

# Comparison of introns grouped into: UP-INTRONS-HeLa-SRRM2-KD, DOWN-INTRONS-HeLa-SRRM2-KD, CR, CS, AS-NC

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Matt version 1.3.0

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## 1 Infos

Visualizations of intron features for different groups of introns. Each intron occurs in exactly one gene, but might occur in several transcripts of that gene. Hence, for some features like the intron length, there is exactly one value for each intron. 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 intron. 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

The Matt paper: *Matt: Unix tools for alternative splicing analysis*, A. Gohr, M. Irimia, *Bioinformatics*, 2018, *bty606*, DOI: [10.1093/bioinformatics/bty606](https://doi.org/10.1093/bioinformatics/bty606)

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](https://doi.org/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](https://doi.org/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](https://doi.org/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:

MATT\_INPUT\_INTRONS\_SRRM2\_HeLa.tab

Selection criteria for defining intron groups:

UP\_INTRONS\_HeLa\_SRRM2-KD : having value UP\_INTRONS\_HeLa\_SRRM2-KD in column GROUP

DOWN\_INTRONS\_HeLa\_SRRM2-KD : having value DOWN\_INTRONS\_HeLa\_SRRM2-KD in column GROUP

CR : having value CR in column GROUP

CS : having value CS in column GROUP

AS\_NC : having value AS\_NC in column GROUP

Intron duplicates removal: yes

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

UP\_INTRONS\_HeLa\_SRRM2-KD: 164 / 155

DOWN\_INTRONS\_HeLa\_SRRM2-KD: 99 / 95

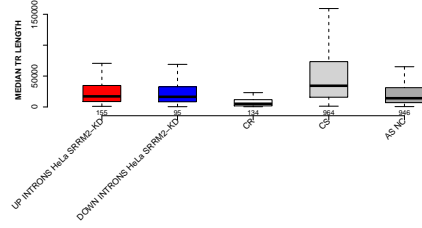
CR: 138 / 134

CS: 1000 / 964

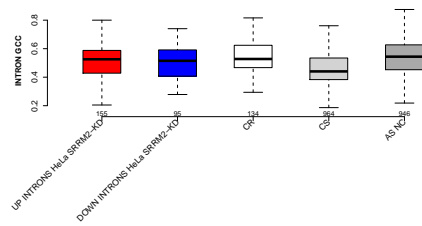
AS\_NC: 1000 / 946

## 5 Overview: Features with statistically significant differences (p-val $\leq 0.05$ )

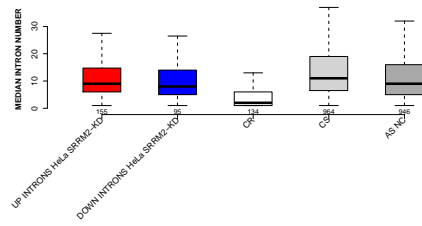
### MEDIAN TR LENGTH



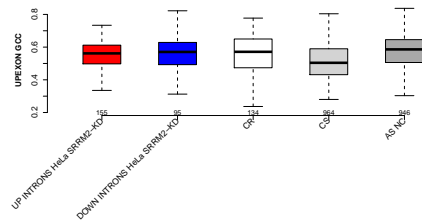
### INTRON GCC



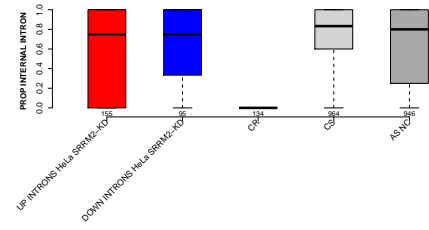
### MEDIAN INTRON NUMBER



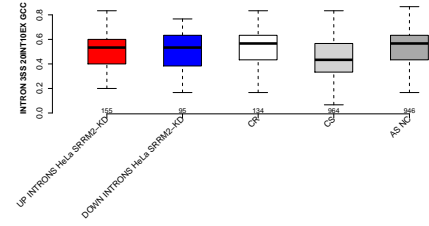
### UPEXON GCC



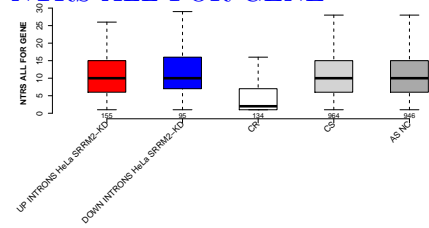
## PROP INTERNAL INTRON



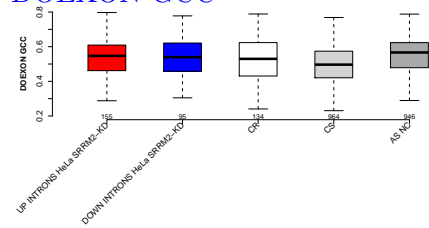
## INTRON 3SS 20INT10EX GCC



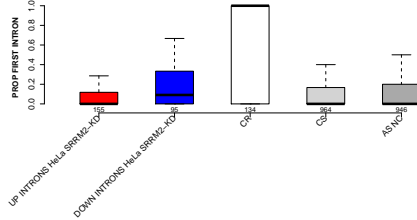
## NTRS ALL FOR GENE



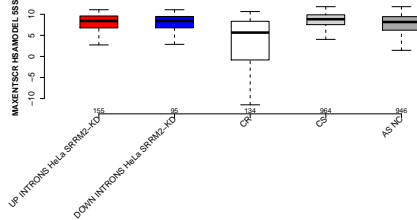
## DOEXON GCC



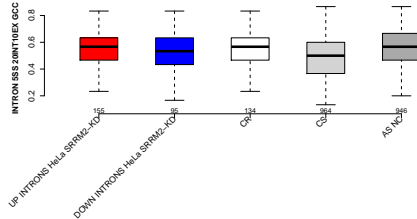
PROP FIRST INTRON



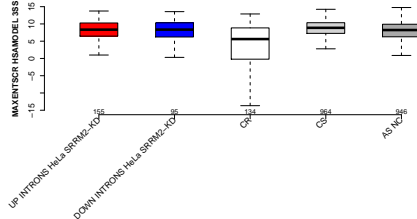
MAXENTSCR HSAMODEL 5SS



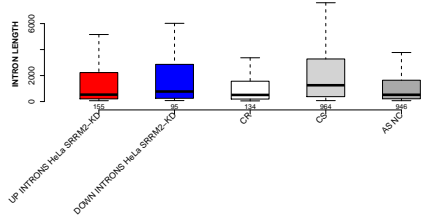
INTRON 5SS 20INT10EX GCC



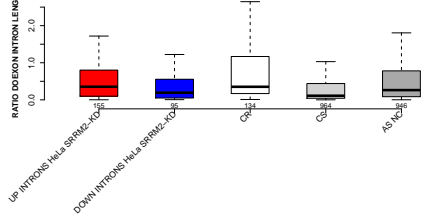
MAXENTSCR HSAMODEL 3SS



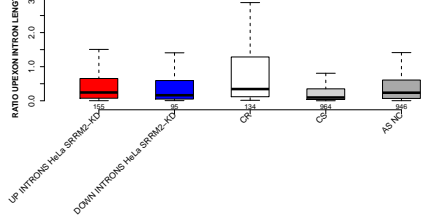
INTRON LENGTH



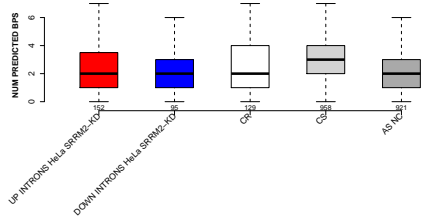
RATIO DOEXON INTRON LENGTH



RATIO UPEXON INTRON LENGTH

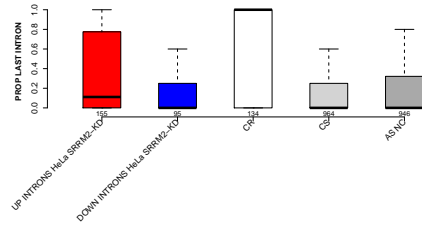


NUM PREDICTED BPS

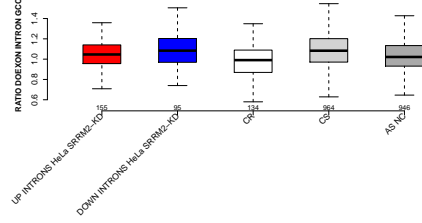




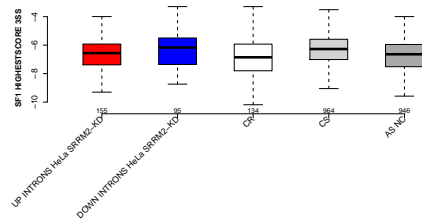
## PROP LAST INTRON



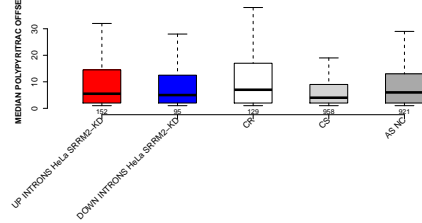
## RATIO DOEXON INTRON GCC



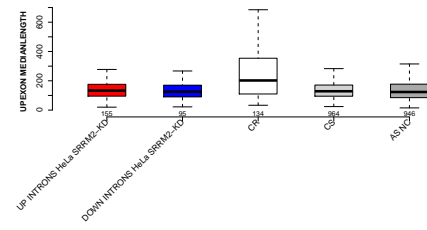
## SF1 HIGHESTSCORE 3SS



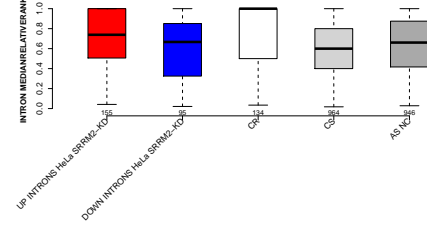
## MEDIAN POLYPYRITRAC OFFSET



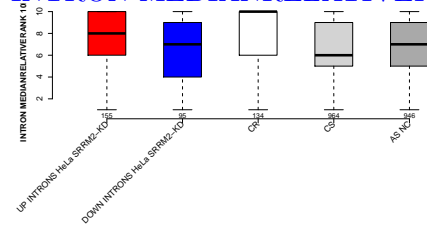
## UPEXON MEDIANLENGTH



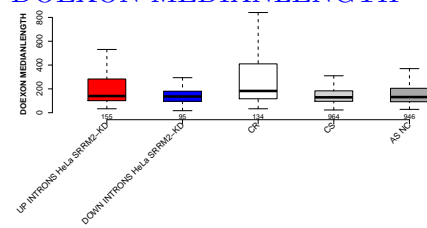
## INTRON MEDIANRELATIVERANK



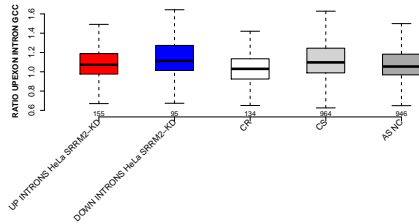
## INTRON MEDIANRELATIVERANK 10BINS



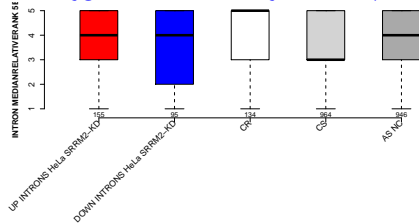
## DOEXON MEDIANLENGTH



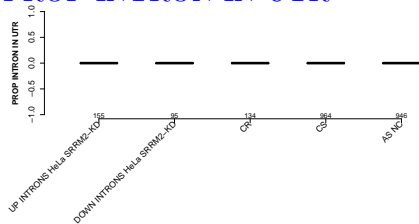
RATIO UPEXON INTRON GCC



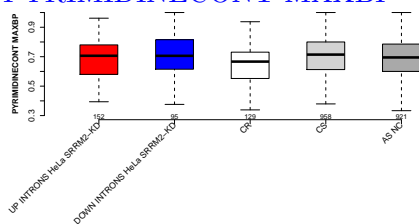
INTRON MEDIANRELATIVERANK 5BINS



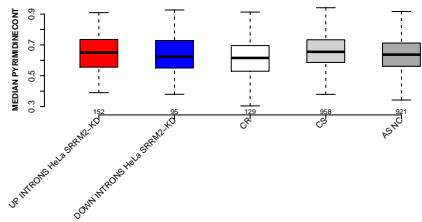
PROP INTRON IN UTR



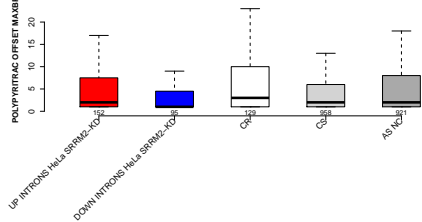
PYRIMIDINECONT MAXBP



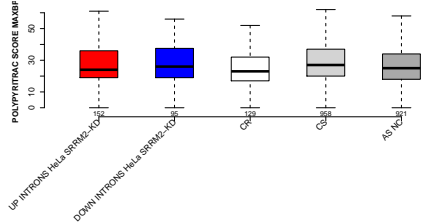
MEDIAN PYRIMIDINECONT



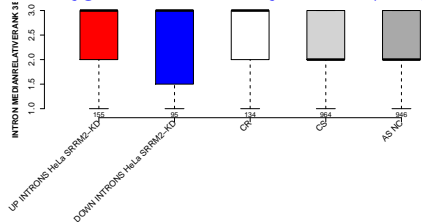
POLYPYRITRAC OFFSET MAXBP



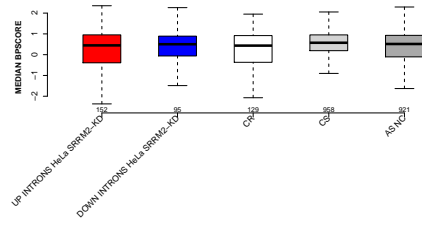
POLYPYRITRAC SCORE MAXBP



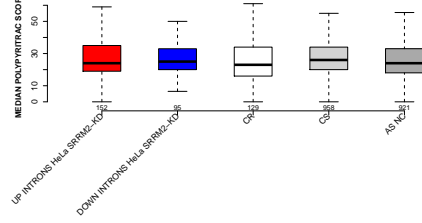
INTRON MEDIANRELATIVERANK 3BINS



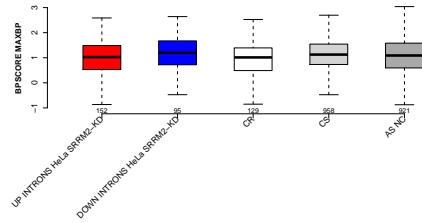
### MEDIAN BPSCORE



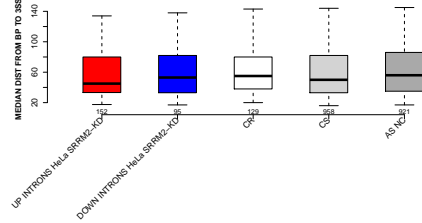
### MEDIAN POLYPYRITRAC SCORE



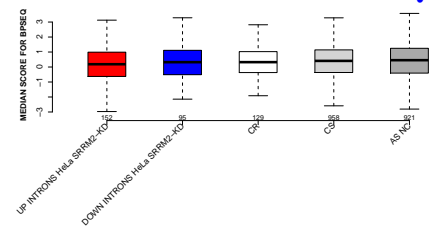
### BPSCORE MAXBP



### MEDIAN DIST FROM BP TO 3SS



## MEDIAN SCORE FOR BPSEQ

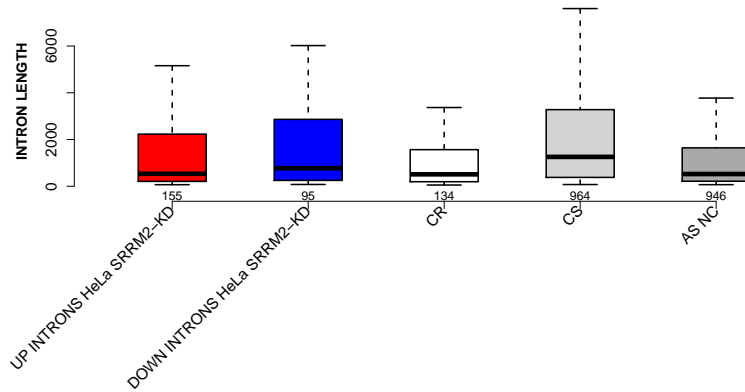


## 6 Details: Box plots and statistical assessments for all features

### 6.1 INTRON LENGTH

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Meaning:



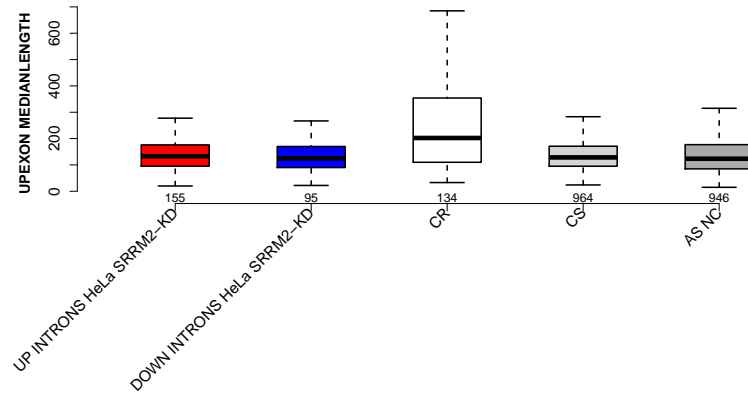
Significant results from Mann-Whitney U test:

- UP\_INTRONS\_HeLa\_SRRM2-KD vs CS : 4.87266e-06  
mean: 2166.0258 < 3879.2459 , median: 533 < 1255.5
- CR vs CS : 1.08129e-07  
mean: 1152.2313 < 3879.2459 , median: 509 < 1255.5
- CS vs AS\_NC : 2.92607e-20  
mean: 3879.2459 > 1716.518 , median: 1255.5 > 521.5

## 6.2 UPEXON MEDIANLENGTH

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Meaning: if intron is in several transcripts, it might have different up-stream exons, and this is the median length of them



Significant results from Mann-Whitney U test:

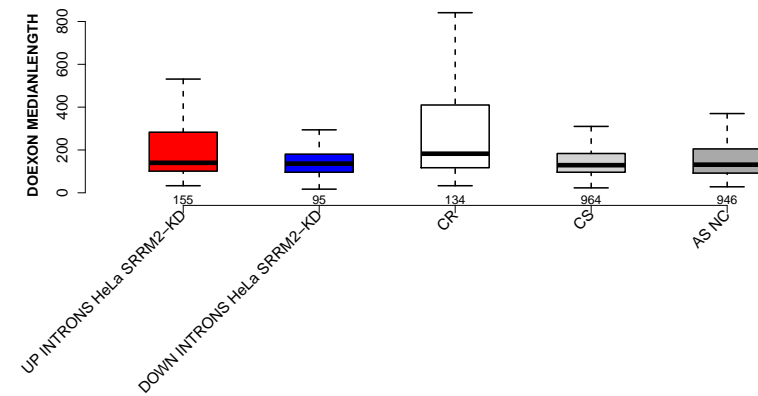
- UP\_INTRONS\_HeLa\_SRRM2-KD vs CR : 3.86644e-06  
mean: 164.8548 < 356.5522 , median: 133 < 202.25
- DOWN\_INTRONS\_HeLa\_SRRM2-KD vs CR : 5.58287e-05  
mean: 183.0789 < 356.5522 , median: 125 < 202.25
- CR vs CS : 3.20885e-10  
mean: 356.5522 > 150.1846 , median: 202.25 > 128.5
- CR vs AS\_NC : 1.57614e-10  
mean: 356.5522 > 160.0751 , median: 202.25 > 123.5



### 6.3 DOEXON MEDIANLENGTH

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Meaning: same as UPEXON MEDIANLENGTH but for down-stream exons



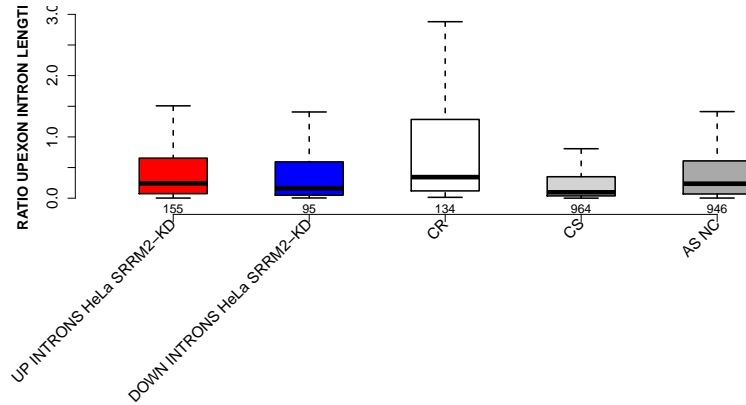
Significant results from Mann-Whitney U test:

- UP\_INTRONS\_HeLa\_SRRM2-KD vs CR : 0.0260182  
mean: 375.7677 > 361.4627 , median: 140 < 182.5
- UP\_INTRONS\_HeLa\_SRRM2-KD vs CS : 0.0182822  
mean: 375.7677 > 246.346 , median: 140 > 129
- DOWN\_INTRONS\_HeLa\_SRRM2-KD vs CR : 0.000480698  
mean: 244.5053 < 361.4627 , median: 136 < 182.5
- CR vs CS : 2.48579e-08  
mean: 361.4627 > 246.346 , median: 182.5 > 129
- CR vs AS\_NC : 5.78224e-06  
mean: 361.4627 > 268.2442 , median: 182.5 > 131.25

## 6.4 RATIO UPEXON INTRON LENGTH

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Meaning: median up-stream exon length / intron length



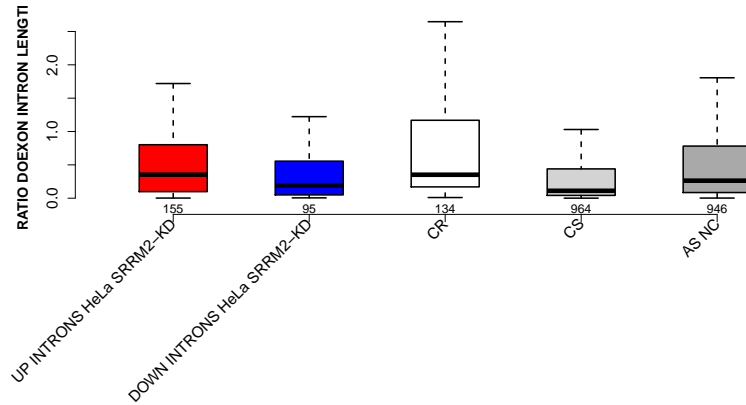
Significant results from Mann-Whitney U test:

- UP\_INTRONS\_HeLa\_SRRM2-KD vs CR : 0.00242493  
mean: 0.475157 < 1.0408 , median: 0.243243 < 0.343735
- UP\_INTRONS\_HeLa\_SRRM2-KD vs CS : 1.23865e-06  
mean: 0.475157 > 0.328647 , median: 0.243243 > 0.0958741
- DOWN\_INTRONS\_HeLa\_SRRM2-KD vs CR : 0.000146514  
mean: 0.442579 < 1.0408 , median: 0.162243 < 0.343735
- DOWN\_INTRONS\_HeLa\_SRRM2-KD vs CS : 0.0326435  
mean: 0.442579 > 0.328647 , median: 0.162243 > 0.0958741
- CR vs CS : 8.2837e-16  
mean: 1.0408 > 0.328647 , median: 0.343735 > 0.0958741
- CR vs AS\_NC : 4.36147e-05  
mean: 1.0408 > 0.47991 , median: 0.343735 > 0.236098
- CS vs AS\_NC : 1.46819e-18  
mean: 0.328647 < 0.47991 , median: 0.0958741 < 0.236098

## 6.5 RATIO DOEXON INTRON LENGTH

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Meaning: median down-stream exon length / intron length



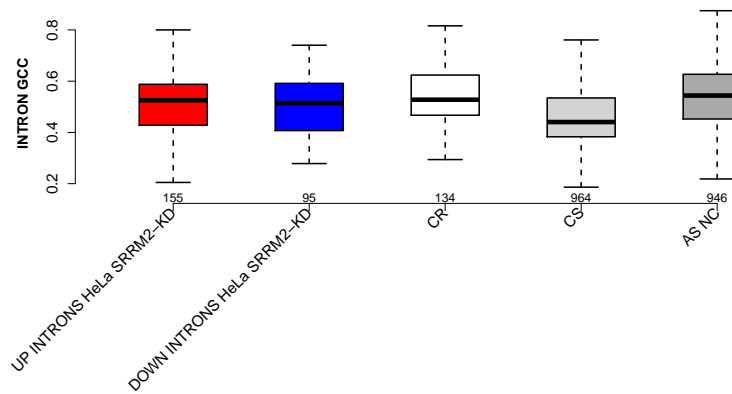
Significant results from Mann-Whitney U test:

- UP\_INTRONS\_HeLa\_SRRM2-KD vs DOWN\_INTRONS\_HeLa\_SRRM2-KD : 0.0176405  
mean: 1.0333 > 0.547007 , median: 0.35315 > 0.191702
- UP\_INTRONS\_HeLa\_SRRM2-KD vs CS : 1.45192e-08  
mean: 1.0333 > 0.467174 , median: 0.35315 > 0.110795
- DOWN\_INTRONS\_HeLa\_SRRM2-KD vs CR : 0.000620765  
mean: 0.547007 < 1.4756 , median: 0.191702 < 0.351779
- DOWN\_INTRONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.0327654  
mean: 0.547007 < 0.802519 , median: 0.191702 < 0.262484
- CR vs CS : 4.59092e-13  
mean: 1.4756 > 0.467174 , median: 0.351779 > 0.110795
- CR vs AS\_NC : 0.00522333  
mean: 1.4756 > 0.802519 , median: 0.351779 > 0.262484
- CS vs AS\_NC : 1.17687e-19  
mean: 0.467174 < 0.802519 , median: 0.110795 < 0.262484

## 6.6 INTRON GCC

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Meaning: GC content of entire intron sequence



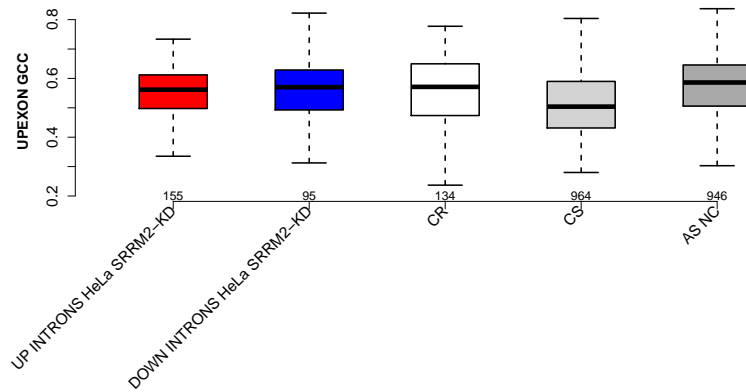
Significant results from Mann-Whitney U test:

- UP\_INTRONS\_HeLa\_SRRM2-KD vs CS : 1.67063e-08  
mean: 0.513464 > 0.462795 , median: 0.525499 > 0.440515
- UP\_INTRONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.0105787  
mean: 0.513464 < 0.538179 , median: 0.525499 < 0.543969
- DOWN\_INTRONS\_HeLa\_SRRM2-KD vs CR : 0.0135932  
mean: 0.500922 < 0.540639 , median: 0.514793 < 0.52764
- DOWN\_INTRONS\_HeLa\_SRRM2-KD vs CS : 0.00185869  
mean: 0.500922 > 0.462795 , median: 0.514793 > 0.440515
- DOWN\_INTRONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.00296322  
mean: 0.500922 < 0.538179 , median: 0.514793 < 0.543969
- CR vs CS : 8.03349e-14  
mean: 0.540639 > 0.462795 , median: 0.52764 > 0.440515
- CS vs AS\_NC : 1.99986e-46  
mean: 0.462795 < 0.538179 , median: 0.440515 < 0.543969

## 6.7 UPEXON GCC

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Meaning: median GC content of up-stream exons for all occurrences of intron



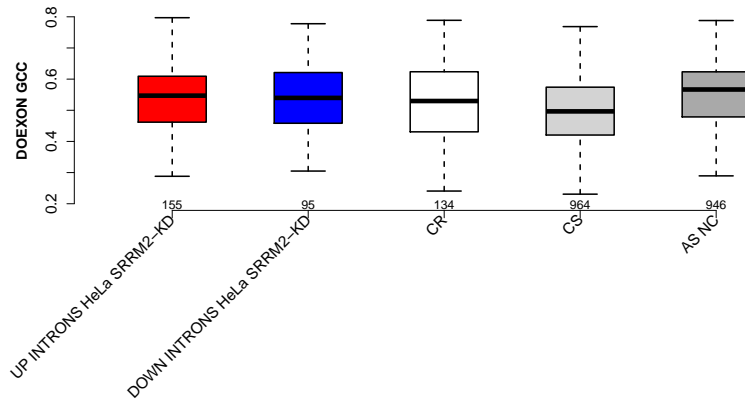
Significant results from Mann-Whitney U test:

- UP\_INTRONS\_HeLa\_SRRM2-KD vs CS : 1.08989e-06  
mean: 0.55085 > 0.513191 , median: 0.561644 > 0.503971
- UP\_INTRONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.00391267  
mean: 0.55085 < 0.572651 , median: 0.561644 < 0.586097
- DOWN\_INTRONS\_HeLa\_SRRM2-KD vs CS : 4.57132e-05  
mean: 0.557332 > 0.513191 , median: 0.57037 > 0.503971
- CR vs CS : 1.99789e-05  
mean: 0.551601 > 0.513191 , median: 0.571212 > 0.503971
- CS vs AS\_NC : 1.17805e-36  
mean: 0.513191 < 0.572651 , median: 0.503971 < 0.586097

## 6.8 DOEXON GCC

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

Meaning: same as UPEXON MEDIANGCC but for down-stream exons



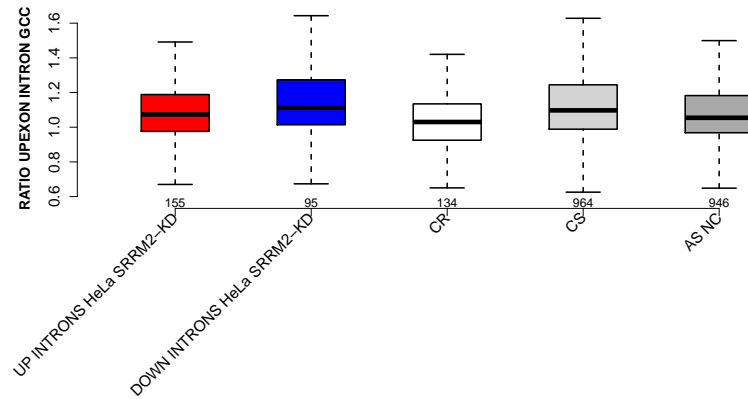
Significant results from Mann-Whitney U test:

- UP\_INTRONS\_HeLa\_SRRM2-KD vs CS : 1.99243e-05  
mean: 0.533688 > 0.498499 , median: 0.546935 > 0.496447
- UP\_INTRONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.045121  
mean: 0.533688 < 0.549441 , median: 0.546935 < 0.566667
- DOWN\_INTRONS\_HeLa\_SRRM2-KD vs CS : 0.000487033  
mean: 0.537607 > 0.498499 , median: 0.539683 > 0.496447
- CR vs CS : 0.00776785  
mean: 0.527008 > 0.498499 , median: 0.529714 > 0.496447
- CR vs AS\_NC : 0.0328866  
mean: 0.527008 < 0.549441 , median: 0.529714 < 0.566667
- CS vs AS\_NC : 2.04679e-29  
mean: 0.498499 < 0.549441 , median: 0.496447 < 0.566667

## 6.9 RATIO UPEXON INTRON GCC

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

Meaning: median GC content of up-stream exons / GC content of intron



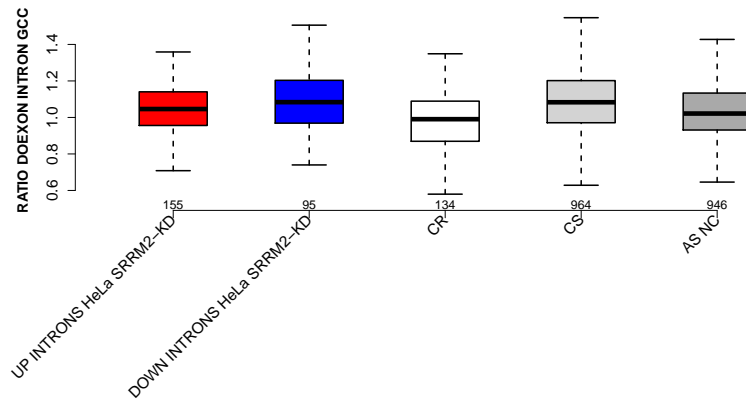
Significant results from Mann-Whitney U test:

- UP\_INTRONS\_HeLa\_SRRM2-KD vs CR : 0.00608431  
mean: 1.1016 > 1.0397 , median: 1.0741 > 1.0302
- DOWN\_INTRONS\_HeLa\_SRRM2-KD vs CR : 0.000128511  
mean: 1.1378 > 1.0397 , median: 1.1134 > 1.0302
- DOWN\_INTRONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.00569266  
mean: 1.1378 > 1.087 , median: 1.1134 > 1.0545
- CR vs CS : 1.09163e-06  
mean: 1.0397 < 1.1365 , median: 1.0302 < 1.0973
- CR vs AS\_NC : 0.00759914  
mean: 1.0397 < 1.087 , median: 1.0302 < 1.0545
- CS vs AS\_NC : 4.92848e-07  
mean: 1.1365 > 1.087 , median: 1.0973 > 1.0545

## 6.10 RATIO DOEXON INTRON GCC

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

Meaning: same as RATIO UPEXON INTRON GCC but for down-stream exons



Significant results from Mann-Whitney U test:

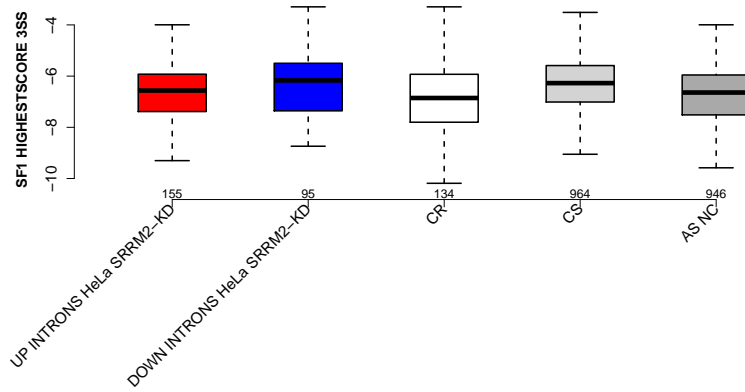
- UP\_INTRONS\_HeLa\_SRRM2-KD vs CR : 0.000725443  
mean: 1.0576 > 0.985322 , median: 1.046 > 0.990465
- UP\_INTRONS\_HeLa\_SRRM2-KD vs CS : 0.00596754  
mean: 1.0576 < 1.1023 , median: 1.046 < 1.0832
- DOWN\_INTRONS\_HeLa\_SRRM2-KD vs CR : 9.31083e-06  
mean: 1.0963 > 0.985322 , median: 1.0837 > 0.990465
- DOWN\_INTRONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.000863889  
mean: 1.0963 > 1.0407 , median: 1.0837 > 1.0214
- CR vs CS : 3.14592e-10  
mean: 0.985322 < 1.1023 , median: 0.990465 < 1.0832
- CR vs AS\_NC : 0.00415084  
mean: 0.985322 < 1.0407 , median: 0.990465 < 1.0214
- CS vs AS\_NC : 2.73176e-14  
mean: 1.1023 > 1.0407 , median: 1.0832 > 1.0214



## 6.11 SF1 HIGHESTSCORE 3SS

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



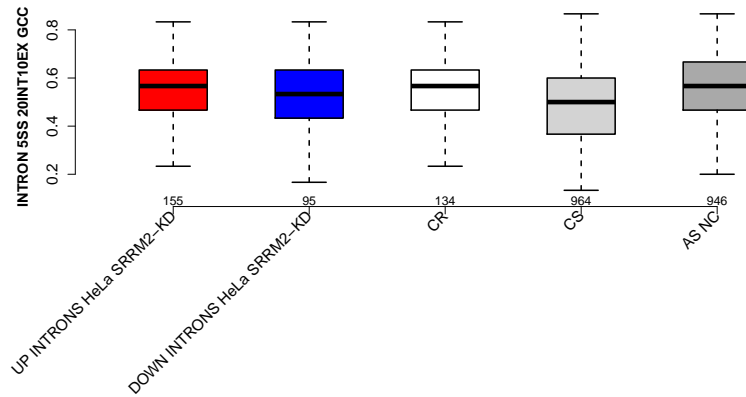
Significant results from Mann-Whitney U test:

- UP\_INTRONS\_HeLa\_SRRM2-KD vs CS : 0.00137915  
mean: -6.595 < -6.30322 , median: -6.56323 < -6.27371
- DOWN\_INTRONS\_HeLa\_SRRM2-KD vs CR : 0.00456293  
mean: -6.34334 > -6.82551 , median: -6.1683 > -6.85534
- DOWN\_INTRONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.0105456  
mean: -6.34334 > -6.66534 , median: -6.1683 > -6.64168
- CR vs CS : 1.69447e-06  
mean: -6.82551 < -6.30322 , median: -6.85534 < -6.27371
- CS vs AS\_NC : 1.14903e-12  
mean: -6.30322 > -6.66534 , median: -6.27371 > -6.64168

## 6.12 INTRON 5SS 20INT10EX GCC

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

Meaning: GC content of last 10 exon and first 20 intron positions at 5 prime end of intron



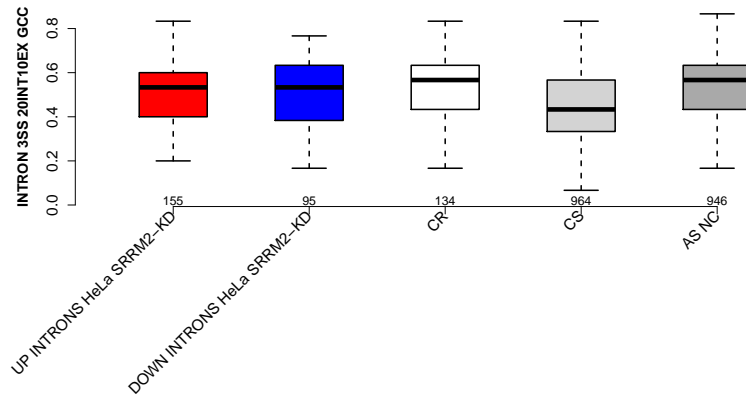
Significant results from Mann-Whitney U test:

- UP\_INTRONS\_HeLa\_SRRM2-KD vs CS : 1.00991e-05  
mean: 0.545591 > 0.492704 , median: 0.566667 > 0.5
- DOWN\_INTRONS\_HeLa\_SRRM2-KD vs CS : 0.0273543  
mean: 0.52386 > 0.492704 , median: 0.533333 > 0.5
- DOWN\_INTRONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.0171307  
mean: 0.52386 < 0.558069 , median: 0.533333 < 0.566667
- CR vs CS : 1.4896e-06  
mean: 0.555721 > 0.492704 , median: 0.566667 > 0.5
- CS vs AS\_NC : 9.22956e-24  
mean: 0.492704 < 0.558069 , median: 0.5 < 0.566667

## 6.13 INTRON 3SS 20INT10EX GCC

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

Meaning: GC content of last 20 intron and first 10 exon positions at 3 prime end of intron



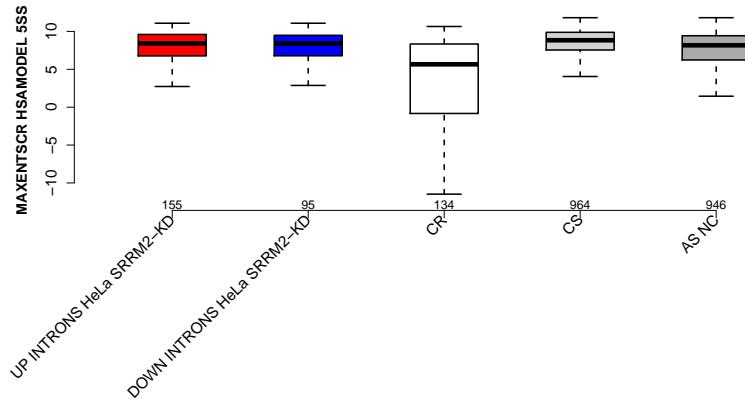
Significant results from Mann-Whitney U test:

- UP\_INTRONS\_HeLa\_SRRM2-KD vs CS : 3.54434e-06  
mean: 0.505806 > 0.449862 , median: 0.533333 > 0.433333
- UP\_INTRONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.0350321  
mean: 0.505806 < 0.530162 , median: 0.533333 < 0.566667
- DOWN\_INTRONS\_HeLa\_SRRM2-KD vs CS : 9.60153e-05  
mean: 0.508772 > 0.449862 , median: 0.533333 > 0.433333
- CR vs CS : 9.34059e-10  
mean: 0.531095 > 0.449862 , median: 0.566667 > 0.433333
- CS vs AS\_NC : 4.86353e-35  
mean: 0.449862 < 0.530162 , median: 0.433333 < 0.566667

## 6.14 MAXENTSCR HSAMODEL 5SS

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

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



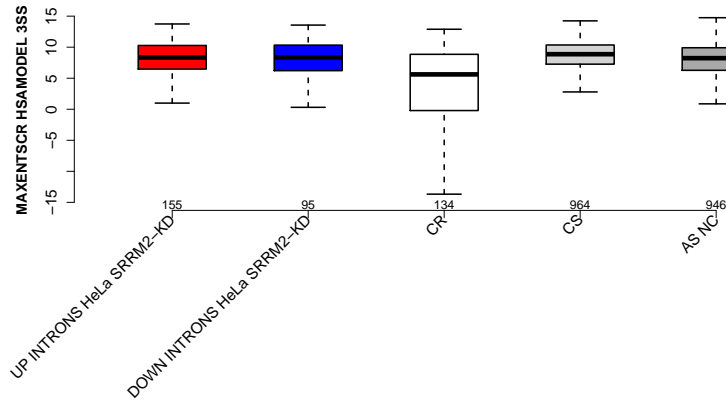
Significant results from Mann-Whitney U test:

- UP\_INTRONS\_HeLa\_SRRM2-KD vs CR : 5.72362e-11  
mean: 7.5978 > 3.059 , median: 8.41 > 5.66
- UP\_INTRONS\_HeLa\_SRRM2-KD vs CS : 0.00540171  
mean: 7.5978 < 8.5015 , median: 8.41 < 8.835
- DOWN\_INTRONS\_HeLa\_SRRM2-KD vs CR : 3.87315e-08  
mean: 7.5123 > 3.059 , median: 8.41 > 5.66
- DOWN\_INTRONS\_HeLa\_SRRM2-KD vs CS : 0.0058917  
mean: 7.5123 < 8.5015 , median: 8.41 < 8.835
- CR vs CS : 7.6399e-26  
mean: 3.059 < 8.5015 , median: 5.66 < 8.835
- CR vs AS\_NC : 2.85077e-14  
mean: 3.059 < 7.4972 , median: 5.66 < 8.17
- CS vs AS\_NC : 1.77517e-16  
mean: 8.5015 > 7.4972 , median: 8.835 > 8.17

## 6.15 MAXENTSCR HSAMODEL 3SS

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

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



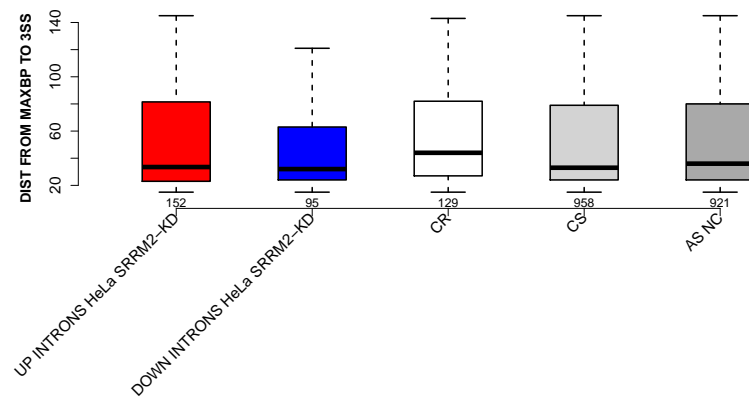
Significant results from Mann-Whitney U test:

- UP\_INTRONS\_HeLa\_SRRM2-KD vs CR : 5.54848e-10  
mean: 8.0493 > 2.8468 , median: 8.34 > 5.615
- DOWN\_INTRONS\_HeLa\_SRRM2-KD vs CR : 2.15187e-07  
mean: 8.0143 > 2.8468 , median: 8.35 > 5.615
- CR vs CS : 4.94648e-21  
mean: 2.8468 < 8.7139 , median: 5.615 < 8.87
- CR vs AS\_NC : 1.83186e-13  
mean: 2.8468 < 7.9216 , median: 5.615 < 8.23
- CS vs AS\_NC : 5.51341e-09  
mean: 8.7139 > 7.9216 , median: 8.87 > 8.23

## 6.16 DIST FROM MAXBP TO 3SS

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

Meaning: Distance to 3ss of best precited BP



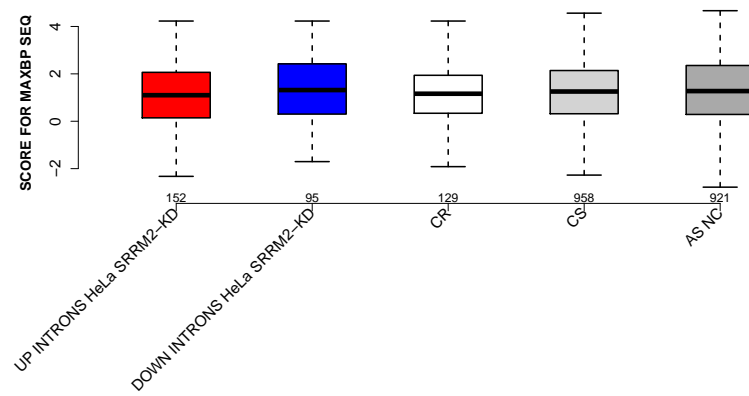
Significant results from Mann-Whitney U test:

- none

## 6.17 SCORE FOR MAXBP SEQ

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

Meaning: BP sequence score of best predicted BP



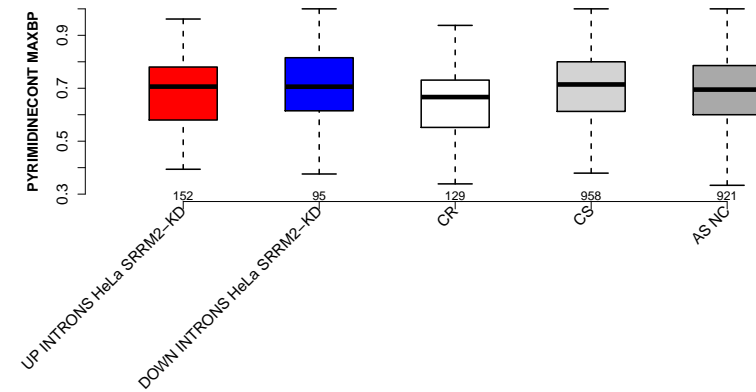
Significant results from Mann-Whitney U test:

- none

## 6.18 PYRIMIDINECONT MAXBP

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

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



Significant results from Mann-Whitney U test:

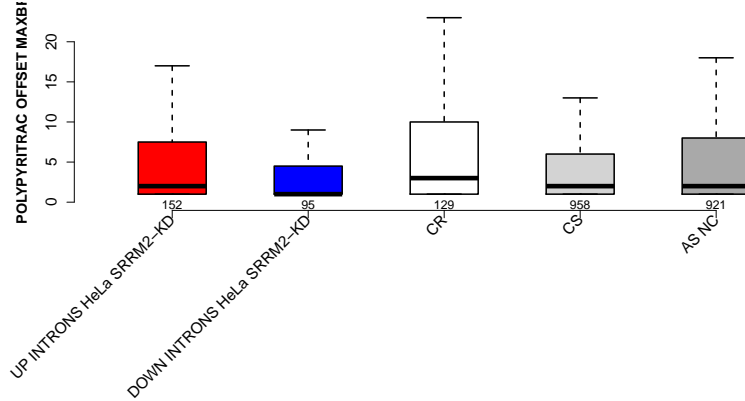
- UP\_INTRONS\_HeLa\_SRRM2-KD vs CR : 0.00710866  
mean: 0.692363 > 0.647842 , median: 0.70619 > 0.666667
- DOWN\_INTRONS\_HeLa\_SRRM2-KD vs CR : 0.000840367  
mean: 0.71519 > 0.647842 , median: 0.705882 > 0.666667
- CR vs CS : 5.61801e-06  
mean: 0.647842 < 0.707598 , median: 0.666667 < 0.714286
- CR vs AS\_NC : 0.000905522  
mean: 0.647842 < 0.690845 , median: 0.666667 < 0.694915
- CS vs AS\_NC : 0.00876255  
mean: 0.707598 > 0.690845 , median: 0.714286 > 0.694915



## 6.19 POLYPYRITRAC OFFSET MAXBP

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

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



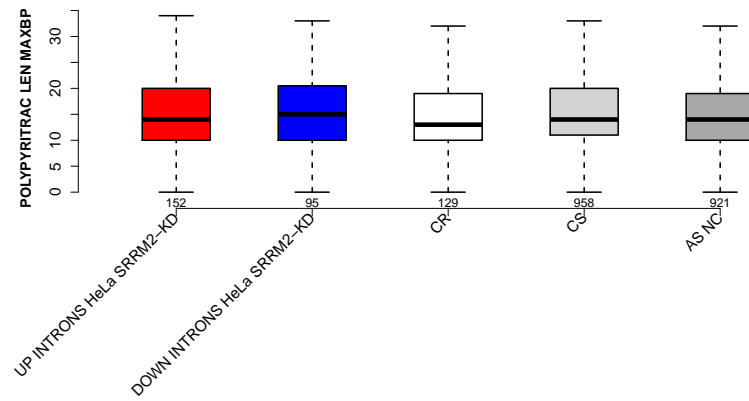
Significant results from Mann-Whitney U test:

- UP\_INTRONS\_HeLa\_SRRM2-KD vs DOWN\_INTRONS\_HeLa\_SRRM2-KD : 0.0471021  
mean: 6.9079 > 3.9368 , median: 2 > 1
- DOWN\_INTRONS\_HeLa\_SRRM2-KD vs CR : 0.0047304  
mean: 3.9368 < 8.3178 , median: 1 < 3
- DOWN\_INTRONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.0072455  
mean: 3.9368 < 6.0239 , median: 1 < 2
- CR vs CS : 0.00158873  
mean: 8.3178 > 4.4927 , median: 3 > 2
- CS vs AS\_NC : 2.41492e-05  
mean: 4.4927 < 6.0239 , median: 2 = 2

## 6.20 POLYPYRITRAC LEN MAXBP

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

Meaning: Polypyrimidine track length for best BP



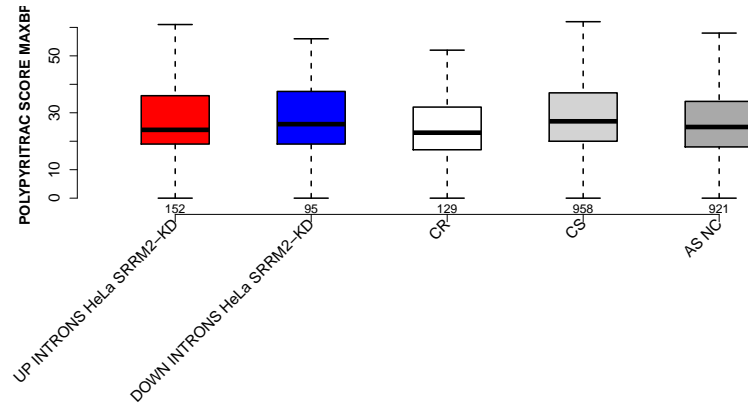
Significant results from Mann-Whitney U test:

- none

## 6.21 POLYPYRITRAC SCORE MAXBP

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

Meaning: Polypyrimidine track score for best BP



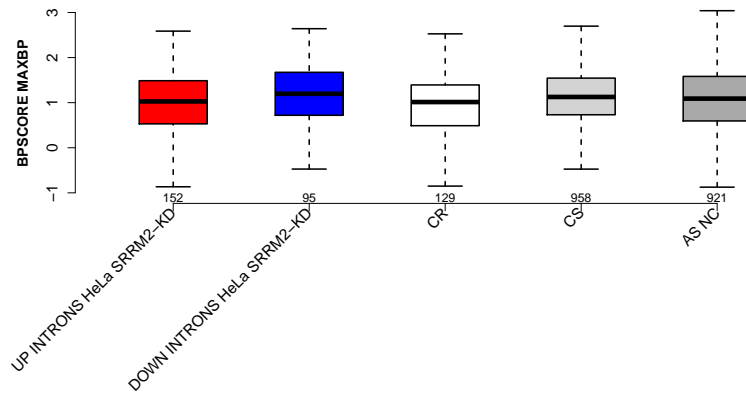
Significant results from Mann-Whitney U test:

- CR vs CS : 0.0016353  
mean: 27.4961 < 30.2213 , median: 23 < 27
- CS vs AS\_NC : 5.8567e-05  
mean: 30.2213 > 28.9761 , median: 27 > 25

## 6.22 BPSCORE MAXBP

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

Meaning: SVM classification score of best BP



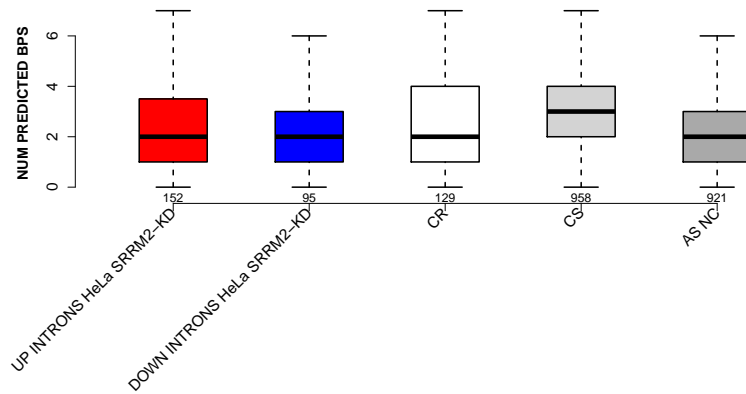
Significant results from Mann-Whitney U test:

- UP\_INTRONS\_HeLa\_SRRM2-KD vs DOWN\_INTRONS\_HeLa\_SRRM2-KD : 0.0306276  
mean: 0.875342 < 1.1583 , median: 1.027 < 1.197
- UP\_INTRONS\_HeLa\_SRRM2-KD vs CS : 0.0159868  
mean: 0.875342 < 1.1101 , median: 1.027 < 1.1261
- DOWN\_INTRONS\_HeLa\_SRRM2-KD vs CR : 0.0133551  
mean: 1.1583 > 0.787115 , median: 1.197 > 1.0133
- CR vs CS : 0.00462666  
mean: 0.787115 < 1.1101 , median: 1.0133 < 1.1261
- CR vs AS\_NC : 0.0379723  
mean: 0.787115 < 1.0158 , median: 1.0133 < 1.0898

## 6.23 NUM PREDICTED BPS

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

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



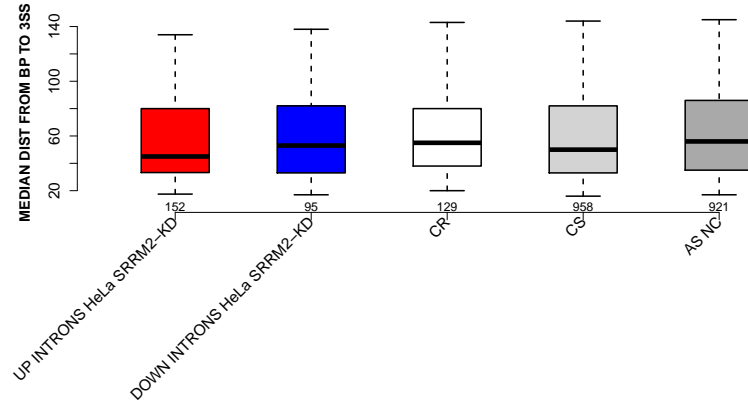
Significant results from Mann-Whitney U test:

- UP\_INTRONS\_HeLa\_SRRM2-KD vs CS : 2.88783e-05  
mean: 2.5263 < 3.2035 , median: 2 < 3
- DOWN\_INTRONS\_HeLa\_SRRM2-KD vs CS : 0.000369413  
mean: 2.4316 < 3.2035 , median: 2 < 3
- CR vs CS : 9.04981e-07  
mean: 2.3566 < 3.2035 , median: 2 < 3
- CS vs AS\_NC : 1.10839e-17  
mean: 3.2035 > 2.4636 , median: 3 > 2

## 6.24 MEDIAN DIST FROM BP TO 3SS

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

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



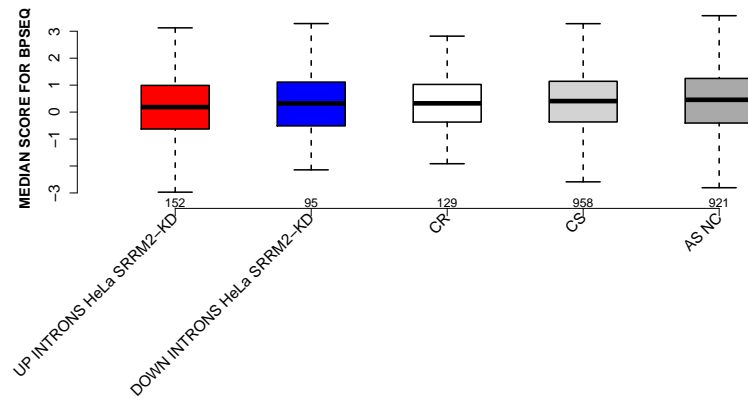
Significant results from Mann-Whitney U test:

- UP\_INTRONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.0390155  
mean: 57.1809 < 62.4001 , median: 45 < 56
- CS vs AS\_NC : 0.00675767  
mean: 58.9358 < 62.4001 , median: 50 < 56

## 6.25 MEDIAN SCORE FOR BPSEQ

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

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



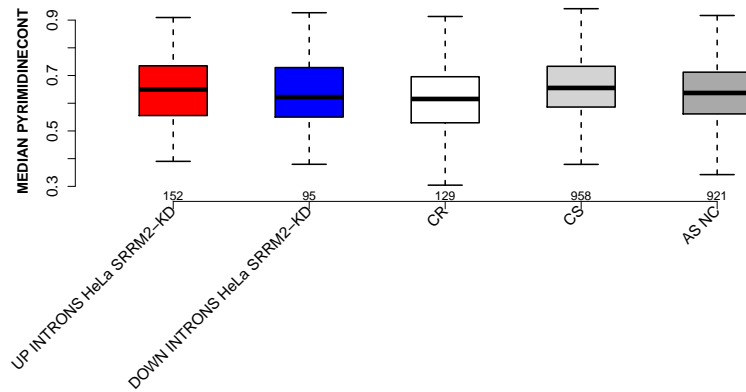
Significant results from Mann-Whitney U test:

- UP\_INTRONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.0211894  
mean: 0.197698 < 0.46408 , median: 0.185756 < 0.455517

## 6.26 MEDIAN PYRIMIDINECONT

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

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



Significant results from Mann-Whitney U test:

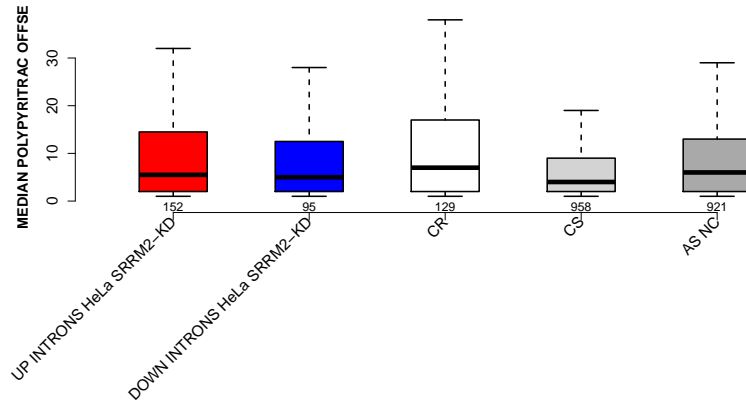
- UP\_INTRONS\_HeLa\_SRRM2-KD vs CR : 0.0123154  
mean: 0.649974 > 0.611269 , median: 0.649675 > 0.615385
- CR vs CS : 9.30364e-06  
mean: 0.611269 < 0.661502 , median: 0.615385 < 0.655172
- CR vs AS\_NC : 0.01555  
mean: 0.611269 < 0.640291 , median: 0.615385 < 0.637036
- CS vs AS\_NC : 2.66141e-05  
mean: 0.661502 > 0.640291 , median: 0.655172 > 0.637036



## 6.27 MEDIAN POLYPYRITRAC OFFSET

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

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



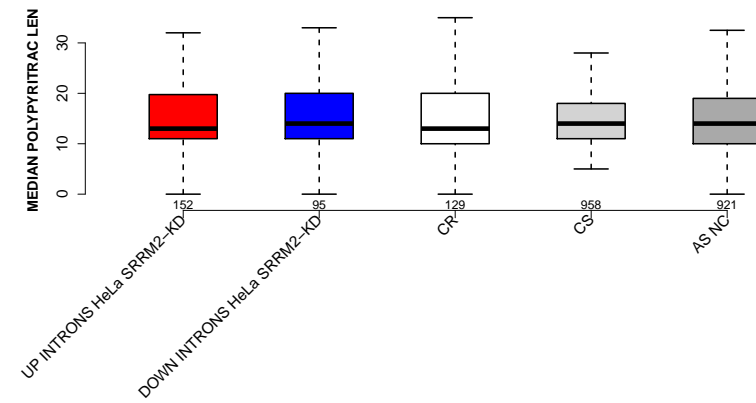
Significant results from Mann-Whitney U test:

- UP\_INTRONS\_HeLa\_SRRM2-KD vs CS : 0.00279852  
mean: 12.6908 > 7.1487 , median: 5.5 > 4
- CR vs CS : 7.87712e-05  
mean: 12.0736 > 7.1487 , median: 7 > 4
- CS vs AS\_NC : 1.37806e-10  
mean: 7.1487 < 10.9783 , median: 4 < 6

## 6.28 MEDIAN POLYPYRITRAC LEN

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

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



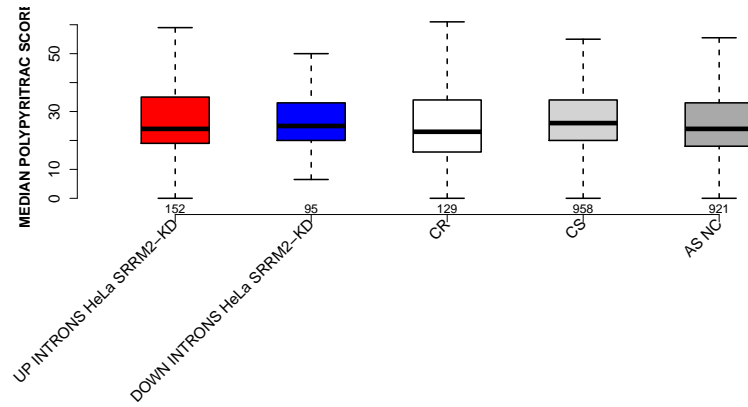
Significant results from Mann-Whitney U test:

- none

## 6.29 MEDIAN POLYPYRITRAC SCORE

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

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



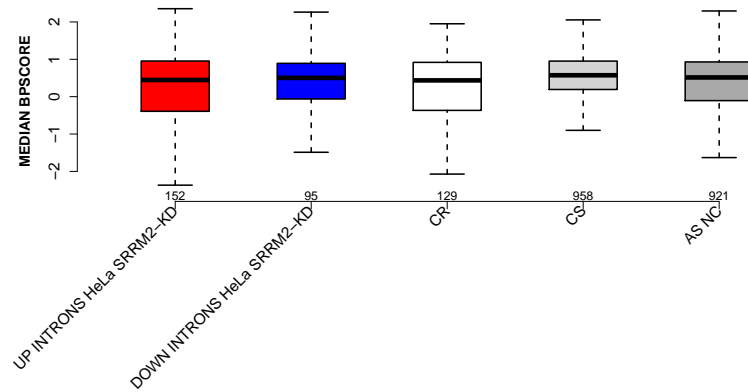
Significant results from Mann-Whitney U test:

- CR vs CS : 0.00373547  
mean: 27.2248 < 28.964 , median: 23 < 26
- CS vs AS\_NC : 0.00110315  
mean: 28.964 > 28.2861 , median: 26 > 24

## 6.30 MEDIAN BPSCORE

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

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



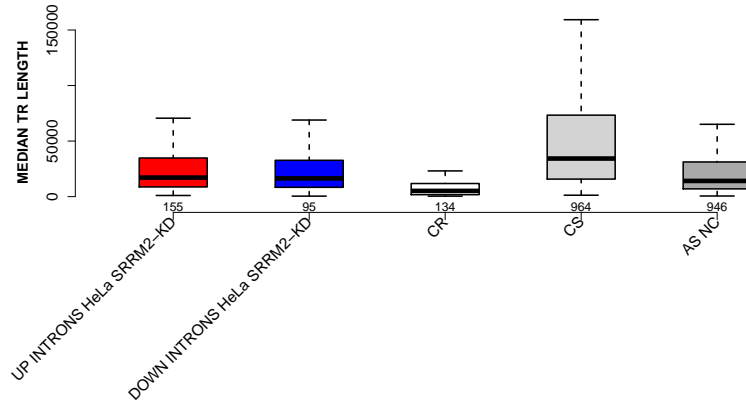
Significant results from Mann-Whitney U test:

- UP\_INTRONS\_HeLa\_SRRM2-KD vs CS : 0.00846798  
mean: 0.0999092 < 0.500233 , median: 0.446996 < 0.572919
- CR vs CS : 0.00199116  
mean: 0.0922574 < 0.500233 , median: 0.435792 < 0.572919
- CS vs AS\_NC : 0.00104682  
mean: 0.500233 > 0.277192 , median: 0.572919 > 0.513934

## 6.31 MEDIAN TR LENGTH

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

Meaning: median length of transcripts the intron occurs in



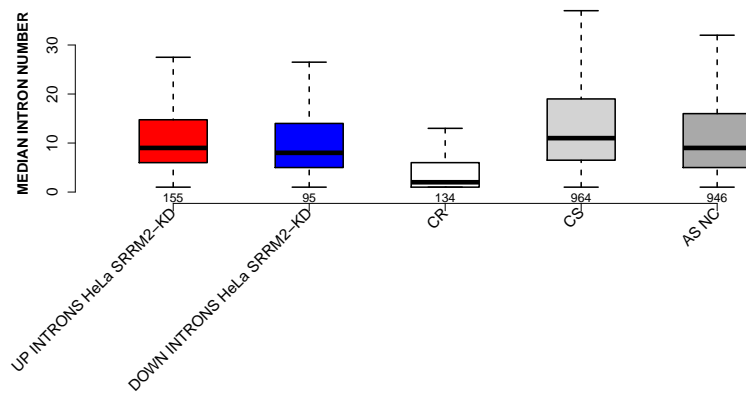
Significant results from Mann-Whitney U test:

- UP\_INTRONS\_HeLa\_SRRM2-KD vs CR : 6.59708e-14  
mean: 31032.071 > 13025.8358 , median: 17128.5 > 5143.25
- UP\_INTRONS\_HeLa\_SRRM2-KD vs CS : 1.97709e-10  
mean: 31032.071 < 57039.4212 , median: 17128.5 < 34287.25
- DOWN\_INTRONS\_HeLa\_SRRM2-KD vs CR : 5.79441e-10  
mean: 29653.3105 > 13025.8358 , median: 16412 > 5143.25
- DOWN\_INTRONS\_HeLa\_SRRM2-KD vs CS : 2.86335e-09  
mean: 29653.3105 < 57039.4212 , median: 16412 < 34287.25
- CR vs CS : 3.44823e-38  
mean: 13025.8358 < 57039.4212 , median: 5143.25 < 34287.25
- CR vs AS\_NC : 9.57145e-17  
mean: 13025.8358 < 26800.0328 , median: 5143.25 < 14123.5
- CS vs AS\_NC : 8.37094e-53  
mean: 57039.4212 > 26800.0328 , median: 34287.25 > 14123.5

## 6.32 MEDIAN INTRON NUMBER

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

Meaning: number of introns of transcripts where intron occurs in



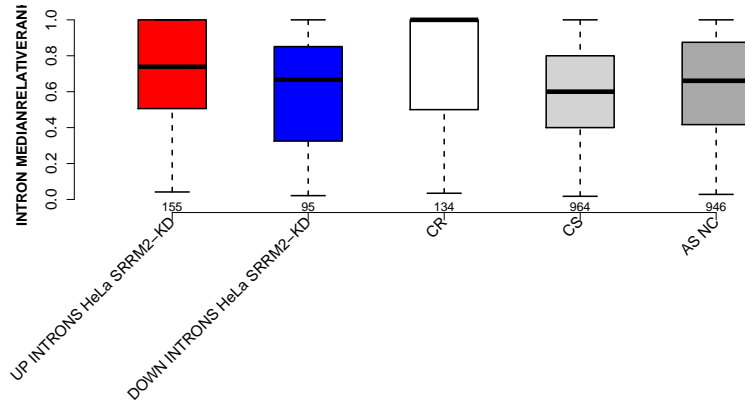
Significant results from Mann-Whitney U test:

- UP\_INTRONS\_HeLa\_SRRM2-KD vs CR : 8.21961e-20  
mean: 11.6 > 4.653 , median: 9 > 2
- UP\_INTRONS\_HeLa\_SRRM2-KD vs CS : 0.00474551  
mean: 11.6 < 14.7329 , median: 9 < 11
- DOWN\_INTRONS\_HeLa\_SRRM2-KD vs CR : 6.49675e-14  
mean: 12.0579 > 4.653 , median: 8 > 2
- DOWN\_INTRONS\_HeLa\_SRRM2-KD vs CS : 0.00365804  
mean: 12.0579 < 14.7329 , median: 8 < 11
- CR vs CS : 1.10678e-39  
mean: 4.653 < 14.7329 , median: 2 < 11
- CR vs AS\_NC : 6.54054e-31  
mean: 4.653 < 12.2193 , median: 2 < 9
- CS vs AS\_NC : 6.33431e-07  
mean: 14.7329 > 12.2193 , median: 11 > 9

### 6.33 INTRON MEDIANRELATIVERANK

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Meaning: similar to INTRON MEDIANRANK, relative rank = rank / number of all introns in transcript, is between 0 and 1



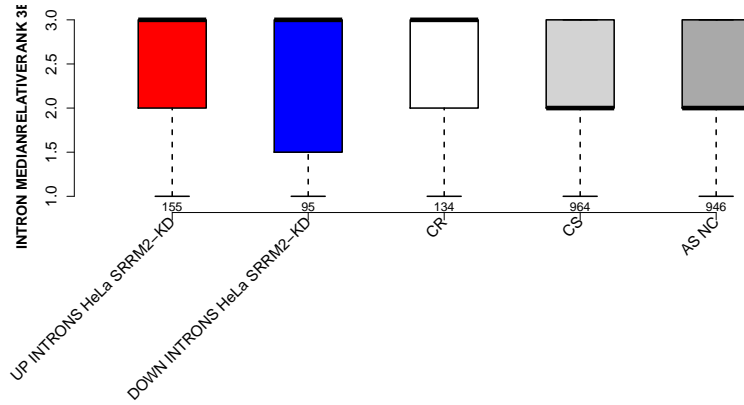
Significant results from Mann-Whitney U test:

- UP\_INTRONS\_HeLa\_SRRM2-KD vs DOWN\_INTRONS\_HeLa\_SRRM2-KD : 0.00664654  
mean: 0.706629 > 0.600236 , median: 0.738636 > 0.666667
- UP\_INTRONS\_HeLa\_SRRM2-KD vs CR : 0.0155778  
mean: 0.706629 < 0.741528 , median: 0.738636 < 1
- UP\_INTRONS\_HeLa\_SRRM2-KD vs CS : 9.66839e-07  
mean: 0.706629 > 0.596326 , median: 0.738636 > 0.6
- UP\_INTRONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.00177639  
mean: 0.706629 > 0.634353 , median: 0.738636 > 0.660714
- DOWN\_INTRONS\_HeLa\_SRRM2-KD vs CR : 4.22325e-05  
mean: 0.600236 < 0.741528 , median: 0.666667 < 1
- CR vs CS : 3.22548e-10  
mean: 0.741528 > 0.596326 , median: 1 > 0.6
- CR vs AS\_NC : 2.83834e-07  
mean: 0.741528 > 0.634353 , median: 1 > 0.660714
- CS vs AS\_NC : 0.00121275  
mean: 0.596326 < 0.634353 , median: 0.6 < 0.660714

## 6.34 INTRON MEDIANRELATIVERANK 3BINS

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



Significant results from Mann-Whitney U test:

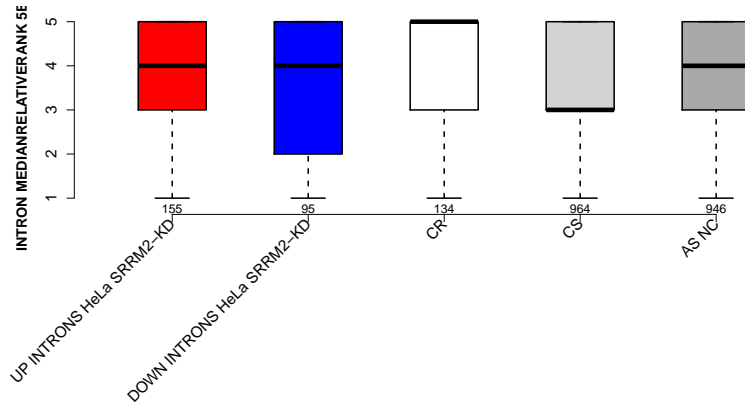
- UP\_INTRONS\_HeLa\_SRRM2-KD vs CS : 0.000912619  
mean: 2.471 > 2.2676 , median: 3 > 2
- UP\_INTRONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.0462794  
mean: 2.471 > 2.3414 , median: 3 > 2
- CR vs CS : 0.000323415  
mean: 2.4776 > 2.2676 , median: 3 > 2
- CR vs AS\_NC : 0.0134824  
mean: 2.4776 > 2.3414 , median: 3 > 2
- CS vs AS\_NC : 0.0151631  
mean: 2.2676 < 2.3414 , median: 2 = 2



## 6.35 INTRON MEDIANRELATIVERANK 5BINS

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Meaning: similar to INTRON MEDIANRELATIVERANK 3BINS with 5 bins



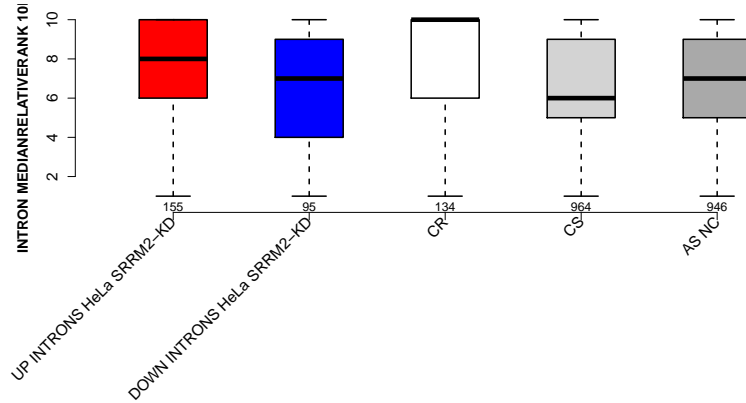
Significant results from Mann-Whitney U test:

- UP\_INTRONS\_HeLa\_SRRM2-KD vs DOWN\_INTRONS\_HeLa\_SRRM2-KD : 0.00772121  
mean: 3.9484 > 3.4526 , median: 4 = 4
- UP\_INTRONS\_HeLa\_SRRM2-KD vs CS : 2.16313e-06  
mean: 3.9484 > 3.4398 , median: 4 > 3
- UP\_INTRONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.00210327  
mean: 3.9484 > 3.6015 , median: 4 = 4
- DOWN\_INTRONS\_HeLa\_SRRM2-KD vs CR : 0.00221592  
mean: 3.4526 < 3.9403 , median: 4 < 5
- CR vs CS : 1.15151e-06  
mean: 3.9403 > 3.4398 , median: 5 > 3
- CR vs AS\_NC : 0.00045711  
mean: 3.9403 > 3.6015 , median: 5 > 4
- CS vs AS\_NC : 0.00284052  
mean: 3.4398 < 3.6015 , median: 3 < 4

## 6.36 INTRON MEDIANRELATIVERANK 10BINS

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Meaning: similar to INTRON MEDIANRELATIVERANK 3BINS with 10 bins



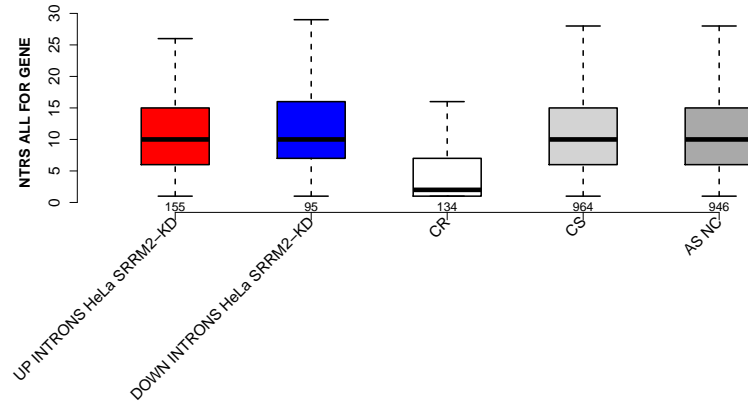
Significant results from Mann-Whitney U test:

- UP\_INTRONS\_HeLa\_SRRM2-KD vs DOWN\_INTRONS\_HeLa\_SRRM2-KD : 0.00634244  
mean: 7.4645 > 6.4737 , median: 8 > 7
- UP\_INTRONS\_HeLa\_SRRM2-KD vs CR : 0.0345051  
mean: 7.4645 < 7.694 , median: 8 < 10
- UP\_INTRONS\_HeLa\_SRRM2-KD vs CS : 2.74931e-06  
mean: 7.4645 > 6.4533 , median: 8 > 6
- UP\_INTRONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.00379649  
mean: 7.4645 > 6.8066 , median: 8 > 7
- DOWN\_INTRONS\_HeLa\_SRRM2-KD vs CR : 5.76052e-05  
mean: 6.4737 < 7.694 , median: 7 < 10
- CR vs CS : 3.04717e-09  
mean: 7.694 > 6.4533 , median: 10 > 6
- CR vs AS\_NC : 3.74844e-06  
mean: 7.694 > 6.8066 , median: 10 > 7
- CS vs AS\_NC : 0.00133839  
mean: 6.4533 < 6.8066 , median: 6 < 7

## 6.37 NTRS ALL FOR GENE

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Meaning: number of transcripts of gene where the intron occurs in



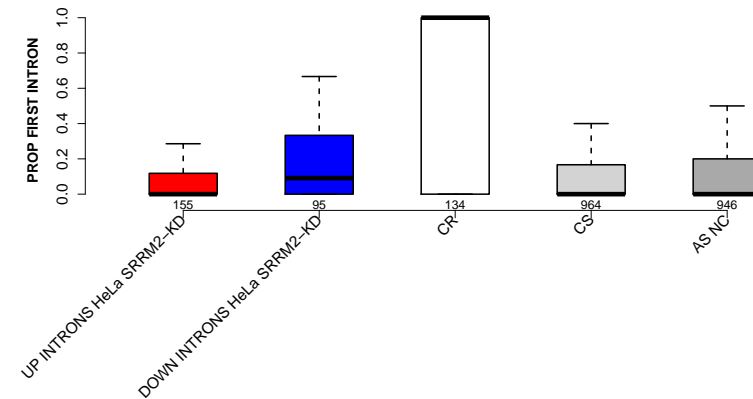
Significant results from Mann-Whitney U test:

- UP\_INTRONS\_HeLa\_SRRM2-KD vs CR : 1.2859e-18  
mean: 11.329 > 5.1119 , median: 10 > 2
- DOWN\_INTRONS\_HeLa\_SRRM2-KD vs CR : 9.90754e-17  
mean: 12.4632 > 5.1119 , median: 10 > 2
- CR vs CS : 4.30137e-30  
mean: 5.1119 < 11.5654 , median: 2 < 10
- CR vs AS\_NC : 7.00098e-29  
mean: 5.1119 < 11.8266 , median: 2 < 10

## 6.38 PROP FIRST INTRON

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Meaning: NTRS WITH INTRON AS FIRST INTRON / NTRS WITH INTRON



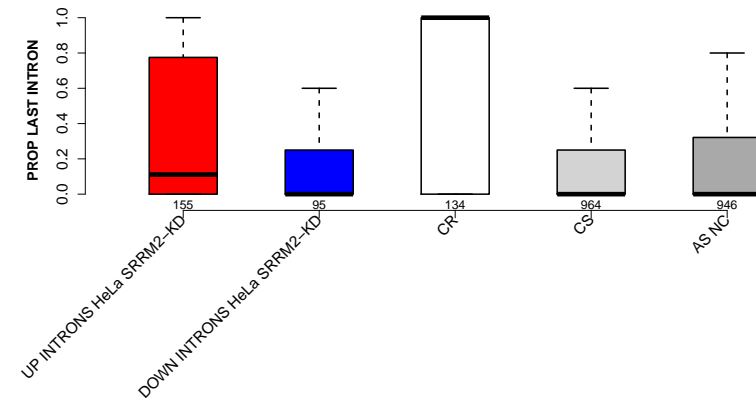
Significant results from Mann-Whitney U test:

- UP\_INTRONS\_HeLa\_SRRM2-KD vs DOWN\_INTRONS\_HeLa\_SRRM2-KD : 0.000683066  
mean: 0.123784 < 0.239339 , median: 0 < 0.0909091
- UP\_INTRONS\_HeLa\_SRRM2-KD vs CR : 9.0133e-17  
mean: 0.123784 < 0.62764 , median: 0 < 1
- DOWN\_INTRONS\_HeLa\_SRRM2-KD vs CR : 1.33844e-07  
mean: 0.239339 < 0.62764 , median: 0.0909091 < 1
- DOWN\_INTRONS\_HeLa\_SRRM2-KD vs CS : 0.000140292  
mean: 0.239339 > 0.126337 , median: 0.0909091 > 0
- DOWN\_INTRONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.0137952  
mean: 0.239339 > 0.187622 , median: 0.0909091 > 0
- CR vs CS : 2.77727e-28  
mean: 0.62764 > 0.126337 , median: 1 > 0
- CR vs AS\_NC : 1.11321e-21  
mean: 0.62764 > 0.187622 , median: 1 > 0
- CS vs AS\_NC : 0.0102985  
mean: 0.126337 < 0.187622 , median: 0 = 0

## 6.39 PROP LAST INTRON

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Meaning: NTRS WITH INTRON AS LAST INTRON / NTRS WITH INTRON



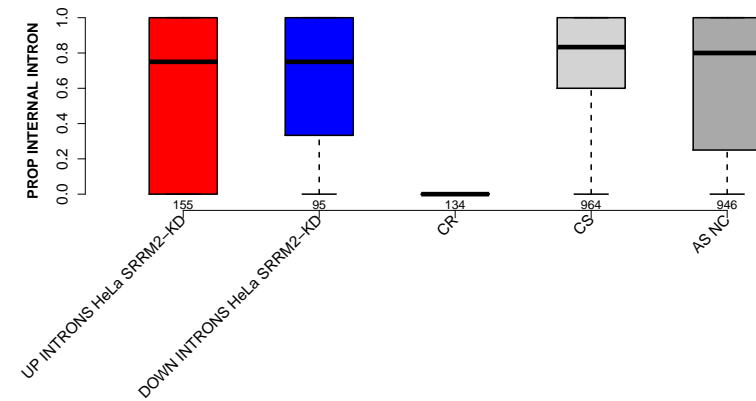
Significant results from Mann-Whitney U test:

- UP\_INTRONS\_HeLa\_SRRM2-KD vs CR : 3.31216e-05  
mean: 0.323509 < 0.581139 , median: 0.111111 < 1
- UP\_INTRONS\_HeLa\_SRRM2-KD vs CS : 0.000193839  
mean: 0.323509 > 0.174989 , median: 0.111111 > 0
- UP\_INTRONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.00684674  
mean: 0.323509 > 0.225521 , median: 0.111111 > 0
- DOWN\_INTRONS\_HeLa\_SRRM2-KD vs CR : 3.77172e-07  
mean: 0.213737 < 0.581139 , median: 0 < 1
- CR vs CS : 2.10845e-17  
mean: 0.581139 > 0.174989 , median: 1 > 0
- CR vs AS\_NC : 4.10561e-14  
mean: 0.581139 > 0.225521 , median: 1 > 0

## 6.40 PROP INTERNAL INTRON

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Meaning: NTRS WITH INTRON AS INTERNAL INTRON / NTRS WITH INTRON



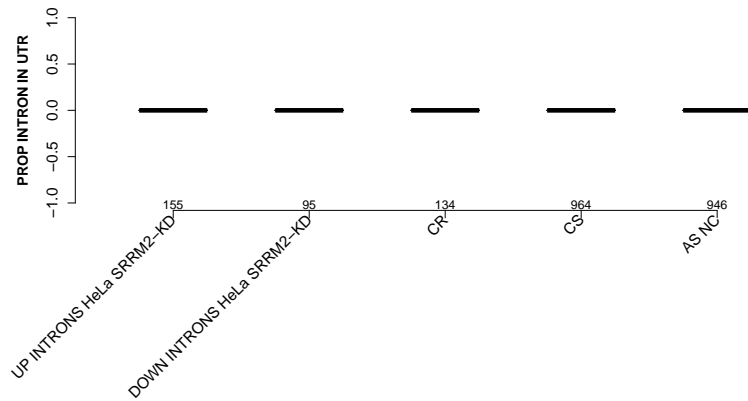
Significant results from Mann-Whitney U test:

- UP\_INTRONS\_HeLa\_SRRM2-KD vs CR : 5.11913e-16  
mean: 0.619586 > 0.185256 , median: 0.75 > 0
- UP\_INTRONS\_HeLa\_SRRM2-KD vs CS : 0.0181204  
mean: 0.619586 < 0.725934 , median: 0.75 < 0.833333
- DOWN\_INTRONS\_HeLa\_SRRM2-KD vs CR : 3.93735e-14  
mean: 0.621332 > 0.185256 , median: 0.75 > 0
- DOWN\_INTRONS\_HeLa\_SRRM2-KD vs CS : 0.00532618  
mean: 0.621332 < 0.725934 , median: 0.75 < 0.833333
- CR vs CS : 2.36114e-35  
mean: 0.185256 < 0.725934 , median: 0 < 0.833333
- CR vs AS\_NC : 3.35221e-26  
mean: 0.185256 < 0.638922 , median: 0 < 0.8
- CS vs AS\_NC : 0.000159711  
mean: 0.725934 > 0.638922 , median: 0.833333 > 0.8

## 6.41 PROP INTRON IN UTR

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Meaning: NTRS WITH INTRON IN UTR / NTRS WITH INTRON



Significant results from Mann-Whitney U test:

- UP\_INTRONS\_HeLa\_SRRM2-KD vs DOWN\_INTRONS\_HeLa\_SRRM2-KD : 0.0348242  
mean: 0.0124322 < 0.0249903 , median: 0 = 0
- DOWN\_INTRONS\_HeLa\_SRRM2-KD vs CS : 2.20266e-06  
mean: 0.0249903 > 0.00707432 , median: 0 = 0
- CR vs CS : 0.00152421  
mean: 0.0265819 > 0.00707432 , median: 0 = 0
- CS vs AS\_NC : 3.32781e-06  
mean: 0.00707432 < 0.0203341 , median: 0 = 0