

Comparison of exons grouped into: silenced, enhanced, unregulated

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1 Infos

Visualizations of exon features for different groups of exons. Each exon occurs in exactly one gene, but might occur in several transcripts of that gene. Hence, for some features like the exon length, there is exactly one value for each exon. For other features, e.g., length of the up-stream exon(s), which could be different in different transcripts, there might be several values for each exon. Consequently, in the latter cases, the median of these value gets reported.

2 Warning: Please read this note carefully

Please keep in mind that some features might affect other features. Especially: all branch-point features get extracted from sub-sequences of introns, by standard the last 150 nt at the 3' end of each intron (if you haven't changed this) always neglecting the first 20 nt at their 5' end. If introns of one set are especially short, i.e., many are shorter than these 150 nt, then the shorter intron length might affect branch-point features. For example, there might be less branch points found in shorter introns or their distance to the 3' intron ends might be generally shorter simply because of their shorter intron length.

3 Notes for publishing results

When publishing results wrt. splice site strengths which you determined for your data using matt, please cite: *Maximum entropy modeling of short sequence motifs with applications to RNA splicing signals*, Yeo et al., 2003, DOI: 10.1089/1066527041410418

When publishing results wrt. branch point features which you determined for your data with matt, please cite: *Genome-wide association between branch point properties and alternative splicing*, Corvelo et al., 2010, DOI: 10.1371/journal.pcbi.1001016

When publishing results with respect to the binding strength of the human Sf1 splicing factor, you might refer to where the Sf1 binding motif comes from: *Analysis of in situ pre-mRNA targets of human splicing factor SF1 reveals a function in alternative splicing*, Margherita Corioni, Nicolas Antih, Goranka Tanackovic, Mihaela Zavolan, and Angela Kramer, 2011, DOI: 10.1093/nar/gkq1042

The Sf1 binding motif is described in supplement, page 13, table S2: Weight matrix of the binding specificity of SF1.

4 Data sets

Input file:

`exons.tab`

Selection criteria for defining exons groups:

`silenced` : having value `silenced` in column `GROUP`

`enhanced` : having value `enhanced` in column `GROUP`

`unregulated` : having value `unregulated` in column `GROUP`

Exon duplicates removal: yes

Numbers of exons per group before / after neglecting exons which were not found in GTF file (gene annotation). For the comparisons only exons which were found in the gene annotation are used. These numbers might change slightly for each feature if NAs occur.

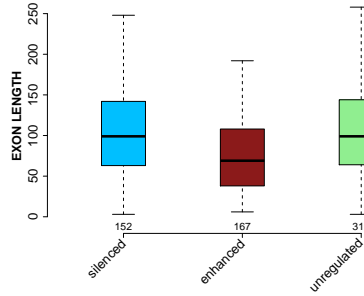
`silenced`: 152 / 152

`enhanced`: 167 / 167

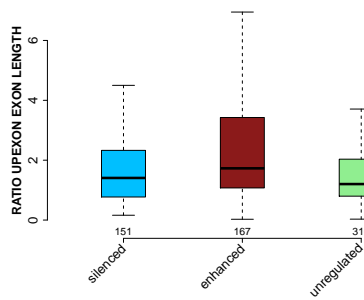
`unregulated`: 322 / 319

5 Overview: Features with statistical significant differences (p-val ≤ 0.05)

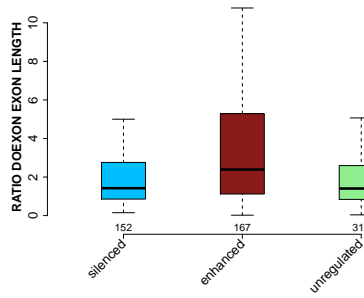
EXON LENGTH



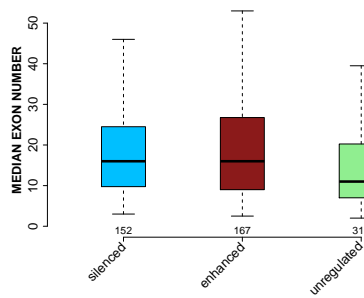
RATIO UPEXON EXON LENGTH



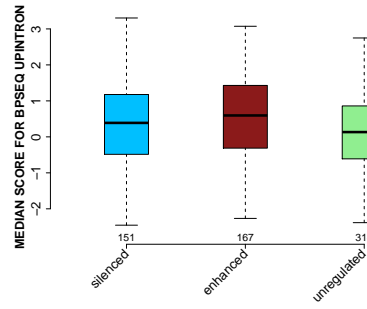
RATIO DOEXON EXON LENGTH



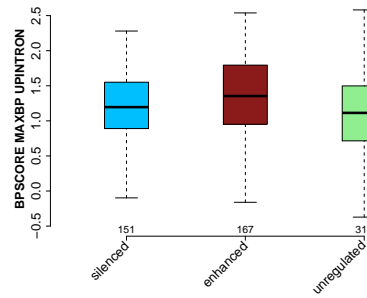
MEDIAN EXON NUMBER



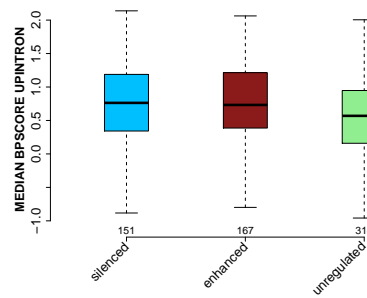
MEDIAN SCORE FOR BPSEQ UPINTRON



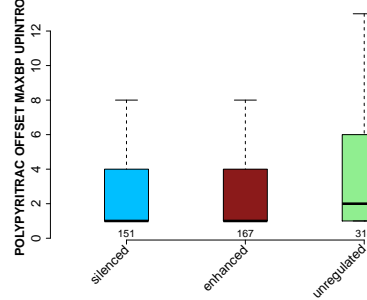
BPSCORE MAXBP UPINTRON



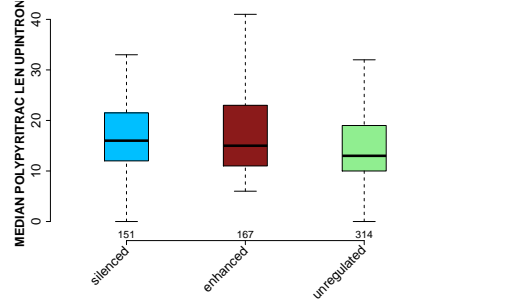
MEDIAN BPSCORE UPINTRON



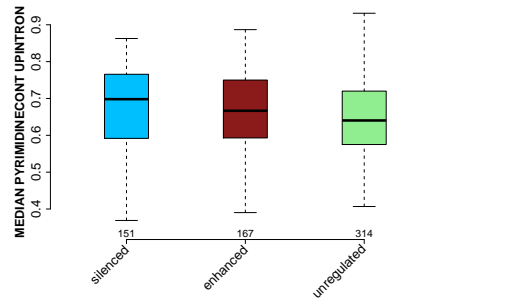
POLYPYRITRAC OFFSET MAXBP UPINTRON



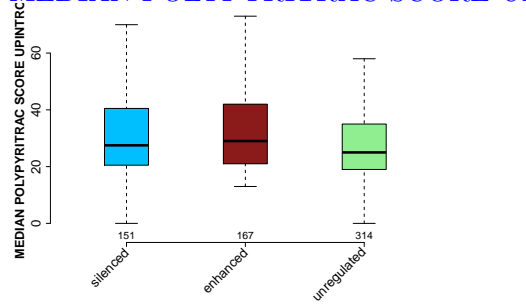
MEDIAN POLYPYRITRAC LEN UPINTRON



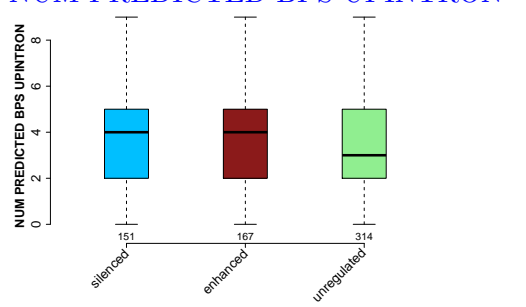
MEDIAN PYRIMIDINECONT UPINTRON



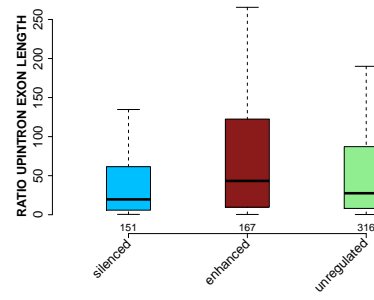
MEDIAN POLYPYRITRAC SCORE UPINTRON



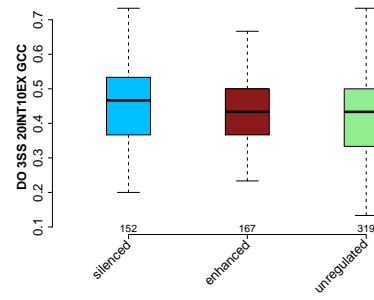
NUM PREDICTED BPS UPINTRON



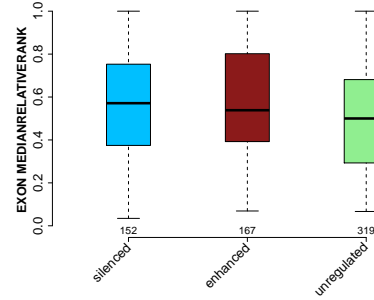
RATIO UPINTRON EXON LENGTH



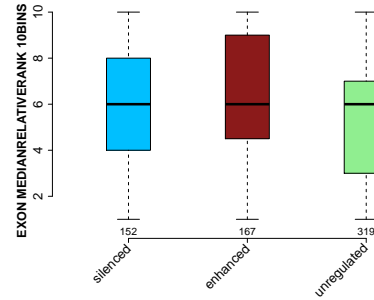
DO 3SS 20INT10EX GCC



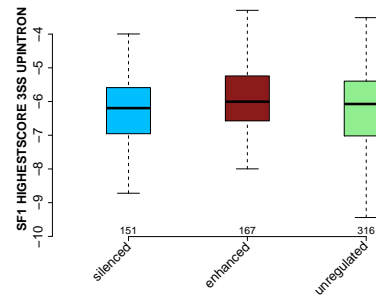
EXON MEDIANRELATIVERANK



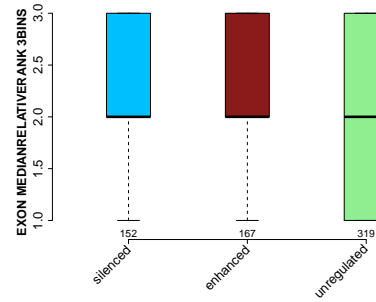
EXON MEDIANRELATIVERANK 10BINS



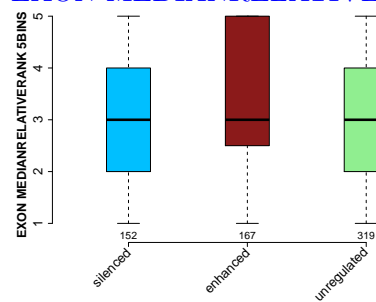
SF1 HIGHESTSCORE 3SS UPINTRON



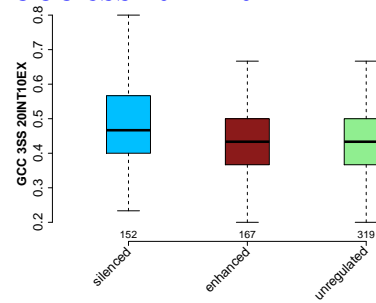
EXON MEDIANRELATIVERANK 3BINS



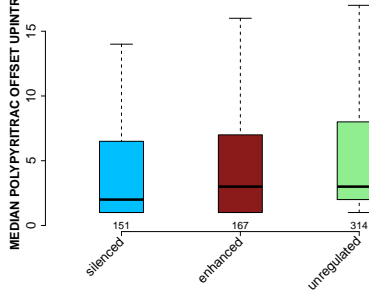
EXON MEDIANRELATIVERANK 5BINS



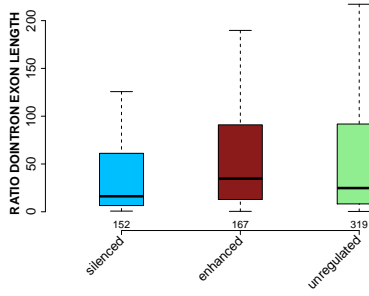
GCC 3SS 20INT10EX



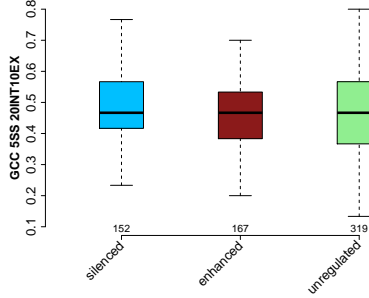
MEDIAN POLYPYRITRAC OFFSET UPINTRON



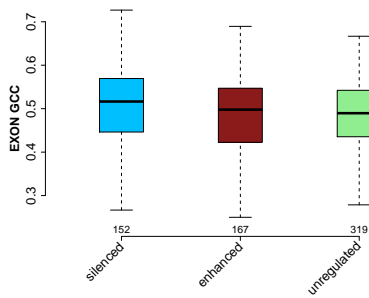
RATIO DOWINTRON EXON LENGTH



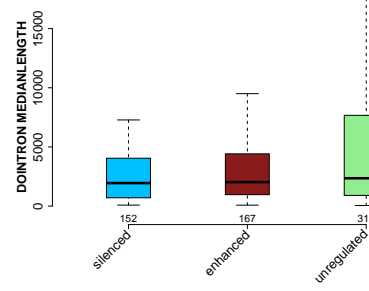
GCC 5SS 20INT10EX



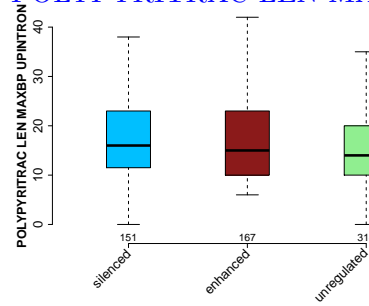
EXON GCC



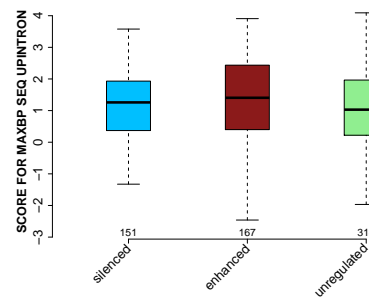
DOINTRON MEDIANLENGTH



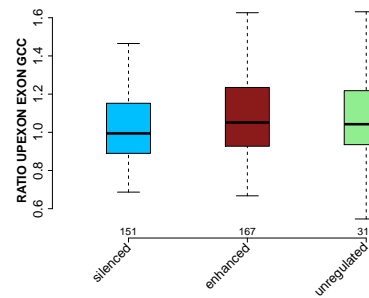
POLYPYRITRAC LEN MAXBP UPINTRON



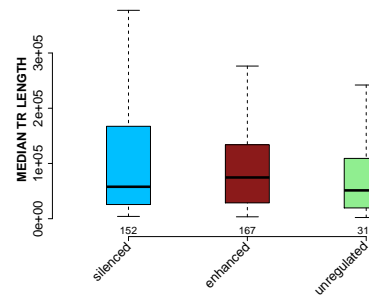
SCORE FOR MAXBP SEQ UPINTRON



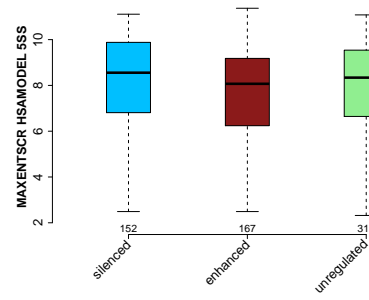
RATIO UPEXON EXON GCC



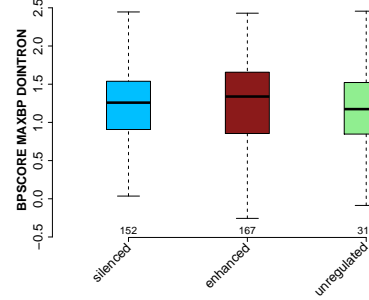
MEDIAN TR LENGTH



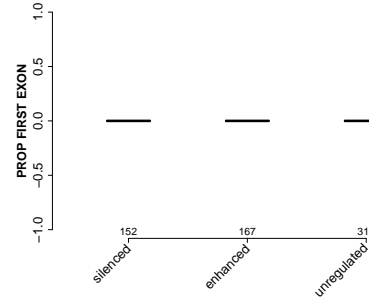
MAXENTSCR HSAMODEL 5SS



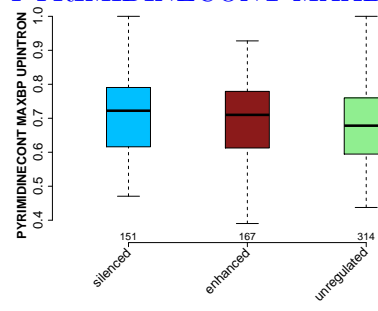
BPScore MAXBP Dointron



PROP FIRST EXON



PYRIMIDINECONT MAXBP UPINTRON

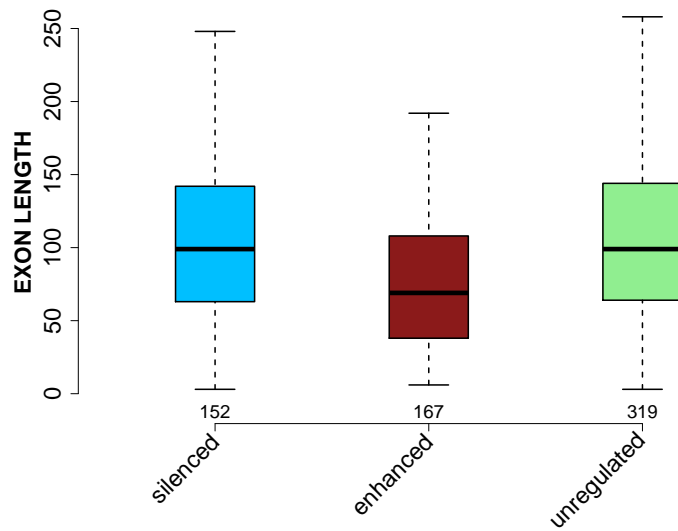


6 Details: Box plots and statistical assessments for all features

6.1 EXON LENGTH

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Meaning:



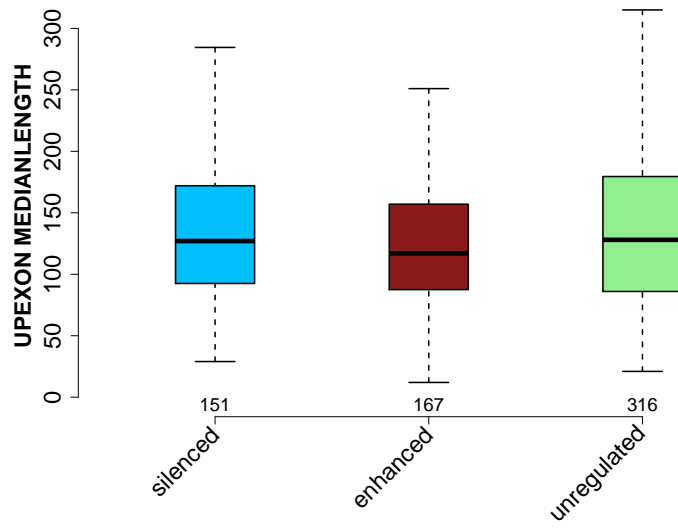
Significant results from Mann-Whitney U test:

- silenced vs enhanced : 1.87431e-05
mean: 115.4145 < 117.6766 , median: 99 > 69
- enhanced vs unregulated : 5.08493e-09
mean: 117.6766 < 141.1787 , median: 69 < 99

6.2 UPEXON MEDIANLENGTH

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Meaning: median length of up-stream exon



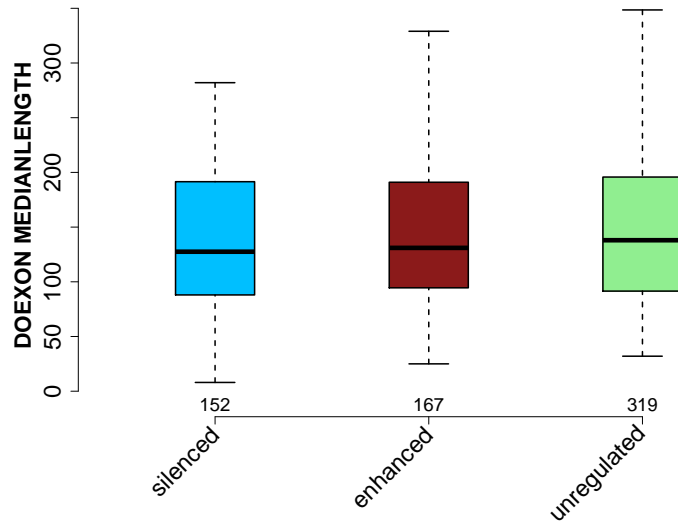
Significant results from Mann-Whitney U test:

- none

6.3 DOEXON MEDIANLENGTH

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Meaning: median length of down-stream exon



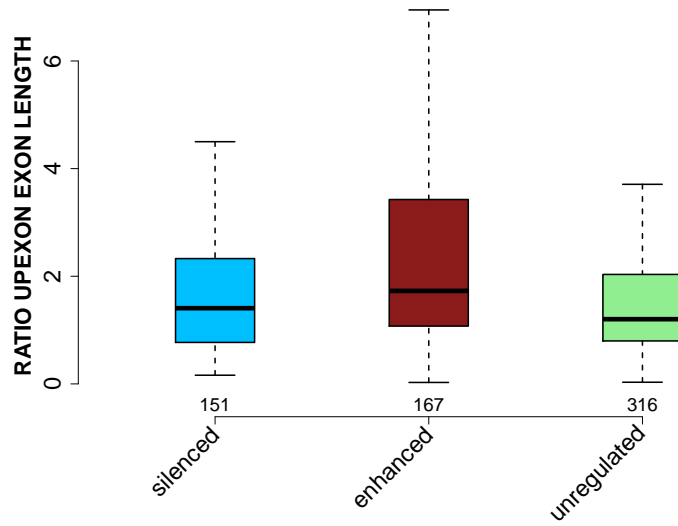
Significant results from Mann-Whitney U test:

- none

6.4 RATIO UPEXON EXON LENGTH

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Meaning: median up-stream exon length / exon length



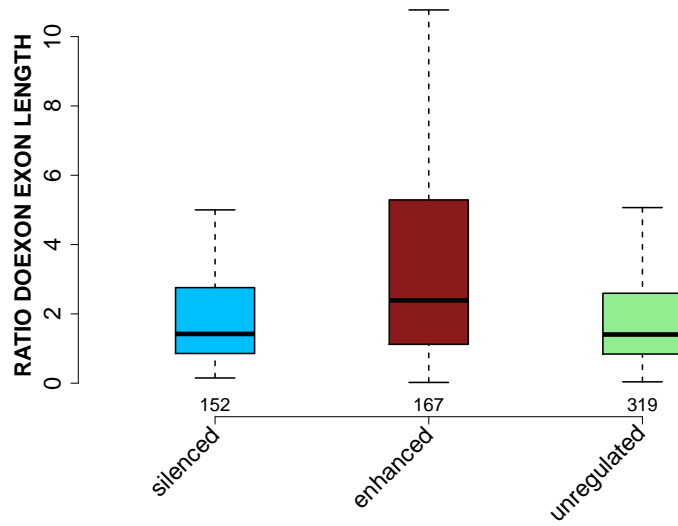
Significant results from Mann-Whitney U test:

- silenced vs enhanced : 0.00407014
mean: 2.8709 < 3.0961 , median: 1.4065 < 1.7284
- enhanced vs unregulated : 5.92597e-06
mean: 3.0961 > 2.2571 , median: 1.7284 > 1.2023

6.5 RATIO DOEXON EXON LENGTH

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Meaning: median down-stream exon length / exon length



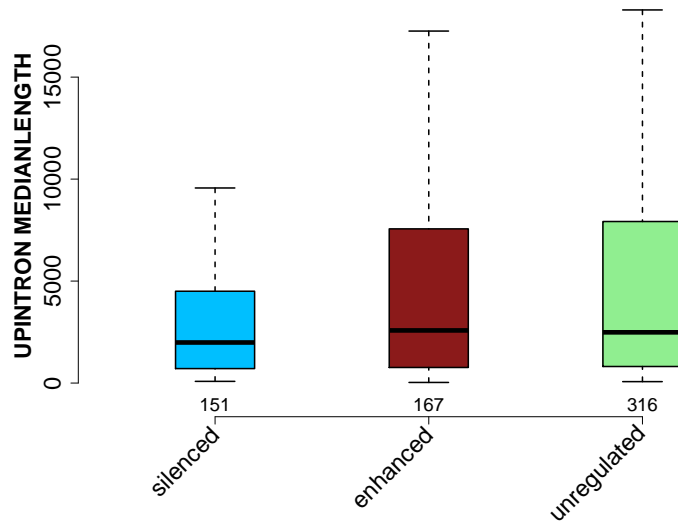
Significant results from Mann-Whitney U test:

- silenced vs enhanced : 0.000173677
mean: 3.7399 < 7.716 , median: 1.4208 < 2.3889
- enhanced vs unregulated : 6.34655e-06
mean: 7.716 > 3.5805 , median: 2.3889 > 1.4049

6.6 UPINTRON MEDIANLENGTH

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Meaning: median length of up-stream introns



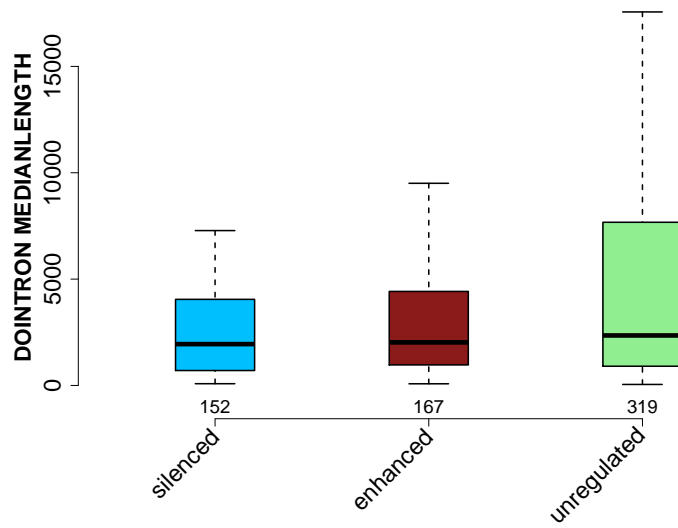
Significant results from Mann-Whitney U test:

- none

6.7 DOINTRON MEDIANLENGTH

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Meaning: median length of down-stream introns



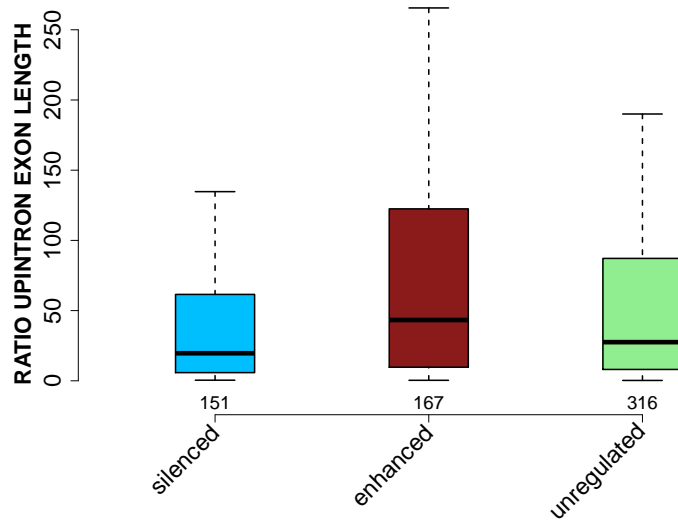
Significant results from Mann-Whitney U test:

- silenced vs unregulated : 0.0148253
mean: 6542.6908 < 7806.0862 , median: 1944 < 2350.5

6.8 RATIO UPINTRON EXON LENGTH

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Meaning: median up-stream intron length / exon length



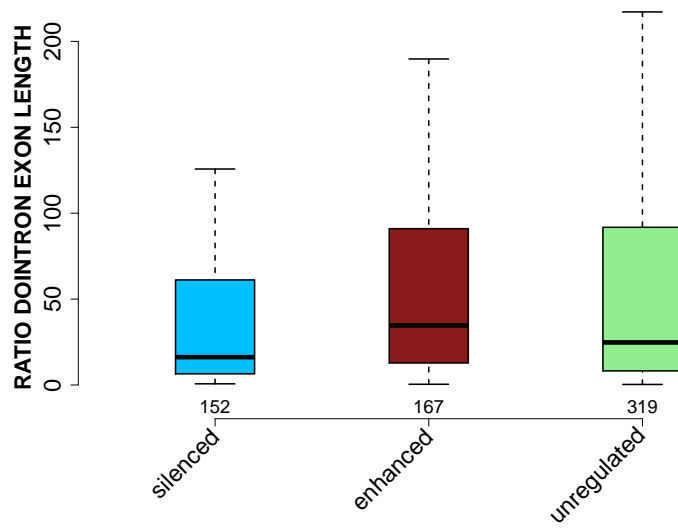
Significant results from Mann-Whitney U test:

- silenced vs enhanced : 0.00125152
mean: 85.0167 < 259.9366 , median: 19.614 < 43.2857
- enhanced vs unregulated : 0.0165469
mean: 259.9366 > 122.7246 , median: 43.2857 > 27.525

6.9 RATIO DOINTRON EXON LENGTH

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Meaning: median down-stream intron length / exon length



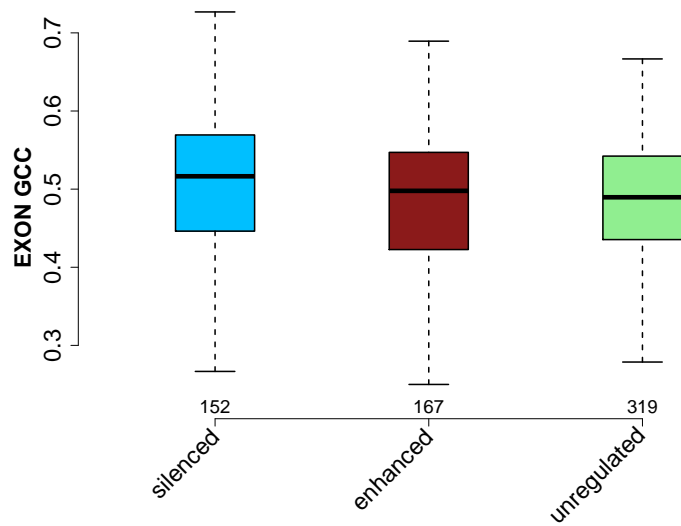
Significant results from Mann-Whitney U test:

- silenced vs enhanced : 0.00864023
mean: 108.7136 > 106.2546 , median: 16.2064 < 34.6522

6.10 EXON GCC

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Meaning: GC content of entire exon sequence



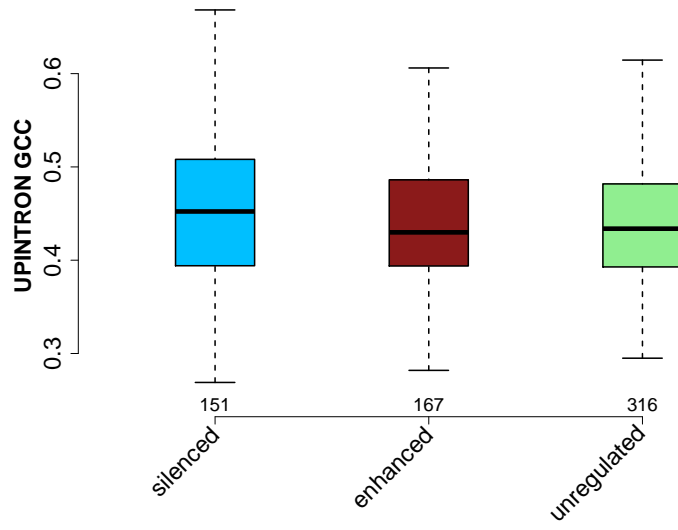
Significant results from Mann-Whitney U test:

- silenced vs enhanced : 0.0223064
mean: 0.511679 > 0.487123 , median: 0.51644 > 0.497817
- silenced vs unregulated : 0.0126749
mean: 0.511679 > 0.492414 , median: 0.51644 > 0.489583

6.11 UPINTRON GCC

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Meaning: GC content of entire up-stream intron sequence



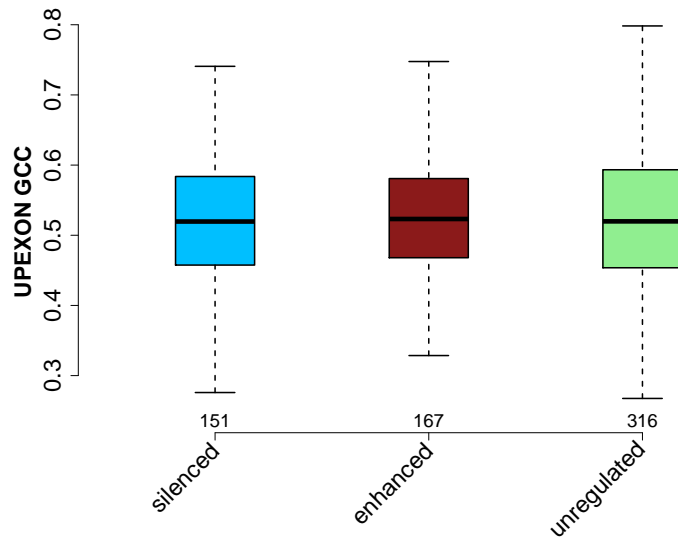
Significant results from Mann-Whitney U test:

- none

6.12 UPEXON GCC

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Meaning: GC content of entire up-stream exon sequence



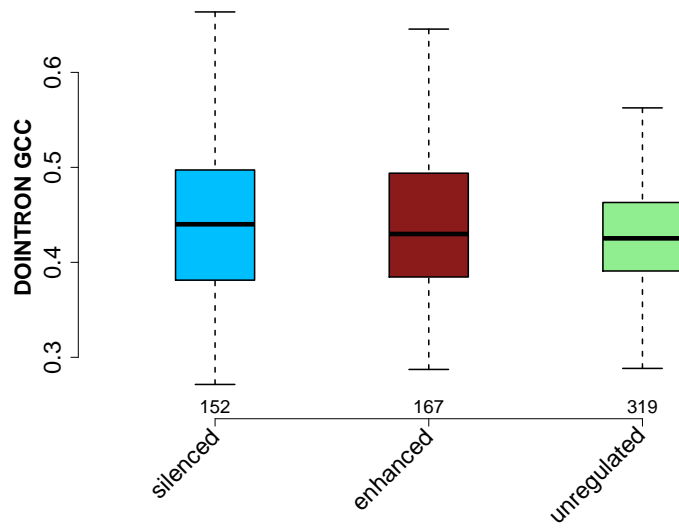
Significant results from Mann-Whitney U test:

- none

6.13 DOINTRON GCC

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Meaning: GC content of entire down-stream intron sequence



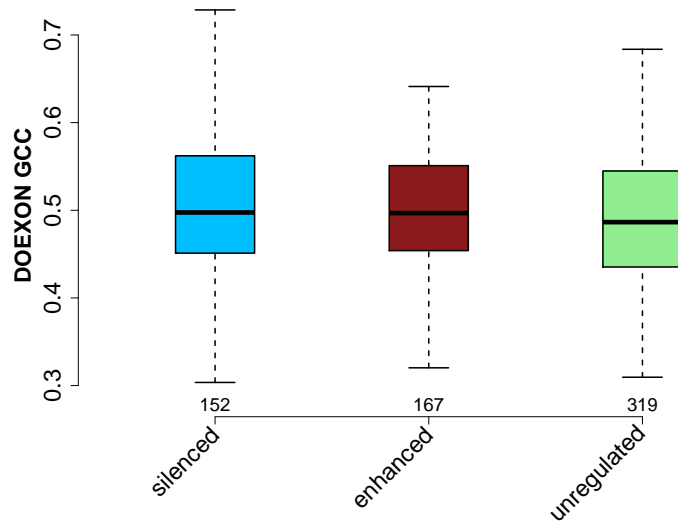
Significant results from Mann-Whitney U test:

- none

6.14 DOEXON GCC

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Meaning: GC content of entire down-stream exon sequence



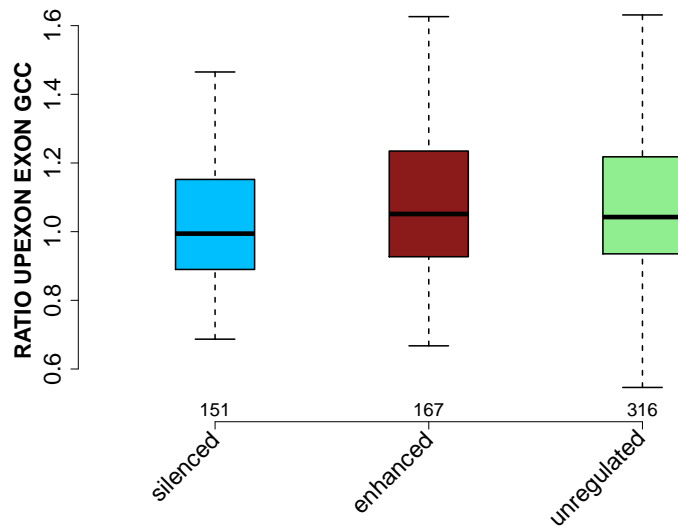
Significant results from Mann-Whitney U test:

- none

6.15 RATIO UPEXON EXON GCC

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Meaning: UPEXON GCC / EXON GCC



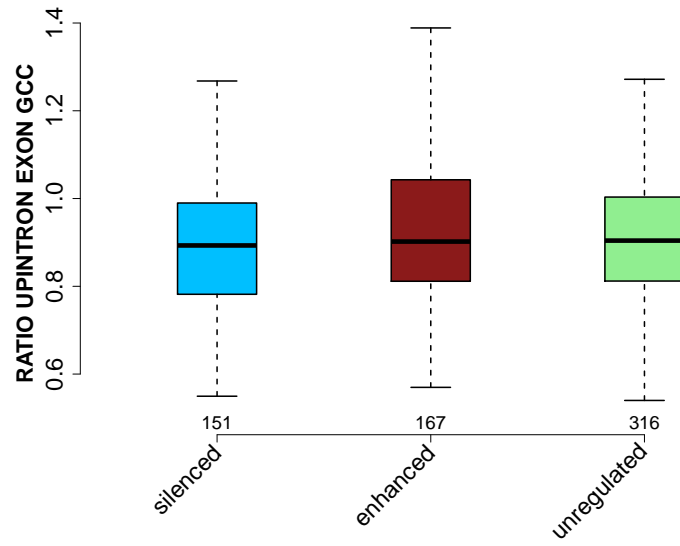
Significant results from Mann-Whitney U test:

- silenced vs enhanced : 0.0176965
mean: 1.0415 < 1.1171 , median: 0.994259 < 1.0514
- silenced vs unregulated : 0.0198832
mean: 1.0415 < 1.0999 , median: 0.994259 < 1.0425

6.16 RATIO UPINTRON GCC

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Meaning: UPINTRON GCC / EXON GCC



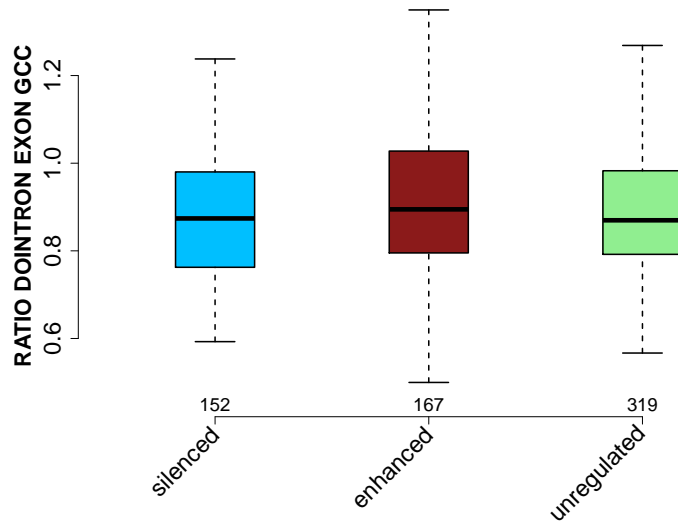
Significant results from Mann-Whitney U test:

- none

6.17 RATIO DOINTRON GCC

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Meaning: DOINTRON GCC / EXON GCC



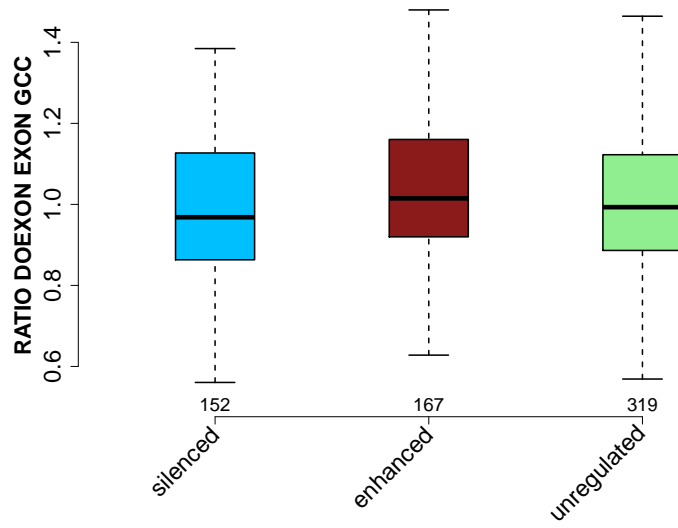
Significant results from Mann-Whitney U test:

- none

6.18 RATIO DOEXON EXON GCC

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Meaning: DOEXON GCC / EXON GCC



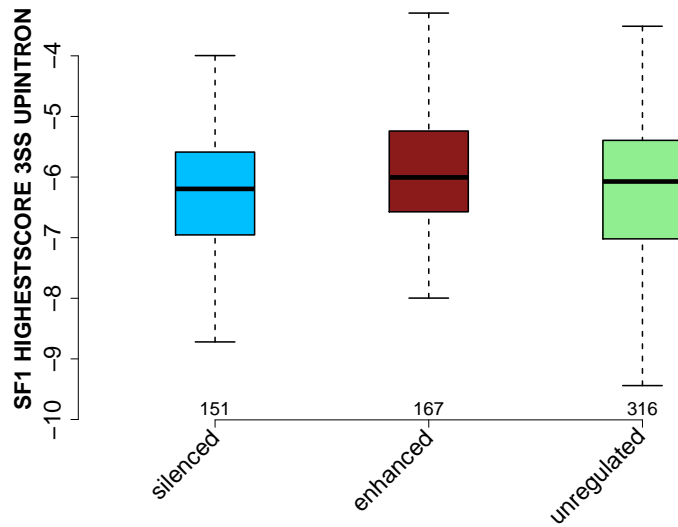
Significant results from Mann-Whitney U test:

- none

6.19 SF1 HIGHESTSCORE 3SS UPINTRON

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Meaning: highest score of a SF1 position weight matrix trained with human data in the last 150 nt 3 prime intron positions of up-stream intron



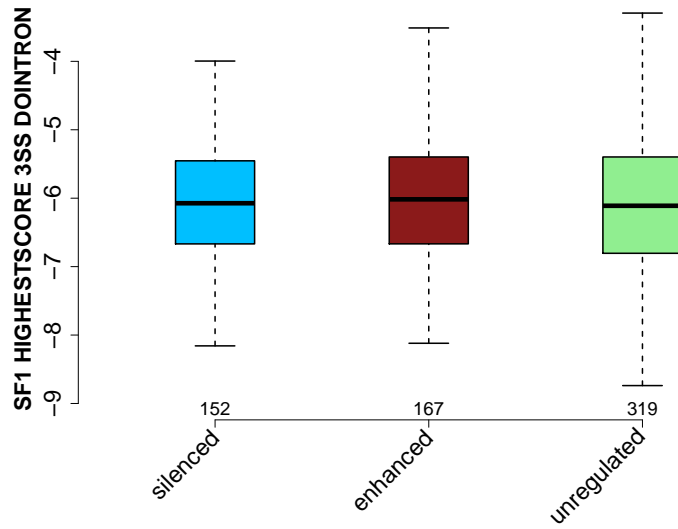
Significant results from Mann-Whitney U test:

- silenced vs enhanced : 0.00306922
mean: -6.29183 < -5.88723 , median: -6.19558 < -6.00556
- enhanced vs unregulated : 0.0448204
mean: -5.88723 > -6.12282 , median: -6.00556 > -6.07364

6.20 SF1 HIGHESTSCORE 3SS DOINTRON

Back to: [Overview](#) | [ToC](#)

Meaning: highest score of a SF1 position weight matrix trained with human data in the last 150 nt 3 prime intron positions of down-stream intron



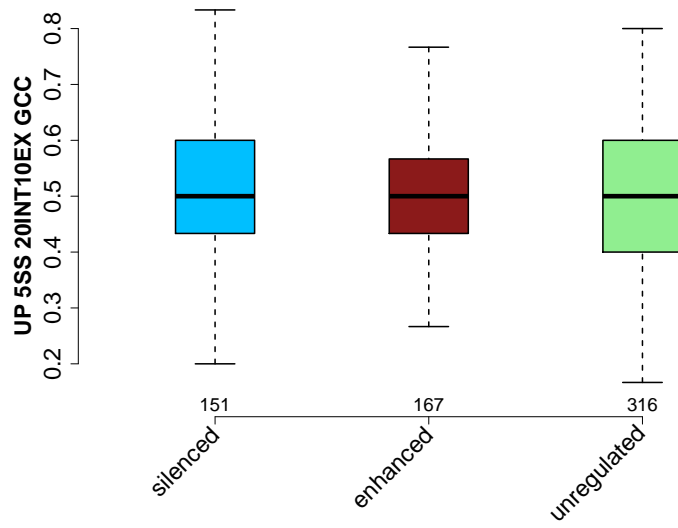
Significant results from Mann-Whitney U test:

- none

6.21 UP 5SS 20INT10EX GCC

Back to: [Overview](#) | [ToC](#)

Meaning: GC content of up-stream 5ss sequence (20int+10ex positions)



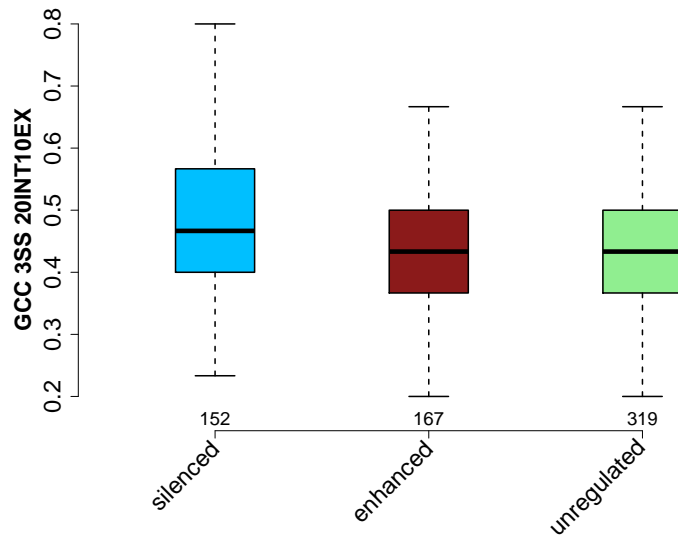
Significant results from Mann-Whitney U test:

- none

6.22 GCC 3SS 20INT10EX

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Meaning: GC content of 3ss sequence (20int+10ex positions)



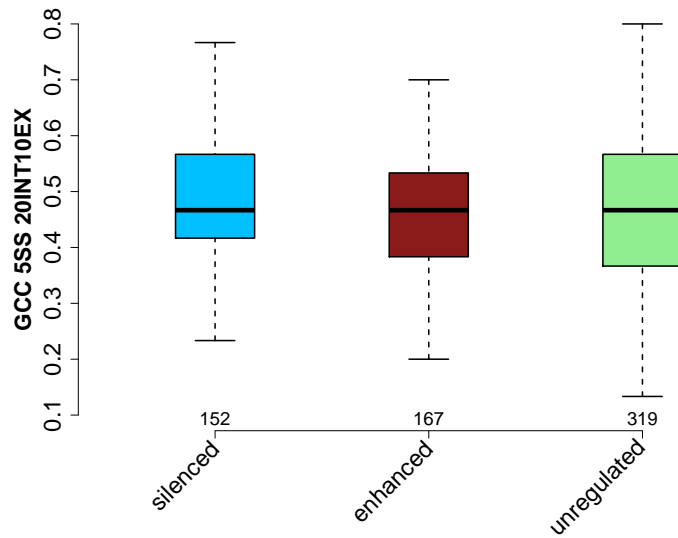
Significant results from Mann-Whitney U test:

- silenced vs enhanced : 0.043068
mean: 0.470614 > 0.443313 , median: 0.466667 > 0.433333
- silenced vs unregulated : 0.00600042
mean: 0.470614 > 0.437618 , median: 0.466667 > 0.433333

6.23 GCC 5SS 20INT10EX

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Meaning: GC content of 5ss sequence (20int+10ex positions)



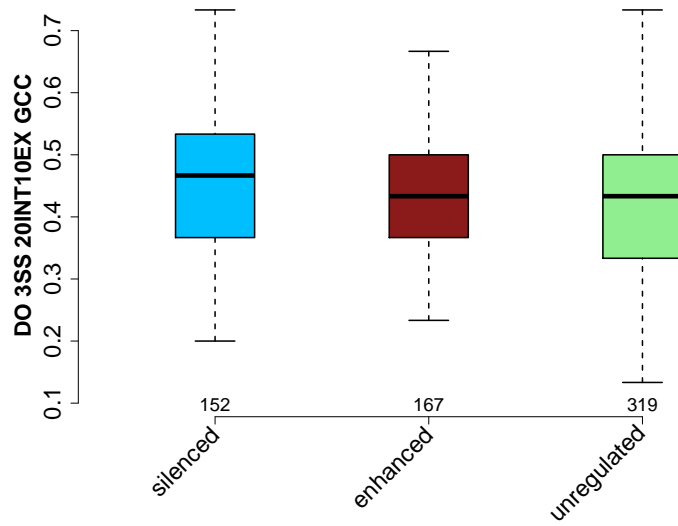
Significant results from Mann-Whitney U test:

- silenced vs enhanced : 0.0106089
mean: 0.489912 > 0.454491 , median: 0.466667 = 0.466667
- silenced vs unregulated : 0.0311947
mean: 0.489912 > 0.46186 , median: 0.466667 = 0.466667

6.24 DO 3SS 20INT10EX GCC

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Meaning: GC content of down-stream 3ss sequence (20int+10ex positions)



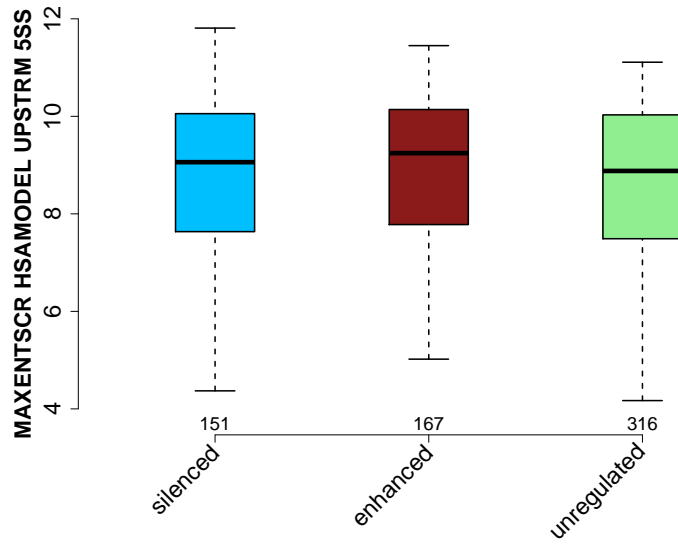
Significant results from Mann-Whitney U test:

- silenced vs unregulated : 0.00134918
mean: 0.457346 > 0.421787 , median: 0.466667 > 0.433333
- enhanced vs unregulated : 0.0286924
mean: 0.442415 > 0.421787 , median: 0.433333 = 0.433333

6.25 MAXENTSCR HSAMODEL UPSTRM 5SS

Back to: [Overview](#) | [ToC](#)

Meaning: maximum entropy score of 5ss of up-stream exon using a model trained with human splice sites



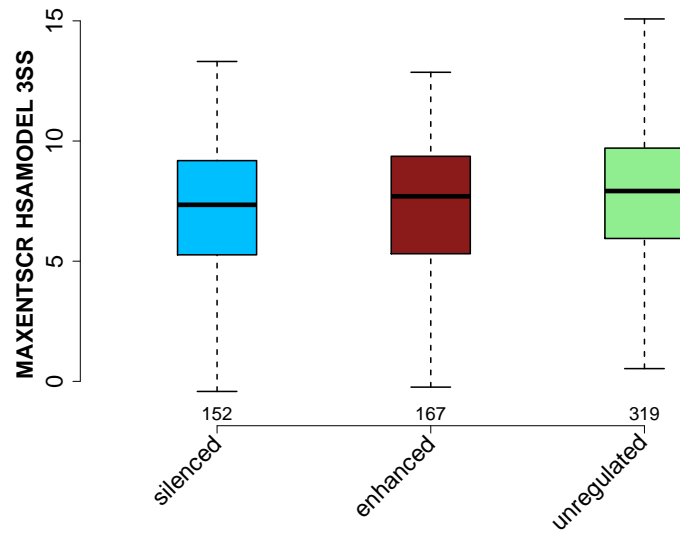
Significant results from Mann-Whitney U test:

- none

6.26 MAXENTSCR HSAMODEL 3SS

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Meaning: maximum entropy score of 3ss using a model trained with human splice sites



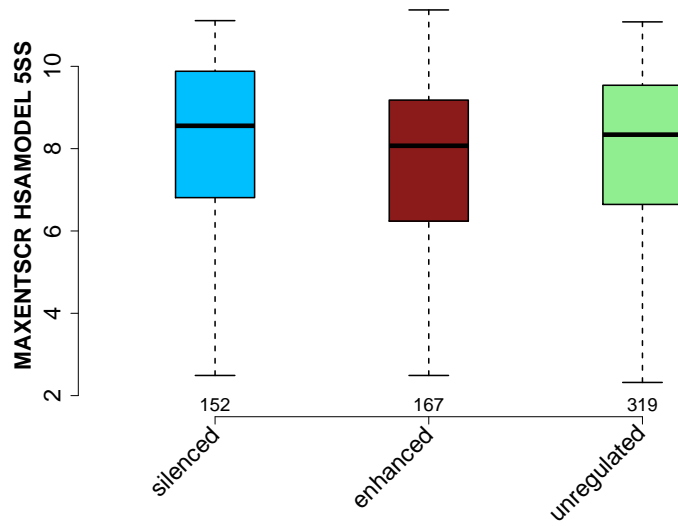
Significant results from Mann-Whitney U test:

- none

6.27 MAXENTSCR HSAMODEL 5SS

Back to: [Overview](#) | [ToC](#)

Meaning: maximum entropy score of 5ss using a model trained with human splice sites



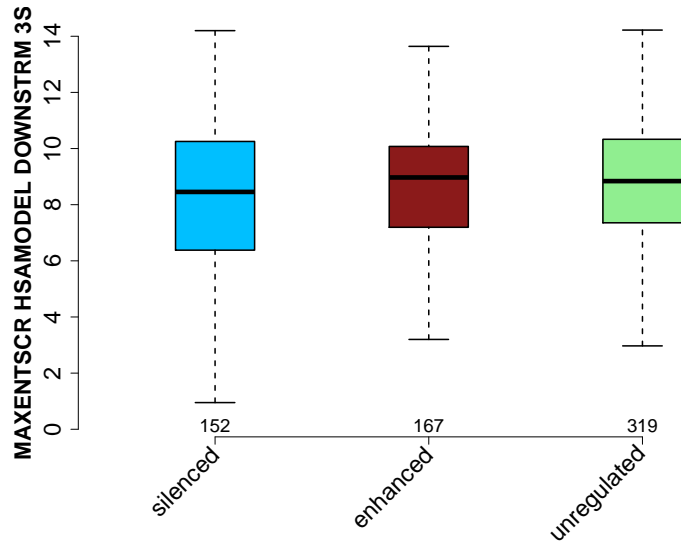
Significant results from Mann-Whitney U test:

- silenced vs enhanced : 0.0294855
mean: 7.7301 > 7.4886 , median: 8.555 > 8.07

6.28 MAXENTSCR HSAMODEL DOWNSTRM 3SS

Back to: [Overview](#) | [ToC](#)

Meaning: maximum entropy score of 3ss of down-stream exon using a model trained with human splice sites



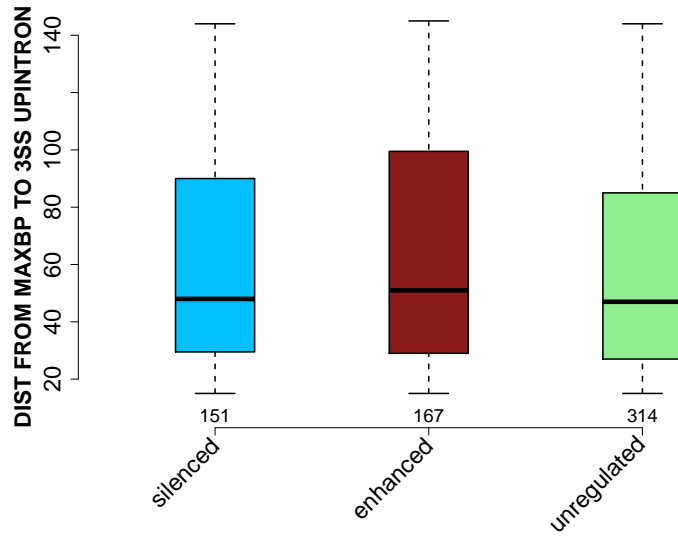
Significant results from Mann-Whitney U test:

- none

6.29 DIST FROM MAXBP TO 3SS UPINTRON

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Meaning: distance to 3ss of best predicted BP



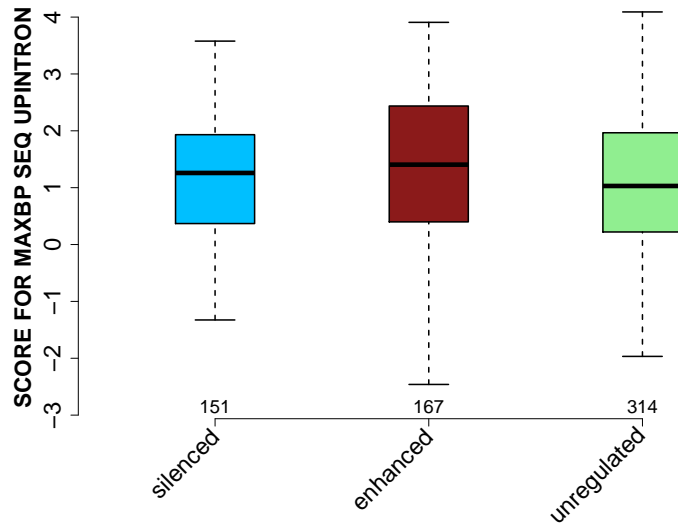
Significant results from Mann-Whitney U test:

- none

6.30 SCORE FOR MAXBP SEQ UPINTRON

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Meaning: BP sequence score of best predicted BP



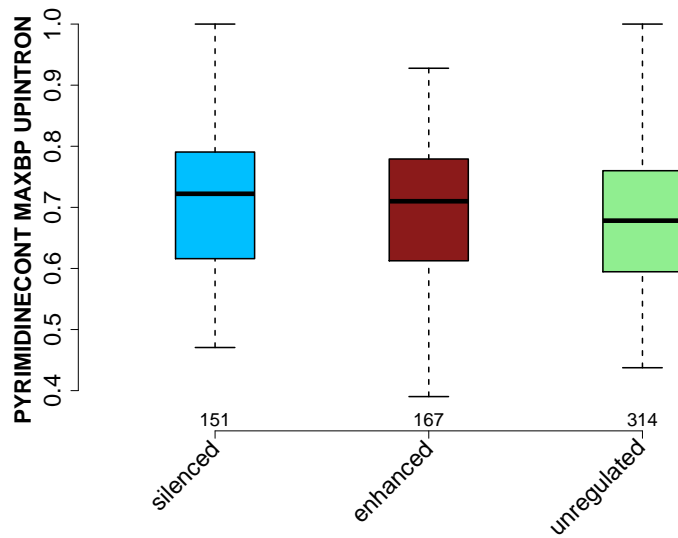
Significant results from Mann-Whitney U test:

- enhanced vs unregulated : 0.0174941
mean: 1.3176 > 1.0377 , median: 1.4049 > 1.03

6.31 PYRIMIDINECONT MAXBP UPINTRON

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Meaning: Pyrimidine content between the BP adenine and the 3 prime splice site for best BP



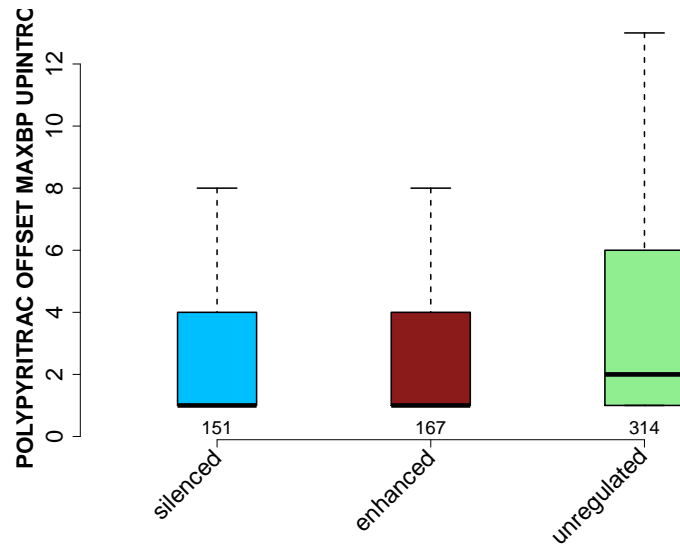
Significant results from Mann-Whitney U test:

- silenced vs unregulated : 0.0406195
mean: 0.706497 > 0.685564 , median: 0.722222 > 0.678235

6.32 POLYPYRITRAC OFFSET MAXBP UPINTRON

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Meaning: Polypyrimidine track offset relative to the BP adenine for best BP



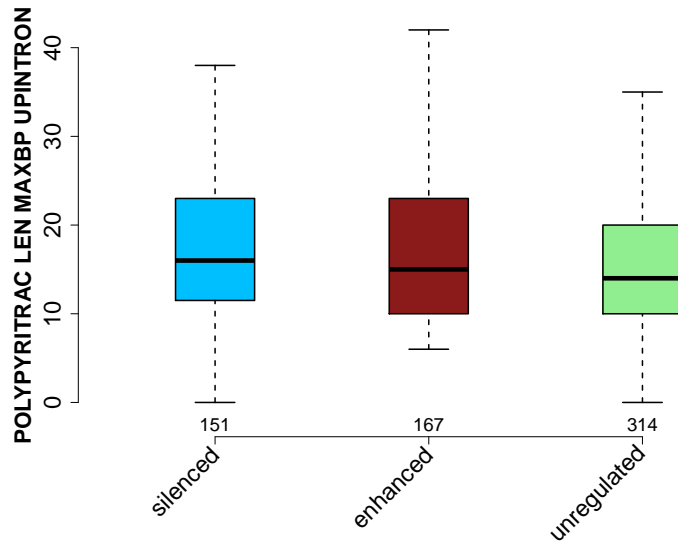
Significant results from Mann-Whitney U test:

- enhanced vs unregulated : 0.000581548
mean: 3.1018 < 4.621 , median: 1 < 2

6.33 POLYPYRITRAC LEN MAXBP UPINTRON

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Meaning: Polypyrimidine track length for best BP



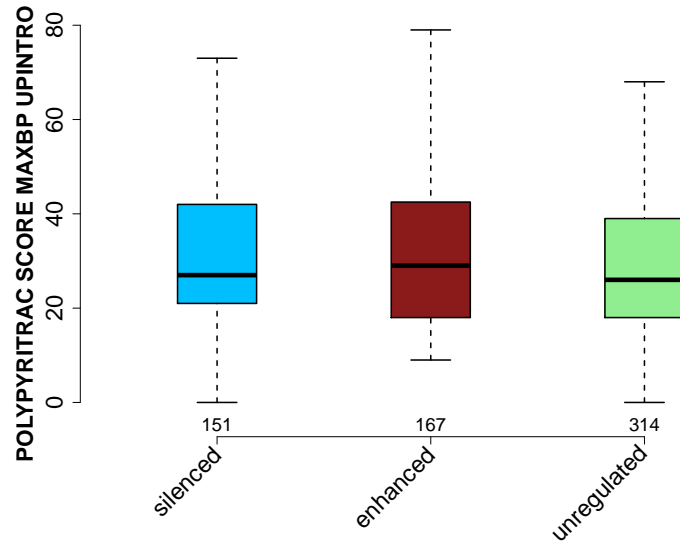
Significant results from Mann-Whitney U test:

- silenced vs unregulated : 0.0160967
mean: 19.7815 > 16.7994 , median: 16 > 14

6.34 POLYPYRITRAC SCORE MAXBP UPINTRON

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Meaning: Polypyrimidine track score for best BP



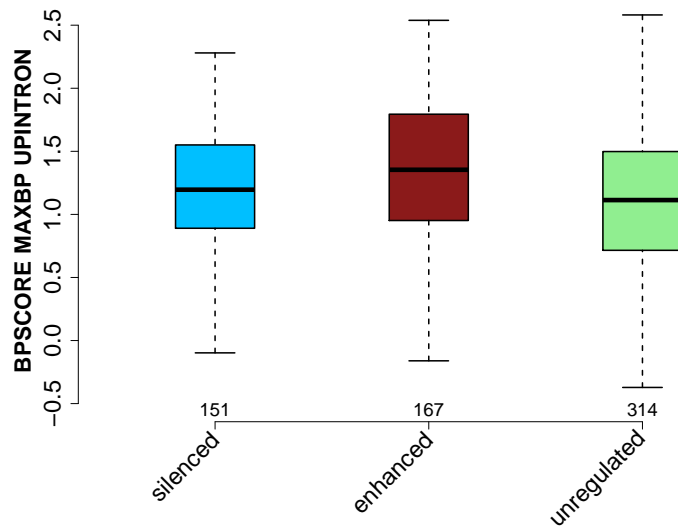
Significant results from Mann-Whitney U test:

- none

6.35 BPSCORE MAXBP UPINTRON

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Meaning: SVM classification score of best BP



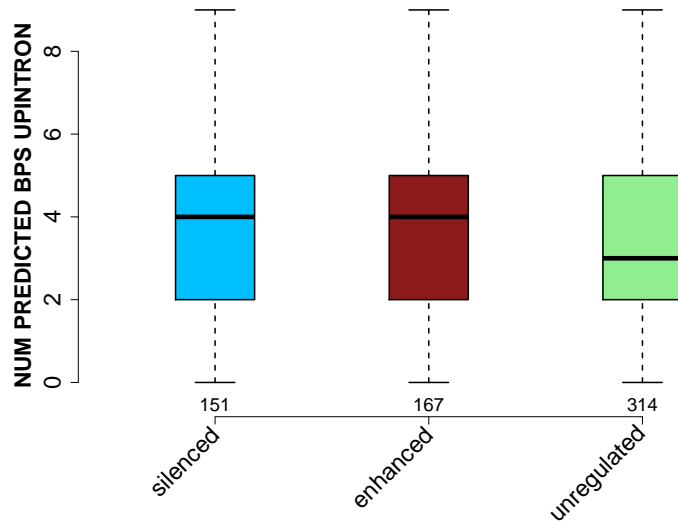
Significant results from Mann-Whitney U test:

- enhanced vs unregulated : 0.000165008
mean: 1.299 > 1.0658 , median: 1.3537 > 1.1135

6.36 NUM PREDICTED BPS UPINTRON

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Meaning: number of all predicted BPs which have a positive BP score



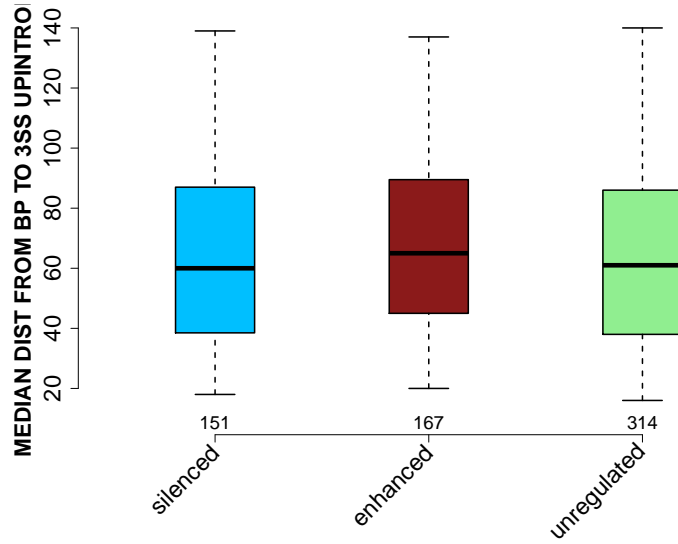
Significant results from Mann-Whitney U test:

- silenced vs unregulated : 0.0128857
mean: 3.9404 > 3.2611 , median: 4 > 3
- enhanced vs unregulated : 0.00111308
mean: 3.9401 > 3.2611 , median: 4 > 3

6.37 MEDIAN DIST FROM BP TO 3SS UPINTRON

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Meaning: like DIST FROM MAXBP TO 3SS but median over top-3 predicted BPs



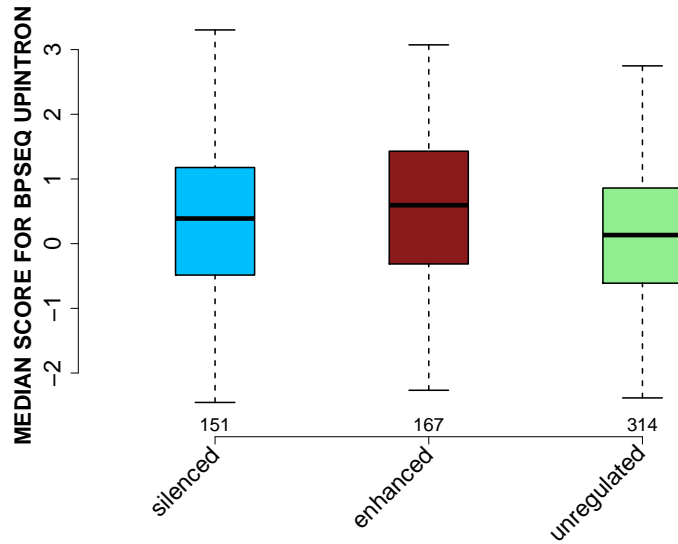
Significant results from Mann-Whitney U test:

- none

6.38 MEDIAN SCORE FOR BPSEQ UPINTRON

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Meaning: like SCORE FOR MAXBP SEQ but median over top-3 predicted BPs



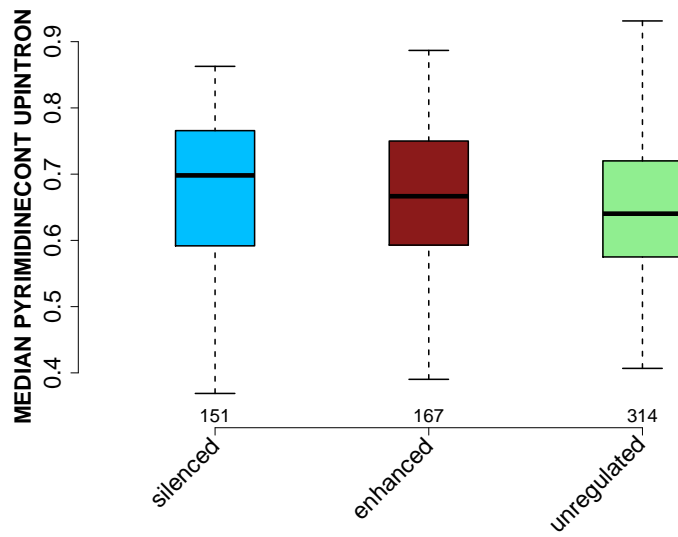
Significant results from Mann-Whitney U test:

- silenced vs unregulated : 0.019083
mean: 0.396912 > 0.124328 , median: 0.388042 > 0.132851
- enhanced vs unregulated : 0.000161402
mean: 0.511624 > 0.124328 , median: 0.59461 > 0.132851

6.39 MEDIAN PYRIMIDINECONT UPINTRON

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Meaning: like PYRIMIDINECONT MAXBP but median over top-3 predicted BPs



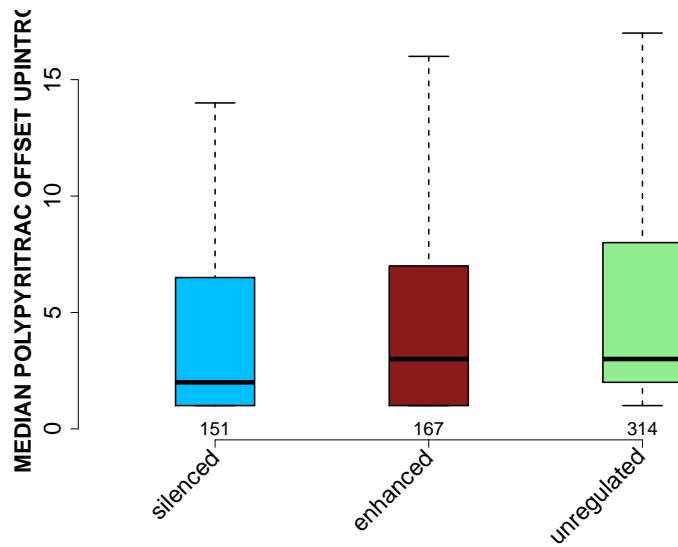
Significant results from Mann-Whitney U test:

- silenced vs unregulated : 0.000910646
mean: 0.683246 > 0.6525 , median: 0.698113 > 0.640313
- enhanced vs unregulated : 0.0296038
mean: 0.6713 > 0.6525 , median: 0.666667 > 0.640313

6.40 MEDIAN POLYPYRITRAC OFFSET UPINTRON

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Meaning: like POLYPYRITRAC OFFSET MAXBP but median over top-3 predicted BPs



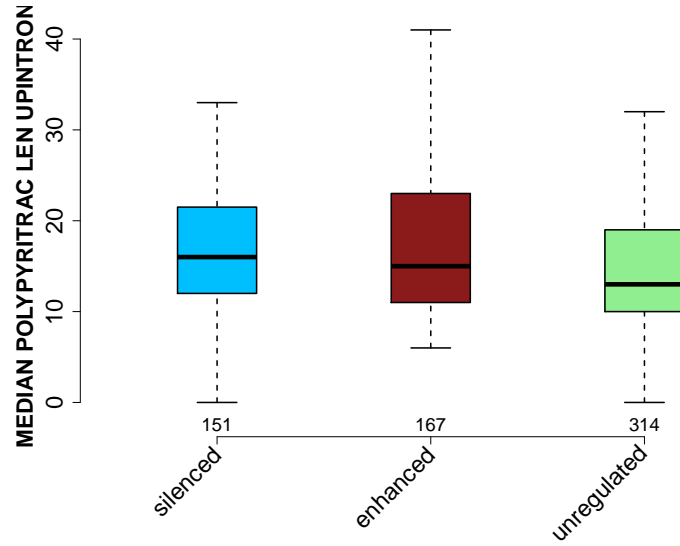
Significant results from Mann-Whitney U test:

- silenced vs unregulated : 0.00603418
mean: 5.4901 < 6.9076 , median: 2 < 3

6.41 MEDIAN POLYPYRITRAC LEN UPINTRON

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Meaning: like POLYPYRITRAC LEN MAXBP but median over top-3 predicted BPs



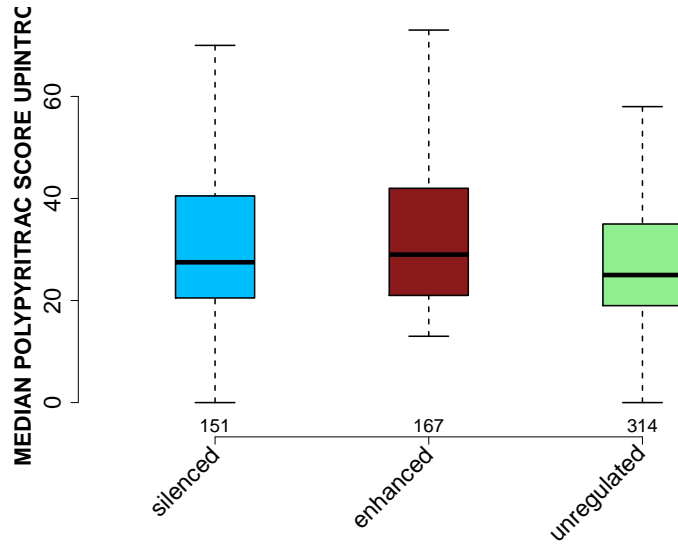
Significant results from Mann-Whitney U test:

- silenced vs unregulated : 0.000977978
mean: 19.4073 > 16.3694 , median: 16 > 13
- enhanced vs unregulated : 0.000885116
mean: 20.2275 > 16.3694 , median: 15 > 13

6.42 MEDIAN POLYPYRITRAC SCORE UPINTRON

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Meaning: like POLYPYRITRAC SCORE MAXBP but median over top-3 predicted BPs



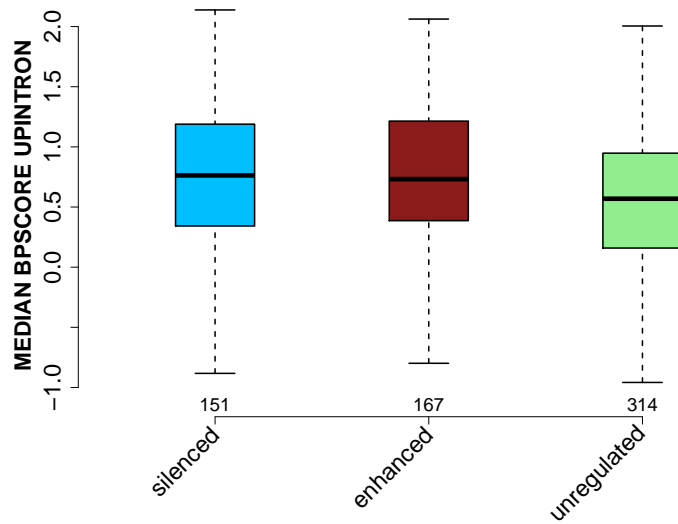
Significant results from Mann-Whitney U test:

- silenced vs unregulated : 0.0103966
mean: 35.6722 > 31.0939 , median: 27.5 > 25
- enhanced vs unregulated : 0.00108801
mean: 38.8503 > 31.0939 , median: 29 > 25

6.43 MEDIAN BPScore UPINTRON

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Meaning: like BPScore MAXBP but median over top-3 predicted BPs



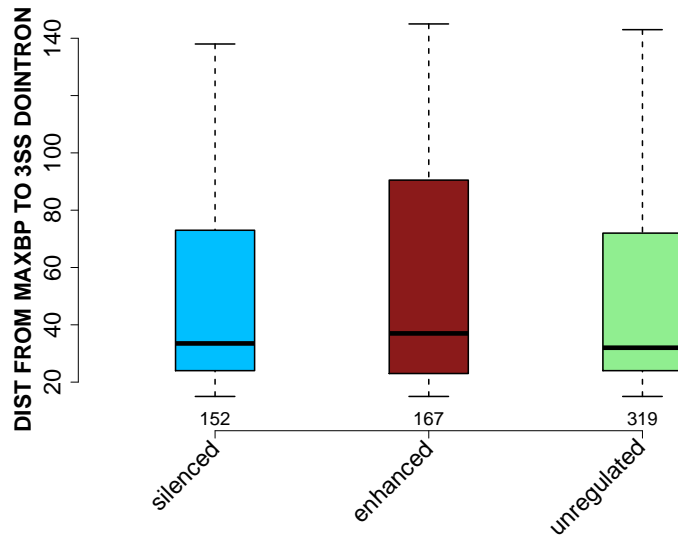
Significant results from Mann-Whitney U test:

- silenced vs unregulated : 0.000608106
mean: 0.673112 > 0.436279 , median: 0.762675 > 0.569037
- enhanced vs unregulated : 0.000239144
mean: 0.696359 > 0.436279 , median: 0.732079 > 0.569037

6.44 DIST FROM MAXBP TO 3SS DOINTRON

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Meaning: distance to 3ss of best predicted BP



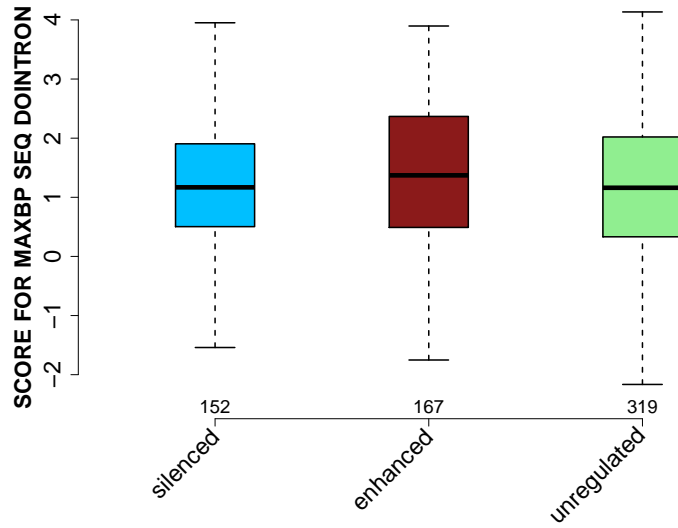
Significant results from Mann-Whitney U test:

- none

6.45 SCORE FOR MAXBP SEQ DOINTRON

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Meaning: BP sequence score of best predicted BP



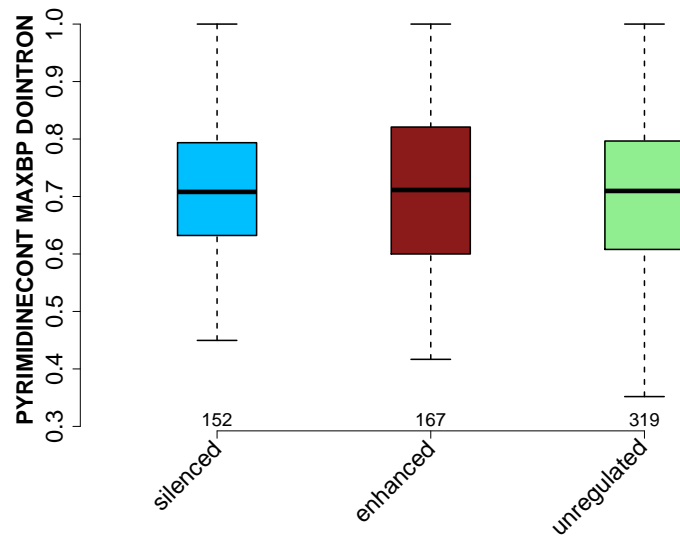
Significant results from Mann-Whitney U test:

- none

6.46 PYRIMIDINECONT MAXBP DOINTRON

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Meaning: Pyrimidine content between the BP adenine and the 3 prime splice site for best BP



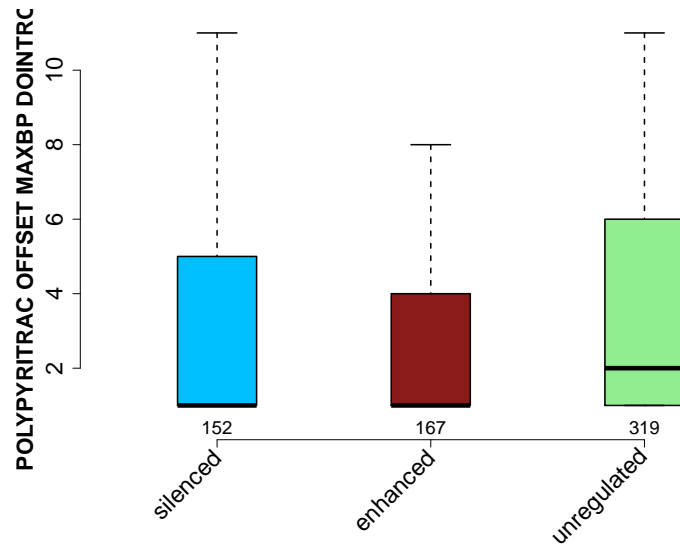
Significant results from Mann-Whitney U test:

- none

6.47 POLYPYRITRAC OFFSET MAXBP DOINTRON

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Meaning: Polypyrimidine track offset relative to the BP adenine for best BP



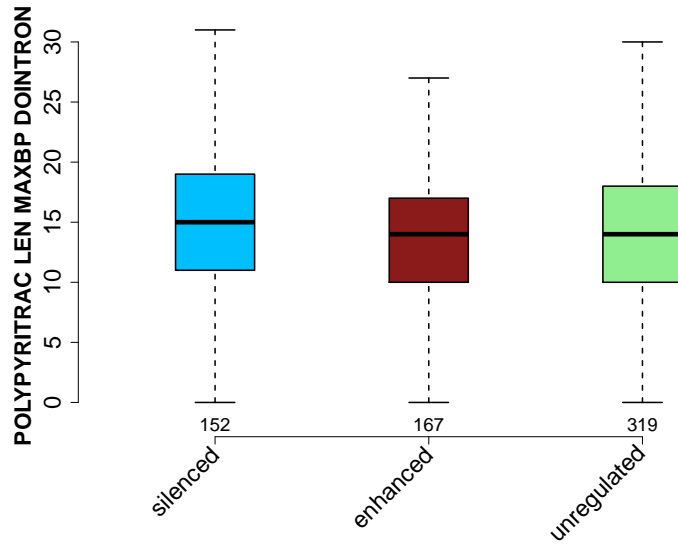
Significant results from Mann-Whitney U test:

- none

6.48 POLYPYRITRAC LEN MAXBP DOINTRON

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Meaning: Polypyrimidine track length for best BP



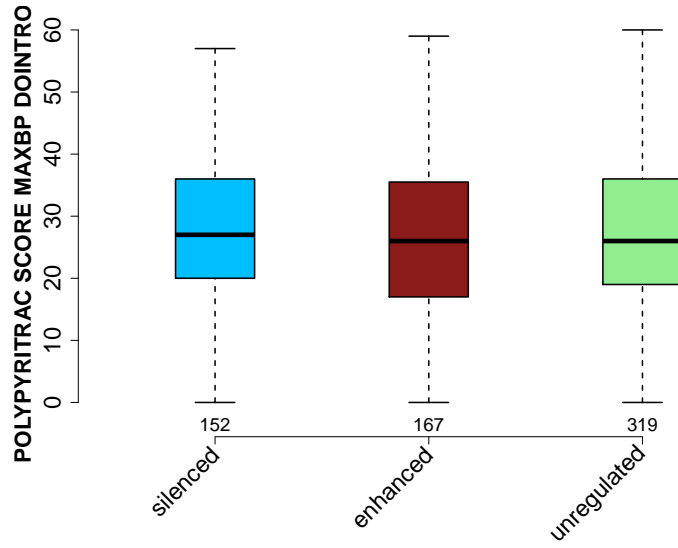
Significant results from Mann-Whitney U test:

- none

6.49 POLYPYRITRAC SCORE MAXBP DOINTRON

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Meaning: Polypyrimidine track score for best BP



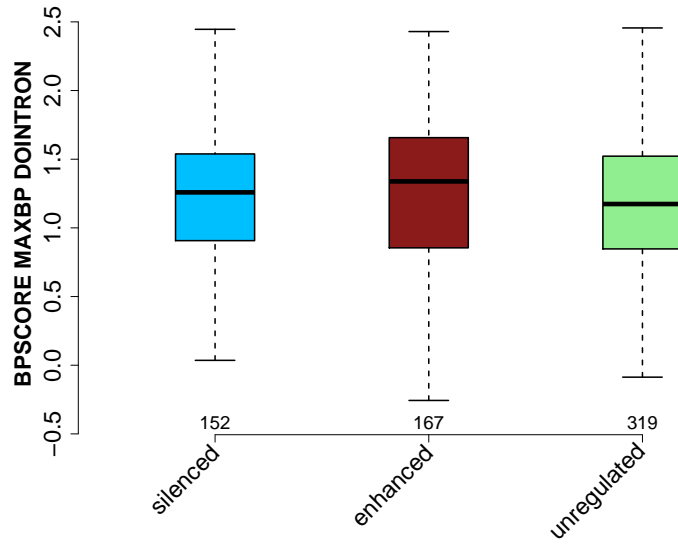
Significant results from Mann-Whitney U test:

- none

6.50 BPSCORE MAXBP DOINTRON

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Meaning: SVM classification score of best BP



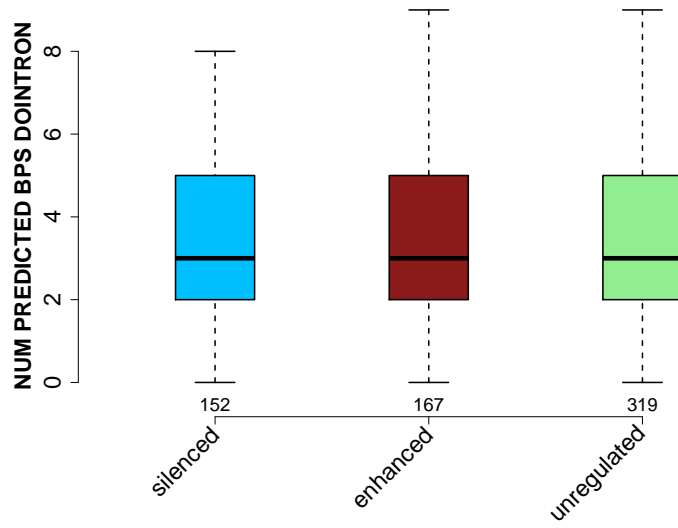
Significant results from Mann-Whitney U test:

- enhanced vs unregulated : 0.0393638
mean: 1.2554 > 1.1678 , median: 1.3385 > 1.1737

6.51 NUM PREDICTED BPS DOINTRON

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Meaning: number of all predicted BPs which have a positive BP score



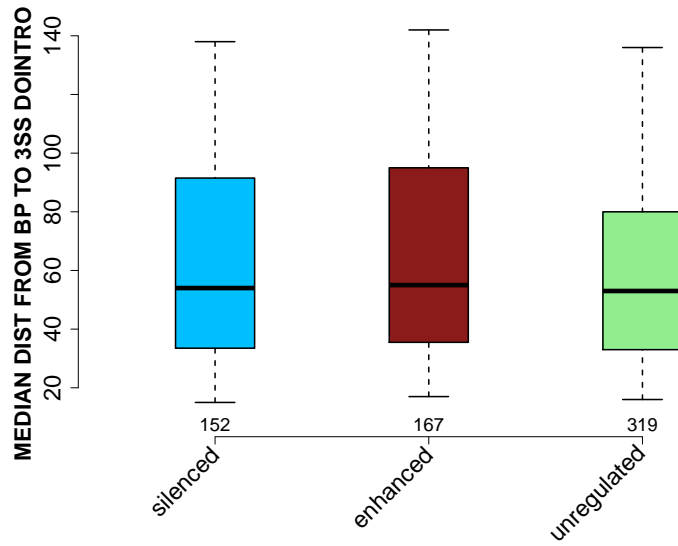
Significant results from Mann-Whitney U test:

- none

6.52 MEDIAN DIST FROM BP TO 3SS DOINTRON

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Meaning: like DIST FROM MAXBP TO 3SS but median over top-3 predicted BPs



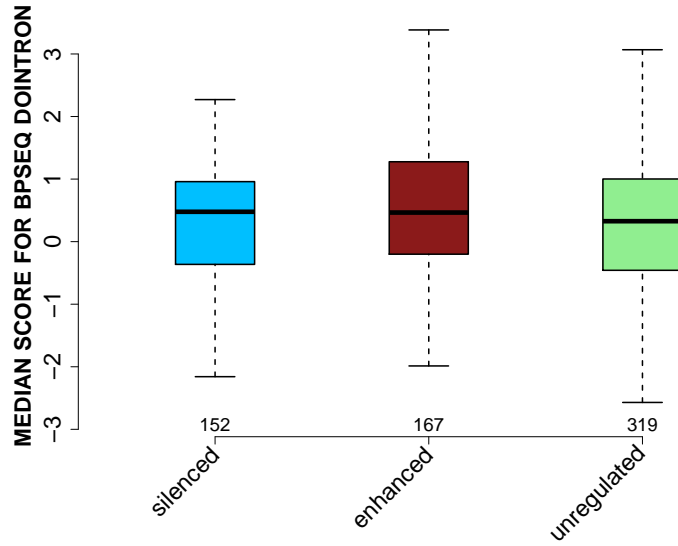
Significant results from Mann-Whitney U test:

- none

6.53 MEDIAN SCORE FOR BPSEQ DOINTRON

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Meaning: like SCORE FOR MAXBP SEQ but median over top-3 predicted BPs



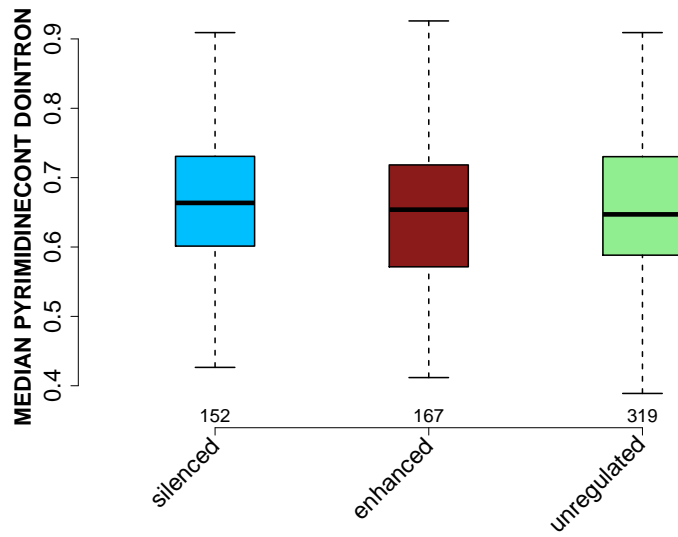
Significant results from Mann-Whitney U test:

- none

6.54 MEDIAN PYRIMIDINECONT DOINTRON

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Meaning: like PYRIMIDINECONT MAXBP but median over top-3 predicted BPs



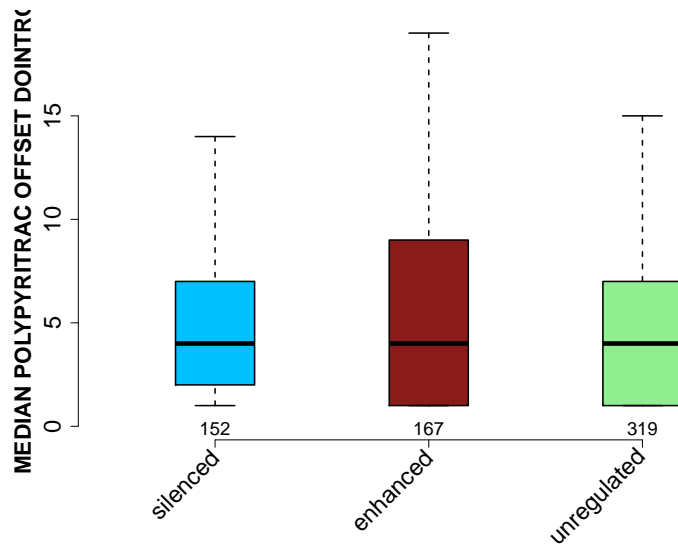
Significant results from Mann-Whitney U test:

- none

6.55 MEDIAN POLYPYRITRAC OFFSET DOWNTON

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Meaning: like POLYPYRITRAC OFFSET MAXBP but median over top-3 predicted BPs



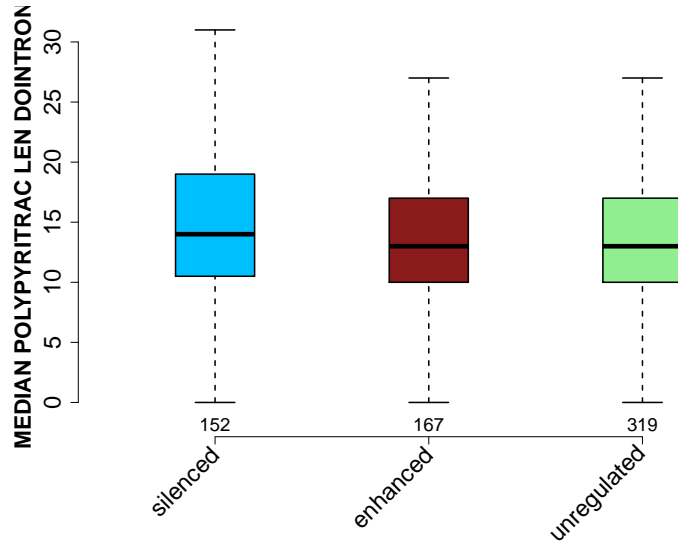
Significant results from Mann-Whitney U test:

- none

6.56 MEDIAN POLYPYRITRAC LEN DOINTRON

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Meaning: like POLYPYRITRAC LEN MAXBP but median over top-3 predicted BPs



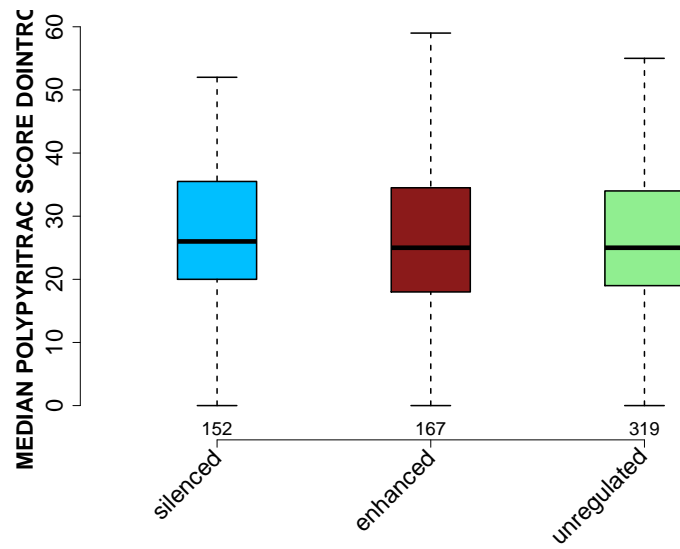
Significant results from Mann-Whitney U test:

- none

6.57 MEDIAN POLYPYRITRAC SCORE DOINTRON

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Meaning: like POLYPYRITRAC SCORE MAXBP but median over top-3 predicted BPs



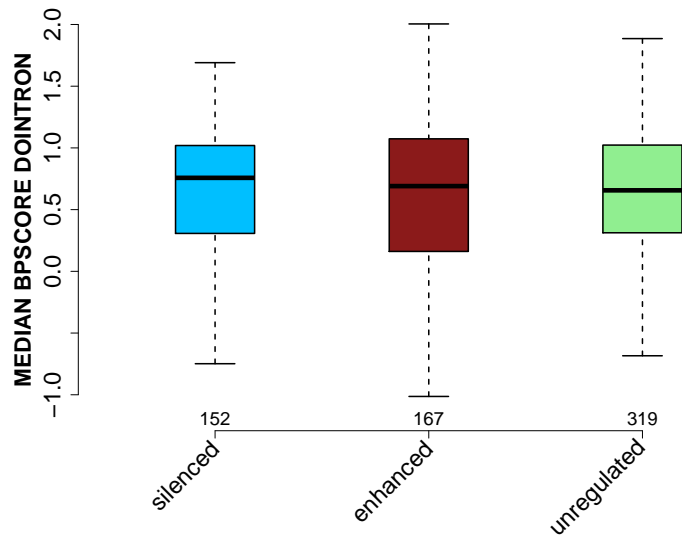
Significant results from Mann-Whitney U test:

- none

6.58 MEDIAN BPScore DOINTRON

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Meaning: like BPScore MAXBP but median over top-3 predicted BPs



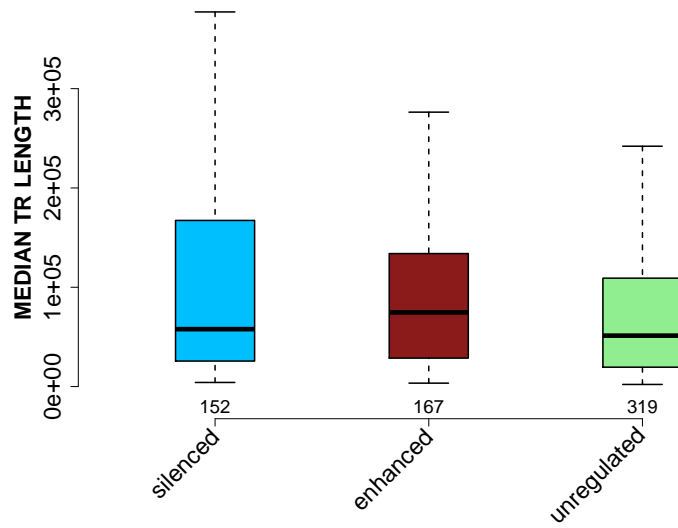
Significant results from Mann-Whitney U test:

- none

6.59 MEDIAN TR LENGTH

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Meaning: median length of transcripts the exon occurs in



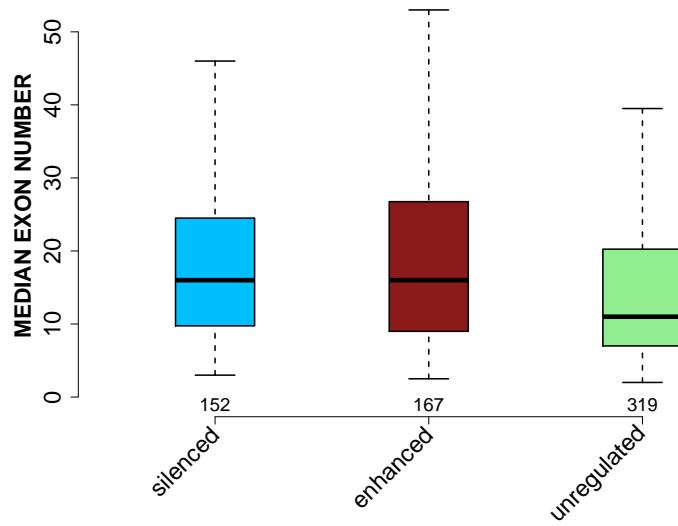
Significant results from Mann-Whitney U test:

- enhanced vs unregulated : 0.0207028
mean: 127677.5689 > 113409.9232 , median: 74647 > 51268

6.60 MEDIAN EXON NUMBER

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Meaning: ... of transcripts where exon was found in



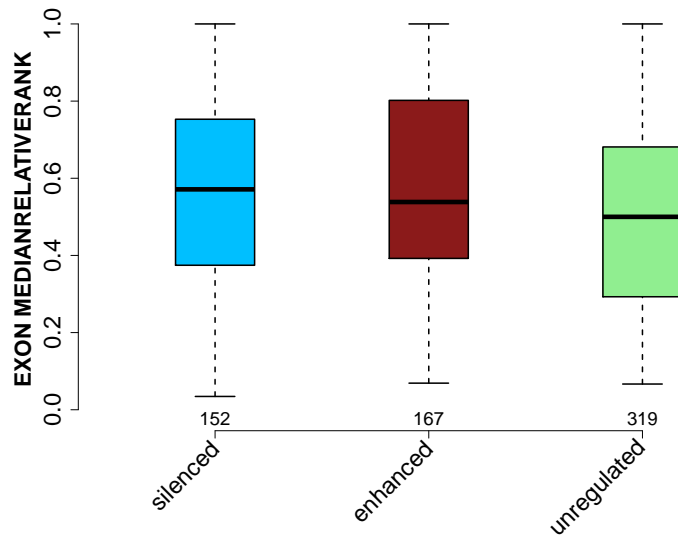
Significant results from Mann-Whitney U test:

- silenced vs unregulated : 4.03497e-05
mean: 19.102 > 14.8135 , median: 16 > 11
- enhanced vs unregulated : 0.000572323
mean: 18.3293 > 14.8135 , median: 16 > 11

6.61 EXON MEDIANRELATIVERANK

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Meaning: relative rank = rank / number of all exons in transcript, is between 0 and 1



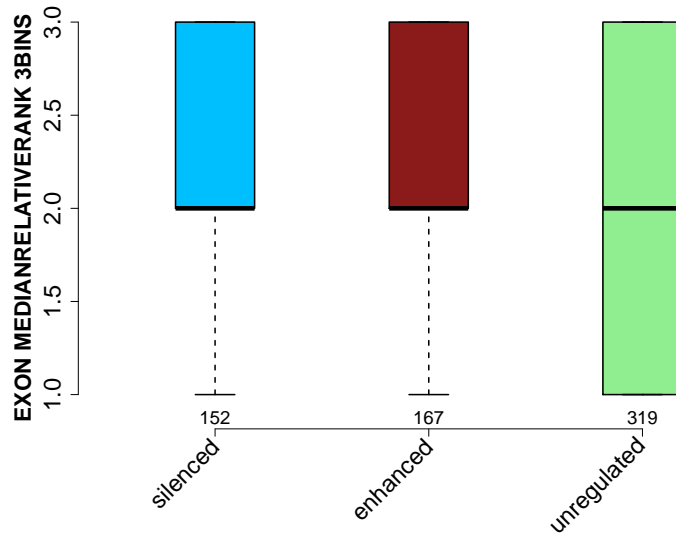
Significant results from Mann-Whitney U test:

- silenced vs unregulated : 0.00819002
mean: 0.566027 > 0.504532 , median: 0.571249 > 0.5
- enhanced vs unregulated : 0.00216876
mean: 0.579442 > 0.504532 , median: 0.538462 > 0.5

6.62 EXON MEDIANRELATIVERANK 3BINS

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Meaning: median bin into which EXON MEDIANRELATIVERANK falls when binning 0-1 into 3 bins



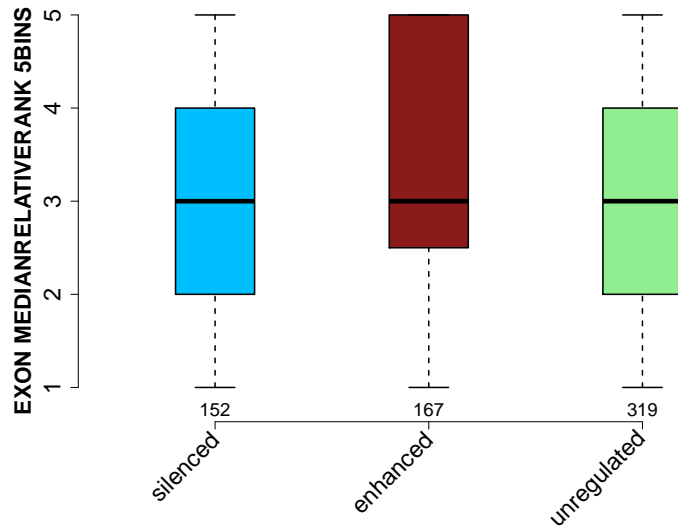
Significant results from Mann-Whitney U test:

- silenced vs unregulated : 0.0040518
mean: 2.2237 > 2.0063 , median: 2 = 2
- enhanced vs unregulated : 0.00429409
mean: 2.2156 > 2.0063 , median: 2 = 2

6.63 EXON MEDIANRELATIVERANK 5BINS

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Meaning: similar to EXON MEDIANRELATIVERANK 3BINS with 5 bins



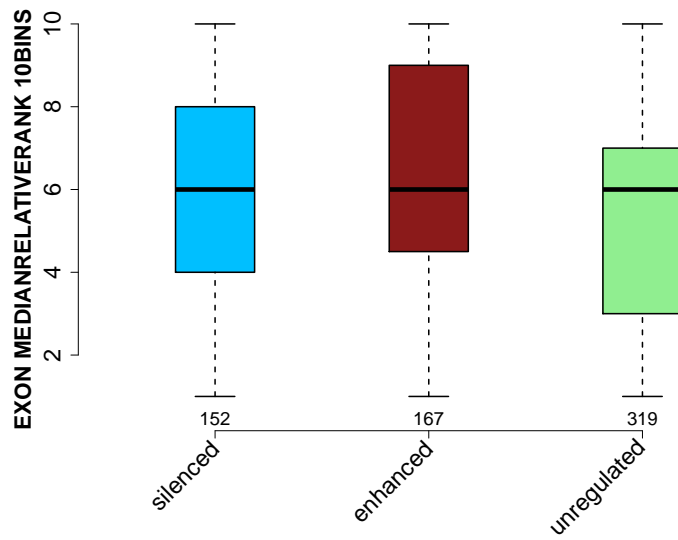
Significant results from Mann-Whitney U test:

- silenced vs unregulated : 0.00673887
mean: 3.3421 > 3.0125 , median: 3 = 3
- enhanced vs unregulated : 0.00451418
mean: 3.3533 > 3.0125 , median: 3 = 3

6.64 EXON MEDIANRELATIVERANK 10BINS

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Meaning: similar to EXON MEDIANRELATIVERANK 3BINS with 10 bins



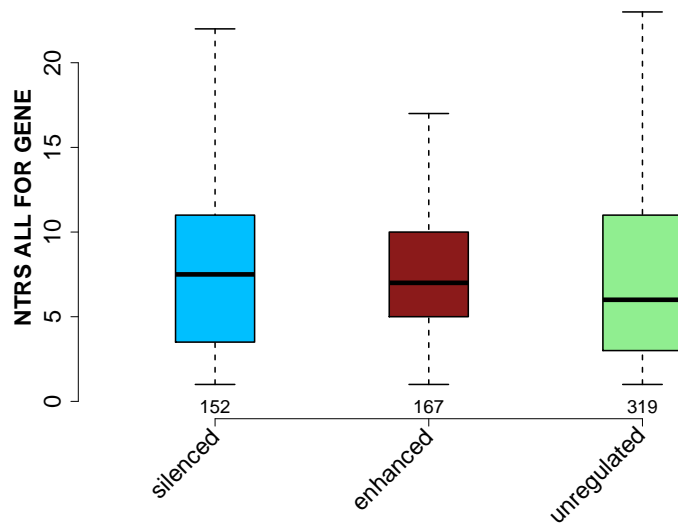
Significant results from Mann-Whitney U test:

- silenced vs unregulated : 0.008429
mean: 6.1842 > 5.5455 , median: 6 = 6
- enhanced vs unregulated : 0.00221307
mean: 6.3174 > 5.5455 , median: 6 = 6

6.65 NTRS ALL FOR GENE

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Meaning: number of transcripts of gene where the exon was found in



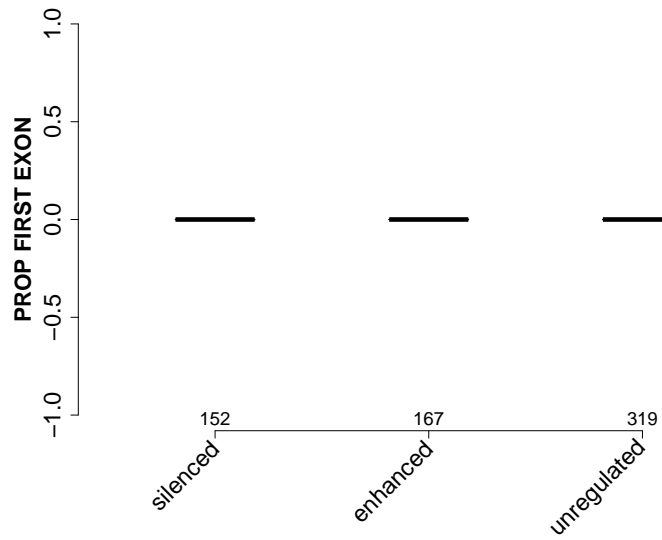
Significant results from Mann-Whitney U test:

- none

6.66 PROP FIRST EXON

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Meaning: NTRS WITH EXON AS FIRST EXON / NTRS WITH EXON



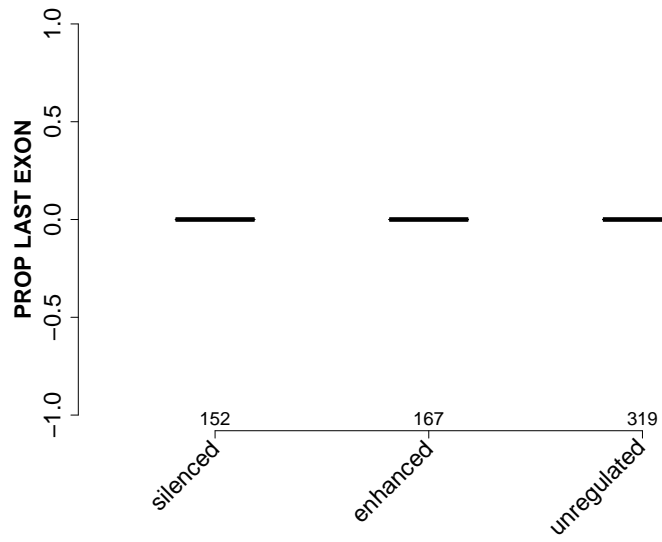
Significant results from Mann-Whitney U test:

- silenced vs unregulated : 0.039493
mean: 0.0199329 < 0.0409892 , median: 0 = 0

6.67 PROP LAST EXON

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Meaning: NTRS WITH EXON AS LAST EXON / NTRS WITH EXON



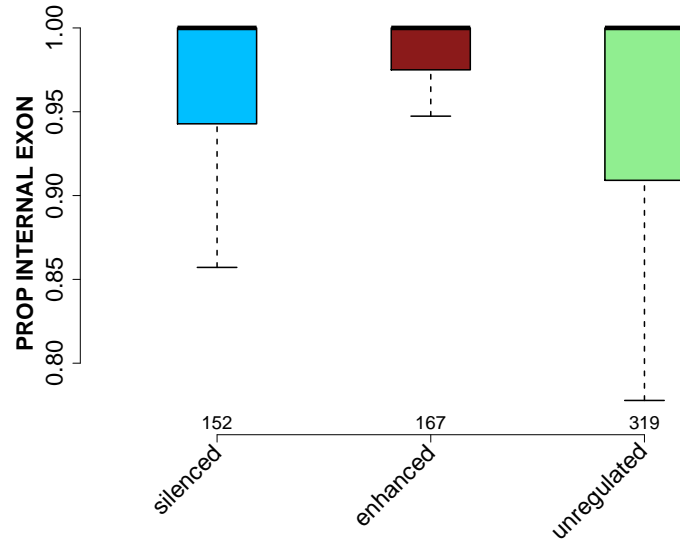
Significant results from Mann-Whitney U test:

- none

6.68 PROP INTERNAL EXON

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Meaning: NTRS WITH EXON AS INTERNAL EXON / NTRS WITH EXON



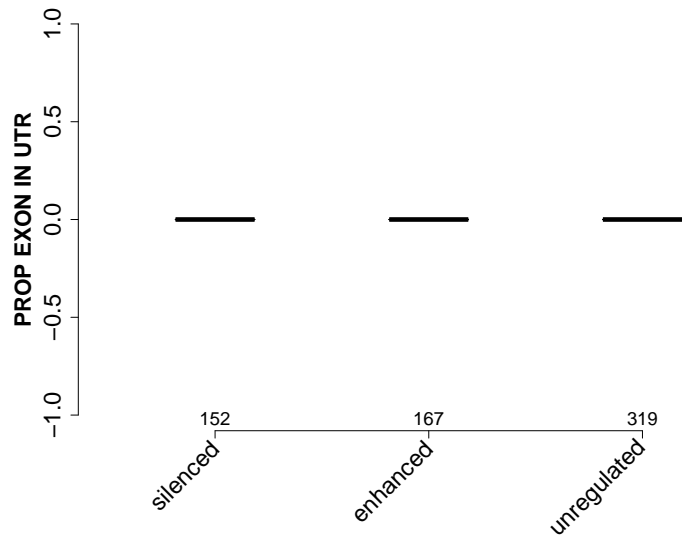
Significant results from Mann-Whitney U test:

- none

6.69 PROP EXON IN UTR

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Meaning: NTRS WITH EXON IN UTR / NTRS WITH EXON



Significant results from Mann-Whitney U test:

- silenced vs enhanced : p value = NA
- silenced vs unregulated : p value = NA
- enhanced vs unregulated : p value = NA