

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

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Matt version 1.3.0

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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

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 Sfl splicing factor, you might refer to where the Sfl 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 Sfl 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\_EXONS\_SRRM2\_HeLa.tab

Selection criteria for defining exons groups:

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

DOWN\_EXONS\_HeLa\_SRRM2-KD : having value DOWN\_EXONS\_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

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.

UP\_EXONS\_HeLa\_SRRM2-KD: 380 / 367

DOWN\_EXONS\_HeLa\_SRRM2-KD: 444 / 434

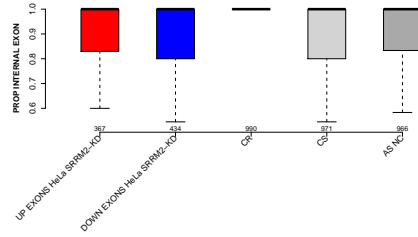
CR: 1000 / 990

CS: 1000 / 971

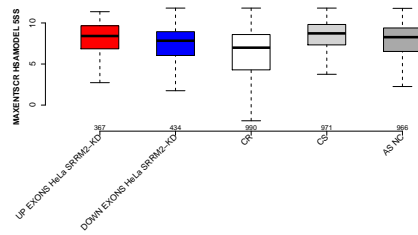
AS\_NC: 1000 / 966

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

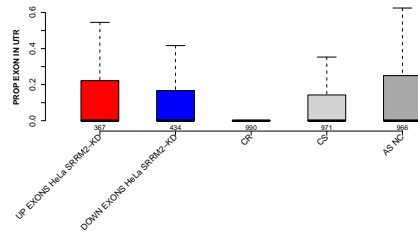
### PROP INTERNAL EXON



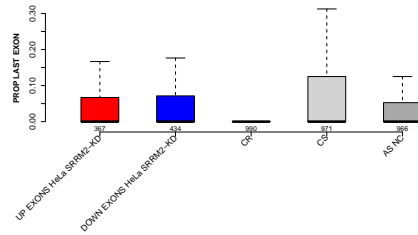
### MAXENTSCR HSAMODEL 5SS



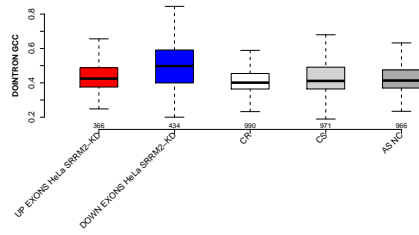
### PROP EXON IN UTR



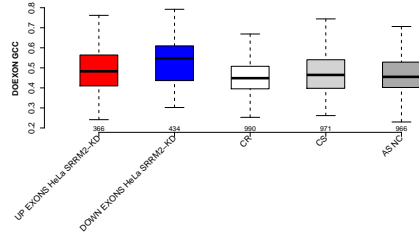
### PROP LAST EXON



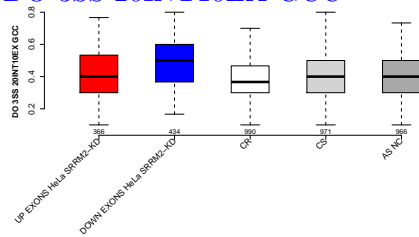
## DOINTRON GCC



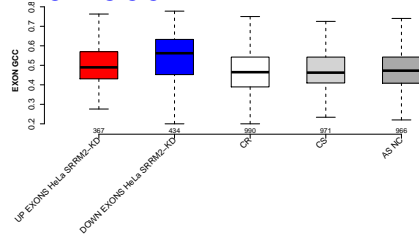
## DOEXON GCC



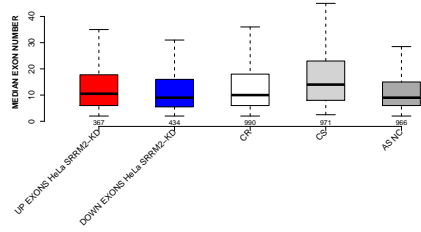
## DO 3SS 20INT10EX GCC



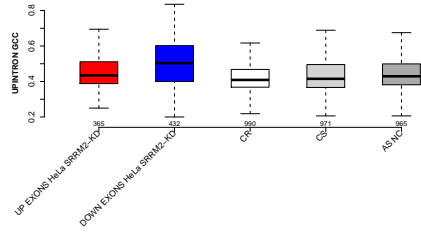
## EXON GCC



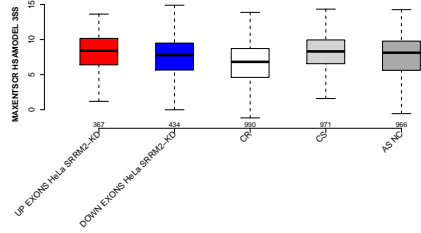
MEDIAN EXON NUMBER



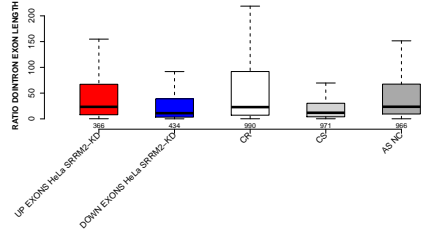
UPINTRON GCC



MAXENTSCR HSAMODEL 3SS

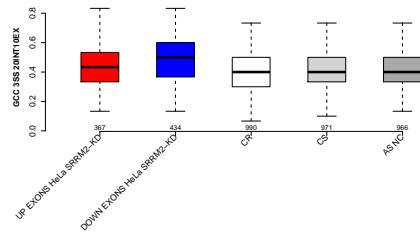


RATIO DONTINRON EXON LENGTH

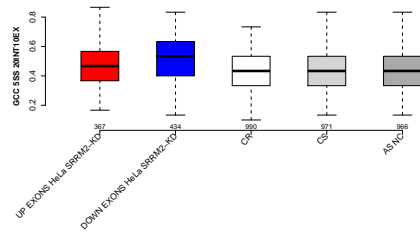




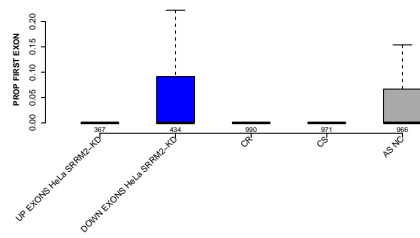
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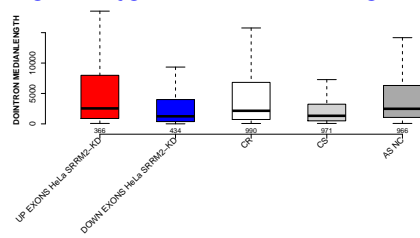
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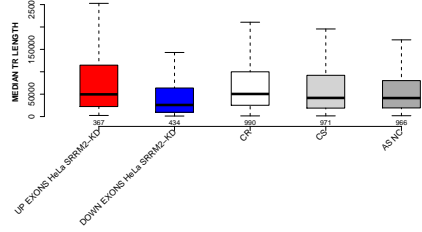
### PROP FIRST EXON



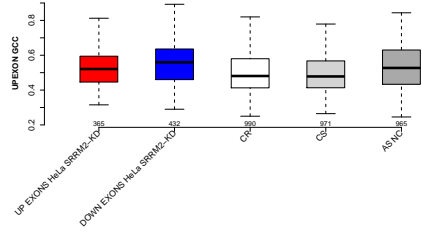
### DOINTRON MEDIANLENGTH



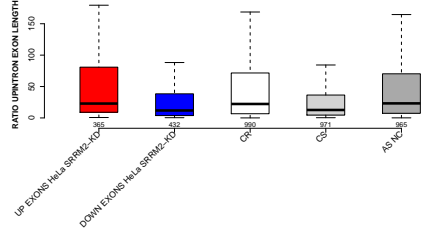
MEDIAN TR LENGTH



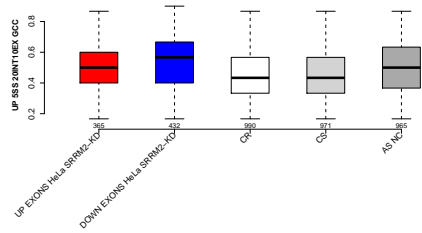
UPEXON GCC



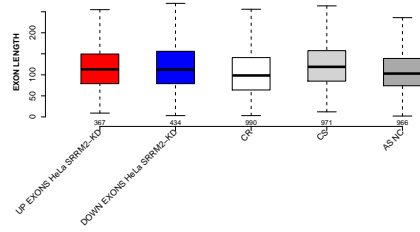
RATIO UPINTRON EXON LENGTH



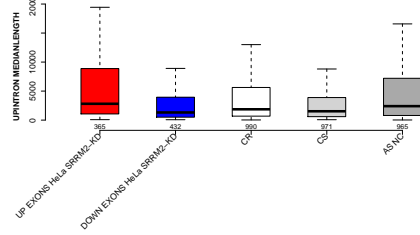
UP 5SS 20INT10EX GCC



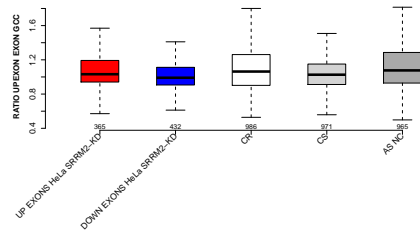
## EXON LENGTH



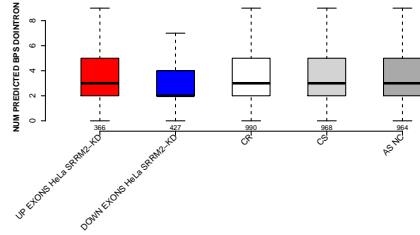
## UPINTRON MEDIANLENGTH



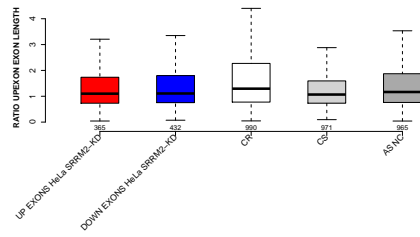
## RATIO UPEXON EXON GCC



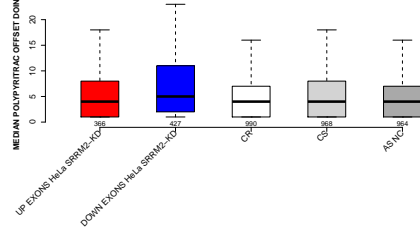
## NUM PREDICTED BPS DOINTRON



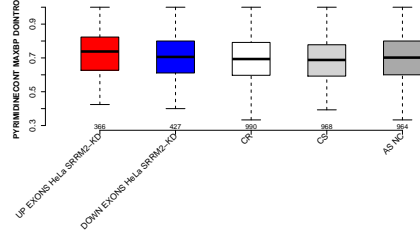
## RATIO UPEXON EXON LENGTH



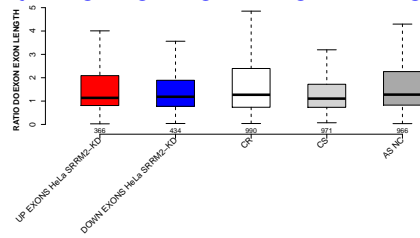
## MEDIAN POLYPYRITRAC OFFSET DOWNT



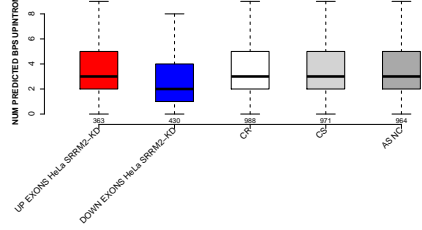
## PYRIMIDINECONT MAXBP DOWNTRO



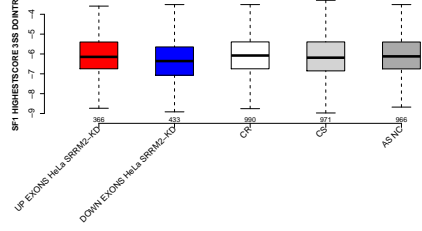
## RATIO DOEXON EXON LENGTH



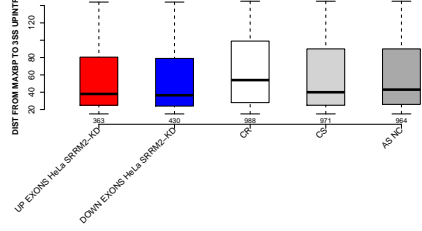
NUM PREDICTED BPS UPINTRON



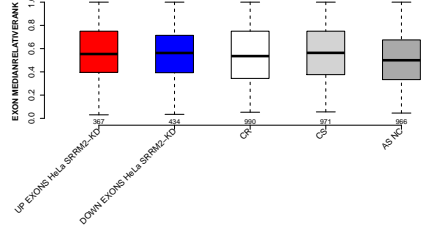
SF1 HIGHESTSCORE 3SS DOWINTRON



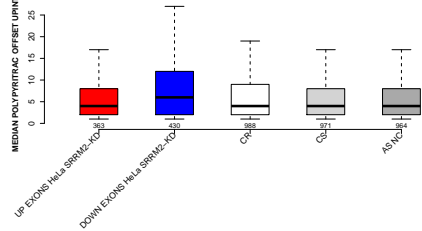
DIST FROM MAXBP TO 3SS UPINTRON



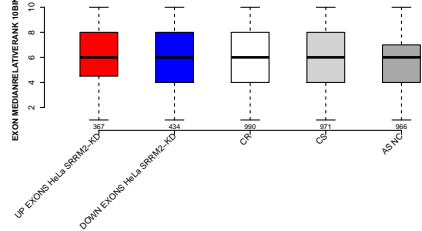
EXON MEDIANRELATIVERANK



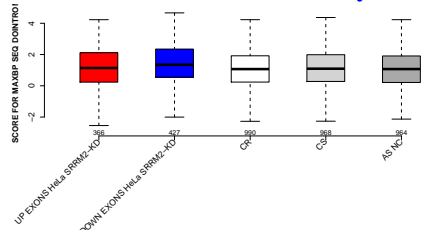
MEDIAN POLYPYRITRAC OFFSET UPINTRON



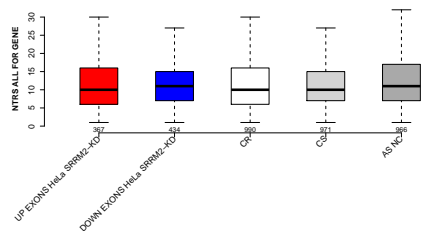
EXON MEDIANRELATIVERANK 10BINS



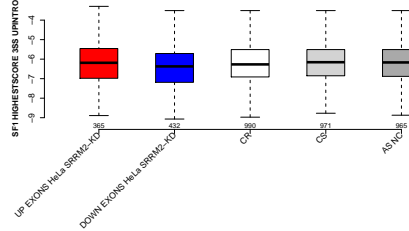
SCORE FOR MAXBP SEQ DOINTRON



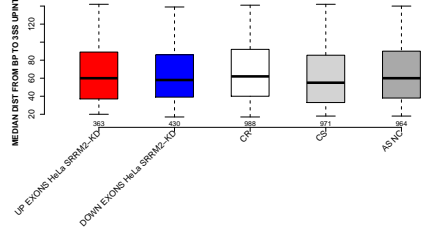
NTRS ALL FOR GENE



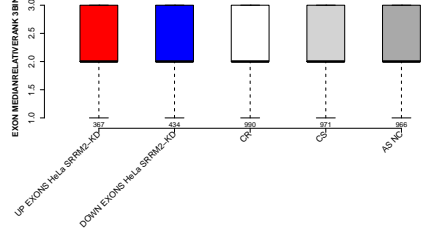
SF1 HIGHESTSCORE 3SS UPINTRON



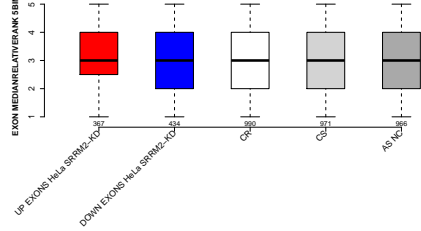
MEDIAN DIST FROM BP TO 3SS UPINTRON



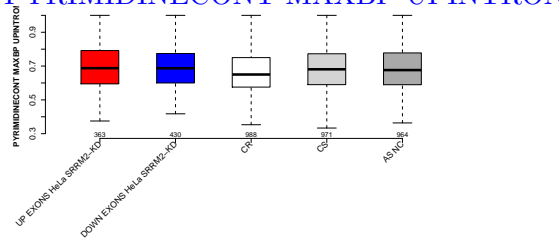
EXON MEDIANRELATIVERANK 3BINS



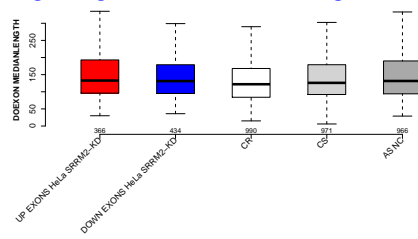
EXON MEDIANRELATIVERANK 5BINS



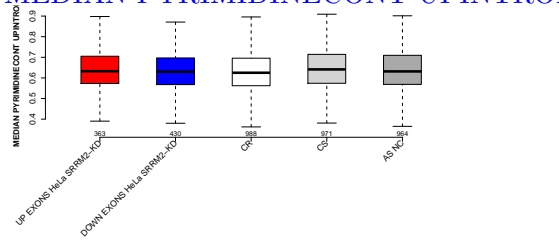
## PYRIMIDINECONT MAXBP UPINTRON



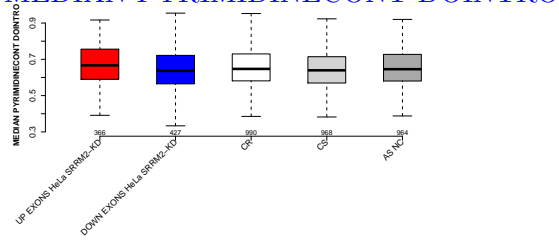
## DOEXON MEDIANLENGTH



## MEDIAN PYRIMIDINECONT UPINTRON

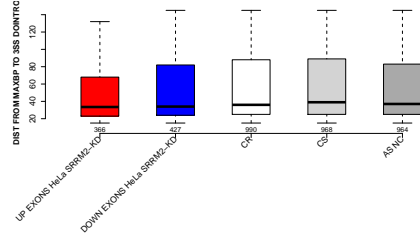


## MEDIAN PYRIMIDINECONT DOWINTRON

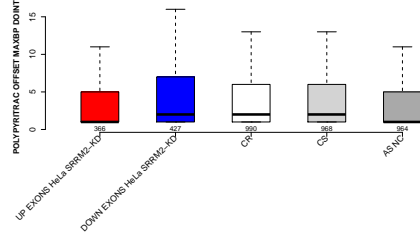




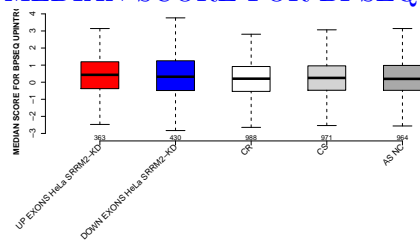
## DIST FROM MAXBP TO 3SS DOWNTON



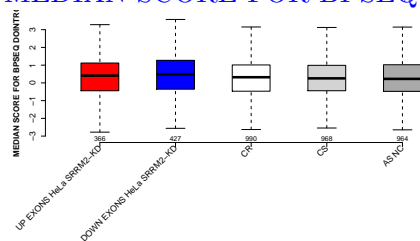
## POLYPYRITRAC OFFSET MAXBP DOWNTON



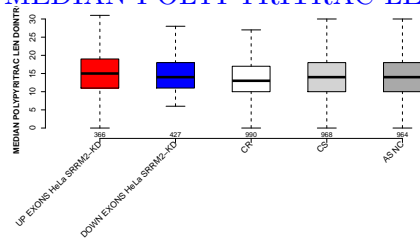
## MEDIAN SCORE FOR BPSEQ UPINTRON



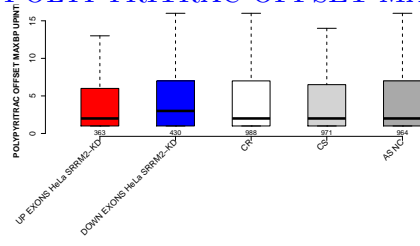
## MEDIAN SCORE FOR BPSEQ DOWNTON



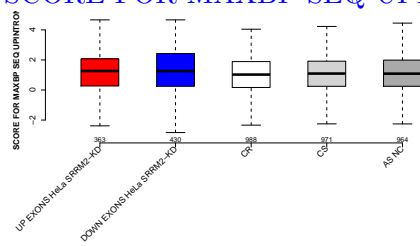
## MEDIAN POLYPYRITRAC LEN DOWINTR



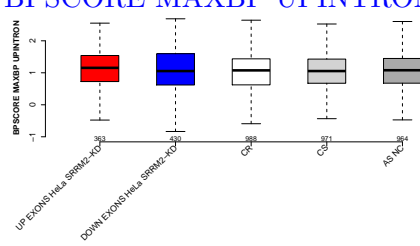
## POLYPYRITRAC OFFSET MAXBP UPINTRON



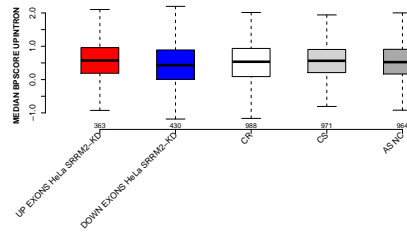
## SCORE FOR MAXBP SEQ UPINTRON



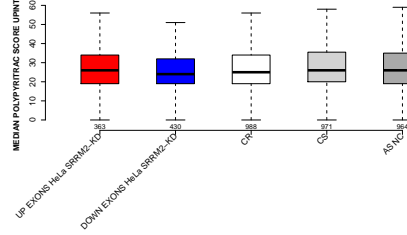
## BPSCORE MAXBP UPINTRON



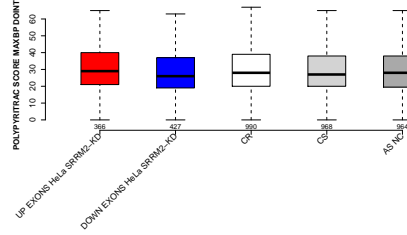
## MEDIAN BPSCORE UPINTRON



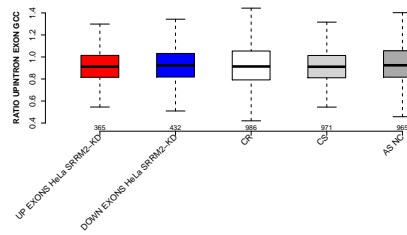
## MEDIAN POLYPYRITRAC SCORE UPINTRON



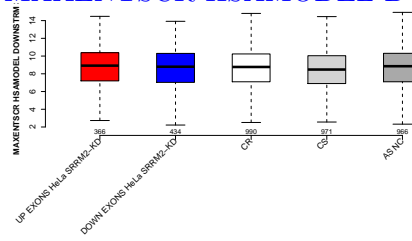
## POLYPYRITRAC SCORE MAXBP DOWINTRON



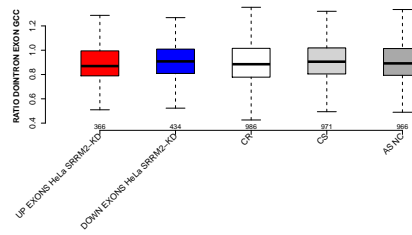
## RATIO UPINTRON EXON GCC



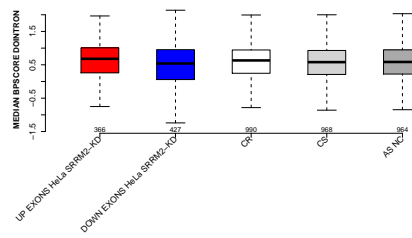
## MAXENTSCR HSAMODEL DOWNSTRM 3SS



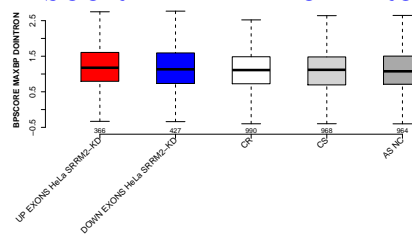
## RATIO DONTON EXON GCC



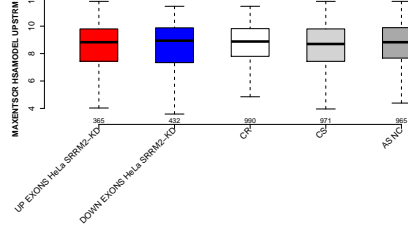
## MEDIAN BPSCORE DONTON



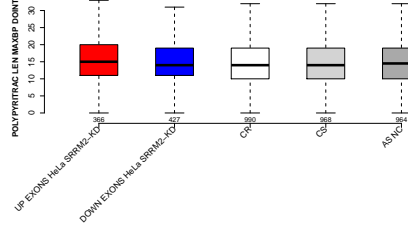
## BPSCORE MAXBP DONTON



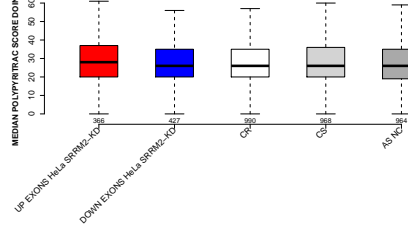
MAXENTSCR HSAMODEL UPSTRM 5SS



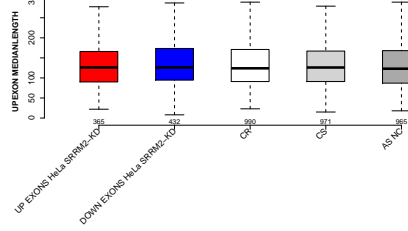
POLYPYRITRAC LEN MAXBP DOINTRON



MEDIAN POLYPYRITRAC SCORE DOINTRON



UPEXON MEDIANLENGTH

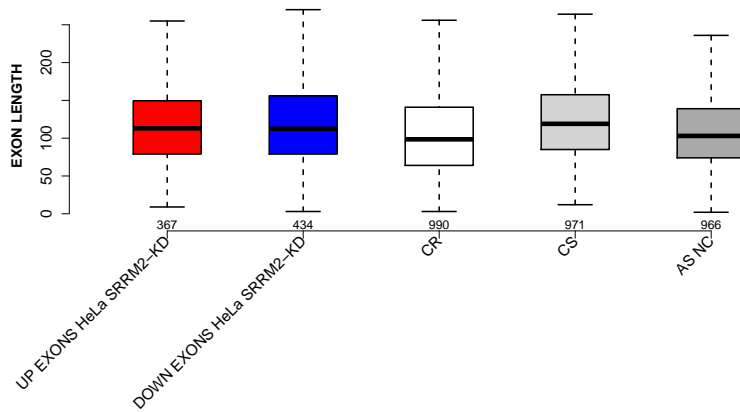


## 6 Details: Box plots and statistical assessments for all features

### 6.1 EXON LENGTH

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

Meaning:



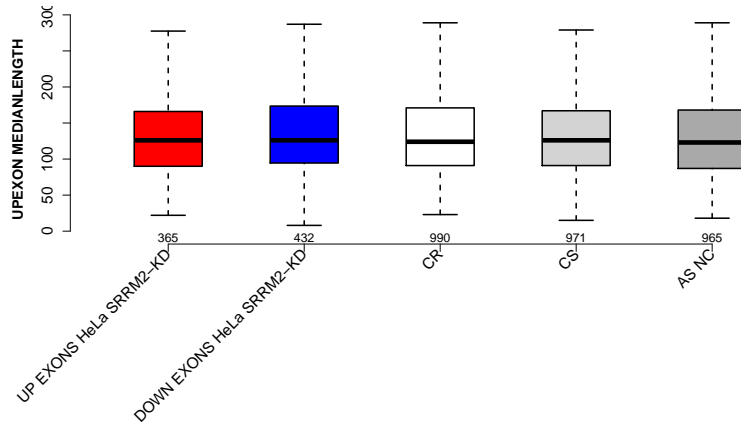
Significant results from Mann-Whitney U test:

- UP\_EXONS\_HeLa\_SRRM2-KD vs CR : 3.37749e-05  
mean: 143.2316 > 118.6434 , median: 113 > 98.5
- UP\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.00267159  
mean: 143.2316 > 126.8747 , median: 113 > 103
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CR : 1.66329e-05  
mean: 145.5276 > 118.6434 , median: 112.5 > 98.5
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.00204301  
mean: 145.5276 > 126.8747 , median: 112.5 > 103
- CR vs CS : 4.80151e-13  
mean: 118.6434 < 134.3944 , median: 98.5 < 119
- CS vs AS\_NC : 4.59401e-09  
mean: 134.3944 > 126.8747 , median: 119 > 103

## 6.2 UPEXON MEDIANLENGTH

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

Meaning: median length of up-stream exon



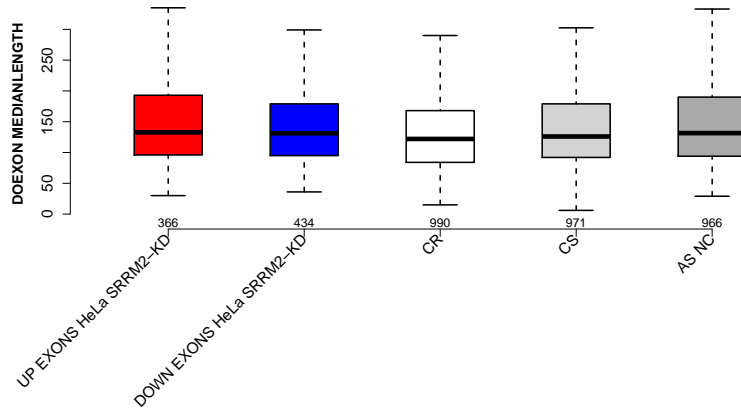
Significant results from Mann-Whitney U test:

- DOWN\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.0433104  
mean: 151.0394 > 145.9187 , median: 126 > 123

### 6.3 DOEXON MEDIANLENGTH

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

Meaning: median length of down-stream exon



Significant results from Mann-Whitney U test:

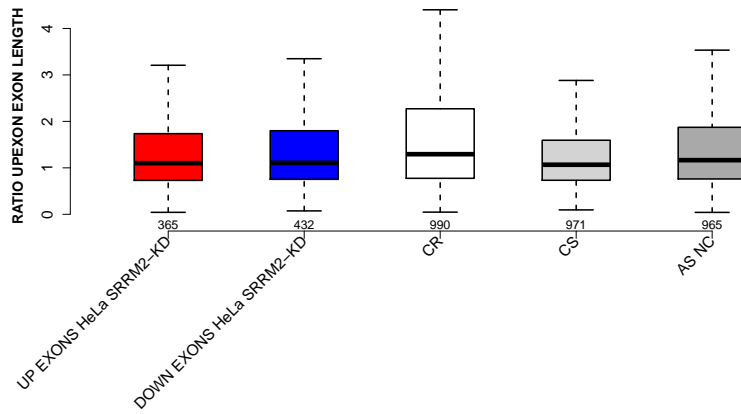
- UP\_EXONS\_HeLa\_SRRM2-KD vs CR : 0.00154108  
mean: 271.8661 > 191.2293 , median: 132.75 > 122
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CR : 0.00300835  
mean: 241.7719 > 191.2293 , median: 131.25 > 122
- CR vs CS : 0.0348148  
mean: 191.2293 < 249.9902 , median: 122 < 126
- CR vs AS\_NC : 0.000279763  
mean: 191.2293 < 267.5751 , median: 122 < 131.5



## 6.4 RATIO UPEXON EXON LENGTH

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

Meaning: median up-stream exon length / exon length



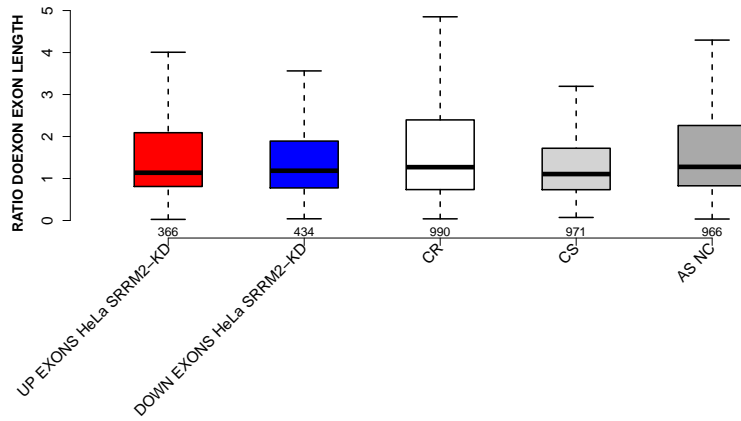
Significant results from Mann-Whitney U test:

- UP\_EXONS\_HeLa\_SRRM2-KD vs CR : 0.000651874  
mean: 1.6281 < 3.4883 , median: 1.1 < 1.2938
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CR : 0.00241235  
mean: 1.6711 < 3.4883 , median: 1.1073 < 1.2938
- CR vs CS : 1.15958e-09  
mean: 3.4883 > 1.3722 , median: 1.2938 > 1.0667
- CR vs AS\_NC : 0.00406776  
mean: 3.4883 > 1.7287 , median: 1.2938 > 1.1653
- CS vs AS\_NC : 0.000650869  
mean: 1.3722 < 1.7287 , median: 1.0667 < 1.1653

## 6.5 RATIO DOEXON EXON LENGTH

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

Meaning: median down-stream exon length / exon length



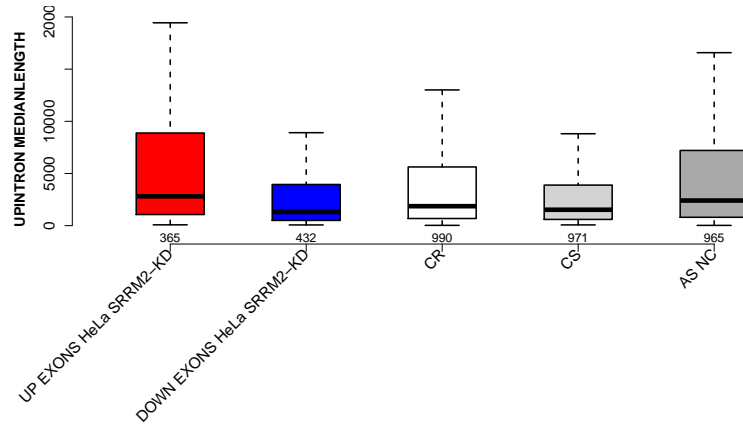
Significant results from Mann-Whitney U test:

- UP\_EXONS\_HeLa\_SRRM2-KD vs CS : 0.0209073  
mean: 2.724 > 2.2626 , median: 1.1371 > 1.1061
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.0239092  
mean: 2.7234 < 3.0366 , median: 1.1852 < 1.277
- CR vs CS : 0.000160718  
mean: 4.2037 > 2.2626 , median: 1.2702 > 1.1061
- CS vs AS\_NC : 2.72097e-07  
mean: 2.2626 < 3.0366 , median: 1.1061 < 1.277

## 6.6 UPINTRON MEDIANLENGTH

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

Meaning: median length of up-stream introns



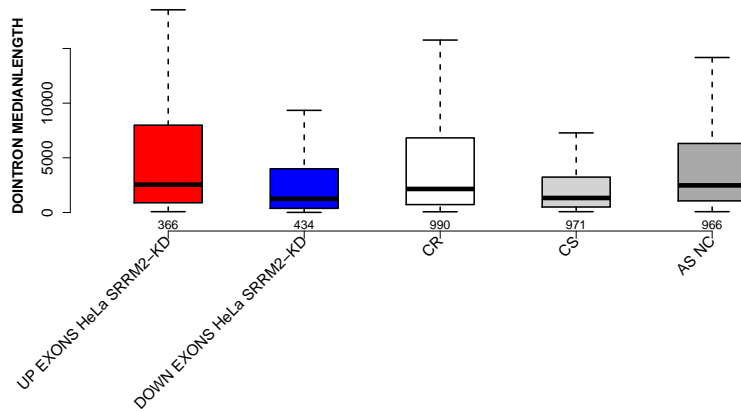
Significant results from Mann-Whitney U test:

- UP\_EXONS\_HeLa\_SRRM2-KD vs DOWN\_EXONS\_HeLa\_SRRM2-KD : 5.96641e-10  
mean: 10242.663 > 5310.7049 , median: 2813 > 1316.5
- UP\_EXONS\_HeLa\_SRRM2-KD vs CR : 0.000206623  
mean: 10242.663 > 6711.3051 , median: 2813 > 1865
- UP\_EXONS\_HeLa\_SRRM2-KD vs CS : 1.3601e-11  
mean: 10242.663 > 4547.5881 , median: 2813 > 1524
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CR : 7.63556e-05  
mean: 5310.7049 < 6711.3051 , median: 1316.5 < 1865
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 4.3952e-09  
mean: 5310.7049 < 7522.4176 , median: 1316.5 < 2406
- CR vs CS : 4.05011e-05  
mean: 6711.3051 > 4547.5881 , median: 1865 > 1524
- CR vs AS\_NC : 0.00874376  
mean: 6711.3051 < 7522.4176 , median: 1865 < 2406
- CS vs AS\_NC : 1.80513e-11  
mean: 4547.5881 < 7522.4176 , median: 1524 < 2406

## 6.7 DOINTRON MEDIANLENGTH

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Meaning: median length of down-stream introns



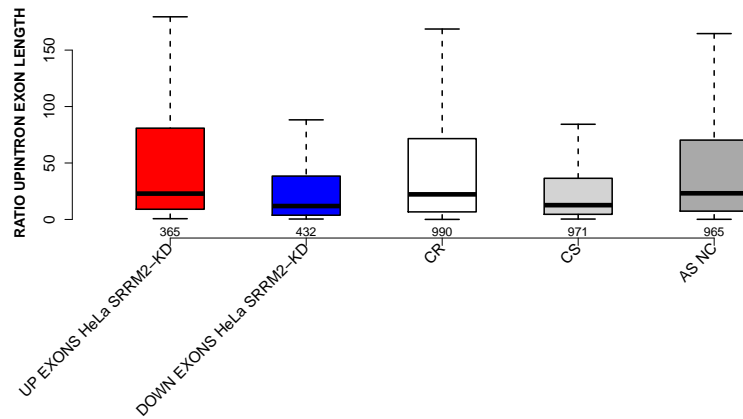
Significant results from Mann-Whitney U test:

- UP\_EXONS\_HeLa\_SRRM2-KD vs DOWN\_EXONS\_HeLa\_SRRM2-KD : 3.09666e-09  
mean: 8074.7883 > 4937.0472 , median: 2545.5 > 1246
- UP\_EXONS\_HeLa\_SRRM2-KD vs CS : 1.98237e-12  
mean: 8074.7883 > 3328.8162 , median: 2545.5 > 1326
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CR : 2.51619e-09  
mean: 4937.0472 < 7524.8823 , median: 1246 < 2150.5
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 4.24293e-14  
mean: 4937.0472 < 6844.3716 , median: 1246 < 2479.5
- CR vs CS : 2.96136e-14  
mean: 7524.8823 > 3328.8162 , median: 2150.5 > 1326
- CS vs AS\_NC : 1.55442e-23  
mean: 3328.8162 < 6844.3716 , median: 1326 < 2479.5

## 6.8 RATIO UPINTRON EXON LENGTH

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

Meaning: median up-stream intron length / exon length



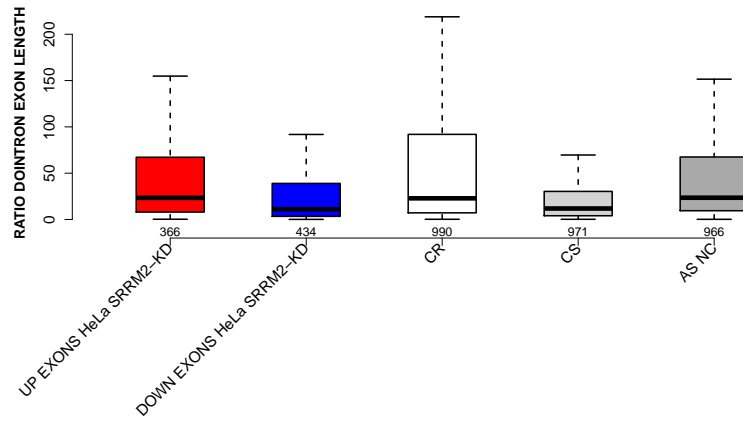
Significant results from Mann-Whitney U test:

- UP\_EXONS\_HeLa\_SRRM2-KD vs DOWN\_EXONS\_HeLa\_SRRM2-KD : 9.48621e-09  
mean: 108.1088 > 46.4838 , median: 22.8824 > 11.8713
- UP\_EXONS\_HeLa\_SRRM2-KD vs CS : 2.31818e-11  
mean: 108.1088 > 43.874 , median: 22.8824 > 12.6522
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CR : 2.129e-09  
mean: 46.4838 < 121.3005 , median: 11.8713 < 22.218
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 2.82076e-10  
mean: 46.4838 < 93.7403 , median: 11.8713 < 23.1736
- CR vs CS : 5.9226e-14  
mean: 121.3005 > 43.874 , median: 22.218 > 12.6522
- CS vs AS\_NC : 1.73003e-15  
mean: 43.874 < 93.7403 , median: 12.6522 < 23.1736

## 6.9 RATIO DONTRON EXON LENGTH

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Meaning: median down-stream intron length / exon length



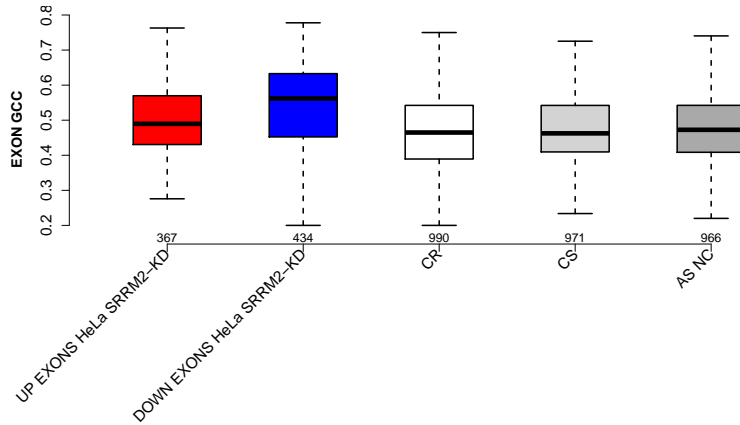
Significant results from Mann-Whitney U test:

- UP\_EXONS\_HeLa\_SRRM2-KD vs DOWN\_EXONS\_HeLa\_SRRM2-KD : 8.47607e-09  
mean: 83.6978 > 69.9979 , median: 23.3551 > 11.0634
- UP\_EXONS\_HeLa\_SRRM2-KD vs CS : 8.92115e-13  
mean: 83.6978 > 32.5529 , median: 23.3551 > 11.8554
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CR : 1.14839e-13  
mean: 69.9979 < 230.4243 , median: 11.0634 < 22.8519
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 7.32623e-16  
mean: 69.9979 < 89.0671 , median: 11.0634 < 23.4998
- CR vs CS : 1.92728e-23  
mean: 230.4243 > 32.5529 , median: 22.8519 > 11.8554
- CS vs AS\_NC : 2.03153e-28  
mean: 32.5529 < 89.0671 , median: 11.8554 < 23.4998

## 6.10 EXON GCC

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

Meaning: GC content of entire exon sequence



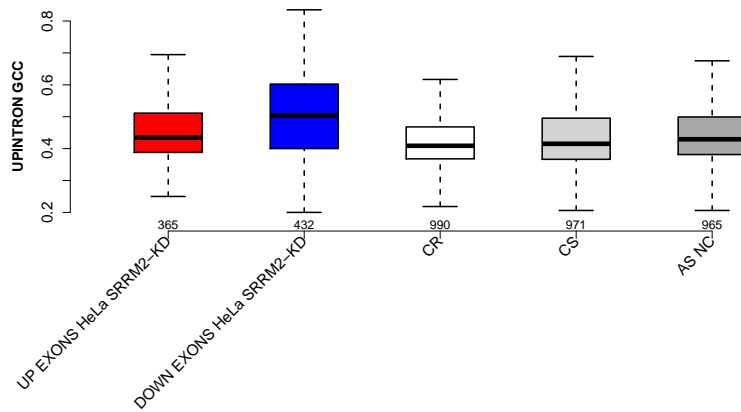
Significant results from Mann-Whitney U test:

- UP\_EXONS\_HeLa\_SRRM2-KD vs DOWN\_EXONS\_HeLa\_SRRM2-KD : 8.7061e-10  
mean: 0.497578 < 0.542795 , median: 0.489583 < 0.561952
- UP\_EXONS\_HeLa\_SRRM2-KD vs CR : 4.29388e-06  
mean: 0.497578 > 0.466662 , median: 0.489583 > 0.464842
- UP\_EXONS\_HeLa\_SRRM2-KD vs CS : 0.000791827  
mean: 0.497578 > 0.478617 , median: 0.489583 > 0.4625
- UP\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.00398792  
mean: 0.497578 > 0.480319 , median: 0.489583 > 0.472582
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CR : 1.04404e-31  
mean: 0.542795 > 0.466662 , median: 0.561952 > 0.464842
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CS : 3.17239e-25  
mean: 0.542795 > 0.478617 , median: 0.561952 > 0.4625
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 7.86391e-24  
mean: 0.542795 > 0.480319 , median: 0.561952 > 0.472582
- CR vs CS : 0.0463023  
mean: 0.466662 < 0.478617 , median: 0.464842 > 0.4625
- CR vs AS\_NC : 0.0159111  
mean: 0.466662 < 0.480319 , median: 0.464842 < 0.472582

## 6.11 UPINTRON GCC

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

Meaning: GC content of entire up-stream intron sequence



Significant results from Mann-Whitney U test:

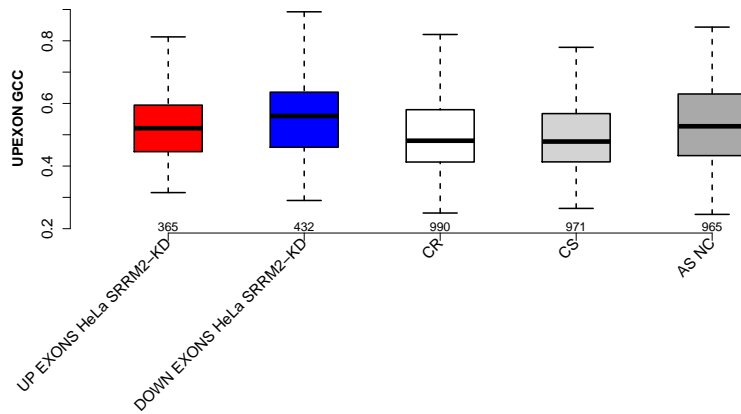
- UP\_EXONS\_HeLa\_SRRM2-KD vs DOWN\_EXONS\_HeLa\_SRRM2-KD : 4.1637e-09  
mean: 0.4535 < 0.504815 , median: 0.434109 < 0.503697
- UP\_EXONS\_HeLa\_SRRM2-KD vs CR : 1.79072e-07  
mean: 0.4535 > 0.426143 , median: 0.434109 > 0.408785
- UP\_EXONS\_HeLa\_SRRM2-KD vs CS : 0.00036756  
mean: 0.4535 > 0.436938 , median: 0.434109 > 0.415066
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CR : 3.73802e-30  
mean: 0.504815 > 0.426143 , median: 0.503697 > 0.408785
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CS : 1.34456e-22  
mean: 0.504815 > 0.436938 , median: 0.503697 > 0.415066
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 8.5218e-17  
mean: 0.504815 > 0.446226 , median: 0.503697 > 0.429279
- CR vs AS\_NC : 7.78529e-07  
mean: 0.426143 < 0.446226 , median: 0.408785 < 0.429279
- CS vs AS\_NC : 0.00380415  
mean: 0.436938 < 0.446226 , median: 0.415066 < 0.429279



## 6.12 UPEXON GCC

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

Meaning: GC content of entire up-stream exon sequence



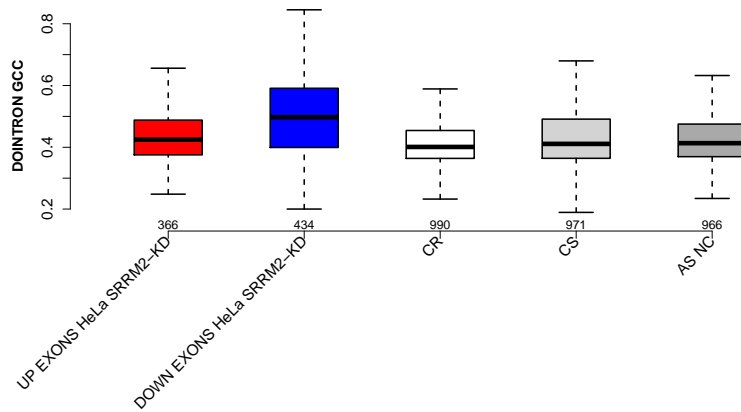
Significant results from Mann-Whitney U test:

- UP\_EXONS\_HeLa\_SRRM2-KD vs DOWN\_EXONS\_HeLa\_SRRM2-KD : 0.00301666  
mean: 0.52882 < 0.549509 , median: 0.520833 < 0.559868
- UP\_EXONS\_HeLa\_SRRM2-KD vs CR : 7.97156e-06  
mean: 0.52882 > 0.502311 , median: 0.520833 > 0.480869
- UP\_EXONS\_HeLa\_SRRM2-KD vs CS : 2.54193e-07  
mean: 0.52882 > 0.494021 , median: 0.520833 > 0.478261
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CR : 2.40493e-13  
mean: 0.549509 > 0.502311 , median: 0.559868 > 0.480869
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CS : 4.19294e-17  
mean: 0.549509 > 0.494021 , median: 0.559868 > 0.478261
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.0219542  
mean: 0.549509 > 0.53578 , median: 0.559868 > 0.527027
- CR vs AS\_NC : 1.07673e-09  
mean: 0.502311 < 0.53578 , median: 0.480869 < 0.527027
- CS vs AS\_NC : 4.97403e-13  
mean: 0.494021 < 0.53578 , median: 0.478261 < 0.527027

## 6.13 DOINTRON GCC

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

Meaning: GC content of entire down-stream intron sequence



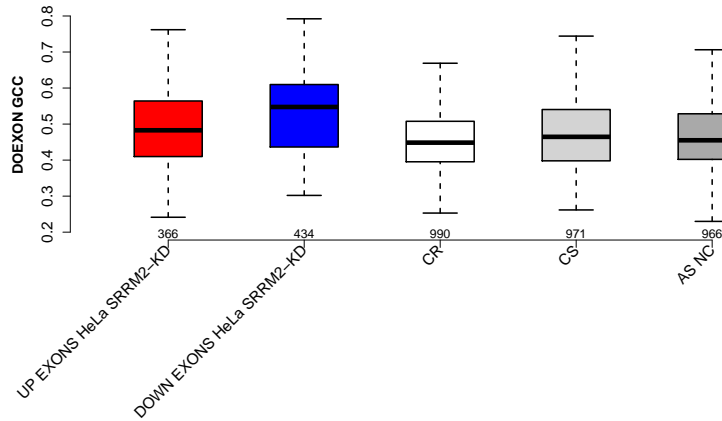
Significant results from Mann-Whitney U test:

- UP\_EXONS\_HeLa\_SRRM2-KD vs DOWN\_EXONS\_HeLa\_SRRM2-KD : 4.71037e-12  
mean: 0.43893 < 0.495065 , median: 0.42467 < 0.497363
- UP\_EXONS\_HeLa\_SRRM2-KD vs CR : 4.17529e-06  
mean: 0.43893 > 0.414595 , median: 0.42467 > 0.401107
- UP\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.0293447  
mean: 0.43893 > 0.429167 , median: 0.42467 > 0.413334
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CR : 4.41092e-34  
mean: 0.495065 > 0.414595 , median: 0.497363 > 0.401107
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CS : 6.65922e-20  
mean: 0.495065 > 0.434245 , median: 0.497363 > 0.410976
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 8.7796e-24  
mean: 0.495065 > 0.429167 , median: 0.497363 > 0.413334
- CR vs CS : 0.00130418  
mean: 0.414595 < 0.434245 , median: 0.401107 < 0.410976
- CR vs AS\_NC : 0.000982023  
mean: 0.414595 < 0.429167 , median: 0.401107 < 0.413334

## 6.14 DOEXON GCC

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

Meaning: GC content of entire down-stream exon sequence



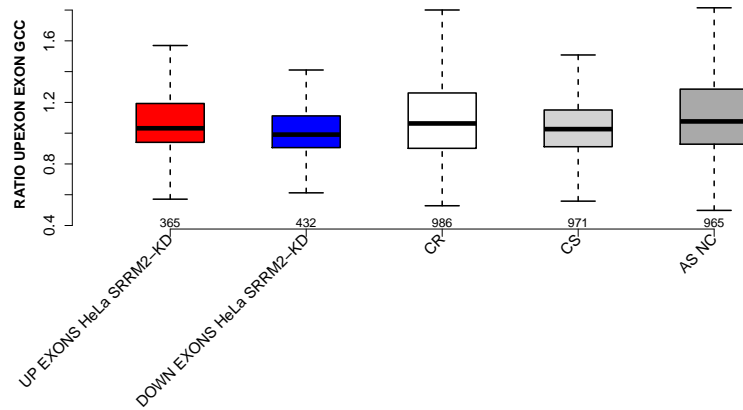
Significant results from Mann-Whitney U test:

- UP\_EXONS\_HeLa\_SRRM2-KD vs DOWN\_EXONS\_HeLa\_SRRM2-KD : 8.26255e-09  
mean: 0.487847 < 0.530139 , median: 0.482759 < 0.547472
- UP\_EXONS\_HeLa\_SRRM2-KD vs CR : 3.00184e-07  
mean: 0.487847 > 0.457746 , median: 0.482759 > 0.44849
- UP\_EXONS\_HeLa\_SRRM2-KD vs CS : 0.0111886  
mean: 0.487847 > 0.473126 , median: 0.482759 > 0.464567
- UP\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.000924438  
mean: 0.487847 > 0.46862 , median: 0.482759 > 0.455013
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CR : 1.39237e-33  
mean: 0.530139 > 0.457746 , median: 0.547472 > 0.44849
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CS : 2.05434e-21  
mean: 0.530139 > 0.473126 , median: 0.547472 > 0.464567
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 6.27616e-25  
mean: 0.530139 > 0.46862 , median: 0.547472 > 0.455013
- CR vs CS : 0.00114095  
mean: 0.457746 < 0.473126 , median: 0.44849 < 0.464567
- CR vs AS\_NC : 0.0130057  
mean: 0.457746 < 0.46862 , median: 0.44849 < 0.455013

## 6.15 RATIO UPEXON EXON GCC

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

Meaning: UPEXON GCC / EXON GCC



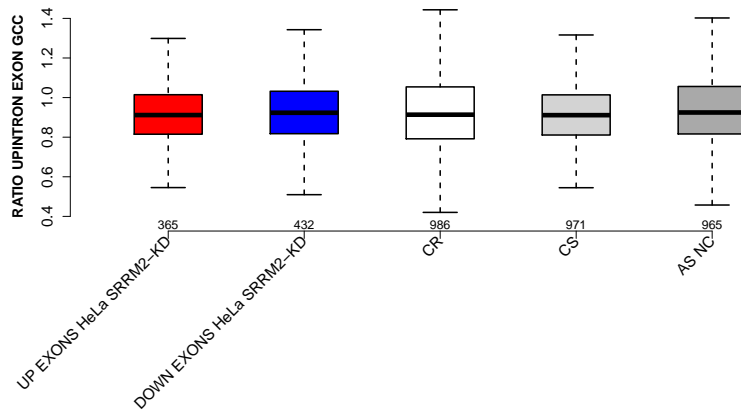
Significant results from Mann-Whitney U test:

- UP\_EXONS\_HeLa\_SRRM2-KD vs DOWN\_EXONS\_HeLa\_SRRM2-KD : 0.000479516  
mean: 1.0897 > 1.0324 , median: 1.0318 > 0.990683
- UP\_EXONS\_HeLa\_SRRM2-KD vs CS : 0.028378  
mean: 1.0897 > 1.0484 , median: 1.0318 > 1.0263
- UP\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.00907359  
mean: 1.0897 < 1.1443 , median: 1.0318 < 1.0764
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CR : 7.96771e-06  
mean: 1.0324 < 1.1079 , median: 0.990683 < 1.0632
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CS : 0.0440282  
mean: 1.0324 < 1.0484 , median: 0.990683 < 1.0263
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 5.59416e-11  
mean: 1.0324 < 1.1443 , median: 0.990683 < 1.0764
- CR vs CS : 0.000145748  
mean: 1.1079 > 1.0484 , median: 1.0632 > 1.0263
- CR vs AS\_NC : 0.0145385  
mean: 1.1079 < 1.1443 , median: 1.0632 < 1.0764
- CS vs AS\_NC : 2.48106e-10  
mean: 1.0484 < 1.1443 , median: 1.0263 < 1.0764

## 6.16 RATIO UPINTRON EXON GCC

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

Meaning: UPINTRON GCC / EXON GCC



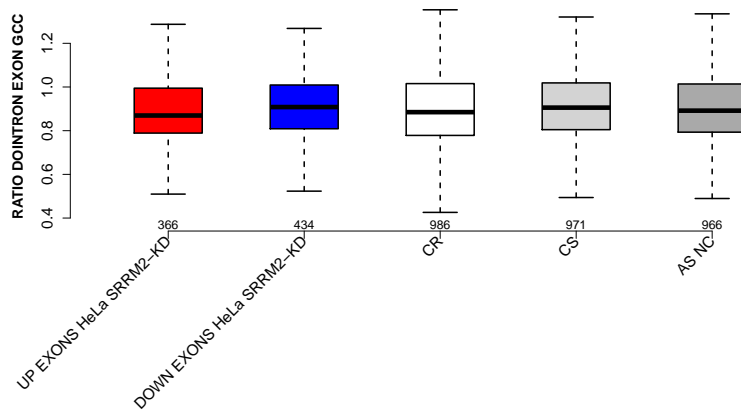
Significant results from Mann-Whitney U test:

- CS vs AS\_NC : 0.010216  
mean: 0.920092 < 0.945663 , median: 0.911243 < 0.924701

## 6.17 RATIO DOINTRON EXON GCC

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

Meaning: DOINTRON GCC / EXON GCC



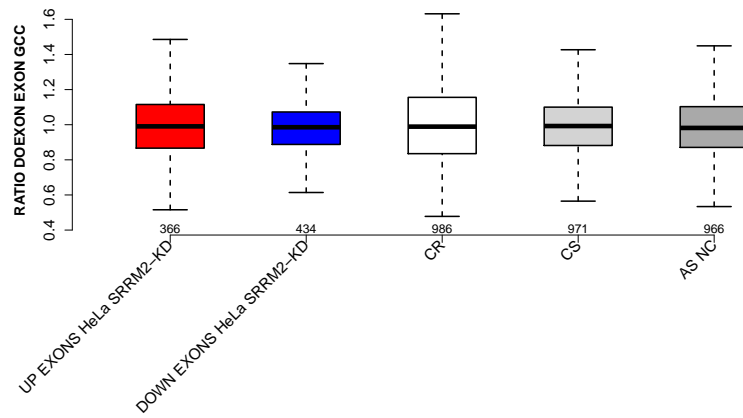
Significant results from Mann-Whitney U test:

- UP\_EXONS\_HeLa\_SRRM2-KD vs DOWN\_EXONS\_HeLa\_SRRM2-KD : 0.0170583  
mean: 0.897102 < 0.922208 , median: 0.869436 < 0.90813
- UP\_EXONS\_HeLa\_SRRM2-KD vs CS : 0.026216  
mean: 0.897102 < 0.914512 , median: 0.869436 < 0.905539

## 6.18 RATIO DOEXON EXON GCC

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

Meaning: DOEXON GCC / EXON GCC



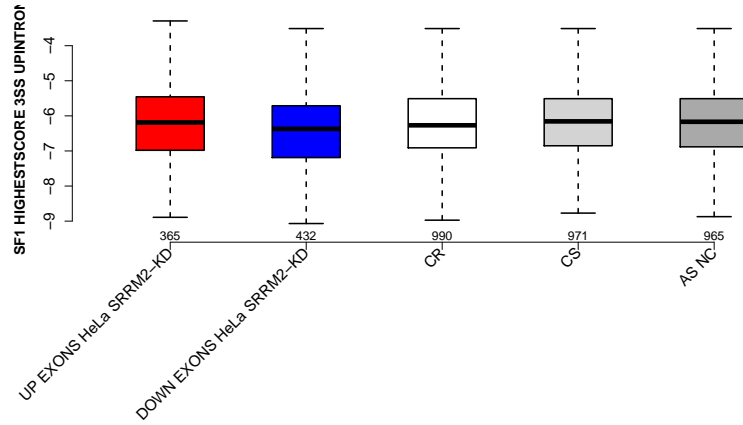
Significant results from Mann-Whitney U test:

- none

## 6.19 SF1 HIGHESTSCORE 3SS UPINTRON

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 up-stream intron



Significant results from Mann-Whitney U test:

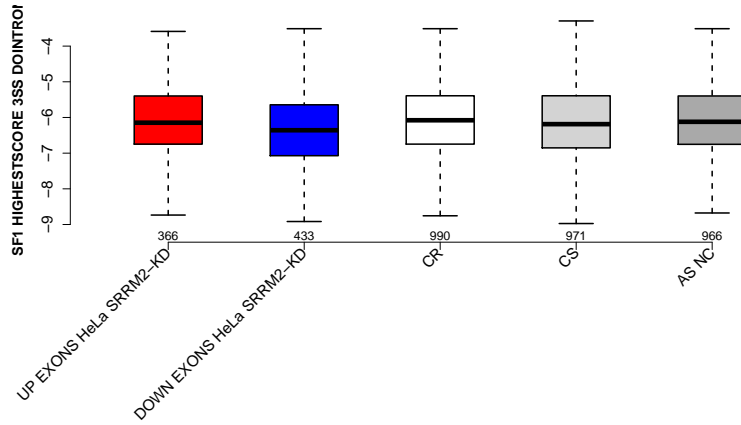
- UP\_EXONS\_HeLa\_SRRM2-KD vs DOWN\_EXONS\_HeLa\_SRRM2-KD : 0.00412607  
mean: -6.18155 > -6.40793 , median: -6.18725 > -6.37142
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CR : 0.000981903  
mean: -6.40793 < -6.18548 , median: -6.37142 < -6.26872
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CS : 4.86795e-05  
mean: -6.40793 < -6.16166 , median: -6.37142 < -6.15674
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 8.71199e-05  
mean: -6.40793 < -6.175 , median: -6.37142 < -6.1683



## 6.20 SF1 HIGHESTSCORE 3SS DOWINTRON

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



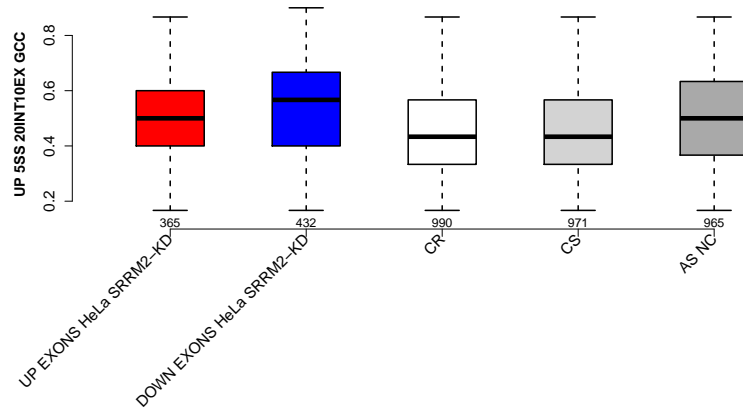
Significant results from Mann-Whitney U test:

- UP\_EXONS\_HeLa\_SRRM2-KD vs DOWN\_EXONS\_HeLa\_SRRM2-KD : 0.000244769  
mean: -6.11141 > -6.38139 , median: -6.14698 > -6.35795
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CR : 7.47846e-07  
mean: -6.38139 < -6.08105 , median: -6.35795 < -6.07814
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CS : 0.000261331  
mean: -6.38139 < -6.13717 , median: -6.35795 < -6.18725
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 8.14539e-07  
mean: -6.38139 < -6.07294 , median: -6.35795 < -6.12133

## 6.21 UP 5SS 20INT10EX GCC

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

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



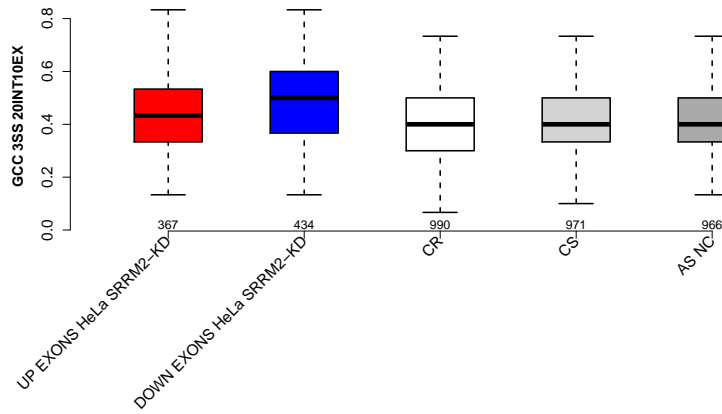
Significant results from Mann-Whitney U test:

- UP\_EXONS\_HeLa\_SRRM2-KD vs DOWN\_EXONS\_HeLa\_SRRM2-KD : 0.000301789  
mean: 0.497534 < 0.532369 , median: 0.5 < 0.566667
- UP\_EXONS\_HeLa\_SRRM2-KD vs CR : 2.43188e-05  
mean: 0.497534 > 0.462508 , median: 0.5 > 0.433333
- UP\_EXONS\_HeLa\_SRRM2-KD vs CS : 0.000166014  
mean: 0.497534 > 0.46459 , median: 0.5 > 0.433333
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CR : 4.10855e-15  
mean: 0.532369 > 0.462508 , median: 0.566667 > 0.433333
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CS : 4.81924e-14  
mean: 0.532369 > 0.46459 , median: 0.566667 > 0.433333
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.000897789  
mean: 0.532369 > 0.504352 , median: 0.566667 > 0.5
- CR vs AS\_NC : 5.87147e-09  
mean: 0.462508 < 0.504352 , median: 0.433333 < 0.5
- CS vs AS\_NC : 8.07591e-08  
mean: 0.46459 < 0.504352 , median: 0.433333 < 0.5

## 6.22 GCC 3SS 20INT10EX

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

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



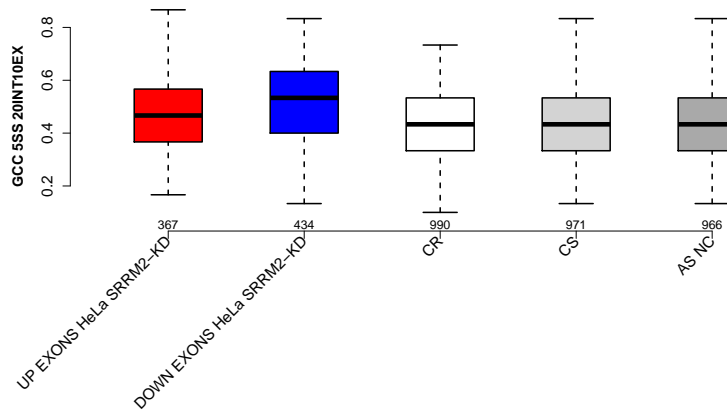
Significant results from Mann-Whitney U test:

- UP\_EXONS\_HeLa\_SRRM2-KD vs DOWN\_EXONS\_HeLa\_SRRM2-KD : 3.86971e-10  
mean: 0.431789 < 0.496697 , median: 0.433333 < 0.5
- UP\_EXONS\_HeLa\_SRRM2-KD vs CR : 0.00168598  
mean: 0.431789 > 0.404343 , median: 0.433333 > 0.4
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CR : 2.40928e-28  
mean: 0.496697 > 0.404343 , median: 0.5 > 0.4
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CS : 1.81944e-20  
mean: 0.496697 > 0.419258 , median: 0.5 > 0.4
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 9.83053e-22  
mean: 0.496697 > 0.416598 , median: 0.5 > 0.4
- CR vs CS : 0.0324977  
mean: 0.404343 < 0.419258 , median: 0.4 = 0.4

## 6.23 GCC 5SS 20INT10EX

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

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



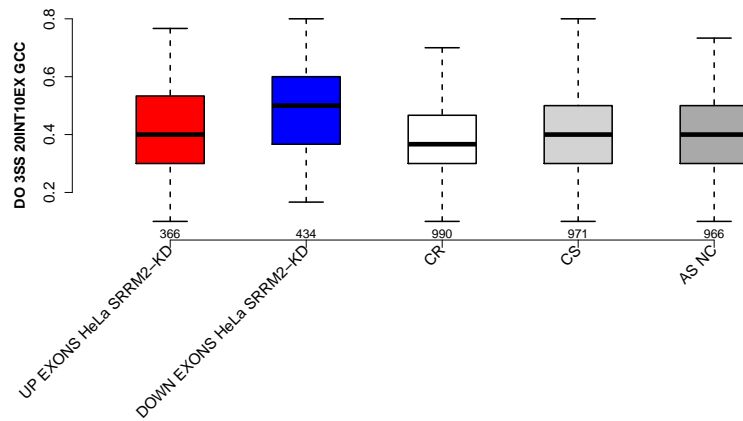
Significant results from Mann-Whitney U test:

- UP\_EXONS\_HeLa\_SRRM2-KD vs DOWN\_EXONS\_HeLa\_SRRM2-KD : 1.0612e-08  
mean: 0.470663 < 0.52788 , median: 0.466667 < 0.533333
- UP\_EXONS\_HeLa\_SRRM2-KD vs CR : 9.41976e-06  
mean: 0.470663 > 0.434747 , median: 0.466667 > 0.433333
- UP\_EXONS\_HeLa\_SRRM2-KD vs CS : 0.00272399  
mean: 0.470663 > 0.448266 , median: 0.466667 > 0.433333
- UP\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.00130321  
mean: 0.470663 > 0.446135 , median: 0.466667 > 0.433333
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CR : 9.09896e-28  
mean: 0.52788 > 0.434747 , median: 0.533333 > 0.433333
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CS : 2.64857e-20  
mean: 0.52788 > 0.448266 , median: 0.533333 > 0.433333
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 7.60984e-22  
mean: 0.52788 > 0.446135 , median: 0.533333 > 0.433333

## 6.24 DO 3SS 20INT10EX GCC

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

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



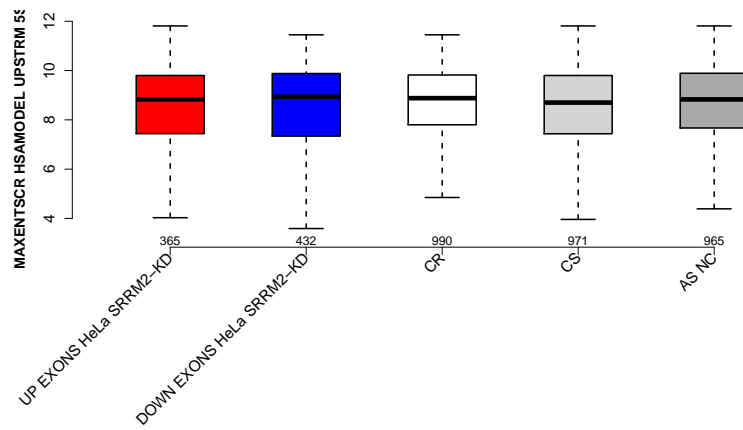
Significant results from Mann-Whitney U test:

- UP\_EXONS\_HeLa\_SRRM2-KD vs DOWN\_EXONS\_HeLa\_SRRM2-KD : 1.56969e-10  
mean: 0.42204 < 0.48725 , median: 0.4 < 0.5
- UP\_EXONS\_HeLa\_SRRM2-KD vs CR : 0.000851897  
mean: 0.42204 > 0.392088 , median: 0.4 > 0.366667
- UP\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.0203796  
mean: 0.42204 > 0.40138 , median: 0.4 = 0.4
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CR : 1.03072e-31  
mean: 0.48725 > 0.392088 , median: 0.5 > 0.366667
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CS : 1.33012e-17  
mean: 0.48725 > 0.417061 , median: 0.5 > 0.4
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 5.99554e-26  
mean: 0.48725 > 0.40138 , median: 0.5 > 0.4
- CR vs CS : 6.14676e-05  
mean: 0.392088 < 0.417061 , median: 0.366667 < 0.4
- CS vs AS\_NC : 0.0106043  
mean: 0.417061 > 0.40138 , median: 0.4 = 0.4

## 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



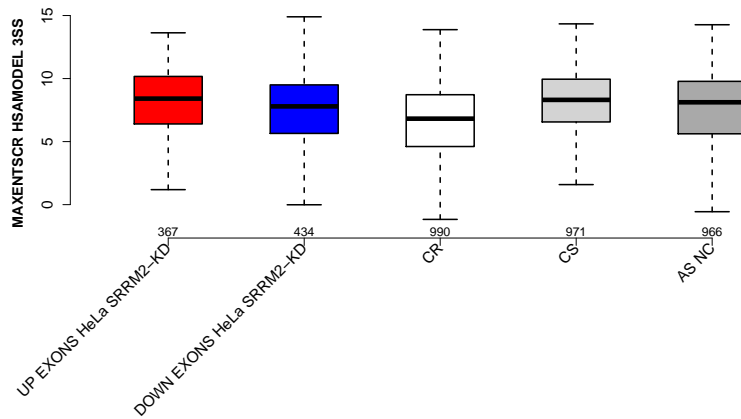
Significant results from Mann-Whitney U test:

- CR vs CS : 0.0253439  
mean: 8.5625 > 8.3674 , median: 8.88 > 8.7

## 6.26 MAXENTSCR HSAMODEL 3SS

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

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



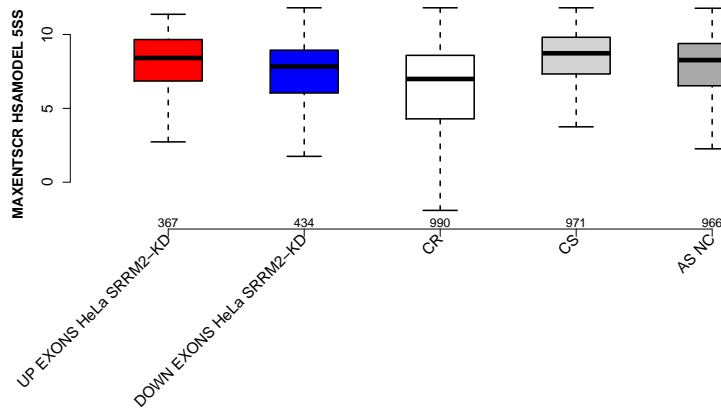
Significant results from Mann-Whitney U test:

- UP\_EXONS\_HeLa\_SRRM2-KD vs DOWN\_EXONS\_HeLa\_SRRM2-KD : 0.000295082  
mean: 7.9072 > 6.9991 , median: 8.41 > 7.795
- UP\_EXONS\_HeLa\_SRRM2-KD vs CR : 8.95128e-17  
mean: 7.9072 > 6.116 , median: 8.41 > 6.82
- UP\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.0110205  
mean: 7.9072 > 7.3247 , median: 8.41 > 8.12
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CR : 4.76243e-06  
mean: 6.9991 > 6.116 , median: 7.795 > 6.82
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CS : 2.56371e-05  
mean: 6.9991 < 7.9083 , median: 7.795 < 8.31
- CR vs CS : 2.04338e-29  
mean: 6.116 < 7.9083 , median: 6.82 < 8.31
- CR vs AS\_NC : 1.32736e-14  
mean: 6.116 < 7.3247 , median: 6.82 < 8.12
- CS vs AS\_NC : 0.00192355  
mean: 7.9083 > 7.3247 , median: 8.31 > 8.12

## 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:

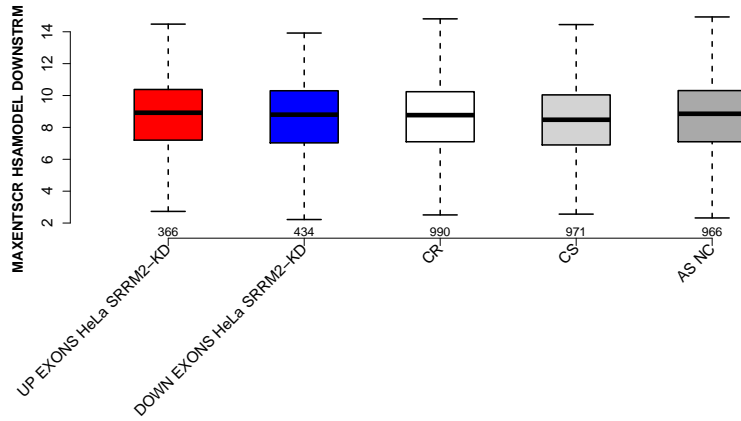
- UP\_EXONS\_HeLa\_SRRM2-KD vs DOWN\_EXONS\_HeLa\_SRRM2-KD : 4.85744e-06  
mean: 7.8765 > 6.7108 , median: 8.41 > 7.835
- UP\_EXONS\_HeLa\_SRRM2-KD vs CR : 2.36346e-21  
mean: 7.8765 > 5.8762 , median: 8.41 > 6.99
- UP\_EXONS\_HeLa\_SRRM2-KD vs CS : 0.0323494  
mean: 7.8765 < 8.2229 , median: 8.41 < 8.73
- UP\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.0169897  
mean: 7.8765 > 7.5422 , median: 8.41 > 8.27
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CR : 4.95122e-07  
mean: 6.7108 > 5.8762 , median: 7.835 > 6.99
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CS : 1.13343e-15  
mean: 6.7108 < 8.2229 , median: 7.835 < 8.73
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.00108818  
mean: 6.7108 < 7.5422 , median: 7.835 < 8.27
- CR vs CS : 1.06918e-55  
mean: 5.8762 < 8.2229 , median: 6.99 < 8.73
- CR vs AS\_NC : 9.15745e-25  
mean: 5.8762 < 7.5422 , median: 6.99 < 8.27
- CS vs AS\_NC : 3.52114e-10  
mean: 8.2229 > 7.5422 , median: 8.73 > 8.27



## 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



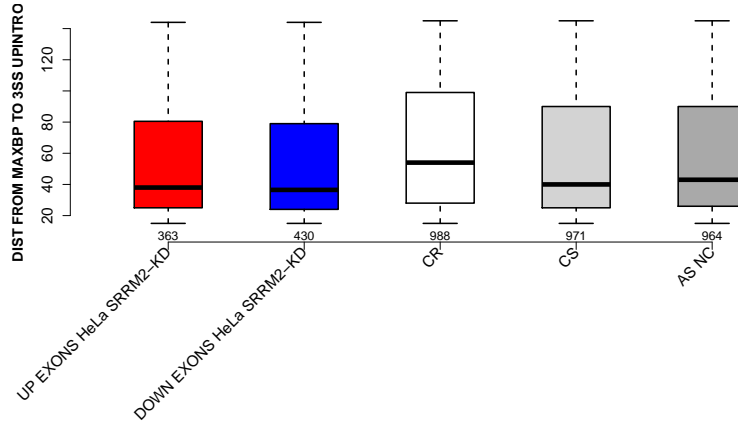
Significant results from Mann-Whitney U test:

- UP\_EXONS\_HeLa\_SRRM2-KD vs CS : 0.0240878  
mean: 8.55 > 8.2961 , median: 8.92 > 8.48
- CR vs CS : 0.0254391  
mean: 8.5701 > 8.2961 , median: 8.77 > 8.48
- CS vs AS\_NC : 0.01275  
mean: 8.2961 < 8.5799 , median: 8.48 < 8.855

## 6.29 DIST FROM MAXBP TO 3SS UPINTRON

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

Meaning: distance to 3ss of best precited BP



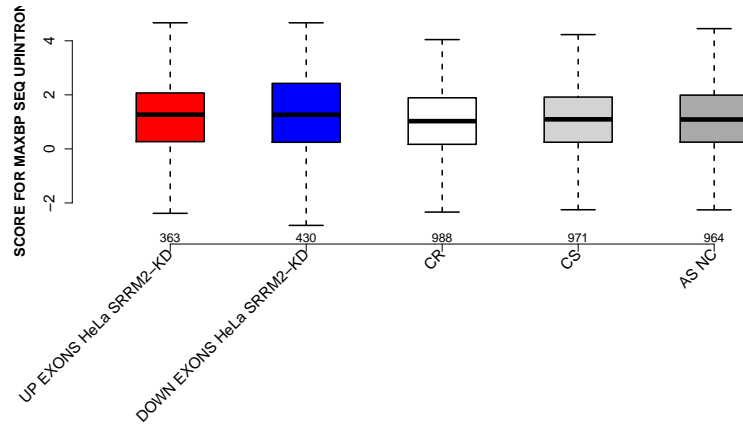
Significant results from Mann-Whitney U test:

- UP\_EXONS\_HeLa\_SRRM2-KD vs CR : 0.000105164  
mean: 54.8457 < 64.3188 , median: 38 < 54
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CR : 1.48045e-06  
mean: 54.3977 < 64.3188 , median: 36.5 < 54
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.0148491  
mean: 54.3977 < 58.862 , median: 36.5 < 43
- CR vs CS : 6.4207e-05  
mean: 64.3188 > 57.965 , median: 54 > 40
- CR vs AS\_NC : 0.00128324  
mean: 64.3188 > 58.862 , median: 54 > 43

## 6.30 SCORE FOR MAXBP SEQ UPINTRON

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

Meaning: BP sequence score of best predicted BP



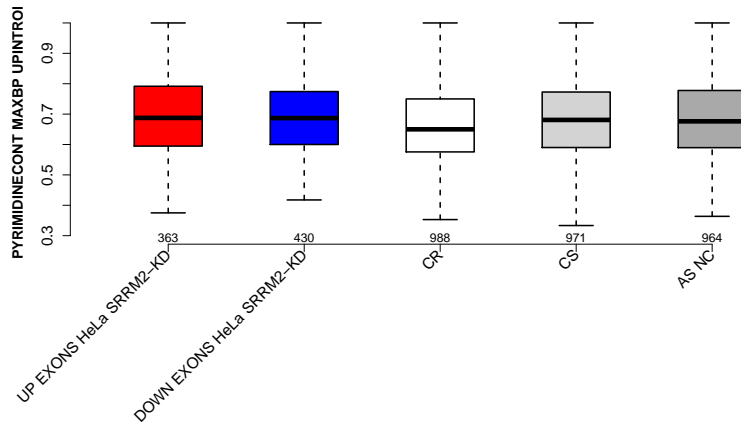
Significant results from Mann-Whitney U test:

- UP\_EXONS\_HeLa\_SRRM2-KD vs CR : 0.0471439  
mean: 1.1764 > 1.0163 , median: 1.2657 > 1.0265
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CR : 0.00464972  
mean: 1.2781 > 1.0163 , median: 1.2618 > 1.0265
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CS : 0.0442659  
mean: 1.2781 > 1.0983 , median: 1.2618 > 1.094

### 6.31 PYRIMIDINECONT MAXBP UPINTRON

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

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



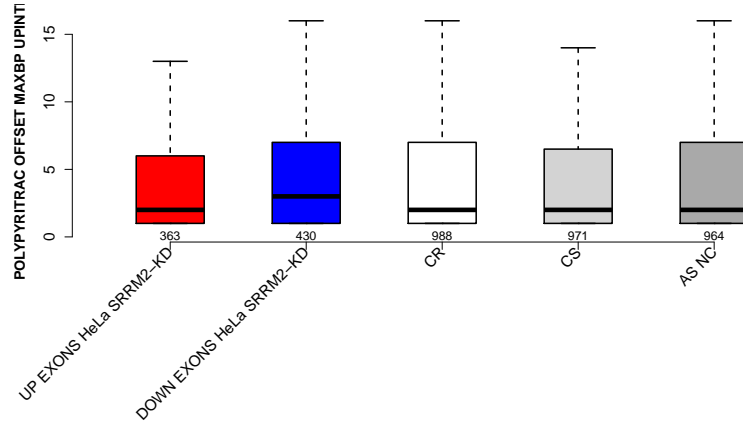
Significant results from Mann-Whitney U test:

- UP\_EXONS\_HeLa\_SRRM2-KD vs CR : 9.34981e-05  
mean: 0.694448 > 0.663459 , median: 0.6875 > 0.65
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CR : 0.000159857  
mean: 0.688082 > 0.663459 , median: 0.686887 > 0.65
- CR vs CS : 0.000128786  
mean: 0.663459 < 0.684265 , median: 0.65 < 0.680851
- CR vs AS\_NC : 0.000303368  
mean: 0.663459 < 0.683134 , median: 0.65 < 0.676263

## 6.32 POLYPYRITRAC OFFSET MAXBP UPINTRON

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

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



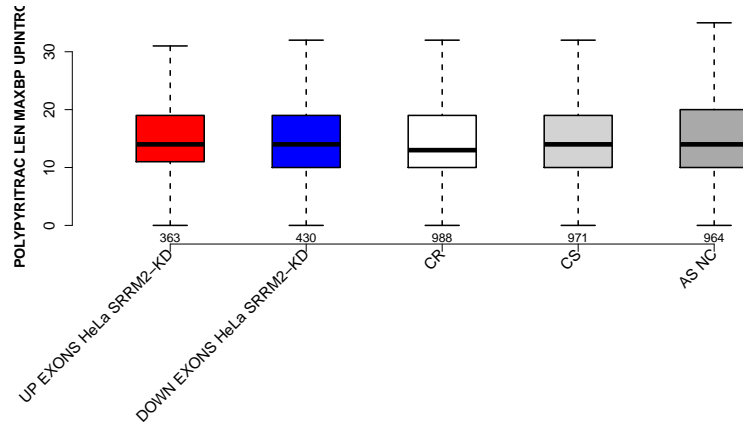
Significant results from Mann-Whitney U test:

- UP\_EXONS\_HeLa\_SRRM2-KD vs DOWN\_EXONS\_HeLa\_SRRM2-KD : 0.00333382  
mean: 4.022 < 5.2512 , median: 2 < 3
- UP\_EXONS\_HeLa\_SRRM2-KD vs CR : 0.0435029  
mean: 4.022 < 4.8097 , median: 2 = 2
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CS : 0.0338954  
mean: 5.2512 > 4.6787 , median: 3 > 2

### 6.33 POLYPYRITRAC LEN MAXBP UPINTRON

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

Meaning: Polypyrimidine track length for best BP



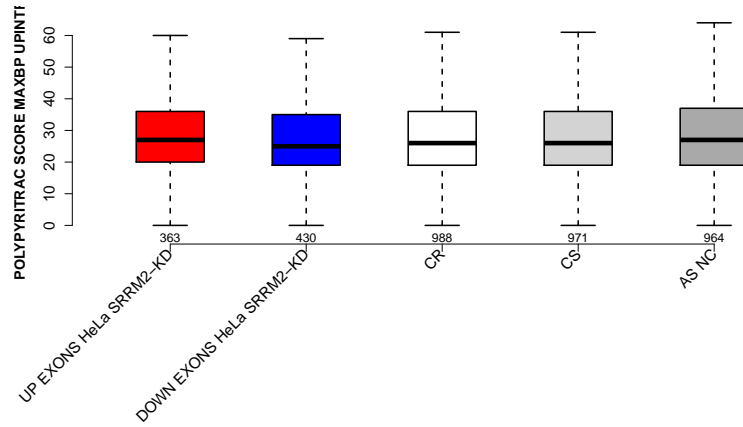
Significant results from Mann-Whitney U test:

- none

## 6.34 POLYPYRITRAC SCORE MAXBP UPINTRON

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

Meaning: Polypyrimidine track score for best BP



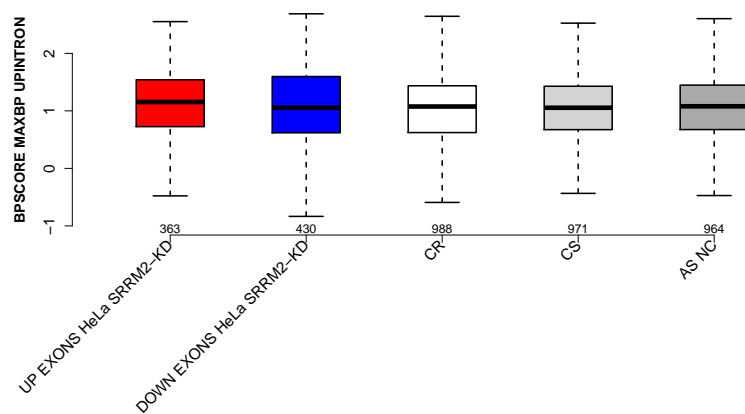
Significant results from Mann-Whitney U test:

- none

## 6.35 BPSCORE MAXBP UPINTRON

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

Meaning: SVM classification score of best BP



Significant results from Mann-Whitney U test:

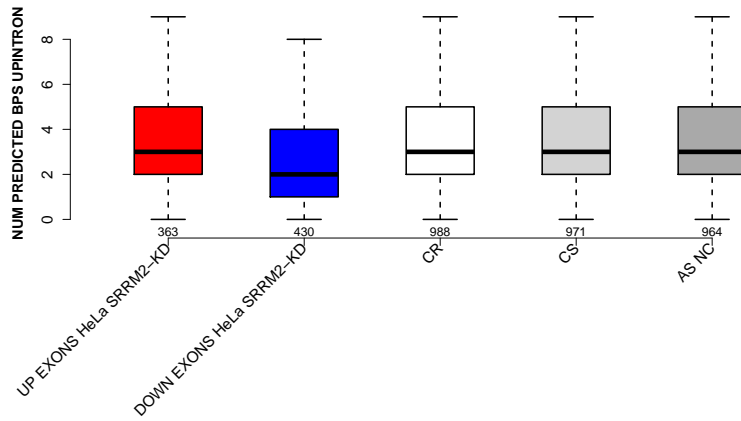
- UP\_EXONS\_HeLa\_SRRM2-KD vs CR : 0.00642225  
mean: 1.1175 > 0.995891 , median: 1.1542 > 1.0755
- UP\_EXONS\_HeLa\_SRRM2-KD vs CS : 0.0229064  
mean: 1.1175 > 1.0327 , median: 1.1542 > 1.0543



## 6.36 NUM PREDICTED BPS UPINTRON

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

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



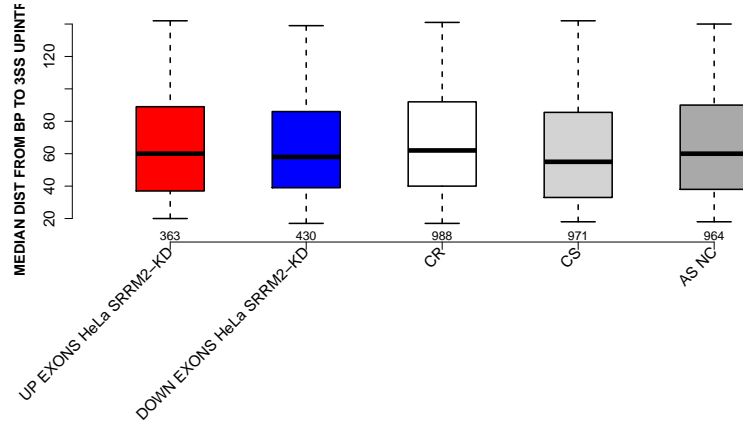
Significant results from Mann-Whitney U test:

- UP\_EXONS\_HeLa\_SRRM2-KD vs DOWN\_EXONS\_HeLa\_SRRM2-KD : 0.000457418  
mean: 3.259 > 2.8256 , median: 3 > 2
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CR : 1.79174e-05  
mean: 2.8256 < 3.3209 , median: 2 < 3
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CS : 4.40556e-07  
mean: 2.8256 < 3.38 , median: 2 < 3
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 5.27356e-06  
mean: 2.8256 < 3.2967 , median: 2 < 3

## 6.37 MEDIAN DIST FROM BP TO 3SS UPINTRON

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

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



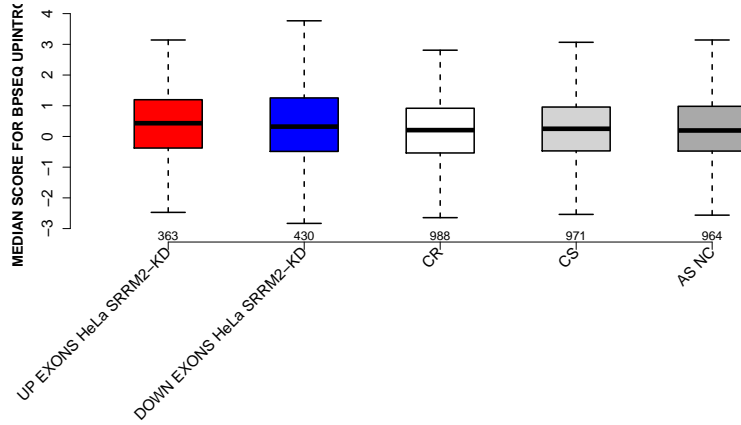
Significant results from Mann-Whitney U test:

- CR vs CS : 5.05486e-05  
mean: 67.0521 > 62.0391 , median: 62 > 55
- CS vs AS\_NC : 0.0114737  
mean: 62.0391 < 65.1291 , median: 55 < 60

## 6.38 MEDIAN SCORE FOR BPSEQ UPINTRON

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



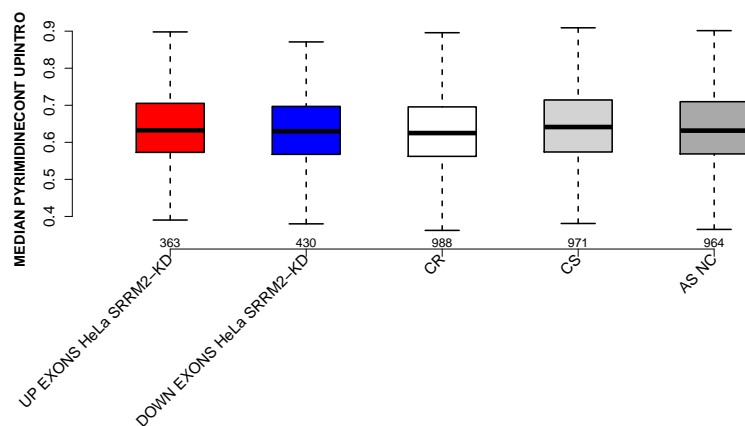
Significant results from Mann-Whitney U test:

- UP\_EXONS\_HeLa\_SRRM2-KD vs CR : 0.00175825  
mean: 0.404782 > 0.17589 , median: 0.431363 > 0.206175
- UP\_EXONS\_HeLa\_SRRM2-KD vs CS : 0.0237284  
mean: 0.404782 > 0.24818 , median: 0.431363 > 0.25016
- UP\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.0136168  
mean: 0.404782 > 0.228412 , median: 0.431363 > 0.194796
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CR : 0.0179424  
mean: 0.40046 > 0.17589 , median: 0.32056 > 0.206175

## 6.39 MEDIAN PYRIMIDINECONT UPINTRON

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

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



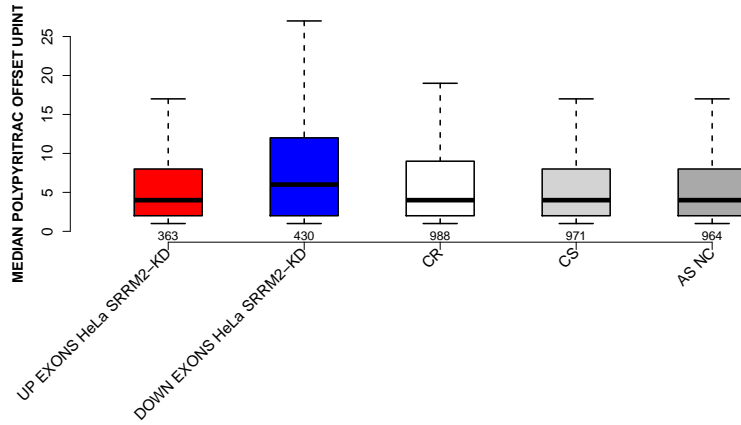
Significant results from Mann-Whitney U test:

- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CS : 0.0416982  
mean: 0.63443 < 0.647334 , median: 0.629949 < 0.641304
- CR vs CS : 0.000347505  
mean: 0.630736 < 0.647334 , median: 0.625 < 0.641304
- CR vs AS\_NC : 0.0404775  
mean: 0.630736 < 0.640556 , median: 0.625 < 0.631579

## 6.40 MEDIAN POLYPYRITRAC OFFSET UPINTRON

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

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



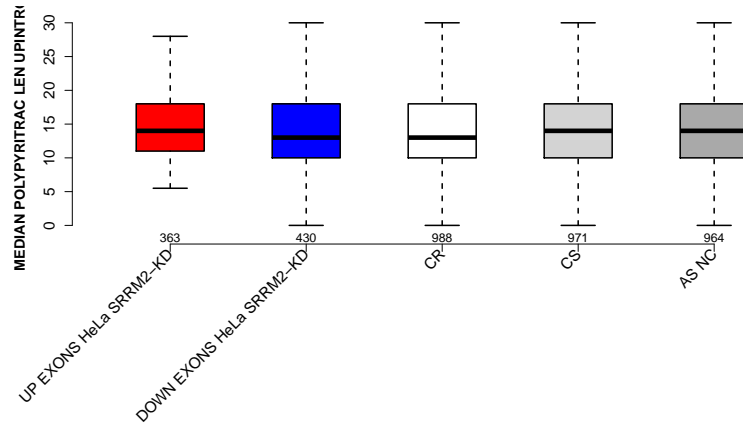
Significant results from Mann-Whitney U test:

- UP\_EXONS\_HeLa\_SRRM2-KD vs DOWN\_EXONS\_HeLa\_SRRM2-KD : 0.00137489  
mean: 7.1033 < 9.9256 , median: 4 < 6
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CR : 0.000138132  
mean: 9.9256 > 6.9408 , median: 6 > 4
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CS : 1.20755e-05  
mean: 9.9256 > 6.7853 , median: 6 > 4
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 4.40517e-05  
mean: 9.9256 > 6.7225 , median: 6 > 4

## 6.41 MEDIAN POLYPYRITRAC LEN UPINTRON

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

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



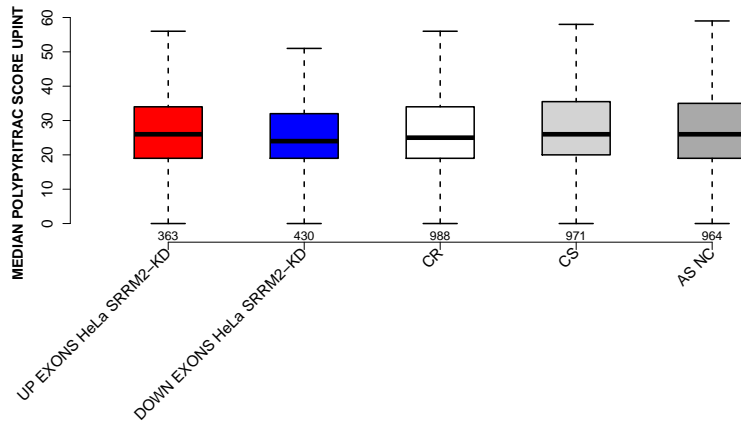
Significant results from Mann-Whitney U test:

- none

## 6.42 MEDIAN POLYPYRITRAC SCORE UPINTRON

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

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



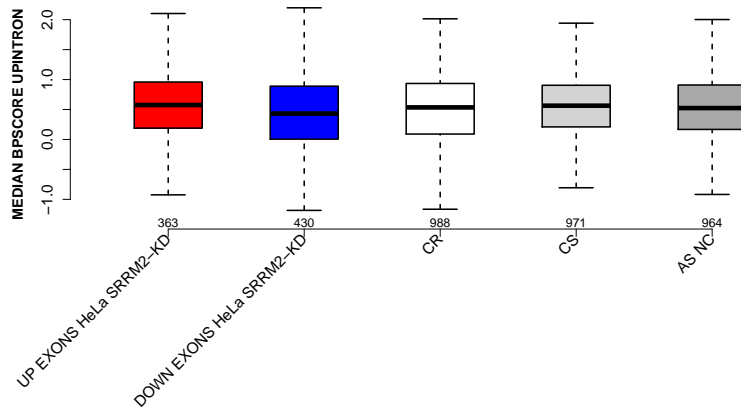
Significant results from Mann-Whitney U test:

- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CS : 0.0075394  
mean: 28.0174 < 29.0623 , median: 24 < 26
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.0447533  
mean: 28.0174 < 29.4803 , median: 24 < 26

## 6.43 MEDIAN BPSCORE UPINTRON

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

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



Significant results from Mann-Whitney U test:

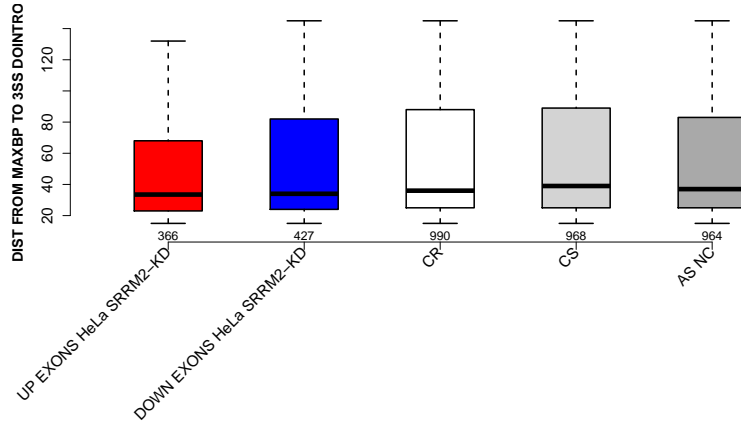
- UP\_EXONS\_HeLa\_SRRM2-KD vs DOWN\_EXONS\_HeLa\_SRRM2-KD : 0.00671989  
mean: 0.493938 > 0.305461 , median: 0.574725 > 0.432173
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CS : 0.00975043  
mean: 0.305461 < 0.464061 , median: 0.432173 < 0.563698
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.039447  
mean: 0.305461 < 0.45823 , median: 0.432173 < 0.524034



## 6.44 DIST FROM MAXBP TO 3SS DONTRO

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

Meaning: distance to 3ss of best precited BP



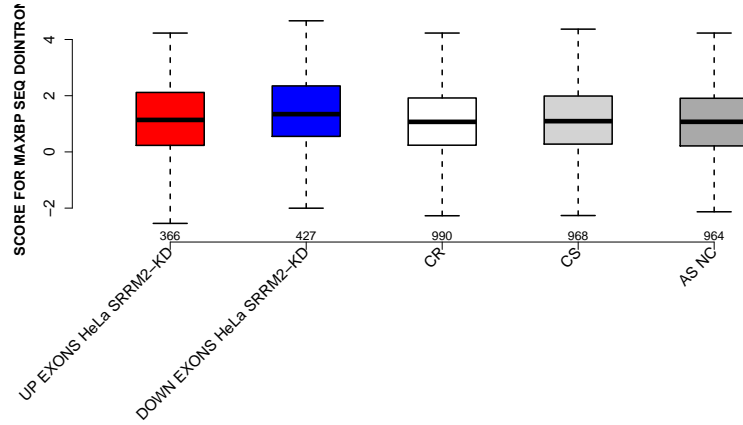
Significant results from Mann-Whitney U test:

- UP\_EXONS\_HeLa\_SRRM2-KD vs CR : 0.00858644  
mean: 50.2787 < 56.1111 , median: 33.5 < 36
- UP\_EXONS\_HeLa\_SRRM2-KD vs CS : 0.00150682  
mean: 50.2787 < 57.4432 , median: 33.5 < 39
- UP\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.0115334  
mean: 50.2787 < 55.3278 , median: 33.5 < 37

## 6.45 SCORE FOR MAXBP SEQ DOINTRON

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

Meaning: BP sequence score of best predicted BP



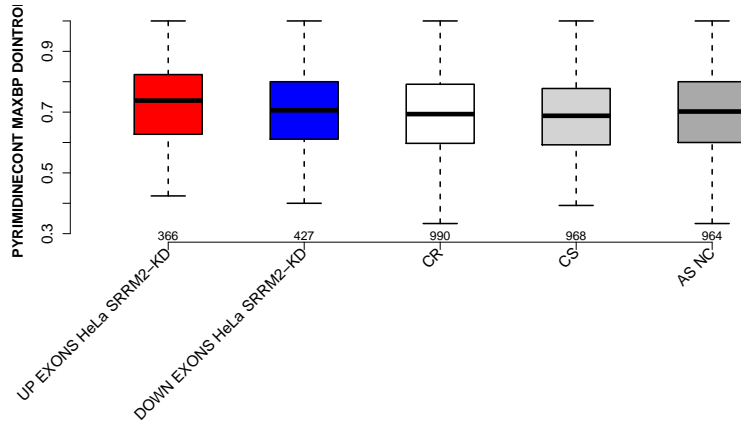
Significant results from Mann-Whitney U test:

- UP\_EXONS\_HeLa\_SRRM2-KD vs DOWN\_EXONS\_HeLa\_SRRM2-KD : 0.0138046  
mean: 1.1394 < 1.4247 , median: 1.1382 < 1.3439
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CR : 1.75231e-05  
mean: 1.4247 > 1.0573 , median: 1.3439 > 1.0693
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CS : 0.000886055  
mean: 1.4247 > 1.1497 , median: 1.3439 > 1.0944
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 1.54644e-05  
mean: 1.4247 > 1.0697 , median: 1.3439 > 1.071

## 6.46 PYRIMIDINECONT MAXBP DONTROI

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

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



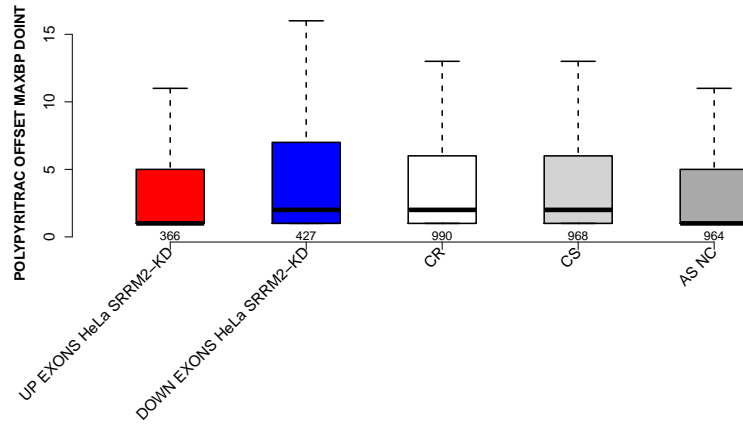
Significant results from Mann-Whitney U test:

- UP\_EXONS\_HeLa\_SRRM2-KD vs DOWN\_EXONS\_HeLa\_SRRM2-KD : 0.00203941  
mean: 0.729466 > 0.702527 , median: 0.737986 > 0.705882
- UP\_EXONS\_HeLa\_SRRM2-KD vs CR : 3.07904e-05  
mean: 0.729466 > 0.698654 , median: 0.737986 > 0.693441
- UP\_EXONS\_HeLa\_SRRM2-KD vs CS : 2.4852e-07  
mean: 0.729466 > 0.690432 , median: 0.737986 > 0.687906
- UP\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.000212971  
mean: 0.729466 > 0.700665 , median: 0.737986 > 0.701941
- CS vs AS\_NC : 0.0469293  
mean: 0.690432 < 0.700665 , median: 0.687906 < 0.701941

## 6.47 POLYPYRITRAC OFFSET MAXBP DONTINRON

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

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



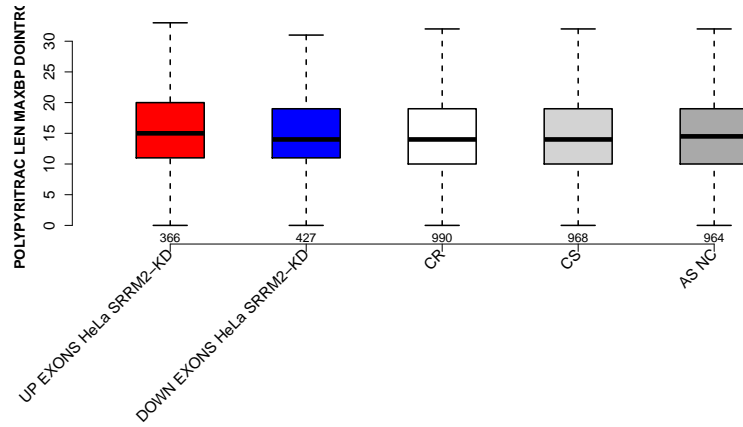
Significant results from Mann-Whitney U test:

- UP\_EXONS\_HeLa\_SRRM2-KD vs DOWN\_EXONS\_HeLa\_SRRM2-KD : 0.00174515  
mean: 3.6284 < 5.0023 , median: 1 < 2
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CR : 0.0464268  
mean: 5.0023 > 4.0576 , median: 2 = 2
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.00175663  
mean: 5.0023 > 3.8029 , median: 2 > 1

## 6.48 POLYPYRITRAC LEN MAXBP DOINTRON

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

Meaning: Polypyrimidine track length for best BP



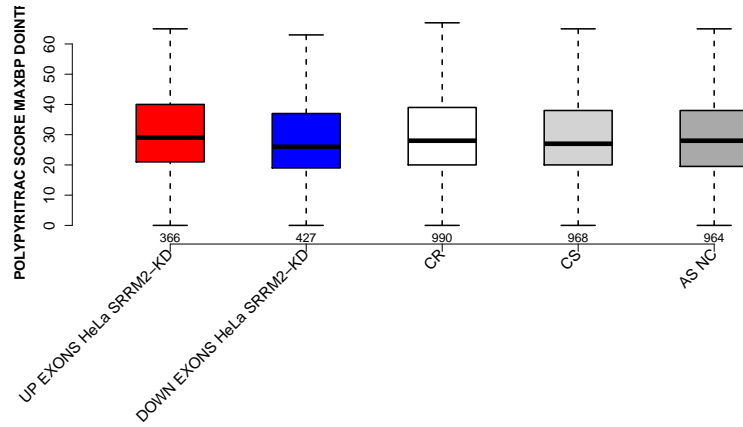
Significant results from Mann-Whitney U test:

- UP\_EXONS\_HeLa\_SRRM2-KD vs CS : 0.0272346  
mean: 16.5902 > 15.657 , median: 15 > 14

## 6.49 POLYPYRITRAC SCORE MAXBP DONTINRON

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

Meaning: Polypyrimidine track score for best BP



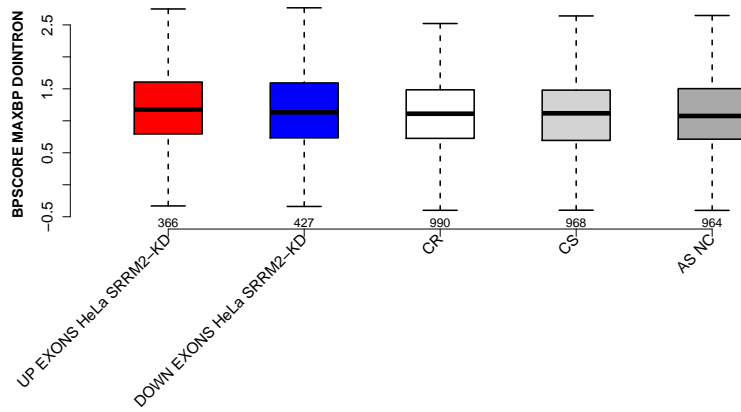
Significant results from Mann-Whitney U test:

- UP\_EXONS\_HeLa\_SRRM2-KD vs DOWN\_EXONS\_HeLa\_SRRM2-KD : 0.00903194  
mean: 32.8962 > 30.3115 , median: 29 > 26
- UP\_EXONS\_HeLa\_SRRM2-KD vs CS : 0.0232612  
mean: 32.8962 > 30.6725 , median: 29 > 27

## 6.50 BPSCORE MAXBP DONTNTRON

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

Meaning: SVM classification score of best BP



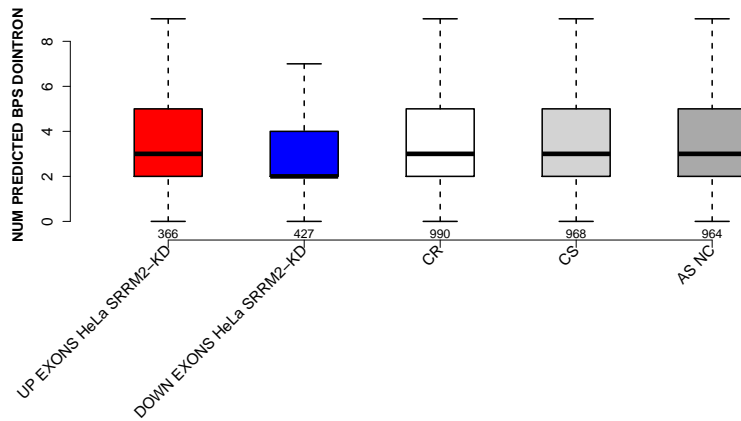
Significant results from Mann-Whitney U test:

- UP\_EXONS\_HeLa\_SRRM2-KD vs CR : 0.0281861  
mean: 1.1603 > 1.0757 , median: 1.1758 > 1.111
- UP\_EXONS\_HeLa\_SRRM2-KD vs CS : 0.0240945  
mean: 1.1603 > 1.0756 , median: 1.1758 > 1.1174
- UP\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.0232608  
mean: 1.1603 > 1.093 , median: 1.1758 > 1.0761
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CS : 0.0401727  
mean: 1.1522 > 1.0756 , median: 1.1323 > 1.1174
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.0384904  
mean: 1.1522 > 1.093 , median: 1.1323 > 1.0761

## 6.51 NUM PREDICTED BPS DOWINTRON

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

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



Significant results from Mann-Whitney U test:

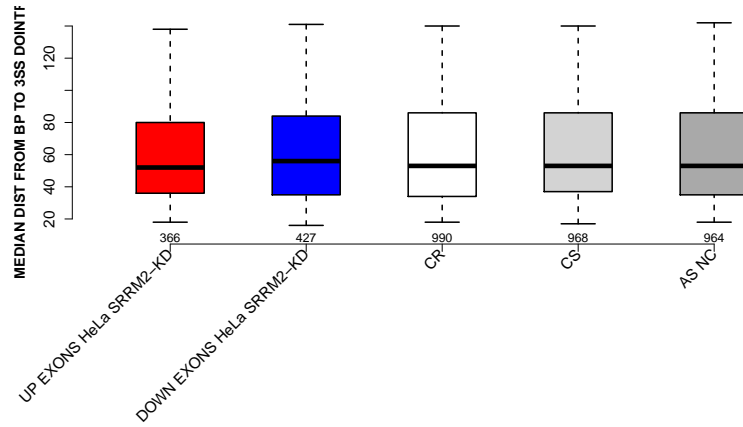
- UP\_EXONS\_HeLa\_SRRM2-KD vs DOWN\_EXONS\_HeLa\_SRRM2-KD : 9.11096e-06  
mean: 3.5137 > 2.9391 , median: 3 > 2
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CR : 1.00471e-09  
mean: 2.9391 < 3.5889 , median: 2 < 3
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CS : 5.61913e-05  
mean: 2.9391 < 3.3554 , median: 2 < 3
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 1.30903e-07  
mean: 2.9391 < 3.555 , median: 2 < 3
- CR vs CS : 0.00806785  
mean: 3.5889 > 3.3554 , median: 3 = 3



## 6.52 MEDIAN DIST FROM BP TO 3SS DOWNTON

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

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



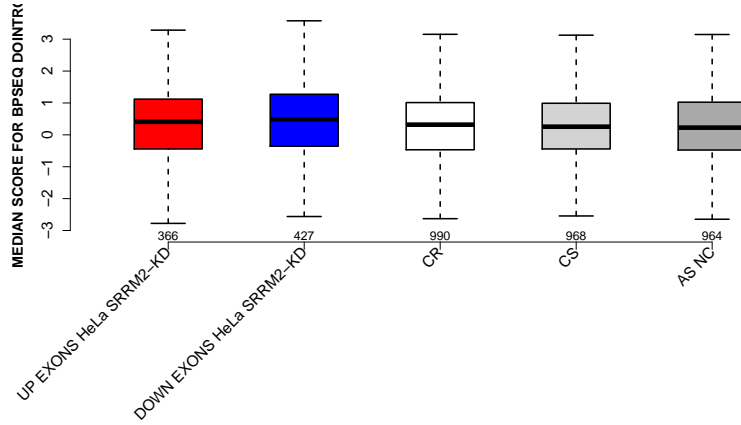
Significant results from Mann-Whitney U test:

- none

## 6.53 MEDIAN SCORE FOR BPSEQ DOINTRON

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

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



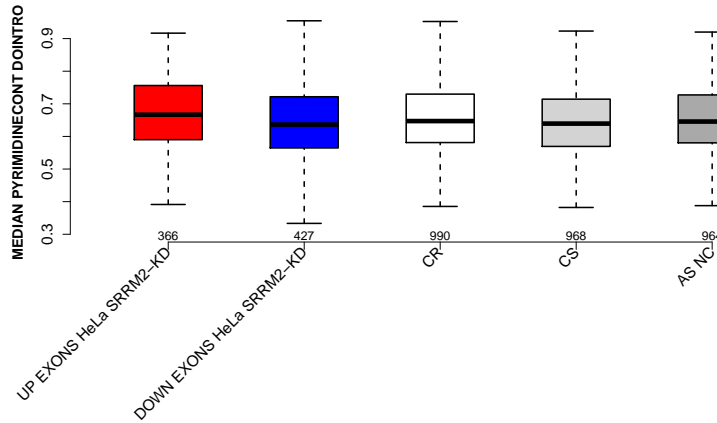
Significant results from Mann-Whitney U test:

- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CR : 0.0116843  
mean: 0.469125 > 0.29346 , median: 0.48498 > 0.318954
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CS : 0.00438641  
mean: 0.469125 > 0.276759 , median: 0.48498 > 0.25525
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.00259727  
mean: 0.469125 > 0.268251 , median: 0.48498 > 0.225732

## 6.54 MEDIAN PYRIMIDINECONT DOINTRON

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

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



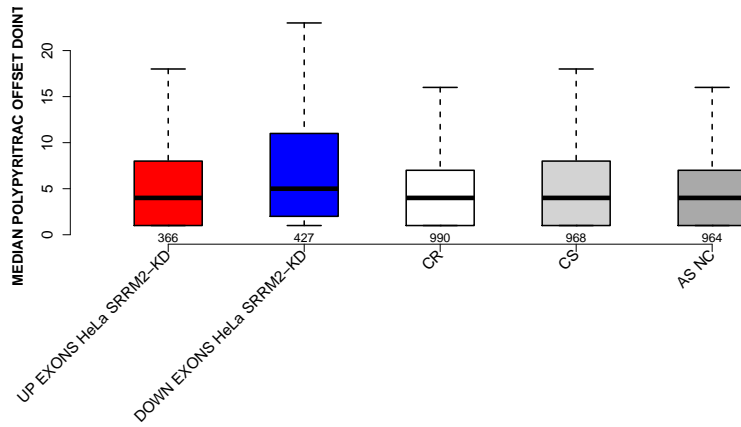
Significant results from Mann-Whitney U test:

- UP\_EXONS\_HeLa\_SRRM2-KD vs DOWN\_EXONS\_HeLa\_SRRM2-KD : 0.00265973  
mean: 0.669052 > 0.64526 , median: 0.666667 > 0.636364
- UP\_EXONS\_HeLa\_SRRM2-KD vs CR : 0.0266018  
mean: 0.669052 > 0.655231 , median: 0.666667 > 0.647059
- UP\_EXONS\_HeLa\_SRRM2-KD vs CS : 0.000450926  
mean: 0.669052 > 0.646648 , median: 0.666667 > 0.639297
- UP\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.0116033  
mean: 0.669052 > 0.652623 , median: 0.666667 > 0.64561
- CR vs CS : 0.0415081  
mean: 0.655231 > 0.646648 , median: 0.647059 > 0.639297

## 6.55 MEDIAN POLYPYRITRAC OFFSET DONTINRON

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

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



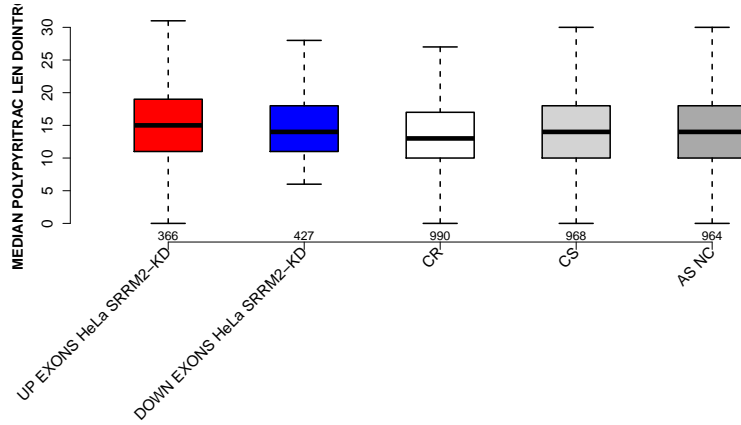
Significant results from Mann-Whitney U test:

- UP\_EXONS\_HeLa\_SRRM2-KD vs DOWN\_EXONS\_HeLa\_SRRM2-KD : 0.00121245  
mean: 7.168 < 9.2951 , median: 4 < 5
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CR : 1.62734e-06  
mean: 9.2951 > 6.2328 , median: 5 > 4
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CS : 0.000100362  
mean: 9.2951 > 6.735 , median: 5 > 4
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 1.94129e-07  
mean: 9.2951 > 5.5991 , median: 5 > 4

## 6.56 MEDIAN POLYPYRITRAC LEN DOINTRON

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

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



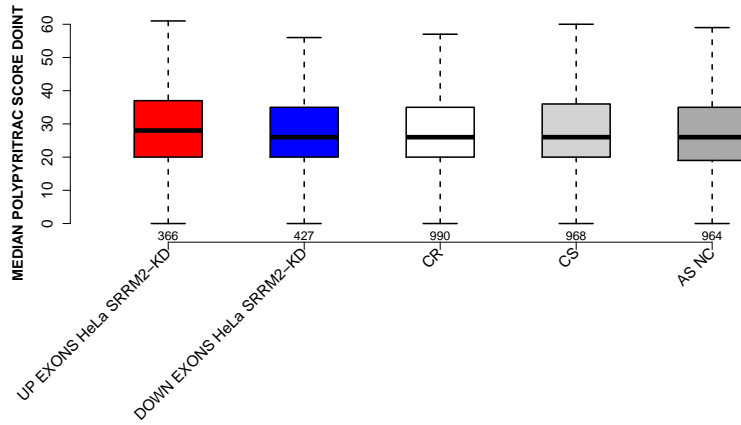
Significant results from Mann-Whitney U test:

- UP\_EXONS\_HeLa\_SRRM2-KD vs CR : 0.00307377  
mean: 16.3784 > 14.8793 , median: 15 > 13
- UP\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.0204886  
mean: 16.3784 > 15.0057 , median: 15 > 14
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CR : 0.043644  
mean: 15.7248 > 14.8793 , median: 14 > 13

## 6.57 MEDIAN POLYPYRITRAC SCORE DOINTRON

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

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



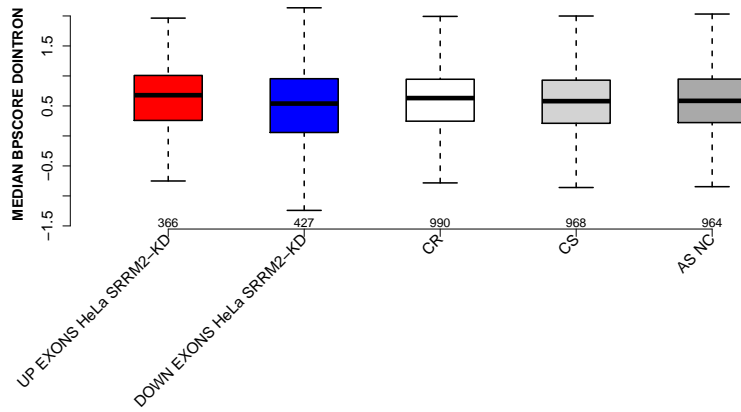
Significant results from Mann-Whitney U test:

- UP\_EXONS\_HeLa\_SRRM2-KD vs DOWN\_EXONS\_HeLa\_SRRM2-KD : 0.0451431  
mean: 31.7842 > 29.1194 , median: 28 > 26
- UP\_EXONS\_HeLa\_SRRM2-KD vs CR : 0.0330349  
mean: 31.7842 > 29.2854 , median: 28 > 26
- UP\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.0273476  
mean: 31.7842 > 28.9907 , median: 28 > 26

## 6.58 MEDIAN BPSCORE DOINTRON

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

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



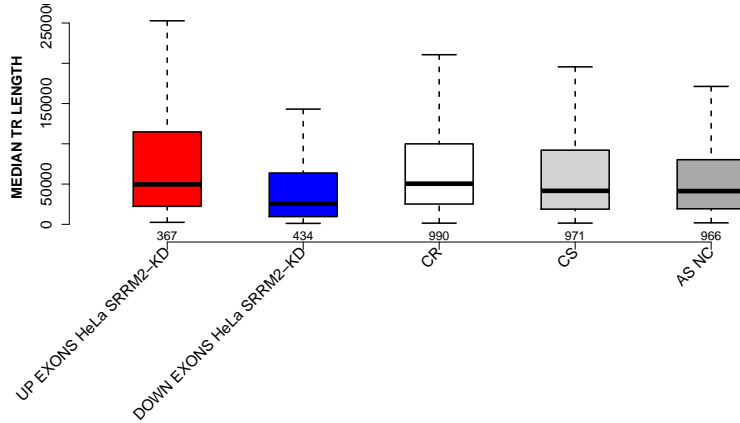
Significant results from Mann-Whitney U test:

- UP\_EXONS\_HeLa\_SRRM2-KD vs DOWN\_EXONS\_HeLa\_SRRM2-KD : 0.0210131  
mean: 0.507982 > 0.384542 , median: 0.678938 > 0.539312
- UP\_EXONS\_HeLa\_SRRM2-KD vs CS : 0.0498484  
mean: 0.507982 > 0.488739 , median: 0.678938 > 0.579906
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CR : 0.047356  
mean: 0.384542 < 0.515359 , median: 0.539312 < 0.630977

## 6.59 MEDIAN TR LENGTH

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

Meaning: median length of transcripts the exon occurs in



Significant results from Mann-Whitney U test:

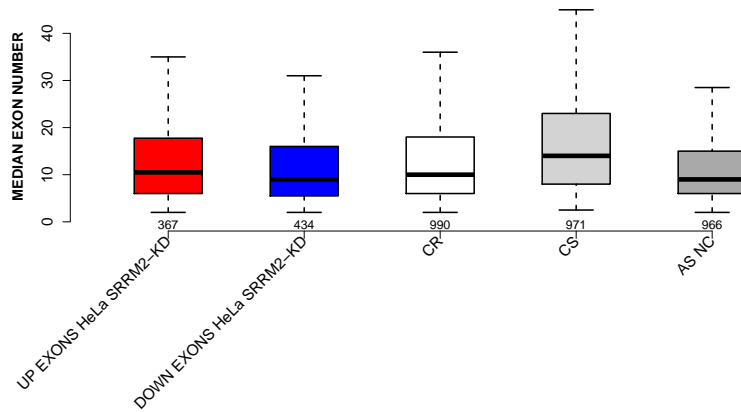
- UP\_EXONS\_HeLa\_SRRM2-KD vs DOWN\_EXONS\_HeLa\_SRRM2-KD : 4.03696e-13  
mean: 88262.4046 > 53265.4908 , median: 49607 > 25834.75
- UP\_EXONS\_HeLa\_SRRM2-KD vs CS : 0.00447684  
mean: 88262.4046 > 68708.6756 , median: 49607 > 41598.5
- UP\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.000645794  
mean: 88262.4046 > 66112.1755 , median: 49607 > 41305
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CR : 3.35973e-20  
mean: 53265.4908 < 81150.9485 , median: 25834.75 < 50445.25
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CS : 1.16178e-09  
mean: 53265.4908 < 68708.6756 , median: 25834.75 < 41598.5
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 8.52665e-09  
mean: 53265.4908 < 66112.1755 , median: 25834.75 < 41305
- CR vs CS : 4.51451e-05  
mean: 81150.9485 > 68708.6756 , median: 50445.25 > 41598.5
- CR vs AS\_NC : 4.75396e-07  
mean: 81150.9485 > 66112.1755 , median: 50445.25 > 41305



## 6.60 MEDIAN EXON NUMBER

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

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



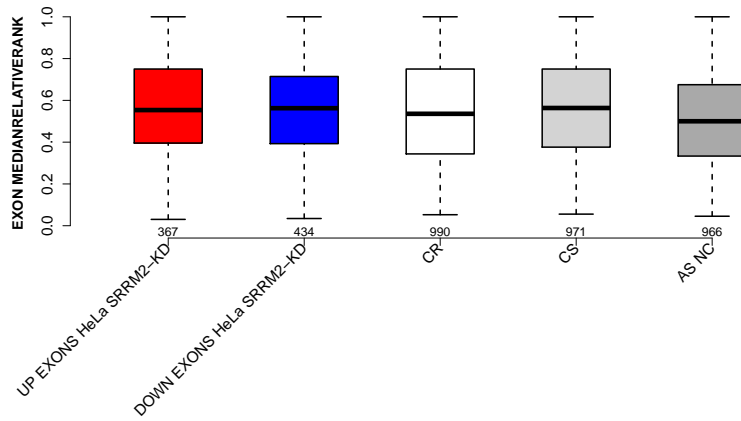
Significant results from Mann-Whitney U test:

- UP\_EXONS\_HeLa\_SRRM2-KD vs CS : 1.28265e-09  
mean: 13.7289 < 18.0505 , median: 10.5 < 14
- UP\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.0295277  
mean: 13.7289 > 12.0538 , median: 10.5 > 9
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CR : 0.00277257  
mean: 12.568 < 13.6091 , median: 9 < 10
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CS : 5.57496e-20  
mean: 12.568 < 18.0505 , median: 9 < 14
- CR vs CS : 2.62364e-16  
mean: 13.6091 < 18.0505 , median: 10 < 14
- CR vs AS\_NC : 0.000430468  
mean: 13.6091 > 12.0538 , median: 10 > 9
- CS vs AS\_NC : 7.58307e-31  
mean: 18.0505 > 12.0538 , median: 14 > 9

## 6.61 EXON MEDIANRELATIVERANK

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

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



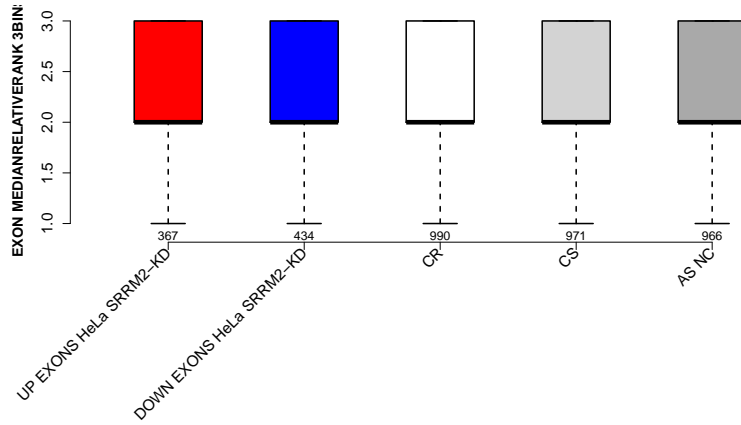
Significant results from Mann-Whitney U test:

- UP\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.00187693  
mean: 0.56138 > 0.518128 , median: 0.553571 > 0.5
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.0015476  
mean: 0.556216 > 0.518128 , median: 0.5625 > 0.5
- CR vs AS\_NC : 0.0022132  
mean: 0.552375 > 0.518128 , median: 0.535714 > 0.5
- CS vs AS\_NC : 7.03048e-06  
mean: 0.562272 > 0.518128 , median: 0.563492 > 0.5

## 6.62 EXON MEDIANRELATIVERANK 3BINS

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

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



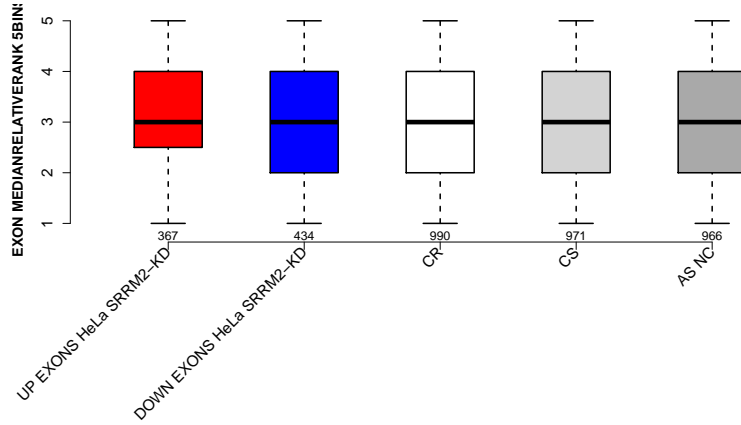
Significant results from Mann-Whitney U test:

- UP\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.00702541  
mean: 2.188 > 2.0673 , median: 2 = 2
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.00313312  
mean: 2.1935 > 2.0673 , median: 2 = 2
- CR vs AS\_NC : 0.0119823  
mean: 2.1495 > 2.0673 , median: 2 = 2
- CS vs AS\_NC : 7.91997e-05  
mean: 2.1988 > 2.0673 , median: 2 = 2

## 6.63 EXON MEDIANRELATIVERANK 5BINS

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

Meaning: similar to EXON MEDIANRELATIVERANK 3BINS with 5 bins



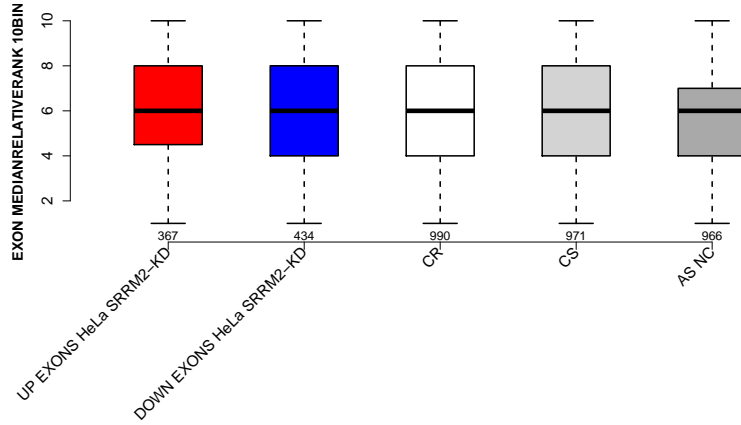
Significant results from Mann-Whitney U test:

- UP\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.00207938  
mean: 3.3052 > 3.0901 , median: 3 = 3
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.00668966  
mean: 3.2696 > 3.0901 , median: 3 = 3
- CR vs AS\_NC : 0.0062452  
mean: 3.2404 > 3.0901 , median: 3 = 3
- CS vs AS\_NC : 8.23835e-05  
mean: 3.3007 > 3.0901 , median: 3 = 3

## 6.64 EXON MEDIANRELATIVERANK 10BINS

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

Meaning: similar to EXON MEDIANRELATIVERANK 3BINS with 10 bins



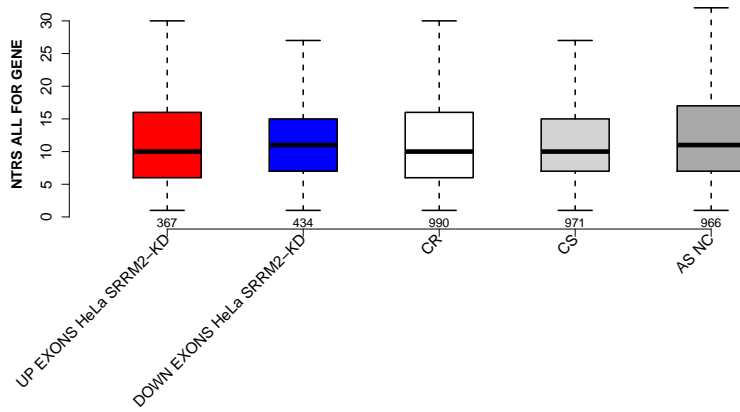
Significant results from Mann-Whitney U test:

- UP\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.00113073  
mean: 6.1608 > 5.7091 , median: 6 = 6
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.00216811  
mean: 6.0829 > 5.7091 , median: 6 = 6
- CR vs AS\_NC : 0.00265021  
mean: 6.0333 > 5.7091 , median: 6 = 6
- CS vs AS\_NC : 1.20853e-05  
mean: 6.1514 > 5.7091 , median: 6 = 6

## 6.65 NTRS ALL FOR GENE

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

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



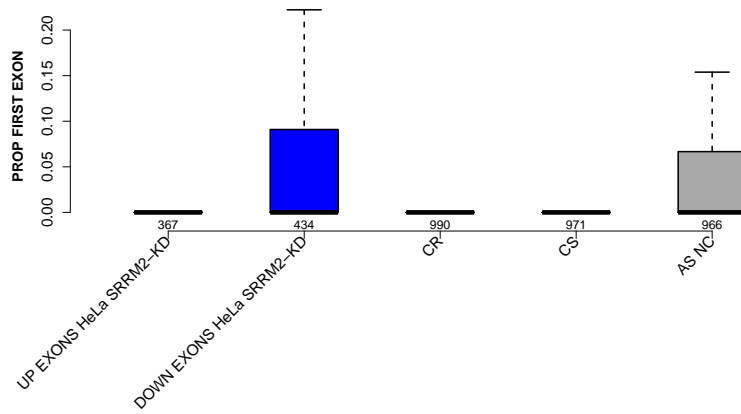
Significant results from Mann-Whitney U test:

- UP\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.00455505  
mean: 12.6649 < 13.2867 , median: 10 < 11
- CR vs AS\_NC : 0.00109117  
mean: 12.4434 < 13.2867 , median: 10 < 11
- CS vs AS\_NC : 2.71284e-05  
mean: 11.724 < 13.2867 , median: 10 < 11

## 6.66 PROP FIRST EXON

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

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



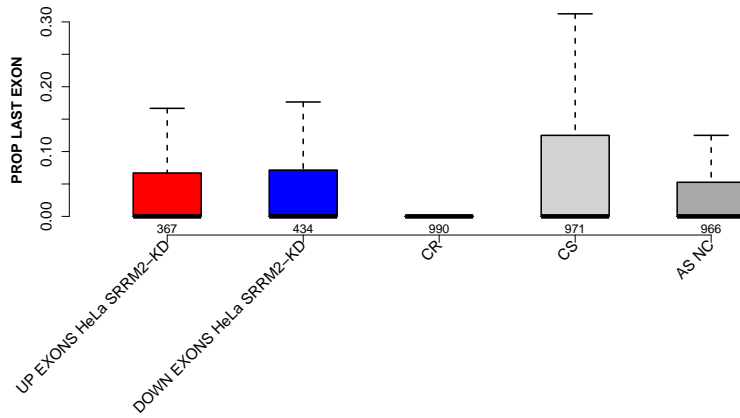
Significant results from Mann-Whitney U test:

- UP\_EXONS\_HeLa\_SRRM2-KD vs DOWN\_EXONS\_HeLa\_SRRM2-KD : 0.0219221  
mean: 0.0488415 < 0.0646191 , median: 0 = 0
- UP\_EXONS\_HeLa\_SRRM2-KD vs CR : 1.02424e-11  
mean: 0.0488415 > 0.0159733 , median: 0 = 0
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CR : 2.69019e-24  
mean: 0.0646191 > 0.0159733 , median: 0 = 0
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CS : 0.00307242  
mean: 0.0646191 > 0.0470158 , median: 0 = 0
- CR vs CS : 2.33653e-16  
mean: 0.0159733 < 0.0470158 , median: 0 = 0
- CR vs AS\_NC : 1.25816e-23  
mean: 0.0159733 < 0.052035 , 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:

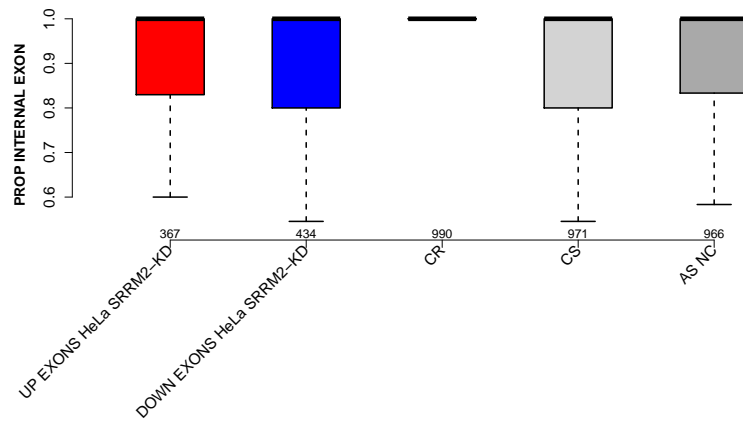
- UP\_EXONS\_HeLa\_SRRM2-KD vs CR : 1.72795e-24  
mean: 0.0586695 > 0.00975332 , median: 0 = 0
- UP\_EXONS\_HeLa\_SRRM2-KD vs CS : 0.0245278  
mean: 0.0586695 < 0.0709814 , median: 0 = 0
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CR : 2.77688e-29  
mean: 0.0588345 > 0.00975332 , median: 0 = 0
- CR vs CS : 9.61347e-49  
mean: 0.00975332 < 0.0709814 , median: 0 = 0
- CR vs AS\_NC : 1.9314e-33  
mean: 0.00975332 < 0.0459006 , median: 0 = 0
- CS vs AS\_NC : 0.000233315  
mean: 0.0709814 > 0.0459006 , median: 0 = 0



## 6.68 PROP INTERNAL EXON

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



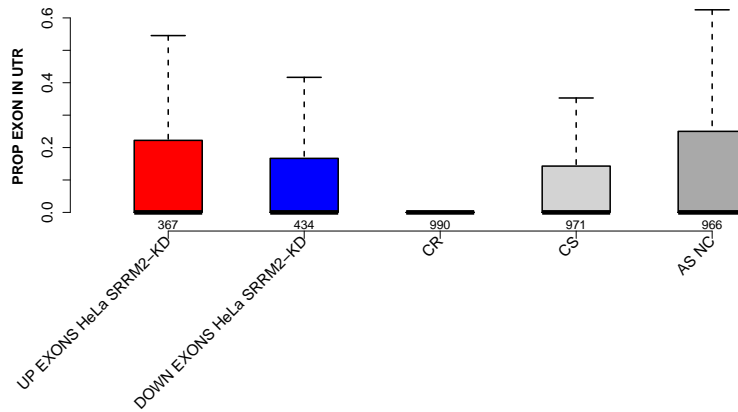
Significant results from Mann-Whitney U test:

- UP\_EXONS\_HeLa\_SRRM2-KD vs CR : 7.823e-29  
mean: 0.892659 < 0.974506 , median: 1 = 1
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CR : 3.07211e-47  
mean: 0.87726 < 0.974506 , median: 1 = 1
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.0204033  
mean: 0.87726 < 0.90406 , median: 1 = 1
- CR vs CS : 5.53837e-59  
mean: 0.974506 > 0.882383 , median: 1 = 1
- CR vs AS\_NC : 5.30105e-50  
mean: 0.974506 > 0.90406 , median: 1 = 1
- CS vs AS\_NC : 0.0115402  
mean: 0.882383 < 0.90406 , median: 1 = 1

## 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:

- UP\_EXONS\_HeLa\_SRRM2-KD vs CR : 2.28704e-21  
mean: 0.138013 > 0.0318968 , median: 0 = 0
- UP\_EXONS\_HeLa\_SRRM2-KD vs CS : 0.016905  
mean: 0.138013 > 0.100925 , median: 0 = 0
- UP\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.0236651  
mean: 0.138013 < 0.153574 , median: 0 = 0
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CR : 1.89143e-23  
mean: 0.11997 > 0.0318968 , median: 0 = 0
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs CS : 0.0281205  
mean: 0.11997 > 0.100925 , median: 0 = 0
- DOWN\_EXONS\_HeLa\_SRRM2-KD vs AS\_NC : 0.00277005  
mean: 0.11997 < 0.153574 , median: 0 = 0
- CR vs CS : 9.76229e-20  
mean: 0.0318968 < 0.100925 , median: 0 = 0
- CR vs AS\_NC : 6.81448e-54  
mean: 0.0318968 < 0.153574 , median: 0 = 0
- CS vs AS\_NC : 9.54238e-11  
mean: 0.100925 < 0.153574 , median: 0 = 0