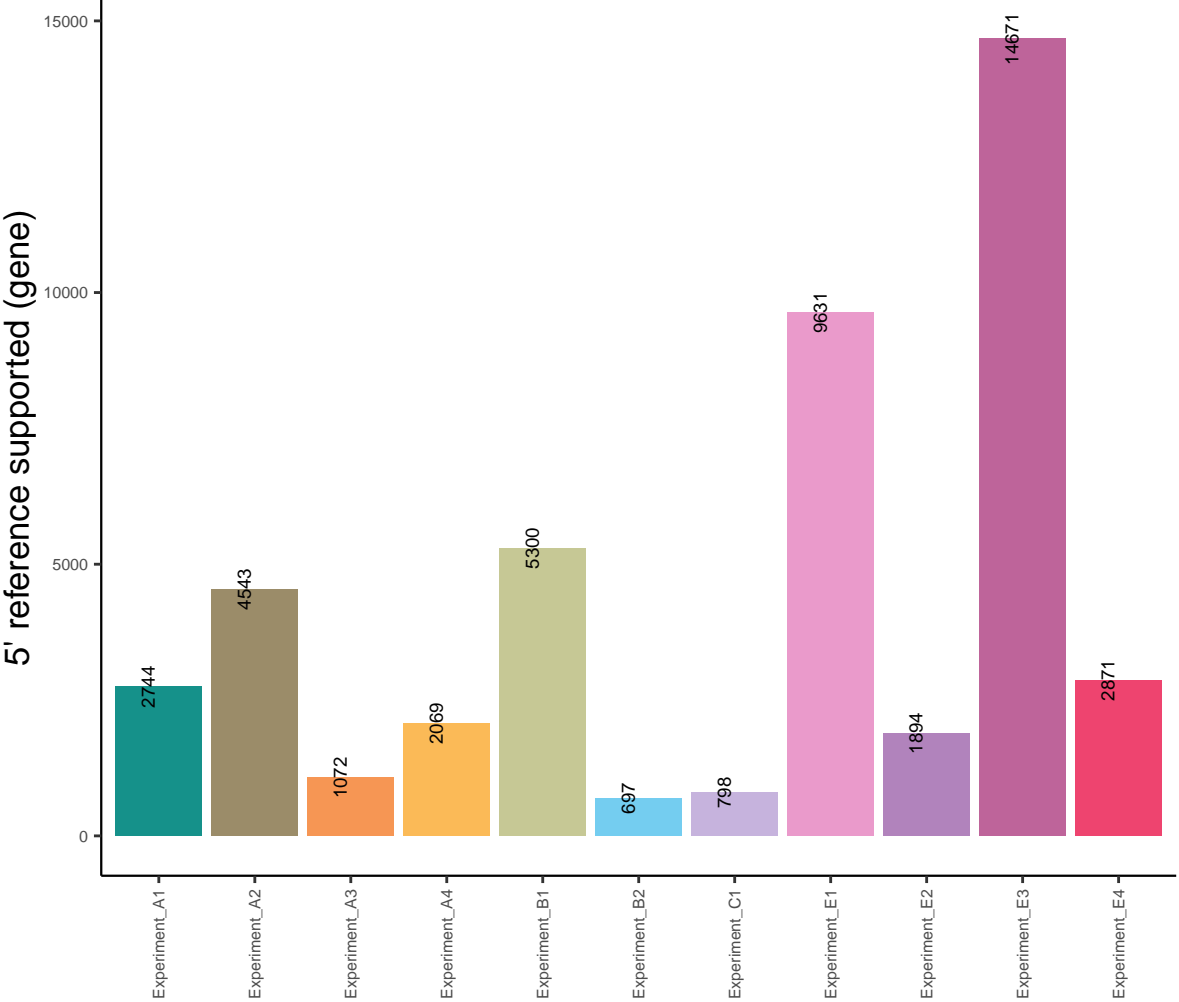
NNC Number of isoforms Comparison



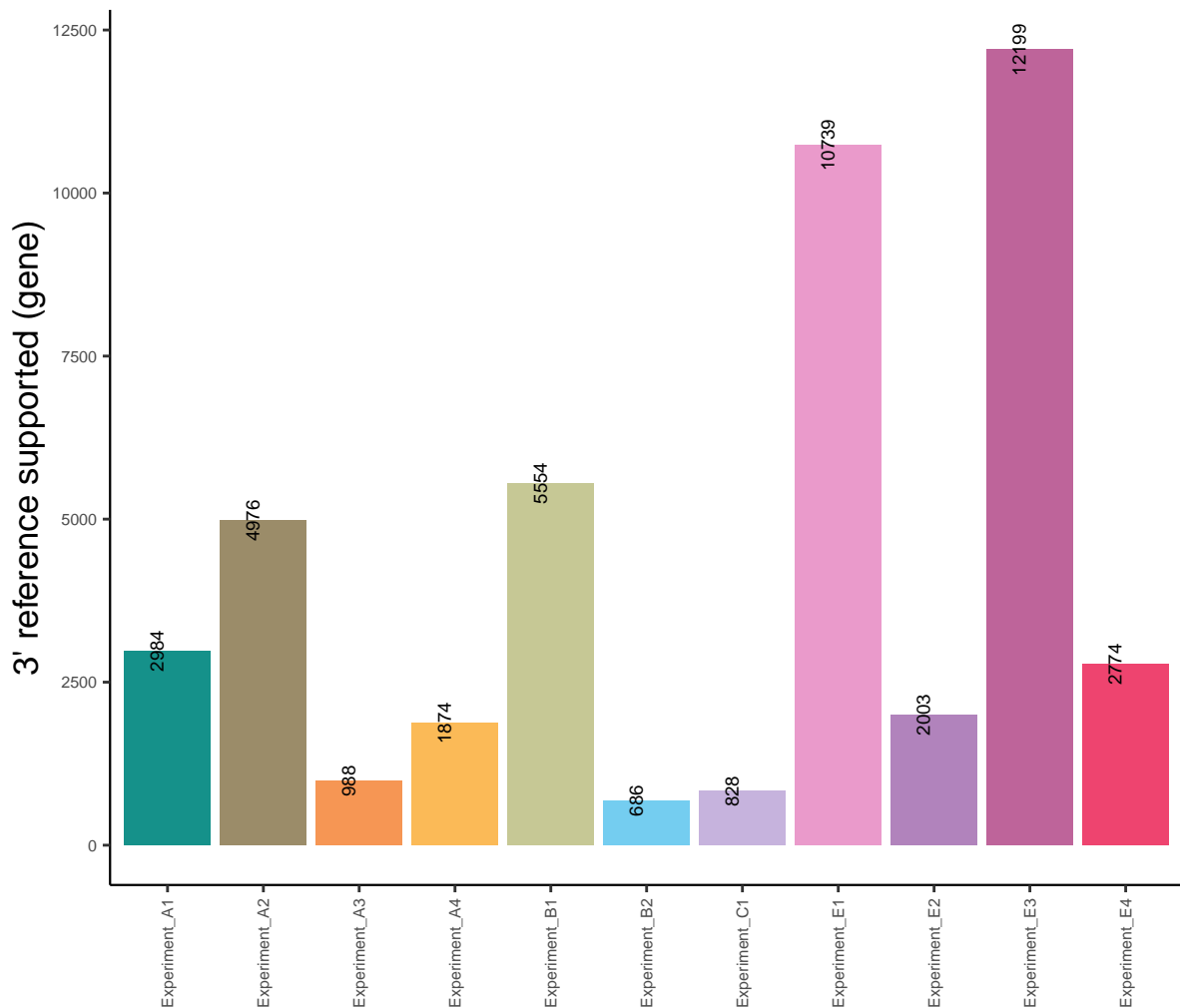
NNC 5' and 3' reference supported (gene) Comparison



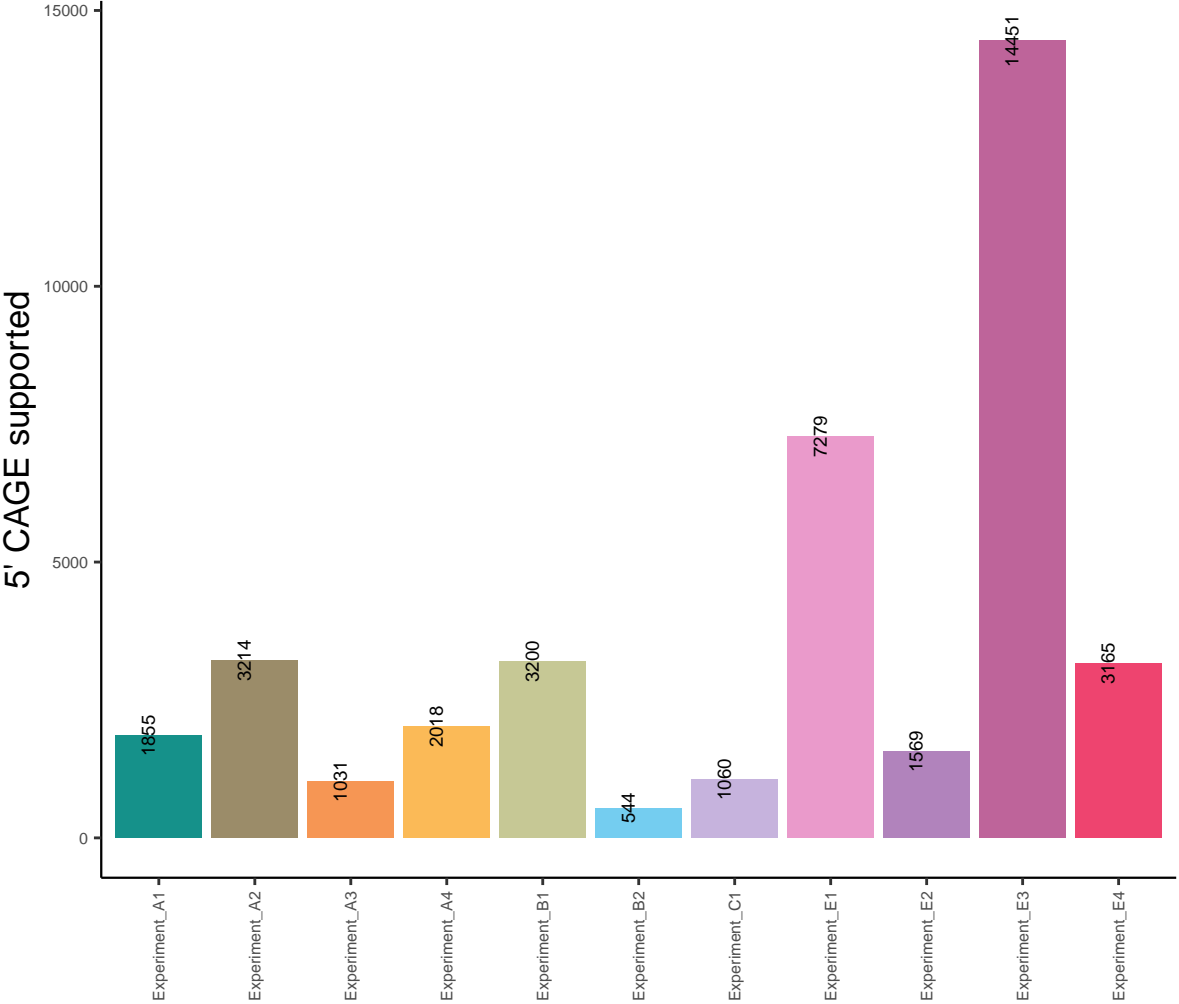
NNC 5' reference supported (gene) Comparison



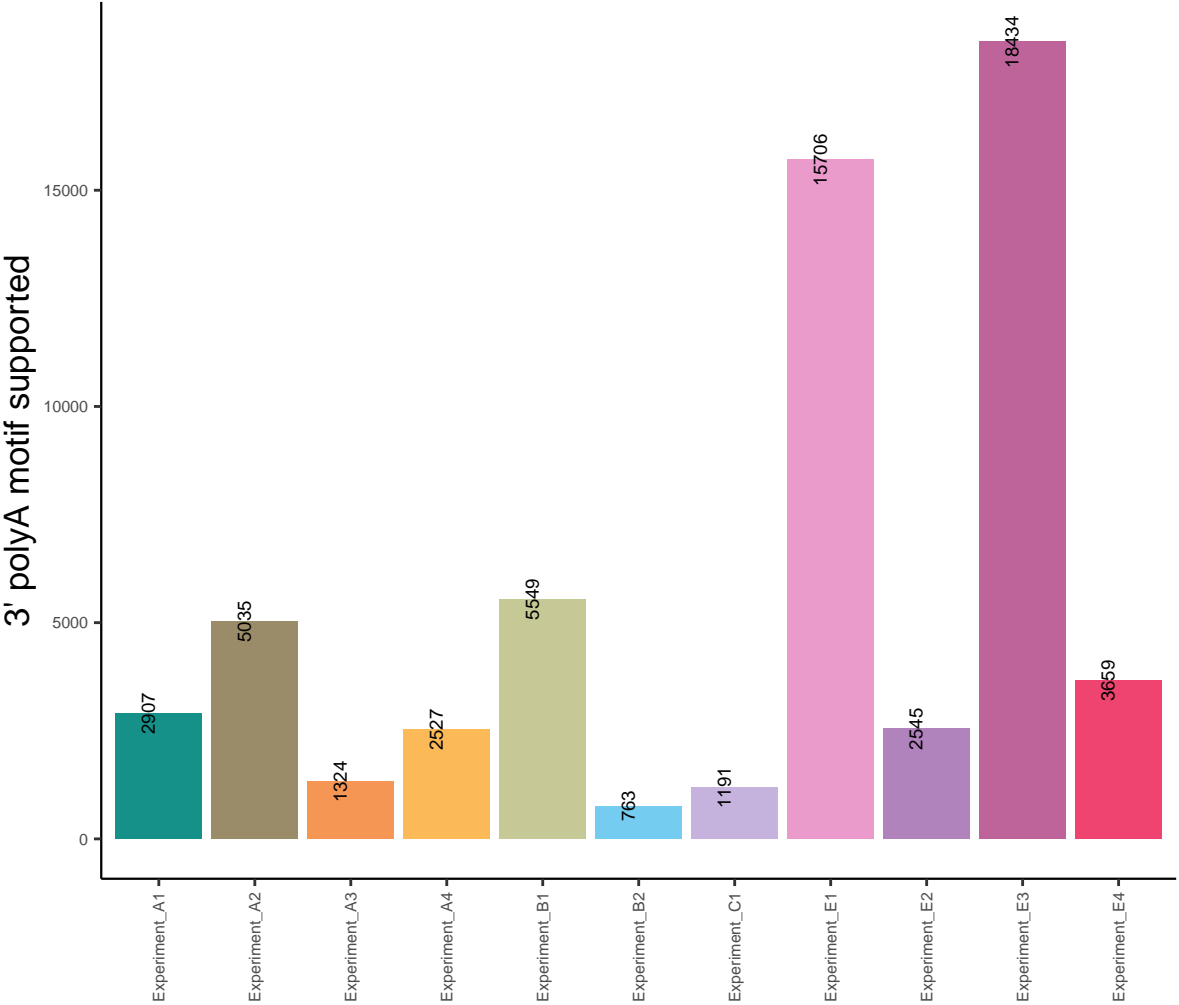
NNC 3' reference supported (gene) Comparison



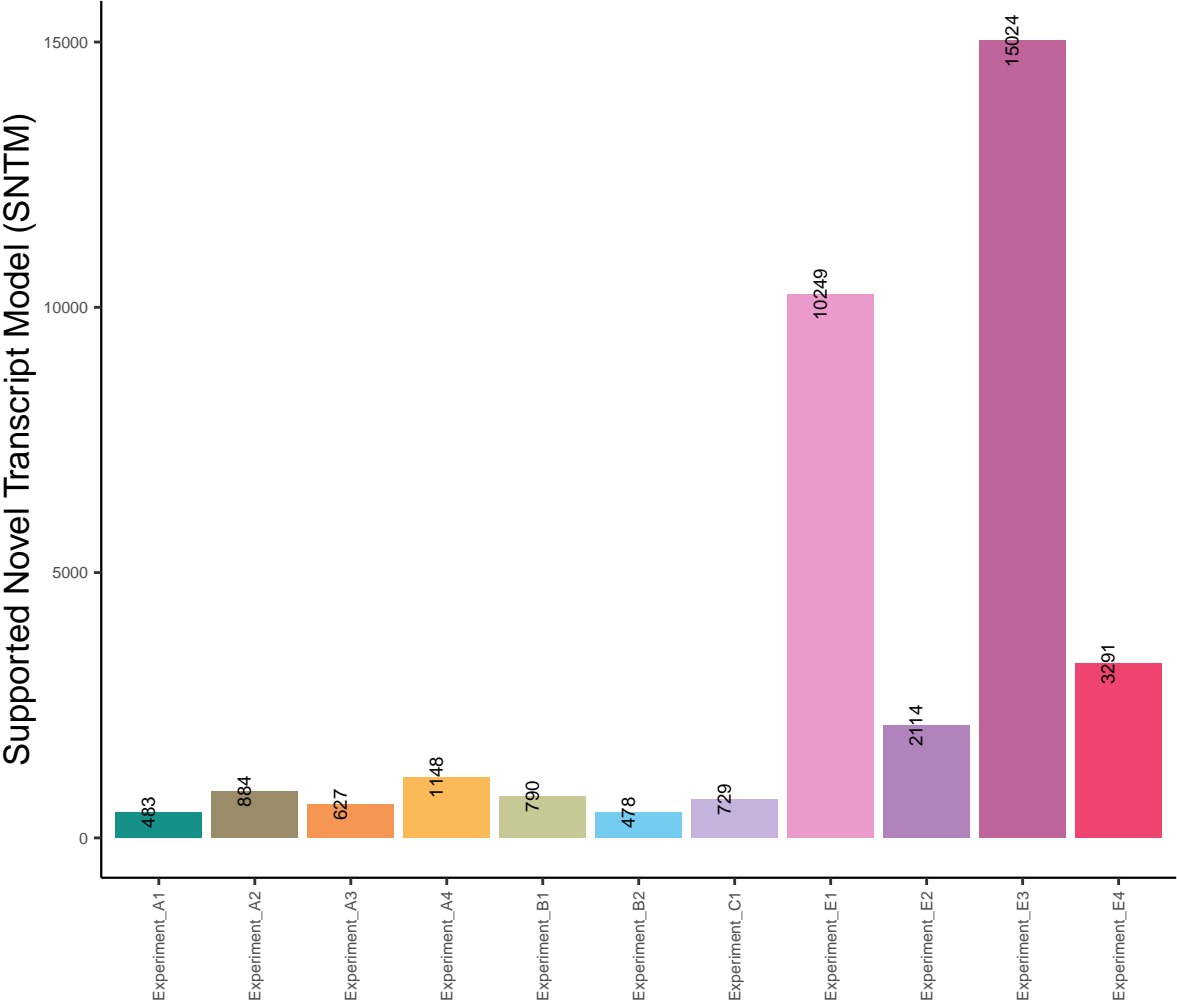
NNC 5' CAGE supported Comparison



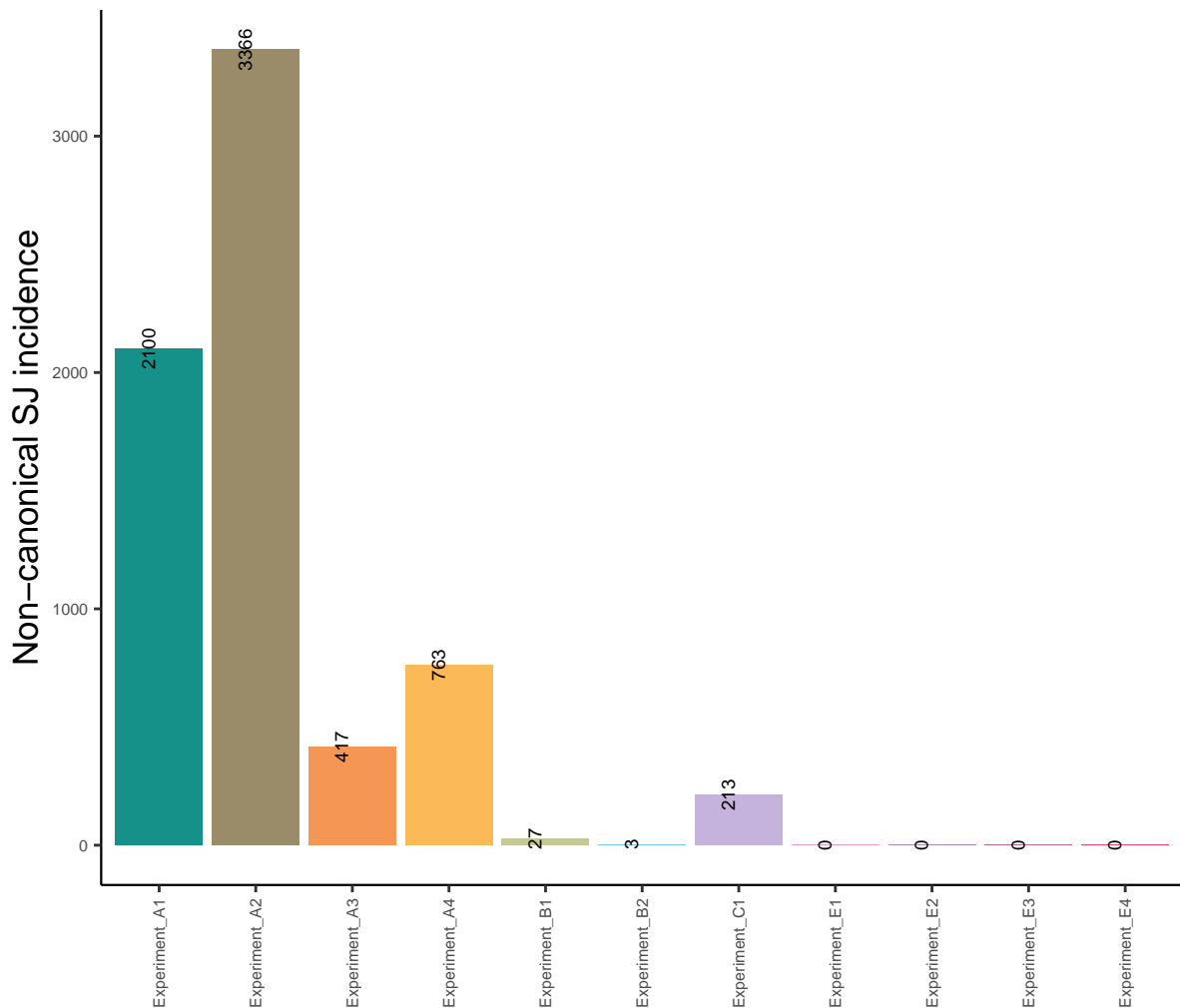
NNC 3' polyA motif supported Comparison



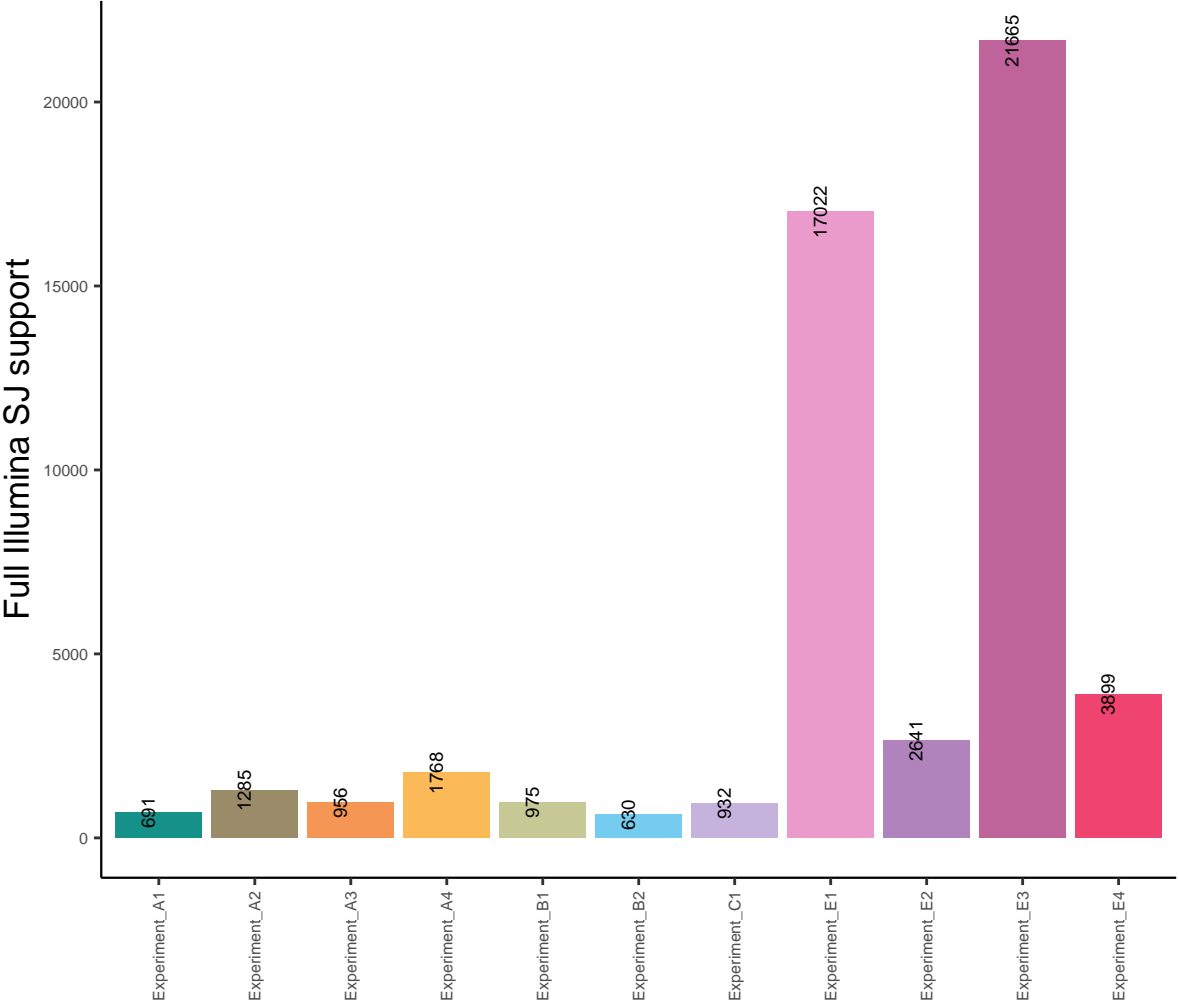
NNC Supported Novel Transcript Model (SNTM) Comparison



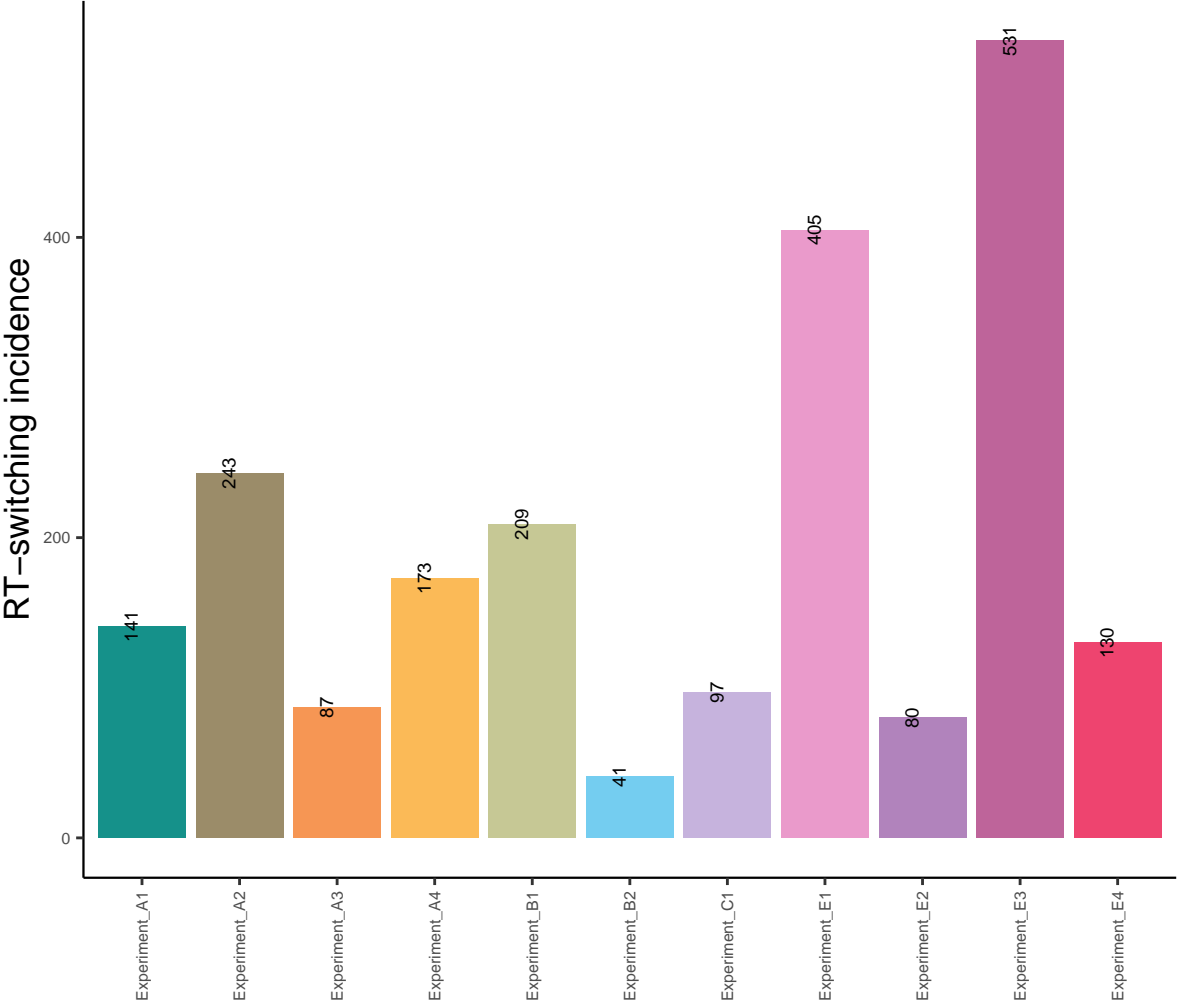
NNC Non-canonical SJ incidence Comparison



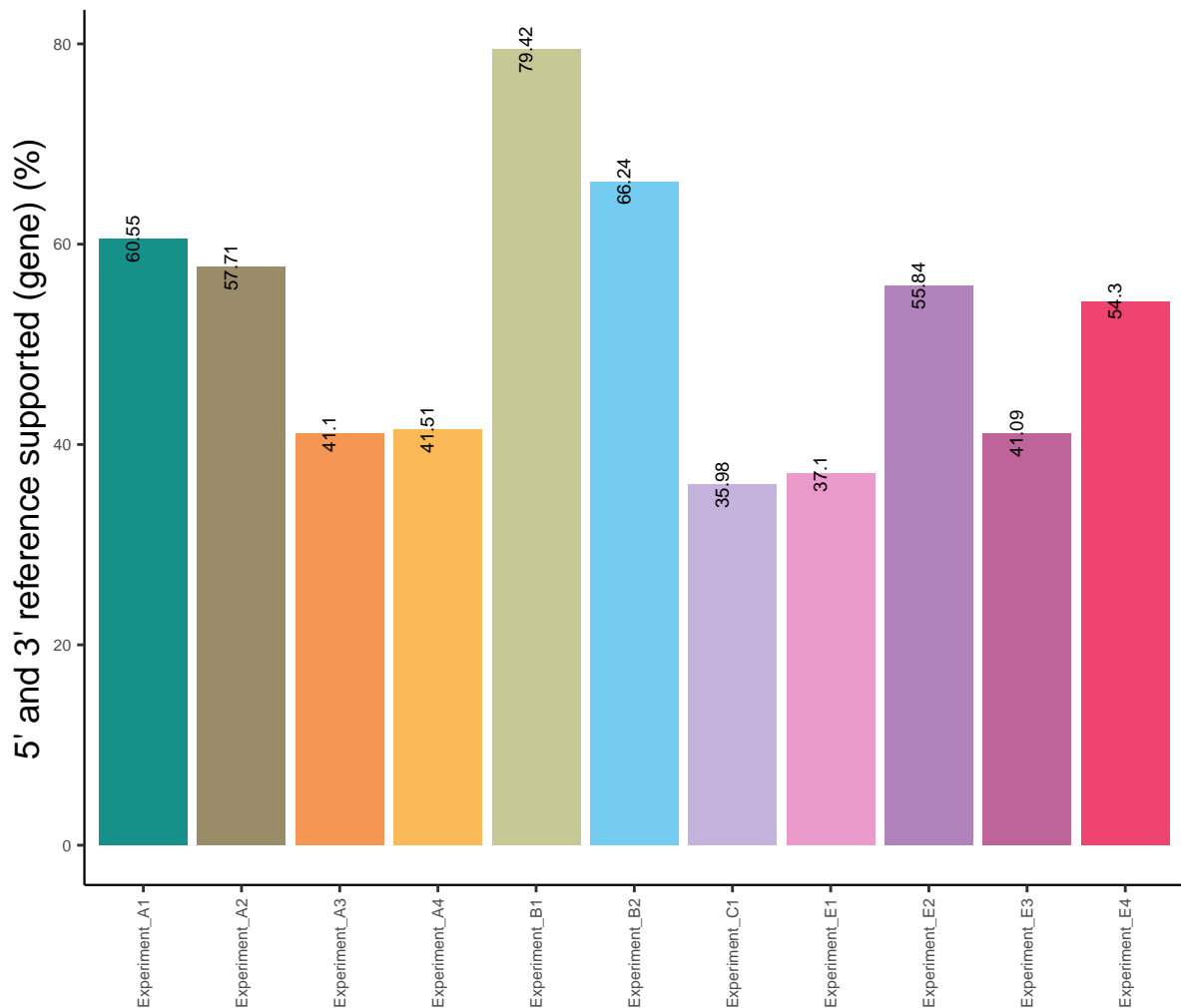
NNC Full Illumina SJ support Comparison



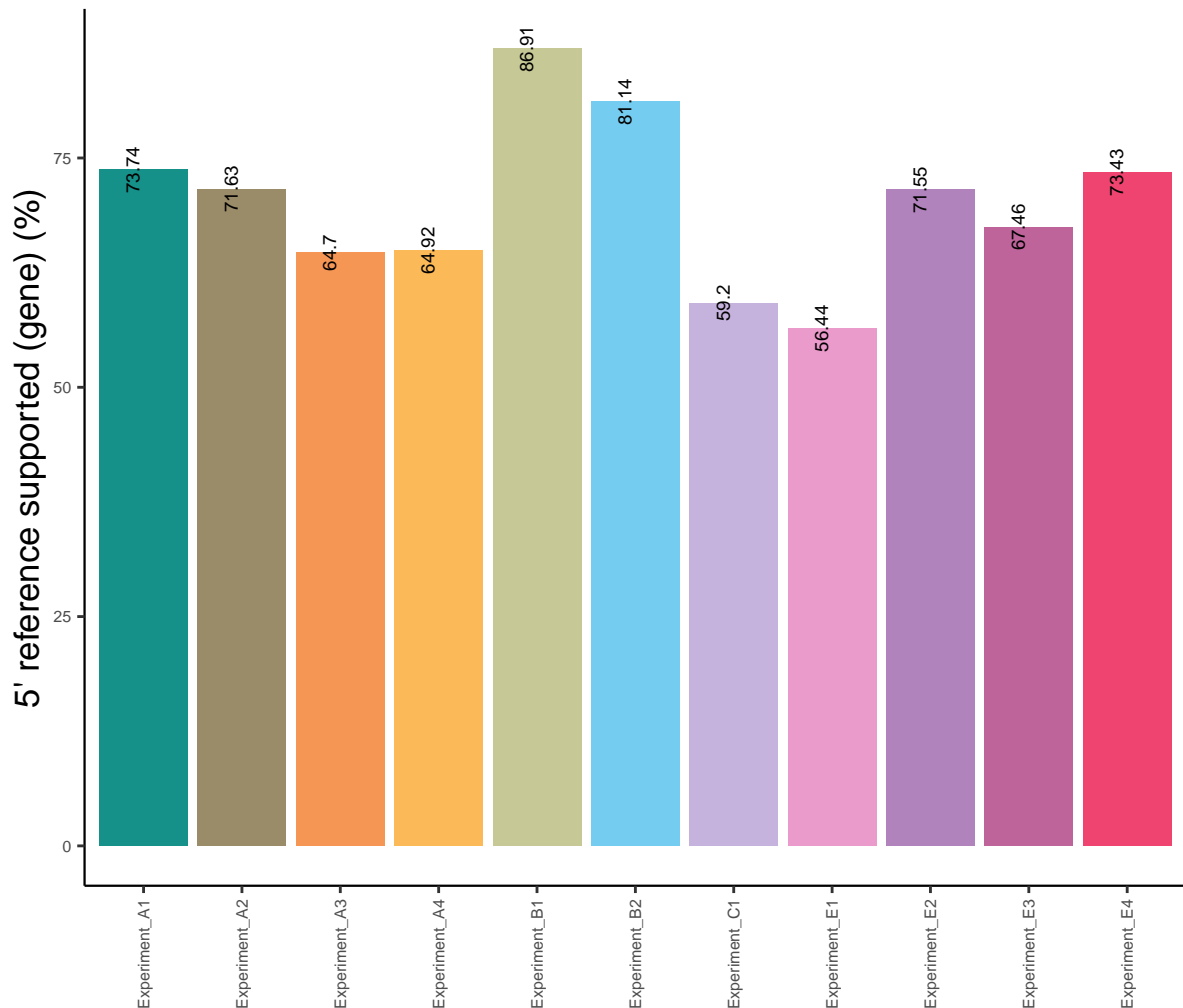
NNC RT-switching incidence Comparison



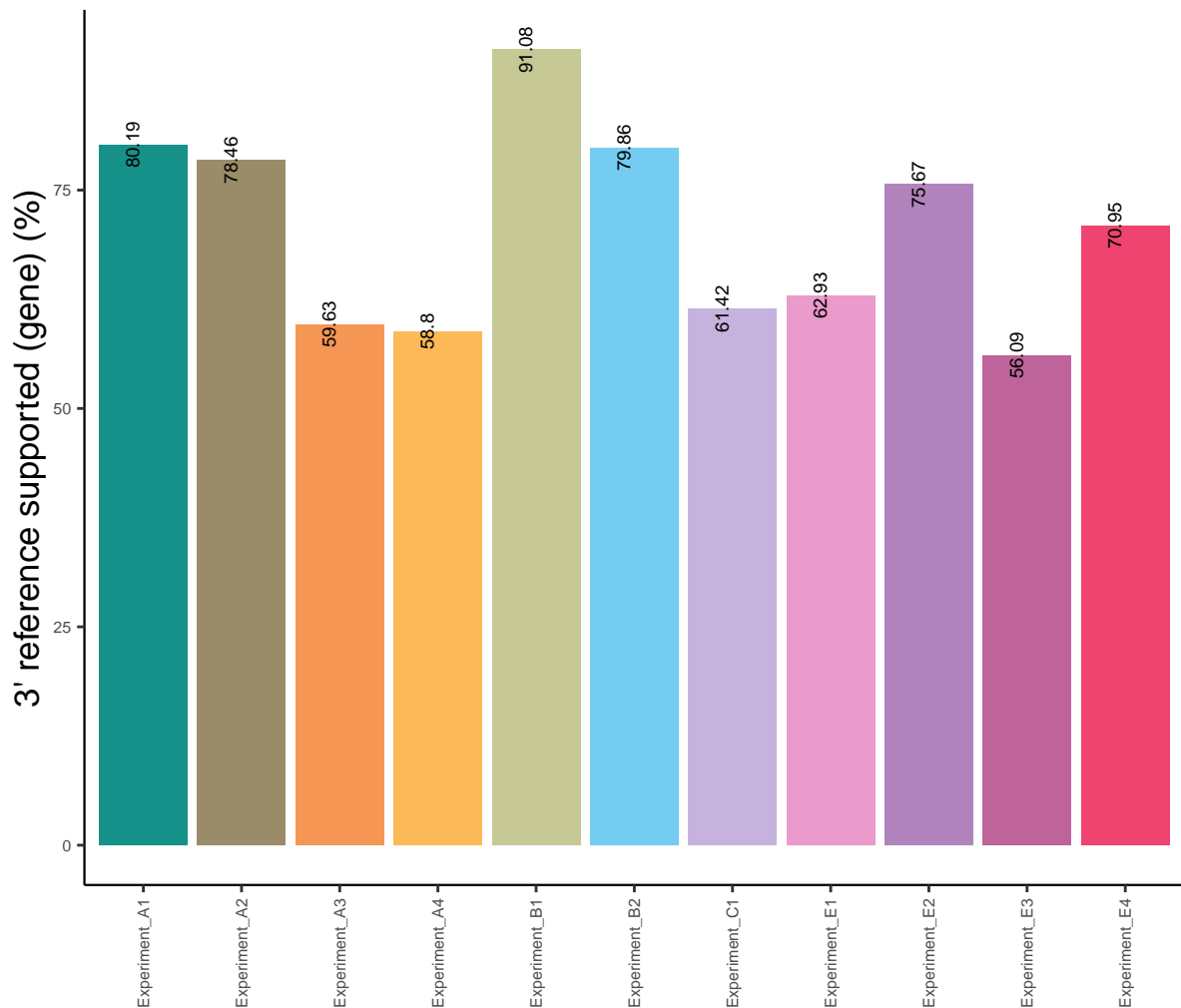
NNC 5' and 3' reference supported (gene) Comparison



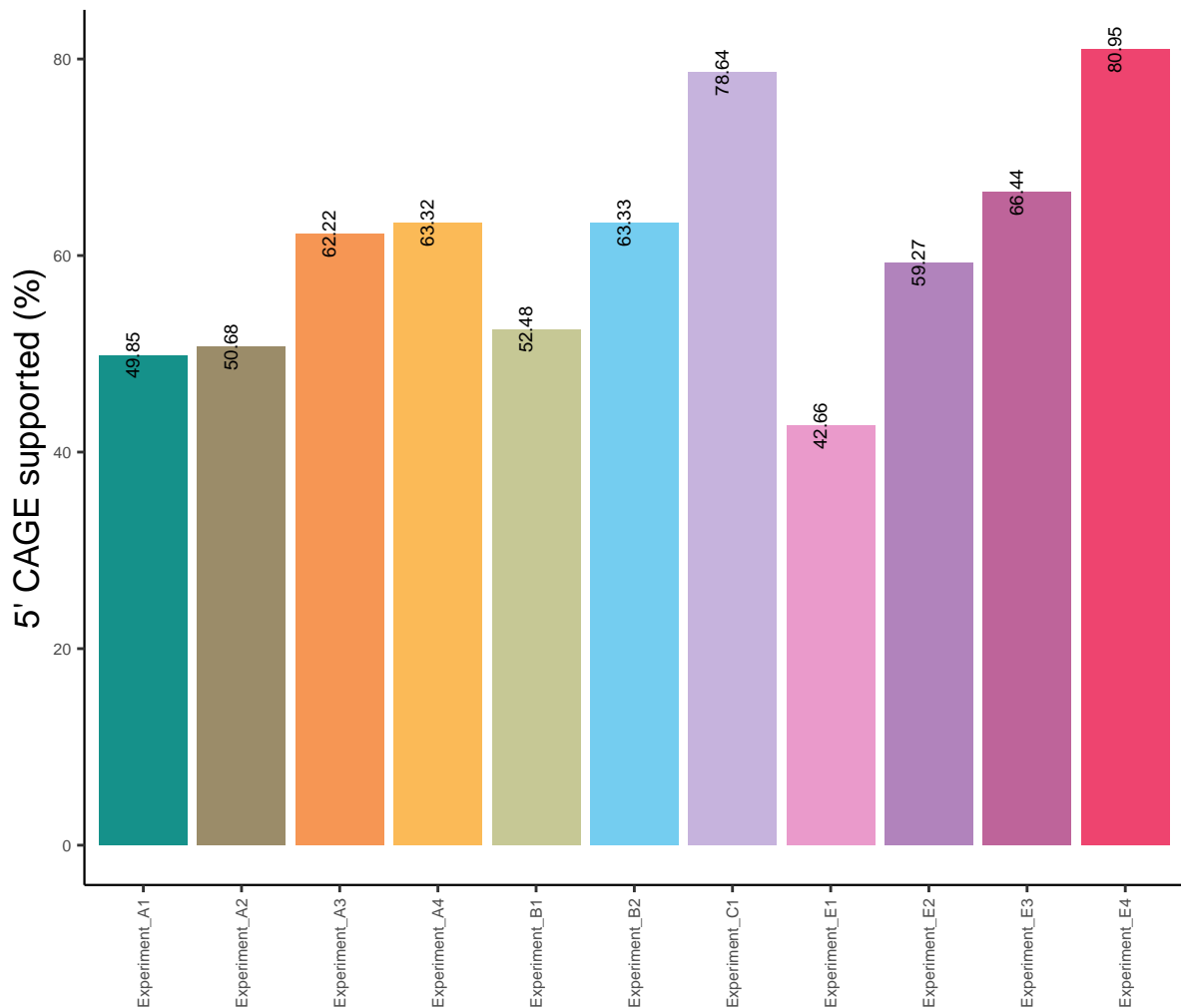
NNC 5' reference supported (gene) Comparison



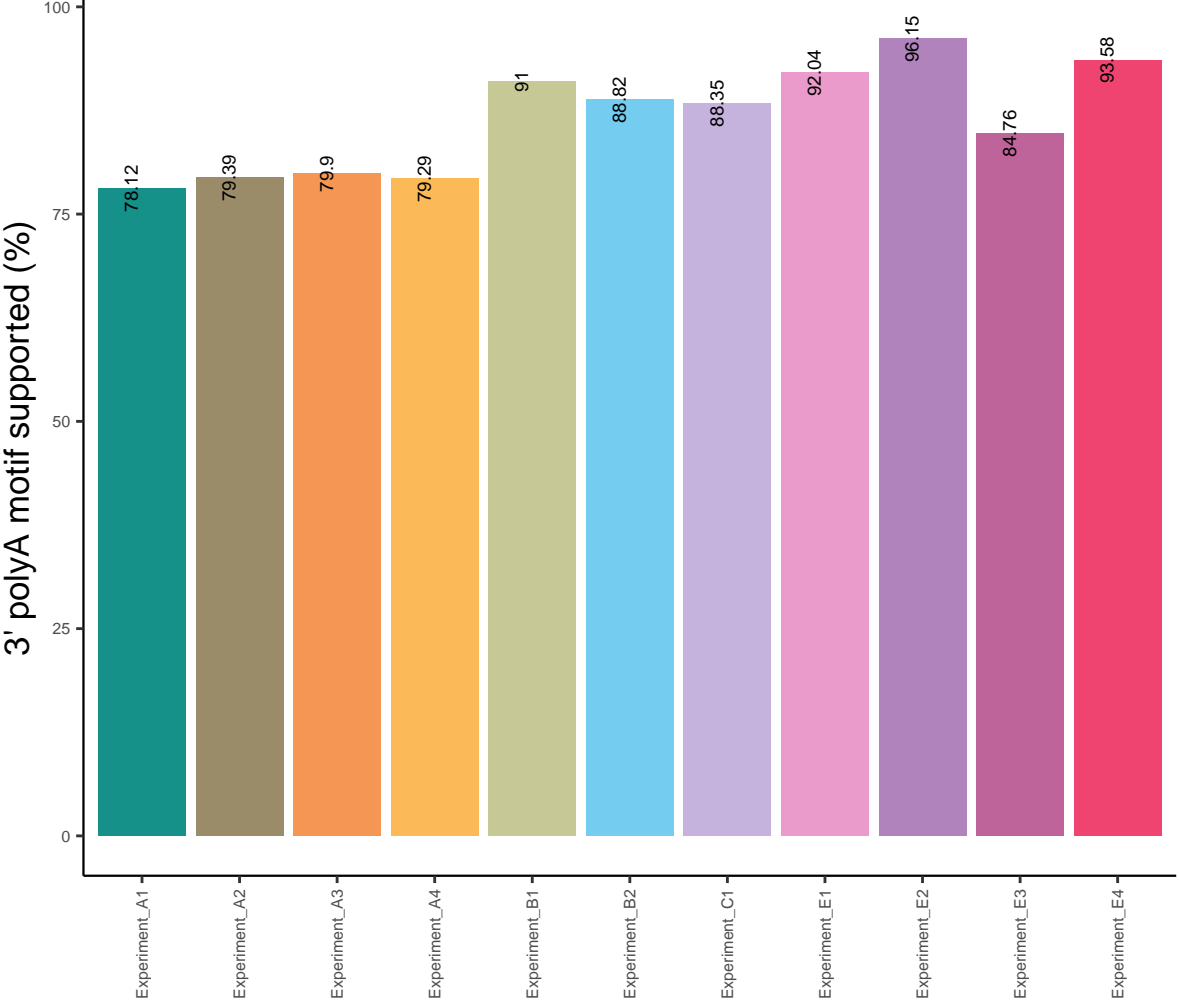
NNC 3' reference supported (gene) Comparison



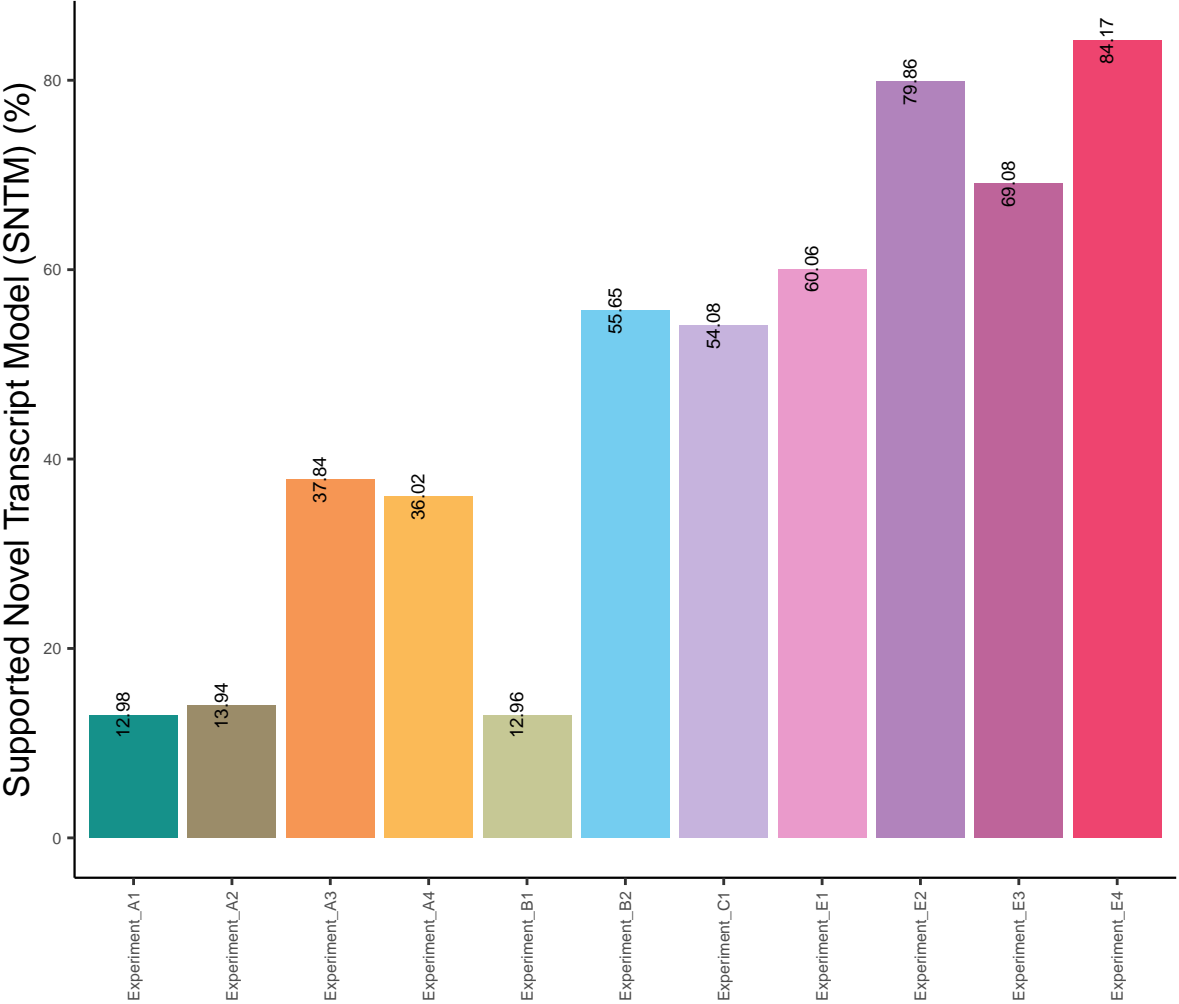
NNC 5' CAGE supported Comparison



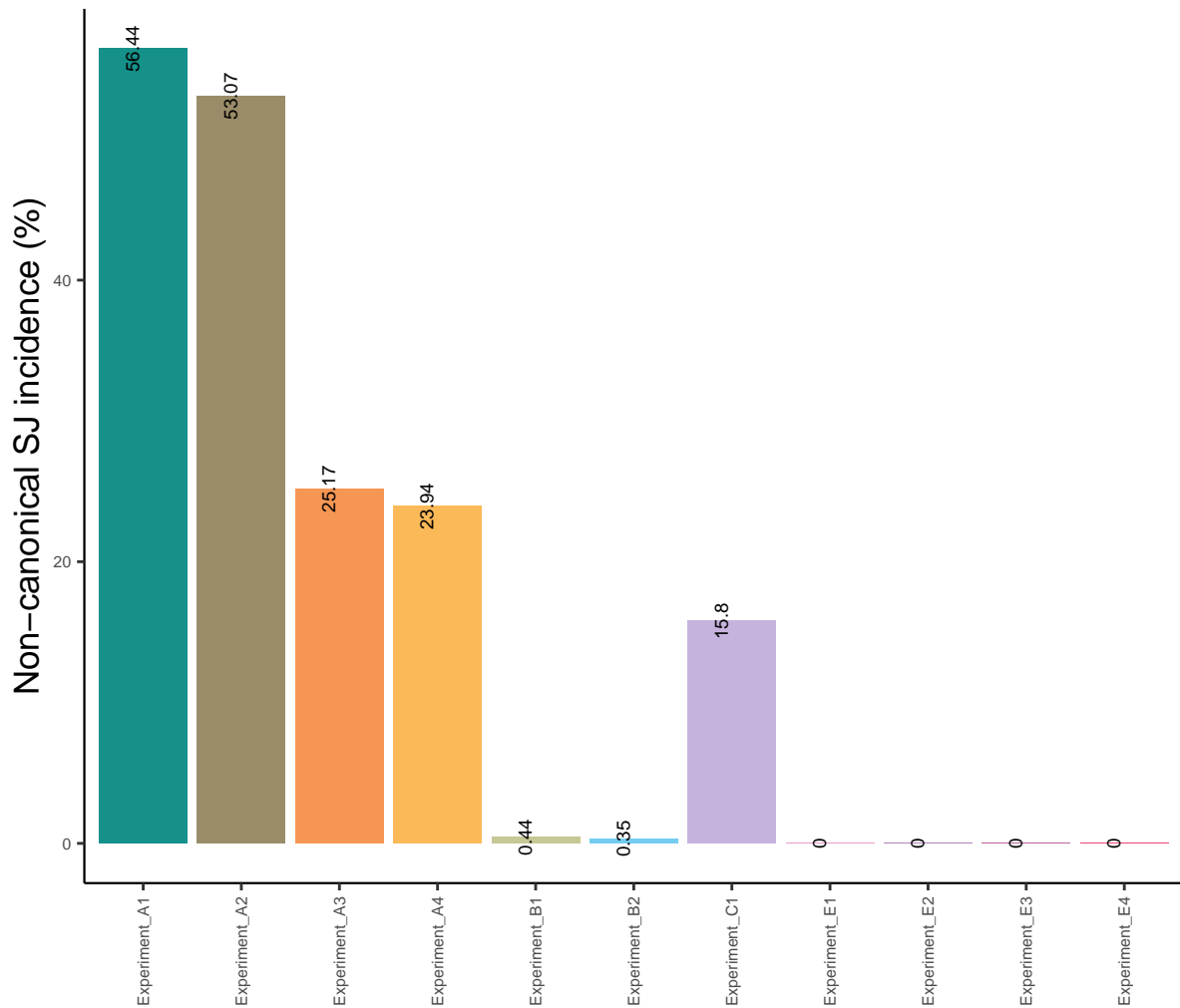
NNC 3' polyA motif supported Comparison



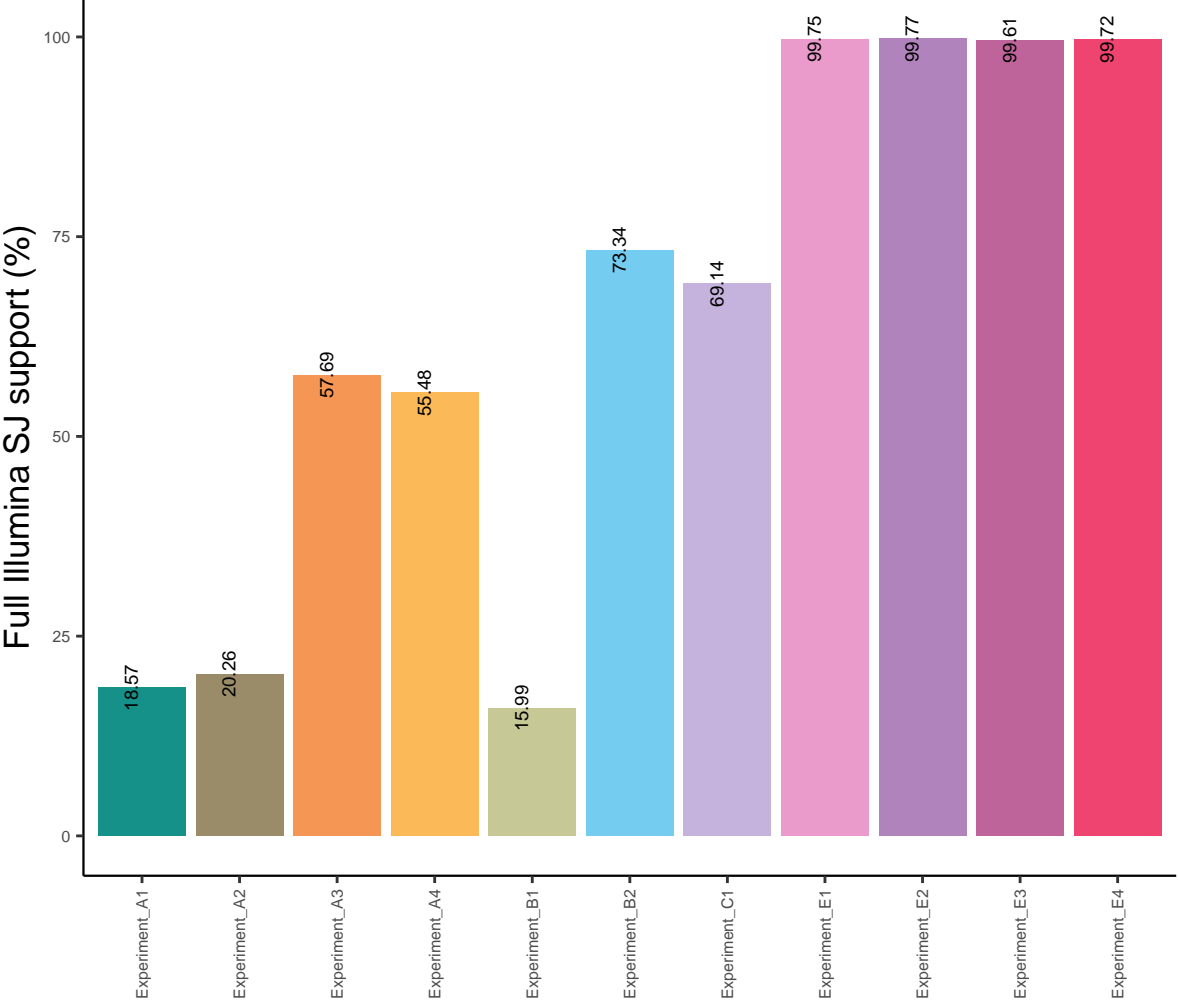
NNC Supported Novel Transcript Model (SNTM) Comparison



NNC Non-canonical SJ incidence Comparison



NNC Full Illumina SJ support Comparison



NNC RT-switching incidence Comparison

