

Comparison of introns grouped into: TAF2-INTRON-UP, TAF2-INTRON-DOWN, CR, AS-NC, CS

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Matt version 1.3.0

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1 Infos

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

2 Warning: Please read this note carefully

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

3 Notes for publishing results

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

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

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

When publishing results with respect to the binding strength of the human 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:

TEST_TAF2_INTRON_UP_ANNO.tab

Selection criteria for defining intron groups:

TAF2_INTRON_UP : having value TAF2_INTRON_UP in column GROUP

TAF2_INTRON_DOWN : having value TAF2_INTRON_DOWN 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

Intron duplicates removal: yes

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

TAF2_INTRON_UP: 126 / 111

TAF2_INTRON_DOWN: 102 / 97

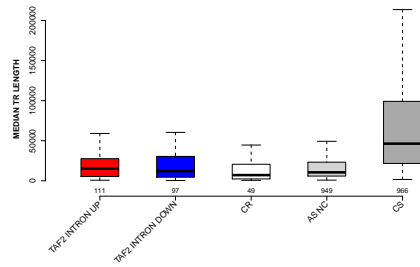
CR: 50 / 49

AS_NC: 1000 / 949

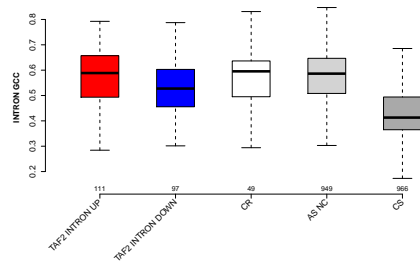
CS: 1000 / 966

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

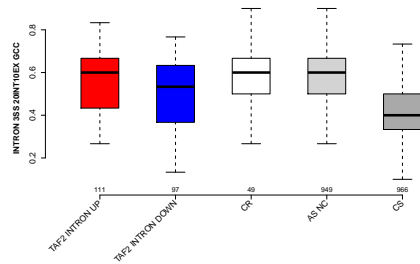
MEDIAN TR LENGTH



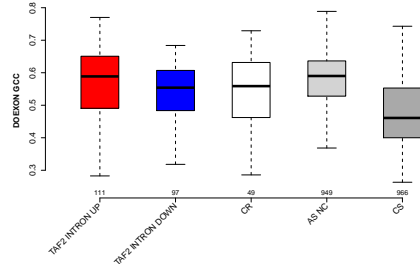
INTRON GCC



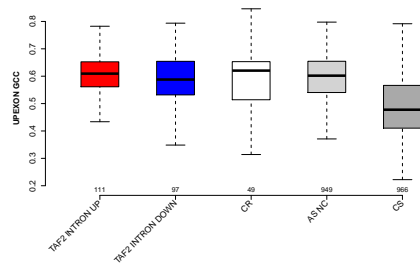
INTRON 3SS 20INT10EX GCC



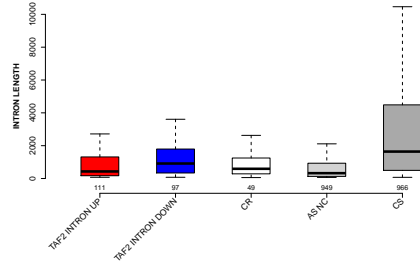
DOEXON GCC



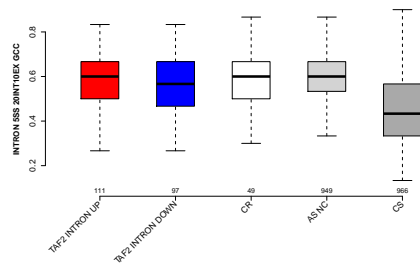
UPEXON GCC



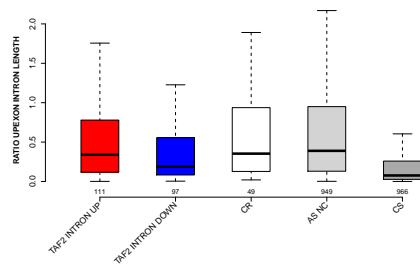
INTRON LENGTH



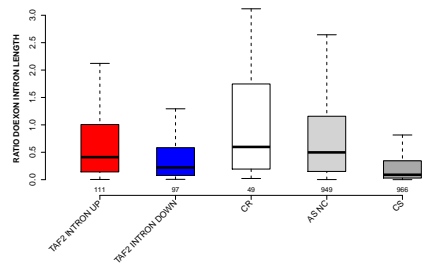
INTRON 5SS 20INT10EX GCC



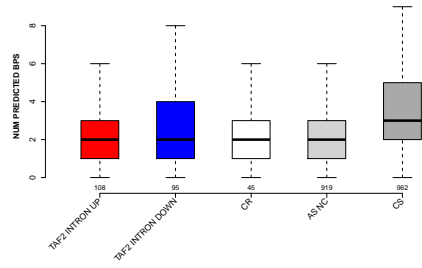
RATIO UPEXON INTRON LENGTH



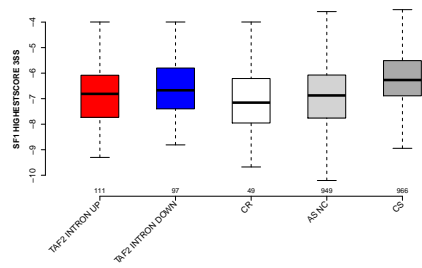
RATIO DOEXON INTRON LENGTH



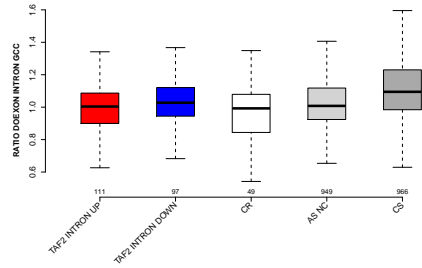
NUM PREDICTED BPS



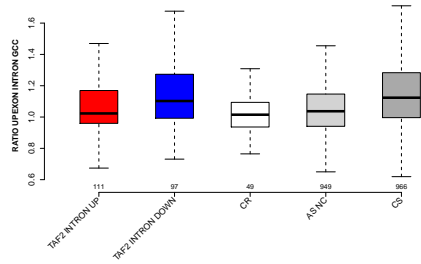
SF1 HIGHESTSCORE 3SS



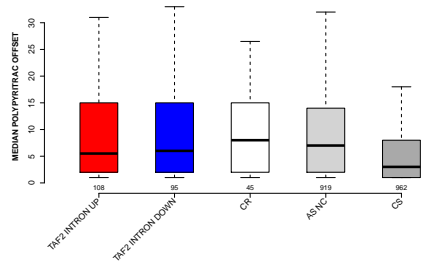
RATIO DOEXON INTRON GCC



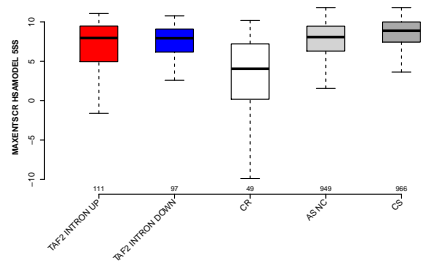
RATIO UPEXON INTRON GCC



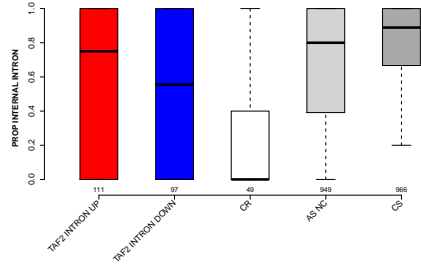
MEDIAN POLYPYRITRAC OFFSET



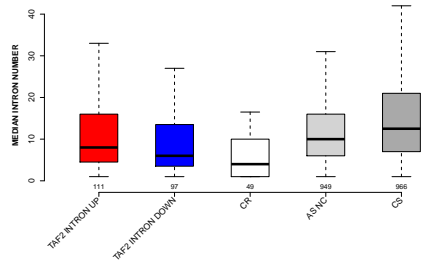
MAXENTSCR HSAMODEL 5SS



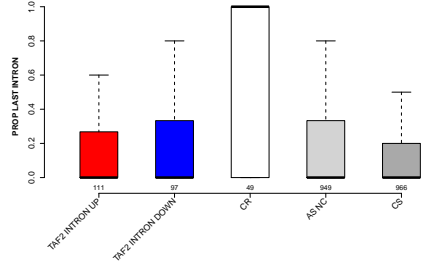
PROP INTERNAL INTRON



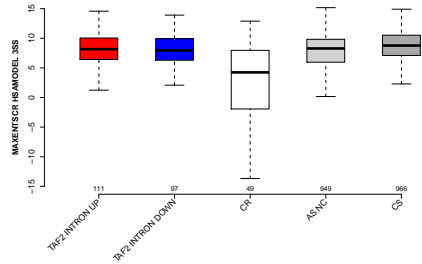
MEDIAN INTRON NUMBER



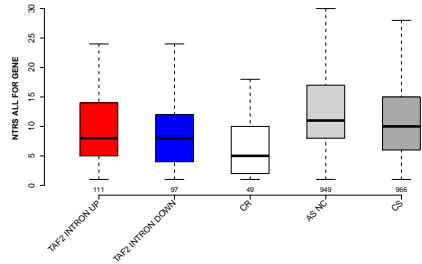
PROP LAST INTRON



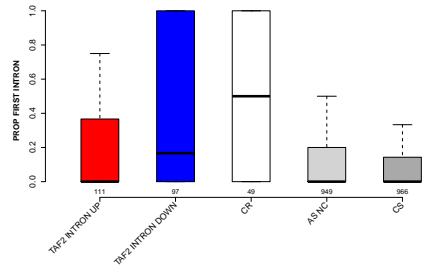
MAXENTSCR HSAMODEL 3SS



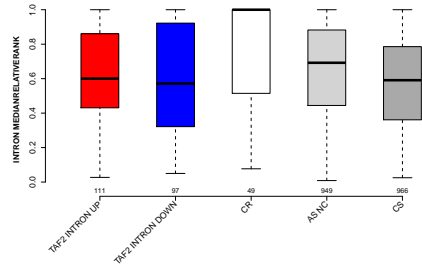
NTRS ALL FOR GENE



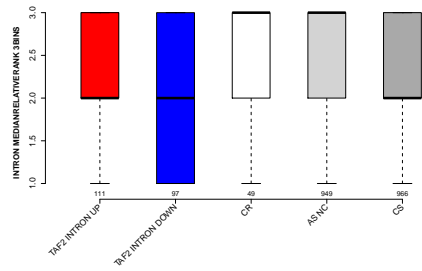
PROP FIRST INTRON



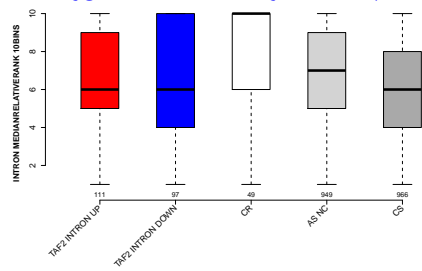
INTRON MEDIANRELATIVERANK



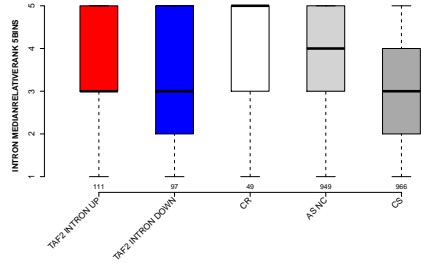
INTRON MEDIANRELATIVERANK 3BINS



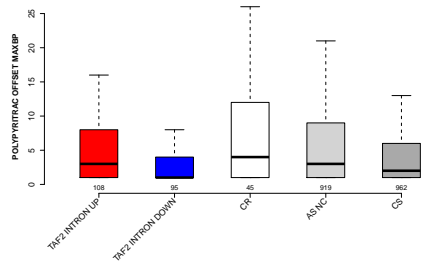
INTRON MEDIANRELATIVERANK 10BINS



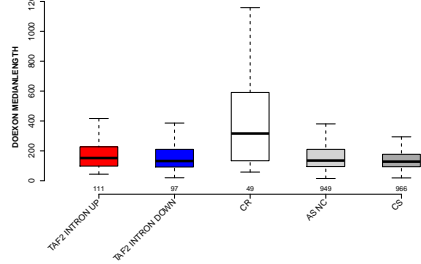
INTRON MEDIANRELATIVERANK 5BINS



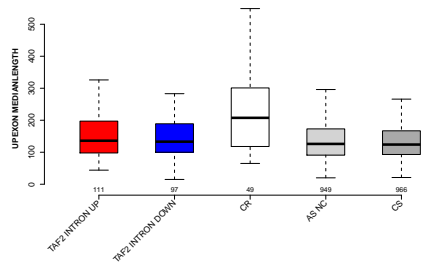
POLYPYRITRAC OFFSET MAXBP



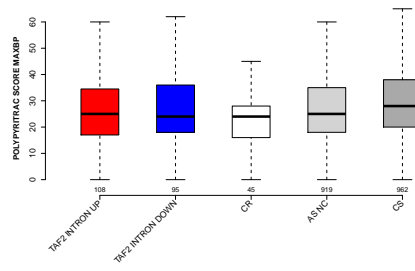
DOEXON MEDIANLENGTH



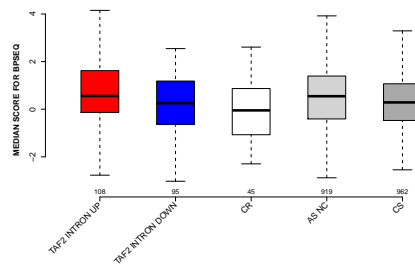
UPEXON MEDIANLENGTH



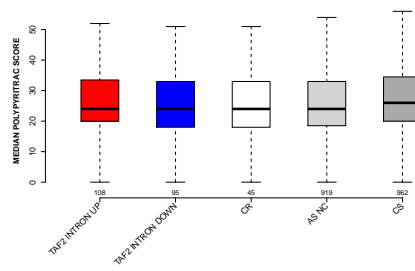
POLYPYRITRAC SCORE MAXBP



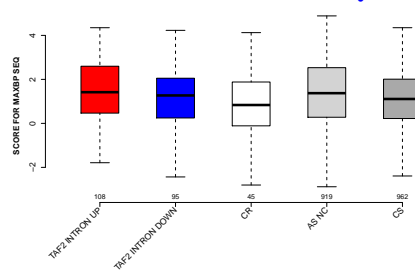
MEDIAN SCORE FOR BPSEQ



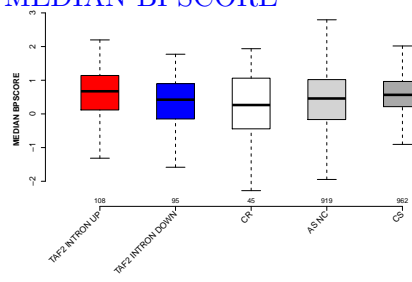
MEDIAN POLYPYRITRAC SCORE



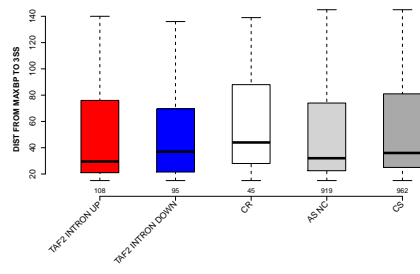
SCORE FOR MAXBP SEQ



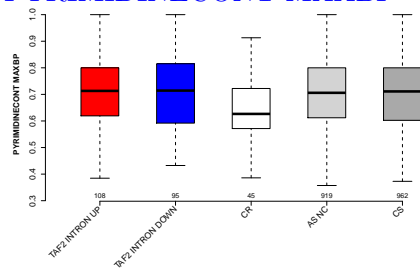
MEDIAN BPSCORE



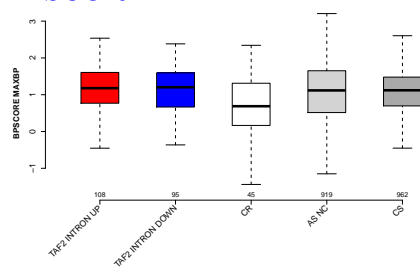
DIST FROM MAXBP TO 3SS



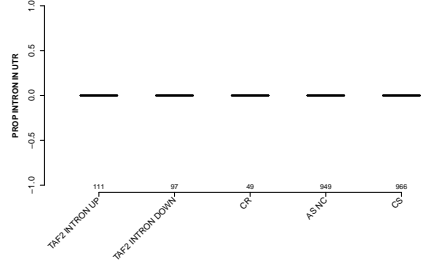
PYRIMIDINECONT MAXBP



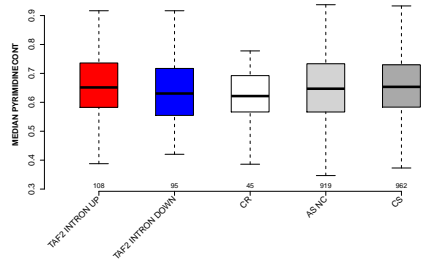
BPSCORE MAXBP



PROP INTRON IN UTR



MEDIAN PYRIMIDINECONT

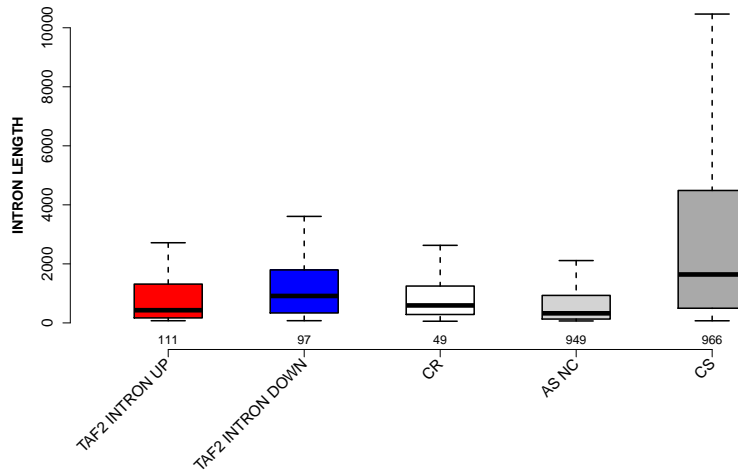


6 Details: Box plots and statistical assessments for all features

6.1 INTRON LENGTH

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Meaning:



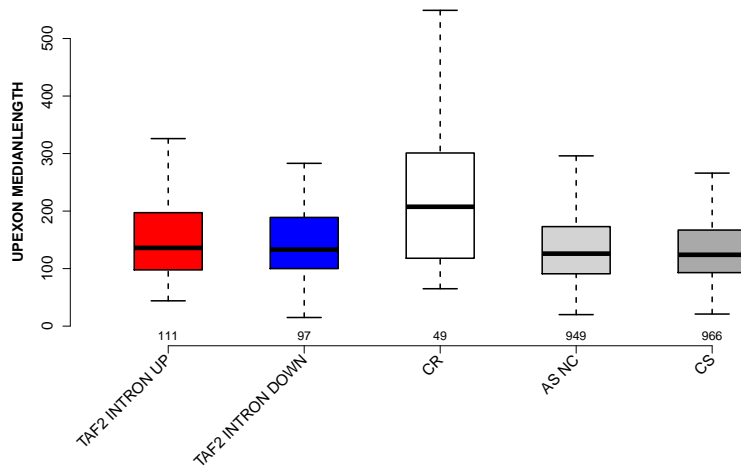
Significant results from Mann-Whitney U test:

- TAF2_INTRON_UP vs TAF2_INTRON_DOWN : 0.0190835
mean: 1897.7027 > 1640.1031 , median: 430 < 913
- TAF2_INTRON_UP vs AS_NC : 0.018135
mean: 1897.7027 > 888.0242 , median: 430 > 325
- TAF2_INTRON_UP vs CS : 3.00282e-11
mean: 1897.7027 < 5064.7308 , median: 430 < 1641
- TAF2_INTRON_DOWN vs AS_NC : 9.12507e-08
mean: 1640.1031 > 888.0242 , median: 913 > 325
- TAF2_INTRON_DOWN vs CS : 5.00329e-05
mean: 1640.1031 < 5064.7308 , median: 913 < 1641
- CR vs AS_NC : 0.0129423
mean: 1180.3673 > 888.0242 , median: 592 > 325
- CR vs CS : 1.42888e-05
mean: 1180.3673 < 5064.7308 , median: 592 < 1641
- AS_NC vs CS : 1.20013e-82
mean: 888.0242 < 5064.7308 , median: 325 < 1641

6.2 UPEXON MEDIANLENGTH

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



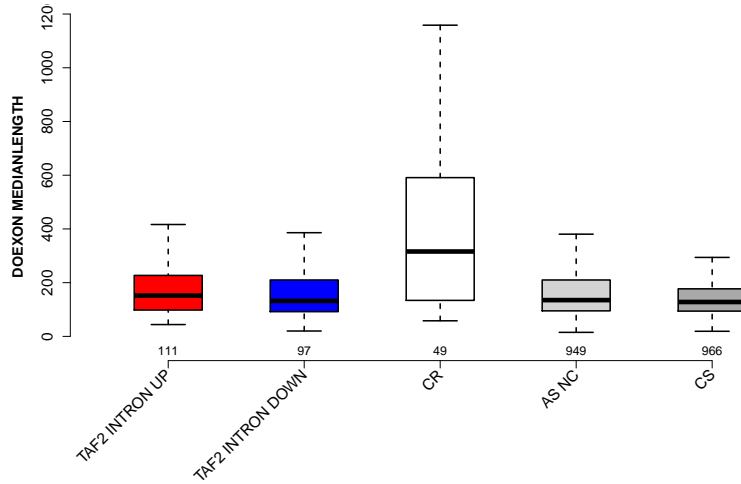
Significant results from Mann-Whitney U test:

- TAF2_INTRON_UP vs CR : 0.00189686
mean: 201.3288 < 382.9694 , median: 136 < 207.5
- TAF2_INTRON_UP vs CS : 0.0347195
mean: 201.3288 > 143.0047 , median: 136 > 124
- TAF2_INTRON_DOWN vs CR : 0.0012626
mean: 181.7577 < 382.9694 , median: 133 < 207.5
- TAF2_INTRON_DOWN vs CS : 0.0483313
mean: 181.7577 > 143.0047 , median: 133 > 124
- CR vs AS_NC : 1.13843e-06
mean: 382.9694 > 163.4842 , median: 207.5 > 126
- CR vs CS : 1.08981e-07
mean: 382.9694 > 143.0047 , median: 207.5 > 124

6.3 DOEXON MEDIANLENGTH

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



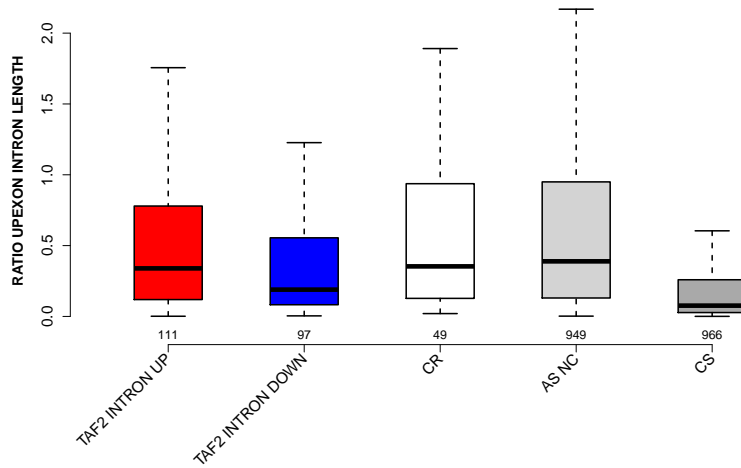
Significant results from Mann-Whitney U test:

- TAF2_INTRON_UP vs CR : 0.00116032
mean: 350.6396 < 521.5306 , median: 152 < 316
- TAF2_INTRON_UP vs CS : 0.00415822
mean: 350.6396 > 257.1242 , median: 152 > 128
- TAF2_INTRON_DOWN vs CR : 5.05231e-05
mean: 234.7887 < 521.5306 , median: 132 < 316
- CR vs AS_NC : 2.11858e-06
mean: 521.5306 > 263.8467 , median: 316 > 135
- CR vs CS : 6.08766e-08
mean: 521.5306 > 257.1242 , median: 316 > 128
- AS_NC vs CS : 0.0136925
mean: 263.8467 > 257.1242 , median: 135 > 128

6.4 RATIO UPEXON INTRON LENGTH

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Meaning: median up-stream exon length / intron length



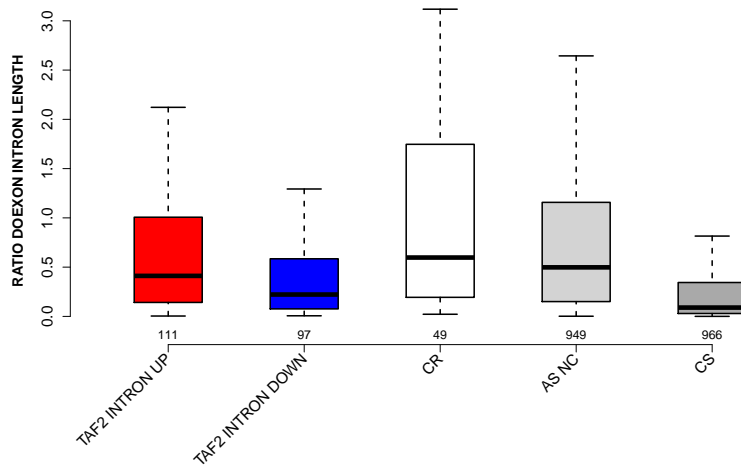
Significant results from Mann-Whitney U test:

- TAF2_INTRON_UP vs TAF2_INTRON_DOWN : 0.0154184
mean: 0.582537 > 0.435989 , median: 0.339207 > 0.189135
- TAF2_INTRON_UP vs CS : 2.77923e-14
mean: 0.582537 > 0.263246 , median: 0.339207 > 0.0762247
- TAF2_INTRON_DOWN vs CR : 0.00751641
mean: 0.435989 < 1.2375 , median: 0.189135 < 0.35337
- TAF2_INTRON_DOWN vs AS_NC : 4.6126e-05
mean: 0.435989 < 0.688341 , median: 0.189135 < 0.388889
- TAF2_INTRON_DOWN vs CS : 2.29273e-06
mean: 0.435989 > 0.263246 , median: 0.189135 > 0.0762247
- CR vs CS : 5.66054e-10
mean: 1.2375 > 0.263246 , median: 0.35337 > 0.0762247
- AS_NC vs CS : 1.89983e-80
mean: 0.688341 > 0.263246 , median: 0.388889 > 0.0762247

6.5 RATIO DOEXON INTRON LENGTH

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Meaning: median down-stream exon length / intron length



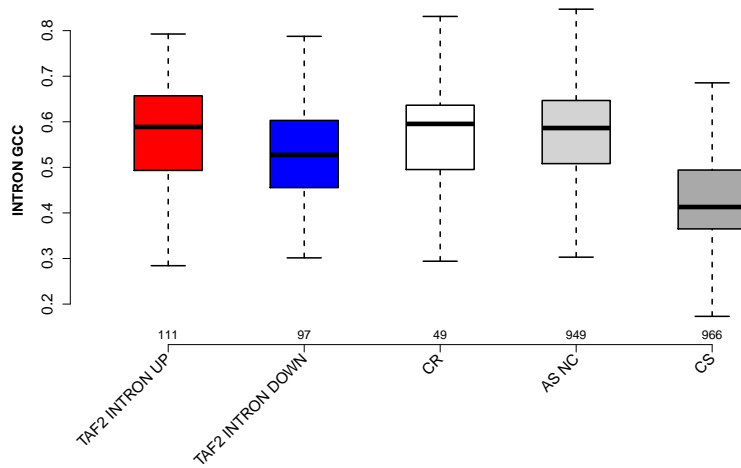
Significant results from Mann-Whitney U test:

- TAF2_INTRON_UP vs TAF2_INTRON_DOWN : 0.00419036
mean: 0.786448 > 0.518959 , median: 0.411215 > 0.221945
- TAF2_INTRON_UP vs CS : 1.13163e-13
mean: 0.786448 > 0.393069 , median: 0.411215 > 0.0895518
- TAF2_INTRON_DOWN vs CR : 0.000647882
mean: 0.518959 < 1.4742 , median: 0.221945 < 0.597403
- TAF2_INTRON_DOWN vs AS_NC : 2.95476e-06
mean: 0.518959 < 1.0008 , median: 0.221945 < 0.497856
- TAF2_INTRON_DOWN vs CS : 4.46143e-05
mean: 0.518959 > 0.393069 , median: 0.221945 > 0.0895518
- CR vs CS : 7.84386e-11
mean: 1.4742 > 0.393069 , median: 0.597403 > 0.0895518
- AS_NC vs CS : 1.75445e-76
mean: 1.0008 > 0.393069 , median: 0.497856 > 0.0895518

6.6 INTRON GCC

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Meaning: GC content of entire intron sequence



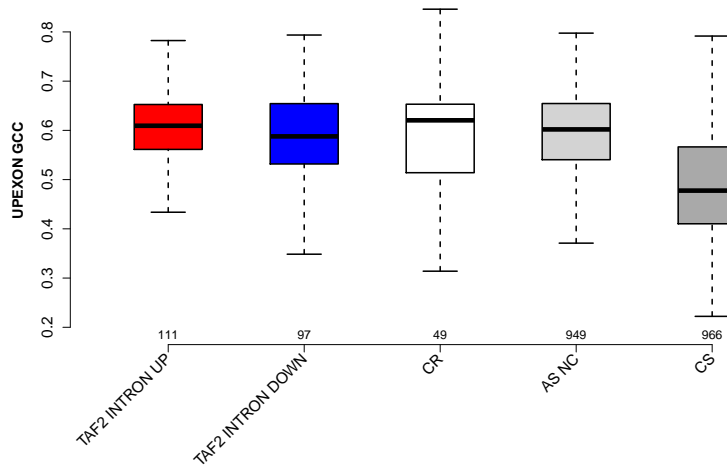
Significant results from Mann-Whitney U test:

- TAF2_INTRON_UP vs TAF2_INTRON_DOWN : 0.005912
mean: 0.568329 > 0.527257 , median: 0.588608 > 0.527378
- TAF2_INTRON_UP vs CS : 1.08842e-23
mean: 0.568329 > 0.436335 , median: 0.588608 > 0.41294
- TAF2_INTRON_DOWN vs CR : 0.0404285
mean: 0.527257 < 0.567094 , median: 0.527378 < 0.595349
- TAF2_INTRON_DOWN vs AS_NC : 7.34343e-05
mean: 0.527257 < 0.573131 , median: 0.527378 < 0.586288
- TAF2_INTRON_DOWN vs CS : 1.68118e-13
mean: 0.527257 > 0.436335 , median: 0.527378 > 0.41294
- CR vs CS : 8.34462e-12
mean: 0.567094 > 0.436335 , median: 0.595349 > 0.41294
- AS_NC vs CS : 2.805e-125
mean: 0.573131 > 0.436335 , median: 0.586288 > 0.41294

6.7 UPEXON GCC

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



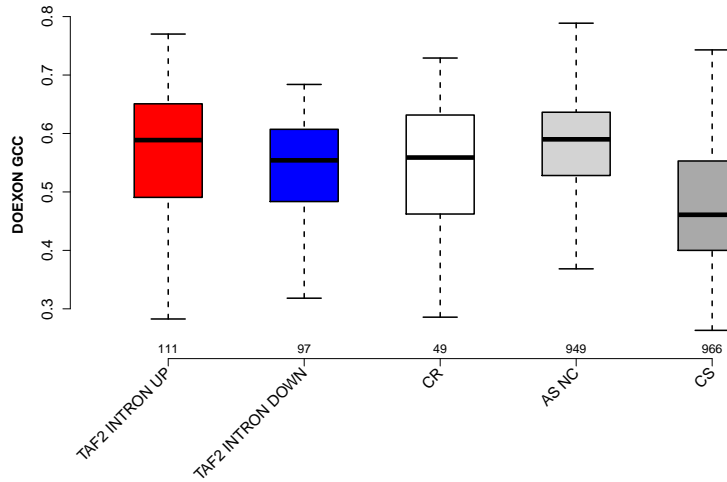
Significant results from Mann-Whitney U test:

- TAF2_INTRON_UP vs CS : 1.35078e-20
mean: 0.593268 > 0.492495 , median: 0.609375 > 0.477628
- TAF2_INTRON_DOWN vs CS : 8.56112e-16
mean: 0.585893 > 0.492495 , median: 0.587786 > 0.477628
- CR vs CS : 2.06025e-07
mean: 0.580403 > 0.492495 , median: 0.62042 > 0.477628
- AS_NC vs CS : 1.61282e-89
mean: 0.592162 > 0.492495 , median: 0.60197 > 0.477628

6.8 DOEXON GCC

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



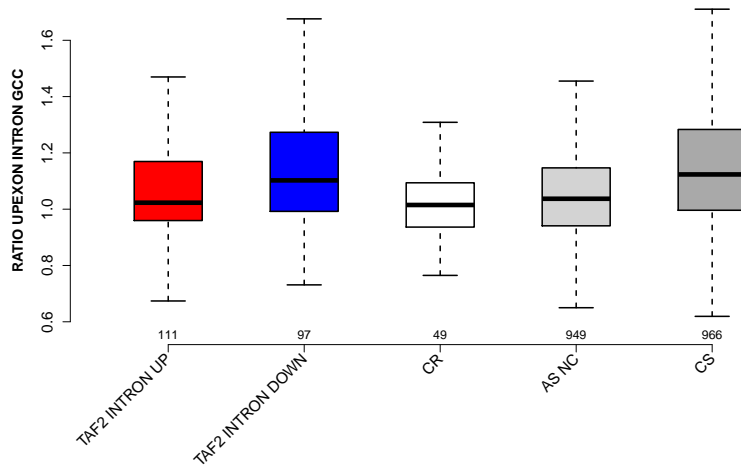
Significant results from Mann-Whitney U test:

- TAF2_INTRON_UP vs TAF2_INTRON_DOWN : 0.0396316
mean: 0.564055 > 0.541121 , median: 0.588672 > 0.554054
- TAF2_INTRON_UP vs CS : 7.55611e-15
mean: 0.564055 > 0.478673 , median: 0.588672 > 0.460893
- TAF2_INTRON_DOWN vs AS_NC : 0.000133148
mean: 0.541121 < 0.578015 , median: 0.554054 < 0.59
- TAF2_INTRON_DOWN vs CS : 1.35923e-09
mean: 0.541121 > 0.478673 , median: 0.554054 > 0.460893
- CR vs AS_NC : 0.0376878
mean: 0.540458 < 0.578015 , median: 0.558824 < 0.59
- CR vs CS : 0.000121241
mean: 0.540458 > 0.478673 , median: 0.558824 > 0.460893
- AS_NC vs CS : 2.08968e-95
mean: 0.578015 > 0.478673 , median: 0.59 > 0.460893

6.9 RATIO UPEXON INTRON GCC

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



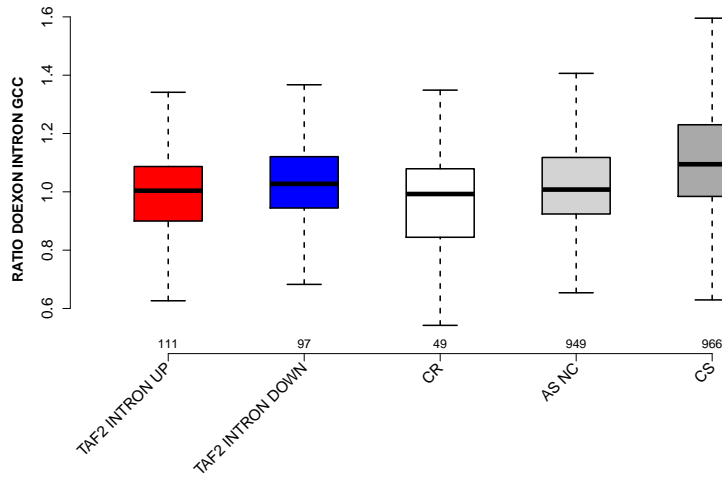
Significant results from Mann-Whitney U test:

- TAF2_INTRON_UP vs TAF2_INTRON_DOWN : 0.0131335
mean: 1.0731 < 1.1428 , median: 1.023 < 1.1023
- TAF2_INTRON_UP vs CS : 9.34929e-05
mean: 1.0731 < 1.1559 , median: 1.023 < 1.1235
- TAF2_INTRON_DOWN vs CR : 0.00655507
mean: 1.1428 > 1.0397 , median: 1.1023 > 1.0149
- TAF2_INTRON_DOWN vs AS_NC : 0.000218418
mean: 1.1428 > 1.0541 , median: 1.1023 > 1.037
- CR vs CS : 0.000345774
mean: 1.0397 < 1.1559 , median: 1.0149 < 1.1235
- AS_NC vs CS : 2.69574e-23
mean: 1.0541 < 1.1559 , median: 1.037 < 1.1235

6.10 RATIO DOEXON INTRON GCC

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



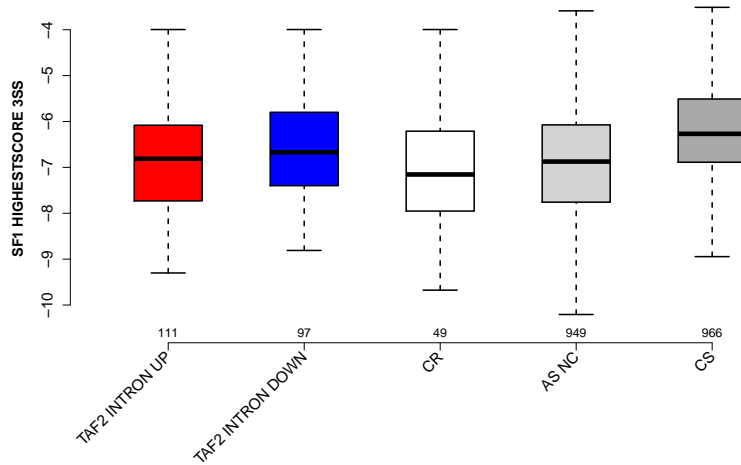
Significant results from Mann-Whitney U test:

- TAF2_INTRON_UP vs CS : 1.17596e-08
mean: 1.0092 < 1.1219 , median: 1.0038 < 1.0946
- TAF2_INTRON_DOWN vs CR : 0.0427087
mean: 1.0486 > 0.969457 , median: 1.0273 > 0.992481
- TAF2_INTRON_DOWN vs CS : 0.000136924
mean: 1.0486 < 1.1219 , median: 1.0273 < 1.0946
- CR vs CS : 7.04813e-07
mean: 0.969457 < 1.1219 , median: 0.992481 < 1.0946
- AS_NC vs CS : 8.35131e-28
mean: 1.0283 < 1.1219 , median: 1.0078 < 1.0946

6.11 SF1 HIGHESTSCORE 3SS

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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



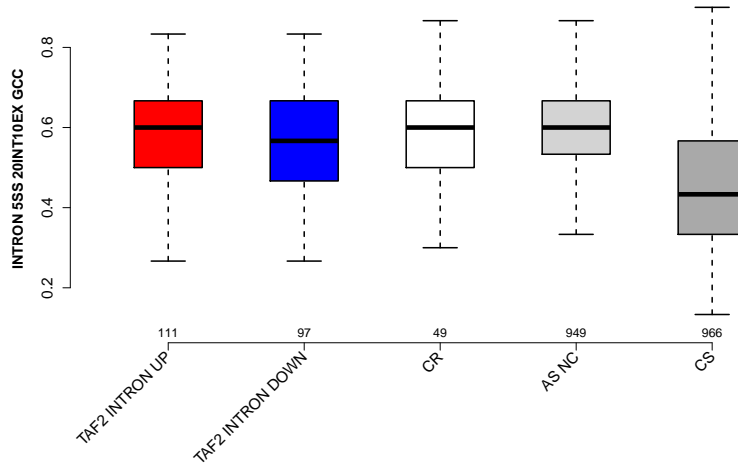
Significant results from Mann-Whitney U test:

- TAF2_INTRON_UP vs CS : 3.53798e-06
mean: -6.73335 < -6.19464 , median: -6.81202 < -6.26872
- TAF2_INTRON_DOWN vs CR : 0.0316435
mean: -6.57328 > -7.07336 , median: -6.67084 > -7.15474
- TAF2_INTRON_DOWN vs CS : 0.00100782
mean: -6.57328 < -6.19464 , median: -6.67084 < -6.26872
- CR vs CS : 1.95145e-06
mean: -7.07336 < -6.19464 , median: -7.15474 < -6.26872
- AS_NC vs CS : 6.28079e-34
mean: -6.83588 < -6.19464 , median: -6.8734 < -6.26872

6.12 INTRON 5SS 20INT10EX GCC

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



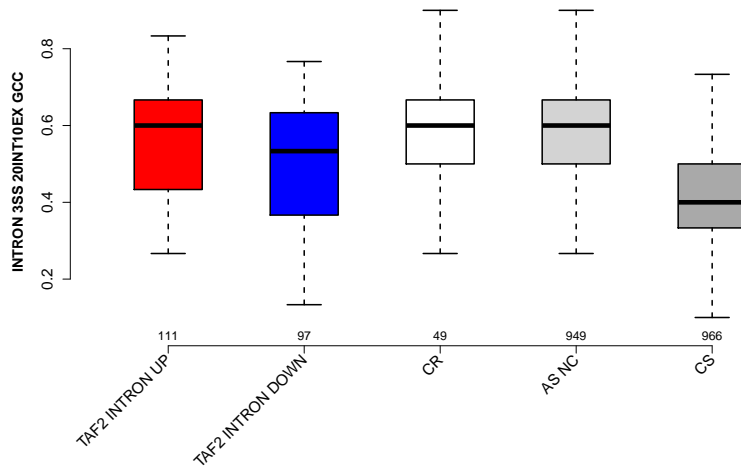
Significant results from Mann-Whitney U test:

- TAF2_INTRON_UP vs CS : 2.51212e-14
mean: 0.576577 > 0.461939 , median: 0.6 > 0.433333
- TAF2_INTRON_DOWN vs AS_NC : 0.0163667
mean: 0.561512 < 0.594766 , median: 0.566667 < 0.6
- TAF2_INTRON_DOWN vs CS : 6.67443e-10
mean: 0.561512 > 0.461939 , median: 0.566667 > 0.433333
- CR vs CS : 2.47e-07
mean: 0.57551 > 0.461939 , median: 0.6 > 0.433333
- AS_NC vs CS : 6.04821e-82
mean: 0.594766 > 0.461939 , median: 0.6 > 0.433333

6.13 INTRON 3SS 20INT10EX GCC

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



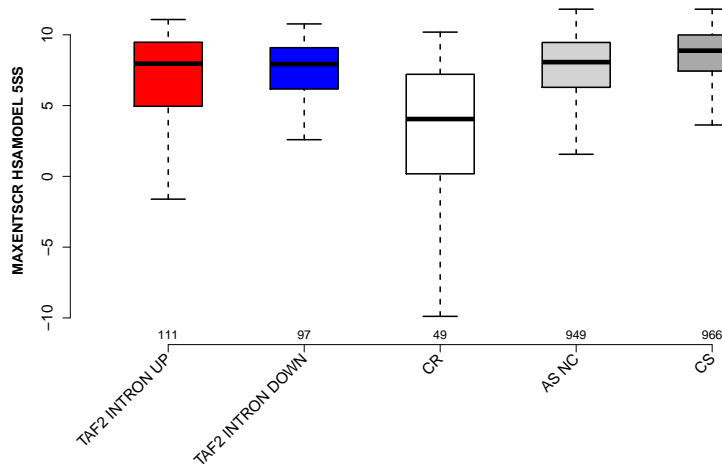
Significant results from Mann-Whitney U test:

- TAF2_INTRON_UP vs TAF2_INTRON_DOWN : 0.00117603
mean: 0.567267 > 0.500344 , median: 0.6 > 0.533333
- TAF2_INTRON_UP vs CS : 2.13779e-20
mean: 0.567267 > 0.418288 , median: 0.6 > 0.4
- TAF2_INTRON_DOWN vs CR : 0.0194048
mean: 0.500344 < 0.565306 , median: 0.533333 < 0.6
- TAF2_INTRON_DOWN vs AS_NC : 1.56959e-05
mean: 0.500344 < 0.568599 , median: 0.533333 < 0.6
- TAF2_INTRON_DOWN vs CS : 3.45365e-08
mean: 0.500344 > 0.418288 , median: 0.533333 > 0.4
- CR vs CS : 1.72611e-10
mean: 0.565306 > 0.418288 , median: 0.6 > 0.4
- AS_NC vs CS : 2.19029e-111
mean: 0.568599 > 0.418288 , median: 0.6 > 0.4

6.14 MAXENTSCR HSAMODEL 5SS

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



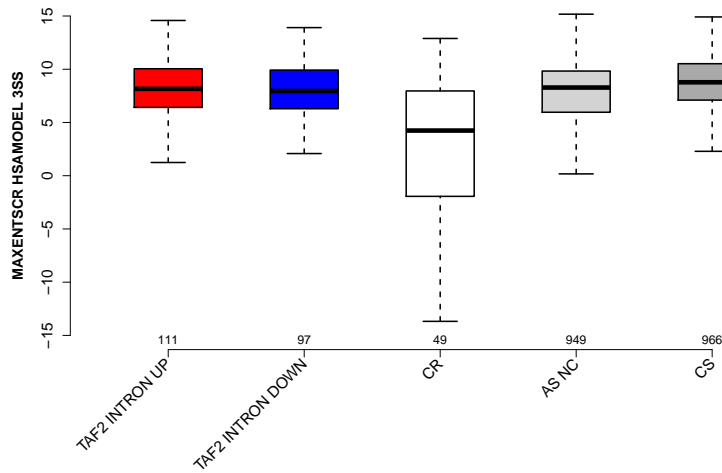
Significant results from Mann-Whitney U test:

- TAF2_INTRON_UP vs CR : 1.42262e-07
mean: 7.2566 > 2.4767 , median: 7.96 > 4.05
- TAF2_INTRON_UP vs CS : 2.94441e-06
mean: 7.2566 < 8.4679 , median: 7.96 < 8.88
- TAF2_INTRON_DOWN vs CR : 1.67402e-07
mean: 7.2361 > 2.4767 , median: 7.93 > 4.05
- TAF2_INTRON_DOWN vs CS : 1.22019e-06
mean: 7.2361 < 8.4679 , median: 7.93 < 8.88
- CR vs AS_NC : 1.19476e-10
mean: 2.4767 < 7.2152 , median: 4.05 < 8.07
- CR vs CS : 2.20109e-17
mean: 2.4767 < 8.4679 , median: 4.05 < 8.88
- AS_NC vs CS : 3.26574e-18
mean: 7.2152 < 8.4679 , median: 8.07 < 8.88

6.15 MAXENTSCR HSAMODEL 3SS

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



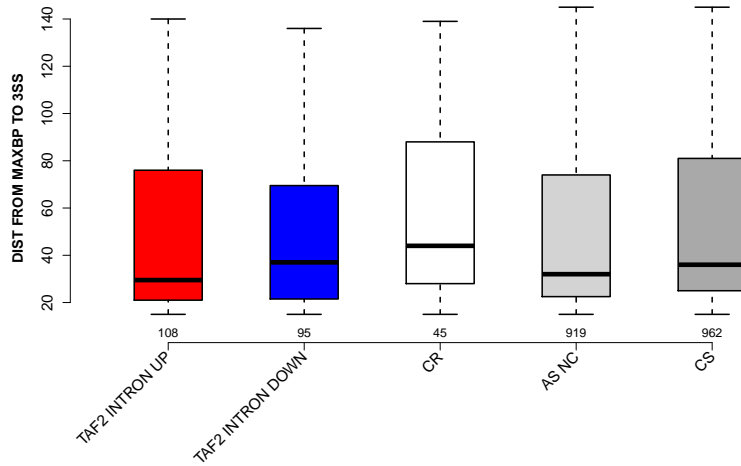
Significant results from Mann-Whitney U test:

- TAF2_INTRON_UP vs CR : 8.66463e-07
mean: 7.8656 > 1.2061 , median: 8.16 > 4.24
- TAF2_INTRON_UP vs CS : 0.0113712
mean: 7.8656 < 8.6681 , median: 8.16 < 8.775
- TAF2_INTRON_DOWN vs CR : 3.89808e-06
mean: 7.7303 > 1.2061 , median: 7.96 > 4.24
- TAF2_INTRON_DOWN vs CS : 0.0103728
mean: 7.7303 < 8.6681 , median: 7.96 < 8.775
- CR vs AS_NC : 3.03037e-08
mean: 1.2061 < 7.6425 , median: 4.24 < 8.28
- CR vs CS : 7.80899e-12
mean: 1.2061 < 8.6681 , median: 4.24 < 8.775
- AS_NC vs CS : 1.42038e-09
mean: 7.6425 < 8.6681 , median: 8.28 < 8.775

6.16 DIST FROM MAXBP TO 3SS

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Meaning: Distance to 3ss of best precited BP



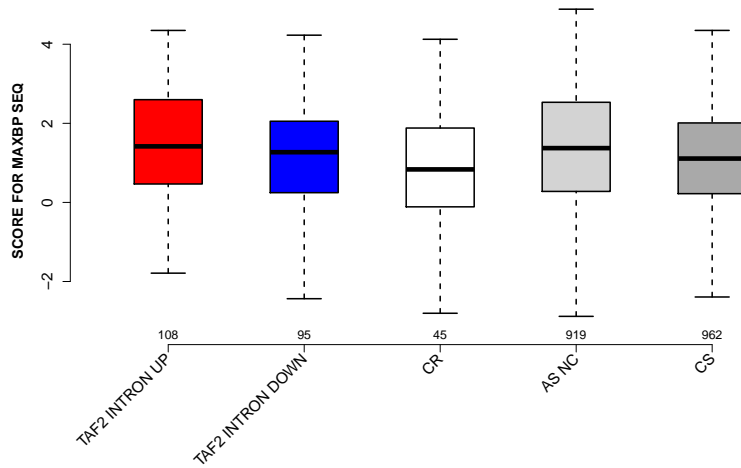
Significant results from Mann-Whitney U test:

- TAF2_INTRON_UP vs CR : 0.0240055
mean: 50.7685 < 60.6889 , median: 29.5 < 44
- TAF2_INTRON_UP vs CS : 0.0300902
mean: 50.7685 < 54.1944 , median: 29.5 < 36
- CR vs AS_NC : 0.0172338
mean: 60.6889 > 50.5473 , median: 44 > 32
- AS_NC vs CS : 0.000701499
mean: 50.5473 < 54.1944 , median: 32 < 36

6.17 SCORE FOR MAXBP SEQ

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Meaning: BP sequence score of best predicted BP



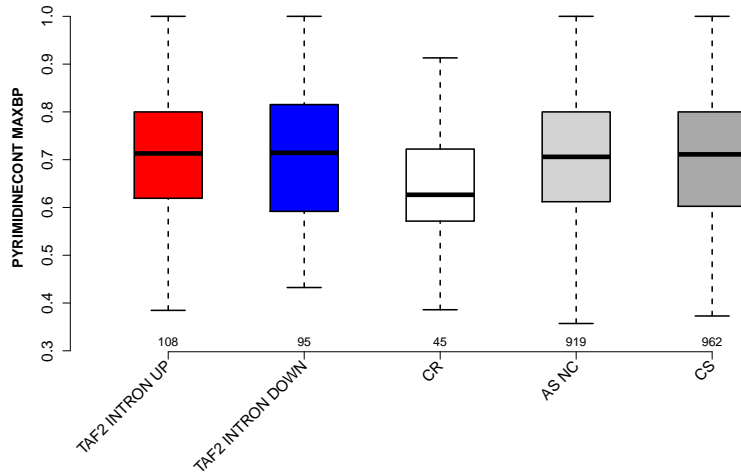
Significant results from Mann-Whitney U test:

- TAF2_INTRON_UP vs CR : 0.00788925
mean: 1.5003 > 0.727067 , median: 1.4172 > 0.834817
- TAF2_INTRON_UP vs CS : 0.0156213
mean: 1.5003 > 1.114 , median: 1.4172 > 1.1088
- CR vs AS_NC : 0.00895556
mean: 0.727067 < 1.3493 , median: 0.834817 < 1.3728
- AS_NC vs CS : 0.000284643
mean: 1.3493 > 1.114 , median: 1.3728 > 1.1088

6.18 PYRIMIDINECONT MAXBP

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



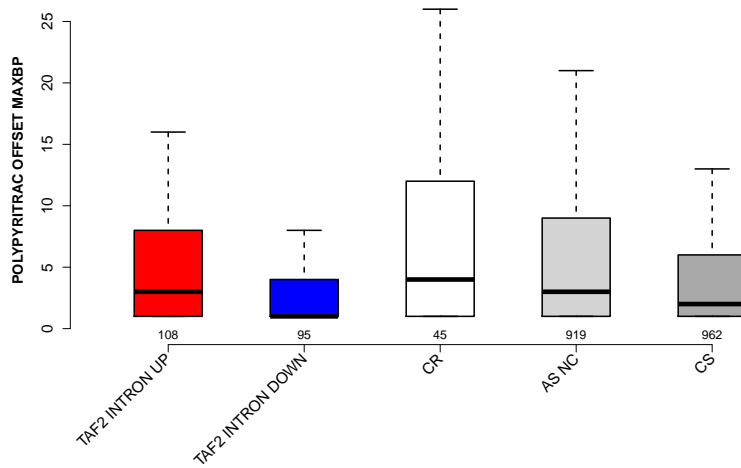
Significant results from Mann-Whitney U test:

- TAF2_INTRON_UP vs CR : 0.00266655
mean: 0.710472 > 0.640034 , median: 0.713075 > 0.626506
- TAF2_INTRON_DOWN vs CR : 0.014205
mean: 0.704809 > 0.640034 , median: 0.714286 > 0.626506
- CR vs AS_NC : 0.00255973
mean: 0.640034 < 0.702141 , median: 0.626506 < 0.705882
- CR vs CS : 0.00178398
mean: 0.640034 < 0.706294 , median: 0.626506 < 0.711111

6.19 POLYPYRITRAC OFFSET MAXBP

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



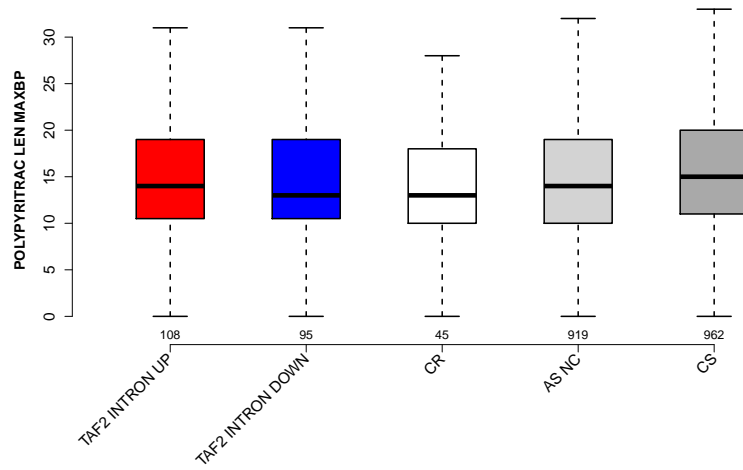
Significant results from Mann-Whitney U test:

- TAF2_INTRON_UP vs TAF2_INTRON_DOWN : 0.0368784
mean: 6.8704 > 6.0632 , median: 3 > 1
- TAF2_INTRON_UP vs CS : 0.0327155
mean: 6.8704 > 4.0541 , median: 3 > 2
- TAF2_INTRON_DOWN vs CR : 0.00299531
mean: 6.0632 < 8.0667 , median: 1 < 4
- TAF2_INTRON_DOWN vs AS_NC : 0.00219637
mean: 6.0632 < 6.445 , median: 1 < 3
- CR vs CS : 0.0013561
mean: 8.0667 > 4.0541 , median: 4 > 2
- AS_NC vs CS : 7.96057e-09
mean: 6.445 > 4.0541 , median: 3 > 2

6.20 POLYPYRITRAC LEN MAXBP

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Meaning: Polypyrimidine track length for best BP



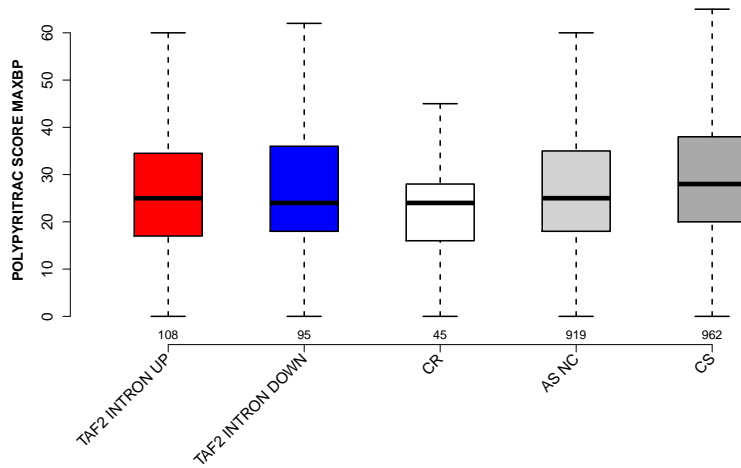
Significant results from Mann-Whitney U test:

- none

6.21 POLYPYRITRAC SCORE MAXBP

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Meaning: Polypyrimidine track score for best BP



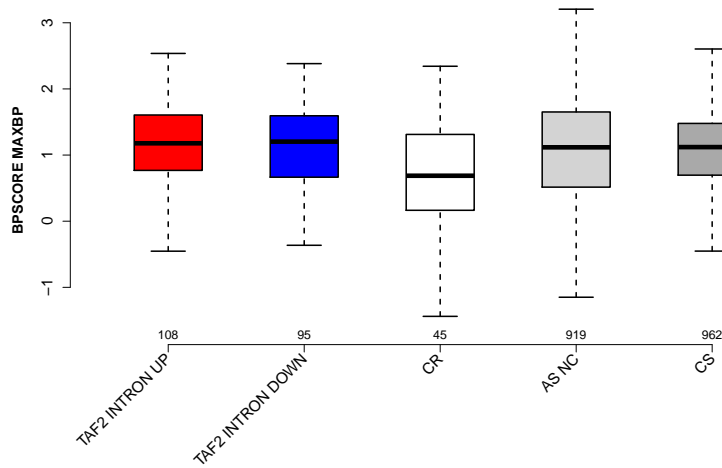
Significant results from Mann-Whitney U test:

- TAF2_INTRON_UP vs CS : 0.0274739
mean: 27.0093 < 31.1403 , median: 25 < 28
- CR vs CS : 0.00935101
mean: 28.0222 < 31.1403 , median: 24 < 28
- AS_NC vs CS : 4.43541e-06
mean: 28.2111 < 31.1403 , median: 25 < 28

6.22 BPSCORE MAXBP

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Meaning: SVM classification score of best BP



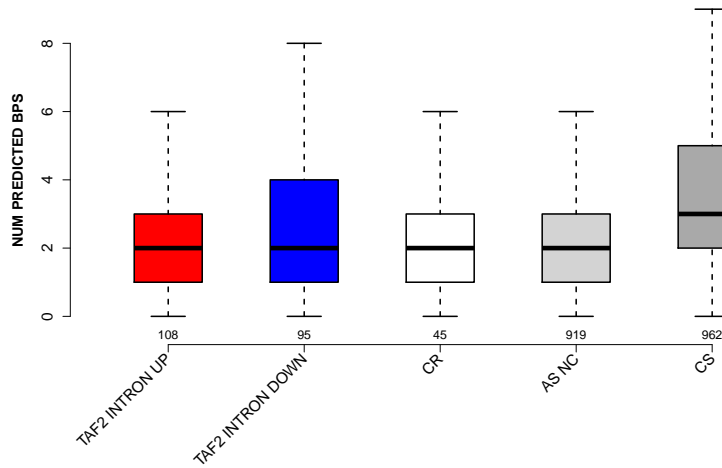
Significant results from Mann-Whitney U test:

- TAF2_INTRON_UP vs CR : 0.0110649
mean: 1.0354 > 0.643616 , median: 1.178 > 0.687251
- TAF2_INTRON_DOWN vs CR : 0.0139531
mean: 0.934106 > 0.643616 , median: 1.2031 > 0.687251
- CR vs AS_NC : 0.0159753
mean: 0.643616 < 1.0117 , median: 0.687251 < 1.1169
- CR vs CS : 0.00395986
mean: 0.643616 < 1.0995 , median: 0.687251 < 1.1203

6.23 NUM PREDICTED BPS

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



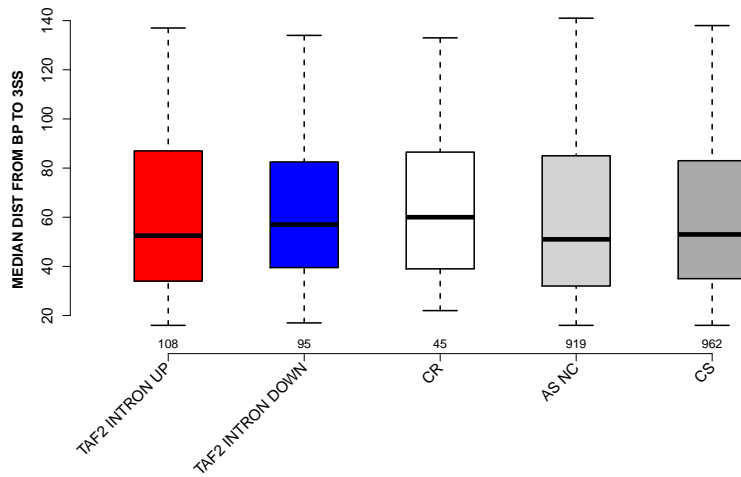
Significant results from Mann-Whitney U test:

- TAF2_INTRON_UP vs AS_NC : 0.0226021
mean: 2.5278 > 2.1132 , median: 2 = 2
- TAF2_INTRON_UP vs CS : 1.35522e-06
mean: 2.5278 < 3.4283 , median: 2 < 3
- TAF2_INTRON_DOWN vs CS : 3.99566e-05
mean: 2.6211 < 3.4283 , median: 2 < 3
- CR vs CS : 0.000223094
mean: 2.4 < 3.4283 , median: 2 < 3
- AS_NC vs CS : 4.30433e-50
mean: 2.1132 < 3.4283 , median: 2 < 3

6.24 MEDIAN DIST FROM BP TO 3SS

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



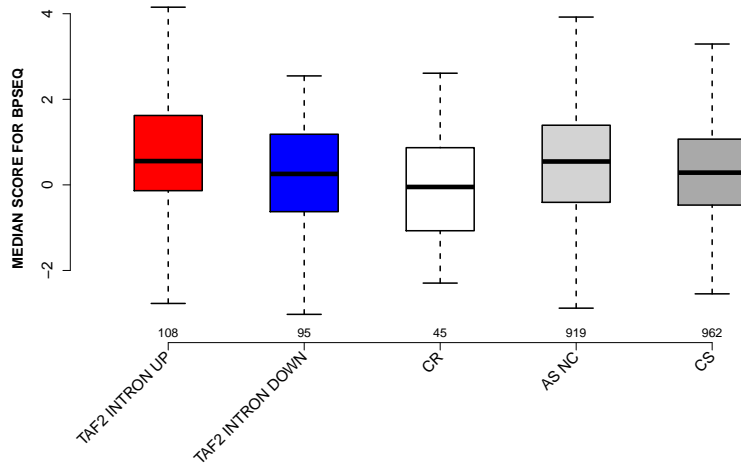
Significant results from Mann-Whitney U test:

- none

6.25 MEDIAN SCORE FOR BPSEQ

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



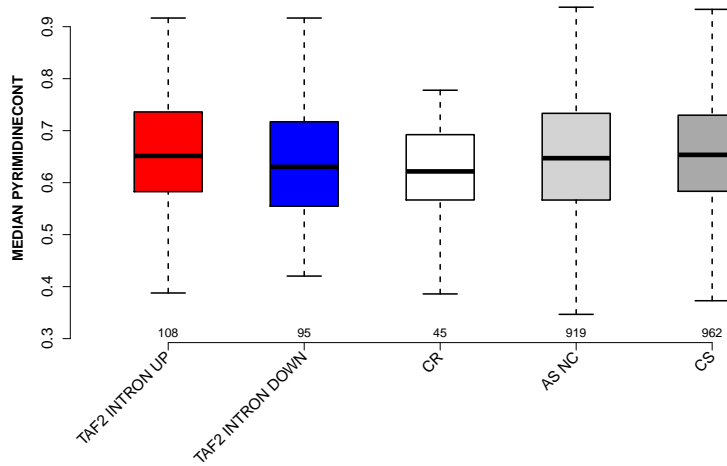
Significant results from Mann-Whitney U test:

- TAF2_INTRON_UP vs TAF2_INTRON_DOWN : 0.0269353
mean: 0.700525 > 0.182839 , median: 0.555944 > 0.25609
- TAF2_INTRON_UP vs CR : 0.00590751
mean: 0.700525 > 0.0265635 , median: 0.555944 > -0.0489897
- TAF2_INTRON_UP vs CS : 0.00185699
mean: 0.700525 > 0.29138 , median: 0.555944 > 0.286001
- CR vs AS_NC : 0.00855432
mean: 0.0265635 < 0.55621 , median: -0.0489897 < 0.546263
- AS_NC vs CS : 4.30369e-05
mean: 0.55621 > 0.29138 , median: 0.546263 > 0.286001

6.26 MEDIAN PYRIMIDINECONT

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



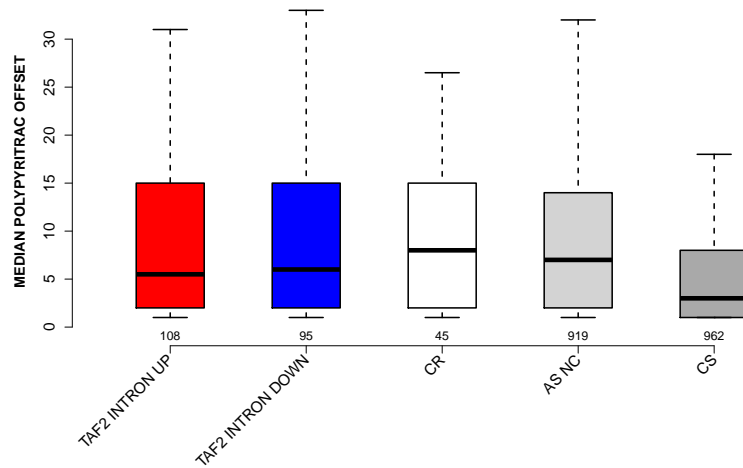
Significant results from Mann-Whitney U test:

- CR vs AS_NC : 0.0432779
mean: 0.608188 < 0.64973 , median: 0.621622 < 0.647059
- CR vs CS : 0.0119525
mean: 0.608188 < 0.658743 , median: 0.621622 < 0.653454

6.27 MEDIAN POLYPYRITRAC OFFSET

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



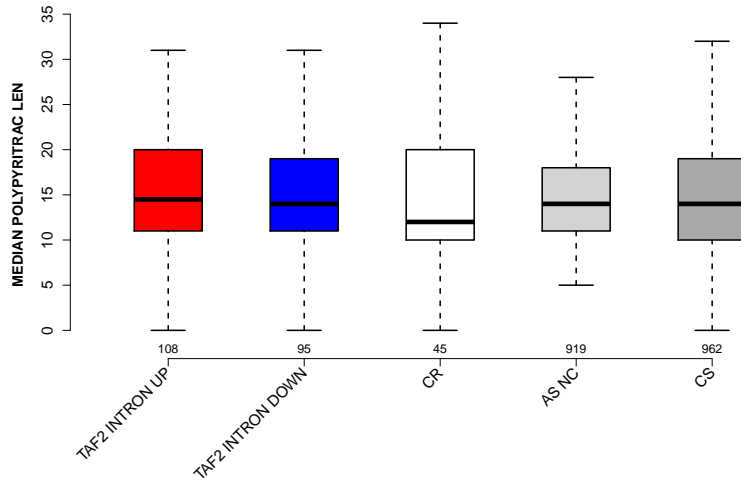
Significant results from Mann-Whitney U test:

- TAF2_INTRON_UP vs CS : 0.00022748
mean: 12.1991 > 6.2386 , median: 5.5 > 3
- TAF2_INTRON_DOWN vs CS : 0.00569816
mean: 12.0421 > 6.2386 , median: 6 > 3
- CR vs CS : 0.0002235
mean: 11.7667 > 6.2386 , median: 8 > 3
- AS_NC vs CS : 1.08241e-22
mean: 11.7198 > 6.2386 , median: 7 > 3

6.28 MEDIAN POLYPYRITRAC LEN

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



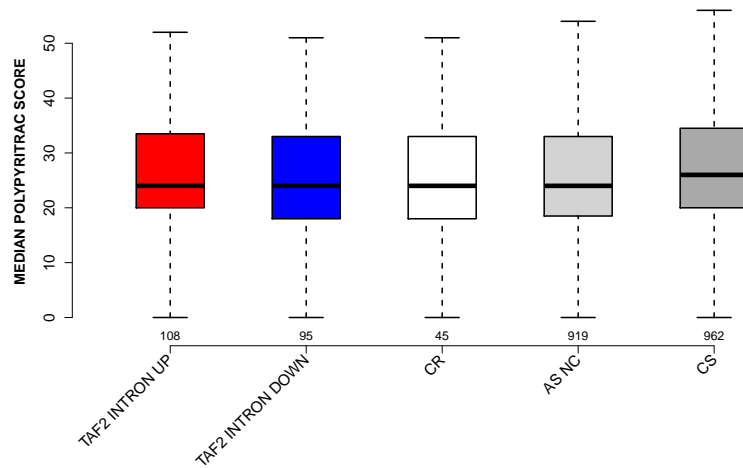
Significant results from Mann-Whitney U test:

- none

6.29 MEDIAN POLYPYRITRAC SCORE

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



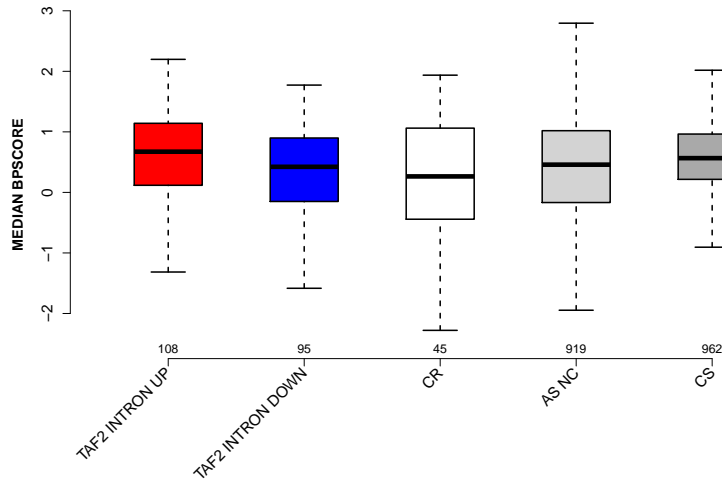
Significant results from Mann-Whitney U test:

- AS_NC vs CS : 0.000237225
mean: 27.2514 < 29.2968 , median: 24 < 26

6.30 MEDIAN BPSCORE

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



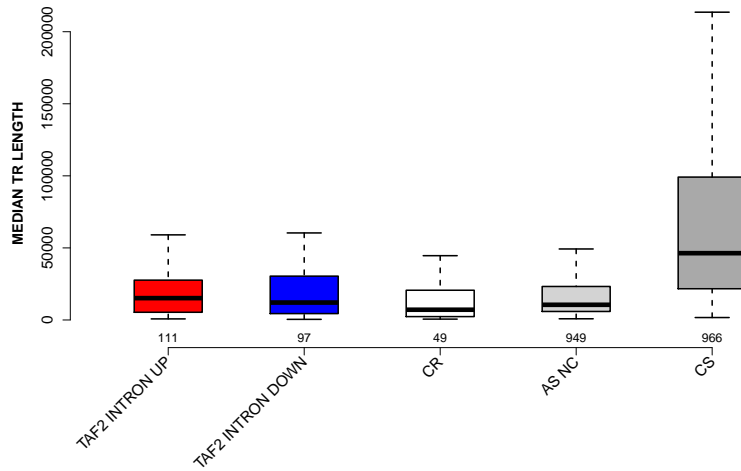
Significant results from Mann-Whitney U test:

- TAF2_INTRON_UP vs CR : 0.0339887
mean: 0.350907 > 0.0460514 , median: 0.672467 > 0.264176
- CR vs CS : 0.00548657
mean: 0.0460514 < 0.523785 , median: 0.264176 < 0.565722
- AS_NC vs CS : 0.000316957
mean: 0.264585 < 0.523785 , median: 0.45818 < 0.565722

6.31 MEDIAN TR LENGTH

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Meaning: median length of transcripts the intron occurs in



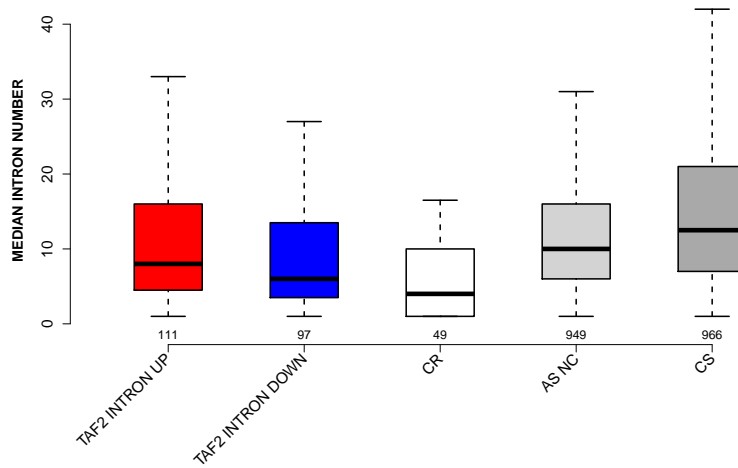
Significant results from Mann-Whitney U test:

- TAF2_INTRON_UP vs CR : 0.0210965
mean: 33301.4685 > 19738.1837 , median: 15146 > 7107
- TAF2_INTRON_UP vs CS : 1.54356e-20
mean: 33301.4685 < 75308.278 , median: 15146 < 46337.5
- TAF2_INTRON_DOWN vs CR : 0.0406311
mean: 29330.5464 > 19738.1837 , median: 12074 > 7107
- TAF2_INTRON_DOWN vs CS : 9.41636e-18
mean: 29330.5464 < 75308.278 , median: 12074 < 46337.5
- CR vs AS_NC : 0.0342503
mean: 19738.1837 < 20284.3203 , median: 7107 < 10531.5
- CR vs CS : 1.02478e-14
mean: 19738.1837 < 75308.278 , median: 7107 < 46337.5
- AS_NC vs CS : 1.04971e-127
mean: 20284.3203 < 75308.278 , median: 10531.5 < 46337.5

6.32 MEDIAN INTRON NUMBER

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Meaning: number of introns of transcripts where intron occurs in



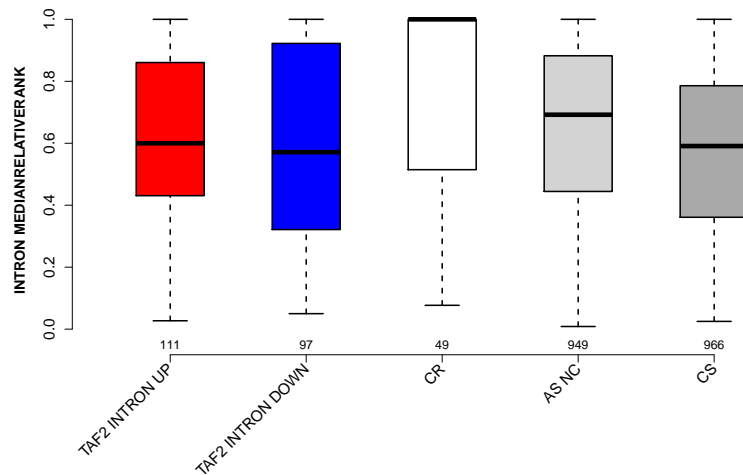
Significant results from Mann-Whitney U test:

- TAF2_INTRON_UP vs CR : 6.57163e-05
mean: 11.5 > 6.2857 , median: 8 > 4
- TAF2_INTRON_UP vs CS : 6.10713e-06
mean: 11.5 < 16.4752 , median: 8 < 12.5
- TAF2_INTRON_DOWN vs CR : 0.00417314
mean: 9.1134 > 6.2857 , median: 6 > 4
- TAF2_INTRON_DOWN vs AS_NC : 4.45197e-05
mean: 9.1134 < 12.7339 , median: 6 < 10
- TAF2_INTRON_DOWN vs CS : 8.51509e-11
mean: 9.1134 < 16.4752 , median: 6 < 12.5
- CR vs AS_NC : 2.5395e-08
mean: 6.2857 < 12.7339 , median: 4 < 10
- CR vs CS : 3.87834e-12
mean: 6.2857 < 16.4752 , median: 4 < 12.5
- AS_NC vs CS : 6.35515e-12
mean: 12.7339 < 16.4752 , median: 10 < 12.5

6.33 INTRON MEDIANRELATIVERANK

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



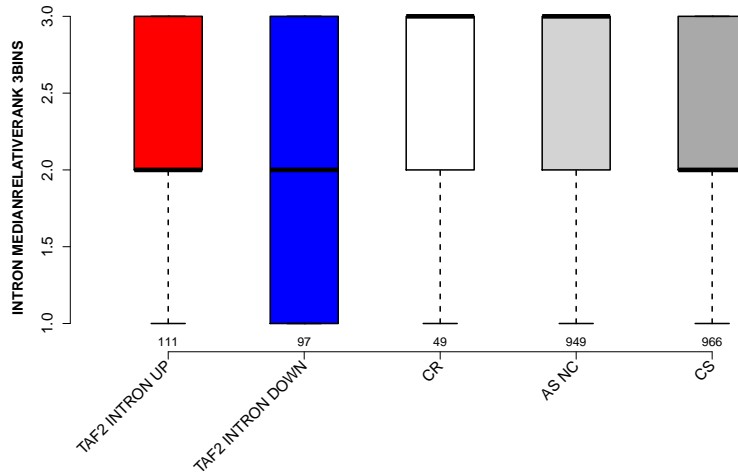
Significant results from Mann-Whitney U test:

- TAF2_INTRON_UP vs CR : 0.000155908
mean: 0.622705 < 0.787237 , median: 0.6 < 1
- TAF2_INTRON_DOWN vs CR : 0.000186628
mean: 0.596808 < 0.787237 , median: 0.571429 < 1
- CR vs AS_NC : 3.6448e-05
mean: 0.787237 > 0.649585 , median: 1 > 0.692105
- CR vs CS : 6.74798e-08
mean: 0.787237 > 0.576095 , median: 1 > 0.590972
- AS_NC vs CS : 1.47703e-09
mean: 0.649585 > 0.576095 , median: 0.692105 > 0.590972

6.34 INTRON MEDIANRELATIVERANK 3BINS

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



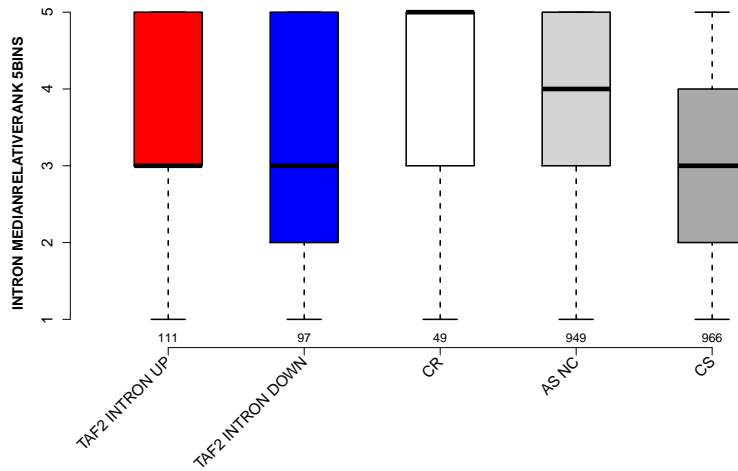
Significant results from Mann-Whitney U test:

- TAF2_INTRON_UP vs CR : 0.0318141
mean: 2.3514 < 2.5714 , median: 2 < 3
- TAF2_INTRON_DOWN vs CR : 0.0105636
mean: 2.2165 < 2.5714 , median: 2 < 3
- TAF2_INTRON_DOWN vs AS_NC : 0.0439243
mean: 2.2165 < 2.3962 , median: 2 < 3
- CR vs CS : 0.00048695
mean: 2.5714 > 2.2039 , median: 3 > 2
- AS_NC vs CS : 4.47311e-09
mean: 2.3962 > 2.2039 , median: 3 > 2

6.35 INTRON MEDIANRELATIVERANK 5BINS

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Meaning: similar to INTRON MEDIANRELATIVERANK 3BINS with 5 bins



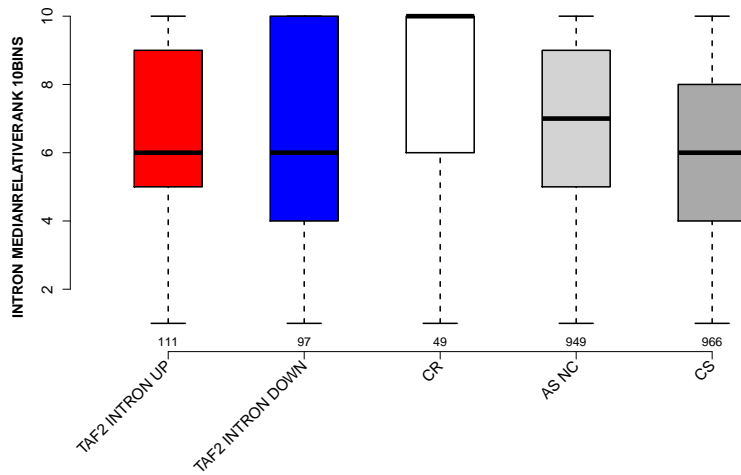
Significant results from Mann-Whitney U test:

- TAF2_INTRON_UP vs CR : 0.000635308
mean: 3.5225 < 4.1633 , median: 3 < 5
- TAF2_INTRON_DOWN vs CR : 0.00158815
mean: 3.3918 < 4.1633 , median: 3 < 5
- CR vs AS_NC : 0.00135058
mean: 4.1633 > 3.6786 , median: 5 > 4
- CR vs CS : 3.21625e-06
mean: 4.1633 > 3.3437 , median: 5 > 3
- AS_NC vs CS : 5.56003e-09
mean: 3.6786 > 3.3437 , median: 4 > 3

6.36 INTRON MEDIANRELATIVERANK 10BINS

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Meaning: similar to INTRON MEDIANRELATIVERANK 3BINS with 10 bins



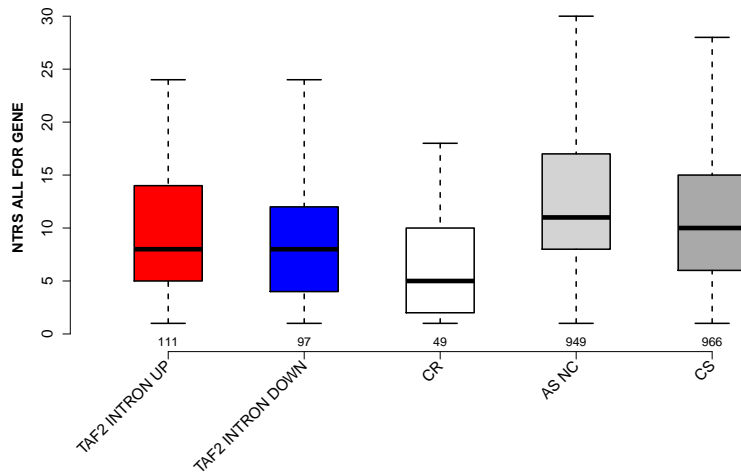
Significant results from Mann-Whitney U test:

- TAF2_INTRON_UP vs CR : 0.000166608
mean: 6.6667 < 8.1429 , median: 6 < 10
- TAF2_INTRON_DOWN vs CR : 0.00048624
mean: 6.4639 < 8.1429 , median: 6 < 10
- CR vs AS_NC : 8.77334e-05
mean: 8.1429 > 6.9442 , median: 10 > 7
- CR vs CS : 2.01587e-07
mean: 8.1429 > 6.2588 , median: 10 > 6
- AS_NC vs CS : 4.90923e-09
mean: 6.9442 > 6.2588 , median: 7 > 6

6.37 NTRS ALL FOR GENE

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



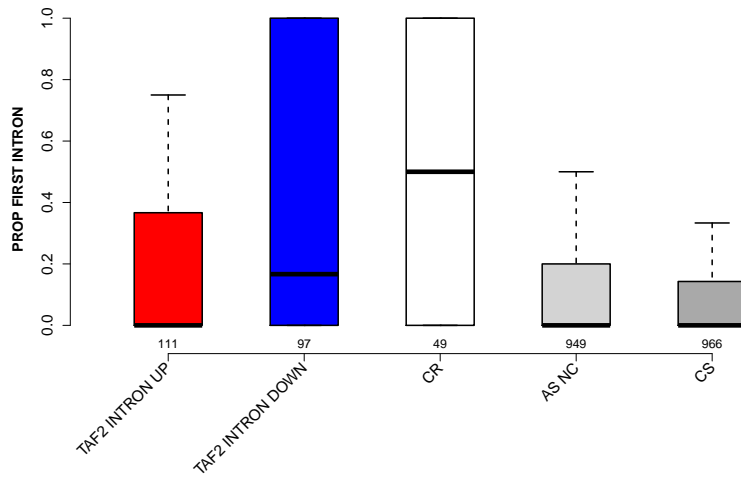
Significant results from Mann-Whitney U test:

- TAF2_INTRON_UP vs CR : 0.00158204
mean: 10.2072 > 7.0204 , median: 8 > 5
- TAF2_INTRON_UP vs AS_NC : 7.86328e-06
mean: 10.2072 < 13.1423 , median: 8 < 11
- TAF2_INTRON_UP vs CS : 0.020986
mean: 10.2072 < 11.266 , median: 8 < 10
- TAF2_INTRON_DOWN vs CR : 0.0190009
mean: 8.8144 > 7.0204 , median: 8 > 5
- TAF2_INTRON_DOWN vs AS_NC : 2.43118e-08
mean: 8.8144 < 13.1423 , median: 8 < 11
- TAF2_INTRON_DOWN vs CS : 0.000323491
mean: 8.8144 < 11.266 , median: 8 < 10
- CR vs AS_NC : 2.7049e-10
mean: 7.0204 < 13.1423 , median: 5 < 11
- CR vs CS : 2.70254e-07
mean: 7.0204 < 11.266 , median: 5 < 10
- AS_NC vs CS : 7.55967e-08
mean: 13.1423 > 11.266 , median: 11 > 10

6.38 PROP FIRST INTRON

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



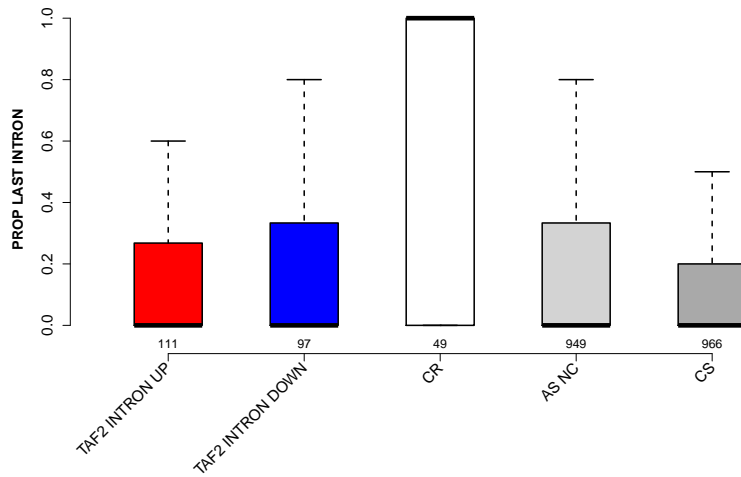
Significant results from Mann-Whitney U test:

- TAF2_INTRON_UP vs TAF2_INTRON_DOWN : 0.0212085
mean: 0.247153 < 0.368205 , median: 0 < 0.166667
- TAF2_INTRON_UP vs CR : 0.00731242
mean: 0.247153 < 0.489456 , median: 0 < 0.5
- TAF2_INTRON_UP vs CS : 0.00453583
mean: 0.247153 > 0.122024 , median: 0 = 0
- TAF2_INTRON_DOWN vs AS_NC : 2.18981e-06
mean: 0.368205 > 0.158179 , median: 0.166667 > 0
- TAF2_INTRON_DOWN vs CS : 5.02564e-10
mean: 0.368205 > 0.122024 , median: 0.166667 > 0
- CR vs AS_NC : 4.14762e-05
mean: 0.489456 > 0.158179 , median: 0.5 > 0
- CR vs CS : 3.50239e-07
mean: 0.489456 > 0.122024 , median: 0.5 > 0
- AS_NC vs CS : 0.000628243
mean: 0.158179 > 0.122024 , median: 0 = 0

6.39 PROP LAST INTRON

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



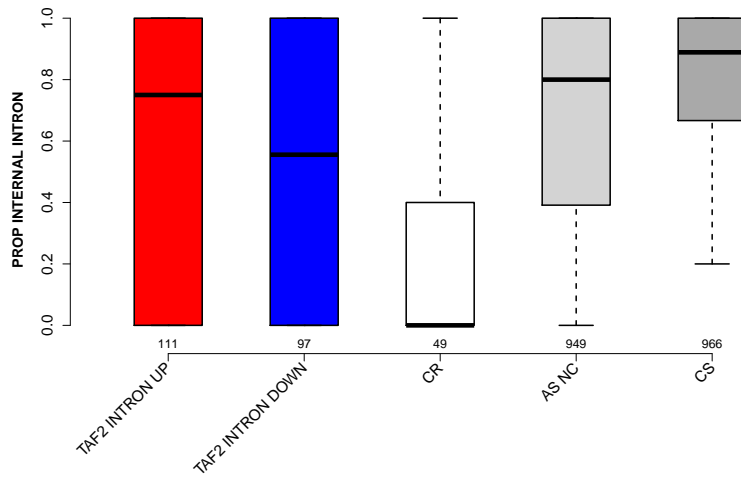
Significant results from Mann-Whitney U test:

- TAF2_INTRON_UP vs CR : 7.24044e-06
mean: 0.23853 < 0.62619 , median: 0 < 1
- TAF2_INTRON_DOWN vs CR : 2.82965e-05
mean: 0.264388 < 0.62619 , median: 0 < 1
- TAF2_INTRON_DOWN vs CS : 0.0442627
mean: 0.264388 > 0.152926 , median: 0 = 0
- CR vs AS_NC : 1.77408e-07
mean: 0.62619 > 0.237764 , median: 1 > 0
- CR vs CS : 6.34572e-12
mean: 0.62619 > 0.152926 , median: 1 > 0
- AS_NC vs CS : 5.66807e-09
mean: 0.237764 > 0.152926 , median: 0 = 0

6.40 PROP INTERNAL INTRON

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



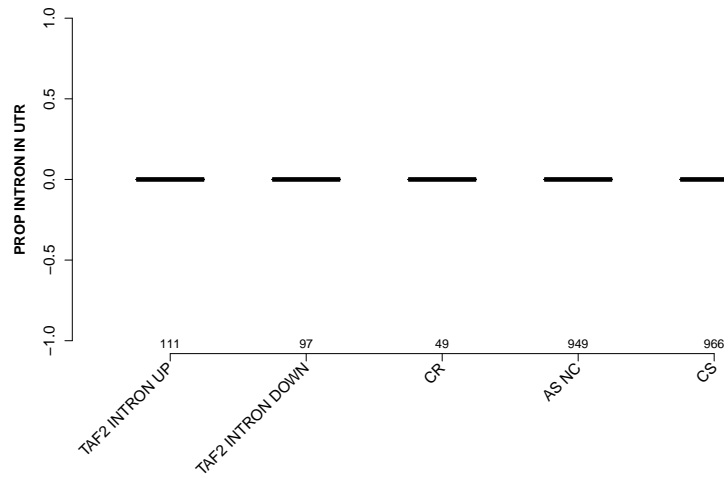
Significant results from Mann-Whitney U test:

- TAF2_INTRON_UP vs TAF2_INTRON_DOWN : 0.0481698
mean: 0.594658 > 0.481781 , median: 0.75 > 0.555556
- TAF2_INTRON_UP vs CR : 1.01407e-05
mean: 0.594658 > 0.242857 , median: 0.75 > 0
- TAF2_INTRON_UP vs CS : 0.00109877
mean: 0.594658 < 0.750345 , median: 0.75 < 0.888889
- TAF2_INTRON_DOWN vs CR : 0.00129454
mean: 0.481781 > 0.242857 , median: 0.555556 > 0
- TAF2_INTRON_DOWN vs AS_NC : 0.000813532
mean: 0.481781 < 0.647068 , median: 0.555556 < 0.8
- TAF2_INTRON_DOWN vs CS : 3.09574e-09
mean: 0.481781 < 0.750345 , median: 0.555556 < 0.888889
- CR vs AS_NC : 1.58787e-08
mean: 0.242857 < 0.647068 , median: 0 < 0.8
- CR vs CS : 1.2596e-12
mean: 0.242857 < 0.750345 , median: 0 < 0.888889
- AS_NC vs CS : 1.08108e-10
mean: 0.647068 < 0.750345 , median: 0.8 < 0.888889

6.41 PROP INTRON IN UTR

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Meaning: NTRS WITH INTRON IN UTR / NTRS WITH INTRON



Significant results from Mann-Whitney U test:

- TAF2_INTRON_UP vs CS : 0.047602
mean: 0.0242507 > 0.0111757 , median: 0 = 0
- TAF2_INTRON_DOWN vs CS : 0.00412622
mean: 0.0398856 > 0.0111757 , median: 0 = 0
- AS_NC vs CS : 0.00606231
mean: 0.0200644 > 0.0111757 , median: 0 = 0