Comparison of exons grouped into: UP-EXONS-BOTH, UP-EXONS-TAF2, UP-EXONS-TAF2dIDR, DOWN-EXONS-BOTH, DOWN-EXONS-TAF2, DOWN-EXONS-TAF2dIDR, CR, AS-NC, CS

December 8, 2023
Matt version 1.3.0

Contents

1 Infos 4

2 Warning: Please read this note carefully 4

3 Notes for publishing results 4

4 Data sets 5

5 Overview: Features with statistically significant differences (p-val ≤ 0.05) 6

6 Details: Box plots and statistical assessments for all features 22
- 6.1 EXON LENGTH . . . 22
- 6.2 UPEXON MEDIANLENGTH . . . 24
- 6.3 DOEXON MEDIANLENGTH . . . 25
- 6.4 RATIO UPEXON EXON LENGTH . . . 26
- 6.5 RATIO DOEXON EXON LENGTH . . . 28
- 6.6 UPINTRON MEDIANLENGTH . . . 29

6.7 DOINTRON MEDIANLENGTH . . . 31
6.8 RATIO UPINTRON EXON LENGTH . . . 33
6.9 RATIO DOINTRON EXON LENGTH . . . 35
6.10 EXON GCC . . . 37
6.11 UPINTRON GCC . . . 38
6.12 UPEXON GCC . . . 39
6.13 DOINTRON GCC . . . 41
6.14 DOEXON GCC . . . 42
6.15 RATIO UPEXON EXON GCC . . . 44
6.16 RATIO UPINTRON EXON GCC . . . 45
6.17 RATIO DOINTRON EXON GCC . . . 46
6.18 RATIO DOEXON EXON GCC . . . 47
6.19 SF1 HIGHESTSCORE 3SS UPINTRON . . . 48
6.20 SF1 HIGHESTSCORE 3SS DOINTRON . . . 49
6.21 UP 5SS 20INT10EX GCC . . . 50
6.22 GCC 3SS 20INT10EX . . . 51
6.23 GCC 5SS 20INT10EX . . . 52
6.24 DO 3SS 20INT10EX GCC . . . 53
6.25 MAXENTSCR HSAMODEL UPSTRM 5SS . . . 54
6.26 MAXENTSCR HSAMODEL 3SS . . . 56
6.27 MAXENTSCR HSAMODEL 5SS . . . 58
6.28 MAXENTSCR HSAMODEL DOWNSTRM 3SS . . . 60
6.29 DIST FROM MAXBP TO 3SS UPINTRON . . . 61
6.30 SCORE FOR MAXBP SEQ UPINTRON . . . 62
6.31 PYRIMIDINECONT MAXBP UPINTRON . . . 63
6.32 POLYPYRITRAC OFFSET MAXBP UPINTRON . . . 64
6.33 POLYPYRITRAC LEN MAXBP UPINTRON . . . 65
6.34 POLYPYRITRAC SCORE MAXBP UPINTRON . . . 66
6.35 BPSCORE MAXBP UPINTRON . . . 67
6.36 NUM PREDICTED BPS UPINTRON . . . 68
6.37 MEDIAN DIST FROM BP TO 3SS UPINTRON . . . 69
6.38 MEDIAN SCORE FOR BPSEQ UPINTRON . . . 70
6.39 MEDIAN PYRIMIDINECONT UPINTRON . . . 71
6.40 MEDIAN POLYPYRITRAC OFFSET UPINTRON . . . 72
6.41 MEDIAN POLYPYRITRAC LEN UPINTRON . . . 73
6.42 MEDIAN POLYPYRITRAC SCORE UPINTRON . . . 74
6.43 MEDIAN BPSCORE UPINTRON . . . 75
6.44 DIST FROM MAXBP TO 3SS DOINTRON . . . 76
6.45 SCORE FOR MAXBP SEQ DOINTRON . . . 77
6.46 PYRIMIDINECONT MAXBP DOINTRON . . . 78
6.47 POLYPYRITRAC OFFSET MAXBP DOINTRON . . . 79
6.48 POLYPYRITRAC LEN MAXBP DOINTRON . . . 80
6.49 POLYPYRITRAC SCORE MAXBP DOINTRON . . . 81
6.50 BPSCORE MAXBP DOINTRON . . . 82

6.51 NUM PREDICTED BPS DOINTRON 83
6.52 MEDIAN DIST FROM BP TO 3SS DOINTRON 84
6.53 MEDIAN SCORE FOR BPSEQ DOINTRON 85
6.54 MEDIAN PYRIMIDINECONT DOINTRON 86
6.55 MEDIAN POLYPYRITRAC OFFSET DOINTRON 87
6.56 MEDIAN POLYPYRITRAC LEN DOINTRON 88
6.57 MEDIAN POLYPYRITRAC SCORE DOINTRON 89
6.58 MEDIAN BPSCORE DOINTRON 90
6.59 MEDIAN TR LENGTH 91
6.60 MEDIAN EXON NUMBER 93
6.61 EXON MEDIANRELATIVERANK 95
6.62 EXON MEDIANRELATIVERANK 3BINS 96
6.63 EXON MEDIANRELATIVERANK 5BINS 97
6.64 EXON MEDIANRELATIVERANK 10BINS 98
6.65 NTRS ALL FOR GENE 99
6.66 PROP FIRST EXON 101
6.67 PROP LAST EXON 102
6.68 PROP INTERNAL EXON 103
6.69 PROP EXON IN UTR 105

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 then 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

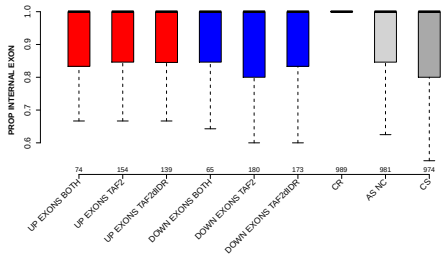
The Matt paper: *Matt: Unix tools for alternative splicing analysis, A. Gohr, M. Irimia, Bioinformatics, 2018, bty606, DOI: 10.1093/bioinformatics/bty606*
When publishing results wrt. splice site strengths which you determined for your data using matt, please cite: *Maximum entropy modeling of short sequence motifs with applications to RNA splicing signals, Yeo et al., 2003, DOI: 10.1089/1066527041410418*
When publishing results wrt. branch point features which you determined for your data with matt, please cite: *Genome-wide association between branch point properties and alternative splicing, Corvelo et al., 2010, DOI: 10.1371/journal.pcbi.1001016*
When publishing results with respect to the binding strength of the human Sf1 splicing factor, you might refert to where the Sf1 binding motif comes from: *Analysis of in situ pre-mRNA targets of human splicing factor SF1 reveals a function in alternative splicing, Margherita Corioni, Nicolas Antih, Goranka Tanackovic, Mihaela Zavolan, and Angela Kramer, 2011, DOI: 10.1093/nar/gkq1042*
The Sf1 binding motif is described in supplement, page 13, table S2: Weight matrix of the binding specificity of SF1.

4 Data sets

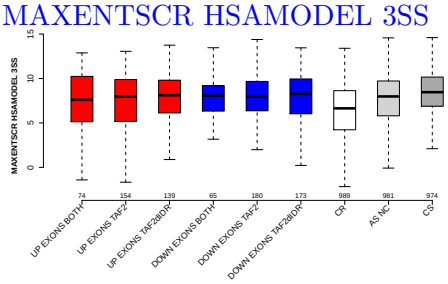
Input file:
ALL_EXONS.tab
Selection criteria for defining exons groups:
UP_EXONS_BOTH : having value UP_EXONS_BOTH in column GROUP
UP_EXONS_TAF2 : having value UP_EXONS_TAF2 in column GROUP
UP_EXONS_TAF2dIDR : having value UP_EXONS_TAF2dIDR in column GROUP
DOWN_EXONS_BOTH : having value DOWN_EXONS_BOTH in column GROUP
DOWN_EXONS_TAF2 : having value DOWN_EXONS_TAF2 in column GROUP
DOWN_EXONS_TAF2dIDR : having value DOWN_EXONS_TAF2dIDR in column GROUP
CR : having value CR in column GROUP
AS_NC : having value AS_NC in column GROUP
CS : having value CS 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_BOTH: 80 / 74
UP_EXONS_TAF2: 159 / 154
UP_EXONS_TAF2dIDR: 147 / 139
DOWN_EXONS_BOTH: 72 / 65
DOWN_EXONS_TAF2: 192 / 180
DOWN_EXONS_TAF2dIDR: 177 / 173
CR: 1000 / 989
AS_NC: 1000 / 981
CS: 1000 / 974

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

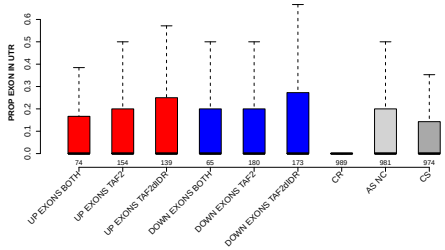
PROP INTERNAL EXON



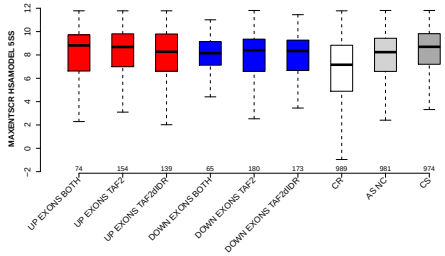
MAXENTSCR HSAMODEL 3SS



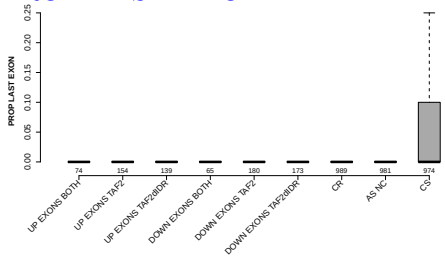
PROP EXON IN UTR



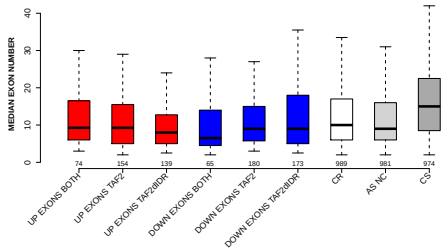
MAXENTSCR HSAMODEL 5SS



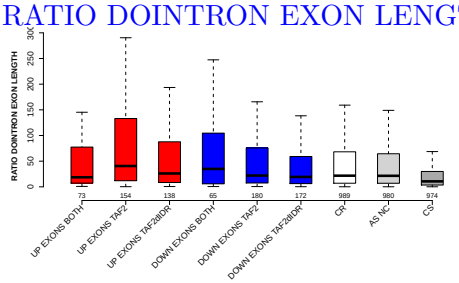
PROP LAST EXON



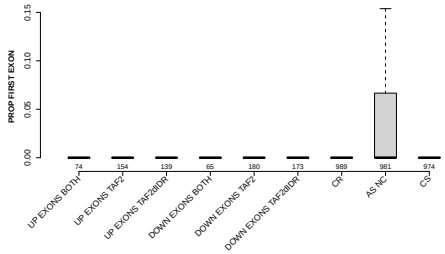
MEDIAN EXON NUMBER



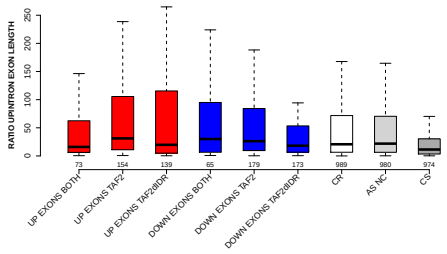
RATIO DOINTRON EXON LENGTH



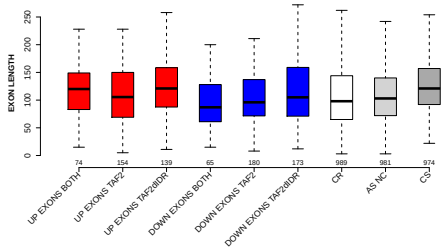
PROP FIRST EXON



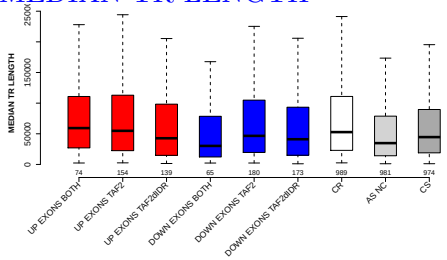
RATIO UPINTRON EXON LENGTH



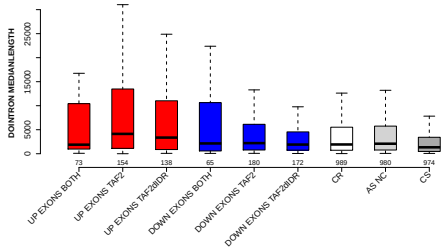
EXON LENGTH



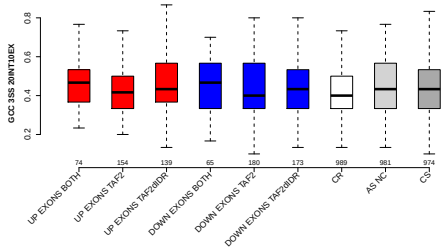
MEDIAN TR LENGTH



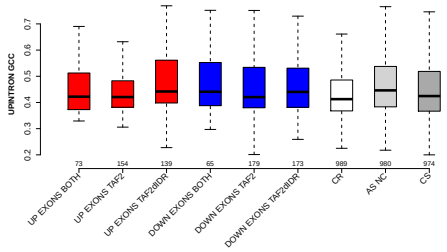
DOINTRON MEDIANLENGTH



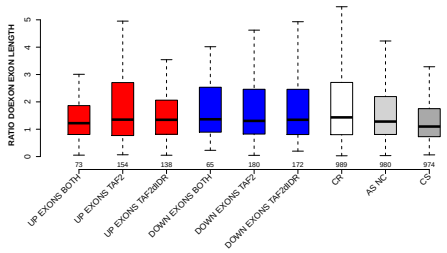
GCC 3SS 20INT10EX



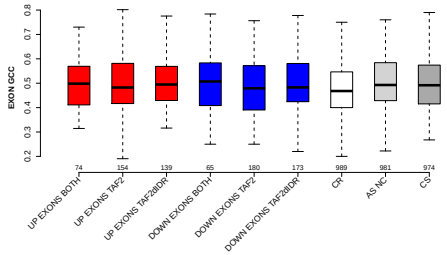
UPINTRON GCC



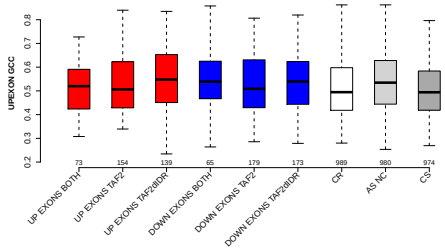
RATIO DOEXON EXON LENGTH



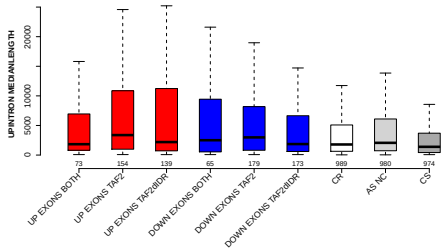
EXON GCC



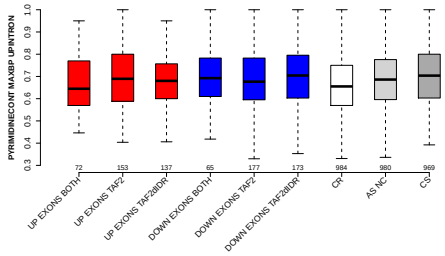
UPEXON GCC



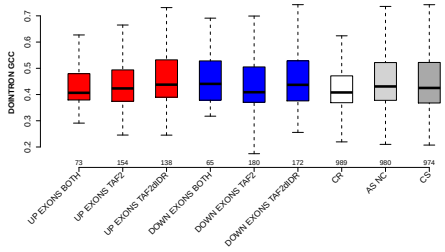
UPINTRON MEDIANLENGTH



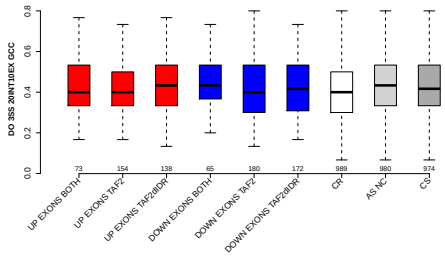
PYRIMIDINECONT MAXBP UPINTRON



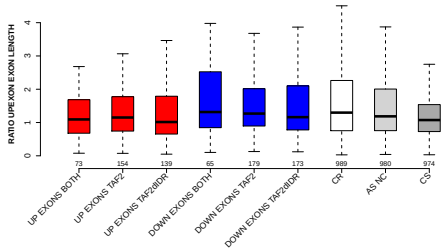
DOINTRON GCC



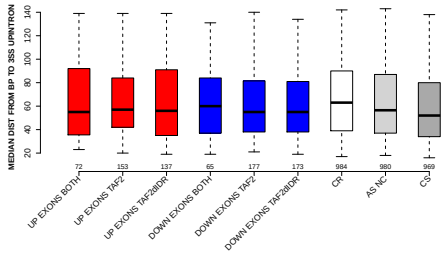
DO 3SS 20INT10EX GCC



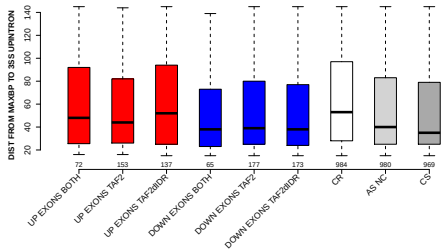
RATIO UPEXON EXON LENGTH



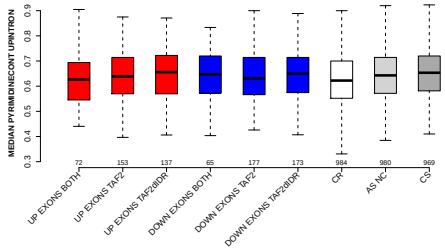
MEDIAN DIST FROM BP TO 3SS UPINTRON



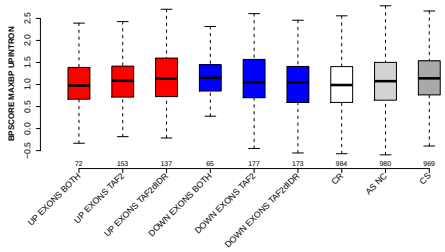
DIST FROM MAXBP TO 3SS UPINTRON



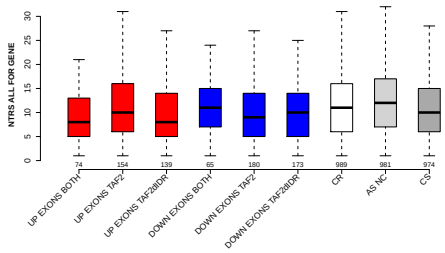
MEDIAN PYRIMIDINECONT UPINTRON



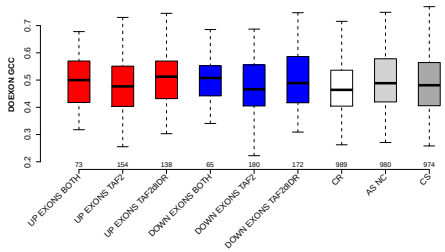
BPSCORE MAXBP UPINTRON



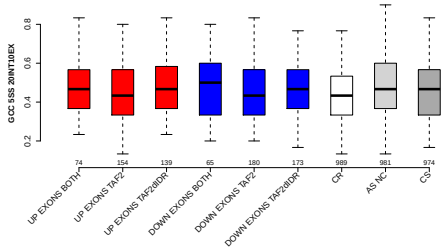
NTRS ALL FOR GENE



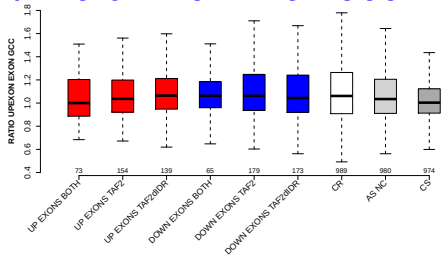
DOEXON GCC



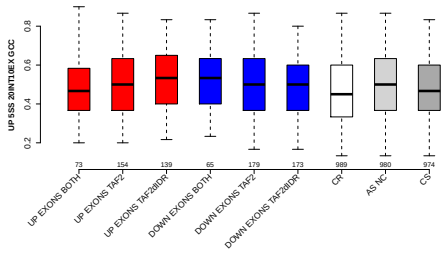
GCC 5SS 20INT10EX



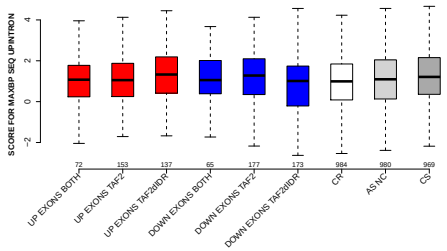
RATIO UPEXON EXON GCC



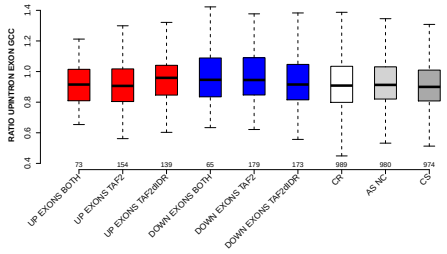
UP 5SS 20INT10EX GCC



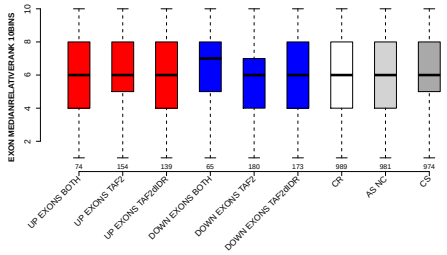
SCORE FOR MAXBP SEQ UPINTRON



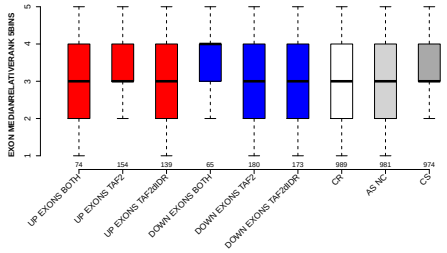
RATIO UPINTRON EXON GCC



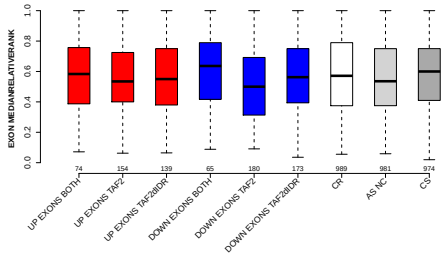
EXON MEDIANRELATIVERANK 10BINS



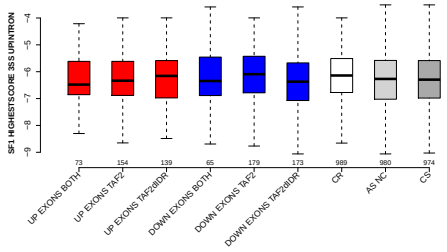
EXON MEDIANRELATIVERANK 5BINS



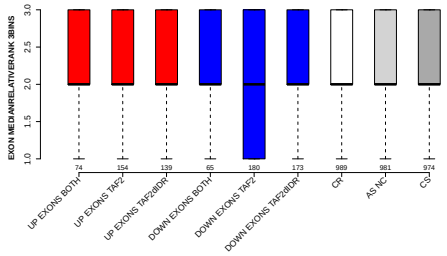
EXON MEDIANRELATIVERANK



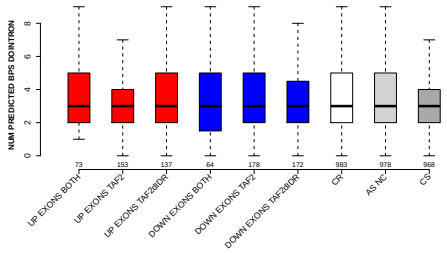
SF1 HIGHESTSCORE 3SS UPINTRON



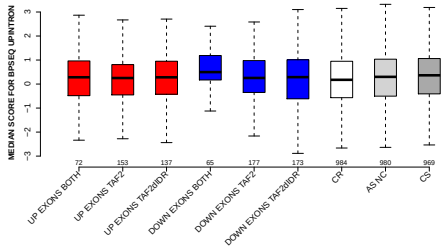
EXON MEDIANRELATIVERANK 3BINS



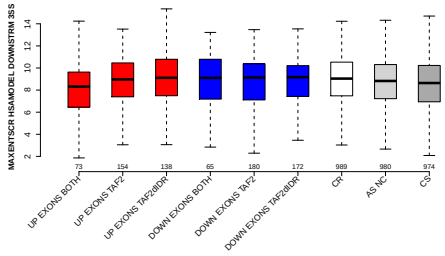
NUM PREDICTED BPS DOINTRON



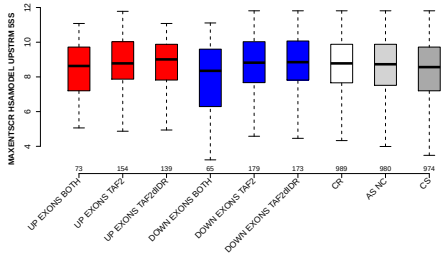
MEDIAN SCORE FOR BPSEQ UPINTRON



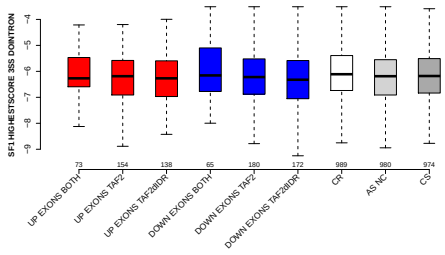
MAXENTSCR HSAMODEL DOWNSTRM 3SS



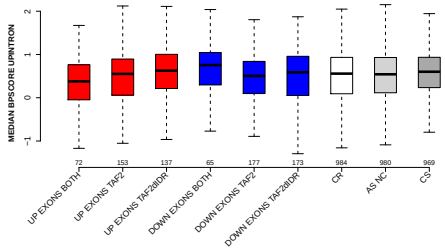
MAXENTSCR HSAMODEL UPSTRM 5SS



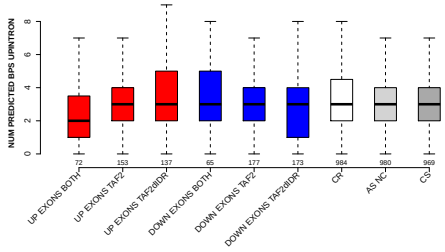
SF1 HIGHESTSCORE 3SS DOINTRON



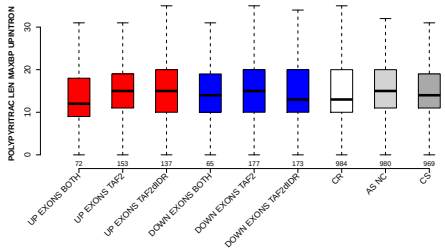
MEDIAN BPSCORE UPINTRON



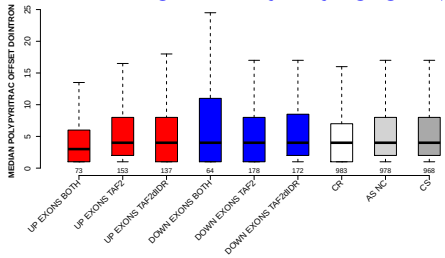
NUM PREDICTED BPS UPINTRON



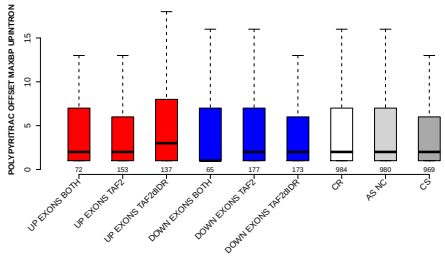
POLYPYRITRAC LEN MAXBP UPINTRON



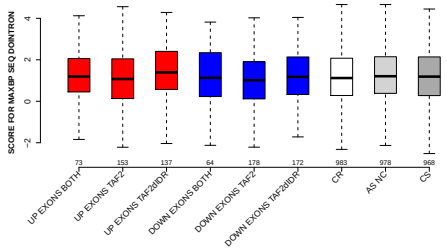
MEDIAN POLYPYRITRAC OFFSET DOINTRON



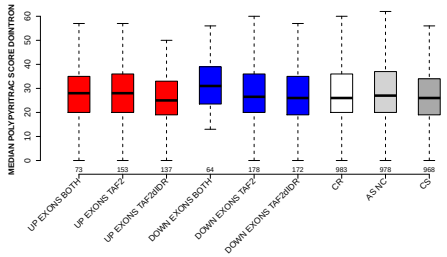
POLYPYRITRAC OFFSET MAXBP UPINTRON



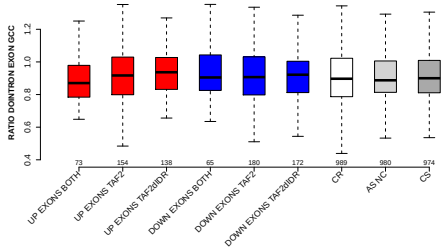
SCORE FOR MAXBP SEQ DOINTRON



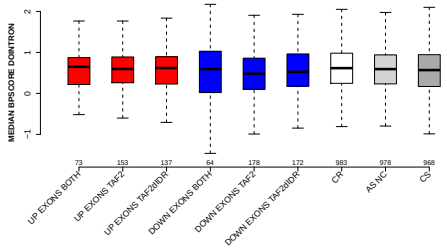
MEDIAN POLYPYRITRAC SCORE DOINTRON



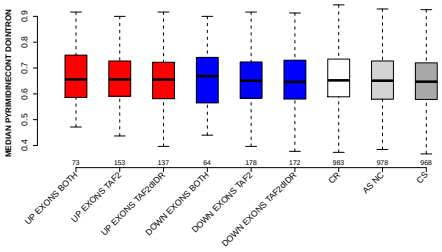
RATIO DOINTRON EXON GCC



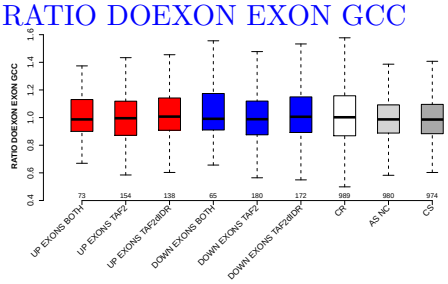
MEDIAN BPSCORE DOINTRON



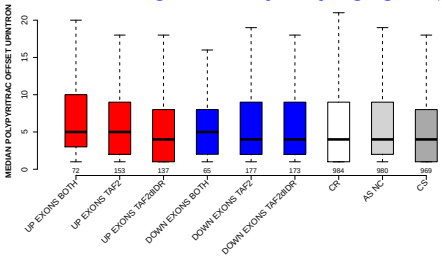
MEDIAN PYRIMIDINECONT DOINTRON



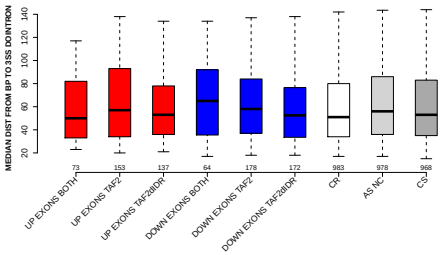
RATIO DOEXON EXON GCC



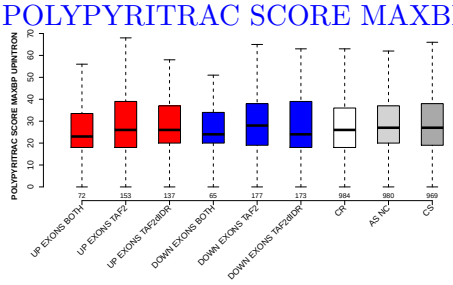
MEDIAN POLYPYRITRAC OFFSET UPINTRON



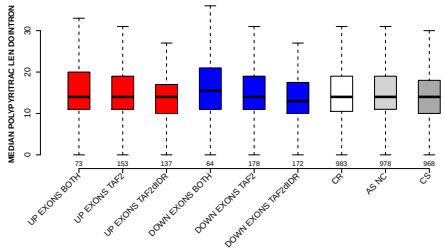
MEDIAN DIST FROM BP TO 3SS DOINTRON



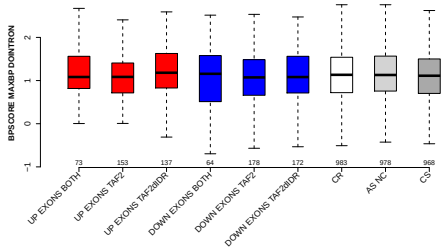
POLYPYRITRAC SCORE MAXBP UPINTRON



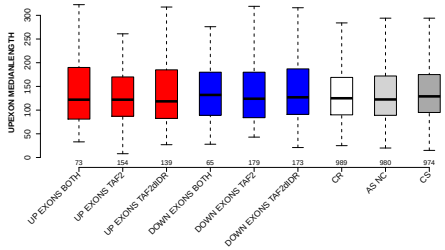
MEDIAN POLYPYRITRAC LEN DOINTRON



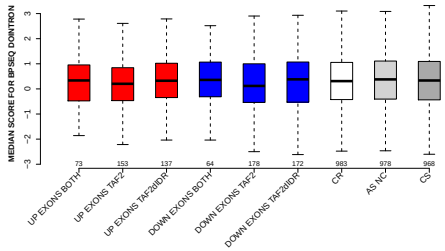
BPSCORE MAXBP DOINTRON



UPEXON MEDIANLENGTH



MEDIAN SCORE FOR BPSEQ DOINTRON

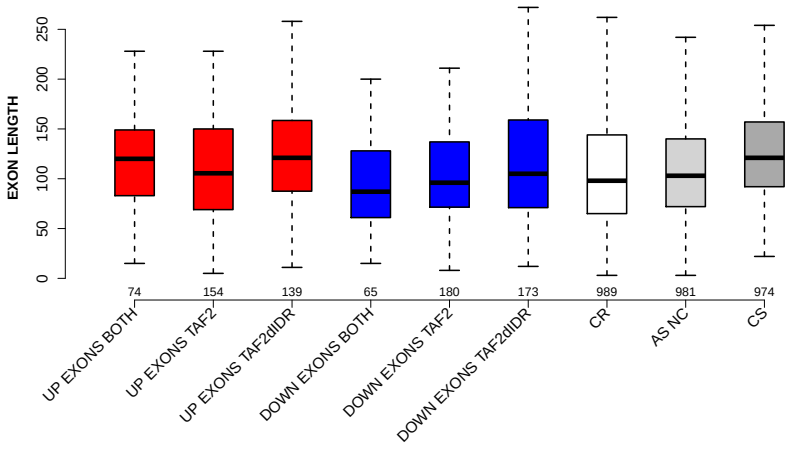


6 Details: Box plots and statistical assessments for all features

6.1 EXON LENGTH

Back to: Overview | ToC

Meaning:



Significant results from Mann-Whitney U test:

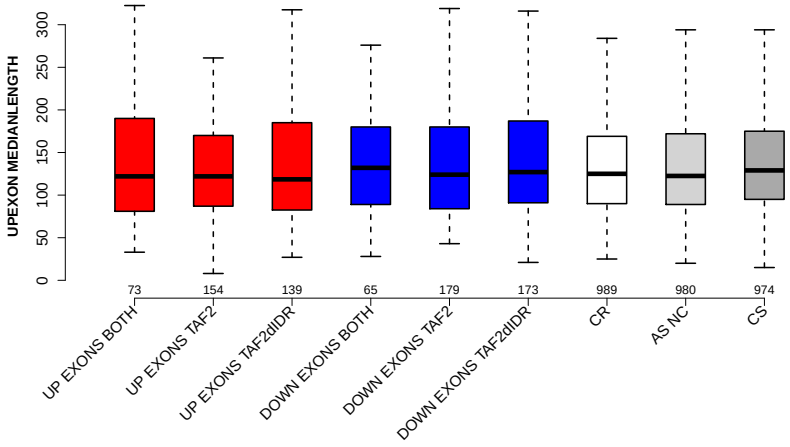
- `UP_EXONS_BOTH` vs `DOWN_EXONS_BOTH` : 0.0128973
  mean: 153.5811 > 113.4615 , median: 120 > 87
- `UP_EXONS_BOTH` vs `DOWN_EXONS_TAF2` : 0.0374477
  mean: 153.5811 > 123.1556 , median: 120 > 96
- `UP_EXONS_BOTH` vs `CR` : 0.0182588
  mean: 153.5811 > 120.4944 , median: 120 > 98
- `UP_EXONS_TAF2` vs `UP_EXONS_TAF2dIDR` : 0.0458467
  mean: 124.013 < 159.8849 , median: 105.5 < 121
- `UP_EXONS_TAF2` vs `CS` : 0.0010214
  mean: 124.013 < 145.0226 , median: 105.5 < 121
- `UP_EXONS_TAF2dIDR` vs `DOWN_EXONS_BOTH` : 0.00181942
  mean: 159.8849 > 113.4615 , median: 121 > 87
- `UP_EXONS_TAF2dIDR` vs `DOWN_EXONS_TAF2` : 0.00188419
  mean: 159.8849 > 123.1556 , median: 121 > 96
- `UP_EXONS_TAF2dIDR` vs `CR` : 0.000174009
  mean: 159.8849 > 120.4944 , median: 121 > 98

- UP_EXONS_TAF2dIDR vs AS_NC : 0.00135921
  mean: 159.8849 > 129.0347 , median: 121 > 103
- DOWN_EXONS_BOTH vs CS : 4.29536e-05
  mean: 113.4615 < 145.0226 , median: 87 < 121
- DOWN_EXONS_TAF2 vs CS : 4.15647e-07
  mean: 123.1556 < 145.0226 , median: 96 < 121
- DOWN_EXONS_TAF2dIDR vs CS : 0.00262271
  mean: 132.3699 < 145.0226 , median: 105 < 121
- CR vs CS : 5.44103e-18
  mean: 120.4944 < 145.0226 , median: 98 < 121
- AS_NC vs CS : 2.3565e-14
  mean: 129.0347 < 145.0226 , median: 103 < 121

6.2 UPEXON MEDIANLENGTH

Back to: Overview | ToC

Meaning: median length of up-stream exon



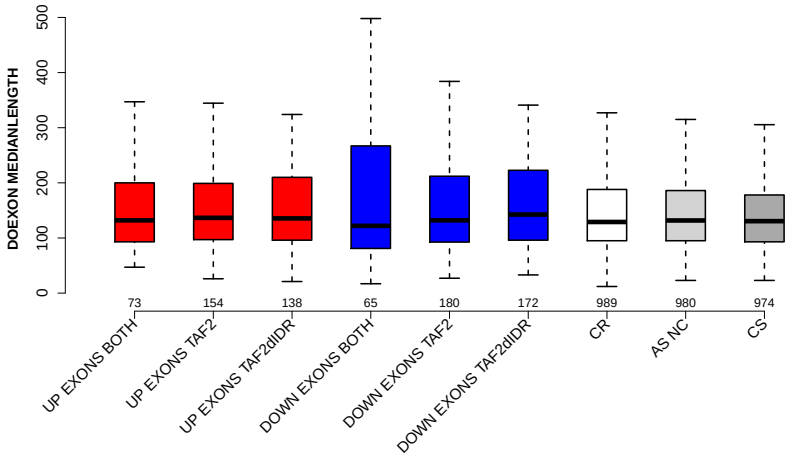
Significant results from Mann-Whitney U test:

- `AS_NC` vs `CS` : 0.0357366
  mean: 153.8842 < 158.056 , median: 122.5 < 129

6.3 DOEXON MEDIANLENGTH

Back to: Overview | ToC

Meaning: median length of down-stream exon



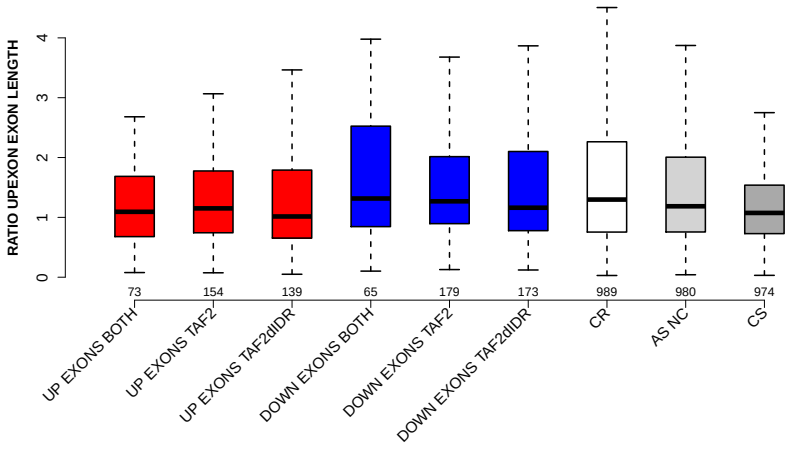
Significant results from Mann-Whitney U test:

- none

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:

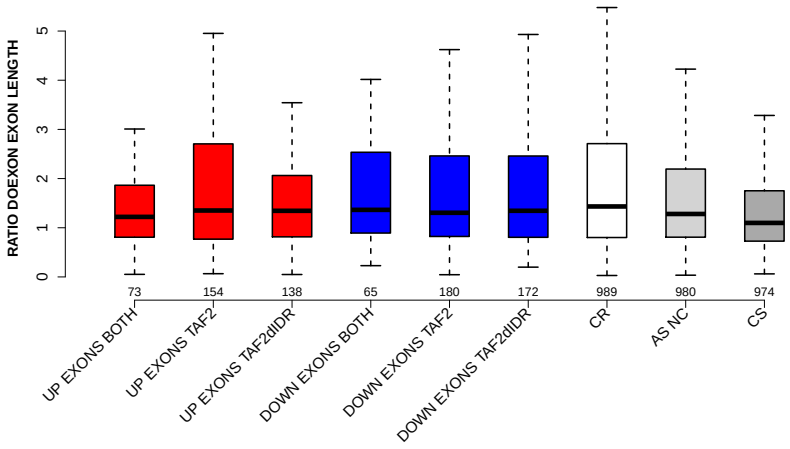
- `UP_EXONS_TAF2dIDR` vs `DOWN_EXONS_BOTH` : 0.00881408
  mean: 1.4397 < 2.1469 , median: 1.0149 < 1.3152
- `UP_EXONS_TAF2dIDR` vs `DOWN_EXONS_TAF2` : 0.00376824
  mean: 1.4397 < 1.8717 , median: 1.0149 < 1.2685
- `UP_EXONS_TAF2dIDR` vs `DOWN_EXONS_TAF2dIDR` : 0.0499621
  mean: 1.4397 < 1.9867 , median: 1.0149 < 1.1613
- `UP_EXONS_TAF2dIDR` vs `CR` : 0.00161569
  mean: 1.4397 < 4.1696 , median: 1.0149 < 1.2974
- `UP_EXONS_TAF2dIDR` vs `AS_NC` : 0.0256711
  mean: 1.4397 < 1.9039 , median: 1.0149 < 1.1855
- `DOWN_EXONS_BOTH` vs `CS` : 0.00320016
  mean: 2.1469 > 1.3862 , median: 1.3152 > 1.0742
- `DOWN_EXONS_TAF2` vs `CS` : 0.0001223
  mean: 1.8717 > 1.3862 , median: 1.2685 > 1.0742
- `DOWN_EXONS_TAF2dIDR` vs `CS` : 0.0154858
  mean: 1.9867 > 1.3862 , median: 1.1613 > 1.0742
- `CR` vs `AS_NC` : 0.0310702
  mean: 4.1696 > 1.9039 , median: 1.2974 > 1.1855
- `CR` vs `CS` : 8.83819e-10
  mean: 4.1696 > 1.3862 , median: 1.2974 > 1.0742

- `AS_NC` vs `CS` : 7.68129e-05
  mean: 1.9039 > 1.3862 , median: 1.1855 > 1.0742

6.5 RATIO DOEXON EXON LENGTH

Back to: Overview | ToC

Meaning: median down-stream exon length / exon length



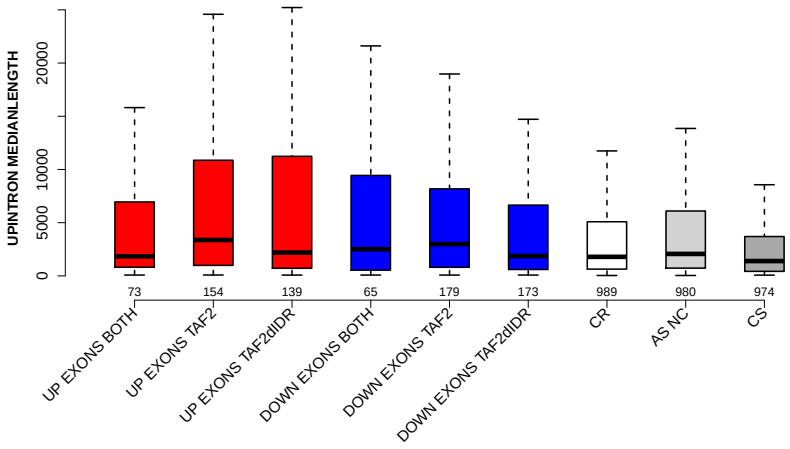
Significant results from Mann-Whitney U test:

- `UP_EXONS_TAF2` vs `CS` : 0.00363817
  mean: 3.9463 > 2.1275 , median: 1.3505 > 1.0982
- `UP_EXONS_TAF2dIDR` vs `CS` : 0.0467108
  mean: 2.6735 > 2.1275 , median: 1.3445 > 1.0982
- `DOWN_EXONS_BOTH` vs `CS` : 0.0128758
  mean: 4.1206 > 2.1275 , median: 1.3639 > 1.0982
- `DOWN_EXONS_TAF2` vs `CS` : 0.00268171
  mean: 3.0248 > 2.1275 , median: 1.3043 > 1.0982
- `DOWN_EXONS_TAF2dIDR` vs `CS` : 0.000665575
  mean: 3.0121 > 2.1275 , median: 1.3451 > 1.0982
- `CR` vs `AS_NC` : 0.0221346
  mean: 4.4465 > 2.7477 , median: 1.4327 > 1.2802
- `CR` vs `CS` : 3.43936e-11
  mean: 4.4465 > 2.1275 , median: 1.4327 > 1.0982
- `AS_NC` vs `CS` : 2.07873e-06
  mean: 2.7477 > 2.1275 , median: 1.2802 > 1.0982

6.6 UPINTRON MEDIANLENGTH

Back to: Overview | ToC

Meaning: median length of up-stream introns



Significant results from Mann-Whitney U test:

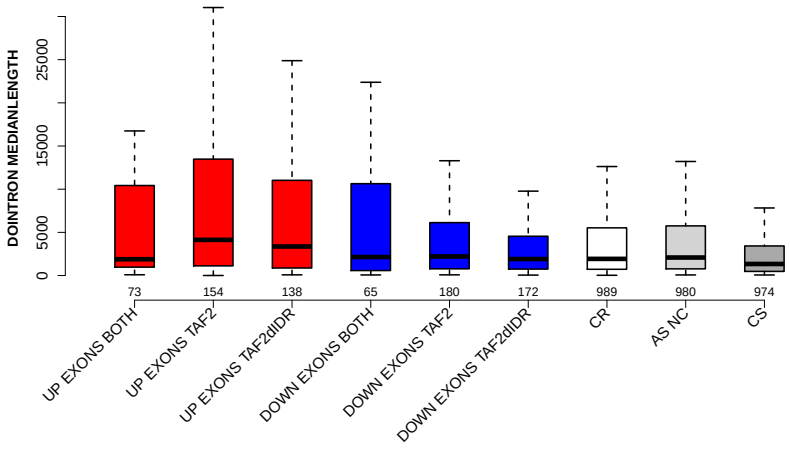
- `UP_EXONS_BOTH` vs `CS` : 0.00453694
  mean: 8666.9726 > 4017.2854 , median: 1835 > 1392.5
- `UP_EXONS_TAF2` vs `DOWN_EXONS_TAF2dIDR` : 0.0155014
  mean: 11683.6656 > 7985.711 , median: 3375 > 1858
- `UP_EXONS_TAF2` vs `CR` : 0.00038802
  mean: 11683.6656 > 6933.5627 , median: 3375 > 1790
- `UP_EXONS_TAF2` vs `AS_NC` : 0.00549059
  mean: 11683.6656 > 6875.8551 , median: 3375 > 2065.5
- `UP_EXONS_TAF2` vs `CS` : 2.12636e-09
  mean: 11683.6656 > 4017.2854 , median: 3375 > 1392.5
- `UP_EXONS_TAF2dIDR` vs `CS` : 8.59043e-05
  mean: 12103.3633 > 4017.2854 , median: 2195 > 1392.5
- `DOWN_EXONS_BOTH` vs `CS` : 0.00834243
  mean: 7935.6769 > 4017.2854 , median: 2508 > 1392.5
- `DOWN_EXONS_TAF2` vs `CR` : 0.0135333
  mean: 8925.1844 > 6933.5627 , median: 2986 > 1790
- `DOWN_EXONS_TAF2` vs `CS` : 2.44371e-07
  mean: 8925.1844 > 4017.2854 , median: 2986 > 1392.5
- `DOWN_EXONS_TAF2dIDR` vs `CS` : 0.00240922
  mean: 7985.711 > 4017.2854 , median: 1858 > 1392.5

- `CR` vs `CS` : 1.42861e-06
  mean: 6933.5627 > 4017.2854 , median: 1790 > 1392.5
- `AS_NC` vs `CS` : 1.79815e-10
  mean: 6875.8551 > 4017.2854 , median: 2065.5 > 1392.5

6.7 DOINTRON MEDIANLENGTH

Back to: Overview | ToC

Meaning: median length of down-stream introns



Significant results from Mann-Whitney U test:

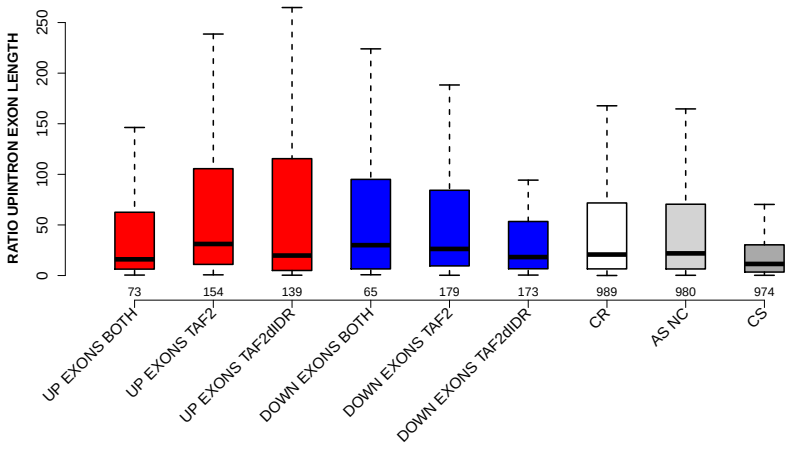
- `UP_EXONS_BOTH` vs `CS` : 0.000511889
  mean: 7906.3014 > 3922.7721 , median: 1885 > 1337.5
- `UP_EXONS_TAF2` vs `DOWN_EXONS_TAF2` : 0.00297989
  mean: 10451.6916 > 9195.1861 , median: 4130.25 > 2208
- `UP_EXONS_TAF2` vs `DOWN_EXONS_TAF2dIDR` : 0.000482079
  mean: 10451.6916 > 8647.5174 , median: 4130.25 > 1908
- `UP_EXONS_TAF2` vs `CR` : 1.34136e-05
  mean: 10451.6916 > 7045.9788 , median: 4130.25 > 1929
- `UP_EXONS_TAF2` vs `AS_NC` : 2.36352e-05
  mean: 10451.6916 > 6229.7811 , median: 4130.25 > 2085.5
- `UP_EXONS_TAF2` vs `CS` : 6.16599e-14
  mean: 10451.6916 > 3922.7721 , median: 4130.25 > 1337.5
- `UP_EXONS_TAF2dIDR` vs `DOWN_EXONS_TAF2dIDR` : 0.0147517
  mean: 9710.337 > 8647.5174 , median: 3361.5 > 1908
- `UP_EXONS_TAF2dIDR` vs `CR` : 0.00374236
  mean: 9710.337 > 7045.9788 , median: 3361.5 > 1929
- `UP_EXONS_TAF2dIDR` vs `AS_NC` : 0.0057794
  mean: 9710.337 > 6229.7811 , median: 3361.5 > 2085.5
- `UP_EXONS_TAF2dIDR` vs `CS` : 3.03338e-09
  mean: 9710.337 > 3922.7721 , median: 3361.5 > 1337.5

- DOWN_EXONS_BOTH vs CS : 0.00627841
  mean: 9586.1 > 3922.7721 , median: 2142 > 1337.5
- DOWN_EXONS_TAF2 vs CS : 5.03898e-05
  mean: 9195.1861 > 3922.7721 , median: 2208 > 1337.5
- DOWN_EXONS_TAF2dIDR vs CS : 0.00153372
  mean: 8647.5174 > 3922.7721 , median: 1908 > 1337.5
- CR vs CS : 2.10602e-10
  mean: 7045.9788 > 3922.7721 , median: 1929 > 1337.5
- AS_NC vs CS : 3.99634e-12
  mean: 6229.7811 > 3922.7721 , median: 2085.5 > 1337.5

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:

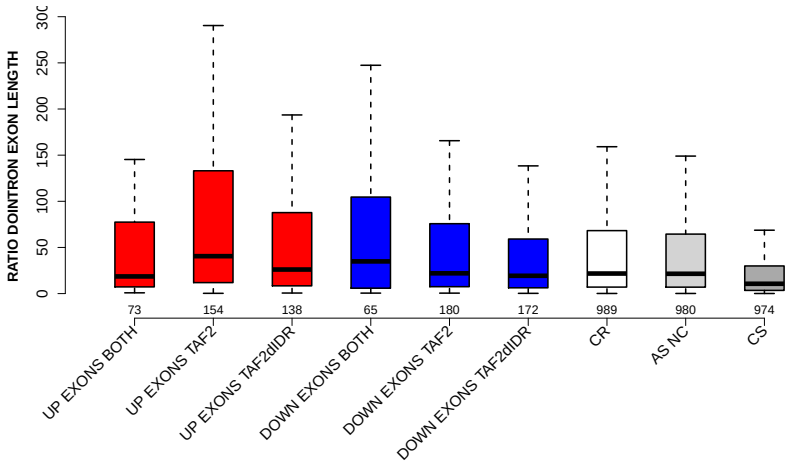
- UP_EXONS_BOTH vs CS : 0.00181773
  mean: 77.1026 > 35.545 , median: 16.0265 > 11.4504
- UP_EXONS_TAF2 vs DOWN_EXONS_TAF2dIDR : 0.00818675
  mean: 118.8299 > 103.5464 , median: 31.176 > 18.2289
- UP_EXONS_TAF2 vs CR : 0.00929941
  mean: 118.8299 < 122.4442 , median: 31.176 > 20.7407
- UP_EXONS_TAF2 vs AS_NC : 0.00698398
  mean: 118.8299 > 77.6027 , median: 31.176 > 21.89
- UP_EXONS_TAF2 vs CS : 3.29972e-13
  mean: 118.8299 > 35.545 , median: 31.176 > 11.4504
- UP_EXONS_TAF2dIDR vs CS : 0.000239577
  mean: 130.1475 > 35.545 , median: 19.7612 > 11.4504
- DOWN_EXONS_BOTH vs CS : 6.2731e-05
  mean: 82.6579 > 35.545 , median: 30.0141 > 11.4504
- DOWN_EXONS_TAF2 vs DOWN_EXONS_TAF2dIDR : 0.0494706
  mean: 103.2265 < 103.5464 , median: 26.2917 > 18.2289
- DOWN_EXONS_TAF2 vs CS : 1.16046e-11
  mean: 103.2265 > 35.545 , median: 26.2917 > 11.4504
- DOWN_EXONS_TAF2dIDR vs CS : 4.35443e-05
  mean: 103.5464 > 35.545 , median: 18.2289 > 11.4504

- `CR` vs `CS` : 2.07358e-18
  mean: 122.4442 > 35.545 , median: 20.7407 > 11.4504
- `AS_NC` vs `CS` : 3.24968e-18
  mean: 77.6027 > 35.545 , median: 21.89 > 11.4504

6.9 RATIO DOINTRON EXON LENGTH

Back to: Overview | ToC

Meaning: median down-stream intron length / exon length



Significant results from Mann-Whitney U test:

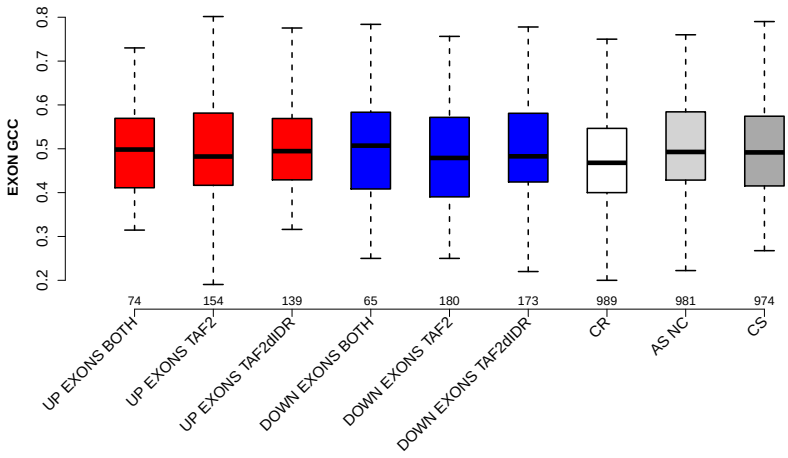
- `UP_EXONS_BOTH` vs `UP_EXONS_TAF2` : 0.0275419
  mean: 80.0172 < 114.1743 , median: 18.5926 < 40.5323
- `UP_EXONS_BOTH` vs `CS` : 0.000613225
  mean: 80.0172 > 33.3658 , median: 18.5926 > 10.6316
- `UP_EXONS_TAF2` vs `DOWN_EXONS_TAF2` : 0.00683171
  mean: 114.1743 > 110.7158 , median: 40.5323 > 21.9719
- `UP_EXONS_TAF2` vs `DOWN_EXONS_TAF2dIDR` : 0.000615693
  mean: 114.1743 > 84.9898 , median: 40.5323 > 19.2845
- `UP_EXONS_TAF2` vs `CR` : 0.000680465
  mean: 114.1743 < 140.2298 , median: 40.5323 > 21.7339
- `UP_EXONS_TAF2` vs `AS_NC` : 7.55356e-05
  mean: 114.1743 > 69.7215 , median: 40.5323 > 21.4731
- `UP_EXONS_TAF2` vs `CS` : 2.53654e-17
  mean: 114.1743 > 33.3658 , median: 40.5323 > 10.6316
- `UP_EXONS_TAF2dIDR` vs `CS` : 1.45121e-08
  mean: 93.5509 > 33.3658 , median: 26.0561 > 10.6316
- `DOWN_EXONS_BOTH` vs `CS` : 2.53462e-05
  mean: 103.7467 > 33.3658 , median: 34.882 > 10.6316
- `DOWN_EXONS_TAF2` vs `CS` : 3.4155e-08
  mean: 110.7158 > 33.3658 , median: 21.9719 > 10.6316

- DOWN_EXONS_TAF2dIDR vs CS : 1.31259e-05
  mean: 84.9898 > 33.3658 , median: 19.2845 > 10.6316
- CR vs CS : 5.05556e-23
  mean: 140.2298 > 33.3658 , median: 21.7339 > 10.6316
- AS_NC vs CS : 4.6611e-20
  mean: 69.7215 > 33.3658 , median: 21.4731 > 10.6316

6.10 EXON GCC

Back to: Overview | ToC

Meaning: GC content of entire exon sequence



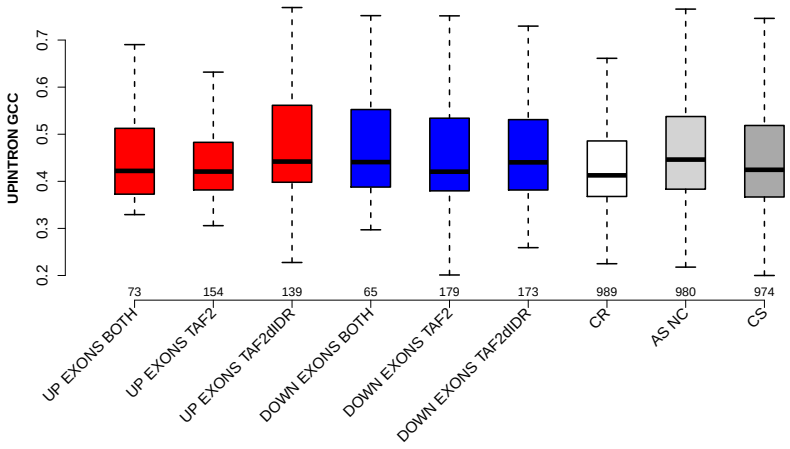
Significant results from Mann-Whitney U test:

- `UP_EXONS_TAF2dIDR` vs `CR` : 0.00824153
  mean: 0.501004 > 0.473215 , median: 0.494624 > 0.46798
- `DOWN_EXONS_TAF2` vs `AS_NC` : 0.00989001
  mean: 0.484878 < 0.506761 , median: 0.479058 < 0.492754
- `DOWN_EXONS_TAF2dIDR` vs `CR` : 0.0104267
  mean: 0.498551 > 0.473215 , median: 0.482824 > 0.46798
- `CR` vs `AS_NC` : 9.57981e-11
  mean: 0.473215 < 0.506761 , median: 0.46798 < 0.492754
- `CR` vs `CS` : 2.64364e-05
  mean: 0.473215 < 0.495129 , median: 0.46798 < 0.491708
- `AS_NC` vs `CS` : 0.0165988
  mean: 0.506761 > 0.495129 , median: 0.492754 > 0.491708

6.11 UPINTRON GCC

Back to: Overview | ToC

Meaning: GC content of entire up-stream intron sequence



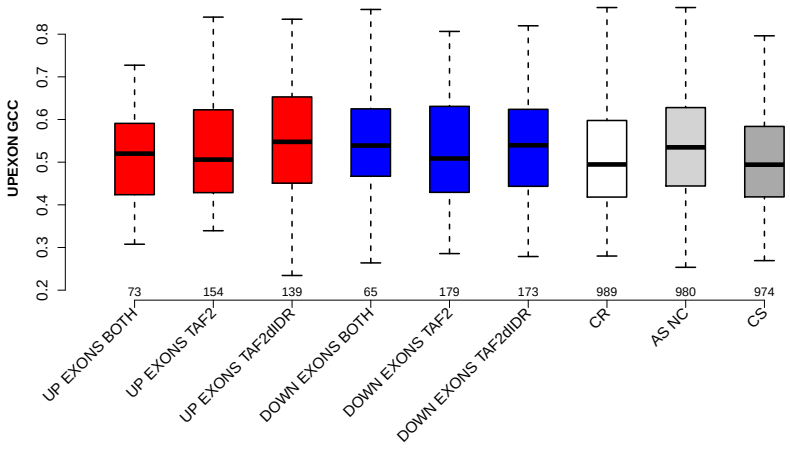
Significant results from Mann-Whitney U test:

- `UP_EXONS_TAF2` vs `UP_EXONS_TAF2dIDR` : 0.0303206
  mean: 0.448093 < 0.474753 , median: 0.42068 < 0.441919
- `UP_EXONS_TAF2` vs `AS_NC` : 0.0295312
  mean: 0.448093 < 0.467422 , median: 0.42068 < 0.446163
- `UP_EXONS_TAF2dIDR` vs `CR` : 1.67255e-05
  mean: 0.474753 > 0.432143 , median: 0.441919 > 0.412684
- `UP_EXONS_TAF2dIDR` vs `CS` : 0.00501733
  mean: 0.474753 > 0.449191 , median: 0.441919 > 0.424454
- `DOWN_EXONS_BOTH` vs `CR` : 0.00769978
  mean: 0.470481 > 0.432143 , median: 0.440823 > 0.412684
- `DOWN_EXONS_TAF2` vs `CR` : 0.0088262
  mean: 0.459668 > 0.432143 , median: 0.420424 > 0.412684
- `DOWN_EXONS_TAF2dIDR` vs `CR` : 0.00317585
  mean: 0.460652 > 0.432143 , median: 0.440279 > 0.412684
- `CR` vs `AS_NC` : 2.5693e-12
  mean: 0.432143 < 0.467422 , median: 0.412684 < 0.446163
- `CR` vs `CS` : 0.0128142
  mean: 0.432143 < 0.449191 , median: 0.412684 < 0.424454
- `AS_NC` vs `CS` : 4.4428e-05
  mean: 0.467422 > 0.449191 , median: 0.446163 > 0.424454

6.12 UPEXON GCC

Back to: Overview | ToC

Meaning: GC content of entire up-stream exon sequence



Significant results from Mann-Whitney U test:

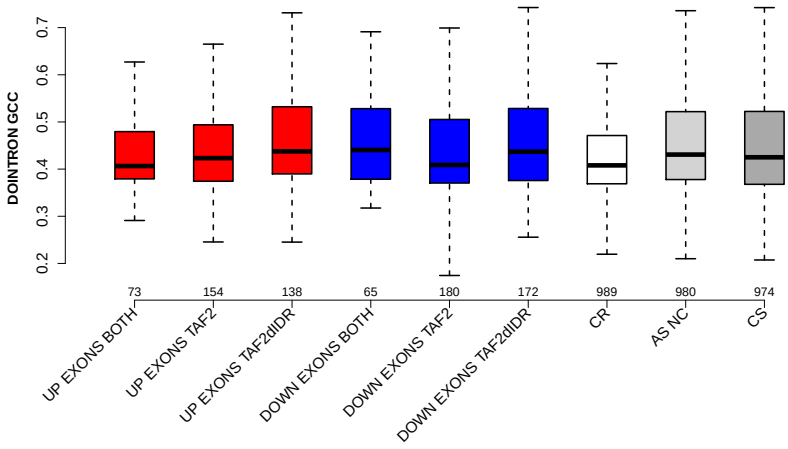
- `UP_EXONS_BOTH` vs `UP_EXONS_TAF2dIDR` : 0.0366132
  mean: 0.514712 < 0.555302 , median: 0.52 < 0.547619
- `UP_EXONS_TAF2` vs `CS` : 0.0342763
  mean: 0.531904 > 0.503564 , median: 0.506 > 0.49412
- `UP_EXONS_TAF2dIDR` vs `CR` : 8.20122e-05
  mean: 0.555302 > 0.50979 , median: 0.547619 > 0.494624
- `UP_EXONS_TAF2dIDR` vs `CS` : 1.00218e-05
  mean: 0.555302 > 0.503564 , median: 0.547619 > 0.49412
- `DOWN_EXONS_BOTH` vs `CR` : 0.0232854
  mean: 0.540802 > 0.50979 , median: 0.538961 > 0.494624
- `DOWN_EXONS_BOTH` vs `CS` : 0.00925009
  mean: 0.540802 > 0.503564 , median: 0.538961 > 0.49412
- `DOWN_EXONS_TAF2` vs `CR` : 0.0423119
  mean: 0.531747 > 0.50979 , median: 0.508621 > 0.494624
- `DOWN_EXONS_TAF2` vs `CS` : 0.0129172
  mean: 0.531747 > 0.503564 , median: 0.508621 > 0.49412
- `DOWN_EXONS_TAF2dIDR` vs `CR` : 0.00647096
  mean: 0.534981 > 0.50979 , median: 0.539589 > 0.494624
- `DOWN_EXONS_TAF2dIDR` vs `CS` : 0.00118905
  mean: 0.534981 > 0.503564 , median: 0.539589 > 0.49412

- `CR` vs `AS_NC` : 3.67945e-08
  mean: 0.50979 < 0.539747 , median: 0.494624 < 0.534724
- `AS_NC` vs `CS` : 1.42543e-10
  mean: 0.539747 > 0.503564 , median: 0.534724 > 0.49412

6.13 DOINTRON GCC

Back to: Overview | ToC

Meaning: GC content of entire down-stream intron sequence



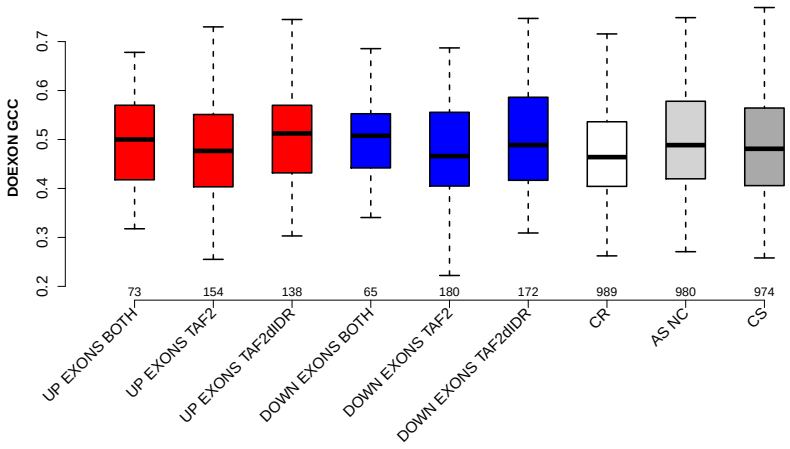
Significant results from Mann-Whitney U test:

- `UP_EXONS_BOTH` vs `UP_EXONS_TAF2dIDR` : 0.0440457
  mean: 0.437631 < 0.465297 , median: 0.406501 < 0.437665
- `UP_EXONS_TAF2` vs `CR` : 0.0151809
  mean: 0.448599 > 0.424278 , median: 0.423264 > 0.407912
- `UP_EXONS_TAF2dIDR` vs `DOWN_EXONS_TAF2` : 0.0158389
  mean: 0.465297 > 0.439764 , median: 0.437665 > 0.408824
- `UP_EXONS_TAF2dIDR` vs `CR` : 9.0568e-06
  mean: 0.465297 > 0.424278 , median: 0.437665 > 0.407912
- `DOWN_EXONS_BOTH` vs `CR` : 0.00562897
  mean: 0.459098 > 0.424278 , median: 0.440588 > 0.407912
- `DOWN_EXONS_TAF2dIDR` vs `CR` : 0.000969258
  mean: 0.454101 > 0.424278 , median: 0.436941 > 0.407912
- `CR` vs `AS_NC` : 4.95333e-10
  mean: 0.424278 < 0.45619 , median: 0.407912 < 0.430774
- `CR` vs `CS` : 1.18618e-05
  mean: 0.424278 < 0.449135 , median: 0.407912 < 0.425062

6.14 DOEXON GCC

Back to: Overview | ToC

Meaning: GC content of entire down-stream exon sequence



Significant results from Mann-Whitney U test:

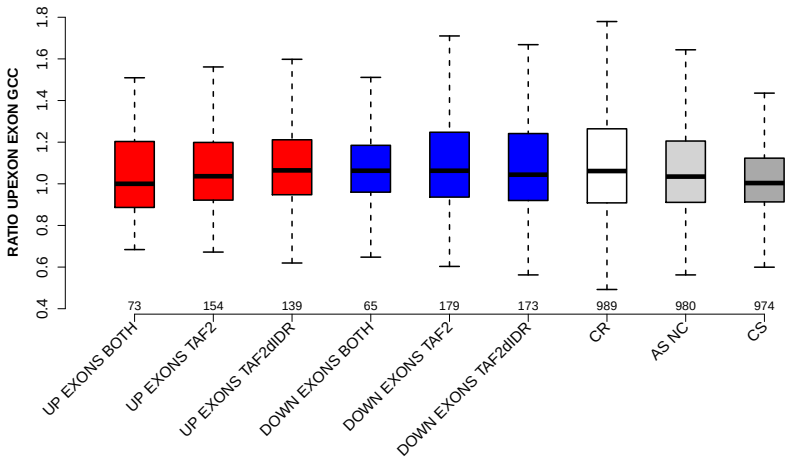
- `UP_EXONS_BOTH` vs `CR` : 0.0438525
  mean: 0.496805 > 0.473391 , median: 0.5 > 0.464
- `UP_EXONS_TAF2` vs `UP_EXONS_TAF2dIDR` : 0.0234347
  mean: 0.483437 < 0.508043 , median: 0.47667 < 0.51241
- `UP_EXONS_TAF2dIDR` vs `DOWN_EXONS_TAF2` : 0.00823883
  mean: 0.508043 > 0.476998 , median: 0.51241 > 0.466067
- `UP_EXONS_TAF2dIDR` vs `CR` : 6.32759e-05
  mean: 0.508043 > 0.473391 , median: 0.51241 > 0.464
- `UP_EXONS_TAF2dIDR` vs `CS` : 0.0251005
  mean: 0.508043 > 0.487881 , median: 0.51241 > 0.481024
- `DOWN_EXONS_BOTH` vs `CR` : 0.00542145
  mean: 0.502038 > 0.473391 , median: 0.507692 > 0.464
- `DOWN_EXONS_TAF2` vs `AS_NC` : 0.014896
  mean: 0.476998 < 0.498185 , median: 0.466067 < 0.488504
- `DOWN_EXONS_TAF2dIDR` vs `CR` : 0.00364403
  mean: 0.49851 > 0.473391 , median: 0.488737 > 0.464
- `CR` vs `AS_NC` : 4.31487e-08
  mean: 0.473391 < 0.498185 , median: 0.464 < 0.488504
- `CR` vs `CS` : 0.00231017
  mean: 0.473391 < 0.487881 , median: 0.464 < 0.481024

- `AS_NC` vs `CS` : 0.0228376
  mean: 0.498185 > 0.487881 , median: 0.488504 > 0.481024

6.15 RATIO UPEXON EXON GCC

Back to: Overview | ToC

Meaning: UPEXON GCC / EXON GCC



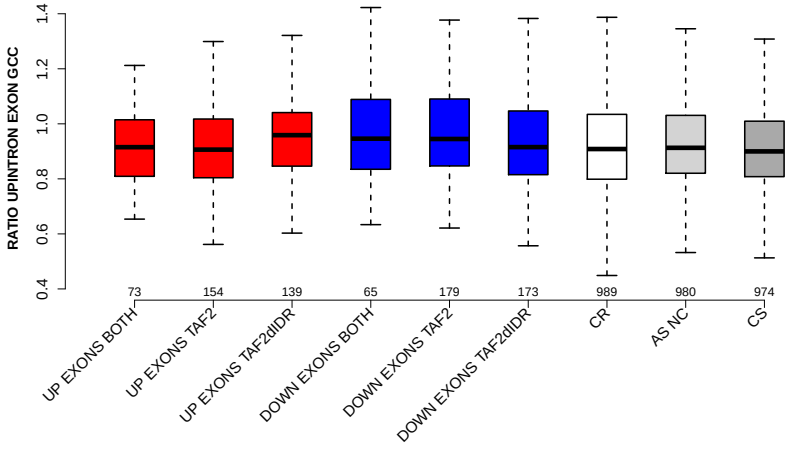
Significant results from Mann-Whitney U test:

- `UP_EXONS_BOTH` vs `UP_EXONS_TAF2dIDR` : 0.0441897
  mean: 1.0577 < 1.135 , median: 1 < 1.0645
- `UP_EXONS_TAF2` vs `CS` : 0.00785793
  mean: 1.1064 > 1.0318 , median: 1.0364 > 1.0036
- `UP_EXONS_TAF2dIDR` vs `CS` : 0.000232019
  mean: 1.135 > 1.0318 , median: 1.0645 > 1.0036
- `DOWN_EXONS_BOTH` vs `CS` : 0.0163145
  mean: 1.1299 > 1.0318 , median: 1.0628 > 1.0036
- `DOWN_EXONS_TAF2` vs `CS` : 0.00065097
  mean: 1.133 > 1.0318 , median: 1.0628 > 1.0036
- `DOWN_EXONS_TAF2dIDR` vs `CS` : 0.00429611
  mean: 1.1075 > 1.0318 , median: 1.0438 > 1.0036
- `CR` vs `CS` : 2.30085e-07
  mean: 1.1225 > 1.0318 , median: 1.0613 > 1.0036
- `AS_NC` vs `CS` : 0.000450082
  mean: 1.092 > 1.0318 , median: 1.0347 > 1.0036

6.16 RATIO UPINTRON EXON GCC

Back to: Overview | ToC

Meaning: UPINTRON GCC / EXON GCC



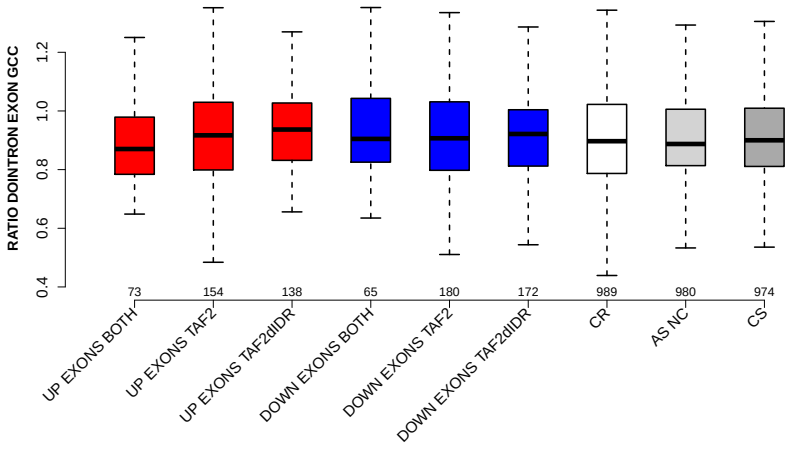
Significant results from Mann-Whitney U test:

- `UP_EXONS_BOTH` vs `DOWN_EXONS_TAF2` : 0.0373066
  mean: 0.915267 < 0.965589 , median: 0.915136 < 0.944942
- `UP_EXONS_TAF2` vs `UP_EXONS_TAF2dIDR` : 0.0463833
  mean: 0.925564 < 0.956319 , median: 0.906199 < 0.958804
- `UP_EXONS_TAF2` vs `DOWN_EXONS_TAF2` : 0.0184271
  mean: 0.925564 < 0.965589 , median: 0.906199 < 0.944942
- `UP_EXONS_TAF2dIDR` vs `CR` : 0.0282432
  mean: 0.956319 > 0.944329 , median: 0.958804 > 0.908418
- `UP_EXONS_TAF2dIDR` vs `CS` : 0.00254181
  mean: 0.956319 > 0.914033 , median: 0.958804 > 0.899821
- `DOWN_EXONS_BOTH` vs `CS` : 0.0313422
  mean: 0.965357 > 0.914033 , median: 0.94601 > 0.899821
- `DOWN_EXONS_TAF2` vs `CR` : 0.00637124
  mean: 0.965589 > 0.944329 , median: 0.944942 > 0.908418
- `DOWN_EXONS_TAF2` vs `AS_NC` : 0.0173143
  mean: 0.965589 > 0.934562 , median: 0.944942 > 0.912835
- `DOWN_EXONS_TAF2` vs `CS` : 0.000233427
  mean: 0.965589 > 0.914033 , median: 0.944942 > 0.899821
- `AS_NC` vs `CS` : 0.0212045
  mean: 0.934562 > 0.914033 , median: 0.912835 > 0.899821

6.17 RATIO DOINTRON EXON GCC

Back to: Overview | ToC

Meaning: DOINTRON GCC / EXON GCC



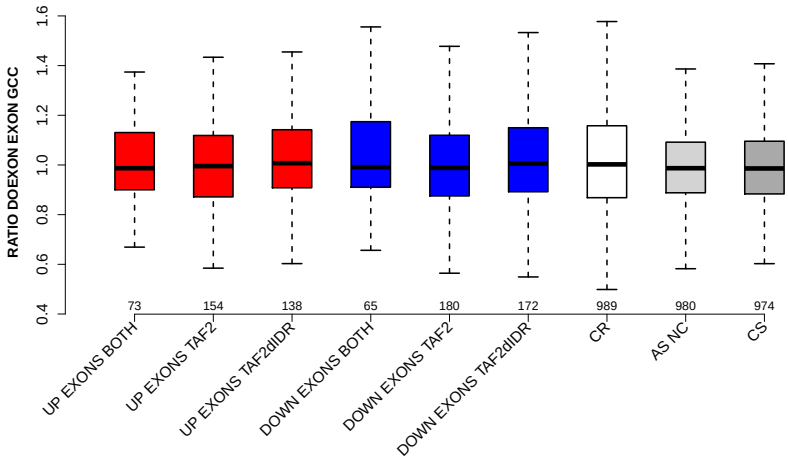
Significant results from Mann-Whitney U test:

- `UP_EXONS_BOTH` vs `UP_EXONS_TAF2dIDR` : 0.0158704
  mean: 0.891846 < 0.939888 , median: 0.870243 < 0.936608
- `UP_EXONS_TAF2dIDR` vs `AS_NC` : 0.032838
  mean: 0.939888 > 0.911736 , median: 0.936608 > 0.887389

6.18 RATIO DOEXON EXON GCC

Back to: Overview | ToC

Meaning: DOEXON GCC / EXON GCC



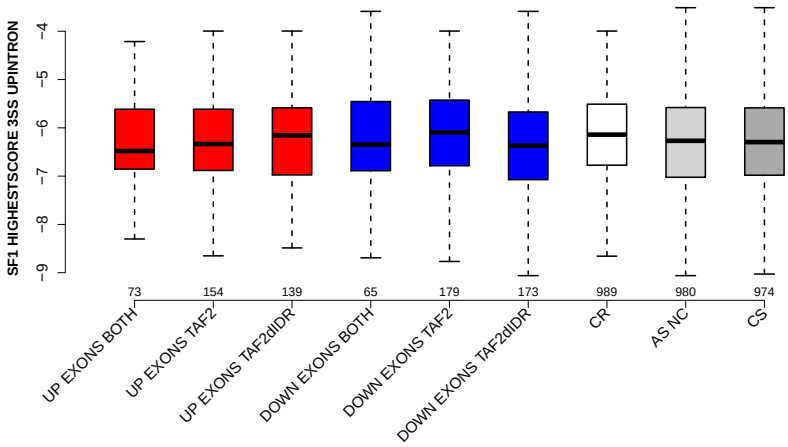
Significant results from Mann-Whitney U test:

- `UP_EXONS_TAF2dIDR` vs `AS_NC` : 0.0393314
  mean: 1.0365 > 1.0003 , median: 1.0071 > 0.986974
- `UP_EXONS_TAF2dIDR` vs `CS` : 0.0474029
  mean: 1.0365 > 0.999579 , median: 1.0071 > 0.985921
- `CR` vs `AS_NC` : 0.02556
  mean: 1.0419 > 1.0003 , median: 1.0023 > 0.986974
- `CR` vs `CS` : 0.0372696
  mean: 1.0419 > 0.999579 , median: 1.0023 > 0.985921

6.19 SF1 HIGHESTSCORE 3SS UPINTRON

Back to: Overview | ToC

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



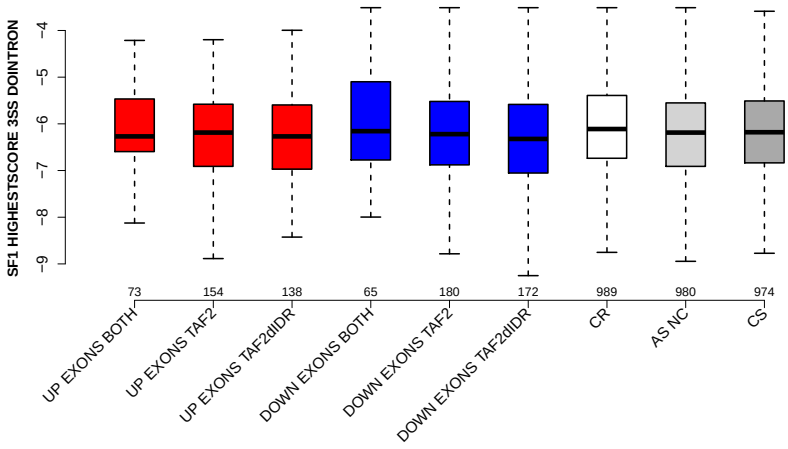
Significant results from Mann-Whitney U test:

- `UP_EXONS_TAF2` vs `CR` : 0.0279716
  mean: -6.30903 < -6.12842 , median: -6.33497 < -6.14071
- `DOWN_EXONS_TAF2` vs `DOWN_EXONS_TAF2dIDR` : 0.0476116
  mean: -6.17385 > -6.34657 , median: -6.09302 > -6.37142
- `DOWN_EXONS_TAF2dIDR` vs `CR` : 0.00566484
  mean: -6.34657 < -6.12842 , median: -6.37142 < -6.14071
- `CR` vs `AS_NC` : 0.0043567
  mean: -6.12842 > -6.26922 , median: -6.14071 > -6.26872
- `CR` vs `CS` : 0.000546325
  mean: -6.12842 > -6.29083 , median: -6.14071 > -6.29538

6.20 SF1 HIGHESTSCORE 3SS DOINTRON

Back to: Overview | ToC

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



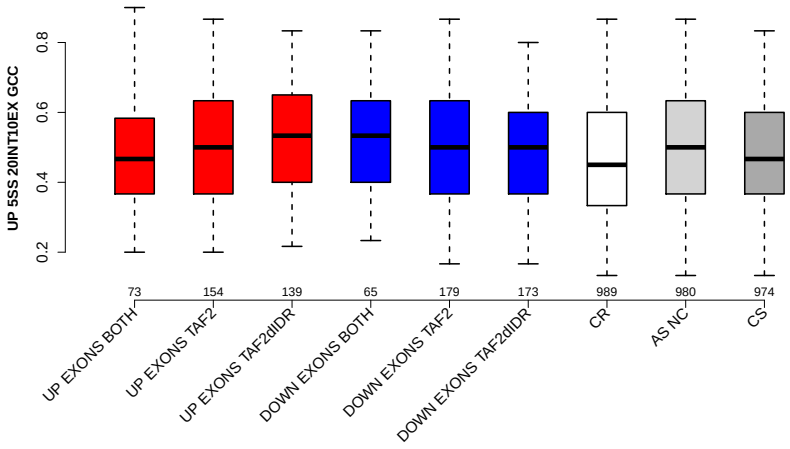
Significant results from Mann-Whitney U test:

- `UP_EXONS_TAF2dIDR` vs `CR` : 0.0473197
  mean: -6.2543 < -6.07791 , median: -6.26872 < -6.11088
- `DOWN_EXONS_TAF2dIDR` vs `CR` : 0.0143318
  mean: -6.31702 < -6.07791 , median: -6.32318 < -6.11088
- `CR` vs `AS_NC` : 0.00275872
  mean: -6.07791 > -6.22114 , median: -6.11088 > -6.18725
- `CR` vs `CS` : 0.035205
  mean: -6.07791 > -6.1712 , median: -6.11088 > -6.17975

6.21 UP 5SS 20INT10EX GCC

Back to: Overview | ToC

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



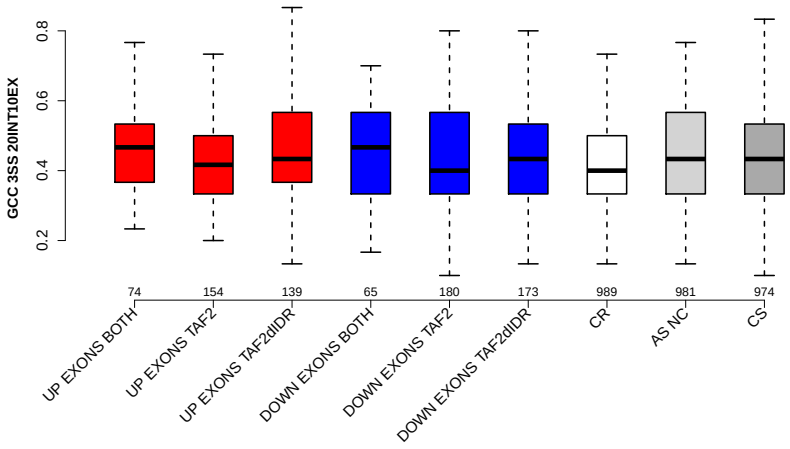
Significant results from Mann-Whitney U test:

- `UP_EXONS_TAF2dIDR` vs `CR` : 0.00066169
  mean: 0.519065 > 0.470206 , median: 0.533333 > 0.45
- `UP_EXONS_TAF2dIDR` vs `CS` : 0.00521155
  mean: 0.519065 > 0.476865 , median: 0.533333 > 0.466667
- `DOWN_EXONS_BOTH` vs `CR` : 0.0104671
  mean: 0.519231 > 0.470206 , median: 0.533333 > 0.45
- `DOWN_EXONS_BOTH` vs `CS` : 0.0314441
  mean: 0.519231 > 0.476865 , median: 0.533333 > 0.466667
- `DOWN_EXONS_TAF2dIDR` vs `CR` : 0.0107854
  mean: 0.500771 > 0.470206 , median: 0.5 > 0.45
- `CR` vs `AS_NC` : 2.75642e-06
  mean: 0.470206 < 0.501207 , median: 0.45 < 0.5
- `AS_NC` vs `CS` : 0.000527655
  mean: 0.501207 > 0.476865 , median: 0.5 > 0.466667

6.22 GCC 3SS 20INT10EX

Back to: Overview | ToC

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



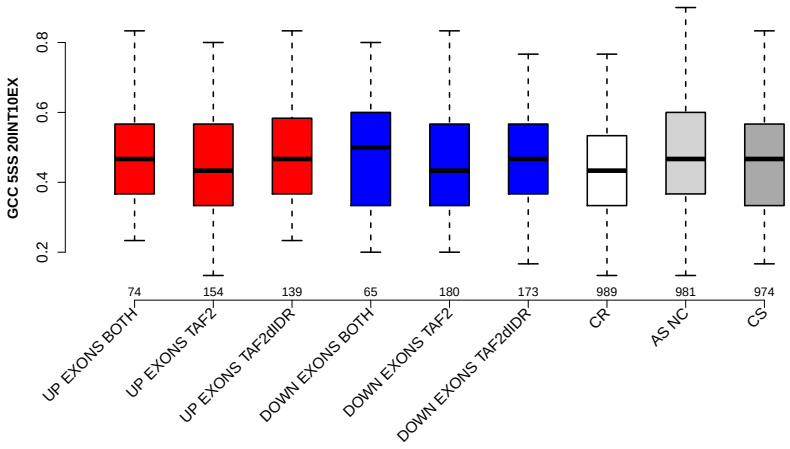
Significant results from Mann-Whitney U test:

- `UP_EXONS_BOTH` vs `CR` : 0.00257028
  mean: 0.454505 > 0.40664 , median: 0.466667 > 0.4
- `UP_EXONS_TAF2` vs `CR` : 0.0215413
  mean: 0.437662 > 0.40664 , median: 0.416667 > 0.4
- `UP_EXONS_TAF2dIDR` vs `CR` : 0.00017059
  mean: 0.455875 > 0.40664 , median: 0.433333 > 0.4
- `DOWN_EXONS_BOTH` vs `CR` : 0.0114112
  mean: 0.450769 > 0.40664 , median: 0.466667 > 0.4
- `DOWN_EXONS_TAF2` vs `CR` : 0.0220727
  mean: 0.436667 > 0.40664 , median: 0.4 = 0.4
- `DOWN_EXONS_TAF2dIDR` vs `CR` : 0.00250524
  mean: 0.443353 > 0.40664 , median: 0.433333 > 0.4
- `CR` vs `AS_NC` : 1.93446e-13
  mean: 0.40664 < 0.454027 , median: 0.4 < 0.433333
- `CR` vs `CS` : 5.86256e-08
  mean: 0.40664 < 0.441273 , median: 0.4 < 0.433333

6.23 GCC 5SS 20INT10EX

Back to: Overview | ToC

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



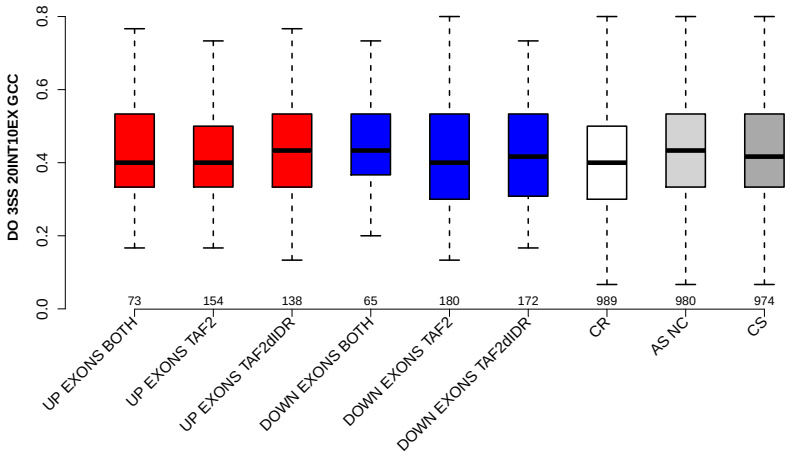
Significant results from Mann-Whitney U test:

- `UP_EXONS_BOTH` vs `CR` : 0.0212354
  mean: 0.479279 > 0.43876 , median: 0.466667 > 0.433333
- `UP_EXONS_TAF2dIDR` vs `CR` : 0.00142564
  mean: 0.480336 > 0.43876 , median: 0.466667 > 0.433333
- `DOWN_EXONS_BOTH` vs `CR` : 0.0363018
  mean: 0.479487 > 0.43876 , median: 0.5 > 0.433333
- `DOWN_EXONS_TAF2dIDR` vs `CR` : 0.0144617
  mean: 0.465511 > 0.43876 , median: 0.466667 > 0.433333
- `CR` vs `AS_NC` : 1.36594e-07
  mean: 0.43876 < 0.474992 , median: 0.433333 < 0.466667
- `CR` vs `CS` : 0.000150613
  mean: 0.43876 < 0.465229 , median: 0.433333 < 0.466667

6.24 DO 3SS 20INT10EX GCC

Back to: Overview | ToC

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



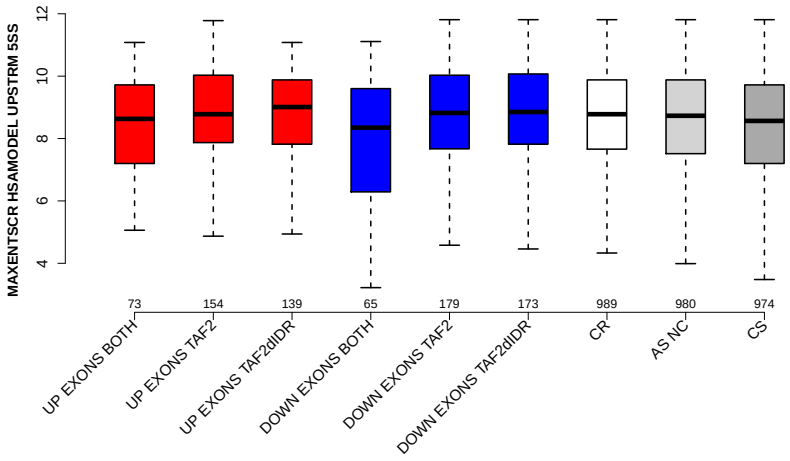
Significant results from Mann-Whitney U test:

- `UP_EXONS_TAF2dIDR` vs `CR` : 0.0028289
  mean: 0.4407 > 0.404398 , median: 0.433333 > 0.4
- `DOWN_EXONS_BOTH` vs `CR` : 0.00556438
  mean: 0.452308 > 0.404398 , median: 0.433333 > 0.4
- `DOWN_EXONS_TAF2` vs `AS_NC` : 0.0443724
  mean: 0.420463 < 0.440748 , median: 0.4 < 0.433333
- `DOWN_EXONS_TAF2dIDR` vs `CR` : 0.0363756
  mean: 0.429457 > 0.404398 , median: 0.416667 > 0.4
- `CR` vs `AS_NC` : 8.68656e-10
  mean: 0.404398 < 0.440748 , median: 0.4 < 0.433333
- `CR` vs `CS` : 1.09636e-05
  mean: 0.404398 < 0.43347 , median: 0.4 < 0.416667

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:

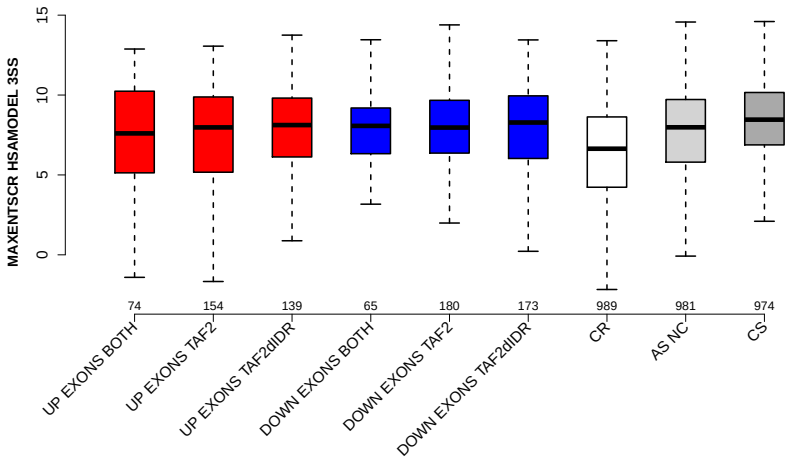
- `UP_EXONS_TAF2` vs `DOWN_EXONS_BOTH` : 0.0324858
  mean: 8.5851 > 7.4092 , median: 8.78 > 8.35
- `UP_EXONS_TAF2` vs `CS` : 0.0405826
  mean: 8.5851 > 8.1698 , median: 8.78 > 8.565
- `UP_EXONS_TAF2dIDR` vs `DOWN_EXONS_BOTH` : 0.00796065
  mean: 8.6461 > 7.4092 , median: 9.01 > 8.35
- `UP_EXONS_TAF2dIDR` vs `CS` : 0.00500756
  mean: 8.6461 > 8.1698 , median: 9.01 > 8.565
- `DOWN_EXONS_BOTH` vs `DOWN_EXONS_TAF2` : 0.0312859
  mean: 7.4092 < 8.5114 , median: 8.35 < 8.82
- `DOWN_EXONS_BOTH` vs `DOWN_EXONS_TAF2dIDR` : 0.0304697
  mean: 7.4092 < 8.5129 , median: 8.35 < 8.85
- `DOWN_EXONS_BOTH` vs `CR` : 0.030028
  mean: 7.4092 < 8.4483 , median: 8.35 < 8.78
- `DOWN_EXONS_BOTH` vs `AS_NC` : 0.0338938
  mean: 7.4092 < 8.3861 , median: 8.35 < 8.73
- `DOWN_EXONS_TAF2` vs `CS` : 0.0278254
  mean: 8.5114 > 8.1698 , median: 8.82 > 8.565

- DOWN_EXONS_TAF2dIDR vs CS : 0.0279796
  mean: 8.5129 > 8.1698 , median: 8.85 > 8.565
- CR vs CS : 0.00265863
  mean: 8.4483 > 8.1698 , median: 8.78 > 8.565
- AS_NC vs CS : 0.00580803
  mean: 8.3861 > 8.1698 , median: 8.73 > 8.565

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:

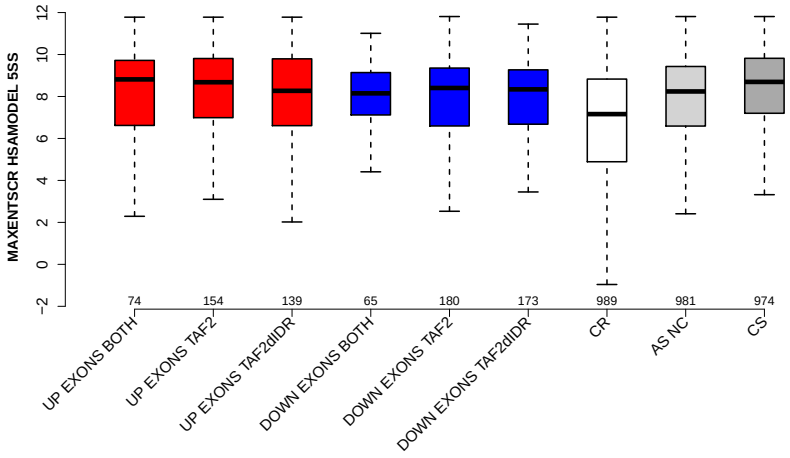
- `UP_EXONS_BOTH` vs `CR` : 0.00367085
  mean: 7.4315 > 5.8246 , median: 7.6 > 6.64
- `UP_EXONS_BOTH` vs `CS` : 0.0230734
  mean: 7.4315 < 8.2122 , median: 7.6 < 8.46
- `UP_EXONS_TAF2` vs `CR` : 3.15197e-05
  mean: 7.0918 > 5.8246 , median: 7.975 > 6.64
- `UP_EXONS_TAF2` vs `CS` : 0.0036242
  mean: 7.0918 < 8.2122 , median: 7.975 < 8.46
- `UP_EXONS_TAF2dIDR` vs `CR` : 3.73002e-07
  mean: 7.3213 > 5.8246 , median: 8.12 > 6.64
- `DOWN_EXONS_BOTH` vs `CR` : 0.000252644
  mean: 7.6985 > 5.8246 , median: 8.07 > 6.64
- `DOWN_EXONS_TAF2` vs `CR` : 2.3322e-08
  mean: 7.5021 > 5.8246 , median: 7.965 > 6.64
- `DOWN_EXONS_TAF2` vs `CS` : 0.00844516
  mean: 7.5021 < 8.2122 , median: 7.965 < 8.46
- `DOWN_EXONS_TAF2dIDR` vs `CR` : 1.96538e-08
  mean: 7.4896 > 5.8246 , median: 8.28 > 6.64
- `DOWN_EXONS_TAF2dIDR` vs `CS` : 0.0395018
  mean: 7.4896 < 8.2122 , median: 8.28 < 8.46

- `CR` vs `AS_NC` : 1.06786e-17
  mean: 5.8246 < 7.2022 , median: 6.64 < 7.98
- `CR` vs `CS` : 1.92866e-46
  mean: 5.8246 < 8.2122 , median: 6.64 < 8.46
- `AS_NC` vs `CS` : 3.91052e-08
  mean: 7.2022 < 8.2122 , median: 7.98 < 8.46

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:

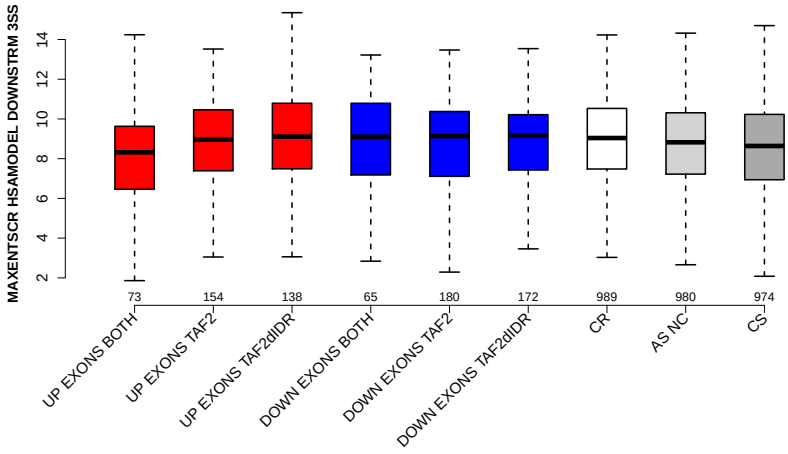
- `UP_EXONS_BOTH` vs `CR` : 0.00011145
  mean: 7.7068 > 6.2218 , median: 8.815 > 7.16
- `UP_EXONS_TAF2` vs `CR` : 2.67805e-11
  mean: 7.9003 > 6.2218 , median: 8.68 > 7.16
- `UP_EXONS_TAF2` vs `AS_NC` : 0.0105682
  mean: 7.9003 > 7.4013 , median: 8.68 > 8.24
- `UP_EXONS_TAF2dIDR` vs `CR` : 1.85548e-05
  mean: 7.2373 > 6.2218 , median: 8.27 > 7.16
- `UP_EXONS_TAF2dIDR` vs `CS` : 0.0263445
  mean: 7.2373 < 8.1678 , median: 8.27 < 8.695
- `DOWN_EXONS_BOTH` vs `CR` : 0.000490528
  mean: 7.9458 > 6.2218 , median: 8.15 > 7.16
- `DOWN_EXONS_TAF2` vs `CR` : 2.64248e-06
  mean: 7.2801 > 6.2218 , median: 8.405 > 7.16
- `DOWN_EXONS_TAF2` vs `CS` : 0.00437063
  mean: 7.2801 < 8.1678 , median: 8.405 < 8.695
- `DOWN_EXONS_TAF2dIDR` vs `CR` : 1.17292e-07
  mean: 7.8679 > 6.2218 , median: 8.34 > 7.16
- `DOWN_EXONS_TAF2dIDR` vs `CS` : 0.00771968
  mean: 7.8679 < 8.1678 , median: 8.34 < 8.695

- `CR` vs `AS_NC` : 4.18395e-17
  mean: 6.2218 < 7.4013 , median: 7.16 < 8.24
- `CR` vs `CS` : 1.30522e-40
  mean: 6.2218 < 8.1678 , median: 7.16 < 8.695
- `AS_NC` vs `CS` : 4.36076e-08
  mean: 7.4013 < 8.1678 , median: 8.24 < 8.695

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



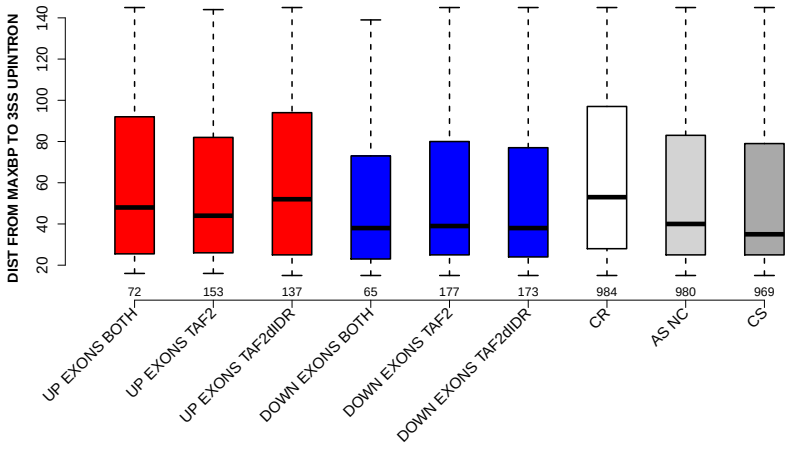
Significant results from Mann-Whitney U test:

- `UP_EXONS_BOTH` vs `UP_EXONS_TAF2dIDR` : 0.0117041
  mean: 8.0936 < 9.0361 , median: 8.32 < 9.11
- `UP_EXONS_BOTH` vs `DOWN_EXONS_TAF2dIDR` : 0.0340167
  mean: 8.0936 < 8.739 , median: 8.32 < 9.17
- `UP_EXONS_BOTH` vs `CR` : 0.00983603
  mean: 8.0936 < 8.8435 , median: 8.32 < 9.04
- `UP_EXONS_TAF2dIDR` vs `CS` : 0.0248078
  mean: 9.0361 > 8.4368 , median: 9.11 > 8.64
- `CR` vs `AS_NC` : 0.0417114
  mean: 8.8435 > 8.5949 , median: 9.04 > 8.825
- `CR` vs `CS` : 0.00153573
  mean: 8.8435 > 8.4368 , median: 9.04 > 8.64

6.29 DIST FROM MAXBP TO 3SS UPINTRON

Back to: Overview | ToC

Meaning: distance to 3ss of best precited BP



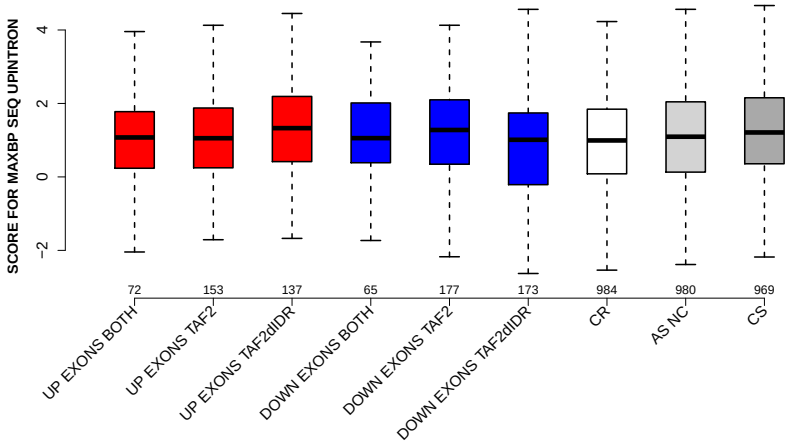
Significant results from Mann-Whitney U test:

- `DOWN_EXONS_BOTH` vs `CR` : 0.0114227
  mean: 51.1385 < 63.5305 , median: 38 < 53
- `DOWN_EXONS_TAF2` vs `CR` : 0.010129
  mean: 55.1921 < 63.5305 , median: 39 < 53
- `DOWN_EXONS_TAF2dIDR` vs `CR` : 0.00654695
  mean: 55.7052 < 63.5305 , median: 38 < 53
- `CR` vs `AS_NC` : 3.90923e-05
  mean: 63.5305 > 56.3327 , median: 53 > 40
- `CR` vs `CS` : 1.295e-08
  mean: 63.5305 > 53.8173 , median: 53 > 35

6.30 SCORE FOR MAXBP SEQ UPINTRON

Back to: Overview | ToC

Meaning: BP sequence score of best predicted BP



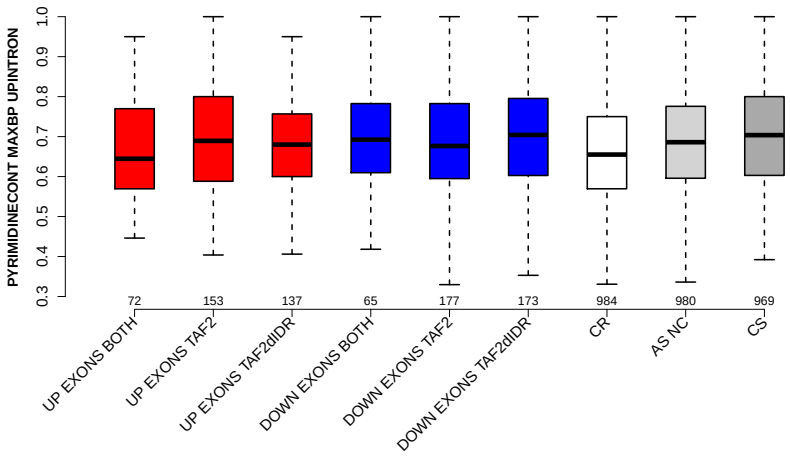
Significant results from Mann-Whitney U test:

- `UP_EXONS_TAF2dIDR` vs `DOWN_EXONS_TAF2dIDR` : 0.0215644
  mean: 1.3299 > 0.94791 , median: 1.3278 > 1.0107
- `UP_EXONS_TAF2dIDR` vs `CR` : 0.00455659
  mean: 1.3299 > 0.957446 , median: 1.3278 > 0.992529
- `DOWN_EXONS_TAF2` vs `CR` : 0.0355819
  mean: 1.1734 > 0.957446 , median: 1.2774 > 0.992529
- `DOWN_EXONS_TAF2dIDR` vs `CS` : 0.0127012
  mean: 0.94791 < 1.2448 , median: 1.0107 < 1.2101
- `CR` vs `AS_NC` : 0.0334407
  mean: 0.957446 < 1.1152 , median: 0.992529 < 1.0943
- `CR` vs `CS` : 9.6107e-06
  mean: 0.957446 < 1.2448 , median: 0.992529 < 1.2101
- `AS_NC` vs `CS` : 0.0326106
  mean: 1.1152 < 1.2448 , median: 1.0943 < 1.2101

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



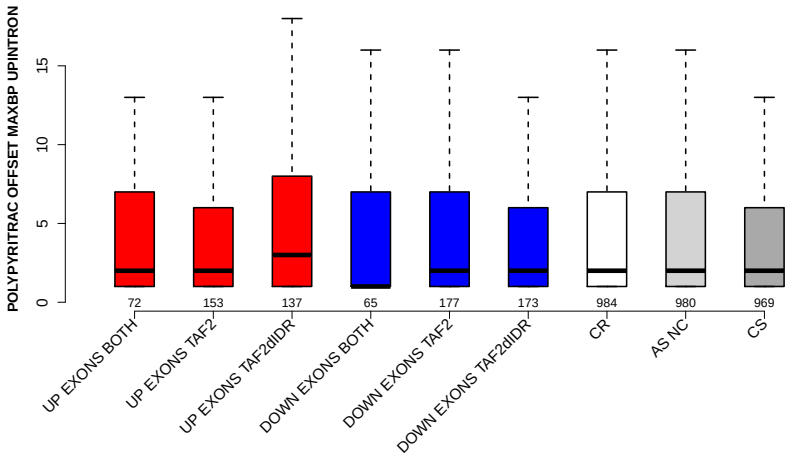
Significant results from Mann-Whitney U test:

- `UP_EXONS_BOTH` vs `CS` : 0.0355337
  mean: 0.66594 < 0.699212 , median: 0.644587 < 0.703704
- `UP_EXONS_TAF2` vs `CR` : 0.00447331
  mean: 0.695246 > 0.661375 , median: 0.68932 > 0.655051
- `DOWN_EXONS_BOTH` vs `CR` : 0.0143665
  mean: 0.700423 > 0.661375 , median: 0.692308 > 0.655051
- `DOWN_EXONS_TAF2` vs `CR` : 0.0271254
  mean: 0.687783 > 0.661375 , median: 0.676471 > 0.655051
- `DOWN_EXONS_TAF2dIDR` vs `CR` : 0.00085158
  mean: 0.695599 > 0.661375 , median: 0.704225 > 0.655051
- `CR` vs `AS_NC` : 5.65413e-06
  mean: 0.661375 < 0.688263 , median: 0.655051 < 0.685994
- `CR` vs `CS` : 4.21948e-10
  mean: 0.661375 < 0.699212 , median: 0.655051 < 0.703704

6.32 POLYPYRITRAC OFFSET MAXBP UPINTRON

Back to: Overview | ToC

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



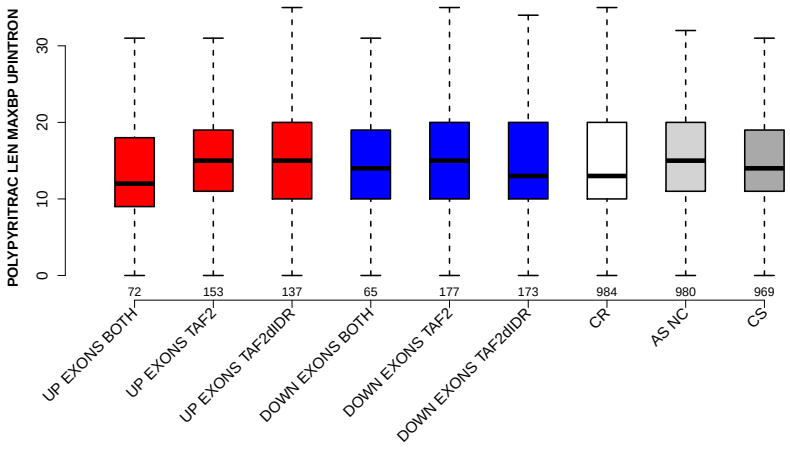
Significant results from Mann-Whitney U test:

- `CR` vs `CS` : 0.0135739
  mean: 5.127 > 4.3808 , median: 2 = 2
- `AS_NC` vs `CS` : 0.0341061
  mean: 4.9286 > 4.3808 , median: 2 = 2

6.33 POLYPYRITRAC LEN MAXBP UPINTRON

Back to: Overview | ToC

Meaning: Polypyrimidine track length for best BP



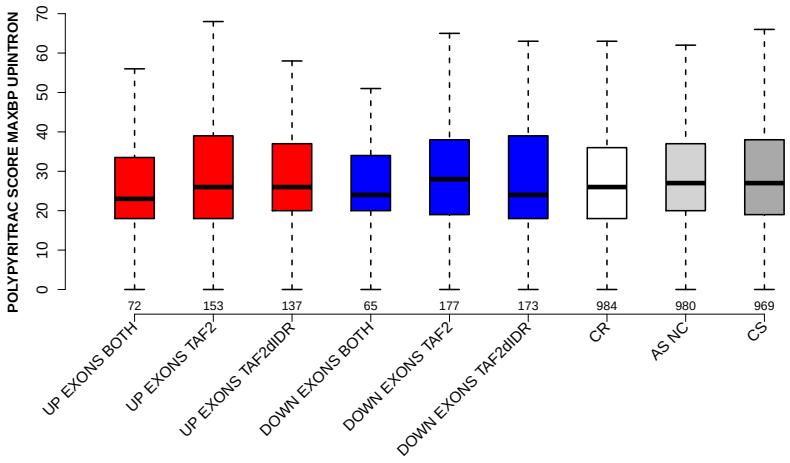
Significant results from Mann-Whitney U test:

- `UP_EXONS_BOTH` vs `UP_EXONS_TAF2` : 0.0226957
  mean: 14.5417 < 16.5948 , median: 12 < 15
- `UP_EXONS_BOTH` vs `UP_EXONS_TAF2dIDR` : 0.0335031
  mean: 14.5417 < 16.781 , median: 12 < 15
- `UP_EXONS_BOTH` vs `DOWN_EXONS_TAF2` : 0.0479479
  mean: 14.5417 < 16.3559 , median: 12 < 15
- `UP_EXONS_BOTH` vs `AS_NC` : 0.0108193
  mean: 14.5417 < 16.6337 , median: 12 < 15
- `UP_EXONS_BOTH` vs `CS` : 0.0232196
  mean: 14.5417 < 15.9319 , median: 12 < 14
- `CR` vs `AS_NC` : 0.014592
  mean: 16.1291 < 16.6337 , median: 13 < 15

6.34 POLYPYRITRAC SCORE MAXBP UPINTRON

Back to: Overview | ToC

Meaning: Polypyrimidine track score for best BP



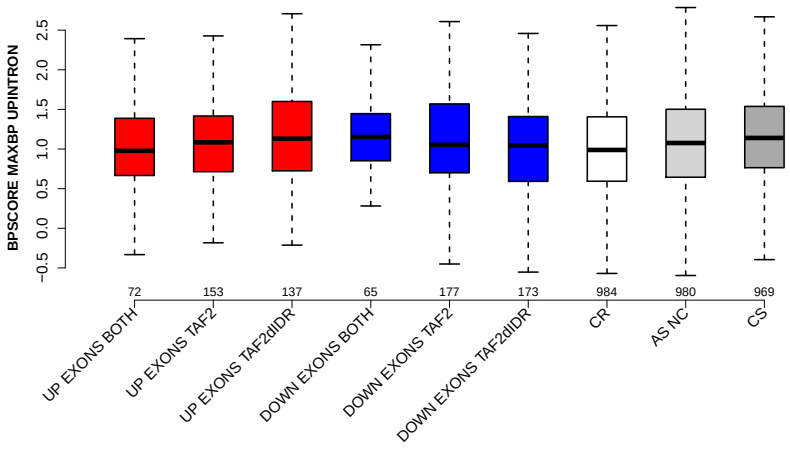
Significant results from Mann-Whitney U test:

- `UP_EXONS_BOTH` vs `AS_NC` : 0.0397432
  mean: 28.6806 < 31.7449 , median: 23 < 27
- `CR` vs `AS_NC` : 0.0326183
  mean: 30.688 < 31.7449 , median: 26 < 27

6.35 BPSCORE MAXBP UPINTRON

Back to: Overview | ToC

Meaning: SVM classification score of best BP



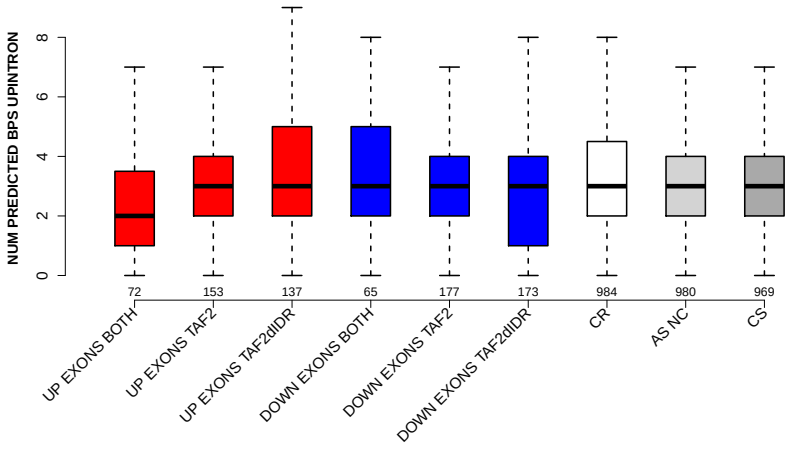
Significant results from Mann-Whitney U test:

- `UP_EXONS_TAF2dIDR` vs `CR` : 0.00812847
  mean: 1.0707 > 0.95162 , median: 1.1303 > 0.988312
- `DOWN_EXONS_TAF2` vs `CR` : 0.0443034
  mean: 1.0533 > 0.95162 , median: 1.0524 > 0.988312
- `DOWN_EXONS_TAF2dIDR` vs `CS` : 0.012904
  mean: 1.002 < 1.1214 , median: 1.0457 < 1.1398
- `CR` vs `AS_NC` : 0.00282501
  mean: 0.95162 < 1.0445 , median: 0.988312 < 1.076
- `CR` vs `CS` : 2.37638e-08
  mean: 0.95162 < 1.1214 , median: 0.988312 < 1.1398
- `AS_NC` vs `CS` : 0.0144174
  mean: 1.0445 < 1.1214 , median: 1.076 < 1.1398

6.36 NUM PREDICTED BPS UPINTRON

Back to: Overview | ToC

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



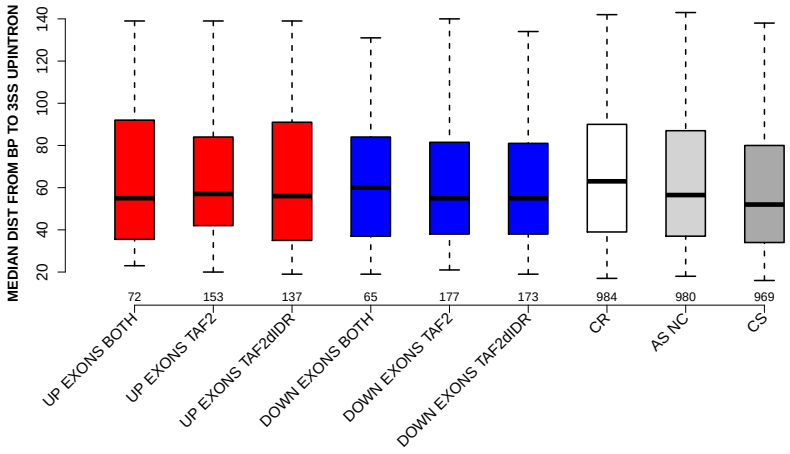
Significant results from Mann-Whitney U test:

- `UP_EXONS_BOTH` vs `UP_EXONS_TAF2dIDR` : 0.00898896
  mean: $2.6528 < 3.3723$, median: $2 < 3$
- `UP_EXONS_BOTH` vs `CR` : 0.00768329
  mean: $2.6528 < 3.3293$, median: $2 < 3$
- `UP_EXONS_BOTH` vs `AS_NC` : 0.0173805
  mean: $2.6528 < 3.2531$, median: $2 < 3$
- `UP_EXONS_BOTH` vs `CS` : 0.00445609
  mean: $2.6528 < 3.3075$, median: $2 < 3$
- `DOWN_EXONS_TAF2` vs `CR` : 0.0448922
  mean: $2.9153 < 3.3293$, median: $3 = 3$
- `DOWN_EXONS_TAF2` vs `CS` : 0.0251059
  mean: $2.9153 < 3.3075$, median: $3 = 3$

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



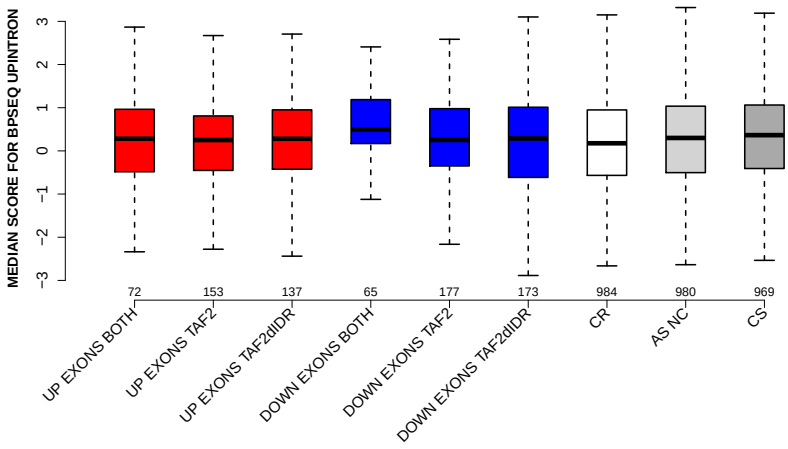
Significant results from Mann-Whitney U test:

- `UP_EXONS_TAF2` vs `CS` : 0.0141171
  mean: 65.9216 > 59.1889 , median: 57 > 52
- `DOWN_EXONS_TAF2` vs `CR` : 0.031458
  mean: 61.7768 < 67.0925 , median: 55 < 63
- `DOWN_EXONS_TAF2dIDR` vs `CR` : 0.0253695
  mean: 61.1908 < 67.0925 , median: 55 < 63
- `CR` vs `AS_NC` : 0.00925672
  mean: 67.0925 > 63.7158 , median: 63 > 56.5
- `CR` vs `CS` : 4.41239e-09
  mean: 67.0925 > 59.1889 , median: 63 > 52
- `AS_NC` vs `CS` : 0.00143796
  mean: 63.7158 > 59.1889 , median: 56.5 > 52

6.38 MEDIAN SCORE FOR BPSEQ UPINTRON

Back to: Overview | ToC

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



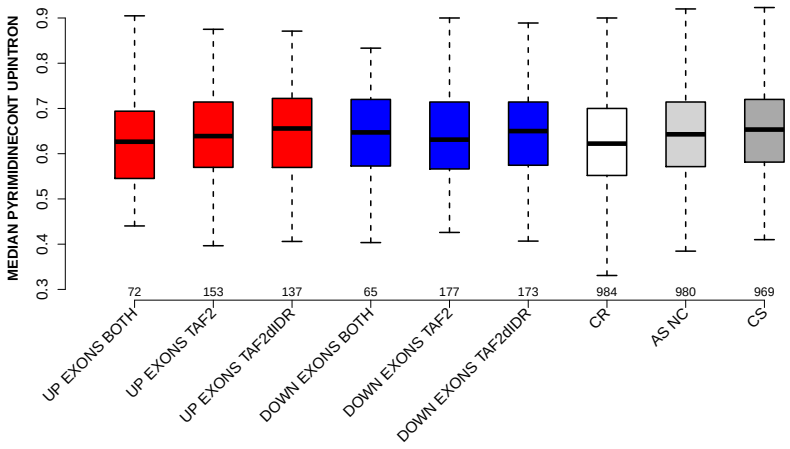
Significant results from Mann-Whitney U test:

- `UP_EXONS_BOTH` vs `DOWN_EXONS_BOTH` : 0.0239009
  mean: 0.199859 < 0.627752 , median: 0.282075 < 0.497757
- `UP_EXONS_TAF2` vs `DOWN_EXONS_BOTH` : 0.00712016
  mean: 0.258781 < 0.627752 , median: 0.250984 < 0.497757
- `UP_EXONS_TAF2dIDR` vs `DOWN_EXONS_BOTH` : 0.0308434
  mean: 0.279247 < 0.627752 , median: 0.281067 < 0.497757
- `DOWN_EXONS_BOTH` vs `DOWN_EXONS_TAF2` : 0.0264949
  mean: 0.627752 > 0.307962 , median: 0.497757 > 0.253786
- `DOWN_EXONS_BOTH` vs `DOWN_EXONS_TAF2dIDR` : 0.0126898
  mean: 0.627752 > 0.152932 , median: 0.497757 > 0.287914
- `DOWN_EXONS_BOTH` vs `CR` : 0.00130383
  mean: 0.627752 > 0.169783 , median: 0.497757 > 0.176331
- `DOWN_EXONS_BOTH` vs `AS_NC` : 0.0111081
  mean: 0.627752 > 0.264037 , median: 0.497757 > 0.299222
- `DOWN_EXONS_BOTH` vs `CS` : 0.0327672
  mean: 0.627752 > 0.352597 , median: 0.497757 > 0.364364
- `CR` vs `CS` : 0.00230752
  mean: 0.169783 < 0.352597 , median: 0.176331 < 0.364364

6.39 MEDIAN PYRIMIDINECONT UPINTRON

Back to: Overview | ToC

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



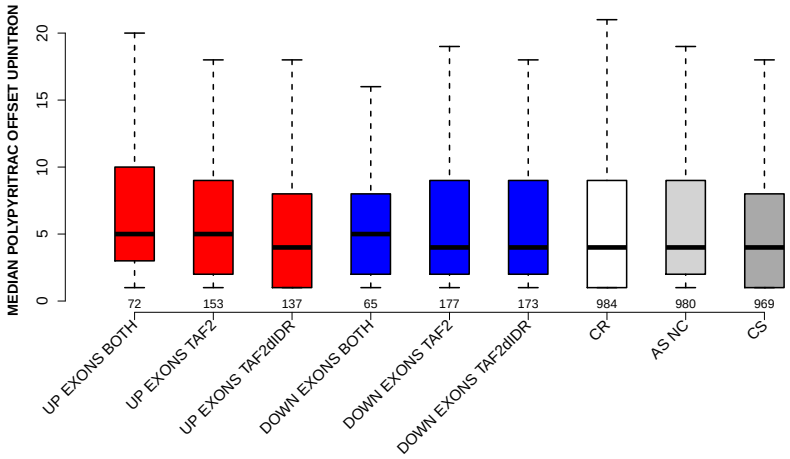
Significant results from Mann-Whitney U test:

- `UP_EXONS_BOTH` vs `CS` : 0.0319645
  mean: 0.630975 < 0.654484 , median: 0.626453 < 0.653333
- `UP_EXONS_TAF2dIDR` vs `CR` : 0.0252743
  mean: 0.64862 > 0.626186 , median: 0.655738 > 0.622296
- `DOWN_EXONS_TAF2dIDR` vs `CR` : 0.00969615
  mean: 0.648608 > 0.626186 , median: 0.65 > 0.622296
- `CR` vs `AS_NC` : 0.000194303
  mean: 0.626186 < 0.645878 , median: 0.622296 < 0.642857
- `CR` vs `CS` : 2.15827e-08
  mean: 0.626186 < 0.654484 , median: 0.622296 < 0.653333

6.40 MEDIAN POLYPYRITRAC OFFSET UPINTRON

Back to: Overview | ToC

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



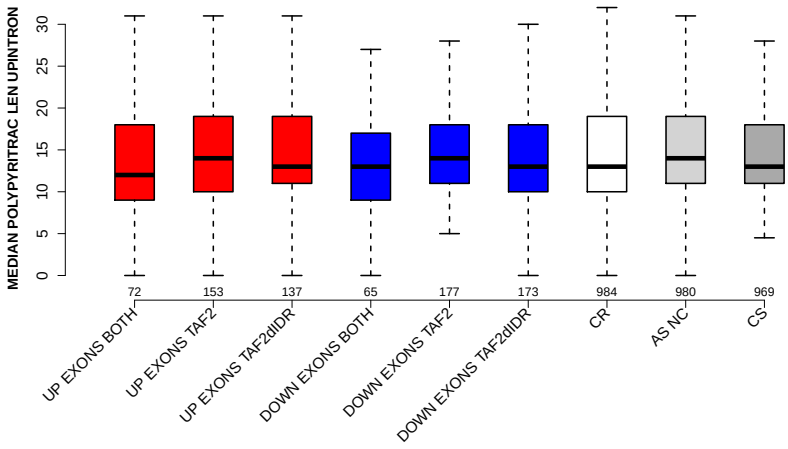
Significant results from Mann-Whitney U test:

- `UP_EXONS_BOTH` vs `CS` : 0.0286505
  mean: 8.7639 > 7.0217 , median: 5 > 4

6.41 MEDIAN POLYPYRITRAC LEN UPINTRON

Back to: Overview | ToC

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



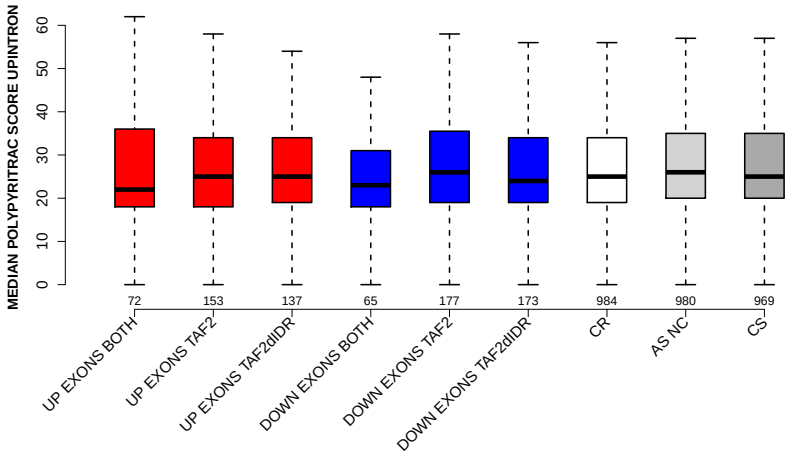
Significant results from Mann-Whitney U test:

- none

6.42 MEDIAN POLYPYRITRAC SCORE UPINTRON

Back to: Overview | ToC

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



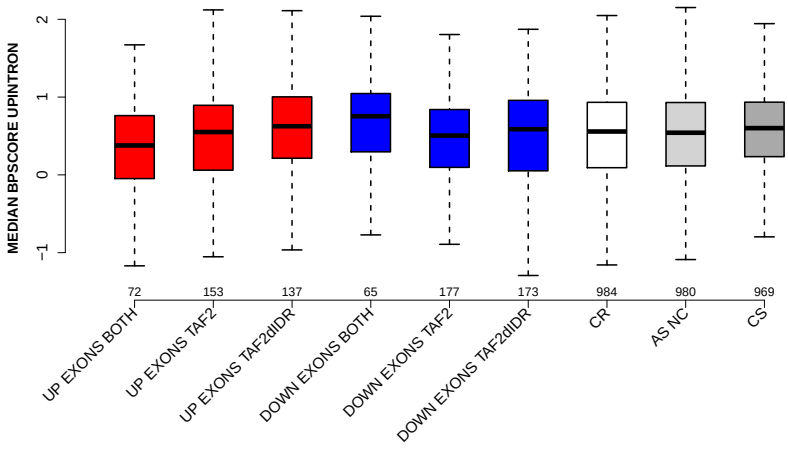
Significant results from Mann-Whitney U test:

- none

6.43 MEDIAN BPSCORE UPINTRON

Back to: Overview | ToC

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



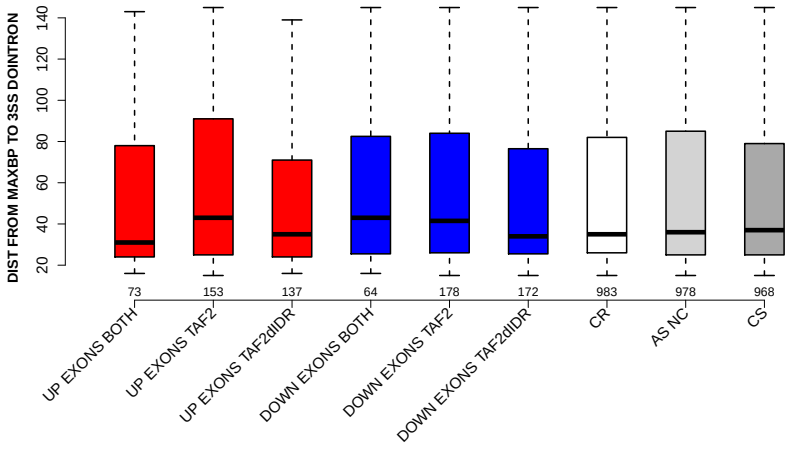
Significant results from Mann-Whitney U test:

- `UP_EXONS_BOTH` vs `UP_EXONS_TAF2dIDR` : 0.0108441
  mean: 0.208414 < 0.43958 , median: 0.37822 < 0.62512
- `UP_EXONS_BOTH` vs `DOWN_EXONS_BOTH` : 0.00729019
  mean: 0.208414 < 0.446045 , median: 0.37822 < 0.754451
- `UP_EXONS_BOTH` vs `CR` : 0.0422611
  mean: 0.208414 < 0.404481 , median: 0.37822 < 0.557488
- `UP_EXONS_BOTH` vs `AS_NC` : 0.0262427
  mean: 0.208414 < 0.430089 , median: 0.37822 < 0.541869
- `UP_EXONS_BOTH` vs `CS` : 0.00296493
  mean: 0.208414 < 0.494375 , median: 0.37822 < 0.600891
- `DOWN_EXONS_BOTH` vs `DOWN_EXONS_TAF2` : 0.0410745
  mean: 0.446045 > 0.387322 , median: 0.754451 > 0.504965
- `CR` vs `CS` : 0.0297797
  mean: 0.404481 < 0.494375 , median: 0.557488 < 0.600891

6.44 DIST FROM MAXBP TO 3SS DOINTRON

Back to: Overview | ToC

Meaning: distance to 3ss of best precited BP



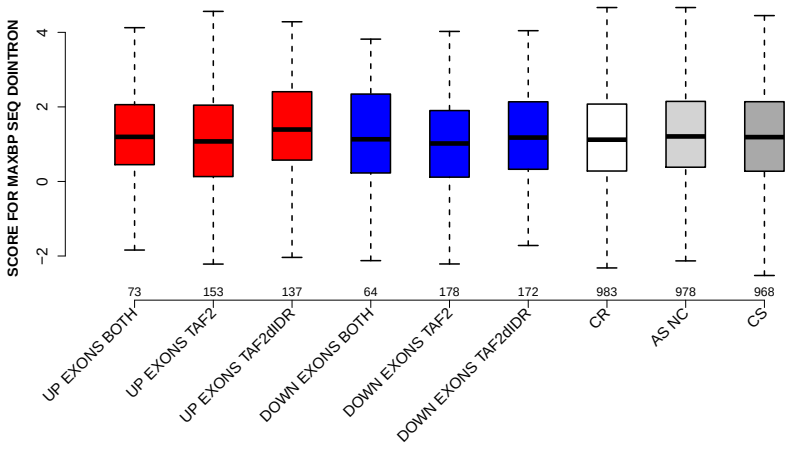
Significant results from Mann-Whitney U test:

- none

6.45 SCORE FOR MAXBP SEQ DOINTRON

Back to: Overview | ToC

Meaning: BP sequence score of best predicted BP



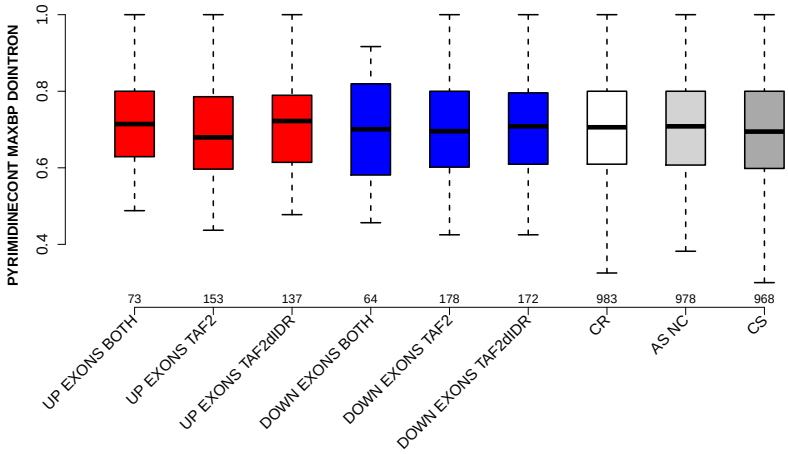
Significant results from Mann-Whitney U test:

- `UP_EXONS_TAF2dIDR` vs `DOWN_EXONS_TAF2` : 0.0137648
  mean: 1.3971 > 1.0157 , median: 1.3927 > 1.0187
- `DOWN_EXONS_TAF2` vs `AS_NC` : 0.0401539
  mean: 1.0157 < 1.2644 , median: 1.0187 < 1.2074

6.46 PYRIMIDINECONT MAXBP DOINTRON

Back to: Overview | ToC

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



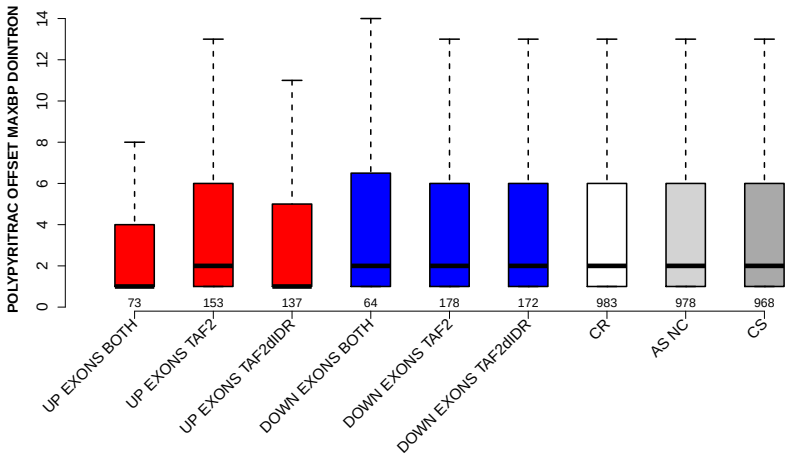
Significant results from Mann-Whitney U test:

- none

6.47 POLYPYRITRAC OFFSET MAXBP DOINTRON

Back to: Overview | ToC

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



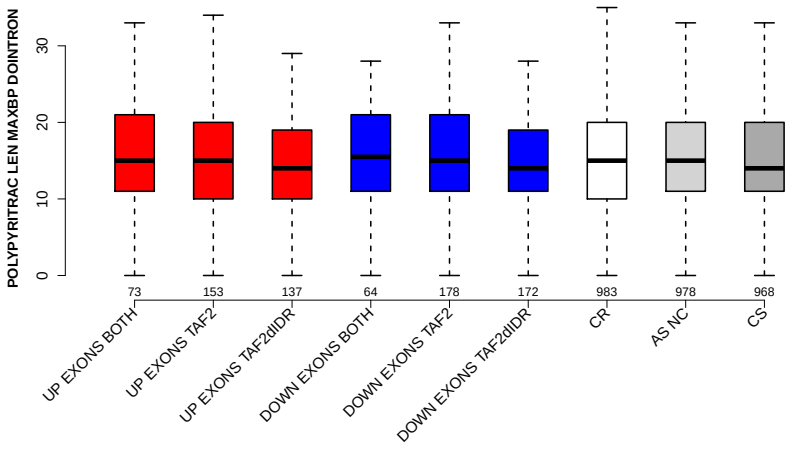
Significant results from Mann-Whitney U test:

- none

6.48 POLYPYRITRAC LEN MAXBP DOINTRON

Back to: Overview | ToC

Meaning: Polypyrimidine track length for best BP



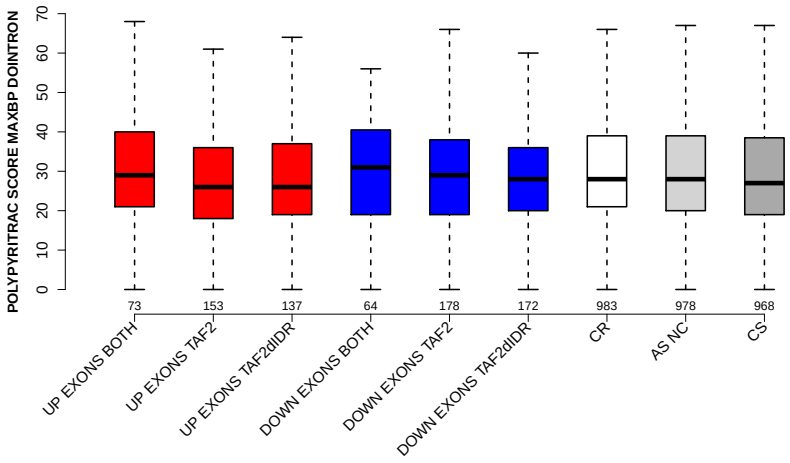
Significant results from Mann-Whitney U test:

- none

6.49 POLYPYRITRAC SCORE MAXBP DOINTRON

Back to: Overview | ToC

Meaning: Polypyrimidine track score for best BP



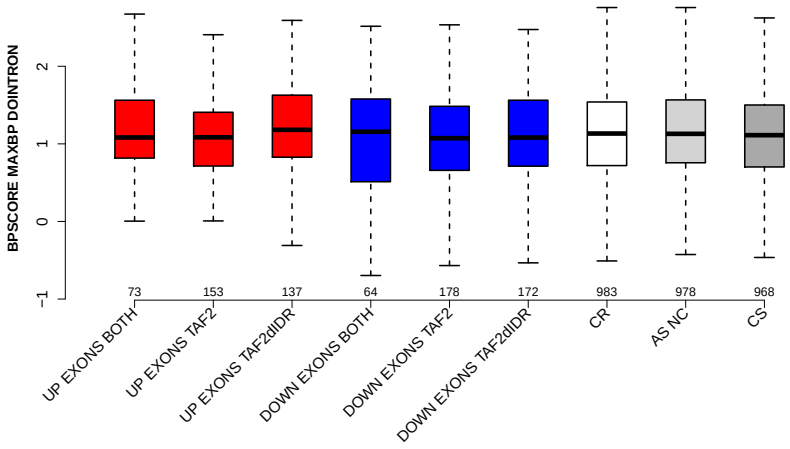
Significant results from Mann-Whitney U test:

- none

6.50 BPSCORE MAXBP DOINTRON

Back to: Overview | ToC

Meaning: SVM classification score of best BP



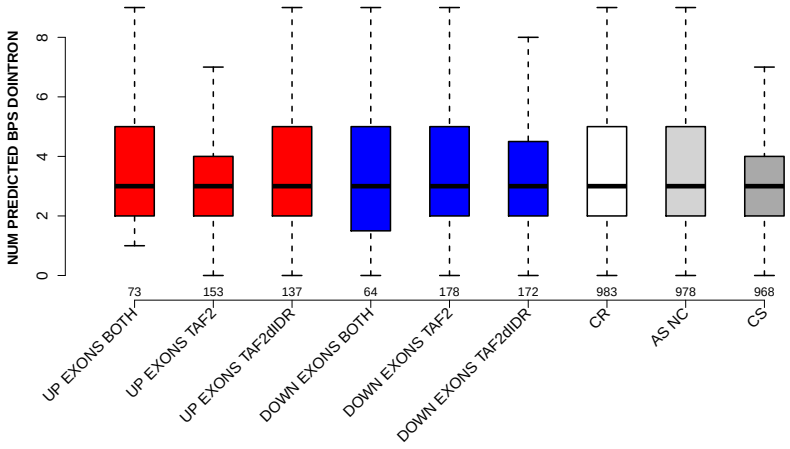
Significant results from Mann-Whitney U test:

- `UP_EXONS_TAF2dIDR` vs `DOWN_EXONS_TAF2` : 0.0429617
  mean: 1.219 > 1.055 , median: 1.1809 > 1.073
- `UP_EXONS_TAF2dIDR` vs `CS` : 0.0355362
  mean: 1.219 > 1.0684 , median: 1.1809 > 1.1118

6.51 NUM PREDICTED BPS DOINTRON

Back to: Overview | ToC

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



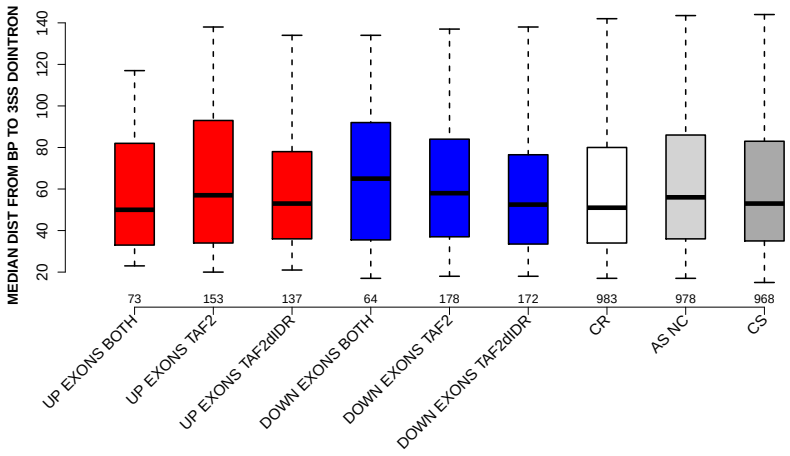
Significant results from Mann-Whitney U test:

- `DOWN_EXONS_TAF2` vs `CR` : 0.0325595
  mean: $3.2584 < 3.5493$, median: $3 = 3$
- `DOWN_EXONS_TAF2dIDR` vs `CR` : 0.0161697
  mean: $3.1802 < 3.5493$, median: $3 = 3$
- `CR` vs `AS_NC` : 0.00437603
  mean: $3.5493 > 3.3497$, median: $3 = 3$
- `CR` vs `CS` : 0.000629348
  mean: $3.5493 > 3.2789$, median: $3 = 3$

6.52 MEDIAN DIST FROM BP TO 3SS DOINTRON

Back to: Overview | ToC

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



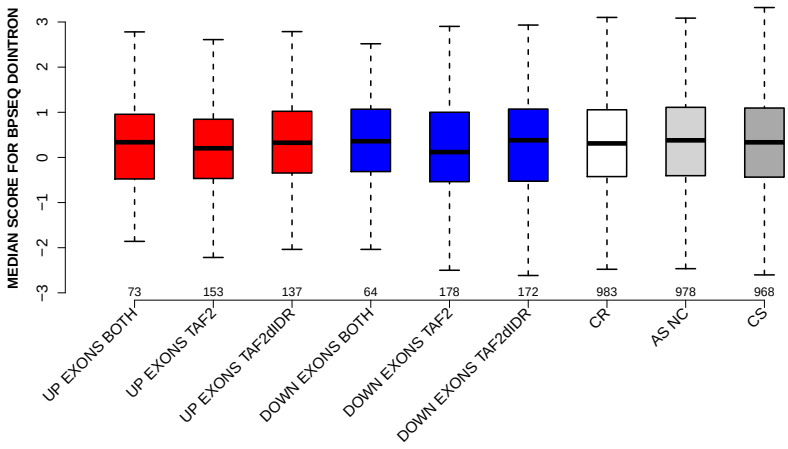
Significant results from Mann-Whitney U test:

- `CR` vs `AS_NC` : 0.0304439
  mean: 60.1562 < 63.407 , median: 51 < 56

6.53 MEDIAN SCORE FOR BPSEQ DOINTRON

Back to: Overview | ToC

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



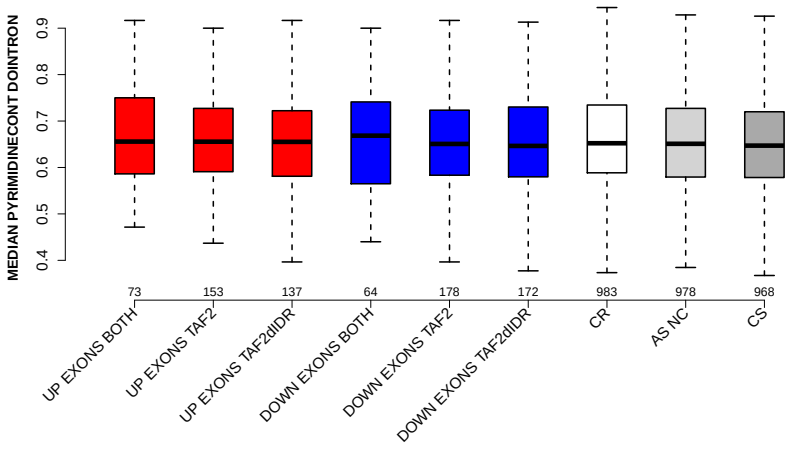
Significant results from Mann-Whitney U test:

- `DOWN_EXONS_TAF2` vs `AS_NC` : 0.0440263
  mean: 0.17012 < 0.368149 , median: 0.118252 < 0.378718

6.54 MEDIAN PYRIMIDINECONT DOINTRON

Back to: Overview | ToC

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



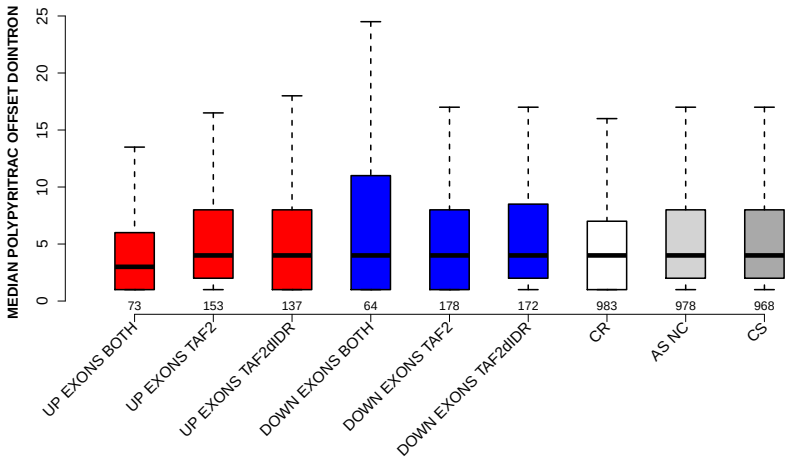
Significant results from Mann-Whitney U test:

- `CR` vs `CS` : 0.0207749
  mean: 0.659389 > 0.648415 , median: 0.652174 > 0.647059

6.55 MEDIAN POLYPYRITRAC OFFSET DOINTRON

Back to: Overview | ToC

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



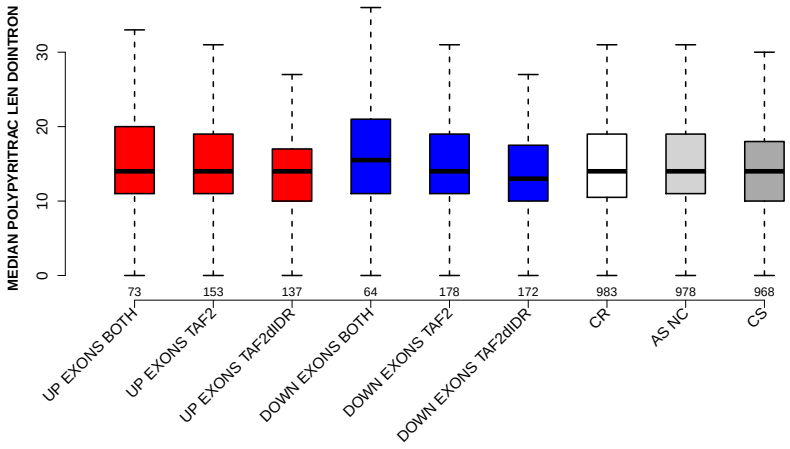
Significant results from Mann-Whitney U test:

- `CR` vs `CS` : 0.0124247
  mean: $6.9318 < 7.0036$, median: $4 = 4$

6.56 MEDIAN POLYPYRITRAC LEN DOINTRON

Back to: Overview | ToC

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



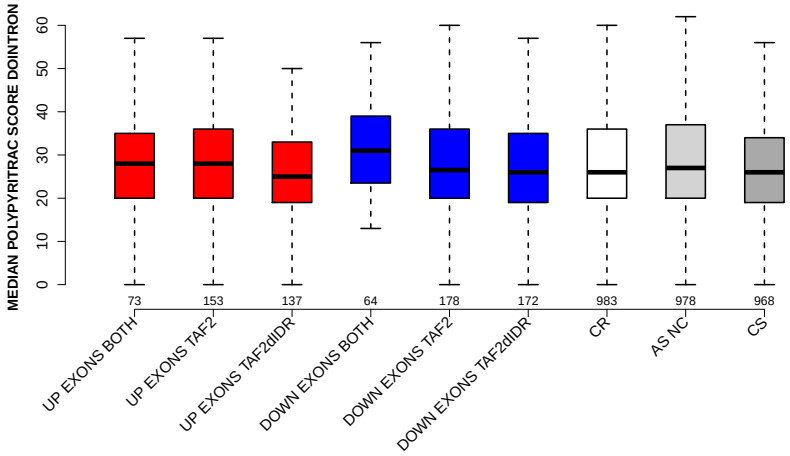
Significant results from Mann-Whitney U test:

- `AS_NC` vs `CS` : 0.0338816
  mean: 15.9463 > 15.1415 , median: 14 = 14

6.57 MEDIAN POLYPYRITRAC SCORE DOINTRON

Back to: Overview | ToC

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



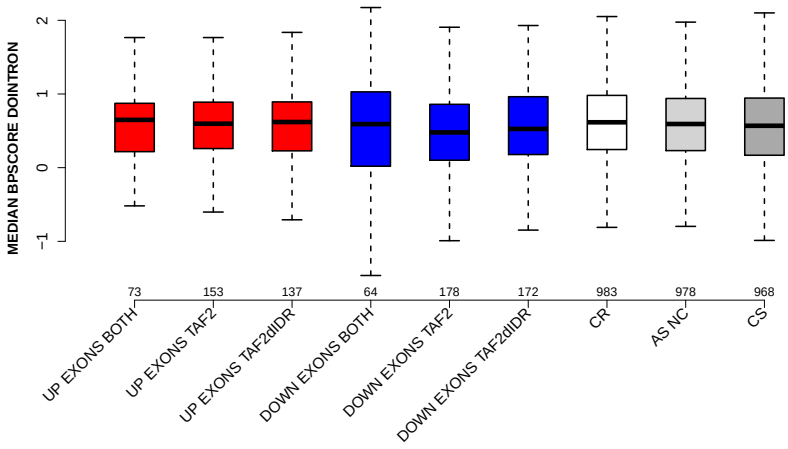
Significant results from Mann-Whitney U test:

- `UP_EXONS_TAF2dIDR` vs `DOWN_EXONS_BOTH` : 0.0150996
  mean: 28.2336 < 31.2266 , median: 25 < 31
- `DOWN_EXONS_BOTH` vs `DOWN_EXONS_TAF2dIDR` : 0.0183047
  mean: 31.2266 > 27.7384 , median: 31 > 26
- `DOWN_EXONS_BOTH` vs `CS` : 0.0170578
  mean: 31.2266 > 28.6958 , median: 31 > 26

6.58 MEDIAN BPSCORE DOINTRON

Back to: Overview | ToC

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



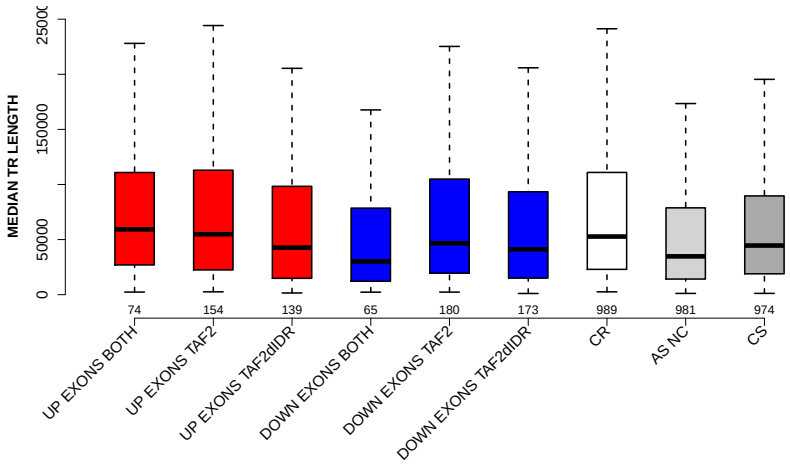
Significant results from Mann-Whitney U test:

- `DOWN_EXONS_TAF2` vs `CR` : 0.0195483
  mean: 0.396572 < 0.494337 , median: 0.478363 < 0.615999
- `DOWN_EXONS_TAF2` vs `AS_NC` : 0.045495
  mean: 0.396572 < 0.494518 , median: 0.478363 < 0.592563

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:

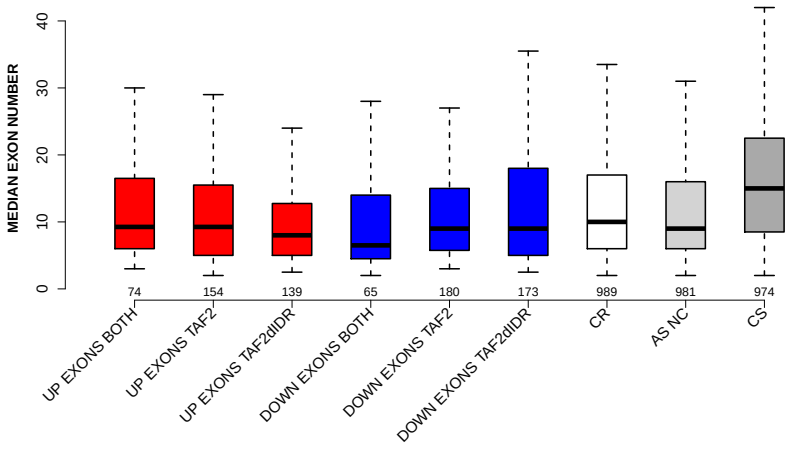
- `UP_EXONS_BOTH` vs `DOWN_EXONS_BOTH` : 0.0406171
  mean: 81414.3986 > 62702.2077 , median: 59294.75 > 30220
- `UP_EXONS_BOTH` vs `AS_NC` : 0.00996476
  mean: 81414.3986 > 62450.4638 , median: 59294.75 > 34777
- `UP_EXONS_TAF2` vs `DOWN_EXONS_BOTH` : 0.0229171
  mean: 87778.8896 > 62702.2077 , median: 54818 > 30220
- `UP_EXONS_TAF2` vs `AS_NC` : 0.000455724
  mean: 87778.8896 > 62450.4638 , median: 54818 > 34777
- `UP_EXONS_TAF2dIDR` vs `CR` : 0.0267584
  mean: 75072.1367 < 85376.6284 , median: 42727 < 52754.5
- `DOWN_EXONS_BOTH` vs `DOWN_EXONS_TAF2` : 0.0498519
  mean: 62702.2077 < 77872.625 , median: 30220 < 46613.5
- `DOWN_EXONS_BOTH` vs `CR` : 0.00284299
  mean: 62702.2077 < 85376.6284 , median: 30220 < 52754.5
- `DOWN_EXONS_TAF2` vs `AS_NC` : 0.00397221
  mean: 77872.625 > 62450.4638 , median: 46613.5 > 34777
- `DOWN_EXONS_TAF2dIDR` vs `CR` : 0.00905896
  mean: 70877.7312 < 85376.6284 , median: 41106 < 52754.5
- `CR` vs `AS_NC` : 4.71087e-14
  mean: 85376.6284 > 62450.4638 , median: 52754.5 > 34777

- `CR` vs `CS` : 1.52863e-05
  mean: 85376.6284 > 67456.8501 , median: 52754.5 > 44592.75
- `AS_NC` vs `CS` : 0.000818899
  mean: 62450.4638 < 67456.8501 , median: 34777 < 44592.75

6.60 MEDIAN EXON NUMBER

Back to: Overview | ToC

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



Significant results from Mann-Whitney U test:

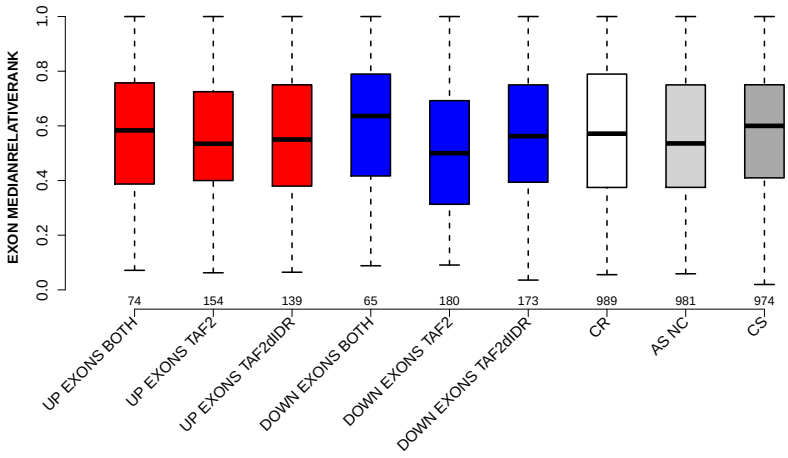
- `UP_EXONS_BOTH` vs `CS` : 4.02442e-06
  mean: 11.7568 < 17.8706 , median: 9.25 < 15
- `UP_EXONS_TAF2` vs `CR` : 0.0263931
  mean: 11.9675 < 13.5794 , median: 9.25 < 10
- `UP_EXONS_TAF2` vs `CS` : 3.77857e-11
  mean: 11.9675 < 17.8706 , median: 9.25 < 15
- `UP_EXONS_TAF2dIDR` vs `DOWN_EXONS_TAF2` : 0.0296821
  mean: 10.6079 < 13.4639 , median: 8 < 9
- `UP_EXONS_TAF2dIDR` vs `CR` : 3.55499e-05
  mean: 10.6079 < 13.5794 , median: 8 < 10
- `UP_EXONS_TAF2dIDR` vs `AS_NC` : 0.00259749
  mean: 10.6079 < 12.3522 , median: 8 < 9
- `UP_EXONS_TAF2dIDR` vs `CS` : 2.33403e-16
  mean: 10.6079 < 17.8706 , median: 8 < 15
- `DOWN_EXONS_BOTH` vs `DOWN_EXONS_TAF2` : 0.0167784
  mean: 9.6615 < 13.4639 , median: 6.5 < 9
- `DOWN_EXONS_BOTH` vs `CR` : 0.000242579
  mean: 9.6615 < 13.5794 , median: 6.5 < 10
- `DOWN_EXONS_BOTH` vs `AS_NC` : 0.00321039
  mean: 9.6615 < 12.3522 , median: 6.5 < 9

- DOWN_EXONS_BOTH vs CS : 2.09088e-10
  mean: 9.6615 < 17.8706 , median: 6.5 < 15
- DOWN_EXONS_TAF2 vs CS : 3.55237e-11
  mean: 13.4639 < 17.8706 , median: 9 < 15
- DOWN_EXONS_TAF2dIDR vs CR : 0.0418873
  mean: 13.1214 < 13.5794 , median: 9 < 10
- DOWN_EXONS_TAF2dIDR vs CS : 1.35406e-10
  mean: 13.1214 < 17.8706 , median: 9 < 15
- CR vs AS_NC : 0.0150464
  mean: 13.5794 > 12.3522 , median: 10 > 9
- CR vs CS : 6.64063e-21
  mean: 13.5794 < 17.8706 , median: 10 < 15
- AS_NC vs CS : 1.23337e-31
  mean: 12.3522 < 17.8706 , median: 9 < 15

6.61 EXON MEDIANRELATIVERANK

Back to: Overview | ToC

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



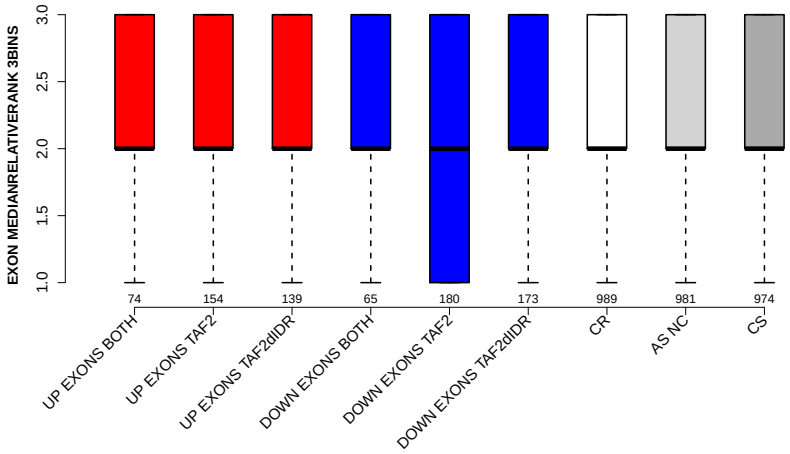
Significant results from Mann-Whitney U test:

- `DOWN_EXONS_BOTH` vs `DOWN_EXONS_TAF2` : 0.0157606
  mean: 0.599686 > 0.514873 , median: 0.636134 > 0.5
- `DOWN_EXONS_TAF2` vs `CR` : 0.00329217
  mean: 0.514873 < 0.57661 , median: 0.5 < 0.571429
- `DOWN_EXONS_TAF2` vs `AS_NC` : 0.0290056
  mean: 0.514873 < 0.558249 , median: 0.5 < 0.535714
- `DOWN_EXONS_TAF2` vs `CS` : 0.000498591
  mean: 0.514873 < 0.580488 , median: 0.5 < 0.59992
- `AS_NC` vs `CS` : 0.0194824
  mean: 0.558249 < 0.580488 , median: 0.535714 < 0.59992

6.62 EXON MEDIANRELATIVERANK 3BINS

Back to: Overview | ToC

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



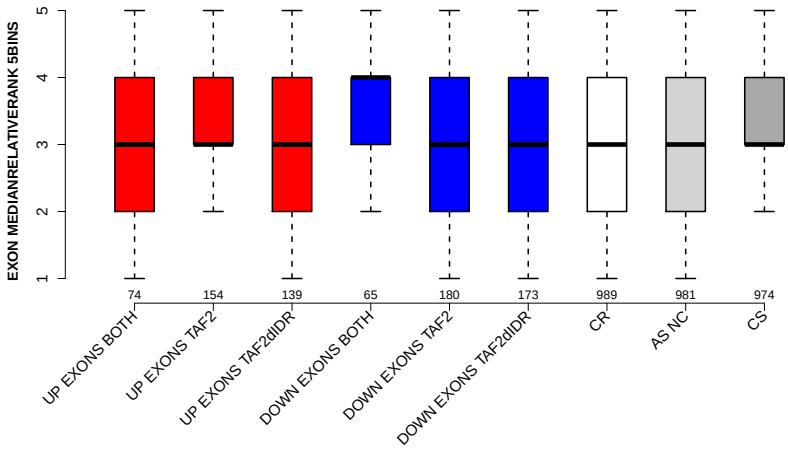
Significant results from Mann-Whitney U test:

- `UP_EXONS_TAF2dIDR` vs `DOWN_EXONS_TAF2` : 0.0432286
  mean: $2.223 > 2.05$, median: $2 = 2$
- `DOWN_EXONS_BOTH` vs `DOWN_EXONS_TAF2` : 0.00522497
  mean: $2.3538 > 2.05$, median: $2 = 2$
- `DOWN_EXONS_TAF2` vs `CR` : 0.00789835
  mean: $2.05 < 2.2113$, median: $2 = 2$
- `DOWN_EXONS_TAF2` vs `AS_NC` : 0.0297333
  mean: $2.05 < 2.1825$, median: $2 = 2$
- `DOWN_EXONS_TAF2` vs `CS` : 0.000615066
  mean: $2.05 < 2.2577$, median: $2 = 2$
- `AS_NC` vs `CS` : 0.0292083
  mean: $2.1825 < 2.2577$, median: $2 = 2$

6.63 EXON MEDIANRELATIVERANK 5BINS

Back to: Overview | ToC

Meaning: similar to EXON MEDIANRELATIVERANK 3BINS with 5 bins



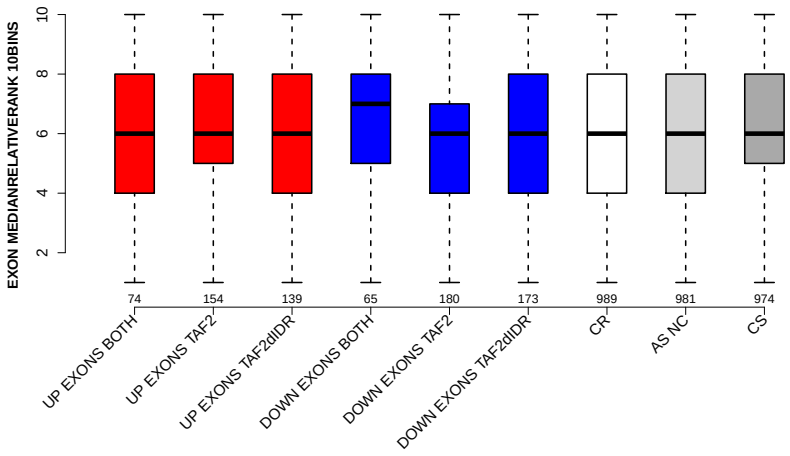
Significant results from Mann-Whitney U test:

- `DOWN_EXONS_BOTH` vs `DOWN_EXONS_TAF2` : 0.00871599
  mean: 3.5231 > 3.0667 , median: 4 > 3
- `DOWN_EXONS_TAF2` vs `DOWN_EXONS_TAF2dIDR` : 0.0483008
  mean: 3.0667 < 3.3179 , median: 3 = 3
- `DOWN_EXONS_TAF2` vs `CR` : 0.0044127
  mean: 3.0667 < 3.36 , median: 3 = 3
- `DOWN_EXONS_TAF2` vs `AS_NC` : 0.0237434
  mean: 3.0667 < 3.2946 , median: 3 = 3
- `DOWN_EXONS_TAF2` vs `CS` : 0.000347239
  mean: 3.0667 < 3.4148 , median: 3 = 3
- `AS_NC` vs `CS` : 0.0147189
  mean: 3.2946 < 3.4148 , median: 3 = 3

6.64 EXON MEDIANRELATIVERANK 10BINS

Back to: Overview | ToC

Meaning: similar to EXON MEDIANRELATIVERANK 3BINS with 10 bins



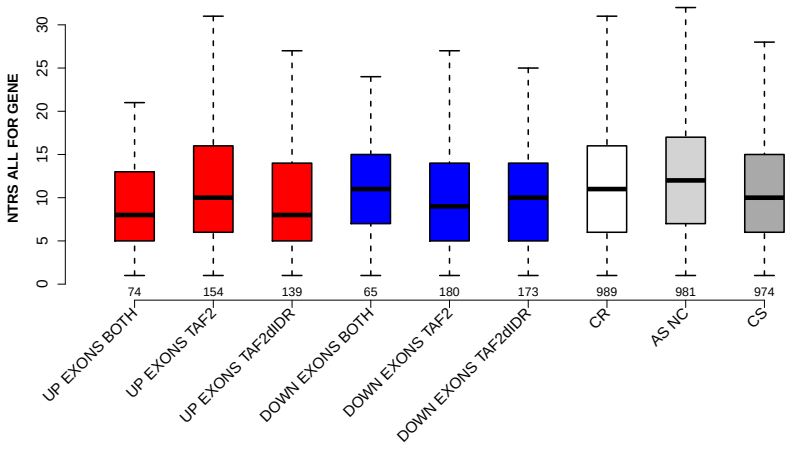
Significant results from Mann-Whitney U test:

- `DOWN_EXONS_BOTH` vs `DOWN_EXONS_TAF2` : 0.0106592
  mean: $6.5231 > 5.6611$, median: $7 > 6$
- `DOWN_EXONS_TAF2` vs `CR` : 0.0032394
  mean: $5.6611 < 6.2528$, median: $6 = 6$
- `DOWN_EXONS_TAF2` vs `AS_NC` : 0.0213173
  mean: $5.6611 < 6.1111$, median: $6 = 6$
- `DOWN_EXONS_TAF2` vs `CS` : 0.000310126
  mean: $5.6611 < 6.3429$, median: $6 = 6$
- `AS_NC` vs `CS` : 0.0175035
  mean: $6.1111 < 6.3429$, 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:

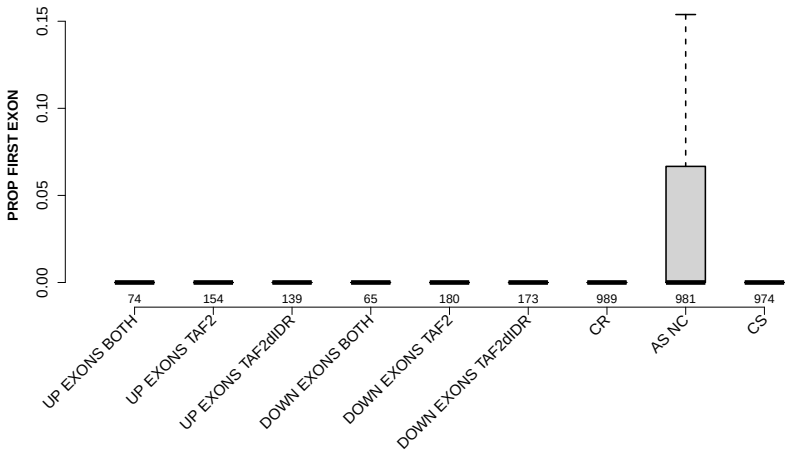
- `UP_EXONS_BOTH` vs `CR` : 0.0330967
  mean: 10.3919 < 12.1163 , median: 8 < 11
- `UP_EXONS_BOTH` vs `AS_NC` : 0.00156367
  mean: 10.3919 < 13.1672 , median: 8 < 12
- `UP_EXONS_TAF2` vs `UP_EXONS_TAF2dIDR` : 0.0179421
  mean: 13.0519 > 10.0719 , median: 10 > 8
- `UP_EXONS_TAF2dIDR` vs `CR` : 0.000514645
  mean: 10.0719 < 12.1163 , median: 8 < 11
- `UP_EXONS_TAF2dIDR` vs `AS_NC` : 2.23675e-06
  mean: 10.0719 < 13.1672 , median: 8 < 12
- `UP_EXONS_TAF2dIDR` vs `CS` : 0.0280462
  mean: 10.0719 < 11.3275 , median: 8 < 10
- `DOWN_EXONS_TAF2` vs `CR` : 0.00749922
  mean: 10.7889 < 12.1163 , median: 9 < 11
- `DOWN_EXONS_TAF2` vs `AS_NC` : 3.53767e-05
  mean: 10.7889 < 13.1672 , median: 9 < 12
- `DOWN_EXONS_TAF2dIDR` vs `CR` : 0.0267
  mean: 11.9827 < 12.1163 , median: 10 < 11
- `DOWN_EXONS_TAF2dIDR` vs `AS_NC` : 0.000251411
  mean: 11.9827 < 13.1672 , median: 10 < 12

- `CR` vs `AS_NC` : 0.00513112
  mean: 12.1163 < 13.1672 , median: 11 < 12
- `CR` vs `CS` : 0.0046396
  mean: 12.1163 > 11.3275 , median: 11 > 10
- `AS_NC` vs `CS` : 3.21291e-08
  mean: 13.1672 > 11.3275 , median: 12 > 10

6.66 PROP FIRST EXON

Back to: Overview | ToC

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



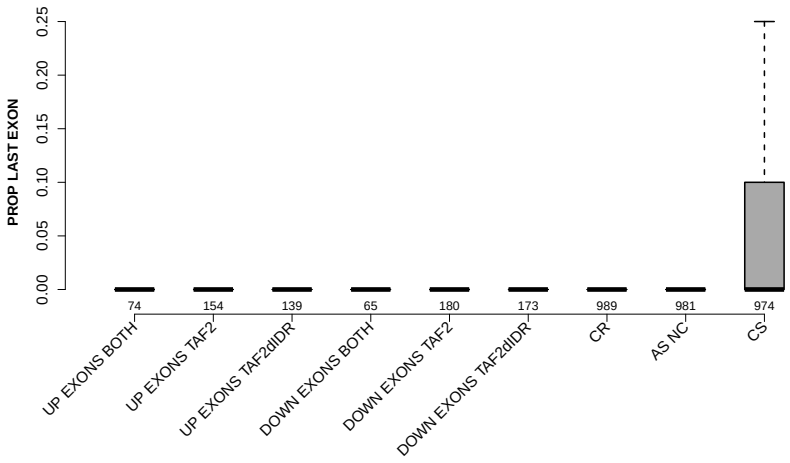
Significant results from Mann-Whitney U test:

- `UP_EXONS_BOTH` vs `CR` : 0.000562603
  mean: 0.0617114 > 0.0186245 , median: 0 = 0
- `UP_EXONS_TAF2` vs `CR` : 1.86301e-06
  mean: 0.050002 > 0.0186245 , median: 0 = 0
- `UP_EXONS_TAF2dIDR` vs `CR` : 0.000580851
  mean: 0.0528993 > 0.0186245 , median: 0 = 0
- `DOWN_EXONS_BOTH` vs `CR` : 0.00336691
  mean: 0.0508858 > 0.0186245 , median: 0 = 0
- `DOWN_EXONS_TAF2` vs `CR` : 1.14305e-05
  mean: 0.0552071 > 0.0186245 , median: 0 = 0
- `DOWN_EXONS_TAF2dIDR` vs `CR` : 2.01076e-06
  mean: 0.0538008 > 0.0186245 , median: 0 = 0
- `CR` vs `AS_NC` : 2.02079e-22
  mean: 0.0186245 < 0.0501965 , median: 0 = 0
- `CR` vs `CS` : 2.71491e-17
  mean: 0.0186245 < 0.0570893 , median: 0 = 0

6.67 PROP LAST EXON

Back to: Overview | ToC

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



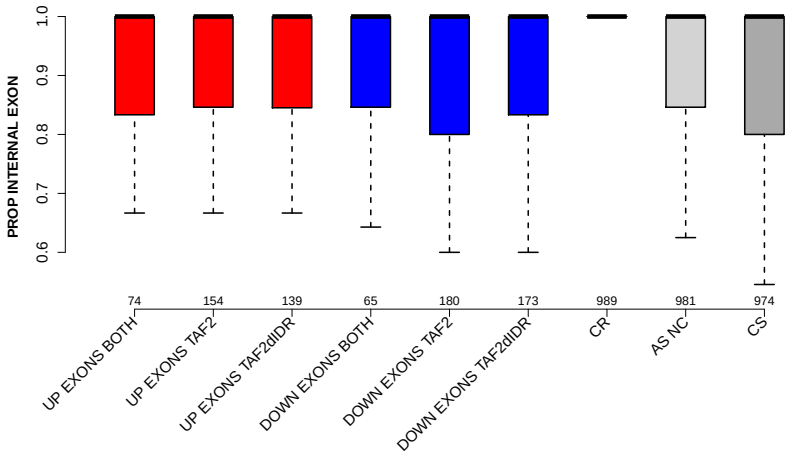
Significant results from Mann-Whitney U test:

- `UP_EXONS_BOTH` vs `CR` : 6.77222e-07
  mean: 0.0612783 > 0.0135426 , median: 0 = 0
- `UP_EXONS_TAF2` vs `CR` : 5.00777e-07
  mean: 0.0379786 > 0.0135426 , median: 0 = 0
- `UP_EXONS_TAF2` vs `CS` : 0.0227779
  mean: 0.0379786 < 0.0648436 , median: 0 = 0
- `UP_EXONS_TAF2dIDR` vs `CR` : 5.97208e-08
  mean: 0.0580468 > 0.0135426 , median: 0 = 0
- `DOWN_EXONS_BOTH` vs `CR` : 7.04215e-05
  mean: 0.043771 > 0.0135426 , median: 0 = 0
- `DOWN_EXONS_TAF2` vs `CR` : 3.5335e-12
  mean: 0.0482259 > 0.0135426 , median: 0 = 0
- `DOWN_EXONS_TAF2dIDR` vs `CR` : 4.76933e-09
  mean: 0.0602372 > 0.0135426 , median: 0 = 0
- `CR` vs `AS_NC` : 3.17694e-25
  mean: 0.0135426 < 0.0468032 , median: 0 = 0
- `CR` vs `CS` : 7.36349e-34
  mean: 0.0135426 < 0.0648436 , median: 0 = 0
- `AS_NC` vs `CS` : 0.014957
  mean: 0.0468032 < 0.0648436 , median: 0 = 0

6.68 PROP INTERNAL EXON

Back to: Overview | ToC

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



Significant results from Mann-Whitney U test:

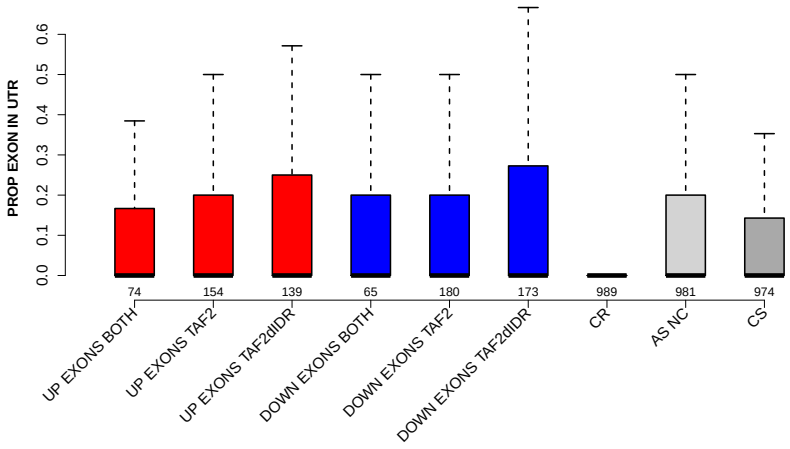
- `UP_EXONS_BOTH` vs `CR` : 9.65439e-08
  mean: 0.87701 < 0.9685 , median: 1 = 1
- `UP_EXONS_TAF2` vs `CR` : 2.10407e-11
  mean: 0.912019 < 0.9685 , median: 1 = 1
- `UP_EXONS_TAF2` vs `CS` : 0.0224197
  mean: 0.912019 > 0.878813 , median: 1 = 1
- `UP_EXONS_TAF2dIDR` vs `CR` : 3.64315e-09
  mean: 0.891281 < 0.9685 , median: 1 = 1
- `UP_EXONS_TAF2dIDR` vs `CS` : 0.0492012
  mean: 0.891281 > 0.878813 , median: 1 = 1
- `DOWN_EXONS_BOTH` vs `CR` : 1.55287e-06
  mean: 0.907266 < 0.9685 , median: 1 = 1
- `DOWN_EXONS_TAF2` vs `CR` : 1.72997e-14
  mean: 0.902222 < 0.9685 , median: 1 = 1
- `DOWN_EXONS_TAF2dIDR` vs `CR` : 3.05834e-12
  mean: 0.888852 < 0.9685 , median: 1 = 1
- `CR` vs `AS_NC` : 2.70646e-40
  mean: 0.9685 > 0.903999 , median: 1 = 1
- `CR` vs `CS` : 1.26316e-49
  mean: 0.9685 > 0.878813 , median: 1 = 1

- `AS_NC` vs `CS` : 0.00929793
  mean: 0.903999 > 0.878813 , median: 1 = 1

6.69 PROP EXON IN UTR

Back to: Overview | ToC

Meaning: NTRS WITH EXON IN UTR / NTRS WITH EXON



Significant results from Mann-Whitney U test:

- `UP_EXONS_BOTH` vs `CR` : 0.000202678
  mean: 0.0998457 > 0.0320912 , median: 0 = 0
- `UP_EXONS_TAF2` vs `CR` : 1.97912e-07
  mean: 0.109251 > 0.0320912 , median: 0 = 0
- `UP_EXONS_TAF2dIDR` vs `CR` : 1.70883e-13
  mean: 0.162536 > 0.0320912 , median: 0 = 0
- `UP_EXONS_TAF2dIDR` vs `CS` : 0.00415122
  mean: 0.162536 > 0.0908769 , median: 0 = 0
- `DOWN_EXONS_BOTH` vs `CR` : 2.02021e-05
  mean: 0.157192 > 0.0320912 , median: 0 = 0
- `DOWN_EXONS_TAF2` vs `CR` : 7.0594e-10
  mean: 0.129475 > 0.0320912 , median: 0 = 0
- `DOWN_EXONS_TAF2dIDR` vs `CR` : 1.12157e-16
  mean: 0.158407 > 0.0320912 , median: 0 = 0
- `DOWN_EXONS_TAF2dIDR` vs `CS` : 0.000848599
  mean: 0.158407 > 0.0908769 , median: 0 = 0
- `CR` vs `AS_NC` : 1.93283e-41
  mean: 0.0320912 < 0.131841 , median: 0 = 0
- `CR` vs `CS` : 4.91851e-16
  mean: 0.0320912 < 0.0908769 , median: 0 = 0

- `AS_NC` vs `CS` : 8.45434e-08
  mean: 0.131841 > 0.0908769 , median: 0 = 0