

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

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Matt version 1.3.0

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1 Infos

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

2 Warning: Please read this note carefully

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

3 Notes for publishing results

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

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

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

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

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

4 Data sets

Input file:

MATT_INPUT_EXONS_TAF2_HeLa.tab

Selection criteria for defining exons groups:

UP_EXONS_TAF2 : having value UP_EXONS_TAF2 in column GROUP

DOWN_EXONS_TAF2 : having value DOWN_EXONS_TAF2 in column GROUP

UP_EXONS_TAF2dIDR : having value UP_EXONS_TAF2dIDR in column GROUP

DOWN_EXONS_TAF2dIDR : having value DOWN_EXONS_TAF2dIDR in column GROUP

CR : having value CR in column GROUP

CS : having value CS in column GROUP

AS_NC : having value AS_NC in column GROUP

Exon duplicates removal: yes

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

UP_EXONS_TAF2: 251 / 239

DOWN_EXONS_TAF2: 275 / 256

UP_EXONS_TAF2dIDR: 234 / 220

DOWN_EXONS_TAF2dIDR: 255 / 244

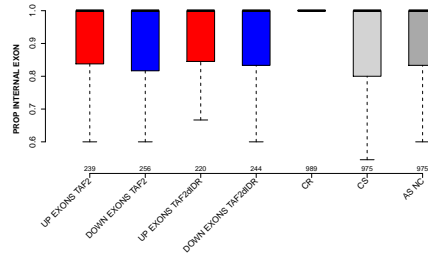
CR: 1000 / 989

CS: 1000 / 975

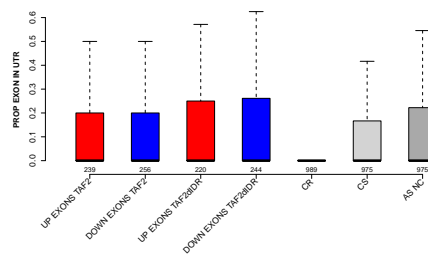
AS_NC: 1000 / 975

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

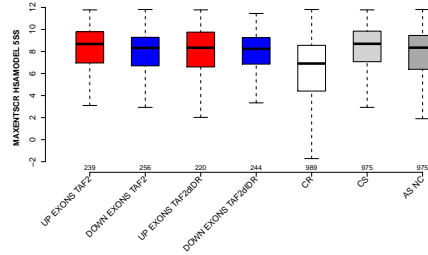
PROP INTERNAL EXON



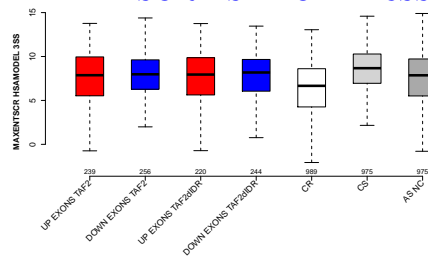
PROP EXON IN UTR



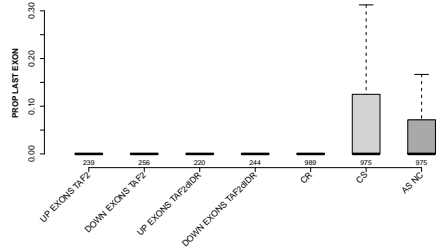
MAXENTSCR HSAMODEL 5SS



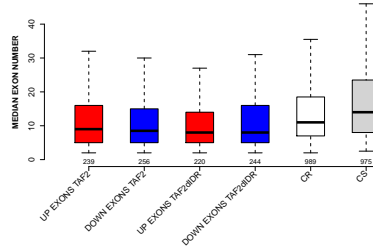
MAXENTSCR HSAMODEL 3SS



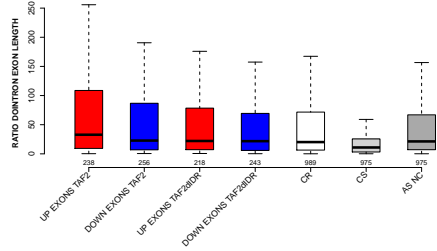
PROP LAST EXON



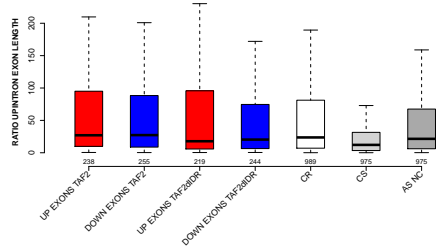
MEDIAN EXON NUMBER



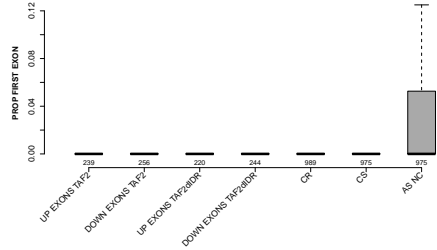
RATIO DONTINON EXON LENGTH



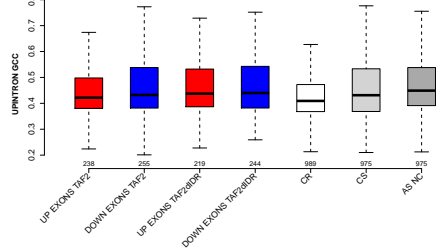
RATIO UPINTRON EXON LENGTH



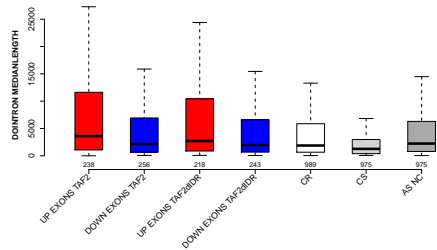
PROP FIRST EXON



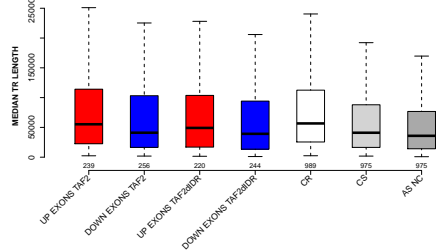
UPINTRON GCC



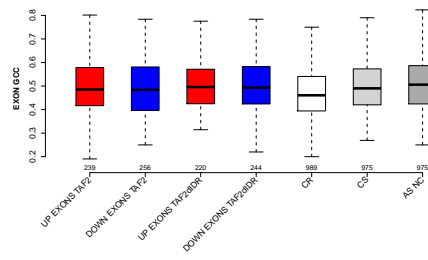
DOINTRON MEDIANLENGTH



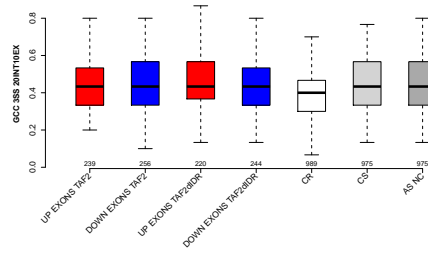
MEDIAN TR LENGTH



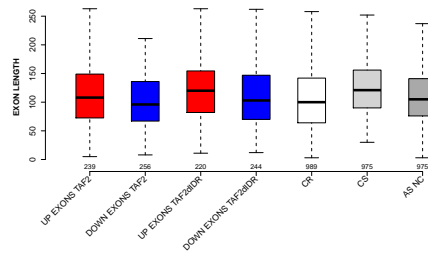
EXON GCC



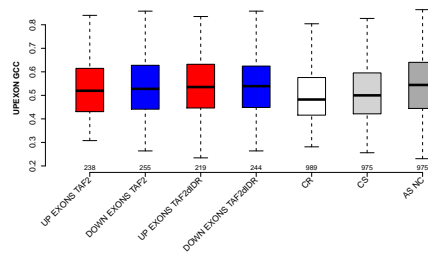
GCC 3SS 20INT10EX



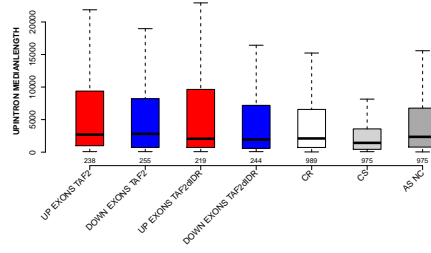
EXON LENGTH



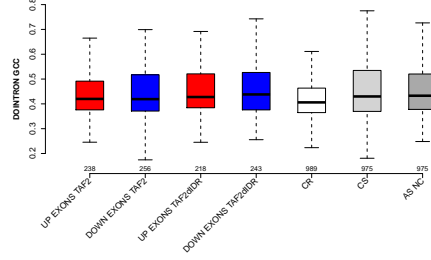
UPEXON GCC



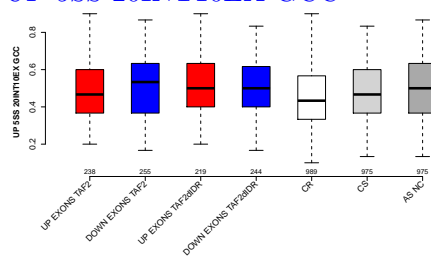
UPINTRON MEDIANLENGTH



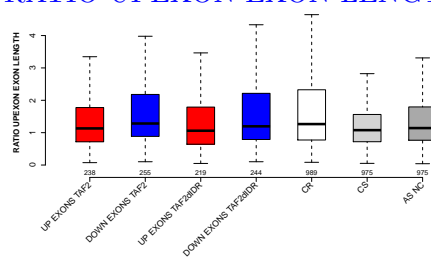
DOINTRON GCC



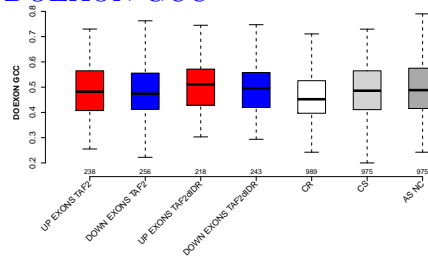
UP 5SS 20INT10EX GCC



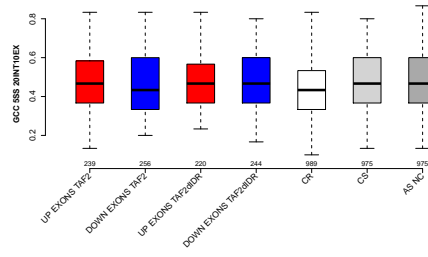
RATIO UPEXON EXON LENGTH



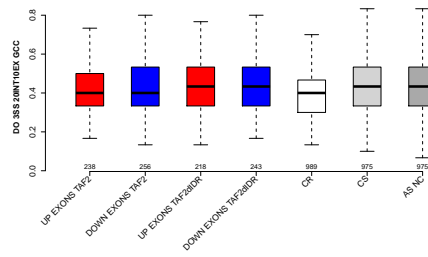
DOEXON GCC



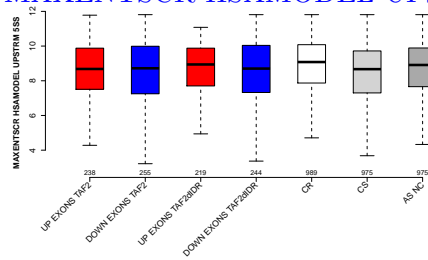
GCC 5SS 20INT10EX



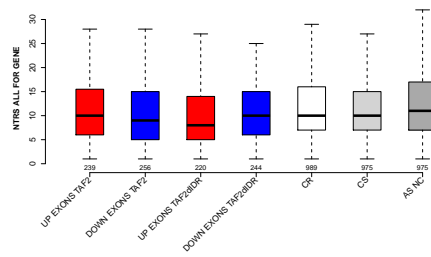
DO 3SS 20INT10EX GCC



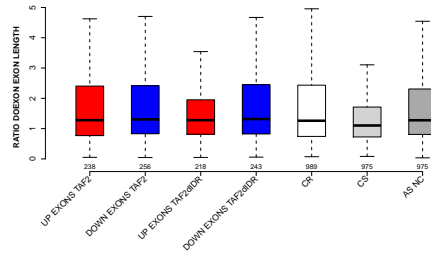
MAXENTSCR HSAMODEL UPSTRM 5SS



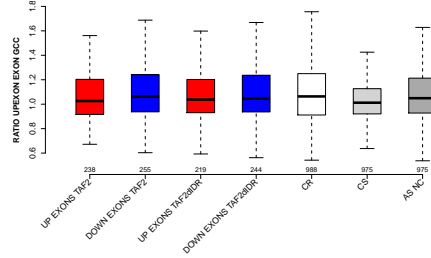
NTRS ALL FOR GENE



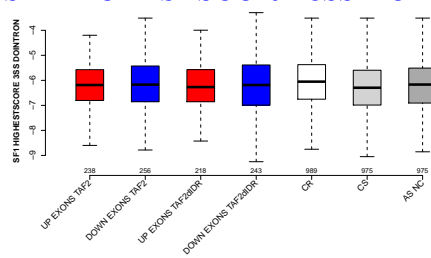
RATIO DOEXON EXON LENGTH



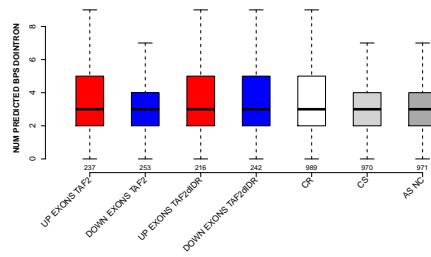
RATIO UPEXON EXON GCC



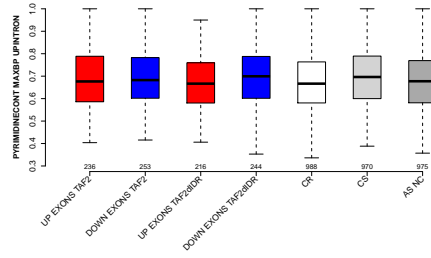
SF1 HIGHESTSCORE 3SS DONTINON



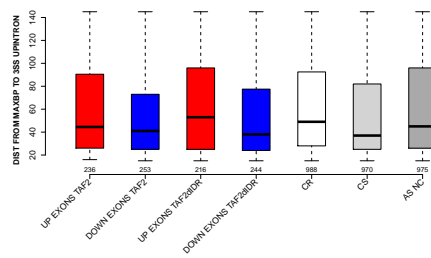
NUM PREDICTED BPS DOWINTRON



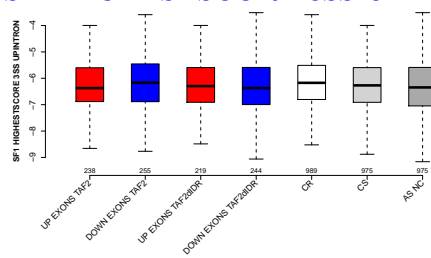
PYRIMIDINECONT MAXBP UPINTRON



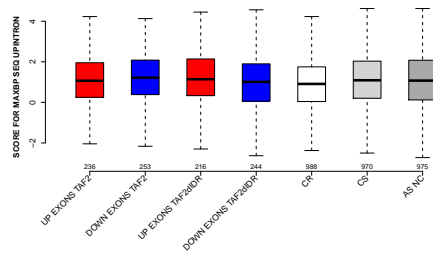
DIST FROM MAXBP TO 3SS UPINTRON



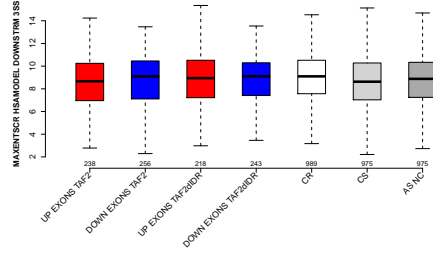
SF1 HIGHESTSCORE 3SS UPINTRON



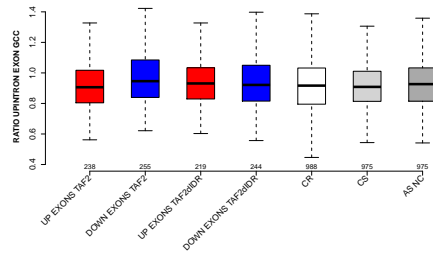
SCORE FOR MAXBP SEQ UPINTRON



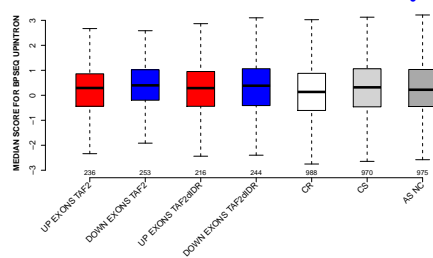
MAXENTSCR HSAMODEL DOWNSTRM 3SS



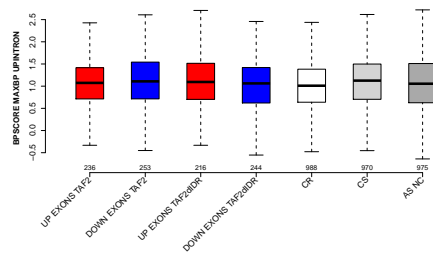
RATIO UPINTRON EXON GCC



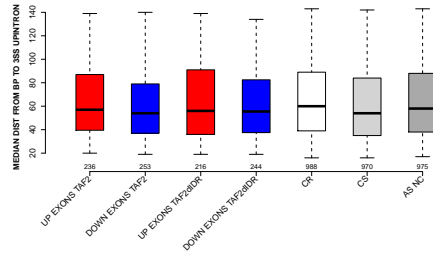
MEDIAN SCORE FOR BPSEQ UPINTRON



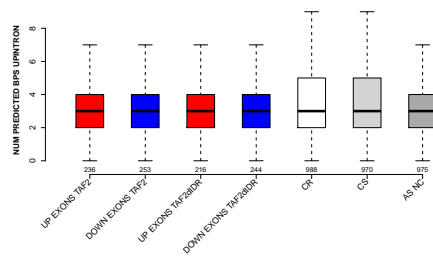
BPSCORE MAXBP UPINTRON



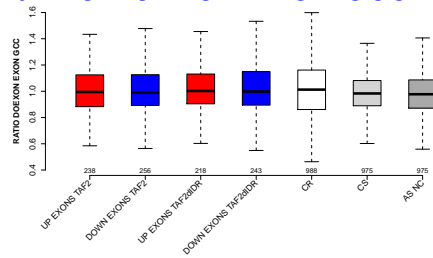
MEDIAN DIST FROM BP TO 3SS UPINTRON



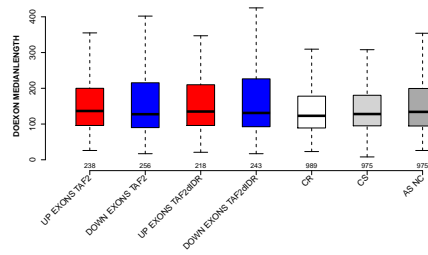
NUM PREDICTED BPS UPINTRON



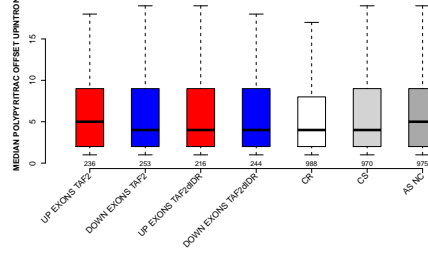
RATIO DOEXON EXON GCC



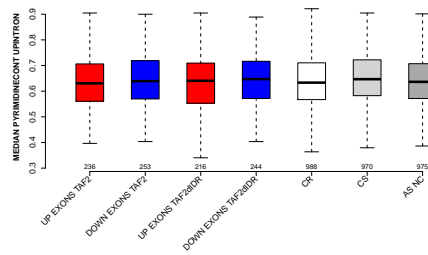
DOEXON MEDIANLENGTH



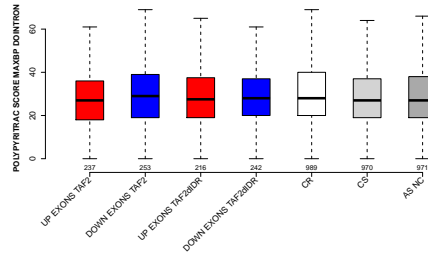
MEDIAN POLYPYRITRAC OFFSET UPINTRON



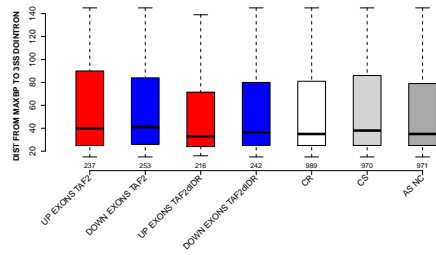
MEDIAN PYRIMIDINECONT UPINTRON



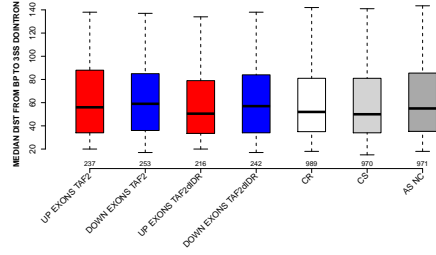
POLYPYRITRAC SCORE MAXBP DOINTRON



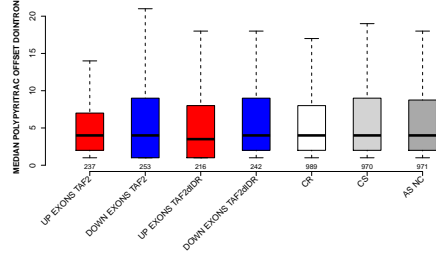
DIST FROM MAXBP TO 3SS DOINTRON



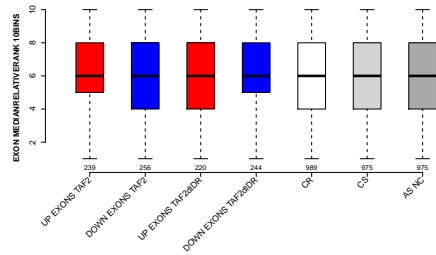
MEDIAN DIST FROM BP TO 3SS DOINTRON



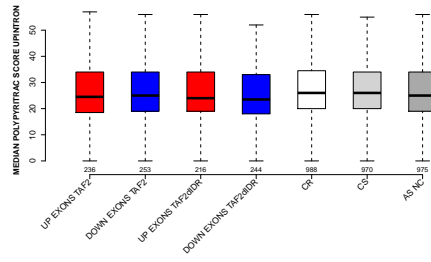
MEDIAN POLYPYRITRAC OFFSET DOINTRON



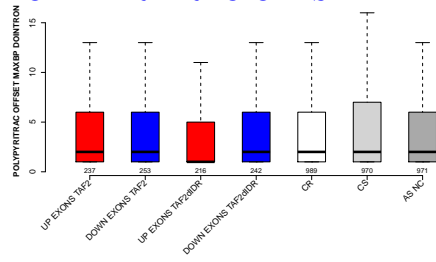
EXON MEDIANRELATIVERANK 10BINS



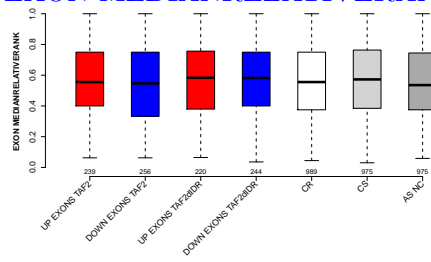
MEDIAN POLYPYRITRAC SCORE UPINTRON



POLYPYRITRAC OFFSET MAXBP DOWINTRON



EXON MEDIANRELATIVERANK

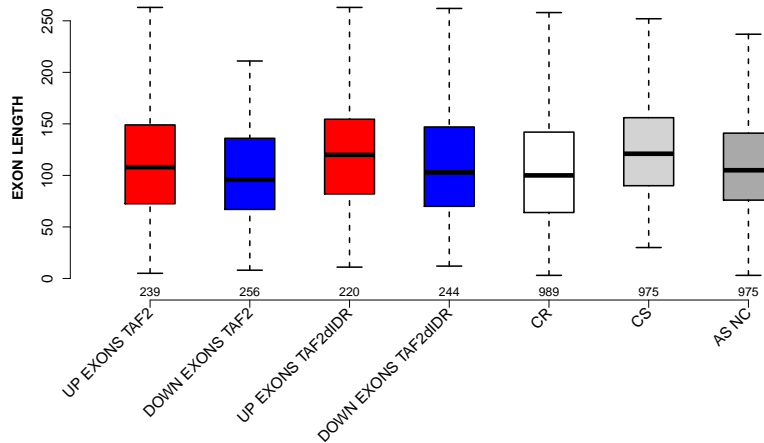


6 Details: Box plots and statistical assessments for all features

6.1 EXON LENGTH

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Meaning:



Significant results from Mann-Whitney U test:

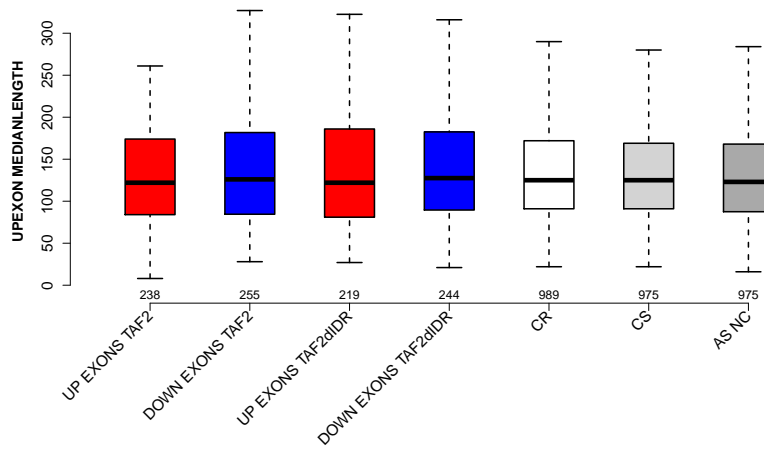
- UP_EXONS_TAF2 vs DOWN_EXONS_TAF2 : 0.0439547
mean: 132.1172 > 119.8789 , median: 108 > 96
- UP_EXONS_TAF2 vs CR : 0.0391829
mean: 132.1172 > 122.4489 , median: 108 > 100
- UP_EXONS_TAF2 vs CS : 0.00282582
mean: 132.1172 < 136.439 , median: 108 < 121
- DOWN_EXONS_TAF2 vs UP_EXONS_TAF2dIDR : 0.000128802
mean: 119.8789 < 156.7273 , median: 96 < 120
- DOWN_EXONS_TAF2 vs CS : 7.01957e-09
mean: 119.8789 < 136.439 , median: 96 < 121
- UP_EXONS_TAF2dIDR vs DOWN_EXONS_TAF2dIDR : 0.0107539
mean: 156.7273 > 135.8975 , median: 120 > 103
- UP_EXONS_TAF2dIDR vs CR : 3.3824e-05
mean: 156.7273 > 122.4489 , median: 120 > 100
- UP_EXONS_TAF2dIDR vs AS_NC : 0.0025018
mean: 156.7273 > 130.7405 , median: 120 > 105

- DOWN_EXONS_TAF2dIDR vs CS : 8.47415e-05
mean: 135.8975 < 136.439 , median: 103 < 121
- CR vs CS : 7.78956e-15
mean: 122.4489 < 136.439 , median: 100 < 121
- CR vs AS_NC : 0.0144618
mean: 122.4489 < 130.7405 , median: 100 < 105
- CS vs AS_NC : 1.50393e-09
mean: 136.439 > 130.7405 , median: 121 > 105

6.2 UPEXON MEDIANLENGTH

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Meaning: median length of up-stream exon



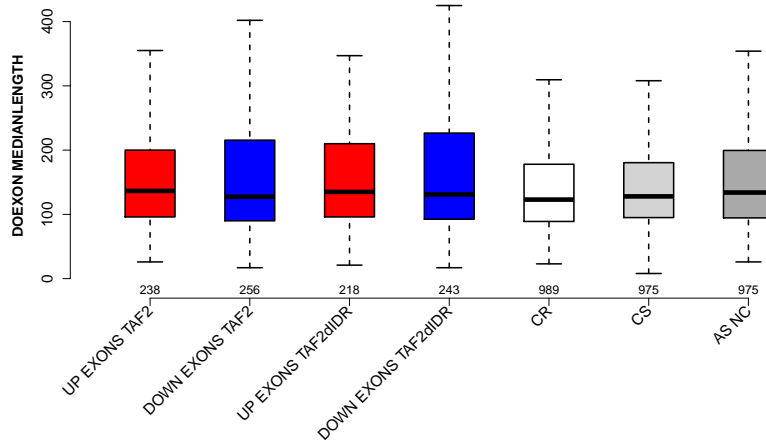
Significant results from Mann-Whitney U test:

- none

6.3 DOEXON MEDIANLENGTH

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Meaning: median length of down-stream exon



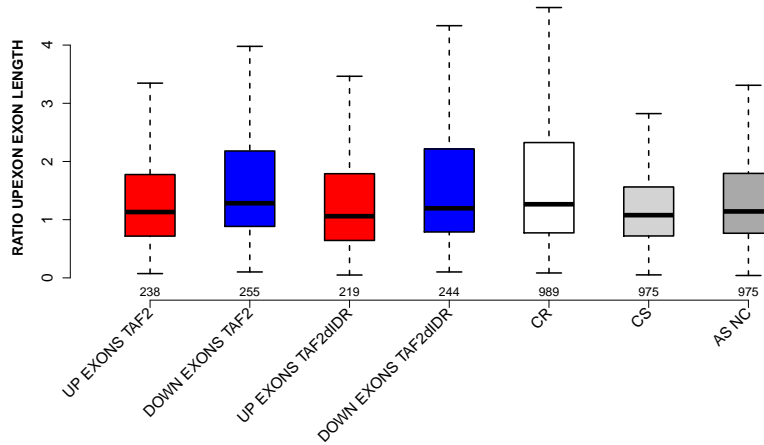
Significant results from Mann-Whitney U test:

- UP_EXONS_TAF2 vs CR : 0.0253166
mean: 343.0126 > 214.4494 , median: 136.5 > 123
- UP_EXONS_TAF2dIDR vs CR : 0.00844088
mean: 305.3784 > 214.4494 , median: 135 > 123
- DOWN_EXONS_TAF2dIDR vs CR : 0.0201404
mean: 278.7407 > 214.4494 , median: 131 > 123
- CR vs AS_NC : 0.00195636
mean: 214.4494 < 253.6615 , median: 123 < 134

6.4 RATIO UPEXON EXON LENGTH

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Meaning: median up-stream exon length / exon length



Significant results from Mann-Whitney U test:

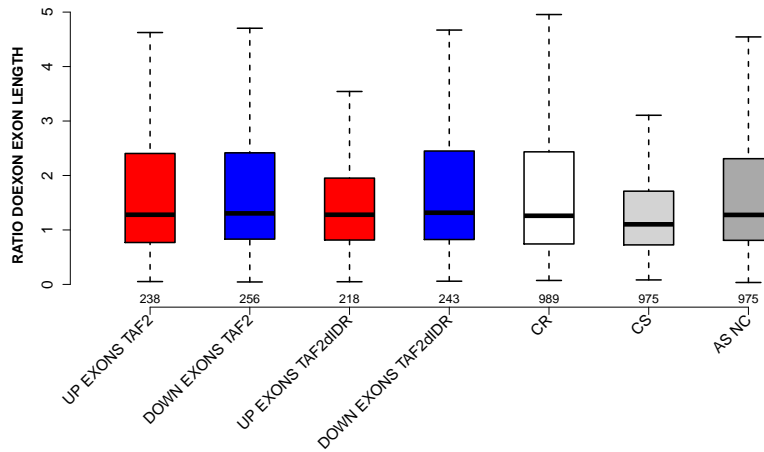
- UP_EXONS_TAF2 vs DOWN_EXONS_TAF2 : 0.01336
mean: 1.8091 < 1.9604 , median: 1.1315 < 1.2827
- UP_EXONS_TAF2 vs CR : 0.0121907
mean: 1.8091 < 2.8807 , median: 1.1315 < 1.2651
- DOWN_EXONS_TAF2 vs UP_EXONS_TAF2dIDR : 0.000627422
mean: 1.9604 > 1.553 , median: 1.2827 > 1.06
- DOWN_EXONS_TAF2 vs CS : 1.13124e-06
mean: 1.9604 > 1.344 , median: 1.2827 > 1.0777
- DOWN_EXONS_TAF2 vs AS_NC : 0.00390398
mean: 1.9604 > 1.6433 , median: 1.2827 > 1.1416
- UP_EXONS_TAF2dIDR vs DOWN_EXONS_TAF2dIDR : 0.0145413
mean: 1.553 < 2.0057 , median: 1.06 < 1.1962
- UP_EXONS_TAF2dIDR vs CR : 0.000486911
mean: 1.553 < 2.8807 , median: 1.06 < 1.2651
- DOWN_EXONS_TAF2dIDR vs CS : 0.000574039
mean: 2.0057 > 1.344 , median: 1.1962 > 1.0777
- CR vs CS : 2.99821e-10
mean: 2.8807 > 1.344 , median: 1.2651 > 1.0777
- CR vs AS_NC : 0.000357305
mean: 2.8807 > 1.6433 , median: 1.2651 > 1.1416

- CS vs AS_NC : 0.003113
mean: 1.344 < 1.6433 , median: 1.0777 < 1.1416

6.5 RATIO DOEXON EXON LENGTH

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Meaning: median down-stream exon length / exon length



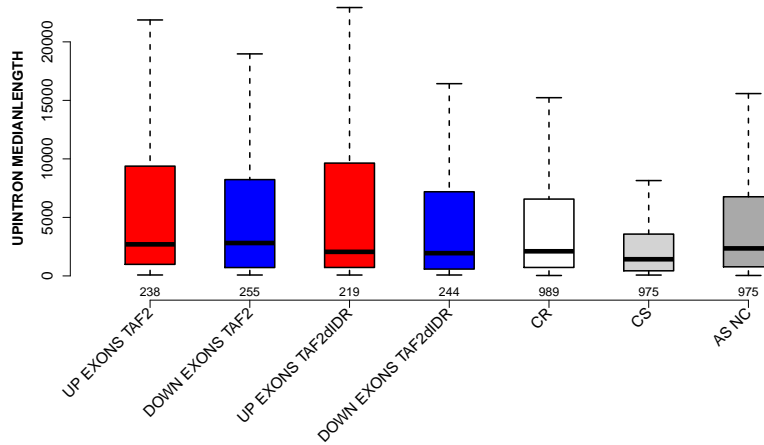
Significant results from Mann-Whitney U test:

- UP_EXONS_TAF2 vs CS : 0.00122404
mean: 3.483 > 2.1532 , median: 1.2792 > 1.1032
- DOWN_EXONS_TAF2 vs CS : 0.000262627
mean: 3.2348 > 2.1532 , median: 1.3043 > 1.1032
- UP_EXONS_TAF2dIDR vs CS : 0.0116085
mean: 2.7238 > 2.1532 , median: 1.2792 > 1.1032
- DOWN_EXONS_TAF2dIDR vs CS : 0.000103871
mean: 3.2573 > 2.1532 , median: 1.3158 > 1.1032
- CR vs CS : 4.88433e-05
mean: 3.4659 > 2.1532 , median: 1.26 > 1.1032
- CS vs AS_NC : 4.46541e-07
mean: 2.1532 < 2.6903 , median: 1.1032 < 1.2759

6.6 UPINTRON MEDIANLENGTH

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Meaning: median length of up-stream introns



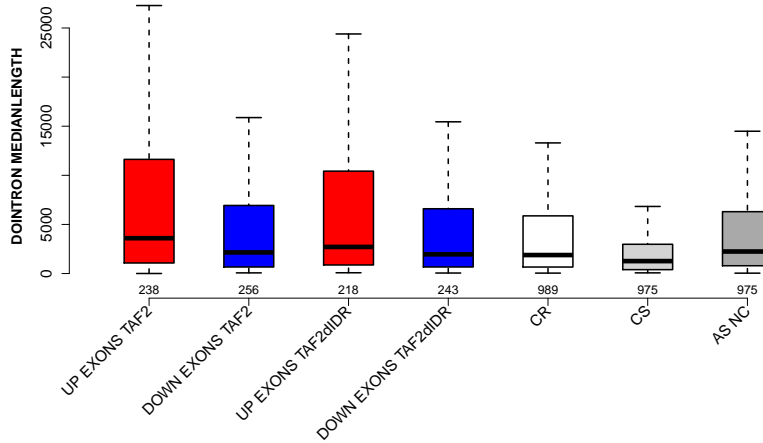
Significant results from Mann-Whitney U test:

- UP_EXONS_TAF2 vs DOWN_EXONS_TAF2dIDR : 0.0281325
mean: 10540.9748 > 7938.9467 , median: 2698.5 > 1944
- UP_EXONS_TAF2 vs CR : 0.0153526
mean: 10540.9748 > 7454.4813 , median: 2698.5 > 2105
- UP_EXONS_TAF2 vs CS : 1.56034e-11
mean: 10540.9748 > 4192.2123 , median: 2698.5 > 1424
- UP_EXONS_TAF2 vs AS_NC : 0.0347486
mean: 10540.9748 > 7070.2631 , median: 2698.5 > 2352
- DOWN_EXONS_TAF2 vs CS : 1.30513e-08
mean: 8743.9843 > 4192.2123 , median: 2810 > 1424
- UP_EXONS_TAF2dIDR vs CS : 5.90098e-07
mean: 11000.1438 > 4192.2123 , median: 2056 > 1424
- DOWN_EXONS_TAF2dIDR vs CS : 6.18304e-05
mean: 7938.9467 > 4192.2123 , median: 1944 > 1424
- CR vs CS : 1.13332e-12
mean: 7454.4813 > 4192.2123 , median: 2105 > 1424
- CS vs AS_NC : 5.47075e-14
mean: 4192.2123 < 7070.2631 , median: 1424 < 2352

6.7 DOINTRON MEDIANLENGTH

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Meaning: median length of down-stream introns



Significant results from Mann-Whitney U test:

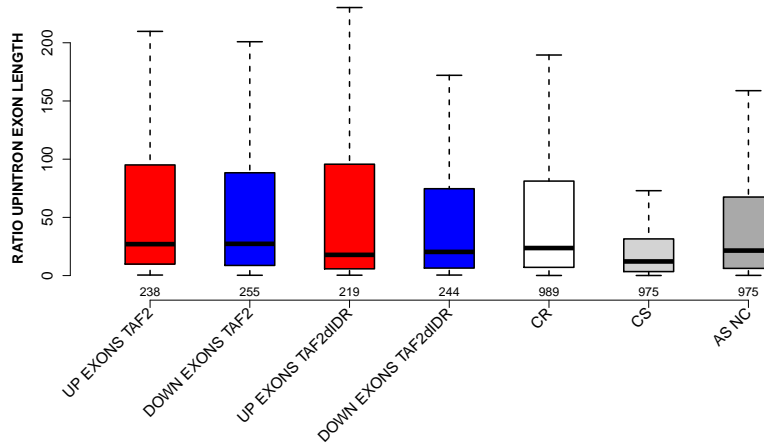
- UP_EXONS_TAF2 vs DOWN_EXONS_TAF2 : 0.00563142
mean: 9540.5336 > 9162 , median: 3597 > 2150.5
- UP_EXONS_TAF2 vs DOWN_EXONS_TAF2dIDR : 0.00312555
mean: 9540.5336 > 8830.1955 , median: 3597 > 1959.5
- UP_EXONS_TAF2 vs CR : 9.09904e-06
mean: 9540.5336 > 6964.5359 , median: 3597 > 1883
- UP_EXONS_TAF2 vs CS : 8.2532e-19
mean: 9540.5336 > 3469.8682 , median: 3597 > 1266
- UP_EXONS_TAF2 vs AS_NC : 0.000406405
mean: 9540.5336 > 6827.9262 , median: 3597 > 2242
- DOWN_EXONS_TAF2 vs CS : 1.01841e-07
mean: 9162 > 3469.8682 , median: 2150.5 > 1266
- UP_EXONS_TAF2dIDR vs CR : 0.00275499
mean: 8876.0298 > 6964.5359 , median: 2709 > 1883
- UP_EXONS_TAF2dIDR vs CS : 4.48405e-13
mean: 8876.0298 > 3469.8682 , median: 2709 > 1266
- UP_EXONS_TAF2dIDR vs AS_NC : 0.0343911
mean: 8876.0298 > 6827.9262 , median: 2709 > 2242
- DOWN_EXONS_TAF2dIDR vs CS : 6.79239e-07
mean: 8830.1955 > 3469.8682 , median: 1959.5 > 1266

- CR vs CS : $7.98293\text{e-}13$
mean: 6964.5359 > 3469.8682 , median: 1883 > 1266
- CS vs AS_NC : $3.34316\text{e-}19$
mean: 3469.8682 < 6827.9262 , median: 1266 < 2242

6.8 RATIO UPINTRON EXON LENGTH

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Meaning: median up-stream intron length / exon length



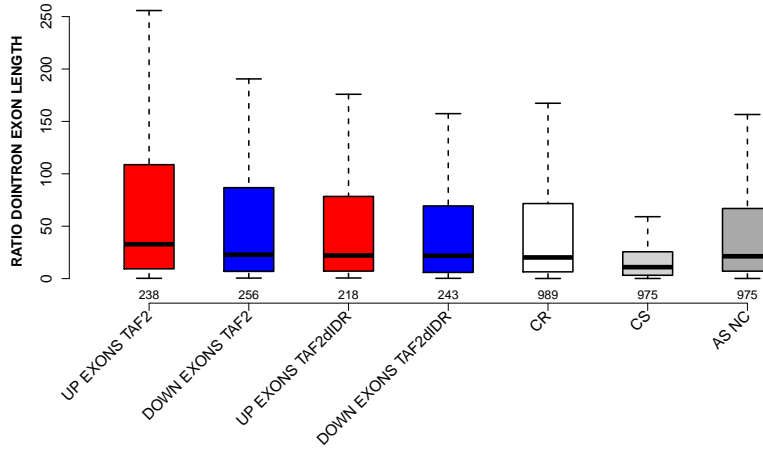
Significant results from Mann-Whitney U test:

- UP_EXONS_TAF2 vs CS : 2.07564e-14
mean: 103.9441 > 38.5547 , median: 27.0098 > 12.1389
- UP_EXONS_TAF2 vs AS_NC : 0.0247406
mean: 103.9441 > 79.0827 , median: 27.0098 > 21.4894
- DOWN_EXONS_TAF2 vs CS : 1.10678e-13
mean: 98.9601 > 38.5547 , median: 27.2677 > 12.1389
- UP_EXONS_TAF2dIDR vs CS : 3.0327e-06
mean: 111.604 > 38.5547 , median: 17.7967 > 12.1389
- DOWN_EXONS_TAF2dIDR vs CS : 4.31711e-07
mean: 96.8487 > 38.5547 , median: 20.3489 > 12.1389
- CR vs CS : 6.781e-23
mean: 115.2639 > 38.5547 , median: 23.6667 > 12.1389
- CS vs AS_NC : 8.63794e-18
mean: 38.5547 < 79.0827 , median: 12.1389 < 21.4894

6.9 RATIO DOWNTON EXON LENGTH

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Meaning: median down-stream intron length / exon length



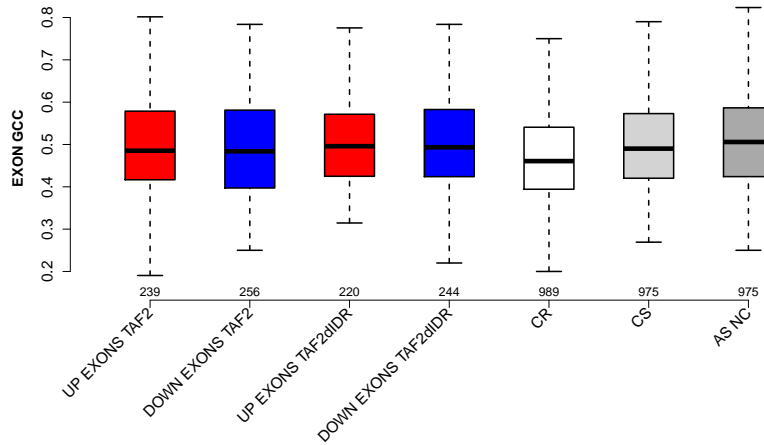
Significant results from Mann-Whitney U test:

- UP_EXONS_TAF2 vs DOWN_EXONS_TAF2 : 0.0486655
mean: 102.7776 < 108.9834 , median: 32.7924 > 22.7676
- UP_EXONS_TAF2 vs DOWN_EXONS_TAF2dIDR : 0.0132441
mean: 102.7776 > 88.9593 , median: 32.7924 > 21.7753
- UP_EXONS_TAF2 vs CR : 0.00193384
mean: 102.7776 < 126.3174 , median: 32.7924 > 20.1944
- UP_EXONS_TAF2 vs CS : 3.18047e-21
mean: 102.7776 > 30.7186 , median: 32.7924 > 10.9298
- UP_EXONS_TAF2 vs AS_NC : 0.000874553
mean: 102.7776 > 75.3214 , median: 32.7924 > 21.324
- DOWN_EXONS_TAF2 vs CS : 2.86577e-12
mean: 108.9834 > 30.7186 , median: 22.7676 > 10.9298
- UP_EXONS_TAF2dIDR vs CS : 1.3087e-11
mean: 86.9808 > 30.7186 , median: 22.073 > 10.9298
- DOWN_EXONS_TAF2dIDR vs CS : 2.33986e-10
mean: 88.9593 > 30.7186 , median: 21.7753 > 10.9298
- CR vs CS : 1.79274e-23
mean: 126.3174 > 30.7186 , median: 20.1944 > 10.9298
- CS vs AS_NC : 2.33453e-24
mean: 30.7186 < 75.3214 , median: 10.9298 < 21.324

6.10 EXON GCC

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Meaning: GC content of entire exon sequence



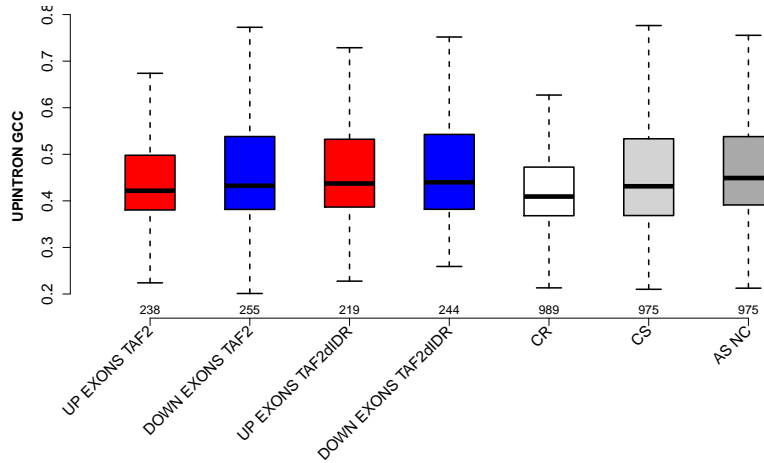
Significant results from Mann-Whitney U test:

- UP_EXONS_TAF2 vs CR : 0.000765651
mean: 0.495189 > 0.467211 , median: 0.485294 > 0.460733
- DOWN_EXONS_TAF2 vs CR : 0.0105512
mean: 0.49005 > 0.467211 , median: 0.483871 > 0.460733
- DOWN_EXONS_TAF2 vs AS_NC : 0.0213582
mean: 0.49005 < 0.508014 , median: 0.483871 < 0.505882
- UP_EXONS_TAF2dIDR vs CR : 5.90943e-05
mean: 0.501028 > 0.467211 , median: 0.495925 > 0.460733
- DOWN_EXONS_TAF2dIDR vs CR : 0.000115689
mean: 0.498434 > 0.467211 , median: 0.49339 > 0.460733
- CR vs CS : 1.96564e-09
mean: 0.467211 < 0.496929 , median: 0.460733 < 0.490196
- CR vs AS_NC : 1.08001e-15
mean: 0.467211 < 0.508014 , median: 0.460733 < 0.505882
- CS vs AS_NC : 0.0270368
mean: 0.496929 < 0.508014 , median: 0.490196 < 0.505882

6.11 UPINTRON GCC

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Meaning: GC content of entire up-stream intron sequence



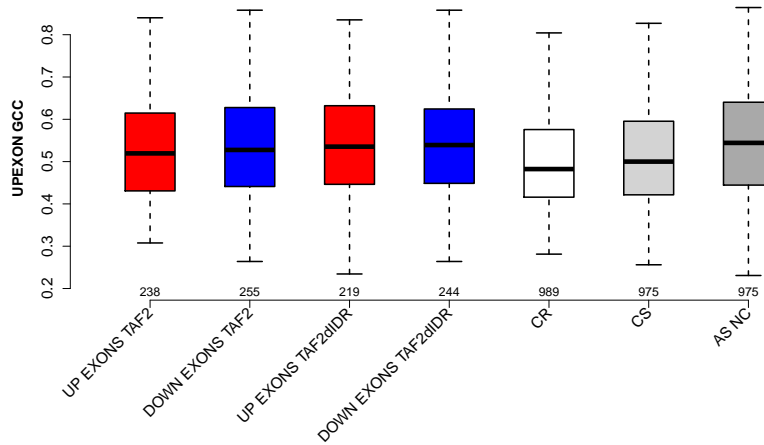
Significant results from Mann-Whitney U test:

- UP_EXONS_TAF2 vs CR : 0.00294742
mean: 0.448702 > 0.425179 , median: 0.421736 > 0.409258
- UP_EXONS_TAF2 vs AS_NC : 0.00267706
mean: 0.448702 < 0.469666 , median: 0.421736 < 0.449019
- DOWN_EXONS_TAF2 vs CR : 4.42313e-06
mean: 0.463756 > 0.425179 , median: 0.432338 > 0.409258
- UP_EXONS_TAF2dIDR vs CR : 9.00721e-07
mean: 0.465765 > 0.425179 , median: 0.437334 > 0.409258
- DOWN_EXONS_TAF2dIDR vs CR : 2.43929e-06
mean: 0.462969 > 0.425179 , median: 0.439965 > 0.409258
- CR vs CS : 1.92517e-07
mean: 0.425179 < 0.453929 , median: 0.409258 < 0.431347
- CR vs AS_NC : 8.55295e-21
mean: 0.425179 < 0.469666 , median: 0.409258 < 0.449019
- CS vs AS_NC : 0.000513981
mean: 0.453929 < 0.469666 , median: 0.431347 < 0.449019

6.12 UPEXON GCC

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Meaning: GC content of entire up-stream exon sequence



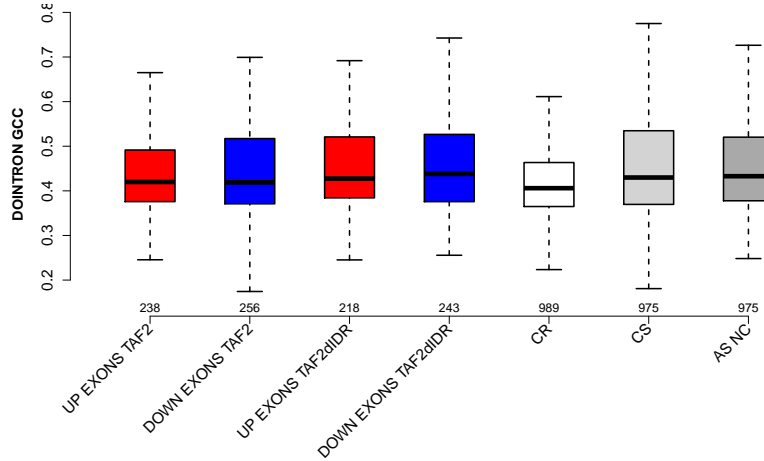
Significant results from Mann-Whitney U test:

- UP_EXONS_TAF2 vs CR : 0.00645386
mean: 0.527072 > 0.503835 , median: 0.519434 > 0.482353
- UP_EXONS_TAF2 vs AS_NC : 0.0329457
mean: 0.527072 < 0.544063 , median: 0.519434 < 0.544218
- DOWN_EXONS_TAF2 vs CR : 7.3167e-05
mean: 0.53618 > 0.503835 , median: 0.527586 > 0.482353
- DOWN_EXONS_TAF2 vs CS : 0.00265821
mean: 0.53618 > 0.509265 , median: 0.527586 > 0.5
- UP_EXONS_TAF2dIDR vs CR : 3.07329e-05
mean: 0.540008 > 0.503835 , median: 0.535354 > 0.482353
- UP_EXONS_TAF2dIDR vs CS : 0.00109562
mean: 0.540008 > 0.509265 , median: 0.535354 > 0.5
- DOWN_EXONS_TAF2dIDR vs CR : 1.56887e-05
mean: 0.536582 > 0.503835 , median: 0.539143 > 0.482353
- DOWN_EXONS_TAF2dIDR vs CS : 0.000949341
mean: 0.536582 > 0.509265 , median: 0.539143 > 0.5
- CR vs AS_NC : 1.71171e-14
mean: 0.503835 < 0.544063 , median: 0.482353 < 0.544218
- CS vs AS_NC : 4.10281e-10
mean: 0.509265 < 0.544063 , median: 0.5 < 0.544218

6.13 DOINTRON GCC

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Meaning: GC content of entire down-stream intron sequence



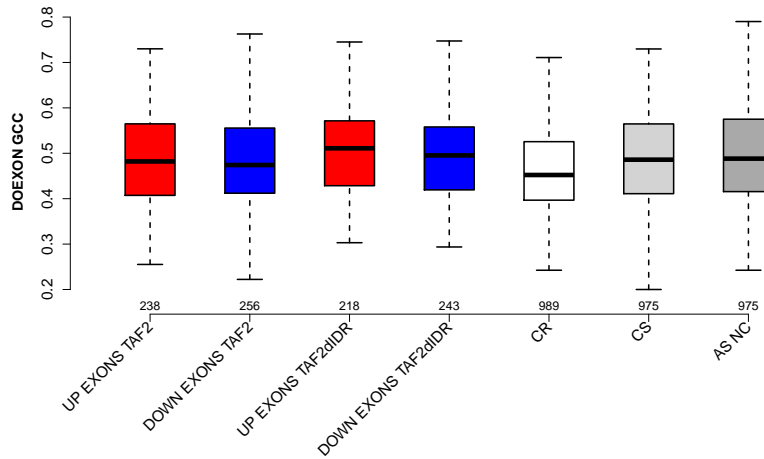
Significant results from Mann-Whitney U test:

- UP_EXONS_TAF2 vs CR : 0.00222039
mean: 0.444184 > 0.421146 , median: 0.419886 > 0.405979
- DOWN_EXONS_TAF2 vs CR : 0.00262272
mean: 0.446379 > 0.421146 , median: 0.419096 > 0.405979
- UP_EXONS_TAF2dIDR vs CR : 5.35259e-06
mean: 0.455708 > 0.421146 , median: 0.427586 > 0.405979
- DOWN_EXONS_TAF2dIDR vs CR : 1.05207e-05
mean: 0.453961 > 0.421146 , median: 0.438 > 0.405979
- CR vs CS : 4.42945e-09
mean: 0.421146 < 0.455097 , median: 0.405979 < 0.429864
- CR vs AS_NC : 1.44284e-12
mean: 0.421146 < 0.454997 , median: 0.405979 < 0.432836

6.14 DOEXON GCC

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Meaning: GC content of entire down-stream exon sequence



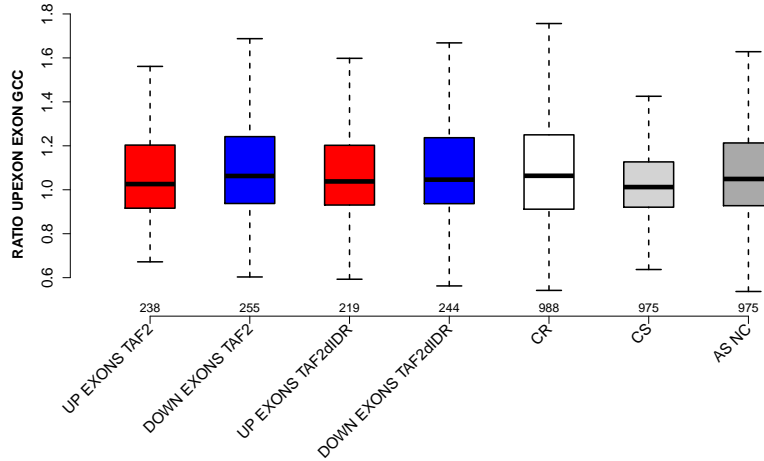
Significant results from Mann-Whitney U test:

- UP_EXONS_TAF2 vs CR : 0.00160709
mean: 0.488385 > 0.466494 , median: 0.48198 > 0.452174
- DOWN_EXONS_TAF2 vs UP_EXONS_TAF2dIDR : 0.0475036
mean: 0.485424 < 0.50401 , median: 0.474106 < 0.510953
- DOWN_EXONS_TAF2 vs CR : 0.00173631
mean: 0.485424 > 0.466494 , median: 0.474106 > 0.452174
- UP_EXONS_TAF2dIDR vs CR : 1.16941e-07
mean: 0.50401 > 0.466494 , median: 0.510953 > 0.452174
- UP_EXONS_TAF2dIDR vs CS : 0.0429119
mean: 0.50401 > 0.488822 , median: 0.510953 > 0.485915
- DOWN_EXONS_TAF2dIDR vs CR : 3.12743e-06
mean: 0.497229 > 0.466494 , median: 0.495294 > 0.452174
- CR vs CS : 1.36501e-07
mean: 0.466494 < 0.488822 , median: 0.452174 < 0.485915
- CR vs AS_NC : 4.48423e-10
mean: 0.466494 < 0.494469 , median: 0.452174 < 0.488189

6.15 RATIO UPEXON EXON GCC

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Meaning: UPEXON GCC / EXON GCC



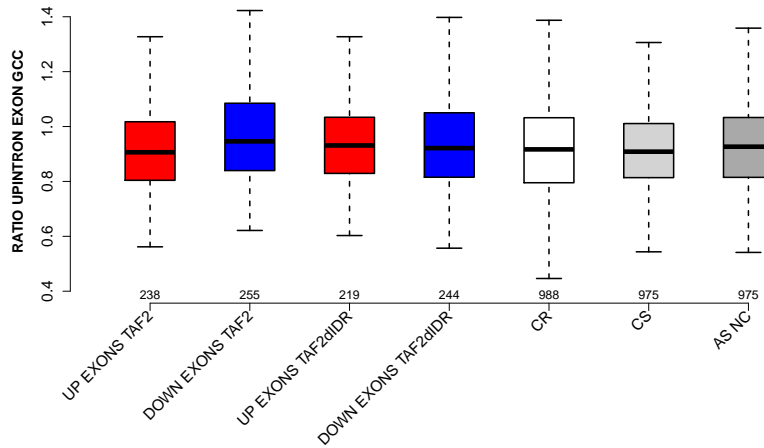
Significant results from Mann-Whitney U test:

- DOWN_EXONS_TAF2 vs CS : 0.000210334
mean: 1.1318 > 1.0385 , median: 1.0628 > 1.0122
- UP_EXONS_TAF2dIDR vs CS : 0.0226995
mean: 1.1022 > 1.0385 , median: 1.0379 > 1.0122
- DOWN_EXONS_TAF2dIDR vs CS : 0.00137964
mean: 1.1127 > 1.0385 , median: 1.046 > 1.0122
- CR vs CS : 2.92826e-06
mean: 1.1195 > 1.0385 , median: 1.0636 > 1.0122
- CS vs AS_NC : 1.64723e-05
mean: 1.0385 < 1.0966 , median: 1.0122 < 1.0491

6.16 RATIO UPINTRON EXON GCC

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Meaning: UPINTRON GCC / EXON GCC



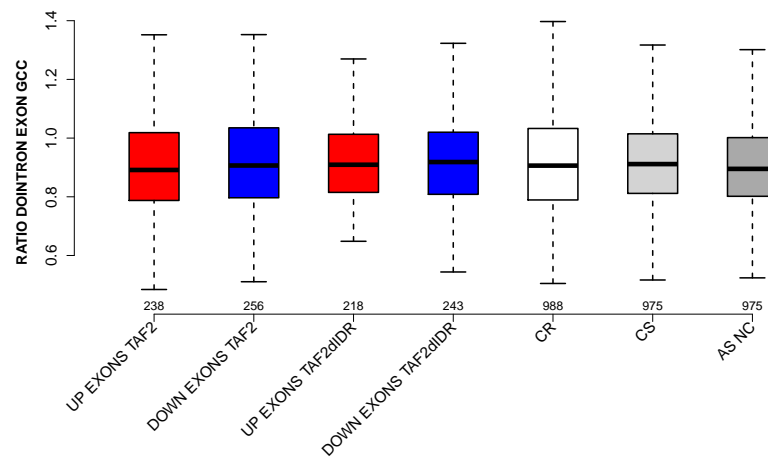
Significant results from Mann-Whitney U test:

- UP_EXONS_TAF2 vs DOWN_EXONS_TAF2 : 0.00374929
mean: 0.921704 < 0.96392 , median: 0.906199 < 0.94601
- DOWN_EXONS_TAF2 vs CR : 0.00388372
mean: 0.96392 > 0.93507 , median: 0.94601 > 0.916773
- DOWN_EXONS_TAF2 vs CS : 0.000317688
mean: 0.96392 > 0.918537 , median: 0.94601 > 0.908418
- DOWN_EXONS_TAF2 vs AS_NC : 0.022033
mean: 0.96392 > 0.93809 , median: 0.94601 > 0.926547

6.17 RATIO DOINTRON EXON GCC

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Meaning: DOINTRON GCC / EXON GCC



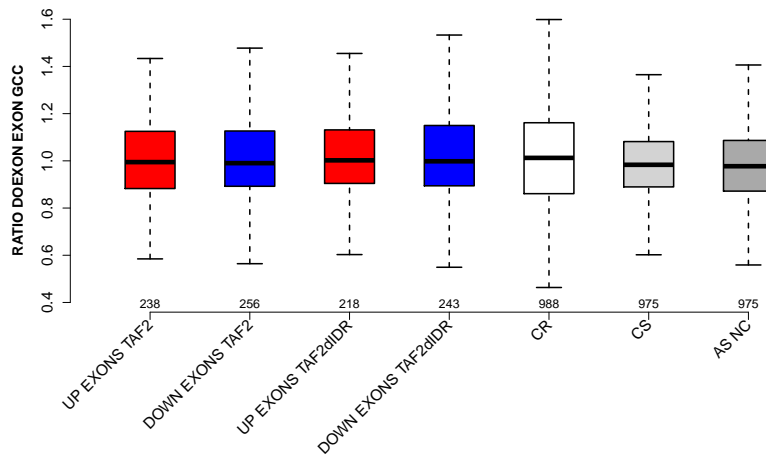
Significant results from Mann-Whitney U test:

- none

6.18 RATIO DOEXON EXON GCC

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Meaning: DOEXON GCC / EXON GCC



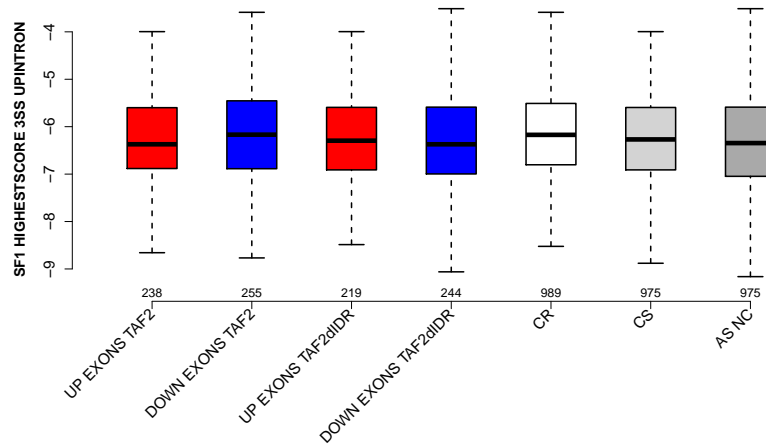
Significant results from Mann-Whitney U test:

- UP_EXONS_TAF2dIDR vs CS : 0.0370682
mean: 1.0259 > 0.995716 , median: 1.0022 > 0.983232
- UP_EXONS_TAF2dIDR vs AS_NC : 0.0091863
mean: 1.0259 > 0.990407 , median: 1.0022 > 0.977208
- DOWN_EXONS_TAF2dIDR vs AS_NC : 0.0387332
mean: 1.0278 > 0.990407 , median: 0.998174 > 0.977208
- CR vs CS : 0.0165655
mean: 1.0332 > 0.995716 , median: 1.0125 > 0.983232
- CR vs AS_NC : 0.00115402
mean: 1.0332 > 0.990407 , median: 1.0125 > 0.977208

6.19 SF1 HIGHESTSCORE 3SS UPINTRON

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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



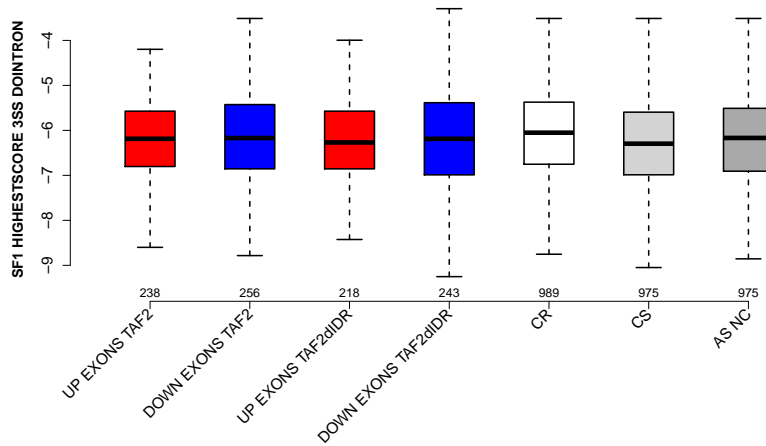
Significant results from Mann-Whitney U test:

- UP_EXONS_TAF2 vs CR : 0.0330878
mean: -6.27676 < -6.13032 , median: -6.37099 < -6.17225
- DOWN_EXONS_TAF2dIDR vs CR : 0.00917635
mean: -6.31153 < -6.13032 , median: -6.37142 < -6.17225
- CR vs CS : 0.0301947
mean: -6.13032 > -6.24475 , median: -6.17225 > -6.26872
- CR vs AS_NC : 4.91987e-05
mean: -6.13032 > -6.32583 , median: -6.17225 > -6.34598

6.20 SF1 HIGHESTSCORE 3SS DOWINTRON

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



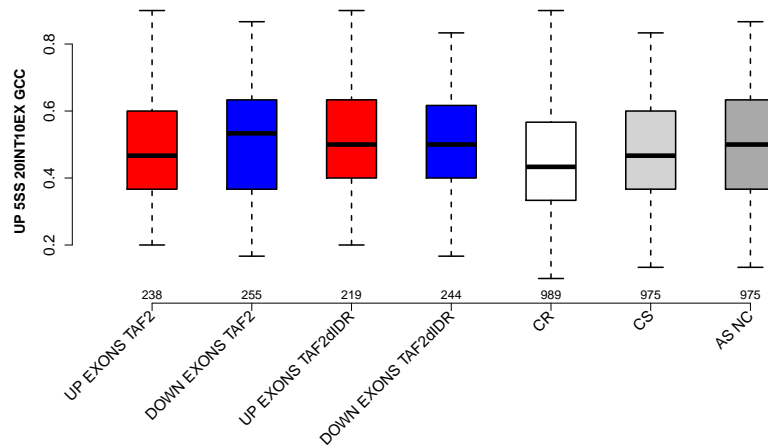
Significant results from Mann-Whitney U test:

- UP_EXONS_TAF2dIDR vs CR : 0.0499153
mean: -6.201 < -6.06511 , median: -6.26872 < -6.05147
- CR vs CS : 4.32869e-06
mean: -6.06511 > -6.29498 , median: -6.05147 > -6.29538
- CR vs AS_NC : 0.00735414
mean: -6.06511 > -6.19824 , median: -6.05147 > -6.1683

6.21 UP 5SS 20INT10EX GCC

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



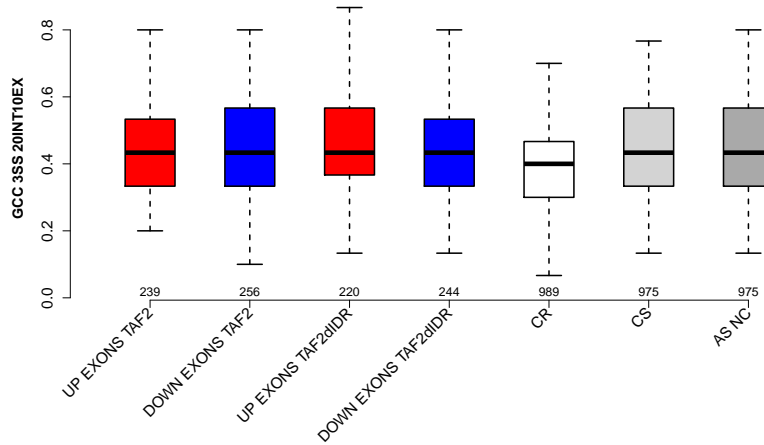
Significant results from Mann-Whitney U test:

- UP_EXONS_TAF2 vs CR : 0.0149628
mean: 0.490126 > 0.46215 , median: 0.466667 > 0.433333
- DOWN_EXONS_TAF2 vs CR : 0.000139668
mean: 0.505359 > 0.46215 , median: 0.533333 > 0.433333
- DOWN_EXONS_TAF2 vs CS : 0.0385738
mean: 0.505359 > 0.480188 , median: 0.533333 > 0.466667
- UP_EXONS_TAF2dIDR vs CR : 0.000252025
mean: 0.504871 > 0.46215 , median: 0.5 > 0.433333
- DOWN_EXONS_TAF2dIDR vs CR : 5.03043e-05
mean: 0.505123 > 0.46215 , median: 0.5 > 0.433333
- DOWN_EXONS_TAF2dIDR vs CS : 0.0248181
mean: 0.505123 > 0.480188 , median: 0.5 > 0.466667
- CR vs CS : 0.00527455
mean: 0.46215 < 0.480188 , median: 0.433333 < 0.466667
- CR vs AS_NC : 8.01664e-11
mean: 0.46215 < 0.507675 , median: 0.433333 < 0.5
- CS vs AS_NC : 0.000158363
mean: 0.480188 < 0.507675 , median: 0.466667 < 0.5

6.22 GCC 3SS 20INT10EX

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



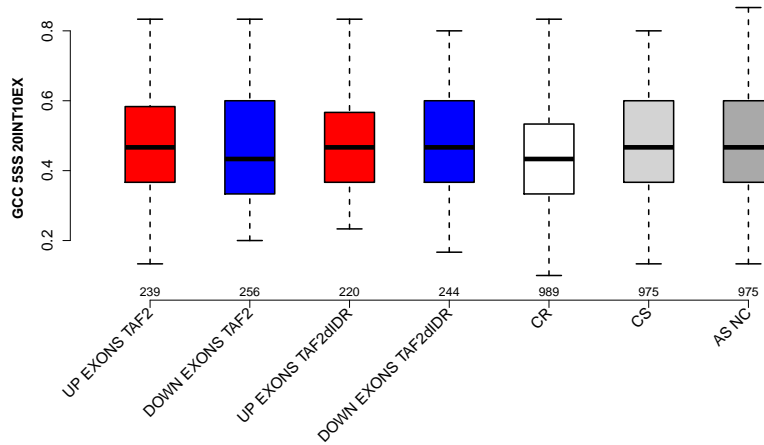
Significant results from Mann-Whitney U test:

- UP_EXONS_TAF2 vs CR : 7.90885e-06
mean: 0.442817 > 0.397742 , median: 0.433333 > 0.4
- DOWN_EXONS_TAF2 vs CR : 9.52554e-06
mean: 0.443229 > 0.397742 , median: 0.433333 > 0.4
- UP_EXONS_TAF2dIDR vs CR : 2.9587e-08
mean: 0.455152 > 0.397742 , median: 0.433333 > 0.4
- DOWN_EXONS_TAF2dIDR vs CR : 3.24629e-06
mean: 0.444399 > 0.397742 , median: 0.433333 > 0.4
- CR vs CS : 9.27503e-12
mean: 0.397742 < 0.442154 , median: 0.4 < 0.433333
- CR vs AS_NC : 4.72057e-15
mean: 0.397742 < 0.447761 , median: 0.4 < 0.433333

6.23 GCC 5SS 20INT10EX

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



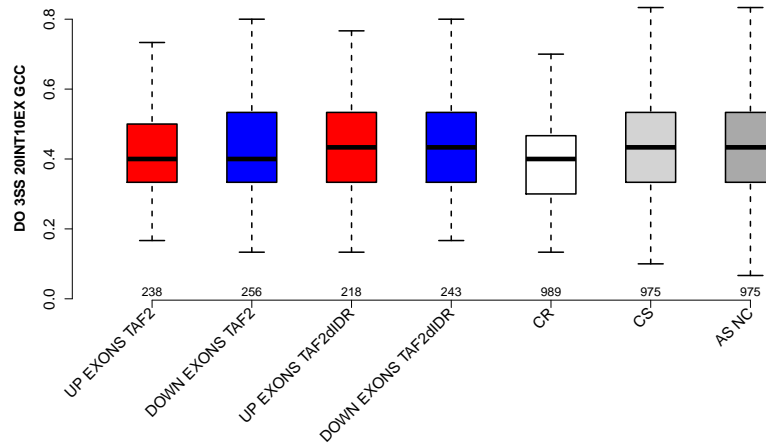
Significant results from Mann-Whitney U test:

- UP_EXONS_TAF2 vs CR : 0.0038584
mean: 0.466806 > 0.434884 , median: 0.466667 > 0.433333
- DOWN_EXONS_TAF2 vs CR : 0.028002
mean: 0.4625 > 0.434884 , median: 0.433333 = 0.433333
- UP_EXONS_TAF2dIDR vs CR : 1.87723e-05
mean: 0.480606 > 0.434884 , median: 0.466667 > 0.433333
- DOWN_EXONS_TAF2dIDR vs CR : 0.000851851
mean: 0.468169 > 0.434884 , median: 0.466667 > 0.433333
- CR vs CS : 4.04717e-07
mean: 0.434884 < 0.46906 , median: 0.433333 < 0.466667
- CR vs AS_NC : 1.38232e-09
mean: 0.434884 < 0.474462 , median: 0.433333 < 0.466667

6.24 DO 3SS 20INT10EX GCC

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



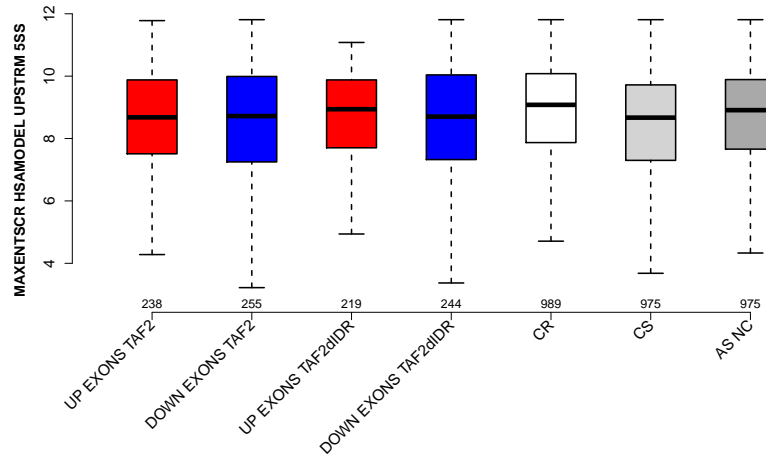
Significant results from Mann-Whitney U test:

- UP_EXONS_TAF2 vs CR : 0.004527
mean: 0.427311 > 0.402022 , median: 0.4 = 0.4
- DOWN_EXONS_TAF2 vs CR : 0.0074089
mean: 0.430924 > 0.402022 , median: 0.4 = 0.4
- UP_EXONS_TAF2dIDR vs CR : 0.000218721
mean: 0.437615 > 0.402022 , median: 0.433333 > 0.4
- DOWN_EXONS_TAF2dIDR vs CR : 0.00144992
mean: 0.433745 > 0.402022 , median: 0.433333 > 0.4
- CR vs CS : 1.88493e-09
mean: 0.402022 < 0.438308 , median: 0.4 < 0.433333
- CR vs AS_NC : 3.34544e-08
mean: 0.402022 < 0.43535 , median: 0.4 < 0.433333

6.25 MAXENTSCR HSAMODEL UPSTRM 5SS

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



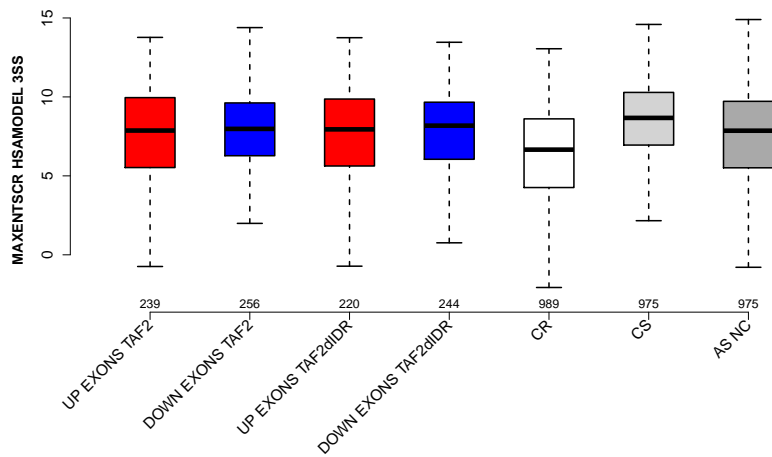
Significant results from Mann-Whitney U test:

- UP_EXONS_TAF2 vs CR : 0.0228766
mean: 8.4229 < 8.7046 , median: 8.68 < 9.08
- DOWN_EXONS_TAF2 vs CR : 0.0203978
mean: 8.2381 < 8.7046 , median: 8.72 < 9.08
- UP_EXONS_TAF2dIDR vs CS : 0.0326245
mean: 8.5027 > 8.1443 , median: 8.94 > 8.67
- DOWN_EXONS_TAF2dIDR vs CR : 0.0148963
mean: 8.2104 < 8.7046 , median: 8.7025 < 9.08
- CR vs CS : 9.32892e-09
mean: 8.7046 > 8.1443 , median: 9.08 > 8.67
- CS vs AS_NC : 7.43271e-05
mean: 8.1443 < 8.5168 , median: 8.67 < 8.91

6.26 MAXENTSCR HSAMODEL 3SS

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



Significant results from Mann-Whitney U test:

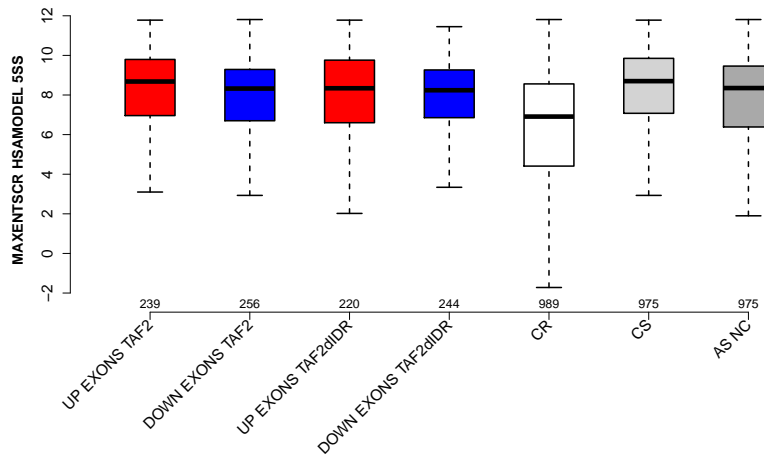
- UP_EXONS_TAF2 vs CR : 3.4701e-07
mean: 7.2557 > 5.9481 , median: 7.87 > 6.66
- UP_EXONS_TAF2 vs CS : 6.6433e-05
mean: 7.2557 < 8.3015 , median: 7.87 < 8.67
- DOWN_EXONS_TAF2 vs CR : 2.4349e-10
mean: 7.5355 > 5.9481 , median: 7.975 > 6.66
- DOWN_EXONS_TAF2 vs CS : 0.000139896
mean: 7.5355 < 8.3015 , median: 7.975 < 8.67
- UP_EXONS_TAF2dIDR vs CR : 6.6899e-08
mean: 7.311 > 5.9481 , median: 7.945 > 6.66
- UP_EXONS_TAF2dIDR vs CS : 0.000663019
mean: 7.311 < 8.3015 , median: 7.945 < 8.67
- DOWN_EXONS_TAF2dIDR vs CR : 7.7401e-10
mean: 7.4417 > 5.9481 , median: 8.18 > 6.66
- DOWN_EXONS_TAF2dIDR vs CS : 0.000512573
mean: 7.4417 < 8.3015 , median: 8.18 < 8.67
- CR vs CS : 4.43837e-51
mean: 5.9481 < 8.3015 , median: 6.66 < 8.67
- CR vs AS_NC : 1.84342e-14
mean: 5.9481 < 7.091 , median: 6.66 < 7.86

- CS vs AS_NC : 4.21667e-12
mean: 8.3015 > 7.091 , median: 8.67 > 7.86

6.27 MAXENTSCR HSAMODEL 5SS

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



Significant results from Mann-Whitney U test:

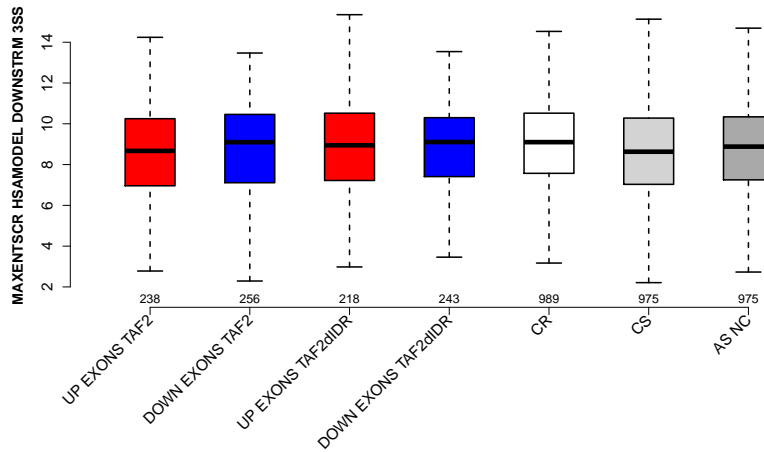
- UP_EXONS_TAF2 vs DOWN_EXONS_TAF2dIDR : 0.0498329
mean: 7.842 < 7.8552 , median: 8.68 > 8.24
- UP_EXONS_TAF2 vs CR : 1.09437e-18
mean: 7.842 > 6.0635 , median: 8.68 > 6.91
- UP_EXONS_TAF2 vs AS_NC : 0.0124058
mean: 7.842 > 7.4267 , median: 8.68 > 8.35
- DOWN_EXONS_TAF2 vs CR : 2.701e-13
mean: 7.4786 > 6.0635 , median: 8.325 > 6.91
- DOWN_EXONS_TAF2 vs CS : 0.000976618
mean: 7.4786 < 8.1169 , median: 8.325 < 8.7
- UP_EXONS_TAF2dIDR vs CR : 2.63803e-11
mean: 7.3772 > 6.0635 , median: 8.34 > 6.91
- UP_EXONS_TAF2dIDR vs CS : 0.0108604
mean: 7.3772 < 8.1169 , median: 8.34 < 8.7
- DOWN_EXONS_TAF2dIDR vs CR : 2.42387e-14
mean: 7.8552 > 6.0635 , median: 8.24 > 6.91
- DOWN_EXONS_TAF2dIDR vs CS : 0.000835459
mean: 7.8552 < 8.1169 , median: 8.24 < 8.7
- CR vs CS : 3.91278e-54
mean: 6.0635 < 8.1169 , median: 6.91 < 8.7

- CR vs AS_NC : 5.24513e-27
mean: 6.0635 < 7.4267 , median: 6.91 < 8.35
- CS vs AS_NC : 6.66362e-08
mean: 8.1169 > 7.4267 , median: 8.7 > 8.35

6.28 MAXENTSCR HSAMODEL DOWNSTRM 3SS

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



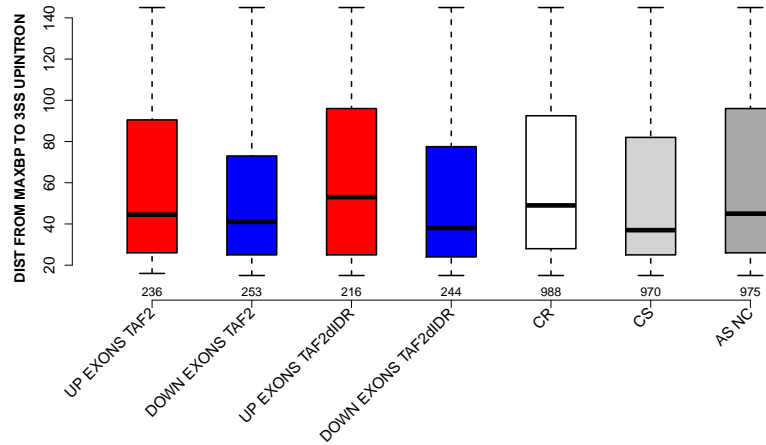
Significant results from Mann-Whitney U test:

- UP_EXONS_TAF2 vs CR : 0.0227406
mean: 8.3161 < 8.8813 , median: 8.67 < 9.1
- CR vs CS : 0.00025107
mean: 8.8813 > 8.4742 , median: 9.1 > 8.63
- CR vs AS_NC : 0.021983
mean: 8.8813 > 8.6556 , median: 9.1 > 8.88

6.29 DIST FROM MAXBP TO 3SS UPINTRON

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Meaning: distance to 3ss of best precited BP



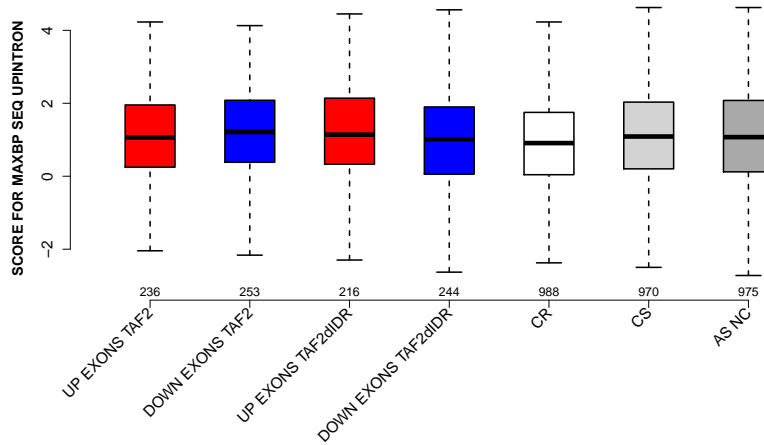
Significant results from Mann-Whitney U test:

- DOWN_EXONS_TAF2 vs UP_EXONS_TAF2dIDR : 0.037155
mean: 53.9289 < 62.8889 , median: 41 < 53
- DOWN_EXONS_TAF2 vs CR : 0.00418314
mean: 53.9289 < 61.7895 , median: 41 < 49
- UP_EXONS_TAF2dIDR vs DOWN_EXONS_TAF2dIDR : 0.0325875
mean: 62.8889 > 54.8525 , median: 53 > 38
- UP_EXONS_TAF2dIDR vs CS : 0.020203
mean: 62.8889 > 55.3268 , median: 53 > 37
- DOWN_EXONS_TAF2dIDR vs CR : 0.00357495
mean: 54.8525 < 61.7895 , median: 38 < 49
- DOWN_EXONS_TAF2dIDR vs AS_NC : 0.0378227
mean: 54.8525 < 60.6082 , median: 38 < 45
- CR vs CS : 2.88861e-05
mean: 61.7895 > 55.3268 , median: 49 > 37
- CS vs AS_NC : 0.00586998
mean: 55.3268 < 60.6082 , median: 37 < 45

6.30 SCORE FOR MAXBP SEQ UPINTRON

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Meaning: BP sequence score of best predicted BP



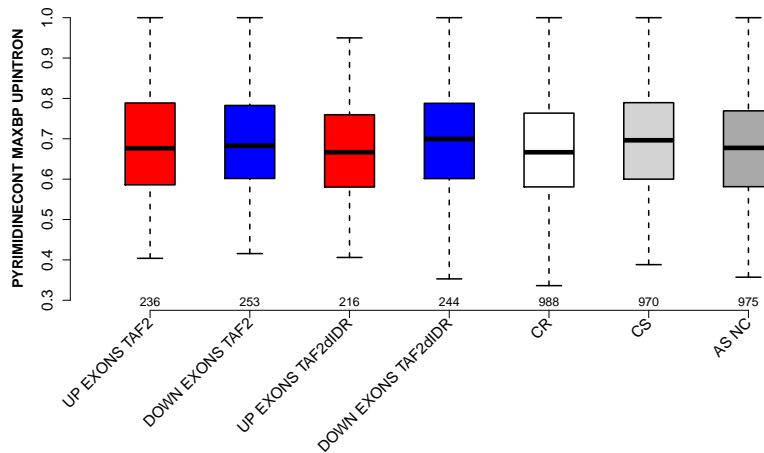
Significant results from Mann-Whitney U test:

- DOWN_EXONS_TAF2 vs CR : 0.00108368
mean: 1.191 > 0.895028 , median: 1.2142 > 0.908554
- UP_EXONS_TAF2dIDR vs CR : 0.00130193
mean: 1.2218 > 0.895028 , median: 1.1408 > 0.908554
- CR vs CS : 0.000184444
mean: 0.895028 < 1.1308 , median: 0.908554 < 1.0889
- CR vs AS_NC : 0.000943299
mean: 0.895028 < 1.1135 , median: 0.908554 < 1.0723

6.31 PYRIMIDINECONT MAXBP UPINTRON

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



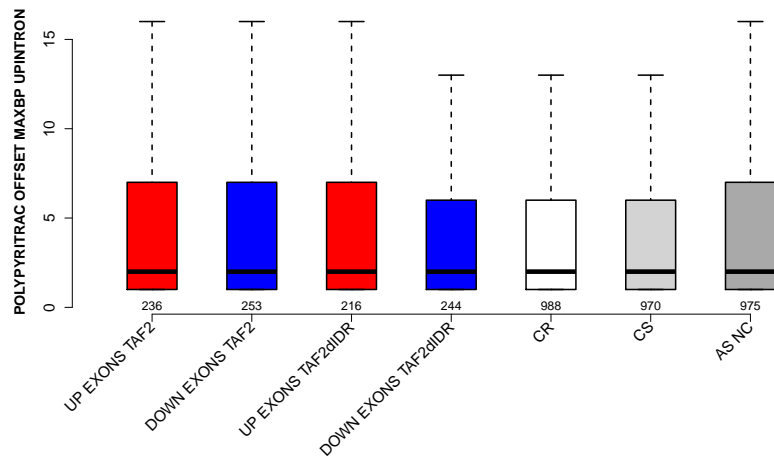
Significant results from Mann-Whitney U test:

- DOWN_EXONS_TAF2 vs CR : 0.0409494
mean: 0.692208 > 0.673727 , median: 0.68254 > 0.666667
- UP_EXONS_TAF2dIDR vs DOWN_EXONS_TAF2dIDR : 0.0361929
mean: 0.671915 < 0.694621 , median: 0.666667 < 0.699462
- UP_EXONS_TAF2dIDR vs CS : 0.00596257
mean: 0.671915 < 0.699287 , median: 0.666667 < 0.696311
- DOWN_EXONS_TAF2dIDR vs CR : 0.0112456
mean: 0.694621 > 0.673727 , median: 0.699462 > 0.666667
- CR vs CS : 1.81279e-05
mean: 0.673727 < 0.699287 , median: 0.666667 < 0.696311
- CS vs AS_NC : 0.000638481
mean: 0.699287 > 0.678683 , median: 0.696311 > 0.677419

6.32 POLYPYRITRAC OFFSET MAXBP UPINTRON

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



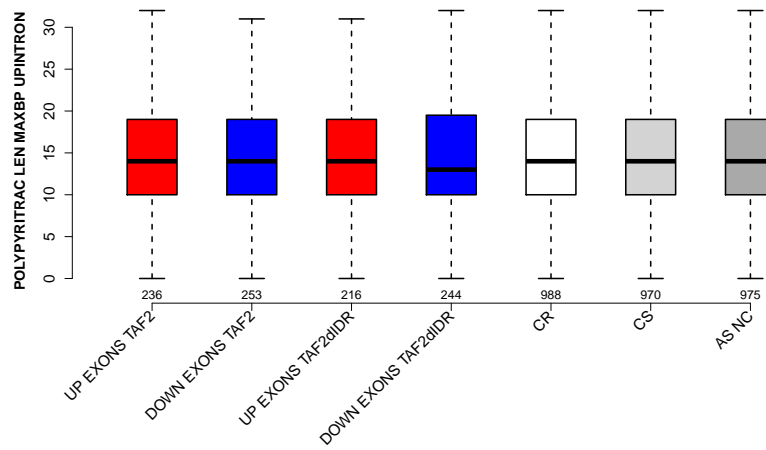
Significant results from Mann-Whitney U test:

- none

6.33 POLYPYRITRAC LEN MAXBP UPINTRON

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Meaning: Polypyrimidine track length for best BP



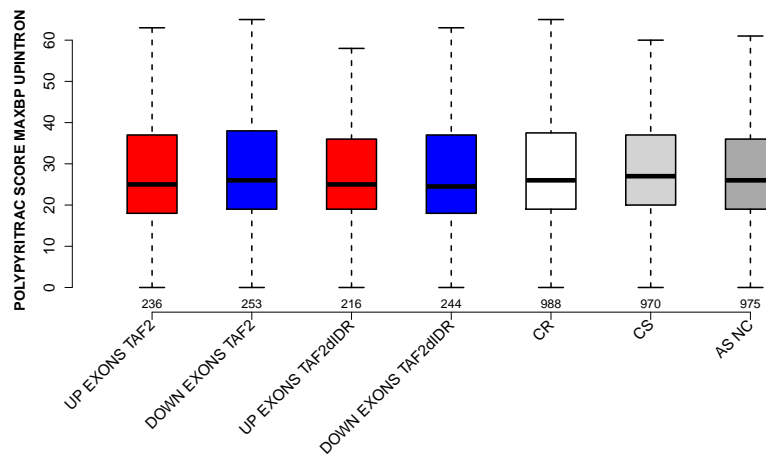
Significant results from Mann-Whitney U test:

- none

6.34 POLYPYRITRAC SCORE MAXBP UPINTRON

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Meaning: Polypyrimidine track score for best BP



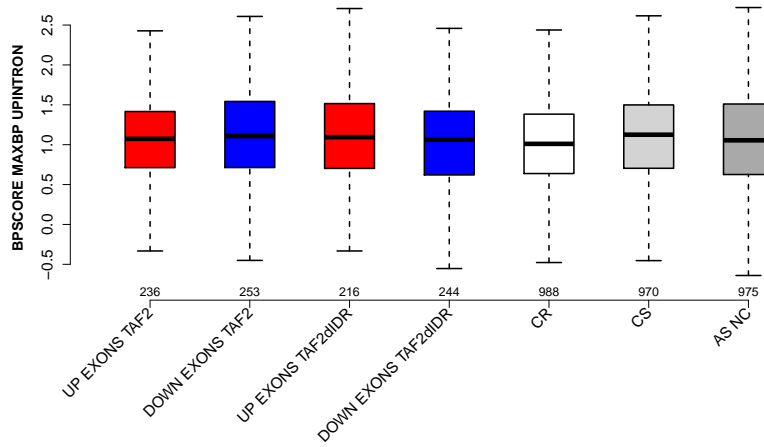
Significant results from Mann-Whitney U test:

- none

6.35 BPSCORE MAXBP UPINTRON

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Meaning: SVM classification score of best BP



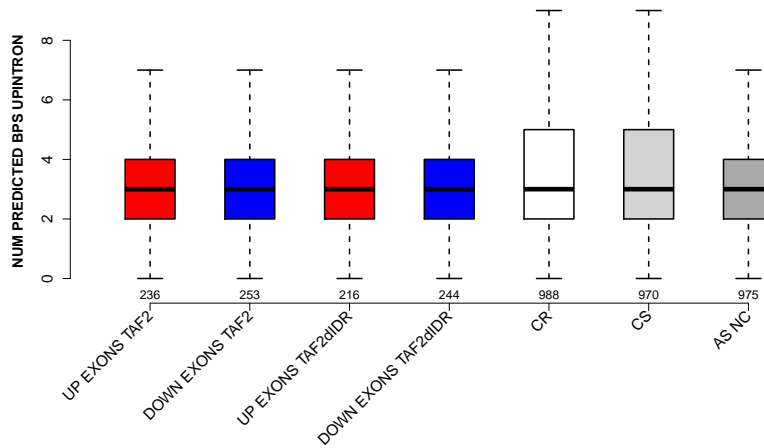
Significant results from Mann-Whitney U test:

- DOWN_EXONS_TAF2 vs CR : 0.0153165
mean: 1.0507 > 0.975256 , median: 1.1083 > 1.0103
- CR vs CS : 0.000645467
mean: 0.975256 < 1.0585 , median: 1.0103 < 1.125
- CR vs AS_NC : 0.0444448
mean: 0.975256 < 1.036 , median: 1.0103 < 1.0551

6.36 NUM PREDICTED BPS UPINTRON

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



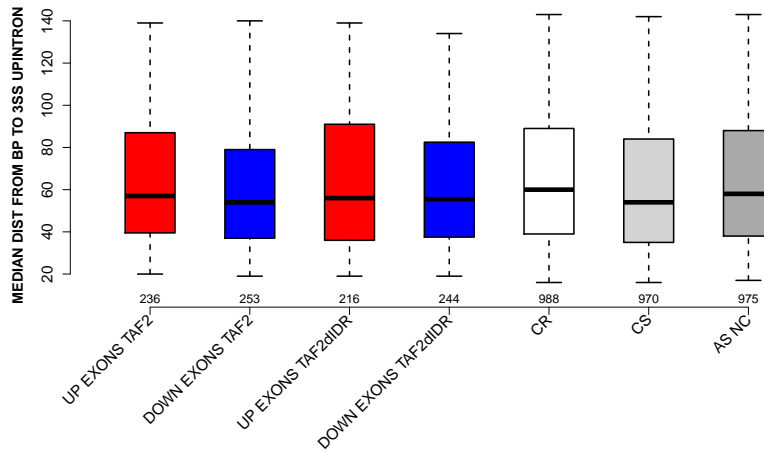
Significant results from Mann-Whitney U test:

- UP_EXONS_TAF2 vs CR : 0.00232384
mean: 2.9831 < 3.3846 , median: 3 = 3
- UP_EXONS_TAF2 vs CS : 0.0112189
mean: 2.9831 < 3.3124 , median: 3 = 3
- DOWN_EXONS_TAF2 vs CR : 0.0212695
mean: 3.0277 < 3.3846 , median: 3 = 3
- DOWN_EXONS_TAF2dIDR vs CR : 0.0351602
mean: 3.0574 < 3.3846 , median: 3 = 3
- CR vs AS_NC : 0.00107347
mean: 3.3846 > 3.1128 , median: 3 = 3
- CS vs AS_NC : 0.0121759
mean: 3.3124 > 3.1128 , median: 3 = 3

6.37 MEDIAN DIST FROM BP TO 3SS UPINTRON

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



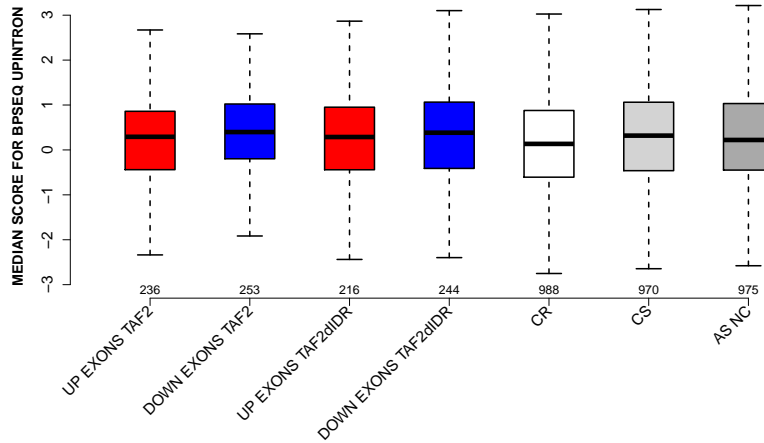
Significant results from Mann-Whitney U test:

- DOWN_EXONS_TAF2 vs CR : 0.0319934
mean: 60.9743 < 65.7379 , median: 54 < 60
- CR vs CS : 0.000906936
mean: 65.7379 > 61.566 , median: 60 > 54
- CS vs AS_NC : 0.0360683
mean: 61.566 < 64.4154 , median: 54 < 58

6.38 MEDIAN SCORE FOR BPSEQ UPINTRON

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



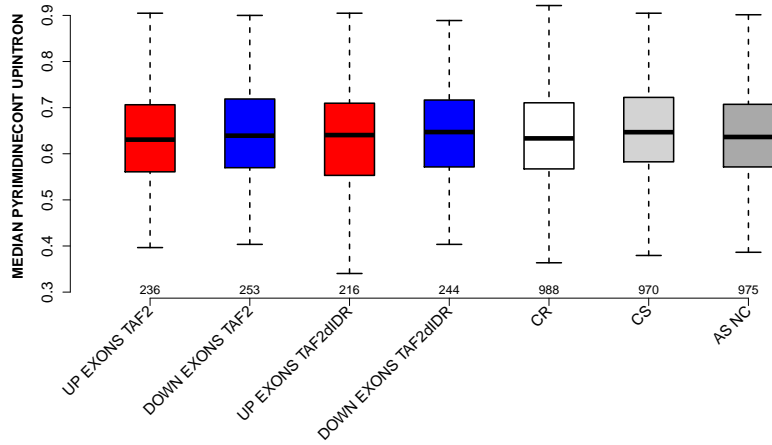
Significant results from Mann-Whitney U test:

- DOWN_EXONS_TAF2 vs CR : 0.000432365
mean: 0.403448 > 0.125194 , median: 0.397847 > 0.134334
- DOWN_EXONS_TAF2dIDR vs CR : 0.0113555
mean: 0.297774 > 0.125194 , median: 0.382922 > 0.134334
- CR vs CS : 0.000836219
mean: 0.125194 < 0.323069 , median: 0.134334 < 0.318296
- CR vs AS_NC : 0.0179472
mean: 0.125194 < 0.267408 , median: 0.134334 < 0.22159

6.39 MEDIAN PYRIMIDINECONT UPINTRON

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



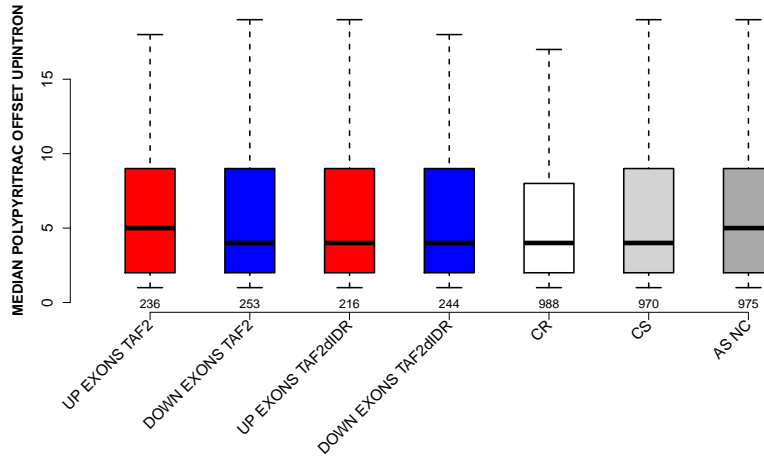
Significant results from Mann-Whitney U test:

- UP_EXONS_TAF2 vs CS : 0.046909
mean: 0.637091 < 0.651158 , median: 0.630604 < 0.646805
- CR vs CS : 0.00771911
mean: 0.639023 < 0.651158 , median: 0.633333 < 0.646805
- CS vs AS_NC : 0.0200711
mean: 0.651158 > 0.640466 , median: 0.646805 > 0.636364

6.40 MEDIAN POLYPYRITRAC OFFSET UPINTRON

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



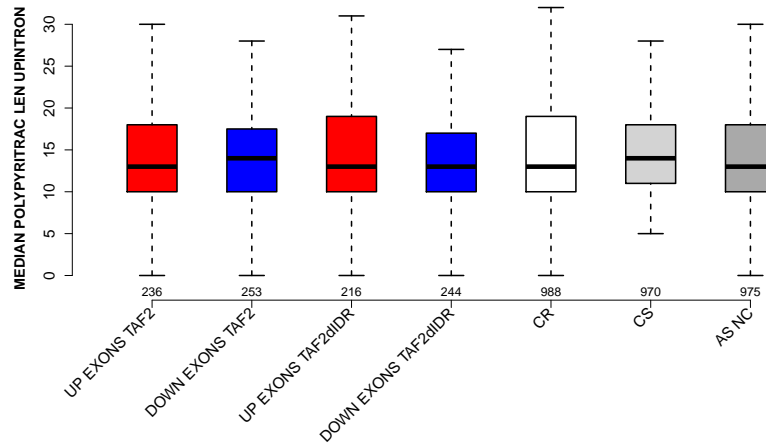
Significant results from Mann-Whitney U test:

- UP_EXONS_TAF2 vs CR : 0.0229141
mean: 8.0593 > 6.5273 , median: 5 > 4
- CR vs AS_NC : 0.00249753
mean: 6.5273 < 7.7056 , median: 4 < 5
- CS vs AS_NC : 0.0333468
mean: 7.3686 < 7.7056 , median: 4 < 5

6.41 MEDIAN POLYPYRITRAC LEN UPINTRON

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



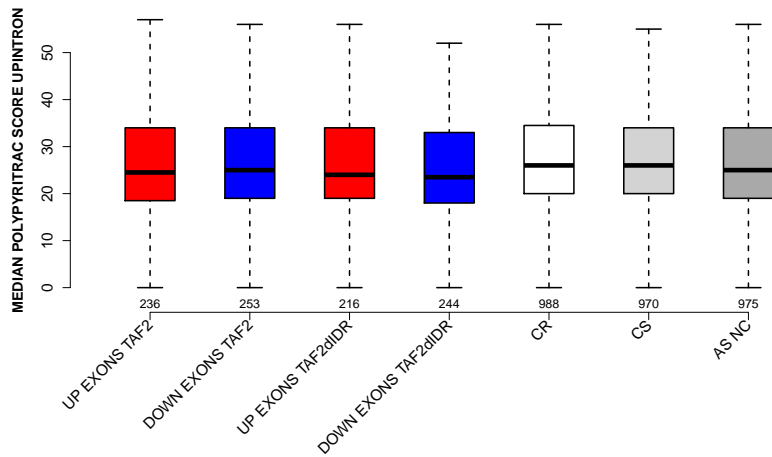
Significant results from Mann-Whitney U test:

- none

6.42 MEDIAN POLYPYRITRAC SCORE UPINTRON

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



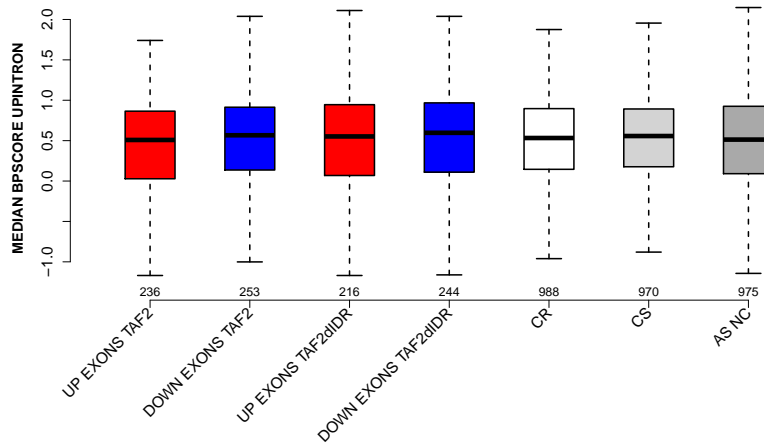
Significant results from Mann-Whitney U test:

- DOWN_EXONS_TAF2dIDR vs CS : 0.0385291
mean: 29.125 > 28.6191 , median: 23.5 < 26

6.43 MEDIAN BPSCORE UPINTRON

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



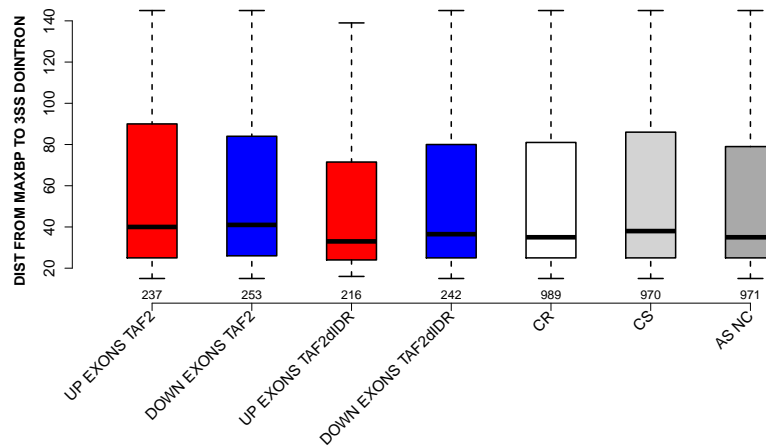
Significant results from Mann-Whitney U test:

- none

6.44 DIST FROM MAXBP TO 3SS DONTNTRON

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Meaning: distance to 3ss of best precited BP



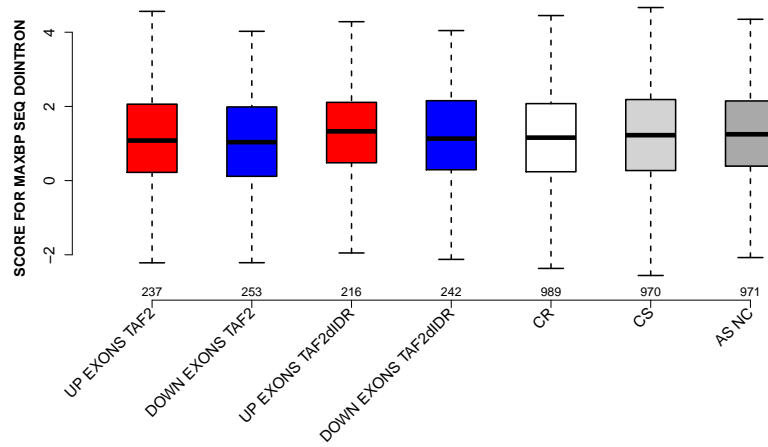
Significant results from Mann-Whitney U test:

- DOWN_EXONS_TAF2 vs UP_EXONS_TAF2dIDR : 0.0144914
mean: 59.4348 > 51.3194 , median: 41 > 33

6.45 SCORE FOR MAXBP SEQ DOINTRON

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Meaning: BP sequence score of best predicted BP



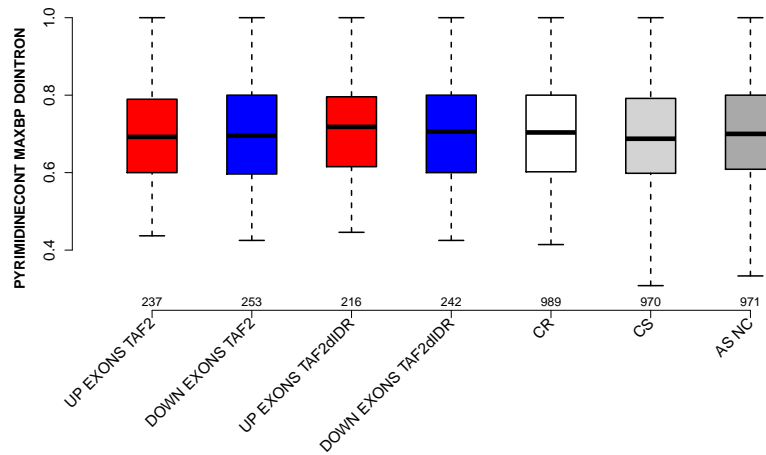
Significant results from Mann-Whitney U test:

- none

6.46 PYRIMIDINECONT MAXBP DONTNTRON

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



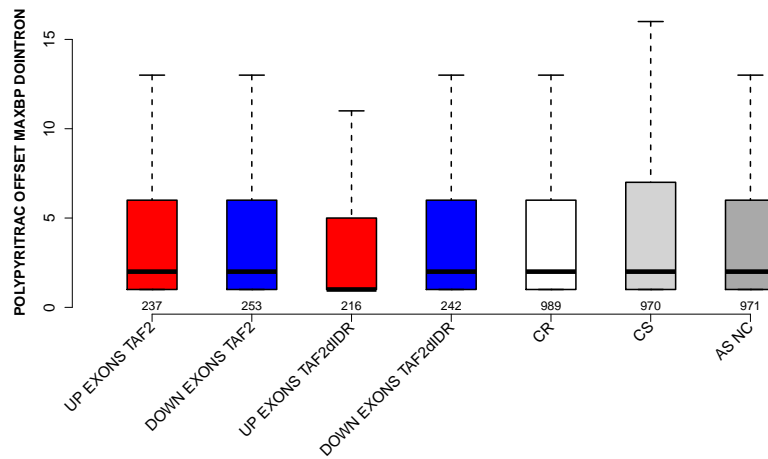
Significant results from Mann-Whitney U test:

- none

6.47 POLYPYRITRAC OFFSET MAXBP DOINTRON

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



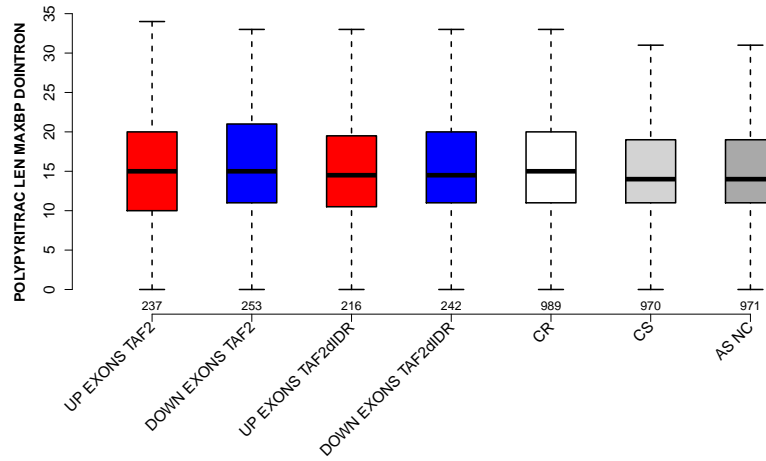
Significant results from Mann-Whitney U test:

- UP_EXONS_TAF2dIDR vs CR : 0.0428699
mean: 3.7639 < 4.7705 , median: 1 < 2
- UP_EXONS_TAF2dIDR vs CS : 0.0404181
mean: 3.7639 < 4.934 , median: 1 < 2

6.48 POLYPYRITRAC LEN MAXBP DONTNTRON

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Meaning: Polypyrimidine track length for best BP



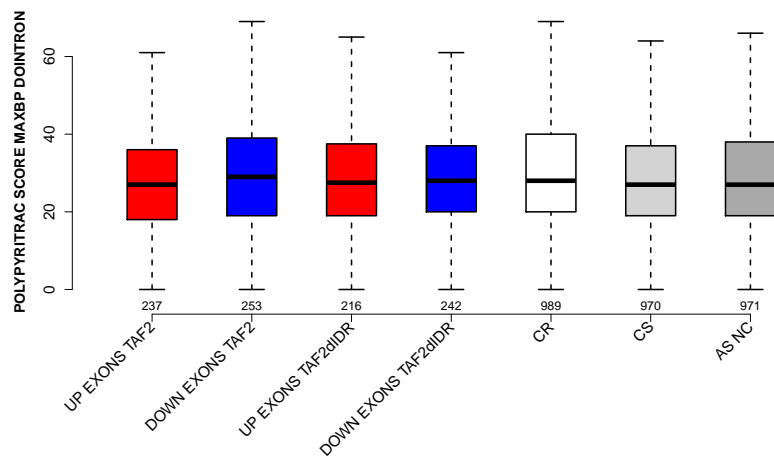
Significant results from Mann-Whitney U test:

- none

6.49 POLYPYRITRAC SCORE MAXBP DONTNTRON

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Meaning: Polypyrimidine track score for best BP



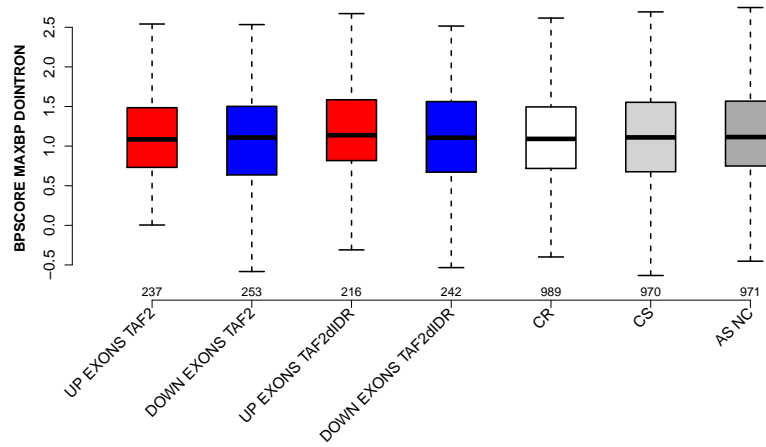
Significant results from Mann-Whitney U test:

- CR vs CS : 0.0110755
mean: 32.0768 > 30.1918 , median: 28 > 27
- CR vs AS_NC : 0.0433664
mean: 32.0768 > 30.5963 , median: 28 > 27

6.50 BPSCORE MAXBP DOINTRON

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Meaning: SVM classification score of best BP



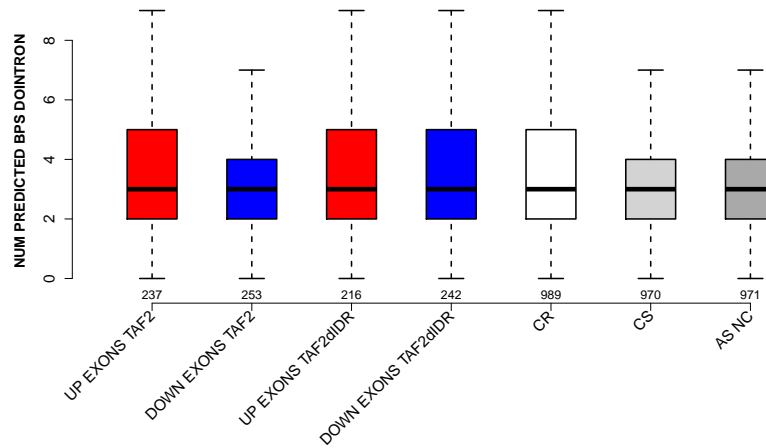
Significant results from Mann-Whitney U test:

- none

6.51 NUM PREDICTED BPS DONTNTRON

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



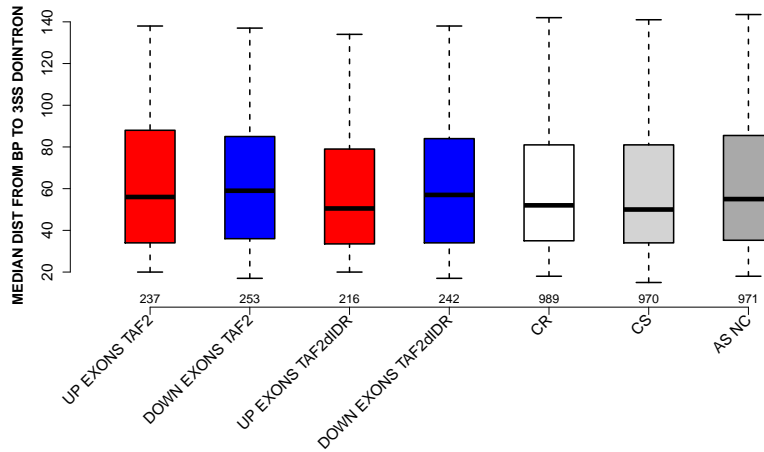
Significant results from Mann-Whitney U test:

- UP_EXONS_TAF2 vs CS : 0.0134093
mean: 3.5316 > 3.1619 , median: 3 = 3
- DOWN_EXONS_TAF2 vs CR : 0.00554276
mean: 3.1976 < 3.5197 , median: 3 = 3
- UP_EXONS_TAF2dIDR vs CS : 0.0350063
mean: 3.5509 > 3.1619 , median: 3 = 3
- DOWN_EXONS_TAF2dIDR vs CR : 0.0119599
mean: 3.1983 < 3.5197 , median: 3 = 3
- CR vs CS : 4.57213e-06
mean: 3.5197 > 3.1619 , median: 3 = 3
- CR vs AS_NC : 0.000588568
mean: 3.5197 > 3.2987 , median: 3 = 3

6.52 MEDIAN DIST FROM BP TO 3SS DONTNTRON

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



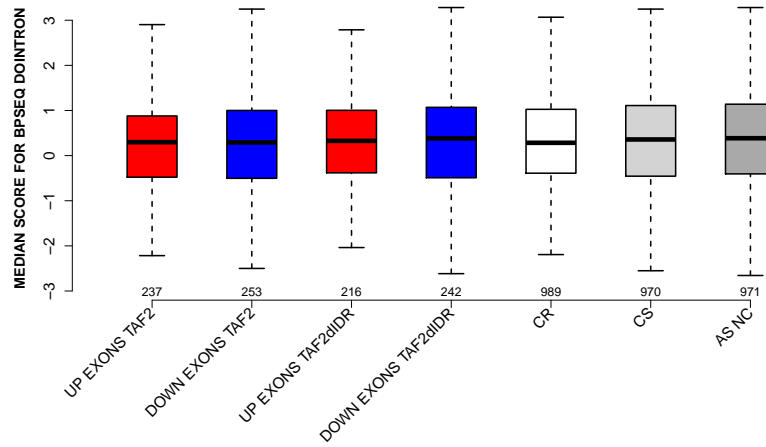
Significant results from Mann-Whitney U test:

- DOWN_EXONS_TAF2 vs CS : 0.0282283
mean: 64.1937 > 59.5237 , median: 59 > 50
- CS vs AS_NC : 0.0375125
mean: 59.5237 < 62.4763 , median: 50 < 55

6.53 MEDIAN SCORE FOR BPSEQ DONTNTRON

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



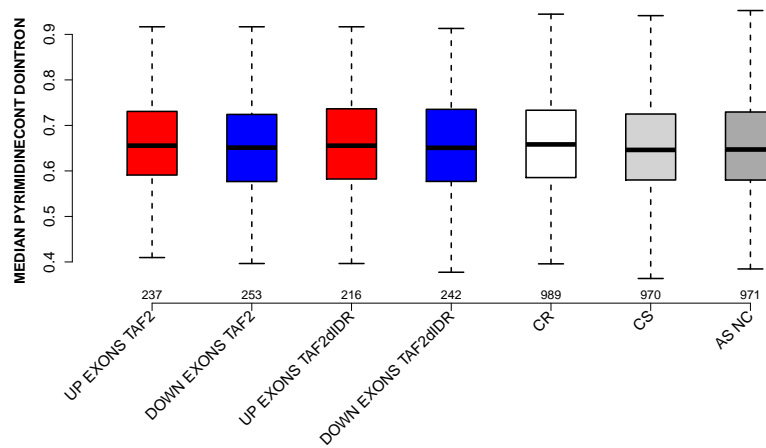
Significant results from Mann-Whitney U test:

- none

6.54 MEDIAN PYRIMIDINECONT DOINTRON

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



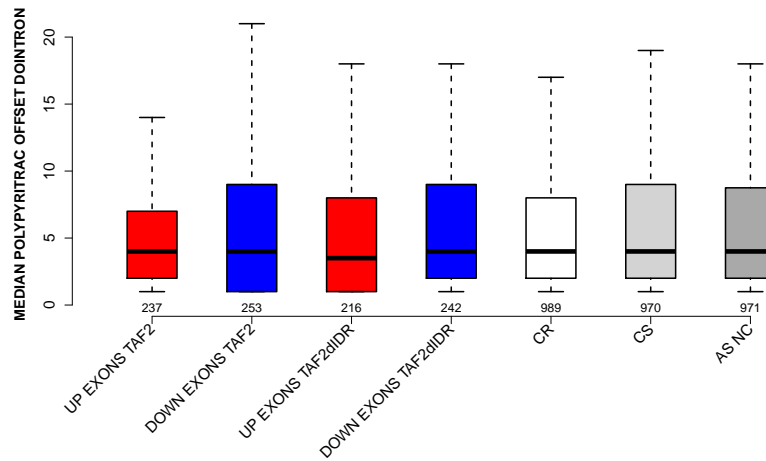
Significant results from Mann-Whitney U test:

- none

6.55 MEDIAN POLYPYRITRAC OFFSET DOINTRON

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



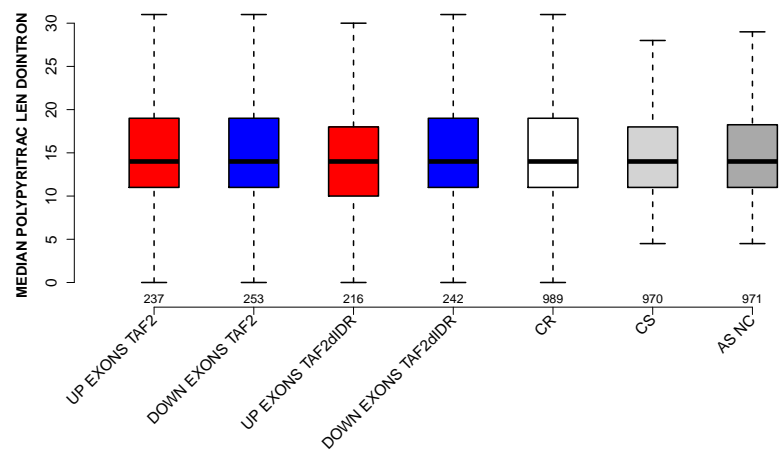
Significant results from Mann-Whitney U test:

- CR vs CS : 0.0311335
mean: 6.7078 < 7.818 , median: 4 = 4

6.56 MEDIAN POLYPYRITRAC LEN DONTNTRON

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



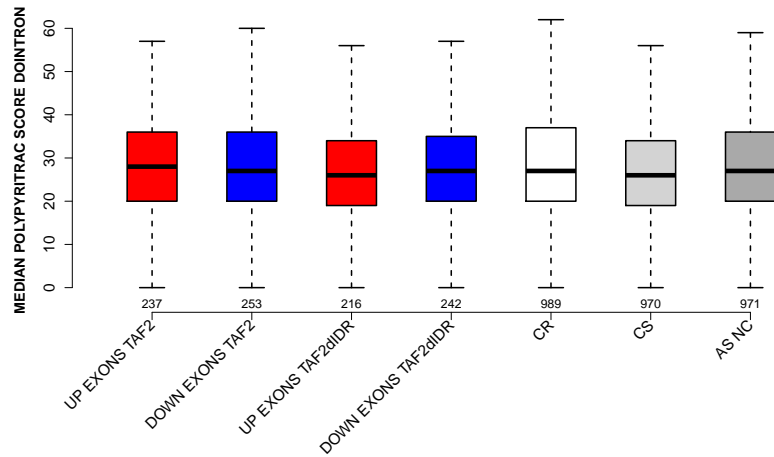
Significant results from Mann-Whitney U test:

- none

6.57 MEDIAN POLYPYRITRAC SCORE DONTNTRON

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



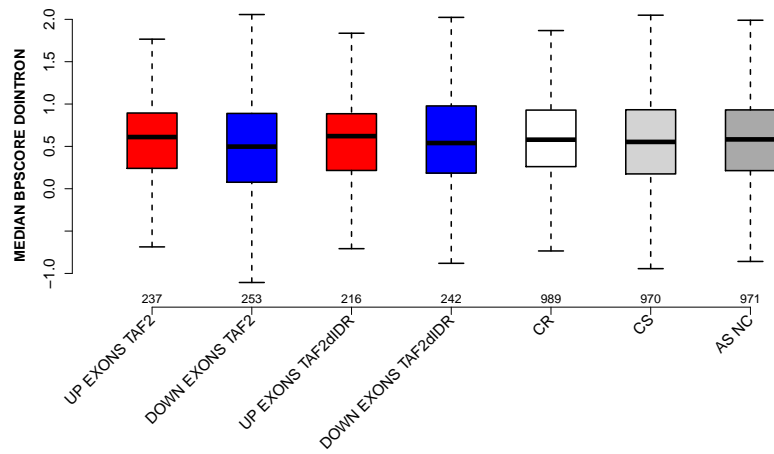
Significant results from Mann-Whitney U test:

- none

6.58 MEDIAN BPSCORE DOINTRON

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



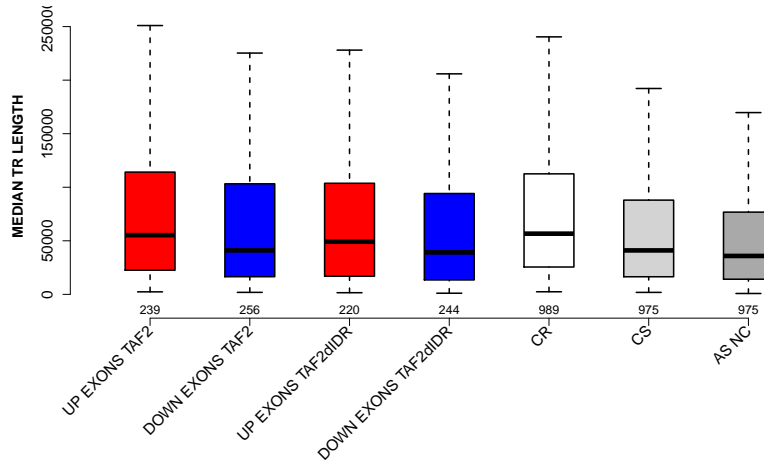
Significant results from Mann-Whitney U test:

- none

6.59 MEDIAN TR LENGTH

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Meaning: median length of transcripts the exon occurs in



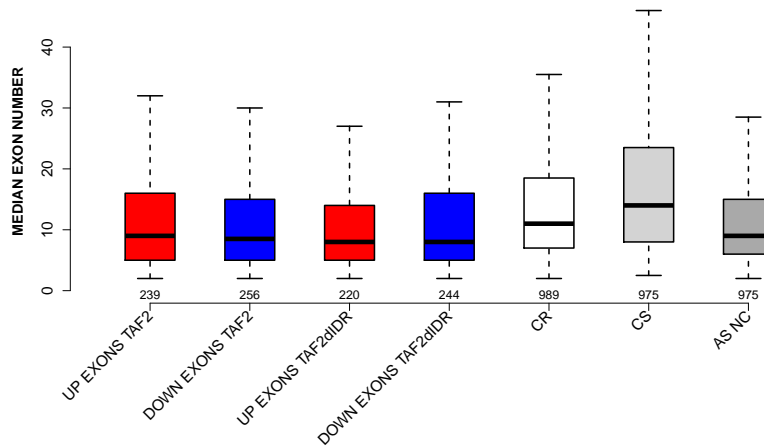
Significant results from Mann-Whitney U test:

- UP_EXONS_TAF2 vs DOWN_EXONS_TAF2dIDR : 0.0159836
mean: 86295.5167 > 69081.9549 , median: 55260.5 > 39210.5
- UP_EXONS_TAF2 vs CS : 0.00437171
mean: 86295.5167 > 67936.5744 , median: 55260.5 > 41036
- UP_EXONS_TAF2 vs AS_NC : 3.36073e-05
mean: 86295.5167 > 61792.2974 , median: 55260.5 > 35858
- DOWN_EXONS_TAF2 vs CR : 0.00030931
mean: 72547.4824 < 89047.3893 , median: 41061.25 < 56666
- UP_EXONS_TAF2dIDR vs CR : 0.0169773
mean: 76627.5364 < 89047.3893 , median: 49121 < 56666
- UP_EXONS_TAF2dIDR vs AS_NC : 0.0150275
mean: 76627.5364 > 61792.2974 , median: 49121 > 35858
- DOWN_EXONS_TAF2dIDR vs CR : 2.0575e-05
mean: 69081.9549 < 89047.3893 , median: 39210.5 < 56666
- CR vs CS : 6.18803e-11
mean: 89047.3893 > 67936.5744 , median: 56666 > 41036
- CR vs AS_NC : 2.41351e-18
mean: 89047.3893 > 61792.2974 , median: 56666 > 35858
- CS vs AS_NC : 0.0327868
mean: 67936.5744 > 61792.2974 , median: 41036 > 35858

6.60 MEDIAN EXON NUMBER

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



Significant results from Mann-Whitney U test:

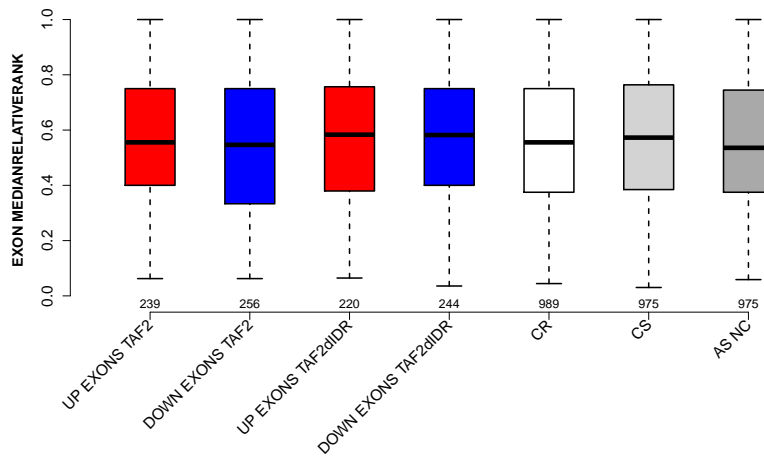
- UP_EXONS_TAF2 vs CR : 0.000230638
mean: 11.9498 < 14.3918 , median: 9 < 11
- UP_EXONS_TAF2 vs CS : 1.4806e-14
mean: 11.9498 < 18.3918 , median: 9 < 14
- DOWN_EXONS_TAF2 vs CR : 1.58284e-05
mean: 12.4414 < 14.3918 , median: 8.5 < 11
- DOWN_EXONS_TAF2 vs CS : 4.53848e-17
mean: 12.4414 < 18.3918 , median: 8.5 < 14
- UP_EXONS_TAF2dIDR vs CR : 4.70062e-07
mean: 10.9659 < 14.3918 , median: 8 < 11
- UP_EXONS_TAF2dIDR vs CS : 7.52545e-19
mean: 10.9659 < 18.3918 , median: 8 < 14
- DOWN_EXONS_TAF2dIDR vs CR : 8.29611e-06
mean: 12.3238 < 14.3918 , median: 8 < 11
- DOWN_EXONS_TAF2dIDR vs CS : 2.00813e-16
mean: 12.3238 < 18.3918 , median: 8 < 14
- CR vs CS : 3.1536e-12
mean: 14.3918 < 18.3918 , median: 11 < 14
- CR vs AS_NC : 2.79907e-09
mean: 14.3918 > 11.7036 , median: 11 > 9

- CS vs AS_NC : 2.6565e-36
mean: 18.3918 > 11.7036 , median: 14 > 9

6.61 EXON MEDIANRELATIVERANK

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



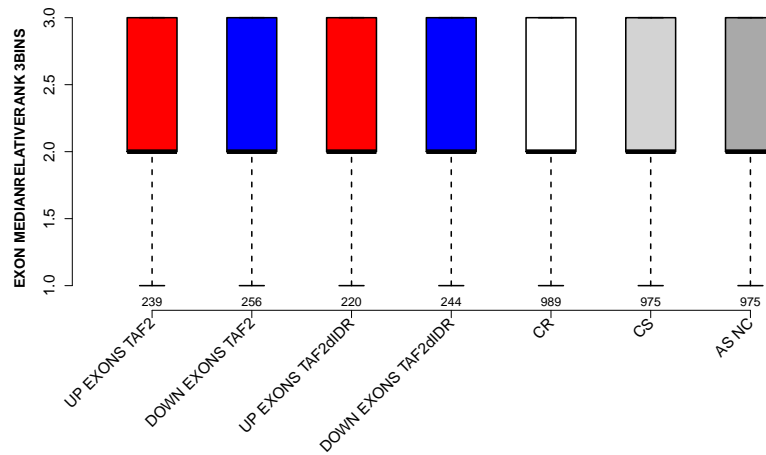
Significant results from Mann-Whitney U test:

- DOWN_EXONS_TAF2 vs CS : 0.045333
mean: 0.53671 < 0.569899 , median: 0.546537 < 0.572727

6.62 EXON MEDIANRELATIVERANK 3BINS

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



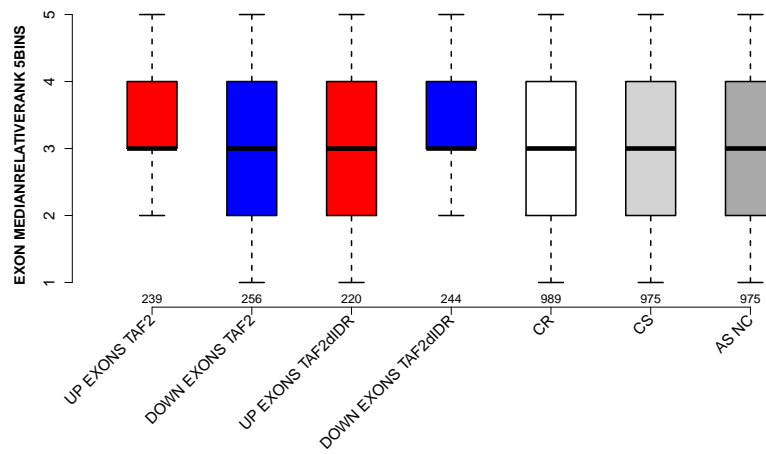
Significant results from Mann-Whitney U test:

- none

6.63 EXON MEDIANRELATIVERANK 5BINS

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Meaning: similar to EXON MEDIANRELATIVERANK 3BINS with 5 bins



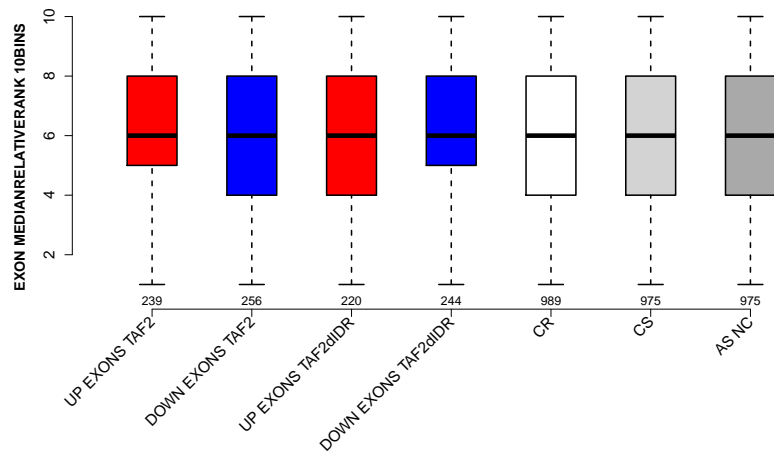
Significant results from Mann-Whitney U test:

- none

6.64 EXON MEDIANRELATIVERANK 10BINS

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Meaning: similar to EXON MEDIANRELATIVERANK 3BINS with 10 bins



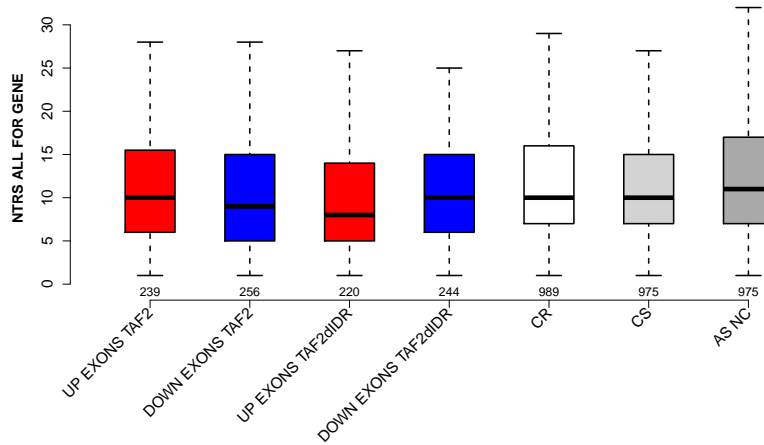
Significant results from Mann-Whitney U test:

- DOWN_EXONS_TAF2 vs CS : 0.034612
mean: $5.8867 < 6.2503$, median: $6 = 6$

6.65 NTRS ALL FOR GENE

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



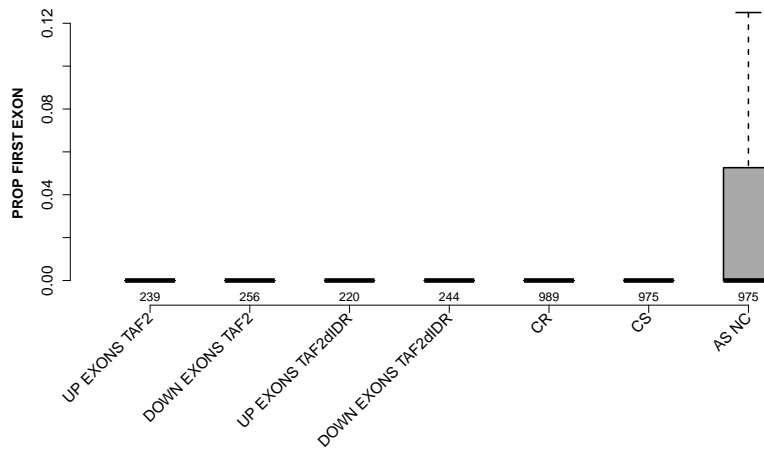
Significant results from Mann-Whitney U test:

- UP_EXONS_TAF2 vs UP_EXONS_TAF2dIDR : 0.0335799
mean: 12.1841 > 10.1545 , median: 10 > 8
- UP_EXONS_TAF2 vs AS_NC : 0.00426027
mean: 12.1841 < 13.4082 , median: 10 < 11
- DOWN_EXONS_TAF2 vs CR : 0.0127851
mean: 10.8984 < 12.3306 , median: 9 < 10
- DOWN_EXONS_TAF2 vs AS_NC : 8.92906e-05
mean: 10.8984 < 13.4082 , median: 9 < 11
- UP_EXONS_TAF2dIDR vs CR : 5.51355e-05
mean: 10.1545 < 12.3306 , median: 8 < 10
- UP_EXONS_TAF2dIDR vs CS : 0.000424607
mean: 10.1545 < 11.7221 , median: 8 < 10
- UP_EXONS_TAF2dIDR vs AS_NC : 9.66731e-08
mean: 10.1545 < 13.4082 , median: 8 < 11
- DOWN_EXONS_TAF2dIDR vs AS_NC : 0.00172541
mean: 11.9098 < 13.4082 , median: 10 < 11
- CR vs AS_NC : 0.0227312
mean: 12.3306 < 13.4082 , median: 10 < 11
- CS vs AS_NC : 0.00057705
mean: 11.7221 < 13.4082 , median: 10 < 11

6.66 PROP FIRST EXON

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



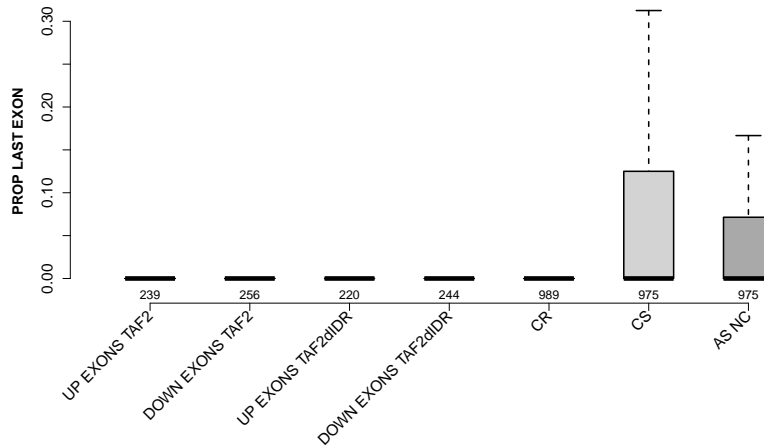
Significant results from Mann-Whitney U test:

- UP_EXONS_TAF2 vs CR : 1.51814e-09
mean: 0.0533646 > 0.0165989 , median: 0 = 0
- DOWN_EXONS_TAF2 vs CR : 1.46175e-08
mean: 0.0538115 > 0.0165989 , median: 0 = 0
- UP_EXONS_TAF2dIDR vs CR : 1.29048e-06
mean: 0.0546853 > 0.0165989 , median: 0 = 0
- DOWN_EXONS_TAF2dIDR vs CR : 6.80679e-09
mean: 0.0531897 > 0.0165989 , median: 0 = 0
- CR vs CS : 6.38481e-17
mean: 0.0165989 < 0.0477305 , median: 0 = 0
- CR vs AS_NC : 2.75593e-22
mean: 0.0165989 < 0.0473486 , median: 0 = 0

6.67 PROP LAST EXON

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



Significant results from Mann-Whitney U test:

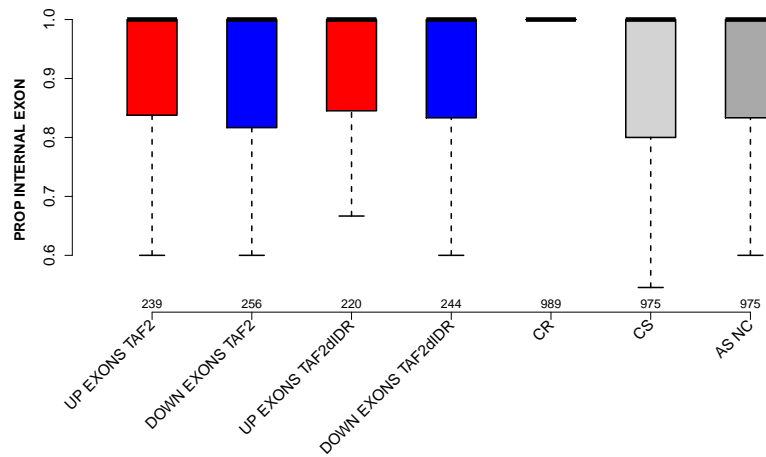
- UP_EXONS_TAF2 vs CR : 8.10066e-12
mean: 0.046033 > 0.0121366 , median: 0 = 0
- UP_EXONS_TAF2 vs CS : 0.00252032
mean: 0.046033 < 0.0705605 , median: 0 = 0
- DOWN_EXONS_TAF2 vs CR : 4.76578e-15
mean: 0.0469509 > 0.0121366 , median: 0 = 0
- DOWN_EXONS_TAF2 vs CS : 0.0142655
mean: 0.0469509 < 0.0705605 , median: 0 = 0
- UP_EXONS_TAF2dIDR vs CR : 4.26495e-12
mean: 0.0584232 > 0.0121366 , median: 0 = 0
- UP_EXONS_TAF2dIDR vs CS : 0.010486
mean: 0.0584232 < 0.0705605 , median: 0 = 0
- DOWN_EXONS_TAF2dIDR vs CR : 8.40137e-11
mean: 0.0543695 > 0.0121366 , median: 0 = 0
- DOWN_EXONS_TAF2dIDR vs CS : 0.00306441
mean: 0.0543695 < 0.0705605 , median: 0 = 0
- CR vs CS : 1.5015e-42
mean: 0.0121366 < 0.0705605 , median: 0 = 0
- CR vs AS_NC : 7.77696e-32
mean: 0.0121366 < 0.0480134 , median: 0 = 0

- CS vs AS_NC : 0.00399334
mean: 0.0705605 > 0.0480134 , median: 0 = 0

6.68 PROP INTERNAL EXON

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



Significant results from Mann-Whitney U test:

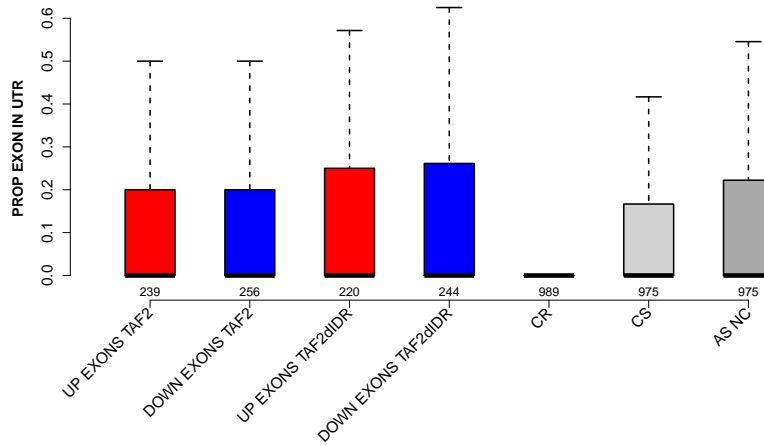
- UP_EXONS_TAF2 vs CR : 3.54675e-19
mean: 0.900602 < 0.972616 , median: 1 = 1
- UP_EXONS_TAF2 vs CS : 0.00927037
mean: 0.900602 > 0.88227 , median: 1 = 1
- DOWN_EXONS_TAF2 vs CR : 1.35732e-21
mean: 0.904136 < 0.972616 , median: 1 = 1
- DOWN_EXONS_TAF2 vs CS : 0.0185011
mean: 0.904136 > 0.88227 , median: 1 = 1
- UP_EXONS_TAF2dIDR vs CR : 3.01299e-16
mean: 0.888298 < 0.972616 , median: 1 = 1
- UP_EXONS_TAF2dIDR vs CS : 0.0147464
mean: 0.888298 > 0.88227 , median: 1 = 1
- DOWN_EXONS_TAF2dIDR vs CR : 4.59764e-18
mean: 0.895002 < 0.972616 , median: 1 = 1
- DOWN_EXONS_TAF2dIDR vs CS : 0.0184073
mean: 0.895002 > 0.88227 , median: 1 = 1
- CR vs CS : 4.20842e-60
mean: 0.972616 > 0.88227 , median: 1 = 1
- CR vs AS_NC : 2.8494e-47
mean: 0.972616 > 0.905467 , median: 1 = 1

- CS vs AS_NC : 0.00419676
mean: 0.88227 < 0.905467 , median: 1 = 1

6.69 PROP EXON IN UTR

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Meaning: NTRS WITH EXON IN UTR / NTRS WITH EXON



Significant results from Mann-Whitney U test:

- UP_EXONS_TAF2 vs CR : 4.29896e-15
mean: 0.107756 > 0.0266206 , median: 0 = 0
- UP_EXONS_TAF2 vs AS_NC : 0.00436873
mean: 0.107756 < 0.140522 , median: 0 = 0
- DOWN_EXONS_TAF2 vs CR : 6.93237e-18
mean: 0.139175 > 0.0266206 , median: 0 = 0
- DOWN_EXONS_TAF2 vs AS_NC : 0.03677
mean: 0.139175 < 0.140522 , median: 0 = 0
- UP_EXONS_TAF2dIDR vs CR : 4.30729e-19
mean: 0.140192 > 0.0266206 , median: 0 = 0
- DOWN_EXONS_TAF2dIDR vs CR : 4.52106e-25
mean: 0.158686 > 0.0266206 , median: 0 = 0
- DOWN_EXONS_TAF2dIDR vs CS : 0.00744388
mean: 0.158686 > 0.100802 , median: 0 = 0
- CR vs CS : 5.55405e-29
mean: 0.0266206 < 0.100802 , median: 0 = 0
- CR vs AS_NC : 3.25277e-59
mean: 0.0266206 < 0.140522 , median: 0 = 0
- CS vs AS_NC : 1.72276e-07
mean: 0.100802 < 0.140522 , median: 0 = 0