

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

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Matt version 1.3.0

## Contents

<b>1</b>	<b>Infos</b>	<b>4</b>
<b>2</b>	<b>Warning: Please read this note carefully</b>	<b>4</b>
<b>3</b>	<b>Notes for publishing results</b>	<b>4</b>
<b>4</b>	<b>Data sets</b>	<b>5</b>
<b>5</b>	<b>Overview: Features with statistically significant differences (<math>p\text{-val} \leq 0.05</math>)</b>	<b>6</b>
<b>6</b>	<b>Details: Box plots and statistical assessments for all features</b>	<b>21</b>
6.1	EXON LENGTH . . . . .	21
6.2	UPEXON MEDIANLENGTH . . . . .	22
6.3	DOEXON MEDIANLENGTH . . . . .	23
6.4	RATIO UPEXON EXON LENGTH . . . . .	24
6.5	RATIO DOEXON EXON LENGTH . . . . .	25
6.6	UPINTRON MEDIANLENGTH . . . . .	26
6.7	DOINTRON MEDIANLENGTH . . . . .	27
6.8	RATIO UPINTRON EXON LENGTH . . . . .	28
6.9	RATIO DOINTRON EXON LENGTH . . . . .	29
6.10	EXON GCC . . . . .	30
6.11	UPINTRON GCC . . . . .	31
6.12	UPEXON GCC . . . . .	32
6.13	DOINTRON GCC . . . . .	33
6.14	DOEXON GCC . . . . .	34

6.15	RATIO UPEXON EXON GCC	35
6.16	RATIO UPINTRON EXON GCC	36
6.17	RATIO DOINTRON EXON GCC	37
6.18	RATIO DOEXON EXON GCC	38
6.19	SF1 HIGHESTSCORE 3SS UPINTRON	39
6.20	SF1 HIGHESTSCORE 3SS DOINTRON	40
6.21	UP 5SS 20INT10EX GCC	41
6.22	GCC 3SS 20INT10EX	42
6.23	GCC 5SS 20INT10EX	43
6.24	DO 3SS 20INT10EX GCC	44
6.25	MAXENTSCR HSAMODEL UPSTRM 5SS	45
6.26	MAXENTSCR HSAMODEL 3SS	46
6.27	MAXENTSCR HSAMODEL 5SS	47
6.28	MAXENTSCR HSAMODEL DOWNSTRM 3SS	48
6.29	DIST FROM MAXBP TO 3SS UPINTRON	49
6.30	SCORE FOR MAXBP SEQ UPINTRON	50
6.31	PYRIMIDINECONT MAXBP UPINTRON	51
6.32	POLYPYRITRAC OFFSET MAXBP UPINTRON	52
6.33	POLYPYRITRAC LEN MAXBP UPINTRON	53
6.34	POLYPYRITRAC SCORE MAXBP UPINTRON	54
6.35	BPSCORE MAXBP UPINTRON	55
6.36	NUM PREDICTED BPS UPINTRON	56
6.37	MEDIAN DIST FROM BP TO 3SS UPINTRON	57
6.38	MEDIAN SCORE FOR BPSEQ UPINTRON	58
6.39	MEDIAN PYRIMIDINECONT UPINTRON	59
6.40	MEDIAN POLYPYRITRAC OFFSET UPINTRON	60
6.41	MEDIAN POLYPYRITRAC LEN UPINTRON	61
6.42	MEDIAN POLYPYRITRAC SCORE UPINTRON	62
6.43	MEDIAN BPSCORE UPINTRON	63
6.44	DIST FROM MAXBP TO 3SS DOINTRON	64
6.45	SCORE FOR MAXBP SEQ DOINTRON	65
6.46	PYRIMIDINECONT MAXBP DOINTRON	66
6.47	POLYPYRITRAC OFFSET MAXBP DOINTRON	67
6.48	POLYPYRITRAC LEN MAXBP DOINTRON	68
6.49	POLYPYRITRAC SCORE MAXBP DOINTRON	69
6.50	BPSCORE MAXBP DOINTRON	70
6.51	NUM PREDICTED BPS DOINTRON	71
6.52	MEDIAN DIST FROM BP TO 3SS DOINTRON	72
6.53	MEDIAN SCORE FOR BPSEQ DOINTRON	73
6.54	MEDIAN PYRIMIDINECONT DOINTRON	74
6.55	MEDIAN POLYPYRITRAC OFFSET DOINTRON	75
6.56	MEDIAN POLYPYRITRAC LEN DOINTRON	76
6.57	MEDIAN POLYPYRITRAC SCORE DOINTRON	77
6.58	MEDIAN BPSCORE DOINTRON	78

6.59	MEDIAN TR LENGTH . . . . .	79
6.60	MEDIAN EXON NUMBER . . . . .	80
6.61	EXON MEDIANRELATIVERANK . . . . .	81
6.62	EXON MEDIANRELATIVERANK 3BINS . . . . .	82
6.63	EXON MEDIANRELATIVERANK 5BINS . . . . .	83
6.64	EXON MEDIANRELATIVERANK 10BINS . . . . .	84
6.65	NTRS ALL FOR GENE . . . . .	85
6.66	PROP FIRST EXON . . . . .	86
6.67	PROP LAST EXON . . . . .	87
6.68	PROP INTERNAL EXON . . . . .	88
6.69	PROP EXON IN UTR . . . . .	89

## 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:

TEST\_TAF2\_EXONS\_UP\_ANNO.tab

Selection criteria for defining exons groups:

TAF2\_UP\_EXONS : having value TAF2\_UP\_EXONS in column GROUP

TAF2\_EXONS\_DOWN : having value TAF2\_EXONS\_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

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.

TAF2\_UP\_EXONS: 270 / 258

TAF2\_EXONS\_DOWN: 296 / 276

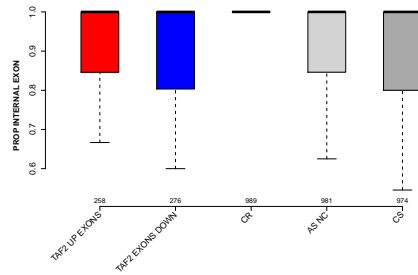
CR: 1000 / 989

AS\_NC: 1000 / 981

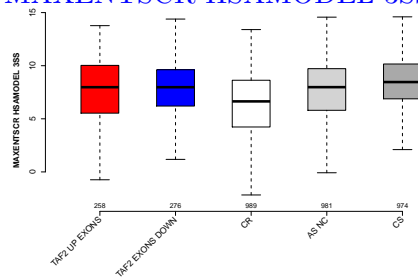
CS: 1000 / 974

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

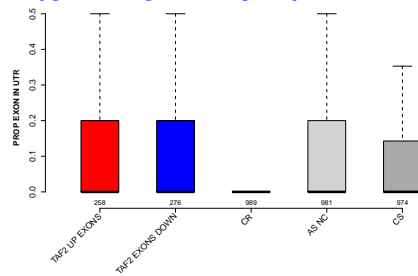
### PROP INTERNAL EXON



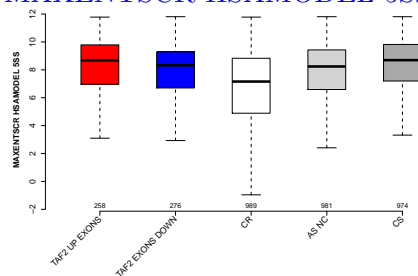
### MAXENTSCR HSAMODEL 3SS



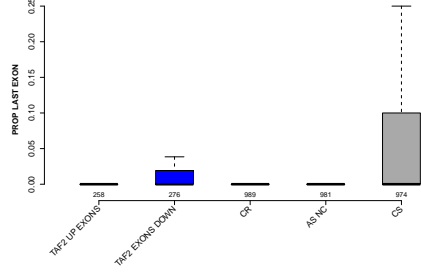
### PROP EXON IN UTR



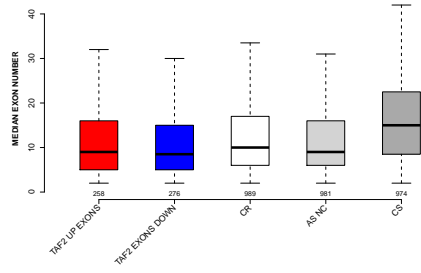
### MAXENTSCR HSAMODEL 5SS



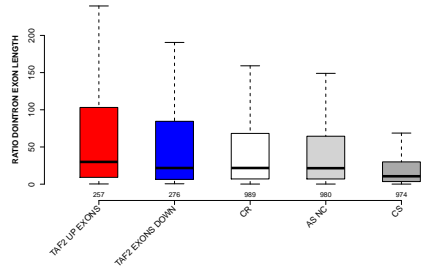
PROP LAST EXON



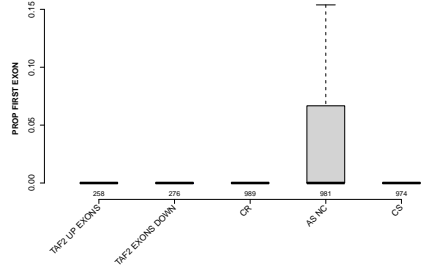
MEDIAN EXON NUMBER



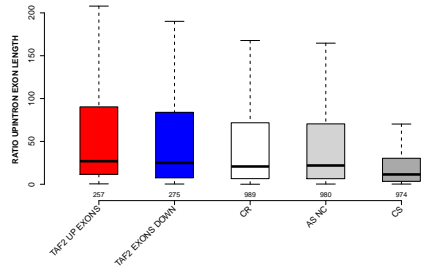
RATIO DONTINON EXON LENGTH



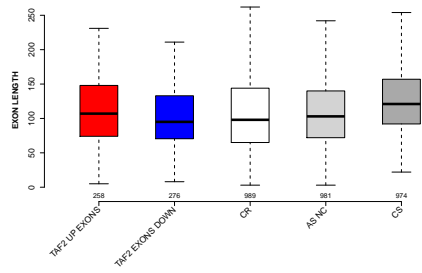
PROP FIRST EXON



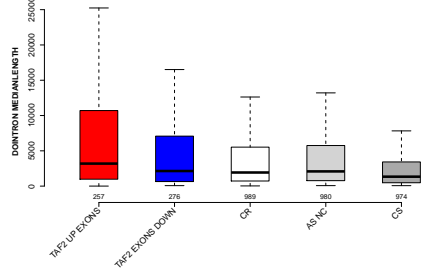
RATIO UPINTRON EXON LENGTH



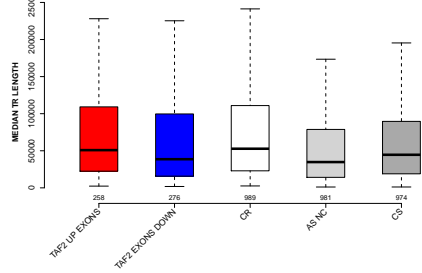
EXON LENGTH



DOINTRON MEDIANLENGTH

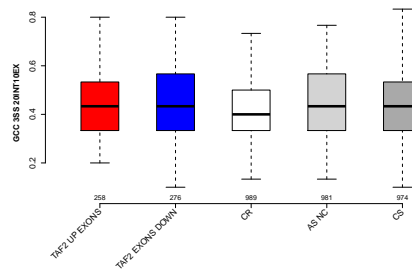


MEDIAN TR LENGTH

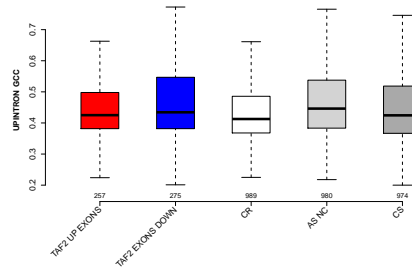




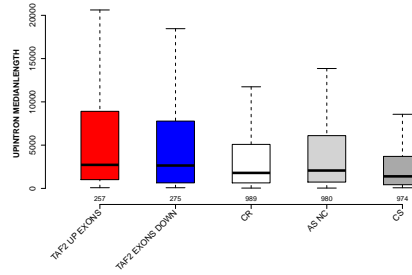
## GCC 3SS 20INT10EX



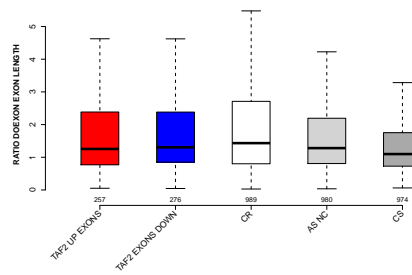
## UPINTRON GCC



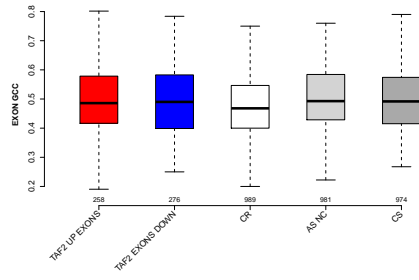
## UPINTRON MEDIANLENGTH



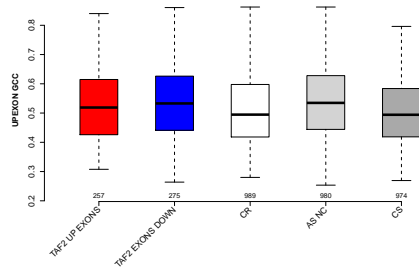
## RATIO DOEXON EXON LENGTH



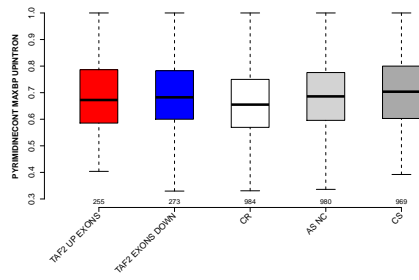
## EXON GCC



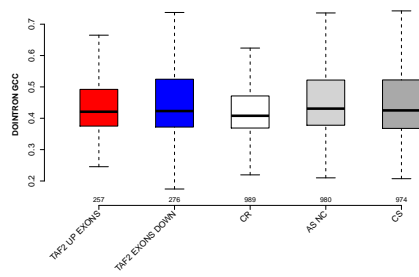
## UPEXON GCC



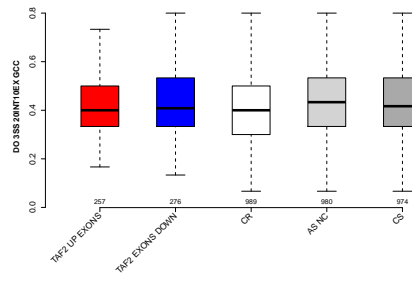
## PYRIMIDINECONT MAXBP UPINTRON



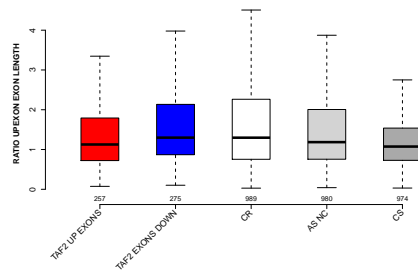
## DOINTRON GCC



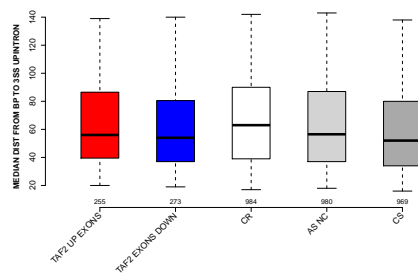
### DO 3SS 20INT10EX GCC



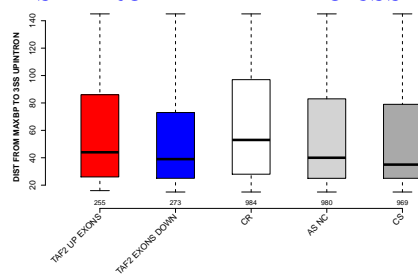
### RATIO UPEXON EXON LENGTH



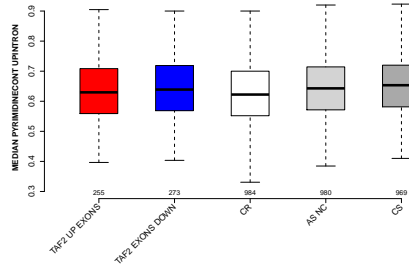
### MEDIAN DIST FROM BP TO 3SS UPINTRON



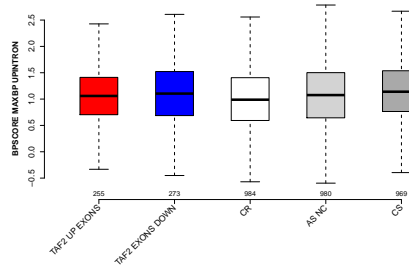
### DIST FROM MAXBP TO 3SS UPINTRON



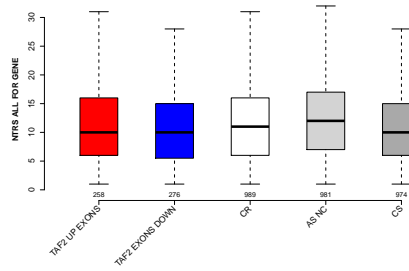
MEDIAN PYRIMIDINECONT UPINTRON



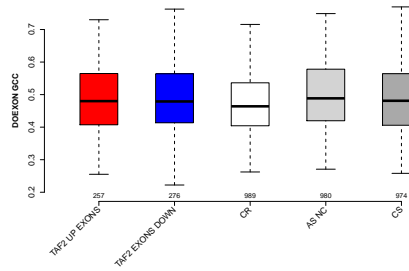
BPSCORE MAXBP UPINTRON



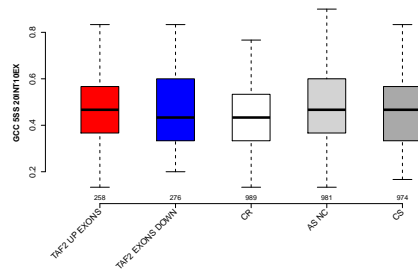
NTRS ALL FOR GENE



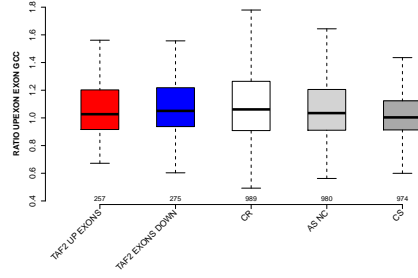
DOEXON GCC



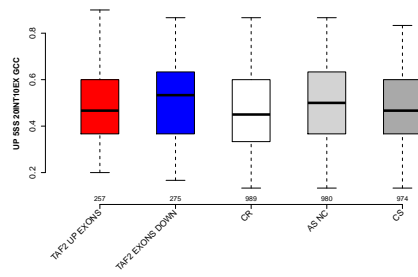
### GCC 5SS 20INT10EX



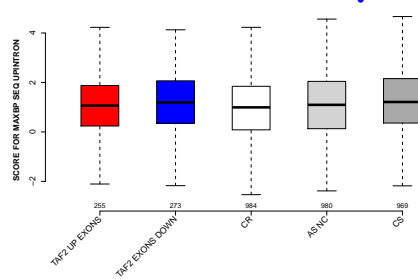
### RATIO UPEXON EXON GCC



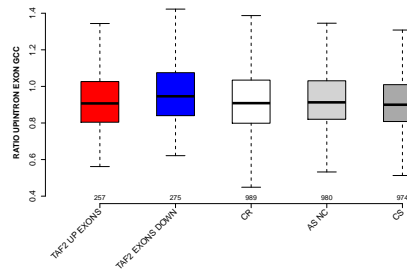
### UP 5SS 20INT10EX GCC



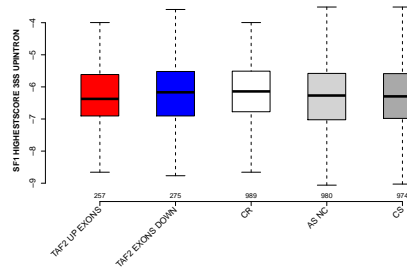
### SCORE FOR MAXBP SEQ UPINTRON



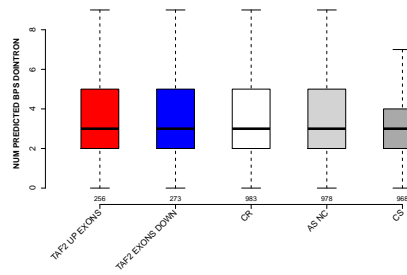
## RATIO UPINTRON EXON GCC



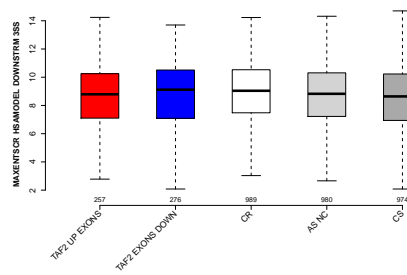
## SF1 HIGHESTSCORE 3SS UPINTRON



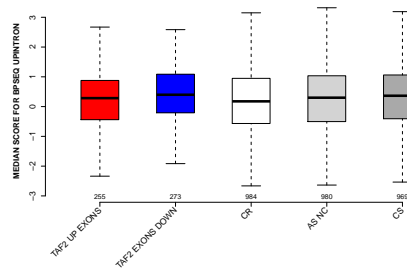
## NUM PREDICTED BPS DOWINTRON



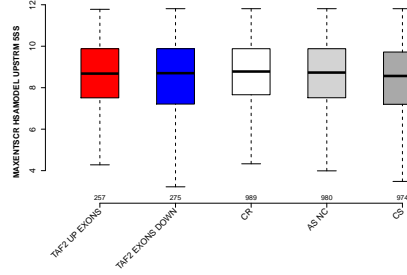
## MAXENTSCR HSAMODEL DOWNSTRM 3SS



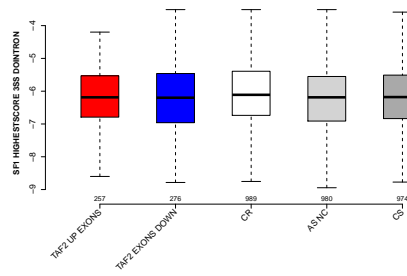
## MEDIAN SCORE FOR BPSEQ UPINTRON



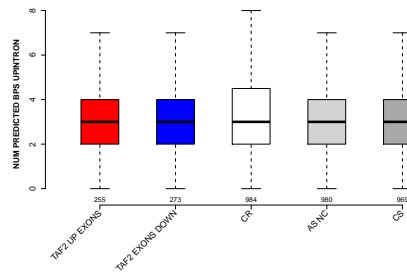
## MAXENTSCR HSAMODEL UPSTRM 5SS



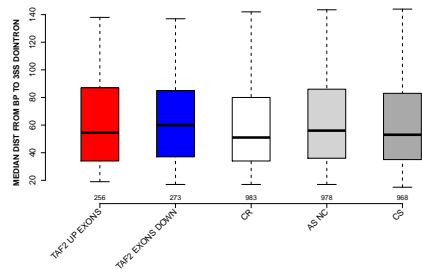
## SF1 HIGHESTSCORE 3SS DONTINON



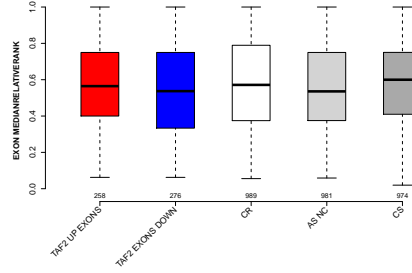
## NUM PREDICTED BPS UPINTRON



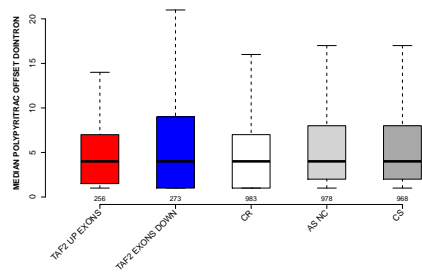
## MEDIAN DIST FROM BP TO 3SS DOWNTON



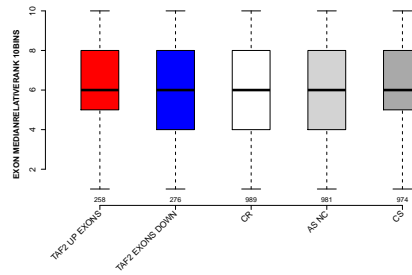
## EXON MEDIANRELATIVERANK



## MEDIAN POLYPYRITRAC OFFSET DOWNTON

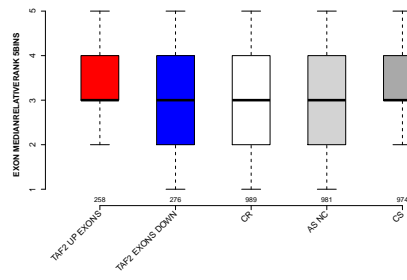


## EXON MEDIANRELATIVERANK 10BINS

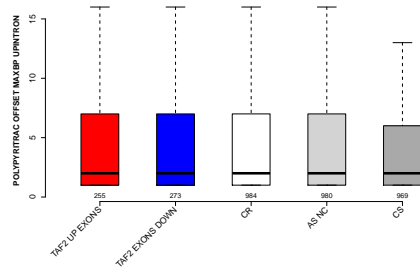




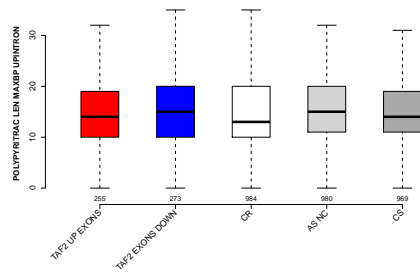
## EXON MEDIANRELATIVERANK 5BINS



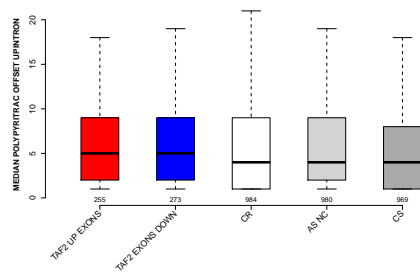
## POLYPYRITRAC OFFSET MAXBP UPINTRON



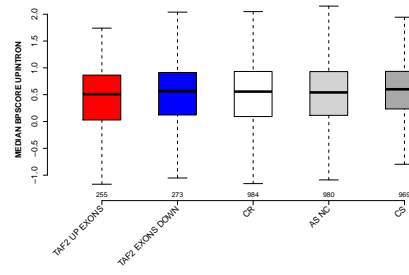
## POLYPYRITRAC LEN MAXBP UPINTRON



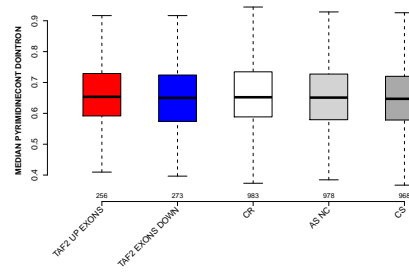
## MEDIAN POLYPYRITRAC OFFSET UPINTRON



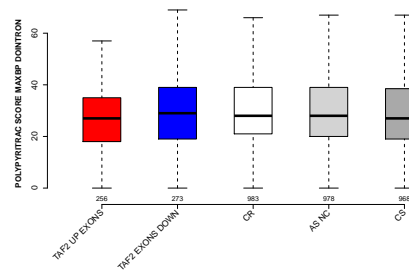
## MEDIAN BPSCORE UPINTRON



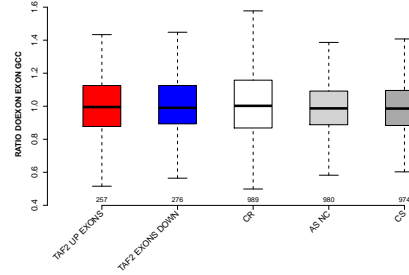
## MEDIAN PYRIMIDINECONT DOINTRON



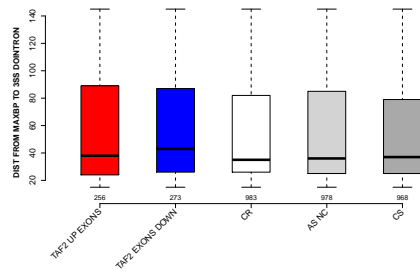
## POLYPYRITRAC SCORE MAXBP DOINTRON



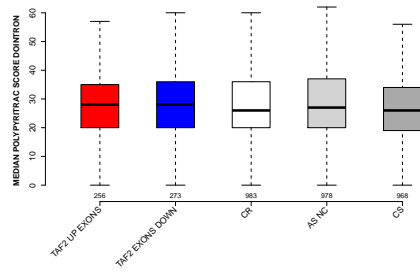
## RATIO DOEXON EXON GCC



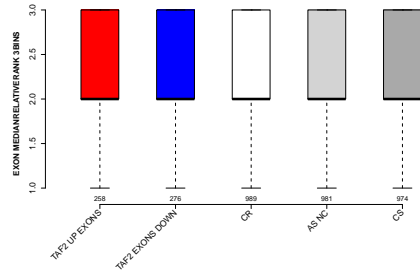
## DIST FROM MAXBP TO 3SS DONTON



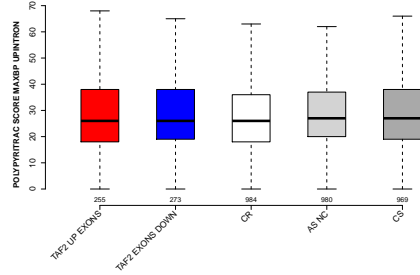
## MEDIAN POLYPYRITRAC SCORE DONTON



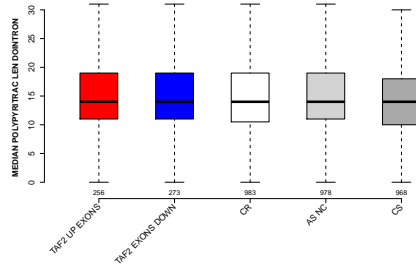
## EXON MEDIANRELATIVERANK 3BINS



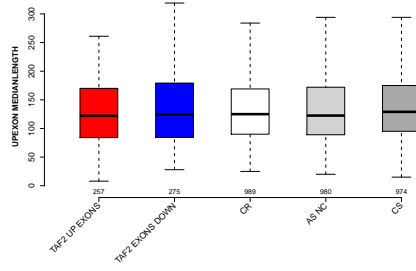
## POLYPYRITRAC SCORE MAXBP UPINTRON



MEDIAN POLYPYRITRAC LEN DOINTRON



UPEXON MEDIANLENGTH

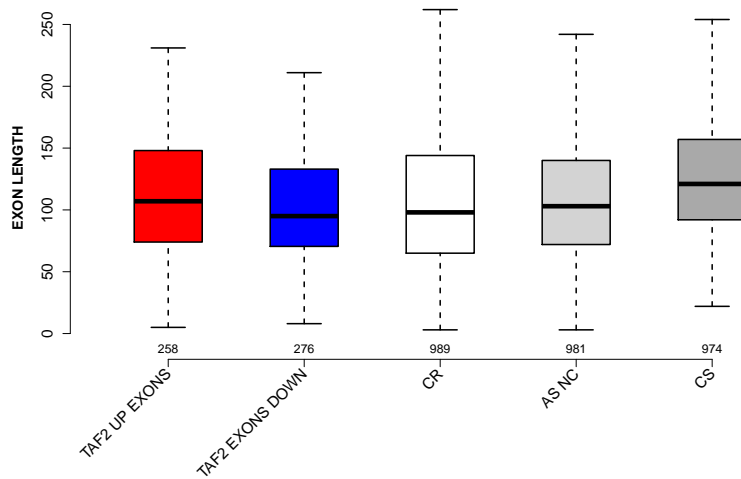


## 6 Details: Box plots and statistical assessments for all features

### 6.1 EXON LENGTH

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

Meaning:



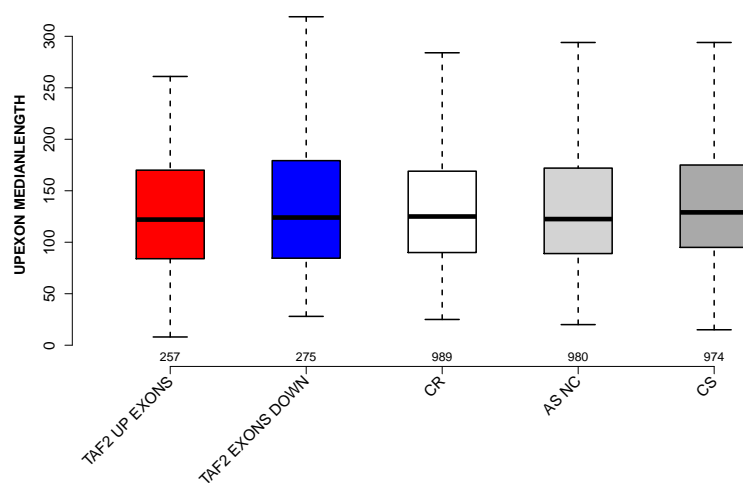
Significant results from Mann-Whitney U test:

- TAF2\_UP\_EXONS vs TAF2\_EXONS\_DOWN : 0.0296385  
mean: 130.2519 > 118.1775 , median: 107 > 95
- TAF2\_UP\_EXONS vs CR : 0.0344785  
mean: 130.2519 > 120.4944 , median: 107 > 98
- TAF2\_UP\_EXONS vs CS : 0.000214108  
mean: 130.2519 < 145.0226 , median: 107 < 121
- TAF2\_EXONS\_DOWN vs CS : 2.0255e-11  
mean: 118.1775 < 145.0226 , median: 95 < 121
- CR vs CS : 5.44103e-18  
mean: 120.4944 < 145.0226 , median: 98 < 121
- AS\_NC vs CS : 2.3565e-14  
mean: 129.0347 < 145.0226 , median: 103 < 121

## 6.2 UPEXON MEDIANLENGTH

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

Meaning: median length of up-stream exon



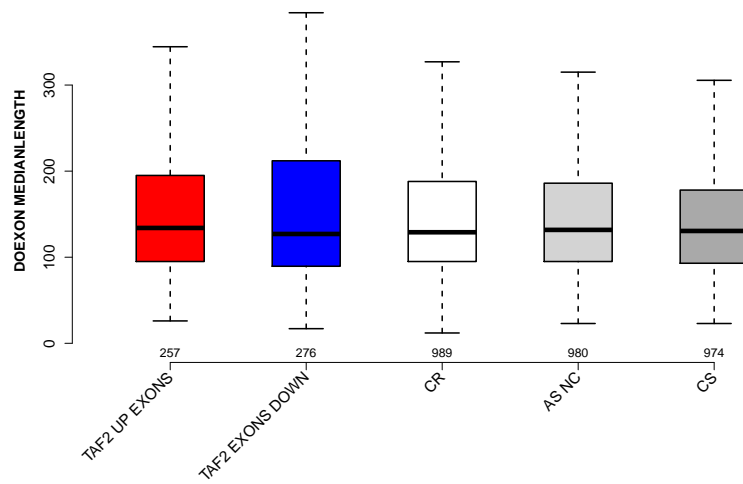
Significant results from Mann-Whitney U test:

- TAF2\_UP\_EXONS vs CS : 0.0479995  
mean: 155.5331 < 158.056 , median: 122 < 129
- AS\_NC vs CS : 0.0357366  
mean: 153.8842 < 158.056 , median: 122.5 < 129

## 6.3 DOEXON MEDIANLENGTH

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

Meaning: median length of down-stream exon



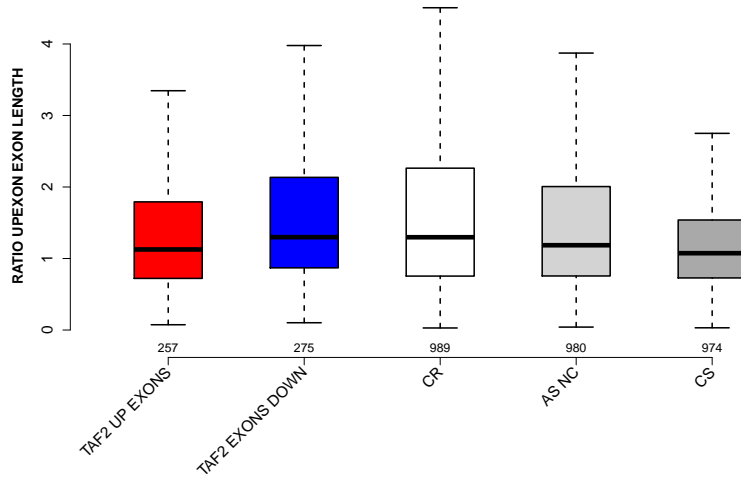
Significant results from Mann-Whitney U test:

- none

## 6.4 RATIO UPEXON EXON LENGTH

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

Meaning: median up-stream exon length / exon length



Significant results from Mann-Whitney U test:

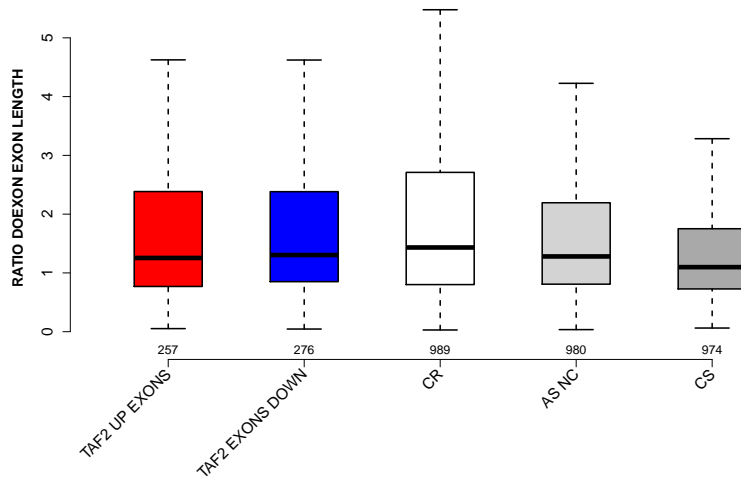
- TAF2\_UP\_EXONS vs TAF2\_EXONS\_DOWN : 0.0133359  
mean: 1.7855 < 1.9183 , median: 1.1263 < 1.2985
- TAF2\_UP\_EXONS vs CR : 0.00987165  
mean: 1.7855 < 4.1696 , median: 1.1263 < 1.2974
- TAF2\_EXONS\_DOWN vs CS : 2.36981e-06  
mean: 1.9183 > 1.3862 , median: 1.2985 > 1.0742
- CR vs AS\_NC : 0.0310702  
mean: 4.1696 > 1.9039 , median: 1.2974 > 1.1855
- CR vs CS : 8.83819e-10  
mean: 4.1696 > 1.3862 , median: 1.2974 > 1.0742
- AS\_NC vs CS : 7.68129e-05  
mean: 1.9039 > 1.3862 , median: 1.1855 > 1.0742



## 6.5 RATIO DOEXON EXON LENGTH

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

Meaning: median down-stream exon length / exon length



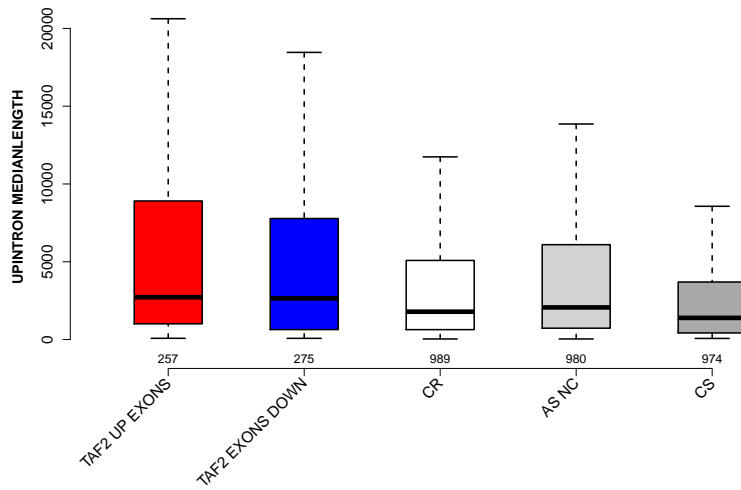
Significant results from Mann-Whitney U test:

- TAF2\_UP\_EXONS vs CS : 0.00214938  
mean: 3.354 > 2.1275 , median: 1.2541 > 1.0982
- TAF2\_EXONS\_DOWN vs CS : 0.00016175  
mean: 3.183 > 2.1275 , median: 1.3043 > 1.0982
- CR vs AS\_NC : 0.0221346  
mean: 4.4465 > 2.7477 , median: 1.4327 > 1.2802
- CR vs CS : 3.43936e-11  
mean: 4.4465 > 2.1275 , median: 1.4327 > 1.0982
- AS\_NC vs CS : 2.07873e-06  
mean: 2.7477 > 2.1275 , median: 1.2802 > 1.0982

## 6.6 UPINTRON MEDIANLENGTH

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

Meaning: median length of up-stream introns



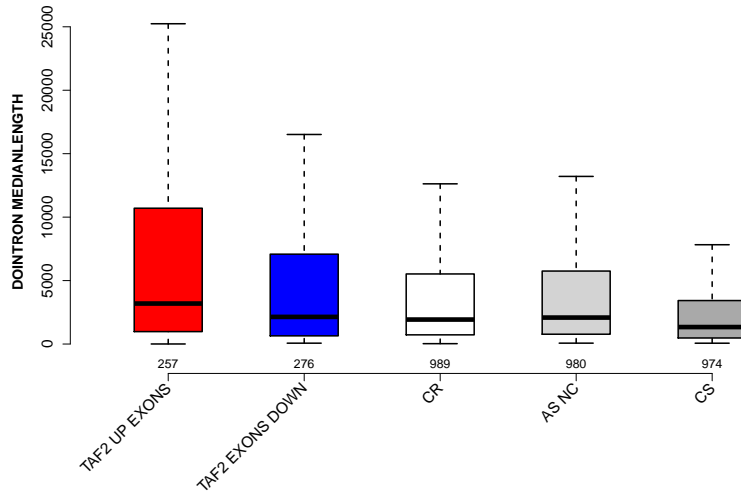
Significant results from Mann-Whitney U test:

- TAF2\_UP\_EXONS vs CR : 0.000214618  
mean: 10108.7004 > 6933.5627 , median: 2719 > 1790
- TAF2\_UP\_EXONS vs AS\_NC : 0.00716632  
mean: 10108.7004 > 6875.8551 , median: 2719 > 2065.5
- TAF2\_UP\_EXONS vs CS : 1.0904e-11  
mean: 10108.7004 > 4017.2854 , median: 2719 > 1392.5
- TAF2\_EXONS\_DOWN vs CS : 5.37926e-07  
mean: 8369.4182 > 4017.2854 , median: 2644 > 1392.5
- CR vs CS : 1.42861e-06  
mean: 6933.5627 > 4017.2854 , median: 1790 > 1392.5
- AS\_NC vs CS : 1.79815e-10  
mean: 6875.8551 > 4017.2854 , median: 2065.5 > 1392.5

## 6.7 DOINTRON MEDIANLENGTH

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

Meaning: median length of down-stream introns



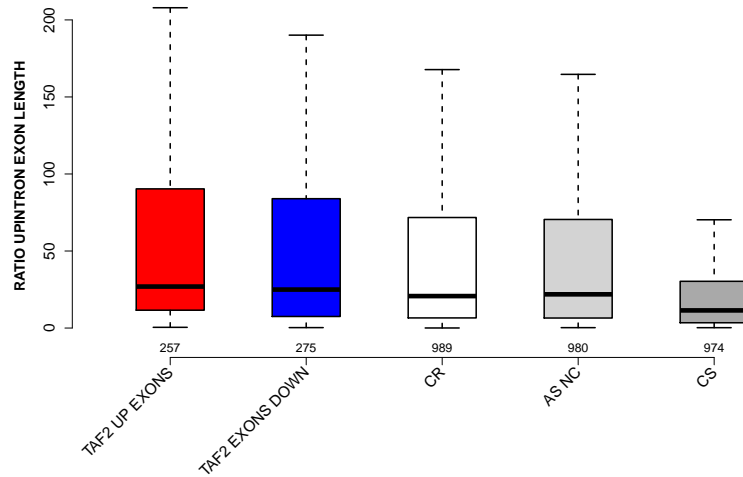
Significant results from Mann-Whitney U test:

- TAF2\_UP\_EXONS vs TAF2\_EXONS\_DOWN : 0.00673644  
mean: 9189.1751 > 8770.3297 , median: 3191 > 2139
- TAF2\_UP\_EXONS vs CR : 0.000112653  
mean: 9189.1751 > 7045.9788 , median: 3191 > 1929
- TAF2\_UP\_EXONS vs AS\_NC : 0.000275153  
mean: 9189.1751 > 6229.7811 , median: 3191 > 2085.5
- TAF2\_UP\_EXONS vs CS : 6.94033e-15  
mean: 9189.1751 > 3922.7721 , median: 3191 > 1337.5
- TAF2\_EXONS\_DOWN vs CS : 2.98936e-05  
mean: 8770.3297 > 3922.7721 , median: 2139 > 1337.5
- CR vs CS : 2.10602e-10  
mean: 7045.9788 > 3922.7721 , median: 1929 > 1337.5
- AS\_NC vs CS : 3.99634e-12  
mean: 6229.7811 > 3922.7721 , median: 2085.5 > 1337.5

## 6.8 RATIO UPINTRON EXON LENGTH

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

Meaning: median up-stream intron length / exon length



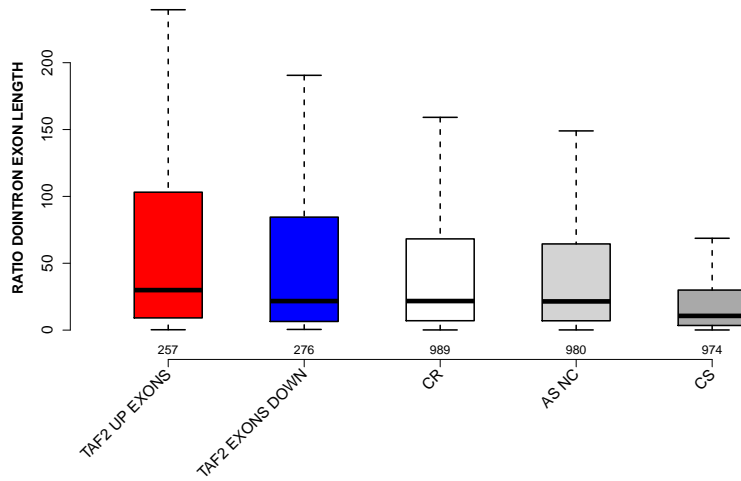
Significant results from Mann-Whitney U test:

- TAF2\_UP\_EXONS vs CR : 0.0235318  
mean: 99.615 < 122.4442 , median: 26.9208 > 20.7407
- TAF2\_UP\_EXONS vs AS\_NC : 0.0167523  
mean: 99.615 > 77.6027 , median: 26.9208 > 21.89
- TAF2\_UP\_EXONS vs CS : 2.97685e-16  
mean: 99.615 > 35.545 , median: 26.9208 > 11.4504
- TAF2\_EXONS\_DOWN vs CS : 7.34547e-13  
mean: 94.4533 > 35.545 , median: 24.9643 > 11.4504
- CR vs CS : 2.07358e-18  
mean: 122.4442 > 35.545 , median: 20.7407 > 11.4504
- AS\_NC vs CS : 3.24968e-18  
mean: 77.6027 > 35.545 , median: 21.89 > 11.4504

## 6.9 RATIO DOWNTON EXON LENGTH

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

Meaning: median down-stream intron length / exon length



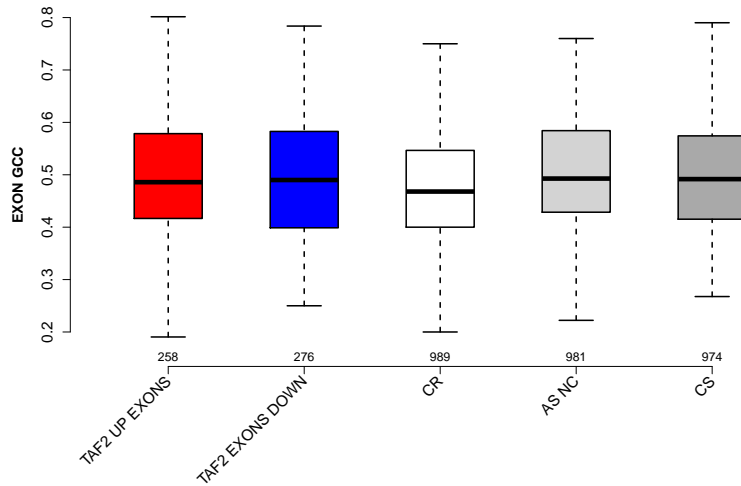
Significant results from Mann-Whitney U test:

- TAF2\_UP\_EXONS vs CR : 0.0174883  
mean: 97.9477 < 140.2298 , median: 29.9143 > 21.7339
- TAF2\_UP\_EXONS vs AS\_NC : 0.00257675  
mean: 97.9477 > 69.7215 , median: 29.9143 > 21.4731
- TAF2\_UP\_EXONS vs CS : 2.42231e-18  
mean: 97.9477 > 33.3658 , median: 29.9143 > 10.6316
- TAF2\_EXONS\_DOWN vs CS : 6.85422e-10  
mean: 103.8057 > 33.3658 , median: 21.71 > 10.6316
- CR vs CS : 5.05556e-23  
mean: 140.2298 > 33.3658 , median: 21.7339 > 10.6316
- AS\_NC vs CS : 4.6611e-20  
mean: 69.7215 > 33.3658 , median: 21.4731 > 10.6316

## 6.10 EXON GCC

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

Meaning: GC content of entire exon sequence



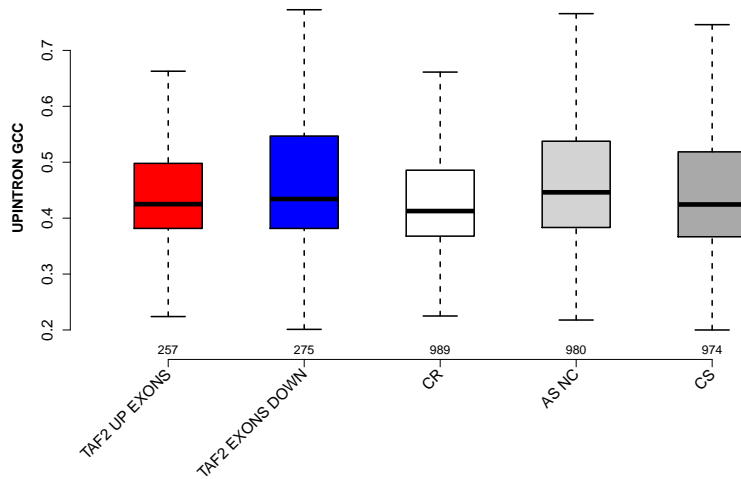
Significant results from Mann-Whitney U test:

- TAF2\_UP\_EXONS vs CR : 0.00795059  
mean: 0.495525 > 0.473215 , median: 0.48589 > 0.46798
- TAF2\_EXONS\_DOWN vs CR : 0.0168948  
mean: 0.494108 > 0.473215 , median: 0.490015 > 0.46798
- CR vs AS\_NC : 9.57981e-11  
mean: 0.473215 < 0.506761 , median: 0.46798 < 0.492754
- CR vs CS : 2.64364e-05  
mean: 0.473215 < 0.495129 , median: 0.46798 < 0.491708
- AS\_NC vs CS : 0.0165988  
mean: 0.506761 > 0.495129 , median: 0.492754 > 0.491708

## 6.11 UPINTRON GCC

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

Meaning: GC content of entire up-stream intron sequence



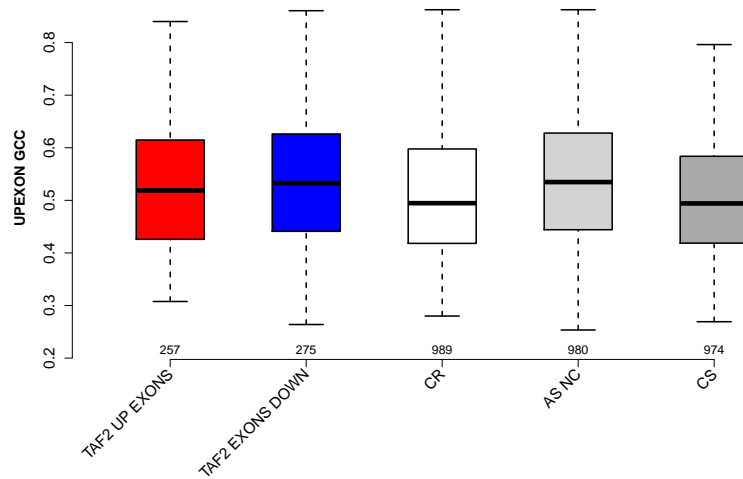
Significant results from Mann-Whitney U test:

- TAF2\_UP\_EXONS vs CR : 0.0238745  
mean: 0.450169 > 0.432143 , median: 0.425046 > 0.412684
- TAF2\_UP\_EXONS vs AS\_NC : 0.0181533  
mean: 0.450169 < 0.467422 , median: 0.425046 < 0.446163
- TAF2\_EXONS\_DOWN vs CR : 4.43842e-05  
mean: 0.466925 > 0.432143 , median: 0.434251 > 0.412684
- TAF2\_EXONS\_DOWN vs CS : 0.0216089  
mean: 0.466925 > 0.449191 , median: 0.434251 > 0.424454
- CR vs AS\_NC : 2.5693e-12  
mean: 0.432143 < 0.467422 , median: 0.412684 < 0.446163
- CR vs CS : 0.0128142  
mean: 0.432143 < 0.449191 , median: 0.412684 < 0.424454
- AS\_NC vs CS : 4.4428e-05  
mean: 0.467422 > 0.449191 , median: 0.446163 > 0.424454

## 6.12 UPEXON GCC

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

Meaning: GC content of entire up-stream exon sequence



Significant results from Mann-Whitney U test:

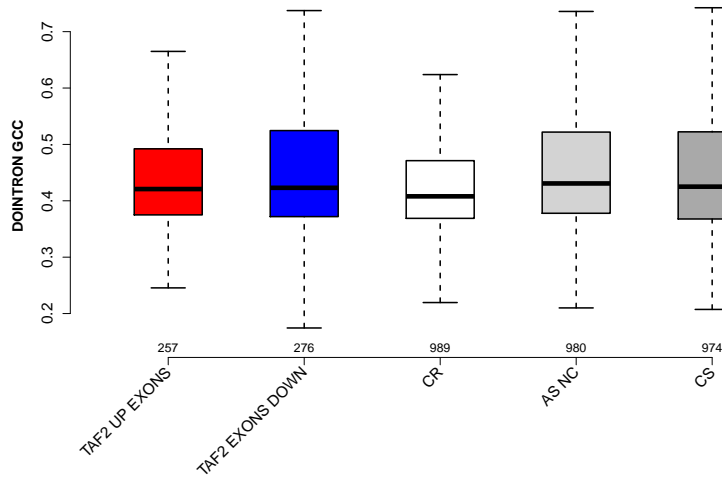
- TAF2\_UP\_EXONS vs CS : 0.0271183  
mean: 0.525439 > 0.503564 , median: 0.518868 > 0.49412
- TAF2\_EXONS\_DOWN vs CR : 0.000935998  
mean: 0.53728 > 0.50979 , median: 0.532847 > 0.494624
- TAF2\_EXONS\_DOWN vs CS : 9.64425e-05  
mean: 0.53728 > 0.503564 , median: 0.532847 > 0.49412
- CR vs AS\_NC : 3.67945e-08  
mean: 0.50979 < 0.539747 , median: 0.494624 < 0.534724
- AS\_NC vs CS : 1.42543e-10  
mean: 0.539747 > 0.503564 , median: 0.534724 > 0.49412



## 6.13 DOINTRON GCC

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

Meaning: GC content of entire down-stream intron sequence



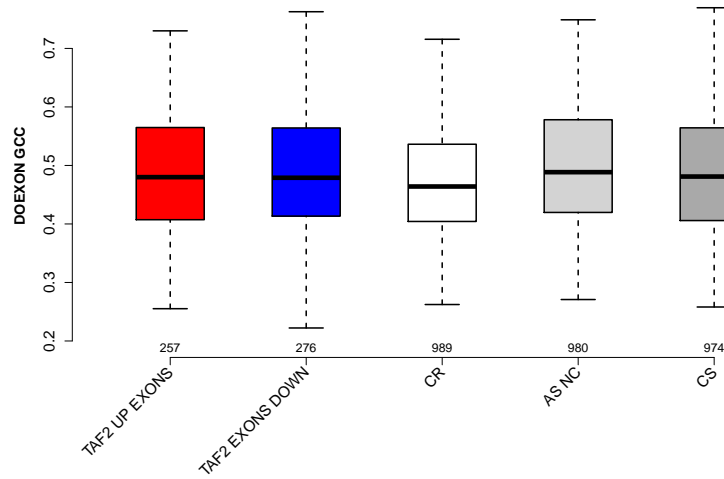
Significant results from Mann-Whitney U test:

- TAF2\_UP\_EXONS vs CR : 0.0141693  
mean: 0.443491 > 0.424278 , median: 0.420808 > 0.407912
- TAF2\_EXONS\_DOWN vs CR : 0.00224459  
mean: 0.450031 > 0.424278 , median: 0.423021 > 0.407912
- CR vs AS\_NC : 4.95333e-10  
mean: 0.424278 < 0.45619 , median: 0.407912 < 0.430774
- CR vs CS : 1.18618e-05  
mean: 0.424278 < 0.449135 , median: 0.407912 < 0.425062

## 6.14 DOEXON GCC

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

Meaning: GC content of entire down-stream exon sequence



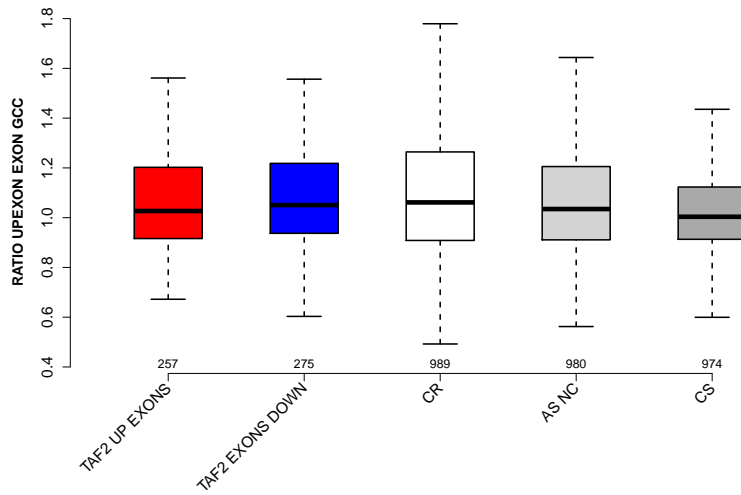
Significant results from Mann-Whitney U test:

- TAF2\_EXONS\_DOWN vs CR : 0.0161561  
mean: 0.489022 > 0.473391 , median: 0.478932 > 0.464
- CR vs AS\_NC : 4.31487e-08  
mean: 0.473391 < 0.498185 , median: 0.464 < 0.488504
- CR vs CS : 0.00231017  
mean: 0.473391 < 0.487881 , median: 0.464 < 0.481024
- AS\_NC vs CS : 0.0228376  
mean: 0.498185 > 0.487881 , median: 0.488504 > 0.481024

## 6.15 RATIO UPEXON EXON GCC

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

Meaning: UPEXON GCC / EXON GCC



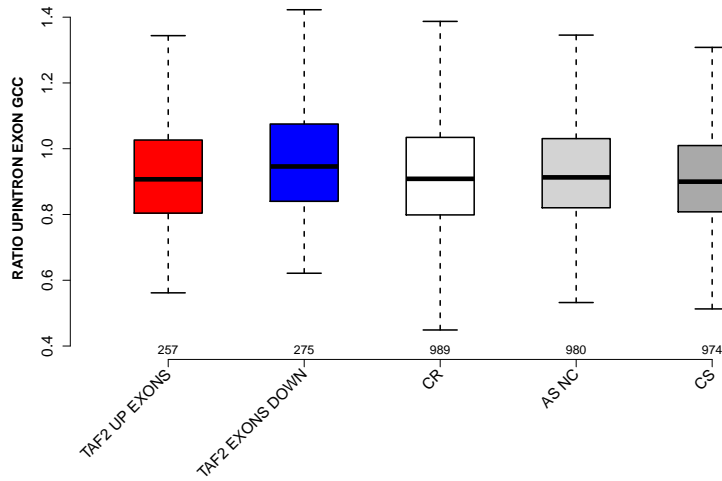
Significant results from Mann-Whitney U test:

- TAF2\_UP\_EXONS vs CS : 0.0221651  
mean: 1.0872 > 1.0318 , median: 1.0268 > 1.0036
- TAF2\_EXONS\_DOWN vs CS : 6.76332e-05  
mean: 1.1238 > 1.0318 , median: 1.0505 > 1.0036
- CR vs CS : 2.30085e-07  
mean: 1.1225 > 1.0318 , median: 1.0613 > 1.0036
- AS\_NC vs CS : 0.000450082  
mean: 1.092 > 1.0318 , median: 1.0347 > 1.0036

## 6.16 RATIO UPINTRON EXON GCC

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

Meaning: UPINTRON GCC / EXON GCC



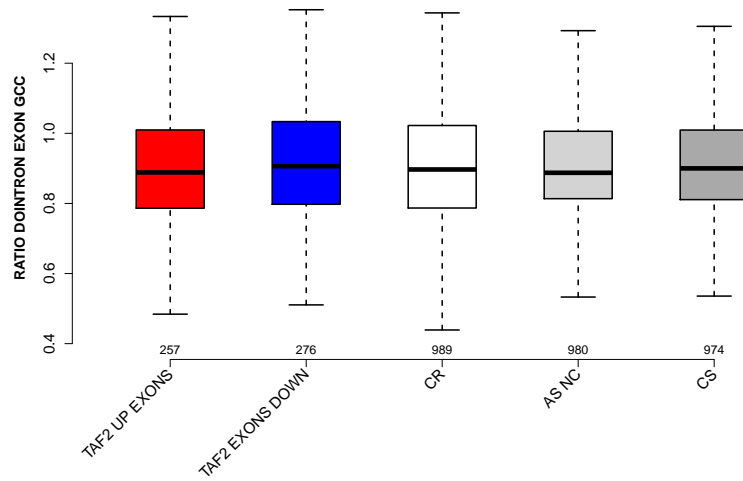
Significant results from Mann-Whitney U test:

- TAF2\_UP\_EXONS vs TAF2\_EXONS\_DOWN : 0.00582089  
mean: 0.925036 < 0.961234 , median: 0.907005 < 0.94601
- TAF2\_EXONS\_DOWN vs CR : 0.00292925  
mean: 0.961234 > 0.944329 , median: 0.94601 > 0.908418
- TAF2\_EXONS\_DOWN vs AS\_NC : 0.0127615  
mean: 0.961234 > 0.934562 , median: 0.94601 > 0.912835
- TAF2\_EXONS\_DOWN vs CS : 4.80096e-05  
mean: 0.961234 > 0.914033 , median: 0.94601 > 0.899821
- AS\_NC vs CS : 0.0212045  
mean: 0.934562 > 0.914033 , median: 0.912835 > 0.899821

## 6.17 RATIO DOINTRON EXON GCC

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

Meaning: DOINTRON GCC / EXON GCC



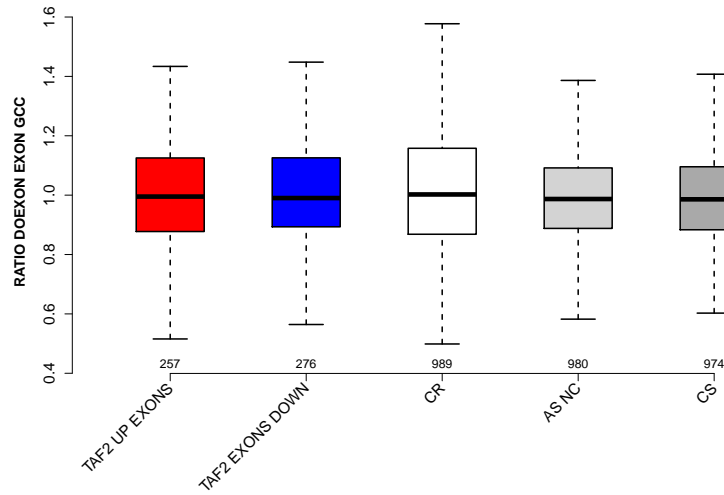
Significant results from Mann-Whitney U test:

- none

## 6.18 RATIO DOEXON EXON GCC

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

Meaning: DOEXON GCC / EXON GCC



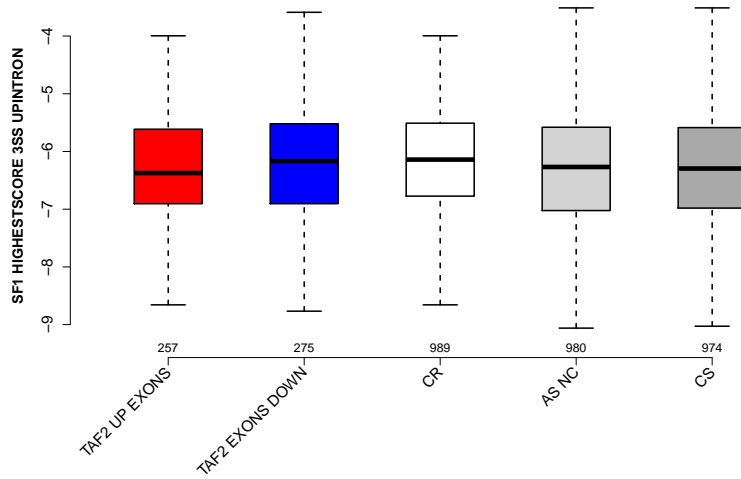
Significant results from Mann-Whitney U test:

- CR vs AS\_NC : 0.02556  
mean: 1.0419 > 1.0003 , median: 1.0023 > 0.986974
- CR vs CS : 0.0372696  
mean: 1.0419 > 0.999579 , median: 1.0023 > 0.985921

## 6.19 SF1 HIGHESTSCORE 3SS UPINTRON

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

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



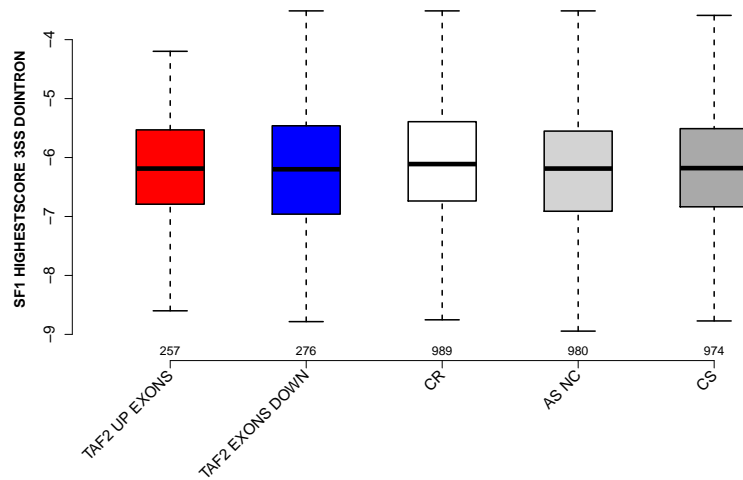
Significant results from Mann-Whitney U test:

- TAF2\_UP\_EXONS vs CR : 0.00424315  
mean: -6.31514 < -6.12842 , median: -6.37398 < -6.14071
- CR vs AS\_NC : 0.0043567  
mean: -6.12842 > -6.26922 , median: -6.14071 > -6.26872
- CR vs CS : 0.000546325  
mean: -6.12842 > -6.29083 , median: -6.14071 > -6.29538

## 6.20 SF1 HIGHESTSCORE 3SS DOWNTON

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

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



Significant results from Mann-Whitney U test:

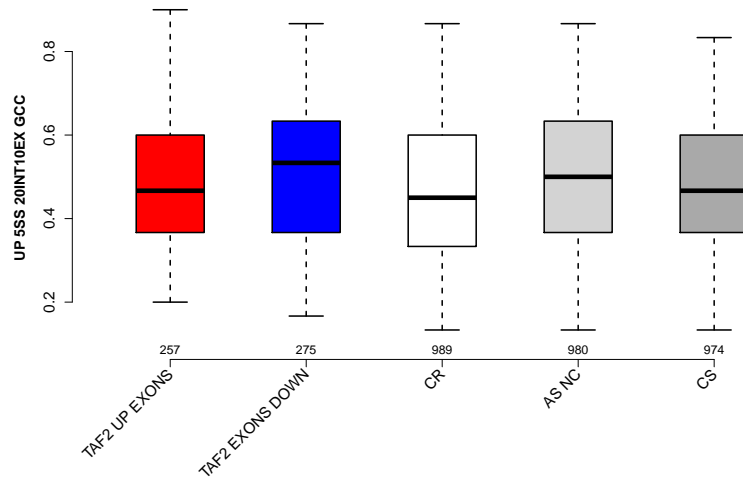
- CR vs AS\_NC : 0.00275872  
mean: -6.07791 > -6.22114 , median: -6.11088 > -6.18725
- CR vs CS : 0.035205  
mean: -6.07791 > -6.1712 , median: -6.11088 > -6.17975



## 6.21 UP 5SS 20INT10EX GCC

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

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



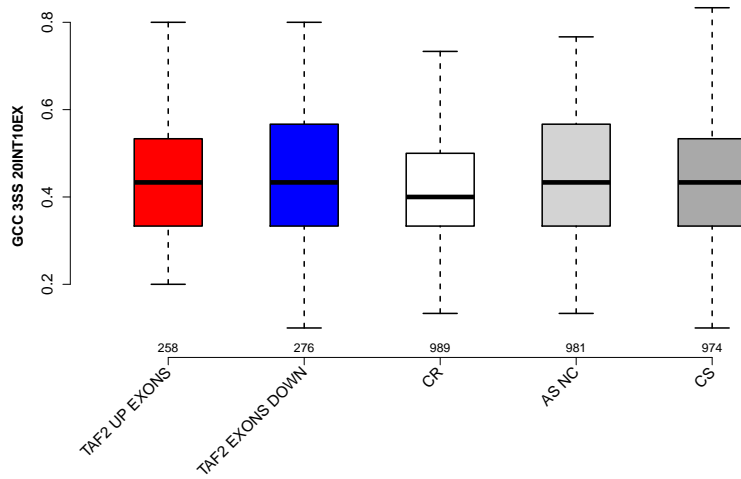
Significant results from Mann-Whitney U test:

- TAF2\_EXONS\_DOWN vs CR : 0.000876224  
mean: 0.506545 > 0.470206 , median: 0.533333 > 0.45
- TAF2\_EXONS\_DOWN vs CS : 0.0100104  
mean: 0.506545 > 0.476865 , median: 0.533333 > 0.466667
- CR vs AS\_NC : 2.75642e-06  
mean: 0.470206 < 0.501207 , median: 0.45 < 0.5
- AS\_NC vs CS : 0.000527655  
mean: 0.501207 > 0.476865 , median: 0.5 > 0.466667

## 6.22 GCC 3SS 20INT10EX

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

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



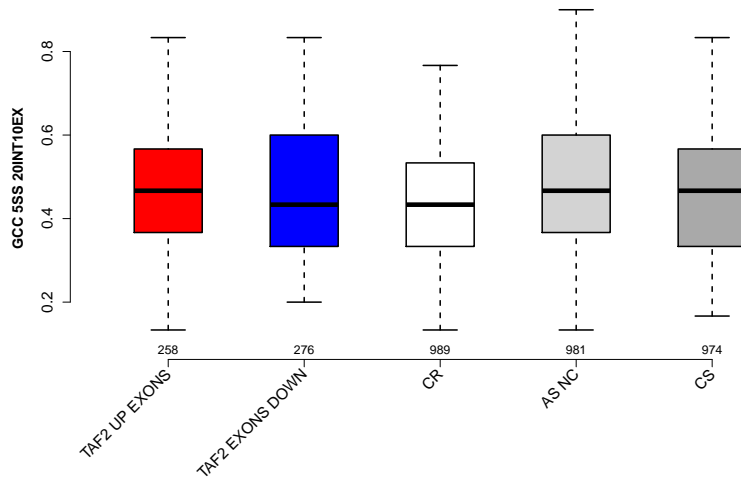
Significant results from Mann-Whitney U test:

- TAF2\_UP\_EXONS vs CR : 0.000509091  
mean: 0.442636 > 0.406664 , median: 0.433333 > 0.4
- TAF2\_EXONS\_DOWN vs CR : 2.43776e-05  
mean: 0.449155 > 0.406664 , median: 0.433333 > 0.4
- CR vs AS\_NC : 1.93446e-13  
mean: 0.406664 < 0.454027 , median: 0.4 < 0.433333
- CR vs CS : 5.86256e-08  
mean: 0.406664 < 0.441273 , median: 0.4 < 0.433333

## 6.23 GCC 5SS 20INT10EX

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

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



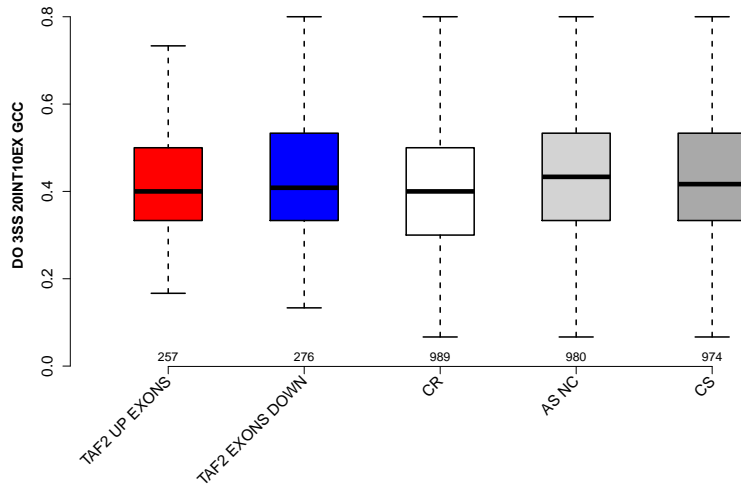
Significant results from Mann-Whitney U test:

- TAF2\_UP\_EXONS vs CR : 0.00443106  
mean: 0.46938 > 0.43876 , median: 0.466667 > 0.433333
- TAF2\_EXONS\_DOWN vs CR : 0.0291487  
mean: 0.465459 > 0.43876 , median: 0.433333 = 0.433333
- CR vs AS\_NC : 1.36594e-07  
mean: 0.43876 < 0.474992 , median: 0.433333 < 0.466667
- CR vs CS : 0.000150613  
mean: 0.43876 < 0.465229 , median: 0.433333 < 0.466667

## 6.24 DO 3SS 20INT10EX GCC

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

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



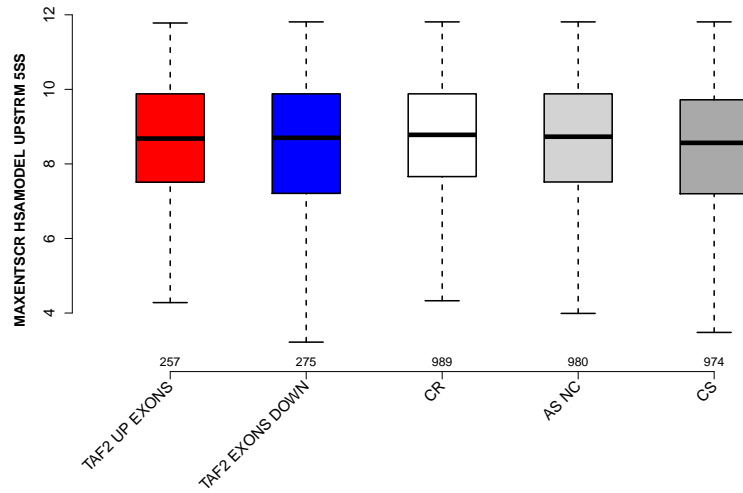
Significant results from Mann-Whitney U test:

- TAF2\_UP\_EXONS vs CR : 0.0160581  
mean: 0.42594 > 0.404398 , median: 0.4 = 0.4
- TAF2\_EXONS\_DOWN vs CR : 0.00296136  
mean: 0.435809 > 0.404398 , median: 0.408333 > 0.4
- CR vs AS\_NC : 8.68656e-10  
mean: 0.404398 < 0.440748 , median: 0.4 < 0.433333
- CR vs CS : 1.09636e-05  
mean: 0.404398 < 0.43347 , median: 0.4 < 0.416667

## 6.25 MAXENTSCR HSAMODEL UPSTRM 5SS

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

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



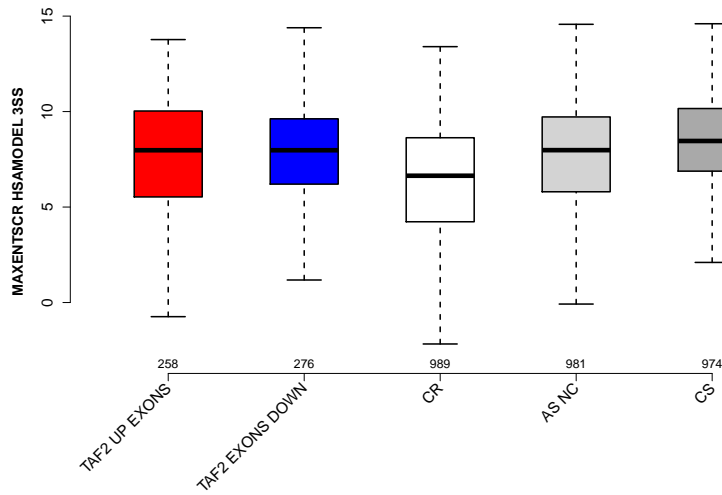
Significant results from Mann-Whitney U test:

- CR vs CS : 0.00265863  
mean: 8.4483 > 8.1698 , median: 8.78 > 8.565
- AS\_NC vs CS : 0.00580803  
mean: 8.3861 > 8.1698 , median: 8.73 > 8.565

## 6.26 MAXENTSCR HSAMODEL 3SS

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

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



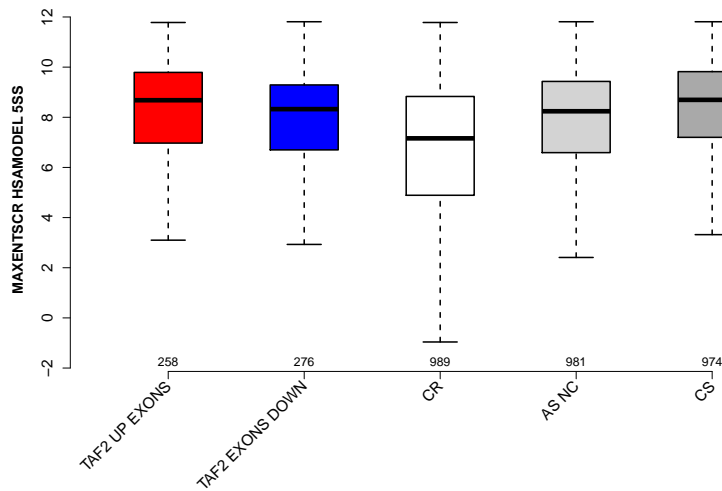
Significant results from Mann-Whitney U test:

- TAF2\_UP\_EXONS vs CR : 3.87443e-08  
mean: 7.3295 > 5.8246 , median: 7.975 > 6.64
- TAF2\_UP\_EXONS vs CS : 0.0011201  
mean: 7.3295 < 8.2122 , median: 7.975 < 8.46
- TAF2\_EXONS\_DOWN vs CR : 1.73939e-10  
mean: 7.5047 > 5.8246 , median: 7.975 > 6.64
- TAF2\_EXONS\_DOWN vs CS : 0.000718752  
mean: 7.5047 < 8.2122 , median: 7.975 < 8.46
- CR vs AS\_NC : 1.06786e-17  
mean: 5.8246 < 7.2022 , median: 6.64 < 7.98
- CR vs CS : 1.92866e-46  
mean: 5.8246 < 8.2122 , median: 6.64 < 8.46
- AS\_NC vs CS : 3.91052e-08  
mean: 7.2022 < 8.2122 , median: 7.98 < 8.46

## 6.27 MAXENTSCR HSAMODEL 5SS

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

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



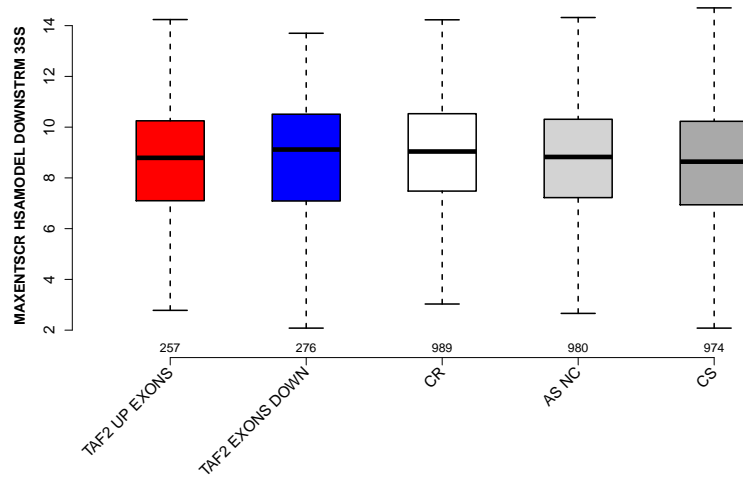
Significant results from Mann-Whitney U test:

- TAF2\_UP\_EXONS vs CR : 1.15842e-14  
mean: 7.8776 > 6.2218 , median: 8.68 > 7.16
- TAF2\_UP\_EXONS vs AS\_NC : 0.0100492  
mean: 7.8776 > 7.4013 , median: 8.68 > 8.24
- TAF2\_EXONS\_DOWN vs CR : 4.43761e-09  
mean: 7.4846 > 6.2218 , median: 8.325 > 7.16
- TAF2\_EXONS\_DOWN vs CS : 0.000732515  
mean: 7.4846 < 8.1678 , median: 8.325 < 8.695
- CR vs AS\_NC : 4.18395e-17  
mean: 6.2218 < 7.4013 , median: 7.16 < 8.24
- CR vs CS : 1.30522e-40  
mean: 6.2218 < 8.1678 , median: 7.16 < 8.695
- AS\_NC vs CS : 4.36076e-08  
mean: 7.4013 < 8.1678 , median: 8.24 < 8.695

## 6.28 MAXENTSCR HSAMODEL DOWNSTRM 3SS

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

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



Significant results from Mann-Whitney U test:

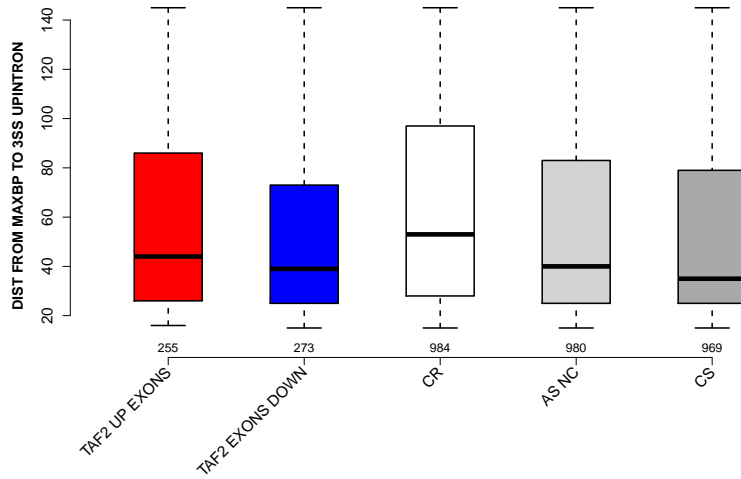
- CR vs AS\_NC : 0.0417114  
mean: 8.8435 > 8.5949 , median: 9.04 > 8.825
- CR vs CS : 0.00153573  
mean: 8.8435 > 8.4368 , median: 9.04 > 8.64



## 6.29 DIST FROM MAXBP TO 3SS UPINTRON

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

Meaning: distance to 3ss of best precited BP



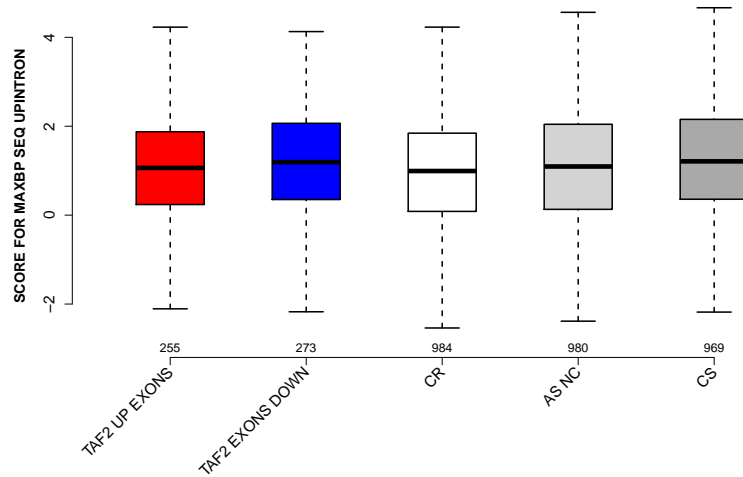
Significant results from Mann-Whitney U test:

- TAF2\_UP\_EXONS vs CS : 0.0333847  
mean: 59.2863 > 53.8173 , median: 44 > 35
- TAF2\_EXONS\_DOWN vs CR : 0.000193813  
mean: 53.3077 < 63.5305 , median: 39 < 53
- CR vs AS\_NC : 3.90923e-05  
mean: 63.5305 > 56.3327 , median: 53 > 40
- CR vs CS : 1.295e-08  
mean: 63.5305 > 53.8173 , median: 53 > 35

## 6.30 SCORE FOR MAXBP SEQ UPINTRON

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

Meaning: BP sequence score of best predicted BP



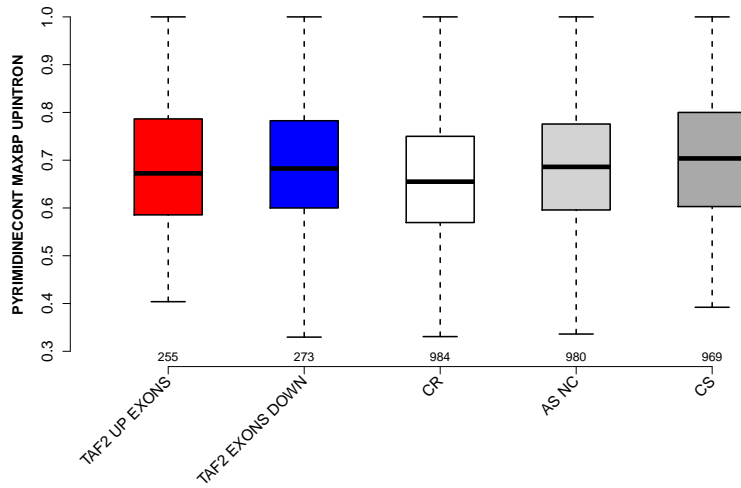
Significant results from Mann-Whitney U test:

- TAF2\_UP\_EXONS vs CS : 0.0371988  
mean: 1.0609 < 1.2448 , median: 1.0628 < 1.2101
- TAF2\_EXONS\_DOWN vs CR : 0.0207174  
mean: 1.1515 > 0.957446 , median: 1.1911 > 0.992529
- CR vs AS\_NC : 0.0334407  
mean: 0.957446 < 1.1152 , median: 0.992529 < 1.0943
- CR vs CS : 9.6107e-06  
mean: 0.957446 < 1.2448 , median: 0.992529 < 1.2101
- AS\_NC vs CS : 0.0326106  
mean: 1.1152 < 1.2448 , median: 1.0943 < 1.2101

## 6.31 PYRIMIDINECONT MAXBP UPINTRON

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

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



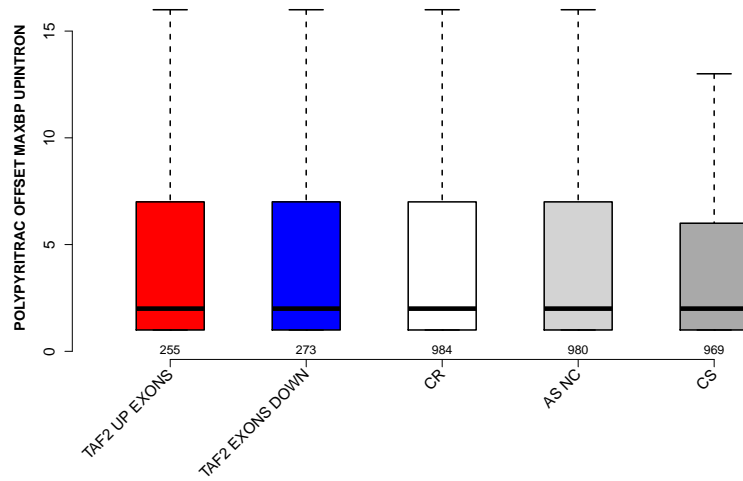
Significant results from Mann-Whitney U test:

- TAF2\_UP\_EXONS vs CR : 0.0249486  
mean: 0.684122 > 0.661375 , median: 0.672414 > 0.655051
- TAF2\_EXONS\_DOWN vs CR : 0.00100009  
mean: 0.69184 > 0.661375 , median: 0.68254 > 0.655051
- CR vs AS\_NC : 5.65413e-06  
mean: 0.661375 < 0.688263 , median: 0.655051 < 0.685994
- CR vs CS : 4.21948e-10  
mean: 0.661375 < 0.699212 , median: 0.655051 < 0.703704

## 6.32 POLYPYRITRAC OFFSET MAXBP UPINTRON

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

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



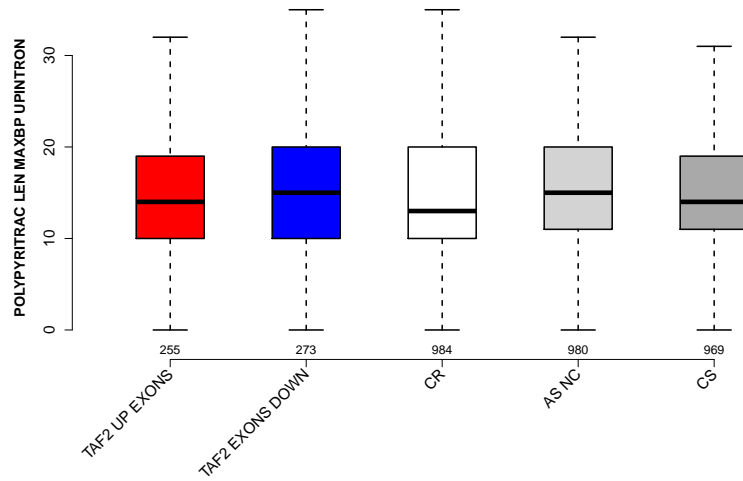
Significant results from Mann-Whitney U test:

- CR vs CS : 0.0135739  
mean: 5.127 > 4.3808 , median: 2 = 2
- AS\_NC vs CS : 0.0341061  
mean: 4.9286 > 4.3808 , median: 2 = 2

### 6.33 POLYPYRITRAC LEN MAXBP UPINTRON

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

Meaning: Polypyrimidine track length for best BP



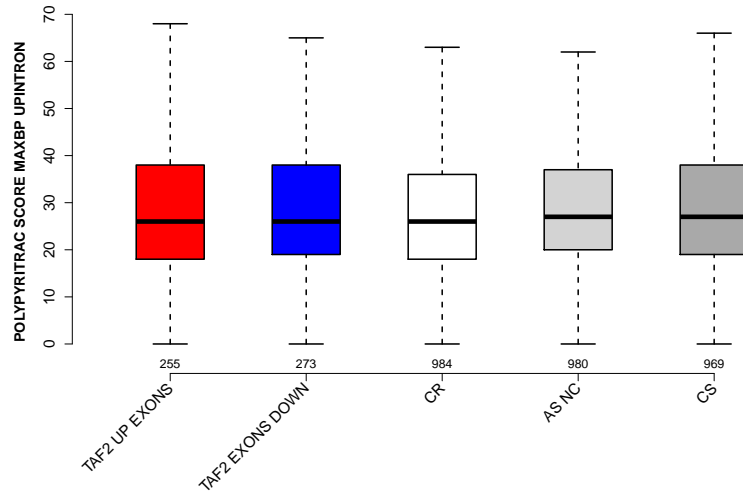
Significant results from Mann-Whitney U test:

- CR vs AS\_NC : 0.014592  
mean: 16.1291 < 16.6337 , median: 13 < 15

## 6.34 POLYPYRITRAC SCORE MAXBP UPINTRON

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

Meaning: Polypyrimidine track score for best BP



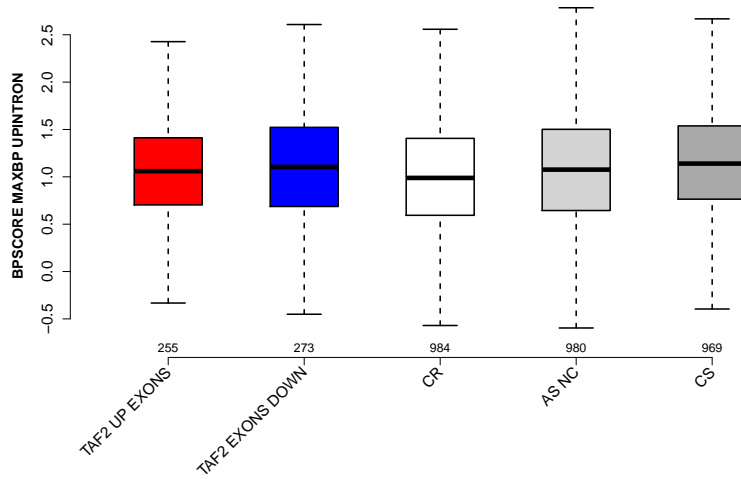
Significant results from Mann-Whitney U test:

- CR vs AS\_NC : 0.0326183  
mean: 30.688 < 31.7449 , median: 26 < 27

## 6.35 BPSCORE MAXBP UPINTRON

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

Meaning: SVM classification score of best BP



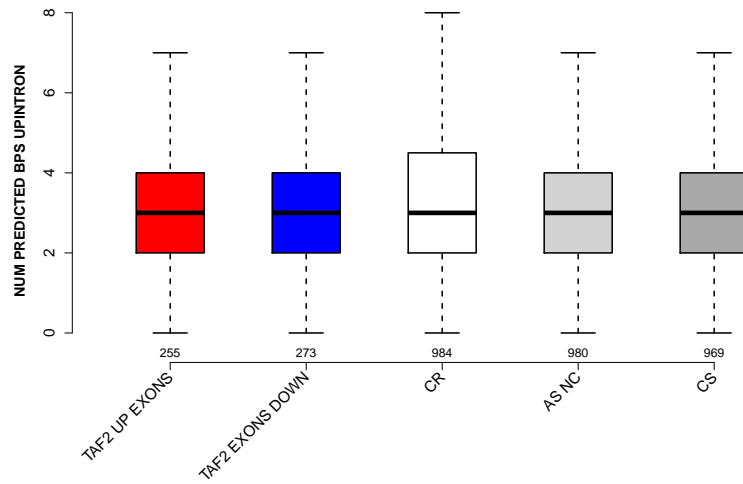
Significant results from Mann-Whitney U test:

- TAF2\_UP\_EXONS vs CS : 0.0387953  
mean: 1.0168 < 1.1214 , median: 1.0592 < 1.1398
- TAF2\_EXONS\_DOWN vs CR : 0.012933  
mean: 1.0347 > 0.95162 , median: 1.1042 > 0.988312
- CR vs AS\_NC : 0.00282501  
mean: 0.95162 < 1.0445 , median: 0.988312 < 1.076
- CR vs CS : 2.37638e-08  
mean: 0.95162 < 1.1214 , median: 0.988312 < 1.1398
- AS\_NC vs CS : 0.0144174  
mean: 1.0445 < 1.1214 , median: 1.076 < 1.1398

## 6.36 NUM PREDICTED BPS UPINTRON

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

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



Significant results from Mann-Whitney U test:

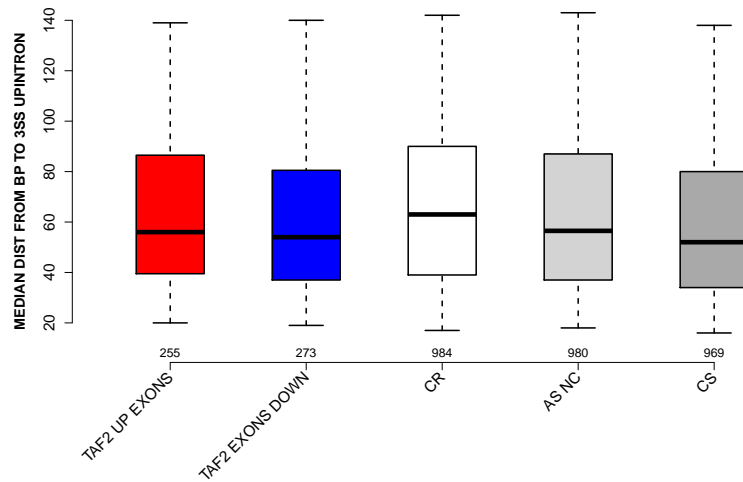
- TAF2\_UP\_EXONS vs CR : 0.00640034  
mean: 2.9529 < 3.3293 , median: 3 = 3
- TAF2\_UP\_EXONS vs AS\_NC : 0.026206  
mean: 2.9529 < 3.2531 , median: 3 = 3
- TAF2\_UP\_EXONS vs CS : 0.00297606  
mean: 2.9529 < 3.3075 , median: 3 = 3
- TAF2\_EXONS\_DOWN vs CR : 0.0236357  
mean: 2.9634 < 3.3293 , median: 3 = 3
- TAF2\_EXONS\_DOWN vs CS : 0.0128047  
mean: 2.9634 < 3.3075 , median: 3 = 3



## 6.37 MEDIAN DIST FROM BP TO 3SS UPINTRON

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

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



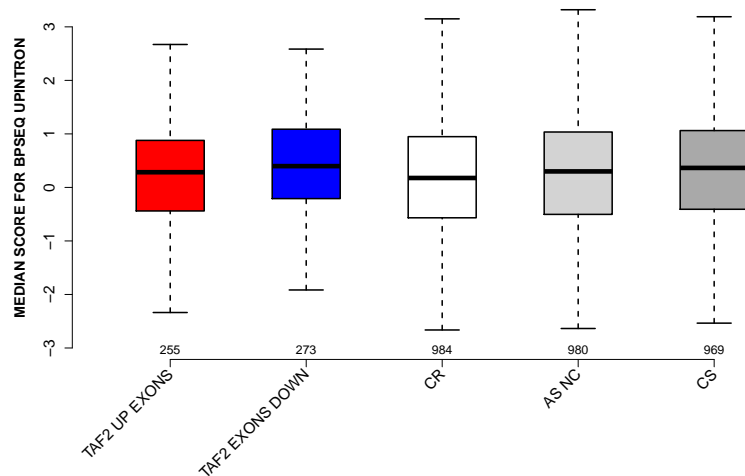
Significant results from Mann-Whitney U test:

- TAF2\_UP\_EXONS vs CS : 0.00619153  
mean: 65.9451 > 59.1889 , median: 56 > 52
- TAF2\_EXONS\_DOWN vs CR : 0.00626334  
mean: 61.2564 < 67.0925 , median: 54 < 63
- CR vs AS\_NC : 0.00925672  
mean: 67.0925 > 63.7158 , median: 63 > 56.5
- CR vs CS : 4.41239e-09  
mean: 67.0925 > 59.1889 , median: 63 > 52
- AS\_NC vs CS : 0.00143796  
mean: 63.7158 > 59.1889 , median: 56.5 > 52

## 6.38 MEDIAN SCORE FOR BPSEQ UPINTRON

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

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



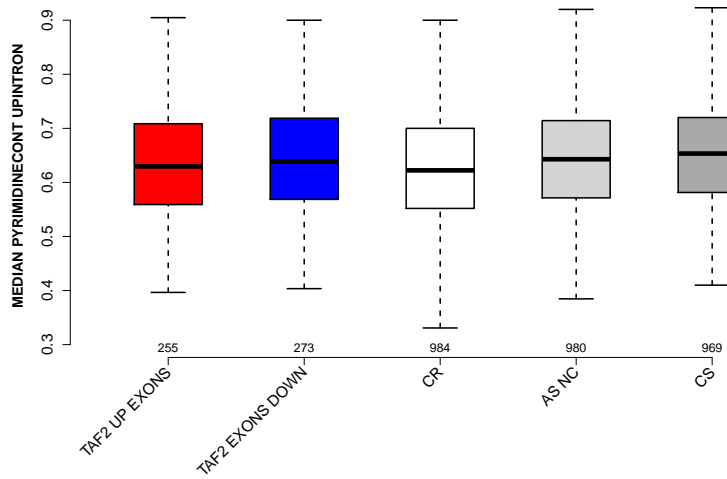
Significant results from Mann-Whitney U test:

- TAF2\_EXONS\_DOWN vs CR : 0.00425729  
mean: 0.386137 > 0.169783 , median: 0.397847 > 0.176331
- CR vs CS : 0.00230752  
mean: 0.169783 < 0.352597 , median: 0.176331 < 0.364364

## 6.39 MEDIAN PYRIMIDINECONT UPINTRON

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

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



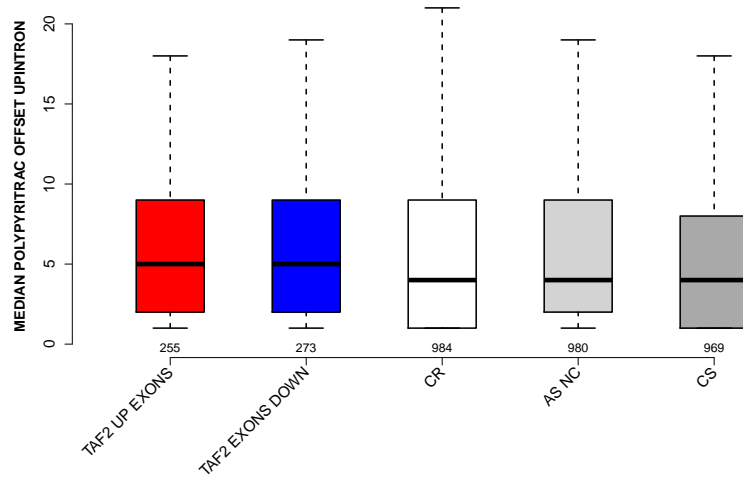
Significant results from Mann-Whitney U test:

- TAF2\_UP\_EXONS vs CS : 0.0152988  
mean: 0.636946 < 0.654484 , median: 0.62963 < 0.653333
- TAF2\_EXONS\_DOWN vs CR : 0.0244487  
mean: 0.643982 > 0.626186 , median: 0.638889 > 0.622296
- CR vs AS\_NC : 0.000194303  
mean: 0.626186 < 0.645878 , median: 0.622296 < 0.642857
- CR vs CS : 2.15827e-08  
mean: 0.626186 < 0.654484 , median: 0.622296 < 0.653333

## 6.40 MEDIAN POLYPYRITRAC OFFSET UPINTRON

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

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



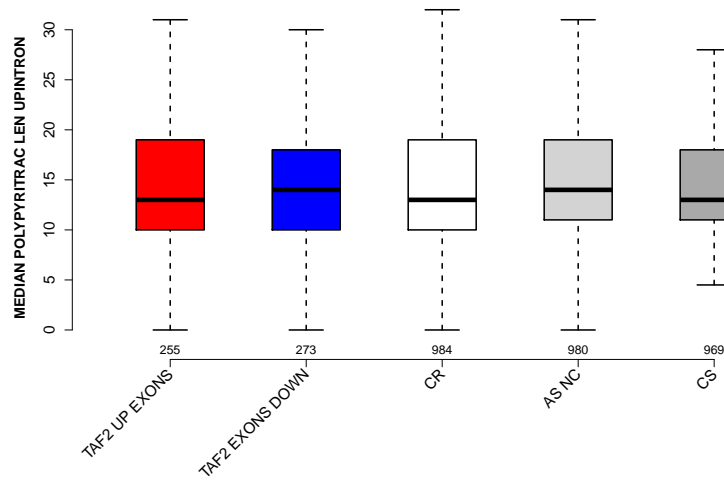
Significant results from Mann-Whitney U test:

- TAF2\_UP\_EXONS vs CS : 0.0157536  
mean: 8.6 > 7.0217 , median: 5 > 4
- TAF2\_EXONS\_DOWN vs CS : 0.0364424  
mean: 8.7473 > 7.0217 , median: 5 > 4

## 6.41 MEDIAN POLYPYRITRAC LEN UPINTRON

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

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



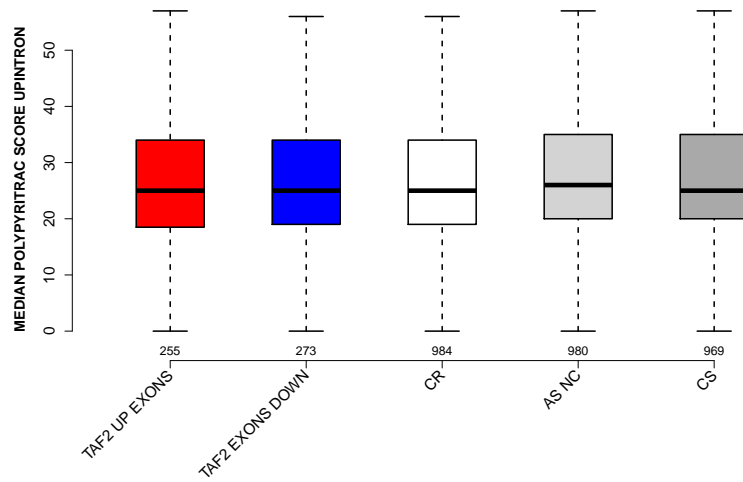
Significant results from Mann-Whitney U test:

- none

## 6.42 MEDIAN POLYPYRITRAC SCORE UPINTRON

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

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



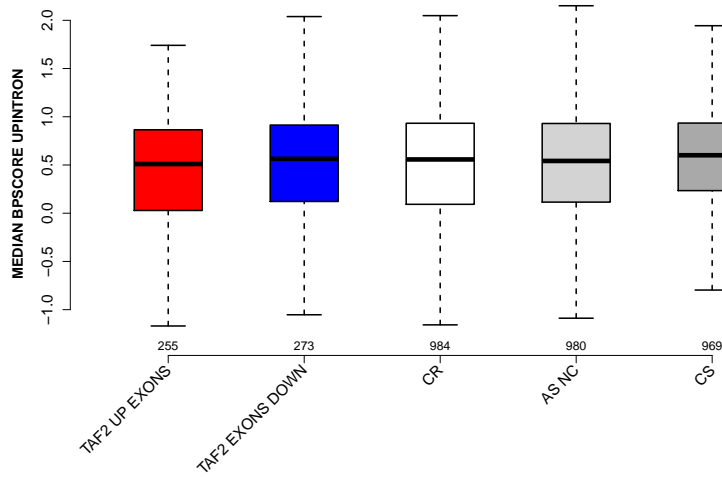
Significant results from Mann-Whitney U test:

- none

## 6.43 MEDIAN BPSCORE UPINTRON

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

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



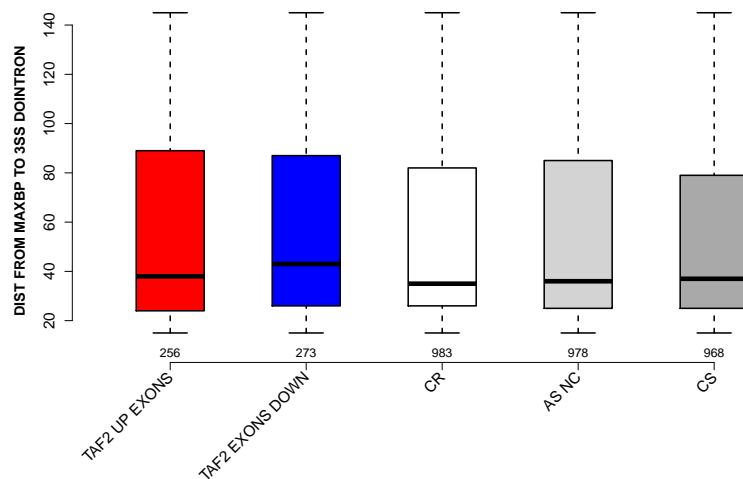
Significant results from Mann-Whitney U test:

- TAF2\_UP\_EXONS vs CS : 0.0172497  
mean: 0.325273 < 0.494375 , median: 0.50975 < 0.600891
- CR vs CS : 0.0297797  
mean: 0.404481 < 0.494375 , median: 0.557488 < 0.600891

## 6.44 DIST FROM MAXBP TO 3SS DOWINTRON

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

Meaning: distance to 3ss of best precited BP



Significant results from Mann-Whitney U test:

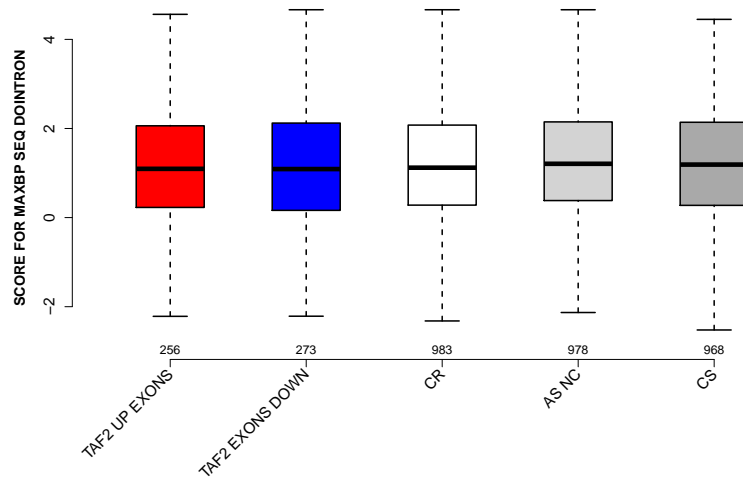
- TAF2\_EXONS\_DOWN vs CR : 0.0348227  
mean: 60.3883 > 54.8637 , median: 43 > 35
- TAF2\_EXONS\_DOWN vs CS : 0.0256629  
mean: 60.3883 > 54.1705 , median: 43 > 37



## 6.45 SCORE FOR MAXBP SEQ DOINTRON

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

Meaning: BP sequence score of best predicted BP



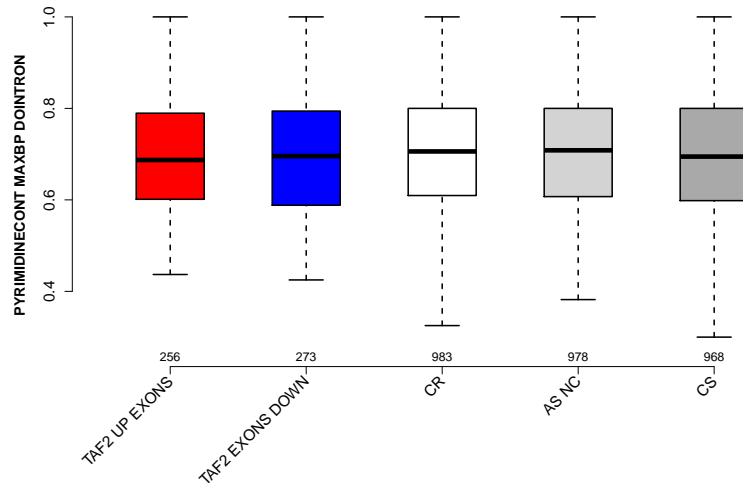
Significant results from Mann-Whitney U test:

- none

## 6.46 PYRIMIDINECONT MAXBP DONTINRON

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

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



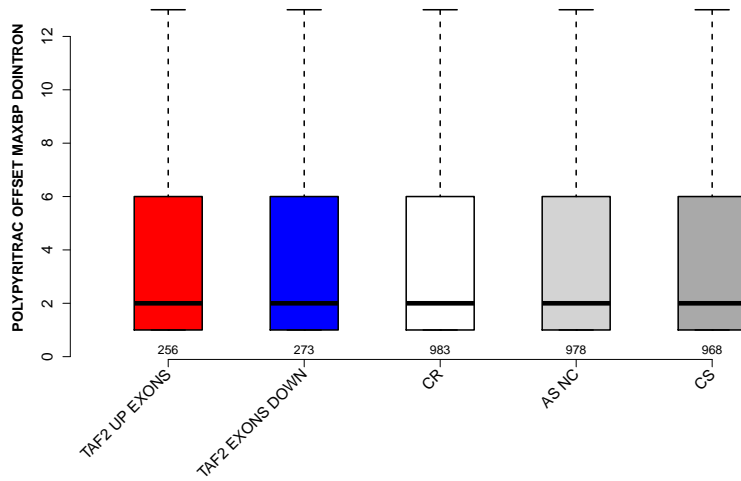
Significant results from Mann-Whitney U test:

- none

## 6.47 POLYPYRITRAC OFFSET MAXBP DONTNTRON

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

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



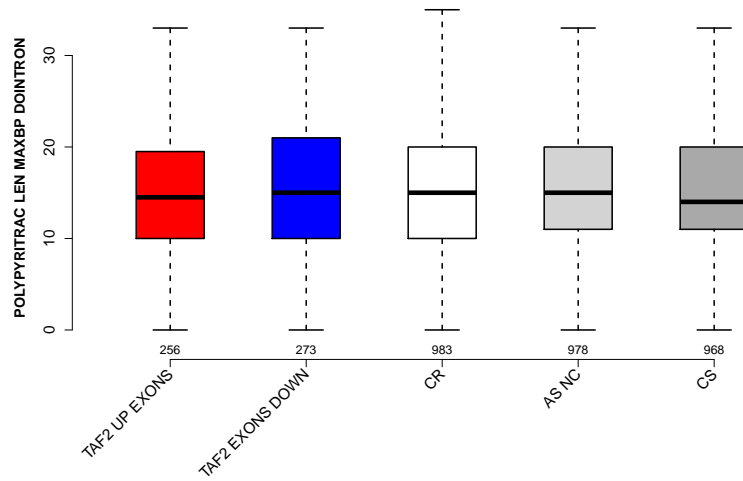
Significant results from Mann-Whitney U test:

- none

## 6.48 POLYPYRITRAC LEN MAXBP DONTNTRON

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

Meaning: Polypyrimidine track length for best BP



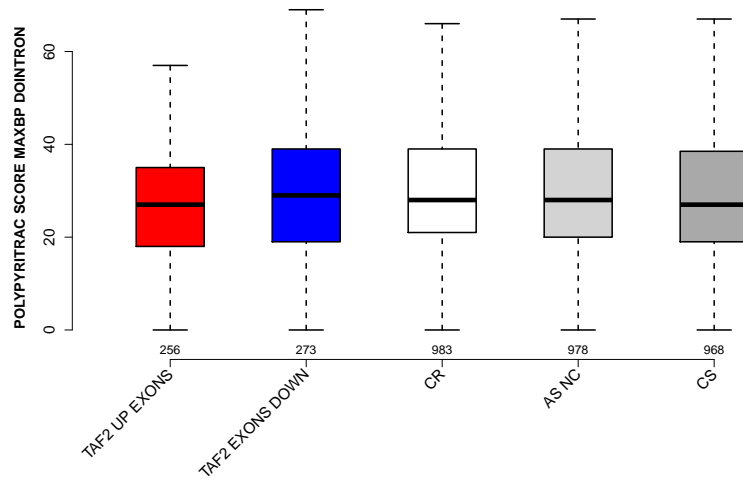
Significant results from Mann-Whitney U test:

- none

## 6.49 POLYPYRITRAC SCORE MAXBP DOINTRON

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

Meaning: Polypyrimidine track score for best BP



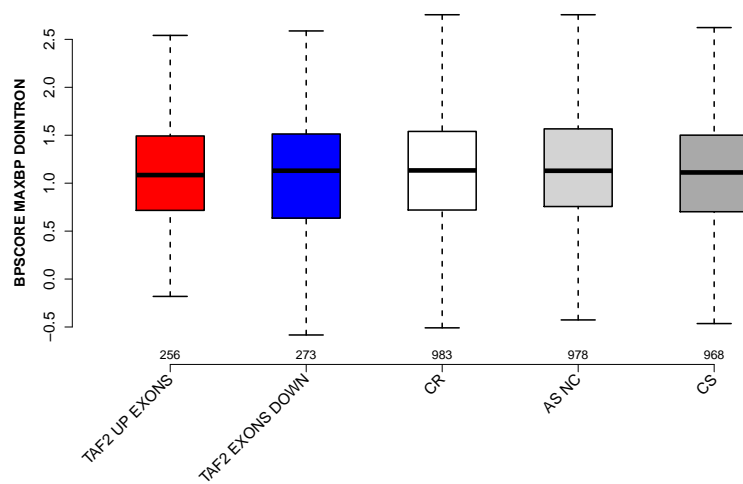
Significant results from Mann-Whitney U test:

- TAF2\_UP\_EXONS vs CR : 0.0250231  
mean: 30.0859 < 32.0122 , median: 27 < 28

## 6.50 BPSCORE MAXBP DONTNTRON

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

Meaning: SVM classification score of best BP



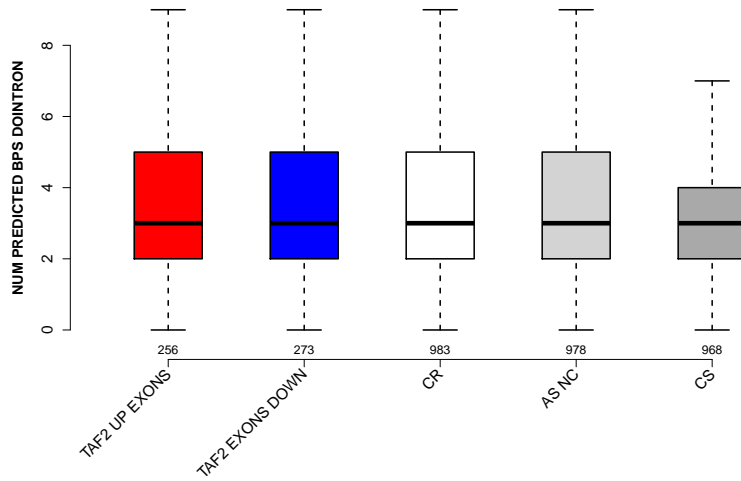
Significant results from Mann-Whitney U test:

- none

## 6.51 NUM PREDICTED BPS DOWINTRON

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

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



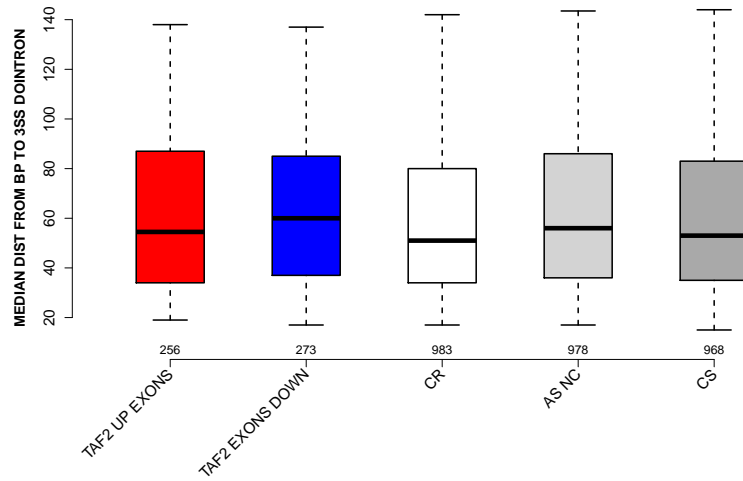
Significant results from Mann-Whitney U test:

- TAF2\_UP\_EXONS vs CS : 0.0487409  
mean: 3.5664 > 3.2789 , median: 3 = 3
- TAF2\_EXONS\_DOWN vs CR : 0.0175177  
mean: 3.293 < 3.5493 , median: 3 = 3
- CR vs AS\_NC : 0.00437603  
mean: 3.5493 > 3.3497 , median: 3 = 3
- CR vs CS : 0.000629348  
mean: 3.5493 > 3.2789 , median: 3 = 3

## 6.52 MEDIAN DIST FROM BP TO 3SS DOWNTON

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

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



Significant results from Mann-Whitney U test:

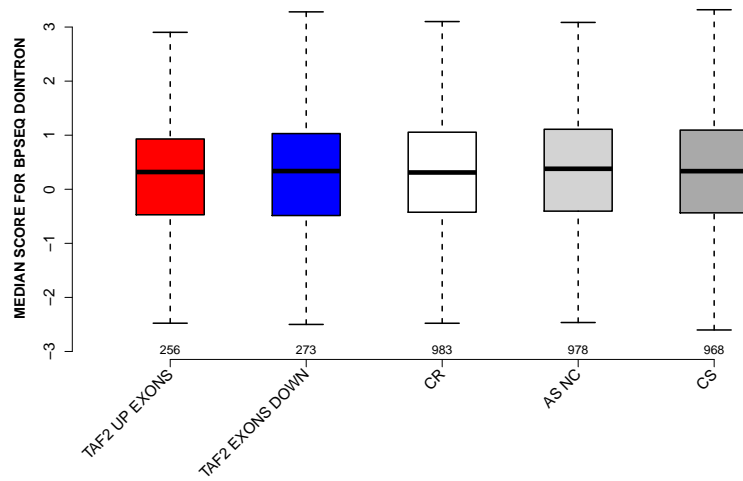
- TAF2\_EXONS\_DOWN vs CR : 0.007995  
mean: 65.5678 > 60.1562 , median: 60 > 51
- TAF2\_EXONS\_DOWN vs CS : 0.0307146  
mean: 65.5678 > 60.7805 , median: 60 > 53
- CR vs AS\_NC : 0.0304439  
mean: 60.1562 < 63.407 , median: 51 < 56



## 6.53 MEDIAN SCORE FOR BPSEQ DQINTRON

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

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



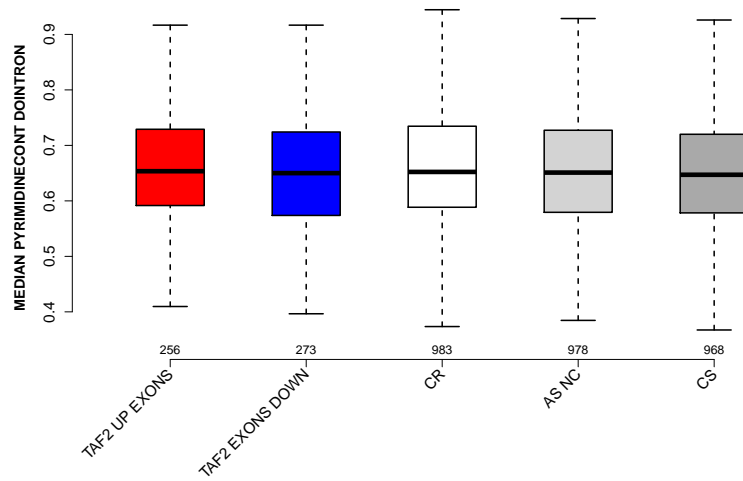
Significant results from Mann-Whitney U test:

- none

## 6.54 MEDIAN PYRIMIDINECONT DONTNTRON

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

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



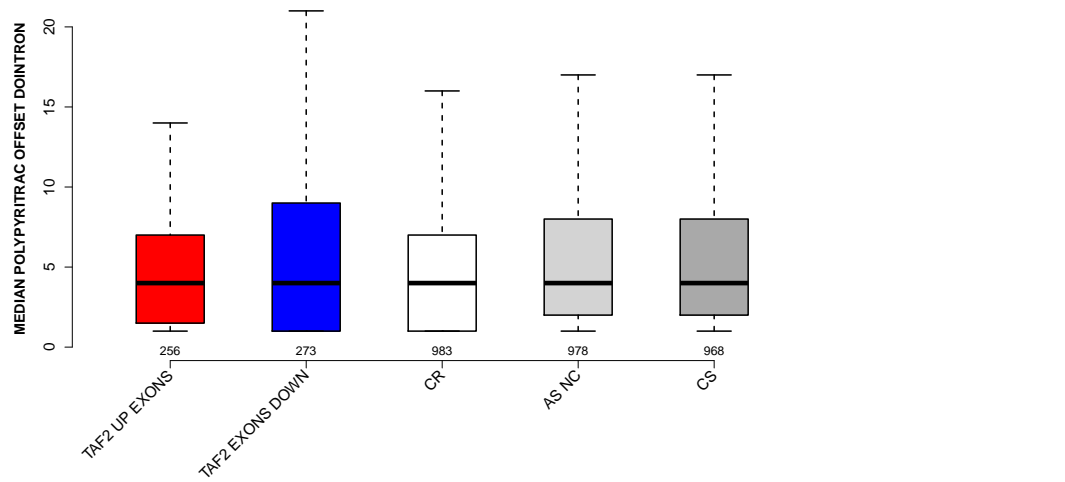
Significant results from Mann-Whitney U test:

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

## 6.55 MEDIAN POLYPYRITRAC OFFSET DONTNTRON

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

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



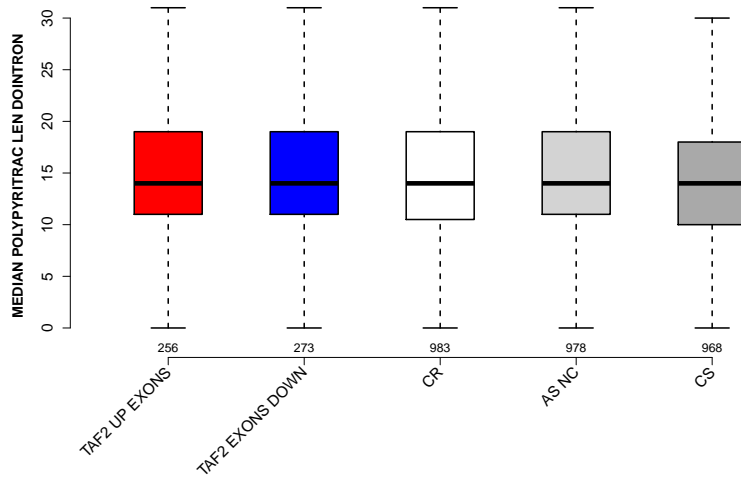
Significant results from Mann-Whitney U test:

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

## 6.56 MEDIAN POLYPYRITRAC LEN DOINTRON

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

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



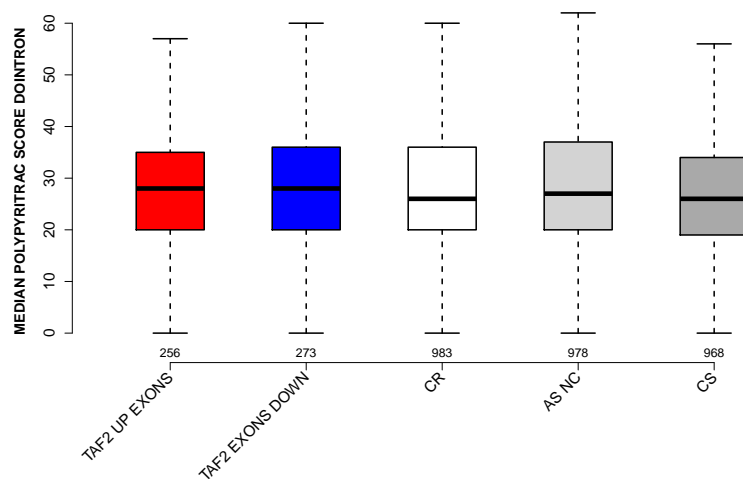
Significant results from Mann-Whitney U test:

- AS\_NC vs CS : 0.0338816  
mean: 15.9463 > 15.1415 , median: 14 = 14

## 6.57 MEDIAN POLYPYRITRAC SCORE DOINTRON

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

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



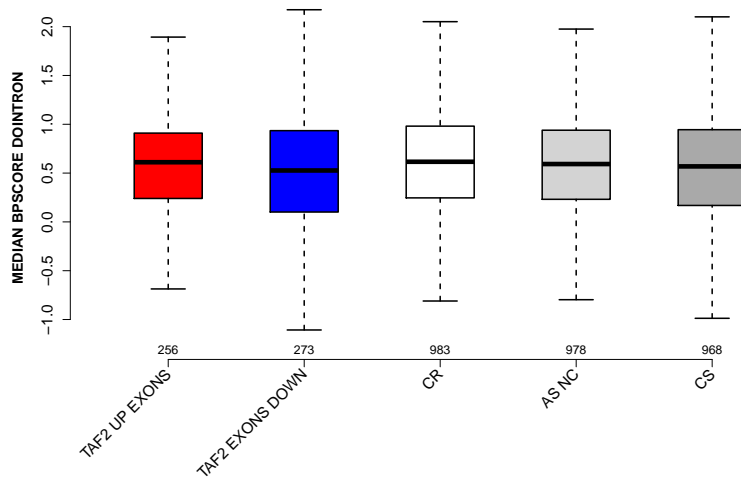
Significant results from Mann-Whitney U test:

- TAF2\_EXONS\_DOWN vs CS : 0.0264364  
mean: 30.6117 > 28.6958 , median: 28 > 26

## 6.58 MEDIAN BPSCORE DOINTRON

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

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



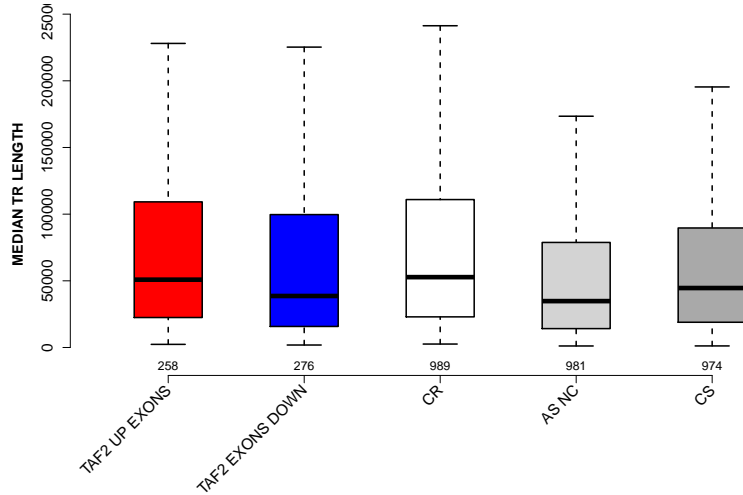
Significant results from Mann-Whitney U test:

- none

## 6.59 MEDIAN TR LENGTH

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

Meaning: median length of transcripts the exon occurs in



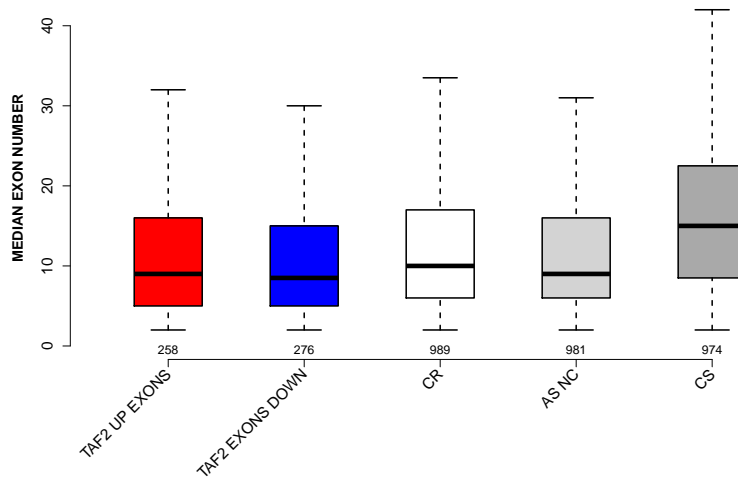
Significant results from Mann-Whitney U test:

- TAF2\_UP\_EXONS vs TAF2\_EXONS\_DOWN : 0.0400977  
mean: 82984.2752 > 70416.6268 , median: 50855.5 > 38620.5
- TAF2\_UP\_EXONS vs AS\_NC : 7.27183e-05  
mean: 82984.2752 > 62450.4638 , median: 50855.5 > 34777
- TAF2\_EXONS\_DOWN vs CR : 0.000518738  
mean: 70416.6268 < 85376.6284 , median: 38620.5 < 52754.5
- CR vs AS\_NC : 4.71087e-14  
mean: 85376.6284 > 62450.4638 , median: 52754.5 > 34777
- CR vs CS : 1.52863e-05  
mean: 85376.6284 > 67456.8501 , median: 52754.5 > 44592.75
- AS\_NC vs CS : 0.000818899  
mean: 62450.4638 < 67456.8501 , median: 34777 < 44592.75

## 6.60 MEDIAN EXON NUMBER

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

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



Significant results from Mann-Whitney U test:

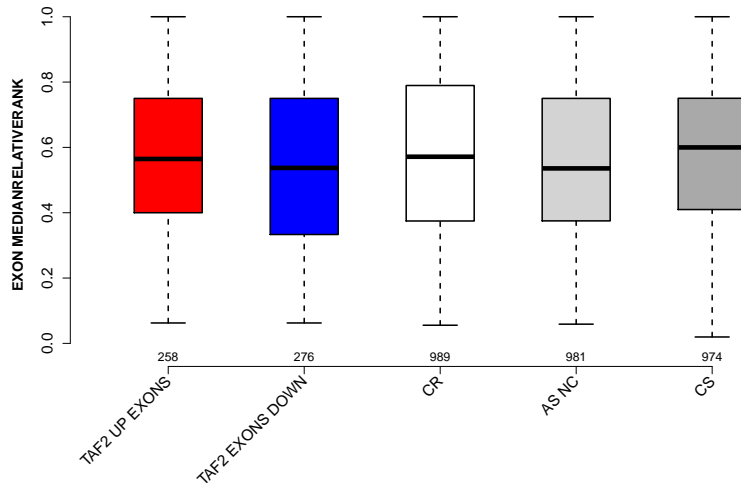
- TAF2\_UP\_EXONS vs CR : 0.010322  
mean: 11.8837 < 13.5794 , median: 9 < 10
- TAF2\_UP\_EXONS vs CS : 3.29592e-16  
mean: 11.8837 < 17.8706 , median: 9 < 15
- TAF2\_EXONS\_DOWN vs CR : 0.00100713  
mean: 12.317 < 13.5794 , median: 8.5 < 10
- TAF2\_EXONS\_DOWN vs CS : 1.72969e-19  
mean: 12.317 < 17.8706 , median: 8.5 < 15
- CR vs AS\_NC : 0.0150464  
mean: 13.5794 > 12.3522 , median: 10 > 9
- CR vs CS : 6.64063e-21  
mean: 13.5794 < 17.8706 , median: 10 < 15
- AS\_NC vs CS : 1.23337e-31  
mean: 12.3522 < 17.8706 , median: 9 < 15



## 6.61 EXON MEDIANRELATIVERANK

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

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



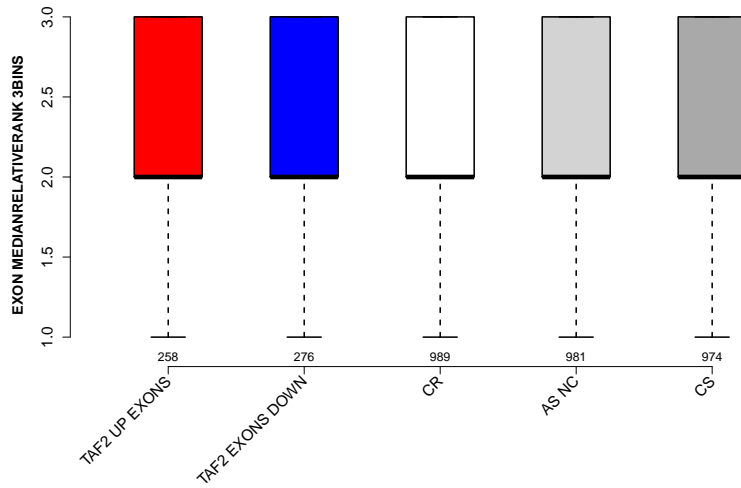
Significant results from Mann-Whitney U test:

- TAF2\_EXONS\_DOWN vs CR : 0.0484867  
mean: 0.540252 < 0.57661 , median: 0.537088 < 0.571429
- TAF2\_EXONS\_DOWN vs CS : 0.0112084  
mean: 0.540252 < 0.580488 , median: 0.537088 < 0.59992
- AS\_NC vs CS : 0.0194824  
mean: 0.558249 < 0.580488 , median: 0.535714 < 0.59992

## 6.62 EXON MEDIANRELATIVERANK 3BINS

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

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



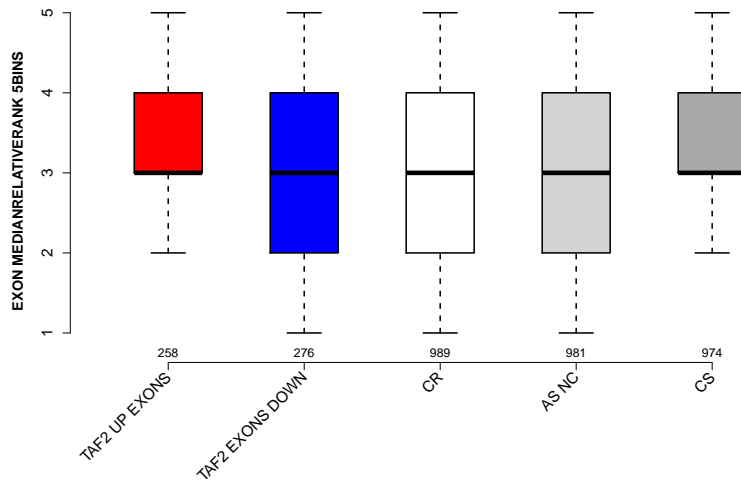
Significant results from Mann-Whitney U test:

- TAF2\_EXONS\_DOWN vs CS : 0.0276061  
mean: 2.1449 < 2.2577 , median: 2 = 2
- AS\_NC vs CS : 0.0292083  
mean: 2.1825 < 2.2577 , median: 2 = 2

## 6.63 EXON MEDIANRELATIVERANK 5BINS

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

Meaning: similar to EXON MEDIANRELATIVERANK 3BINS with 5 bins



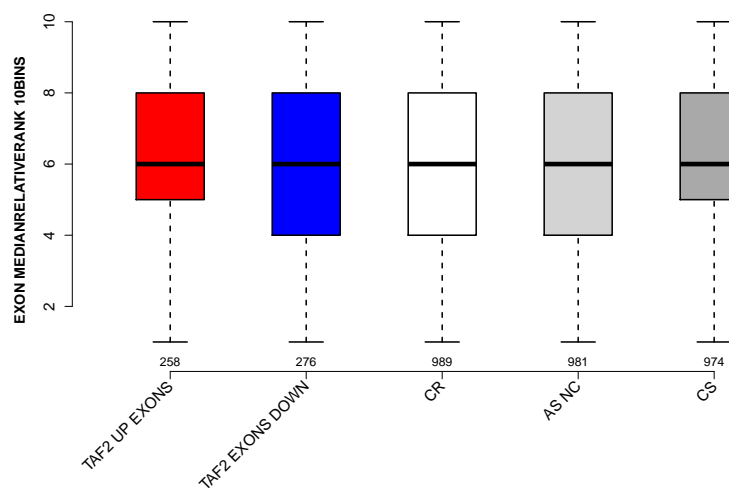
Significant results from Mann-Whitney U test:

- TAF2\_EXONS\_DOWN vs CS : 0.0129309  
mean: 3.2101 < 3.4148 , median: 3 = 3
- AS\_NC vs CS : 0.0147189  
mean: 3.2946 < 3.4148 , median: 3 = 3

## 6.64 EXON MEDIANRELATIVERANK 10BINS

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

Meaning: similar to EXON MEDIANRELATIVERANK 3BINS with 10 bins



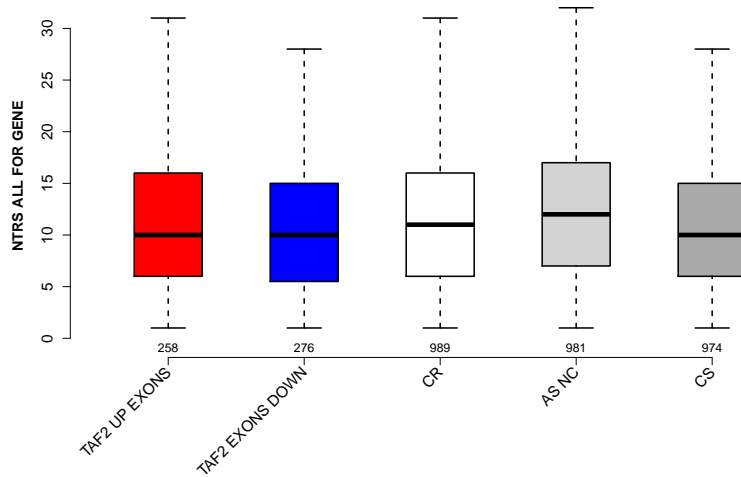
Significant results from Mann-Whitney U test:

- TAF2\_EXONS\_DOWN vs CS : 0.0125634  
mean: 5.942 < 6.3429 , median: 6 = 6
- AS\_NC vs CS : 0.0175035  
mean: 6.1111 < 6.3429 , median: 6 = 6

## 6.65 NTRS ALL FOR GENE

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

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



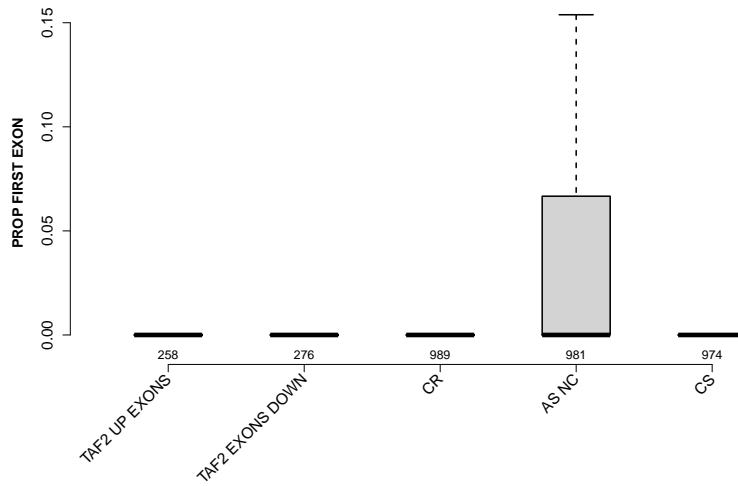
Significant results from Mann-Whitney U test:

- TAF2\_UP\_EXONS vs AS\_NC : 0.00215384  
mean: 12.1977 < 13.1672 , median: 10 < 12
- TAF2\_EXONS\_DOWN vs AS\_NC : 0.000282682  
mean: 11.2355 < 13.1672 , median: 10 < 12
- CR vs AS\_NC : 0.00513112  
mean: 12.1163 < 13.1672 , median: 11 < 12
- CR vs CS : 0.0046396  
mean: 12.1163 > 11.3275 , median: 11 > 10
- AS\_NC vs CS : 3.21291e-08  
mean: 13.1672 > 11.3275 , median: 12 > 10

## 6.66 PROP FIRST EXON

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

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



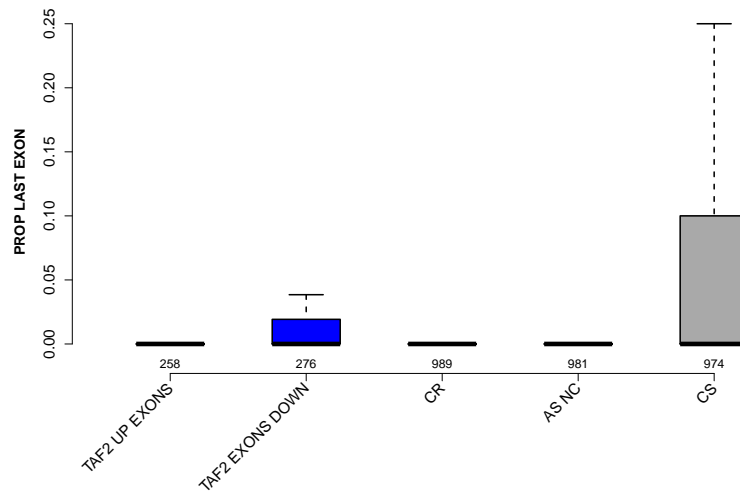
Significant results from Mann-Whitney U test:

- TAF2\_UP\_EXONS vs CR : 2.67727e-09  
mean: 0.0535136 > 0.0186245 , median: 0 = 0
- TAF2\_EXONS\_DOWN vs CR : 1.03491e-09  
mean: 0.0556743 > 0.0186245 , median: 0 = 0
- CR vs AS\_NC : 2.02079e-22  
mean: 0.0186245 < 0.0501965 , median: 0 = 0
- CR vs CS : 2.71491e-17  
mean: 0.0186245 < 0.0570893 , median: 0 = 0

## 6.67 PROP LAST EXON

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

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



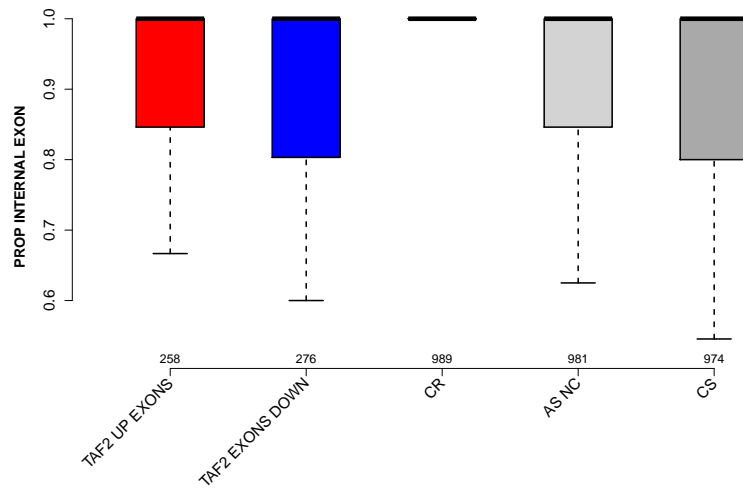
Significant results from Mann-Whitney U test:

- TAF2\_UP\_EXONS vs CR : 2.75269e-10  
mean: 0.0438058 > 0.0135426 , median: 0 = 0
- TAF2\_UP\_EXONS vs CS : 0.0103891  
mean: 0.0438058 < 0.0648436 , median: 0 = 0
- TAF2\_EXONS\_DOWN vs CR : 5.54608e-16  
mean: 0.0471762 > 0.0135426 , median: 0 = 0
- CR vs AS\_NC : 3.17694e-25  
mean: 0.0135426 < 0.0468032 , median: 0 = 0
- CR vs CS : 7.36349e-34  
mean: 0.0135426 < 0.0648436 , median: 0 = 0
- AS\_NC vs CS : 0.014957  
mean: 0.0468032 < 0.0648436 , median: 0 = 0

## 6.68 PROP INTERNAL EXON

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

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



Significant results from Mann-Whitney U test:

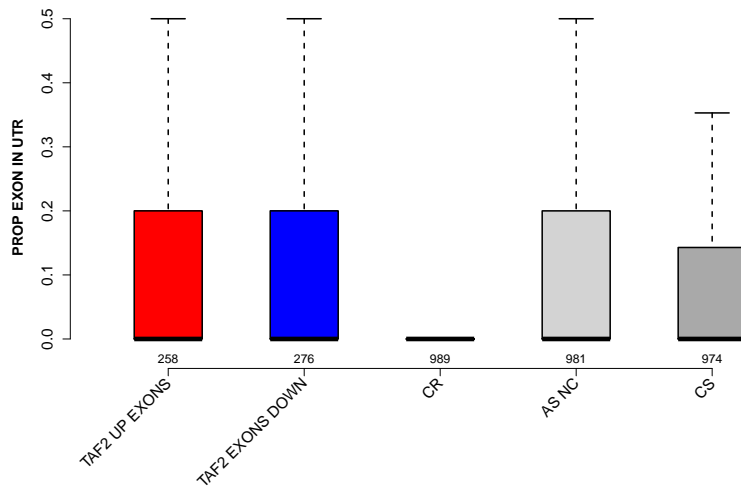
- TAF2\_UP\_EXONS vs CR : 3.58123e-16  
mean: 0.902681 < 0.9685 , median: 1 = 1
- TAF2\_UP\_EXONS vs CS : 0.0115336  
mean: 0.902681 > 0.878813 , median: 1 = 1
- TAF2\_EXONS\_DOWN vs CR : 1.52714e-20  
mean: 0.901693 < 0.9685 , median: 1 = 1
- CR vs AS\_NC : 2.70646e-40  
mean: 0.9685 > 0.903999 , median: 1 = 1
- CR vs CS : 1.26316e-49  
mean: 0.9685 > 0.878813 , median: 1 = 1
- AS\_NC vs CS : 0.00929793  
mean: 0.903999 > 0.878813 , median: 1 = 1



## 6.69 PROP EXON IN UTR

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

Meaning: NTRS WITH EXON IN UTR / NTRS WITH EXON



Significant results from Mann-Whitney U test:

- TAF2\_UP\_EXONS vs CR : 2.21006e-12  
mean: 0.108413 > 0.0320912 , median: 0 = 0
- TAF2\_UP\_EXONS vs AS\_NC : 0.0475832  
mean: 0.108413 < 0.131841 , median: 0 = 0
- TAF2\_EXONS\_DOWN vs CR : 1.02423e-15  
mean: 0.140855 > 0.0320912 , median: 0 = 0
- TAF2\_EXONS\_DOWN vs CS : 0.0156657  
mean: 0.140855 > 0.0908769 , median: 0 = 0
- CR vs AS\_NC : 1.93283e-41  
mean: 0.0320912 < 0.131841 , median: 0 = 0
- CR vs CS : 4.91851e-16  
mean: 0.0320912 < 0.0908769 , median: 0 = 0
- AS\_NC vs CS : 8.45434e-08  
mean: 0.131841 > 0.0908769 , median: 0 = 0