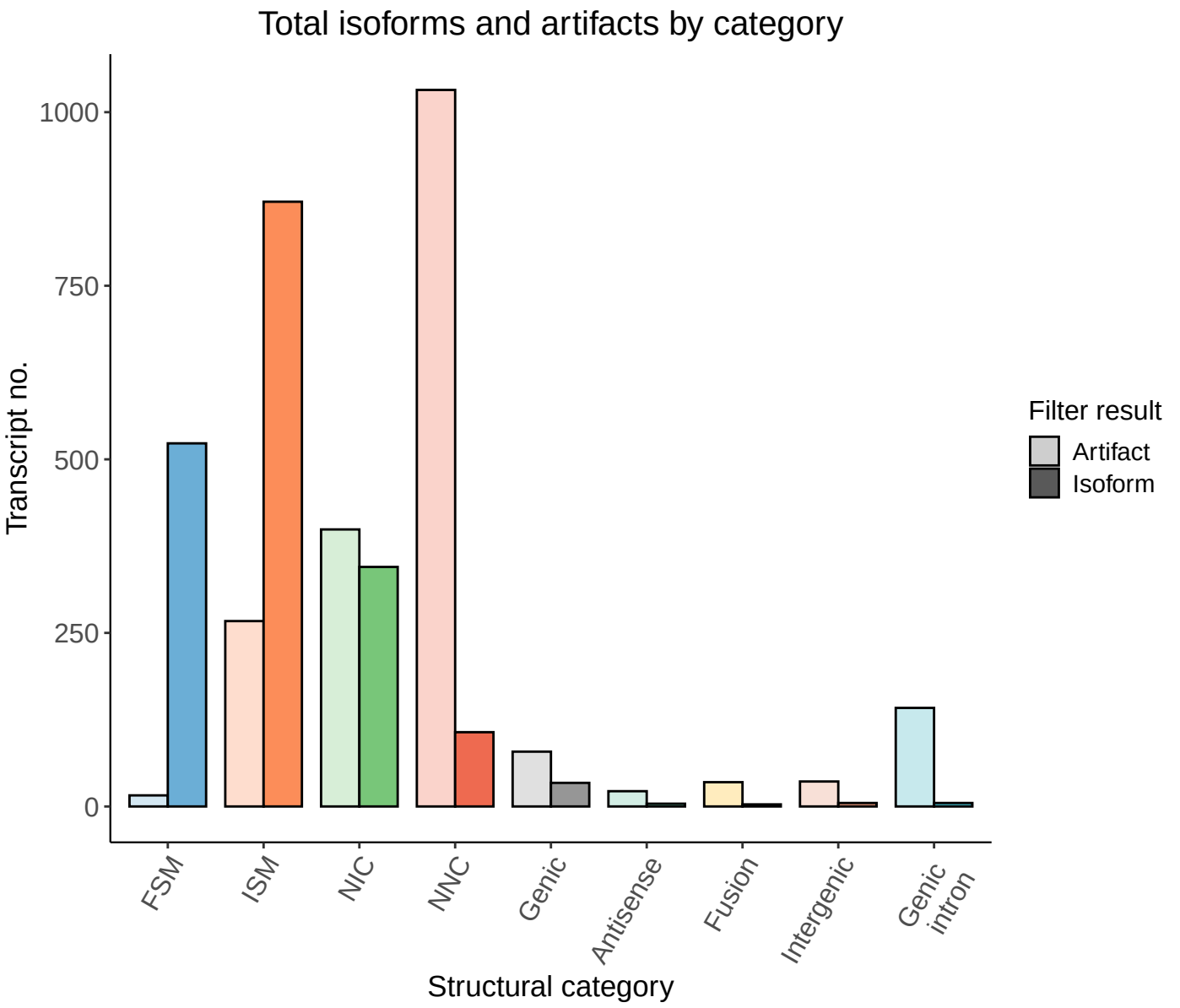
SQANTI3 filter report

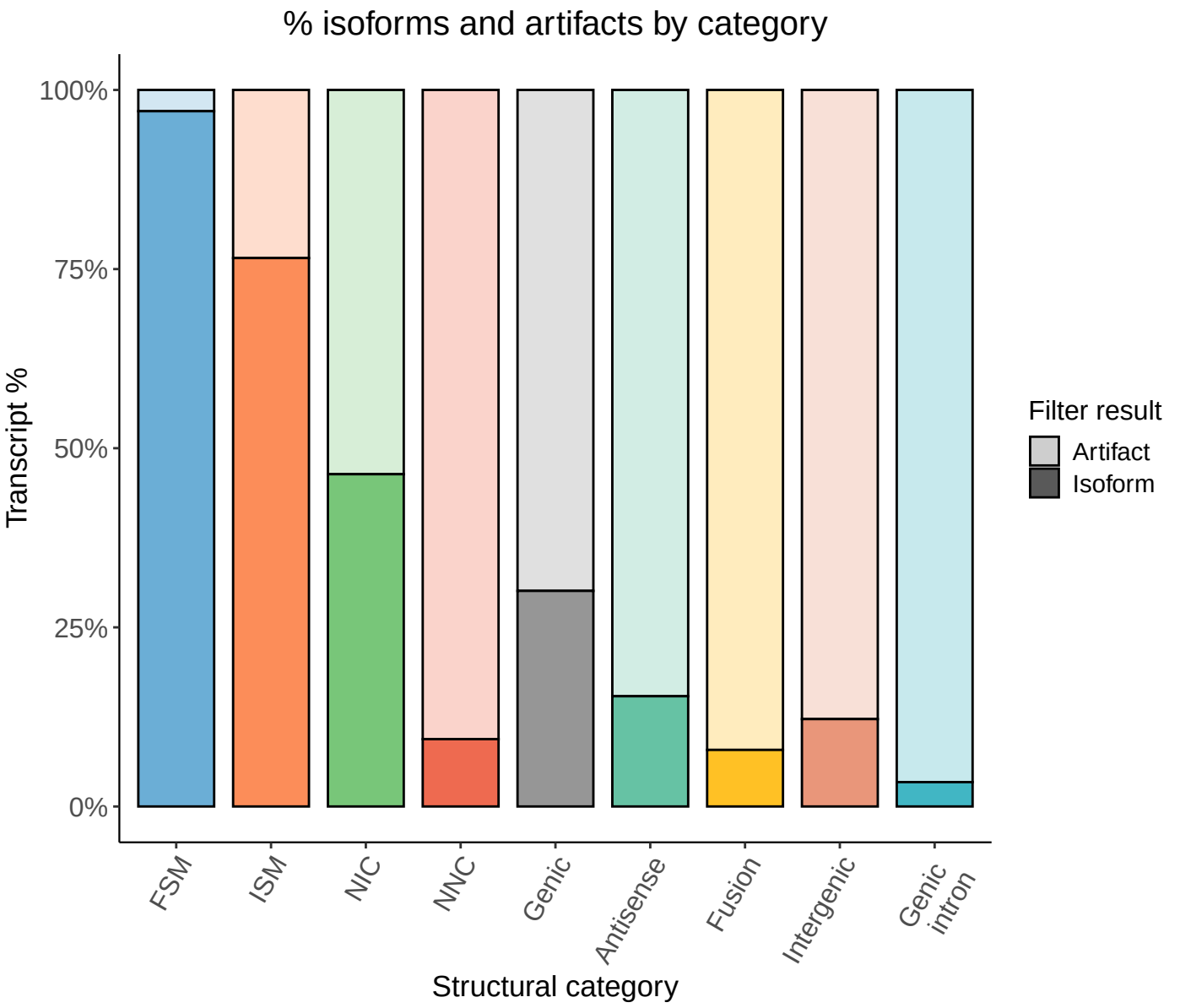
Total Genes: 656

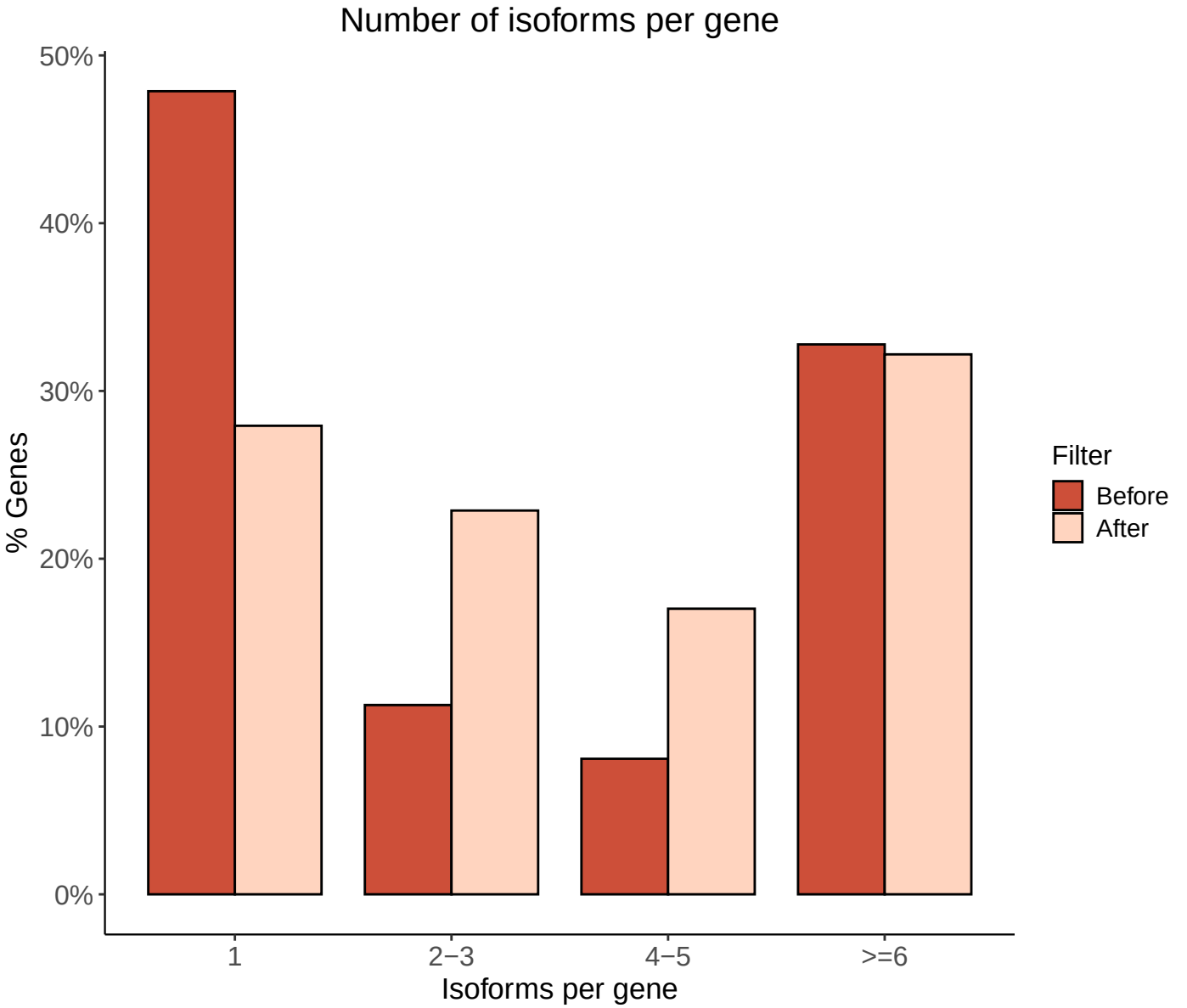
Total Transcripts: 3925
− Isoforms: 1897 (48%)
− Artifacts: 2028 (52%)

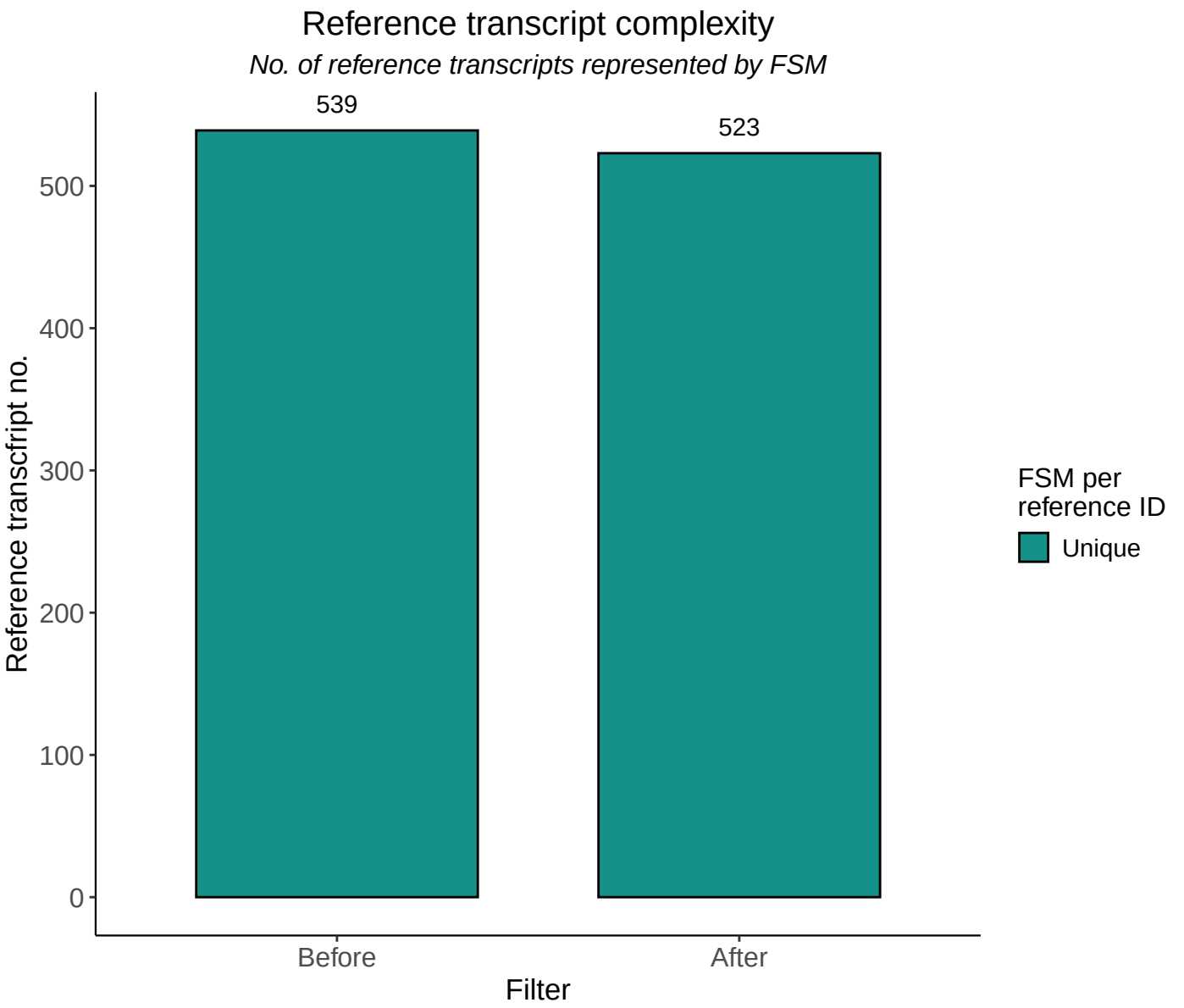
Gene category	Gene no.	No. of genes with artifacts only
Annotated	443	81
Novel	213	199

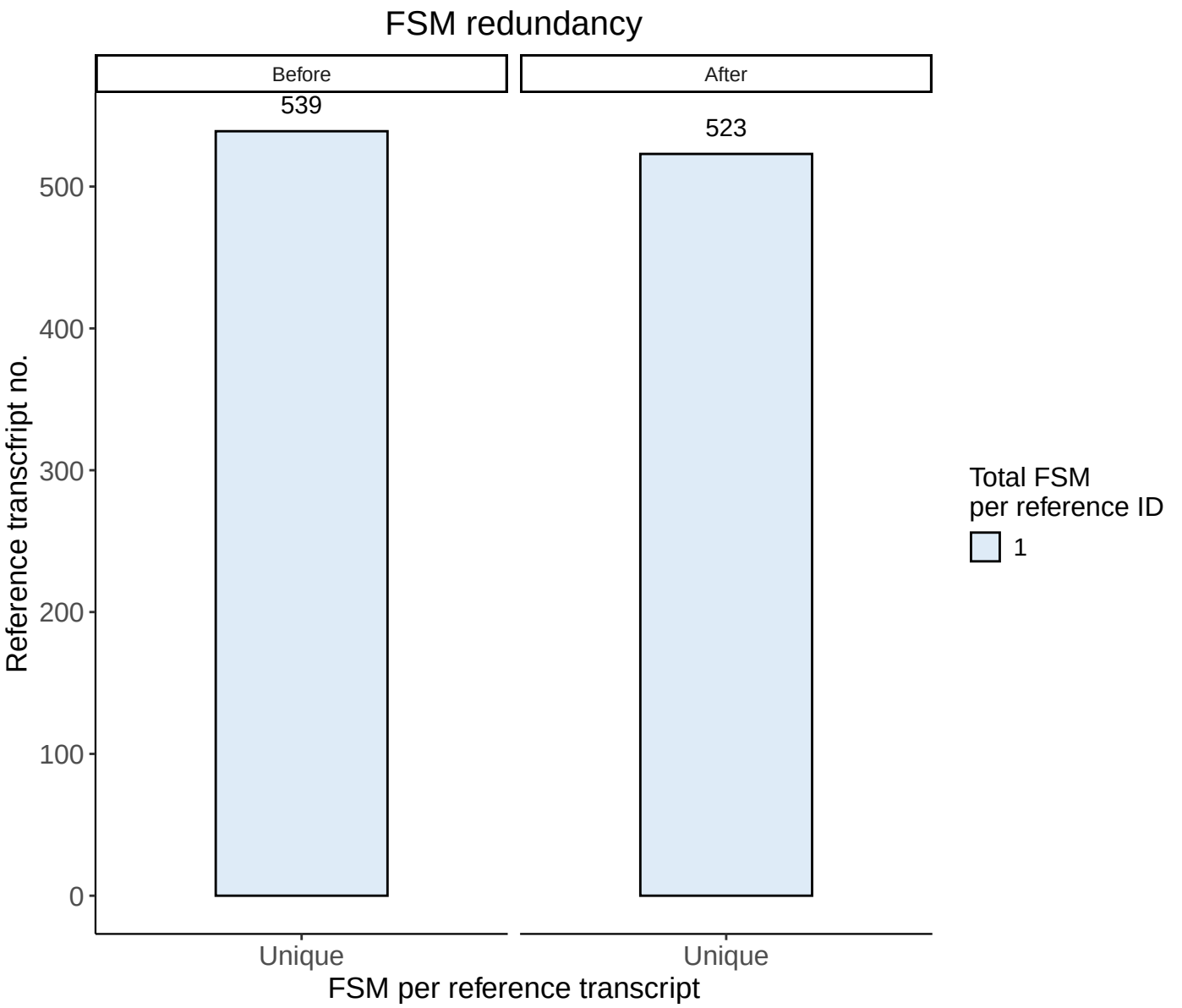
Structural category	Artifact no.	Isoform no.
FSM	16	523
ISM	267	871
NIC	399	345
NNC	1032	107
Genic	79	34
Antisense	22	4
Fusion	35	3
Intergenic	36	5
Genic intron	142	5

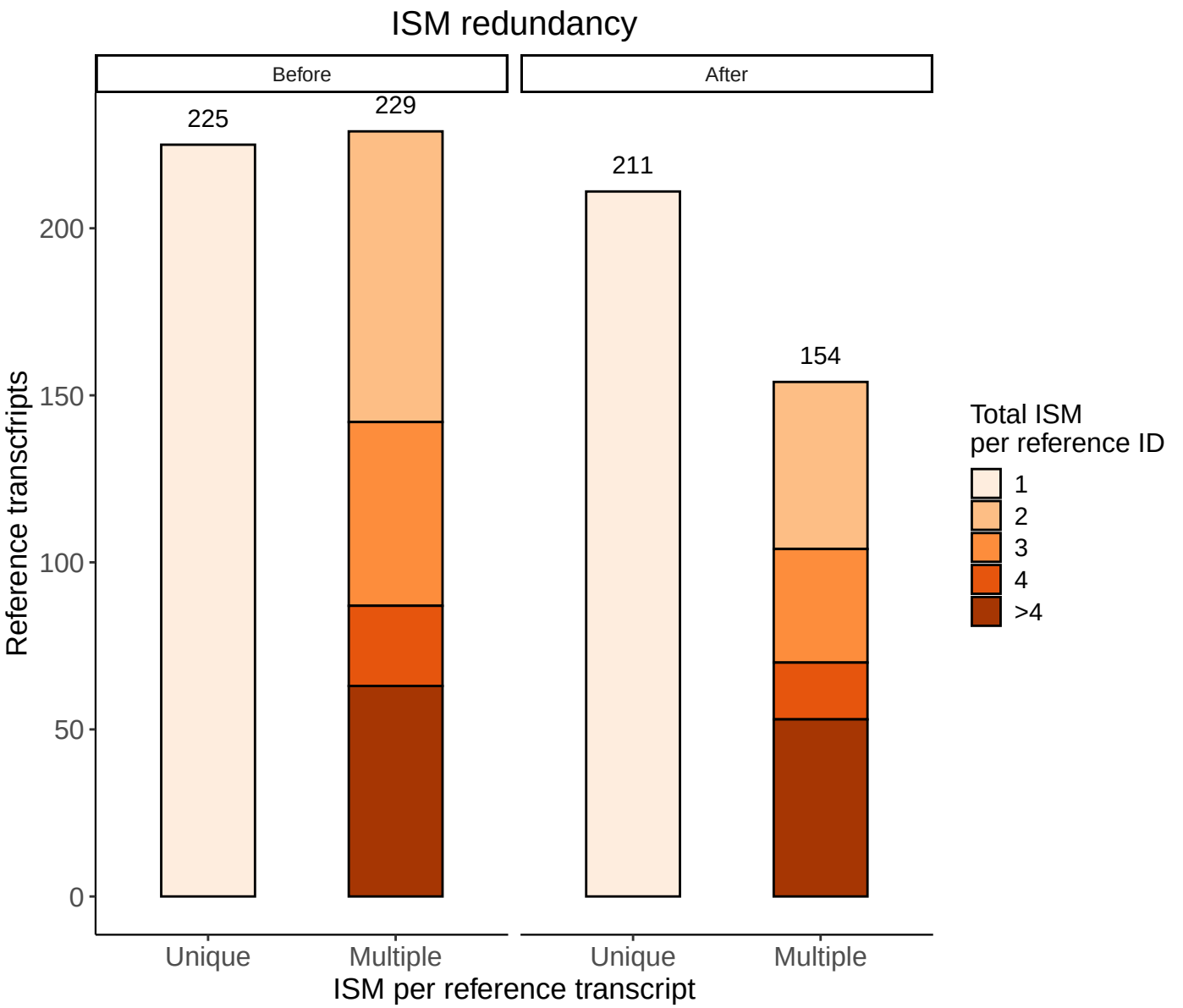

Total isoforms and artifacts by category
Transcript no.
1000
750
500
250
0
FSM
ISM
NIC
NNC
Genic
Antisense
Fusion
Intergenic
Genic intron
Structural category
Filter result
Artifact
Isoform

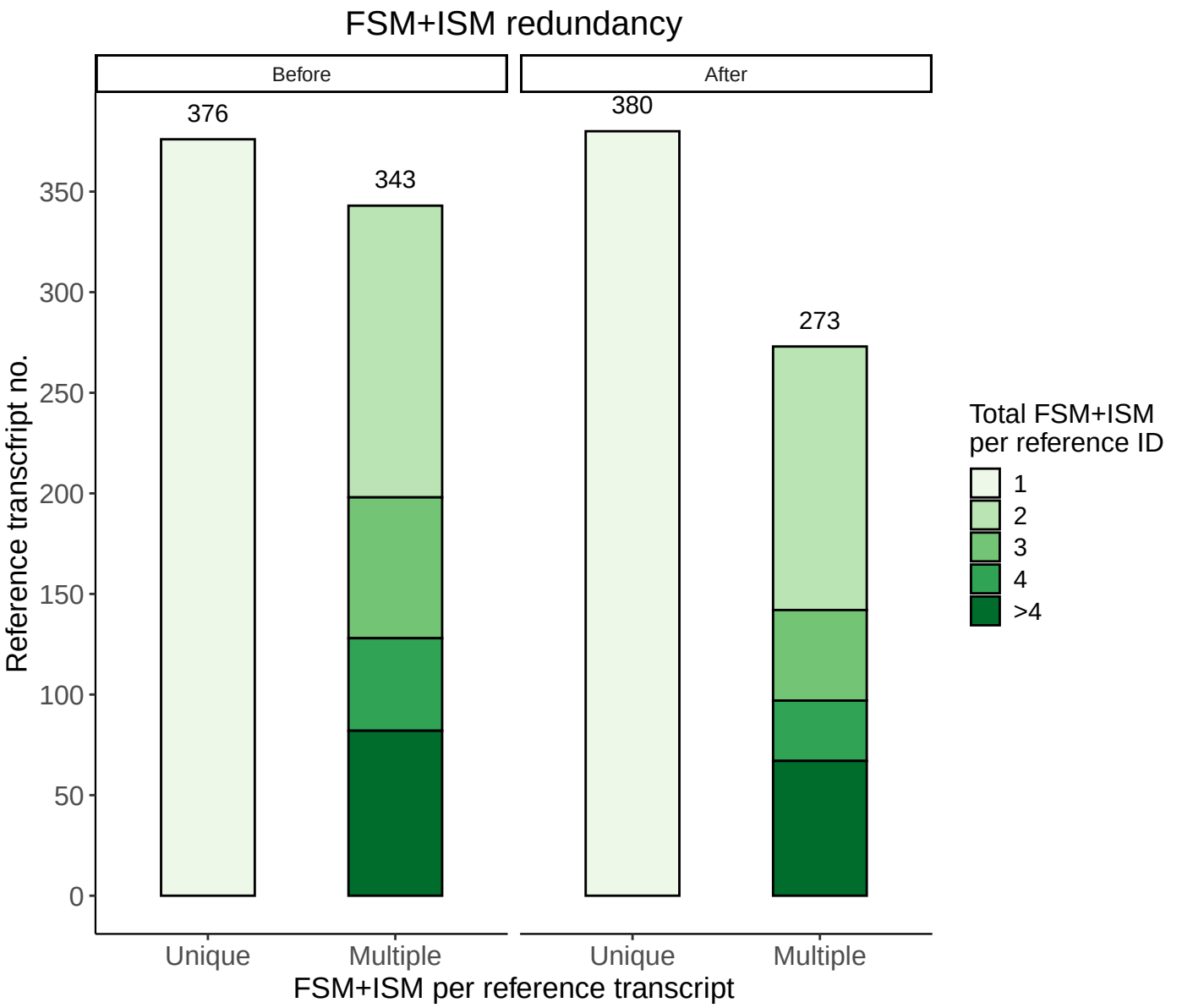

% isoforms and artifacts by category
100%
75%
50%
25%
0%
Transcript %
FSM
ISM
NIC
NNC
Genic
Antisense
Fusion
Intergenic
Genic intron
Structural category
Filter result
Artifact
Isoform


Number of isoforms per gene
50%
40%
30%
20%
10%
0%
% Genes
1
2−3
4−5
>=6
Isoforms per gene
Filter
Before
After


Reference transcript complexity
No. of reference transcripts represented by FSM
539
523
500
400
300
200
100
0
Reference transcfript no.
Before
After
Filter
FSM per reference ID
Unique


FSM redundancy
Before
After
539
523
500
400
300
200
100
0
Reference transcfript no.
Unique
Unique
FSM per reference transcript
Total FSM
per reference ID
1


ISM redundancy
Before
After
225
229
211
154
200
150
100
50
0
Reference transcfripts
Unique
Multiple
Unique
Multiple
ISM per reference transcript
Total ISM
per reference ID
1
2
3
4
>4


FSM+ISM redundancy
Before
After
376
343
380
273
350
300
250
200
150
100
50
0
Reference transcfript no.
Unique
Multiple
Unique
Multiple
FSM+ISM per reference transcript
Total FSM+ISM per reference ID
1
2
3
4
>4

ML classifier performance report

Classification model performance on test set

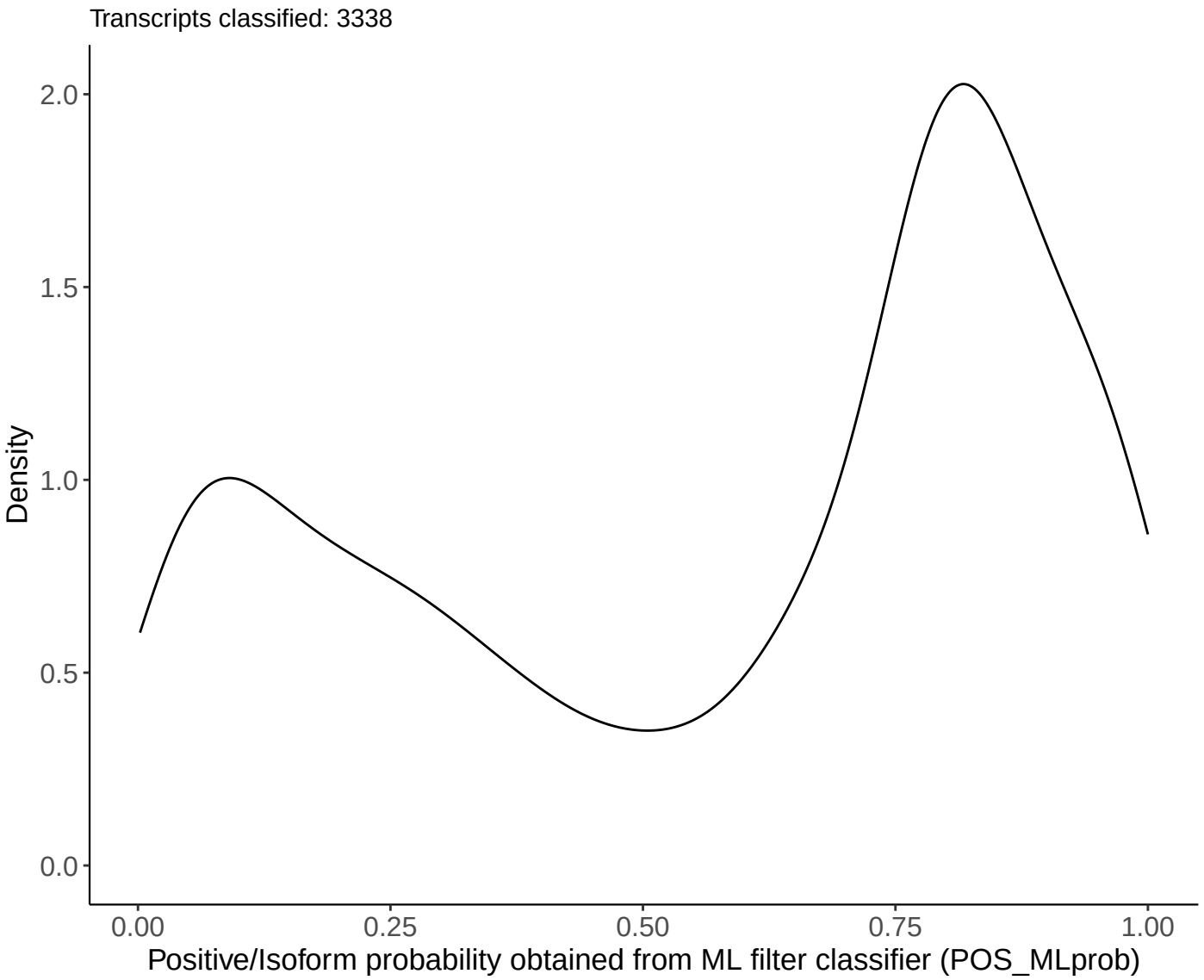
Performance metrics

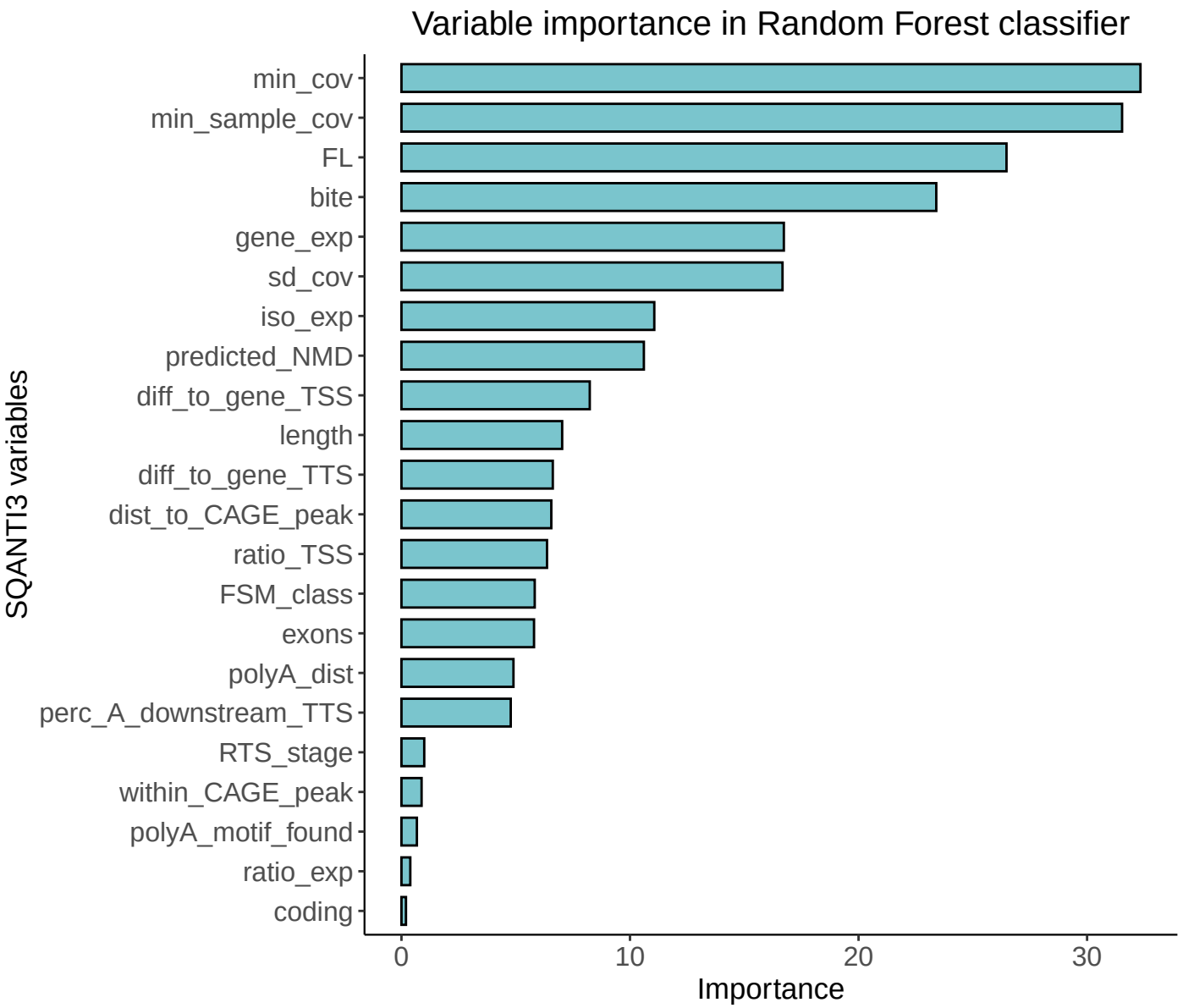
Metric	Value
Accuracy	0.895
Kappa	0.789
AccuracyLower	0.823
AccuracyUpper	0.944
AccuracyNull	0.5
McnemarPValue	0.0433
Sensitivity	0.825
Specificity	0.965
Pos Pred Value	0.959
Neg Pred Value	0.846
Precision	0.959
Recall	0.825
F1	0.887
Prevalence	0.5
Detection Rate	0.412
Detection Prevalence	0.430
Balanced Accuracy	0.895

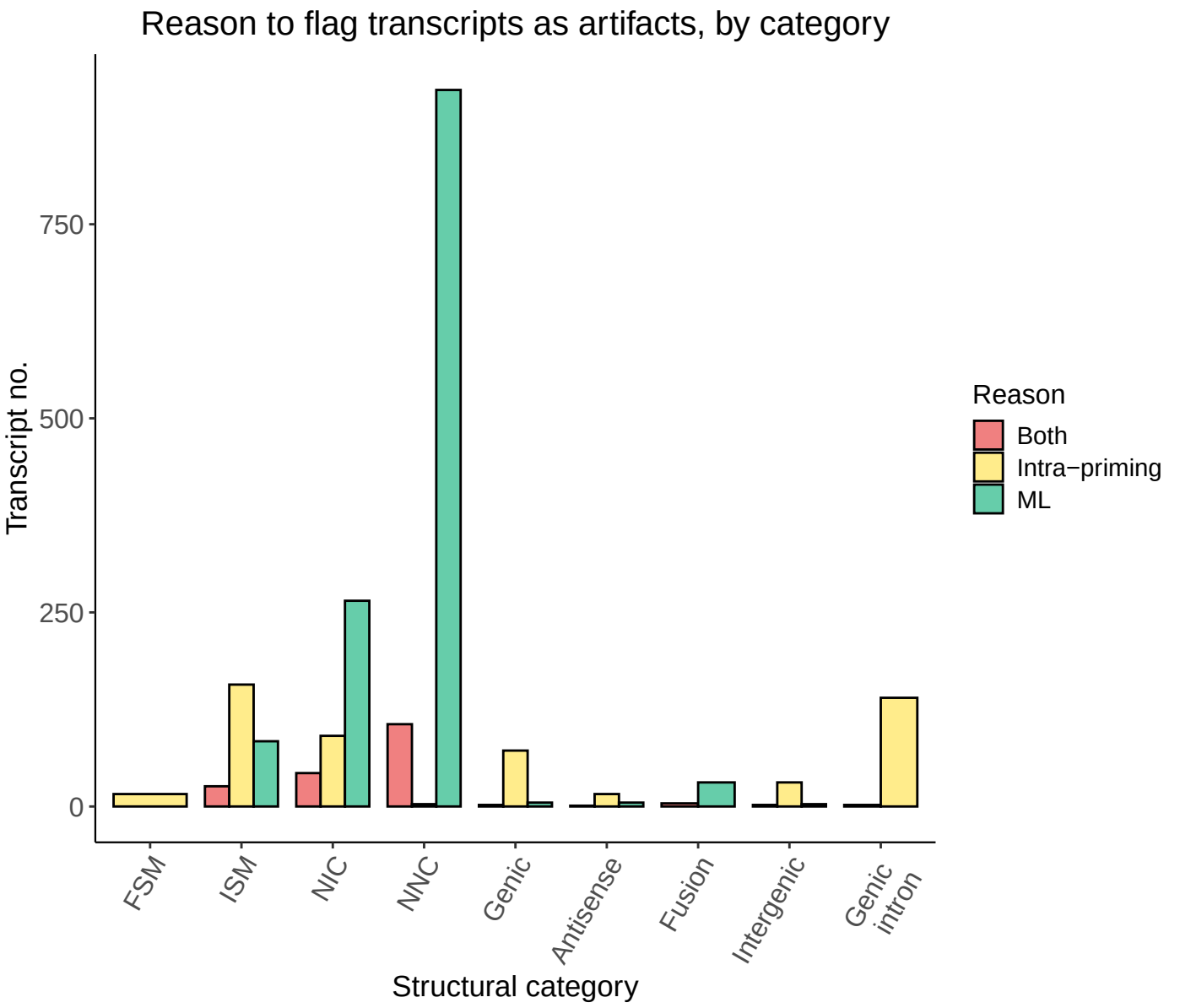
AccuracyPValue	3.005249e−19

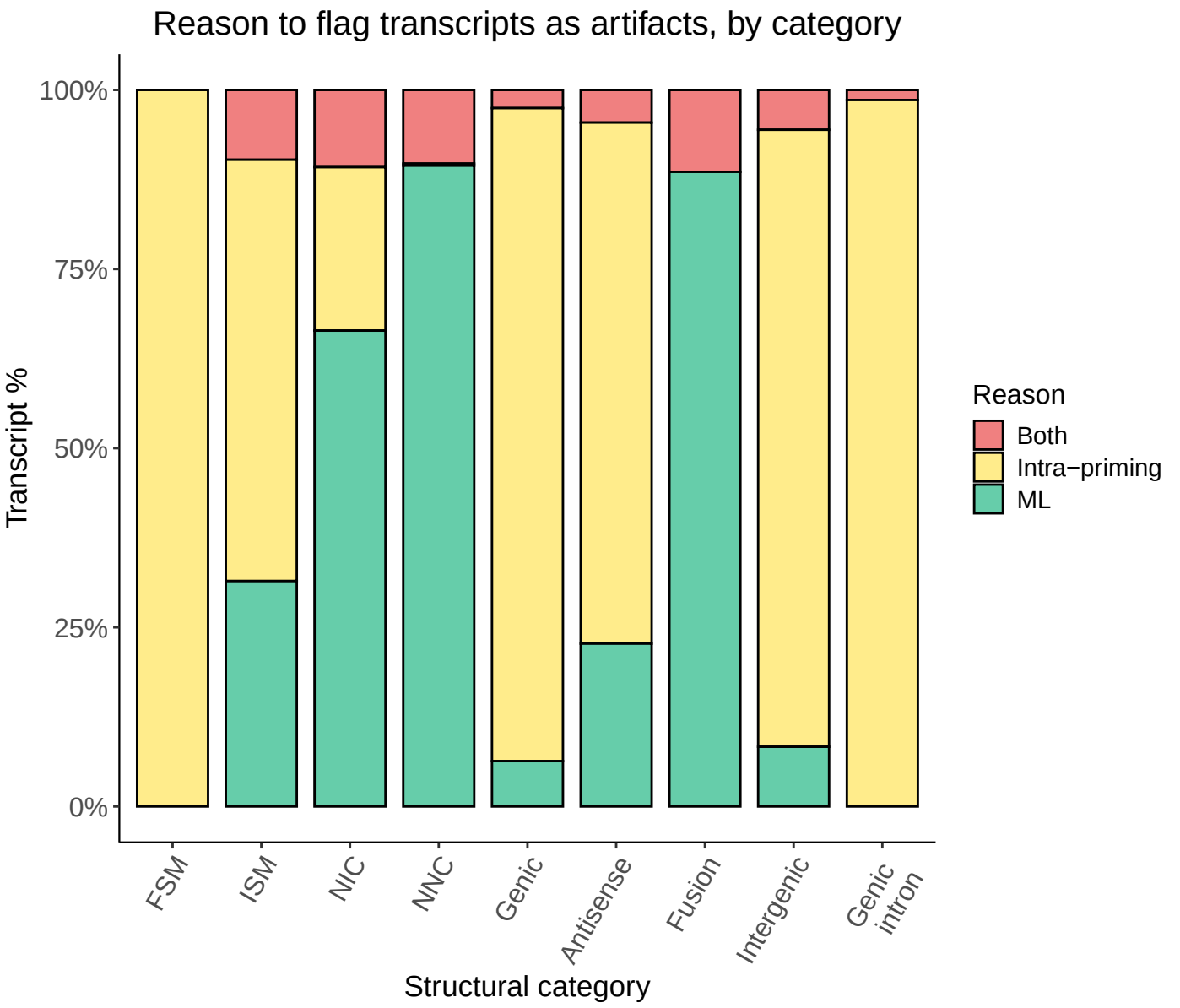
Confusion matrix

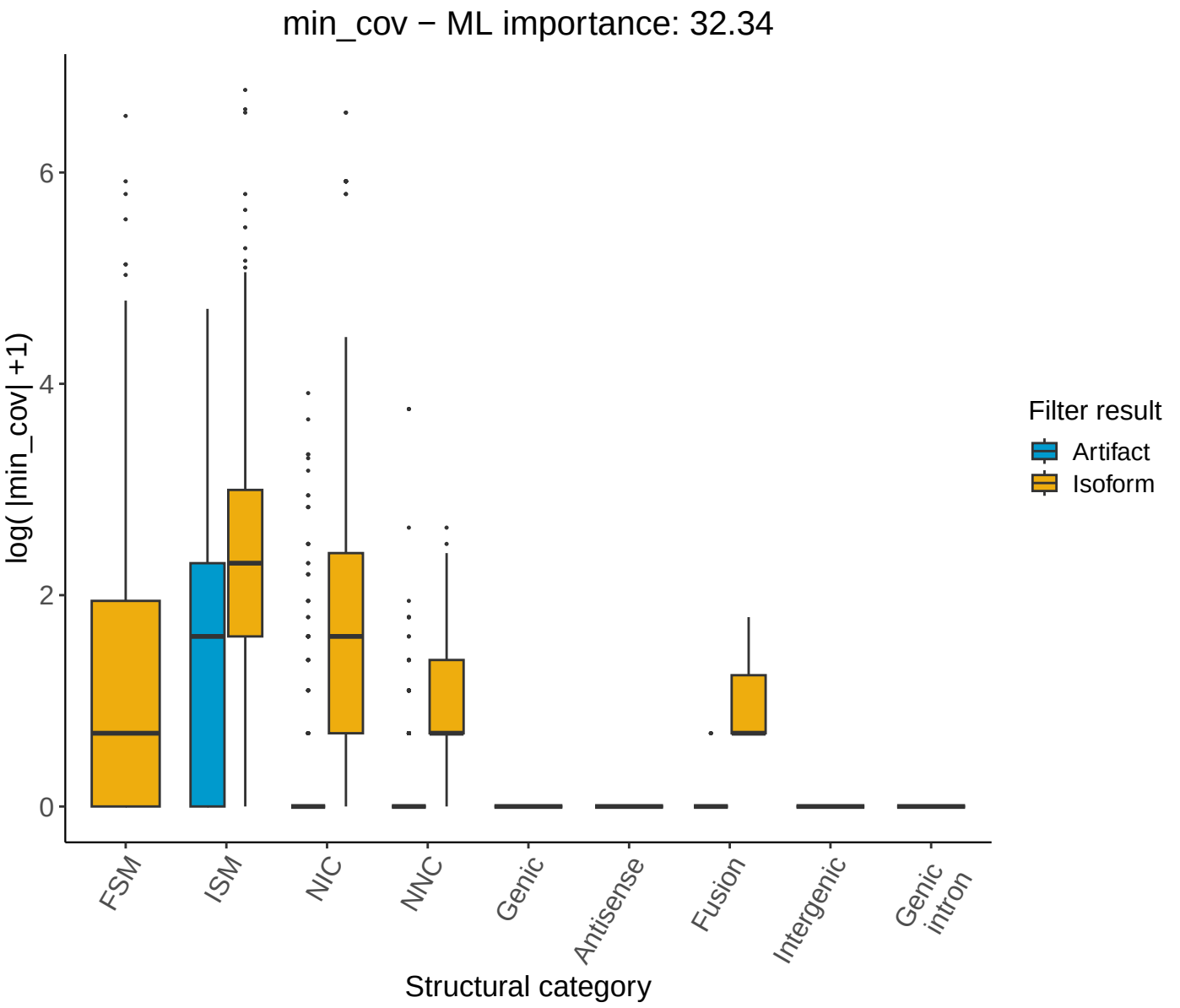
Prediction	Reference	Freq
POS	POS	47
NEG	POS	10
POS	NEG	2
NEG	NEG	55

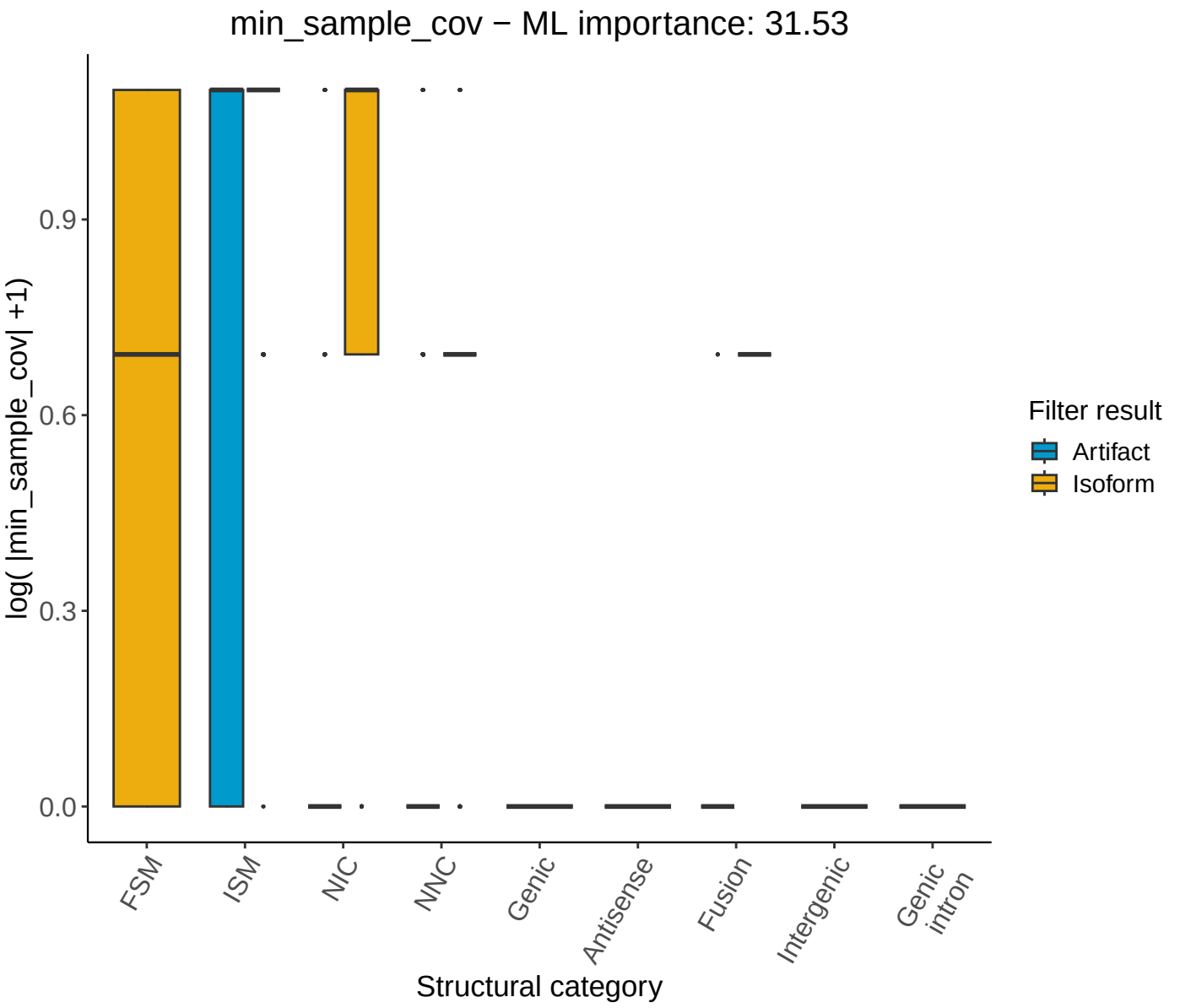

Transcripts classified: 3338
Density
2.0
1.5
1.0
0.5
0.0
0.00
0.25
0.50
0.75
1.00
Positive/Isoform probability obtained from ML filter classifier (POS_MLprob)

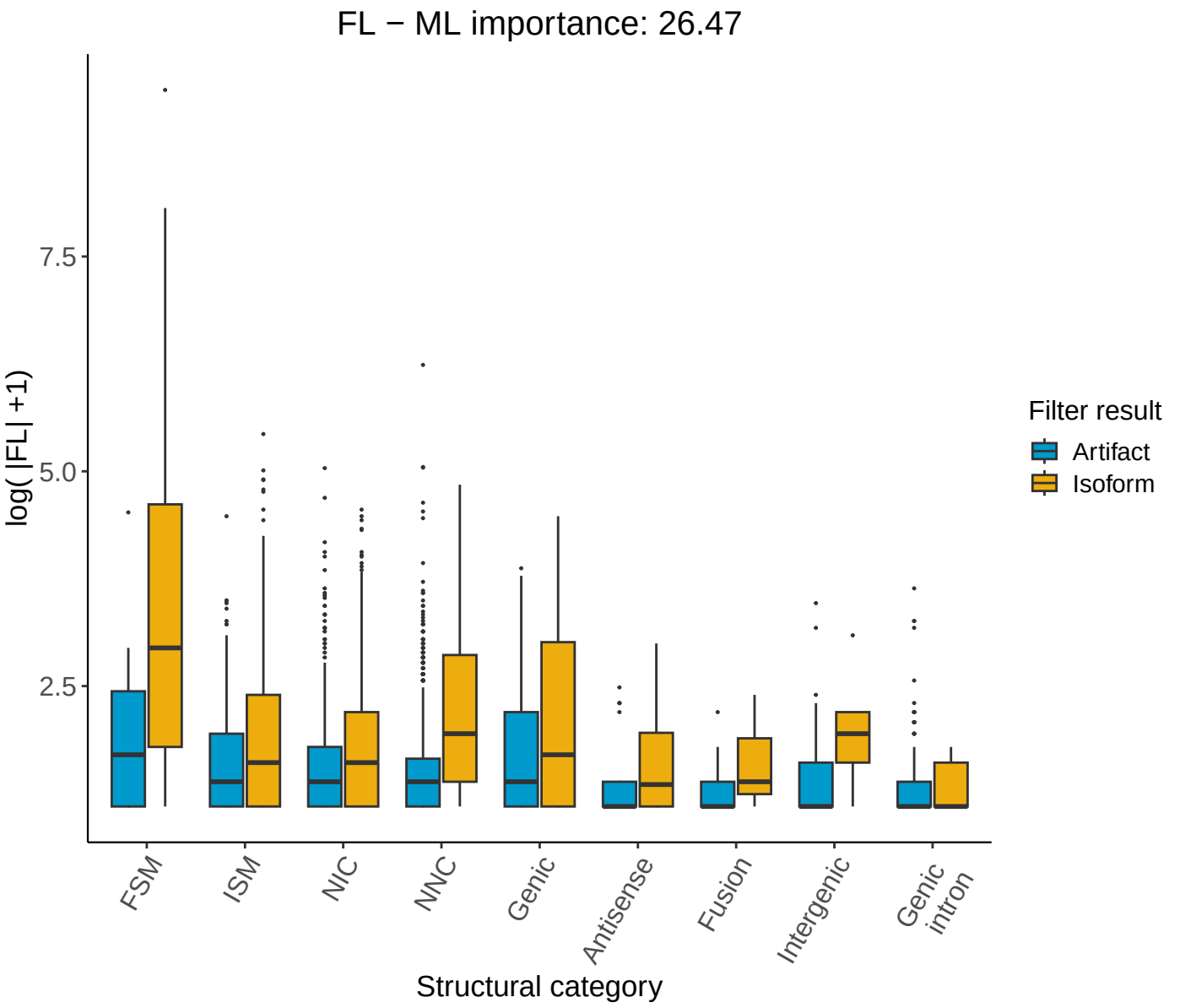

Variable importance in Random Forest classifier
SQANTI3 variables
min_cov
min_sample_cov
FL
bite
gene_exp
sd_cov
iso_exp
predicted_NMD
diff_to_gene_TSS
length
diff_to_gene_TTS
dist_to_CAGE_peak
ratio_TSS
FSM_class
exons
polyA_dist
perc_A_downstream_TTS
RTS_stage
within_CAGE_peak
polyA_motif_found
ratio_exp
coding
0
10
20
30
Importance

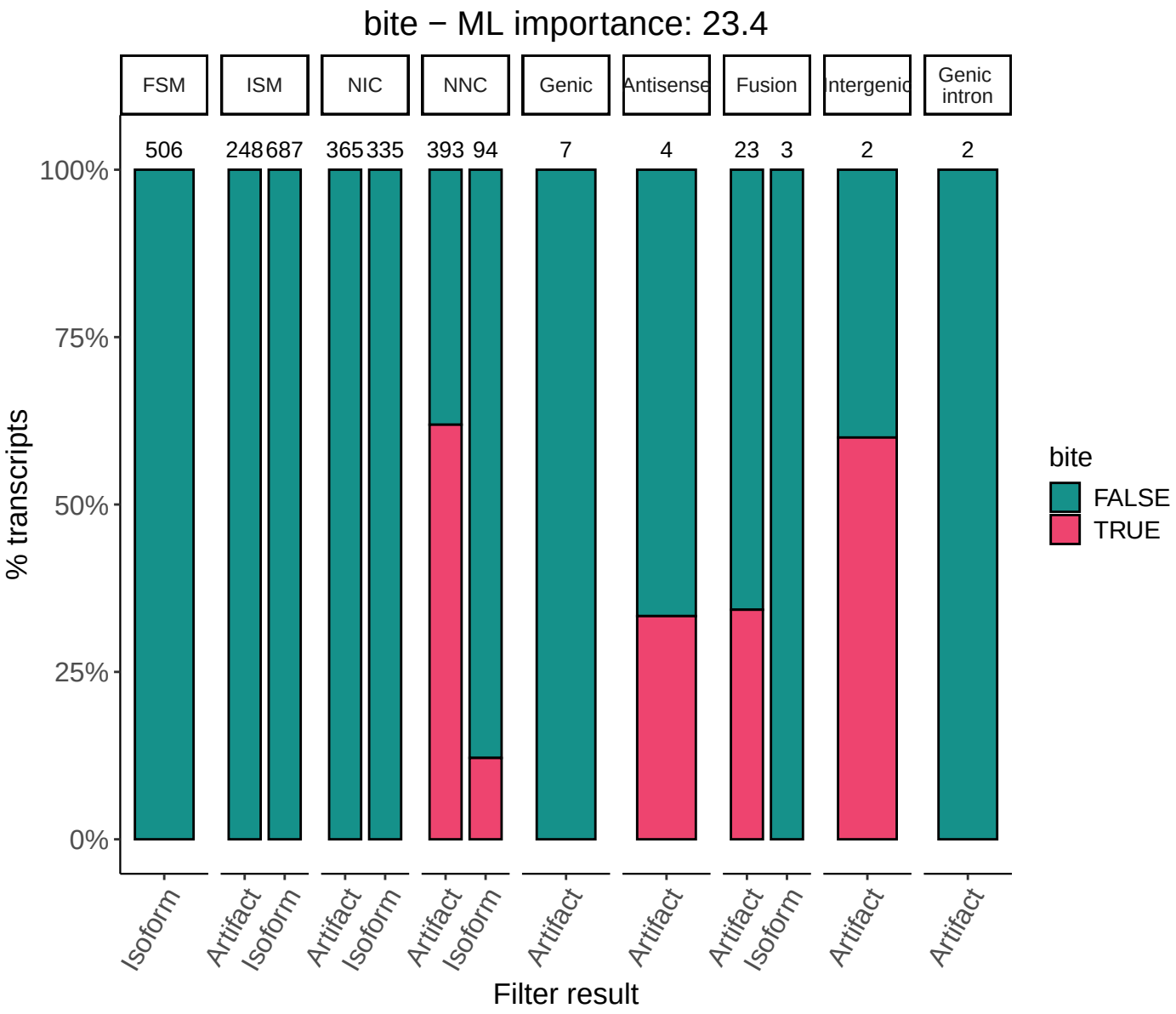

Reason to flag transcripts as artifacts, by category
Transcript no.
0
250
500
750
FSM
ISM
NIC
NNC
Genic
Antisense
Fusion
Intergenic
Genic intron
Structural category
Reason
Both
Intra−priming
ML

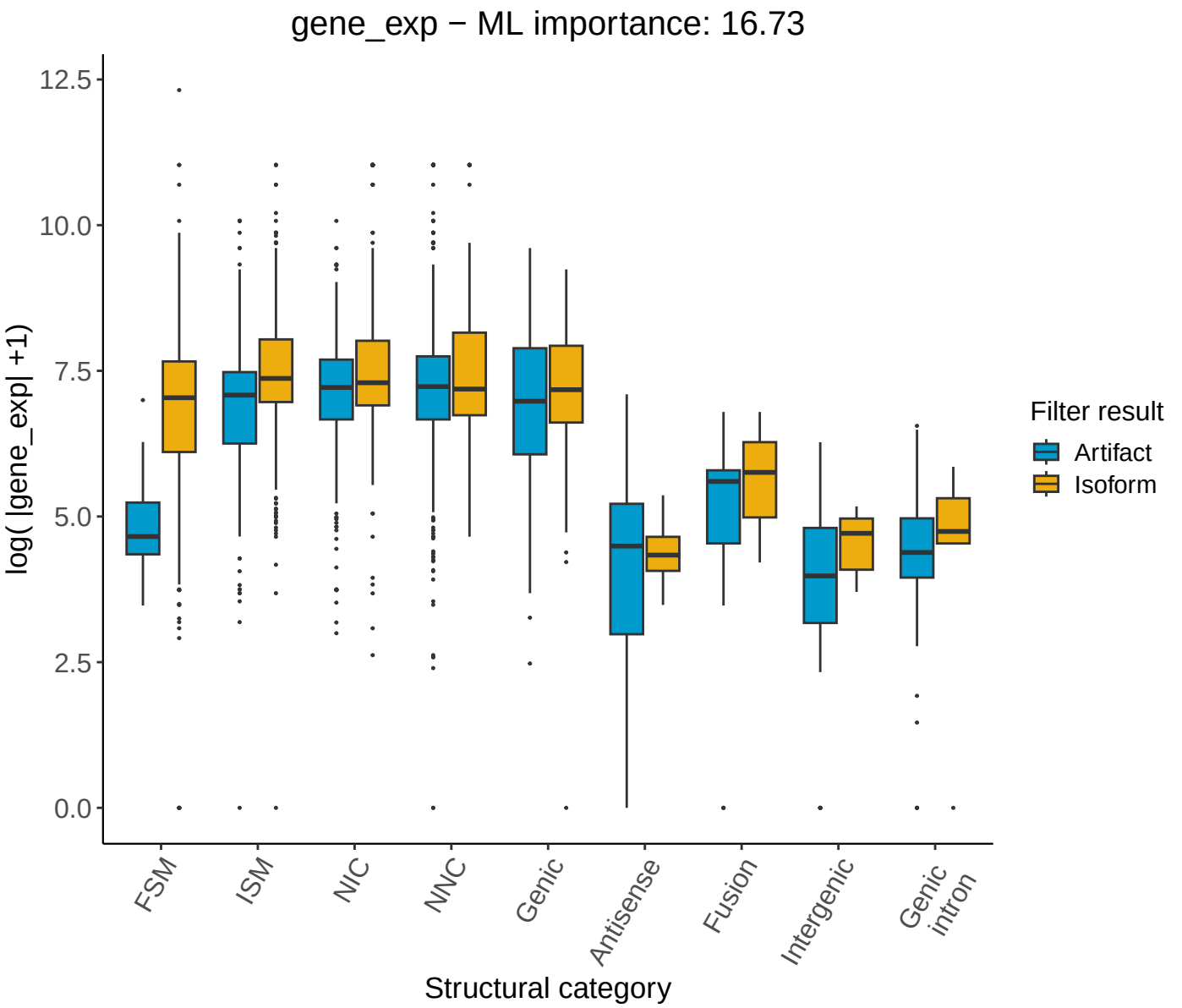

Reason to flag transcripts as artifacts, by category
100%
75%
50%
25%
0%
Transcript %
FSM
ISM
NIC
NNC
Genic
Antisense
Fusion
Intergenic
Genic intron
Structural category
Reason
Both
Intra−priming
ML

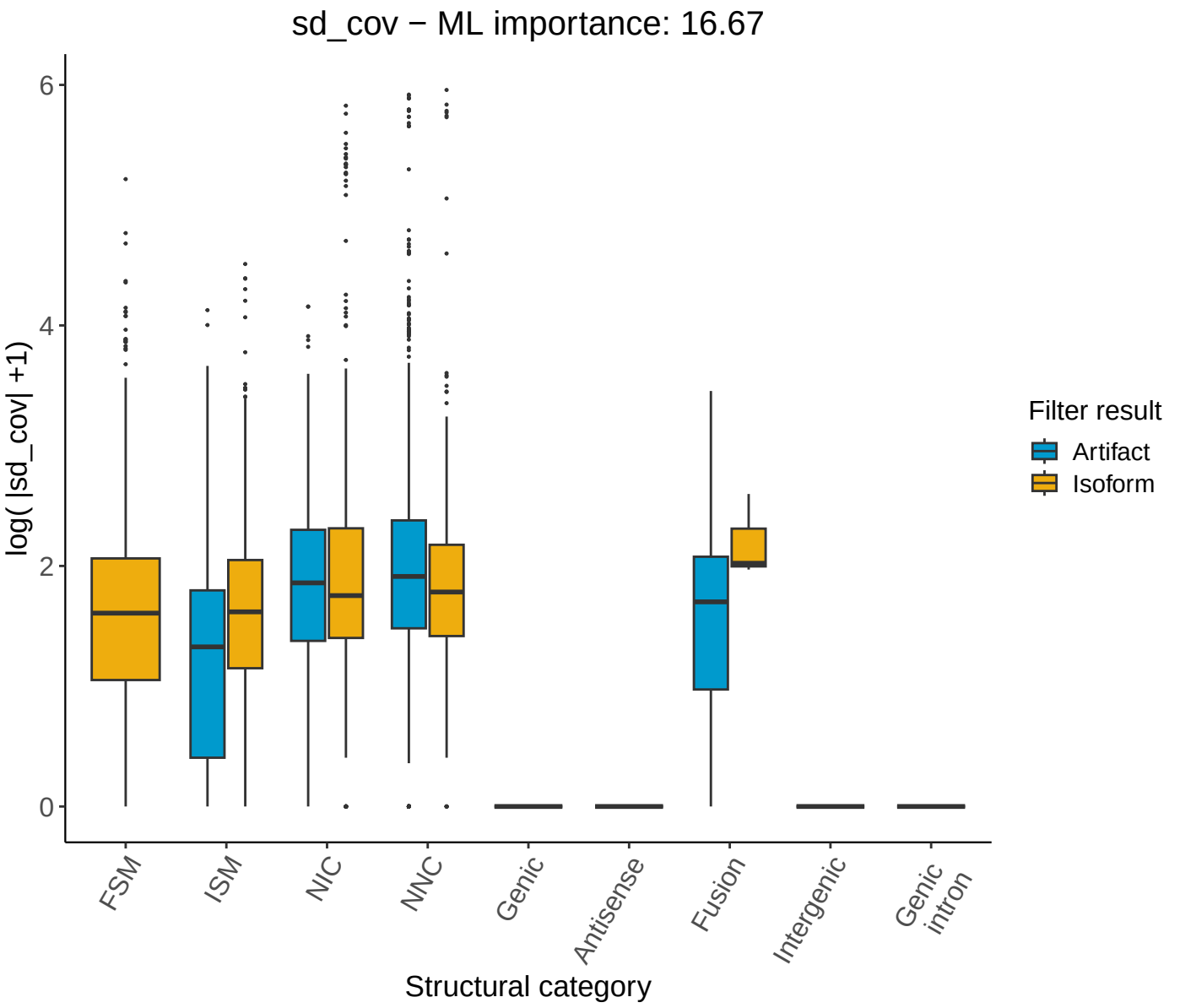

min_cov − ML importance: 32.34
log(|min_cov| +1)
6
4
2
0
FSM
ISM
NIC
NNC
Genic
Antisense
Fusion
Intergenic
Genic intron
Structural category
Filter result
Artifact
Isoform

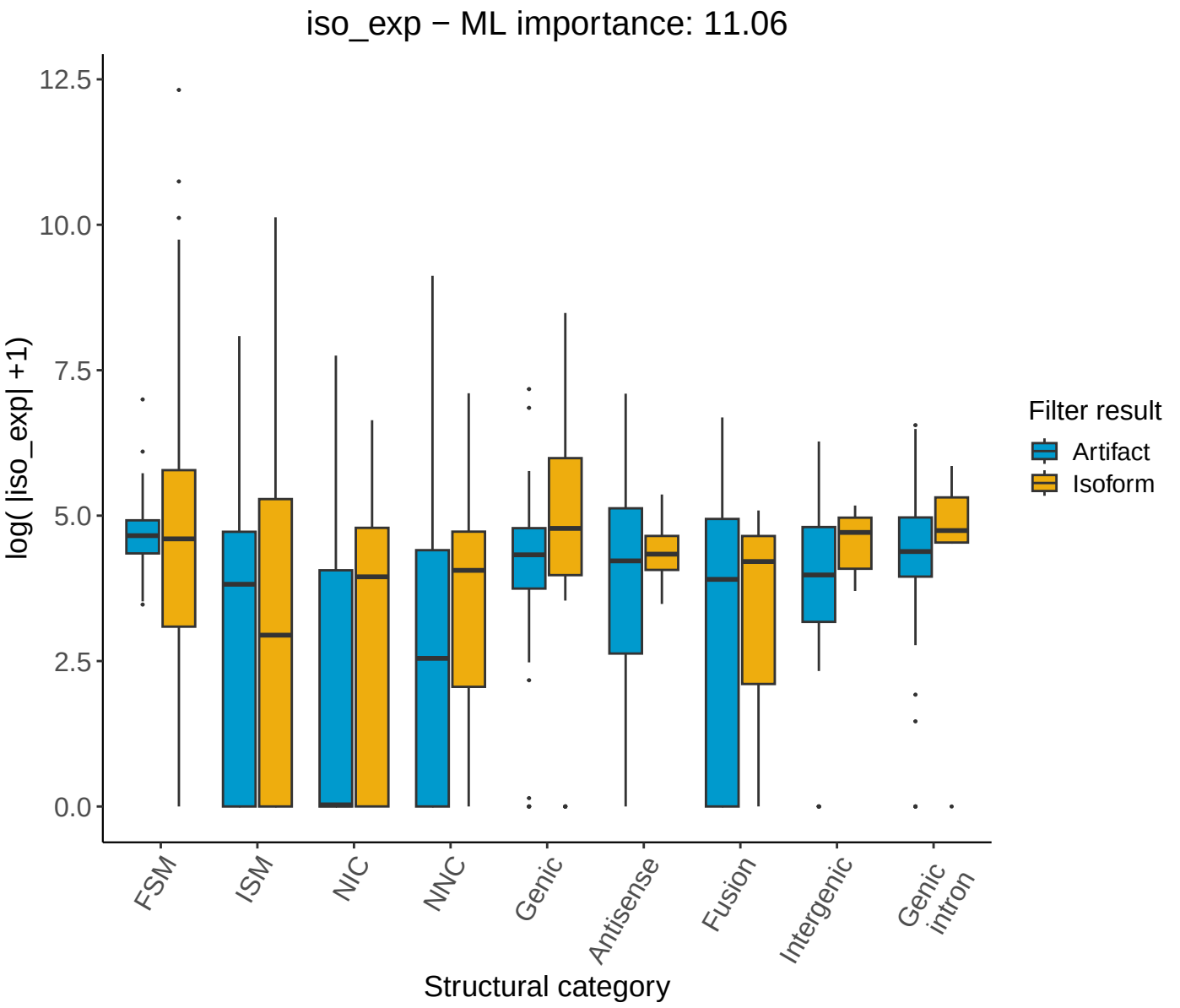

min_sample_cov − ML importance: 31.53
log(|min_sample_cov| +1)
0.0
0.3
0.6
0.9
FSM
ISM
NIC
NNC
Genic
Antisense
Fusion
Intergenic
Genic intron
Structural category
Filter result
Artifact
Isoform

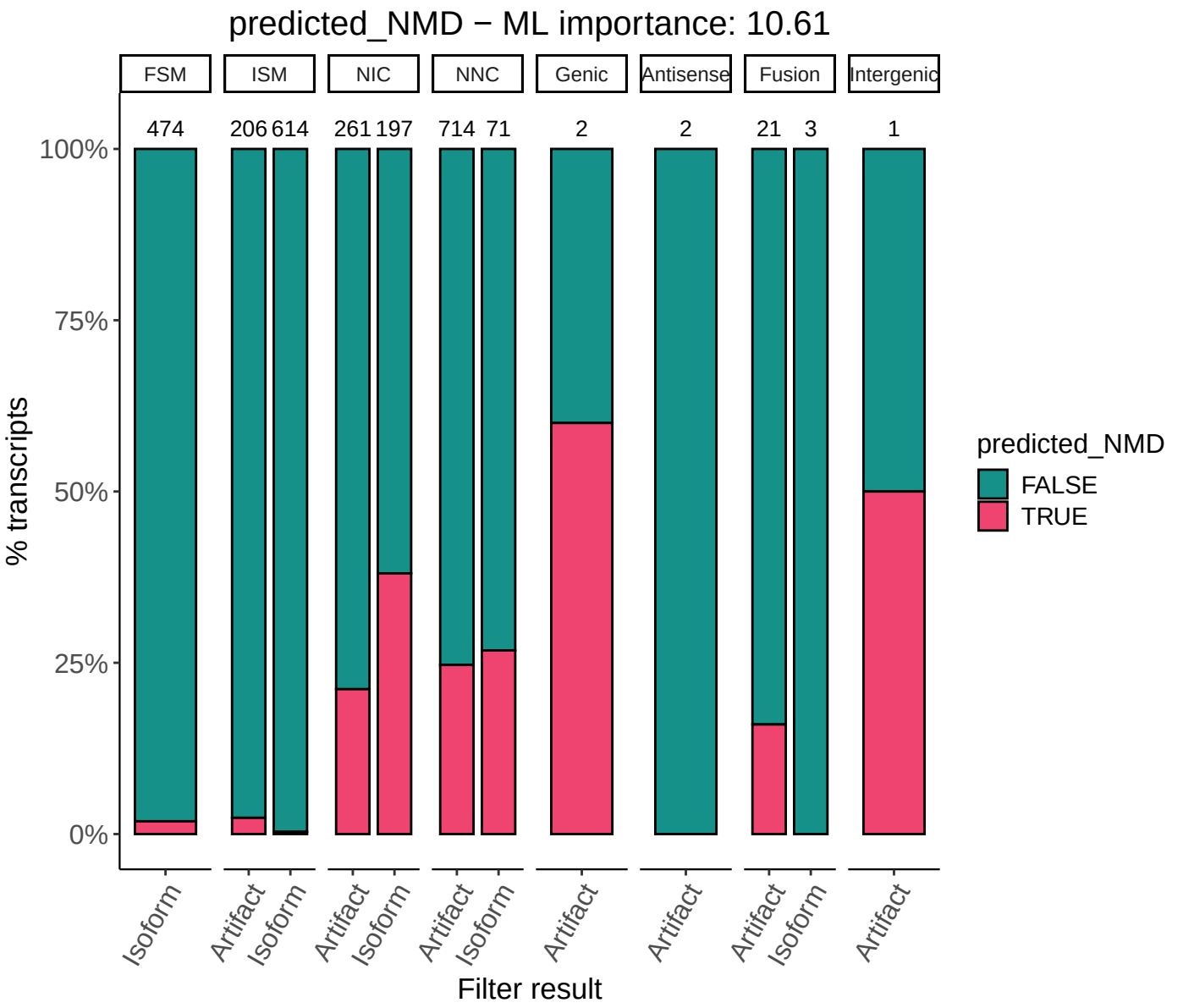

FL − ML importance: 26.47
log(|FL| +1)
7.5
5.0
2.5
FSM
ISM
NIC
NNC
Genic
Antisense
Fusion
Intergenic
Genic intron
Structural category
Filter result
Artifact
Isoform

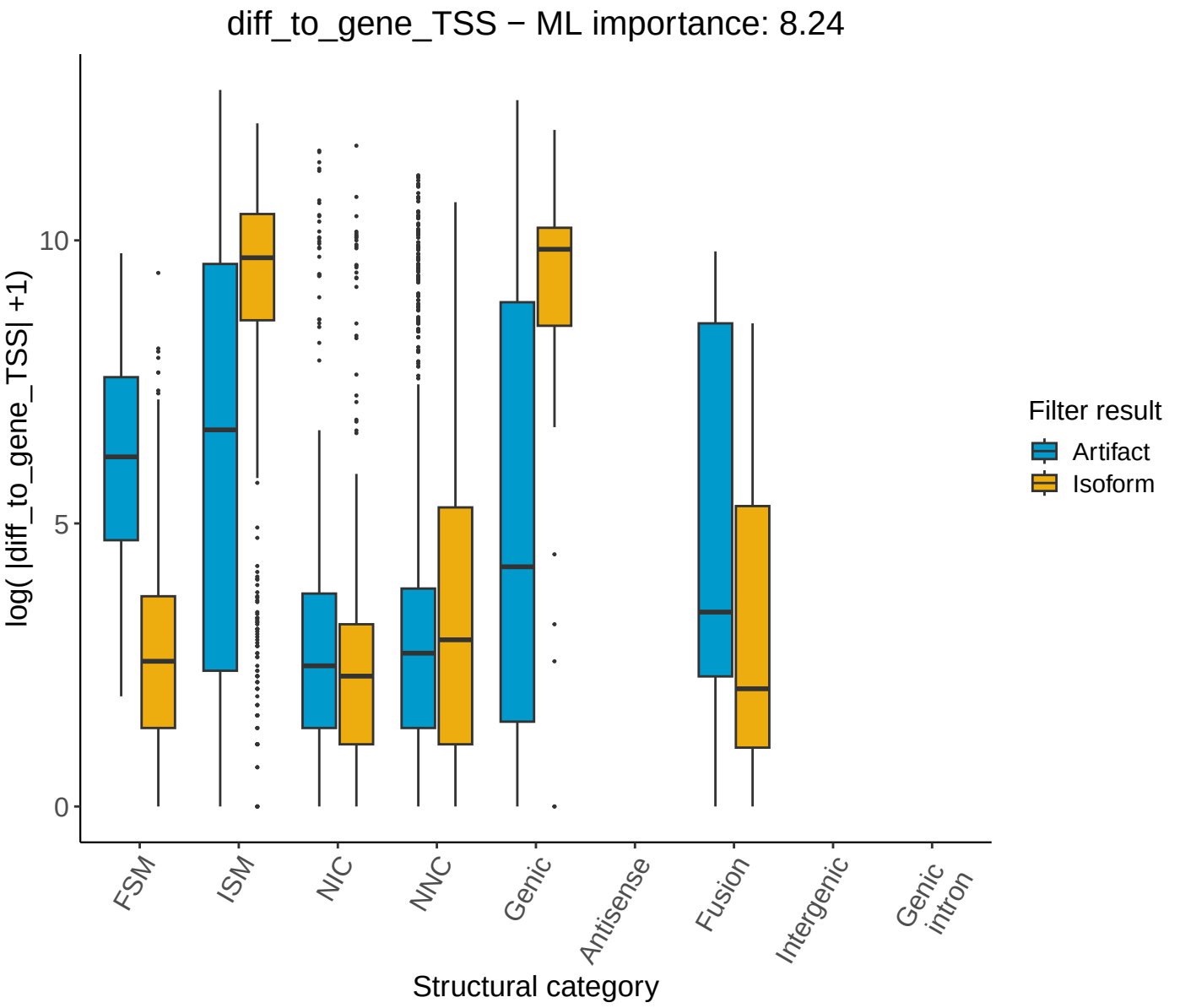

bite − ML importance: 23.4
FSM
ISM
NIC
NNC
Genic
Antisense
Fusion
Intergenic
Genic intron
506
248
687
365
335
393
94
7
4
23
3
2
2
100%
75%
50%
25%
0%
% transcripts
Isoform
Artifact
Isoform
Artifact
Isoform
Artifact
Isoform
Artifact
Artifact
Artifact
Isoform
Artifact
Artifact
Filter result
bite
FALSE
TRUE

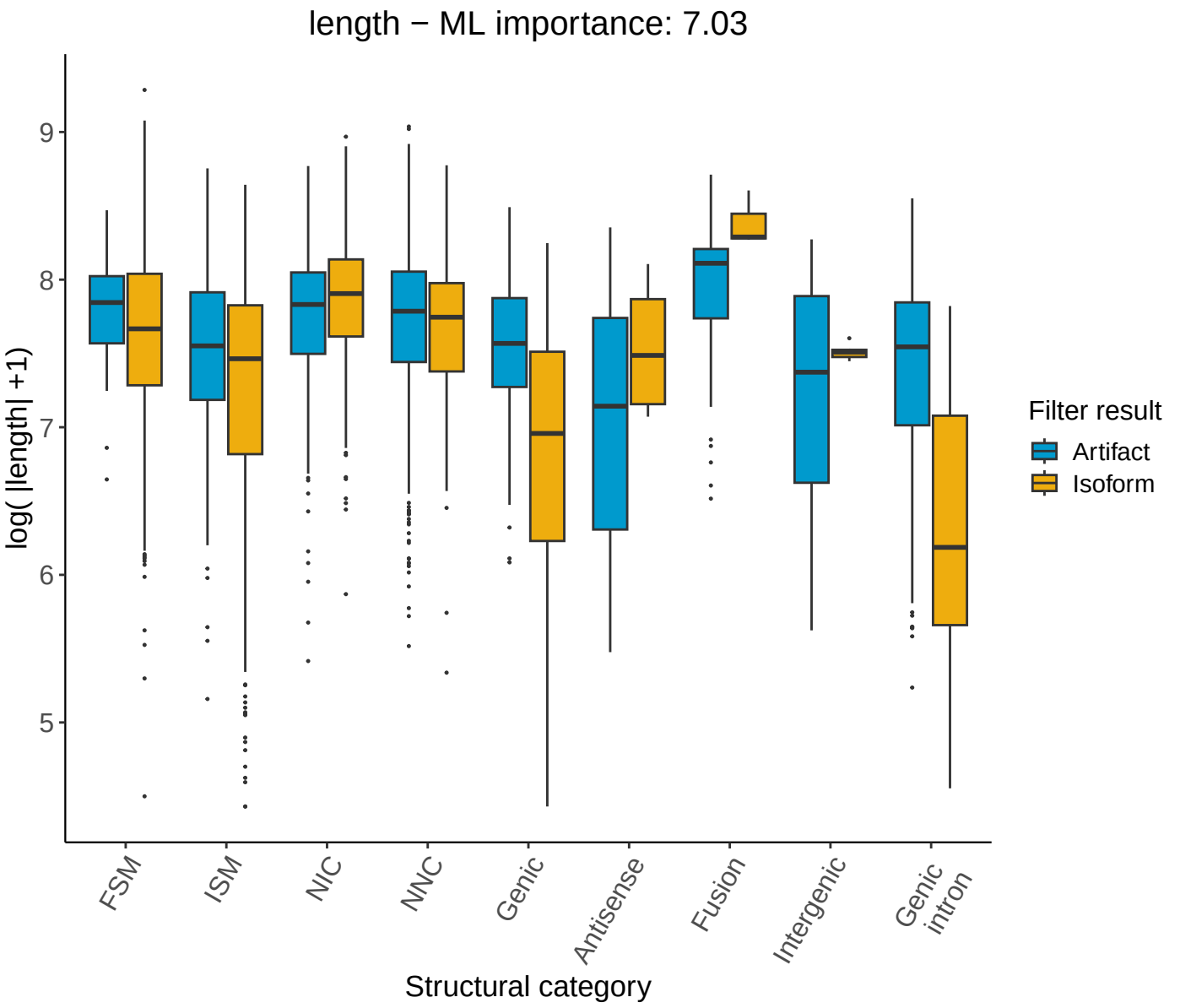

gene_exp − ML importance: 16.73
log(|gene_exp| +1)
12.5
10.0
7.5
5.0
2.5
0.0
FSM
ISM
NIC
NNC
Genic
Antisense
Fusion
Intergenic
Genic intron
Structural category
Filter result
Artifact
Isoform

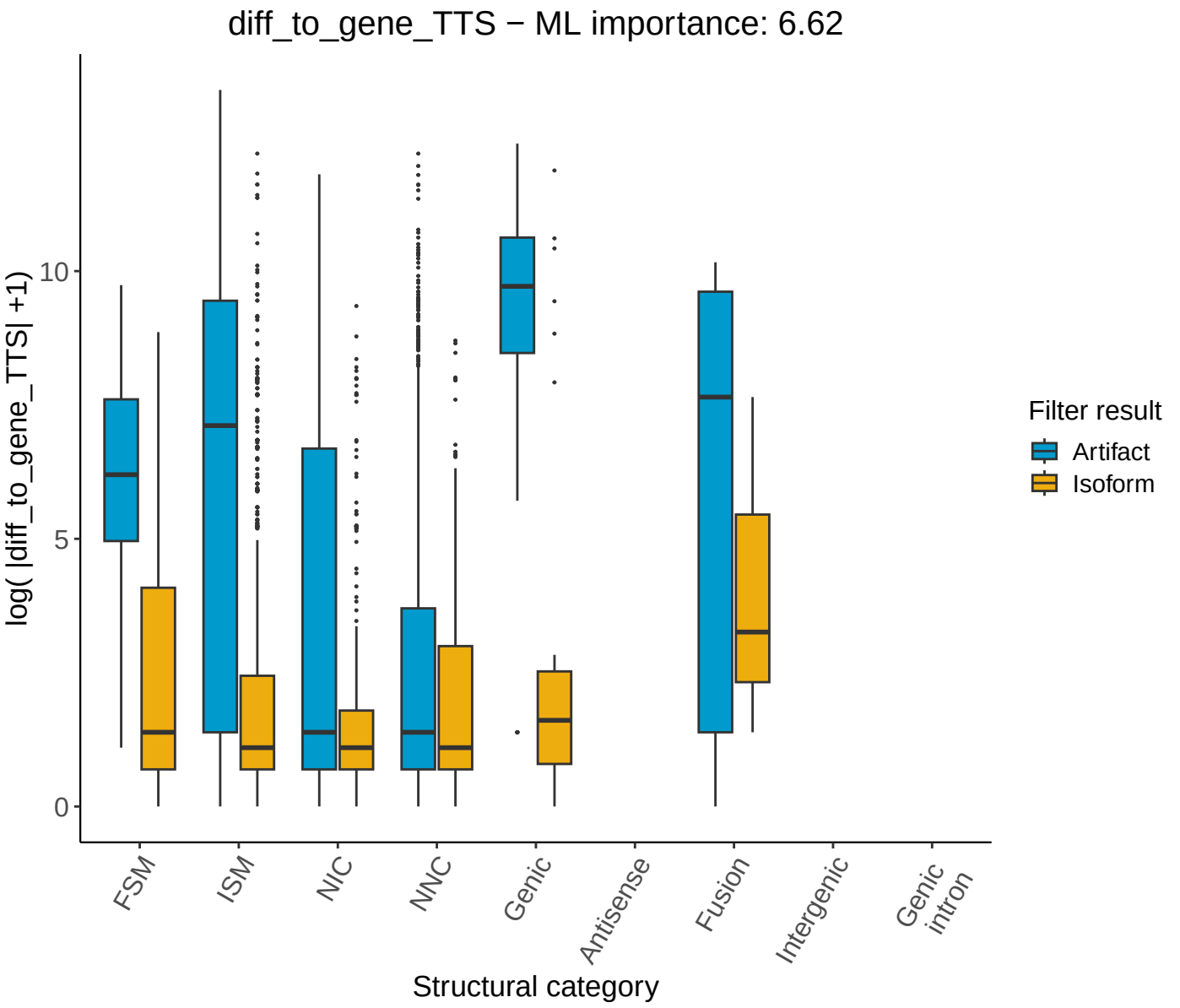

sd_cov − ML importance: 16.67
log(|sd_cov| +1)
6
4
2
0
FSM
ISM
NIC
NNC
Genic
Antisense
Fusion
Intergenic
Genic intron
Structural category
Filter result
Artifact
Isoform

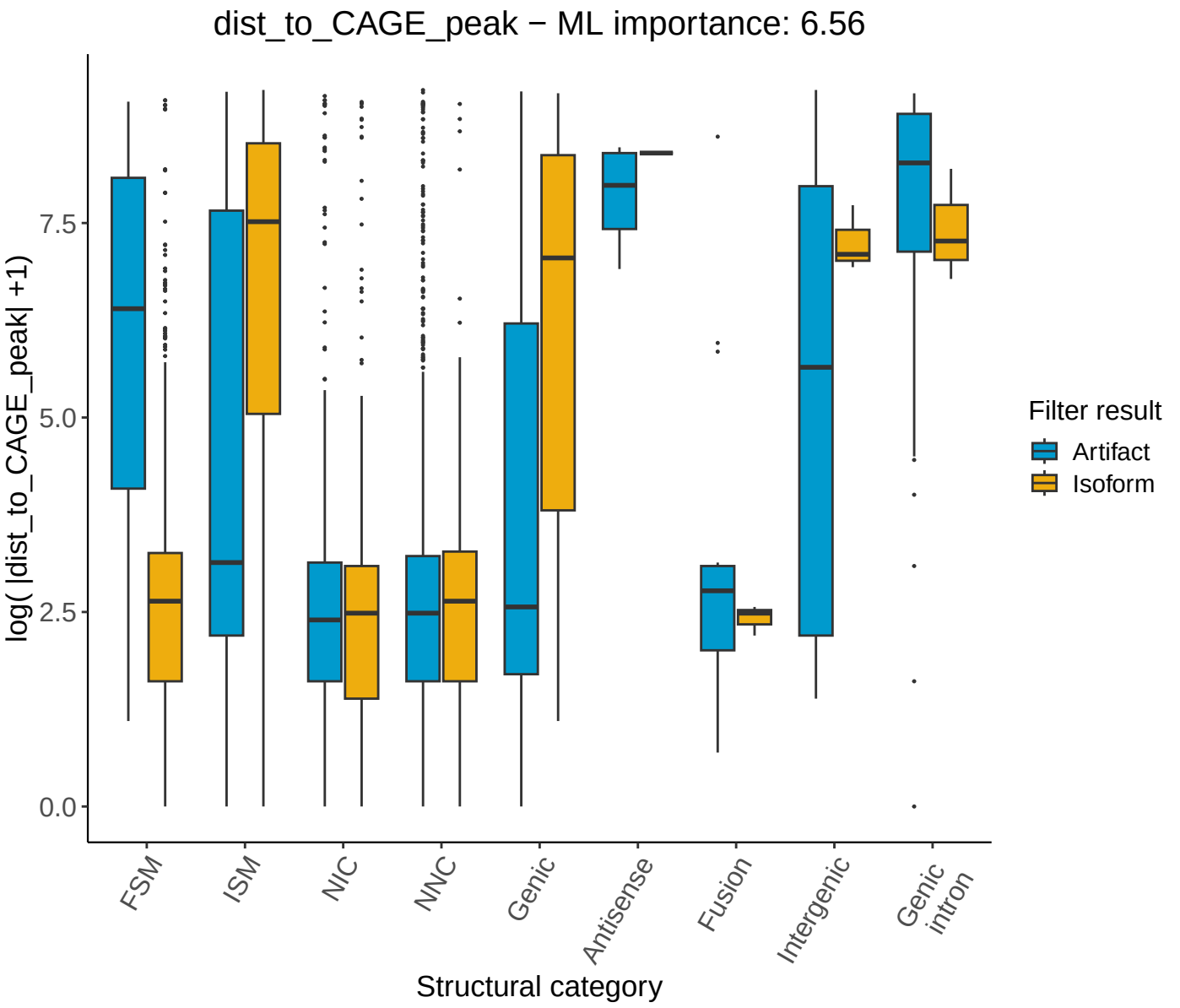

iso_exp − ML importance: 11.06
log(|iso_exp| +1)
12.5
10.0
7.5
5.0
2.5
0.0
FSM
ISM
NIC
NNC
Genic
Antisense
Fusion
Intergenic
Genic intron
Structural category
Filter result
Artifact
Isoform

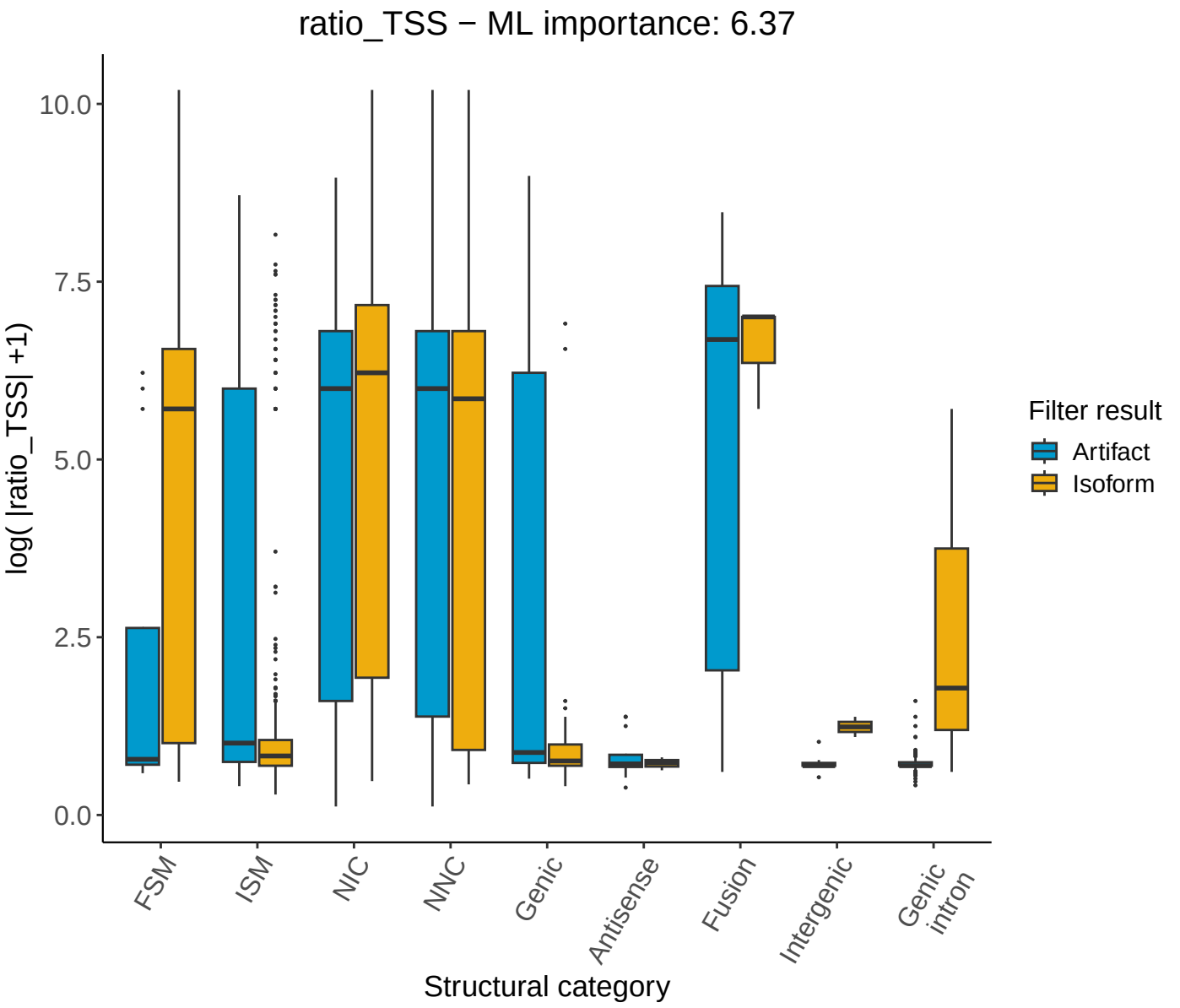

predicted_NMD − ML importance: 10.61
FSM
ISM
NIC
NNC
Genic
Antisense
Fusion
Intergenic
474
206
614
261
197
714
71
2
2
21
3
1
100%
75%
50%
25%
0%
% transcripts
Isoform
Artifact
Isoform
Artifact
Isoform
Artifact
Isoform
Artifact
Artifact
Artifact
Isoform
Artifact
Filter result
predicted_NMD
FALSE
TRUE

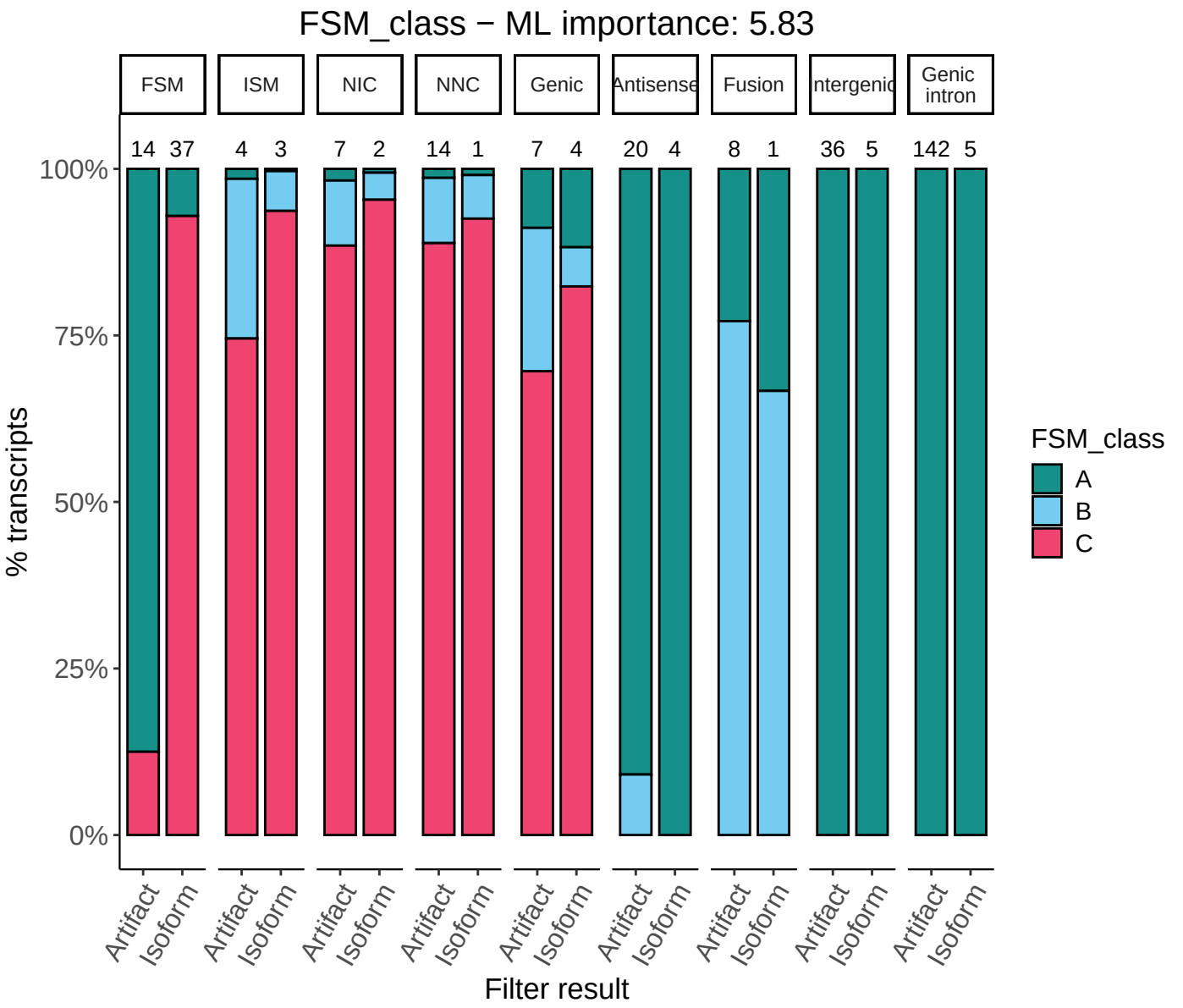

diff_to_gene_TSS − ML importance: 8.24
log(|diff_to_gene_TSS| +1)
10
5
0
FSM
ISM
NIC
NNC
Genic
Antisense
Fusion
Intergenic
Genic intron
Structural category
Filter result
Artifact
Isoform

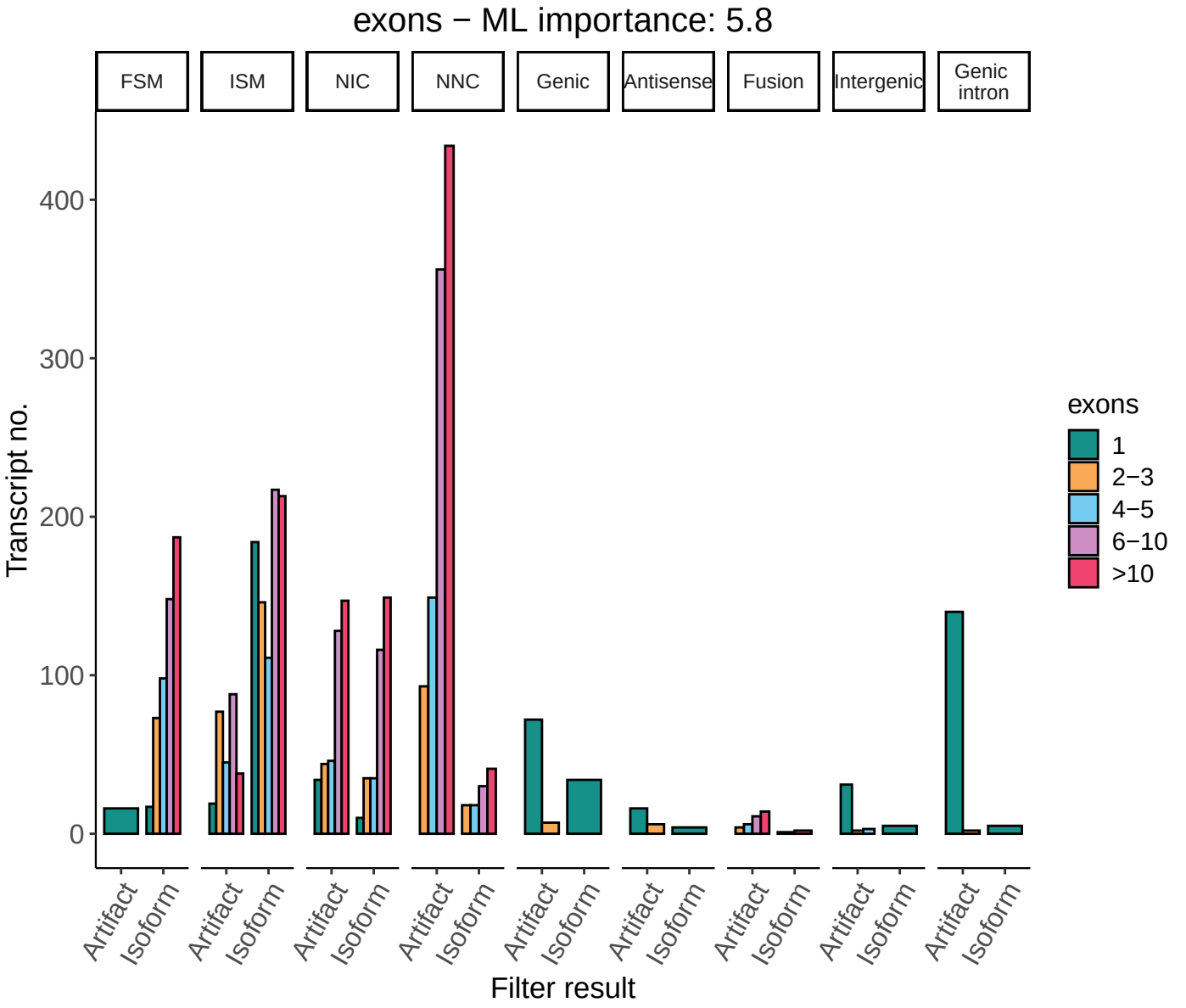

length − ML importance: 7.03
log(|length| +1)
9
8
7
6
5
FSM
ISM
NIC
NNC
Genic
Antisense
Fusion
Intergenic
Genic intron
Structural category
Filter result
Artifact
Isoform

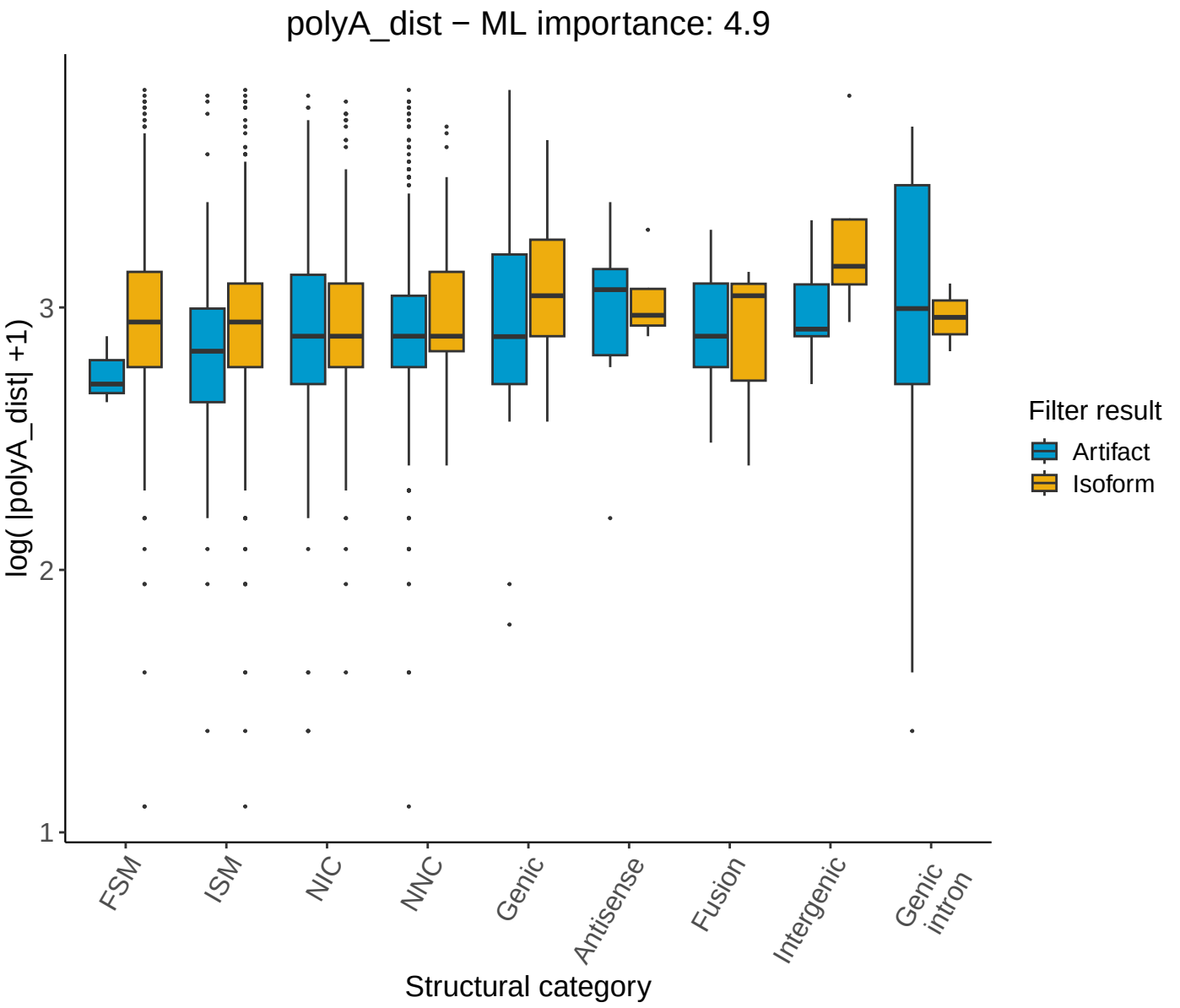

diff_to_gene_TTS − ML importance: 6.62
log(|diff_to_gene_TTS| +1)
10
5
0
FSM
ISM
NIC
NNC
Genic
Antisense
Fusion
Intergenic
Genic intron
Structural category
Filter result
Artifact
Isoform

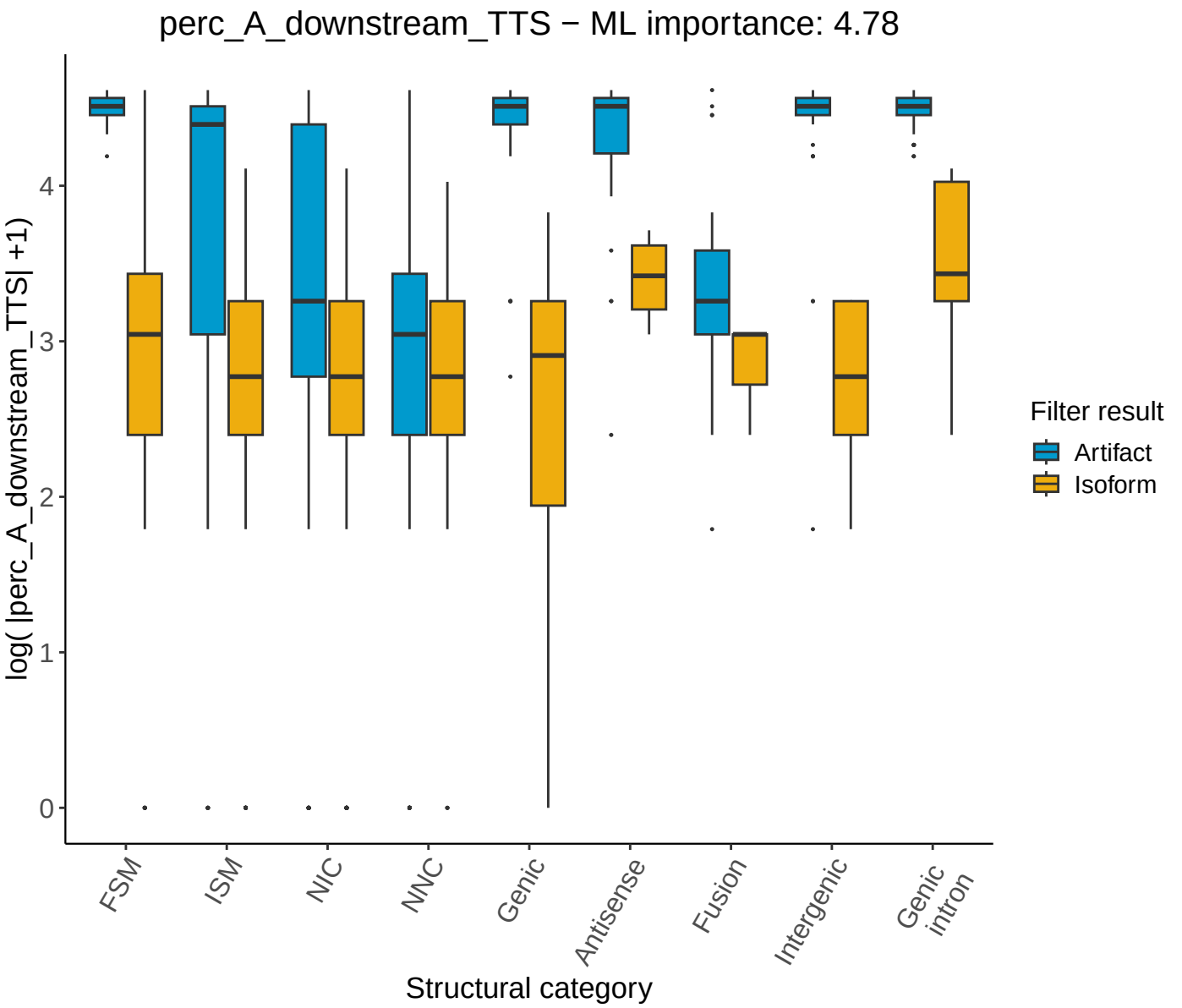

dist_to_CAGE_peak − ML importance: 6.56
log(|dist_to_CAGE_peak| +1)
7.5
5.0
2.5
0.0
FSM
ISM
NIC
NNC
Genic
Antisense
Fusion
Intergenic
Genic intron
Structural category
Filter result
Artifact
Isoform

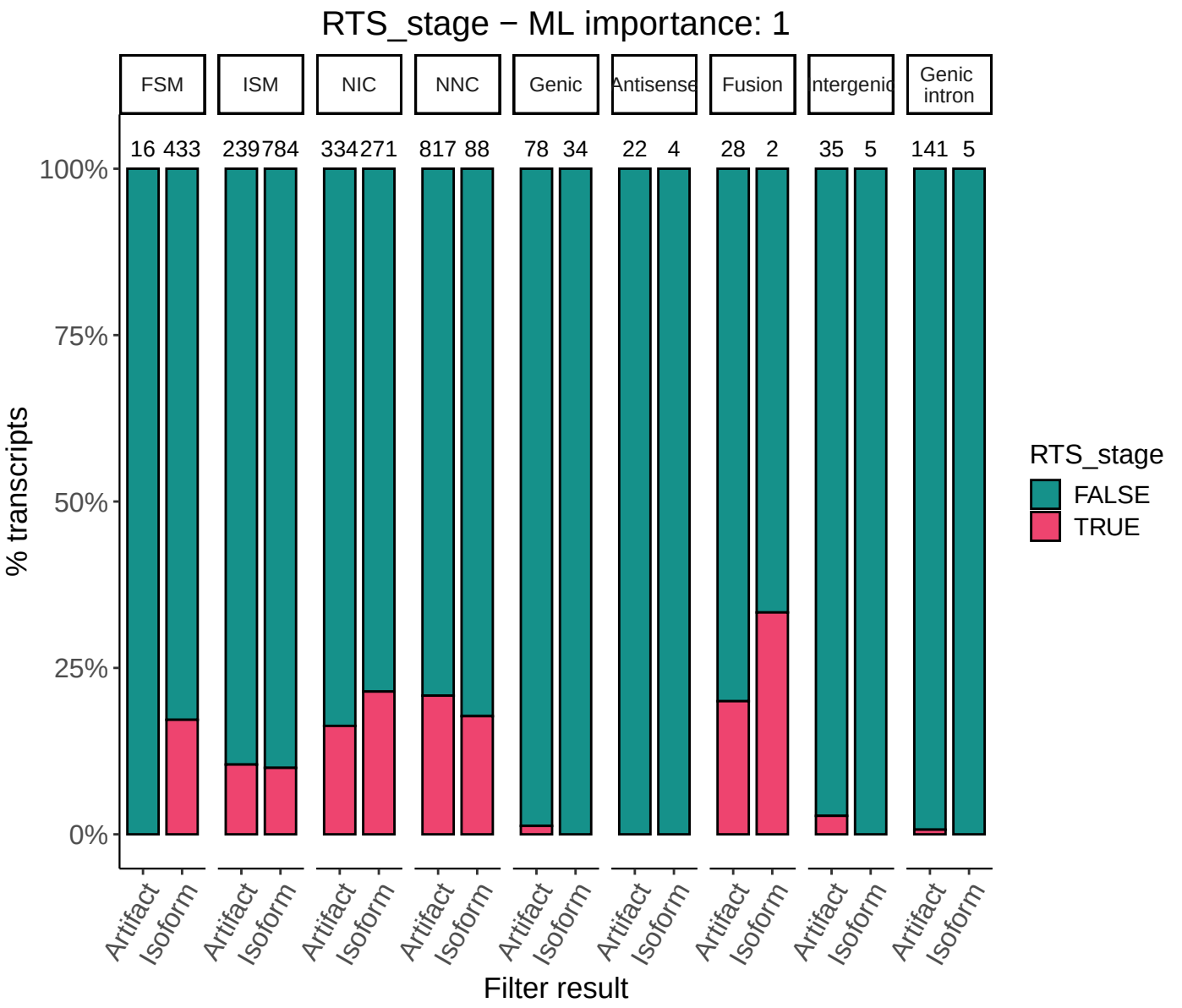

ratio_TSS − ML importance: 6.37
log(|ratio_TSS| +1)
10.0
7.5
5.0
2.5
0.0
FSM
ISM
NIC
NNC
Genic
Antisense
Fusion
Intergenic
Genic intron
Structural category
Filter result
Artifact
Isoform

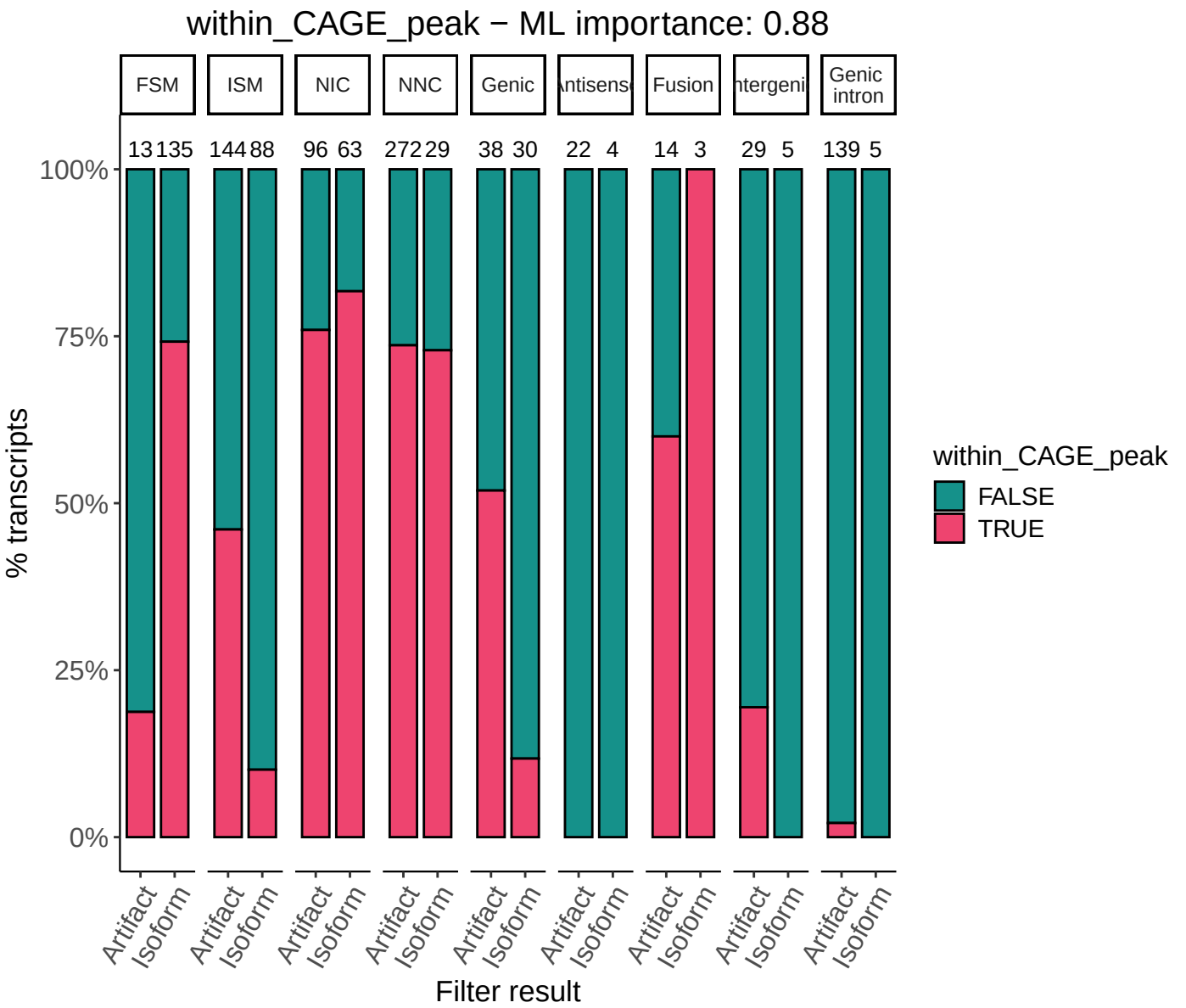

FSM_class − ML importance: 5.83
FSM
ISM
NIC
NNC
Genic
Antisense
Fusion
ntergenic
Genic intron
14 37
4 3
7 2
14 1
7 4
20 4
8 1
36 5
142 5
100%
75%
50%
25%
0%
% transcripts
Artifact
Isoform
Filter result
FSM_class
A
B
C

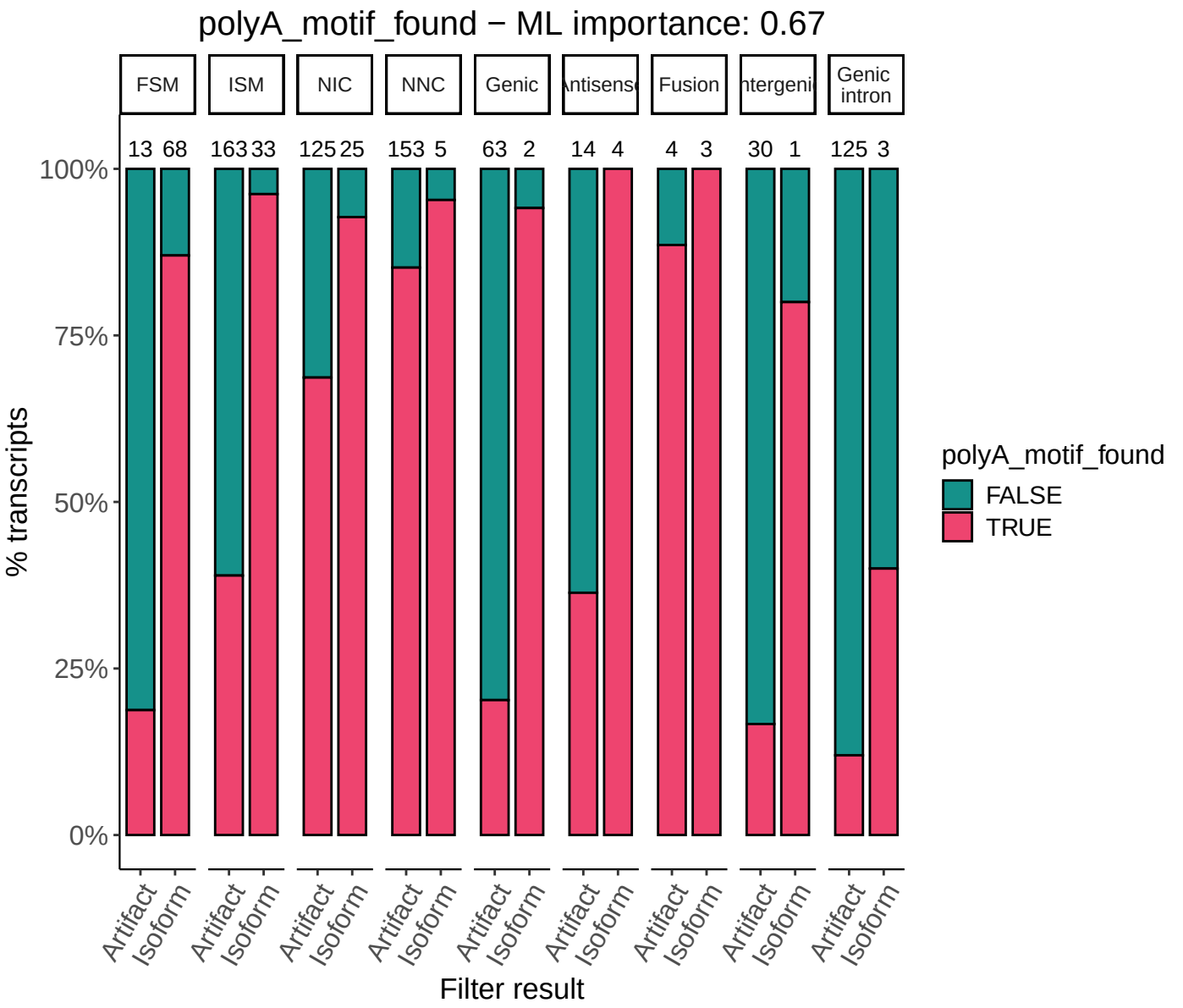

exons − ML importance: 5.8
FSM
ISM
NIC
NNC
Genic
Antisense
Fusion
Intergenic
Genic intron
Transcript no.
0
100
200
300
400
Artifact
Isoform
Filter result
exons
1
2−3
4−5
6−10
>10

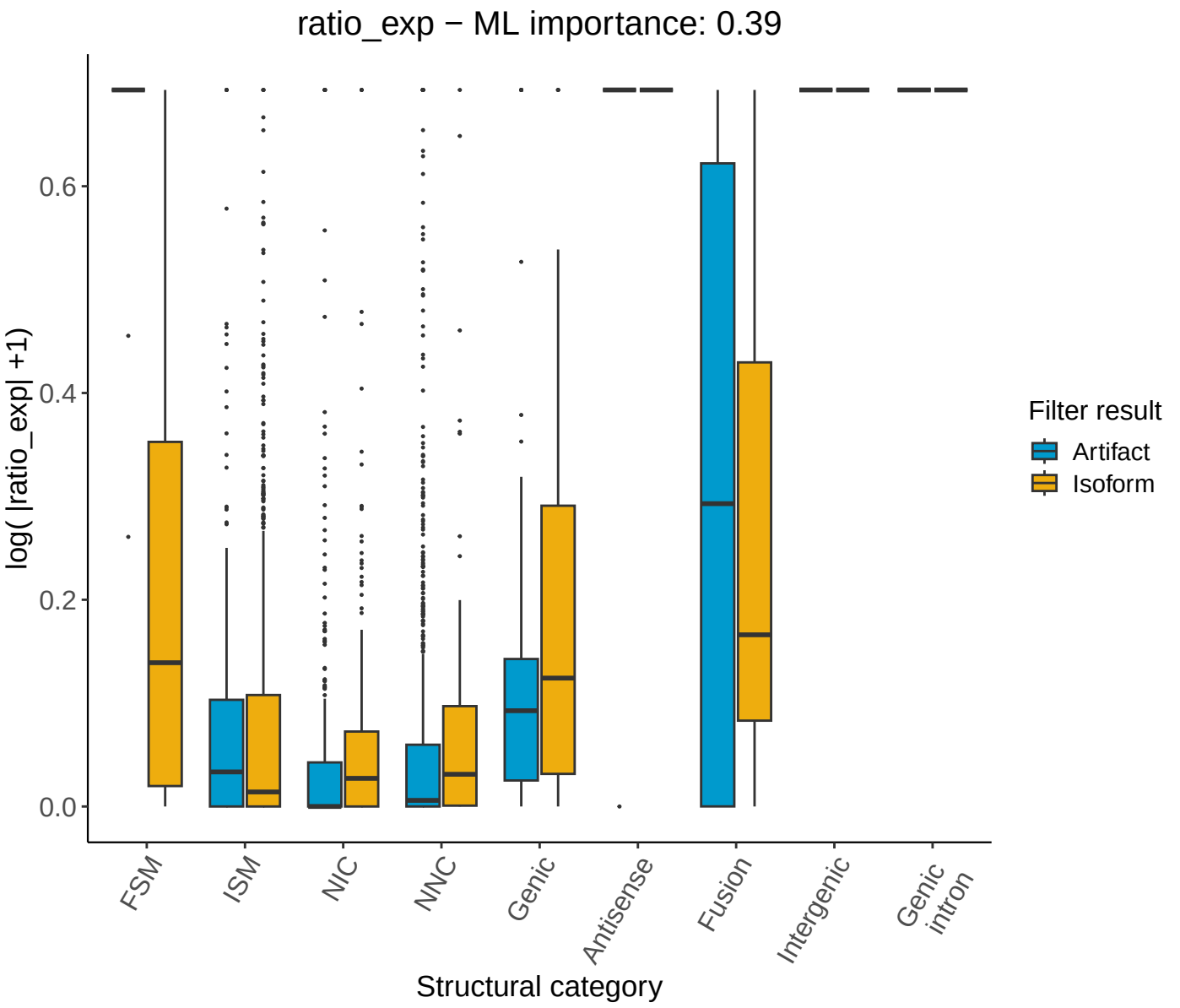

polyA_dist − ML importance: 4.9
log(|polyA_dist| +1)
3
2
1
FSM
ISM
NIC
NNC
Genic
Antisense
Fusion
Intergenic
Genic intron
Structural category
Filter result
Artifact
Isoform

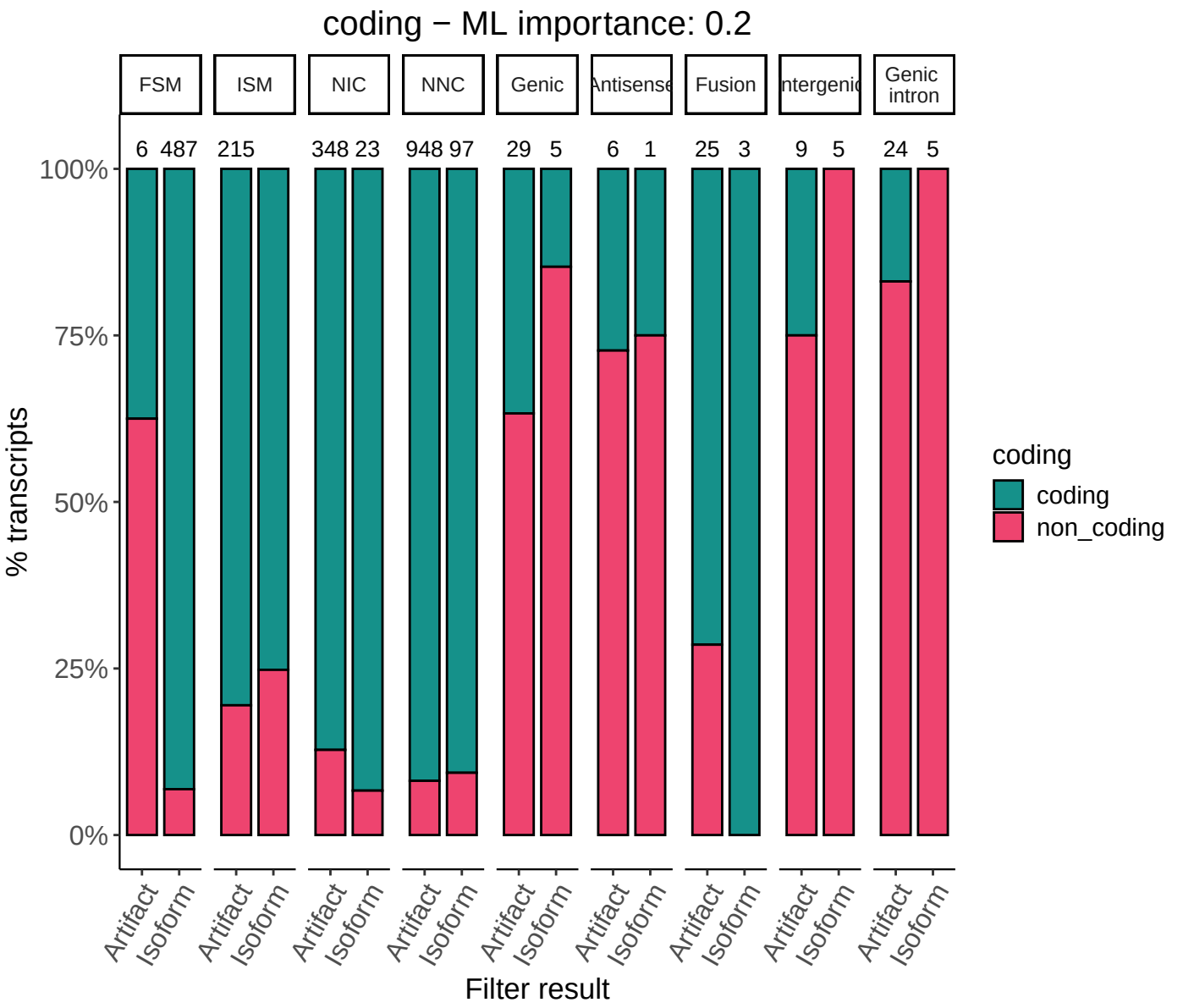

perc_A_downstream_TTS − ML importance: 4.78
log(|perc_A_downstream_TTS| +1)
0
1
2
3
4
FSM
ISM
NIC
NNC
Genic
Antisense
Fusion
Intergenic
Genic intron
Structural category
Filter result
Artifact
Isoform


RTS_stage − ML importance: 1
FSM
ISM
NIC
NNC
Genic
Antisense
Fusion
ntergenic
Genic intron
16 433
239 784
334 271
817 88
78 34
22 4
28 2
35 5
141 5
100%
75%
50%
25%
0%
% transcripts
Artifact
Isoform
Filter result
RTS_stage
FALSE
TRUE

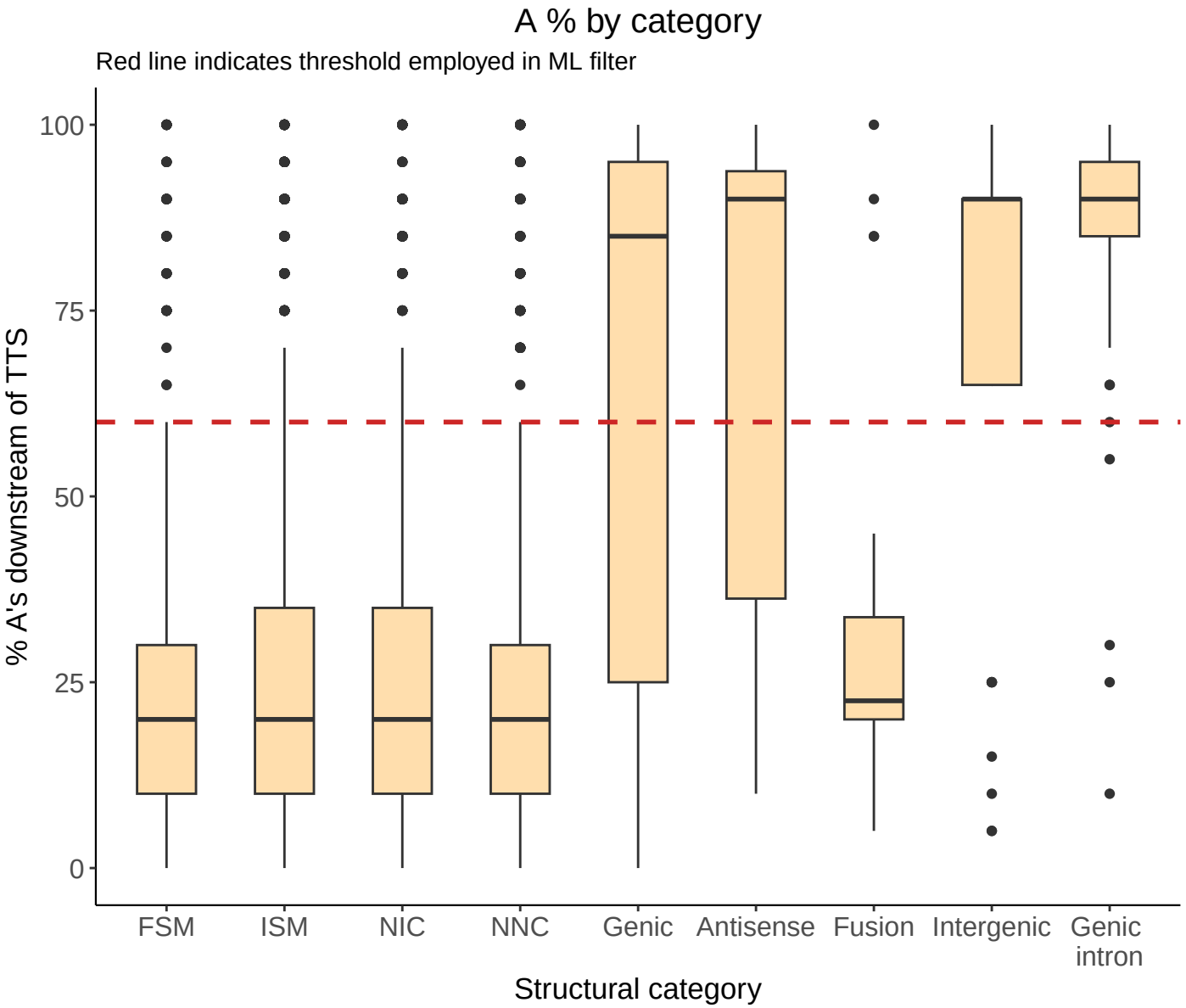

within_CAGE_peak − ML importance: 0.88
FSM
ISM
NIC
NNC
Genic
ntisens
Fusion
ntergeni
Genic intron
13 135
144 88
96 63
272 29
38 30
22 4
14 3
29 5
139 5
100%
75%
50%
25%
0%
% transcripts
Artifact
Isoform
Filter result
within_CAGE_peak
FALSE
TRUE

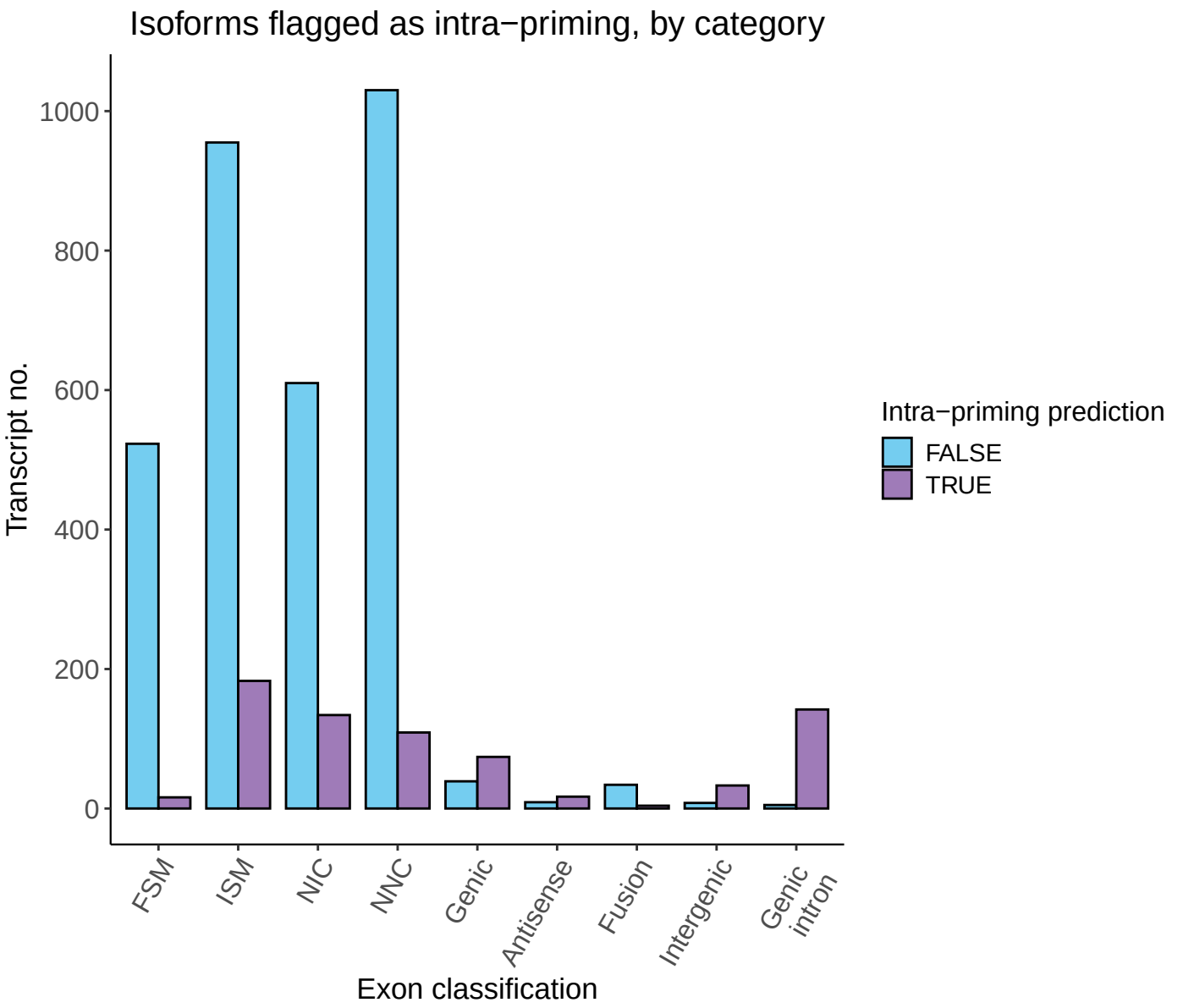

polyA_motif_found − ML importance: 0.67
FSM
ISM
NIC
NNC
Genic
ntisens
Fusion
ntergeni
Genic intron
13 68
163 33
125 25
153 5
63 2
14 4
4 3
30 1
125 3
100%
75%
50%
25%
0%
% transcripts
Artifact
Isoform
Filter result
polyA_motif_found
FALSE
TRUE

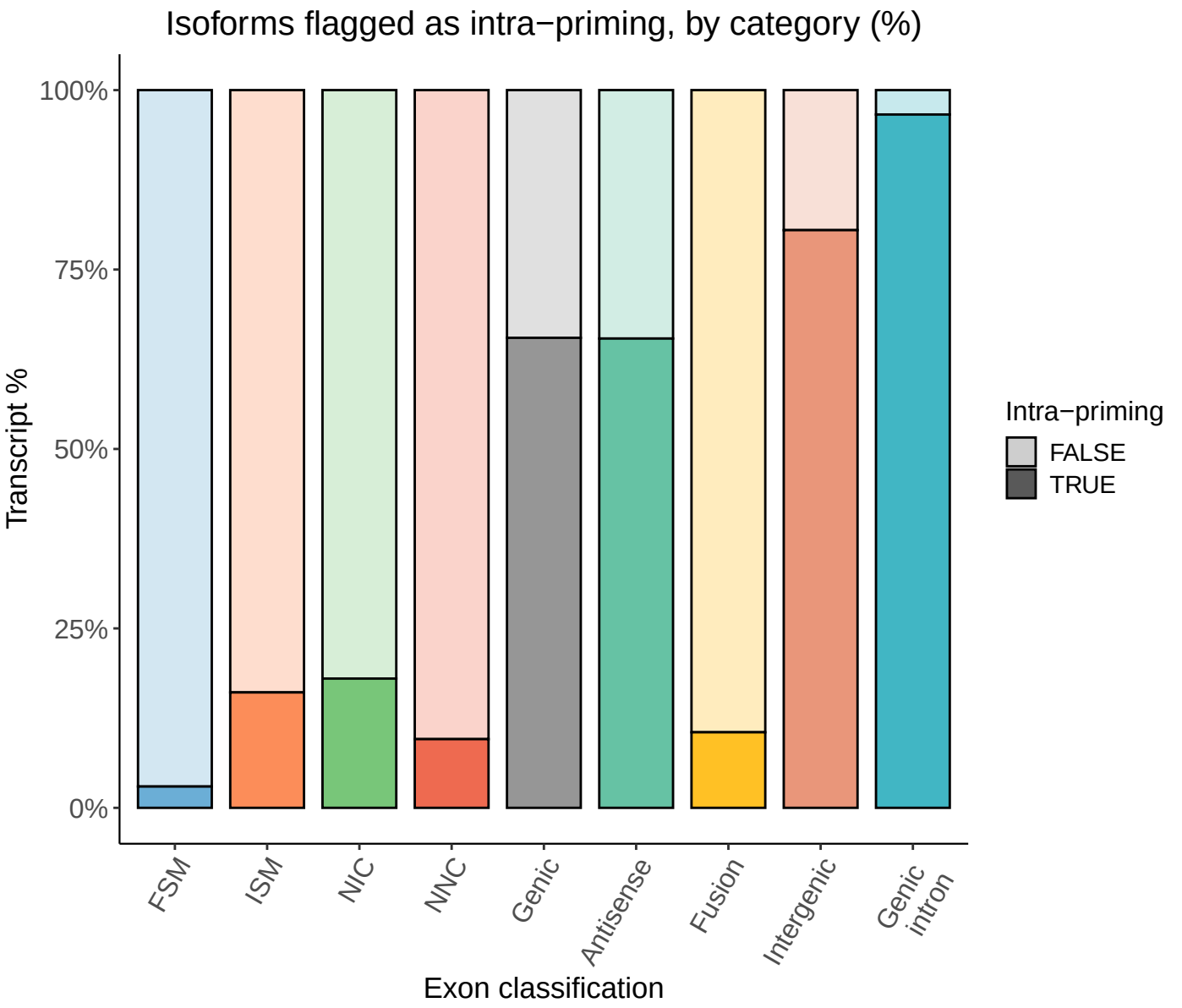

ratio_exp − ML importance: 0.39
log(|ratio_exp| +1)
0.0
0.2
0.4
0.6
FSM
ISM
NIC
NNC
Genic
Antisense
Fusion
Intergenic
Genic intron
Structural category
Filter result
Artifact
Isoform

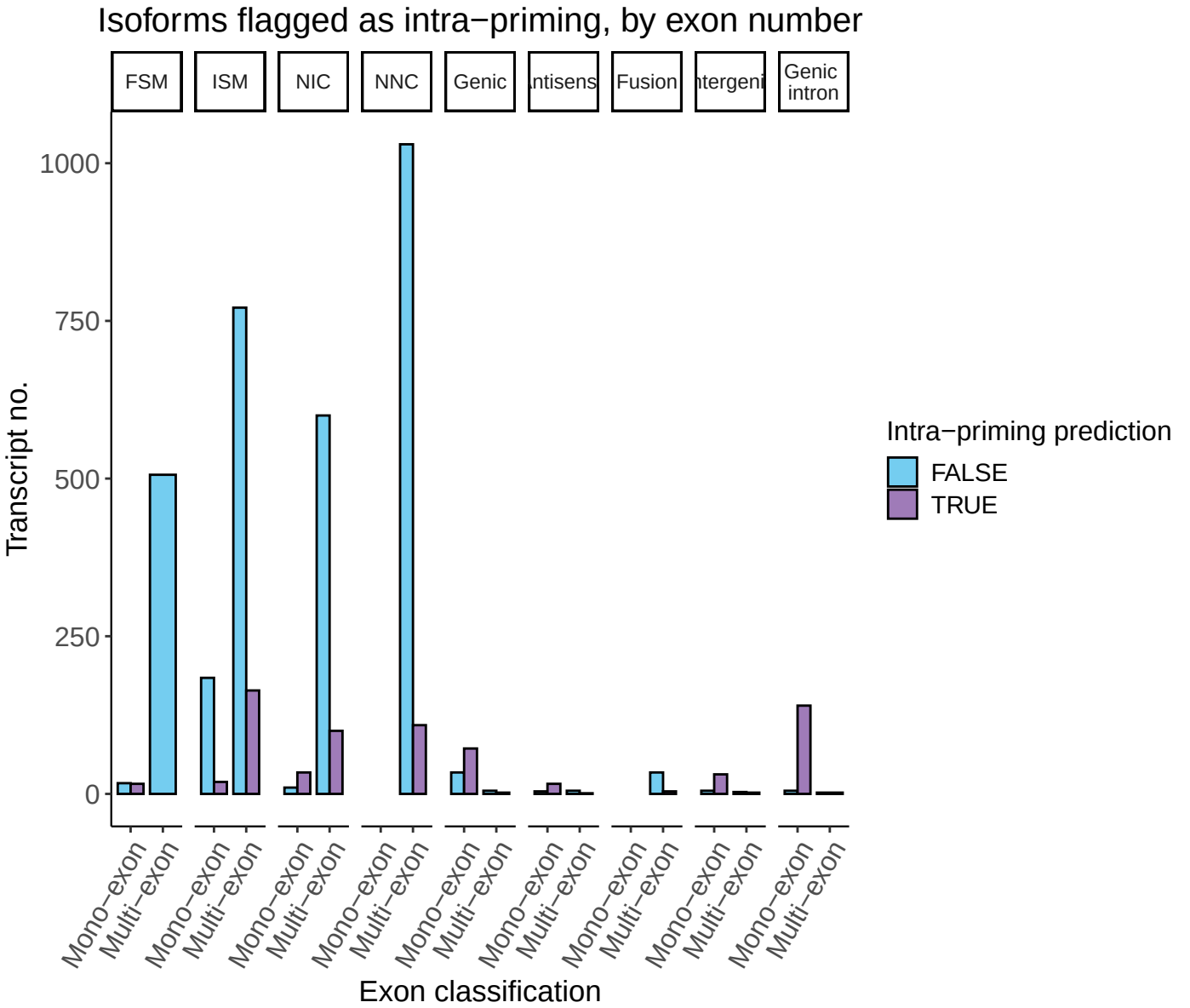

coding − ML importance: 0.2
FSM
ISM
NIC
NNC
Genic
Antisense
Fusion
Intergenic
Genic intron
6 487
215
348 23
948 97
29 5
6 1
25 3
9 5
24 5
100%
75%
50%
25%
0%
% transcripts
Artifact
Isoform
Filter result
coding
coding
non_coding

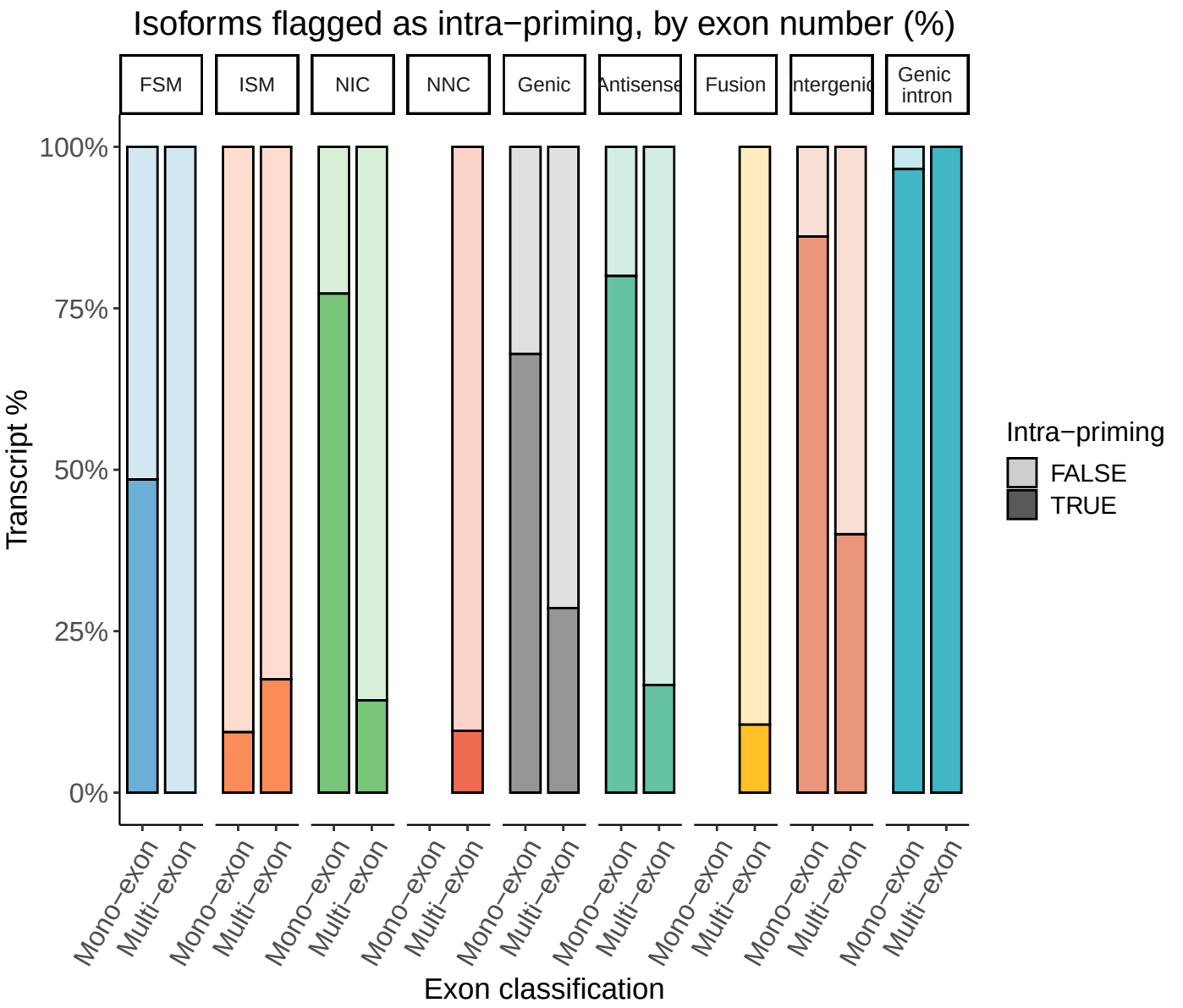
Intra−primming filter report


A % by category
Red line indicates threshold employed in ML filter
% A's downstream of TTS
100
75
50
25
0
FSM
ISM
NIC
NNC
Genic
Antisense
Fusion
Intergenic
Genic intron
Structural category


Isoforms flagged as intra−priming, by category
Transcript no.
1000
800
600
400
200
0
FSM
ISM
NIC
NNC
Genic
Antisense
Fusion
Intergenic
Genic intron
Exon classification
Intra−priming prediction
FALSE
TRUE


Isoforms flagged as intra−priming, by category (%)
Transcript %
100%
75%
50%
25%
0%
FSM
ISM
NIC
NNC
Genic
Antisense
Fusion
Intergenic
Genic intron
Exon classification
Intra−priming
FALSE
TRUE


Isoforms flagged as intra−priming, by exon number
FSM
ISM
NIC
NNC
Genic
ntisens
Fusion
ntergeni
Genic intron
1000
750
500
250
0
Transcript no.
Mono−exon
Multi−exon
Exon classification
Intra−priming prediction
FALSE
TRUE


Isoforms flagged as intra−priming, by exon number (%)
FSM
ISM
NIC
NNC
Genic
Antisense
Fusion
ntergenic
Genic intron
100%
75%
50%
25%
0%
Transcript %
Mono−exon
Multi−exon
Exon classification
Intra−priming
FALSE
TRUE