

Supp. Figure 1 (pages 1-194). isomiR boxplots. Shown are boxplots for all 194 miRBase miRNAs and their associated isomiRs. For each plot, the Y-axis is the quantile normalized sequence read counts for each isomiR. The miRBase reference is green and the isomiRs are red.

Supp. Figure 2 (pages 195-199). Differentially expressed isomiRs for each population. Shown are individual heatmaps for each of the five different population groups examined. Plotted are the population comparisons (columns) and the rows are the different isomiRs. Cells shown in light gray correspond to cases that did not reach statistical significance for the corresponding isomiR/population combination. All other cells correspond to statistically significant combinations with an associated FDR value ≤ 0.05 . The color intensity scale is logarithmic (log2).

Supp. Figure 3 (pages 199-204). Differentially expressed isomiRs for males only. Shown are individual heatmaps for each of the male subjects from the five different population groups examined. Plotted are the population comparisons (columns) and the rows are the different isomiRs. Cells shown in light gray correspond to cases that did not reach statistical significance for the corresponding isomiR/population combination. All other cells correspond to statistically significant combinations with an associated FDR value ≤ 0.05 . The color intensity scale is logarithmic (log2).

Supp. Figure 4 (pages 205-209). Differentially expressed isomiRs for females only. Shown are individual heatmaps for each of the female subjects from the five different population groups examined. Plotted are the population comparisons (columns) and the rows are the different isomiRs. Cells shown in light gray correspond to cases that did not reach statistical significance for the corresponding isomiR/population combination. All other cells correspond to statistically significant combinations with an associated FDR value ≤ 0.05 . The color intensity scale is logarithmic (log2).

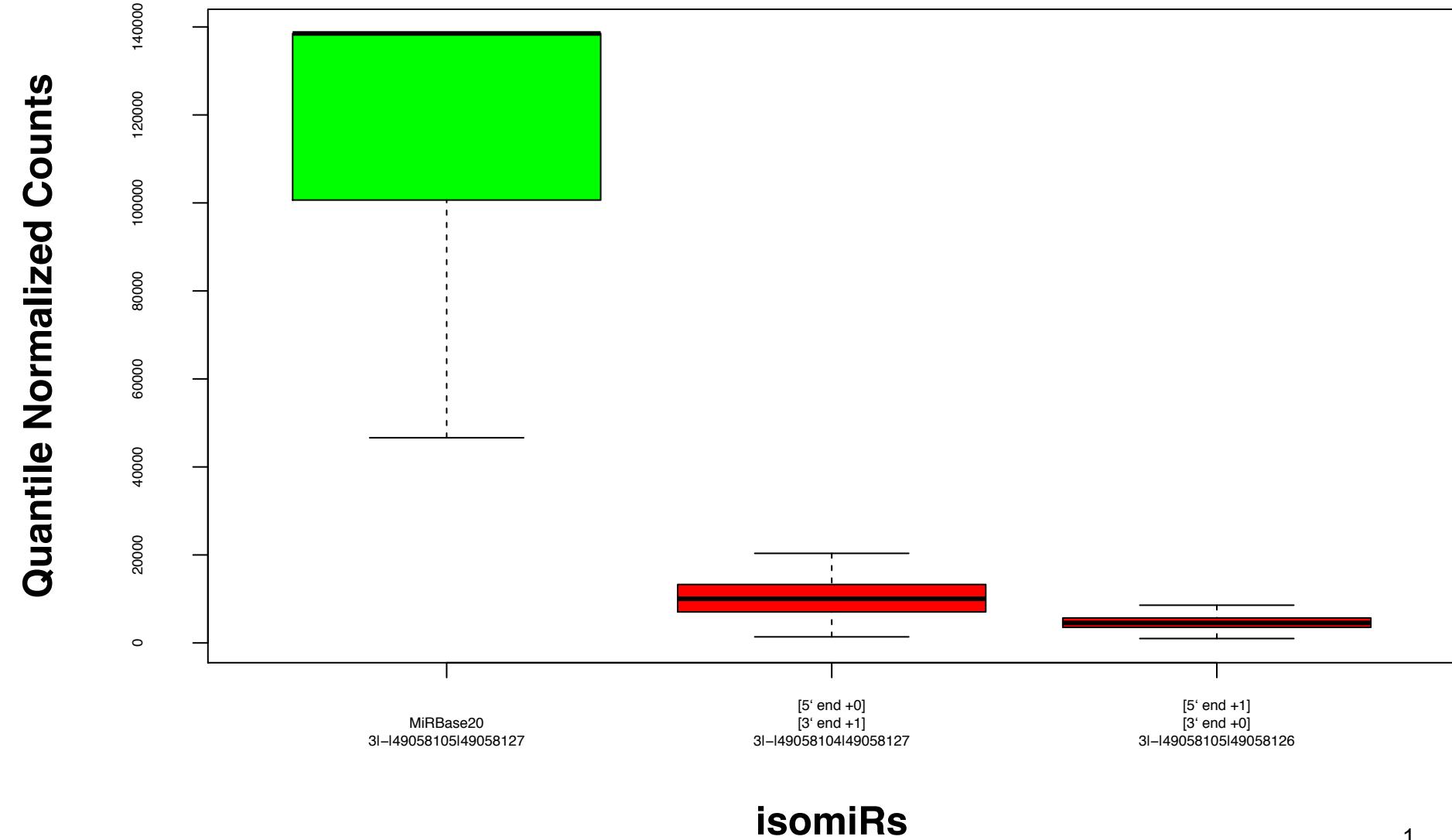
Supp. Figure 5 (page 210). Distribution of isomiR termini. Shown is a schematic representation of the distribution of 5' and 3' terminus of the isomiRs. The 22 nts of the miRBase reference entry is shown in blue with each box and each box extending past represents an additional nucleotide position. The graphs show the distribution of bases at each nucleotide position either extending past the miRBase reference terminus or before the terminus.

Supp. Table 1 (page 211). Statistics for each population separately for the single most abundant isomiR produced from a given precursor arm. The most abundant isomiR's identity was determined by analyzing the technical replicates separately for each of the populations. At each locus, we also generated the "conservative" estimate by requiring that the most abundant isomiR have higher expression than the miRBase reference by at least 0.585 log2 units.

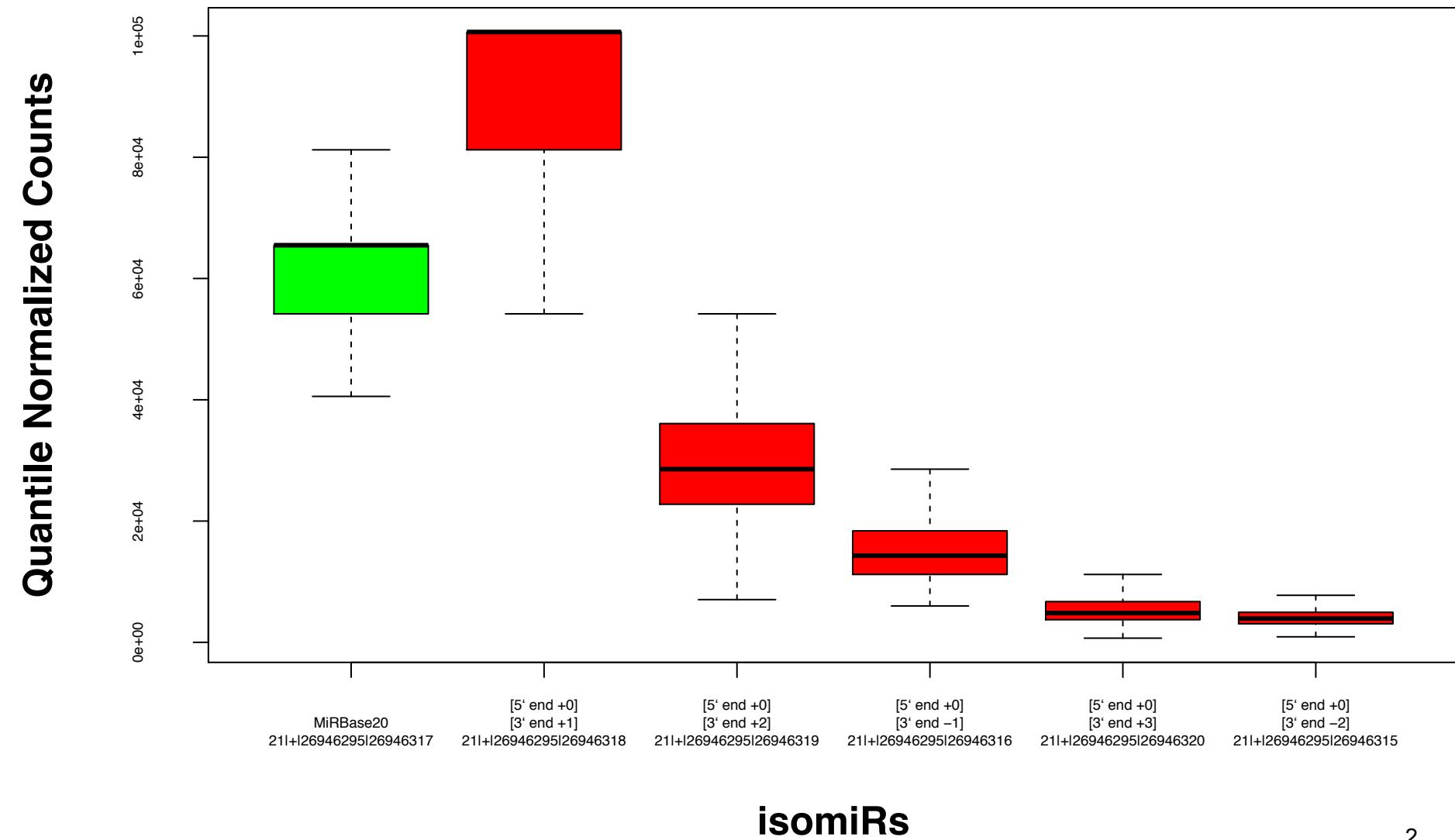
Supp. Table 2 (page 212). Statistics for each population separately for the single most abundant isomiR produced from a given precursor arm – using only females. The most abundant isomiR's identity was determined by analyzing the entire collection of all unique datasets that passed quality control and belonged to females. At each locus, we also generated the "conservative" estimate by requiring that the most abundant isomiR have higher expression than the miRBase reference by at least 0.585 log2 units.

Supp. Table 3 (page 213). Statistics for each population separately for the single most abundant isomiR produced from a given precursor arm – using only males. The most abundant isomiR's identity was determined by analyzing the entire collection of all unique datasets that passed quality control and belonged to males. At each locus, we also generated the "conservative" estimate by requiring that the most abundant isomiR have higher expression than the miRBase reference by at least 0.585 log2 units.

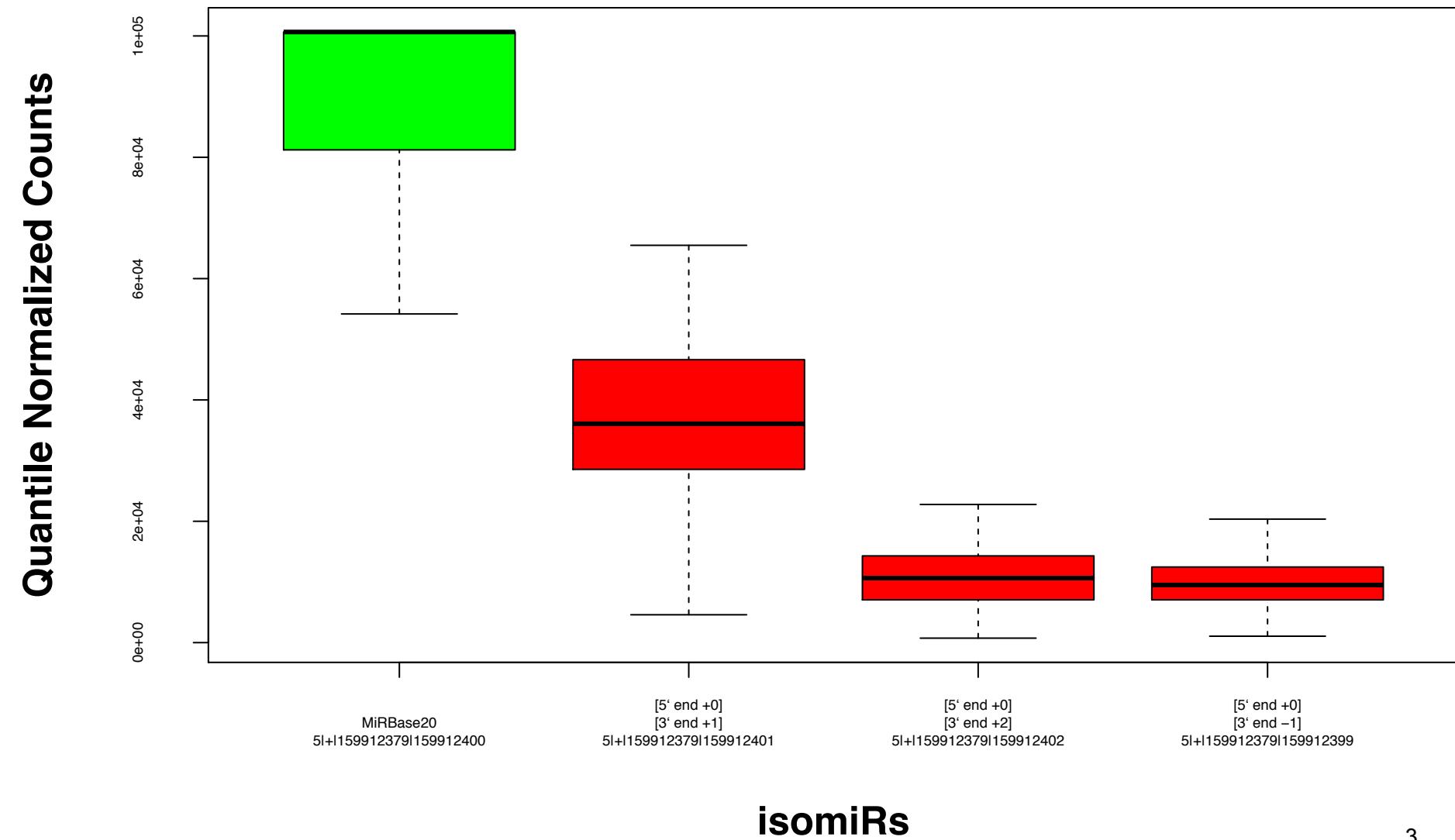
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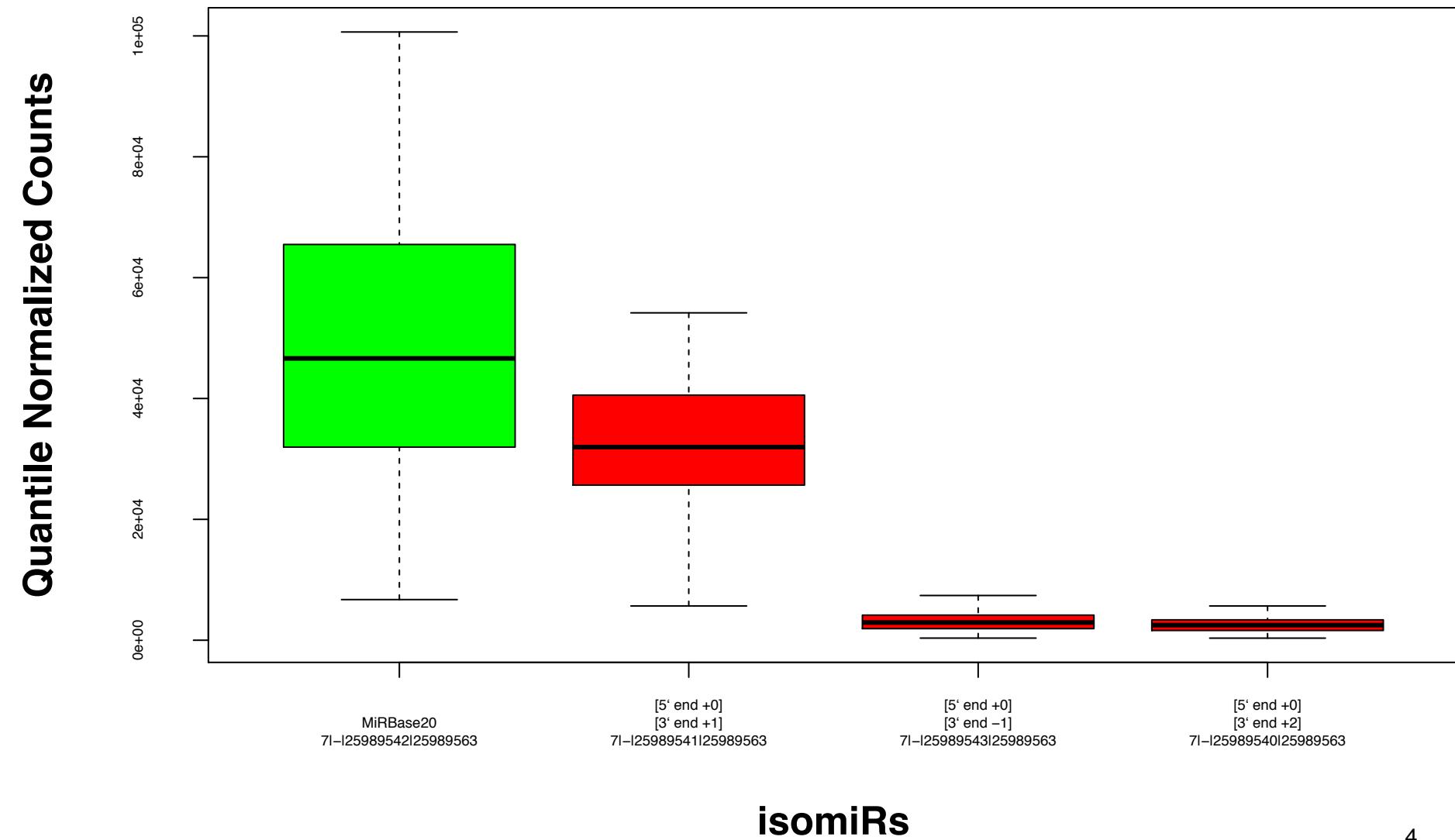
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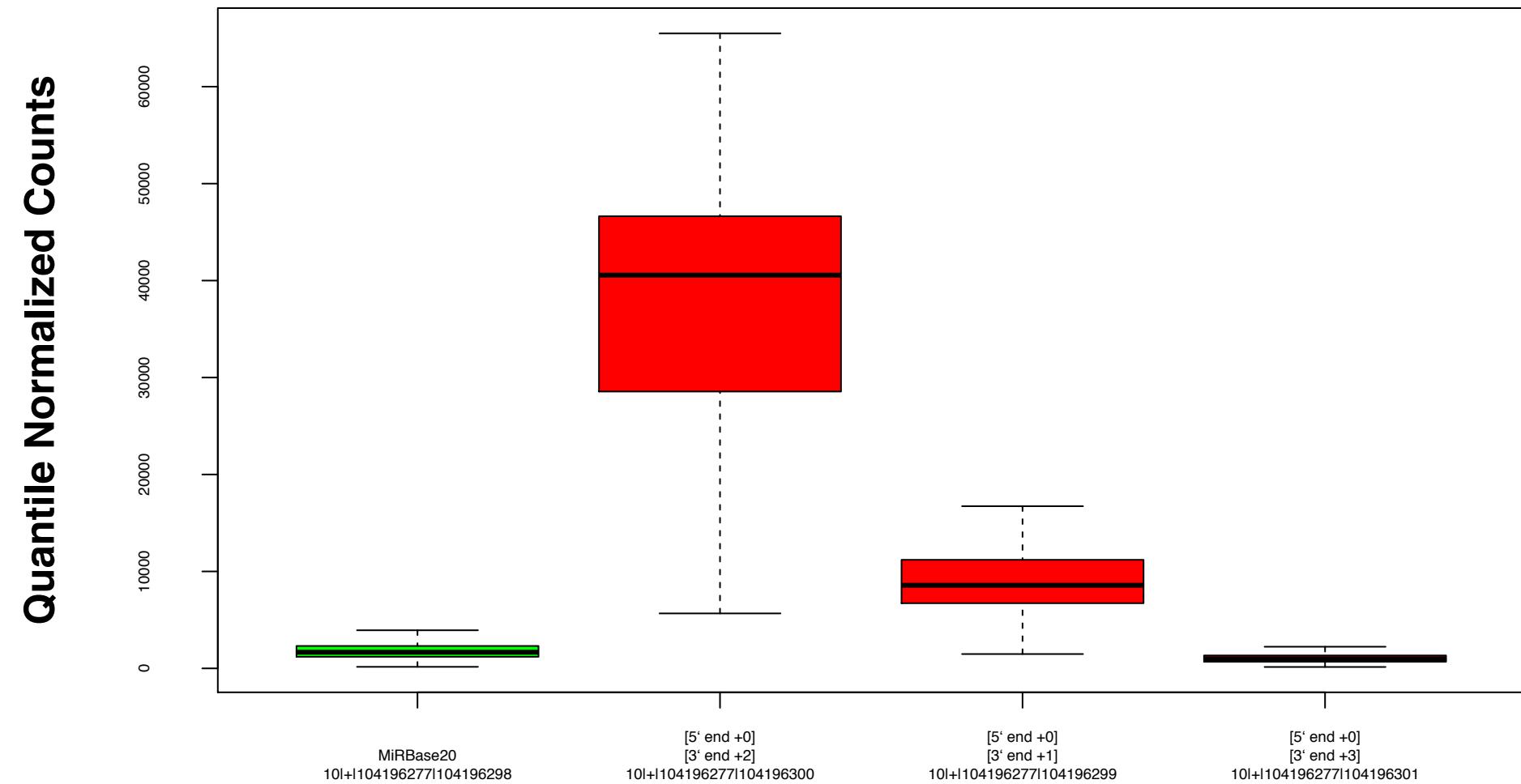
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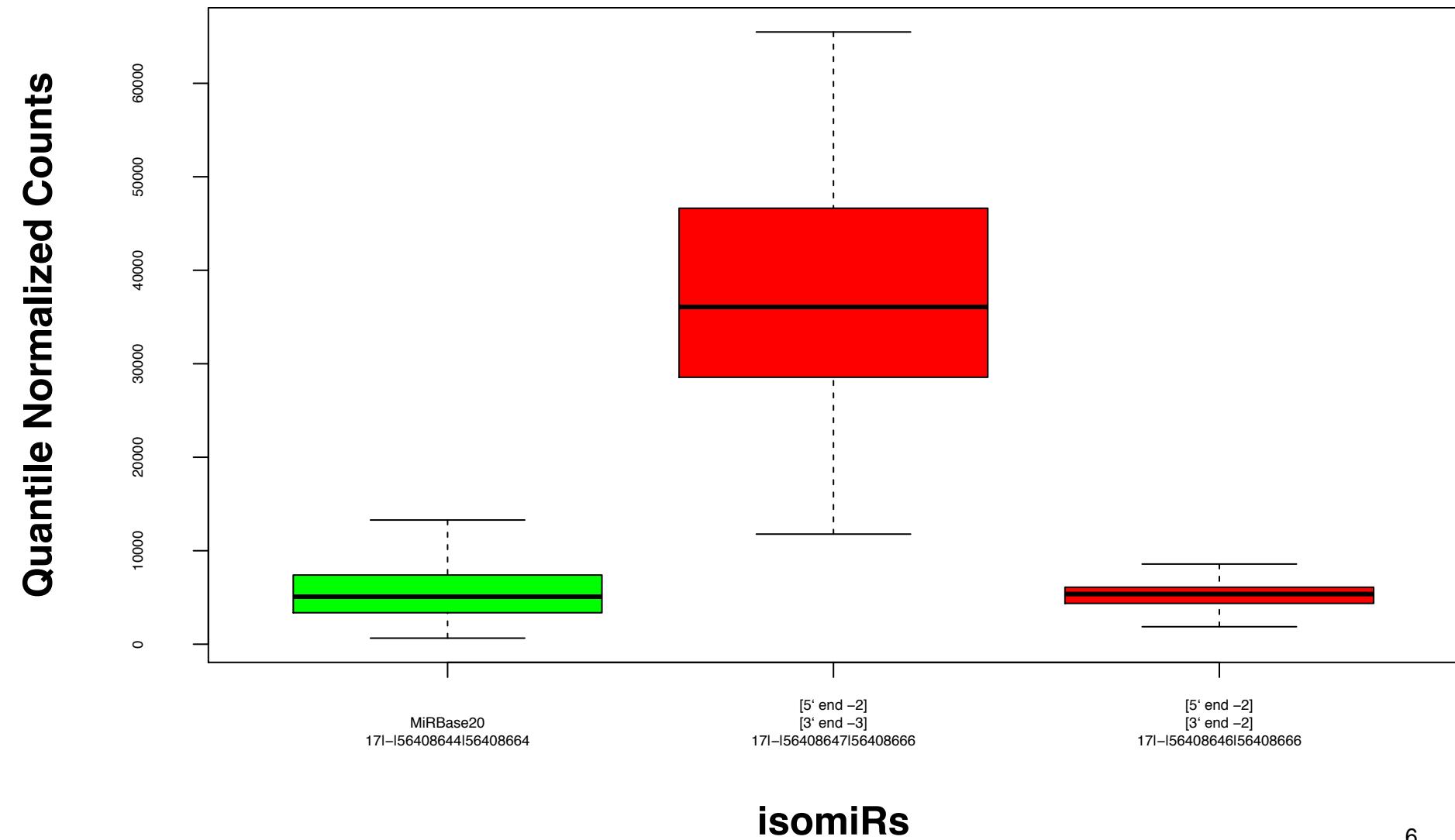


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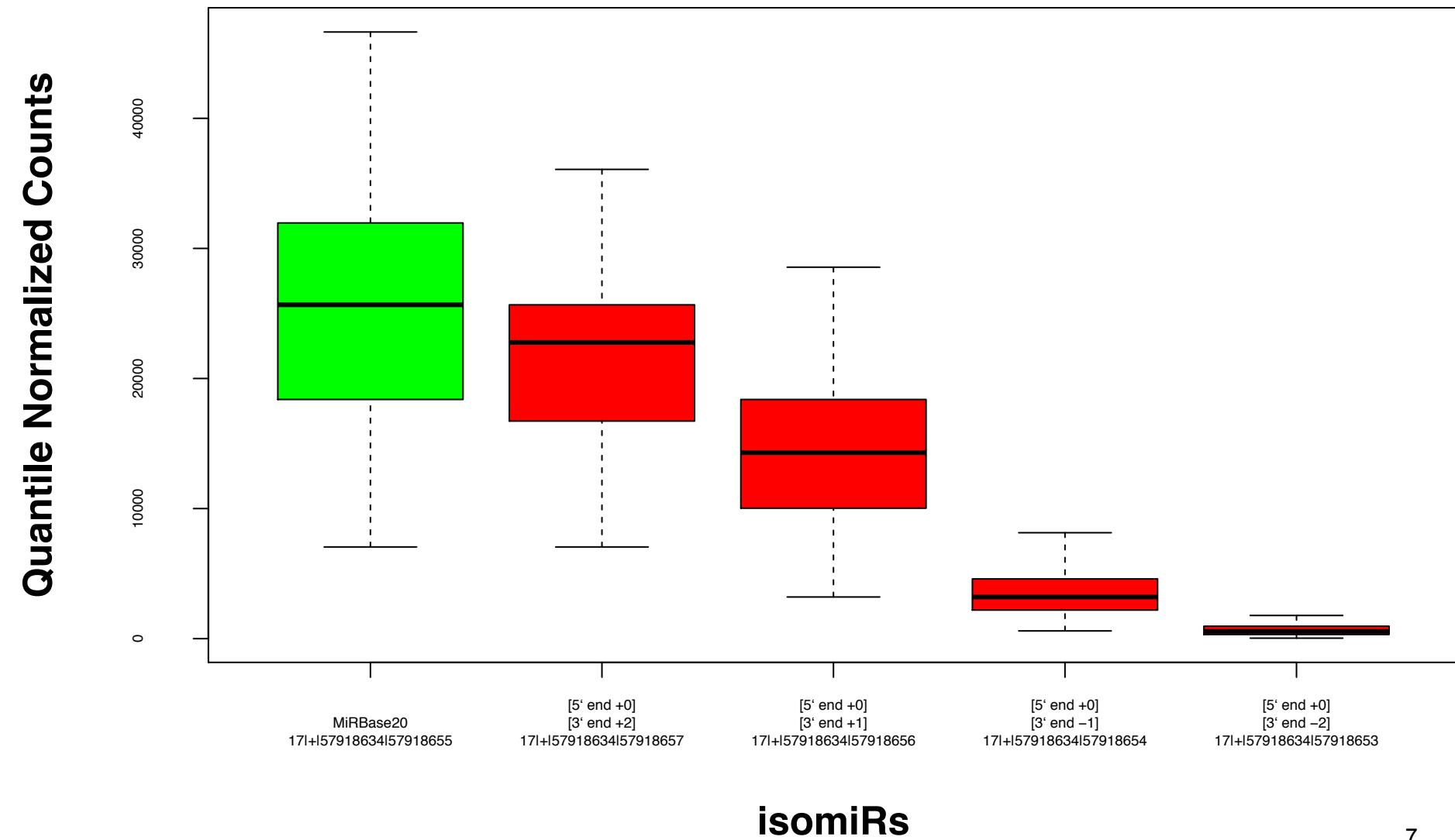


isomiRs

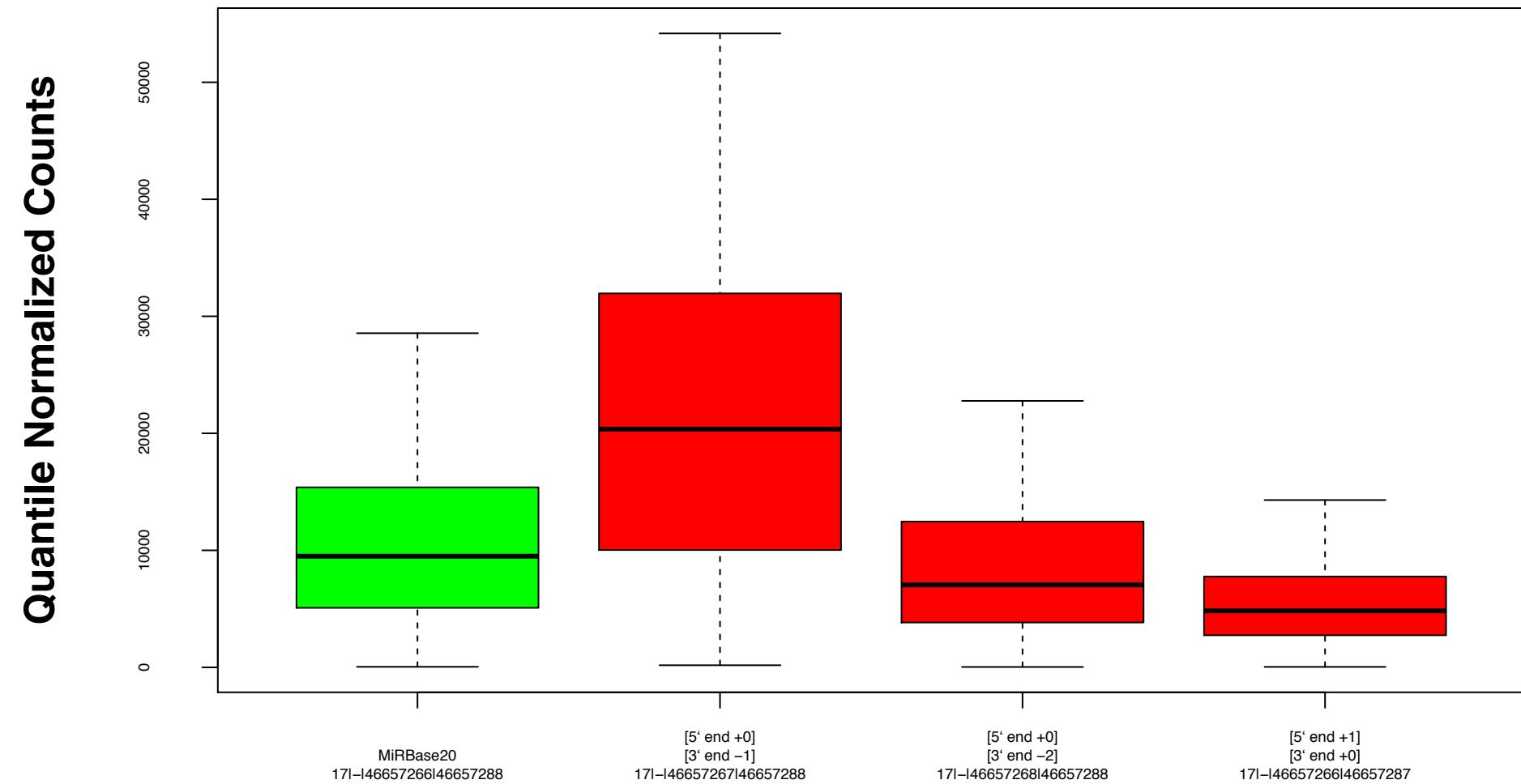
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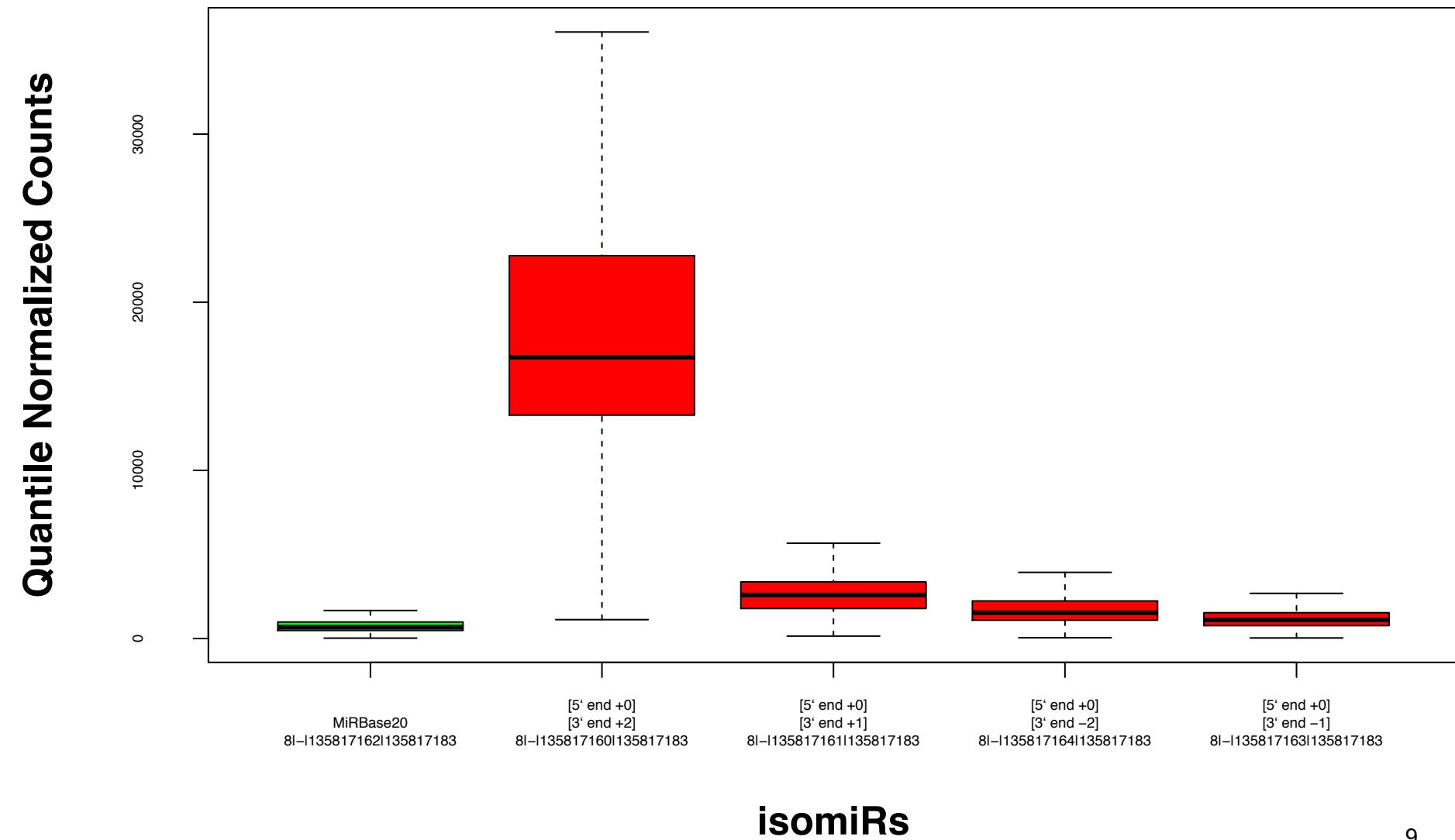
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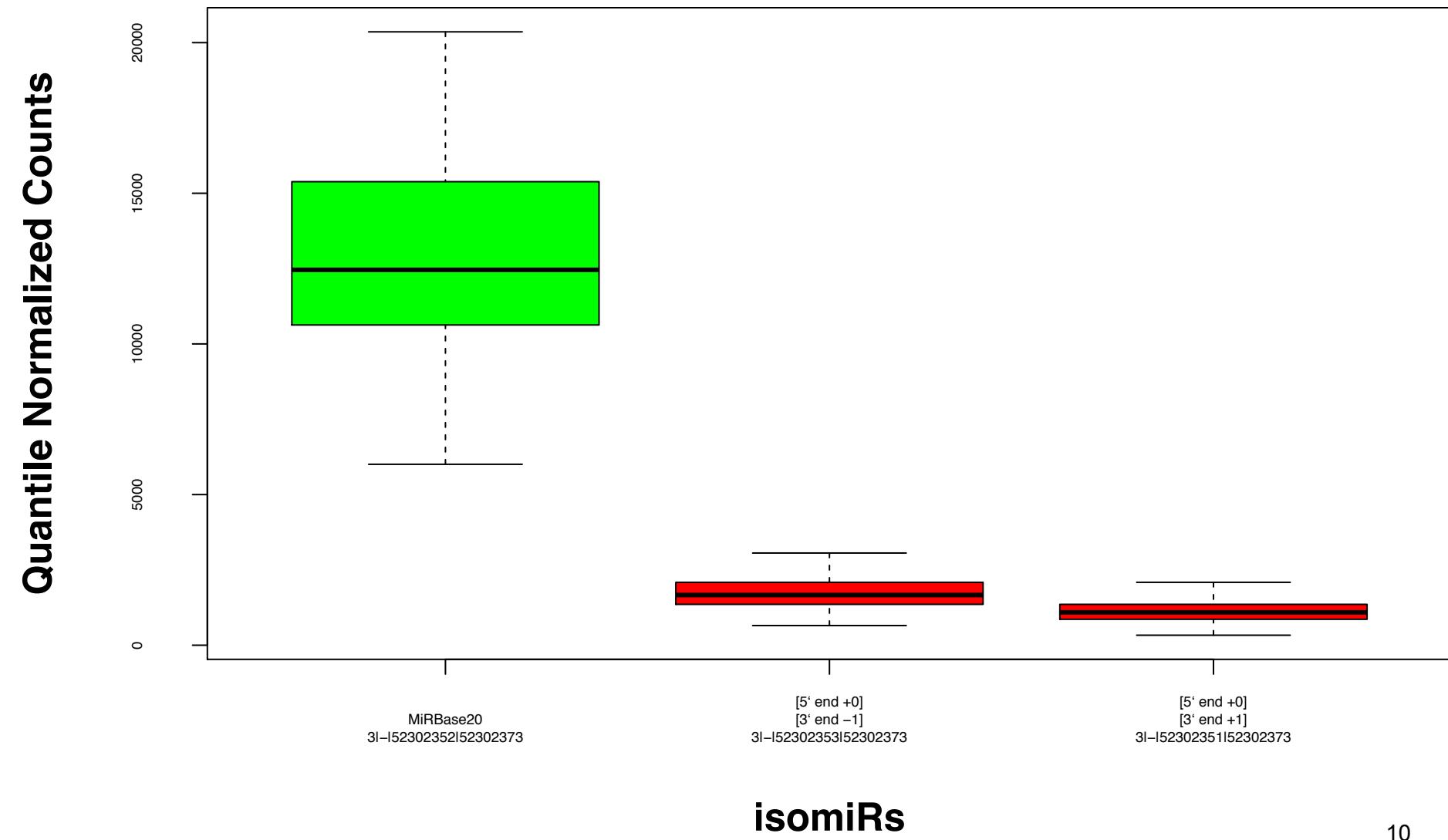
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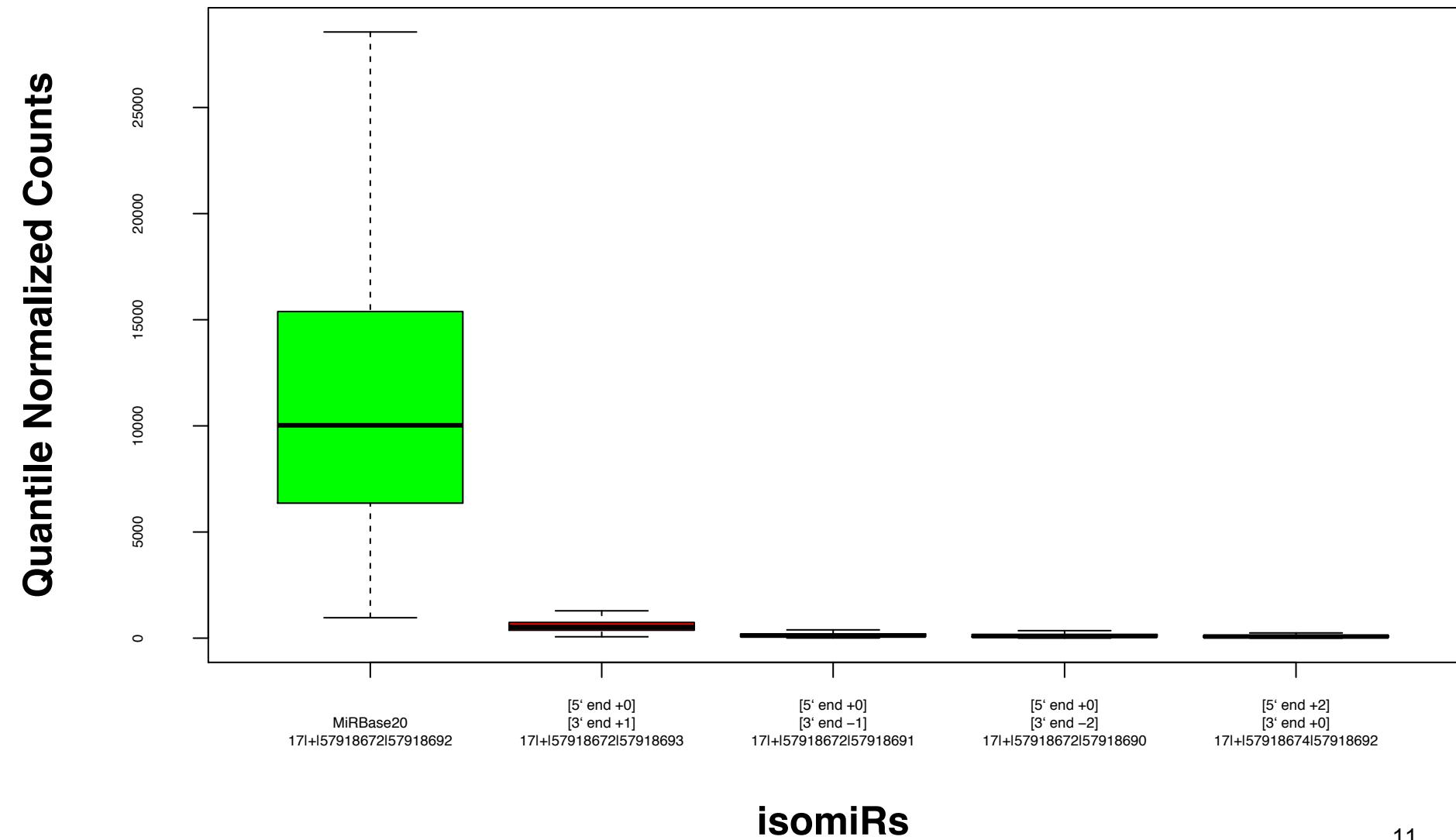
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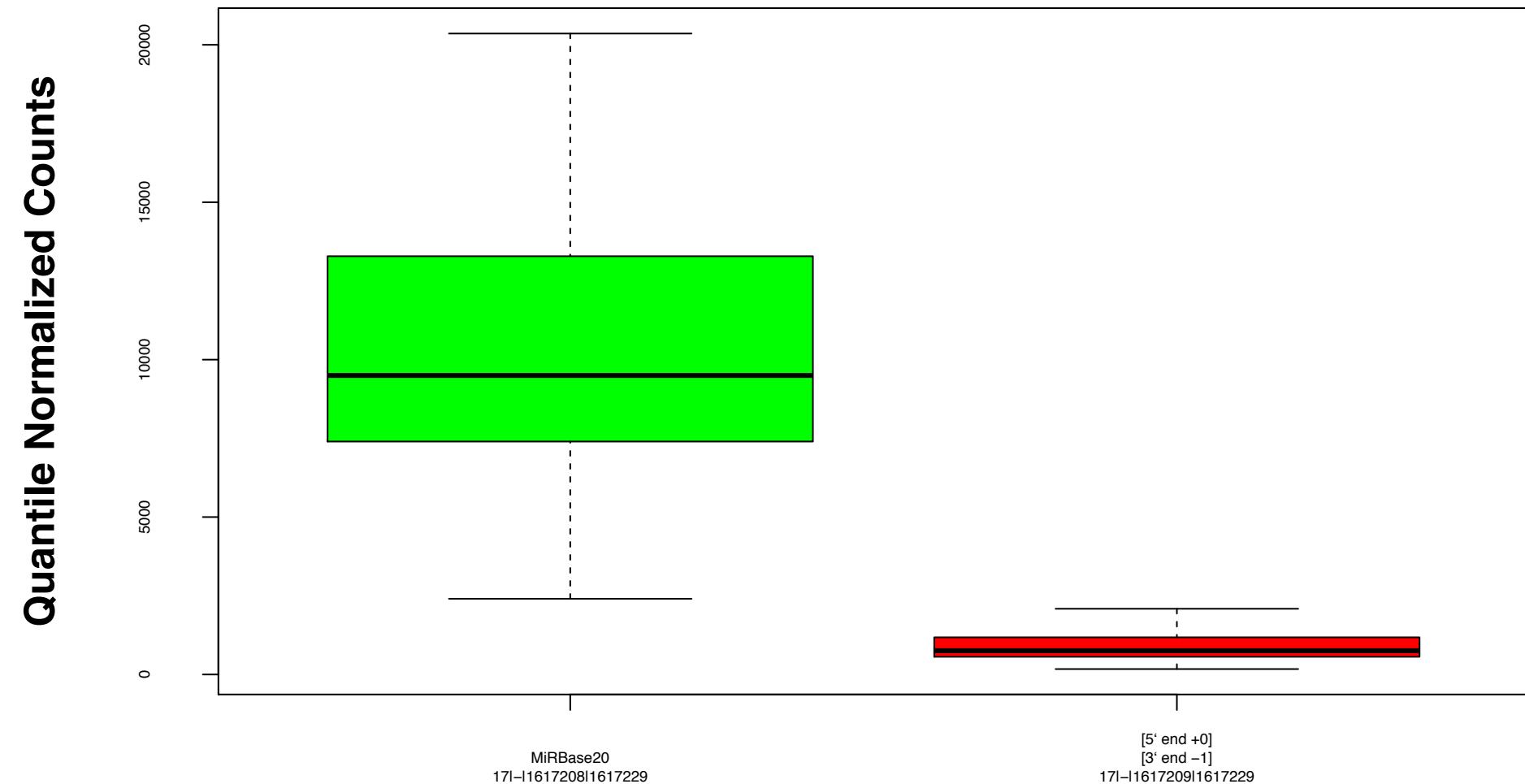
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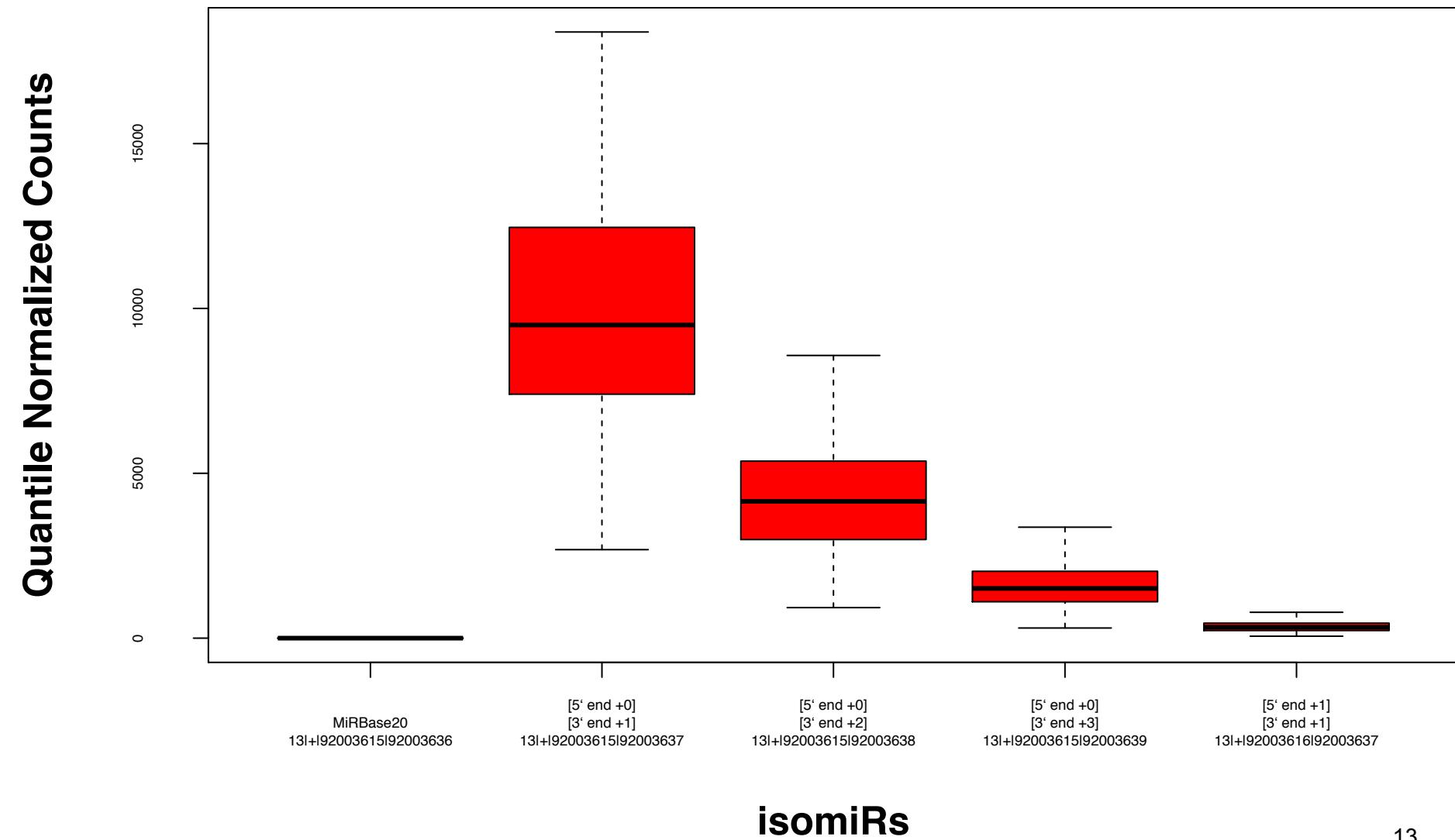
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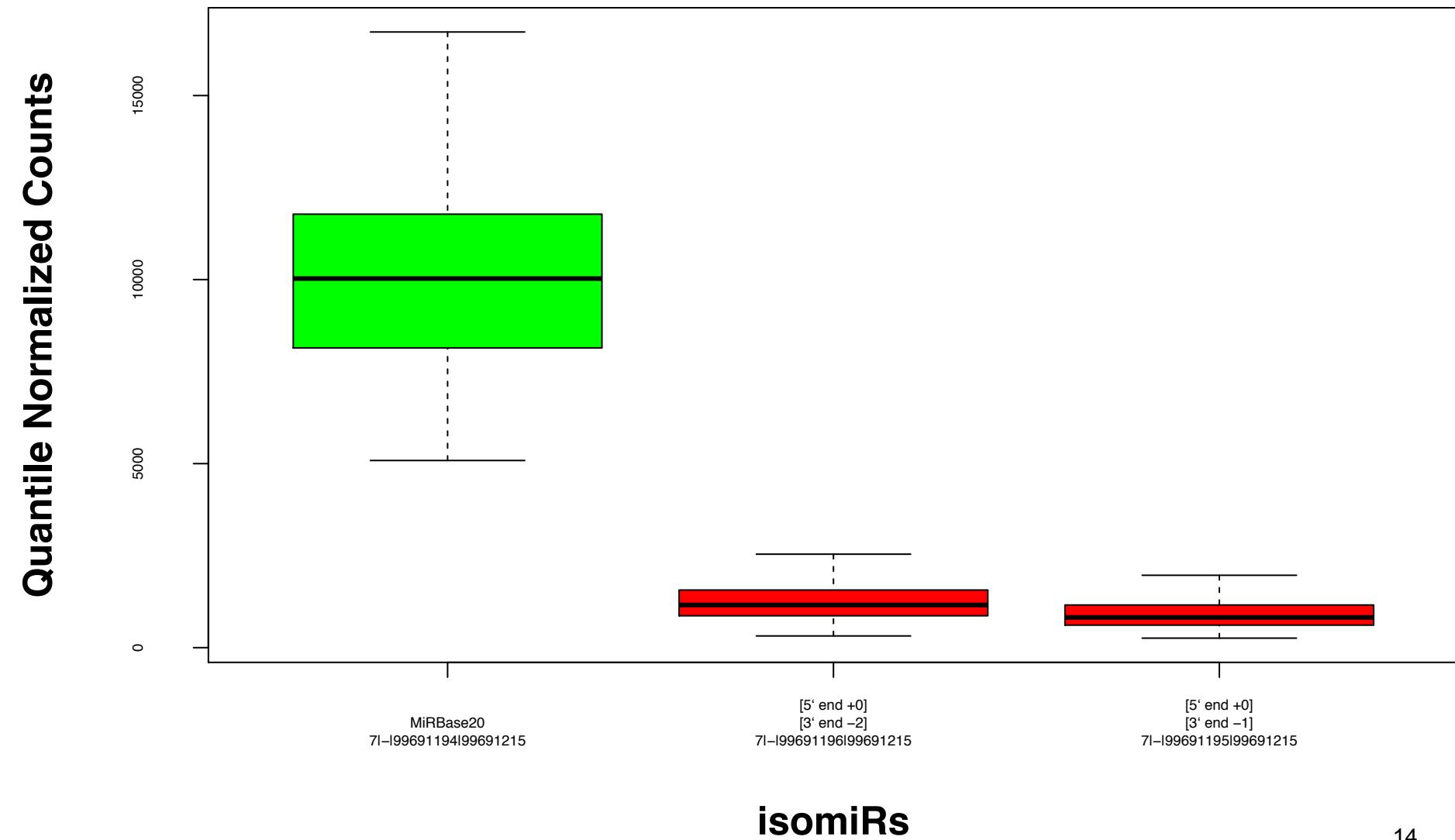
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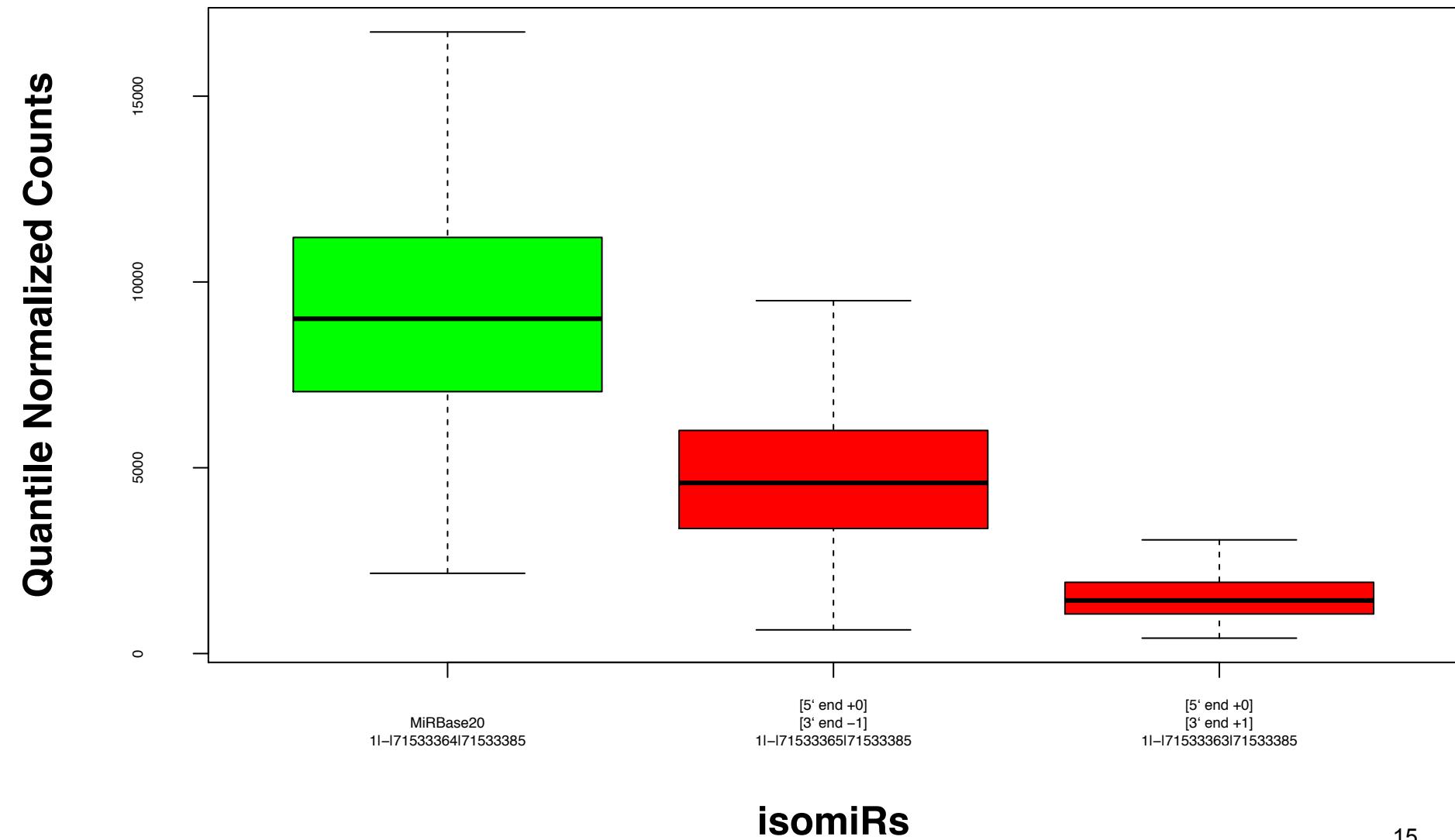
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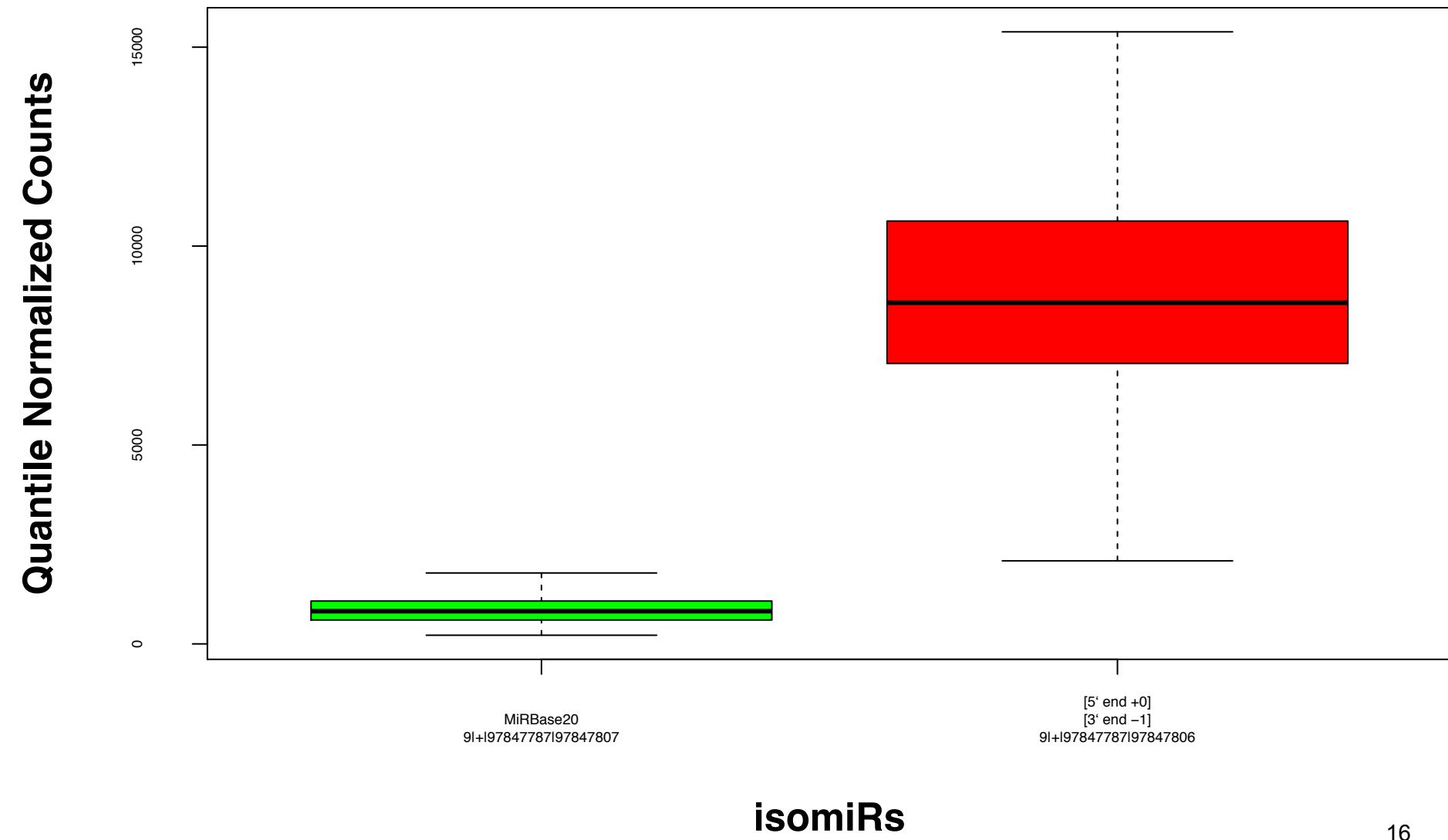
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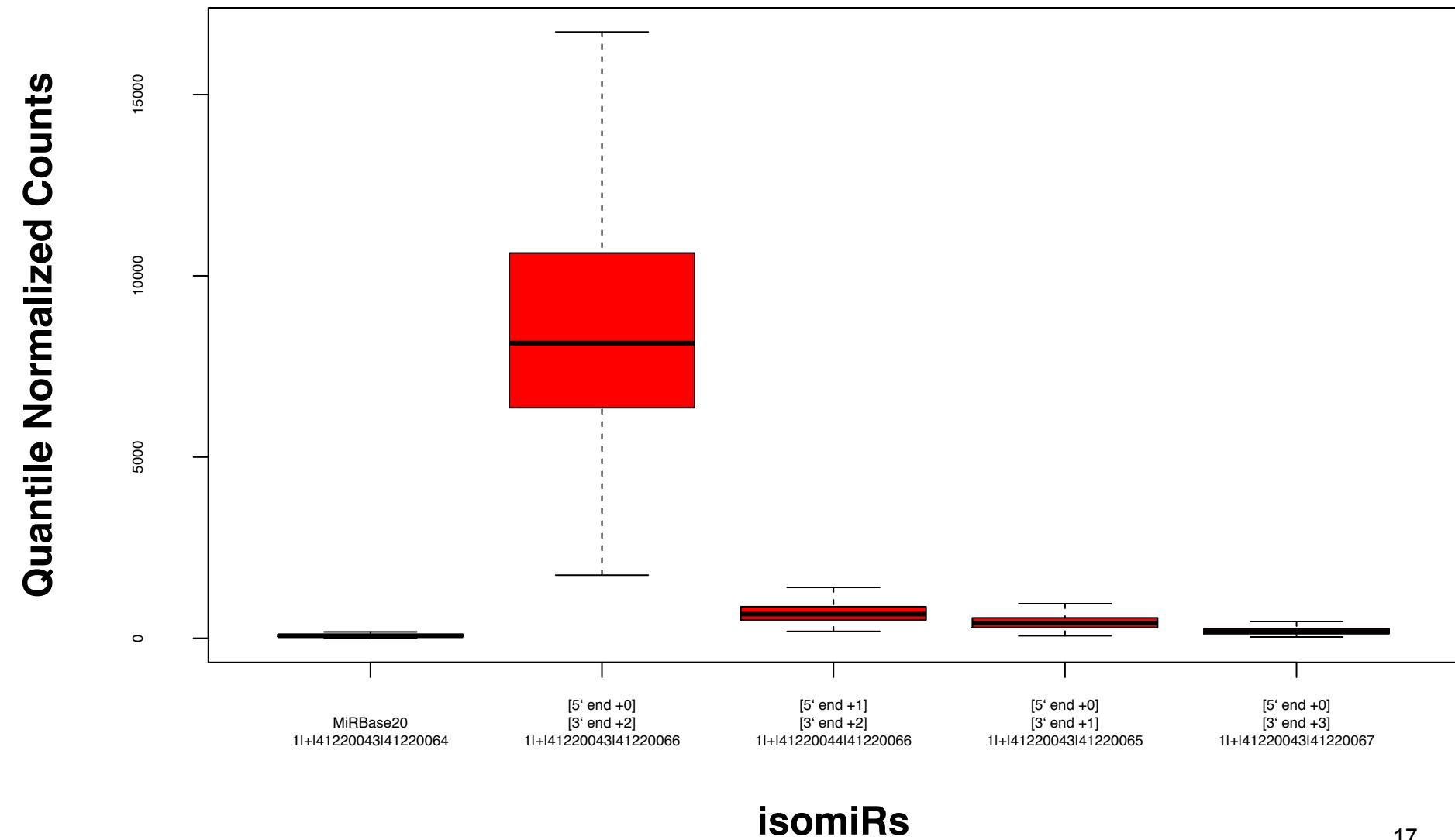
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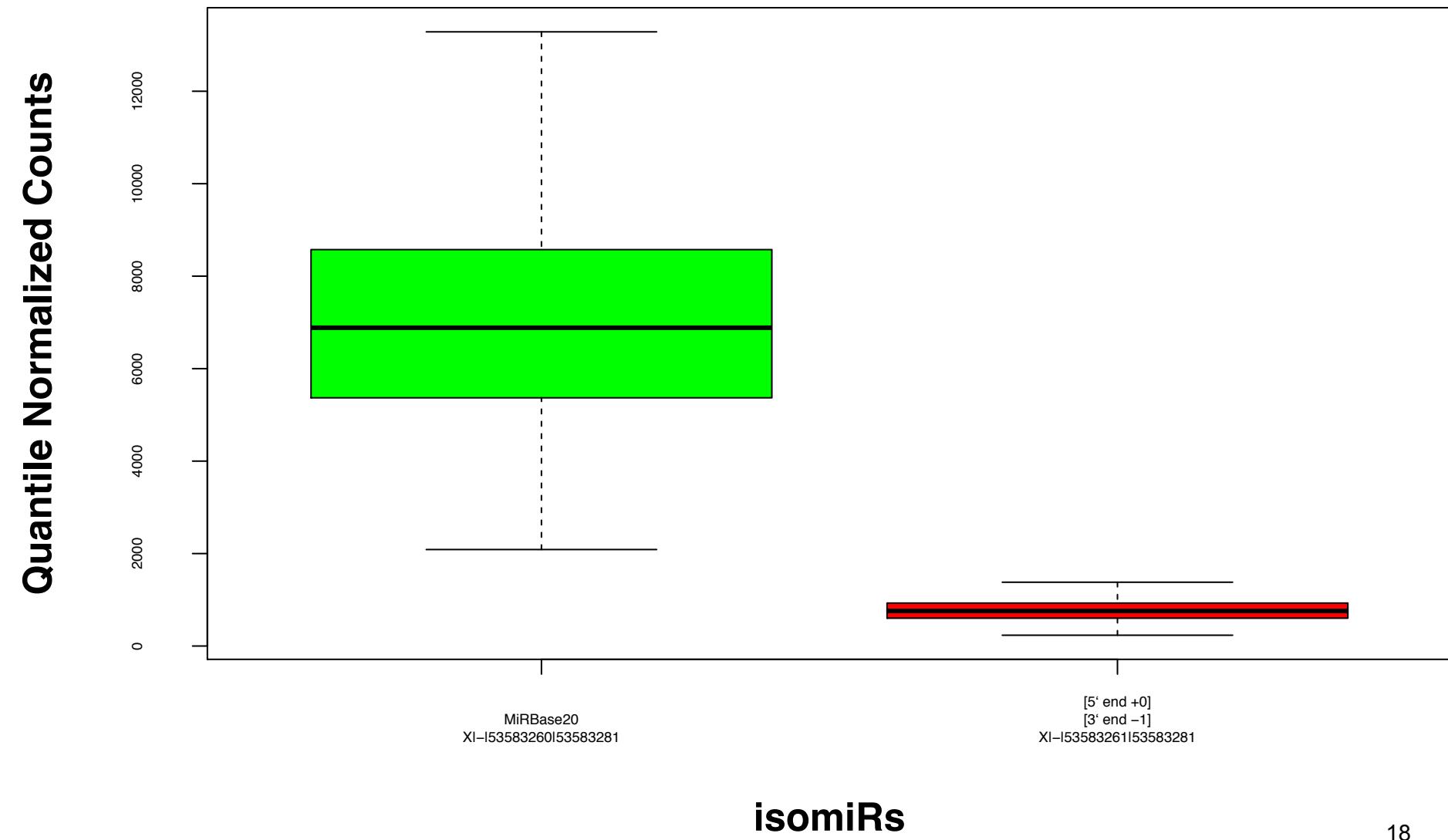
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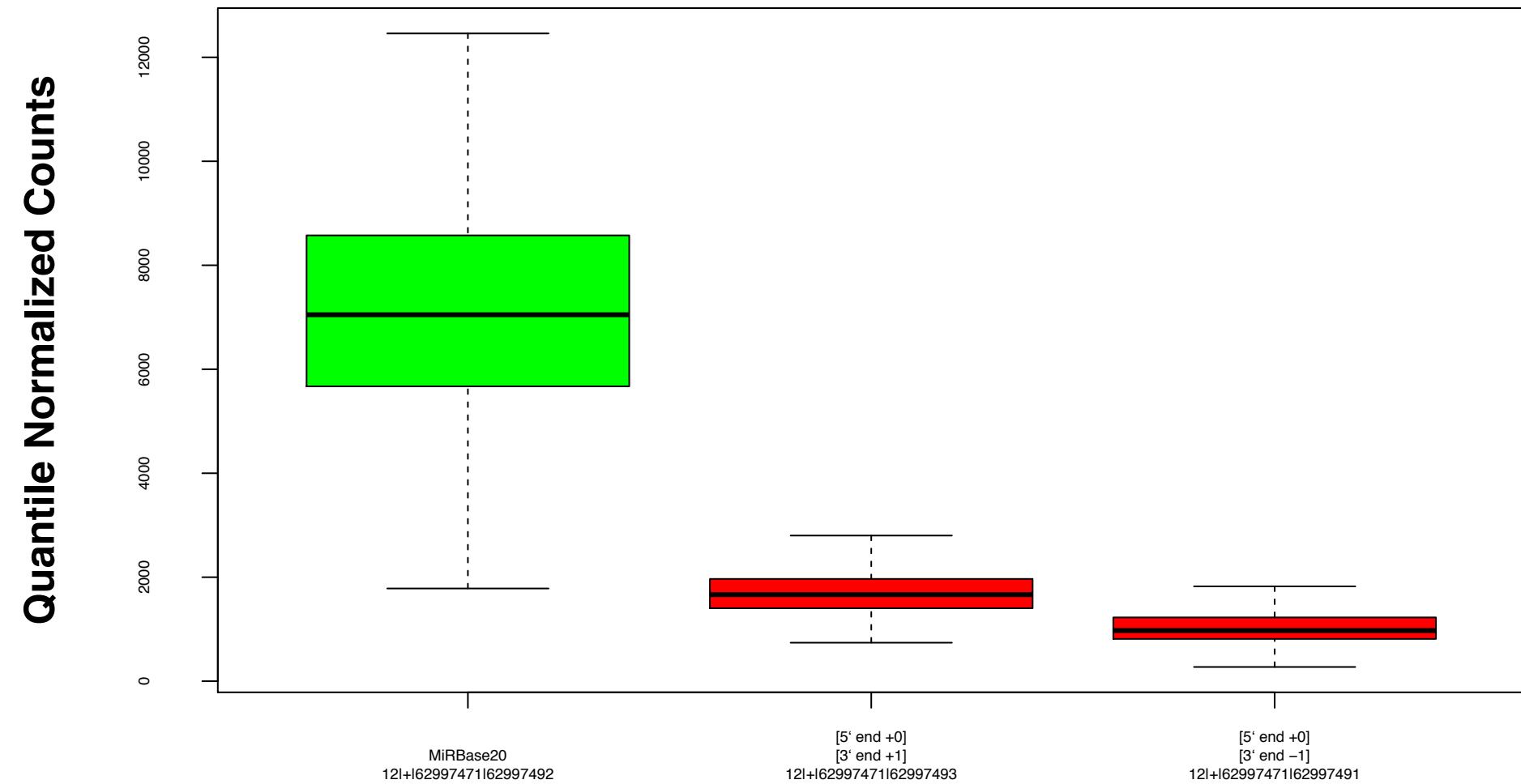
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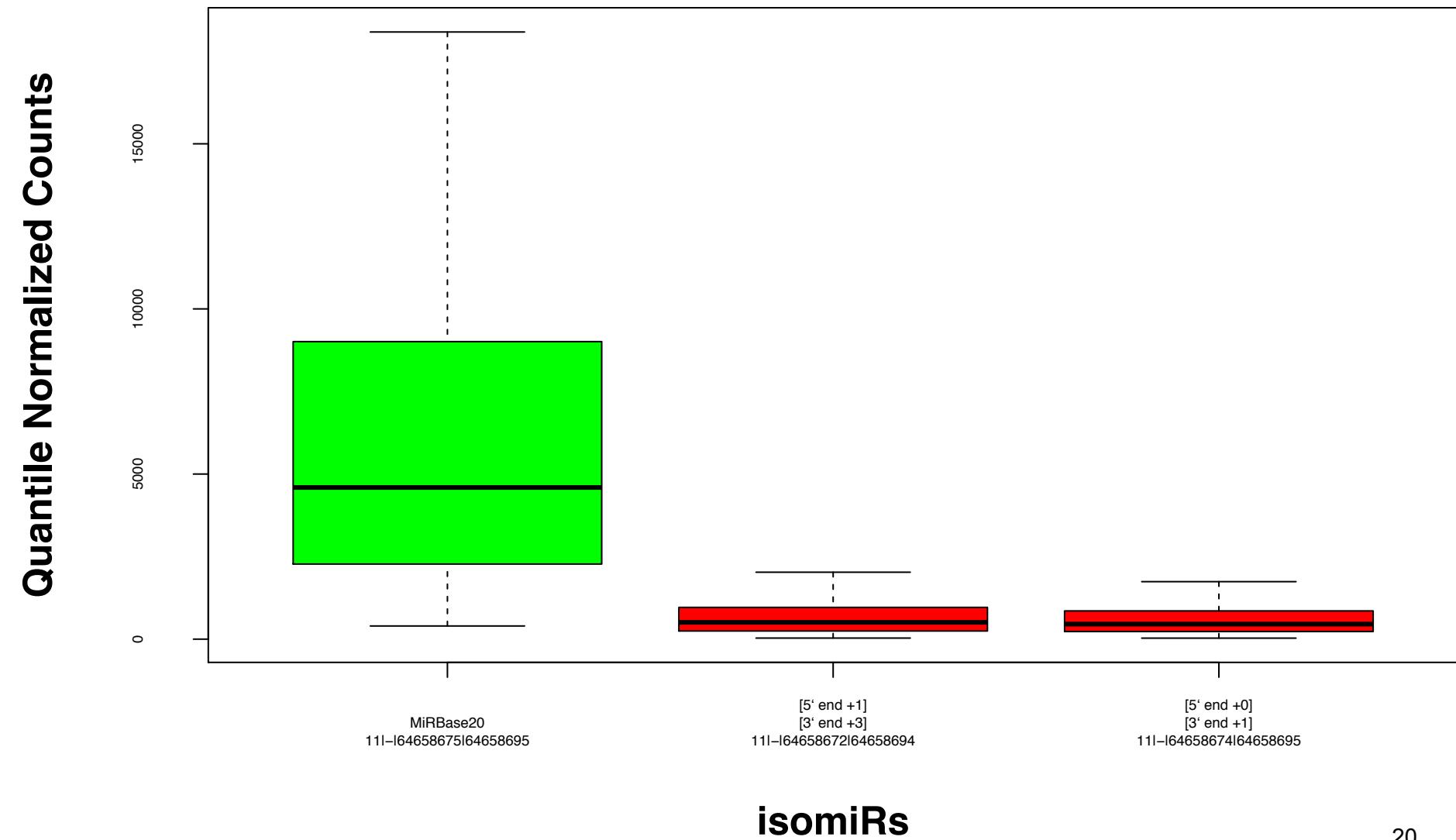
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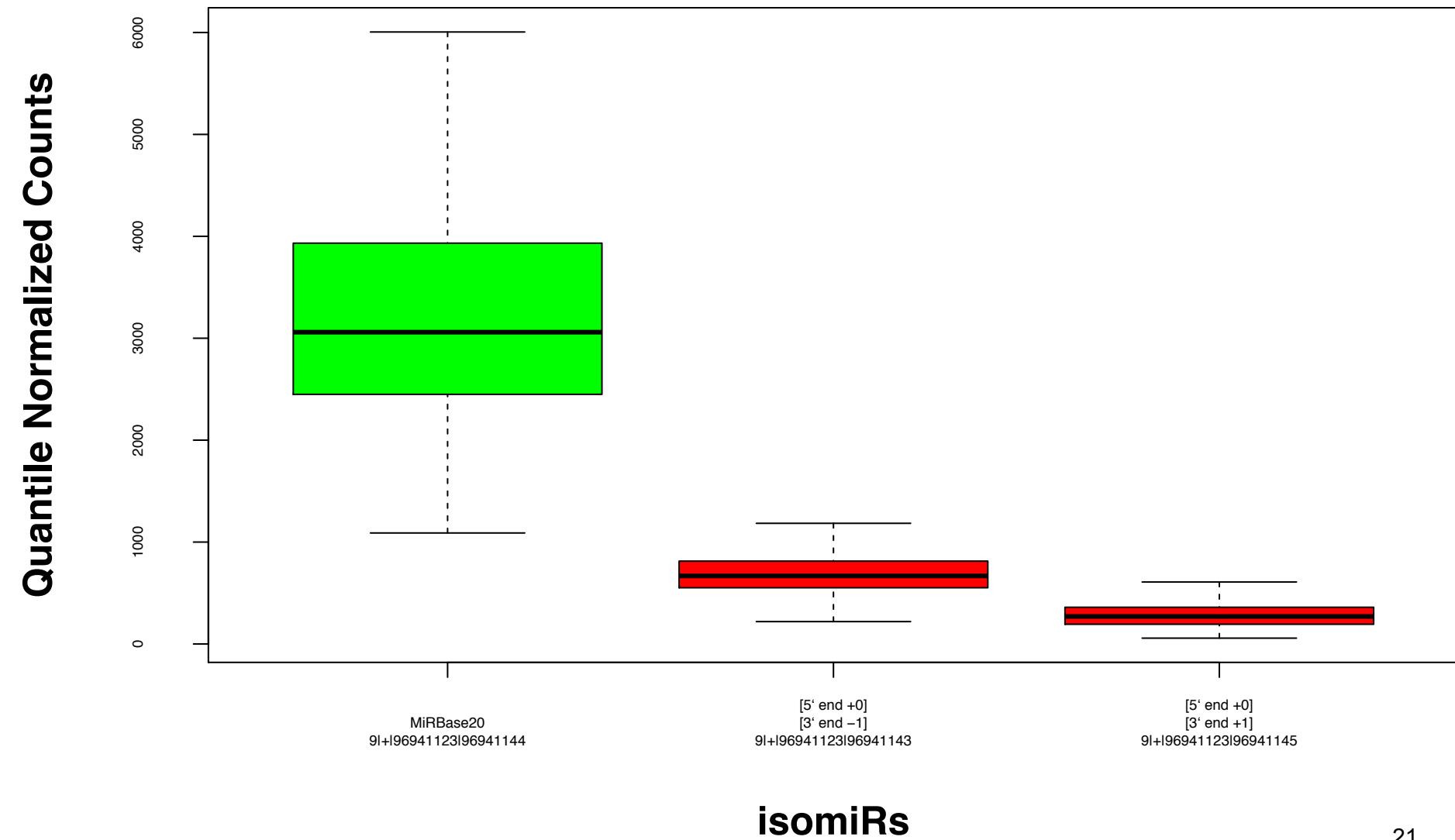
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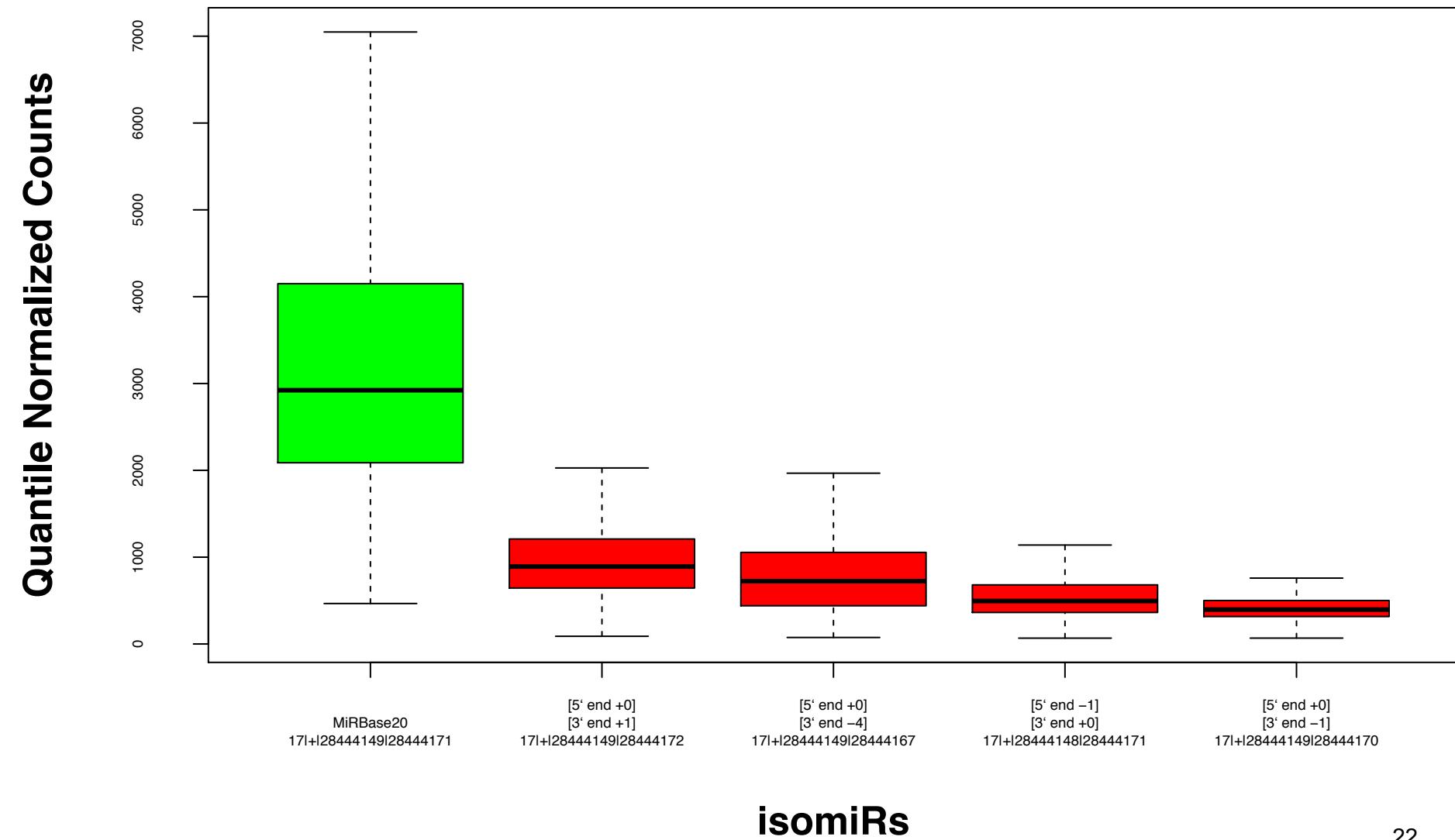
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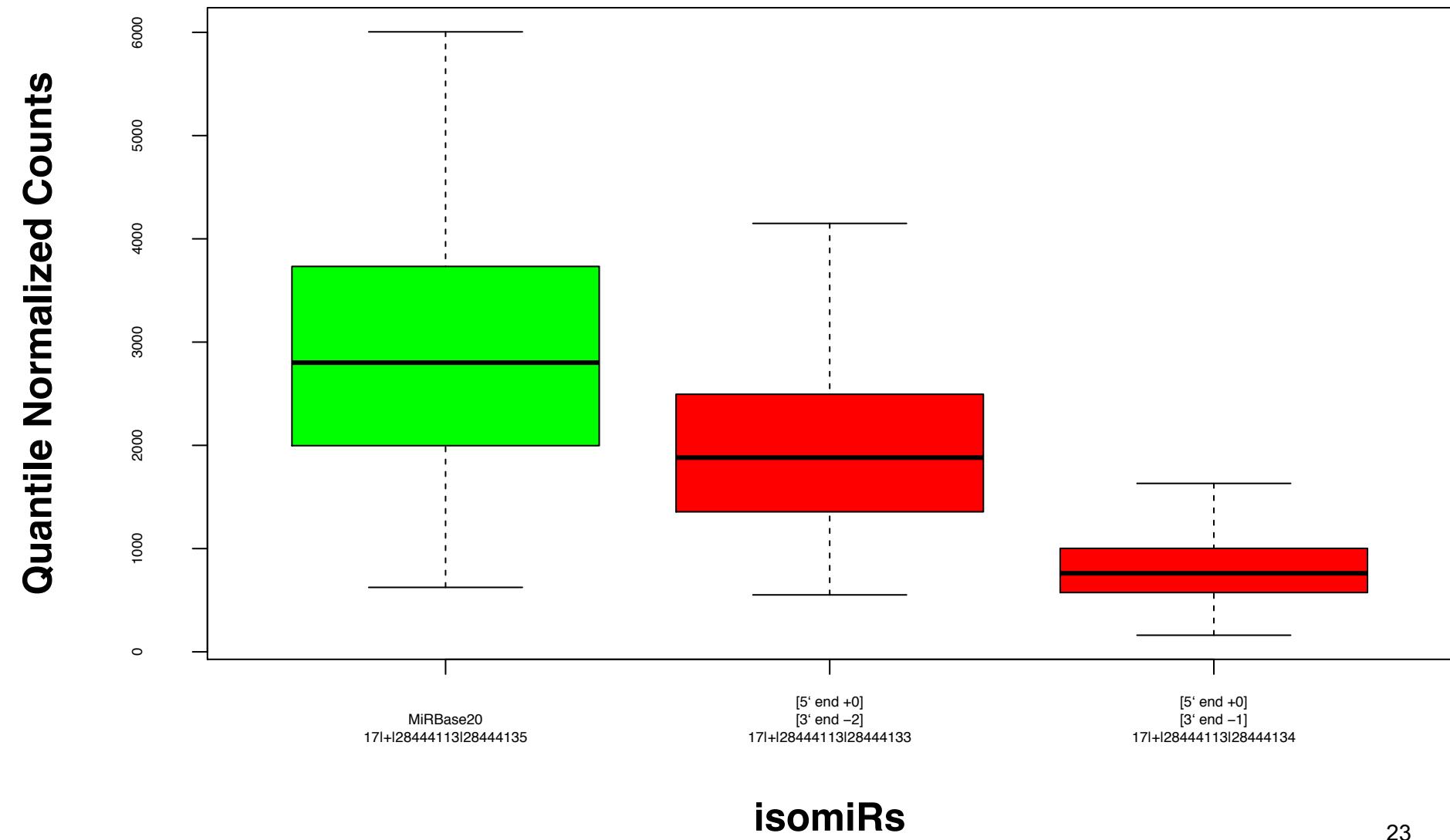
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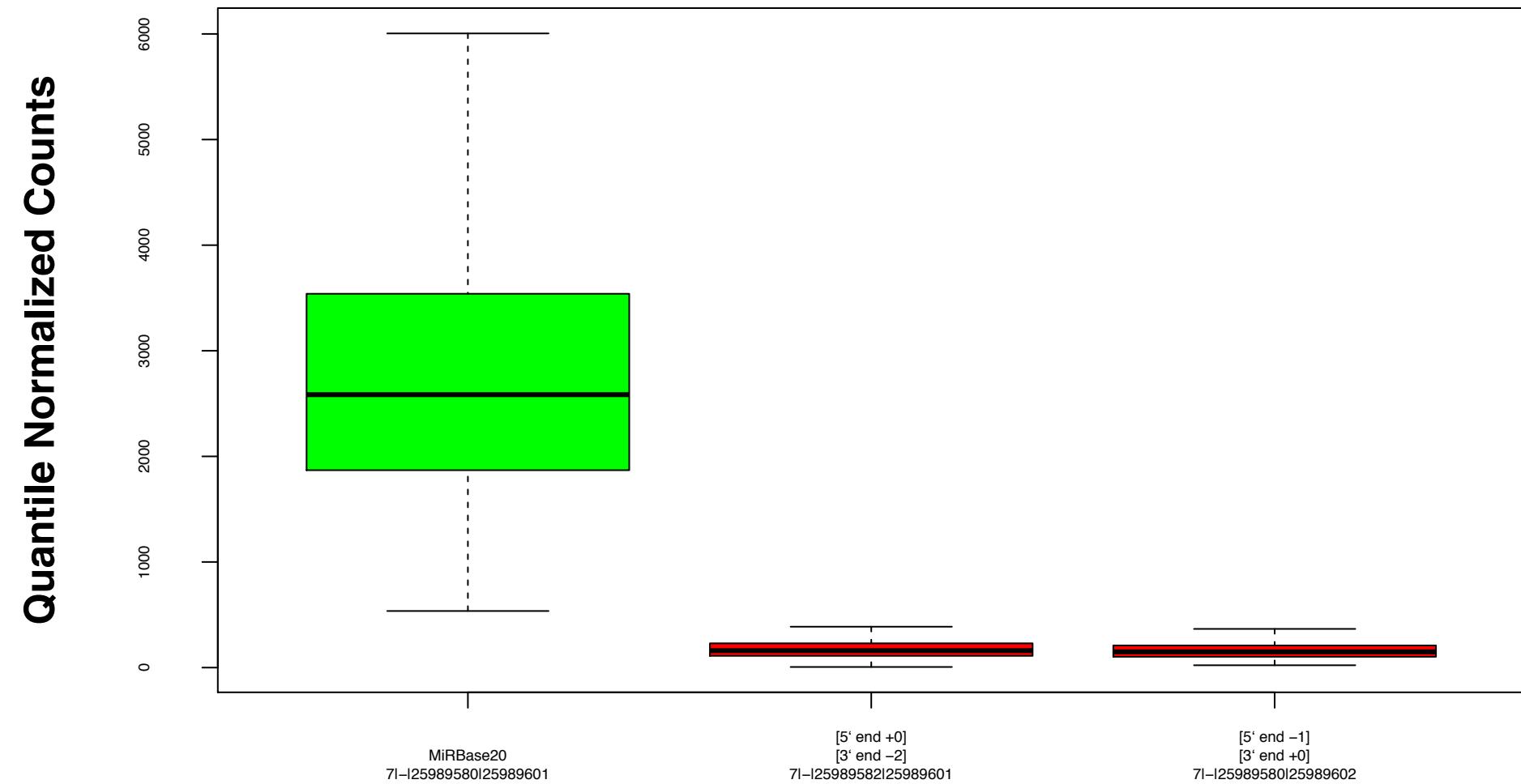
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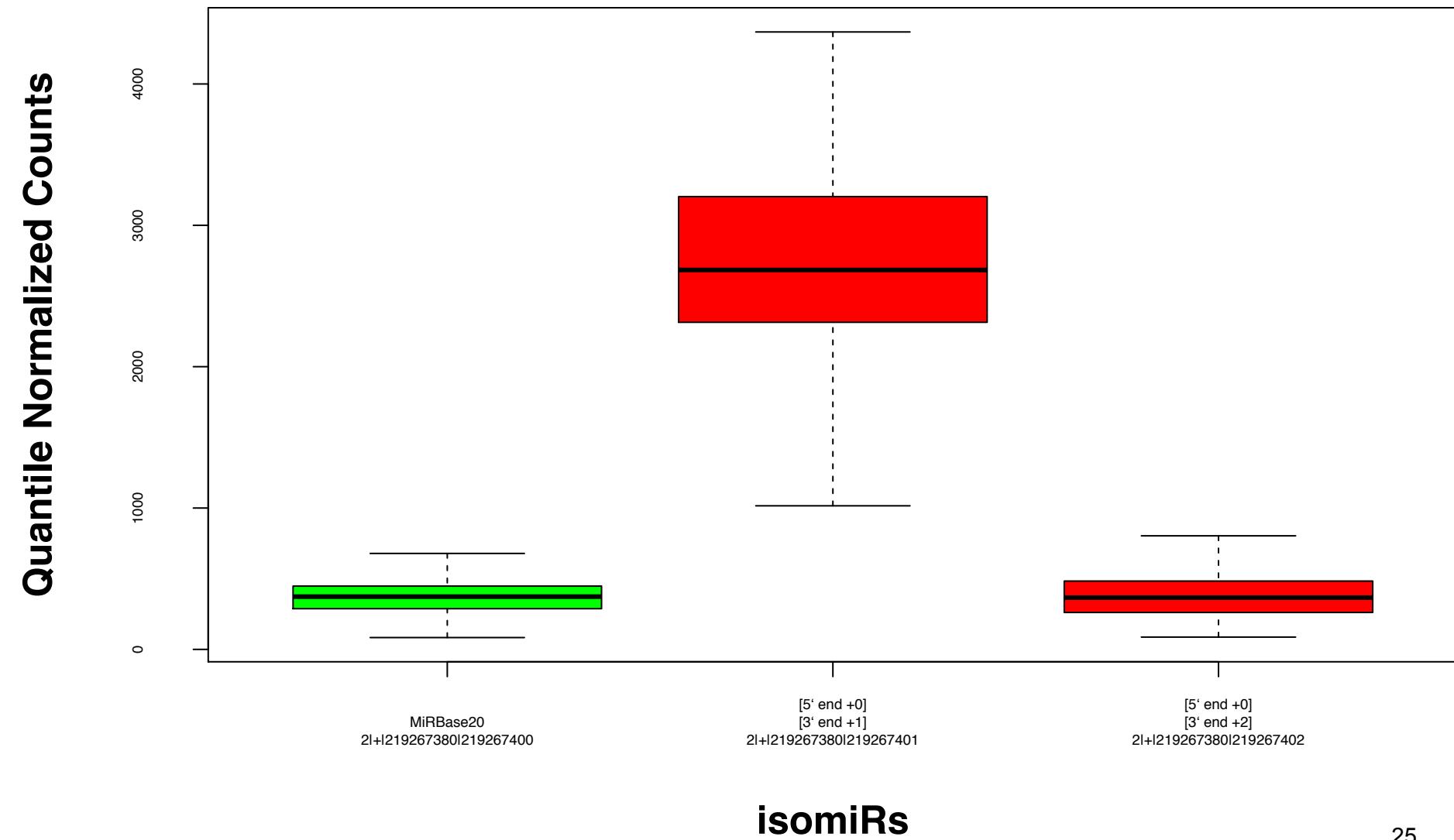
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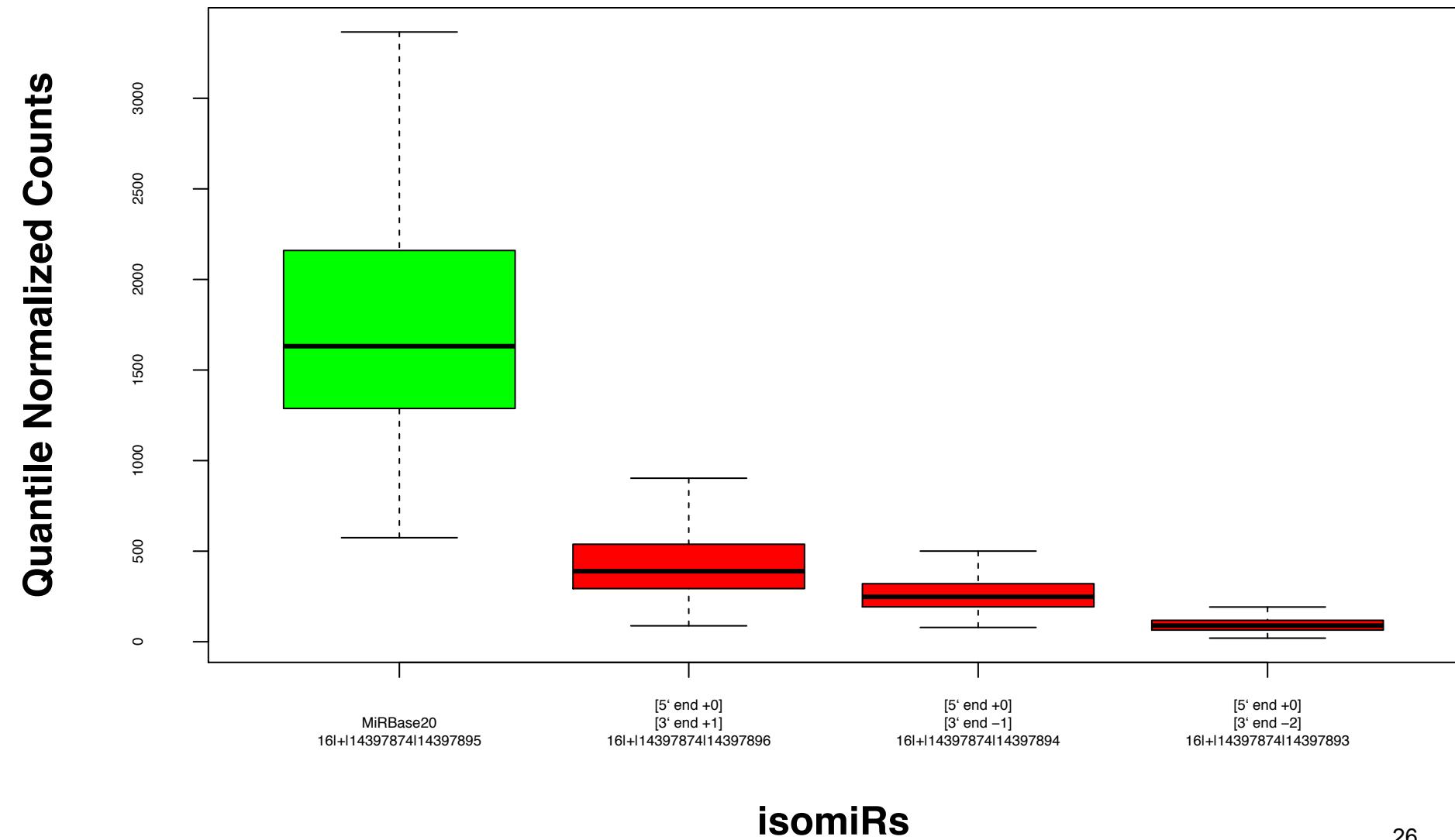


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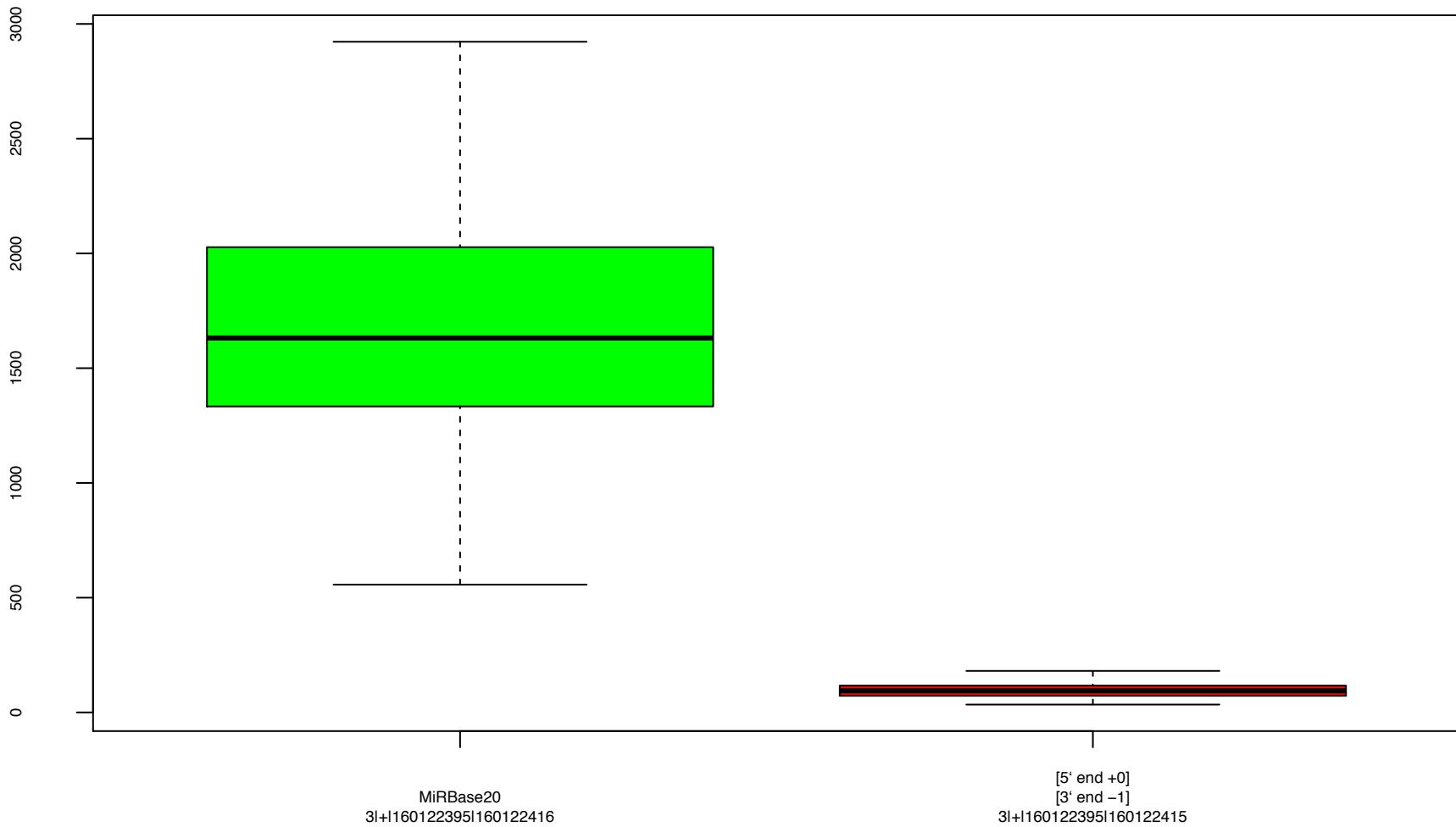
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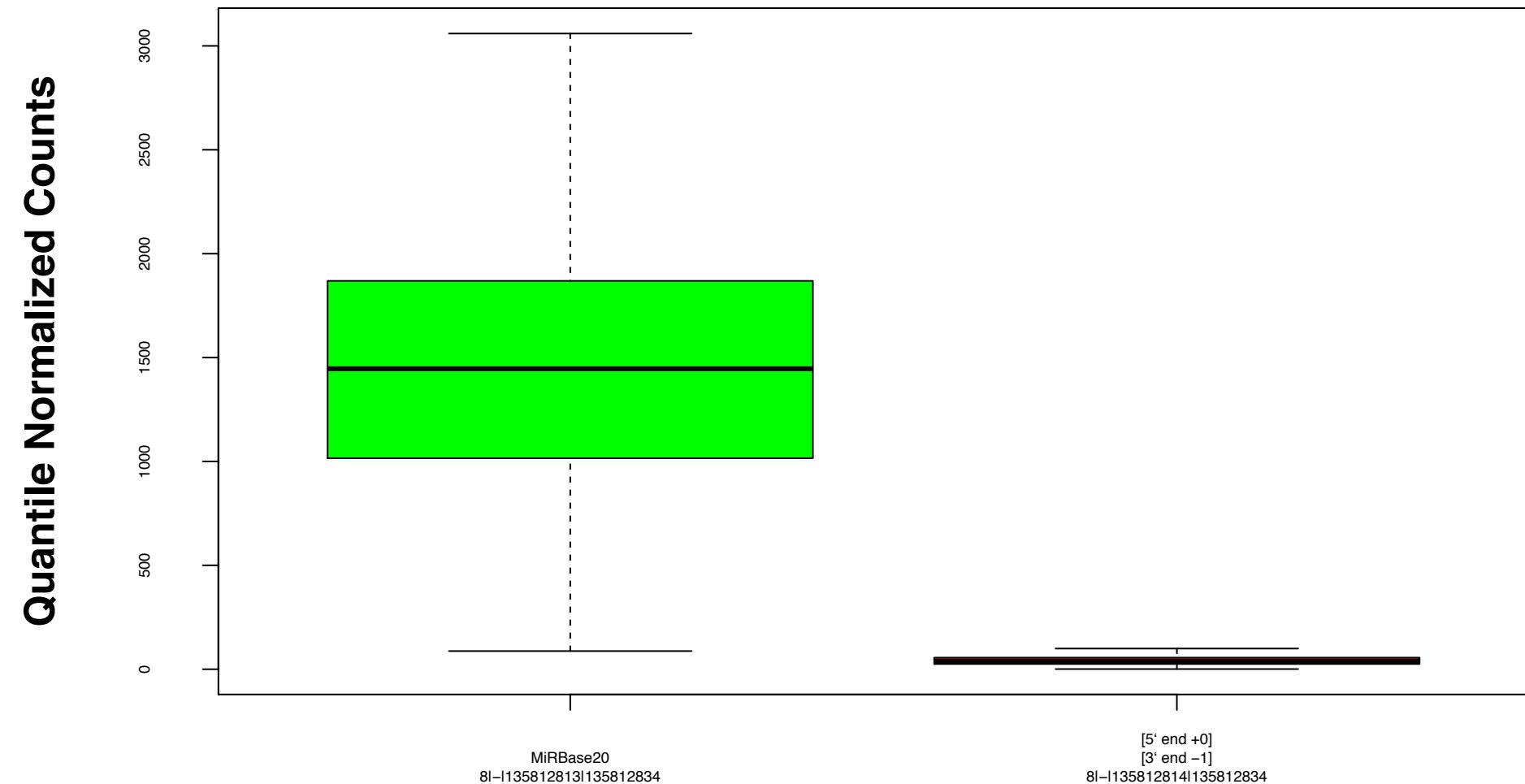
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Quantile Normalized Counts



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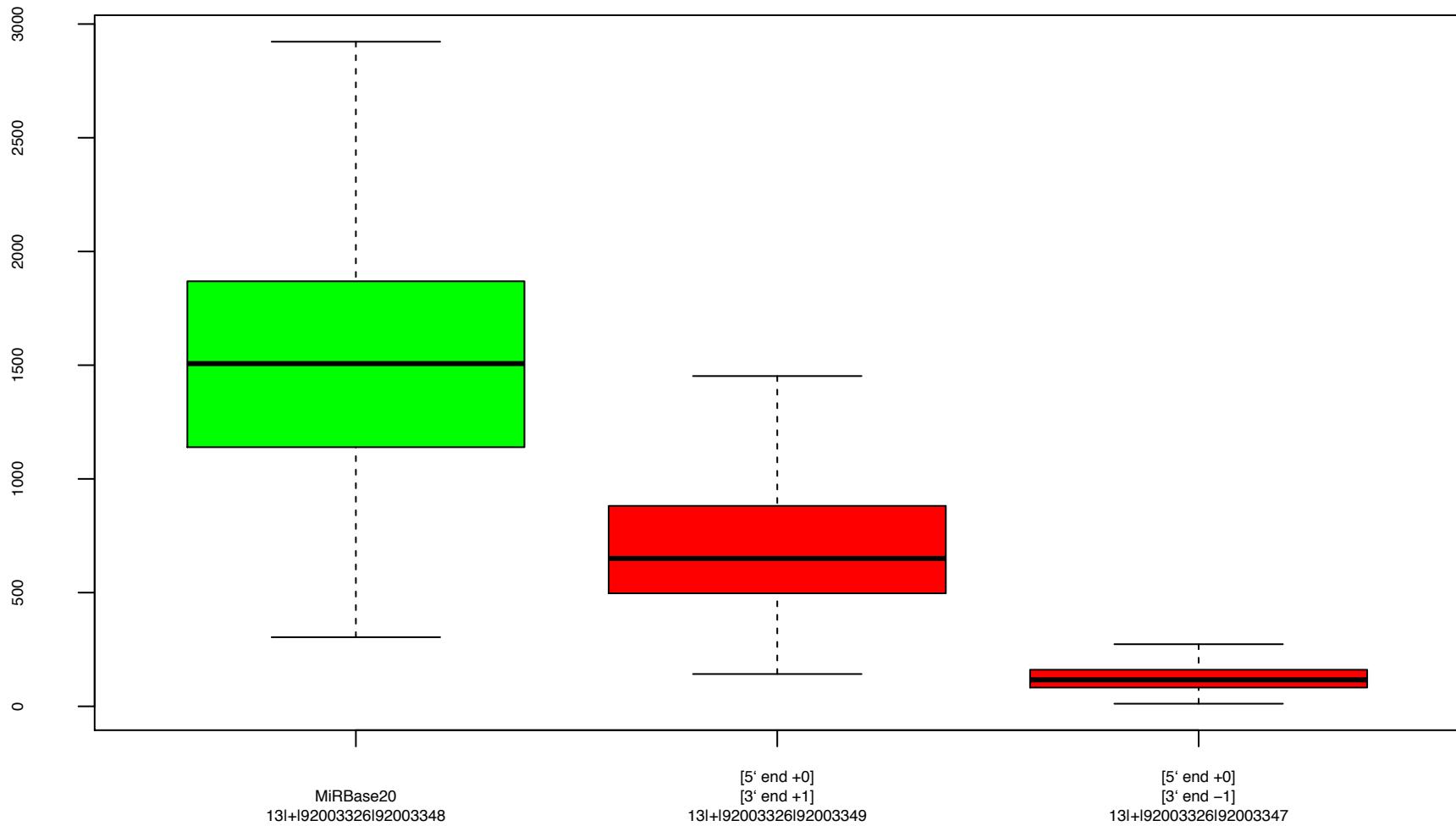
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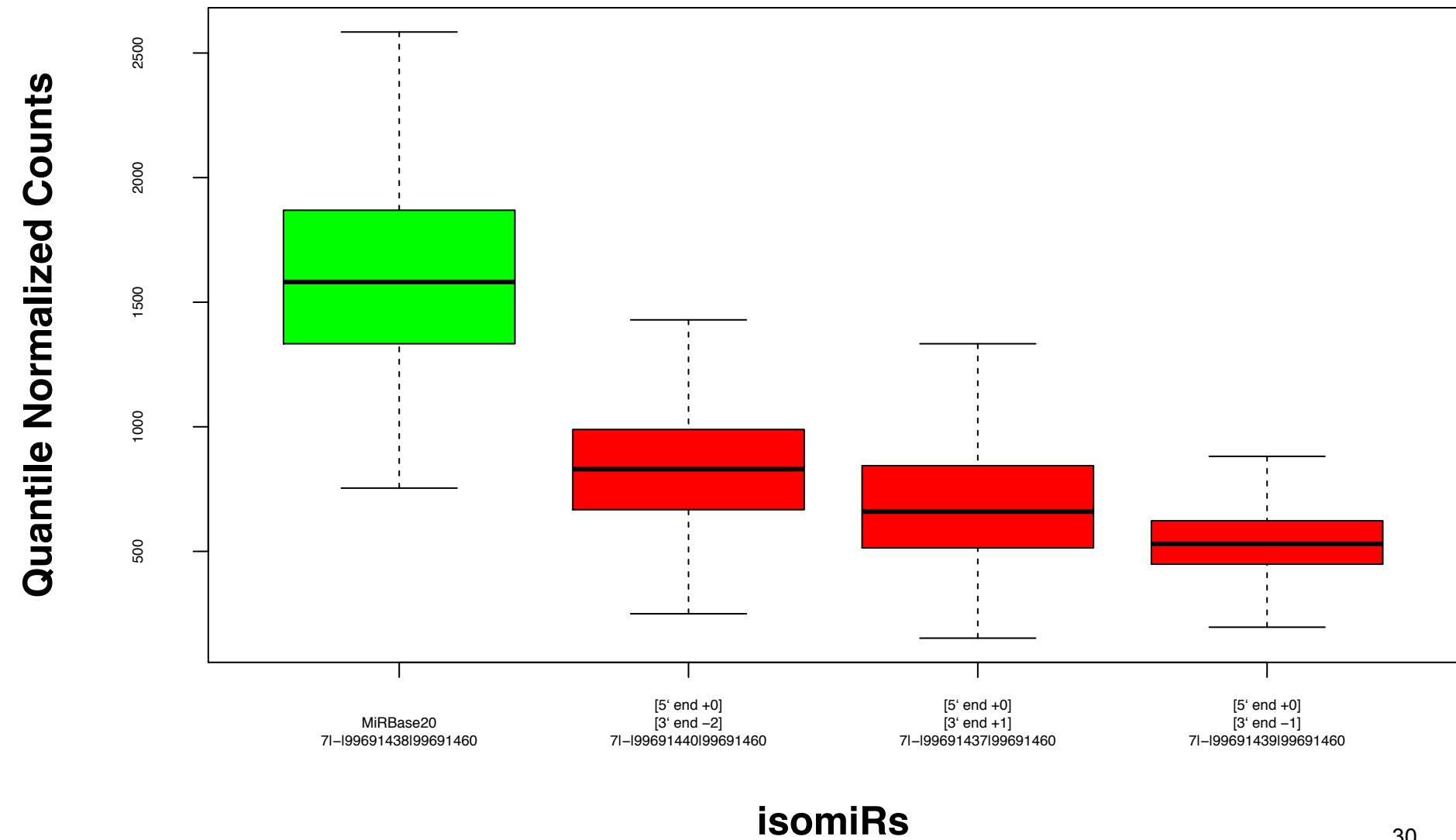
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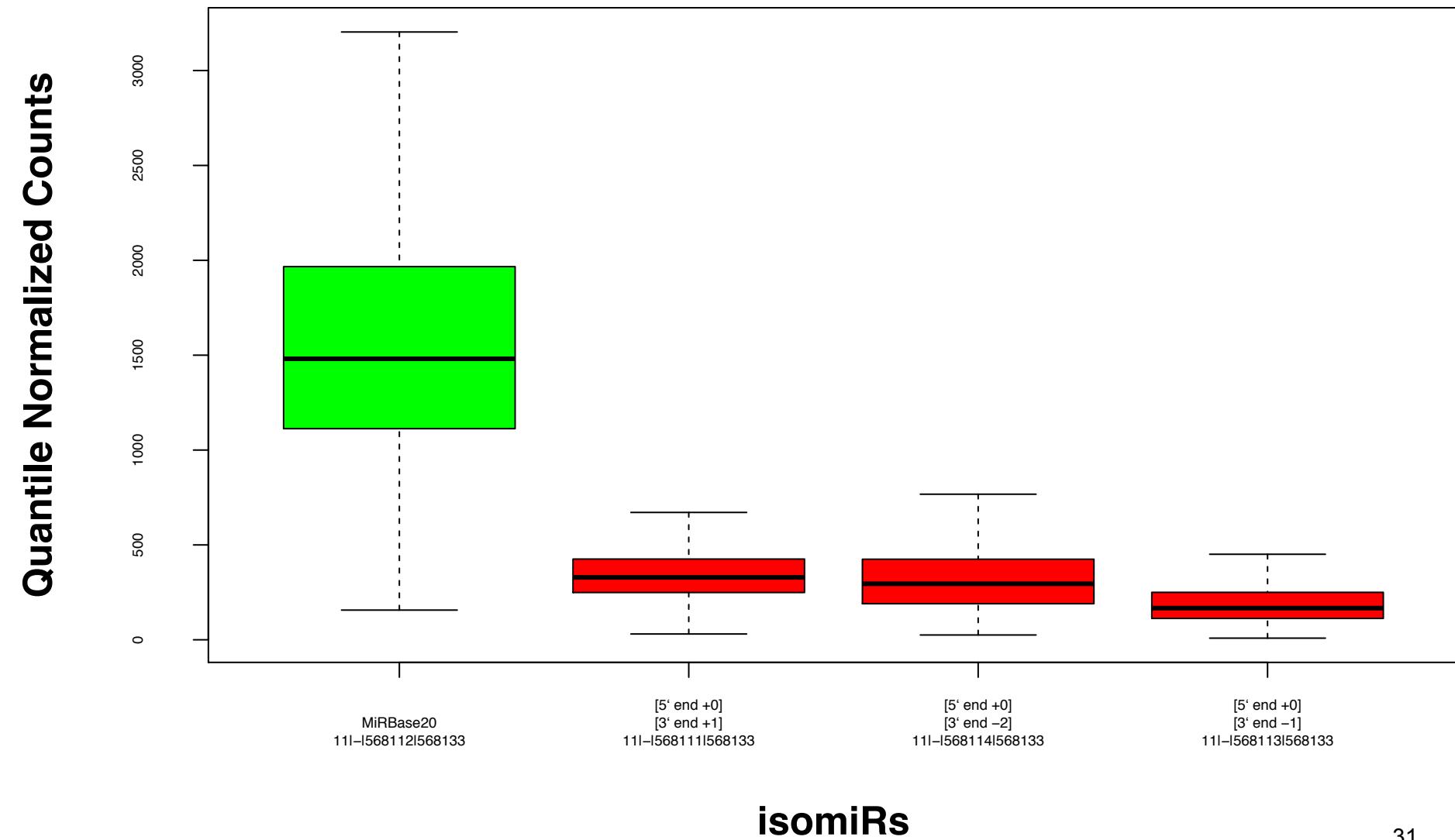


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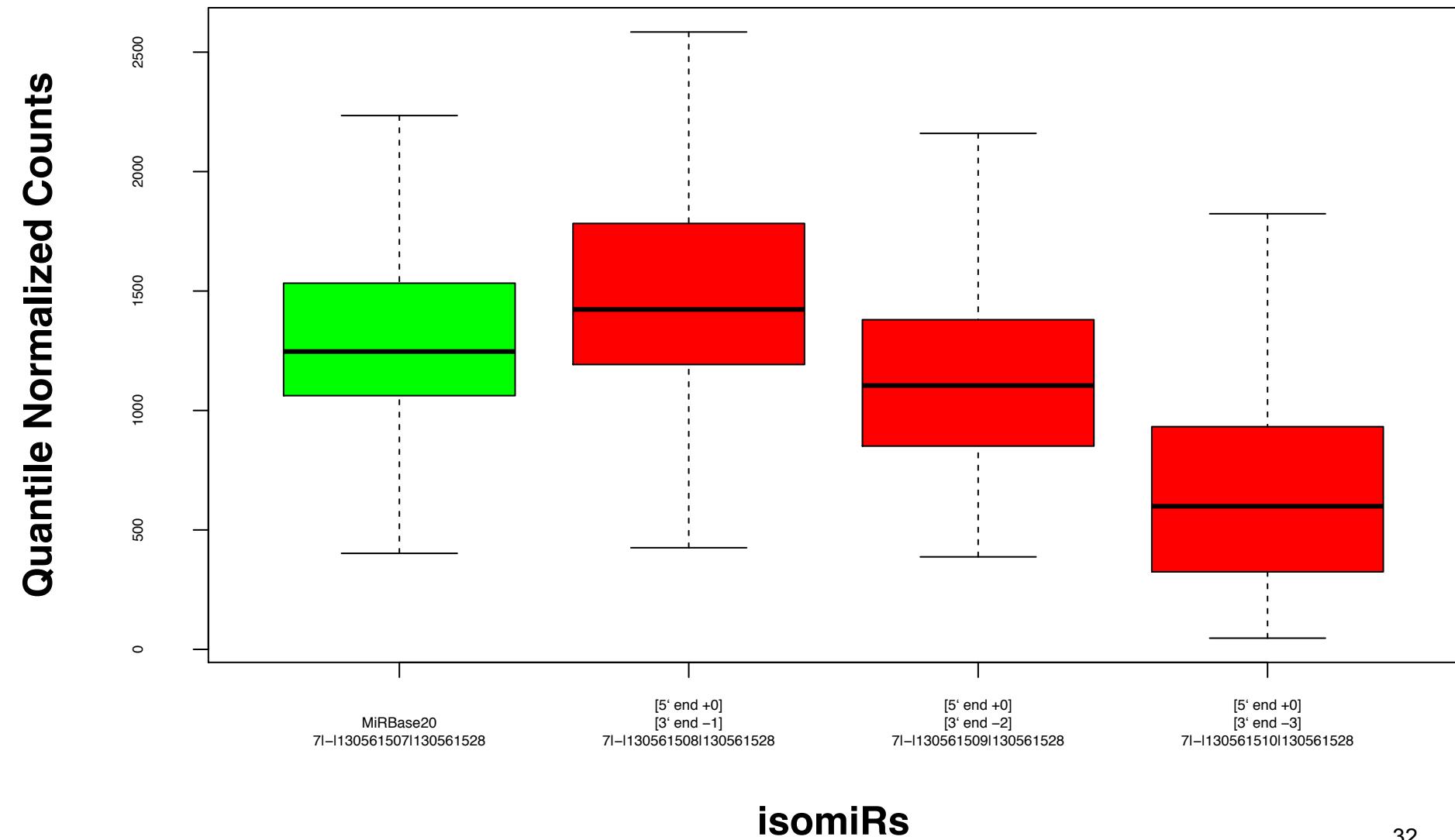
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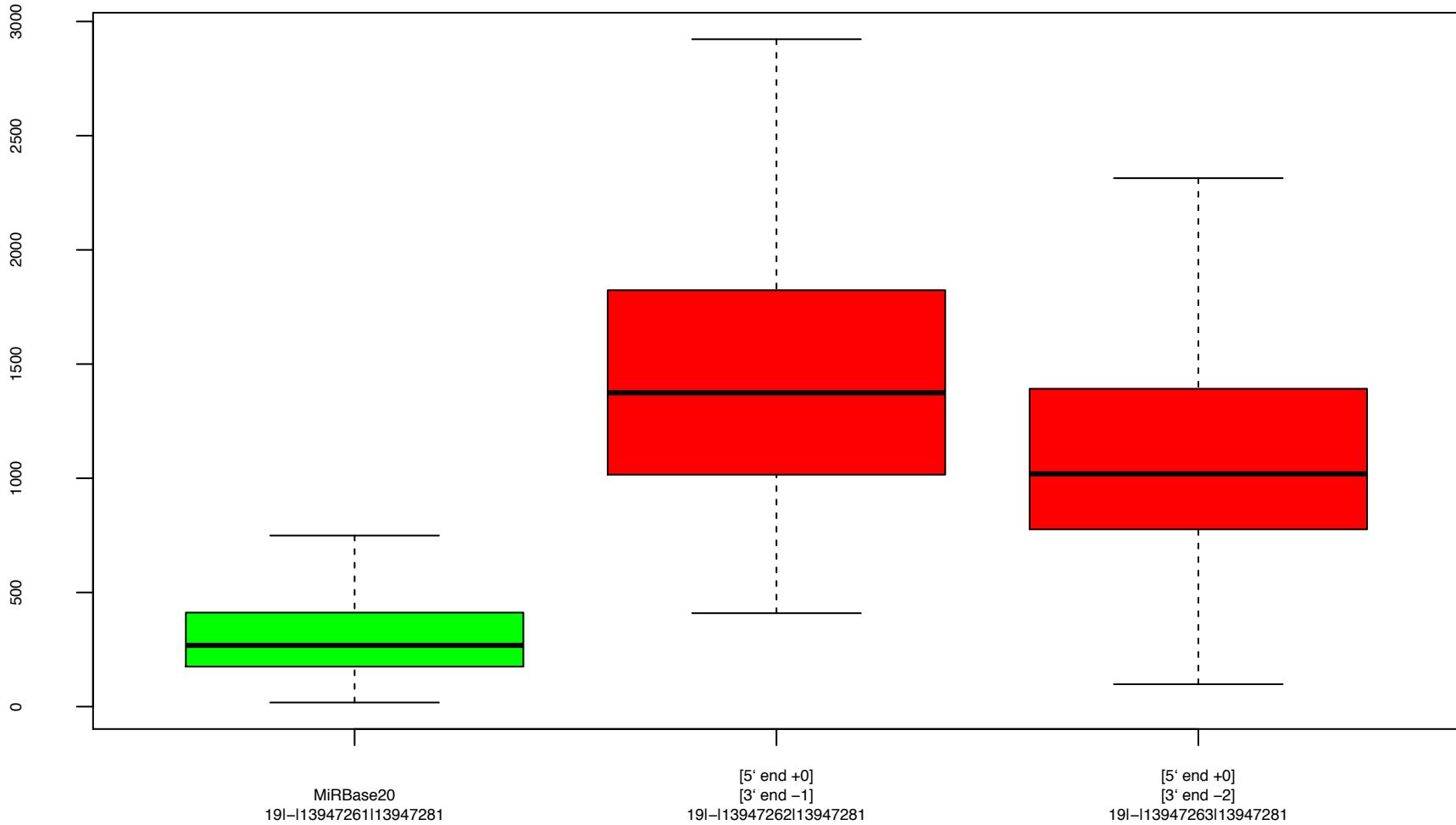


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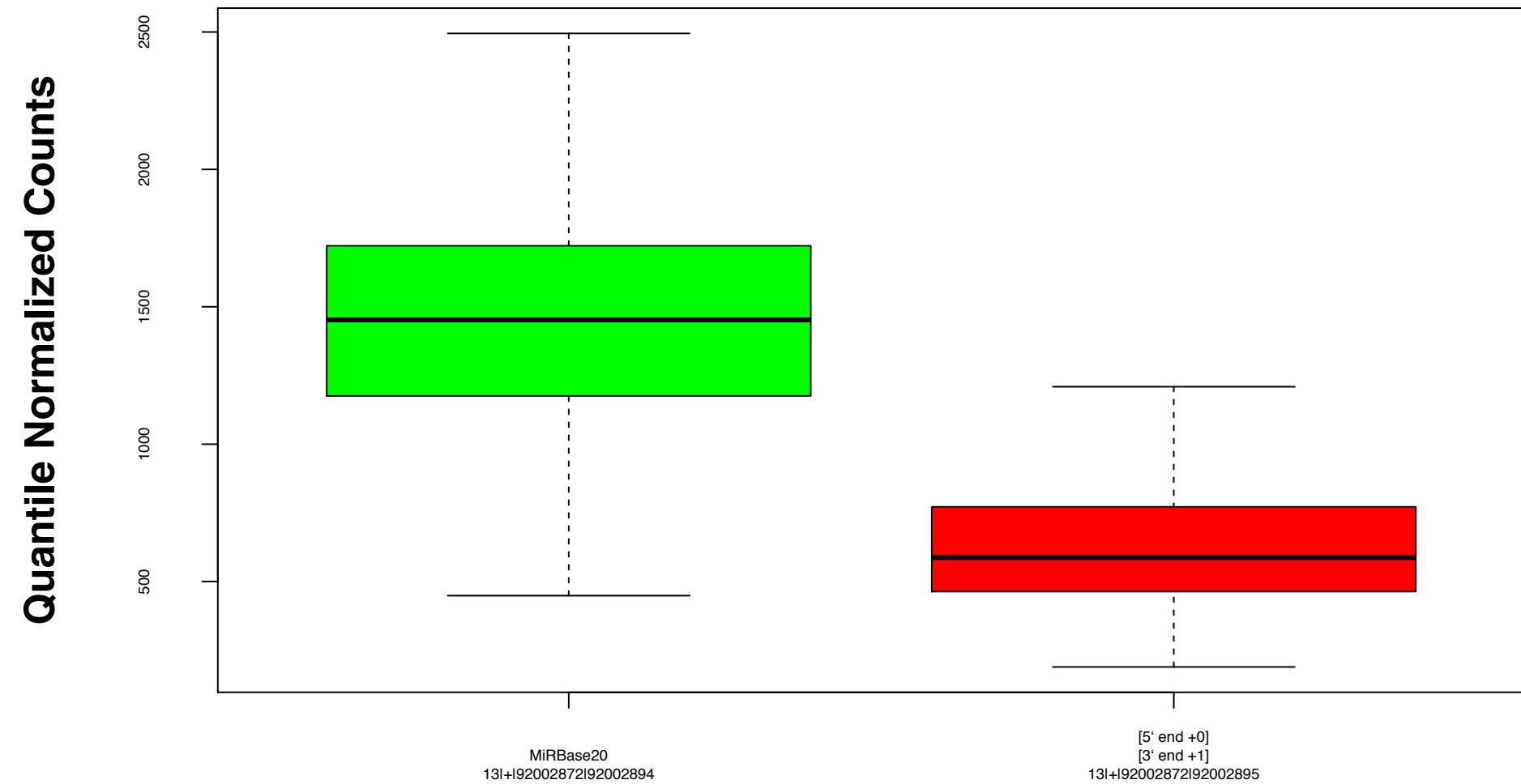
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Quantile Normalized Counts



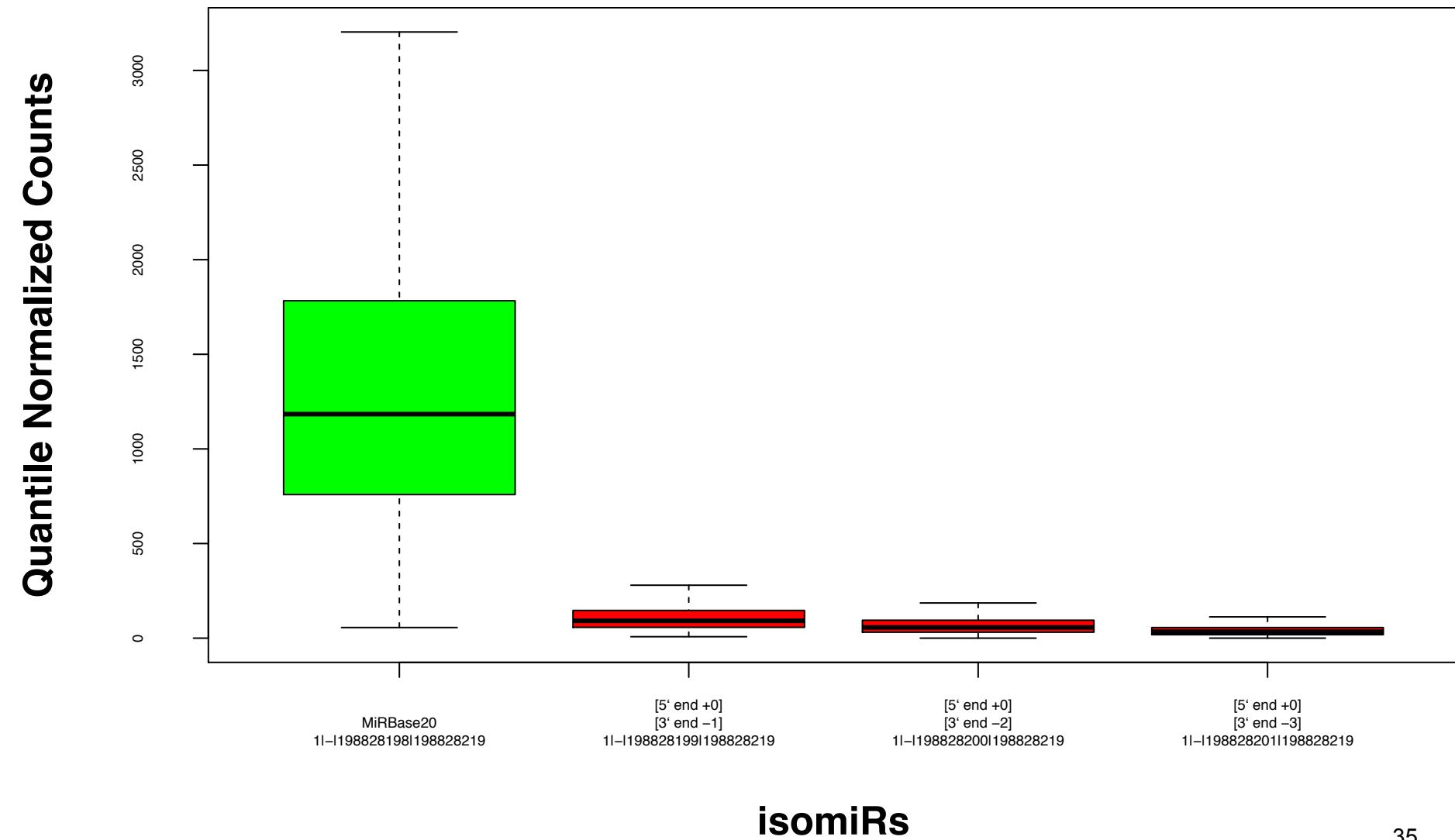
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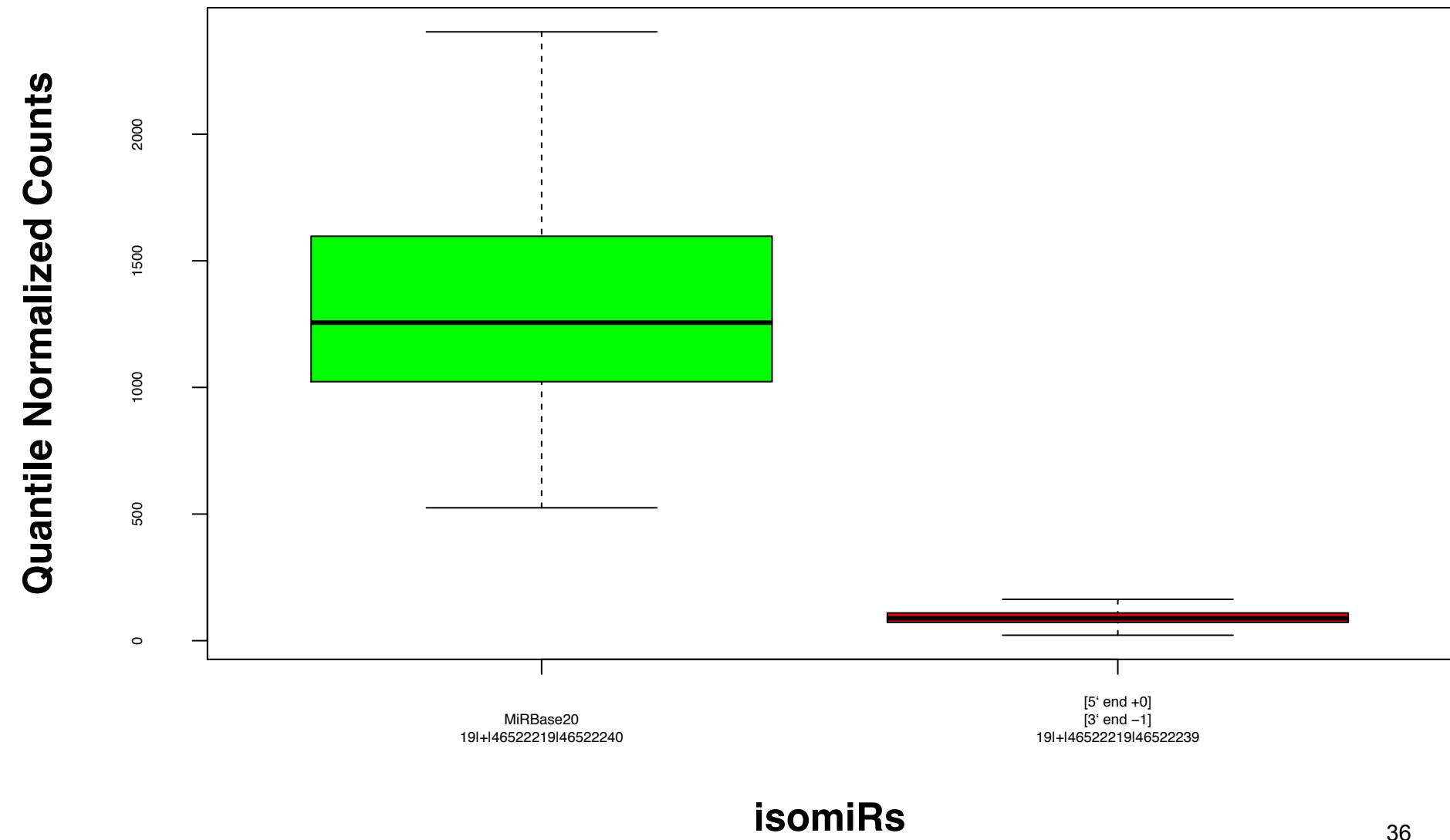


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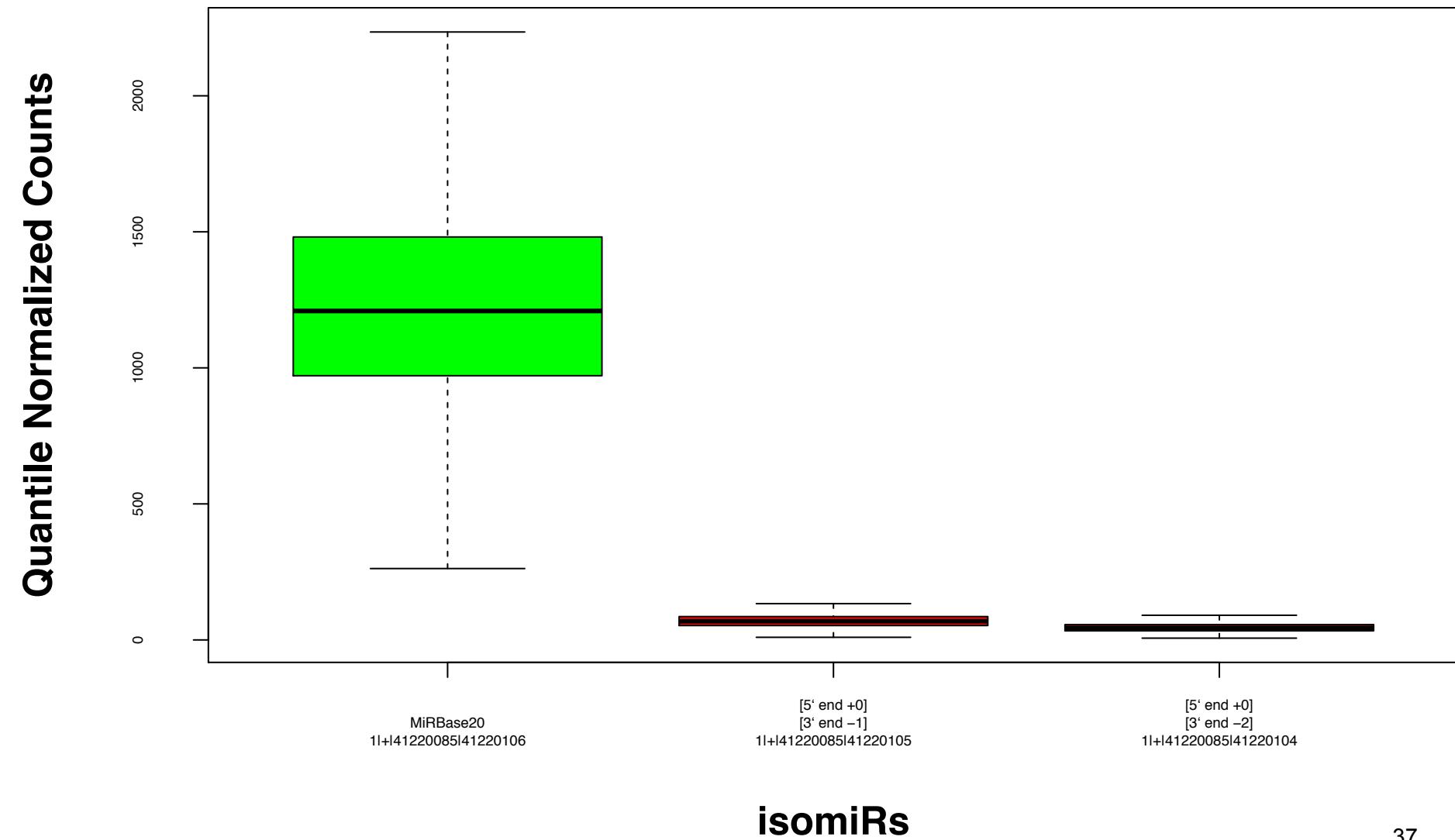
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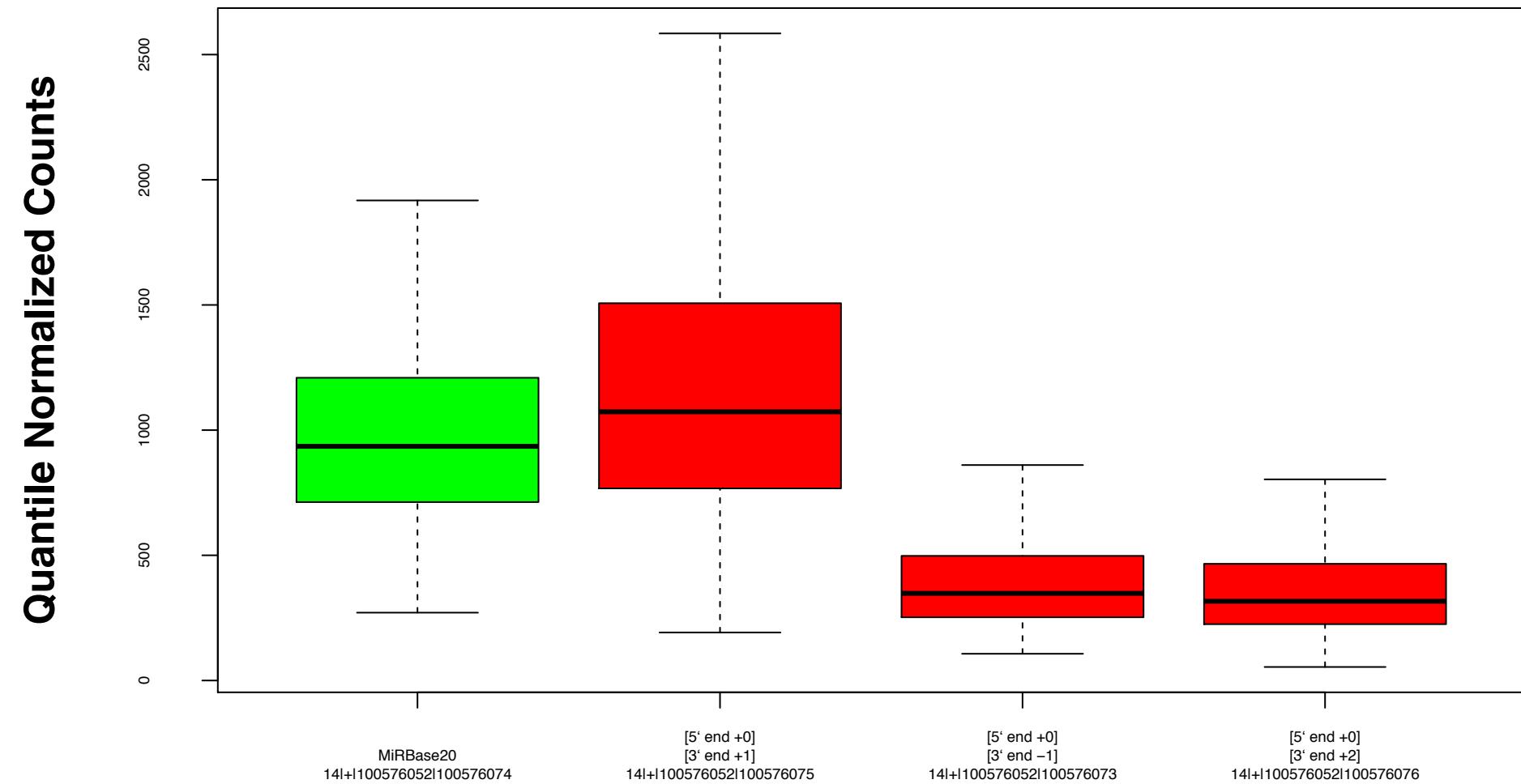
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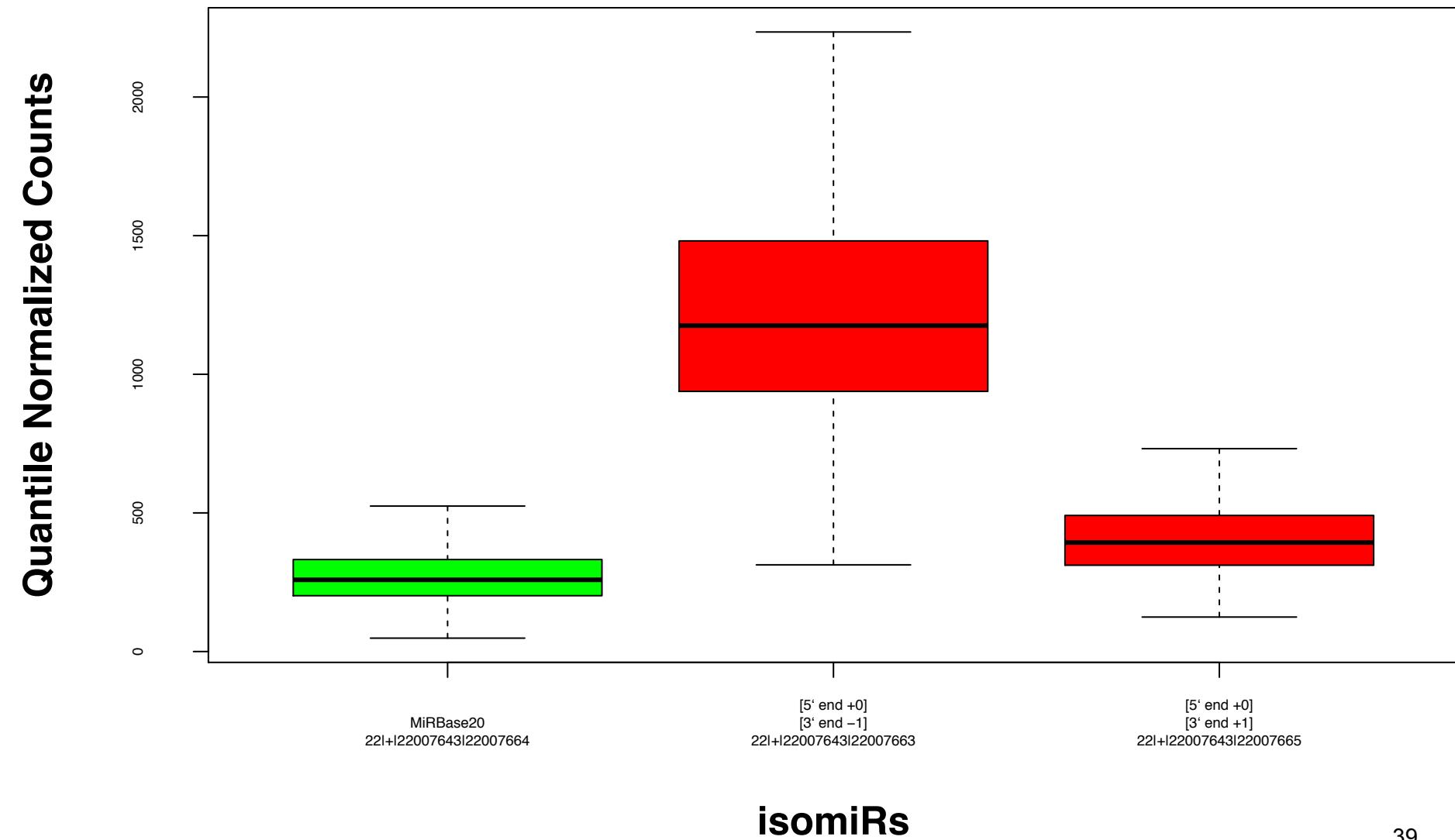
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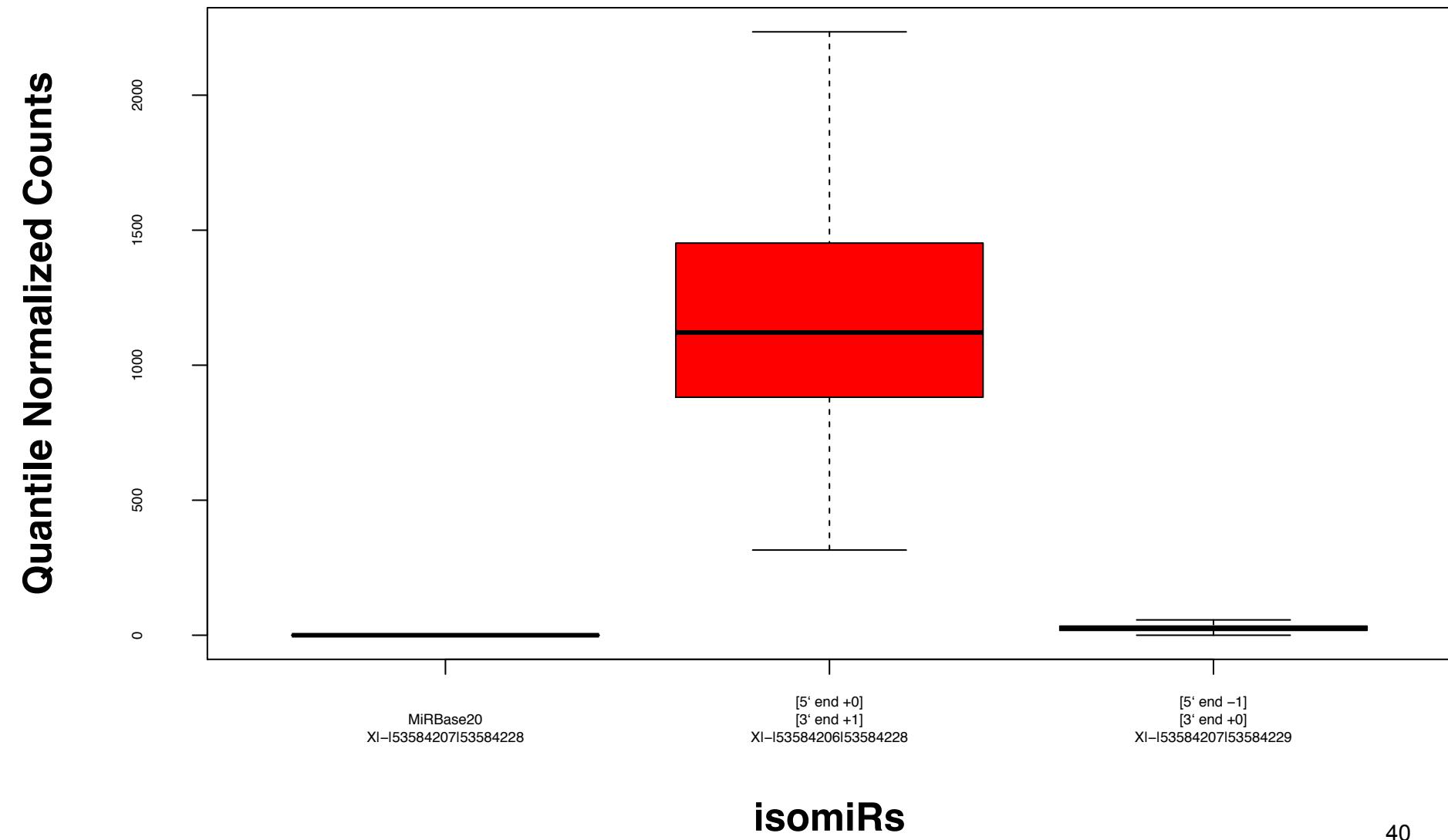
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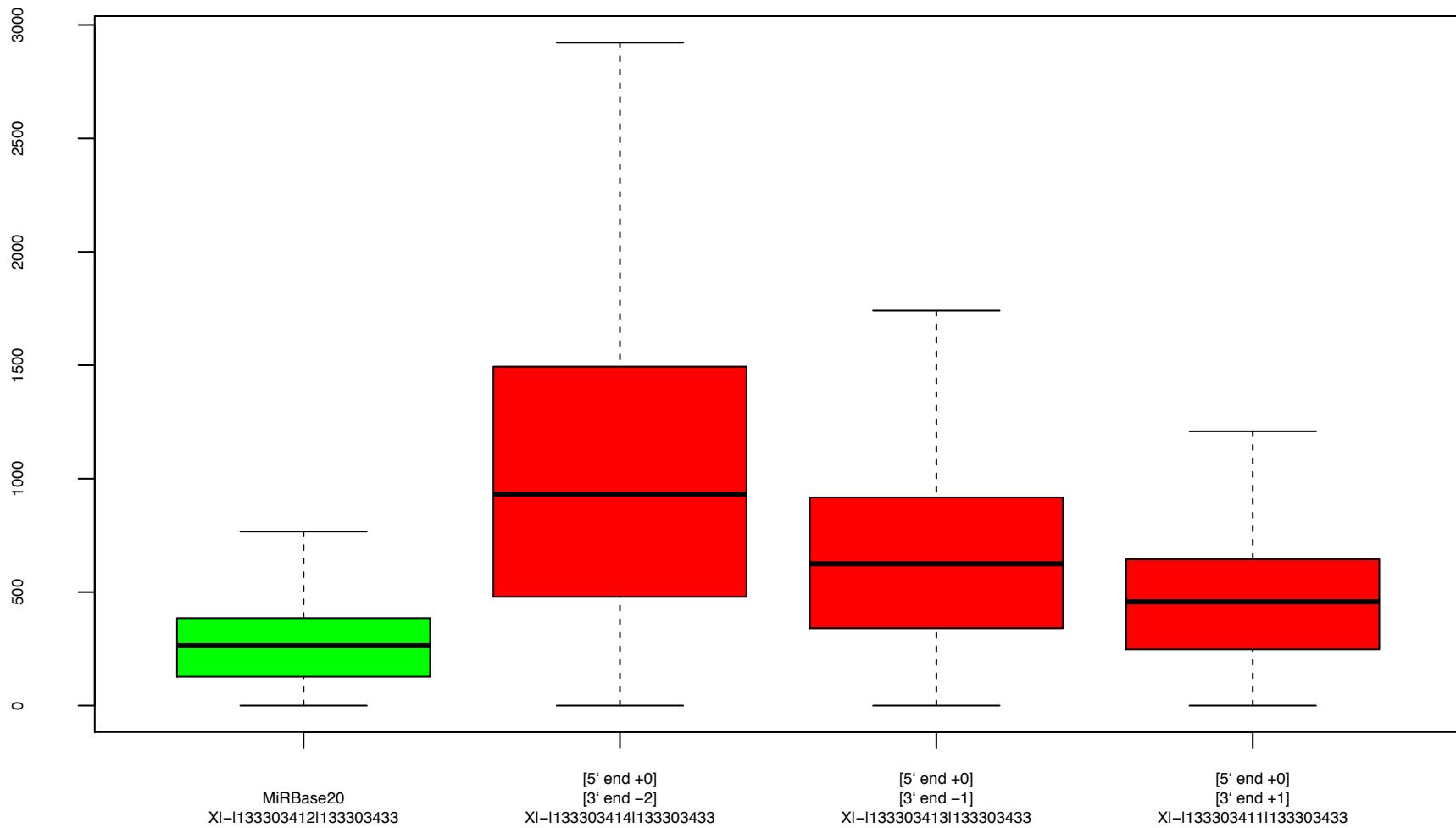


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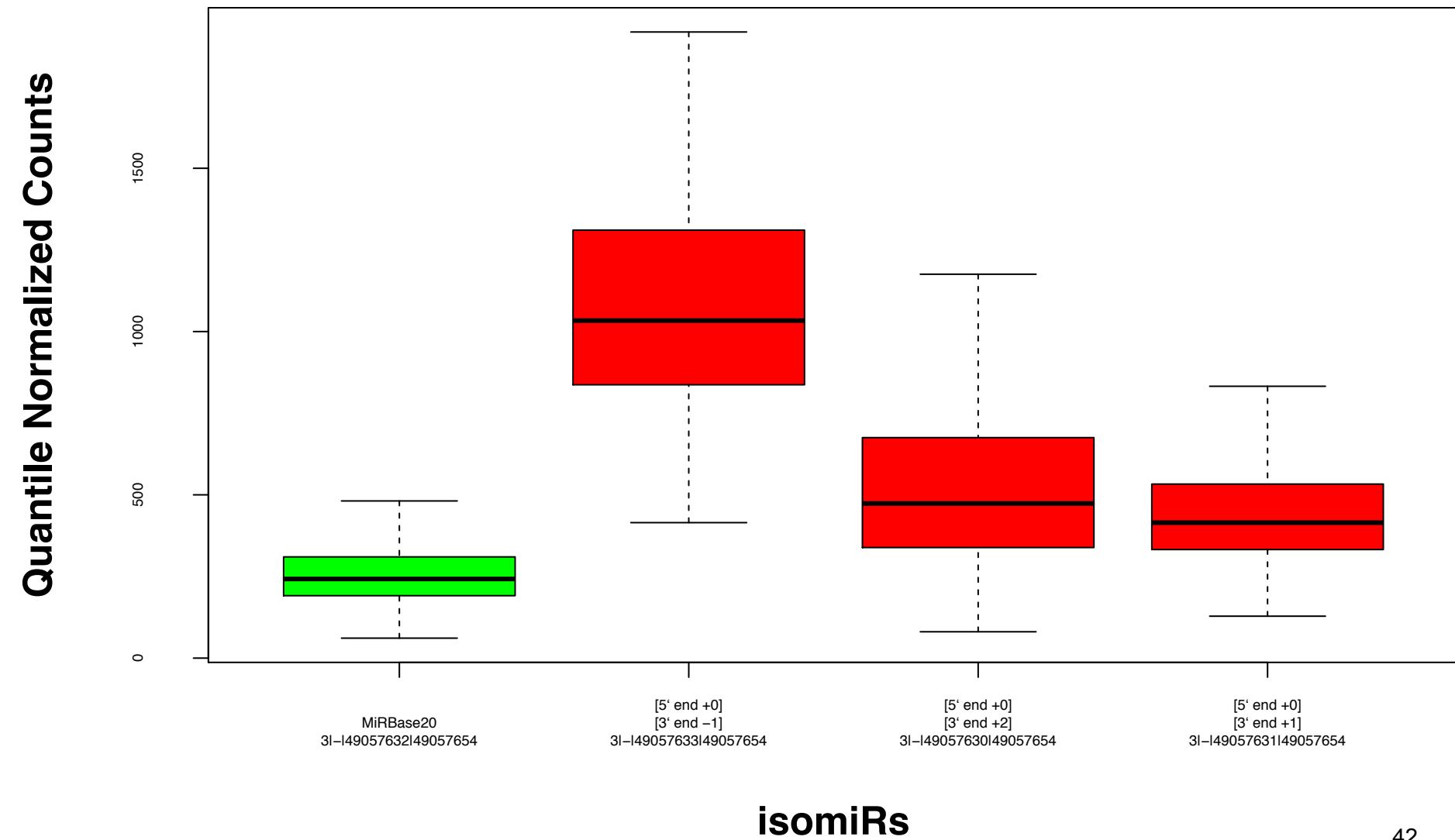
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Quantile Normalized Counts



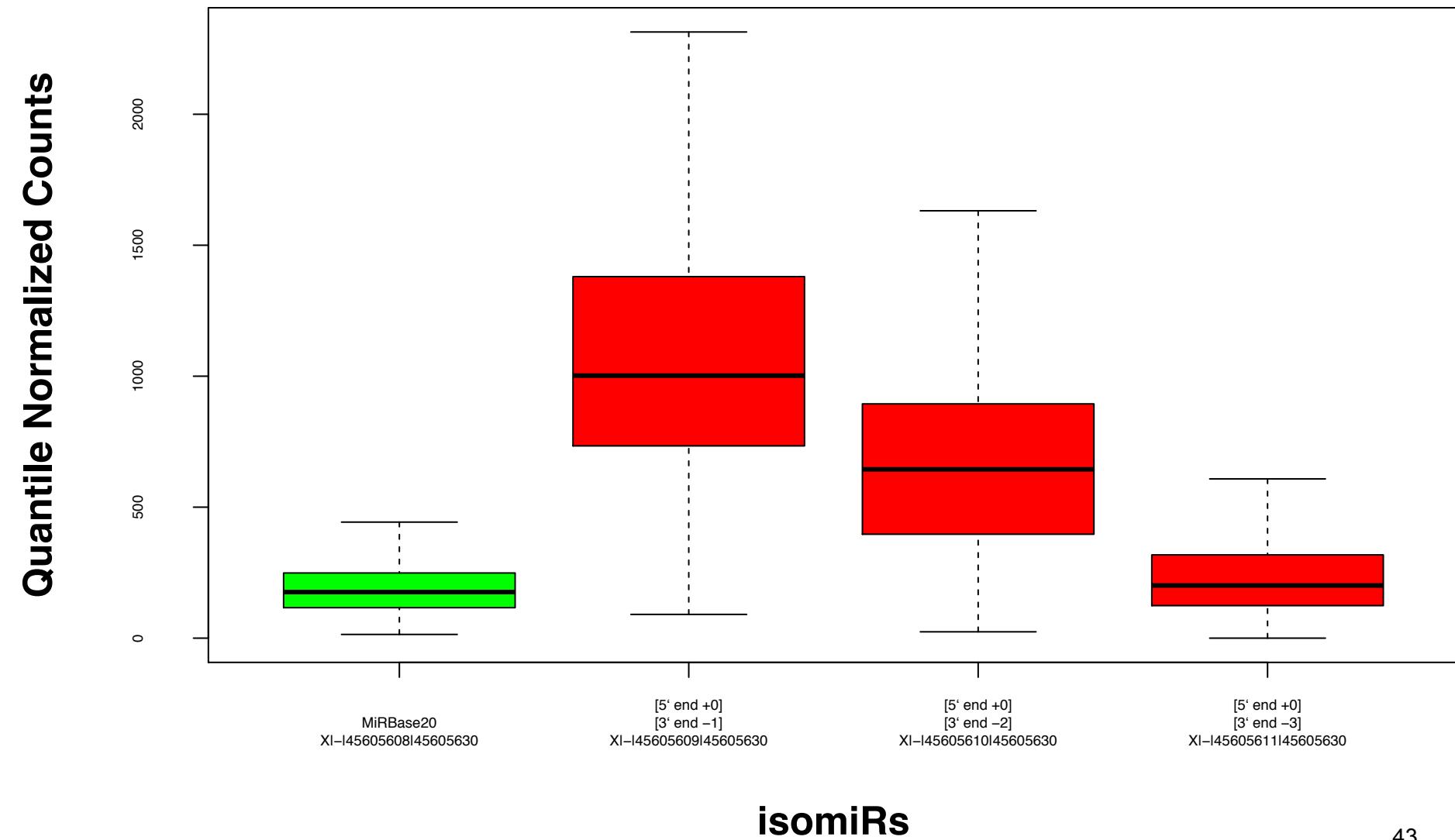
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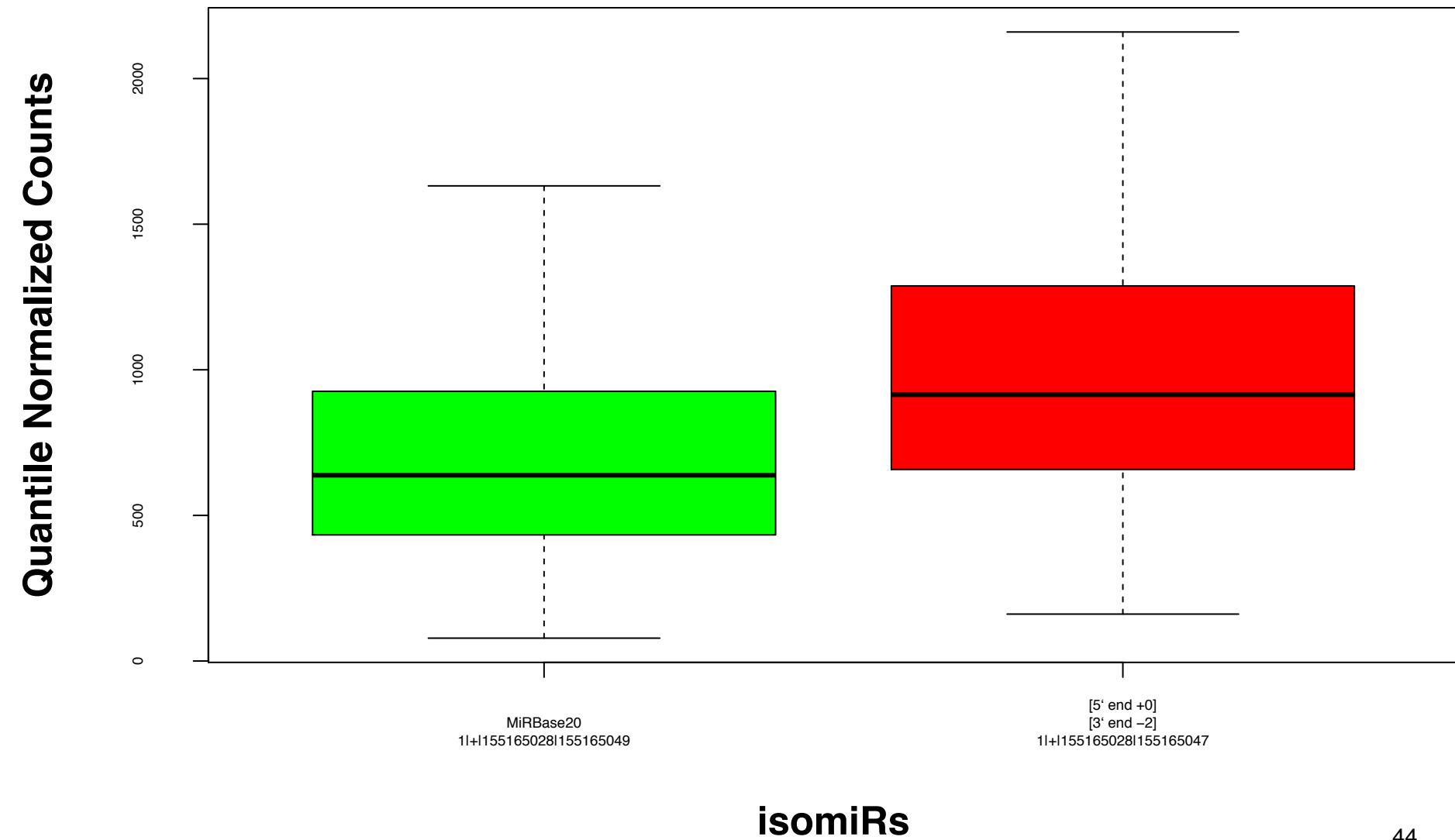


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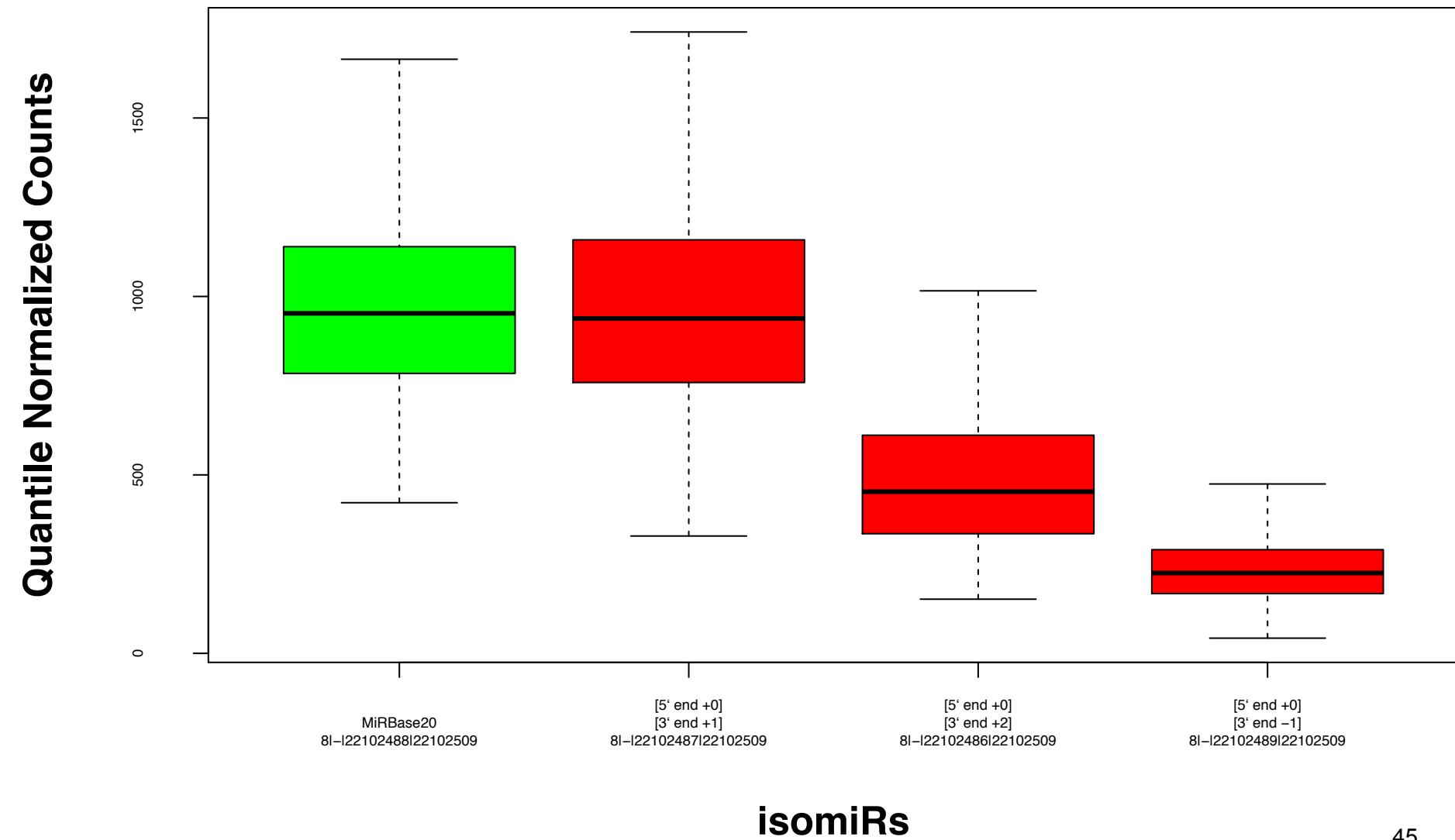


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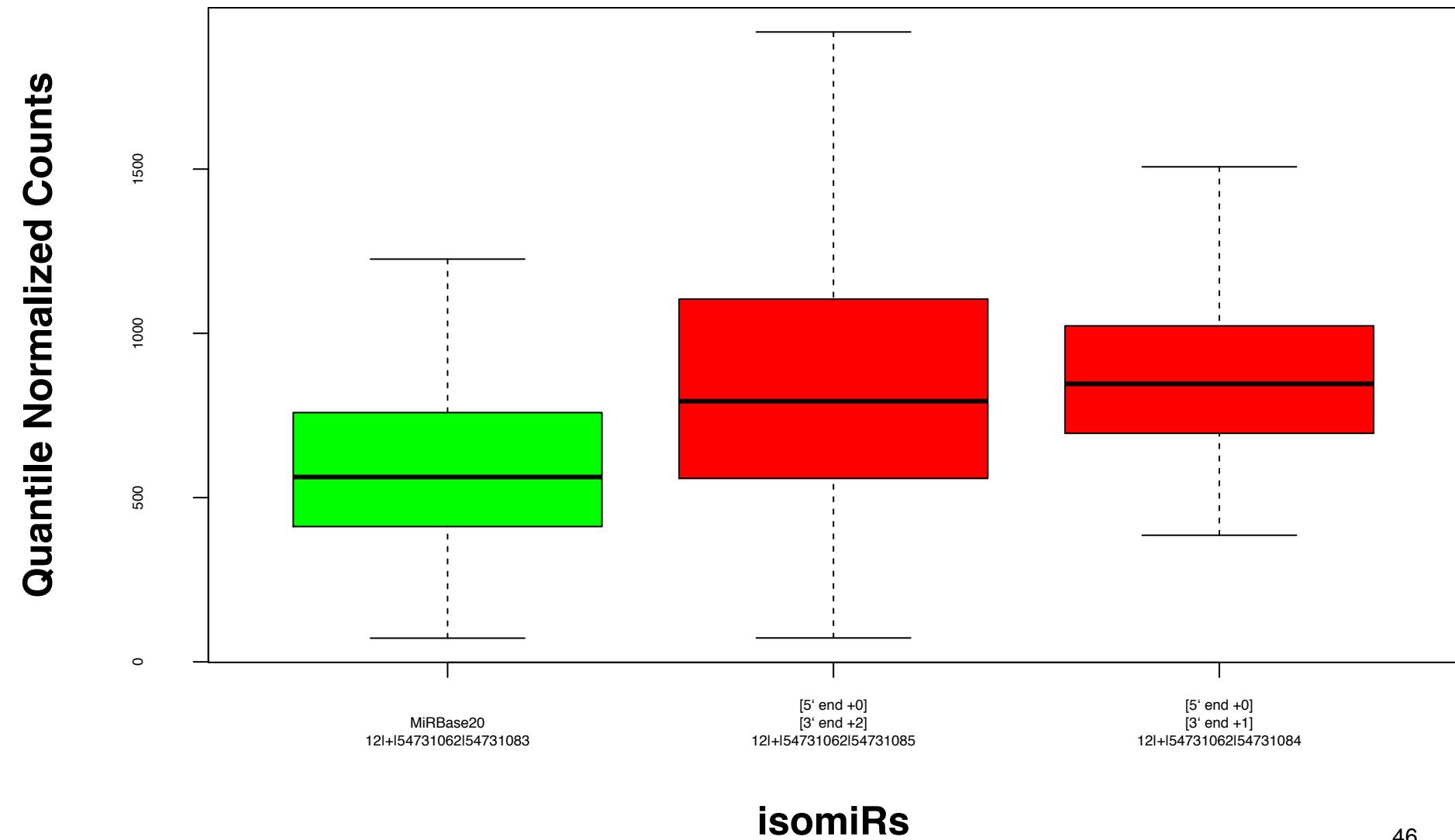


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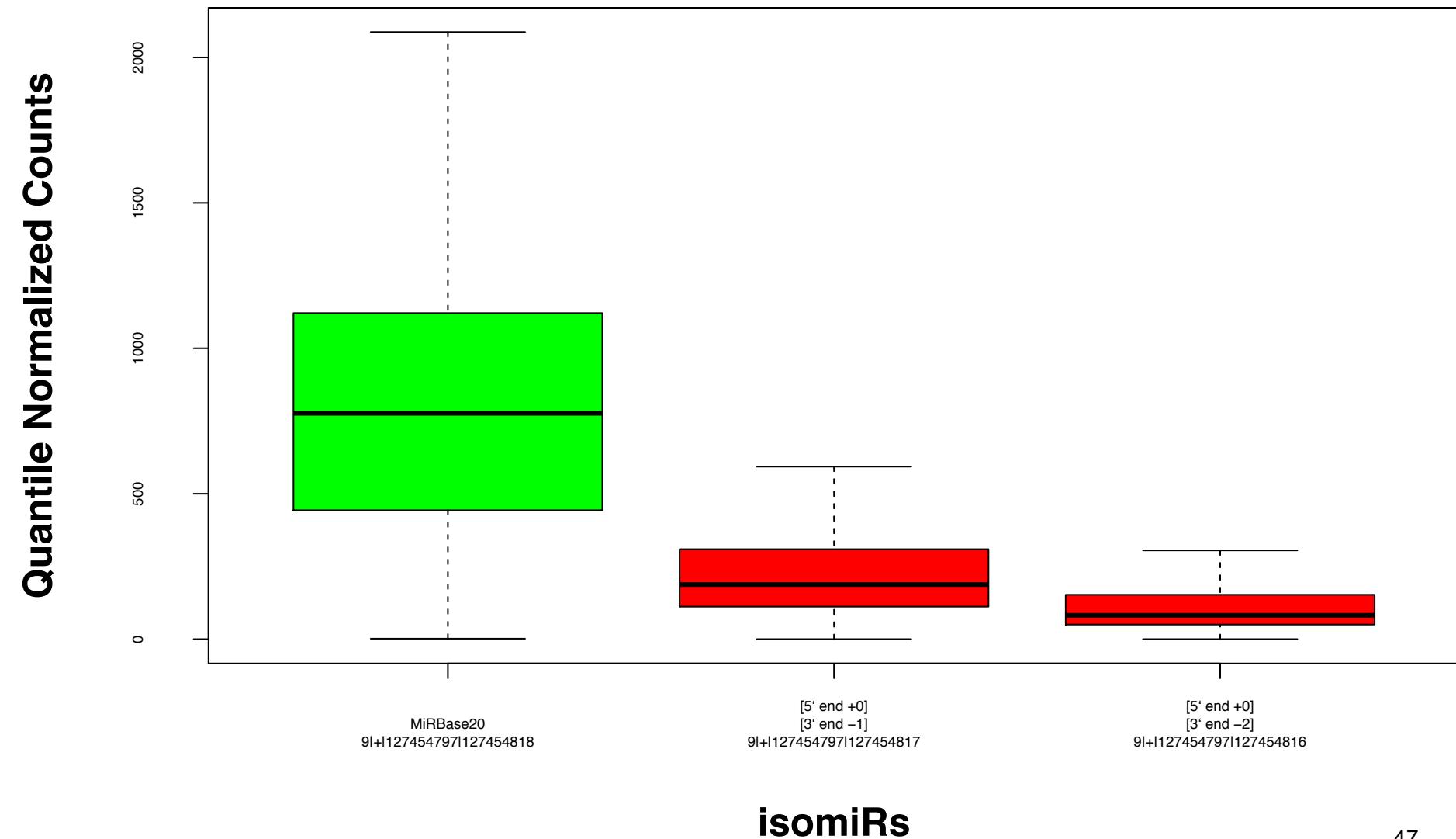
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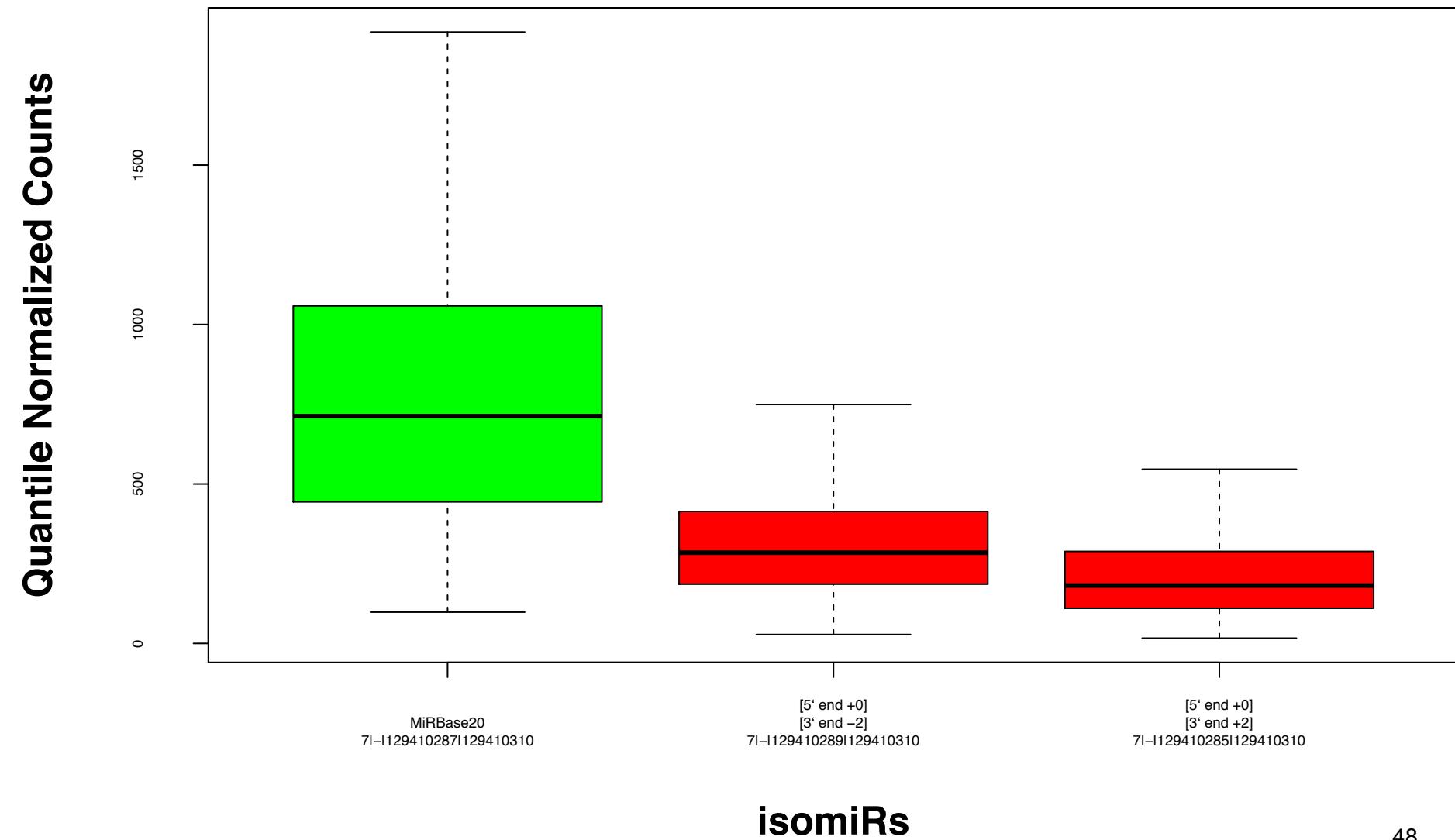
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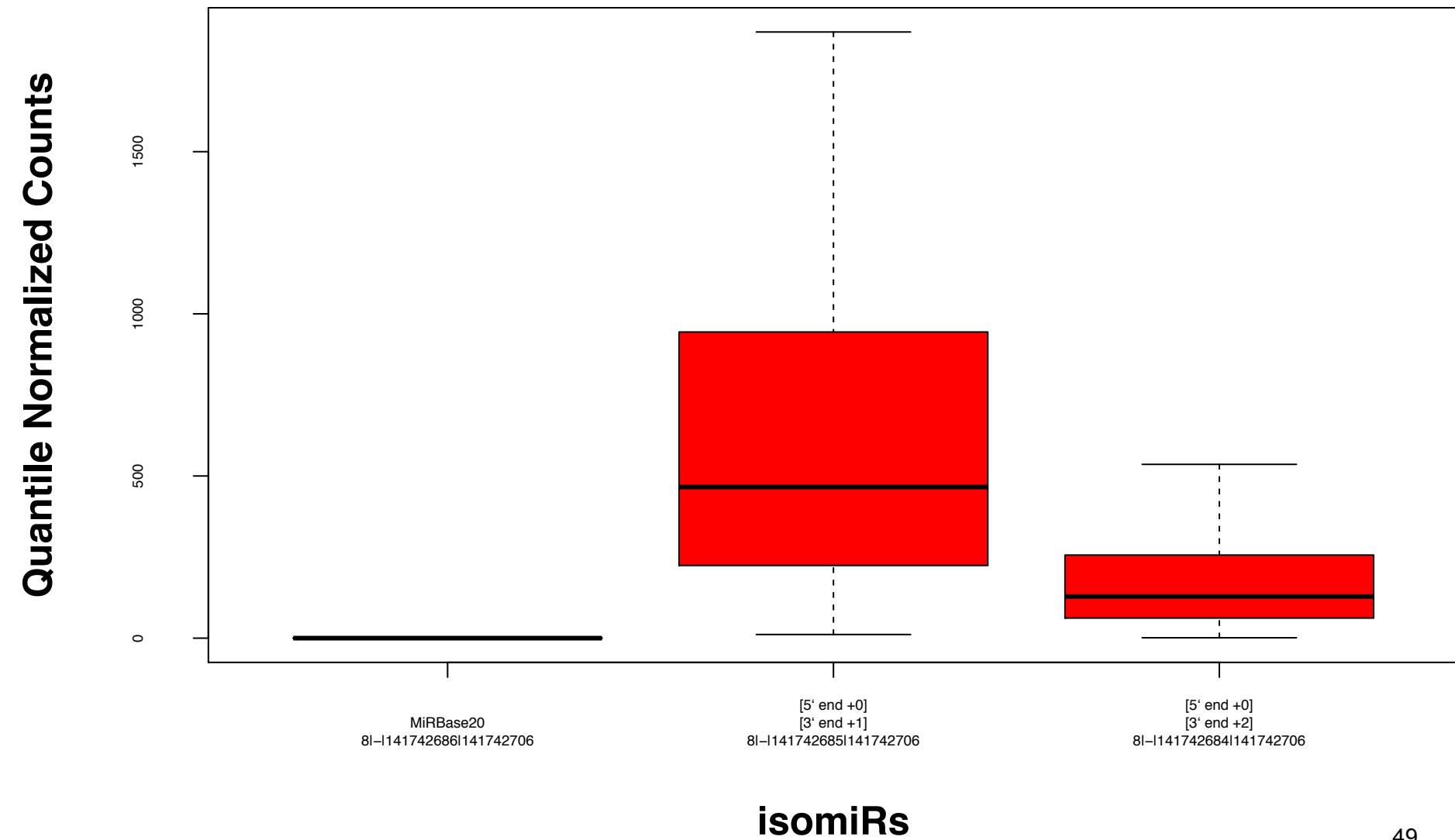
Supp. Figure 1
(pages 1 to 194) **MIMAT0004558=hsa-miR-181a-2-3p=MI0000269**



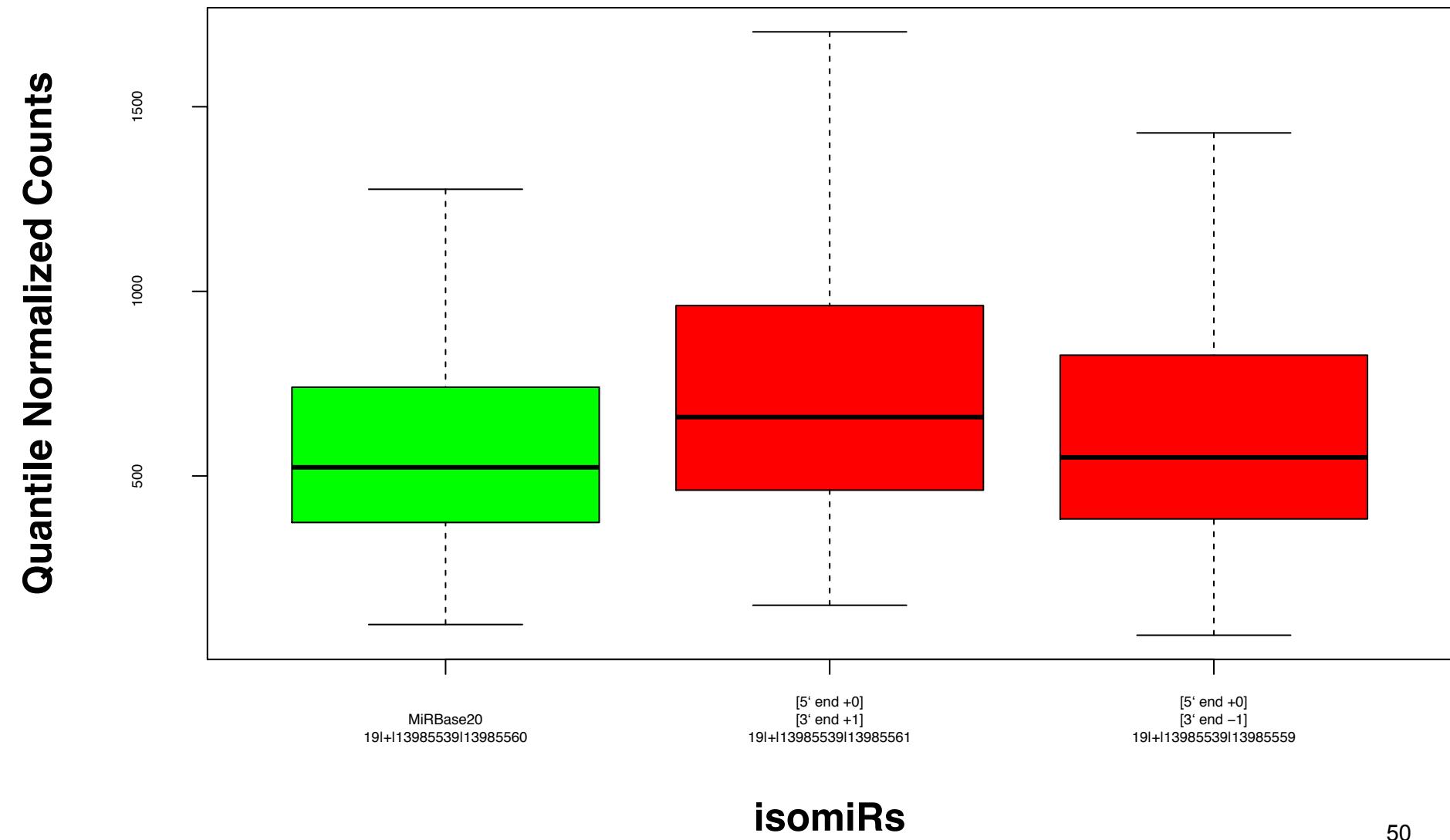
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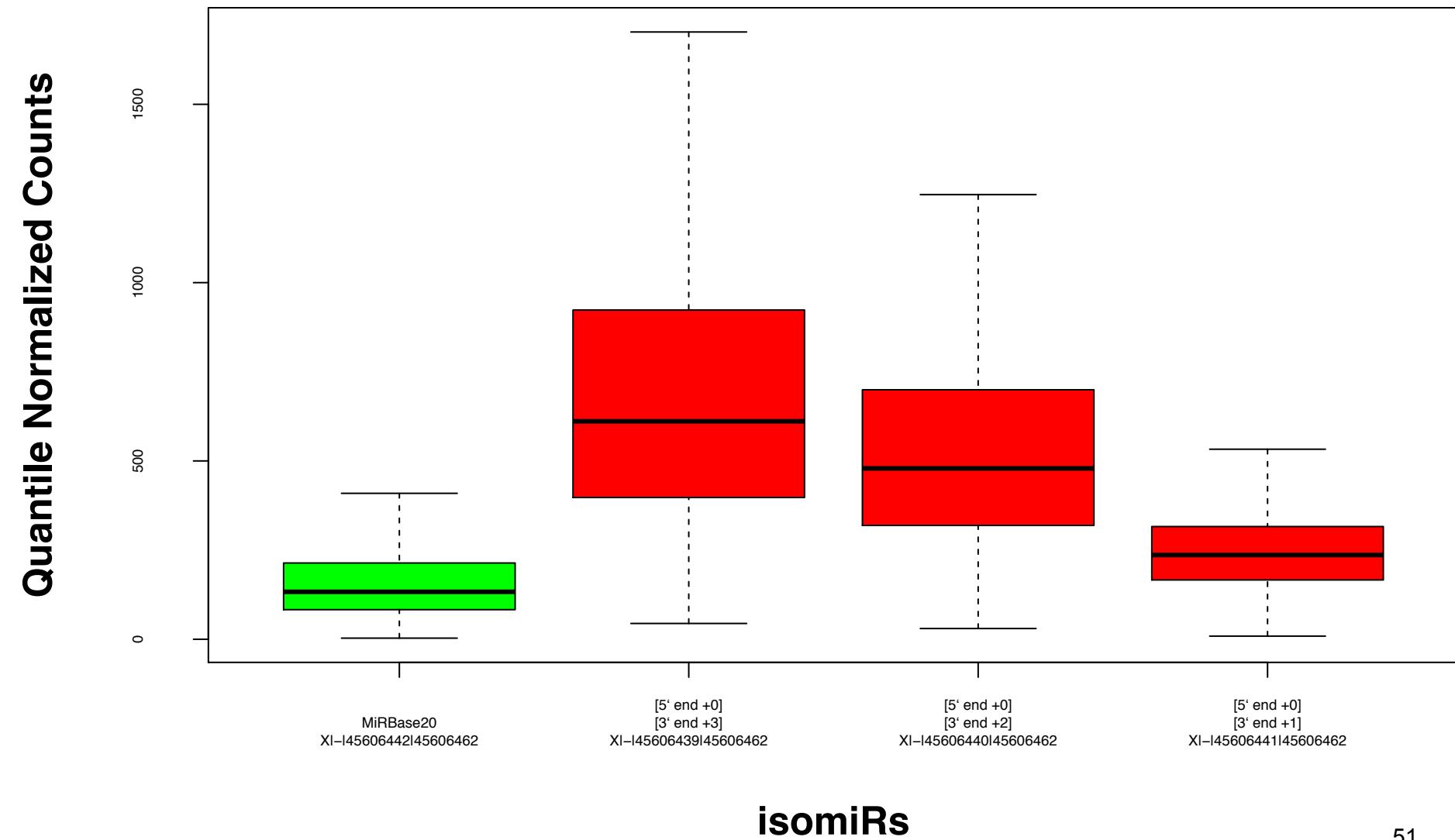


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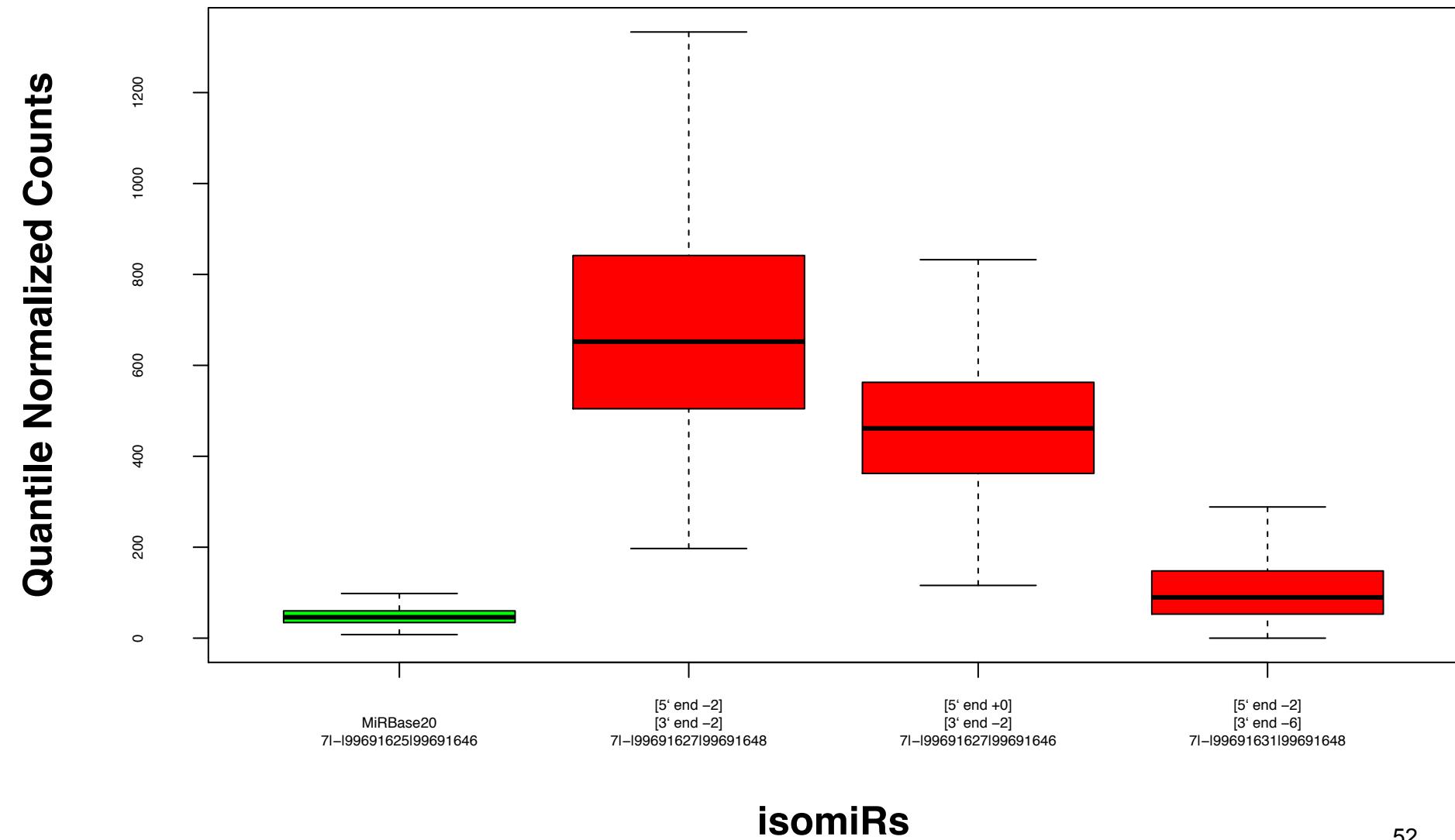


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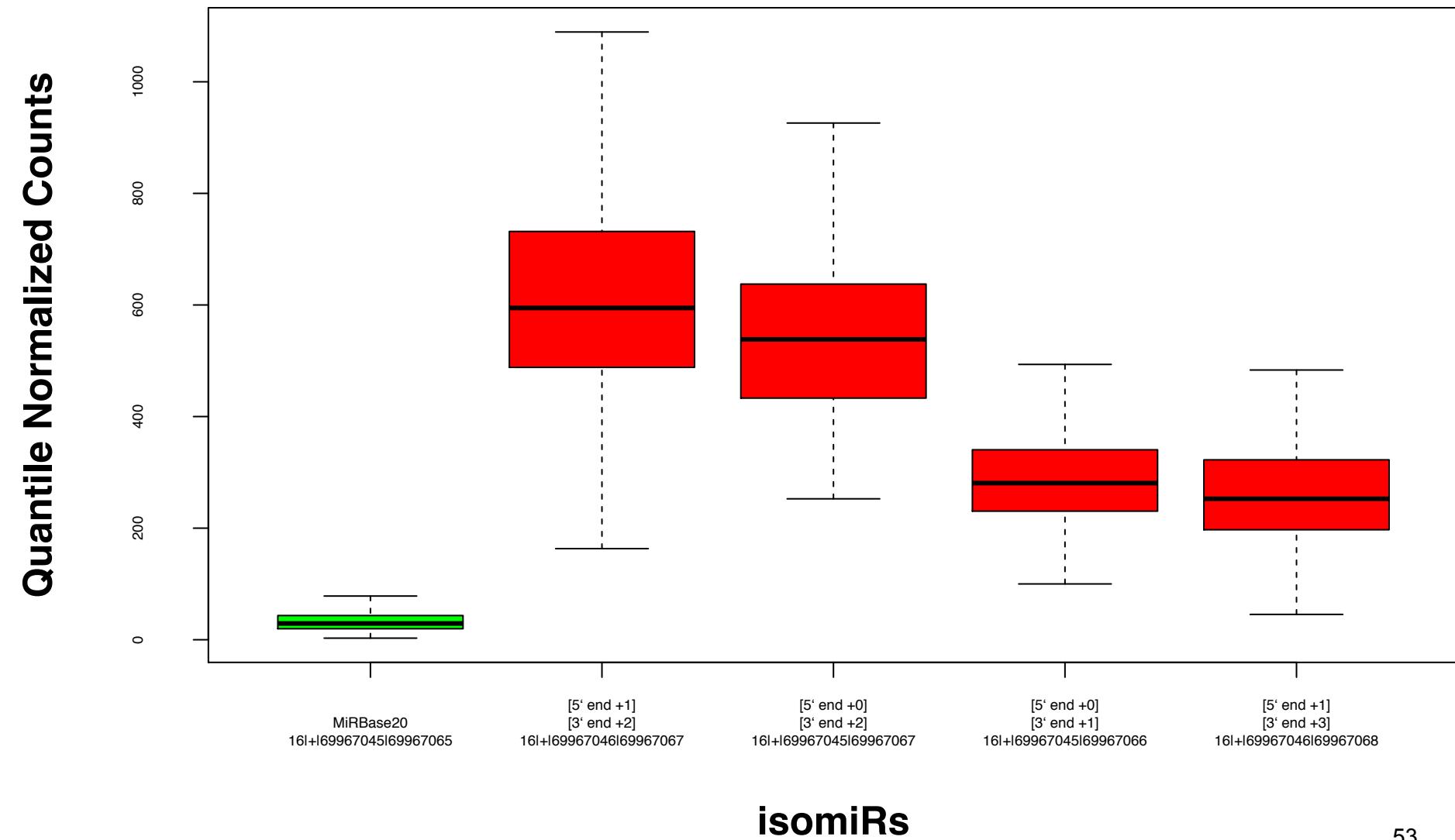
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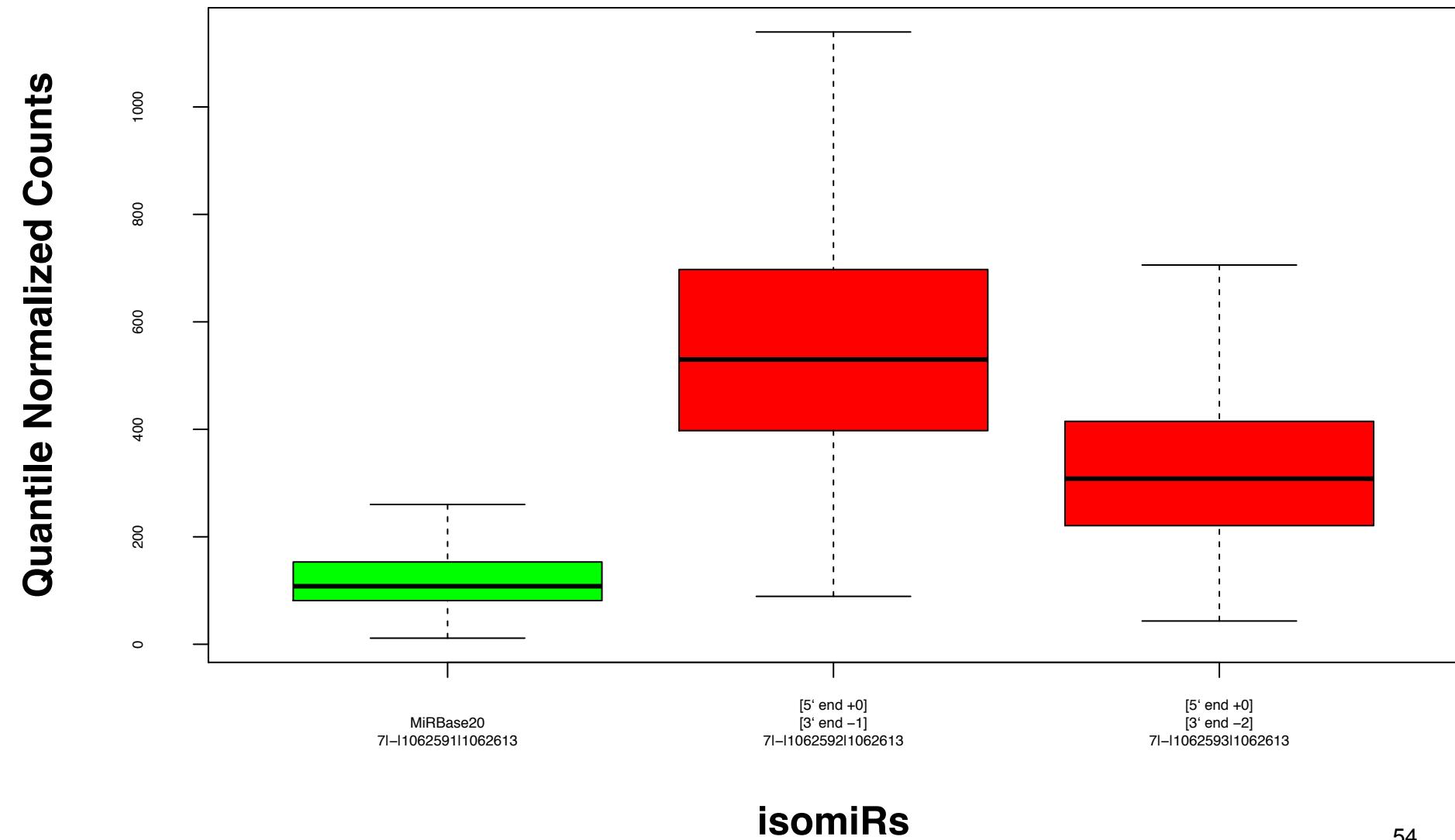
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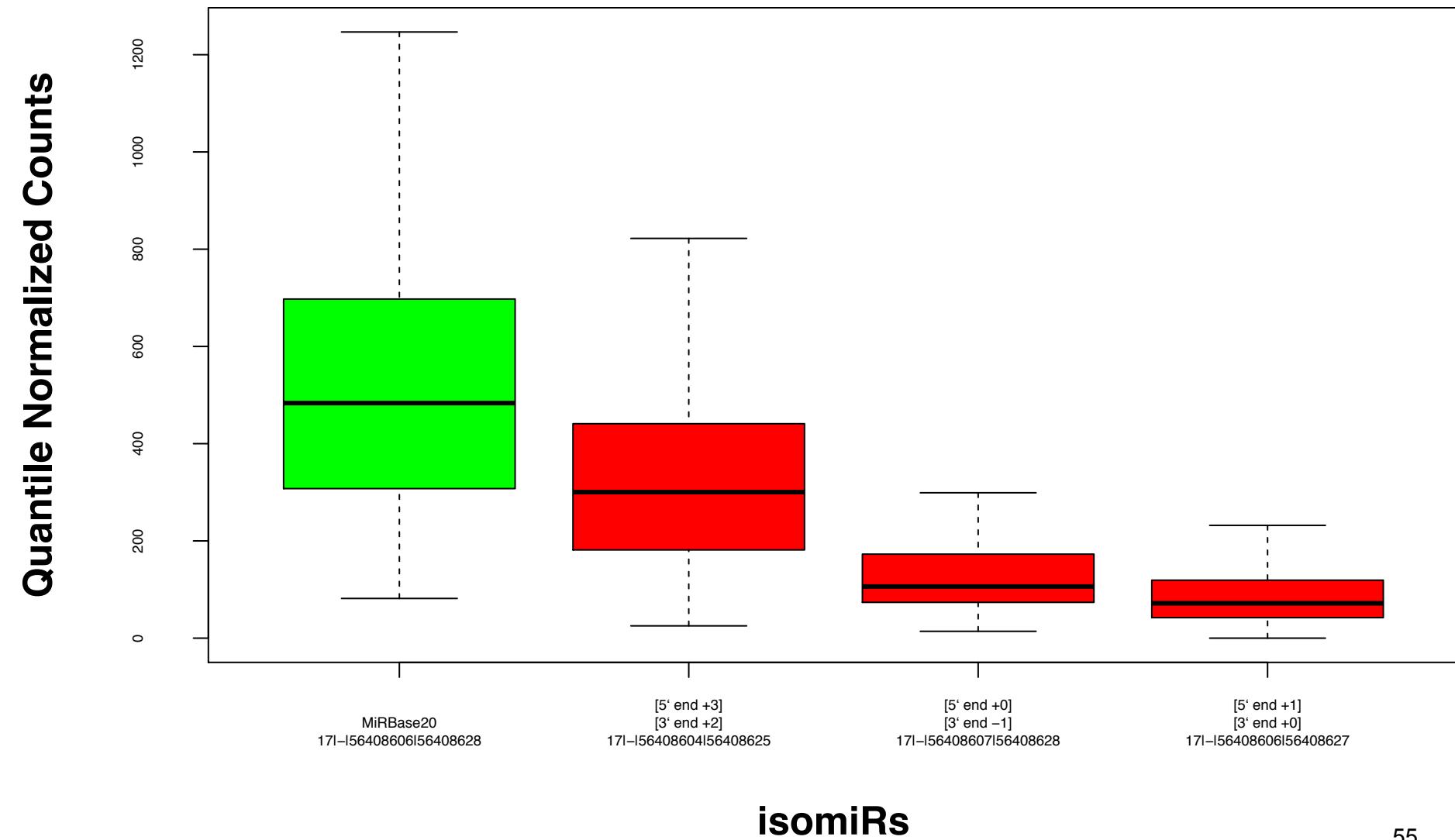
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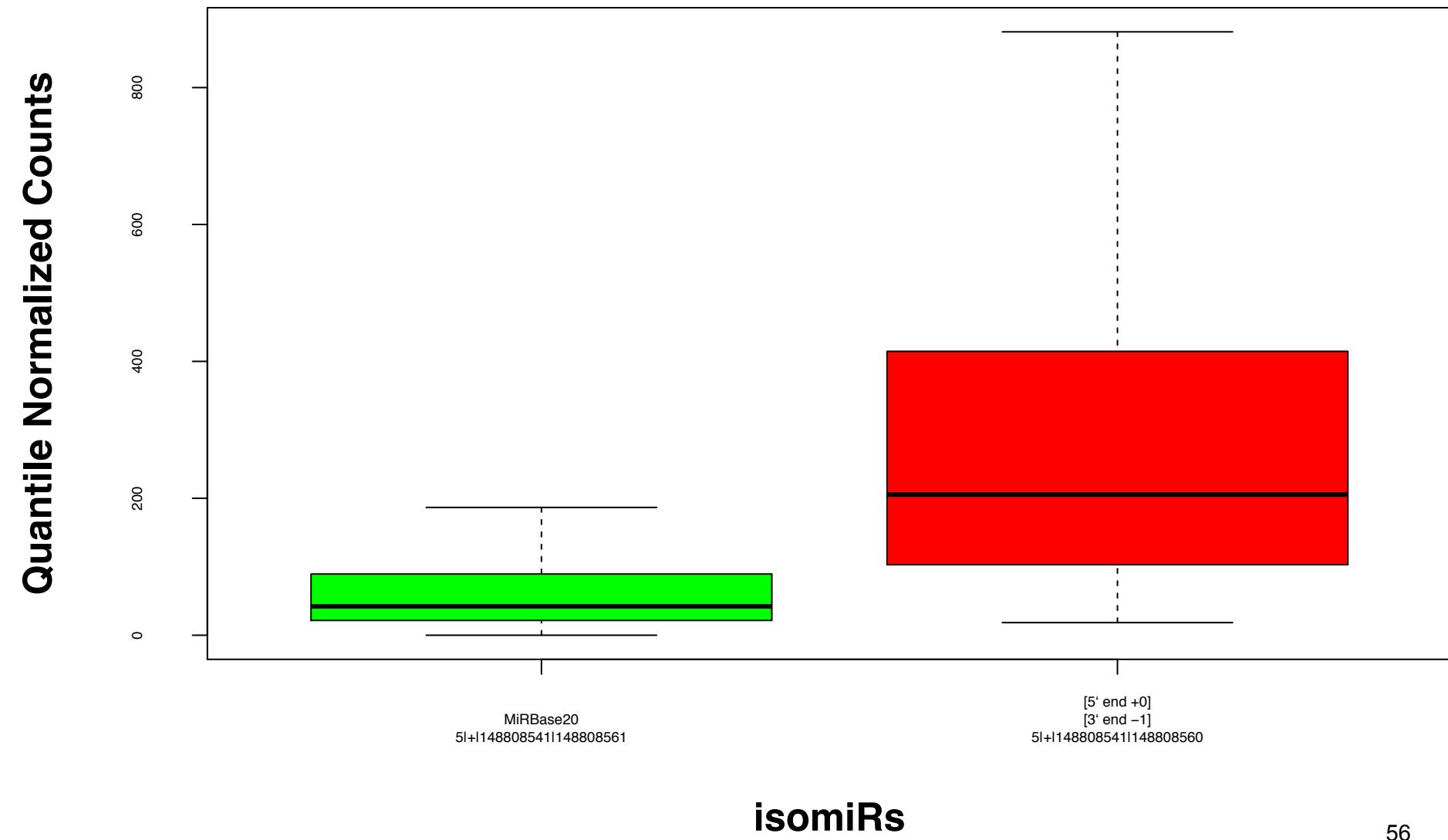
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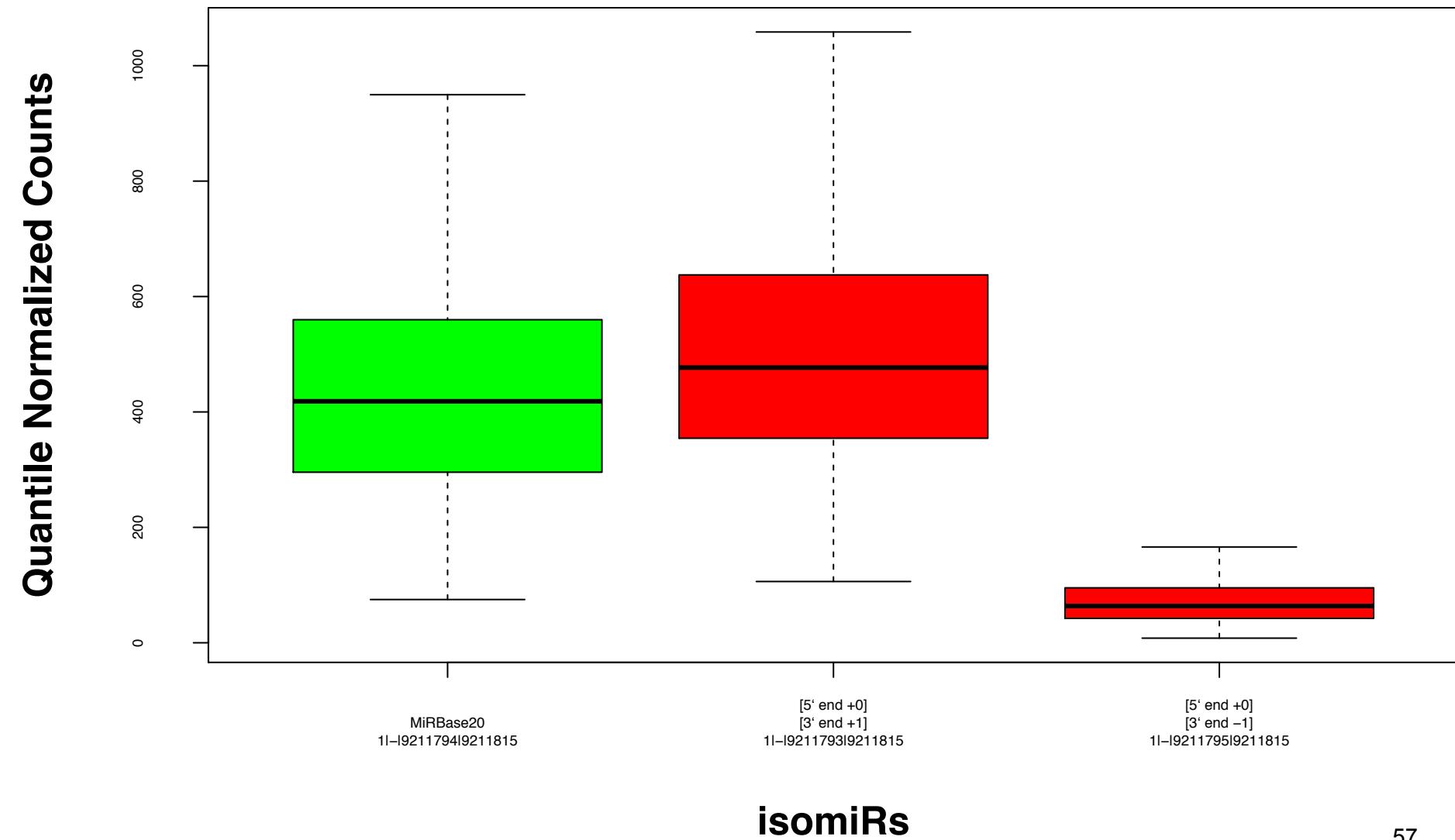
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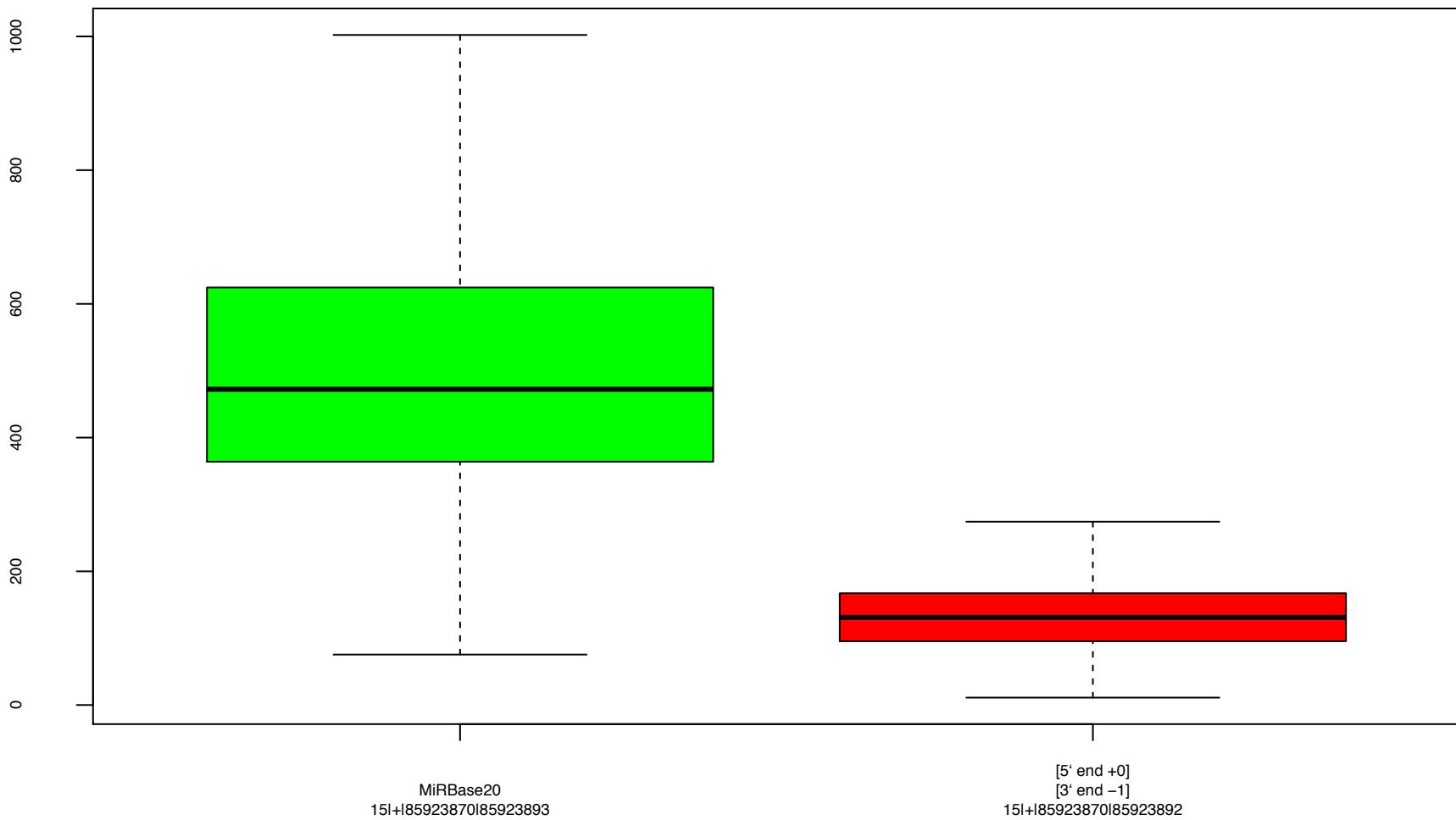


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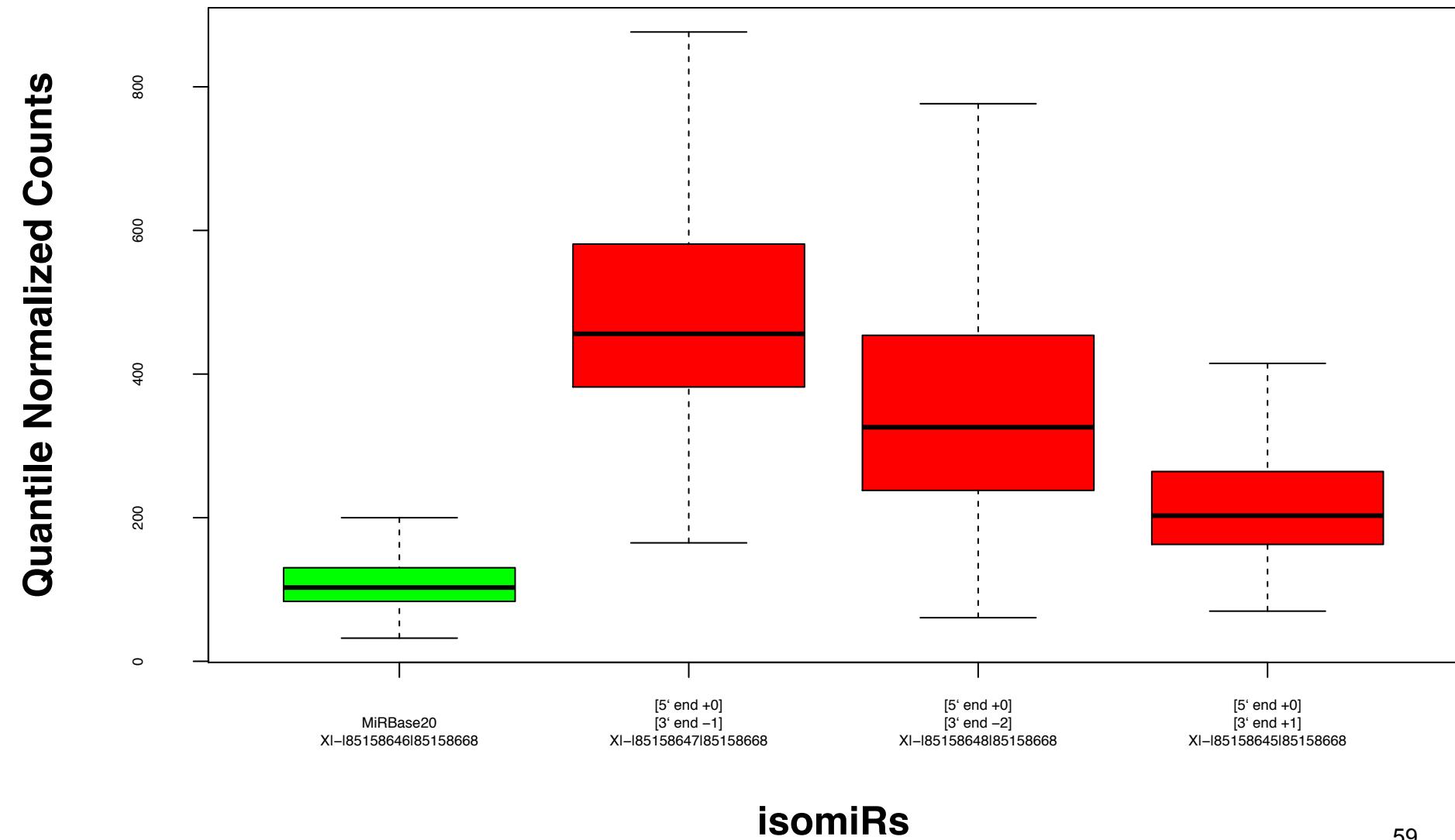
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Quantile Normalized Counts

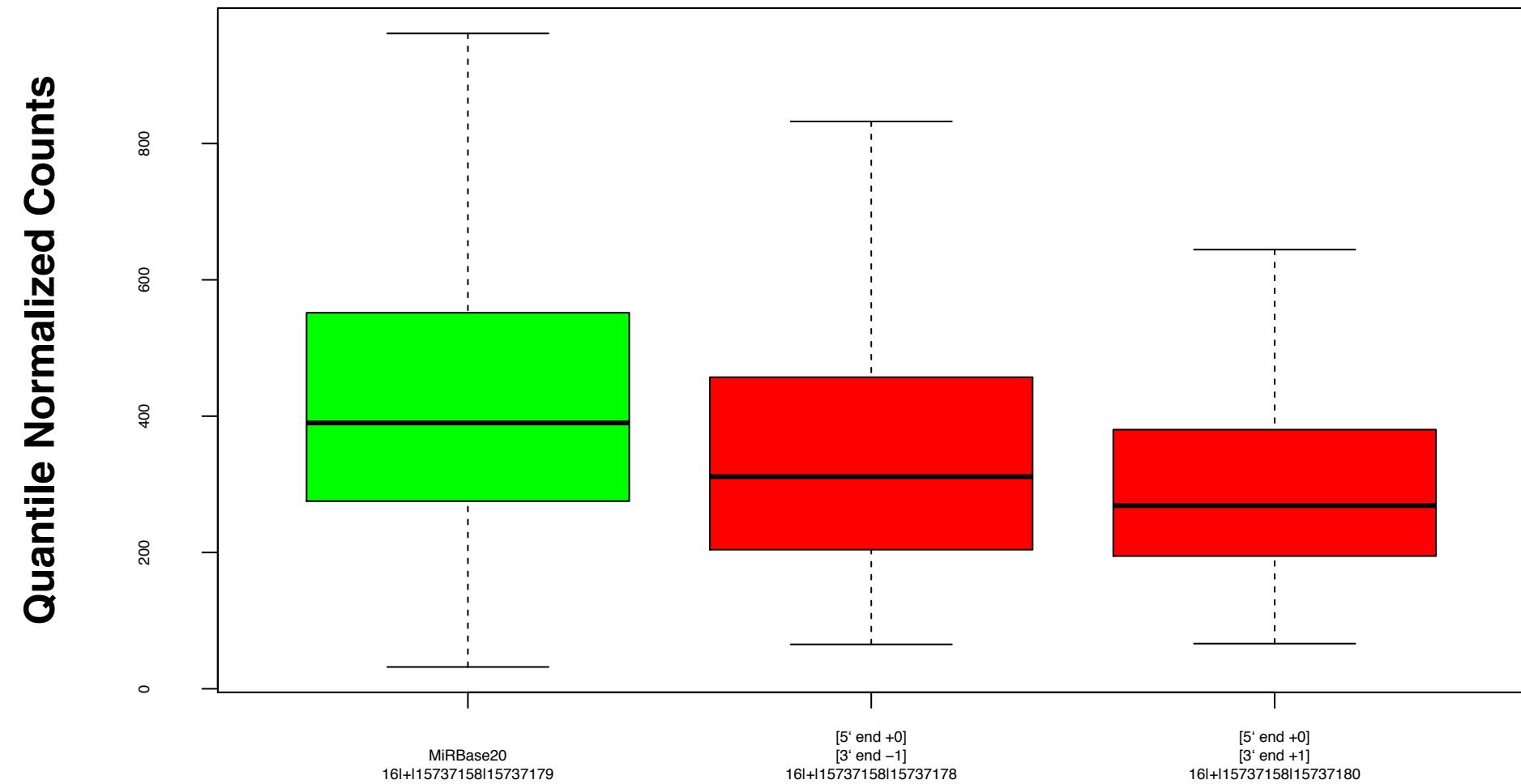


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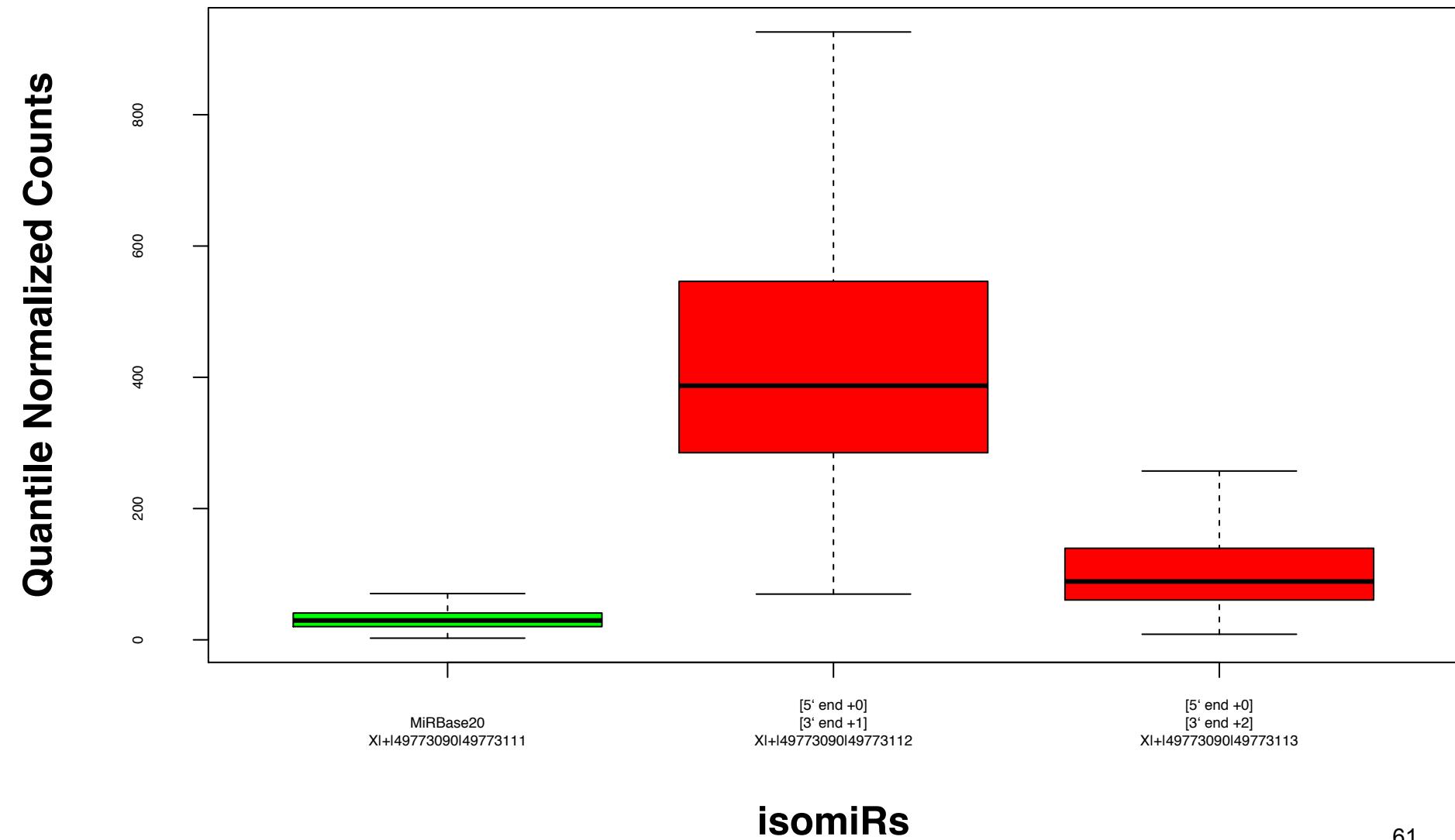
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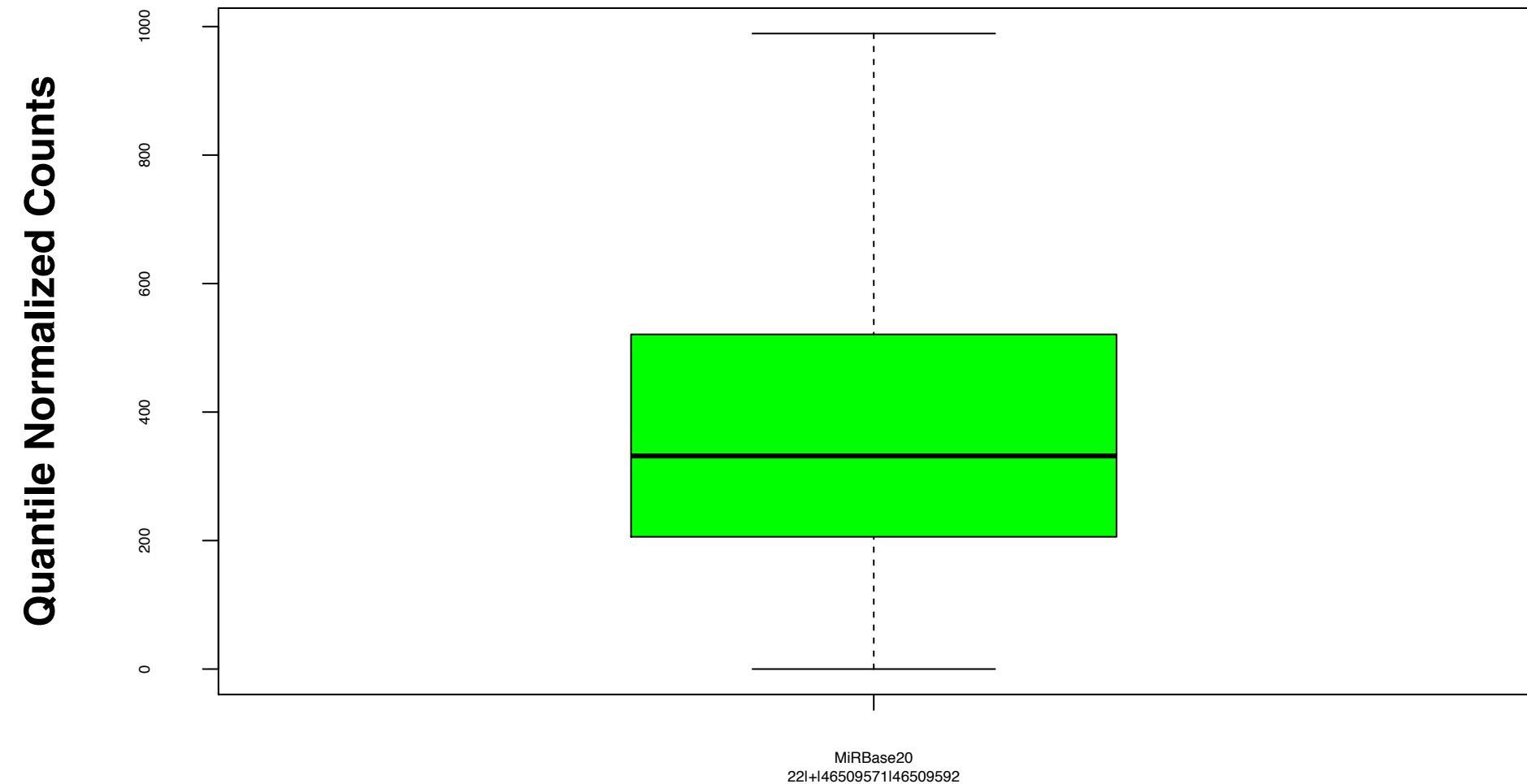


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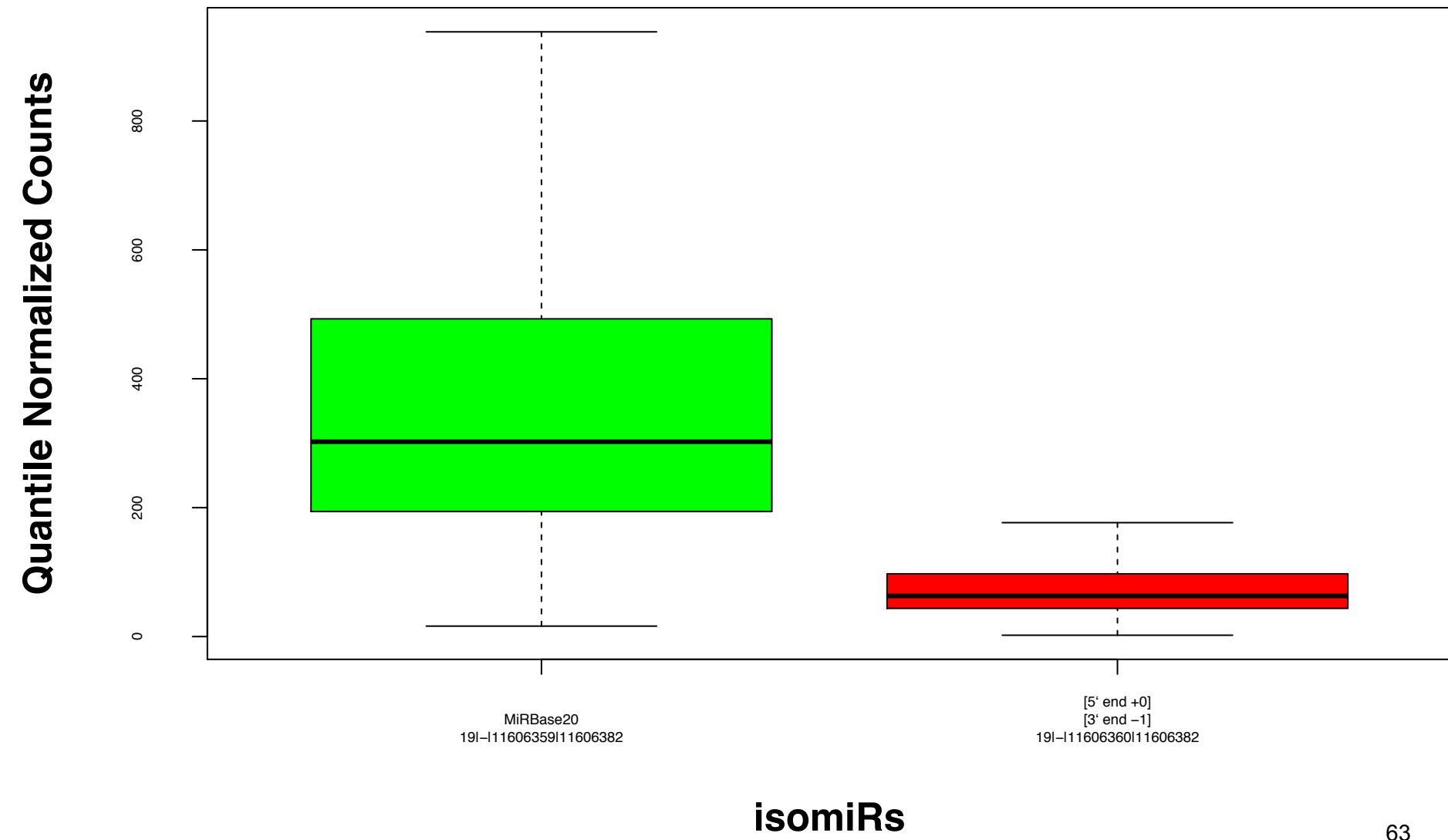


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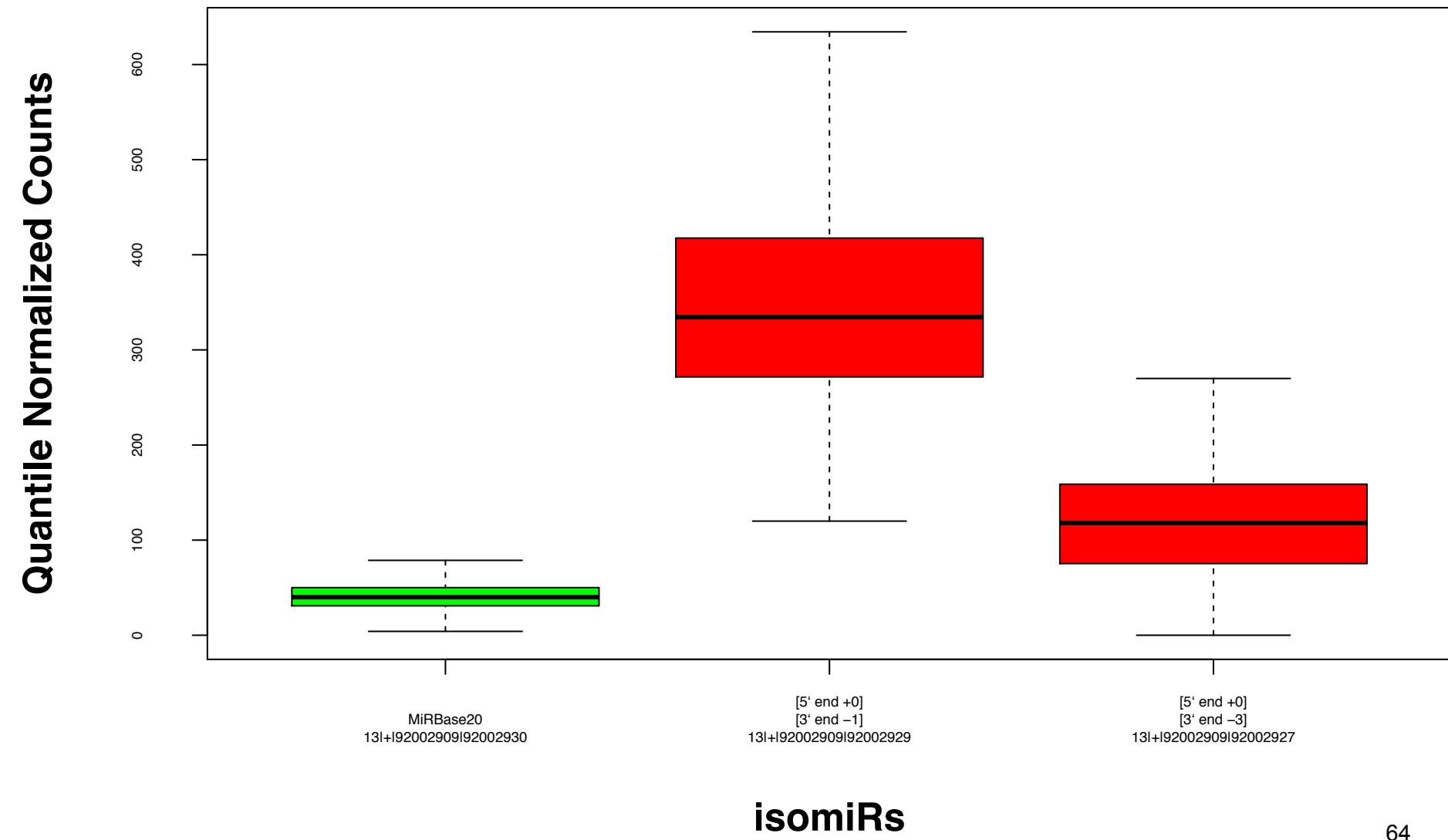
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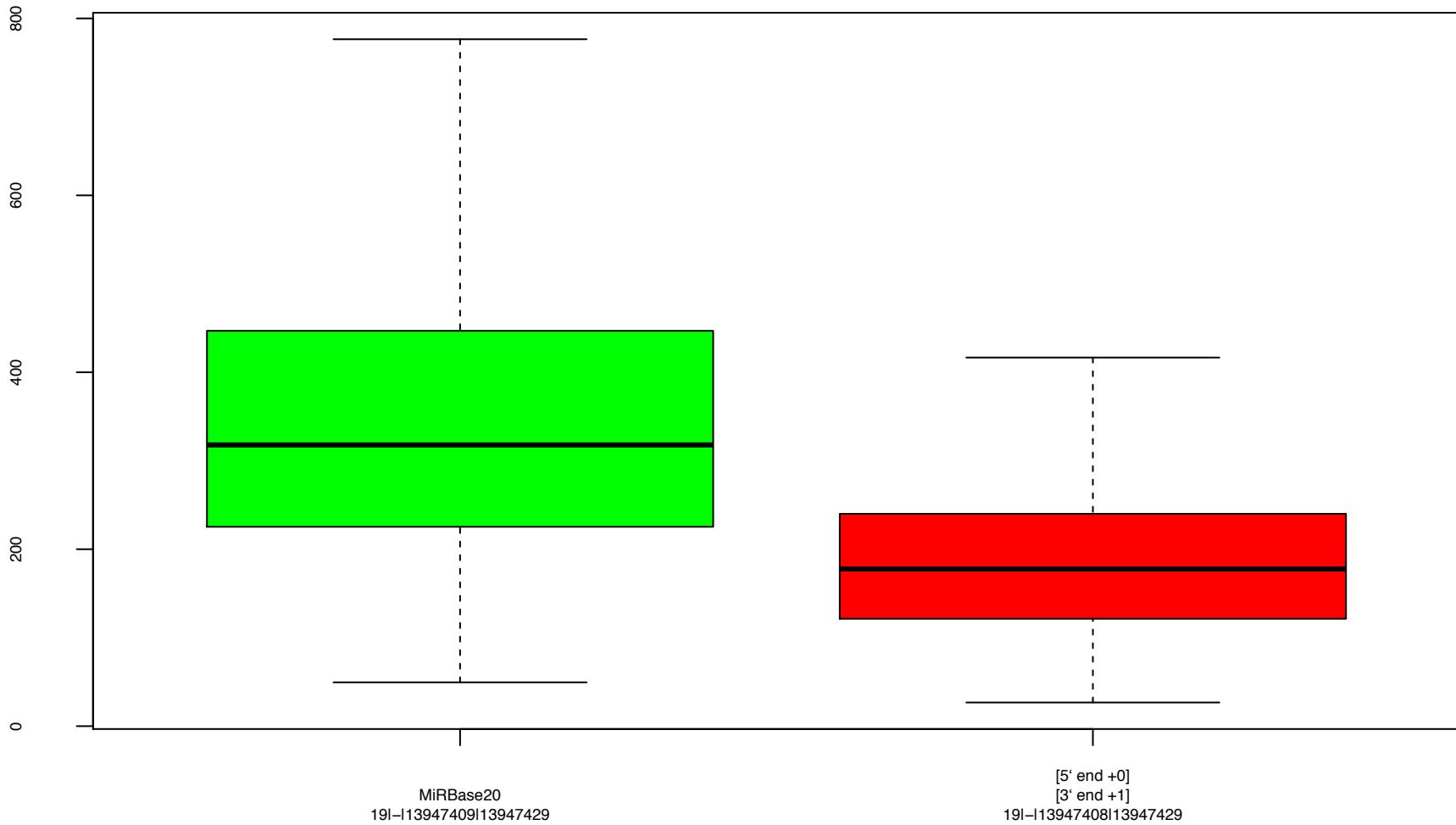


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Quantile Normalized Counts

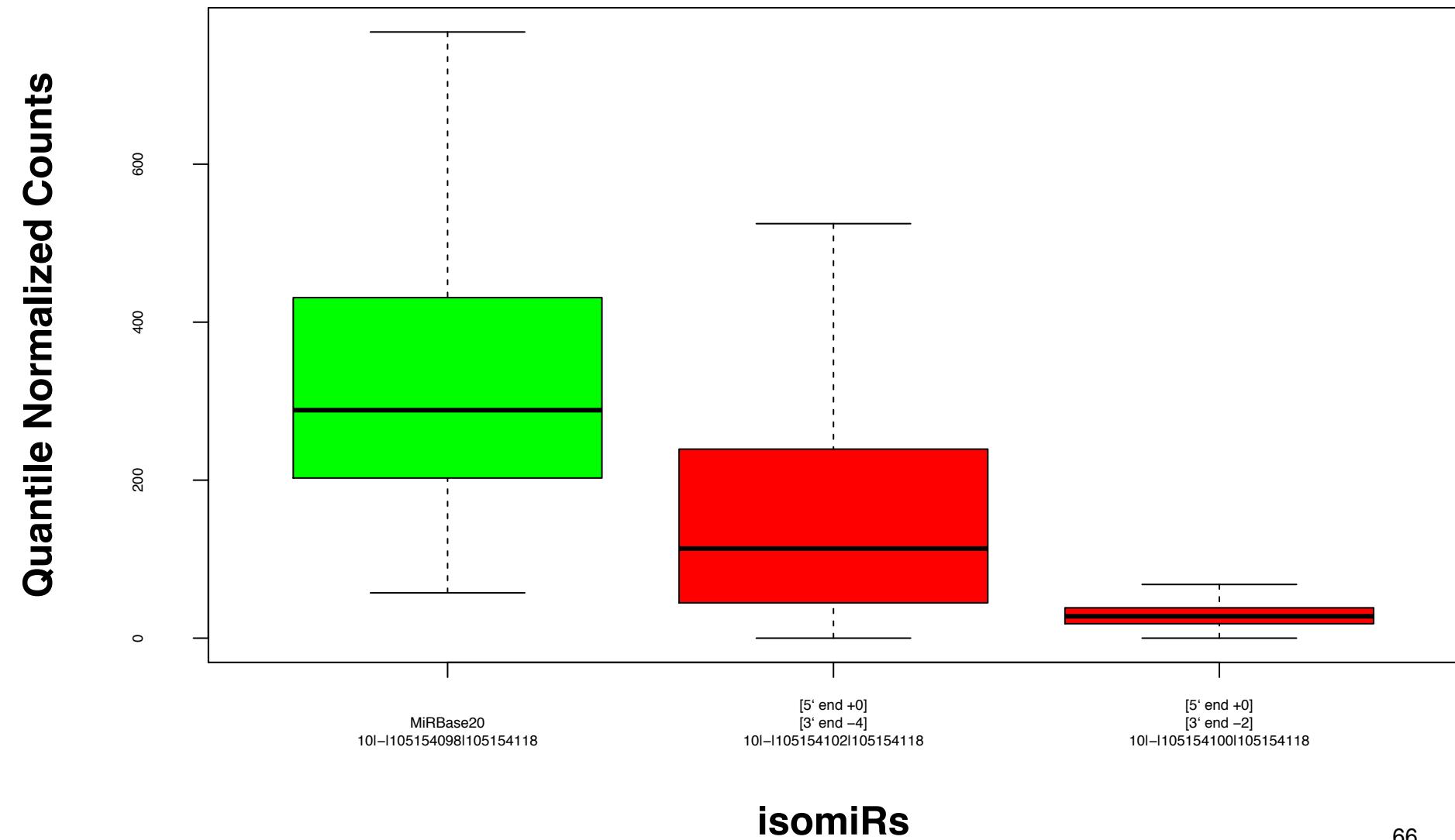


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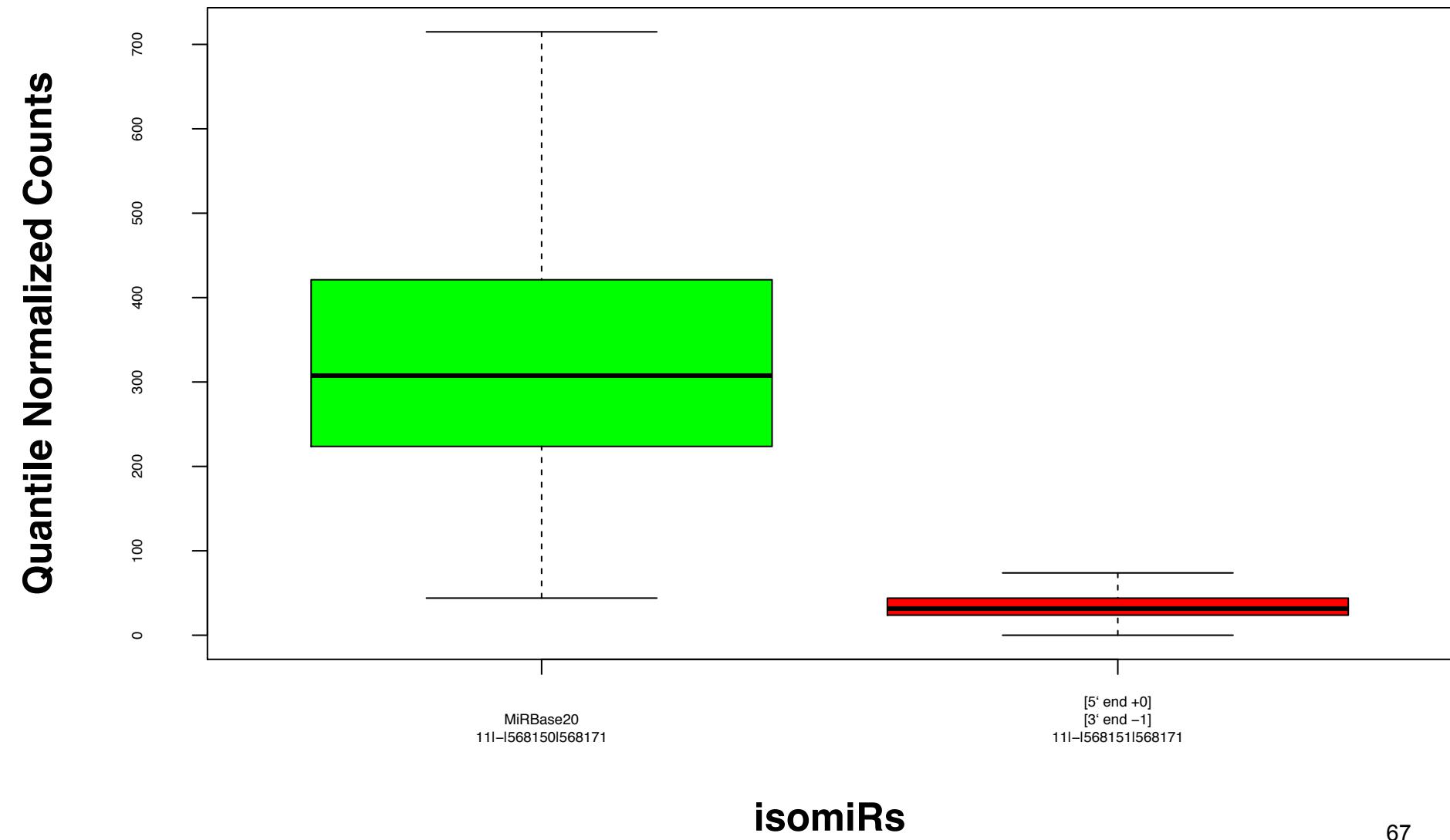
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isomiRs

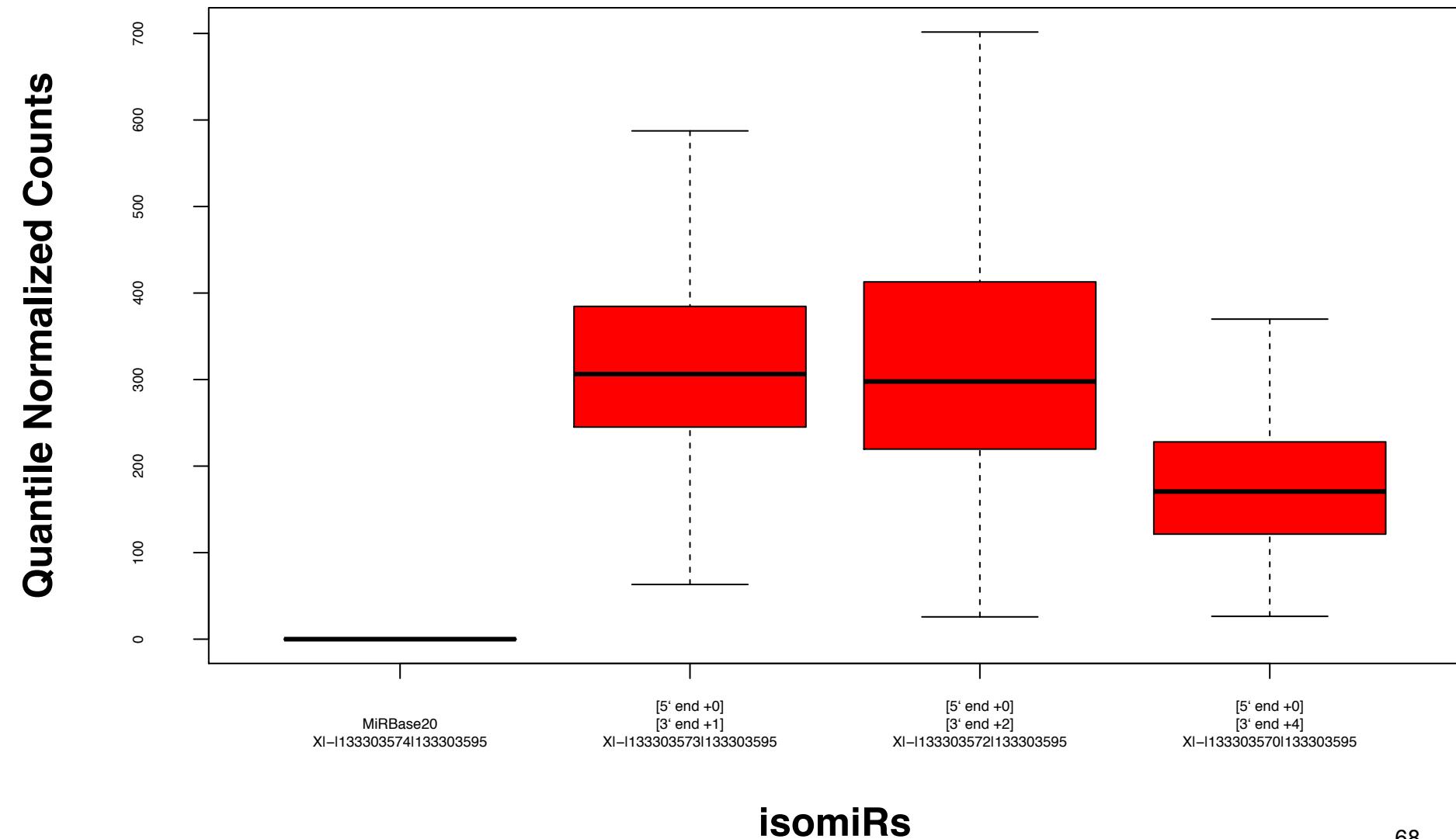
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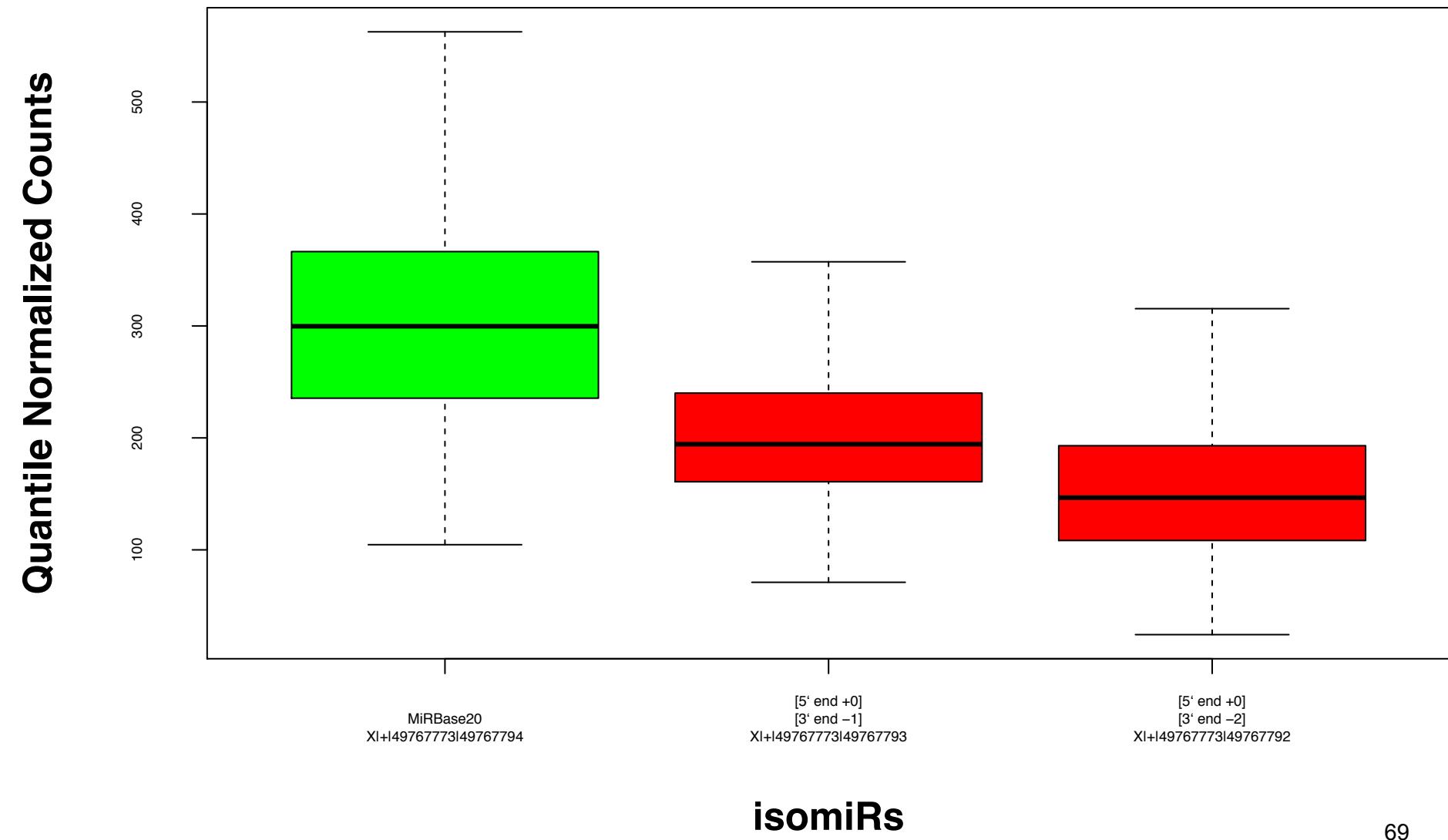
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MIMAT0000092_1=hsa-miR-92a-3p=MI0000094

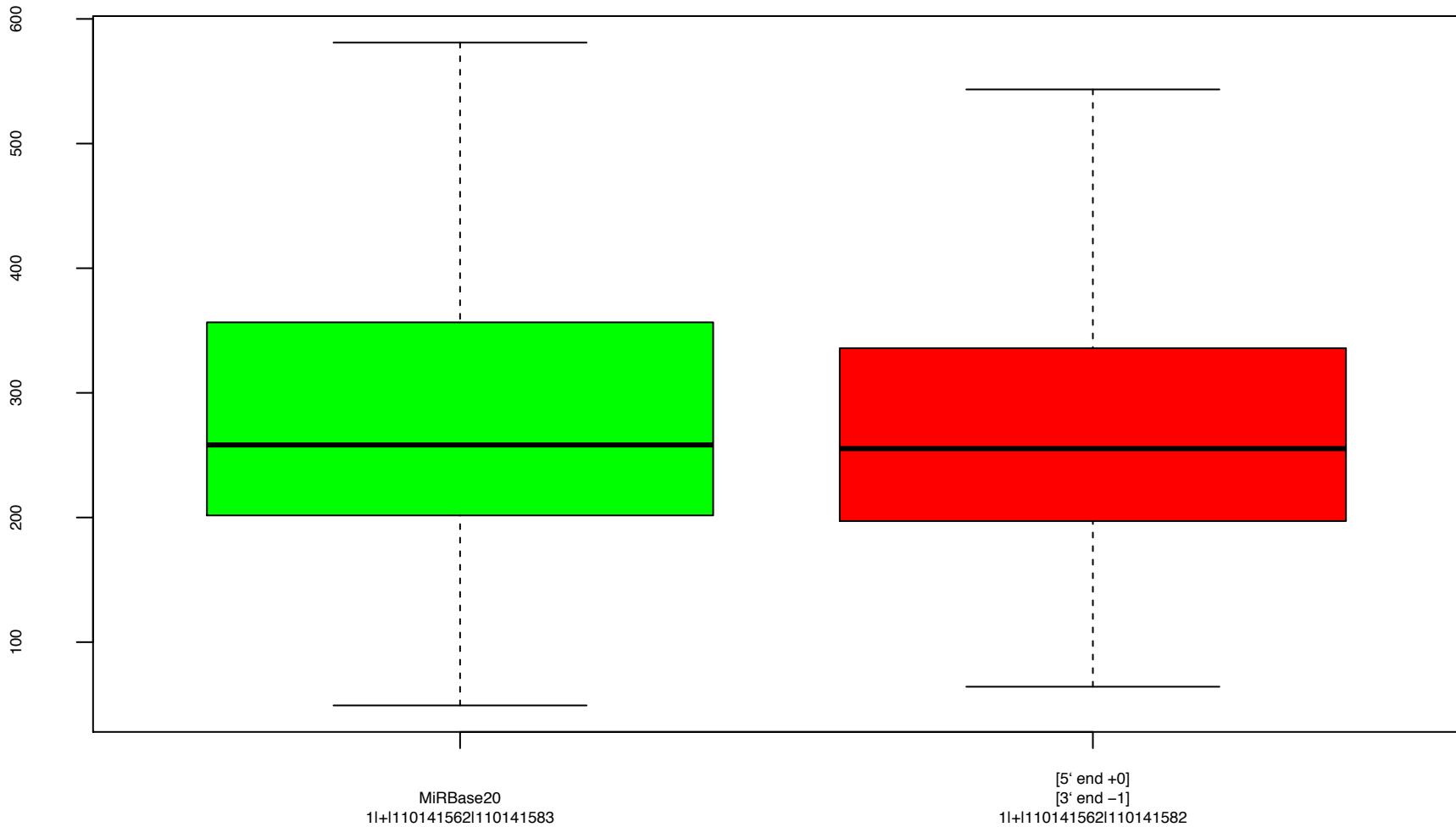


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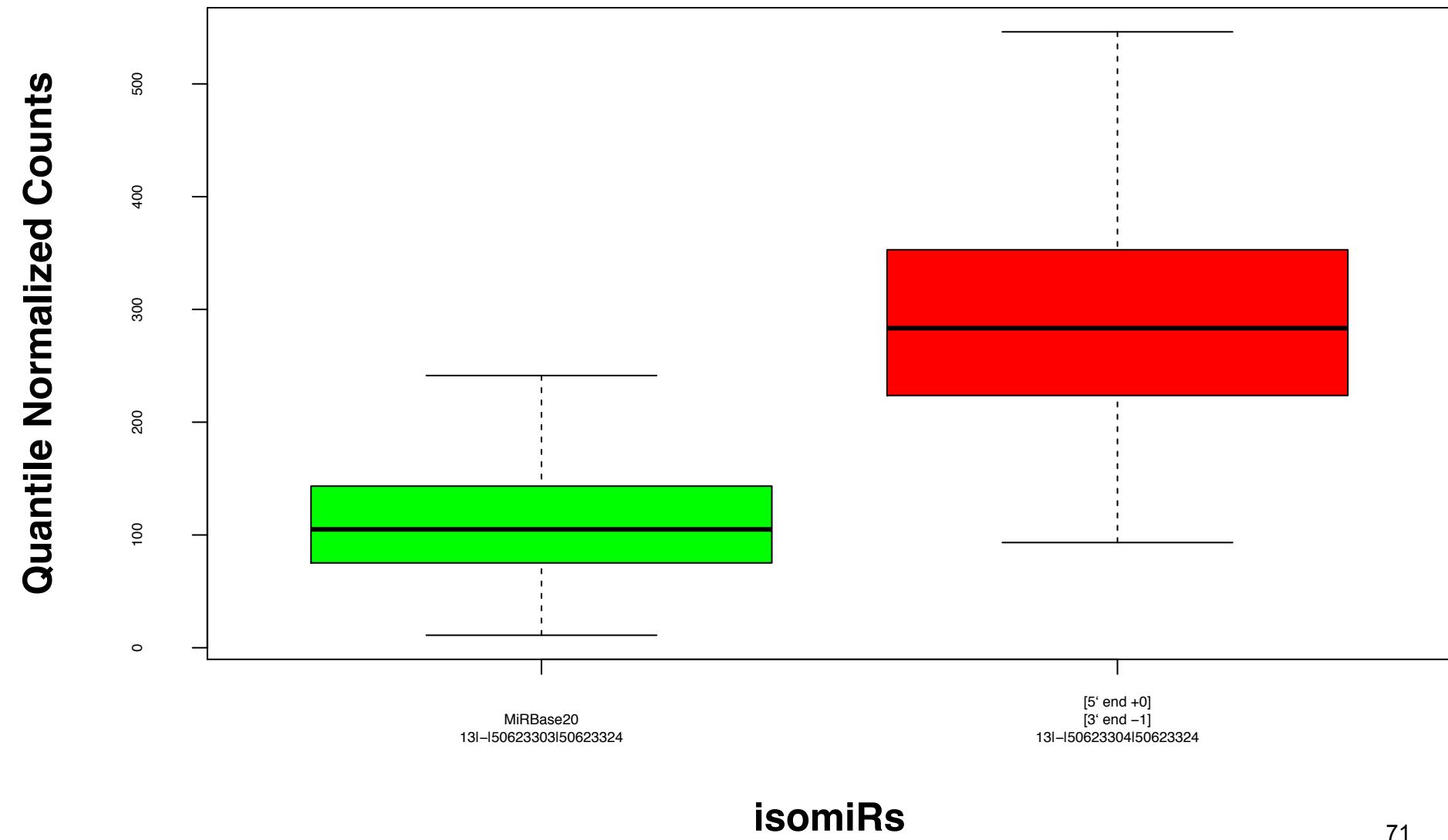
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Quantile Normalized Counts

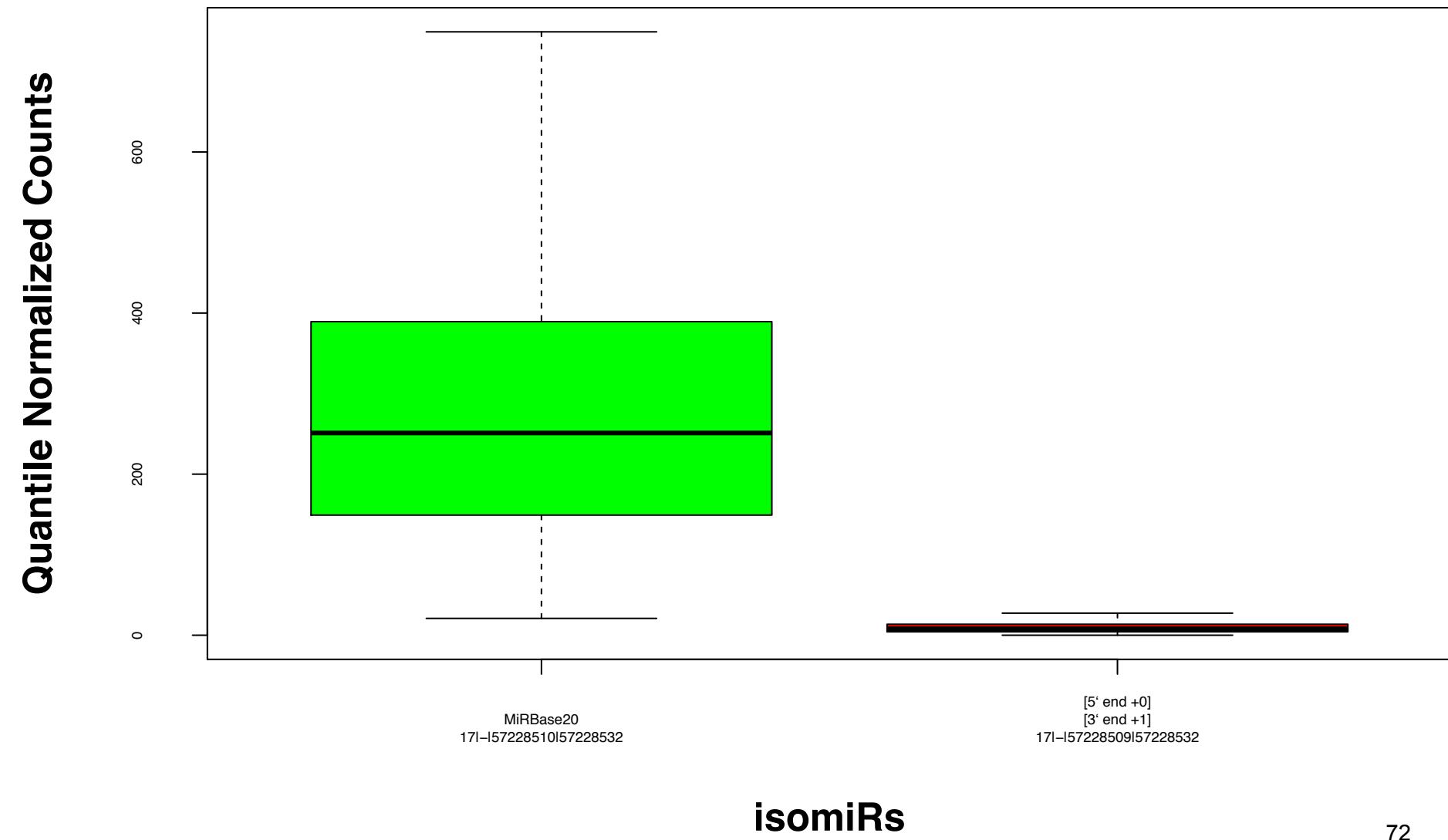


isomiRs

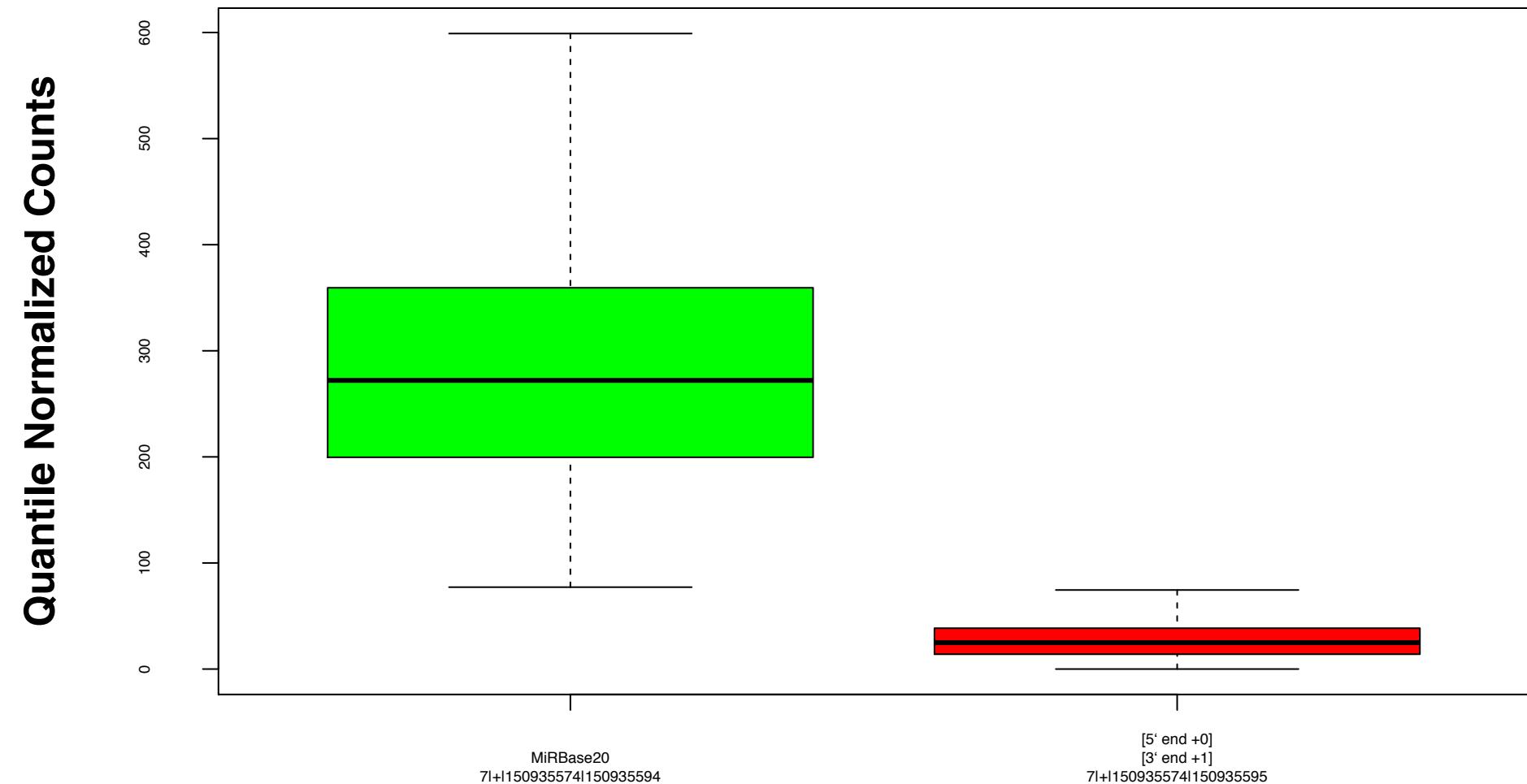
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MIMAT0000688=hsa-miR-301a-3p=MI0000745



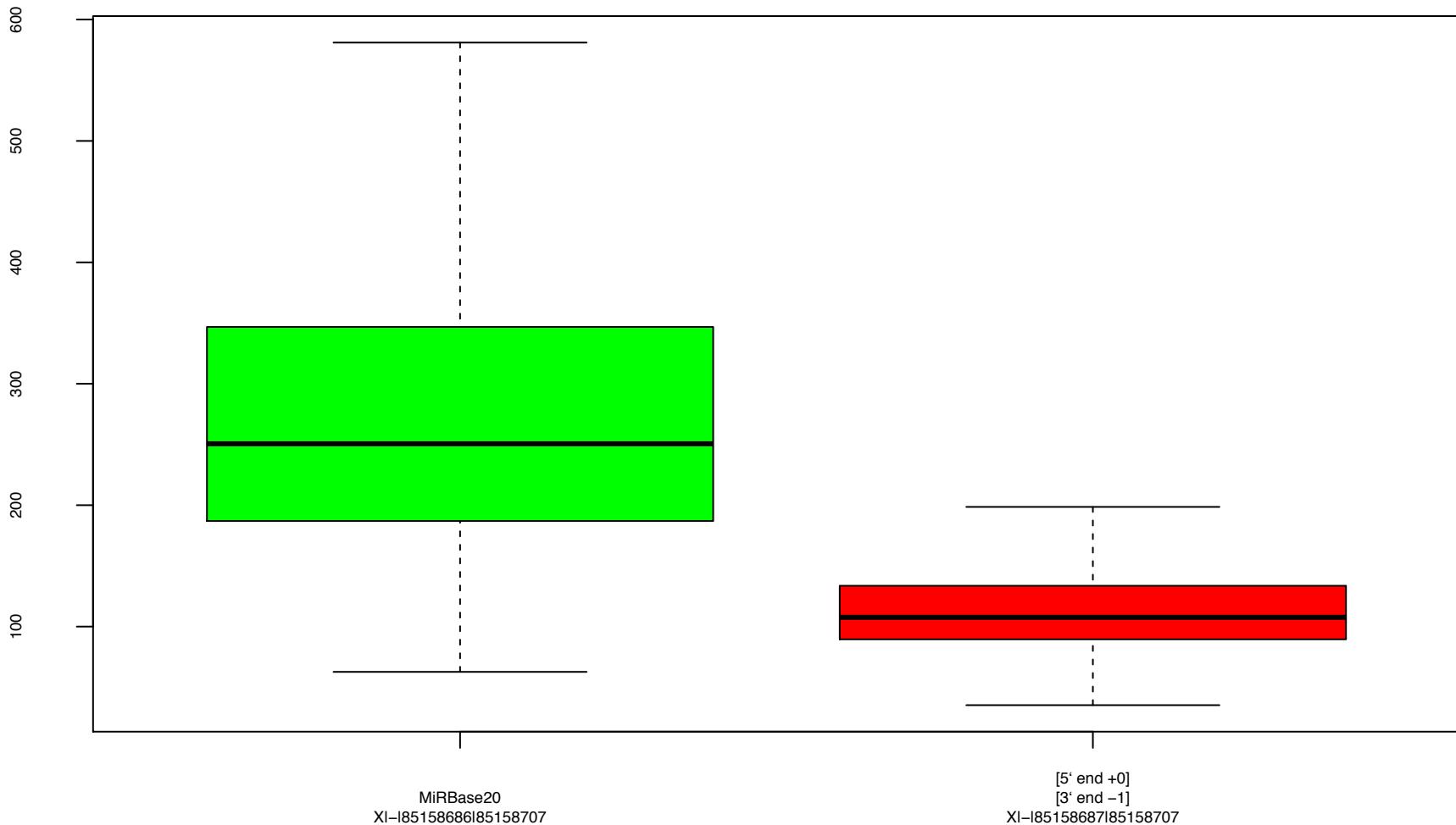
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isomiRs

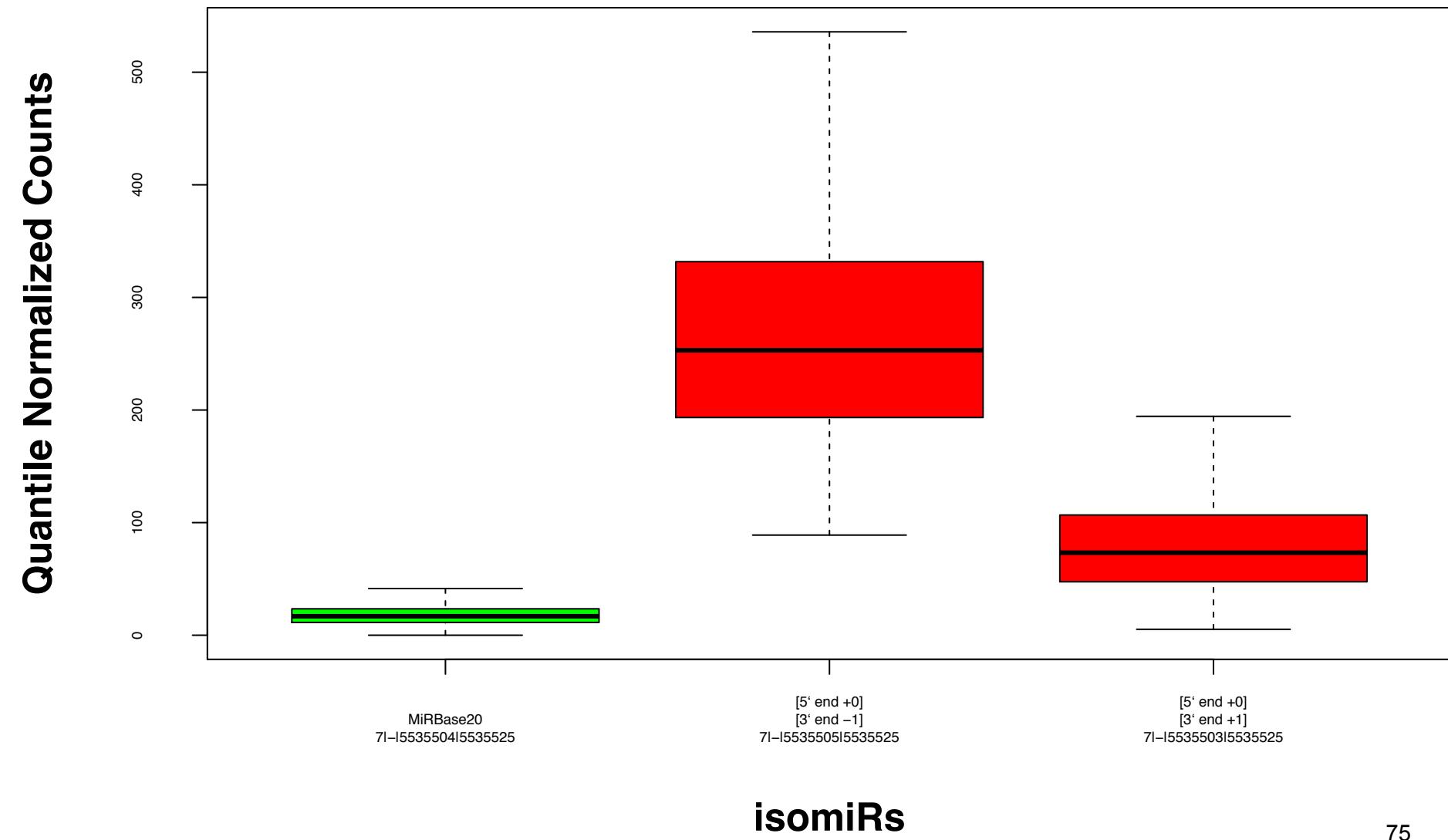
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Quantile Normalized Counts

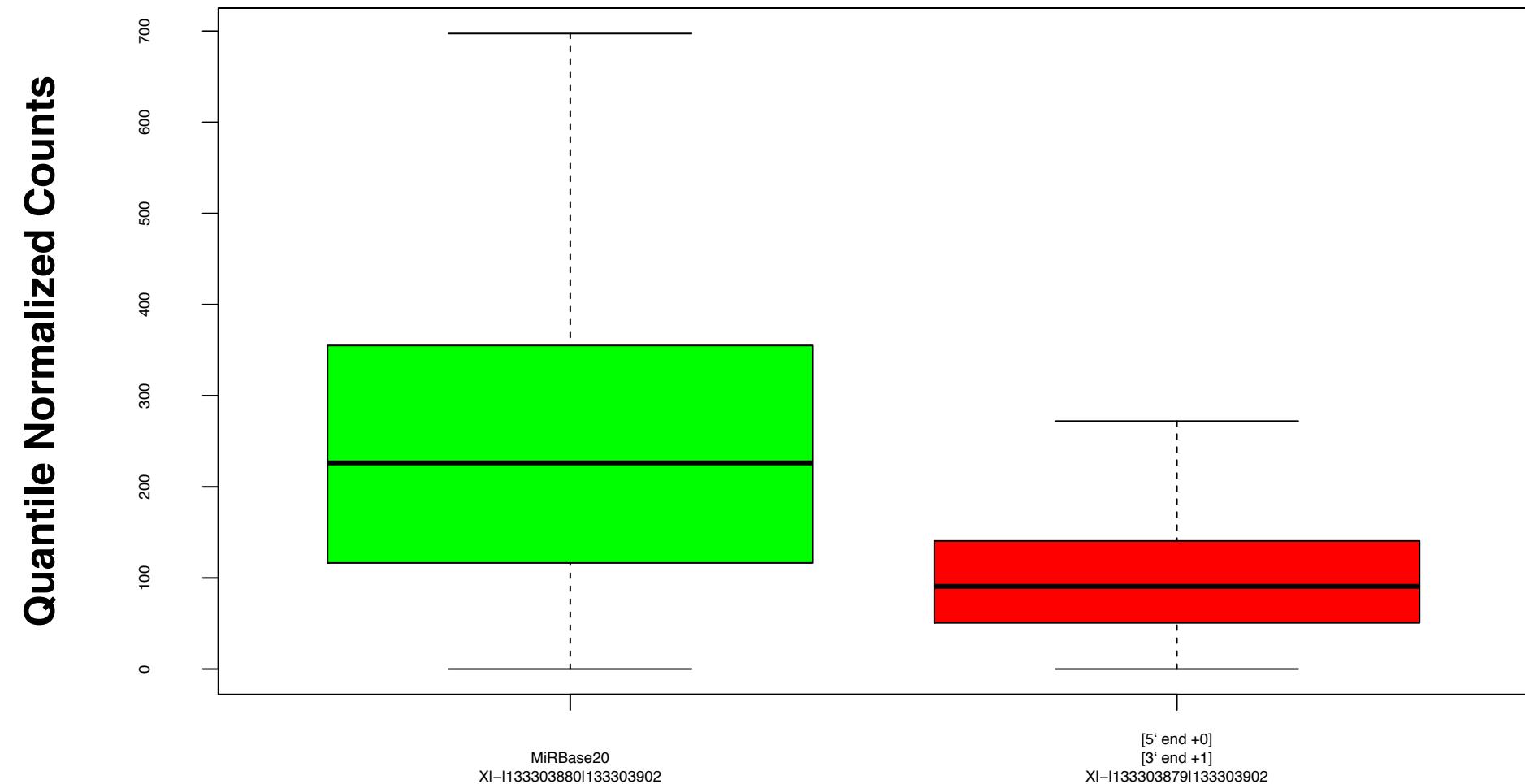


isomiRs

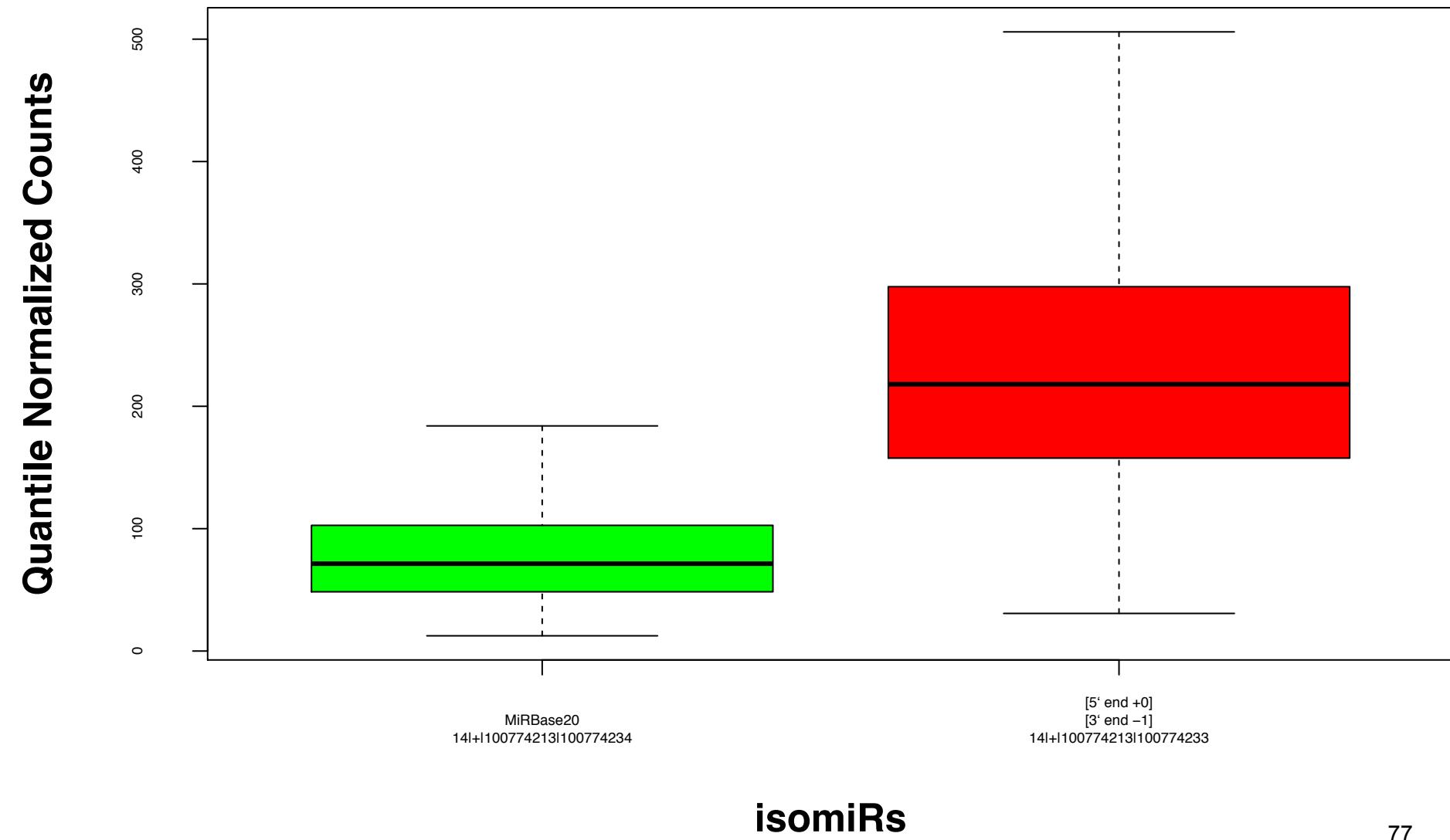
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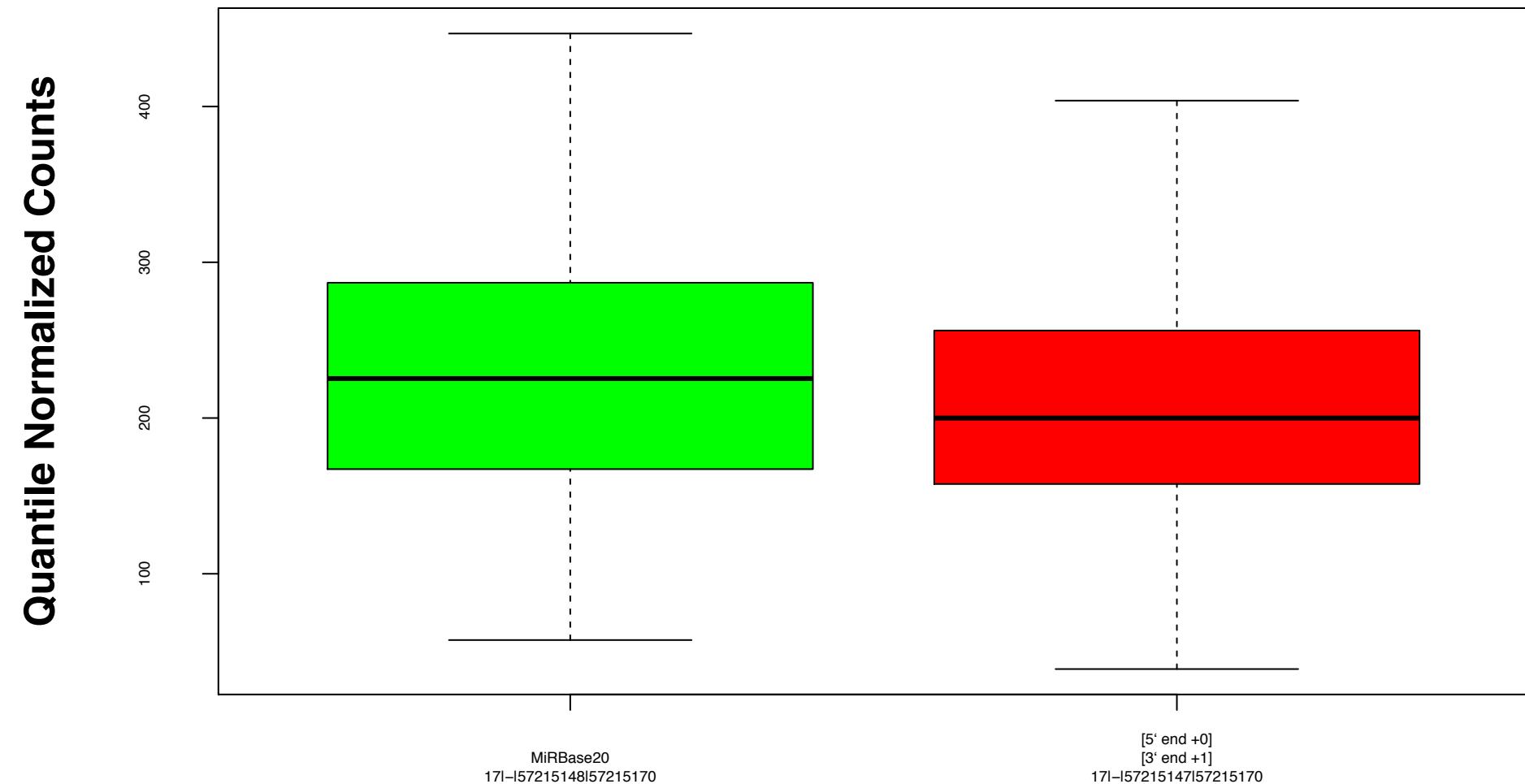
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MIMAT0000772=hsa-miR-345-5p=MI0000825

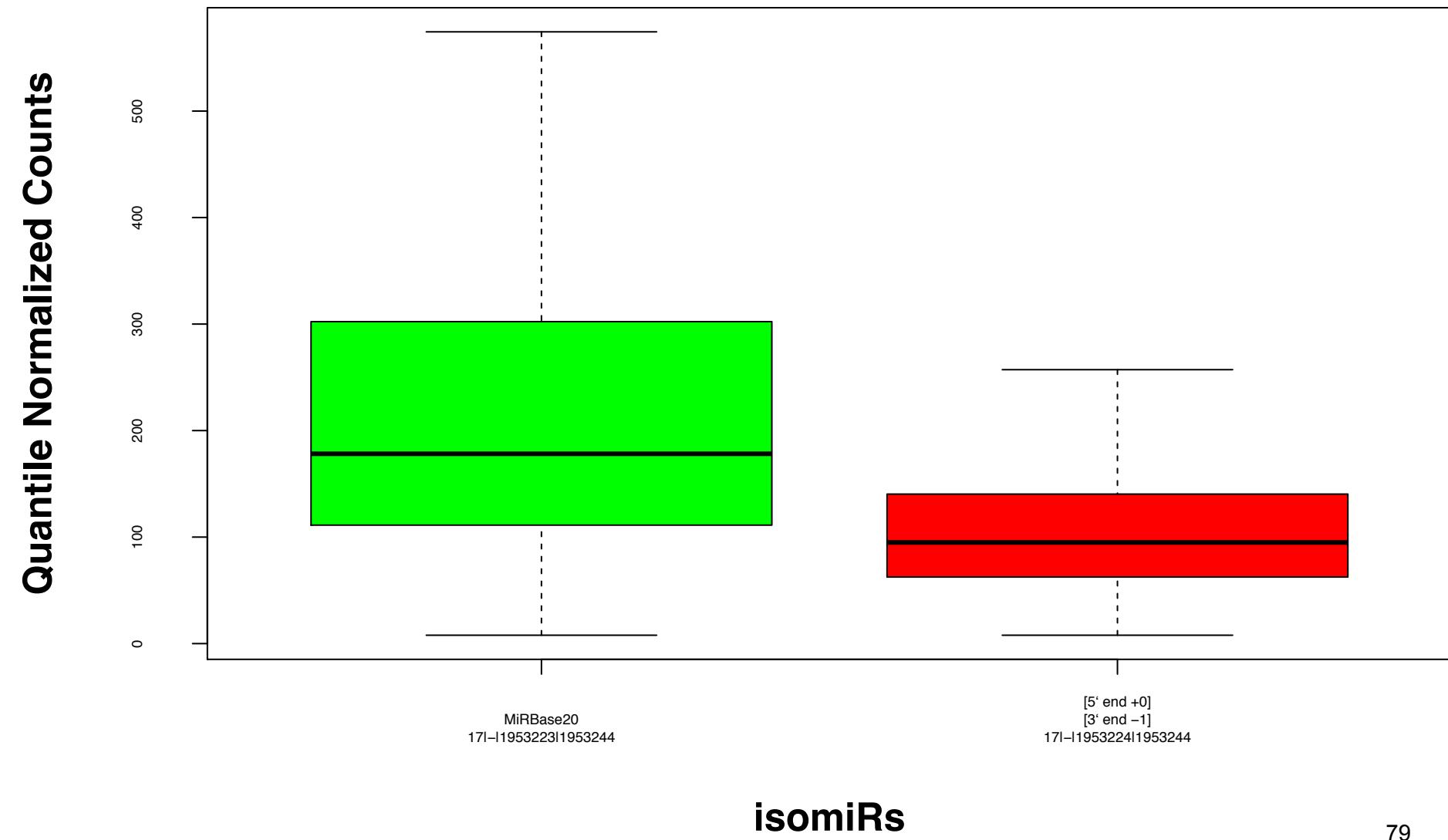


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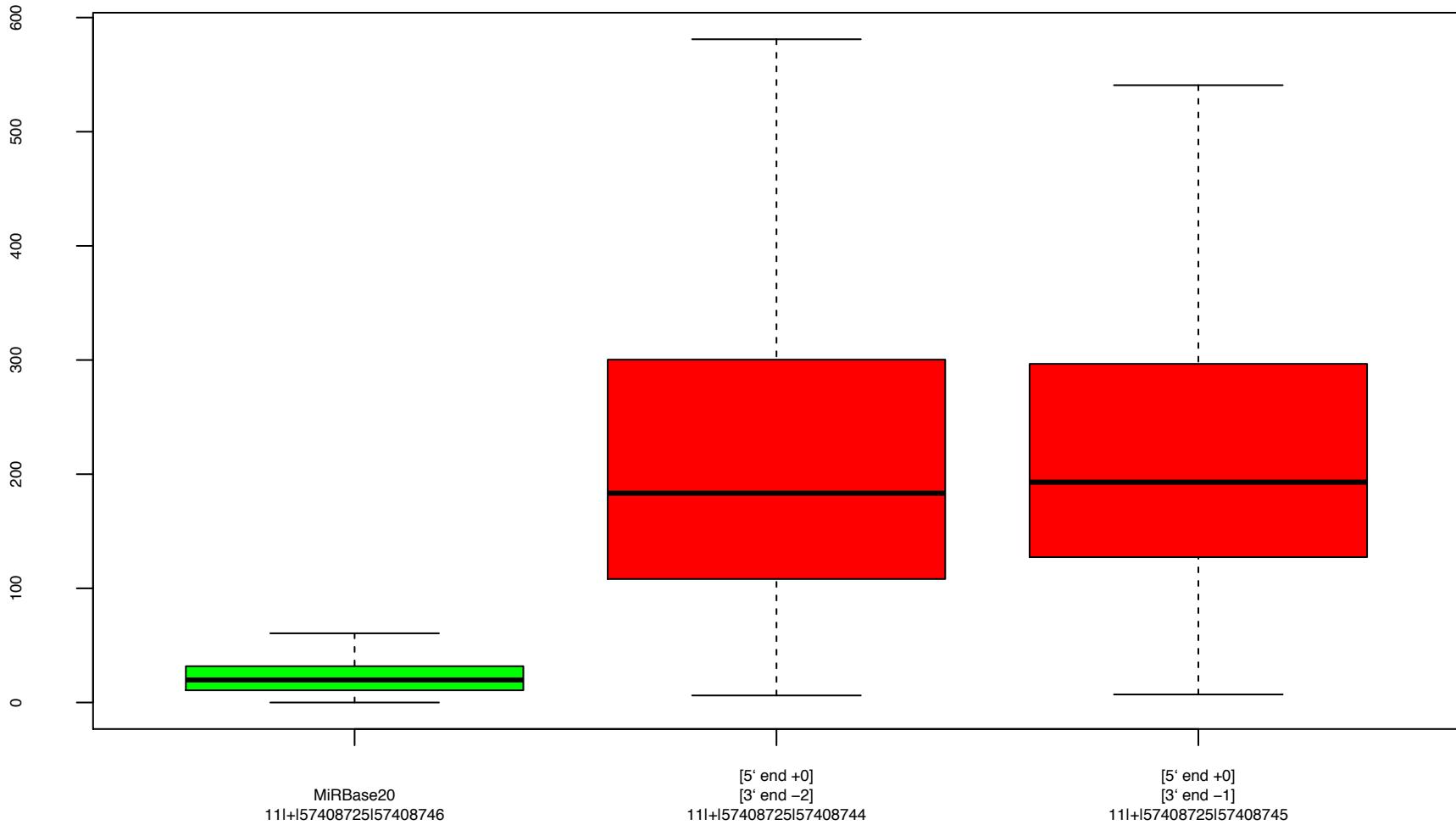
isomiRs

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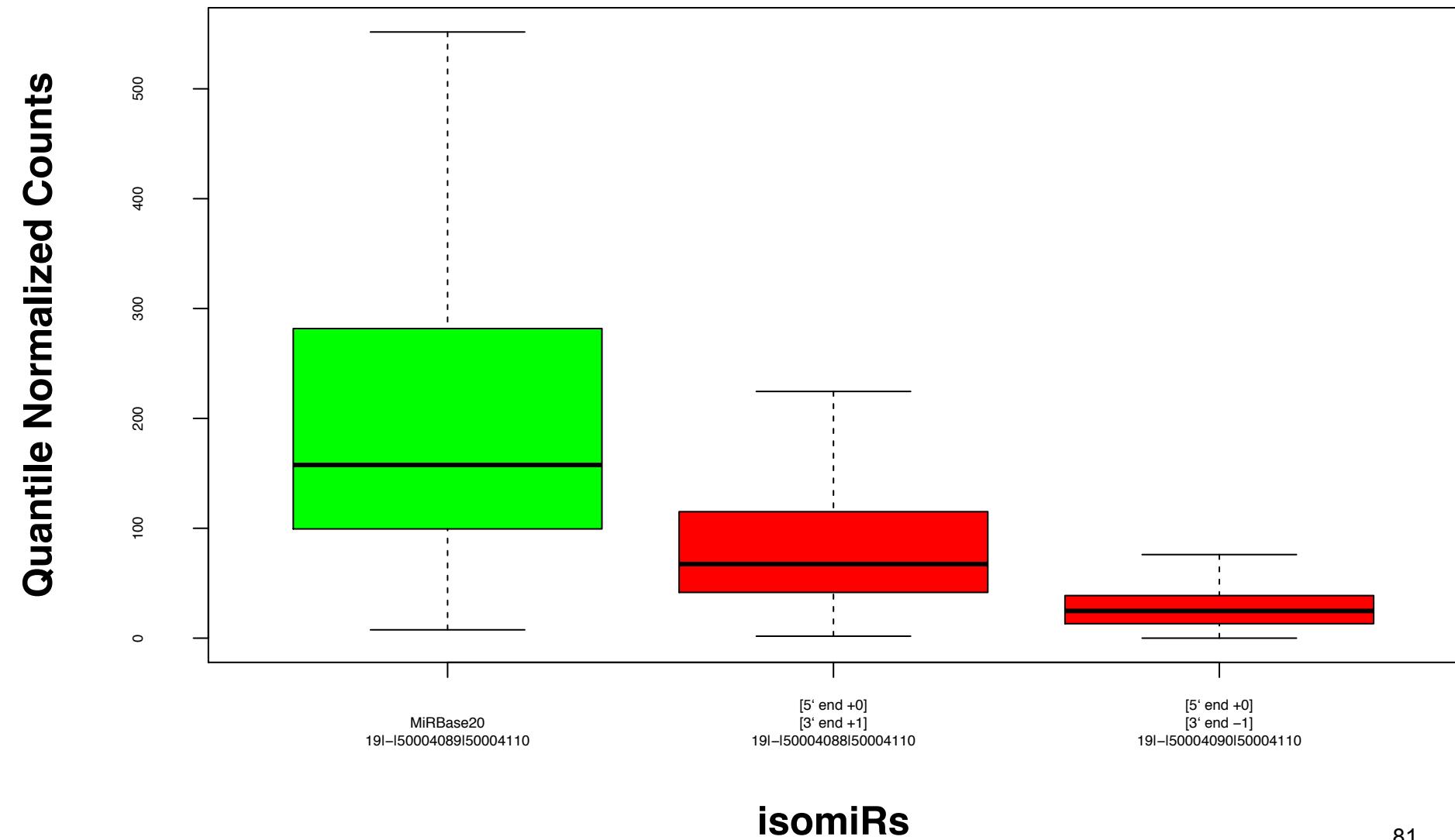
MIMAT0000425=hsa-miR-130a-3p=MI0000448

Quantile Normalized Counts

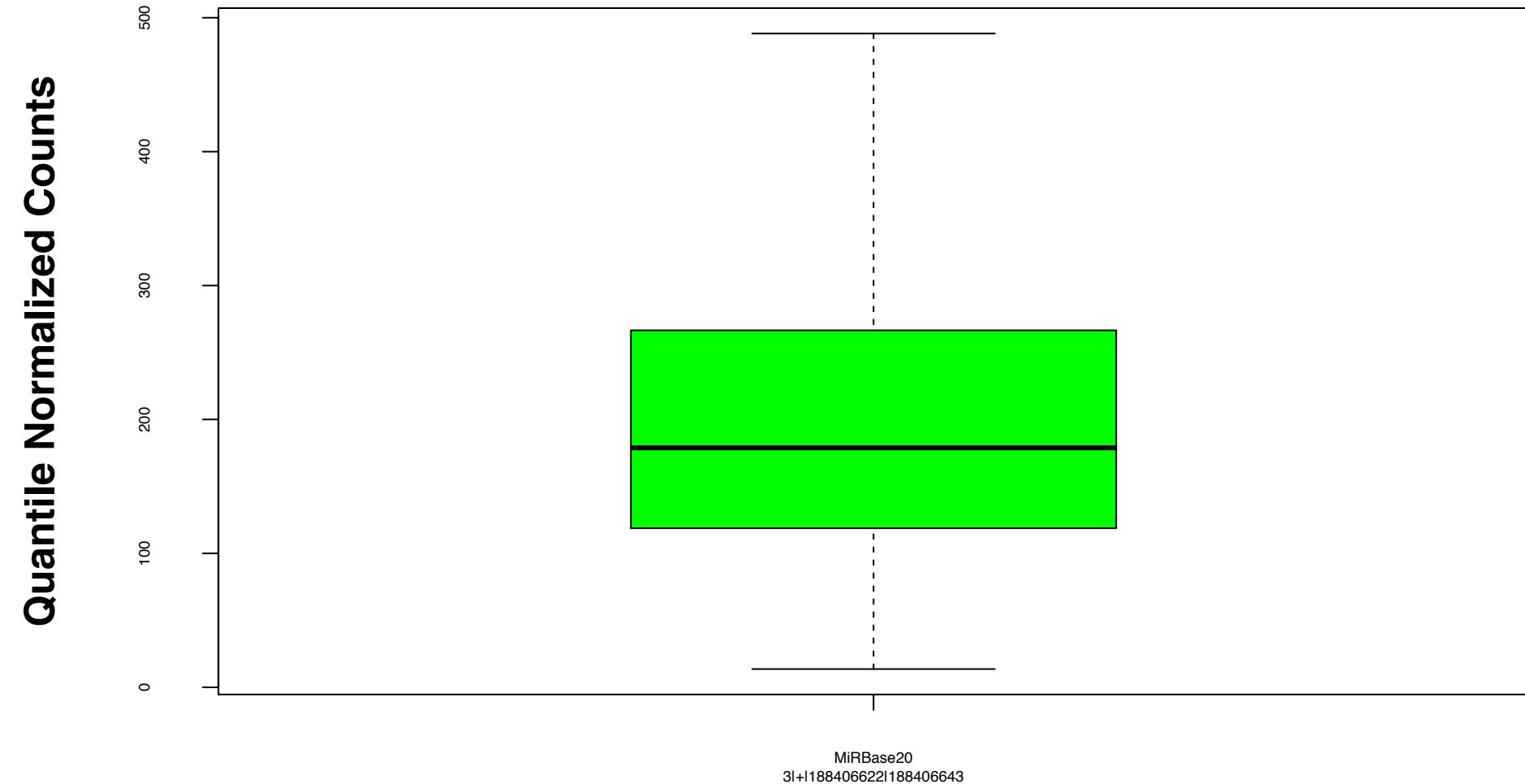


isomiRs

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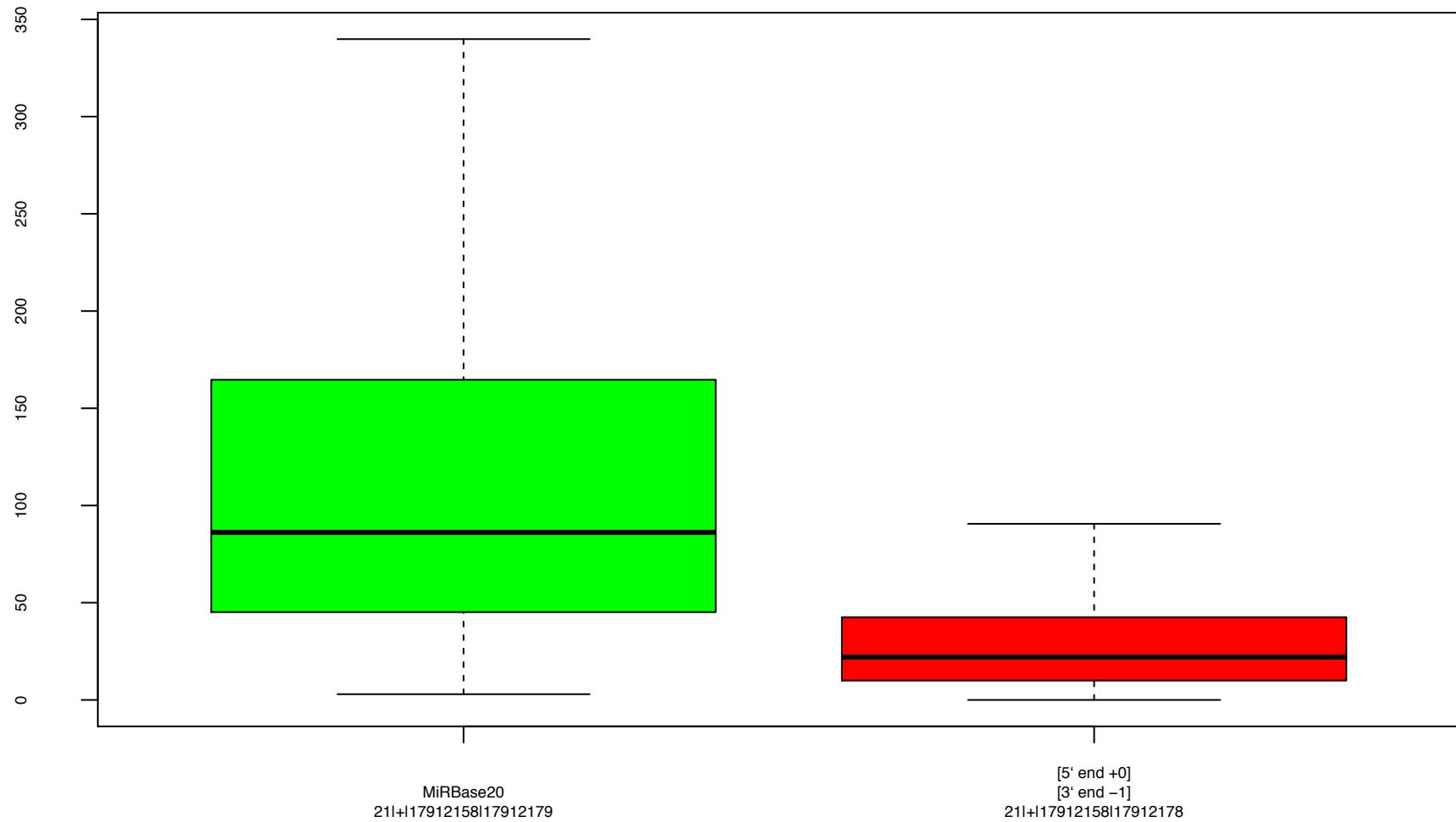


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MIMAT0000064=hsa-let-7c-5p=MI0000064

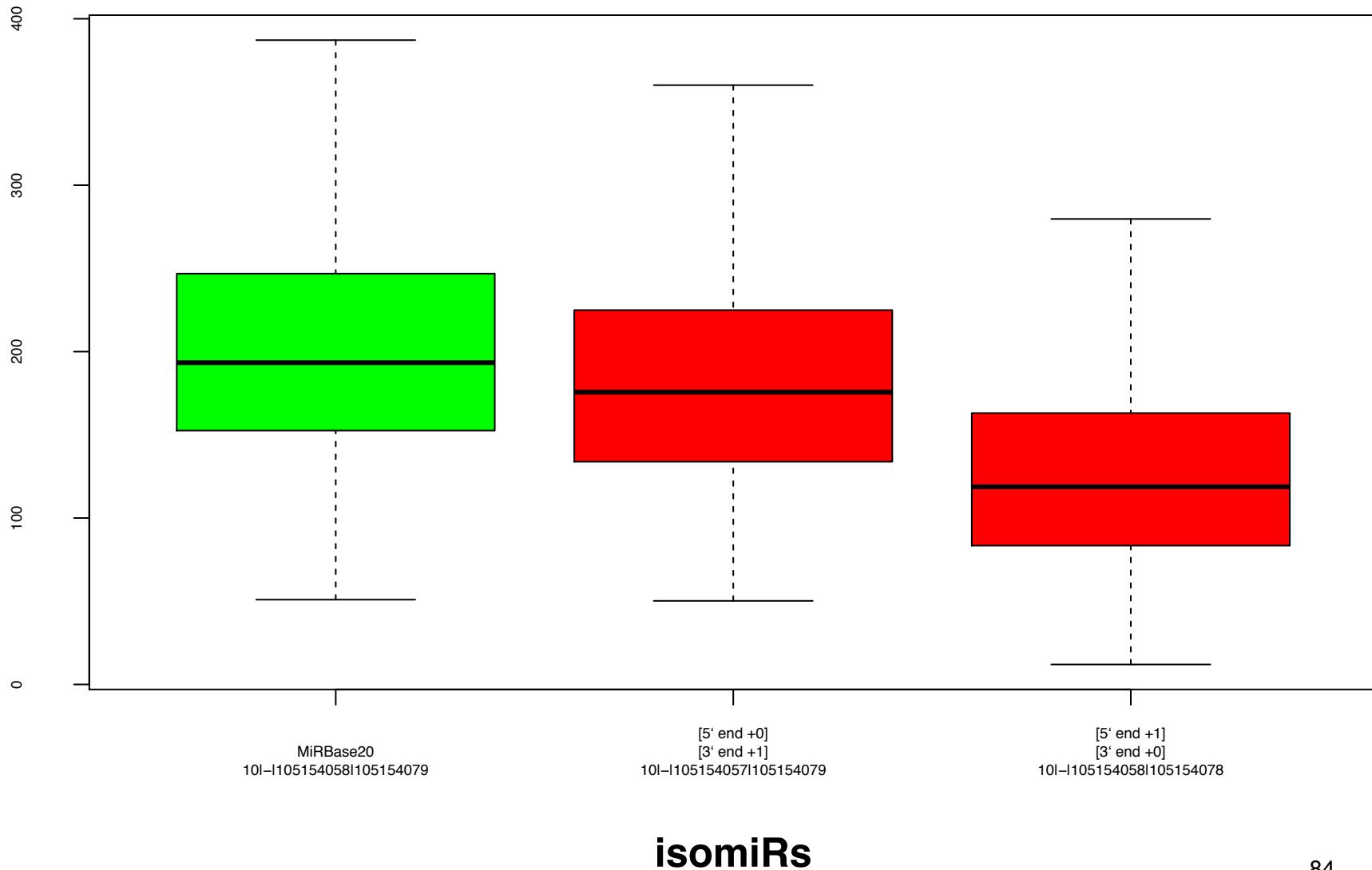
Quantile Normalized Counts



isomiRs

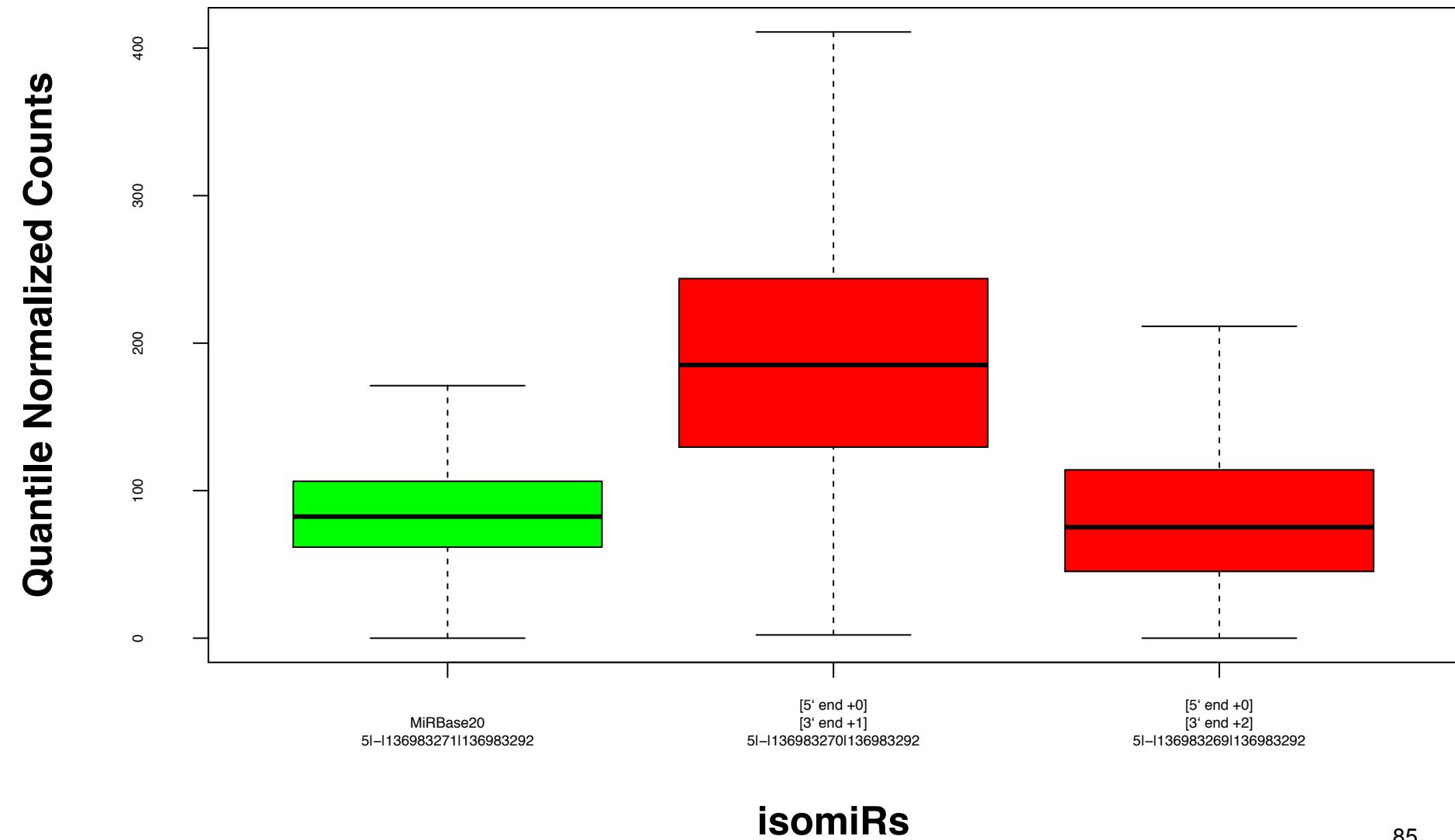
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Quantile Normalized Counts

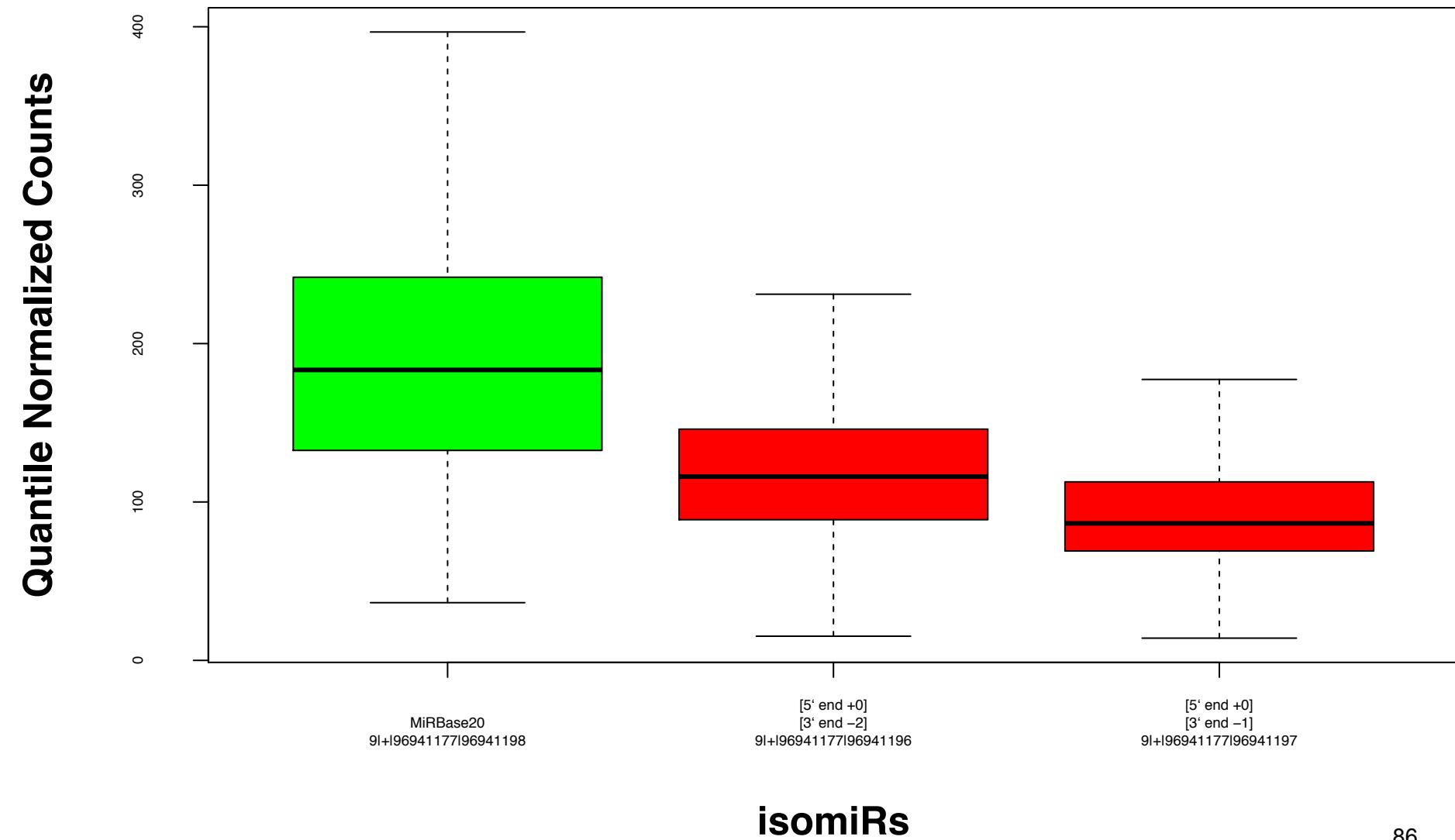


isomiRs

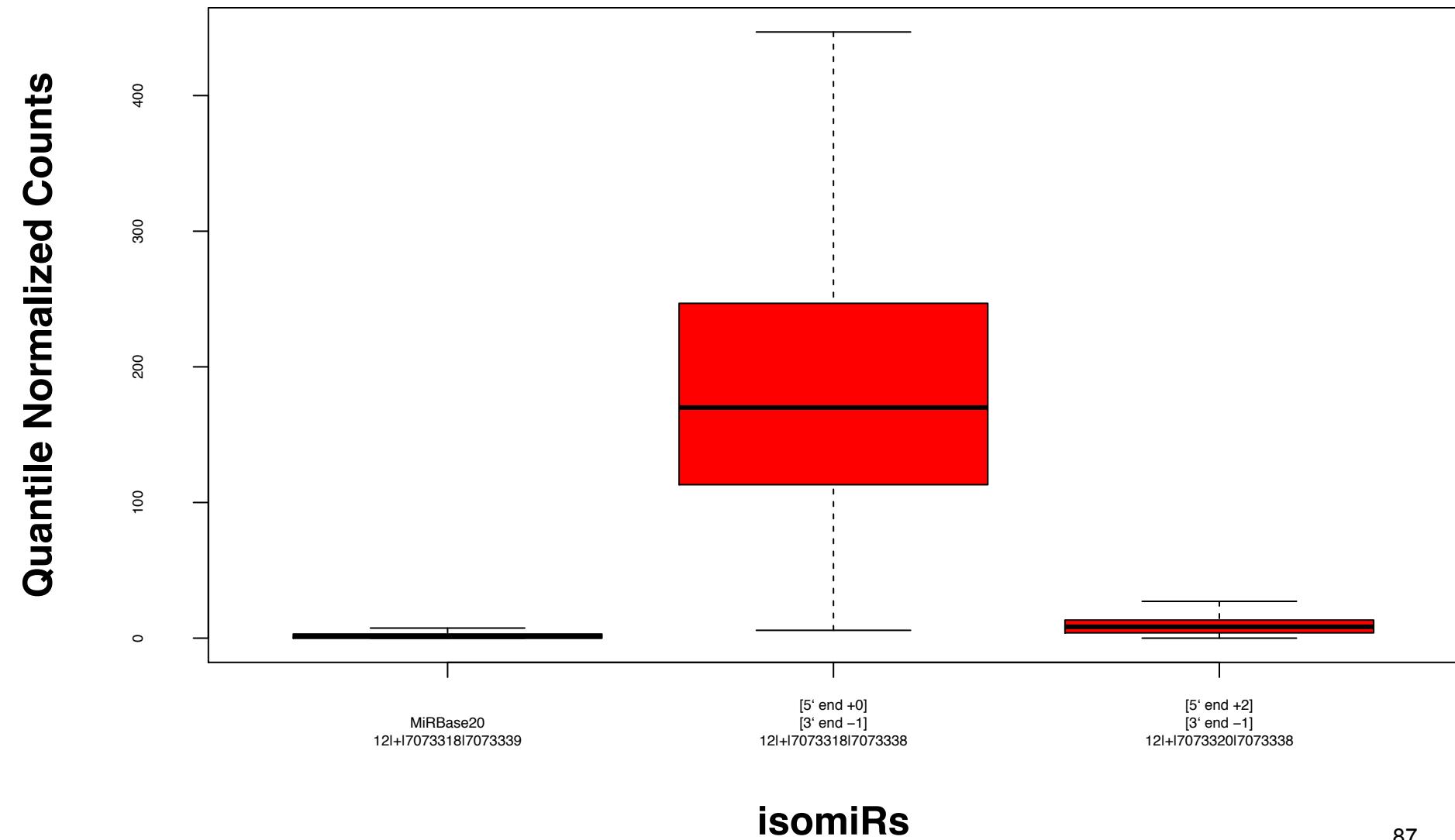
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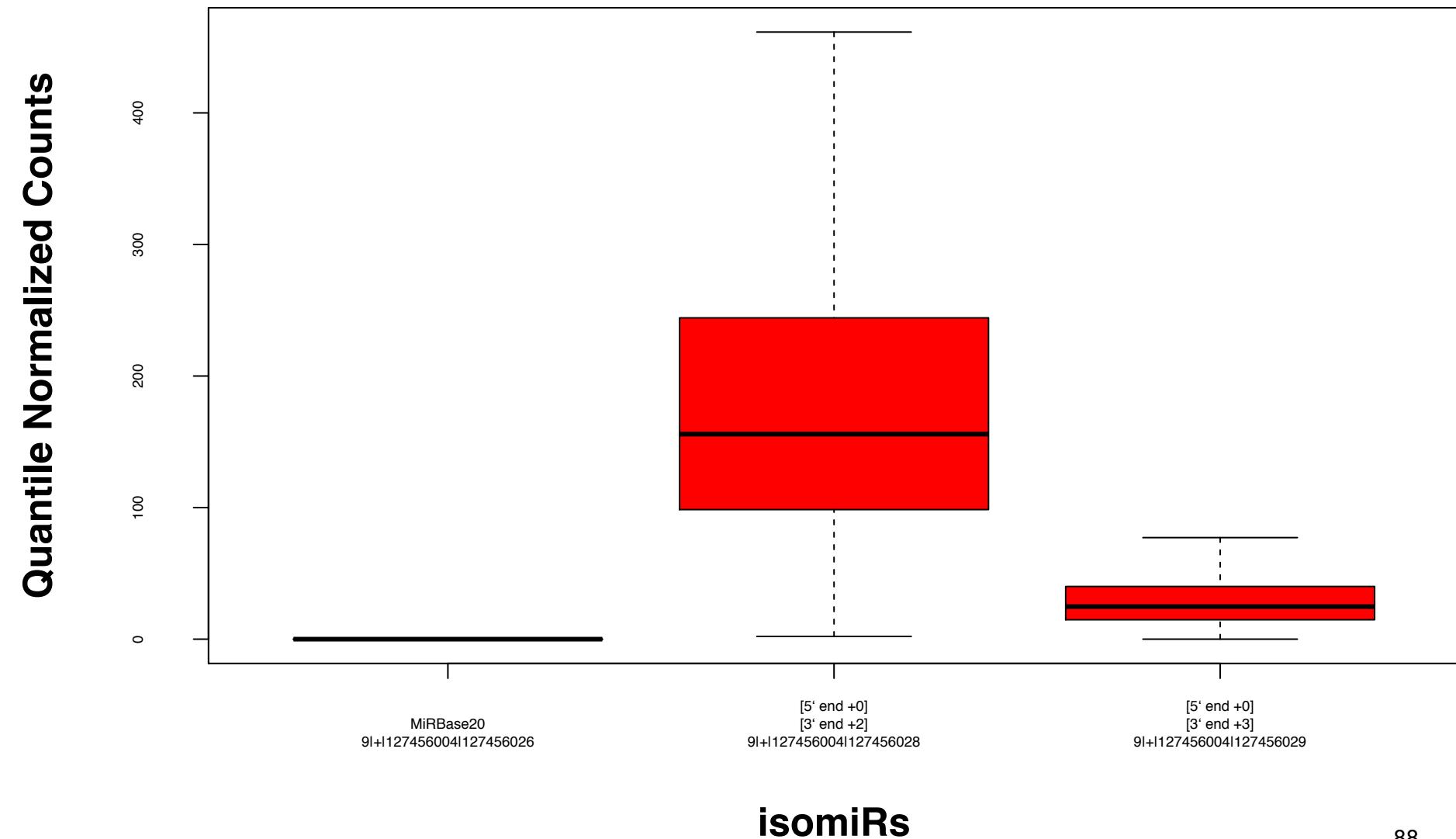


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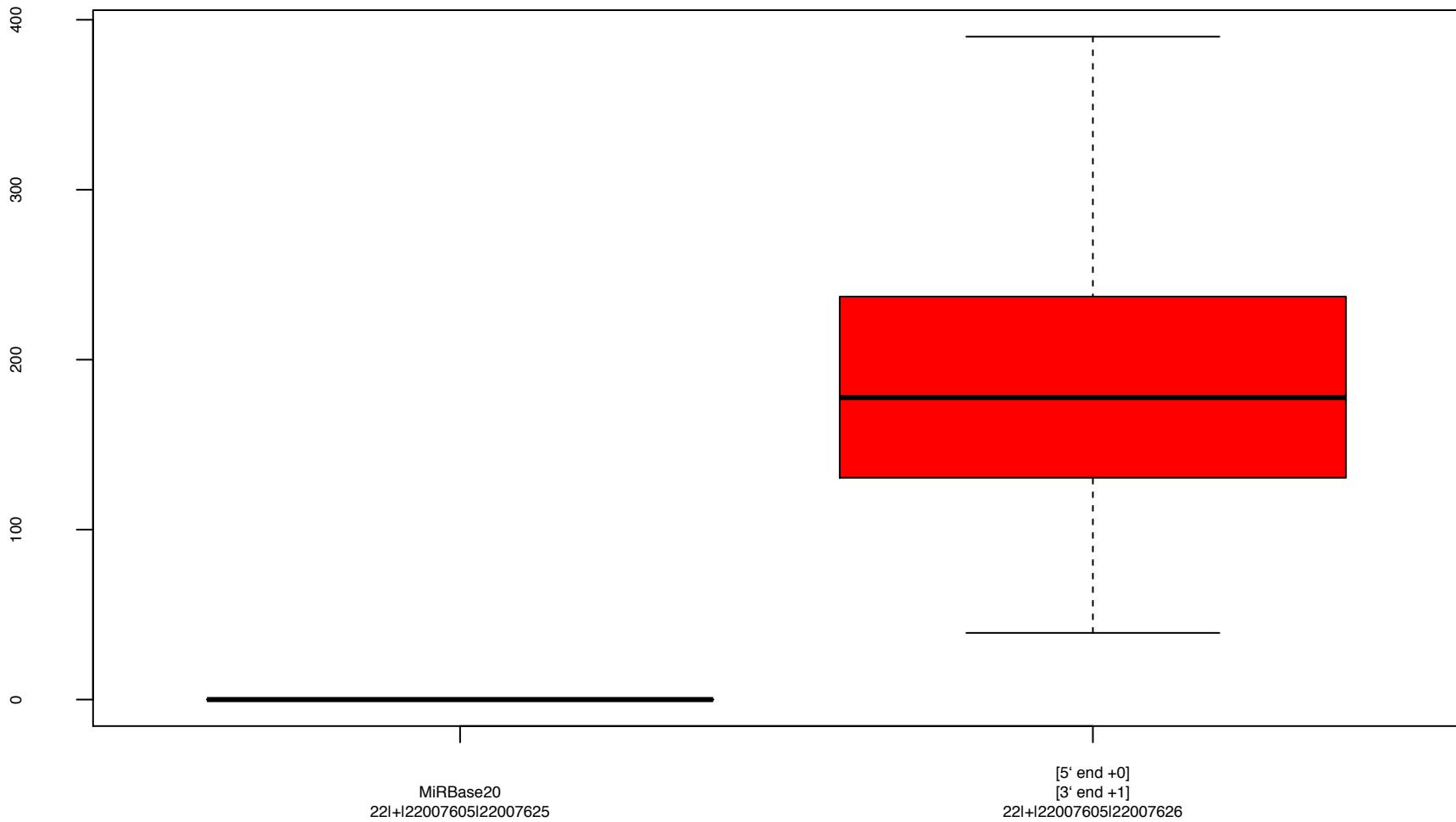
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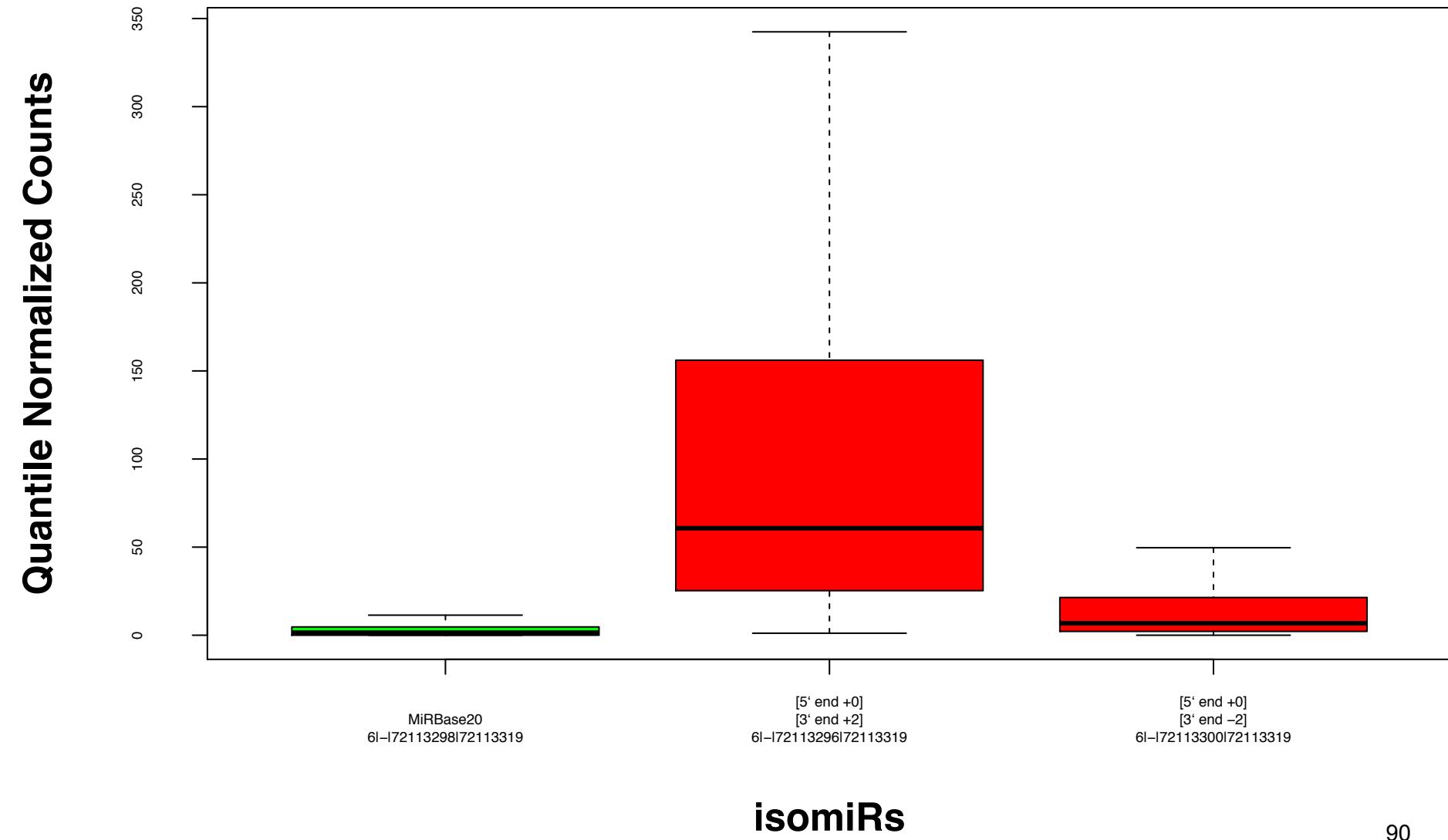
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Quantile Normalized Counts



isomiRs

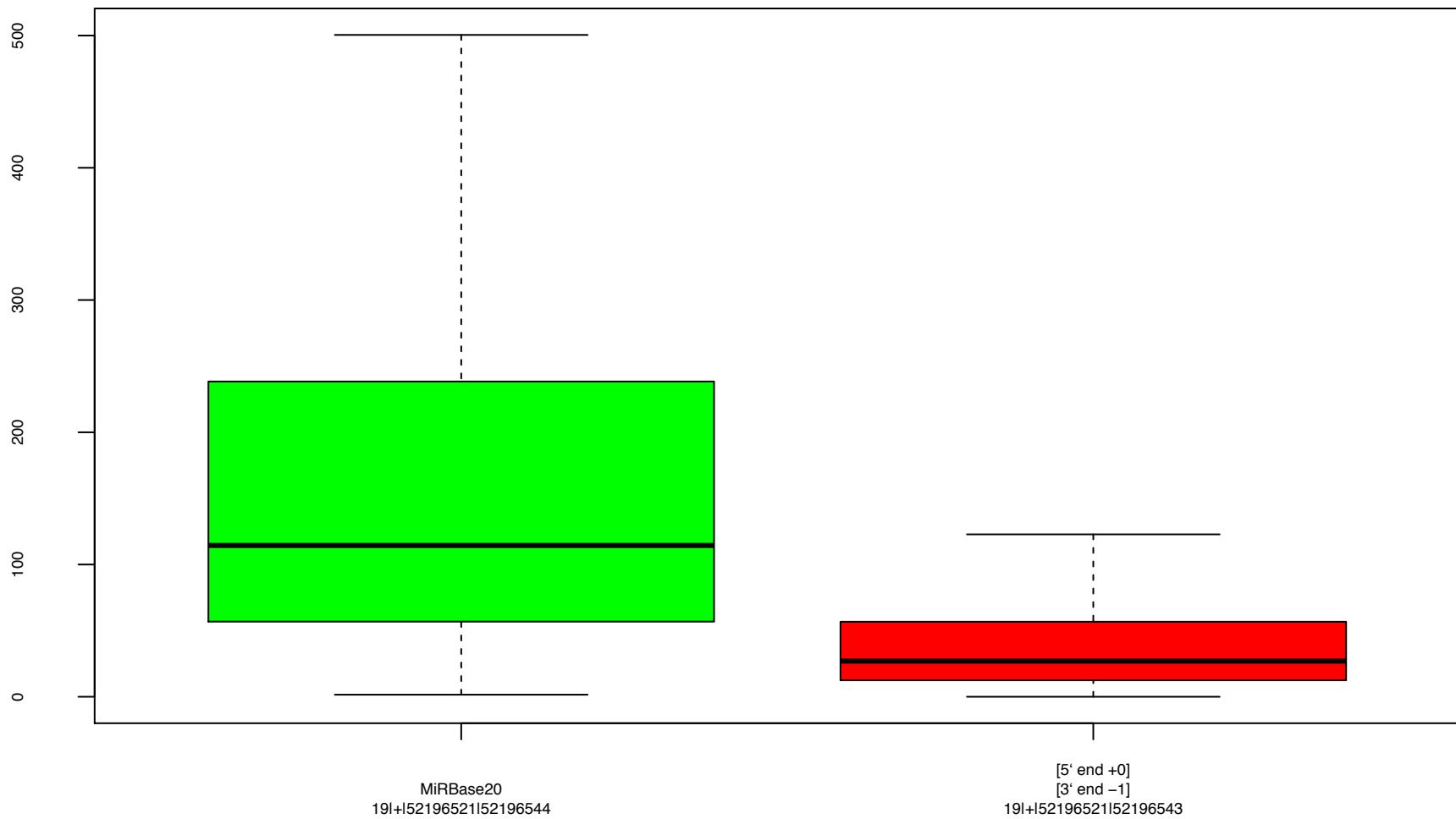
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isomiRs

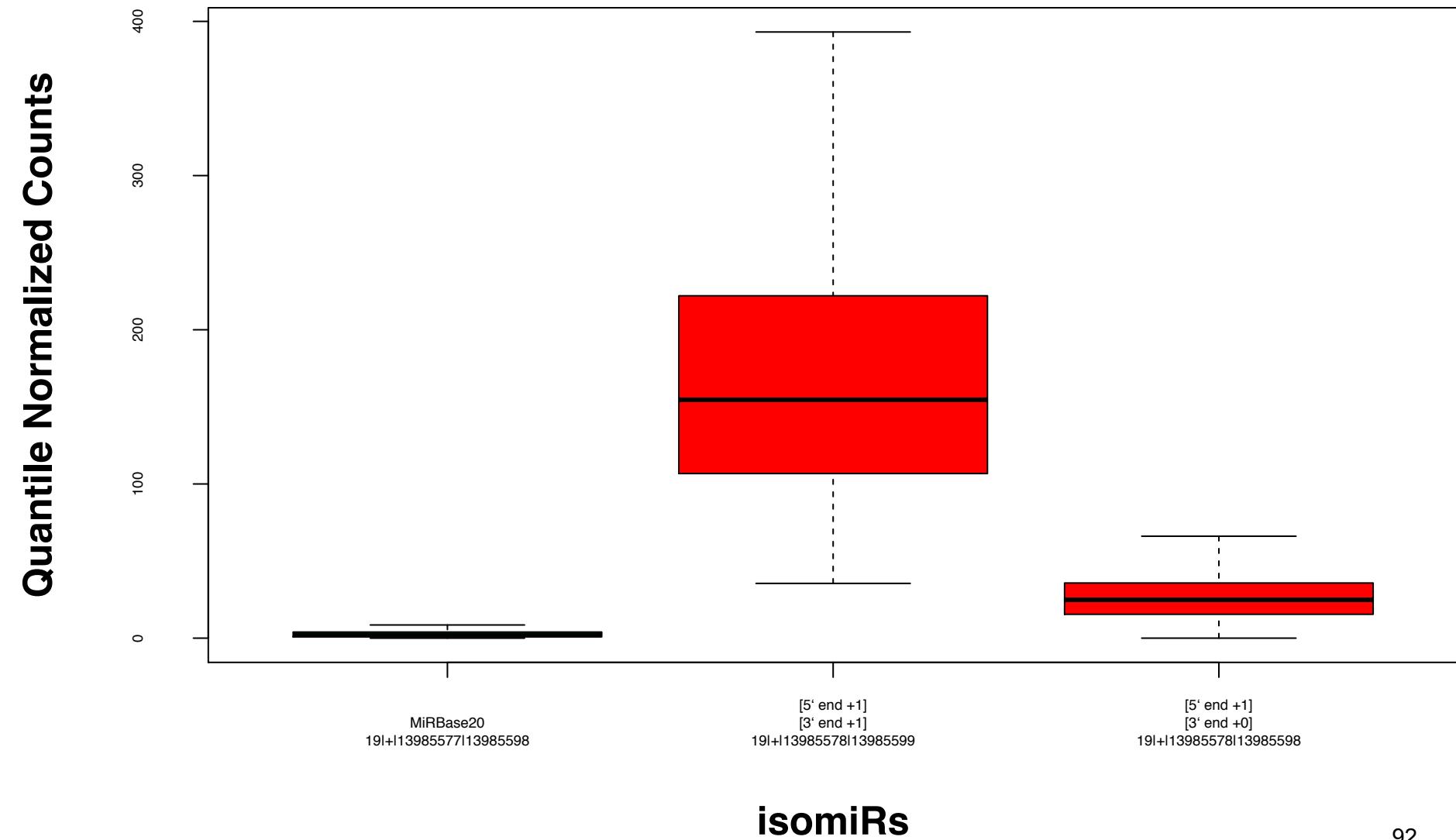
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Quantile Normalized Counts

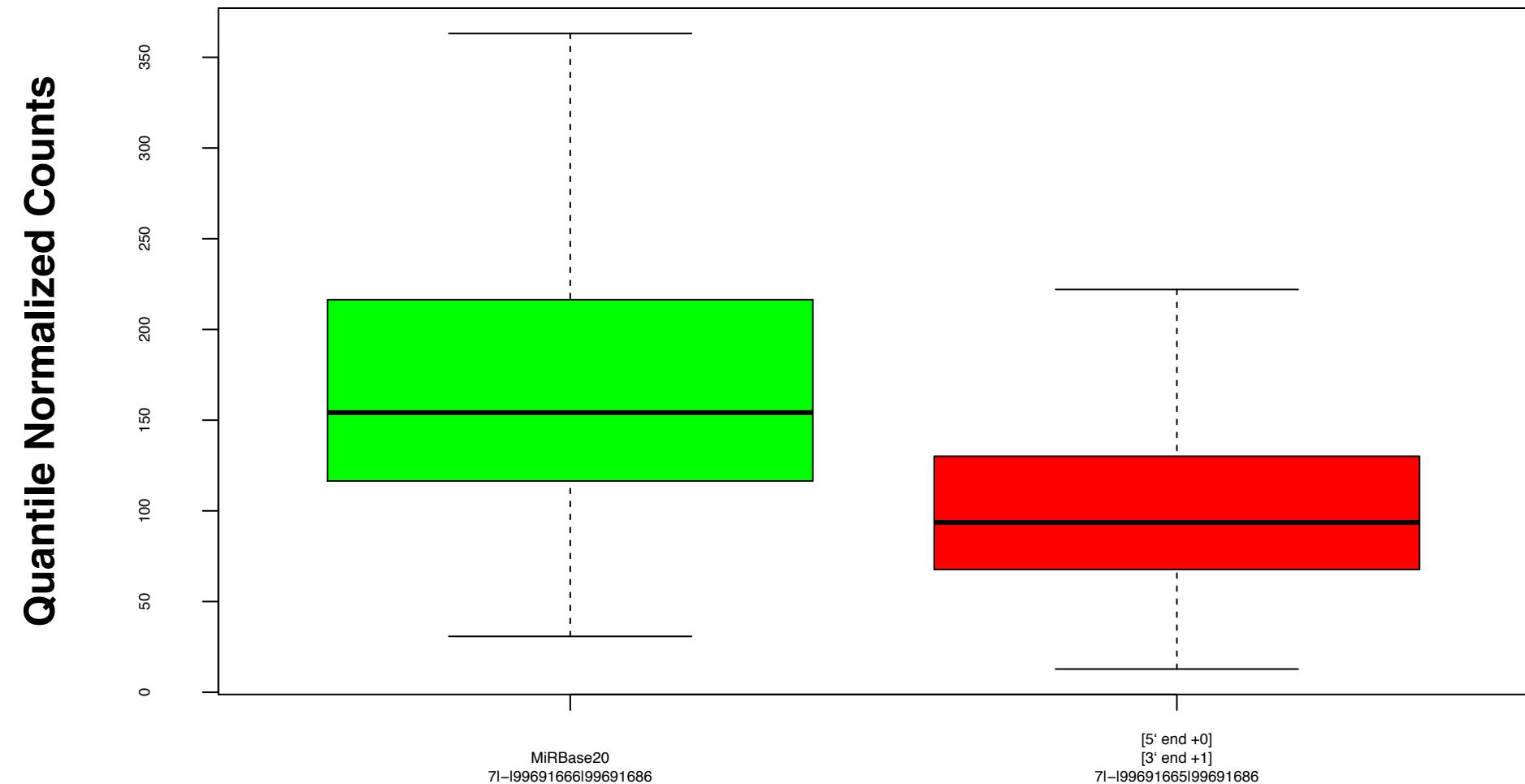


isomiRs

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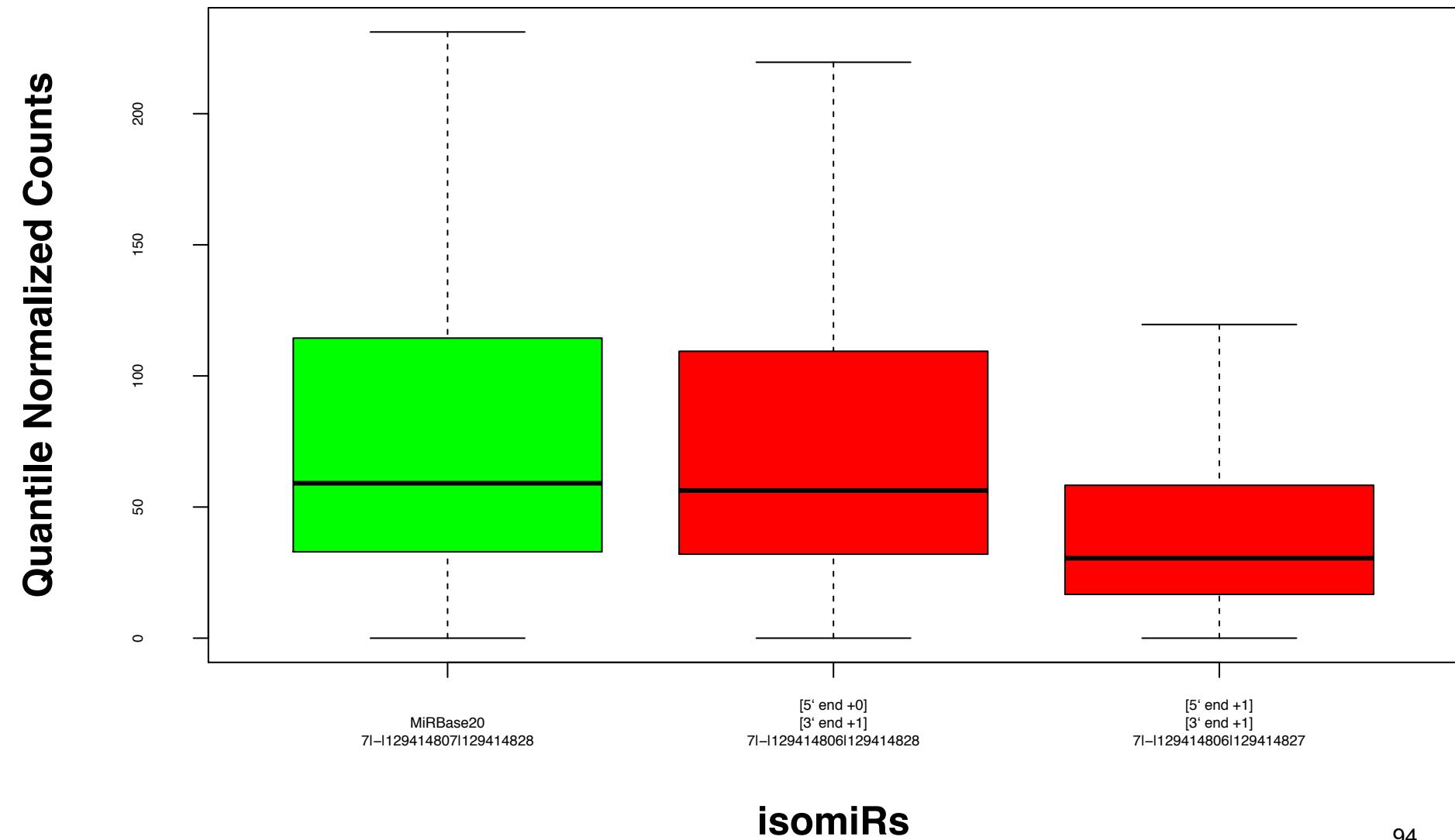


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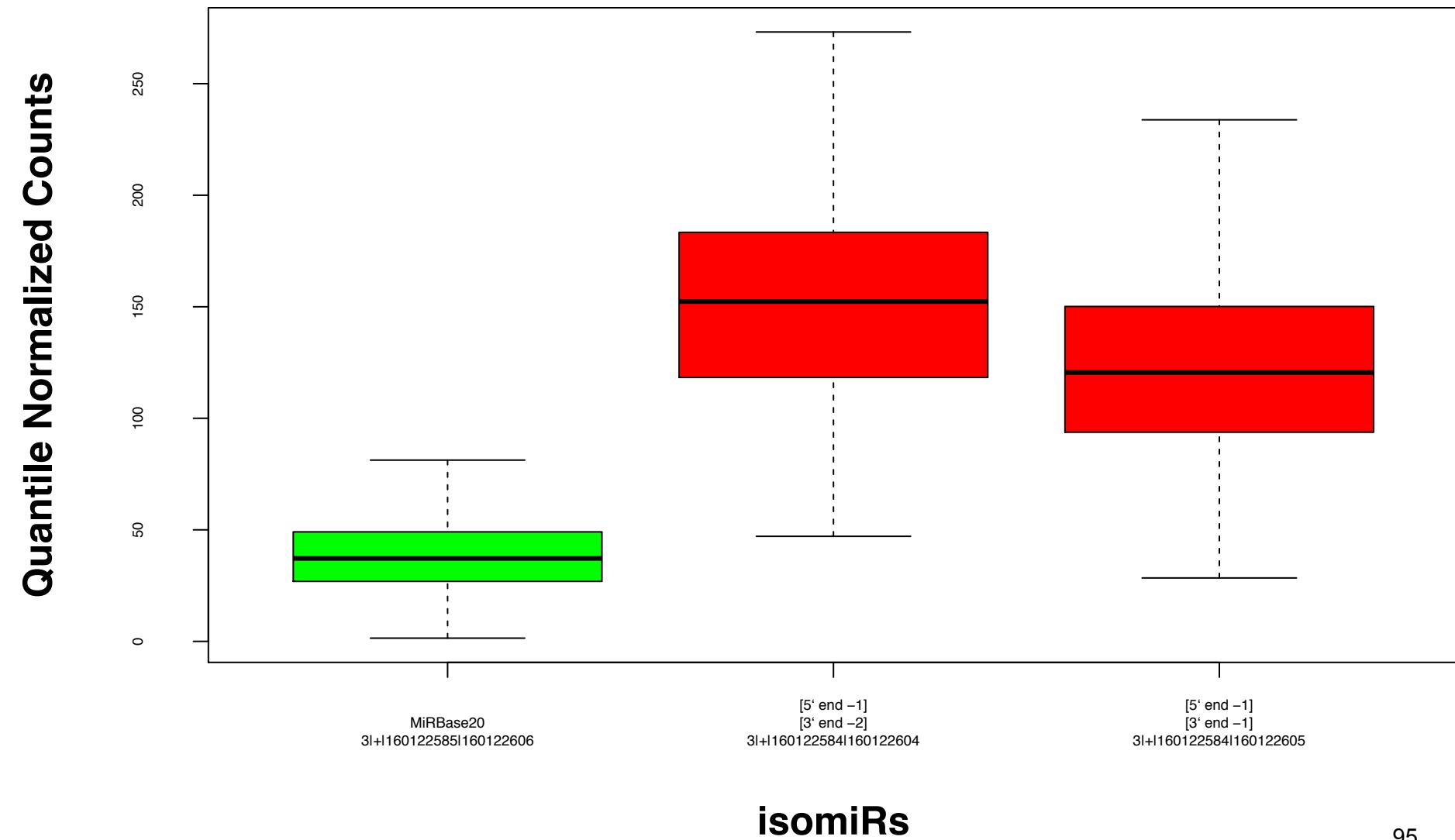


isomiRs

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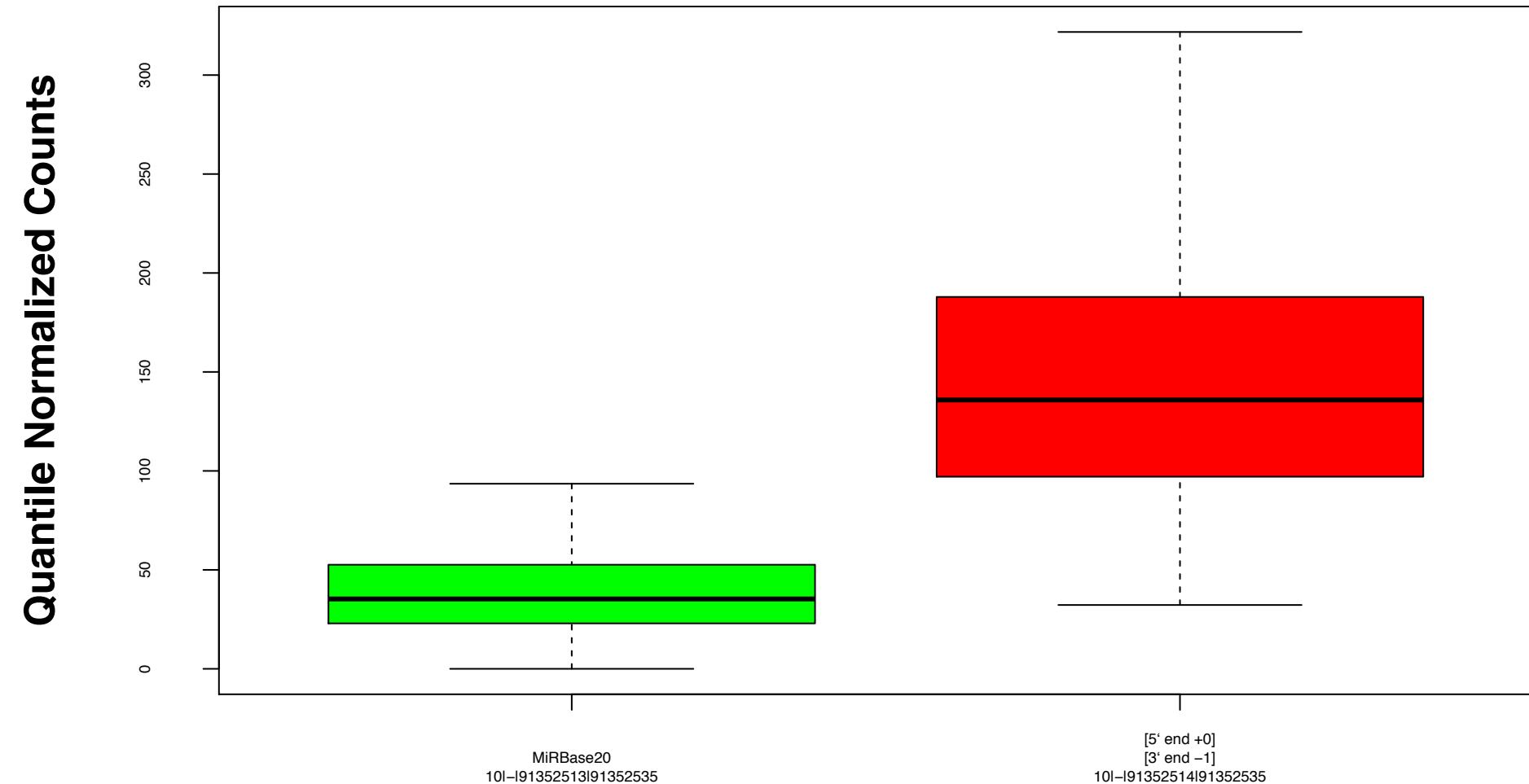


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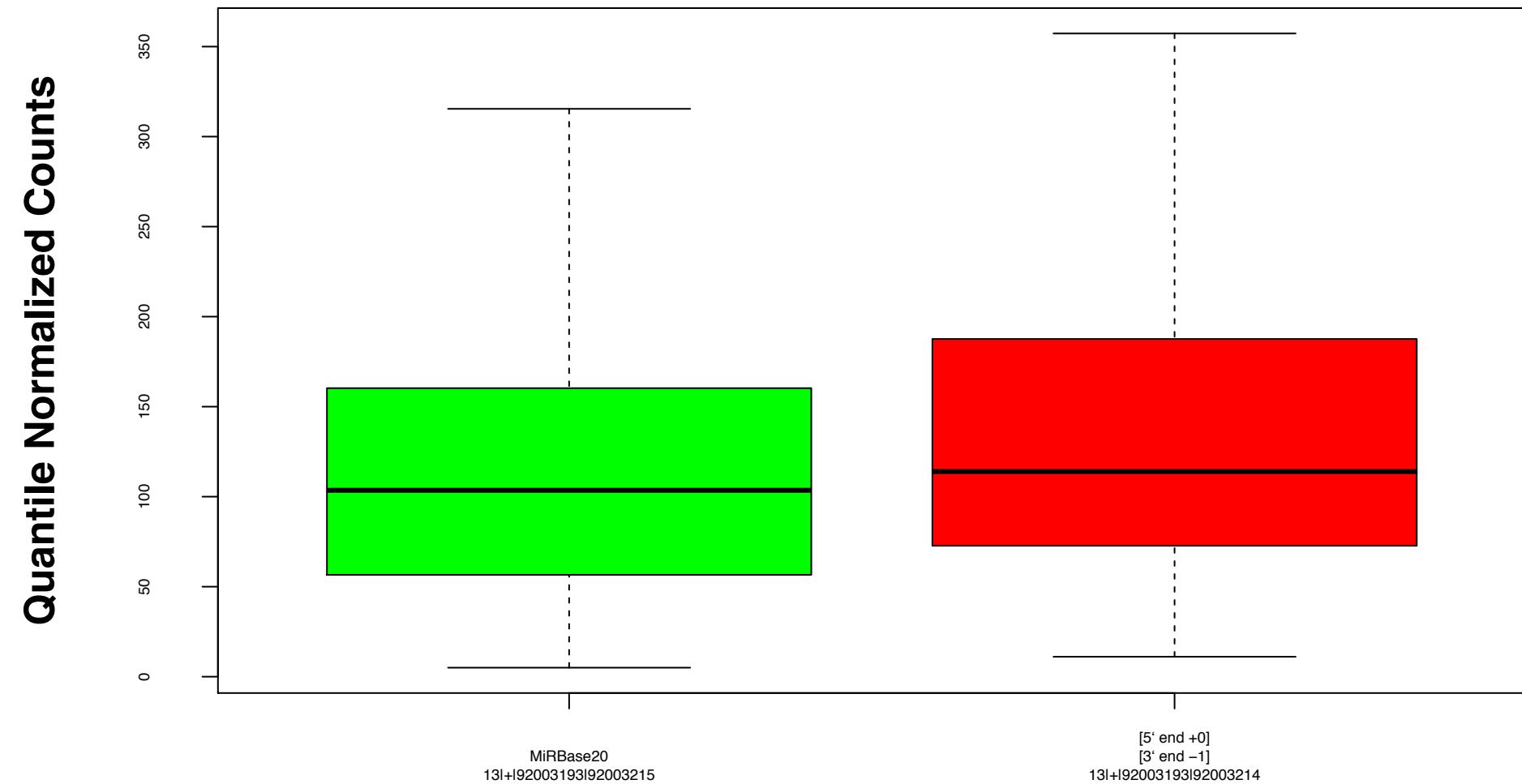
isomiRs

MIMAT0000104=hsa-miR-107=MI0000114

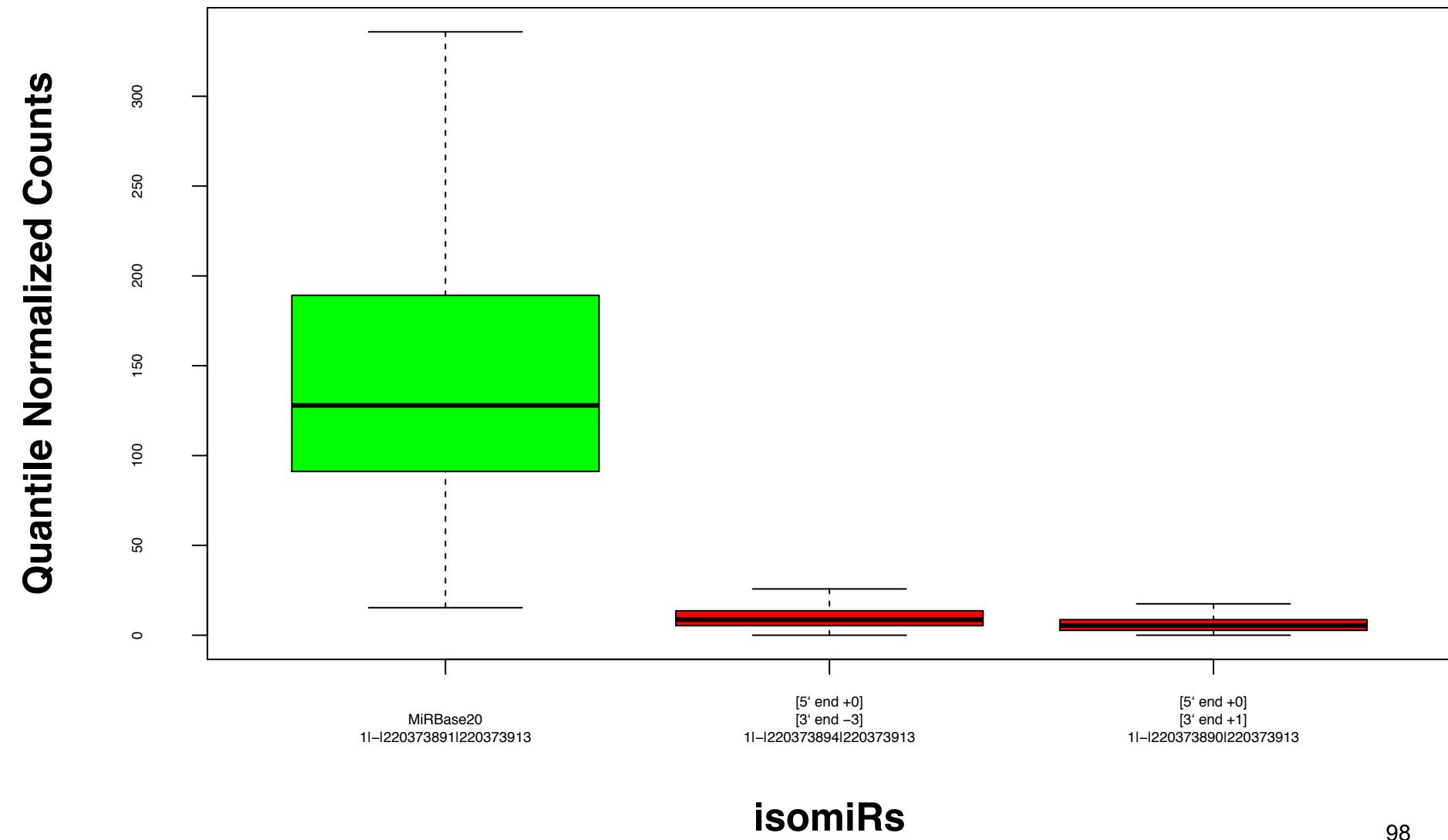


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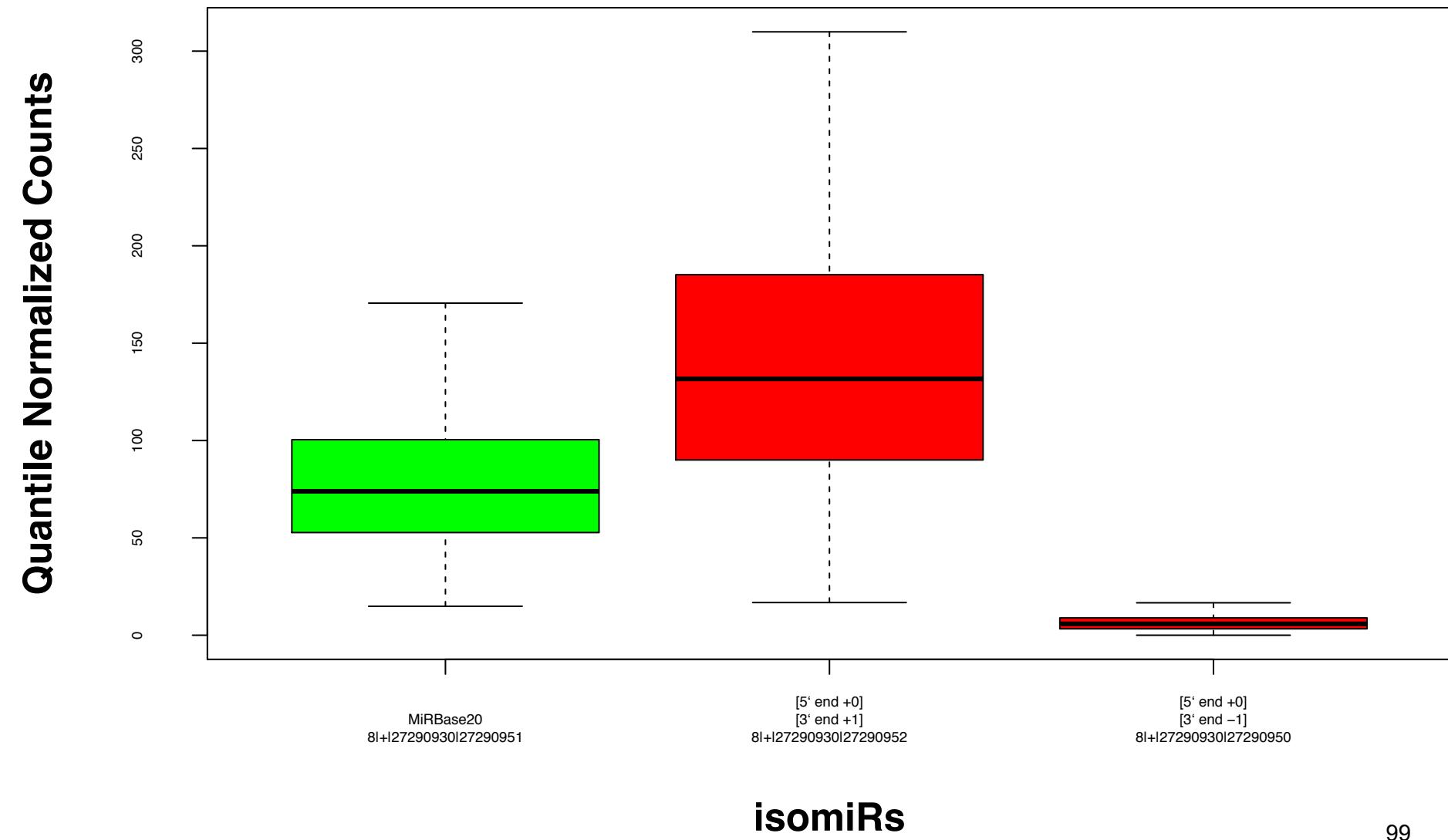
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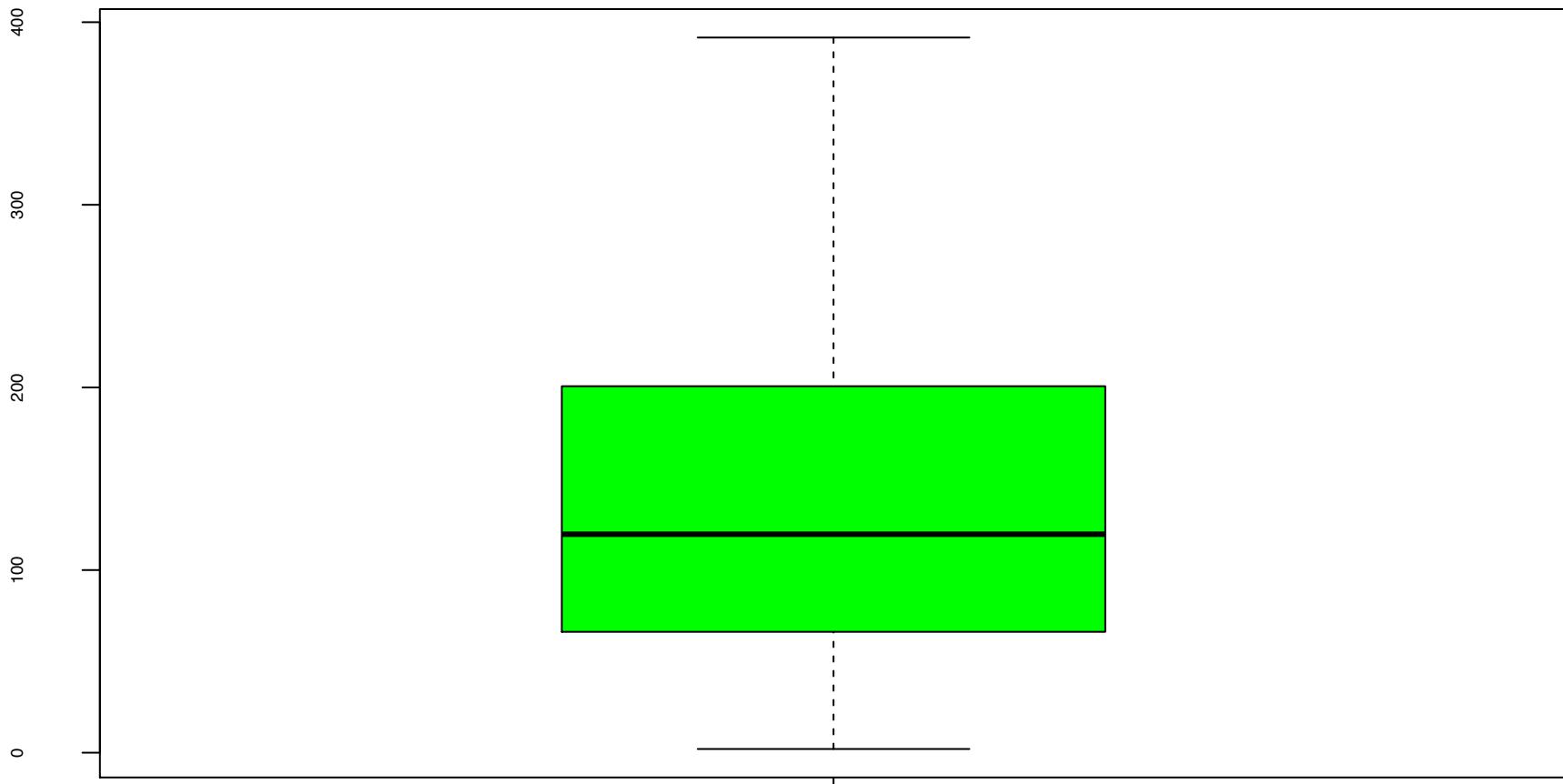


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Quantile Normalized Counts

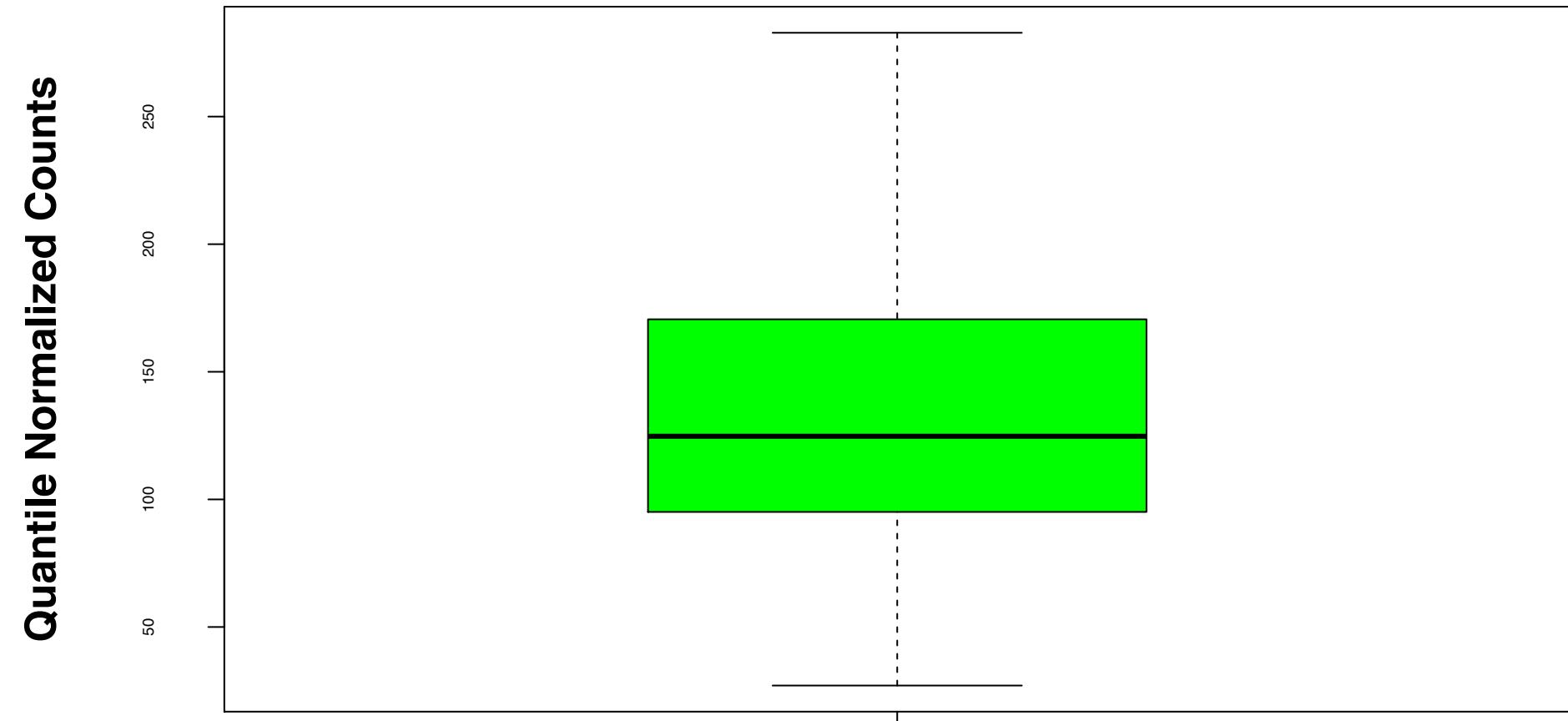


MiRBase20
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isomiRs

100

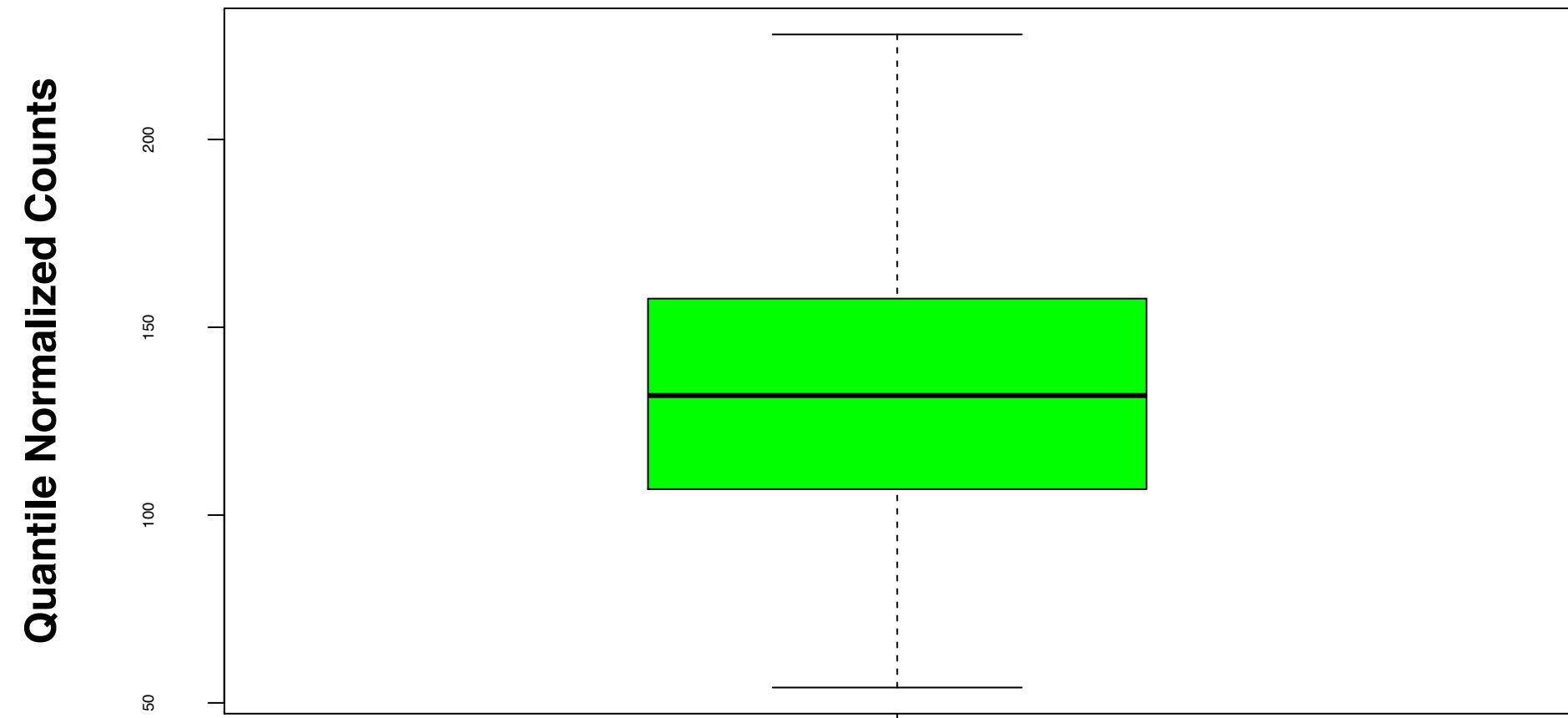
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MiRBase20
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isomiRs

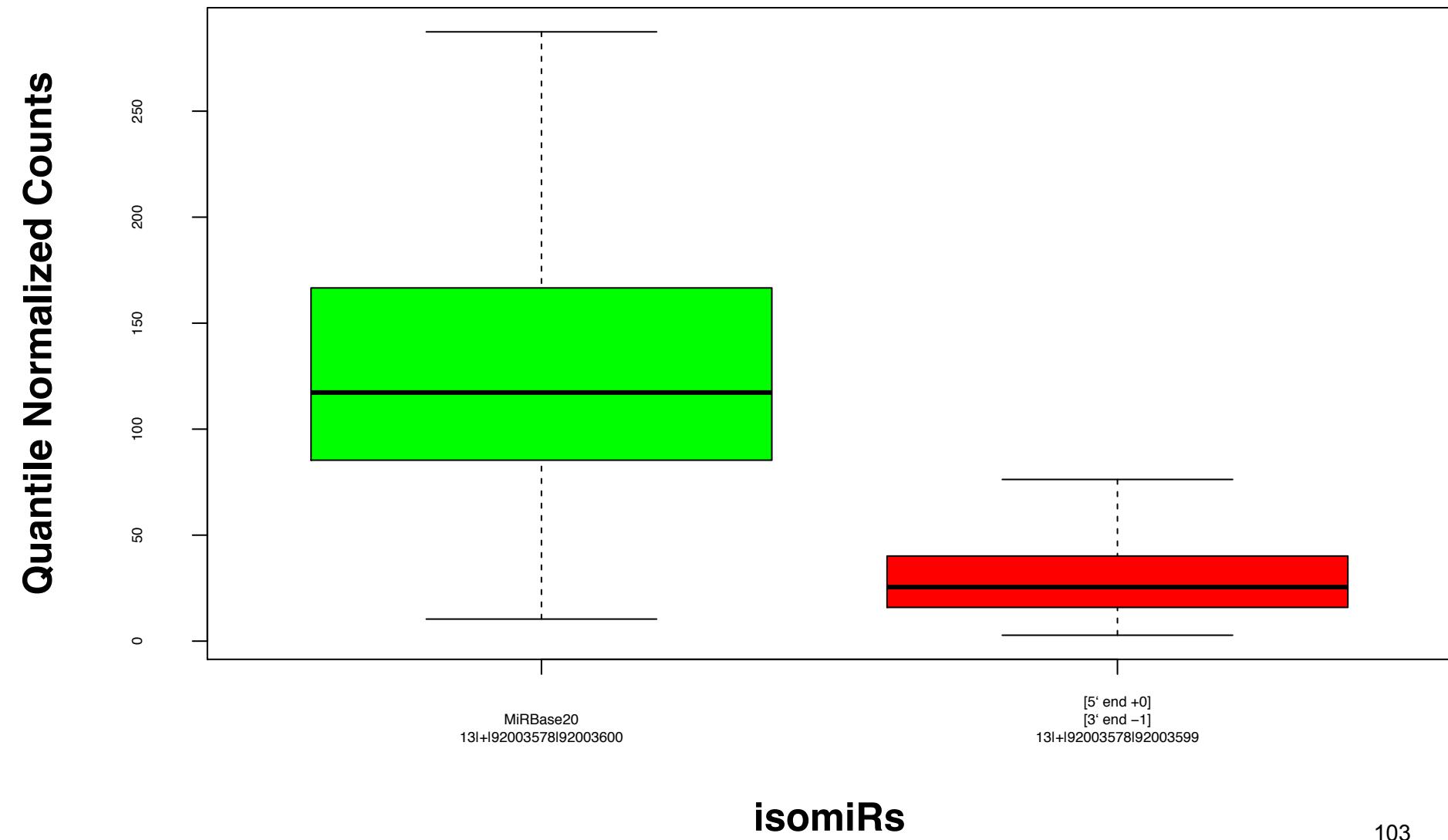
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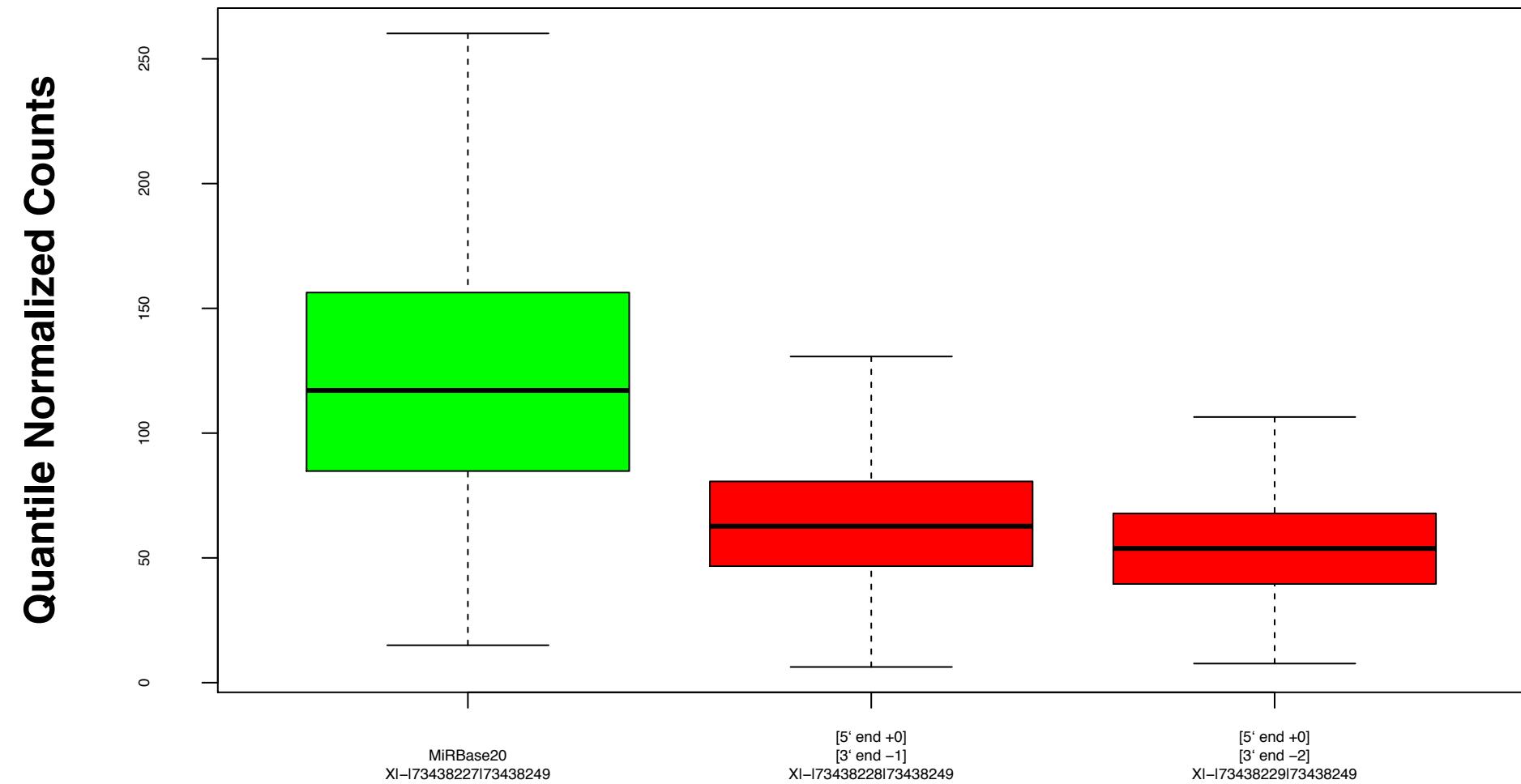
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isomiRs

MIMAT0004507=hsa-miR-92a-1-5p=MI0000093

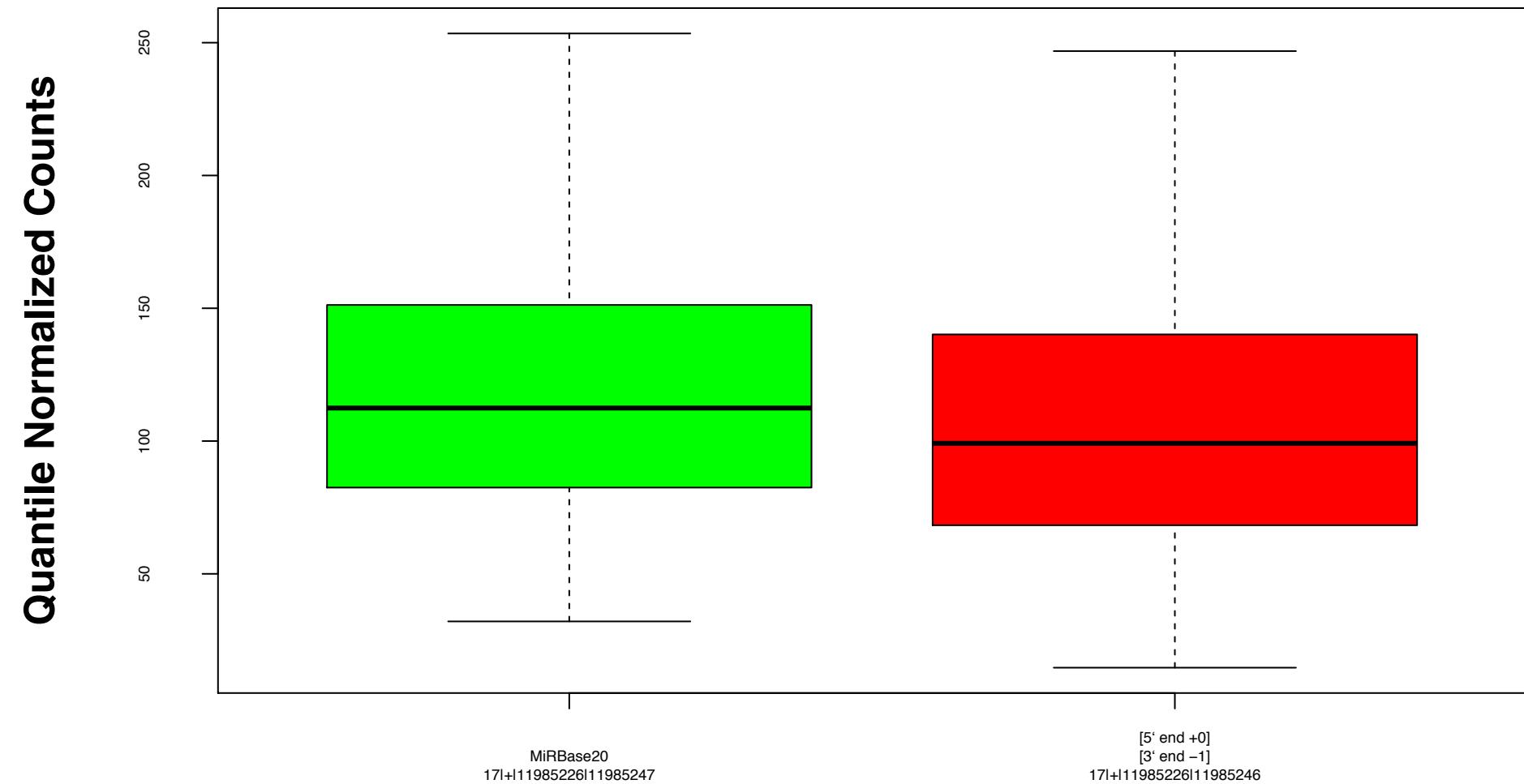


MIMAT0003339=hsa-miR-421=MI0003685

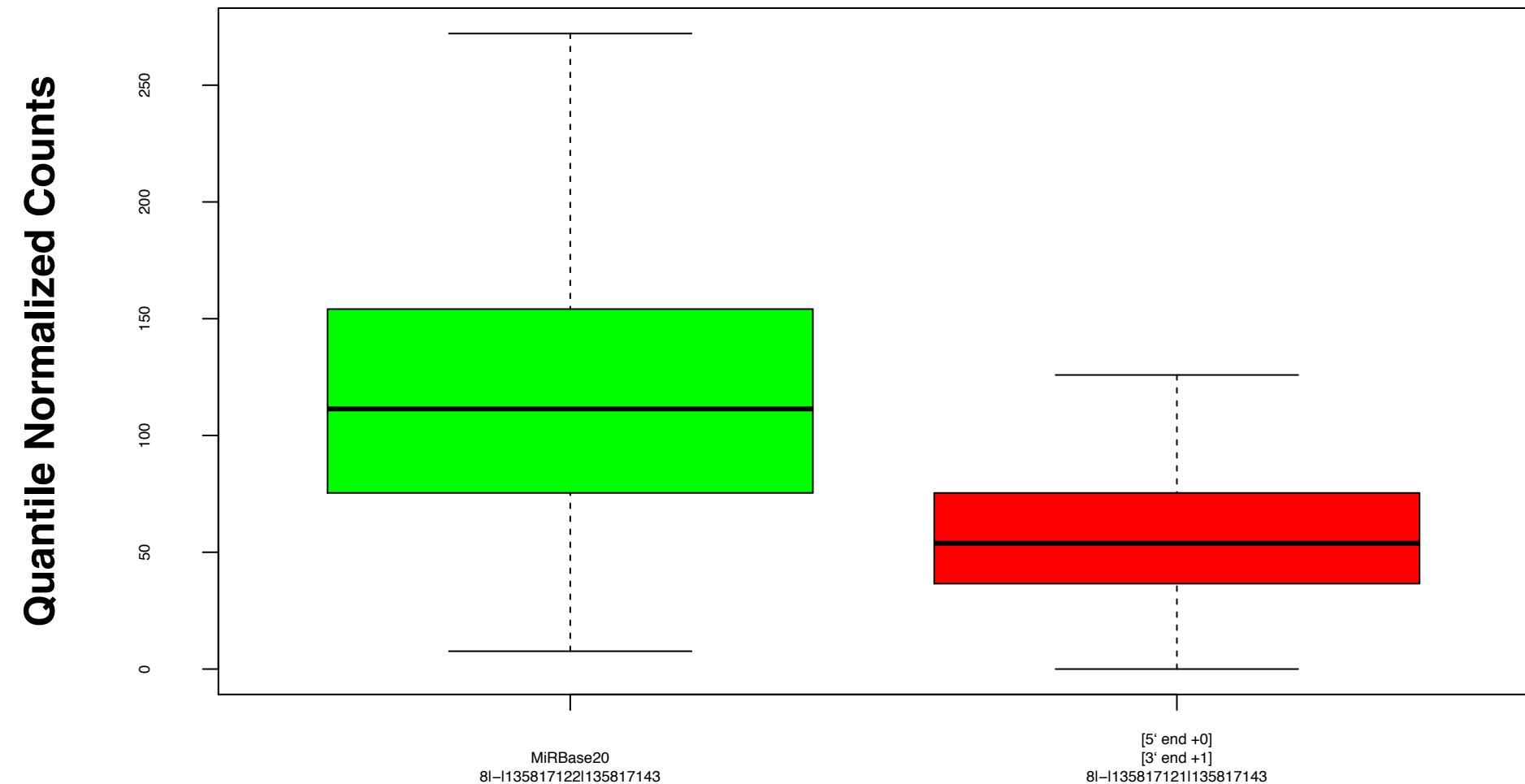


isomiRs

MIMAT0004945=hsa-miR-744-5p=MI0005559

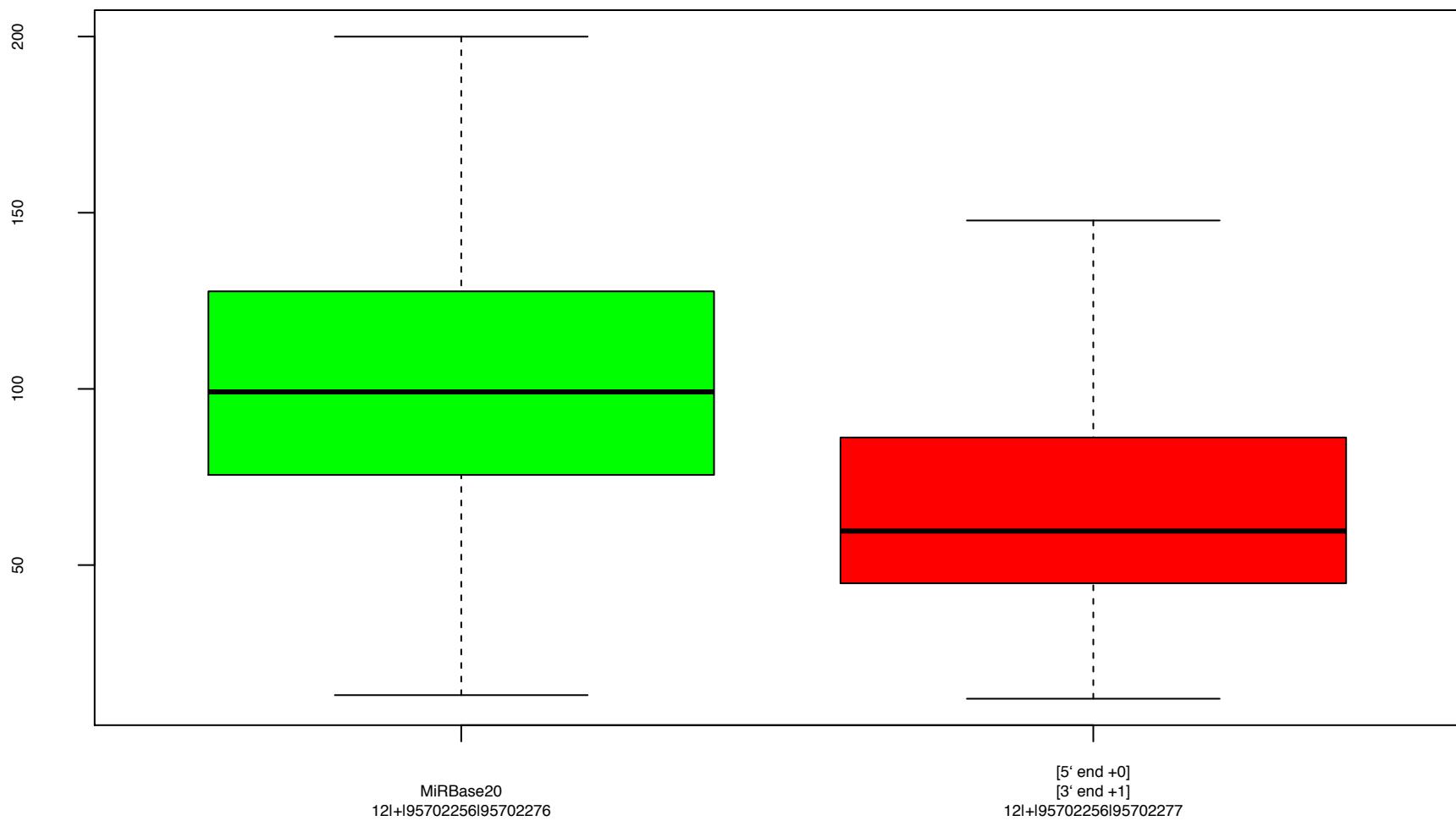


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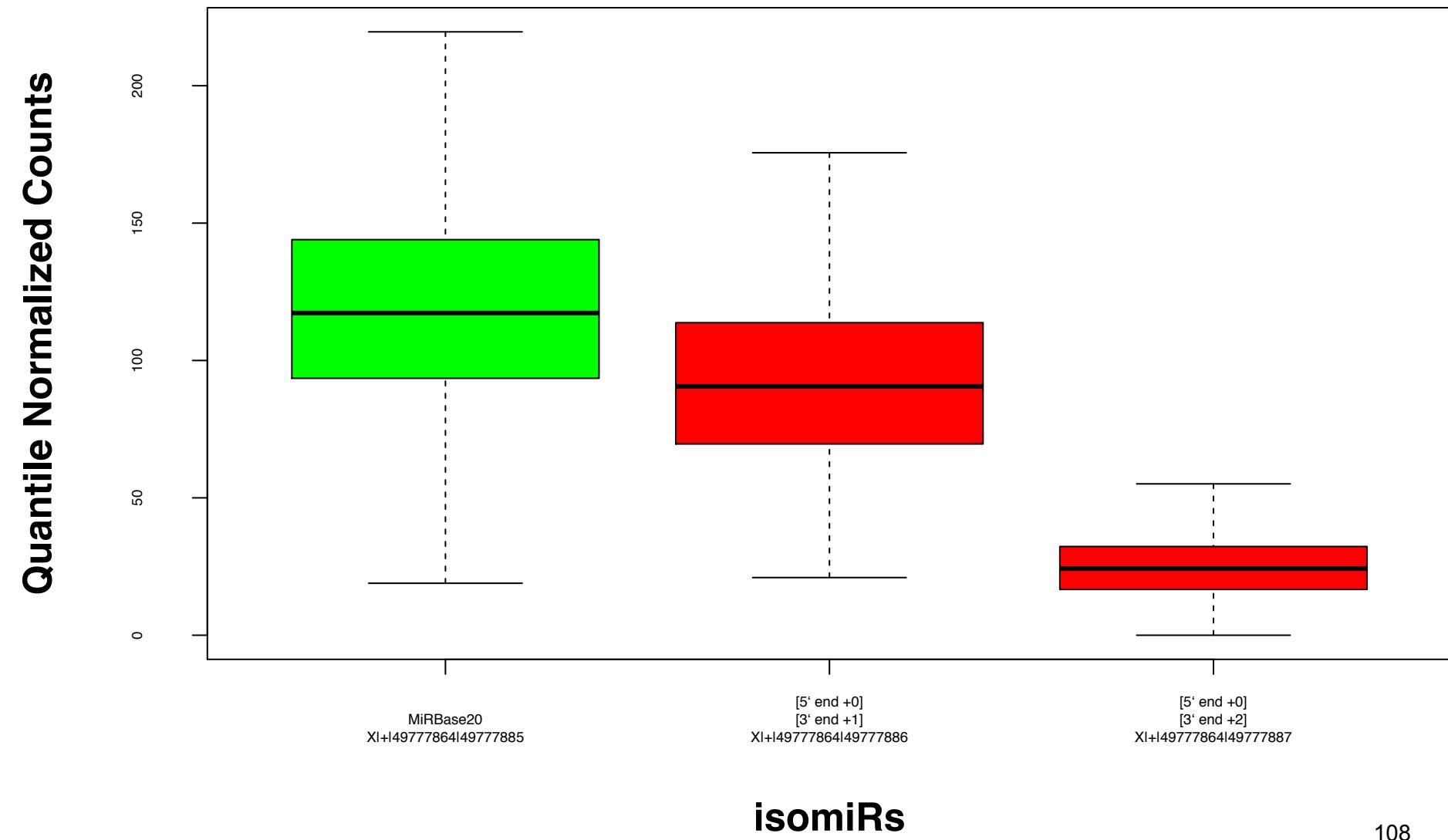
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Quantile Normalized Counts

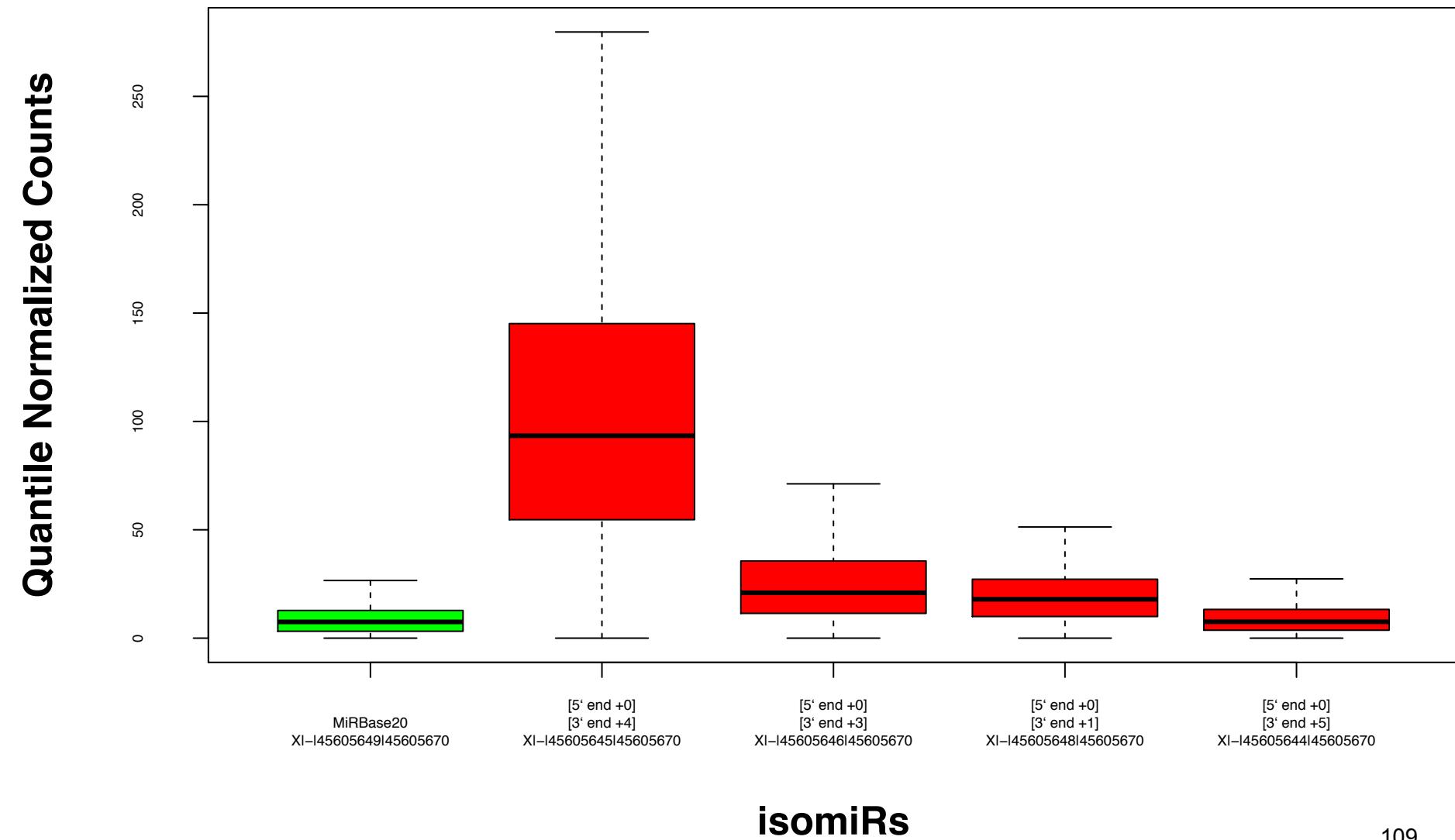


isomiRs

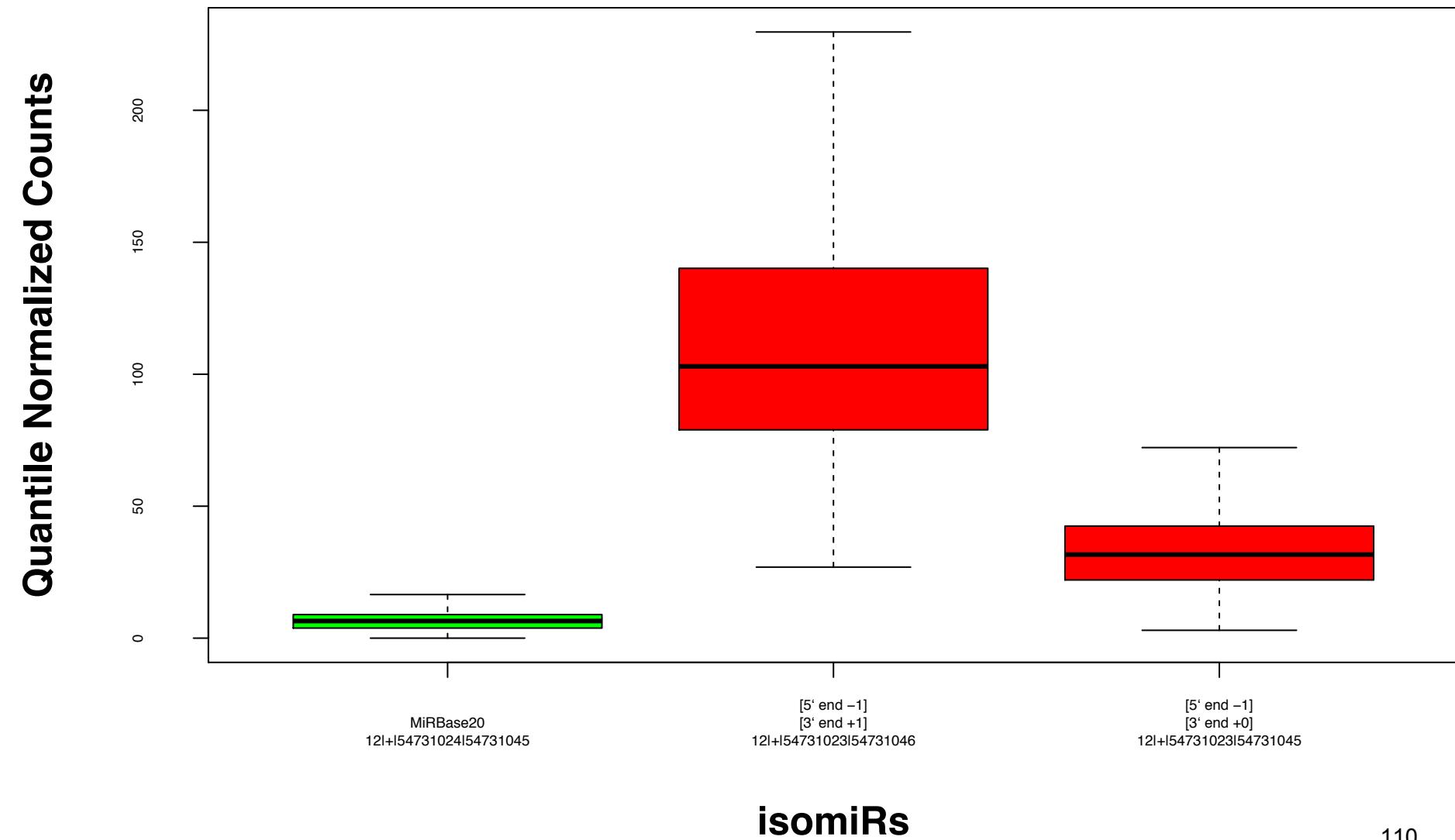
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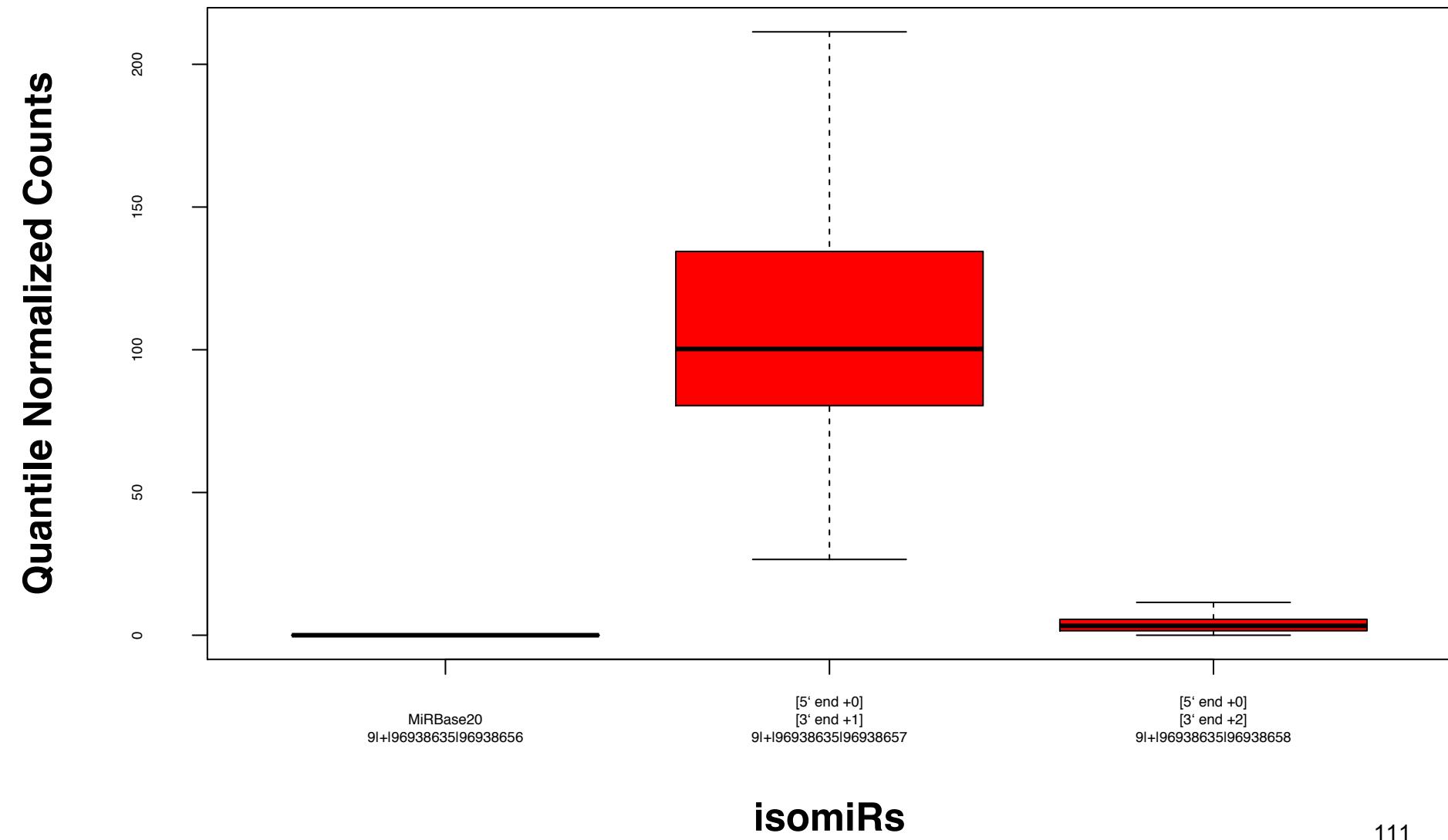


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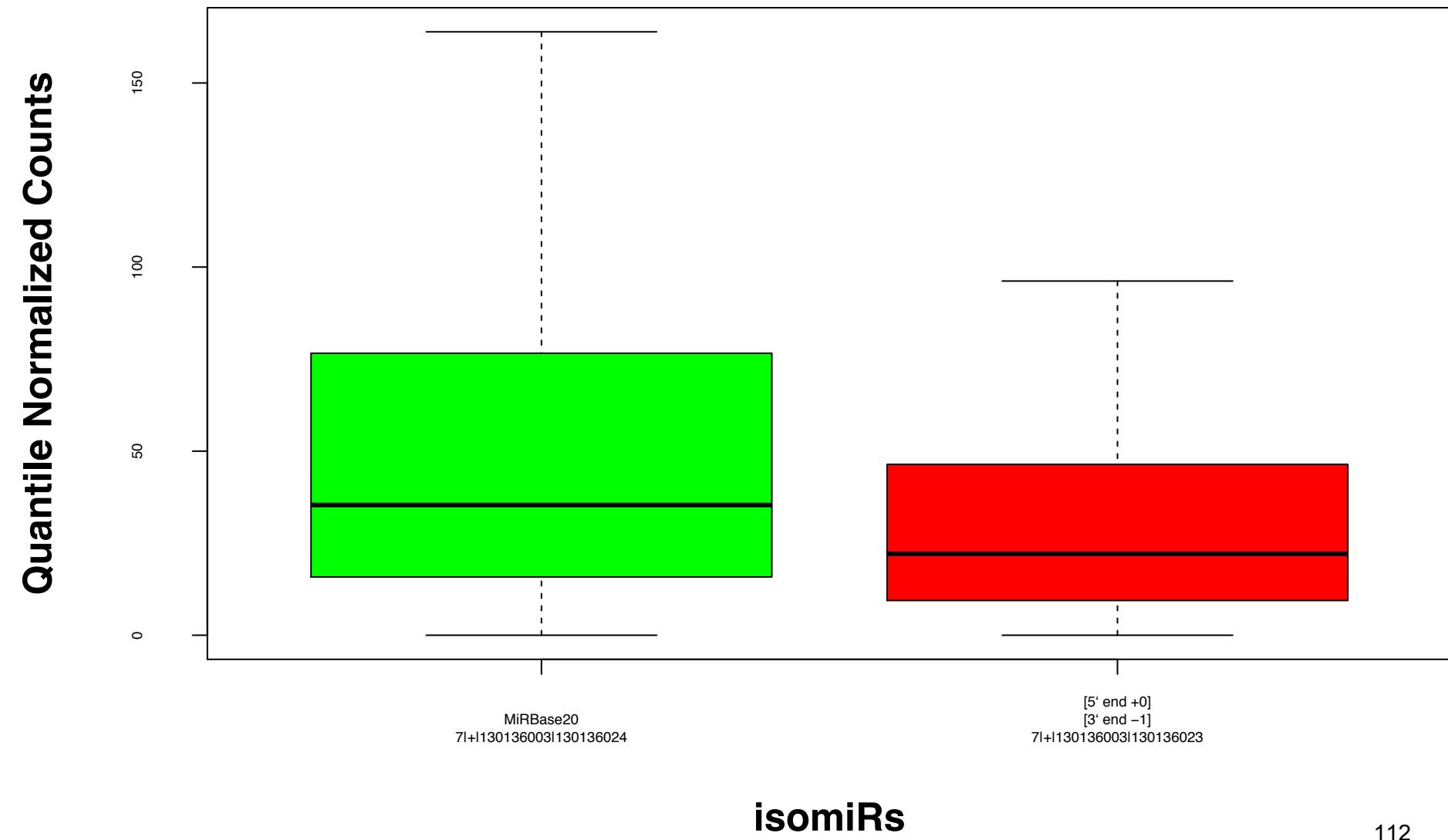


isomiRs

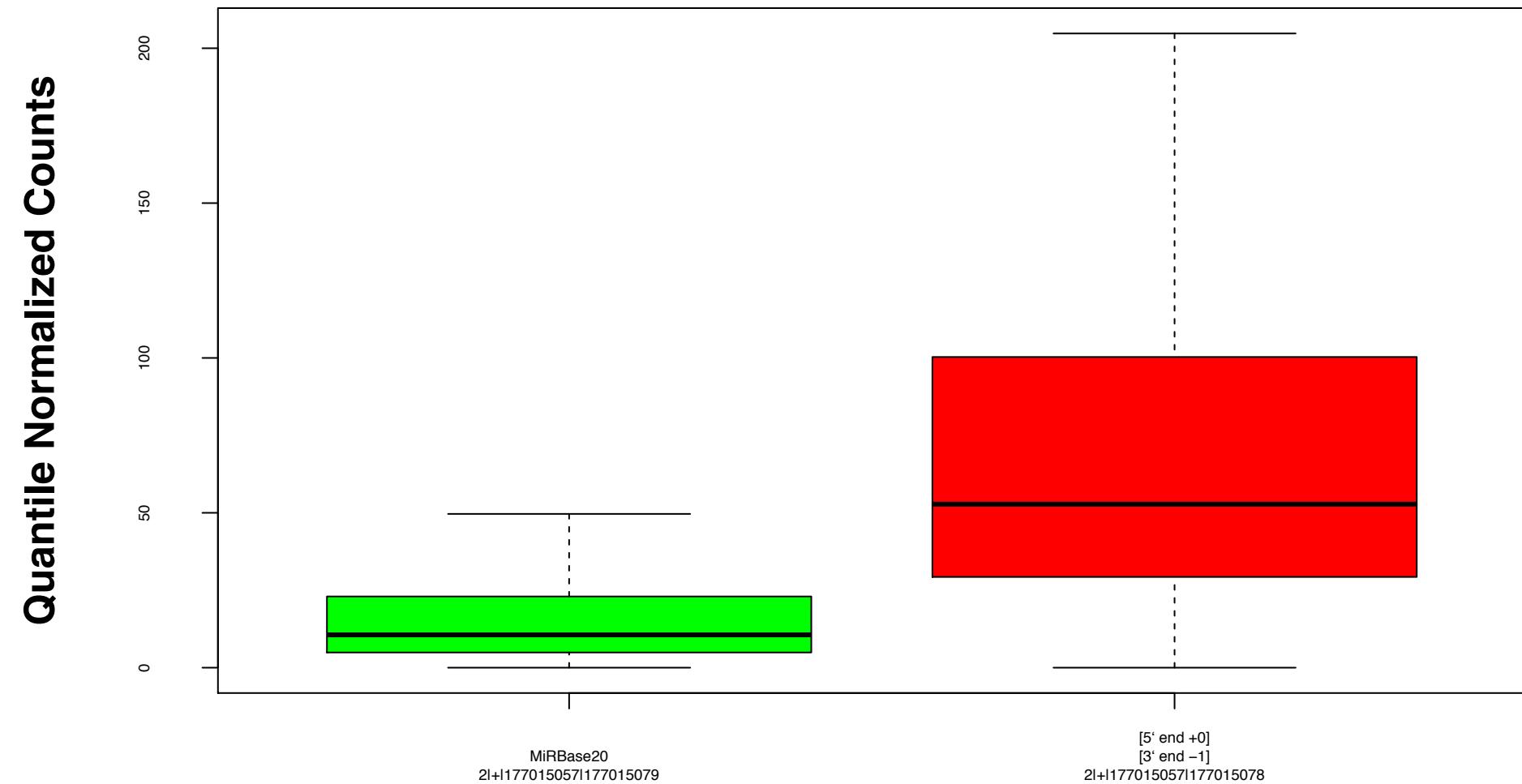
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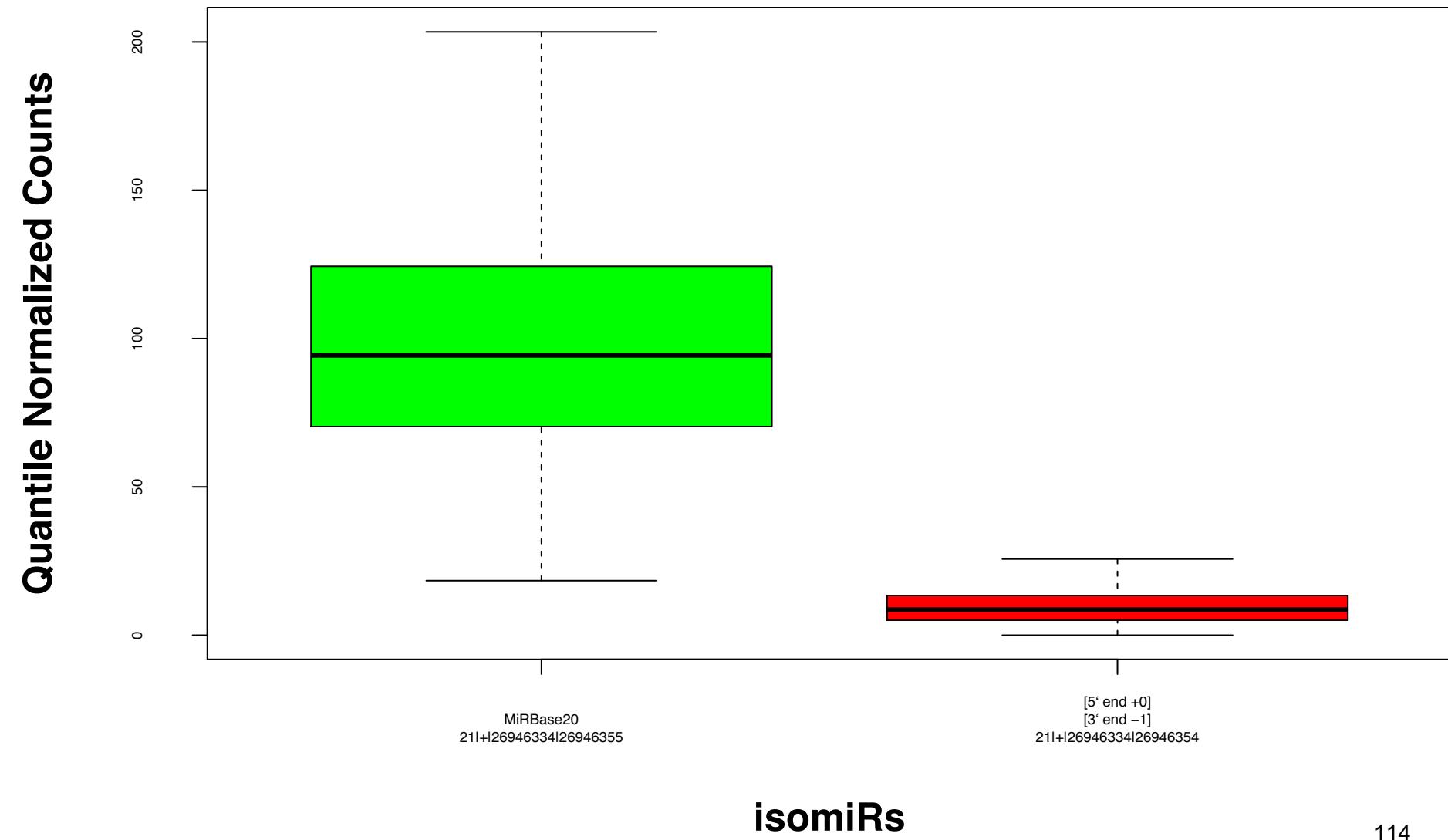
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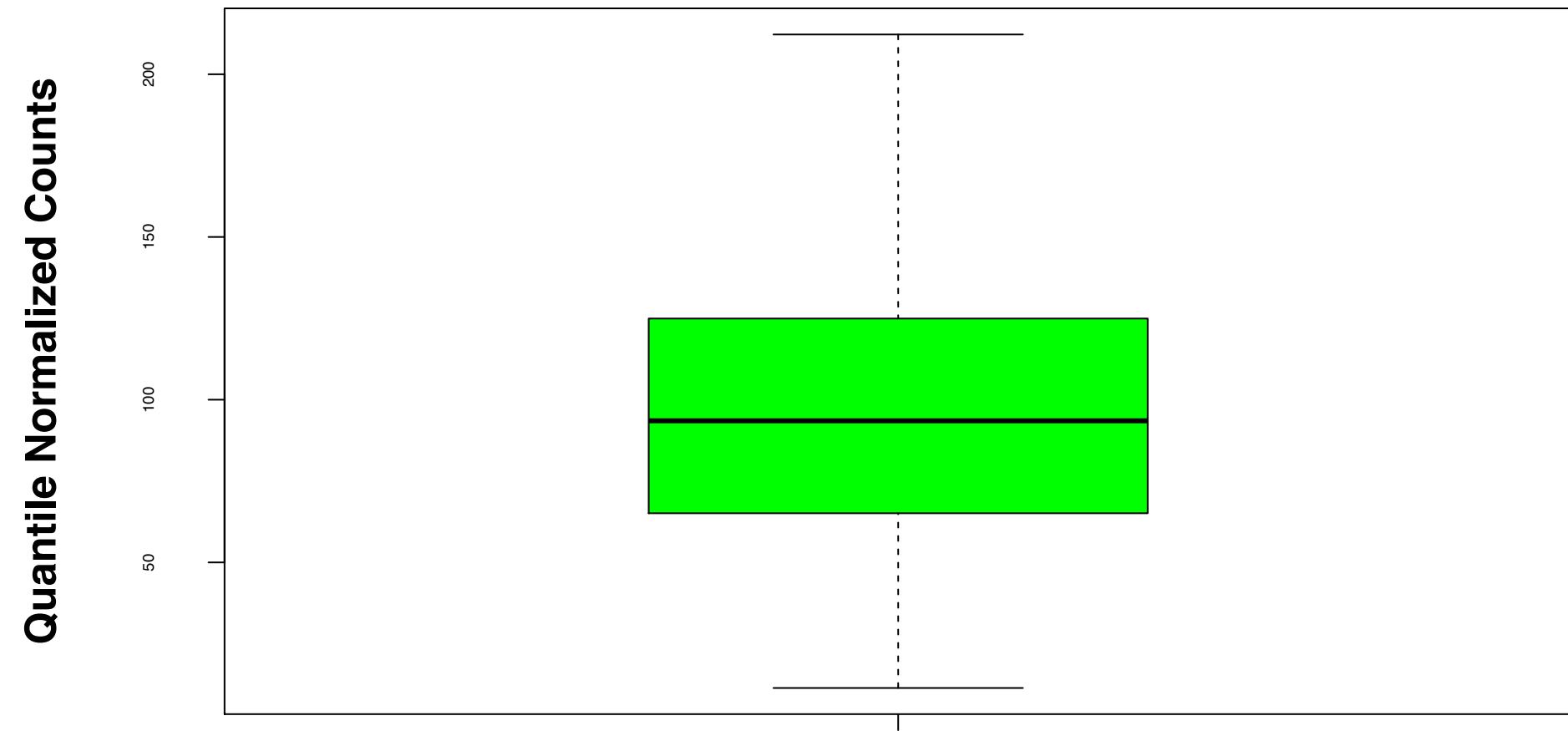
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MIMAT0004658=hsa-miR-155-3p=MI0000681



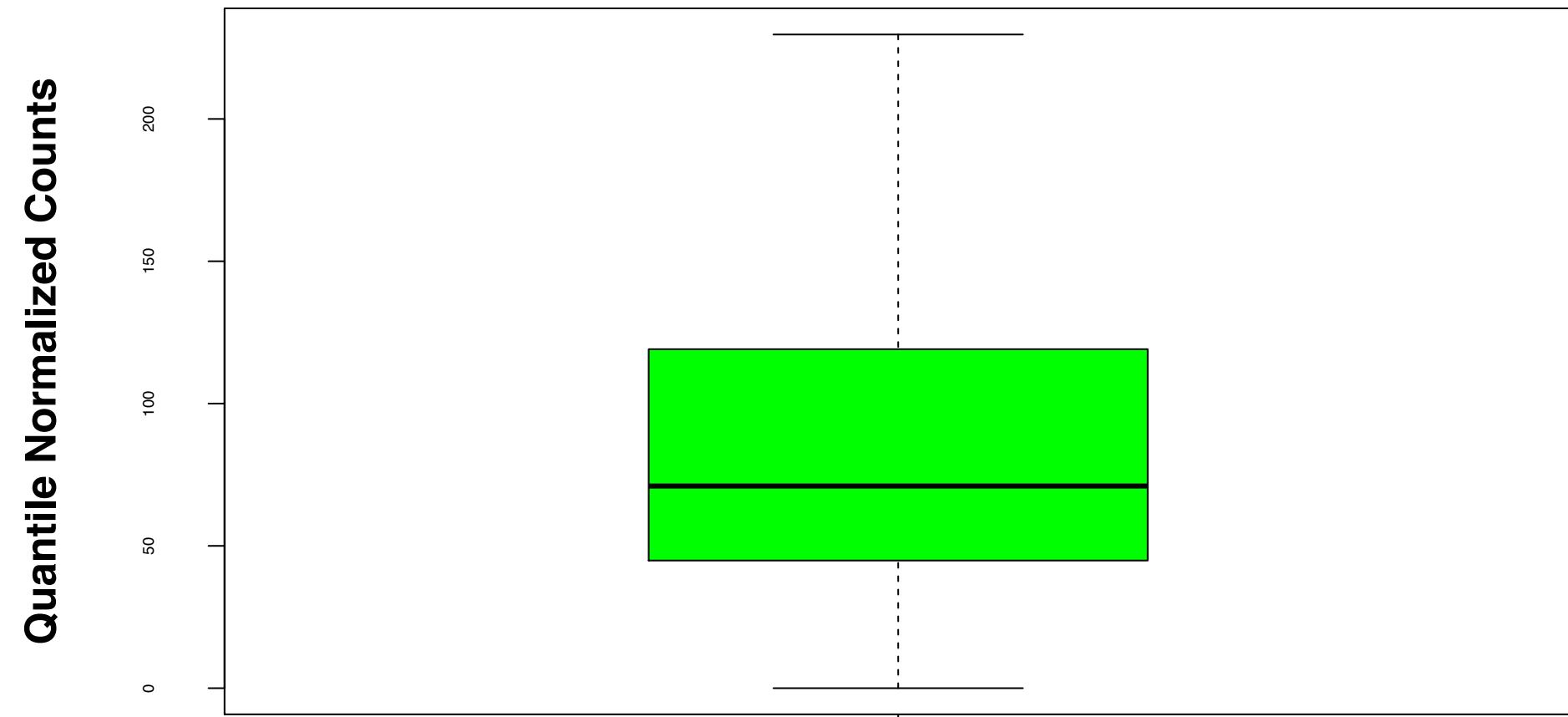
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MiRBase20
21+136422981+136423003

isomiRs

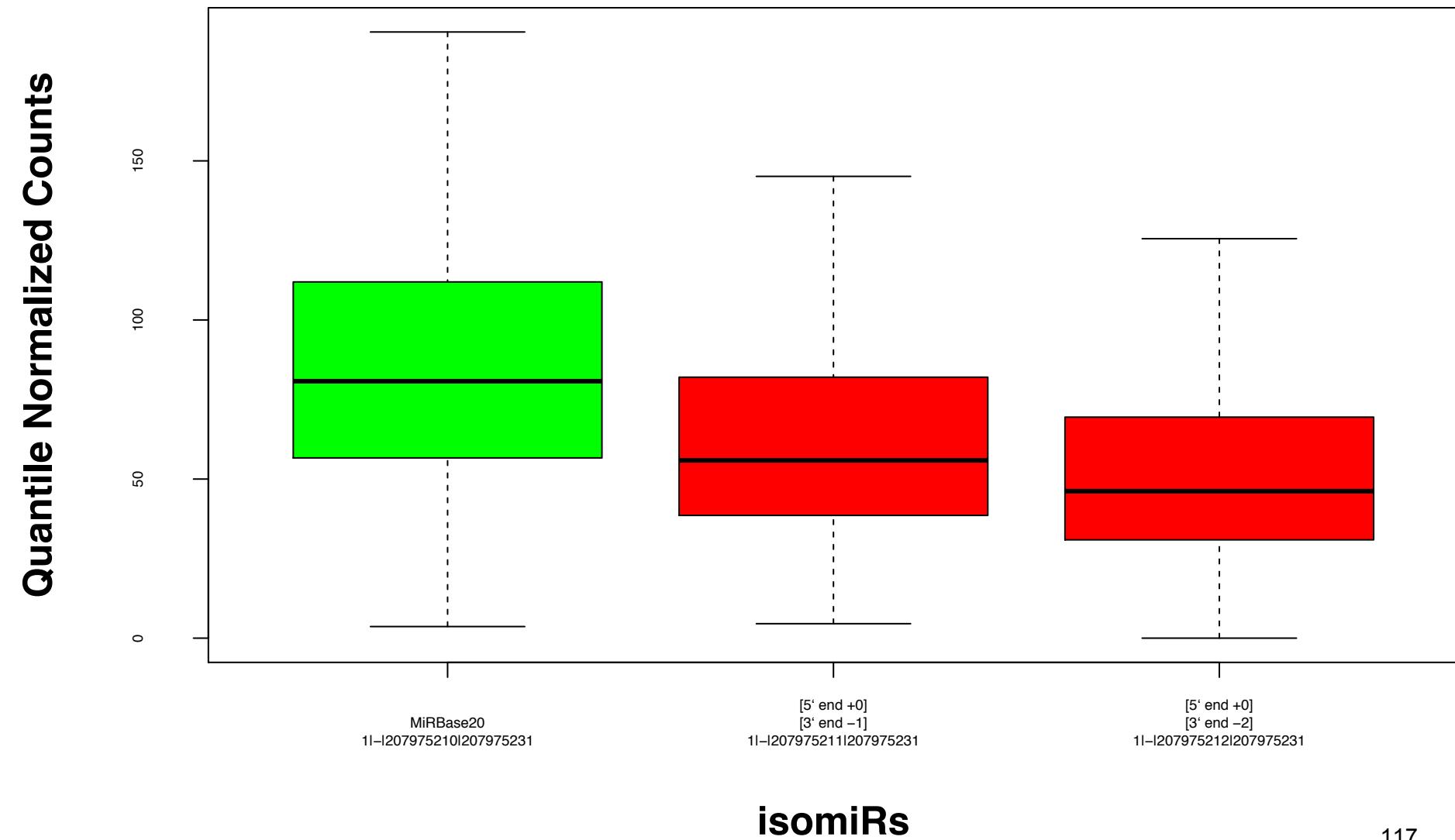
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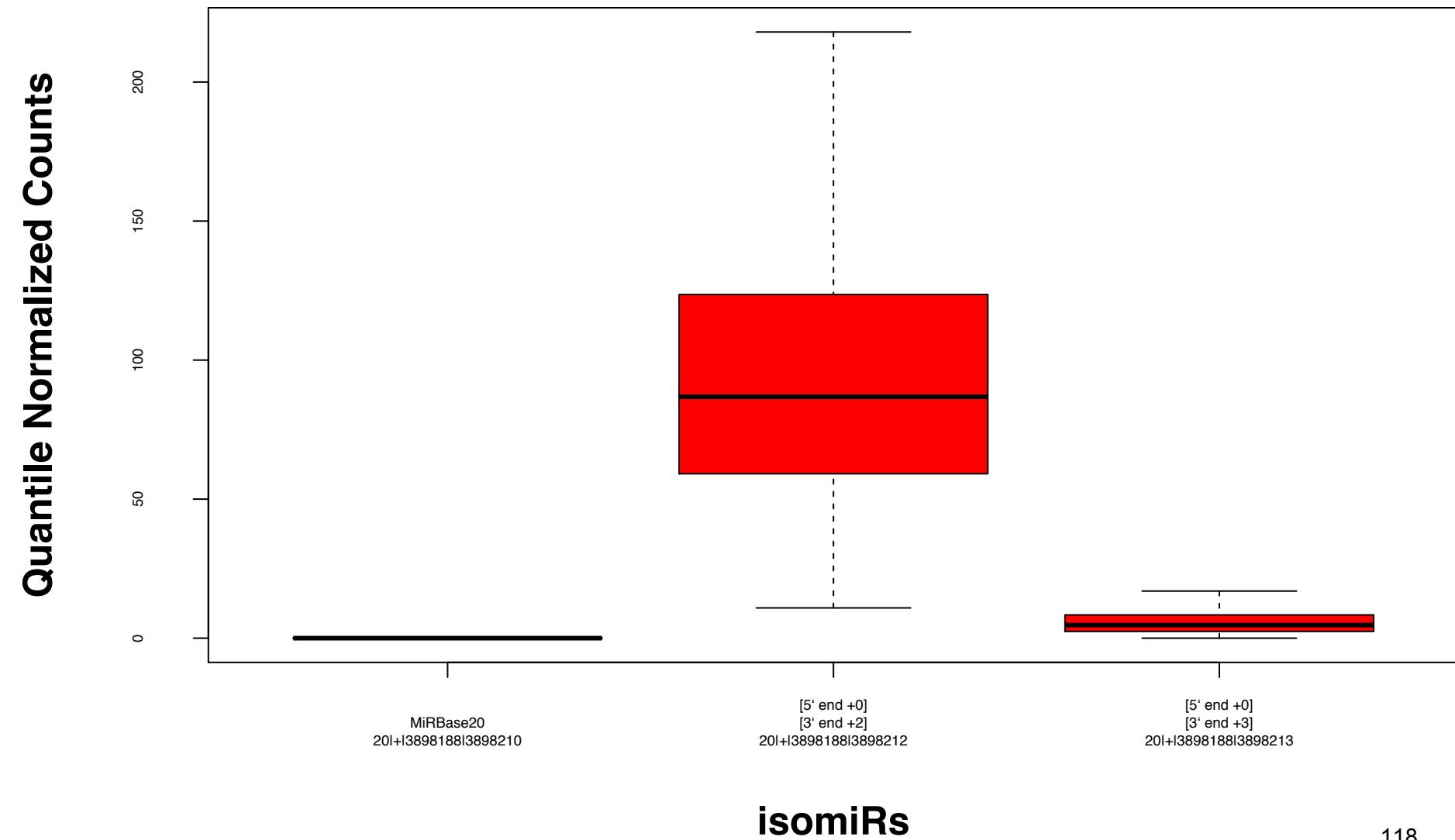
MiRBase20
19l+I52196046l52196067

isomiRs

MIMAT0000681=hsa-miR-29c-3p=MI0000735

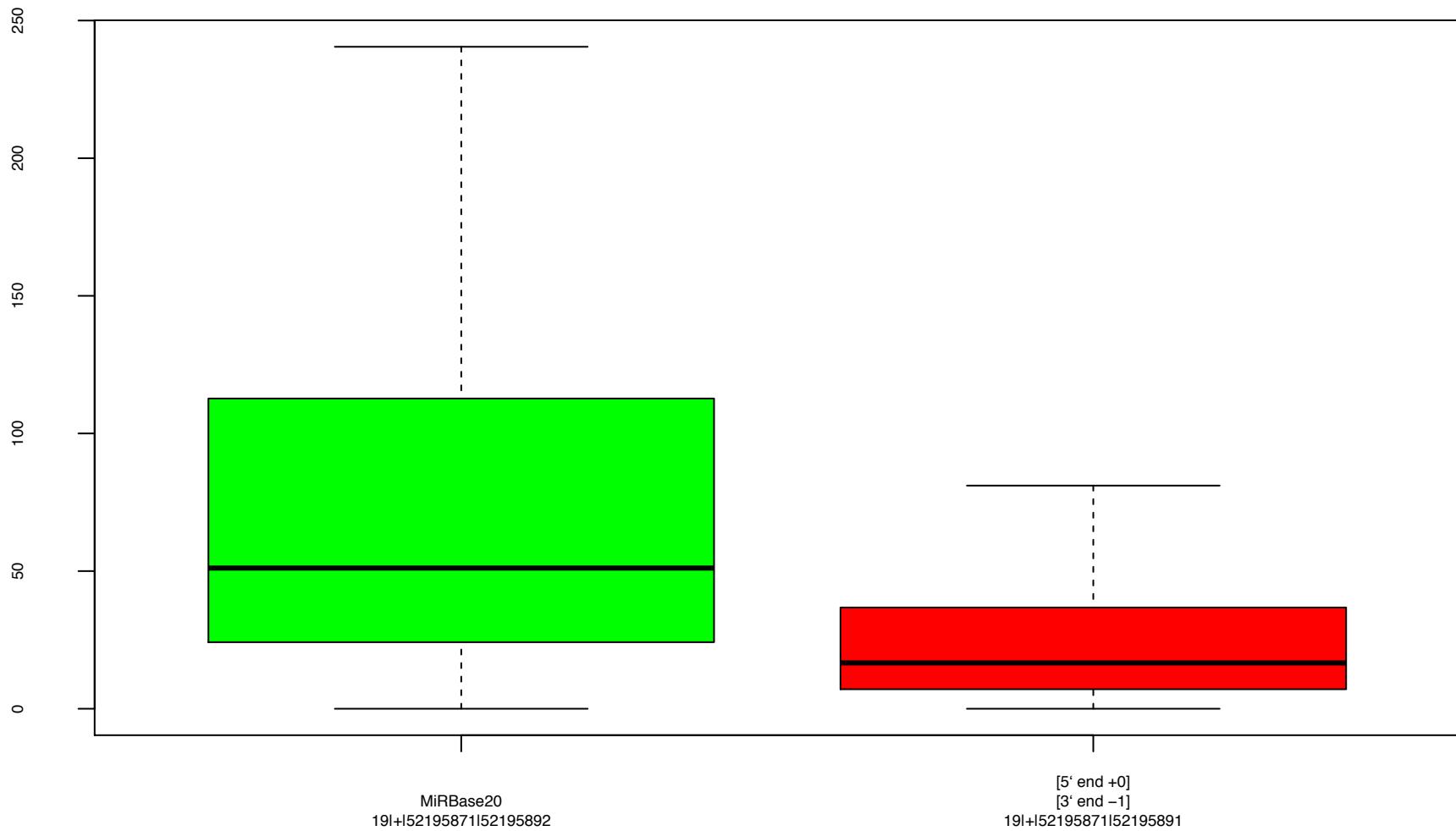


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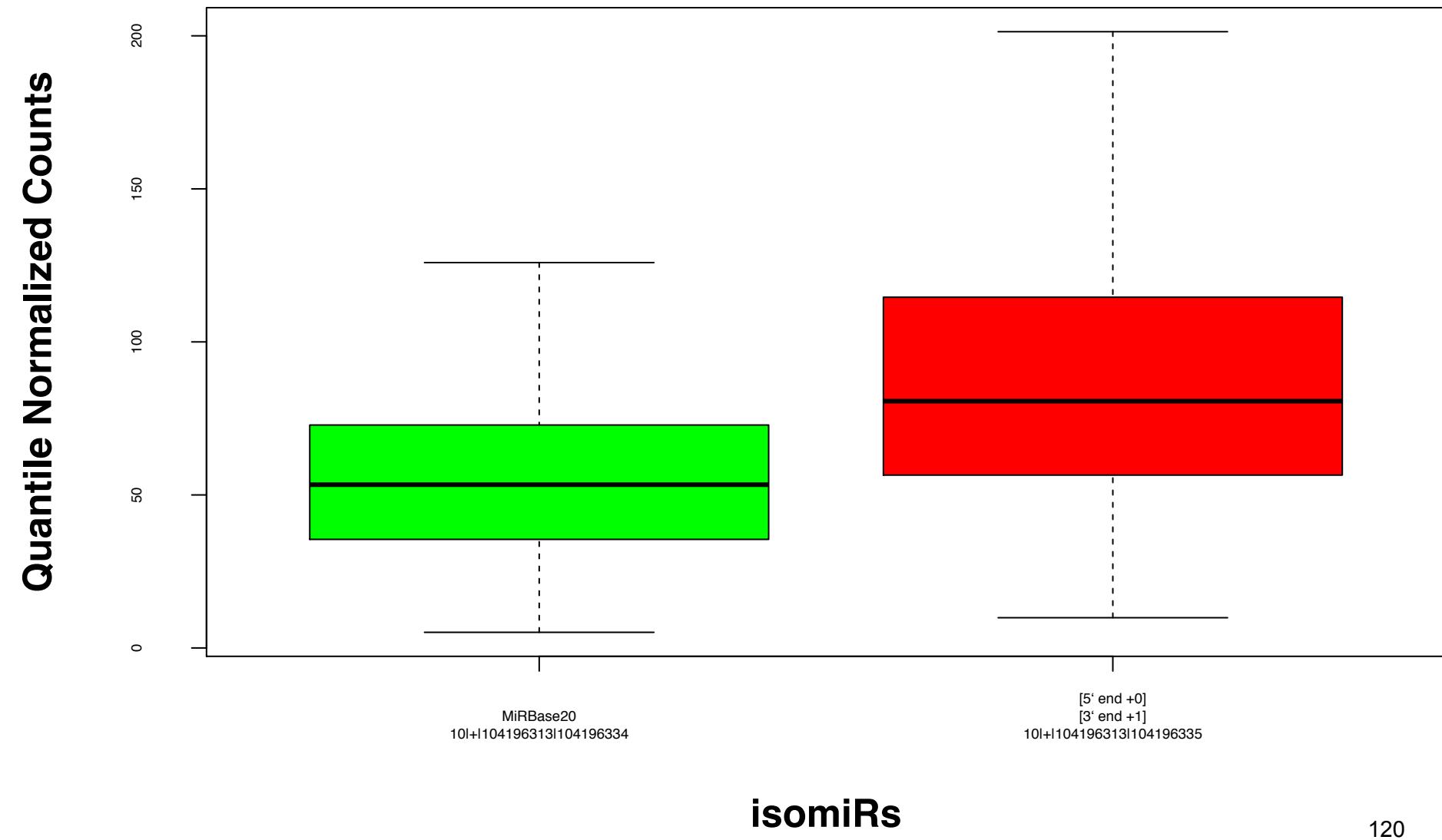
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Quantile Normalized Counts



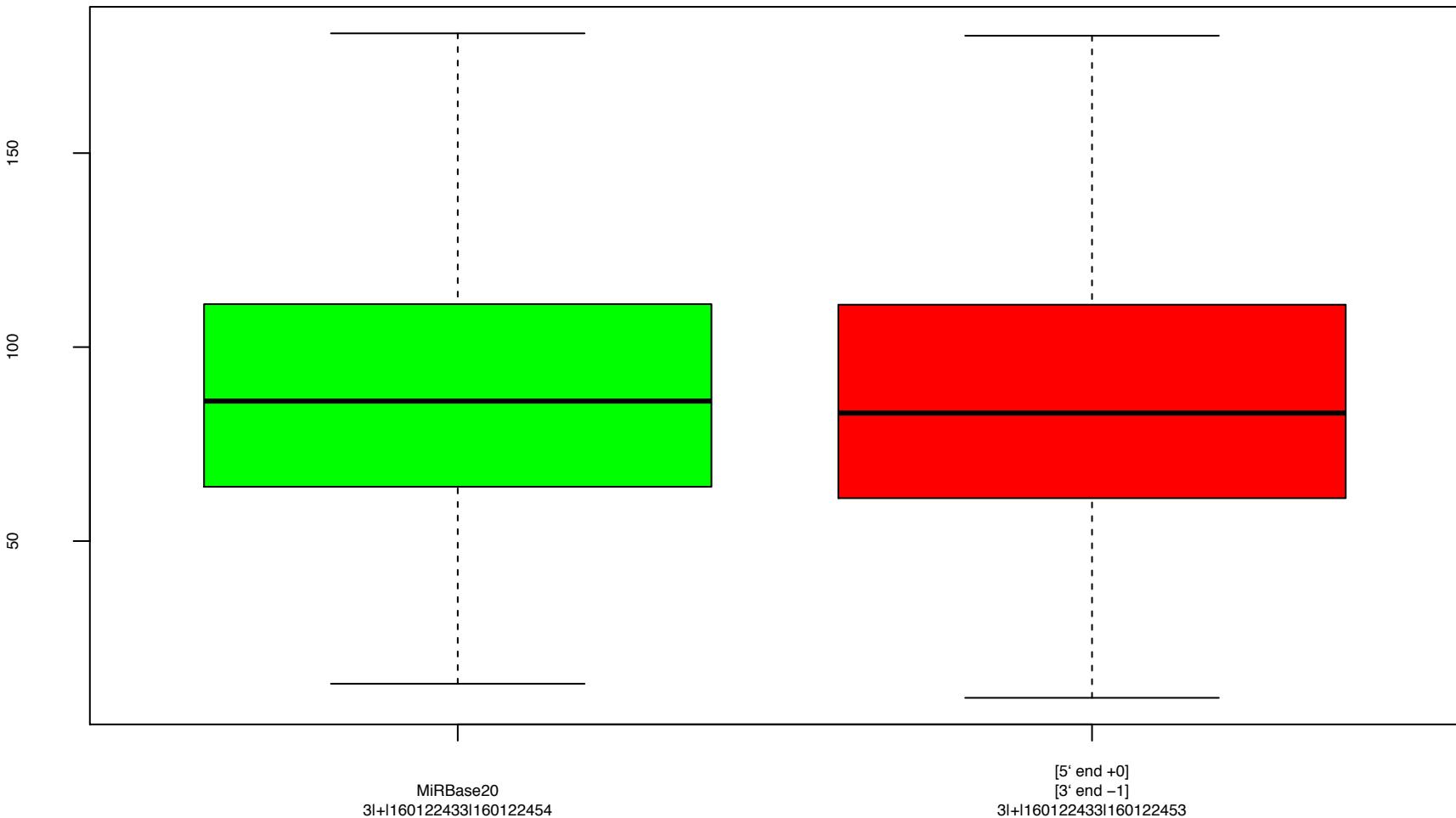
isomiRs

MIMAT0004766=hsa-miR-146b-3p=MI0003129



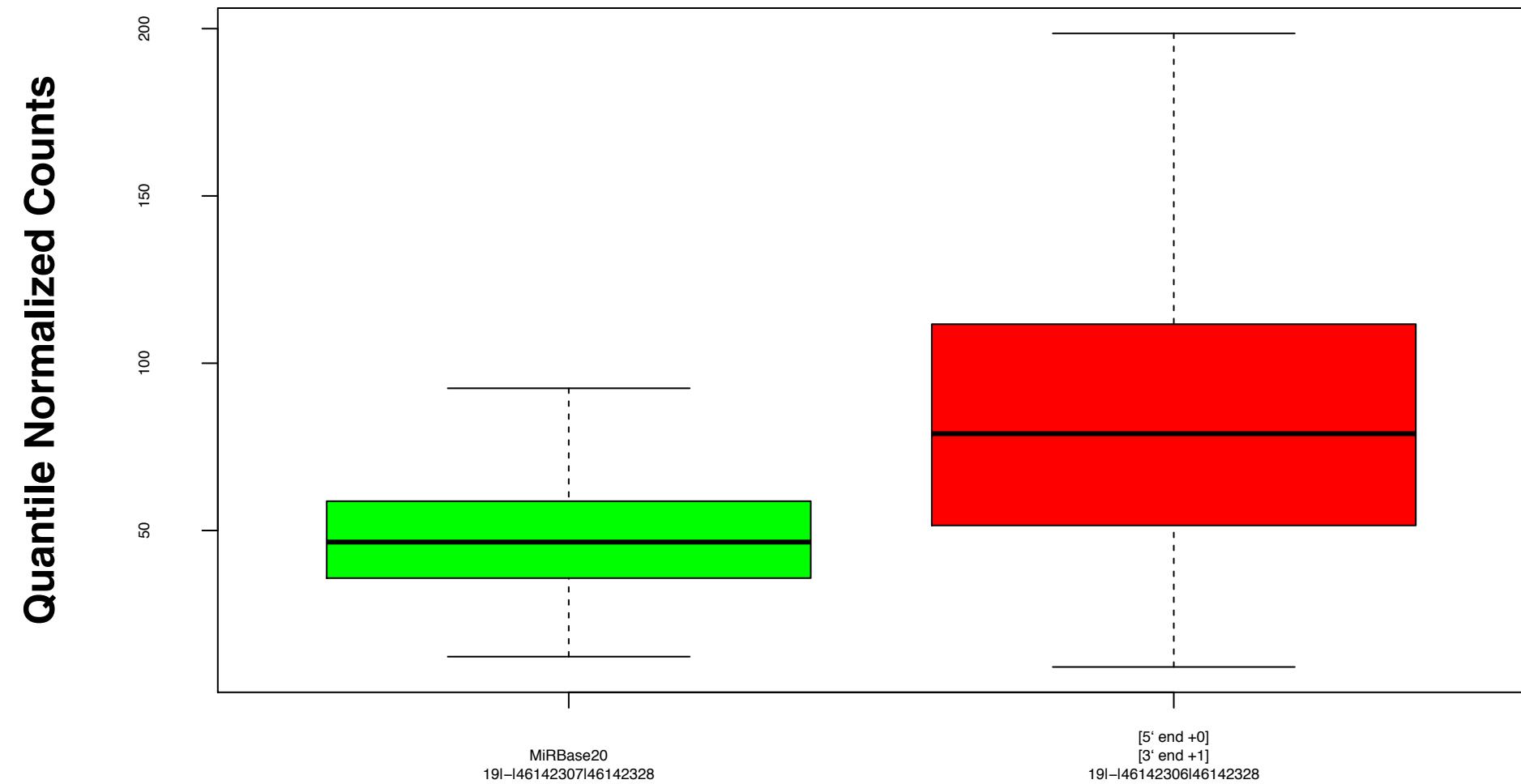
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Quantile Normalized Counts



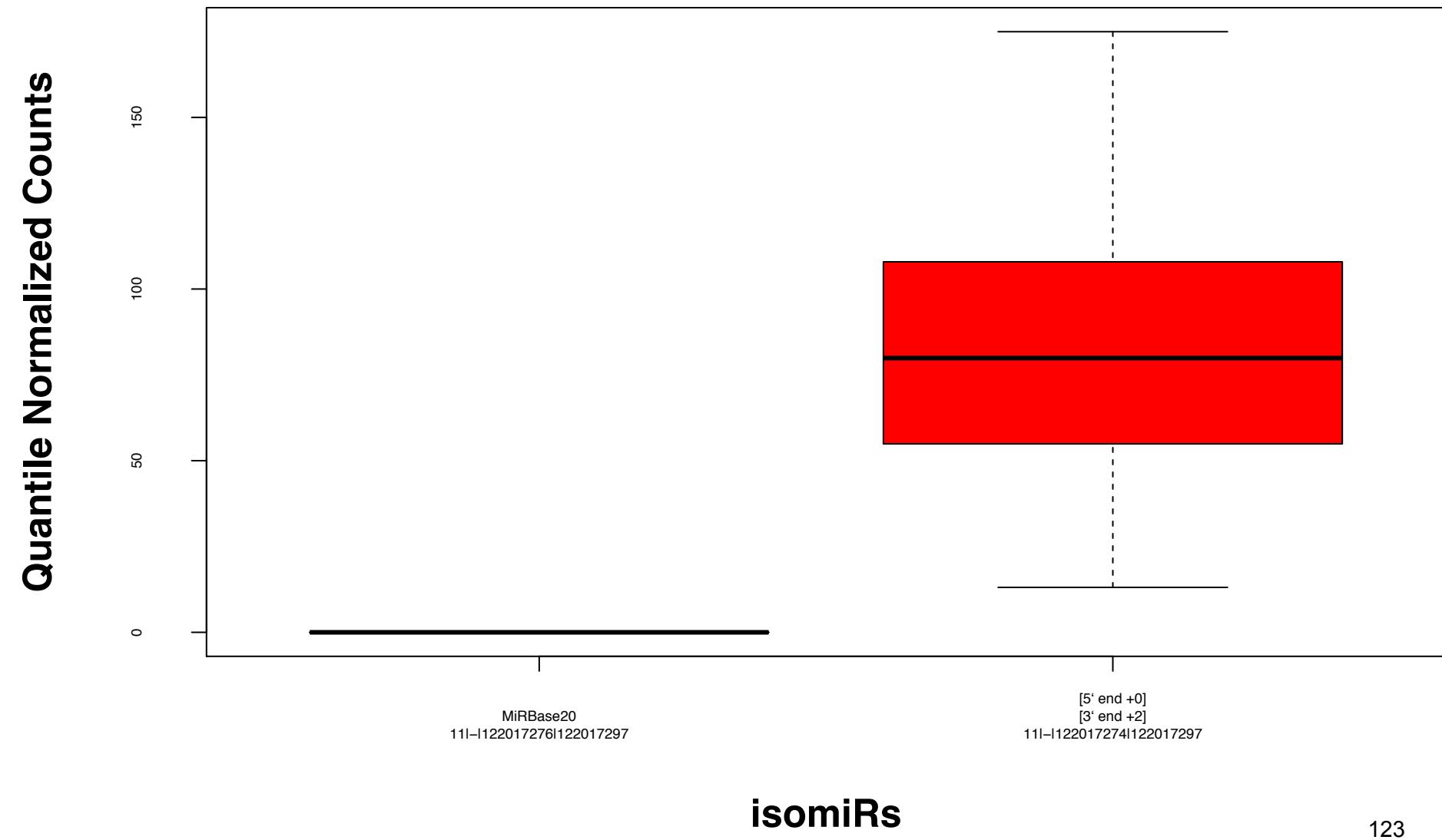
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MIMAT0004693=hsa-miR-330-5p=MI0000803

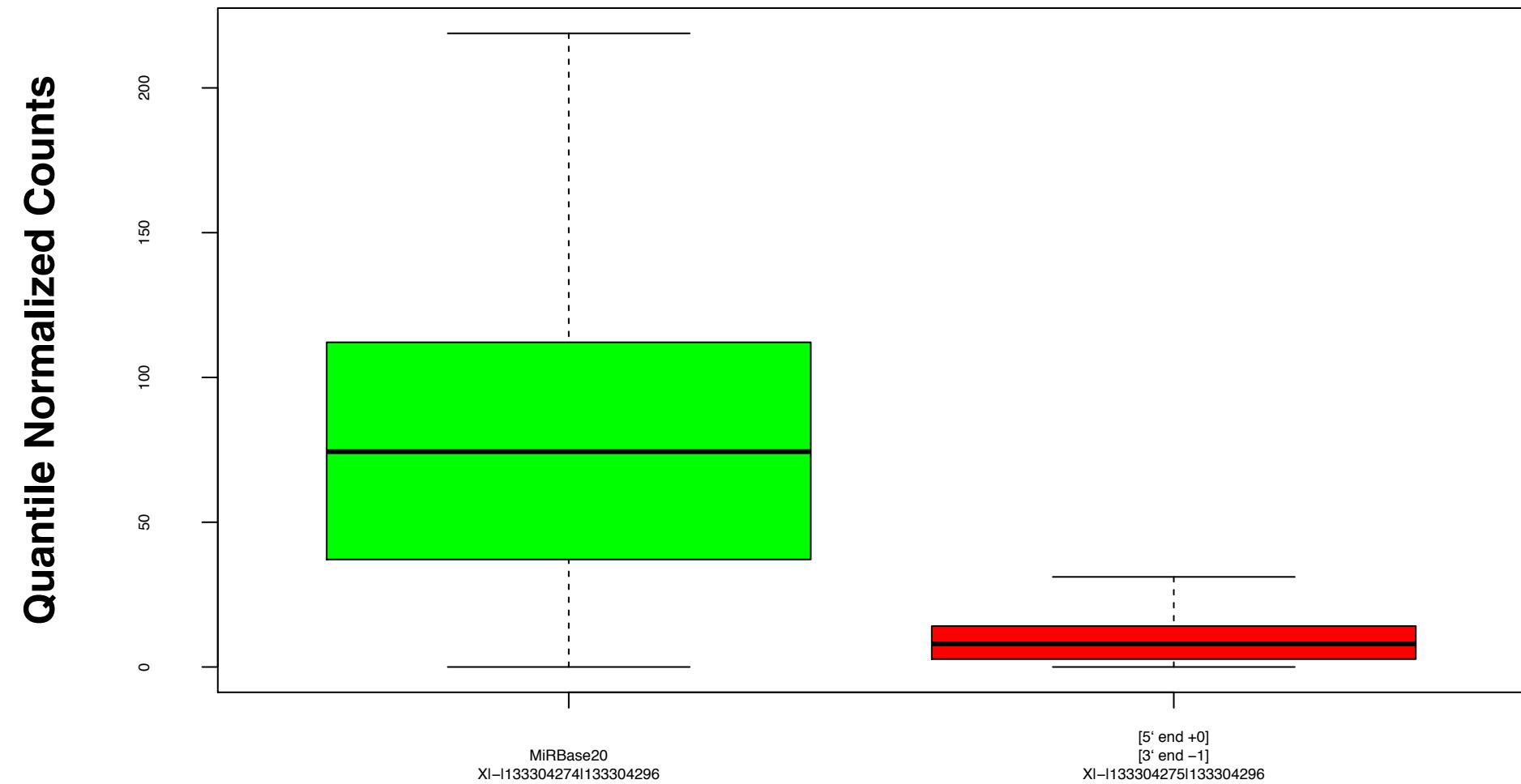


isomiRs

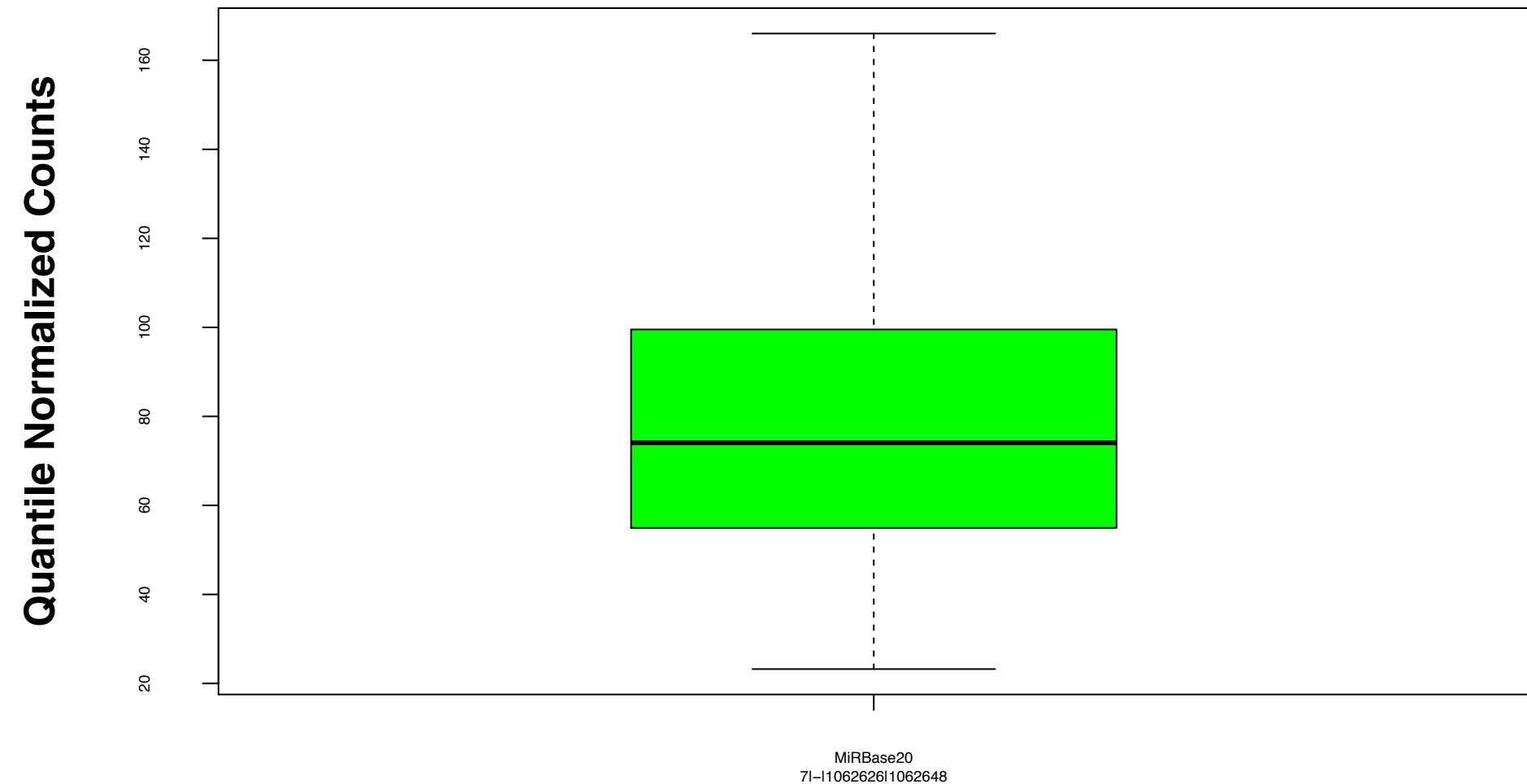
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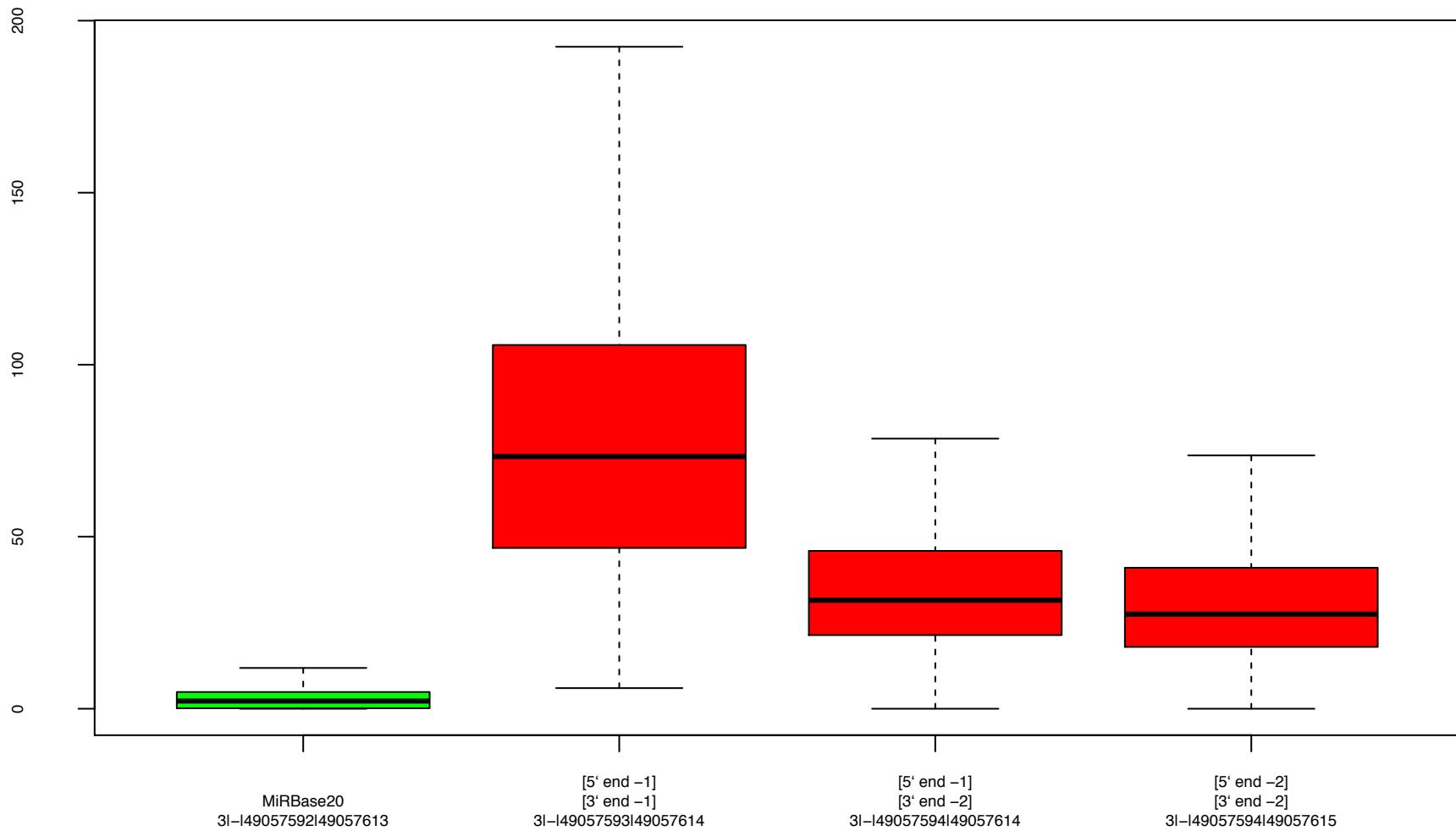


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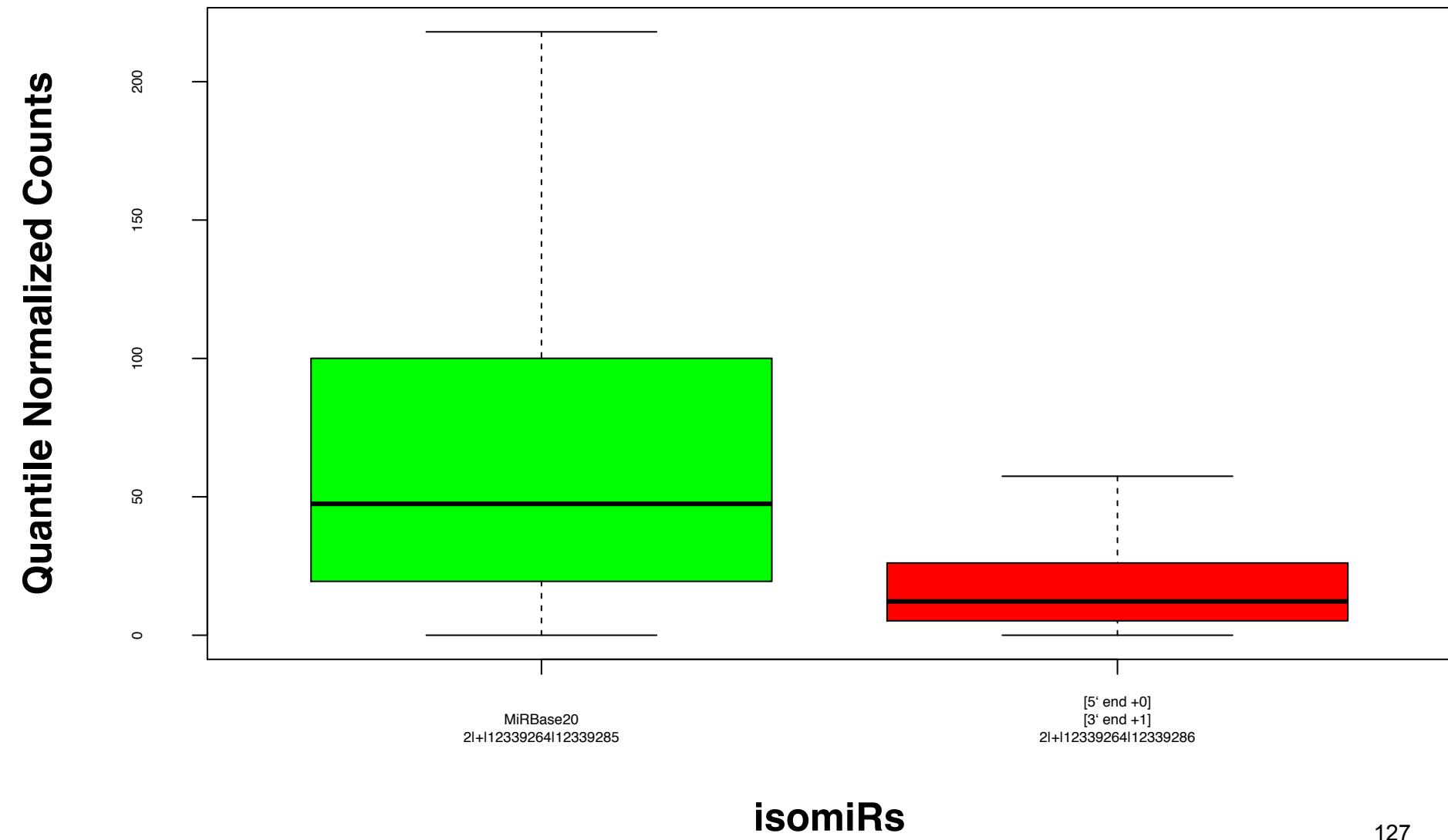
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Quantile Normalized Counts

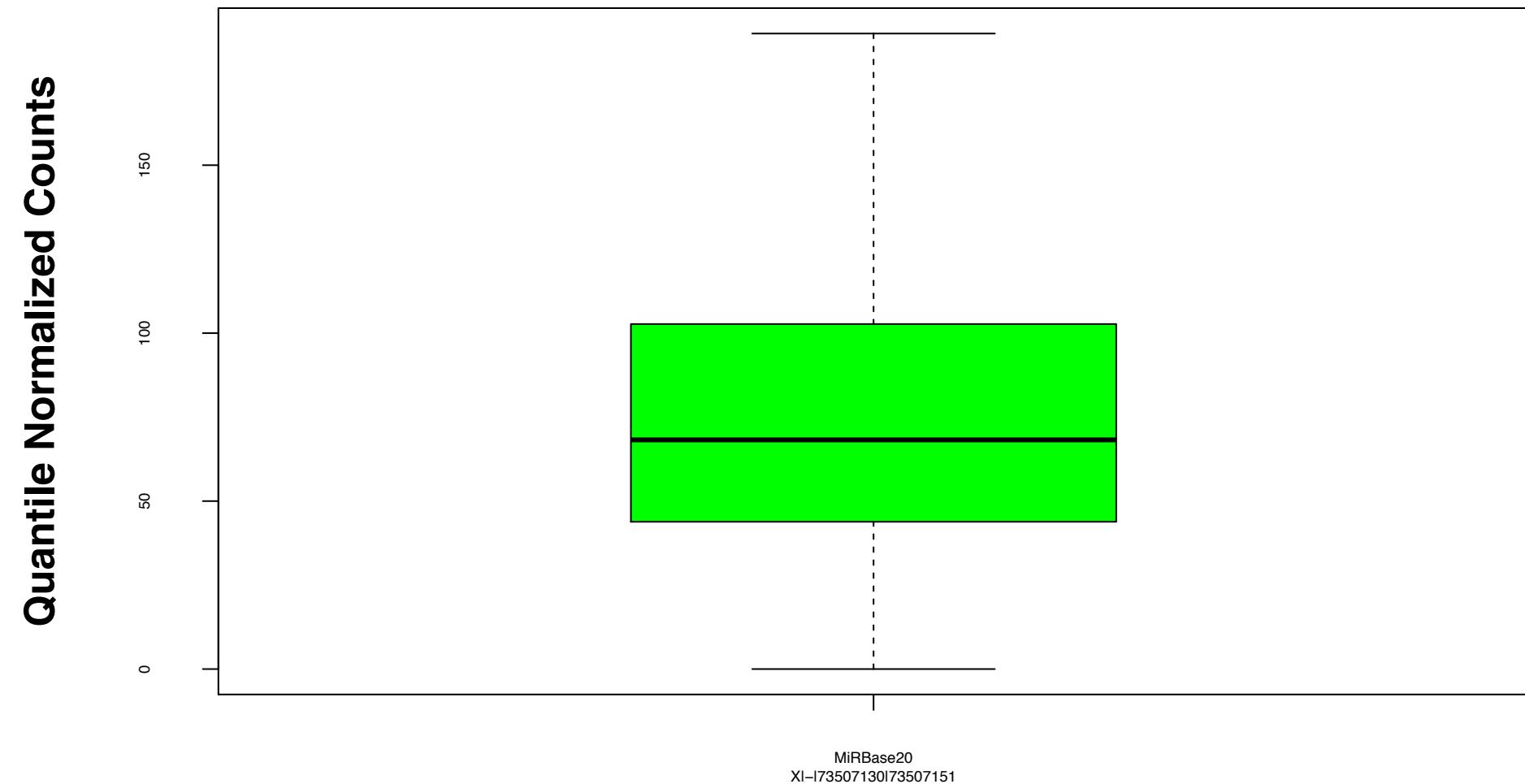


isomiRs

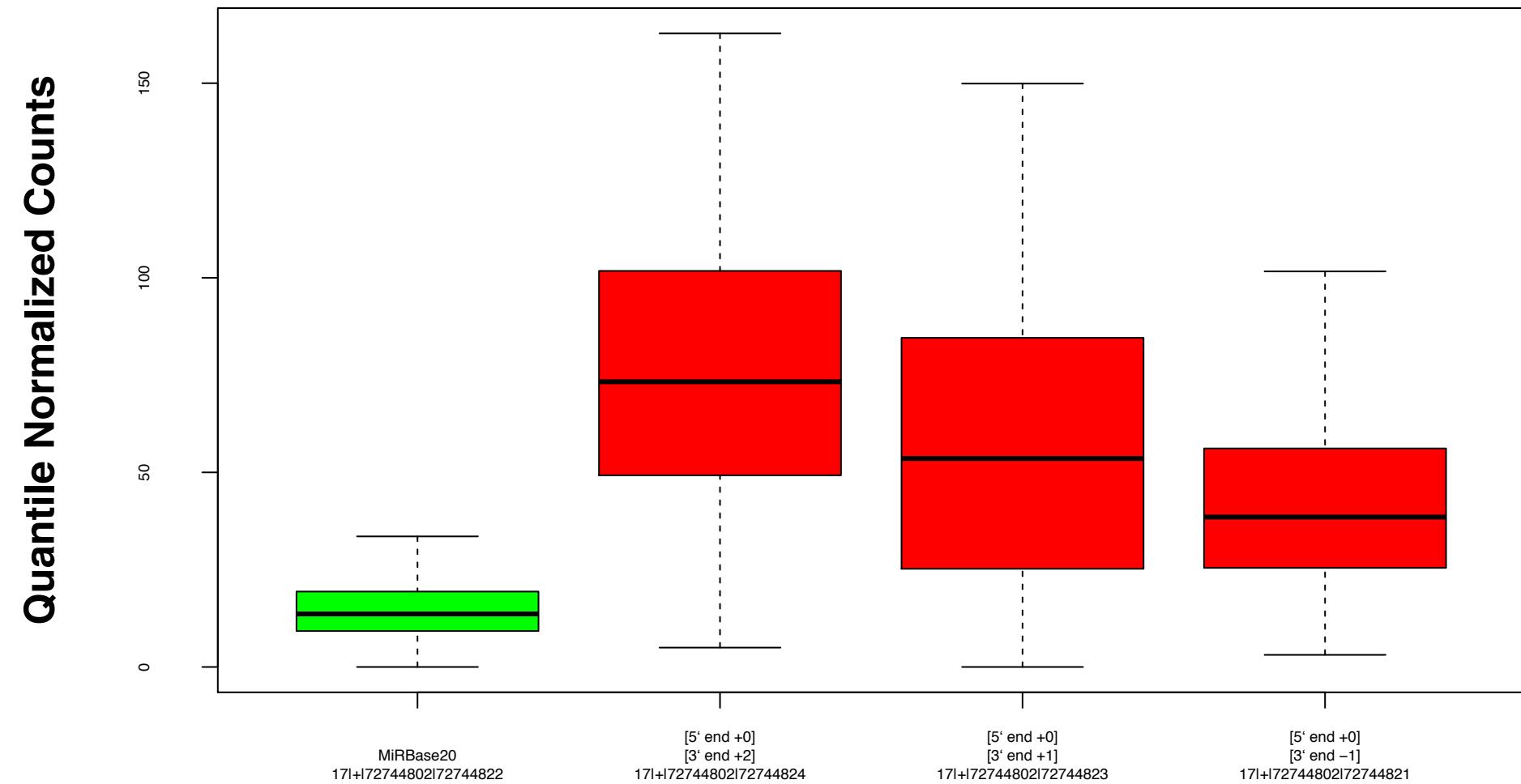
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MIMAT0004688=hsa-miR-374a-3p=MI0000782

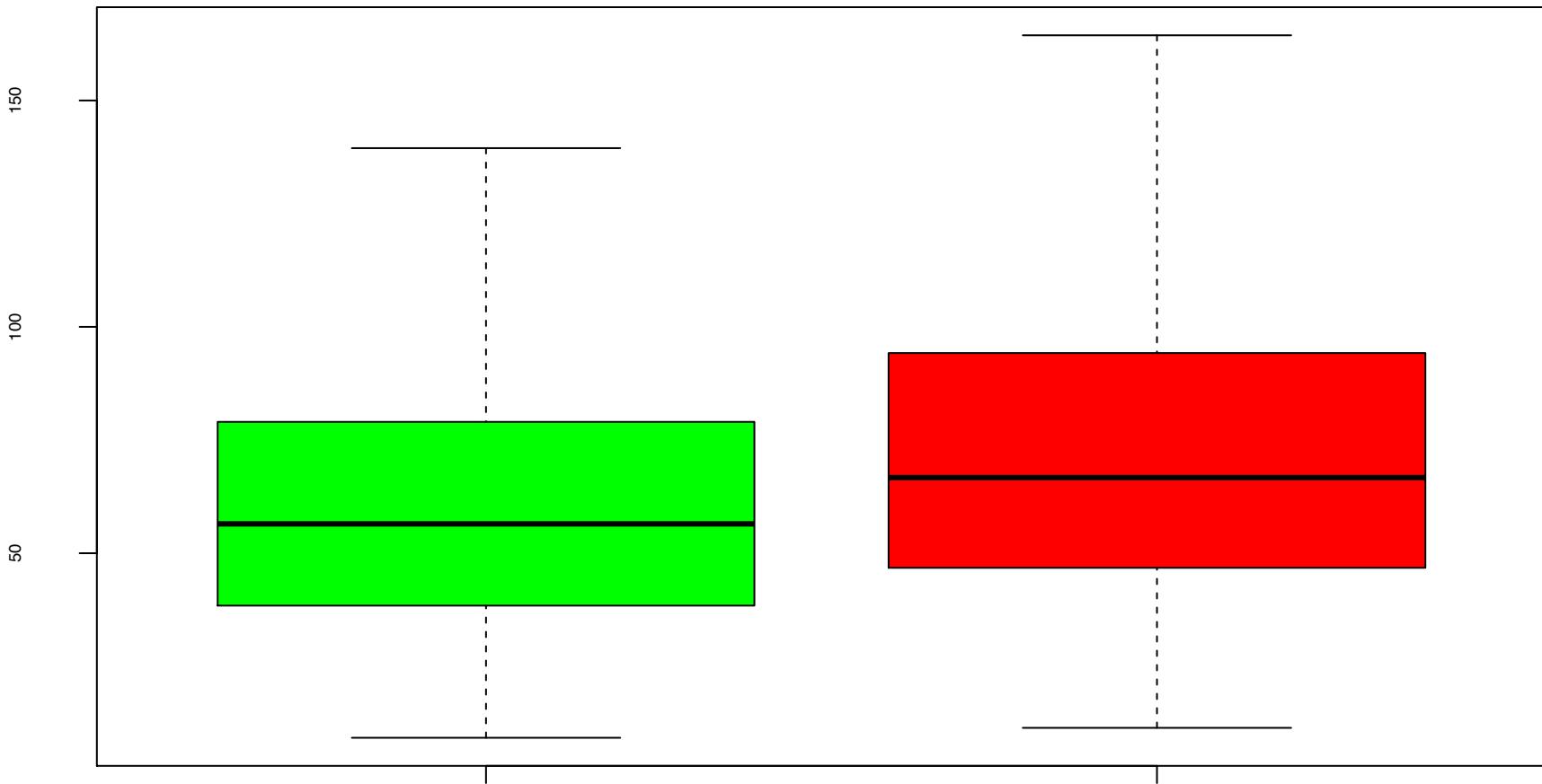


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MIMAT0002821=hsa-miR-181d-5p=MI0003139

Quantile Normalized Counts

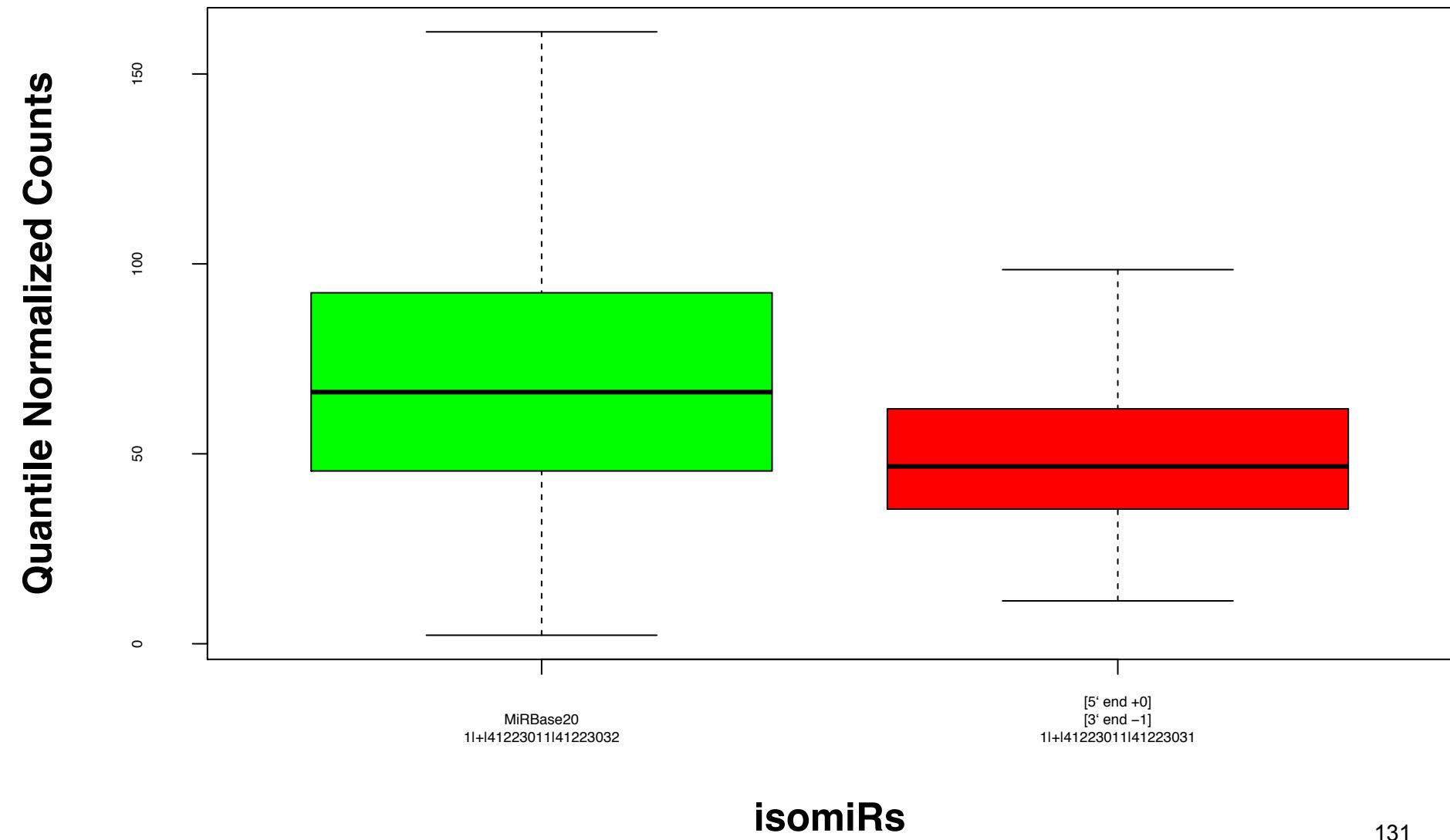


MiRBase20
19l+13985724l13985746

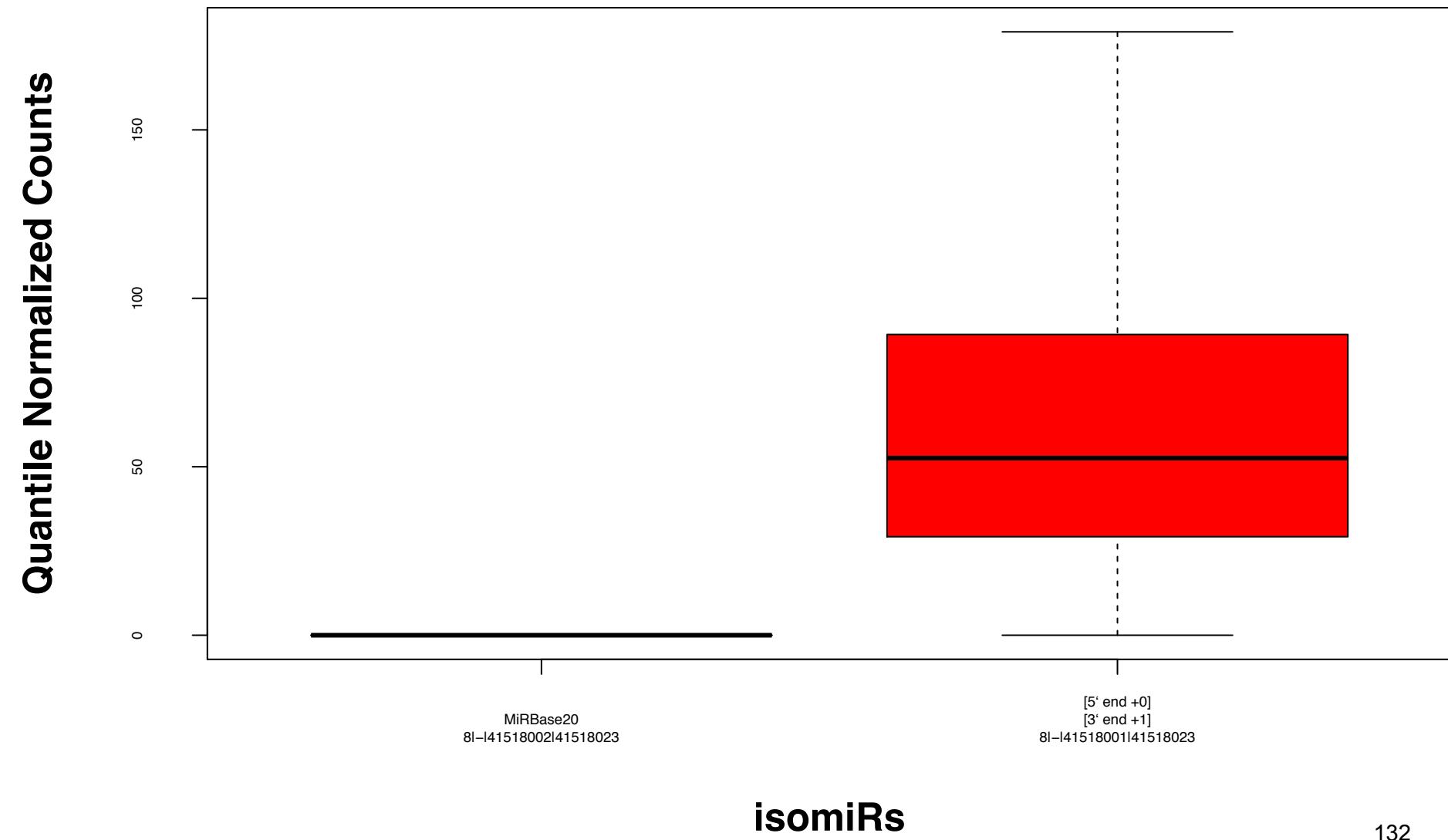
[5' end +0]
[3' end +1]
19l+13985724l13985747

isomiRs

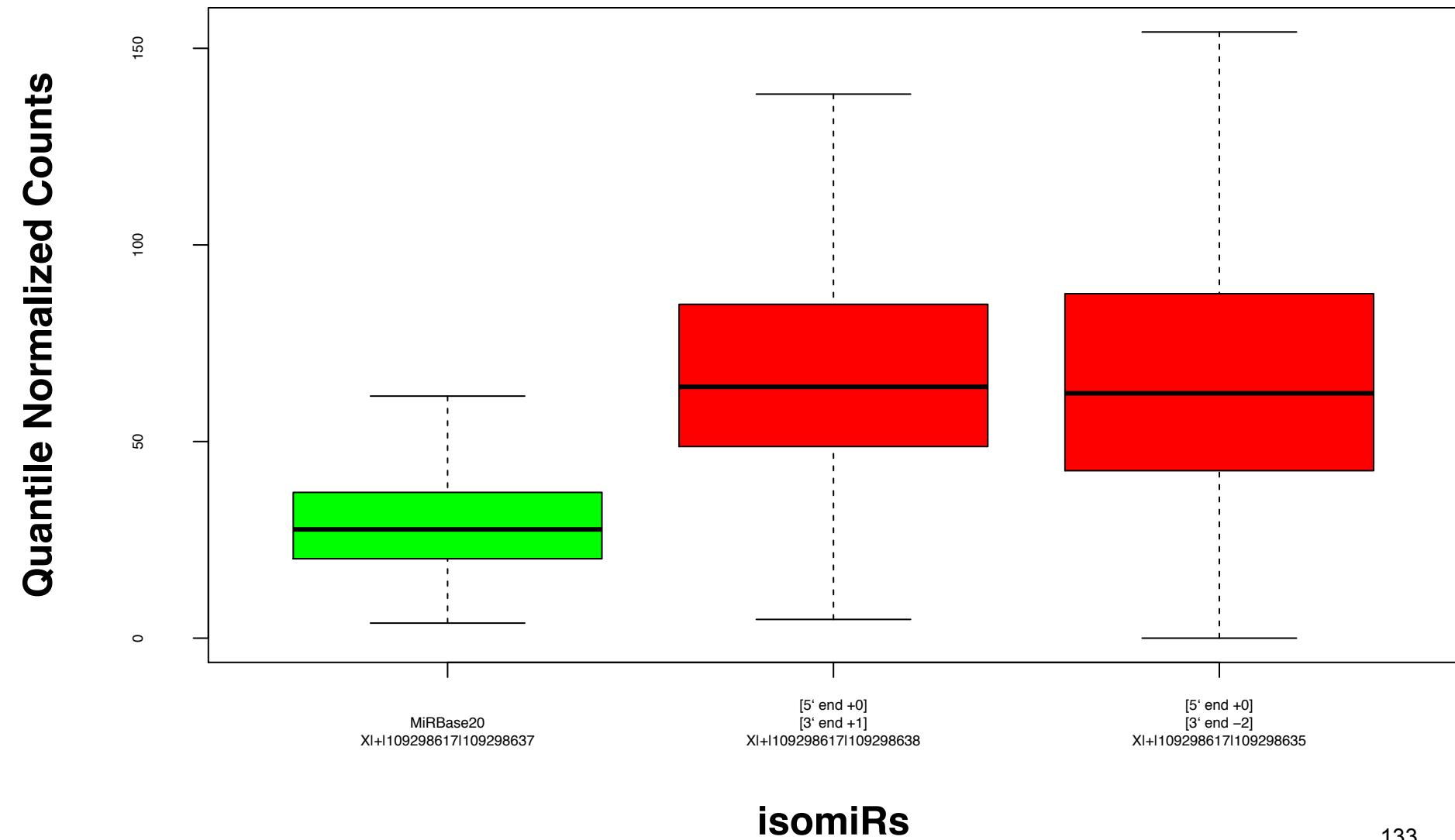
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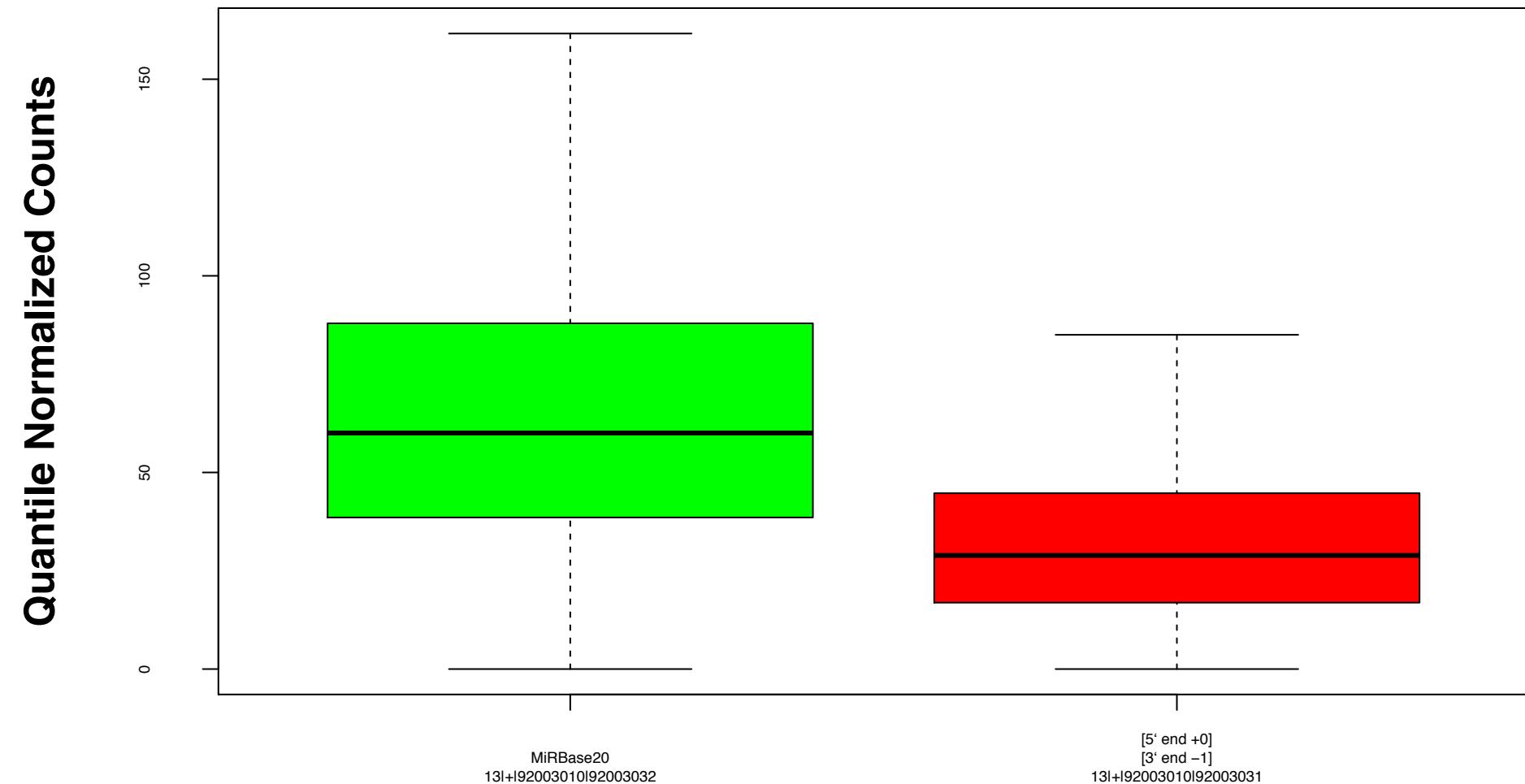
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MIMAT0003322=hsa-miR-652-3p=MI0003667

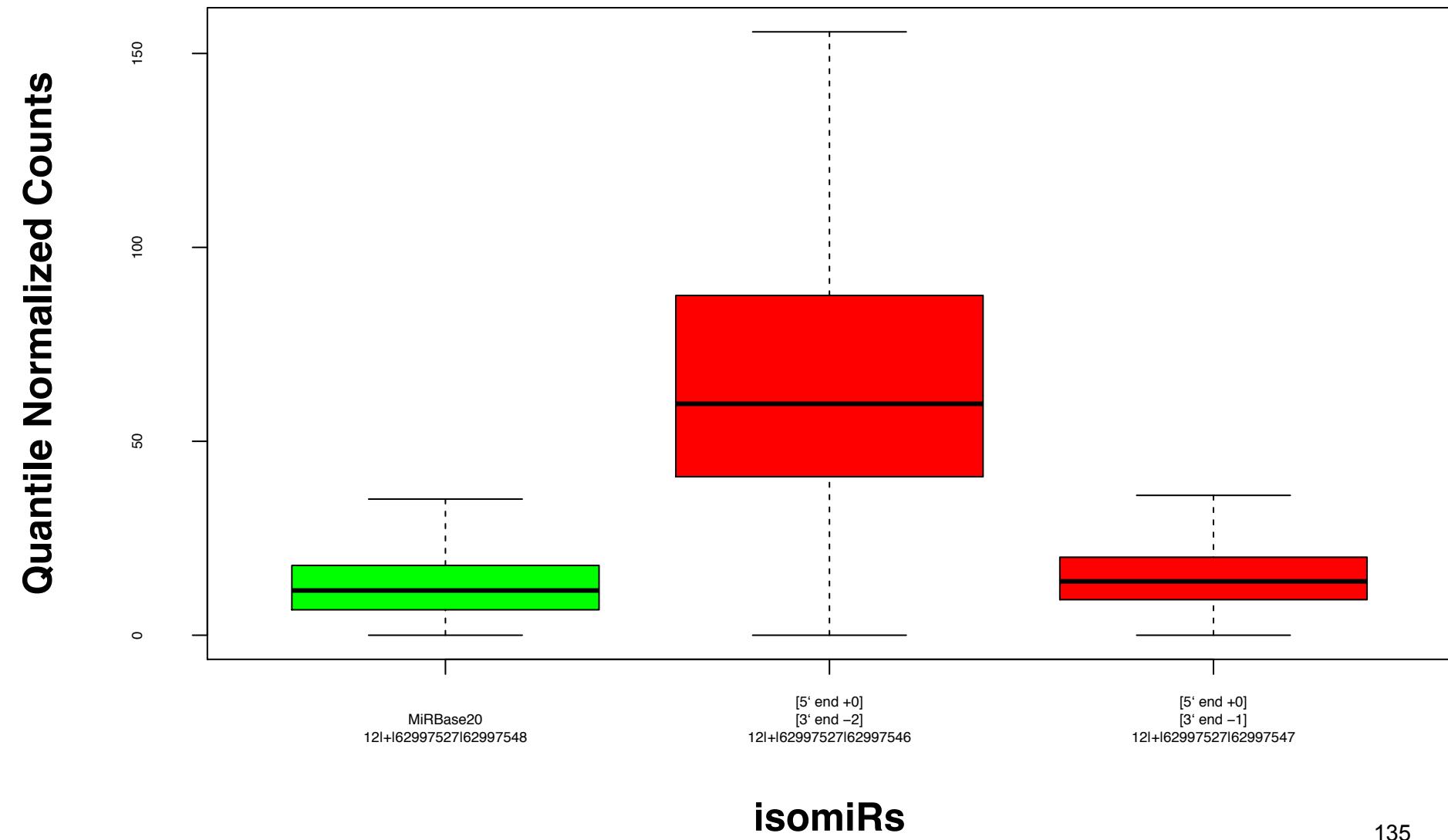


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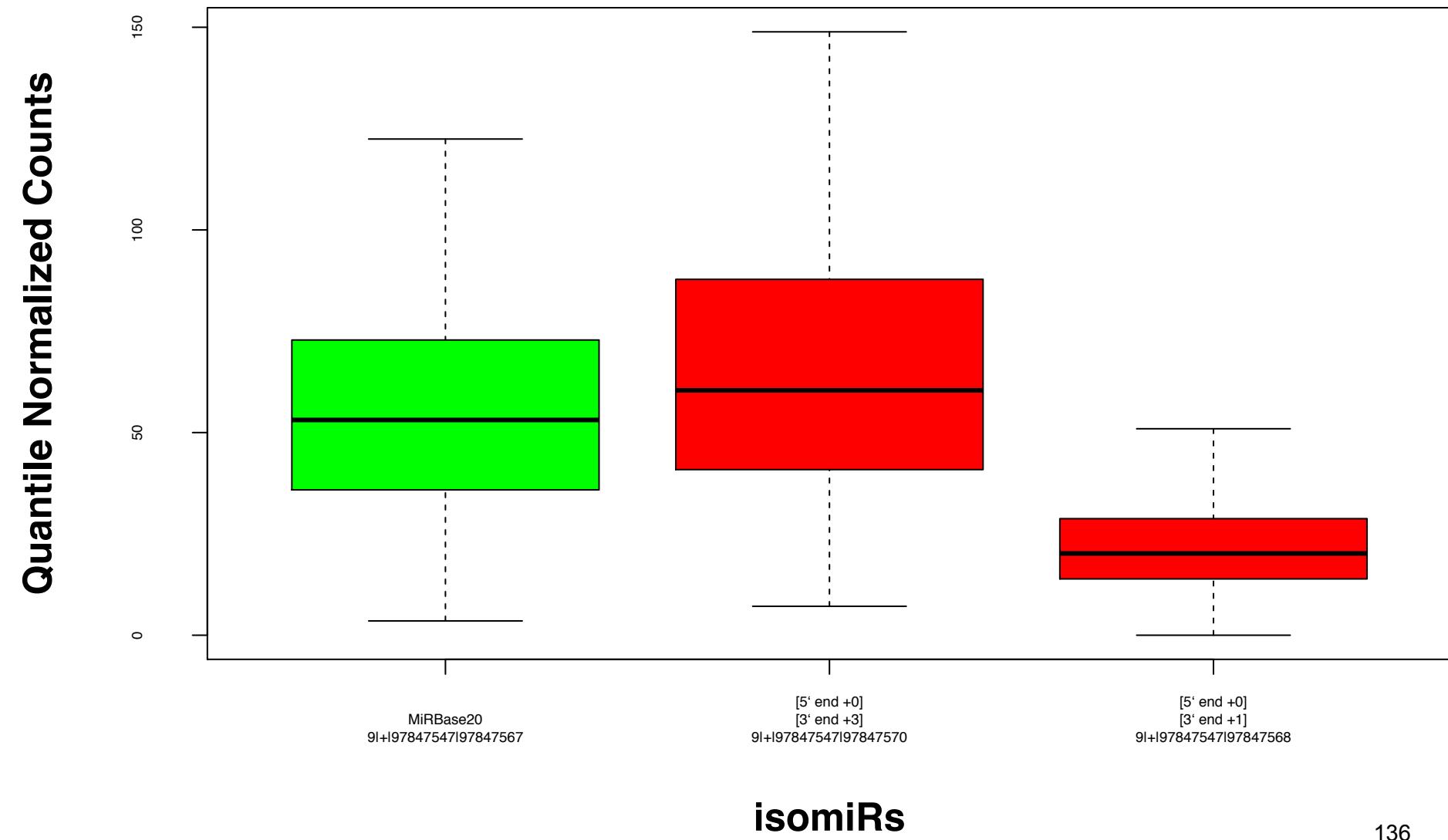


isomiRs

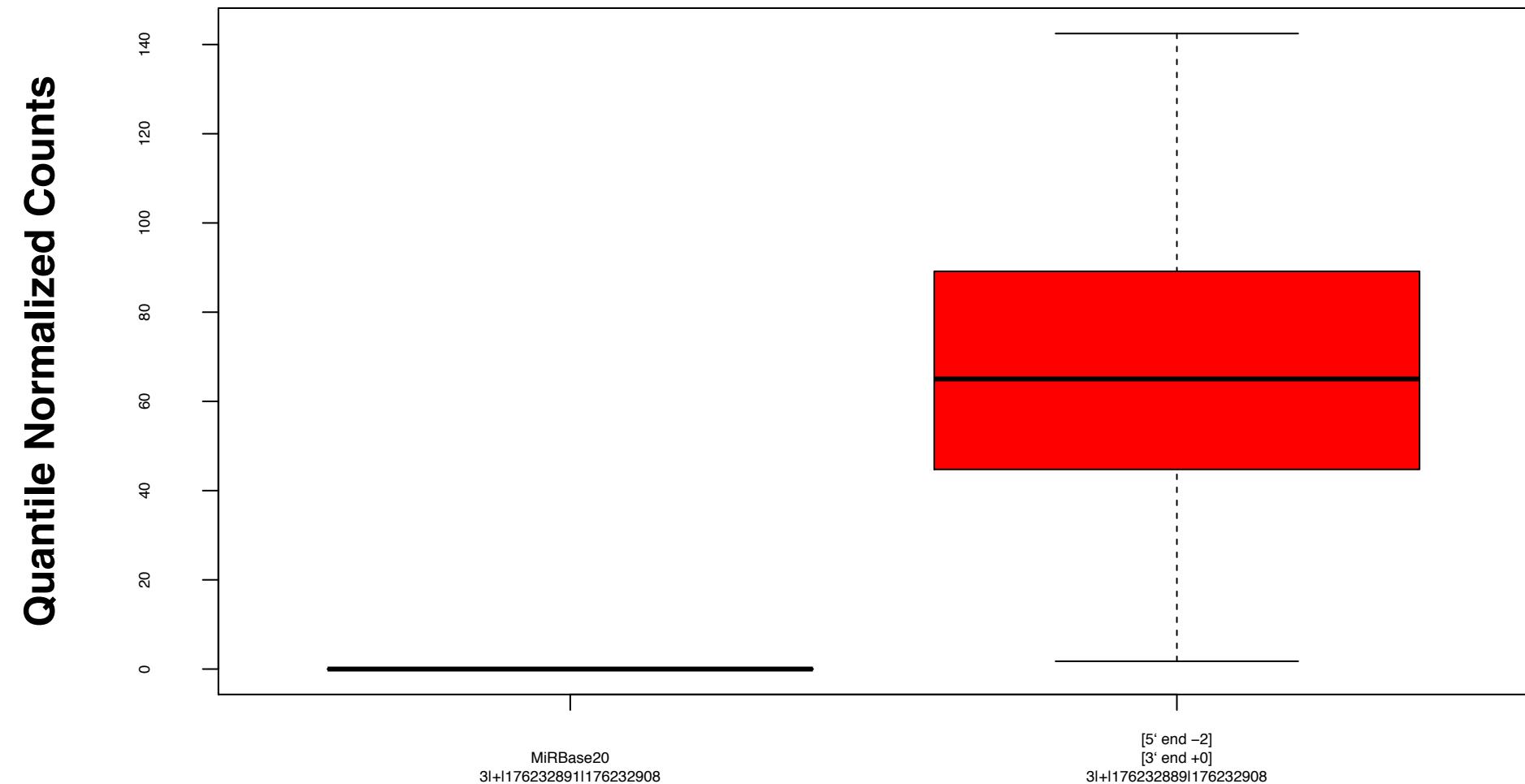
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MIMAT0000418=hsa-miR-23b-3p=MI0000439

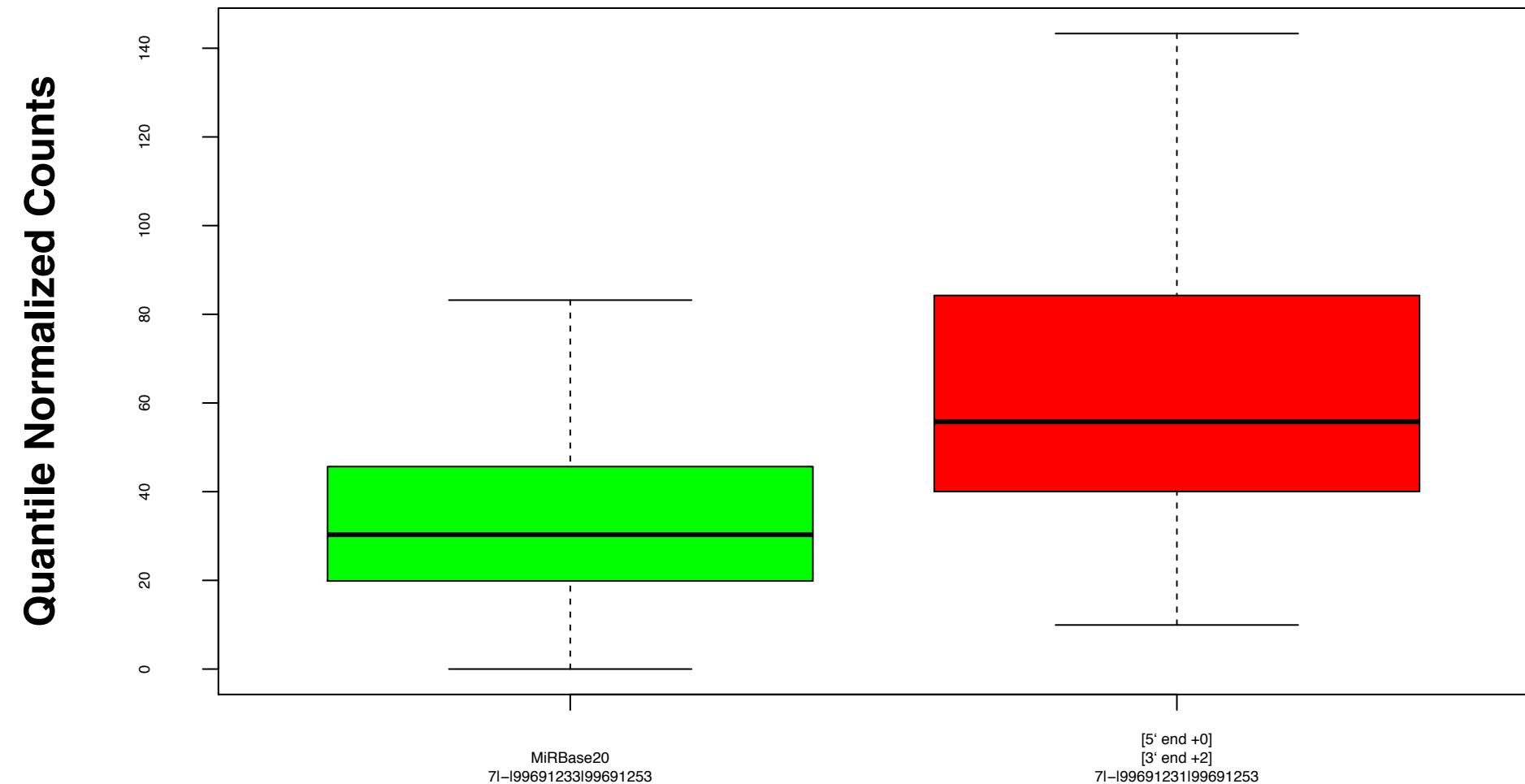


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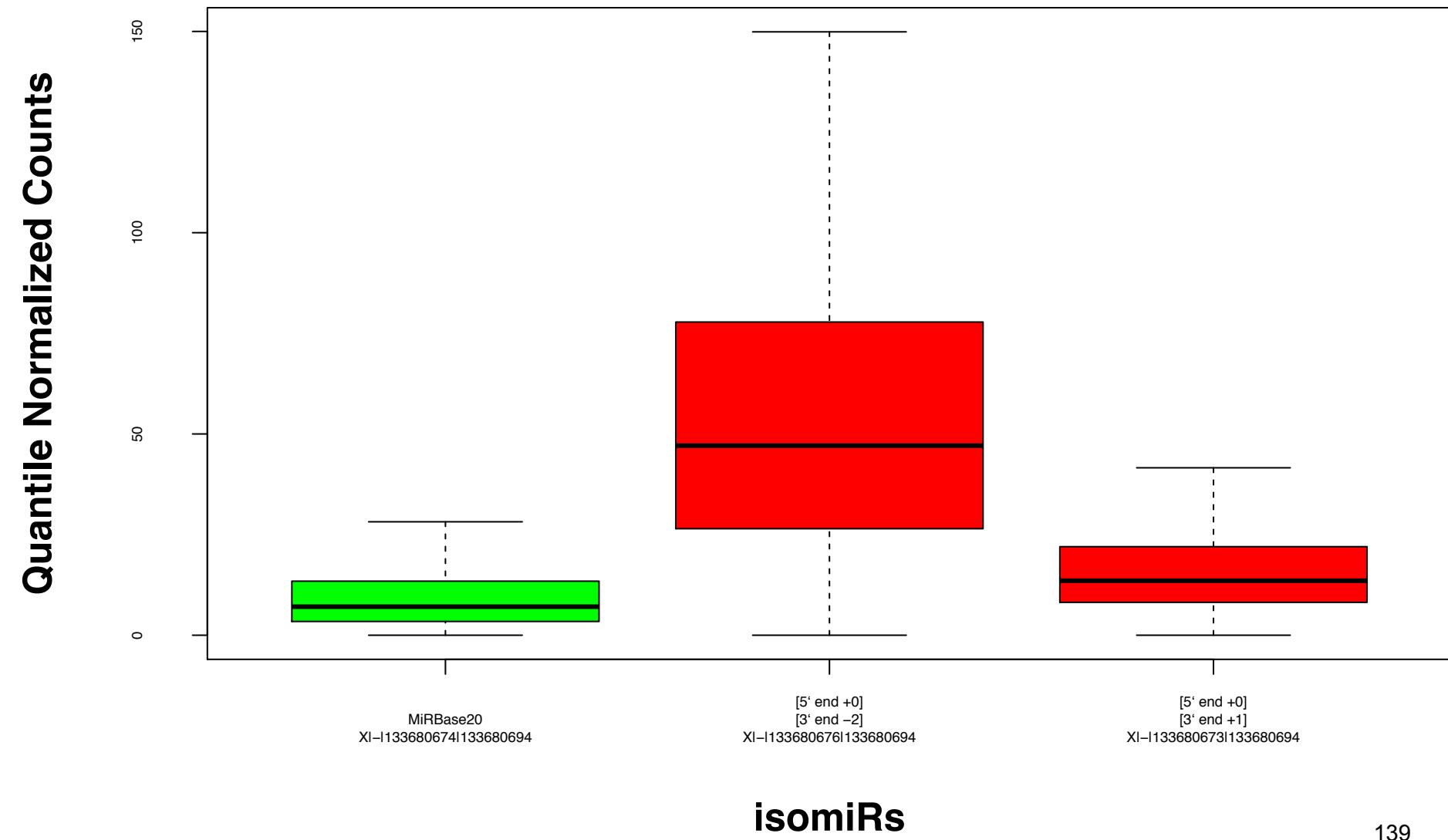
isomiRs

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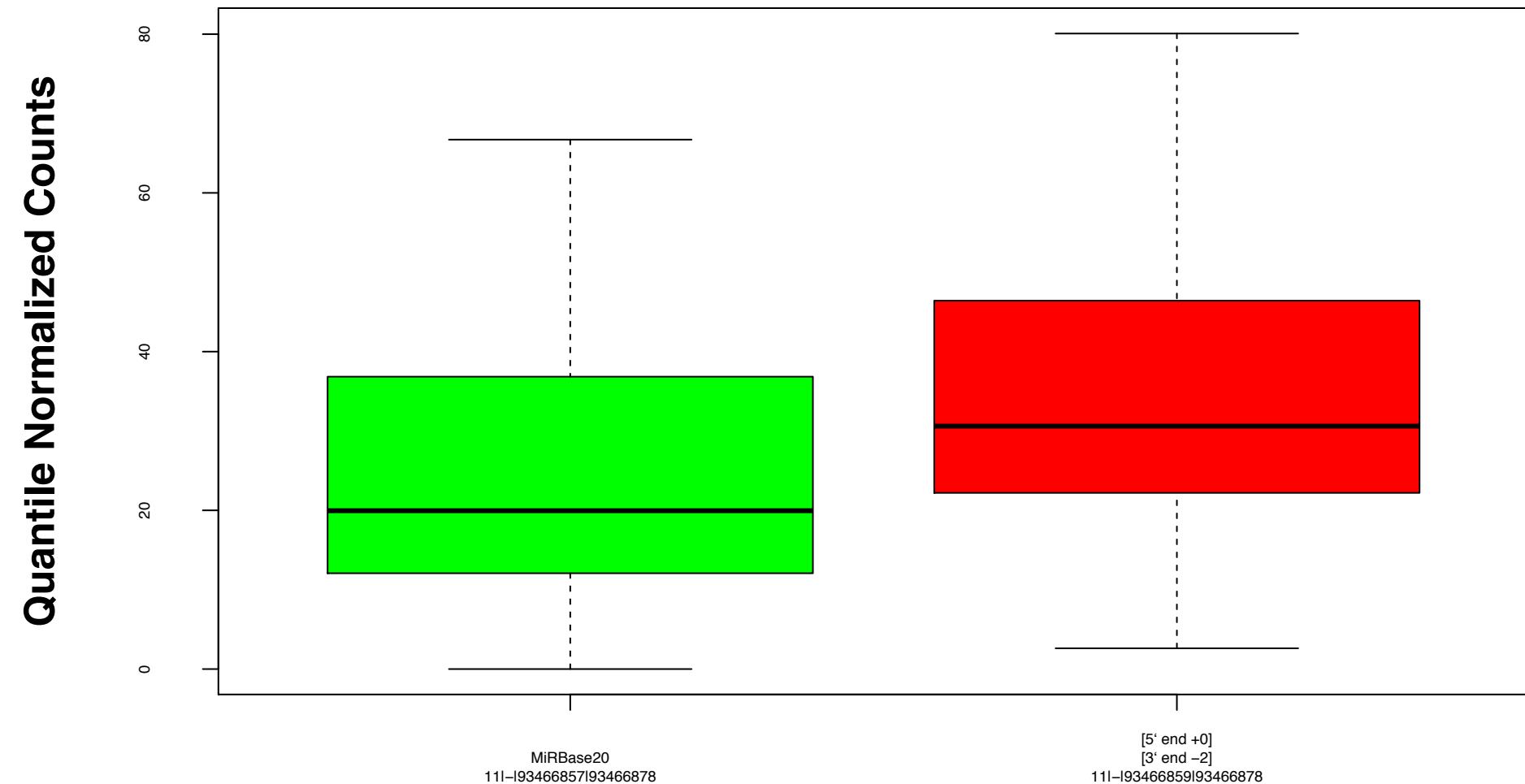


isomiRs

MIMAT0004749=hsa-miR-424-3p=MI0001446

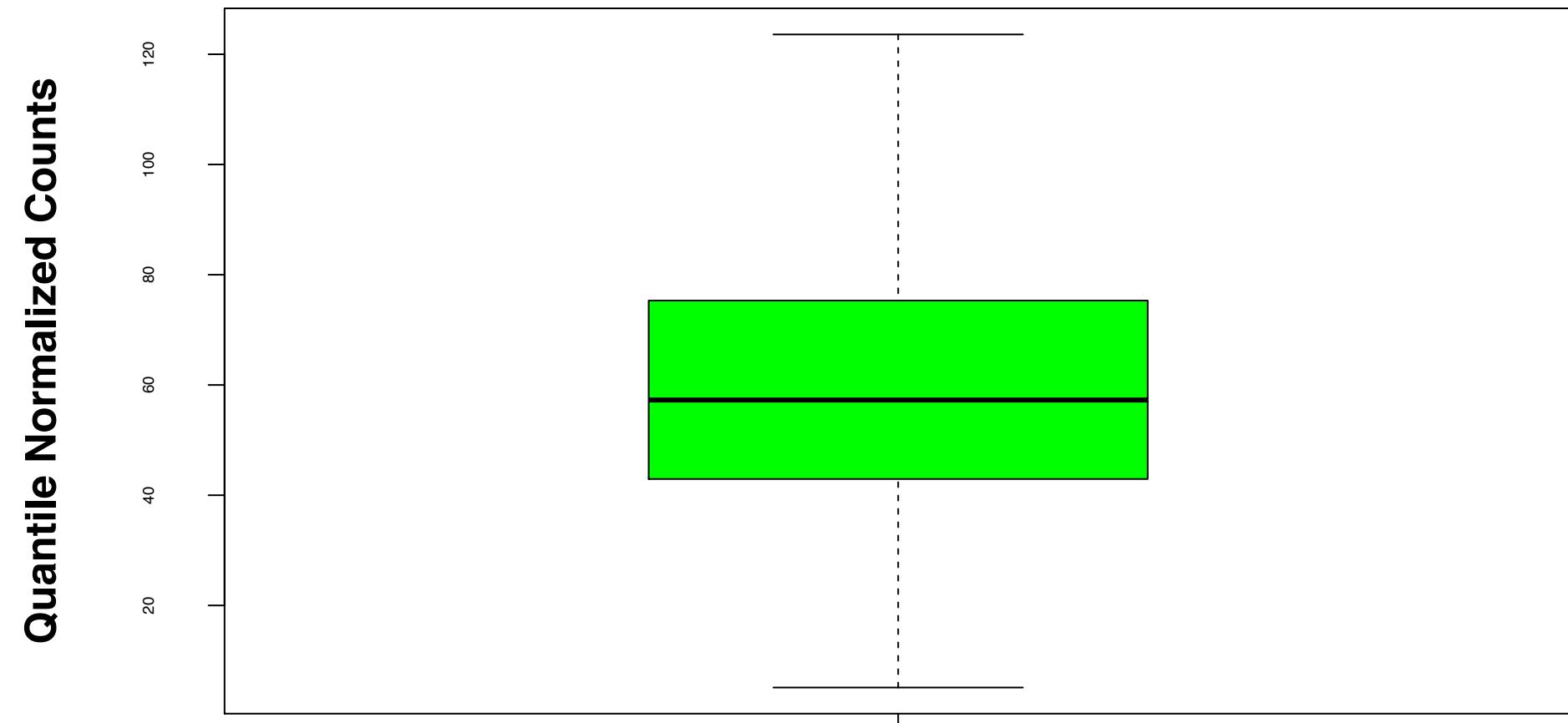


MIMAT0022720=hsa-miR-1304-3p=MI0006371



isomiRs

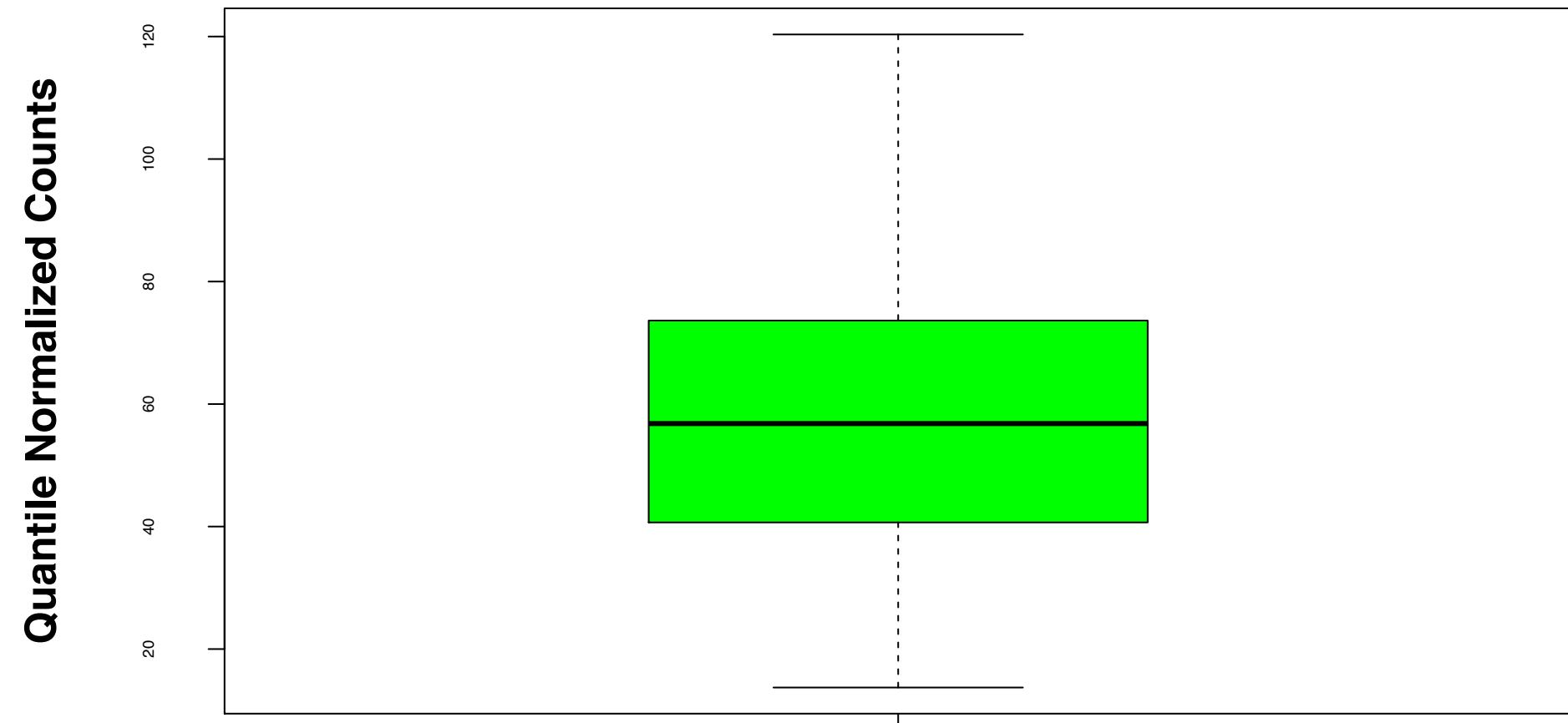
MIMAT0004496=hsa-miR-23a-5p=MI0000079



MiRBase20
19|I-13947444|13947465

isomiRs

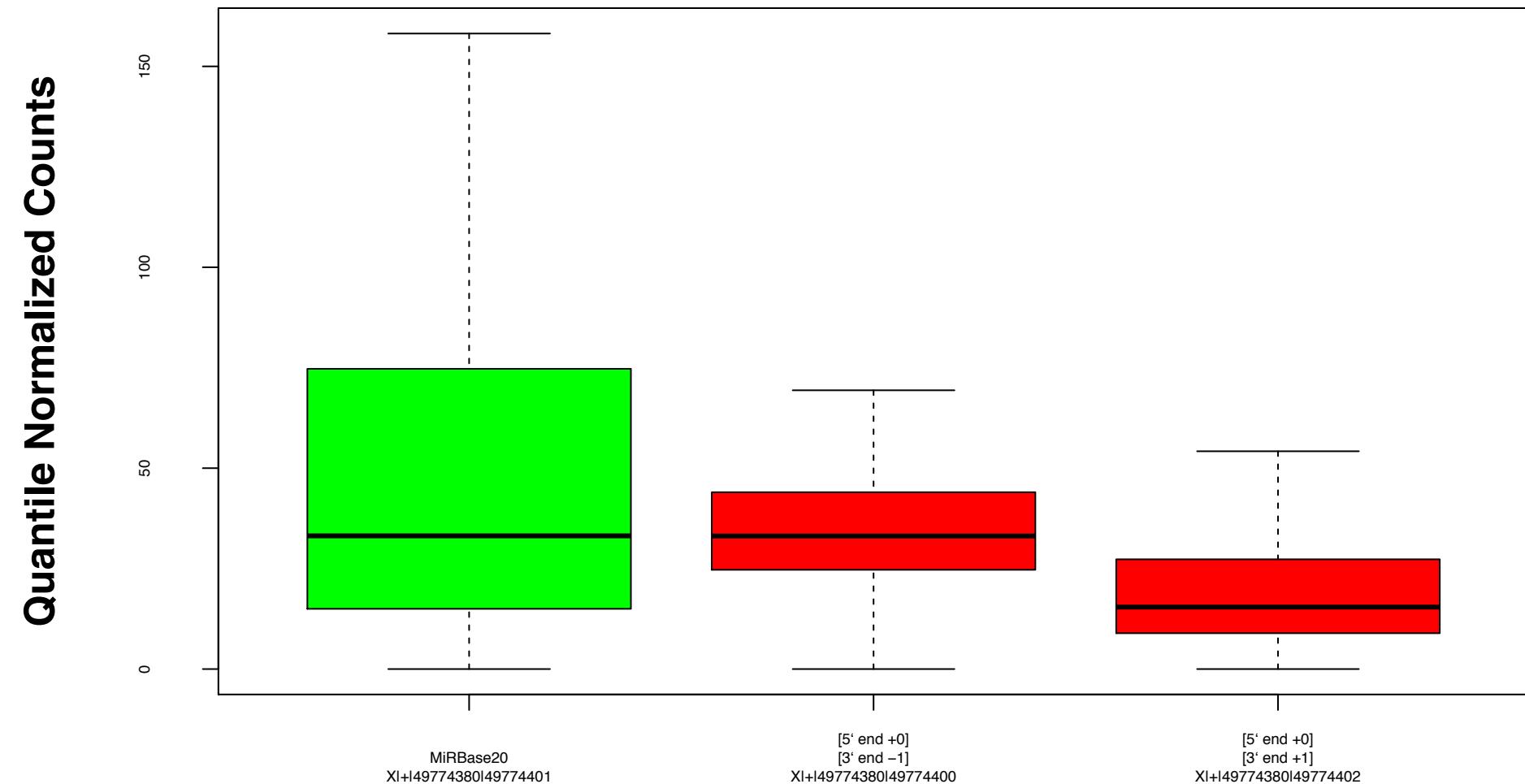
MIMAT0005882=hsa-miR-548k=MI0006354



MiRBase20
11l+I70130092|70130113

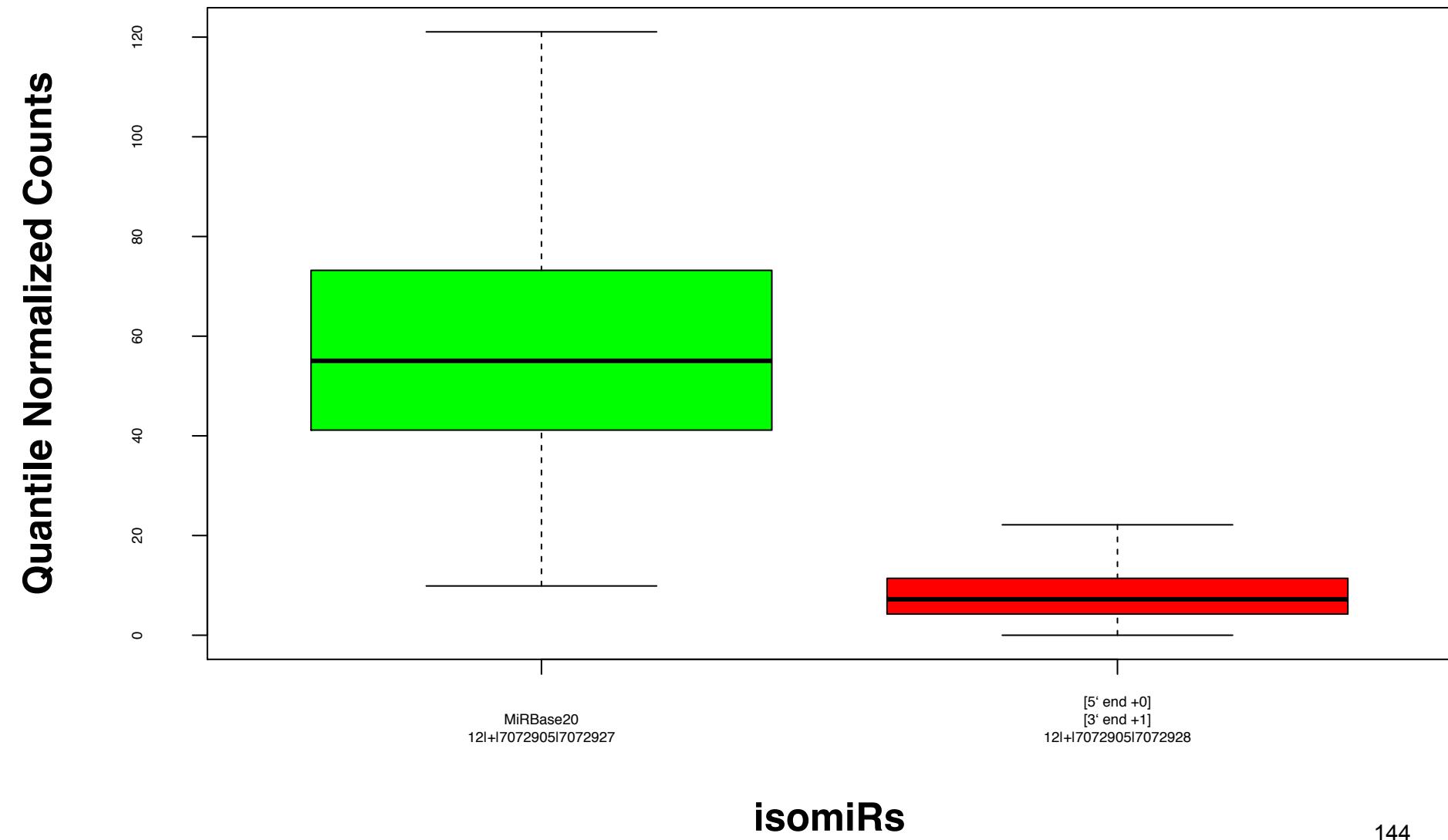
isomiRs

MIMAT0004774=hsa-miR-501-3p=MI0003185

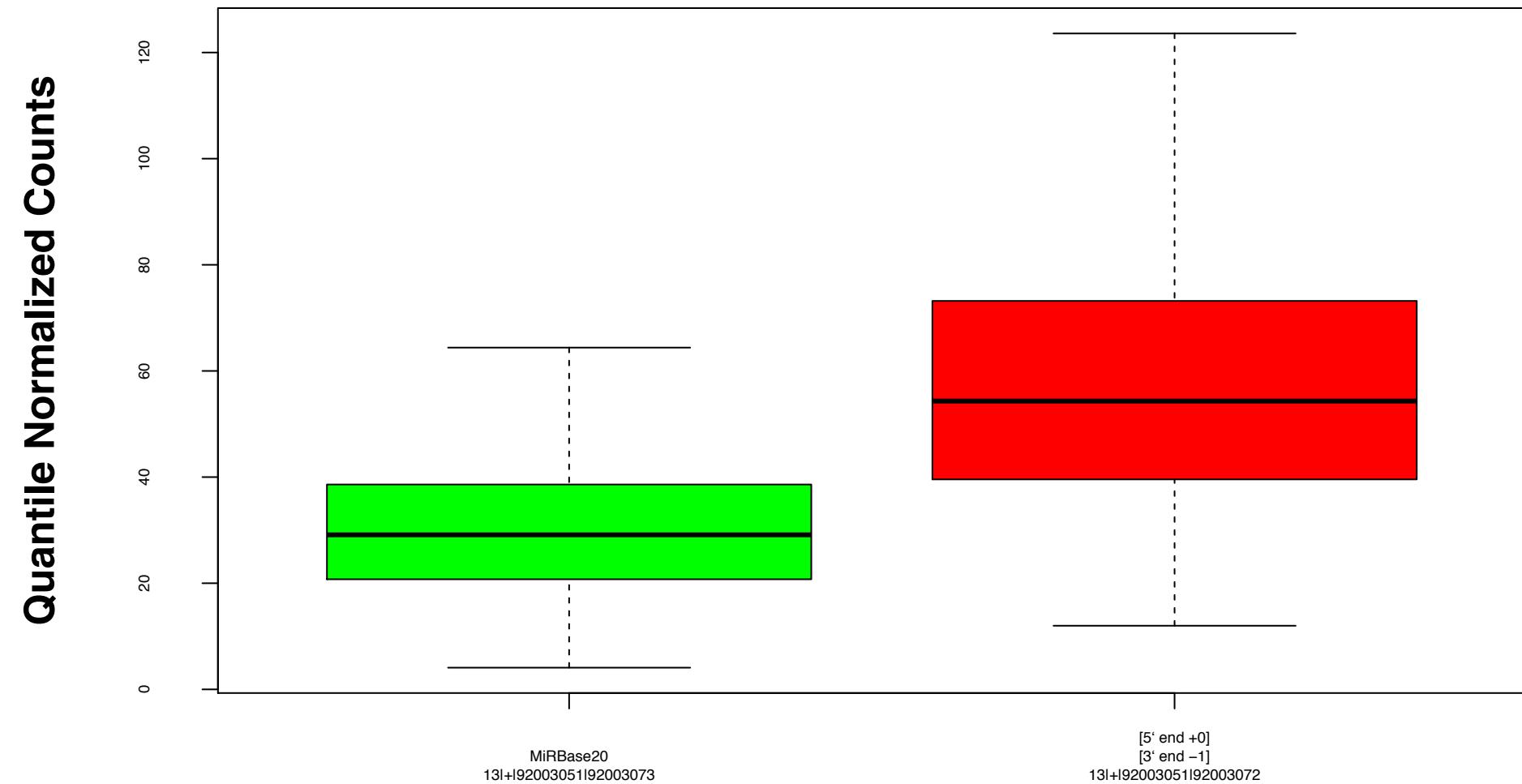


isomiRs

MIMAT0000617=hsa-miR-200c-3p=MI0000650

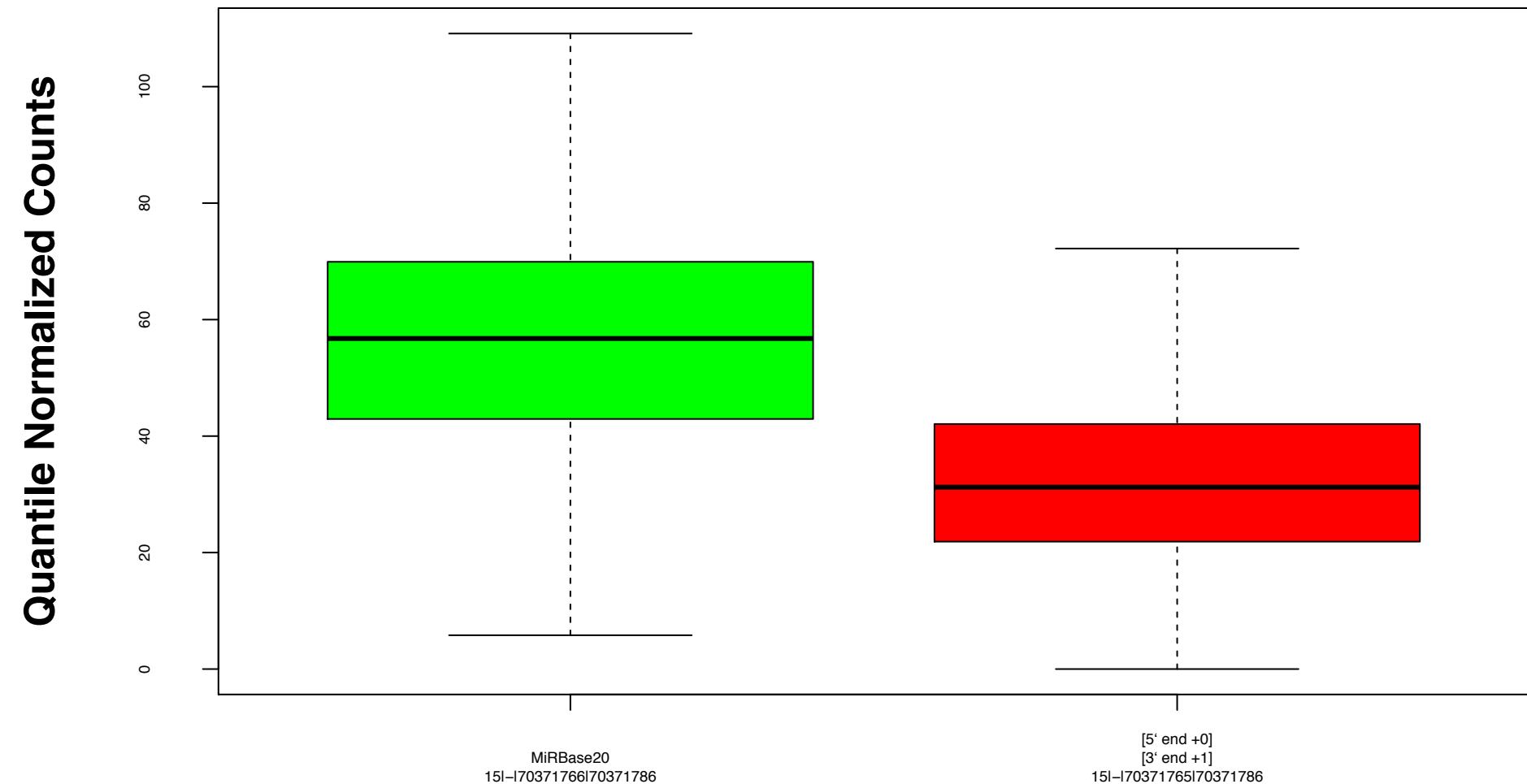


MIMAT0002891=hsa-miR-18a-3p=MI0000072

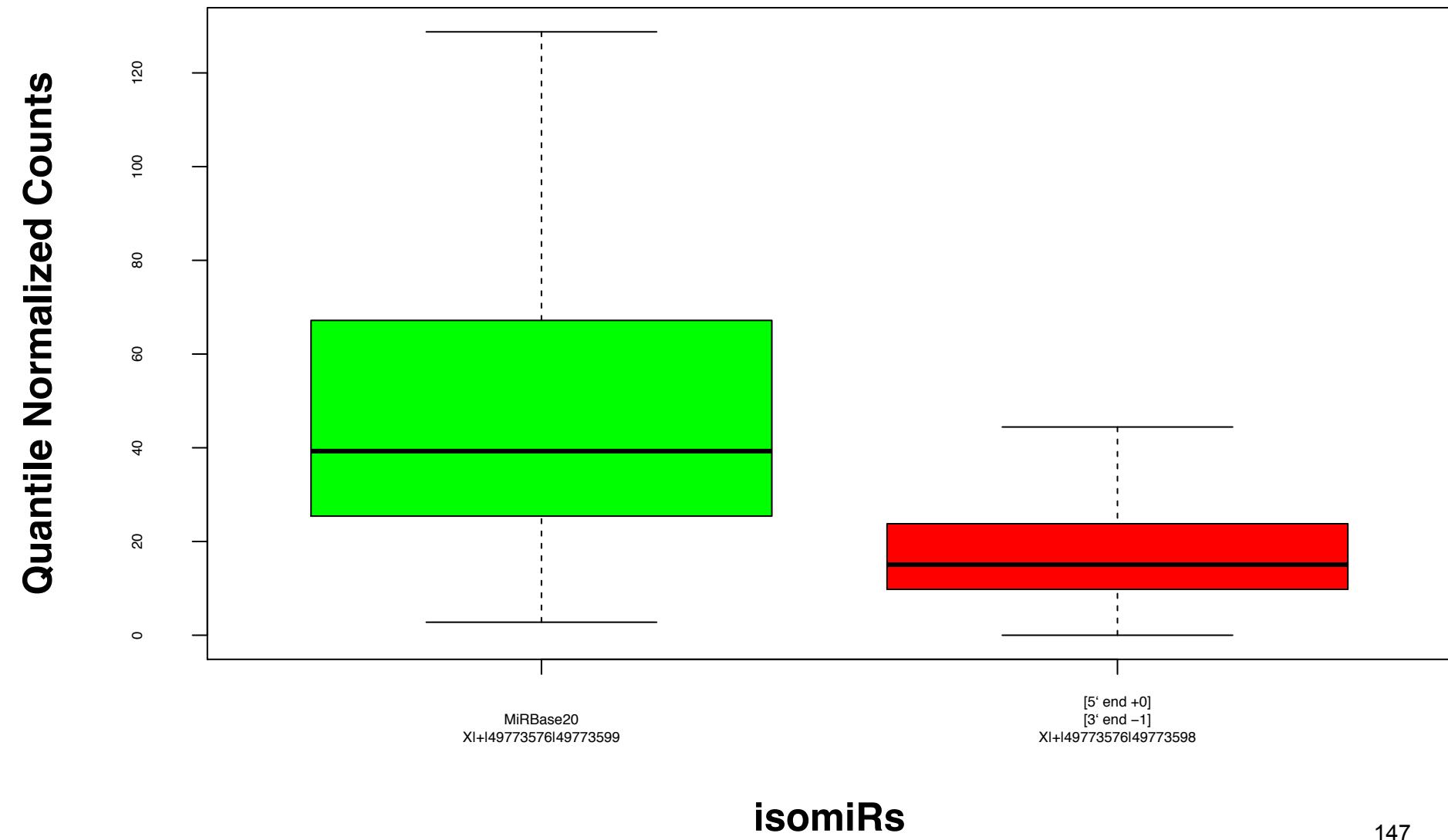


isomiRs

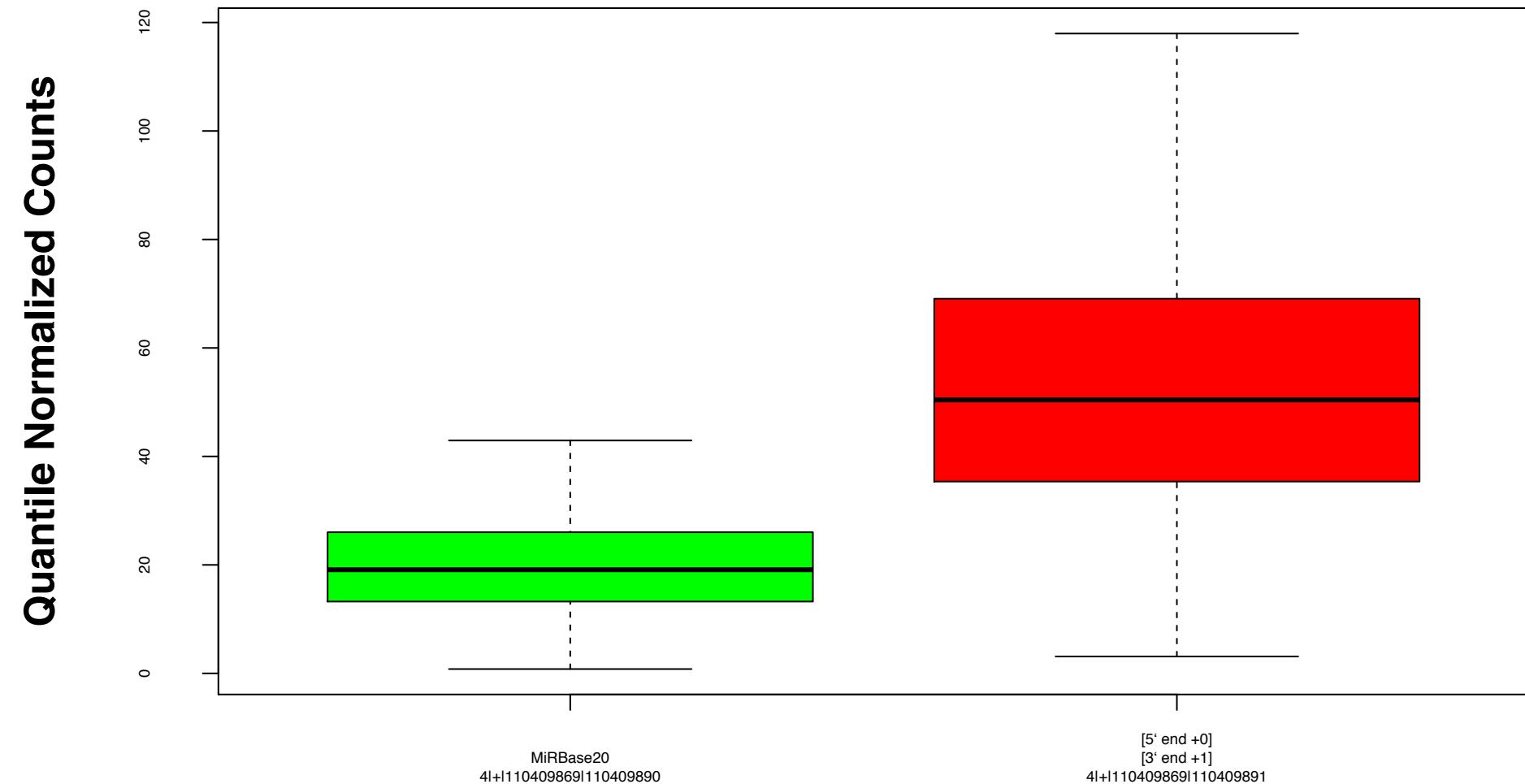
MIMAT0004810=hsa-miR-629-5p=MI0003643



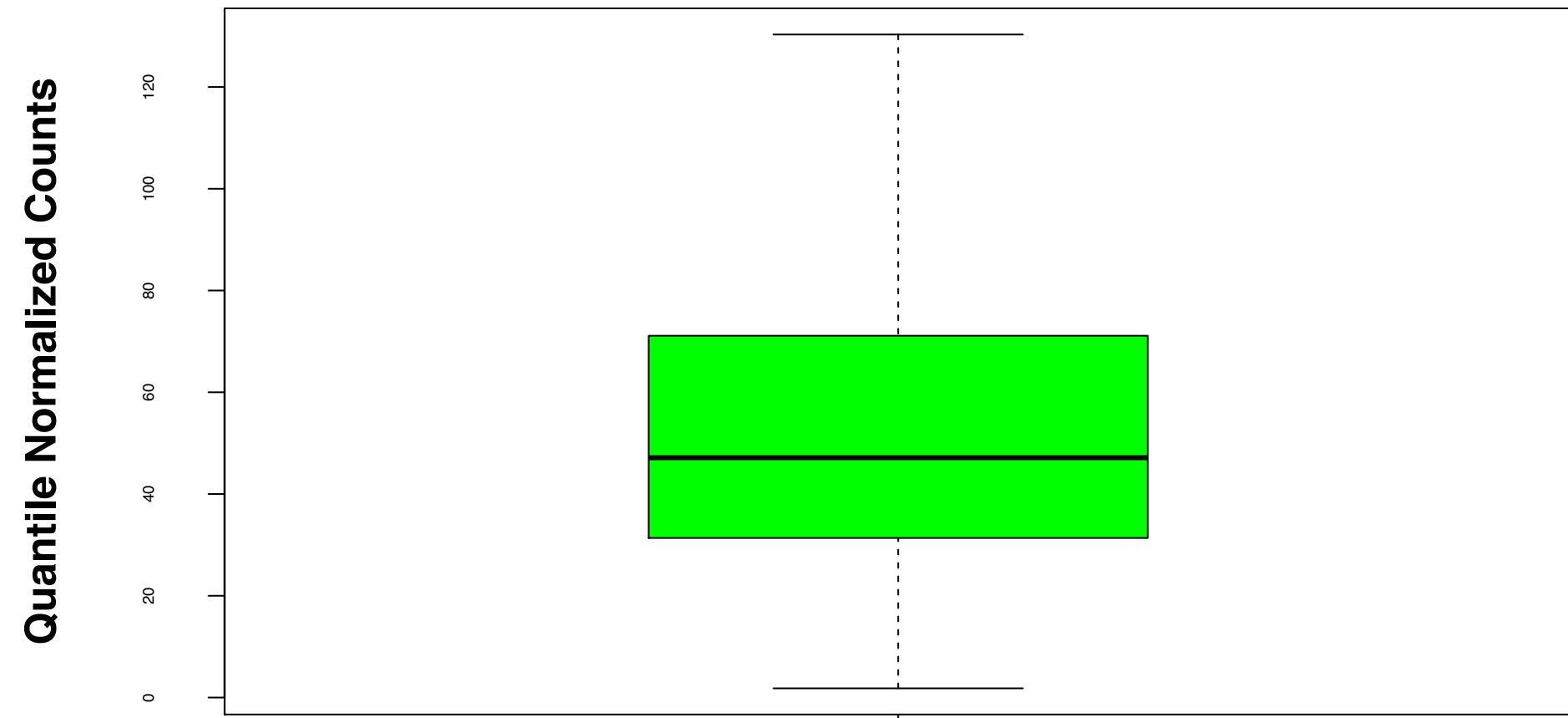
MIMAT0000705=hsa-miR-362-5p=MI0000762



MIMAT0003241=hsa-miR-576-5p=MI0003583



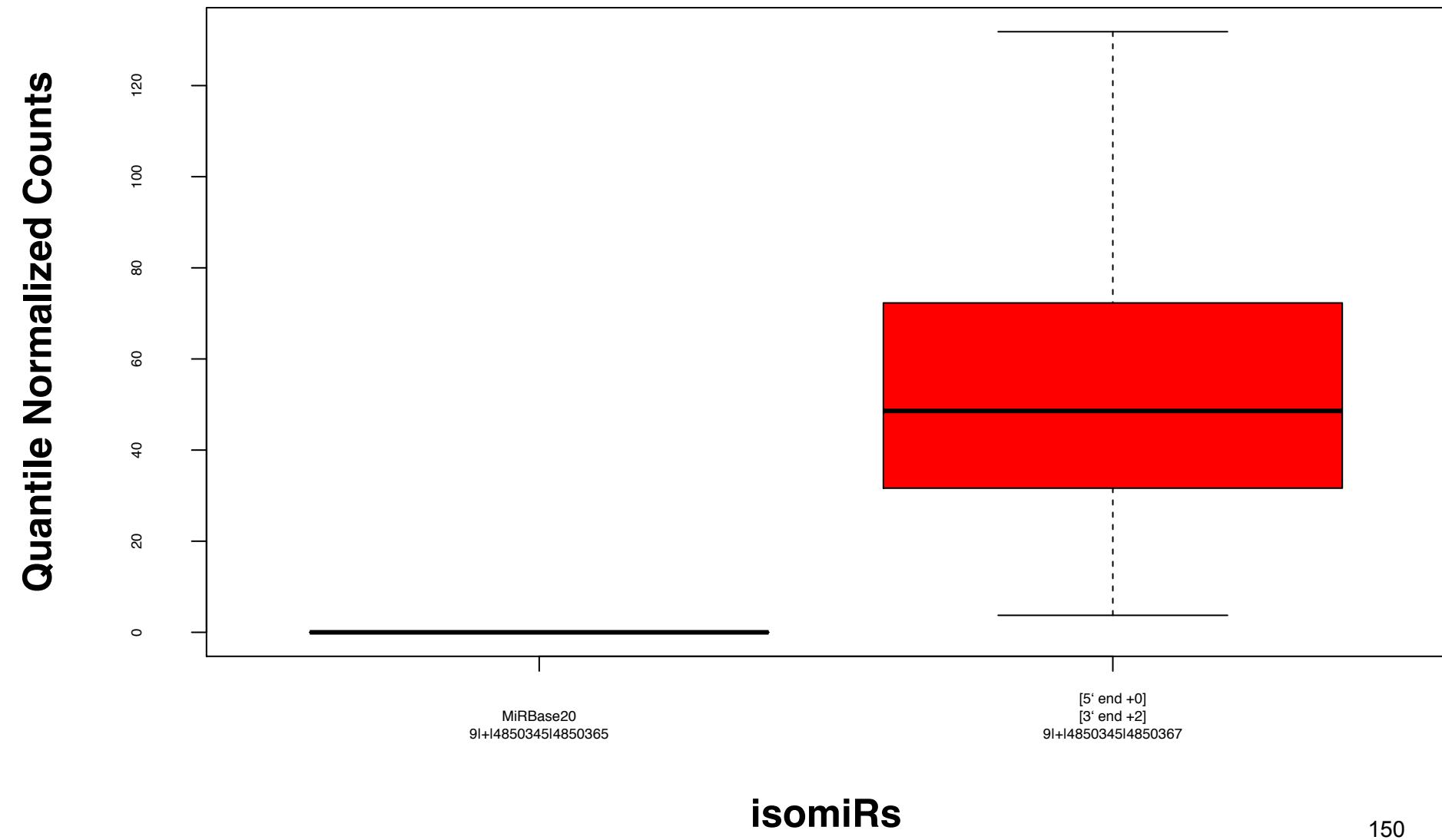
MIMAT0003239=hsa-miR-574-3p=MI0003581



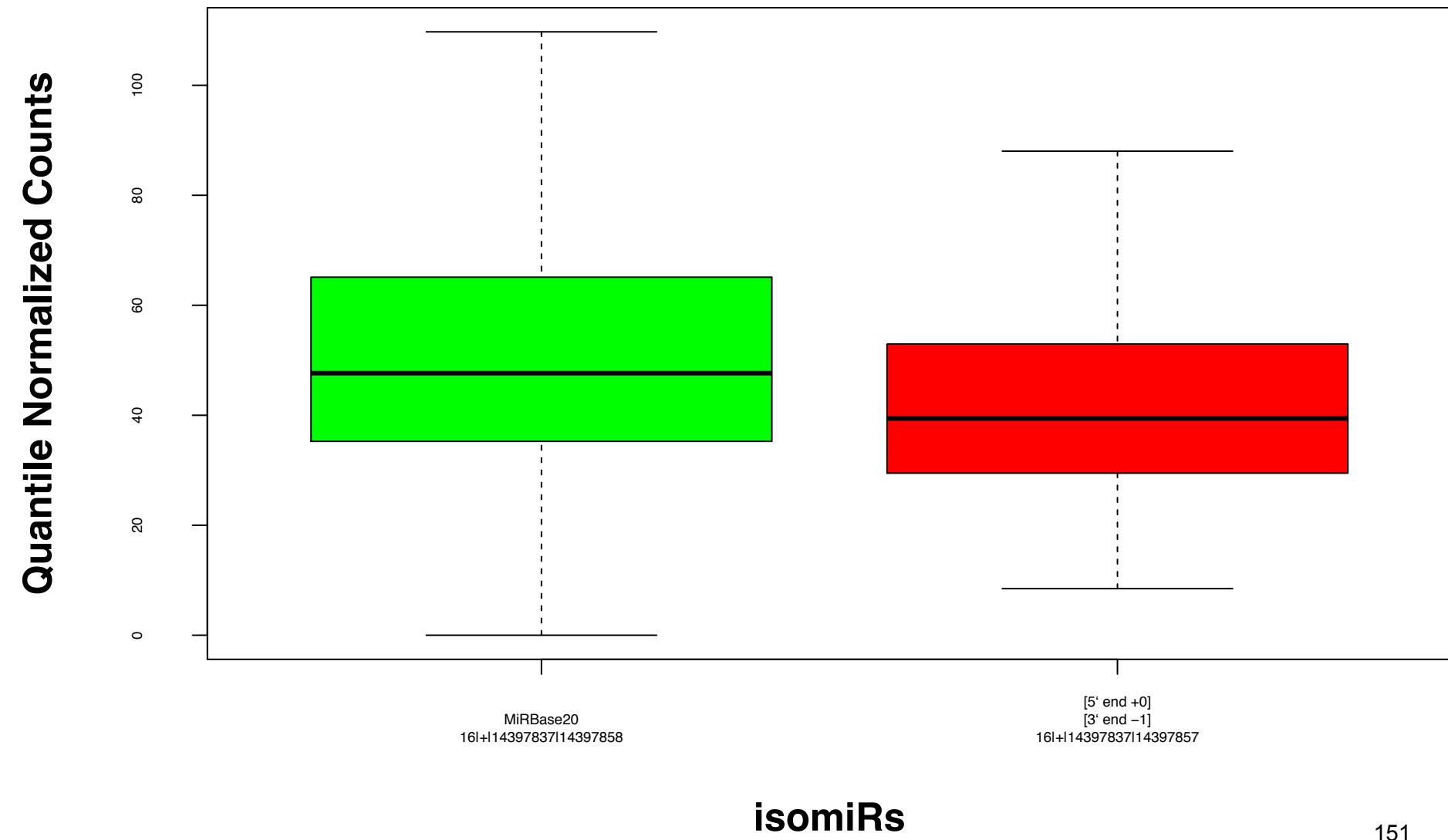
MiRBase20
4l+I38869713lI38869734

isomiRs

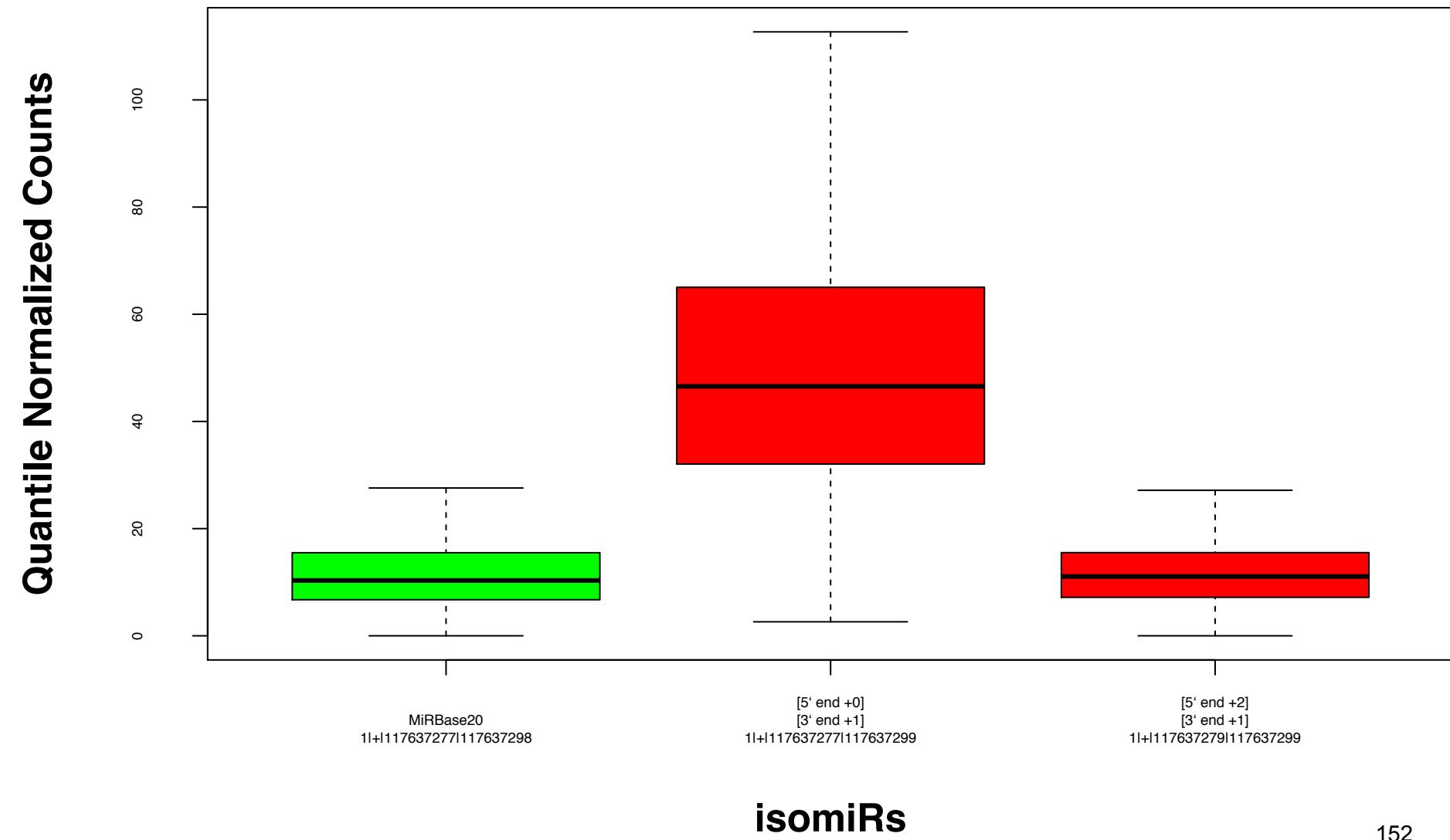
MIMAT0000099_1=hsa-miR-101-3p=MI0000739



MIMAT0004767=hsa-miR-193b-5p=MI0003137

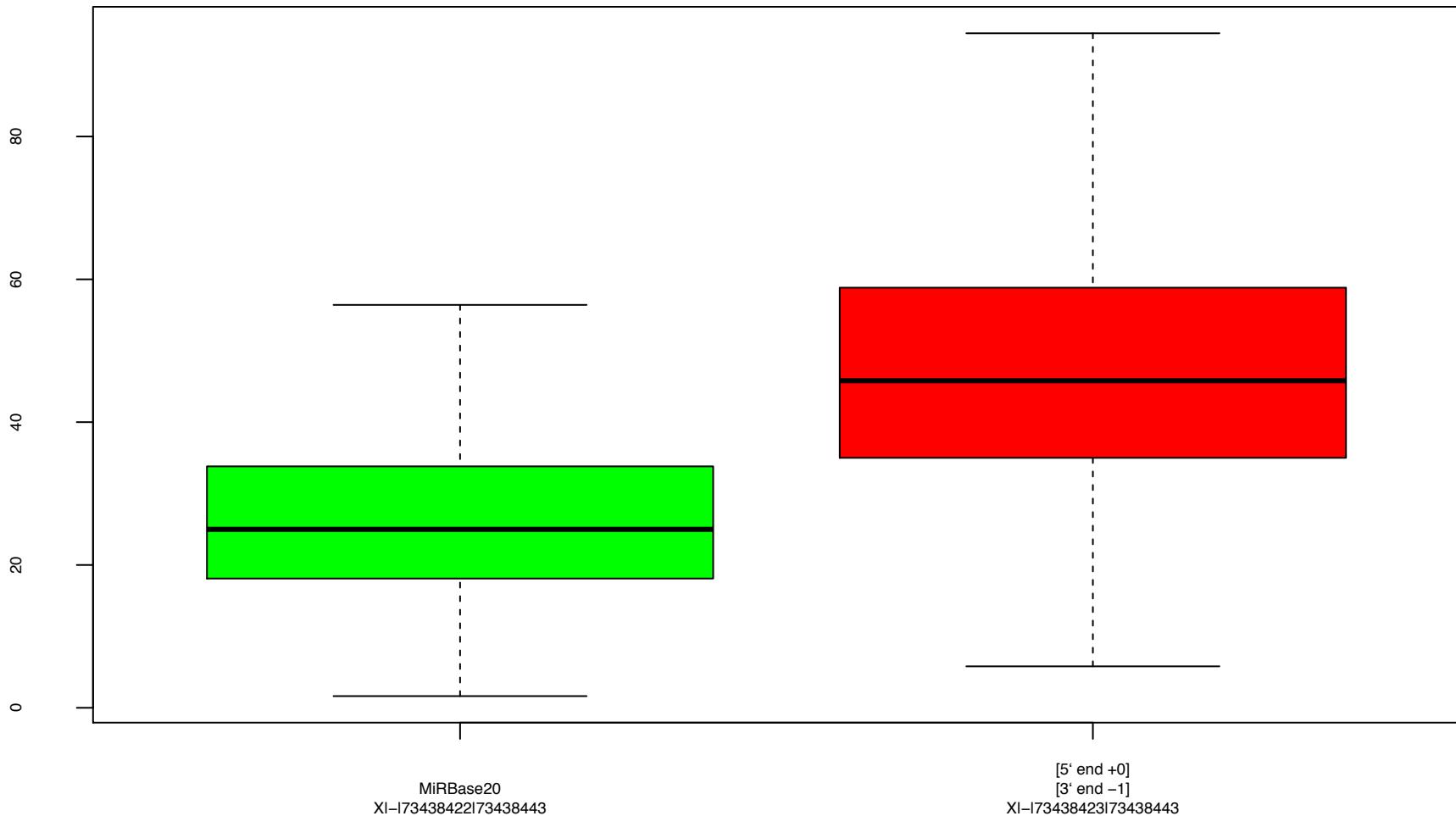


MIMAT0004985=hsa-miR-942-5p=MI0005767



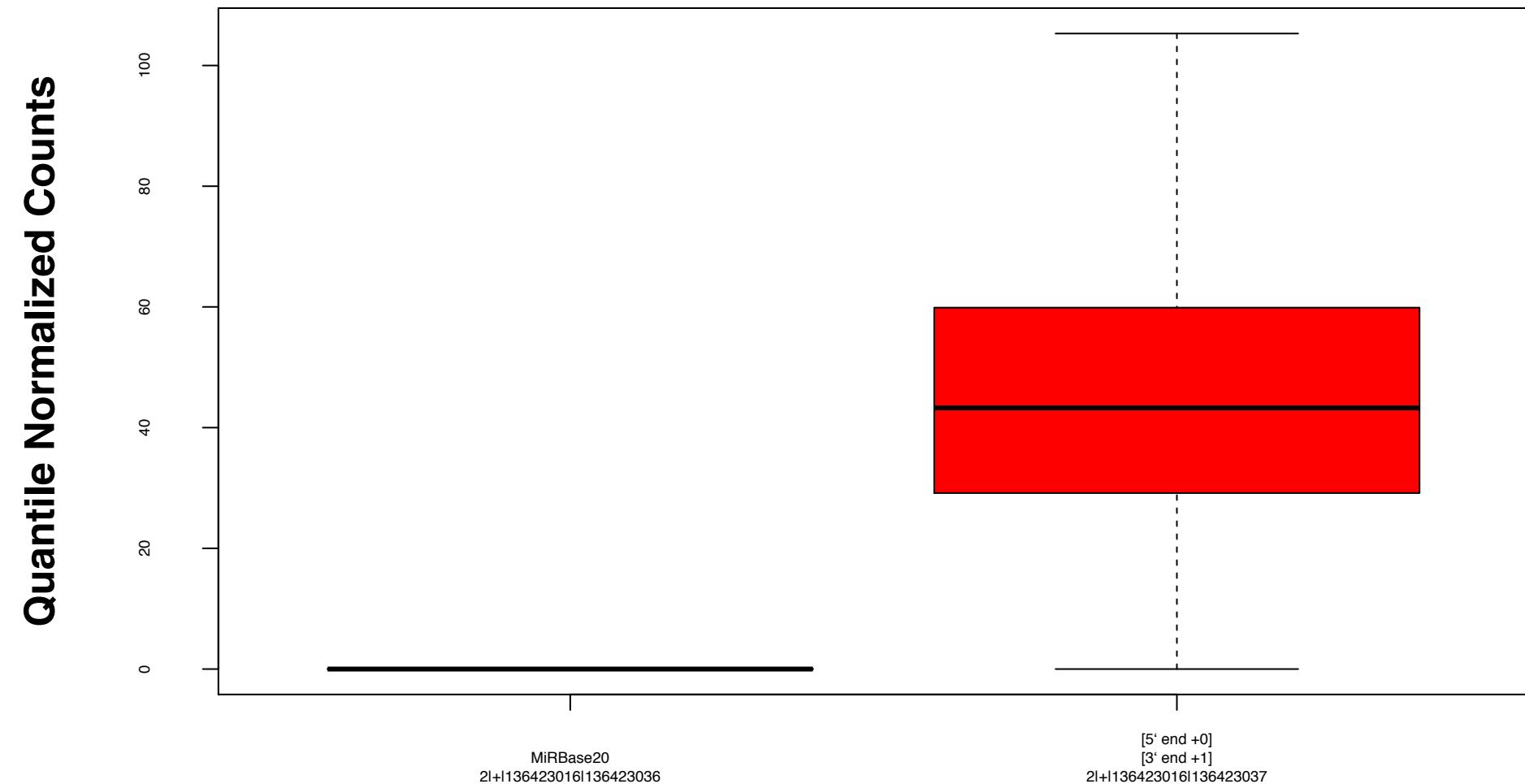
MIMAT0004955=hsa-miR-374b-5p=MI0005566

Quantile Normalized Counts

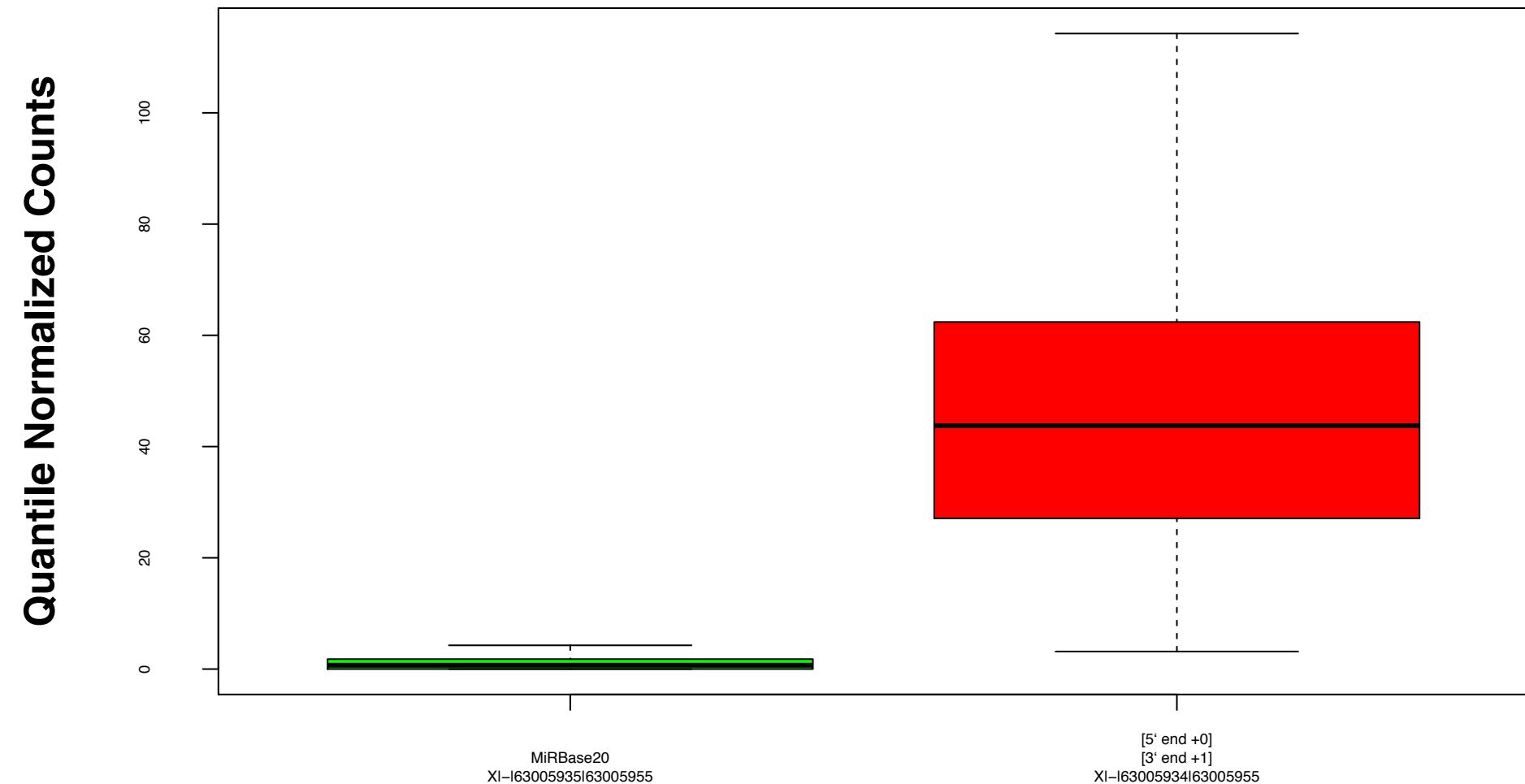


isomiRs

MIMAT0000424=hsa-miR-128-3p=MI0000447

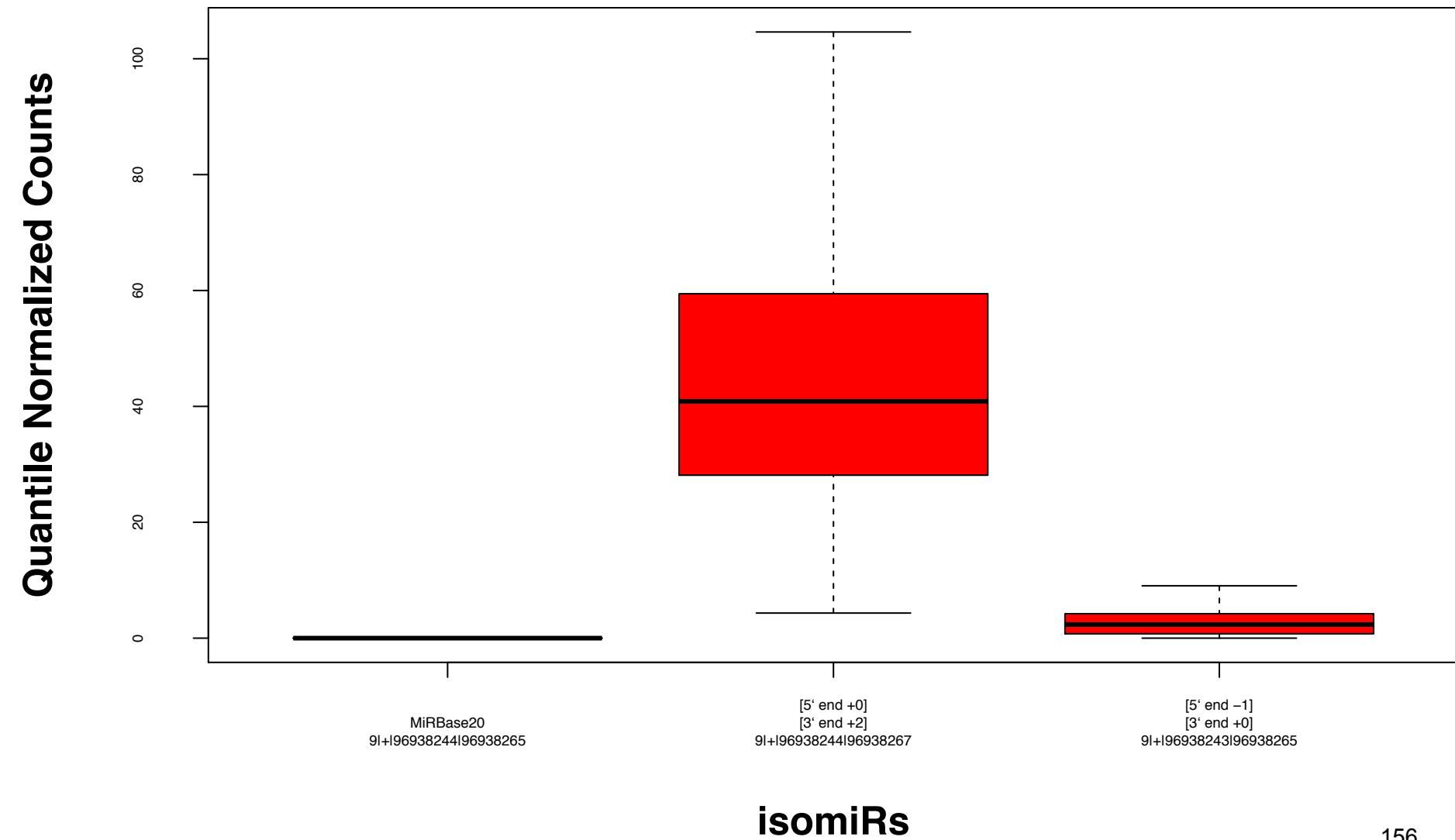


MIMAT0006789=hsa-miR-1468-5p=MI0003782



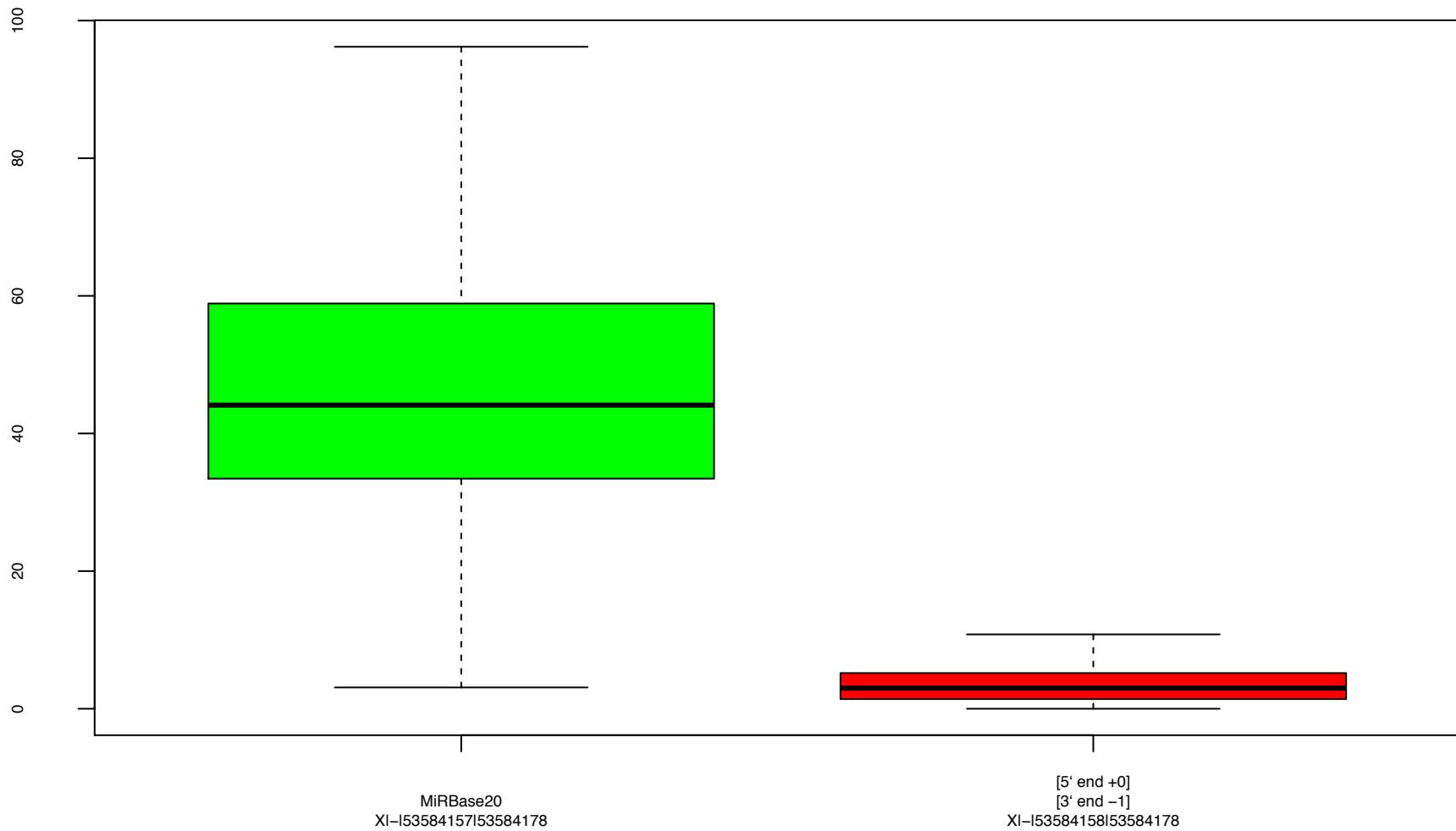
isomiRs

MIMAT0000062_2=hsa-let-7a-5p=MI0000060



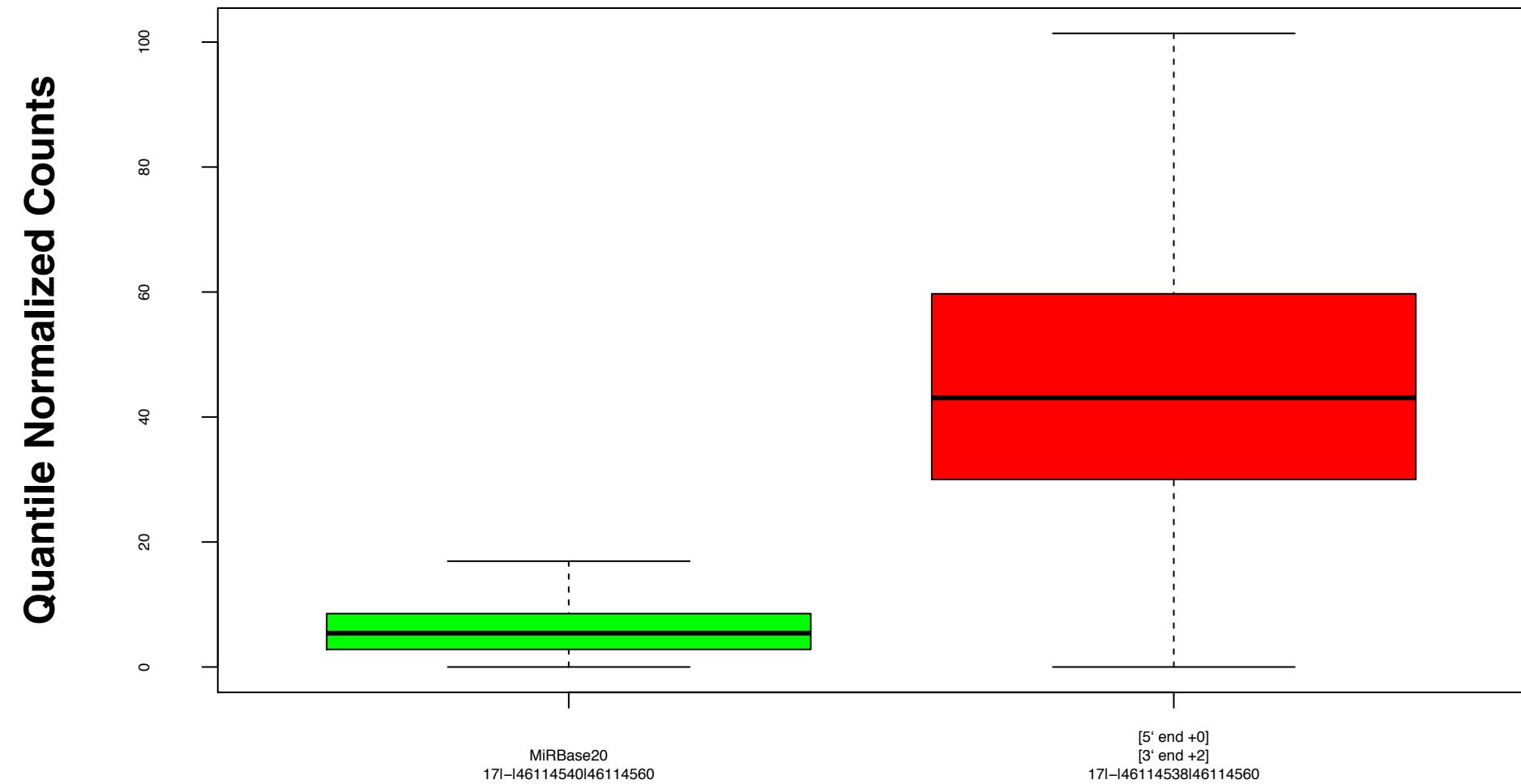
MIMAT0004487=hsa-let-7f-2-3p=MI0000068

Quantile Normalized Counts

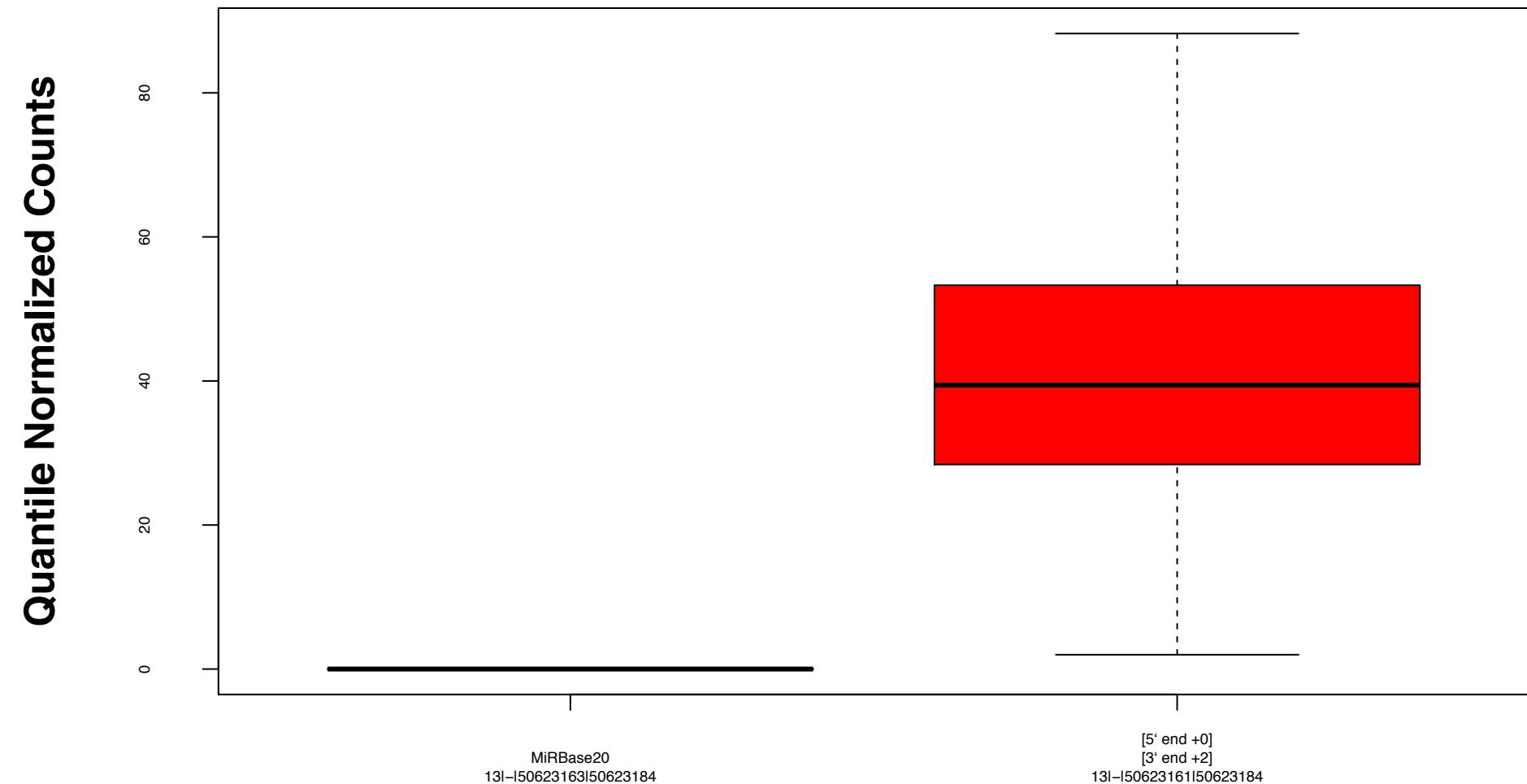


isomiRs

MIMAT0000438=hsa-miR-152-3p=MI0000462

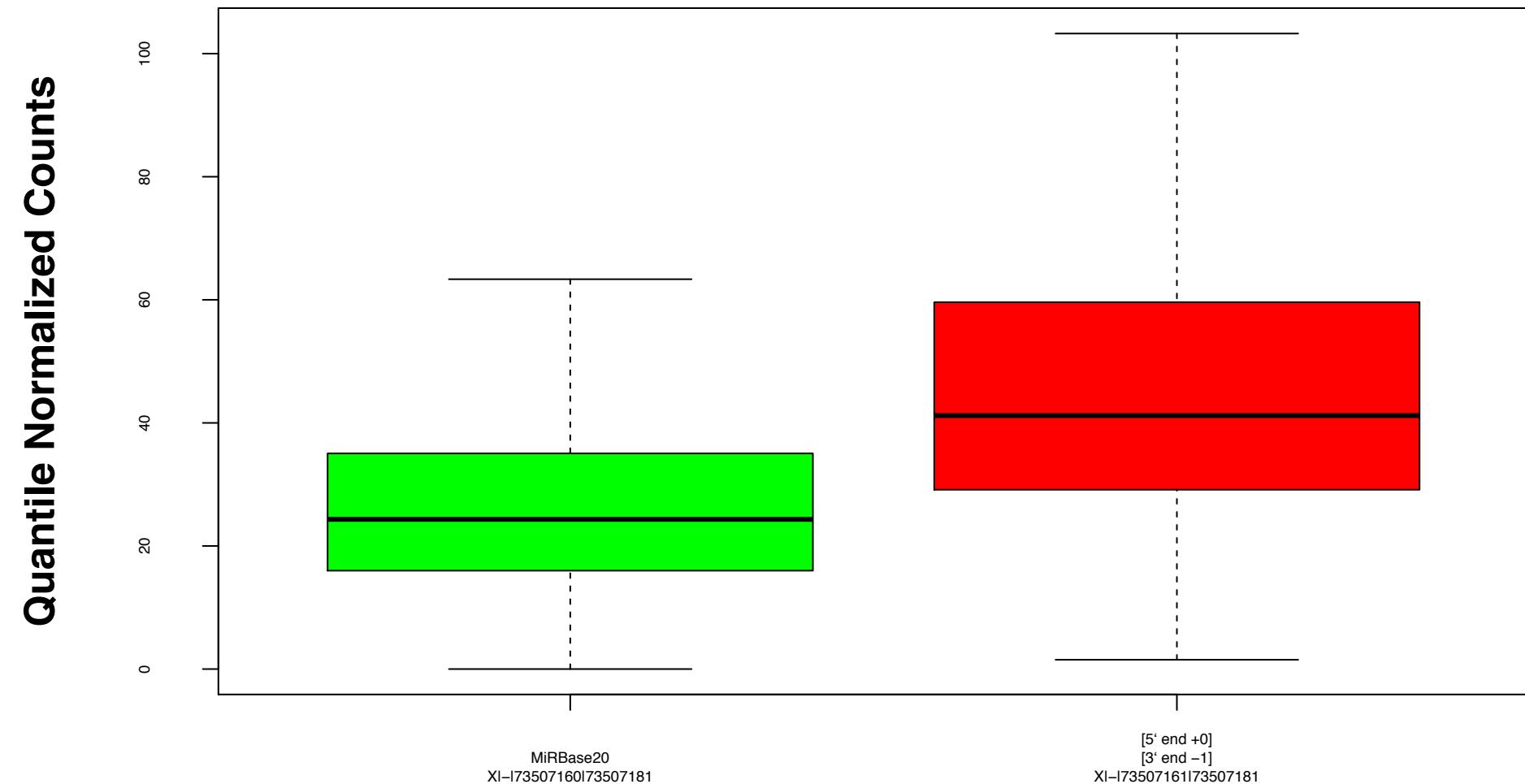


MIMAT0000069=hsa-miR-16-5p=MI0000070



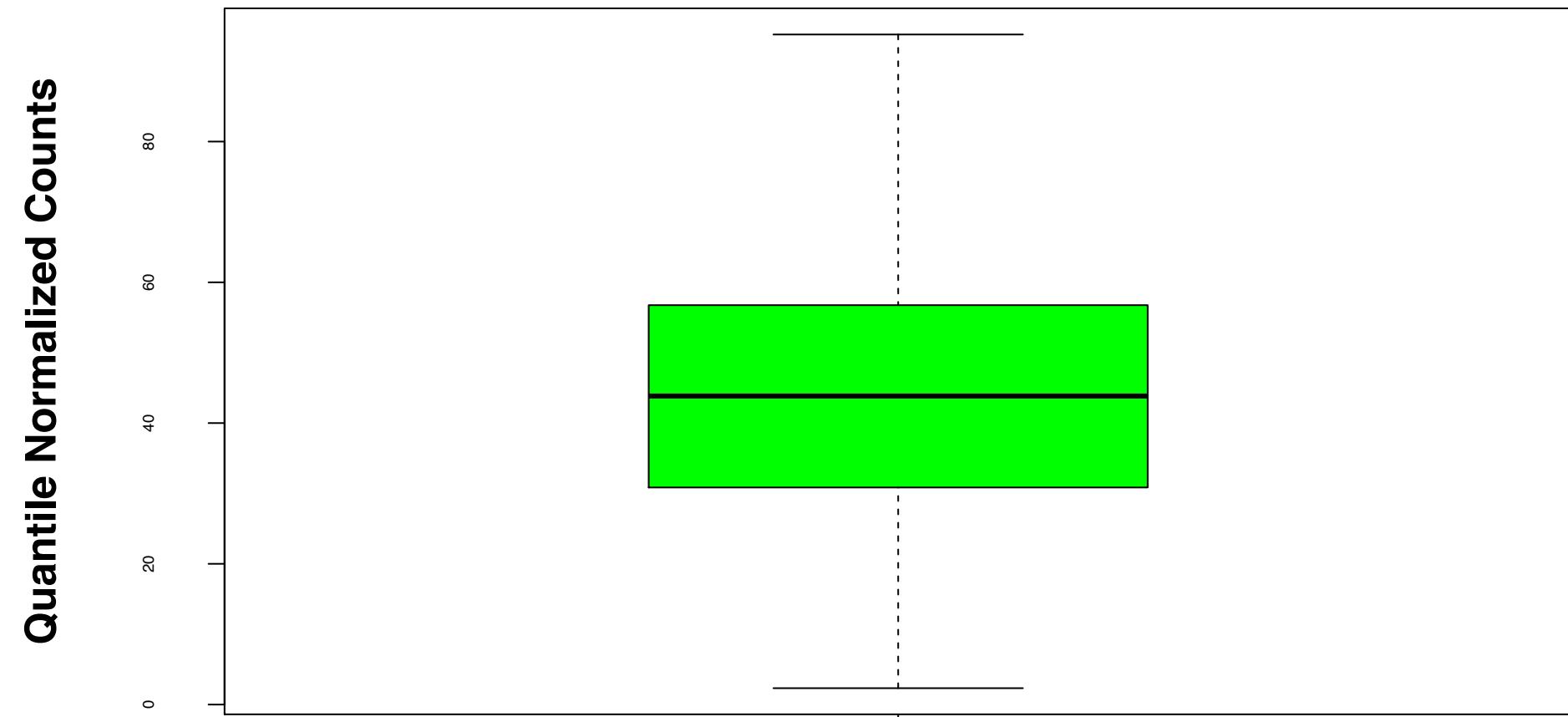
isomiRs

MIMAT0000727=hsa-miR-374a-5p=MI0000782



isomiRs

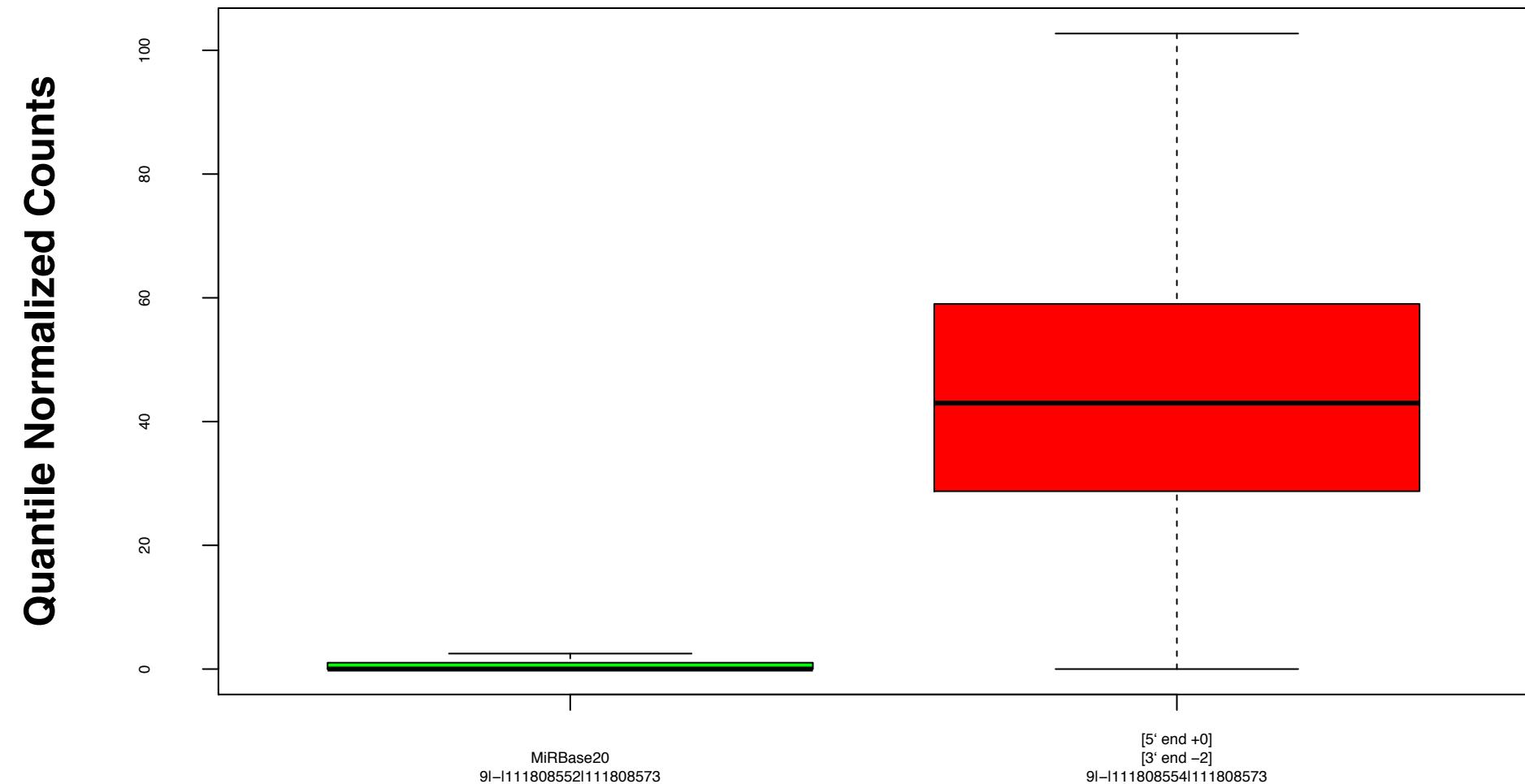
MIMAT0019761=hsa-miR-4677-3p=MI0017308



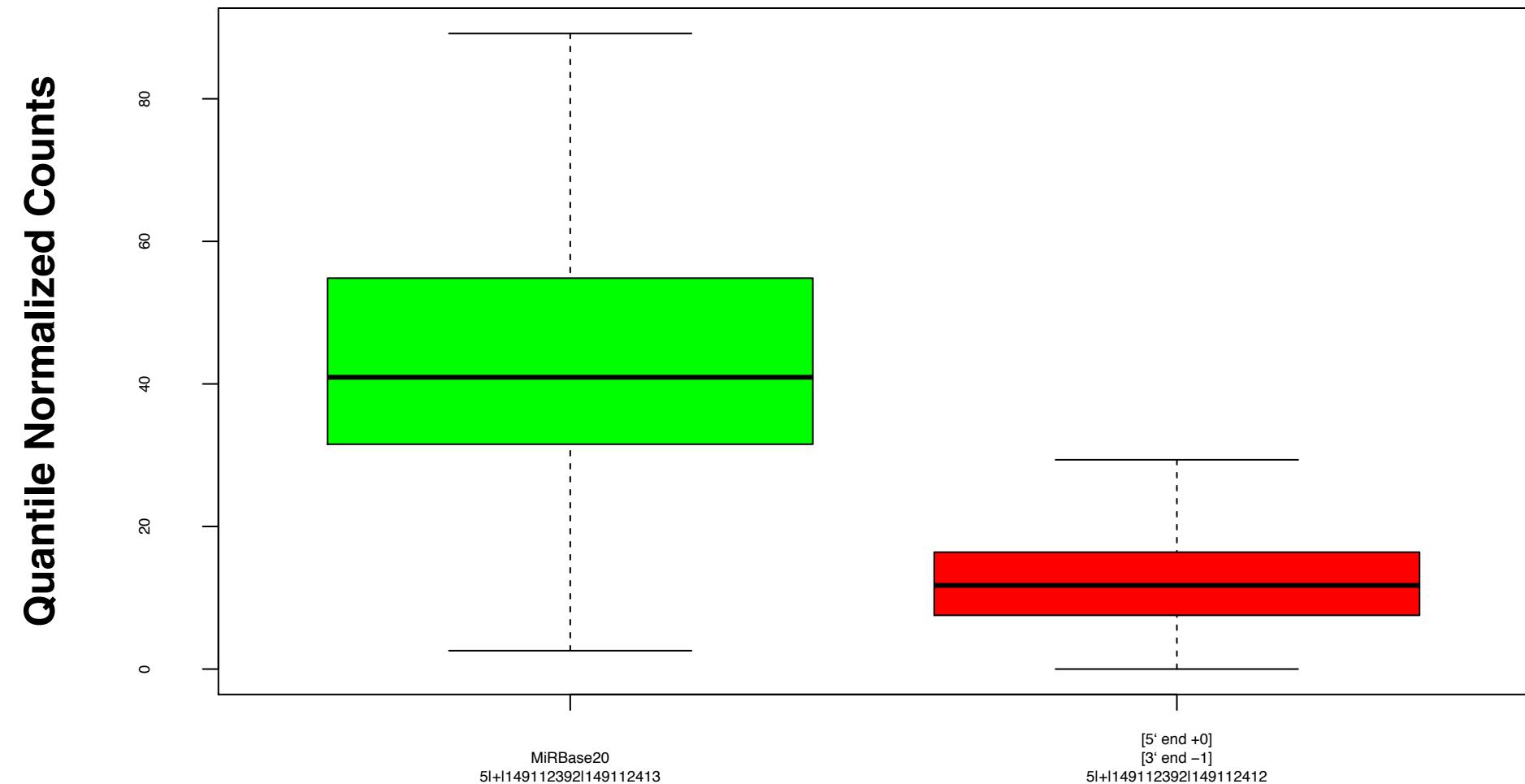
MiRBase20
1|+|243509527|243509548

isomiRs

MIMAT0000090=hsa-miR-32-5p=MI0000090

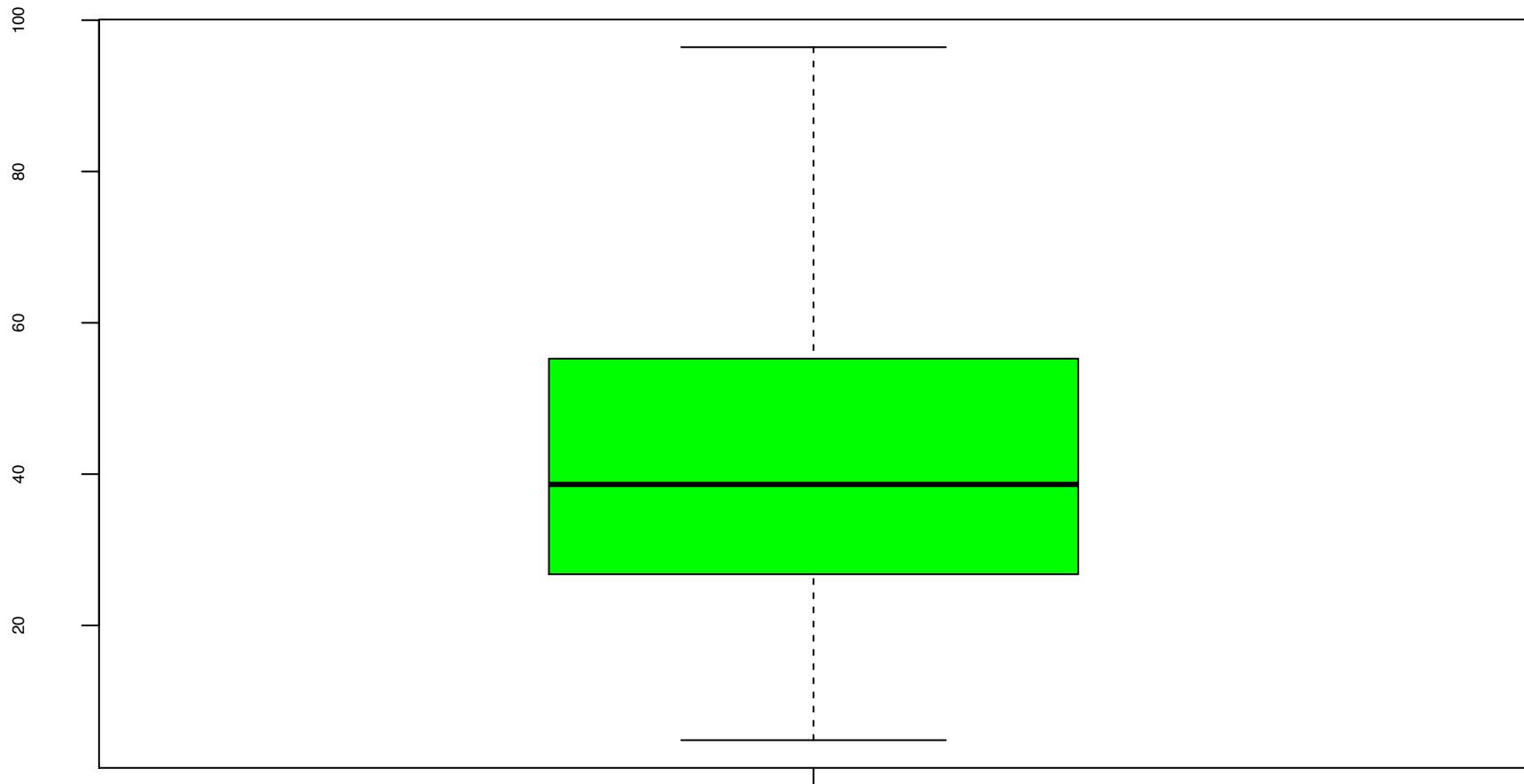


MIMAT0000731=hsa-miR-378a-5p=MI0000786



MIMAT0000455=hsa-miR-185-5p=MI0000482

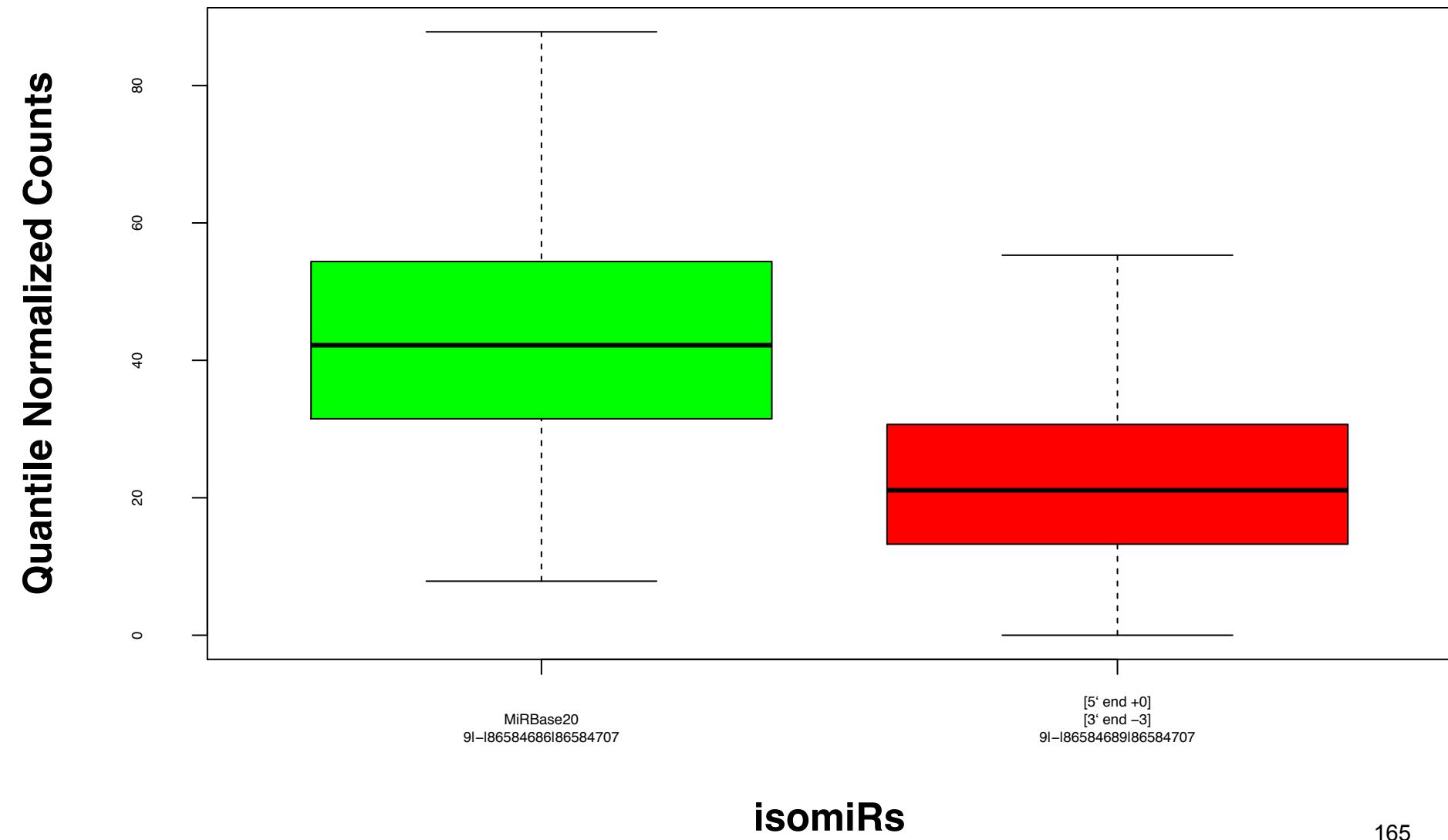
Quantile Normalized Counts



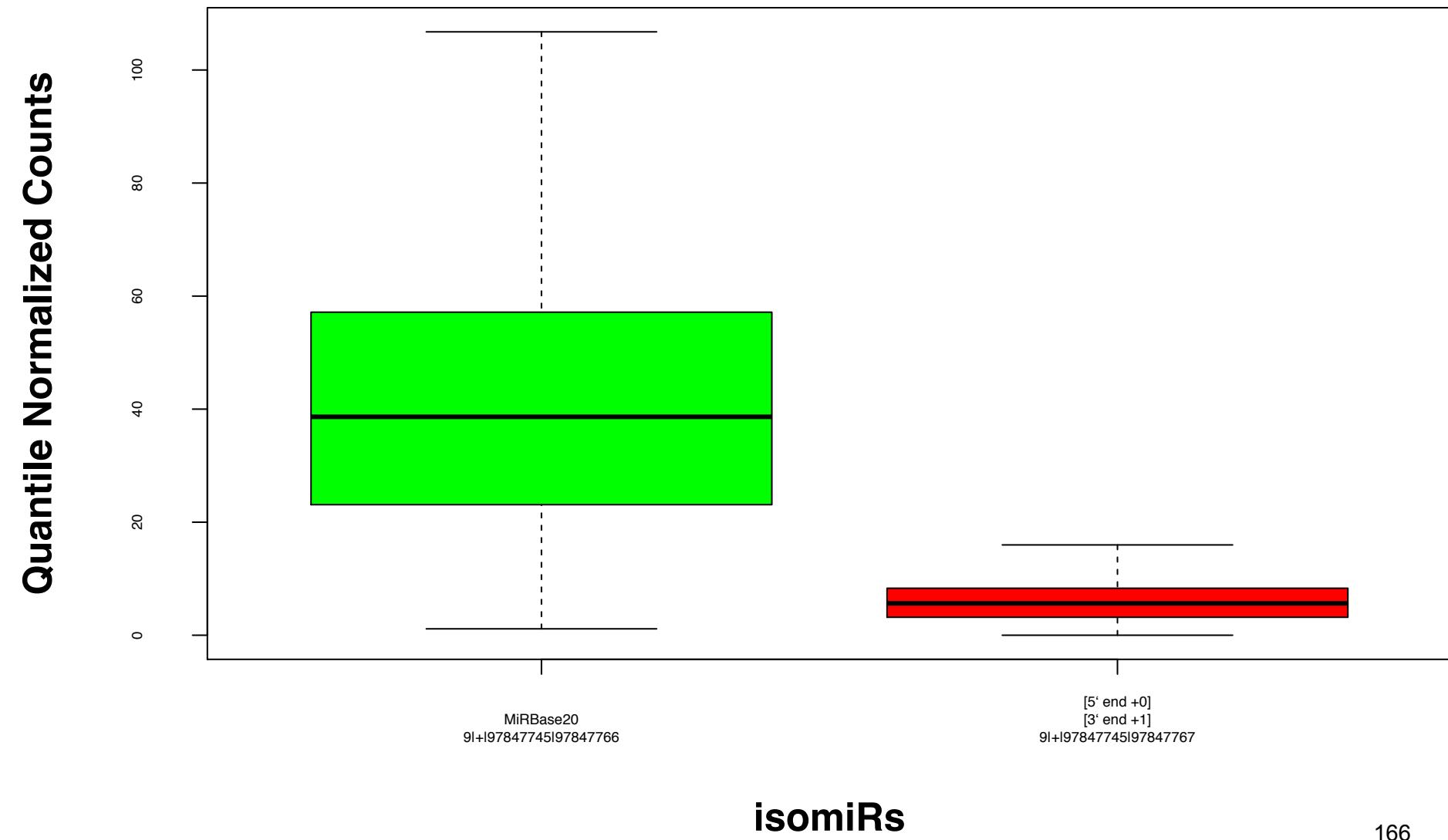
MiRBase20
22l+I20020676|20020697

isomiRs

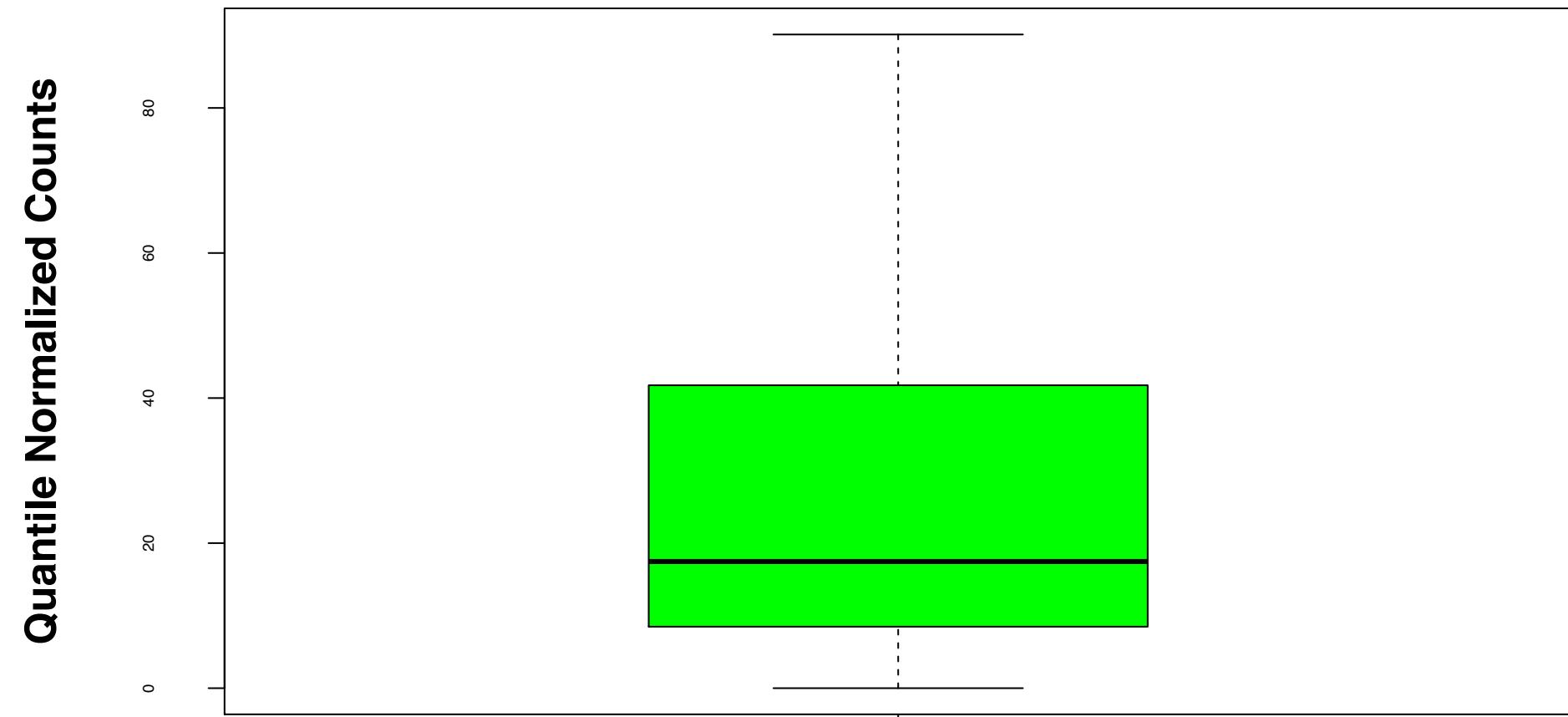
MIMAT0004553=hsa-miR-7-1-3p=MI0000263



MIMAT0004588=hsa-miR-27b-5p=MI0000440



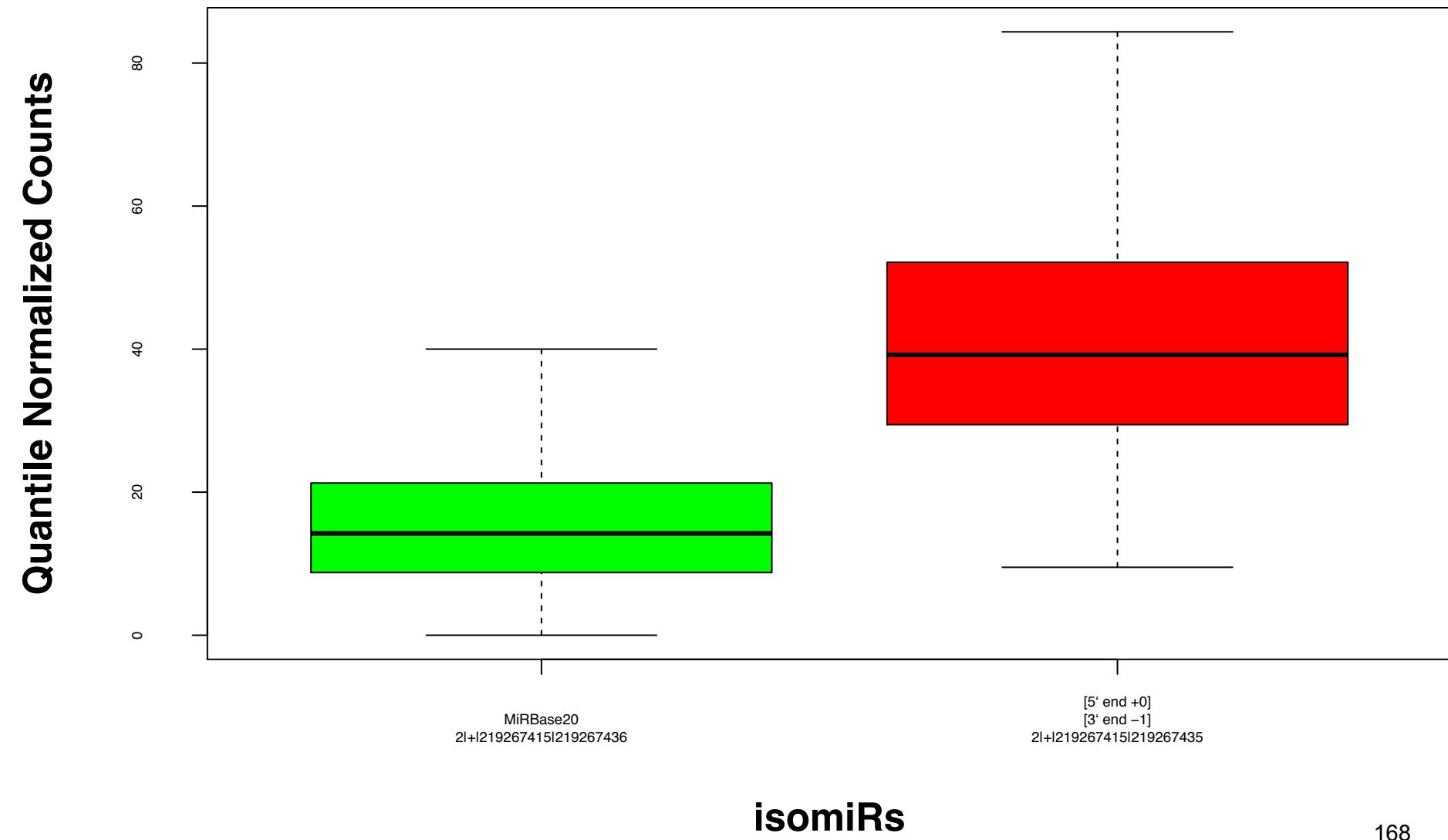
MIMAT0030019=hsa-miR-7704=MI0025240



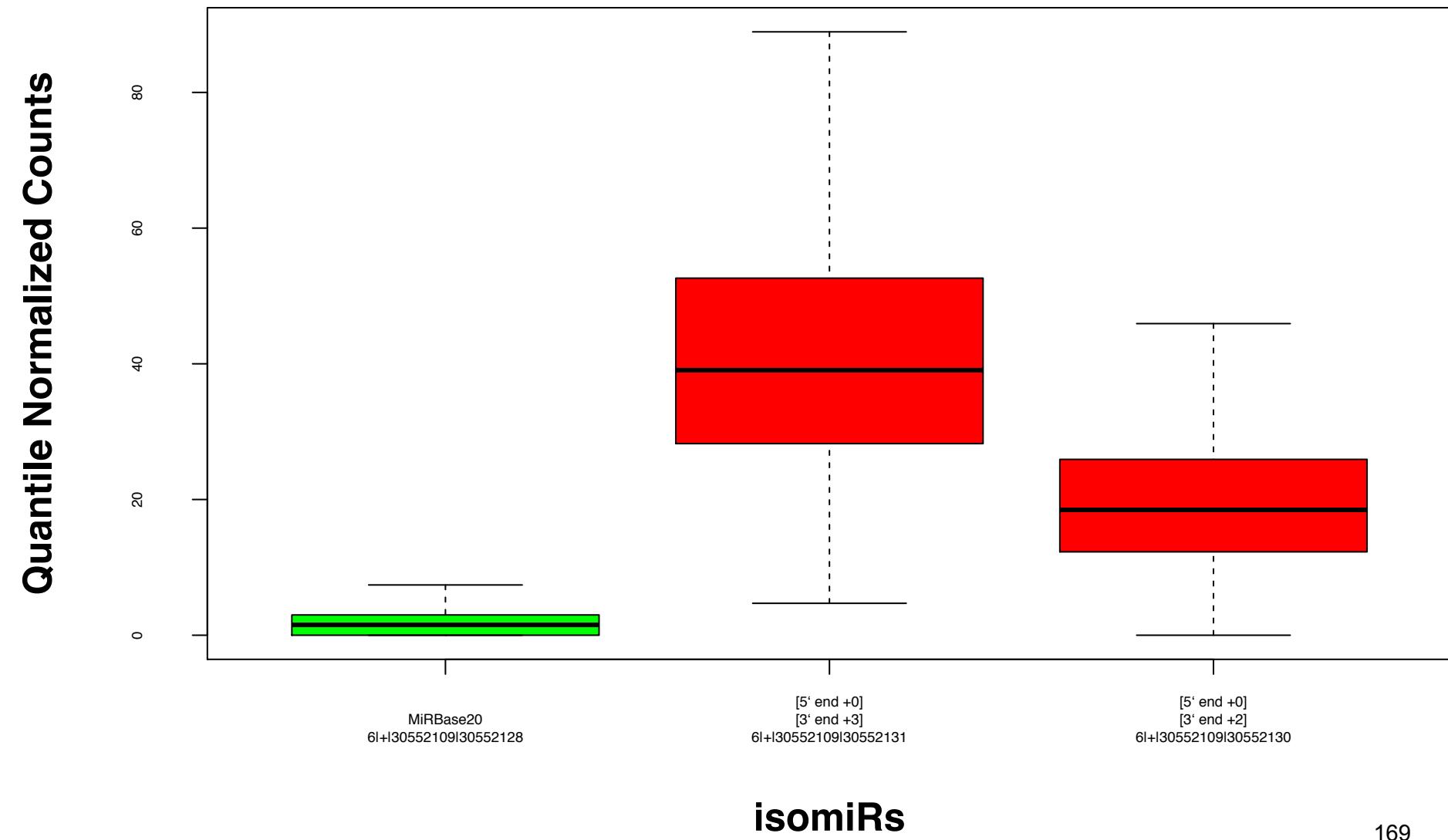
MiRBase20
2l+177053571l177053589

isomiRs

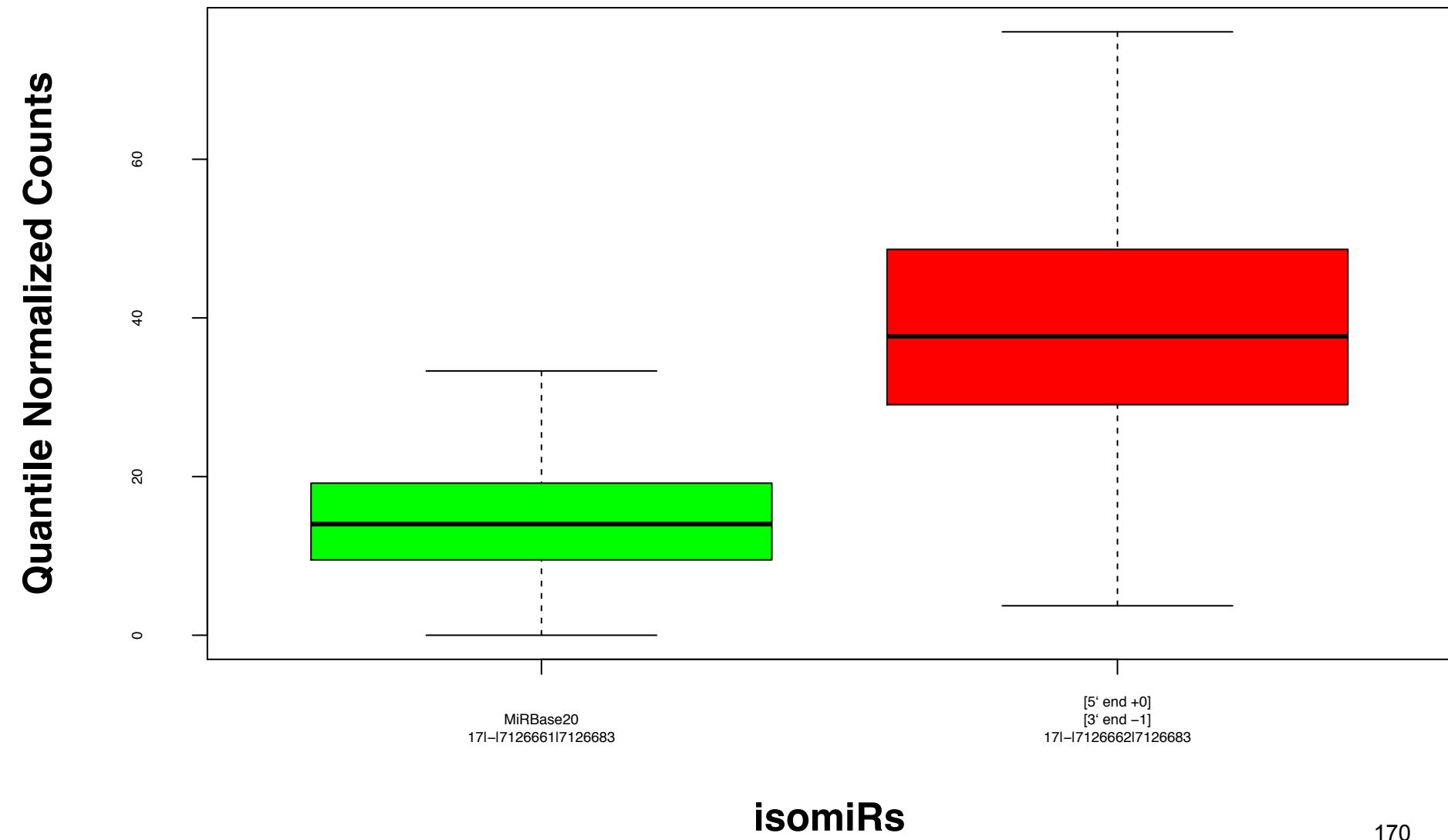
MIMAT0004500=hsa-miR-26b-3p=MI0000084



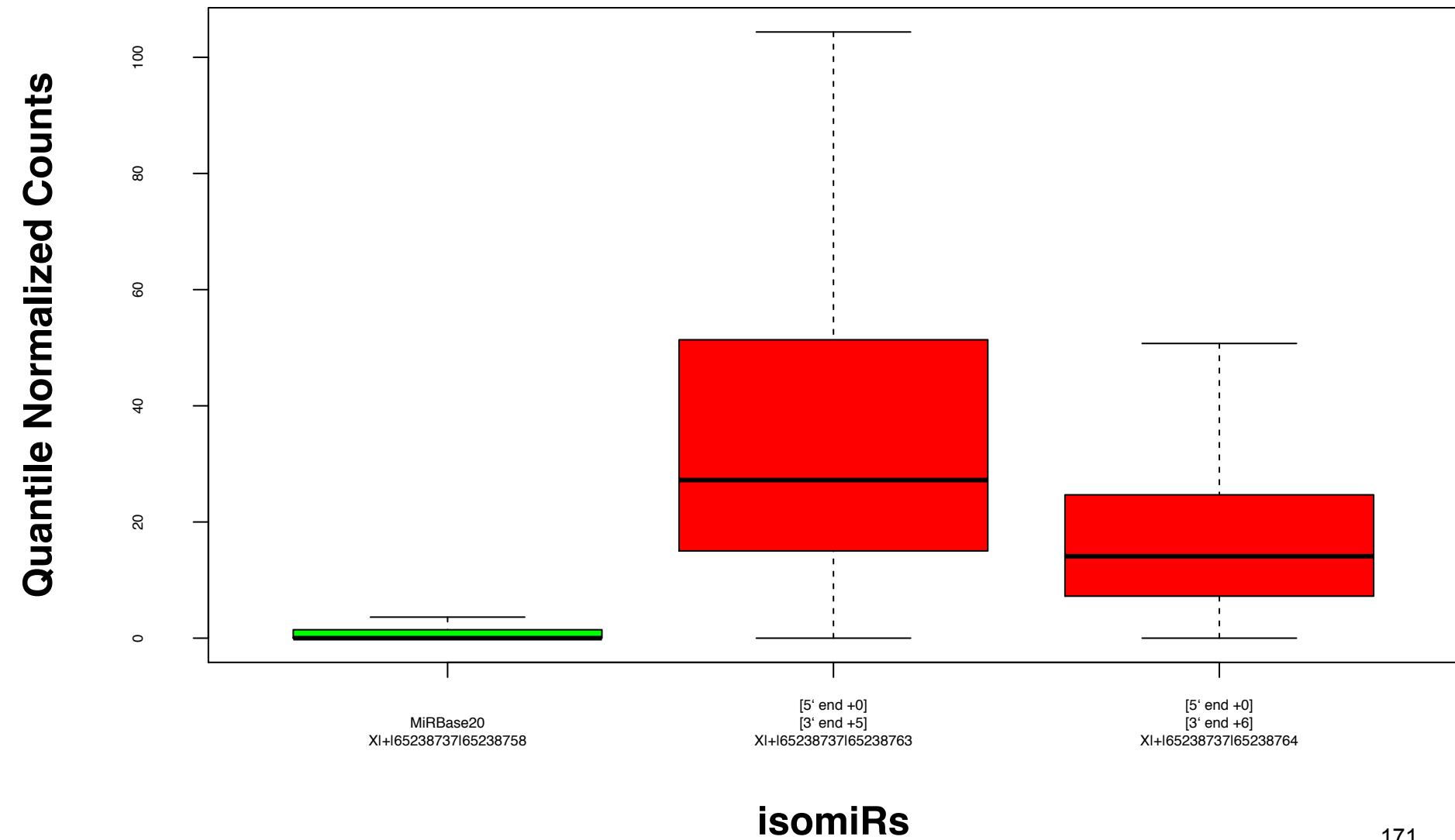
MIMAT0004949=hsa-miR-877-5p=MI0005561



MIMAT0000761=hsa-miR-324-5p=MI0000813

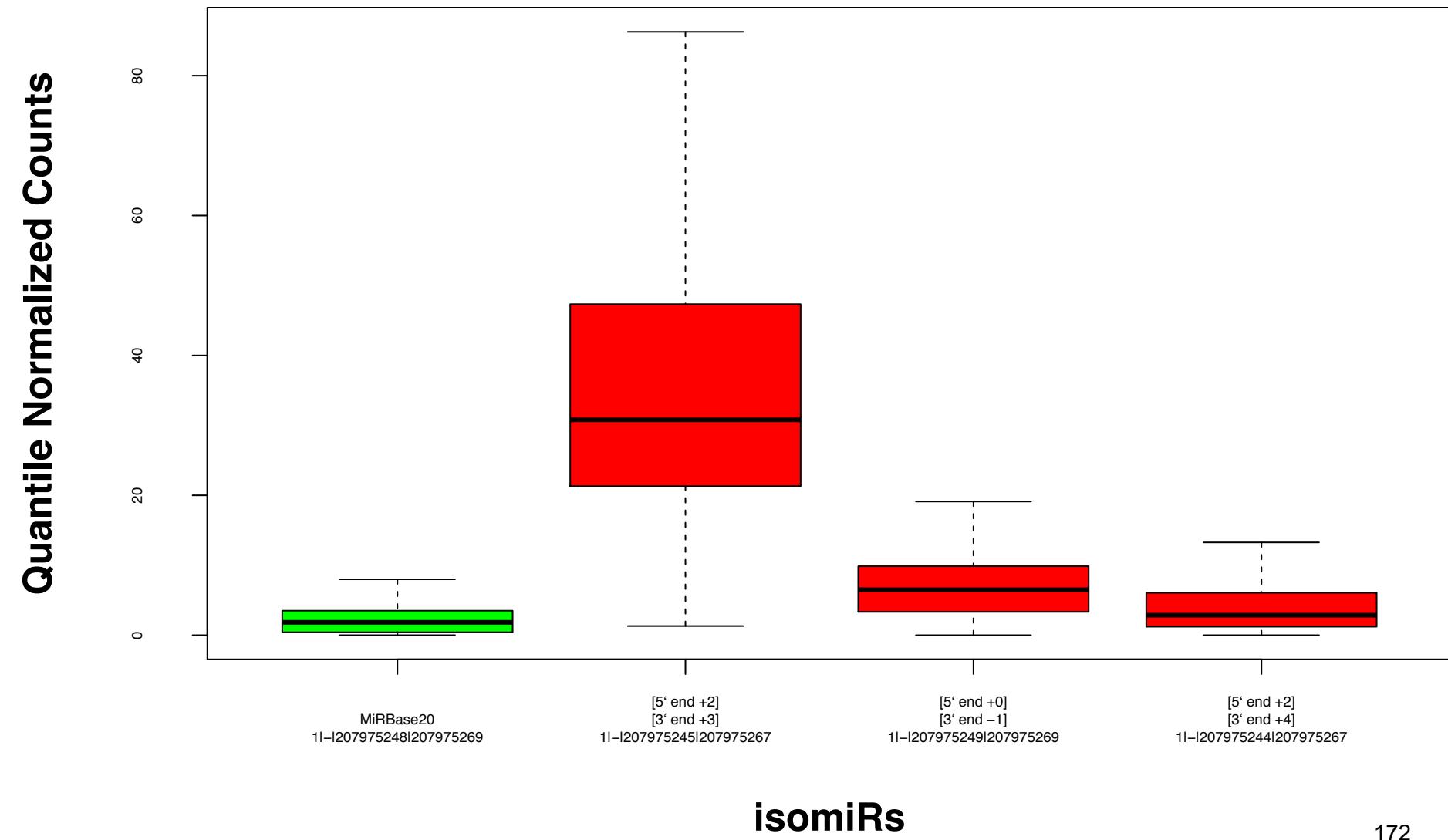


MIMAT0004570=hsa-miR-223-5p=MI0000300

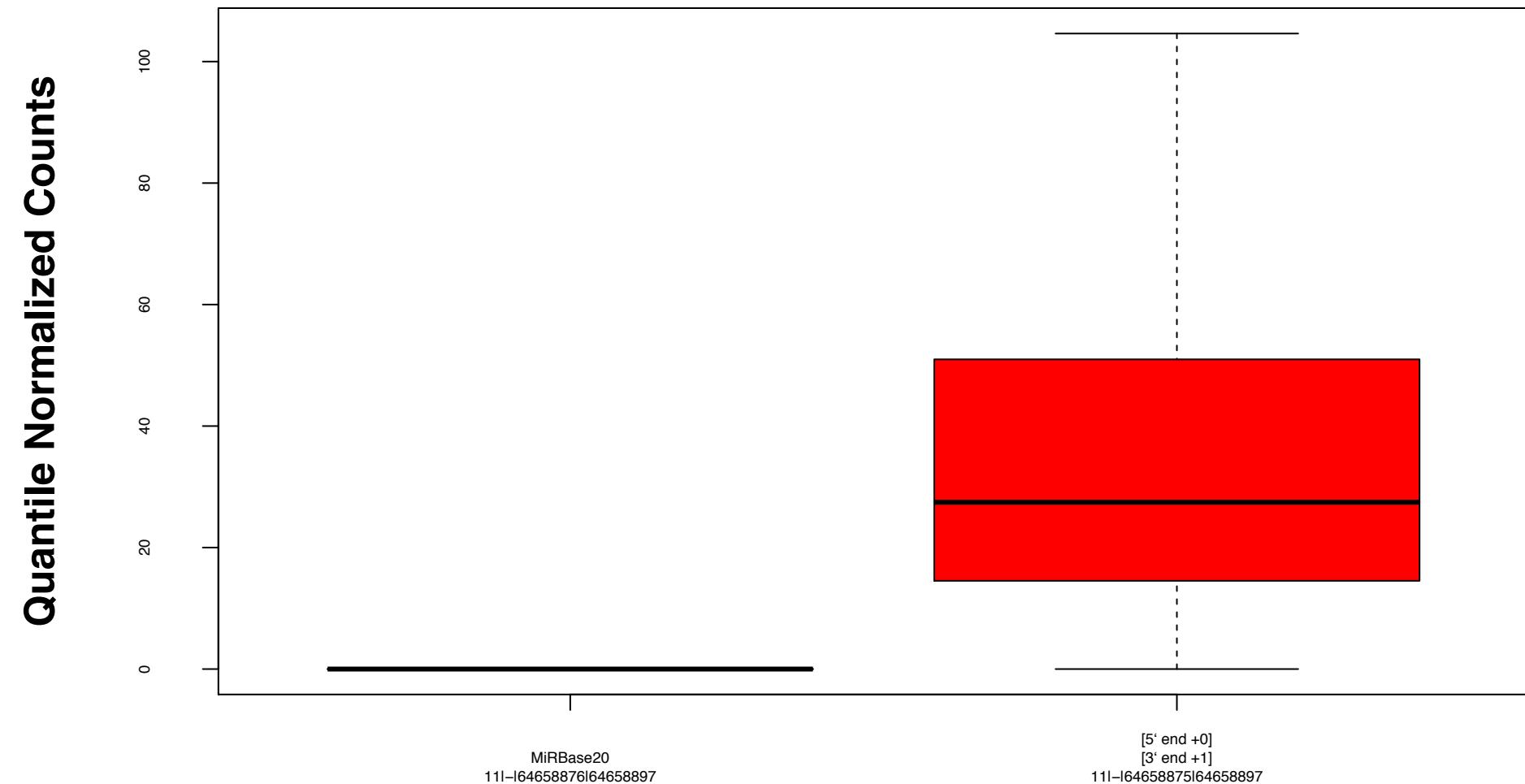


isomiRs

MIMAT0004673=hsa-miR-29c-5p=MI0000735

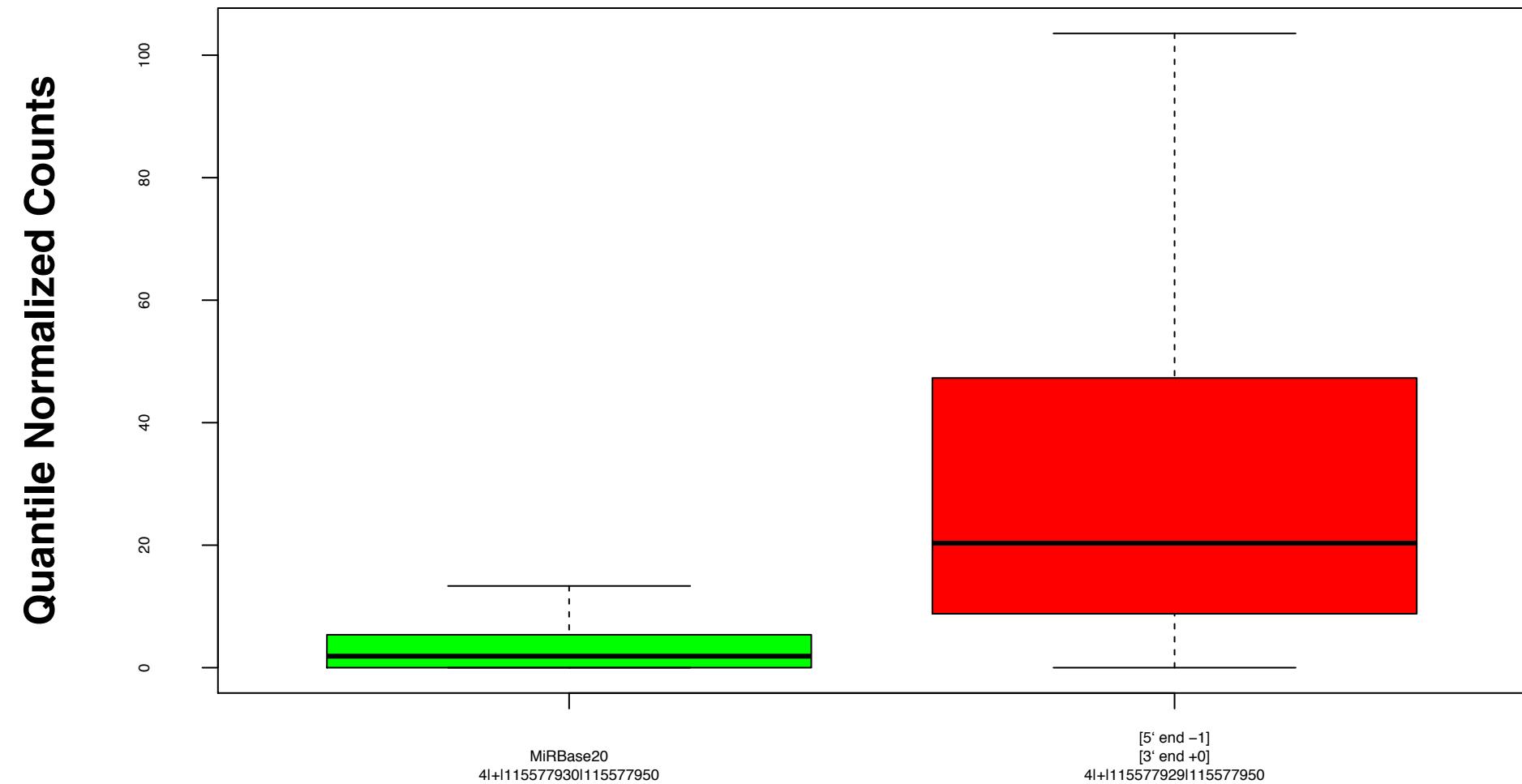


MIMAT0000460_1=hsa-miR-194-5p=MI0000732

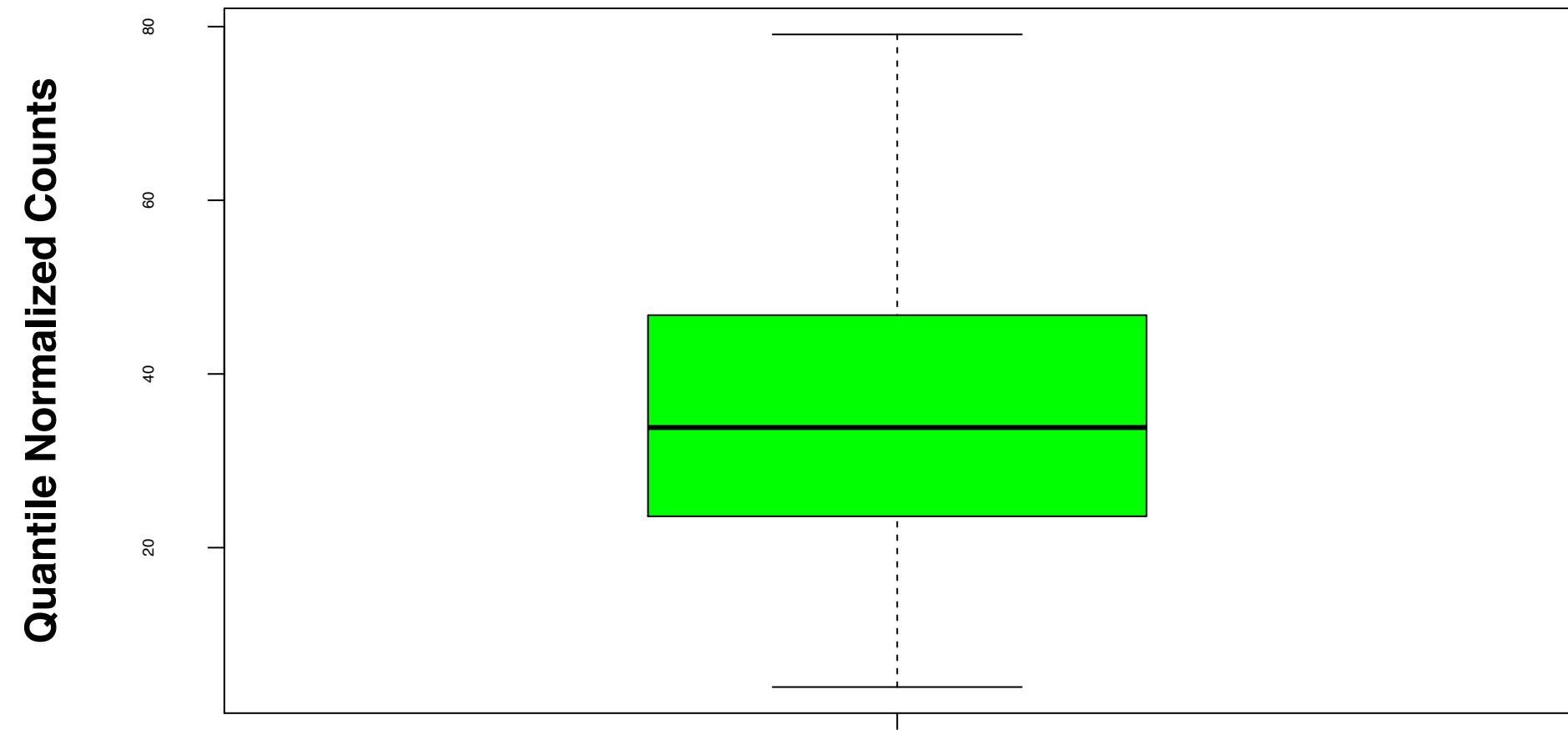


isomiRs

MIMAT0003242=hsa-miR-577=MI0003584



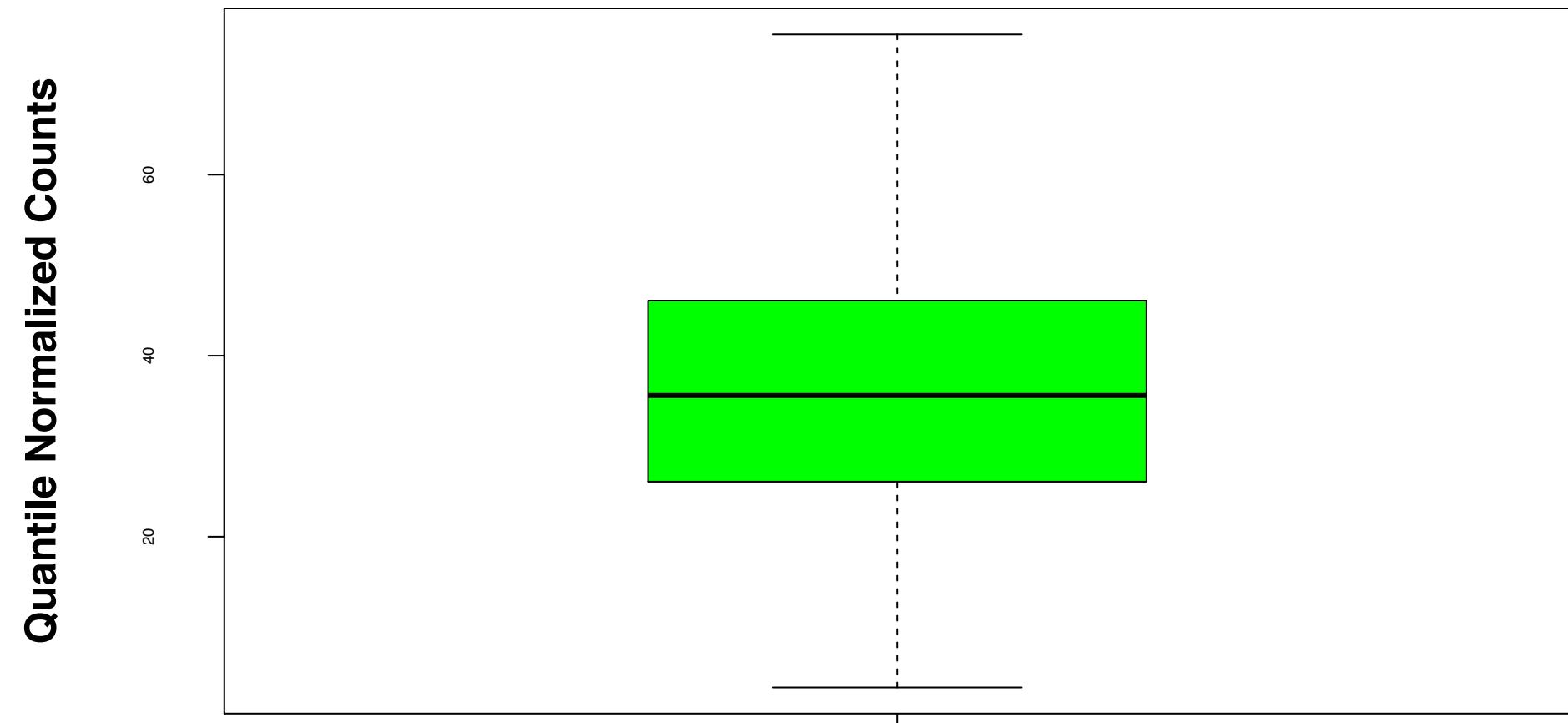
MIMAT0003884=hsa-miR-454-5p=MI0003820



MiRBase20
17l-l57215189|l57215210

isomiRs

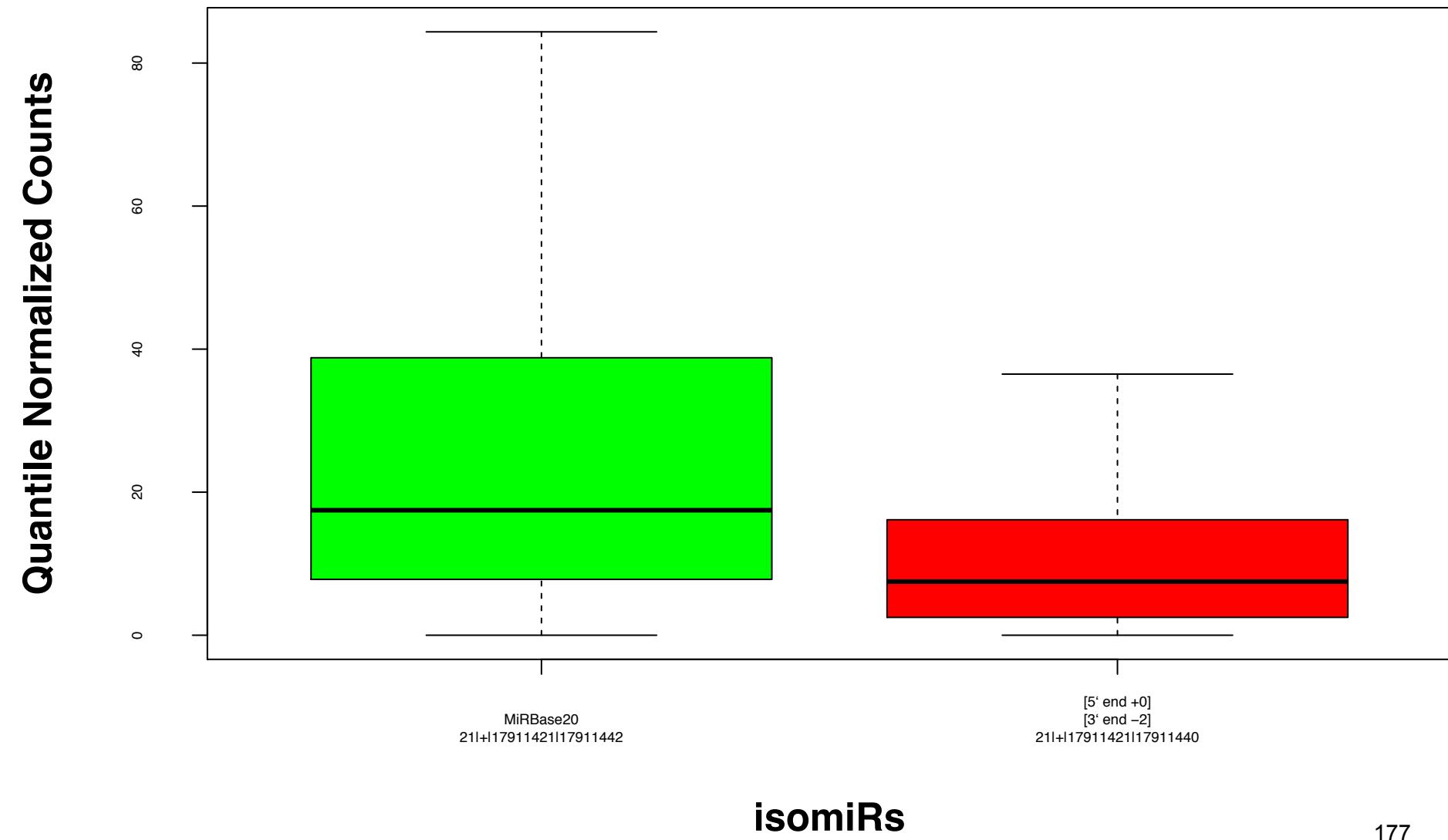
MIMAT0003266=hsa-miR-598-3p=MI0003610



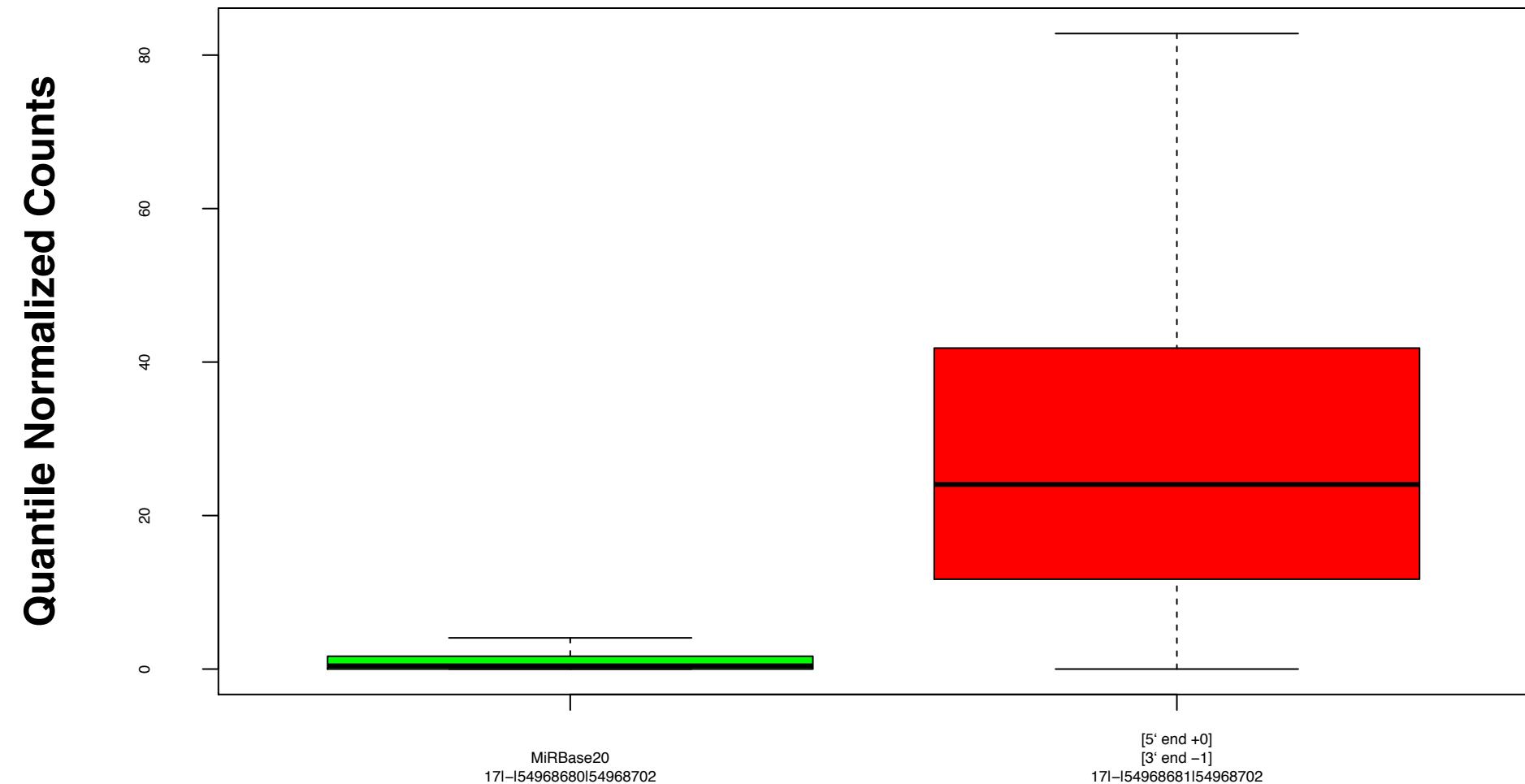
MiRBase20
8l-l10892731l10892752

isomiRs

MIMAT0000097=hsa-miR-99a-5p=MI0000101

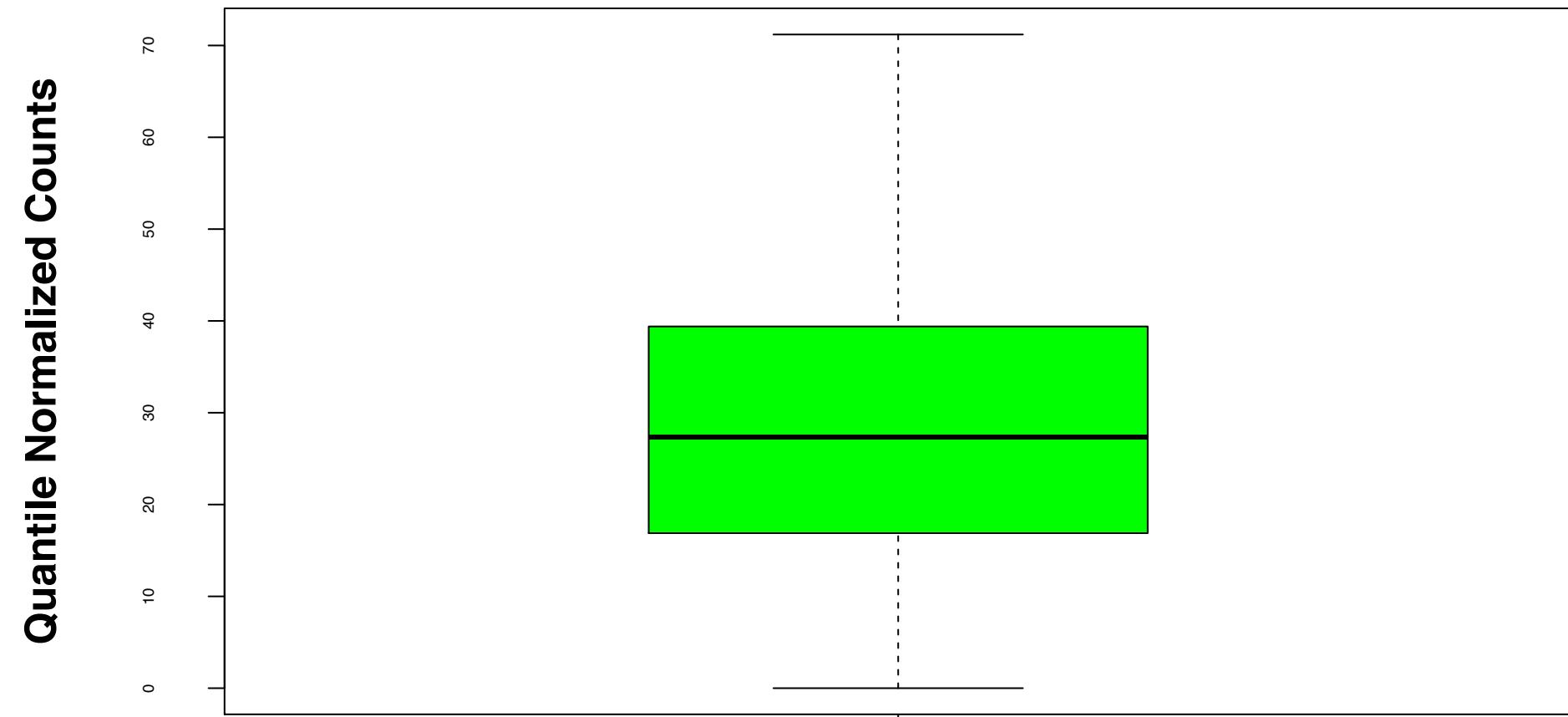


MIMAT0017992=hsa-miR-3614-5p=MI0016004



isomiRs

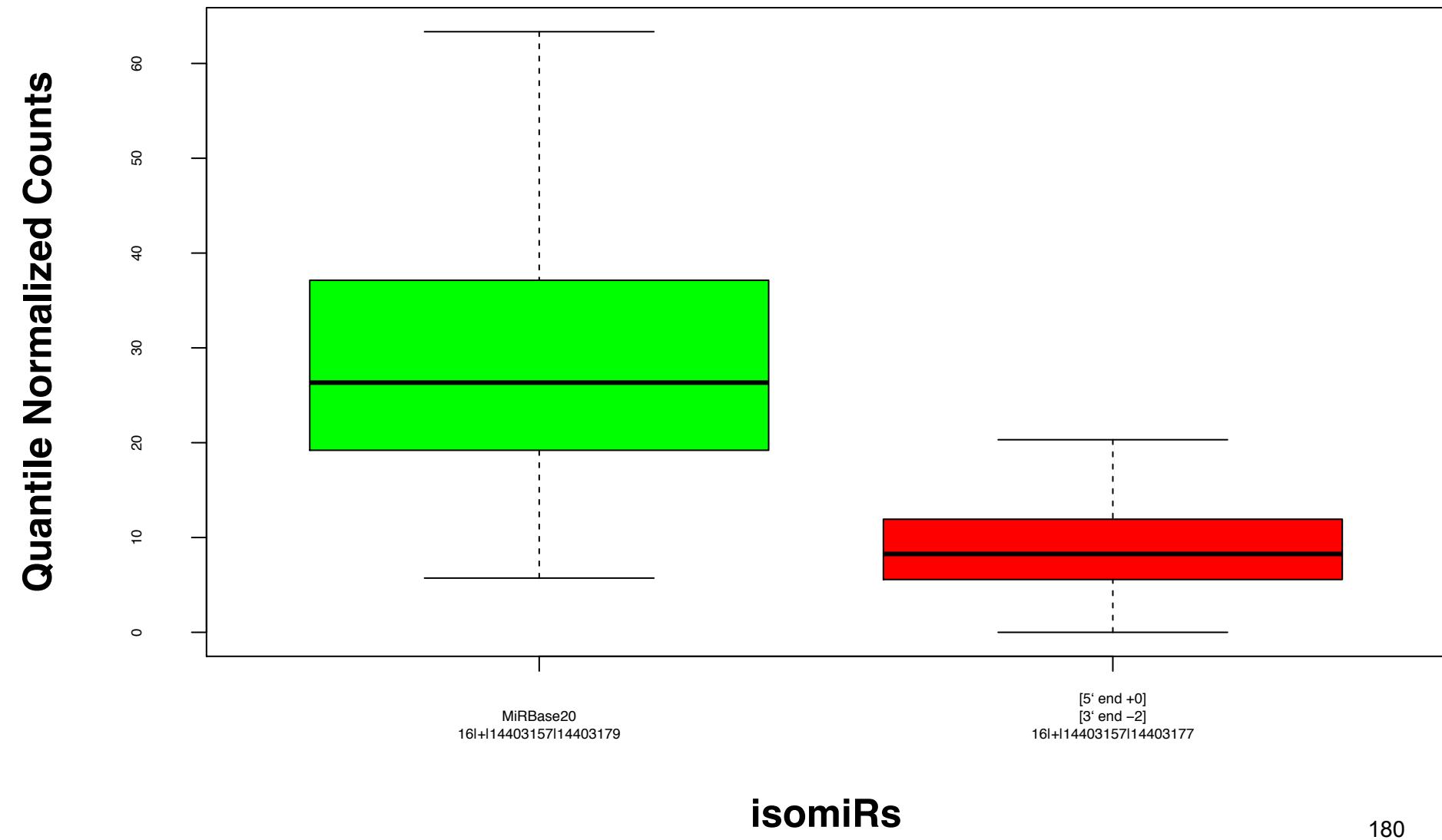
MIMAT0004589=hsa-miR-30b-3p=MI0000441



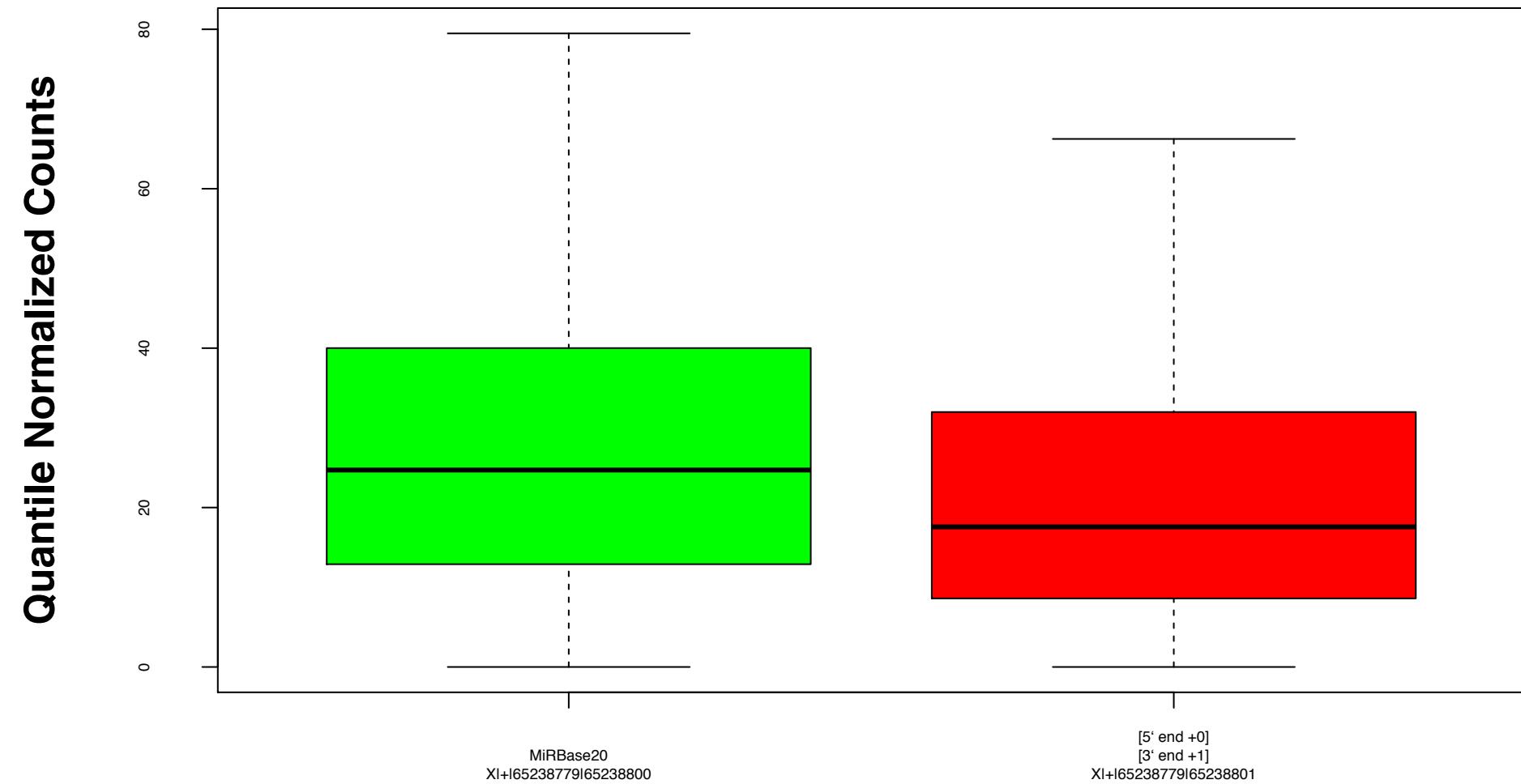
MiRBase20
8I-I135812775I135812796

isomiRs

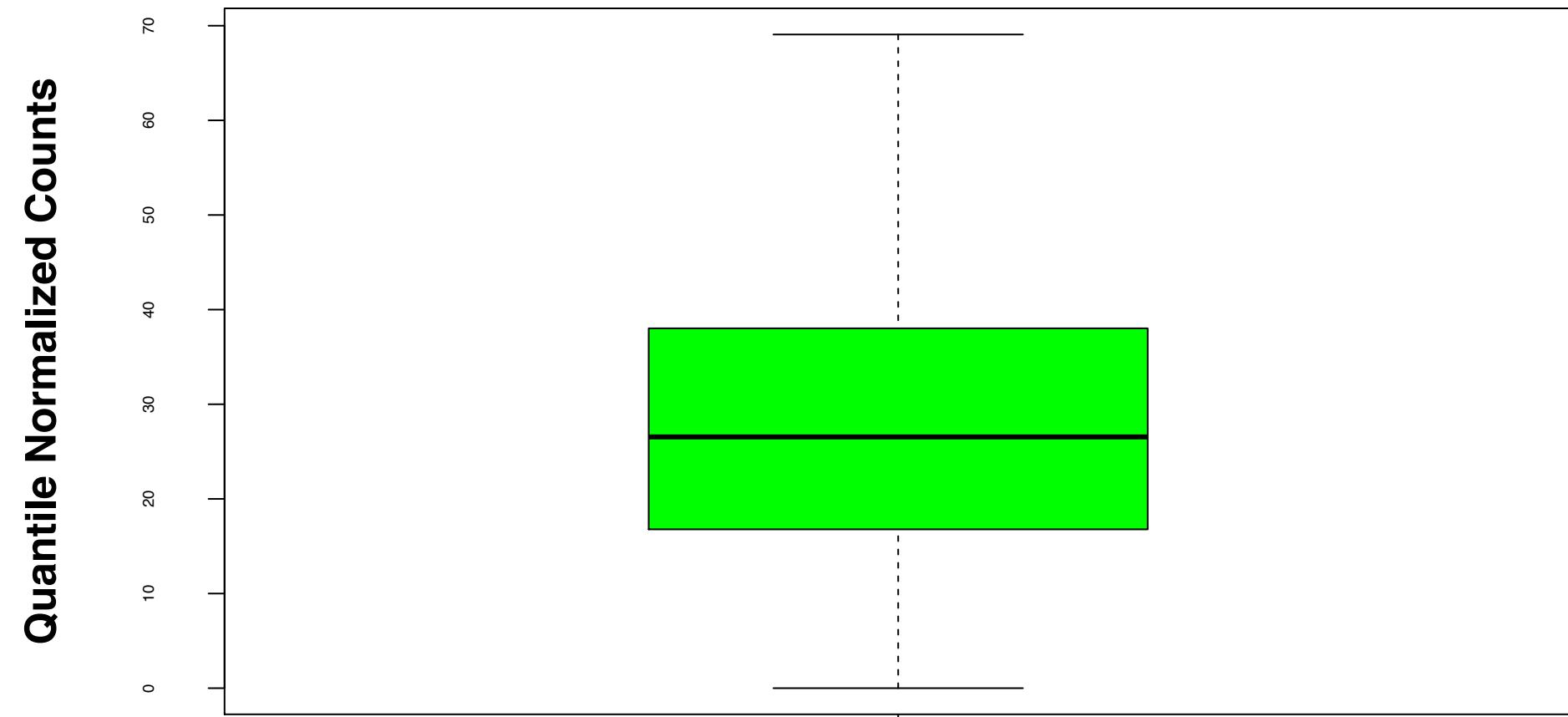
MIMAT0009199=hsa-miR-365a-5p=MI0000767



MIMAT0000280=hsa-miR-223-3p=MI0000300



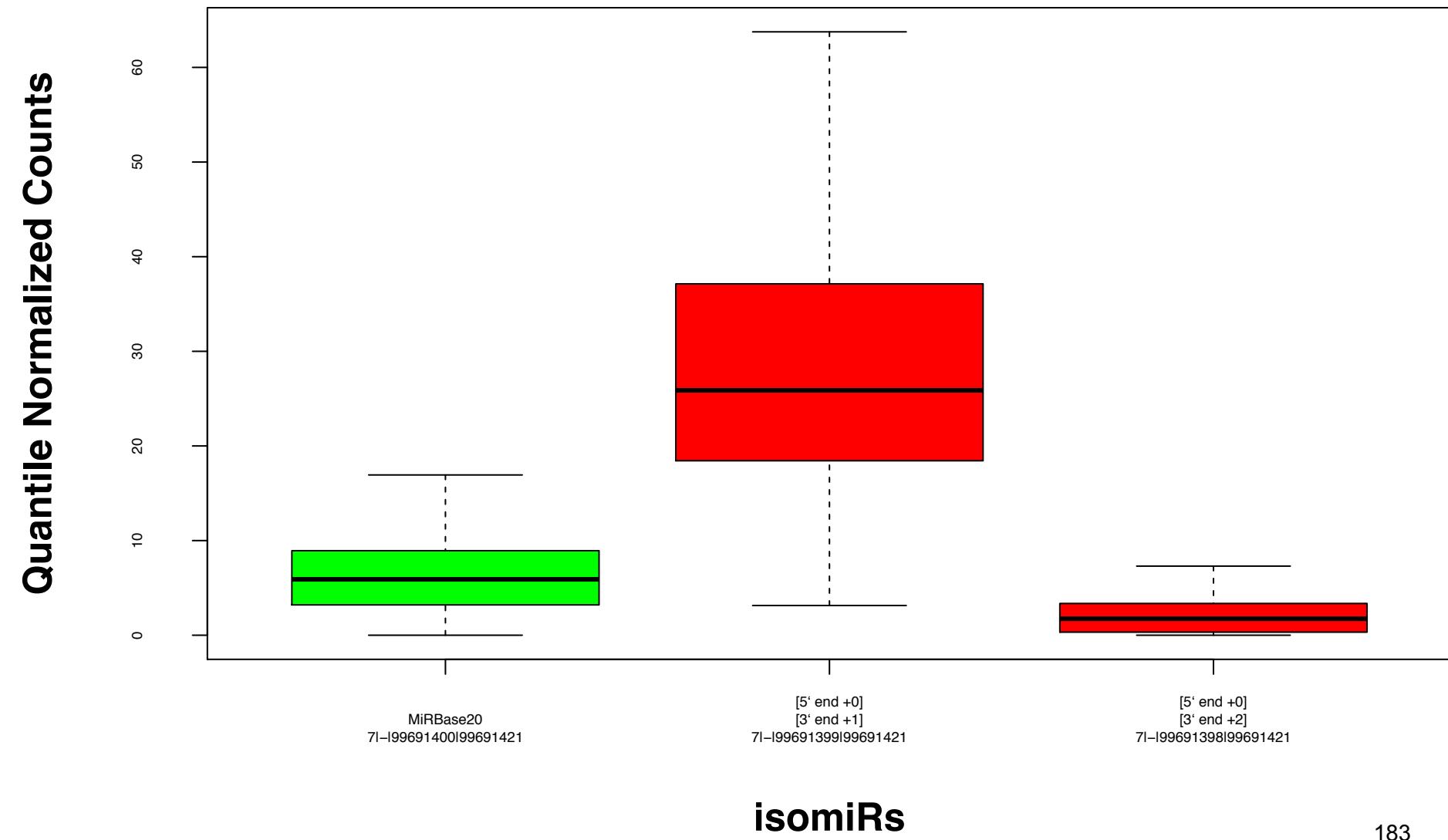
MIMAT0005825=hsa-miR-1180-3p=MI0006273



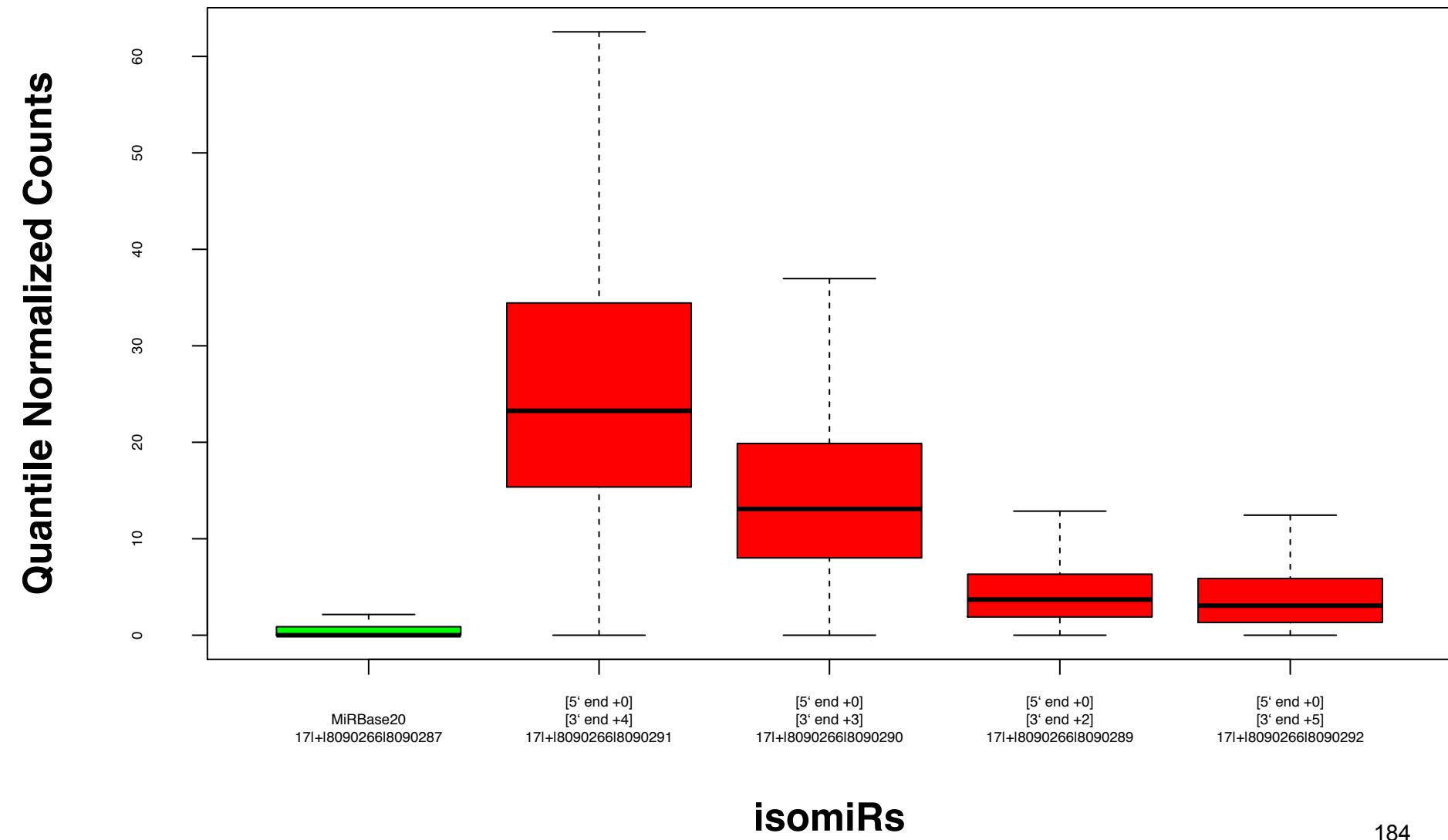
MiRBase20
17I-I19247826|19247847

isomiRs

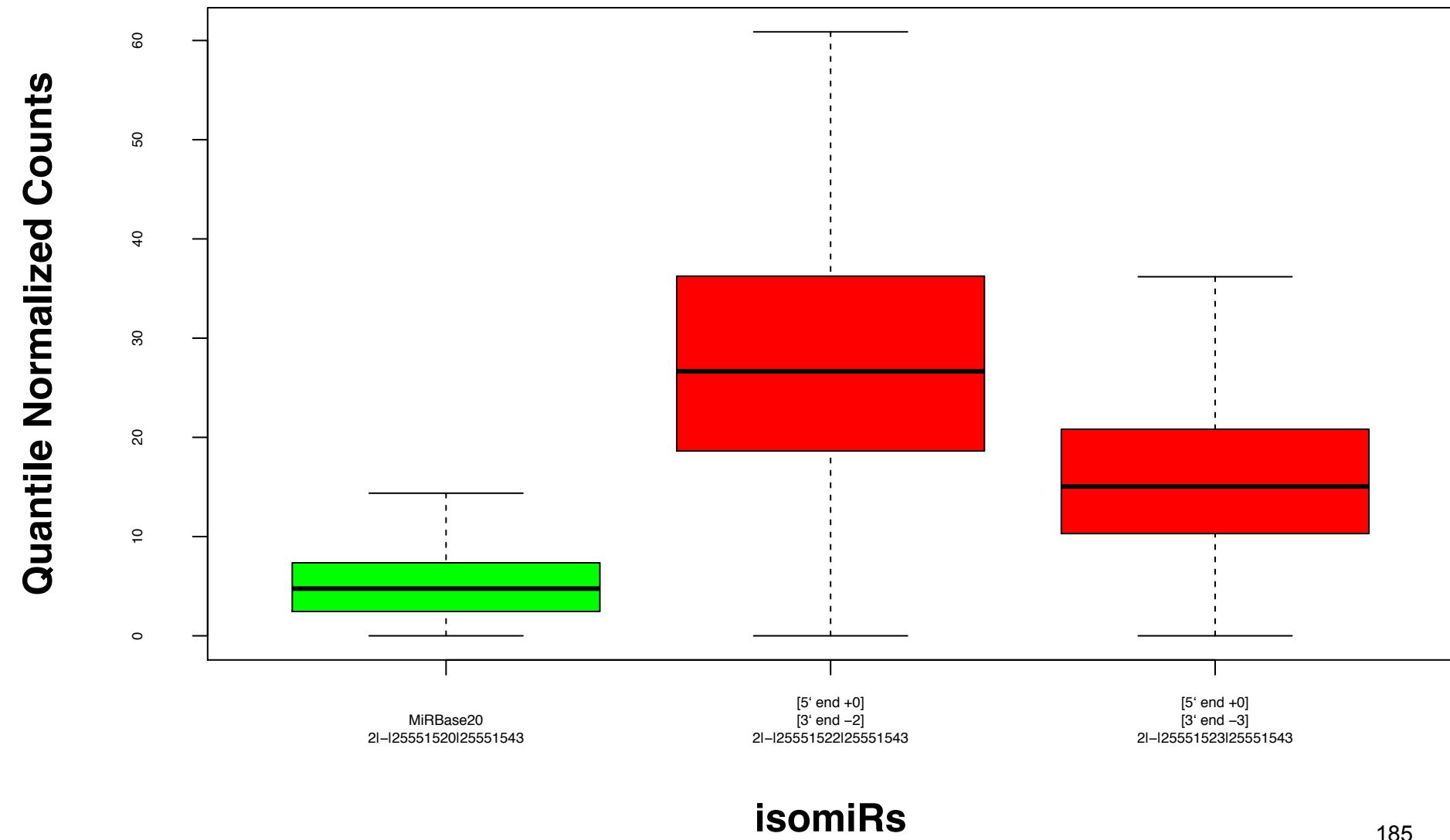
MIMAT0004509=hsa-miR-93-3p=MI0000095



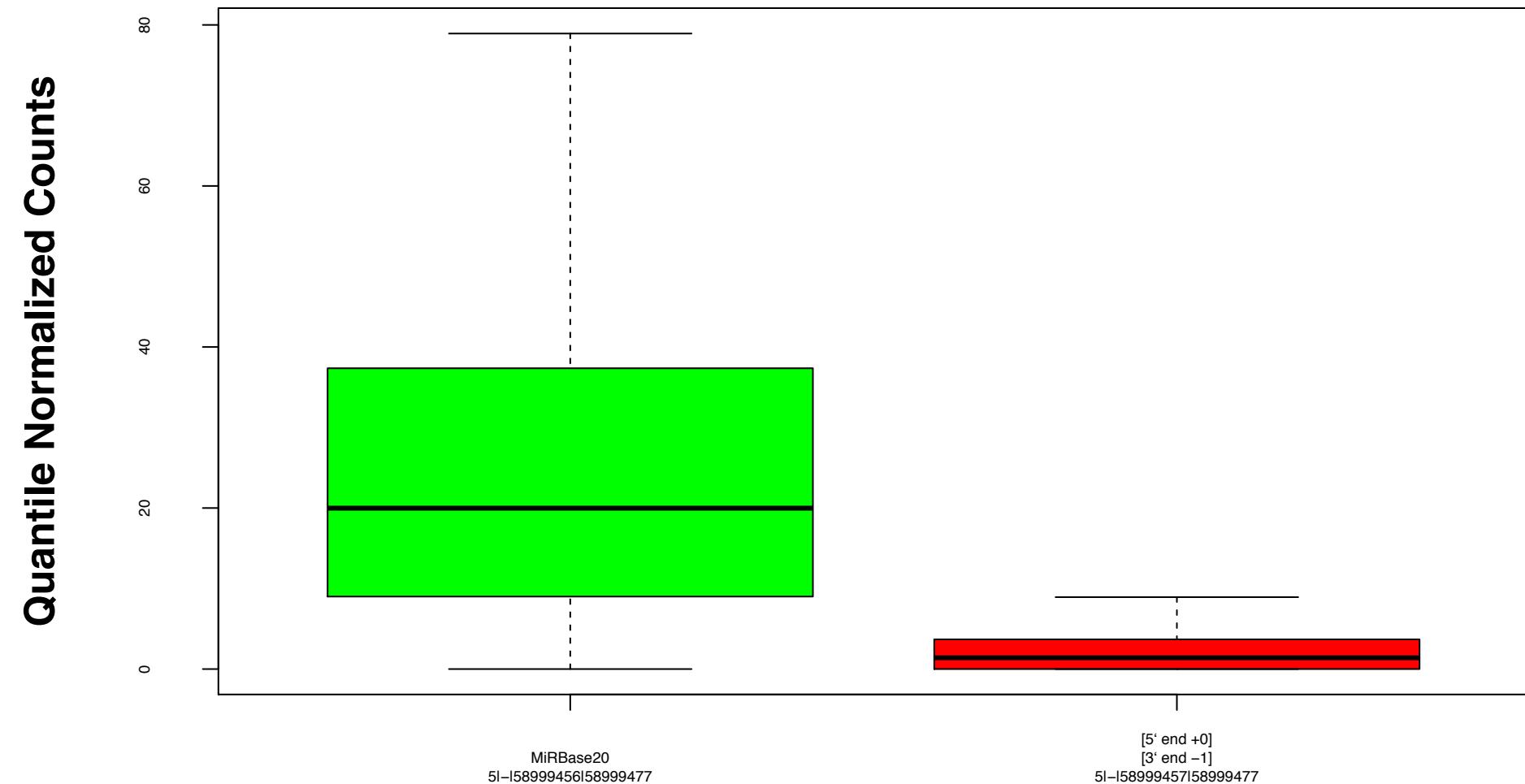
MIMAT0019058=hsa-miR-4521=MI0016887



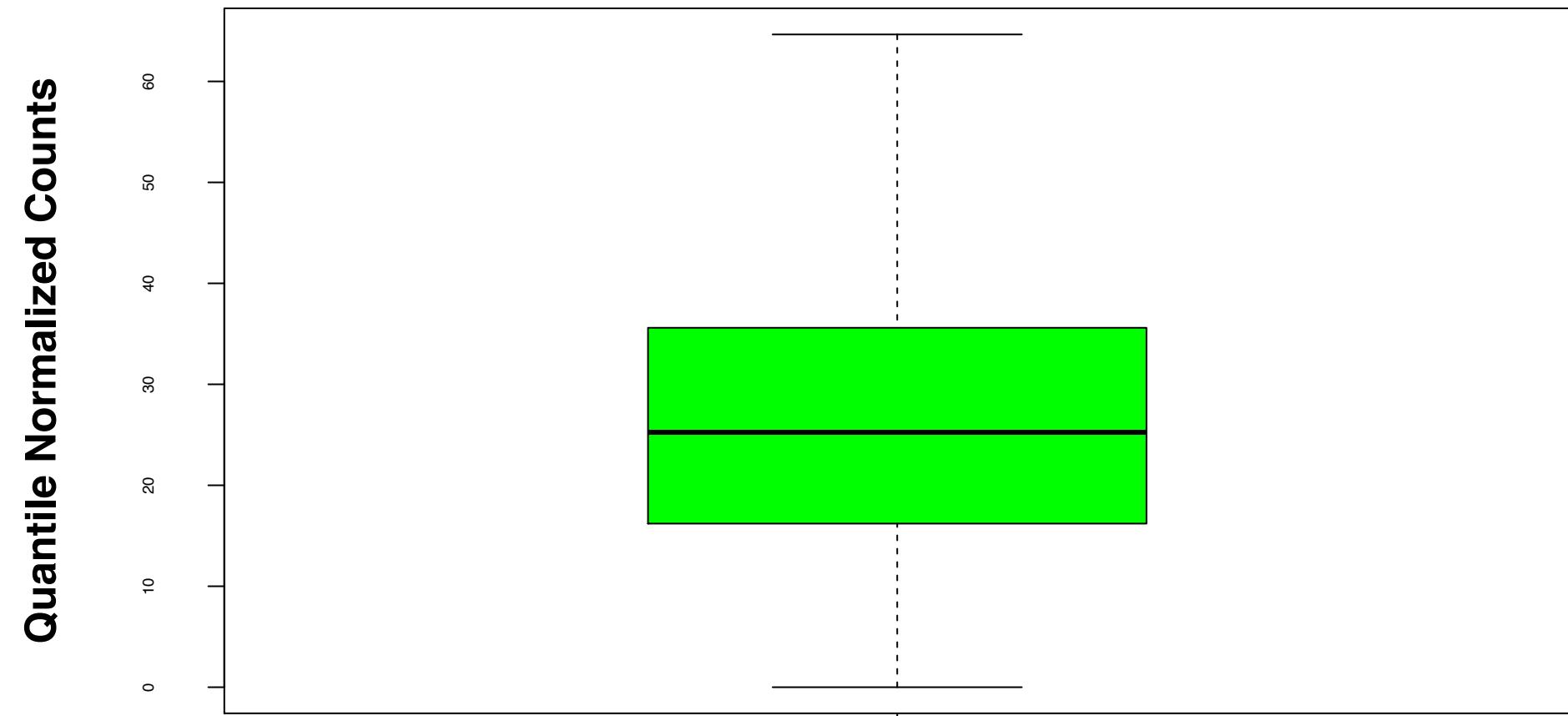
MIMAT0005797=hsa-miR-1301-3p=MI0003815



MIMAT0004797=hsa-miR-582-3p=MI0003589



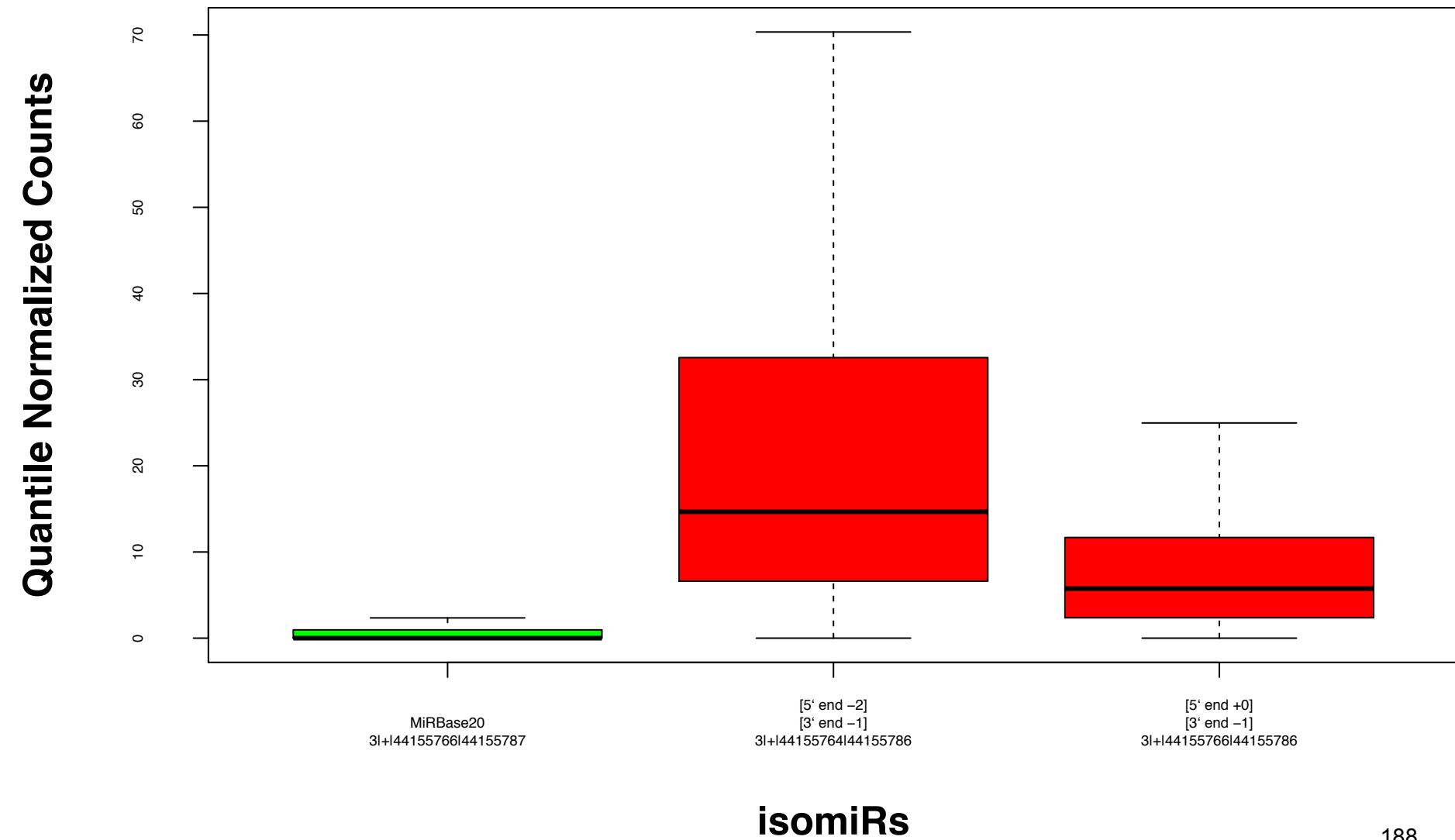
MIMAT0004486=hsa-let-7f-1-3p=MI0000067



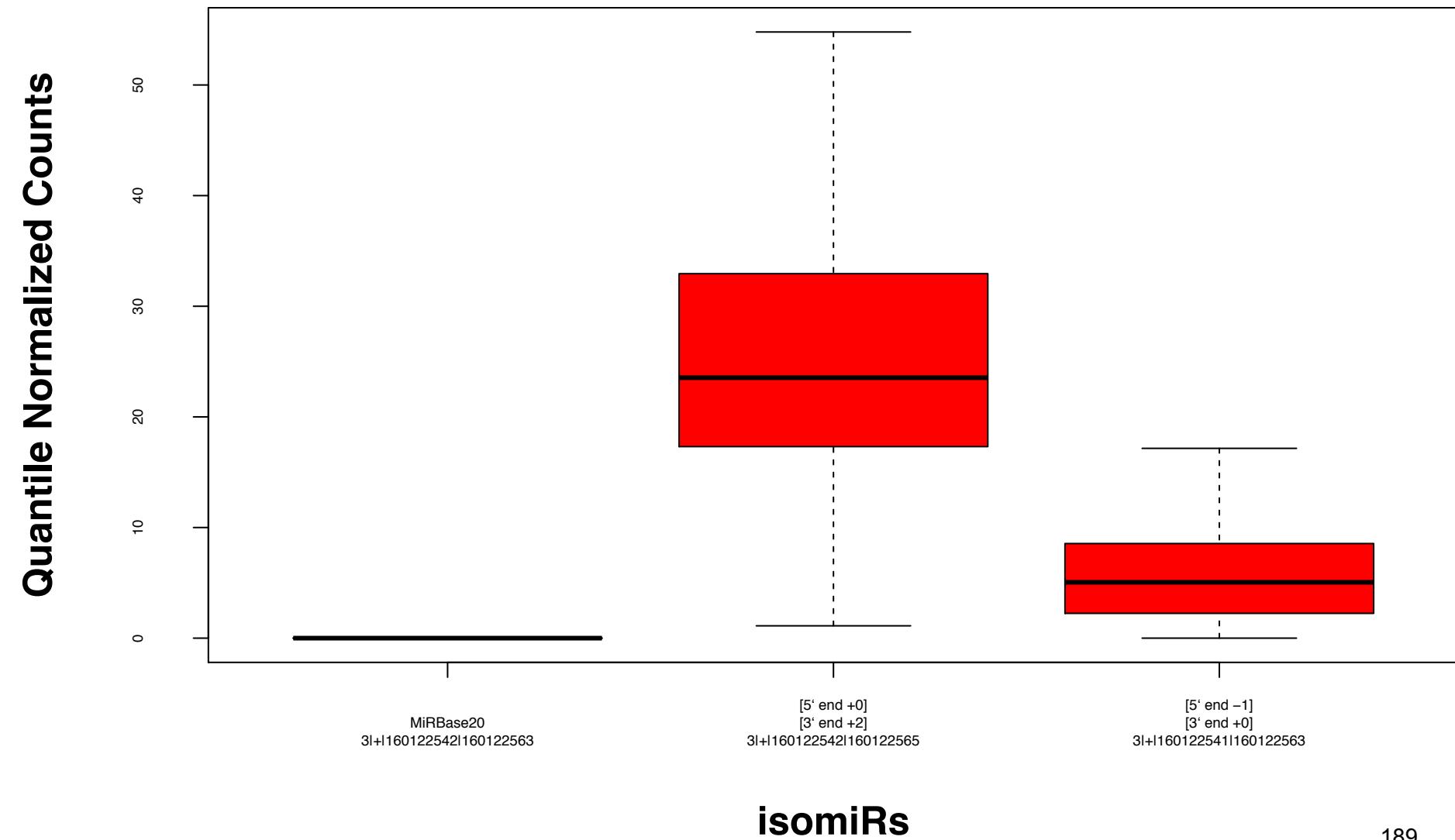
MiRBase20
91+96938691|96938712

isomiRs

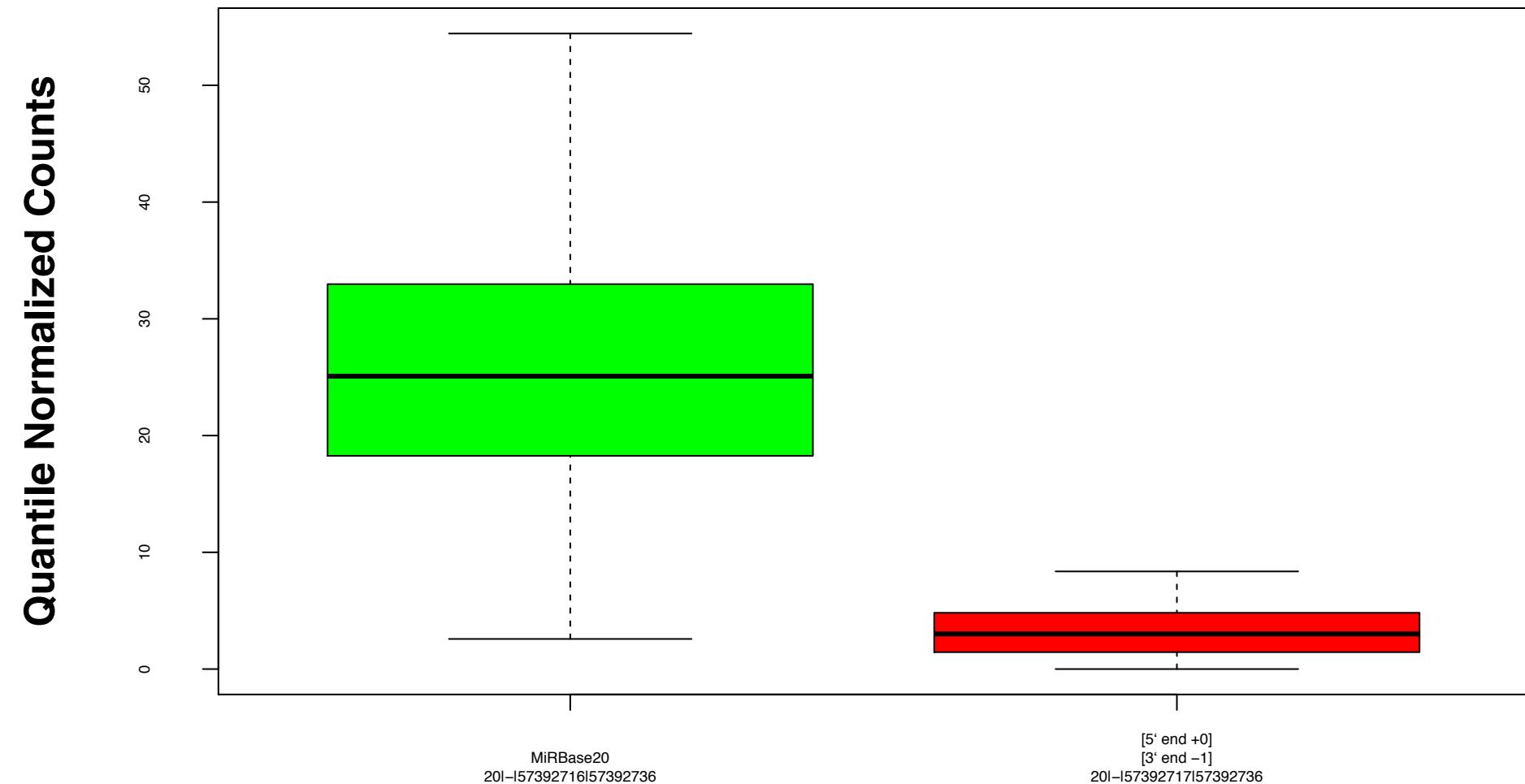
MIMAT0004607=hsa-miR-138-1-3p=MI0000476



MIMAT0000069_1=hsa-miR-16-5p=MI0000115



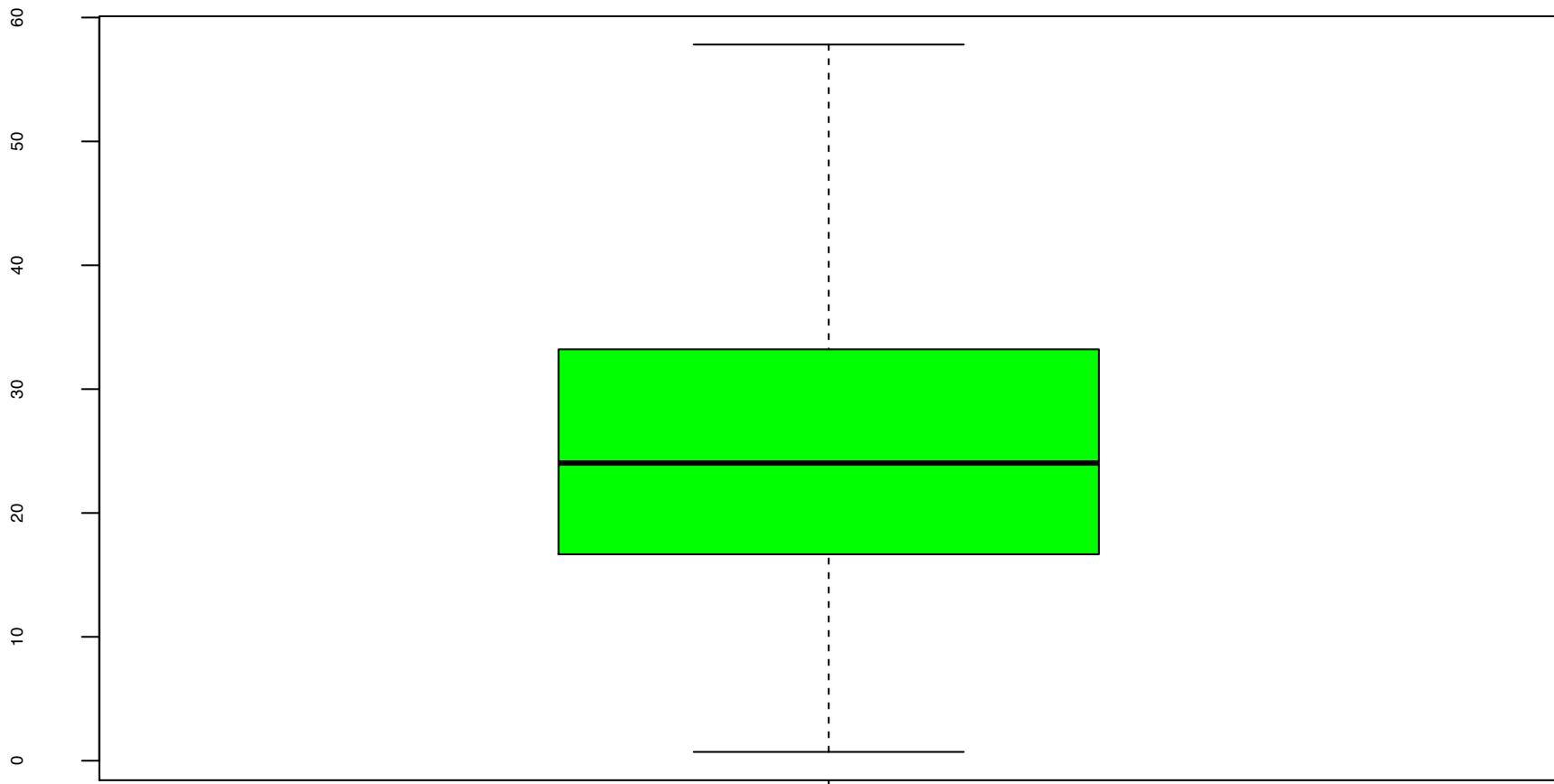
MIMAT0000690=hsa-miR-296-5p=MI0000747



isomiRs

MIMAT0019880=hsa-miR-4746-5p=MI0017385

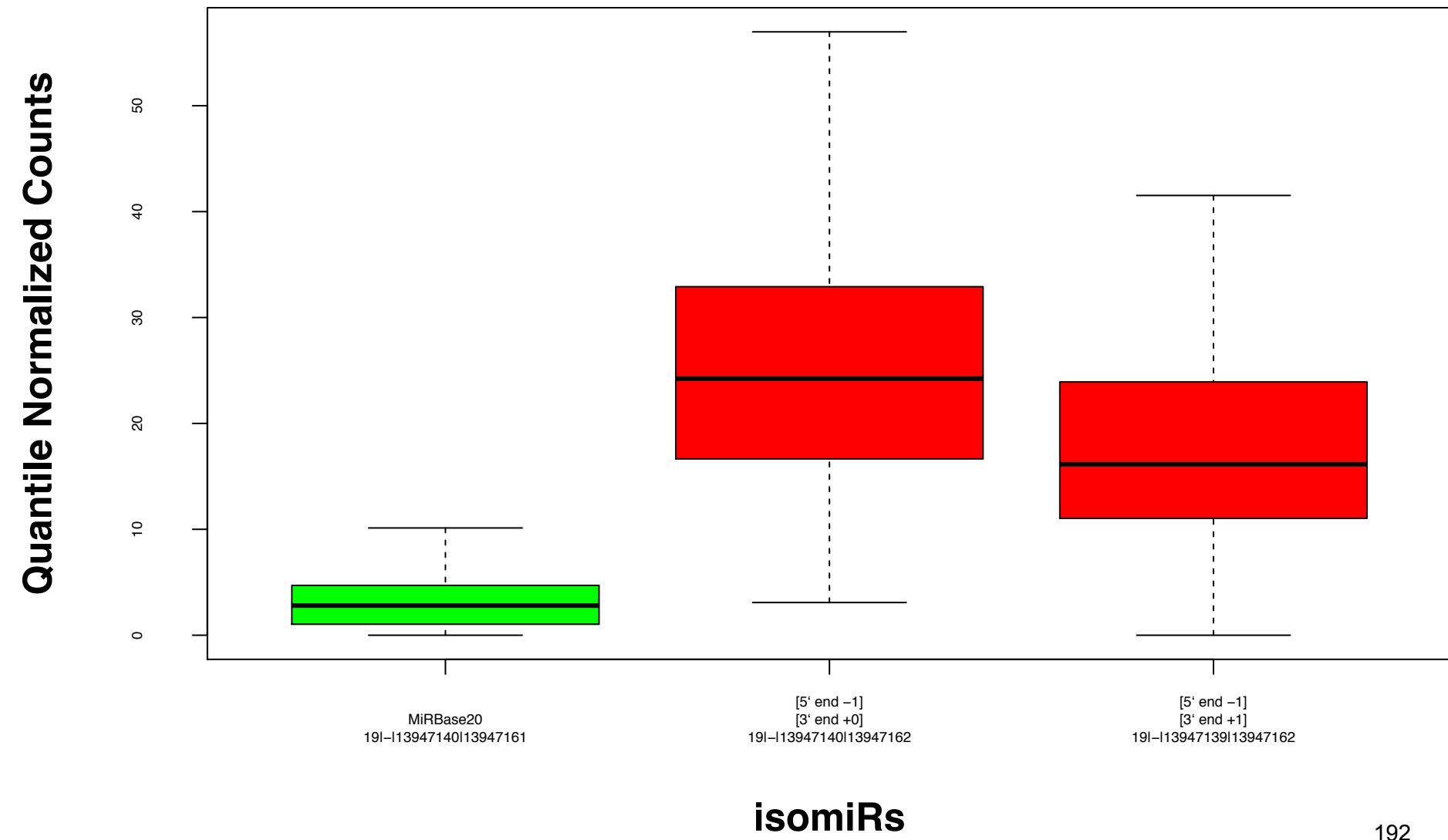
Quantile Normalized Counts



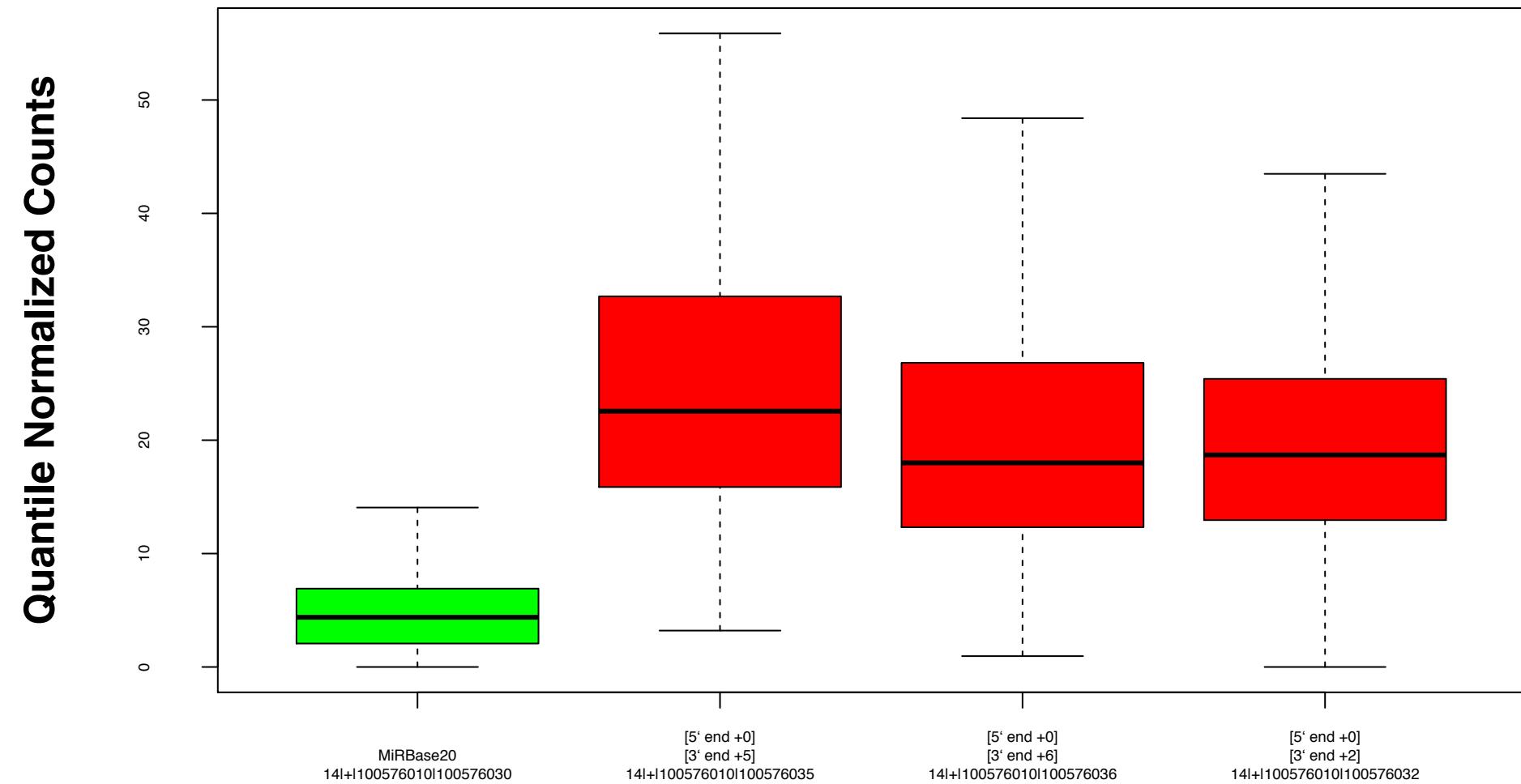
MiRBase20
191+14445984|4446006

isomiRs

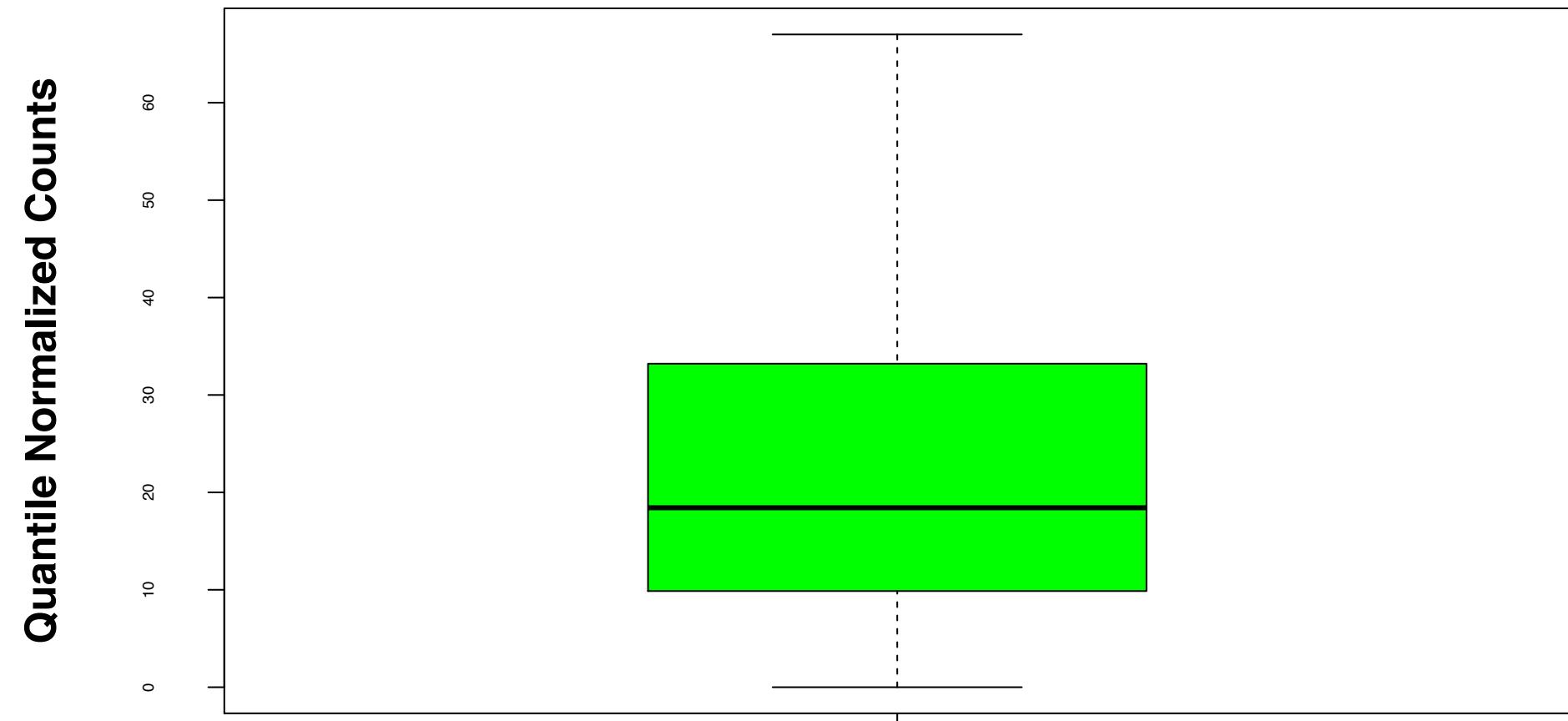
MIMAT0004497=hsa-miR-24-2-5p=MI0000081



MIMAT0004694=hsa-miR-342-5p=MI0000805



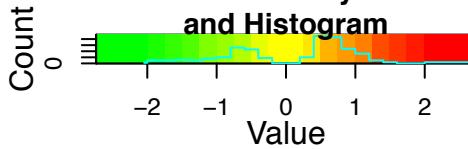
MIMAT0000269=hsa-miR-212-3p=MI0000288



MiRBase20
17I-I1953584|1953604

isomiRs

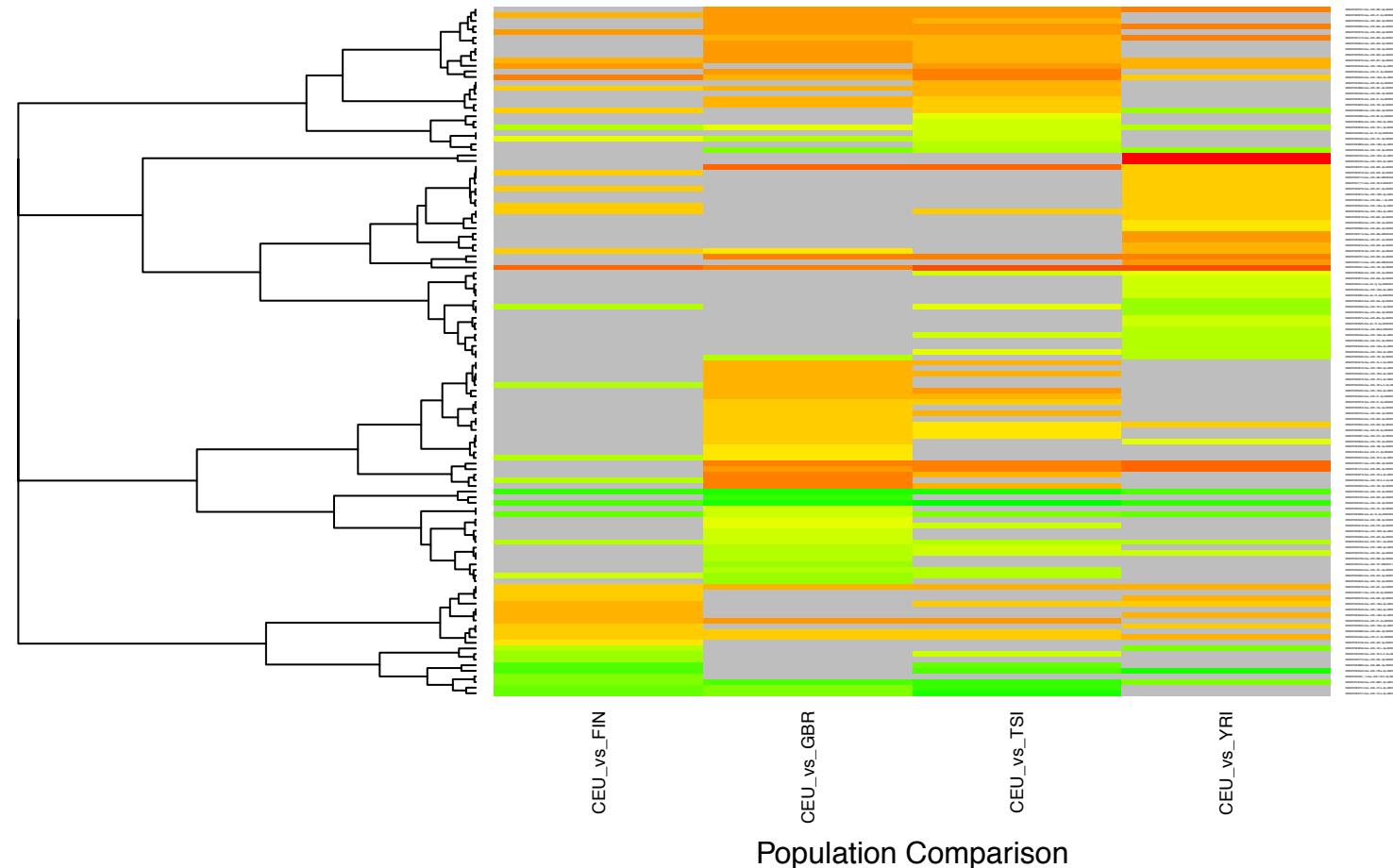
Color Key
and Histogram



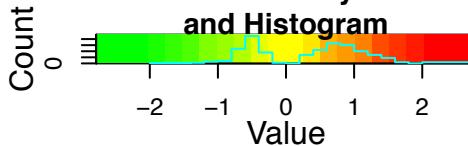
CEU vs All

Sup. Figure 2
(pages 195 to 199)

isomir



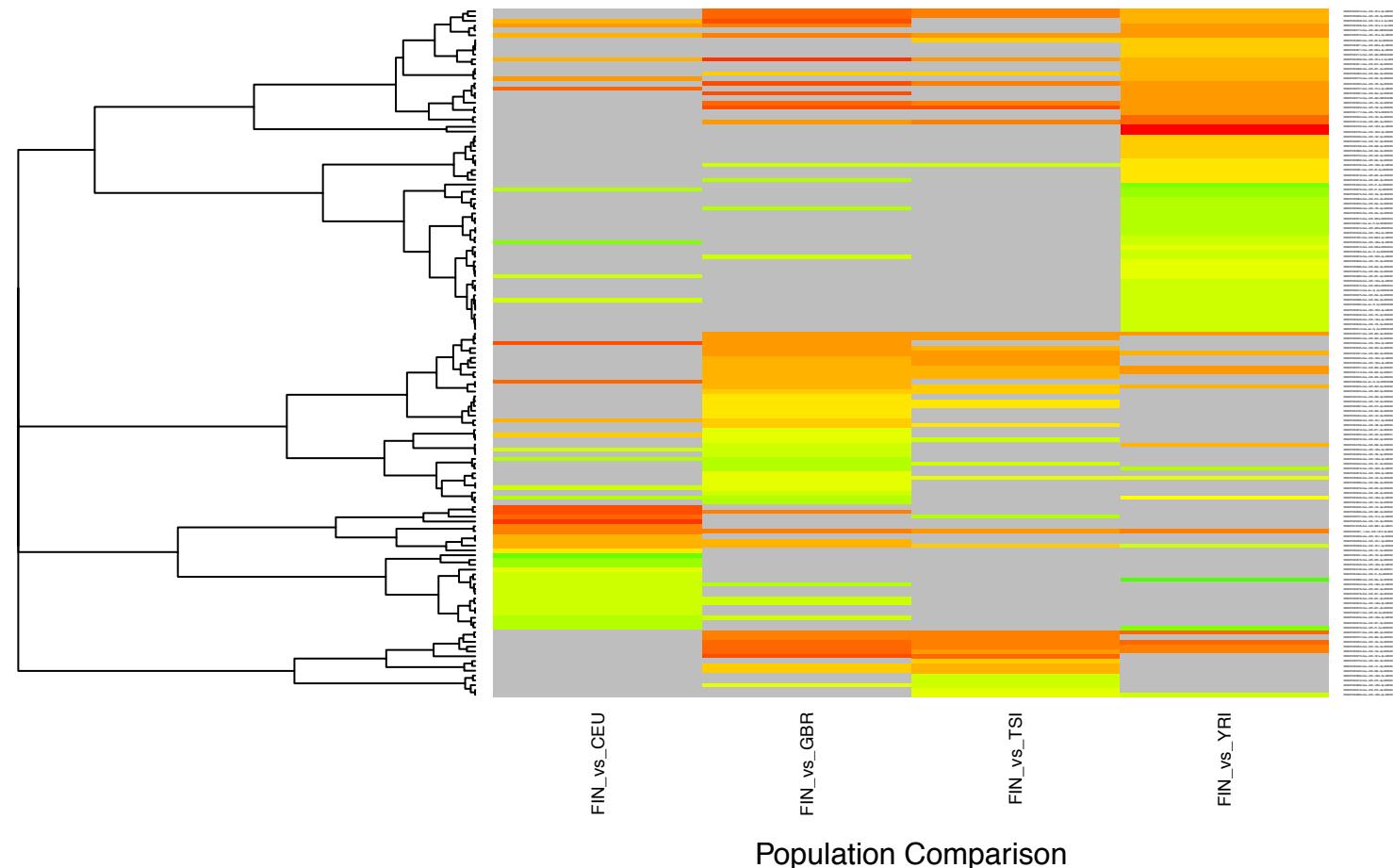
**Color Key
and Histogram**



FIN vs All

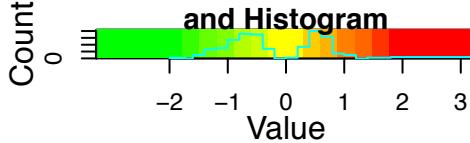
Sup. Figure 2
(pages 195 to 199)

isomir



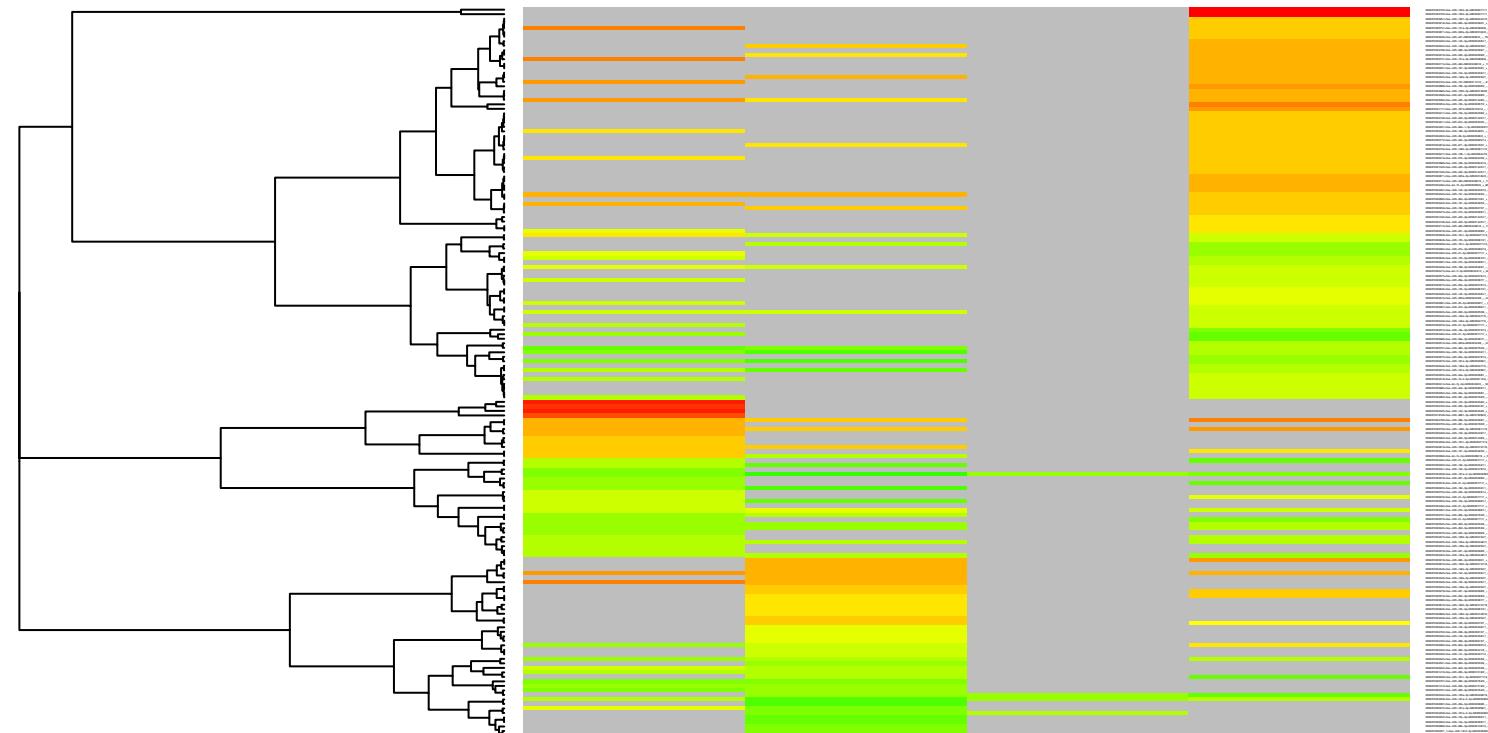
Color Key

and Histogram



GBR vs All

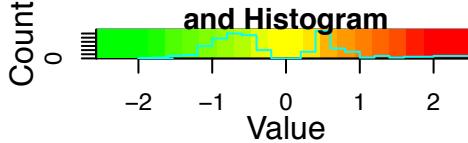
Sup. Figure 2
(pages 195 to 199)



Population Comparison

Color Key

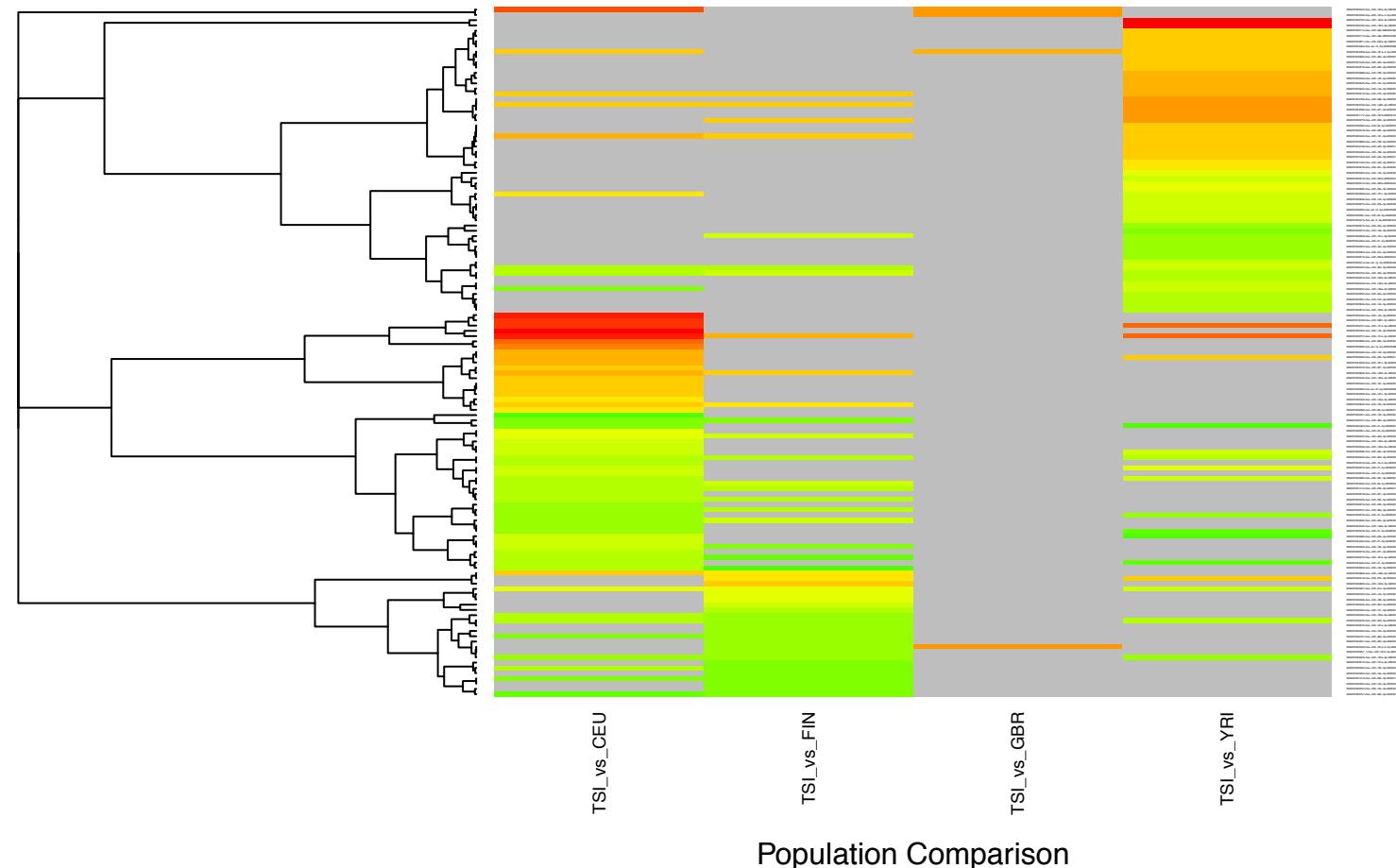
and Histogram



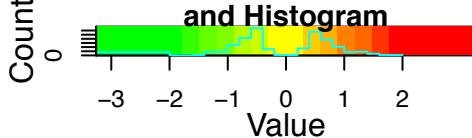
TSI vs All

Supp. Figure 2
(pages 195 to 199)

isomir



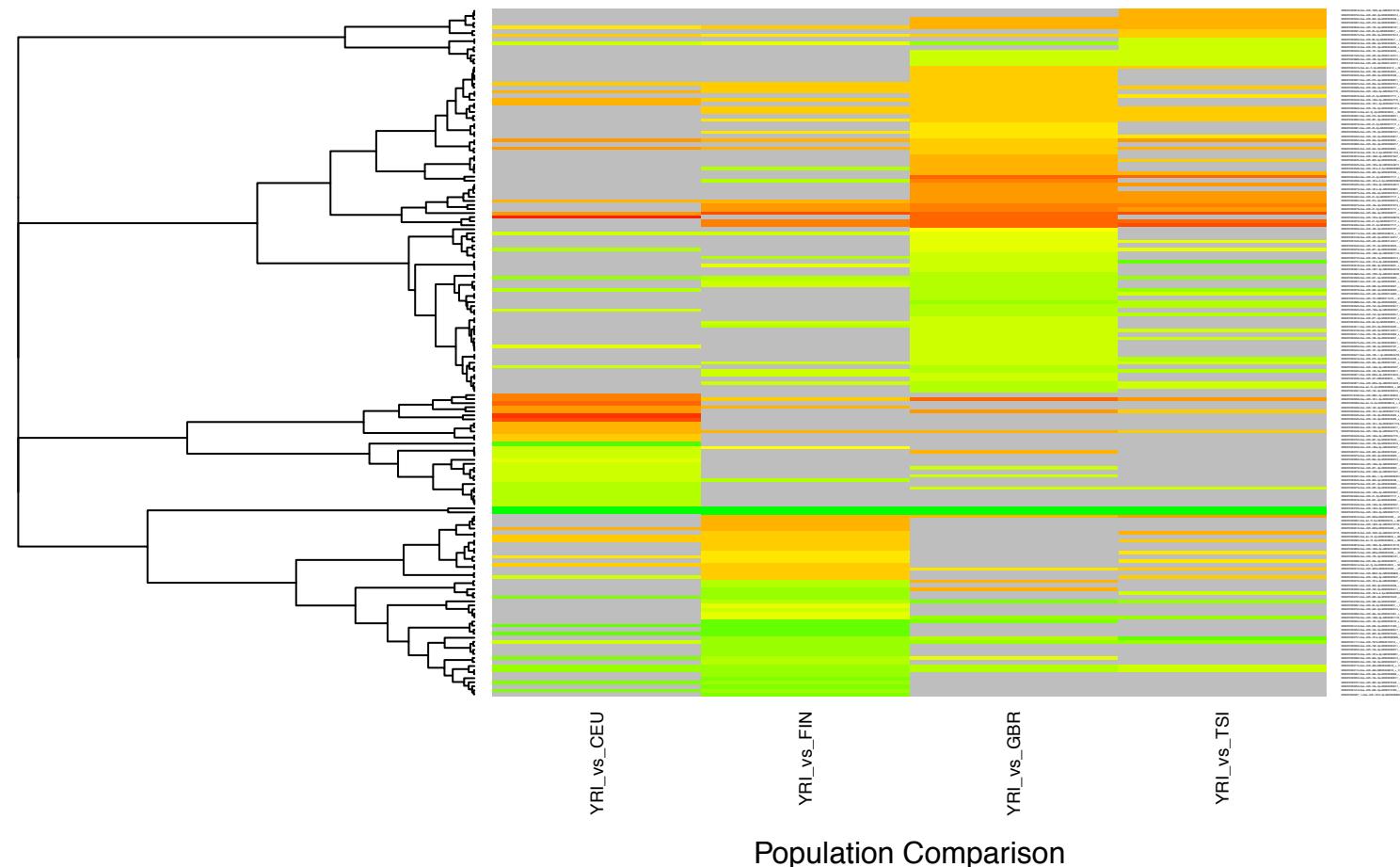
Color Key and Histogram

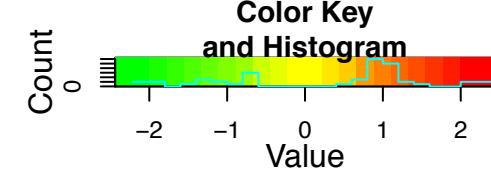


YRI vs All

Supp. Figure 2
(pages 195 to 199)

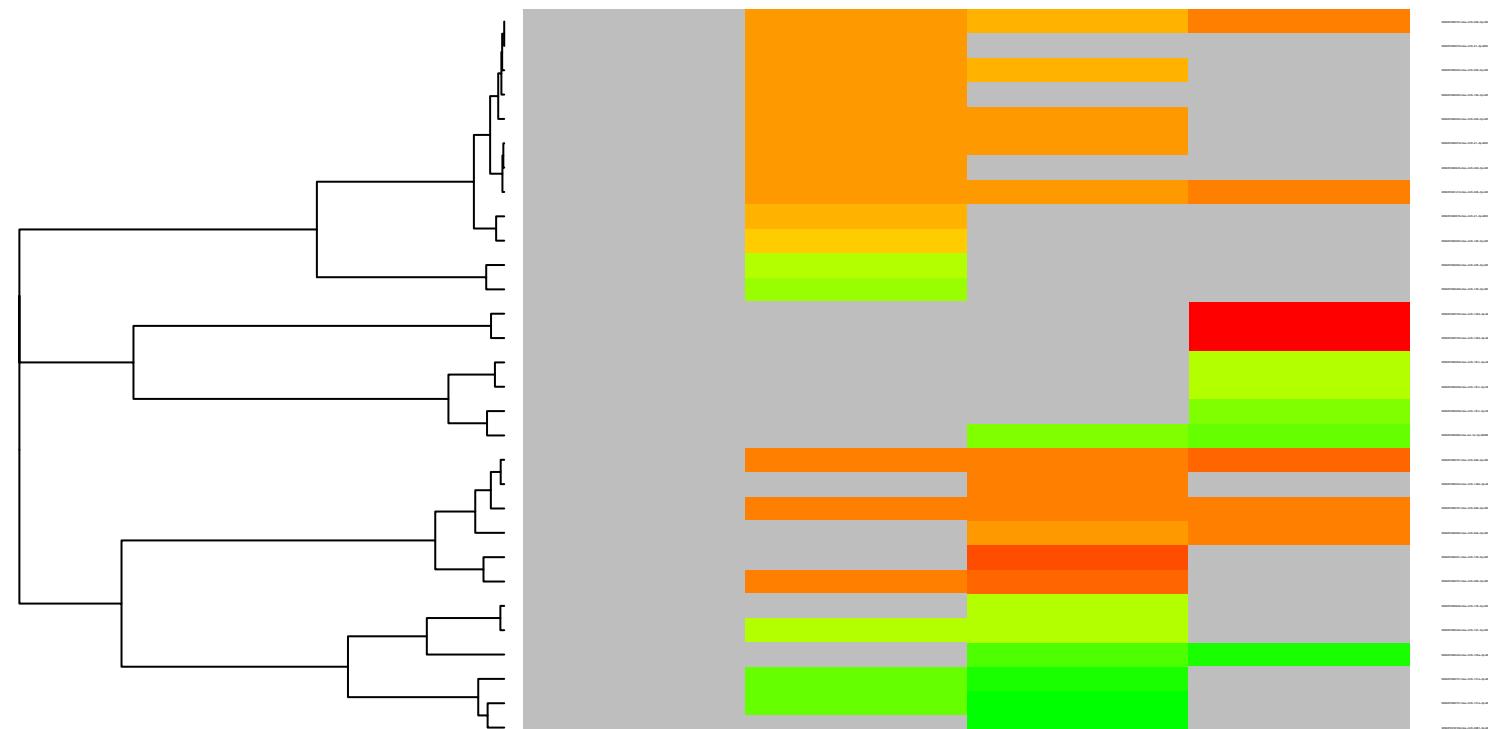
isomir



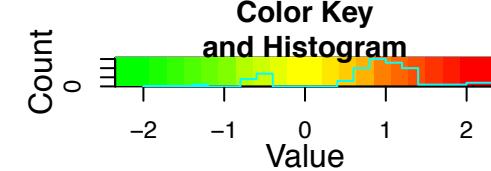


MalesOnly: CEU vs All

Sup. Figure 3
(pages 200 to 204)

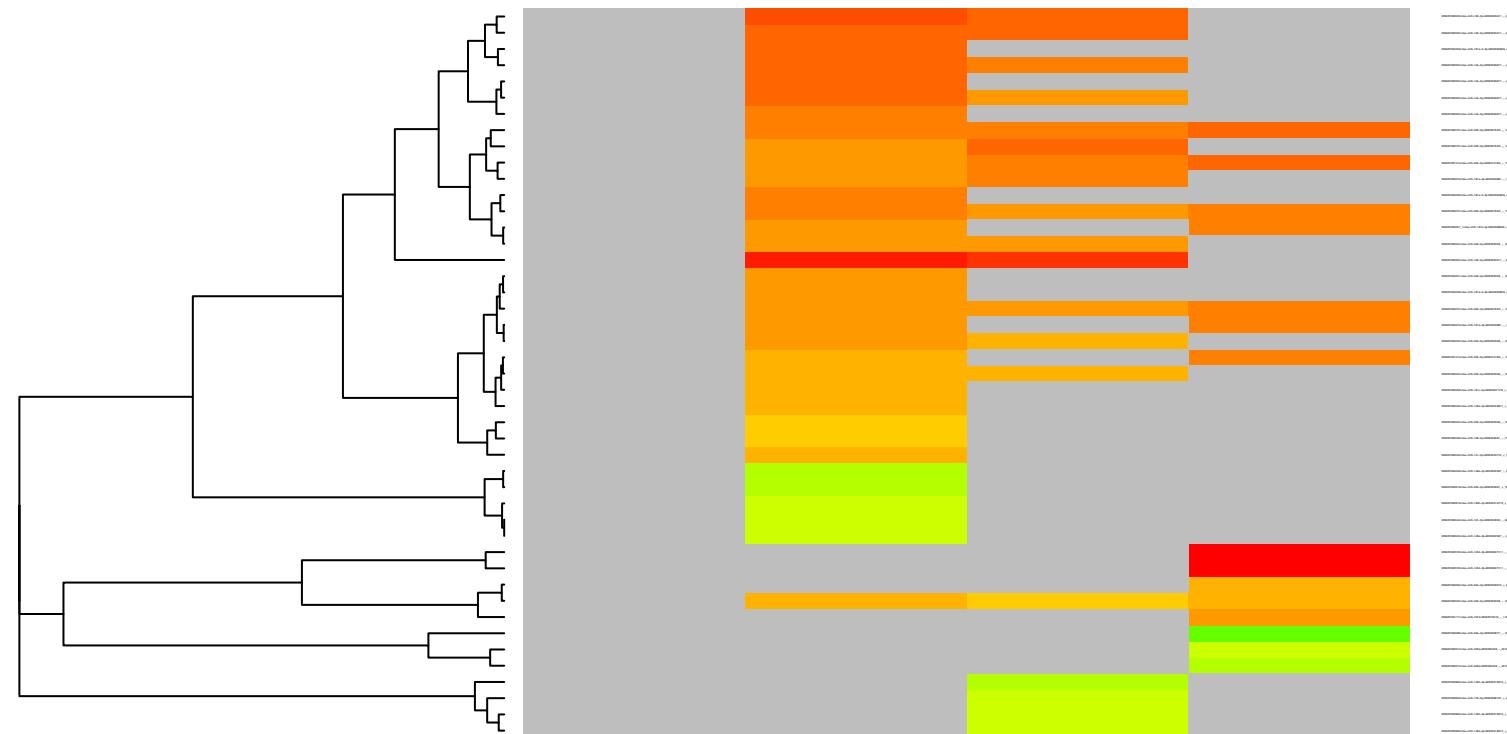


Population Comparison



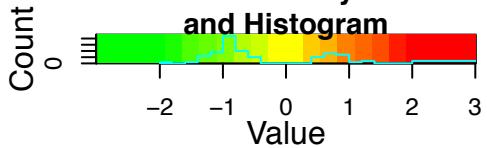
MalesOnly: FIN vs All

Sup. Figure 3
(pages 200 to 204)



Population Comparison

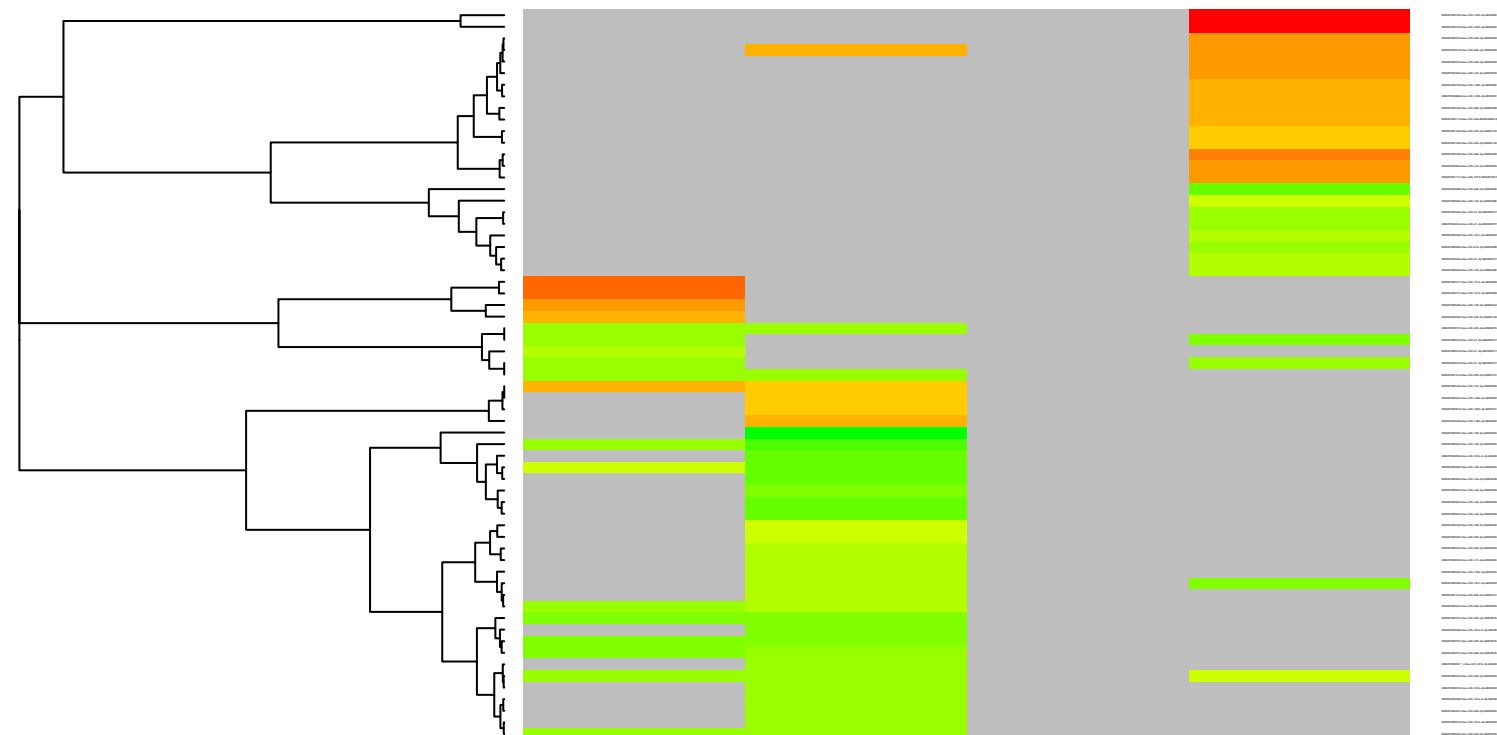
Color Key
and Histogram



MalesOnly: GBR vs All

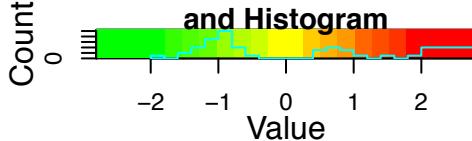
Sup. Figure 3
(pages 200 to 204)

isomir



Color Key

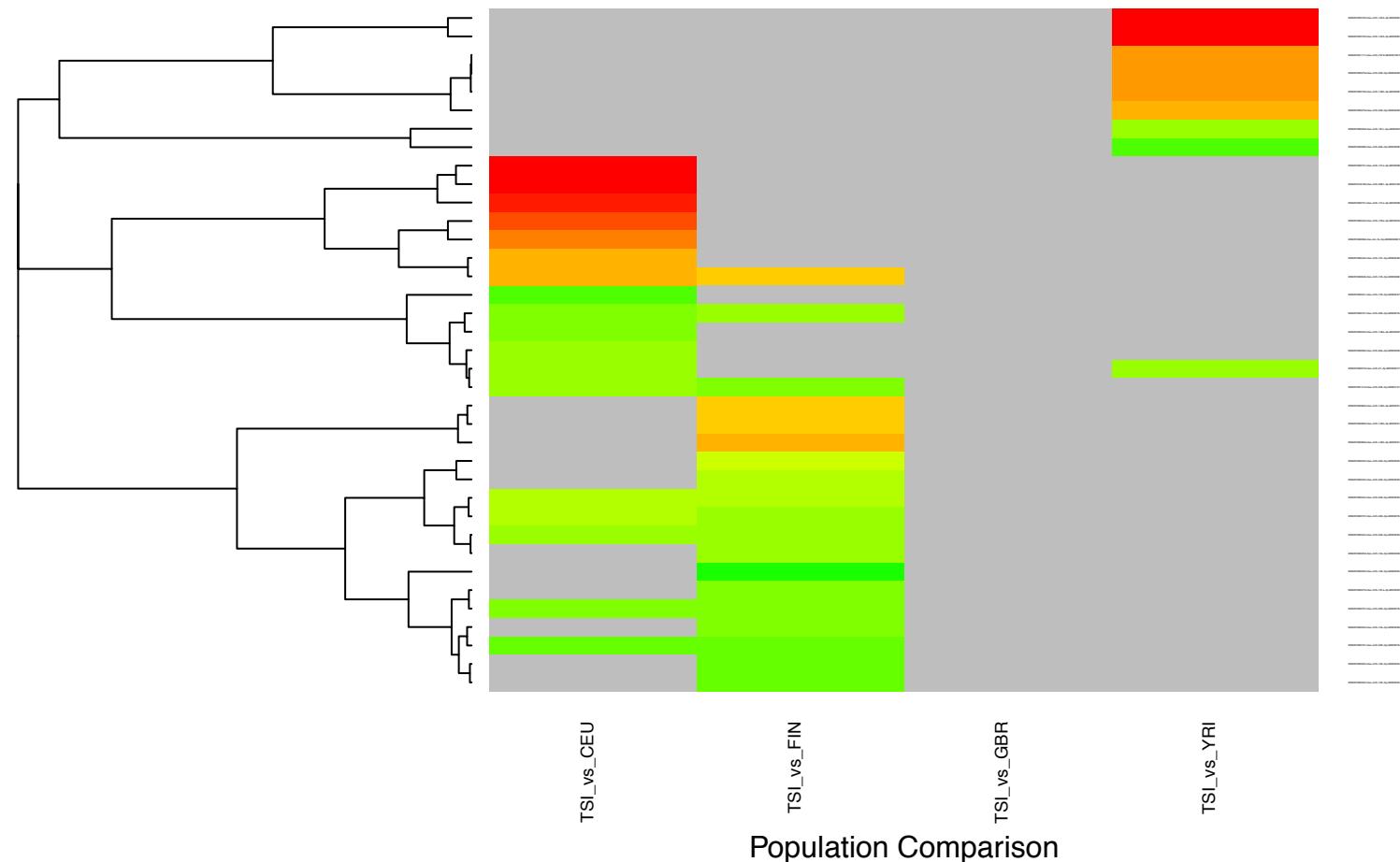
and Histogram



MalesOnly: TSI vs All

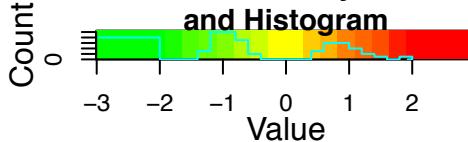
Sup. Figure 3
(pages 200 to 204)

isomir



Color Key

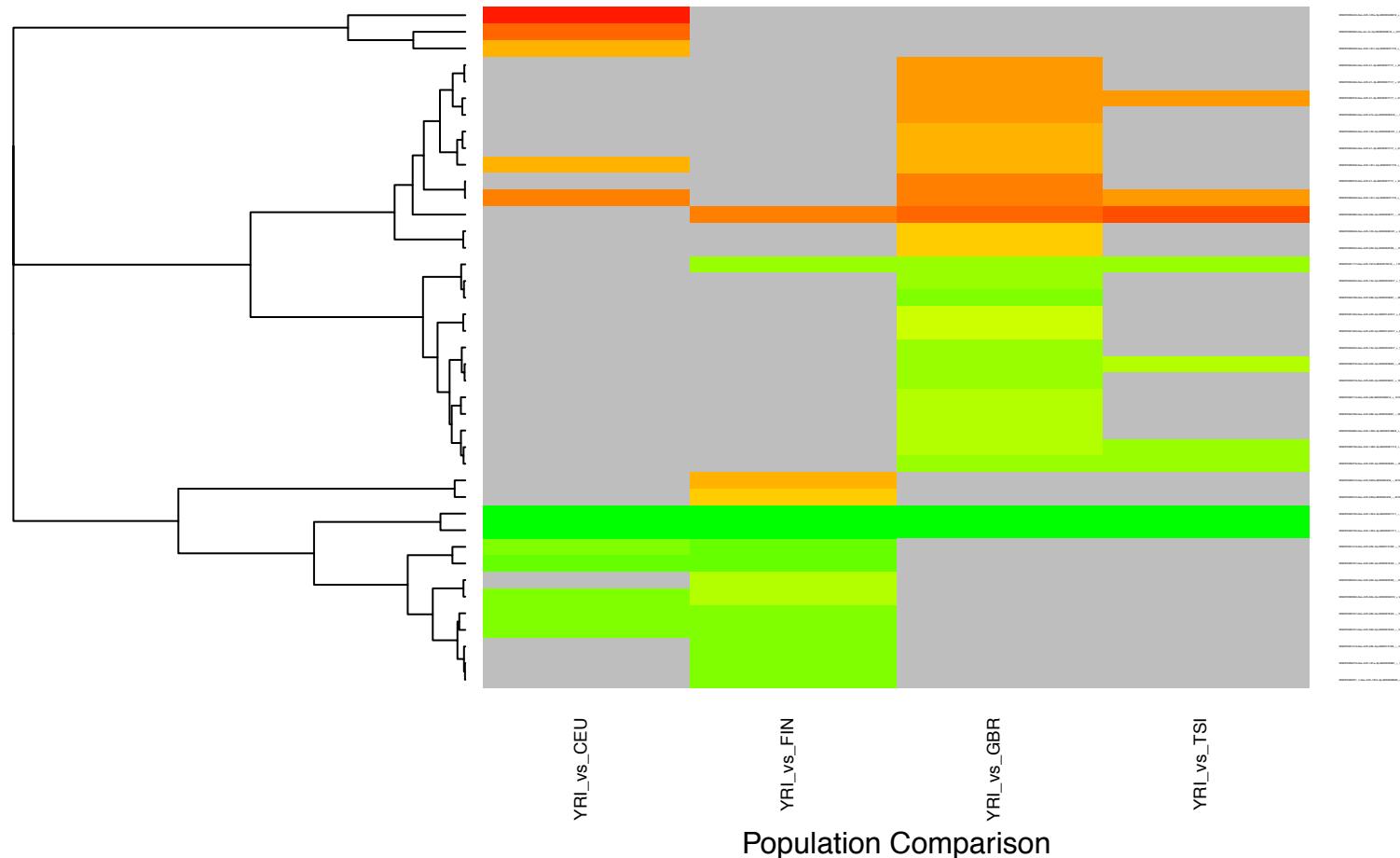
and Histogram

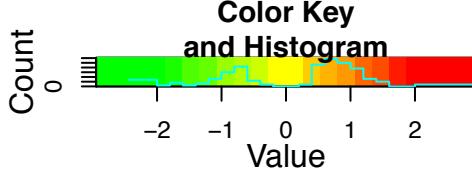


MalesOnly: YRI vs All

Sup. Figure 3
(pages 200 to 204)

isomir

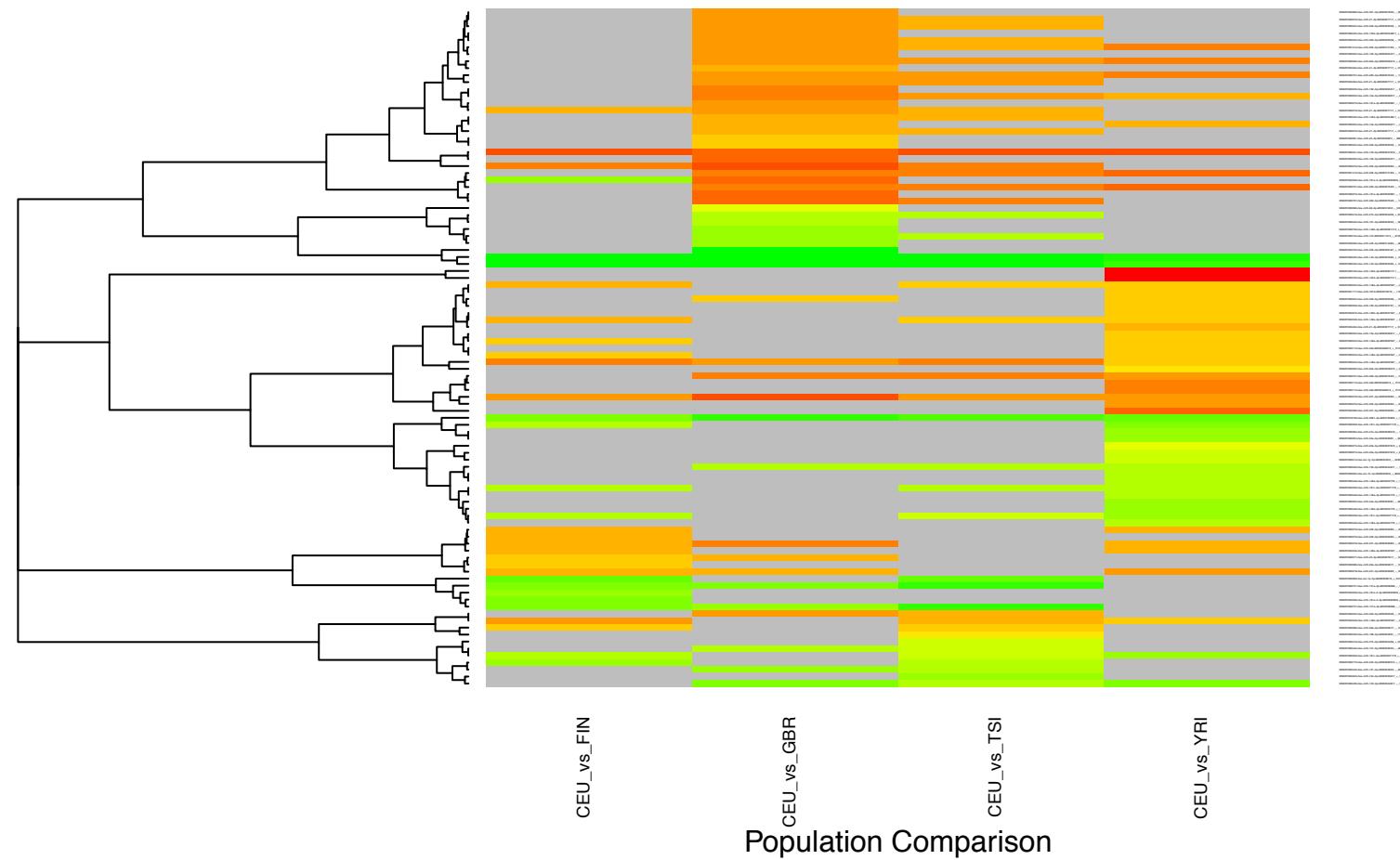




FemalesOnly: CEU vs All

Supp. Figure 4
(pages 205-209)

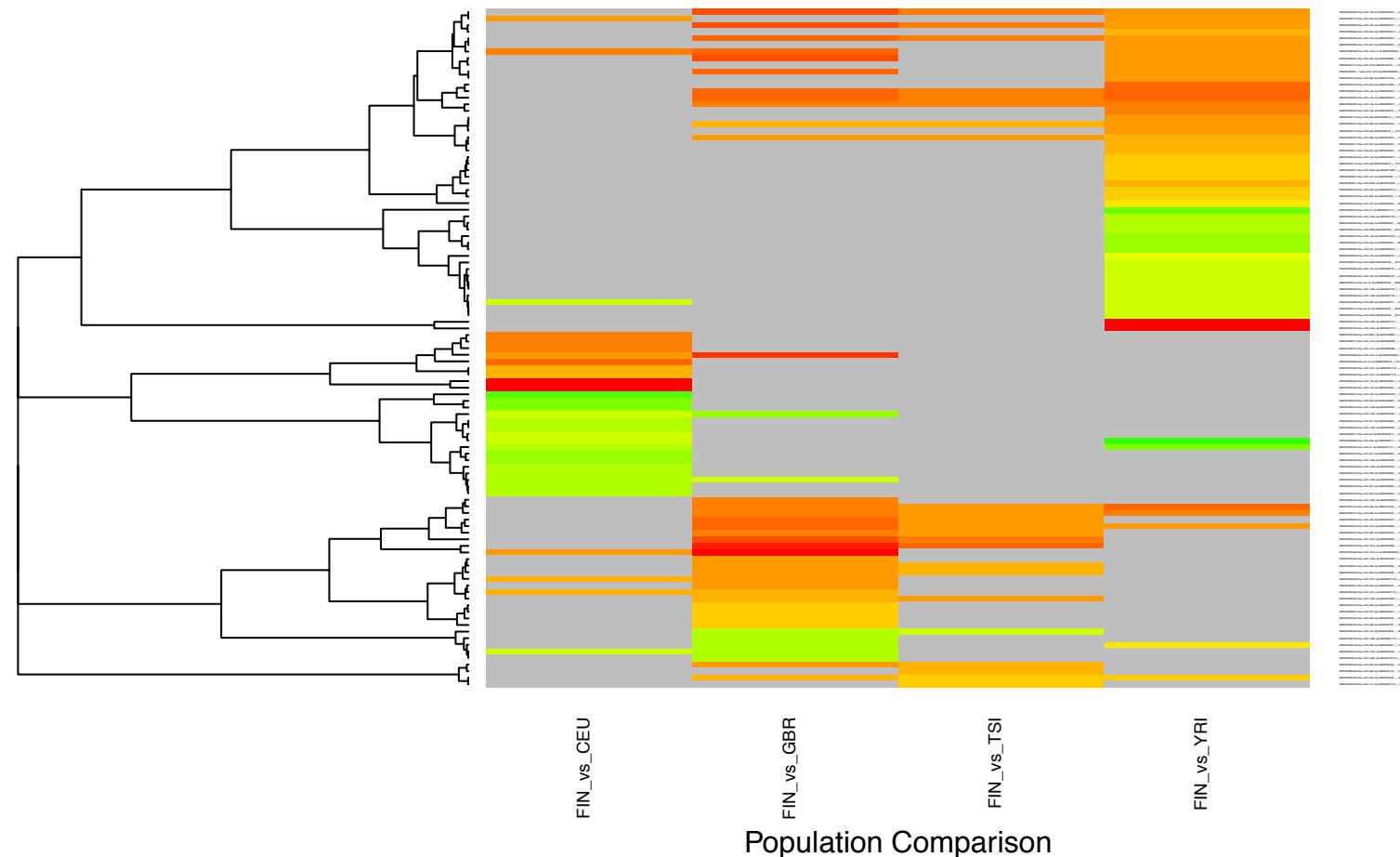
isomir





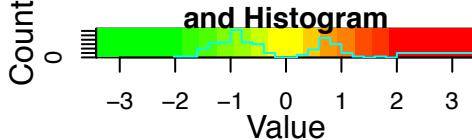
FemalesOnly: FIN vs All

Supp. Figure 4
(pages 205-209)



Color Key

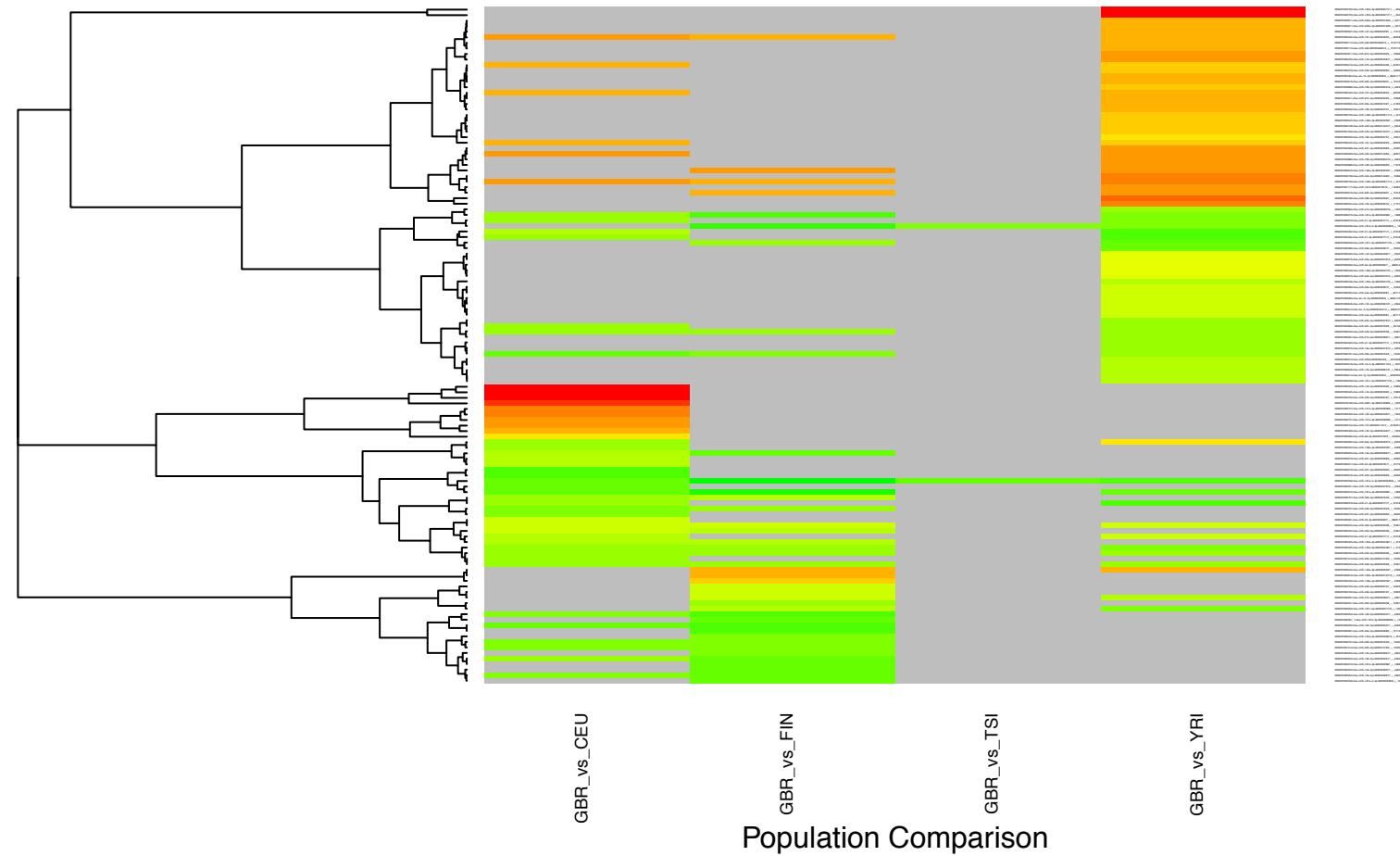
and Histogram



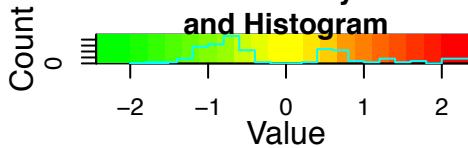
FemalesOnly: GBR vs All

Supp. Figure 4
(pages 205-209)

isomir



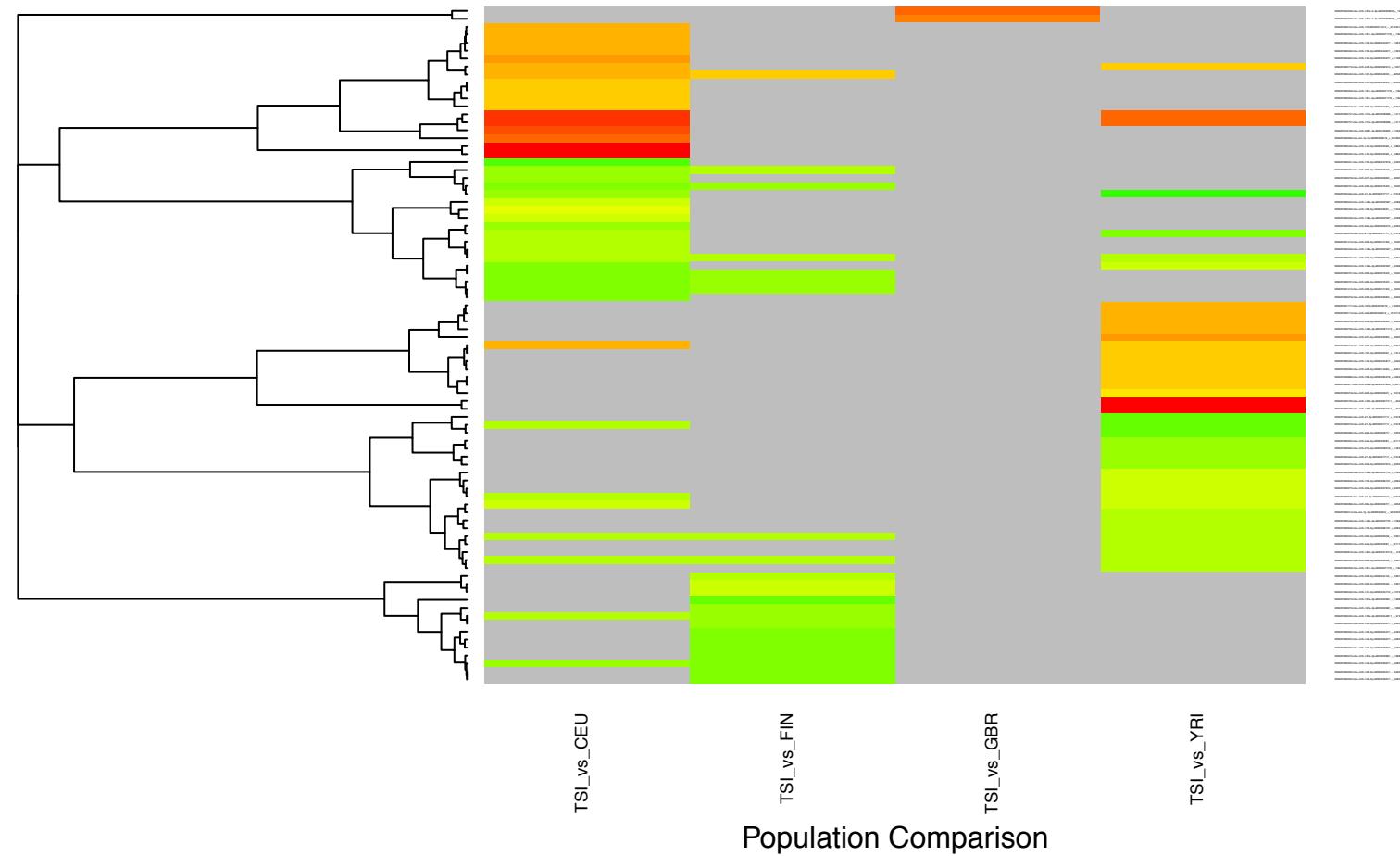
Color Key
and Histogram



FemalesOnly: TSI vs All

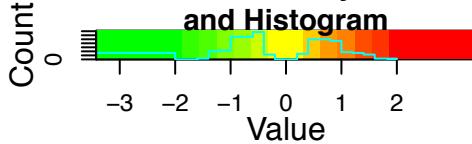
Supp. Figure 4
(pages 205-209)

isomir



Color Key

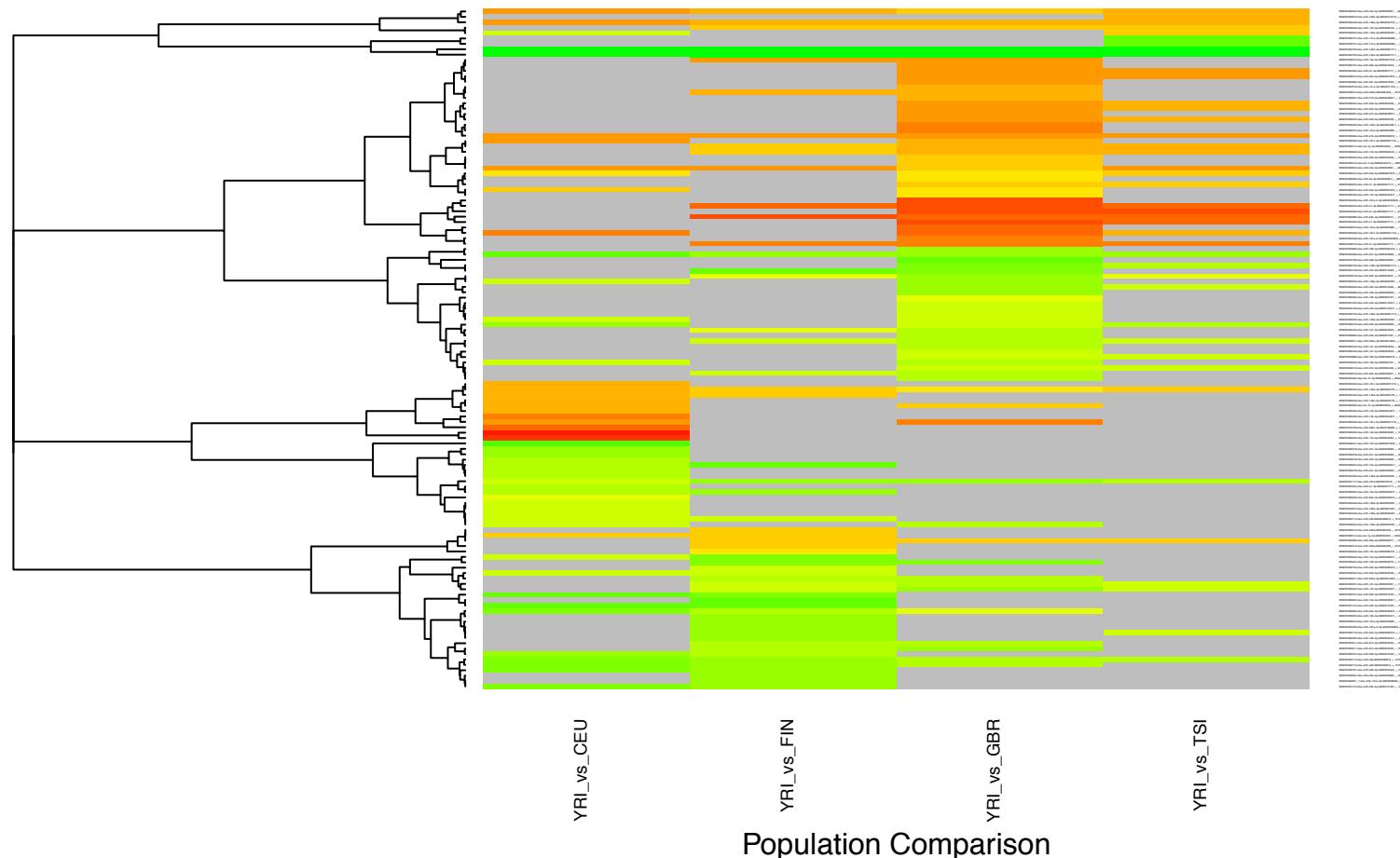
and Histogram



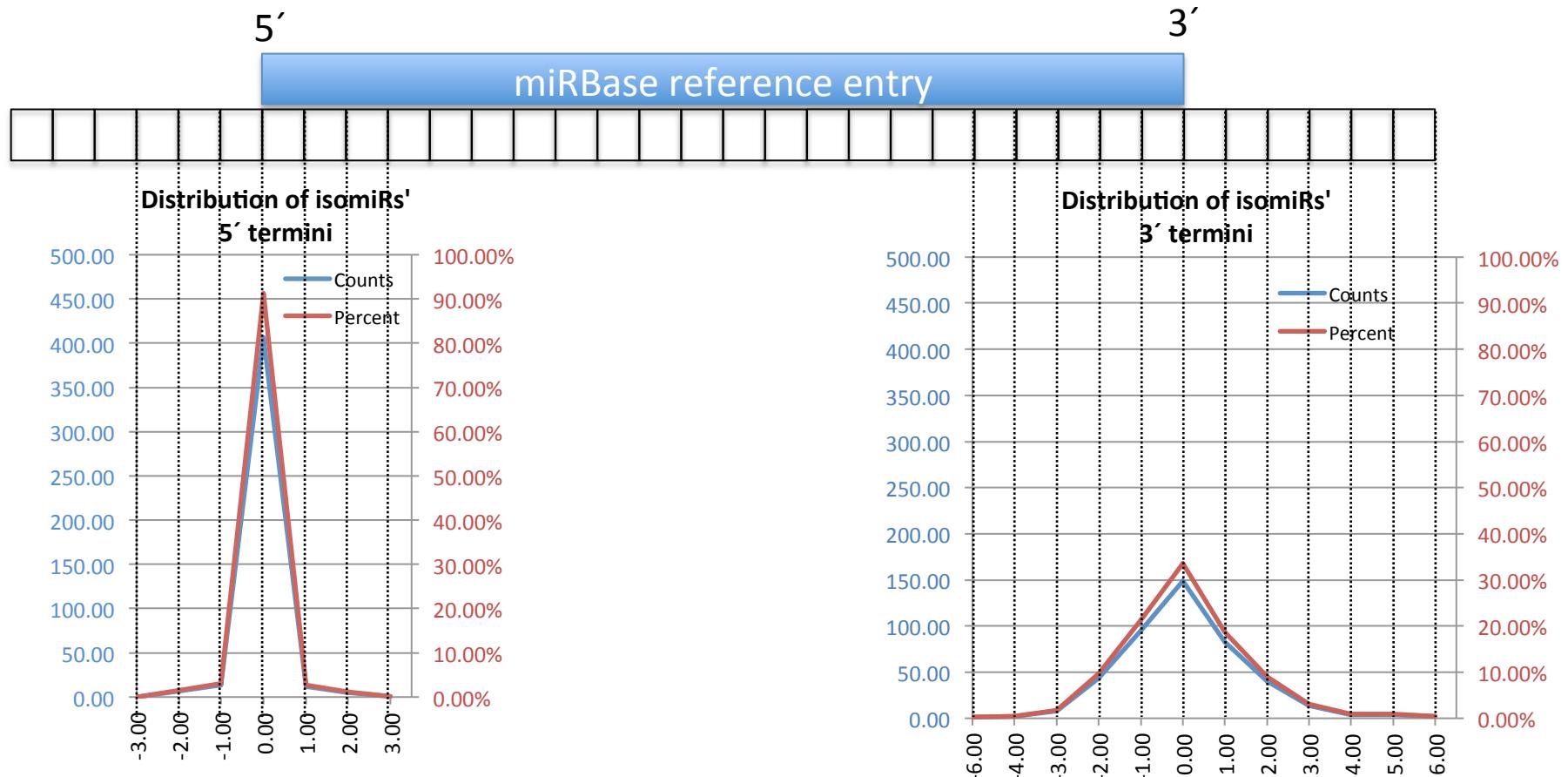
FemalesOnly: YRI vs All

Supp. Figure 4
(pages 205-209)

isomir



Supp. Figure 5
(page 210)



Supp. Table 1. Statistics for each population separately for the single most abundant isomiR produced from a given precursor arm. The most abundant isomiR's identity was determined by analyzing the technical replicates separately for each of the populations. At each locus, we also generated the “conservative” estimate by requiring that the most abundant isomiR have higher expression than the miRBase reference by at least 0.585 log₂ units.

	CEU		FIN		GBR		TSI		YRI	
	Number	Percentage								
MiRNA precursor arms considered	197		190		170		192		188	
MiRBase miRNA sequence not among the 95-th percentile	63	32%	61	32%	56	33%	66	34%	57	30%
Top isomiR not in agreement with miRBase	99	50%	93	49%	92	54%	97	51%	96	51%
Top isomiR (conservative) not in agreement with miRBase	86	44%	84	44%	77	45%	87	45%	83	44%
Top isomiR disagrees with miRBase at 5' end	13	7%	13	7%	10	6%	13	7%	10	5%
Top isomiR disagrees with miRBase at 5' end only	3	2%	2	1%	2	1%	3	2%	2	1%
Top isomiR disagrees with miRBase at 3' end	96	49%	91	48%	90	53%	94	49%	94	50%
Top isomiR disagrees with miRBase at 3' end only	86	44%	80	42%	82	48%	84	44%	86	46%
Top isomiR disagrees with miRBase at both ends	10	5%	11	6%	8	5%	10	5%	8	4%

Supp. Table 2. Statistics for each population separately for the single most abundant isomiR produced from a given precursor arm – using only females. The most abundant isomiR's identity was determined by analyzing the entire collection of all unique datasets that passed quality control and belonged to females. At each locus, we also generated the “conservative” estimate by requiring that the most abundant isomiR have higher expression than the miRBase reference by at least 0.585 log₂ units.

	CEU		FIN		GBR		TSI		YRI	
	Number	Percentage								
MiRNA precursor arms considered	198		189		193		182		199	
MiRBase miRNA sequence not among the 95-th percentile	57	30%	52	28%	58	31%	56	30%	59	30%
Top isomiR not in agreement with miRBase	94	47%	91	48%	95	49%	87	48%	97	49%
Top isomiR (conservative) not in agreement with miRBase	84	42%	81	43%	87	45%	79	43%	87	44%
Top isomiR disagrees with miRBase at 5' end	13	7%	12	6%	12	6%	10	5%	13	7%
Top isomiR disagrees with miRBase at 5' end only	2	1%	3	2%	3	2%	1	1%	2	1%
Top isomiR disagrees with miRBase at 3' end	92	46%	88	47%	92	48%	86	47%	95	48%
Top isomiR disagrees with miRBase at 3' end only	81	41%	79	42%	83	43%	77	42%	84	42%
Top isomiR disagrees with miRBase at both ends	11	6%	9	5%	9	5%	9	5%	11	6%

Supp. Table 3. Statistics for each population separately for the single most abundant isomiR produced from a given precursor arm – using only males. The most abundant isomiR's identity was determined by analyzing the entire collection of all unique datasets that passed quality control and belonged to males. At each locus, we also generated the “conservative” estimate by requiring that the most abundant isomiR have higher expression than the miRBase reference by at least 0.585 log₂ units.

	CEU		FIN		GBR		TSI		YRI	
	Number	Percentage								
MiRNA precursor arms considered	192		183		187		189		195	
MiRBase miRNA sequence not among the 95-th percentile	63	32%	58	31%	60	31%	54	30%	62	31%
Top isomiR not in agreement with miRBase	92	48%	87	48%	91	49%	92	49%	93	48%
Top isomiR (conservative) not in agreement with miRBase	81	42%	79	43%	82	44%	83	44%	82	42%
Top isomiR disagrees with miRBase at 5' end	13	7%	11	6%	10	5%	11	6%	11	6%
Top isomiR disagrees with miRBase at 5' end only	2	1%	3	2%	3	2%	2	1%	3	2%
Top isomiR disagrees with miRBase at 3' end	90	47%	84	46%	88	47%	90	48%	90	46%
Top isomiR disagrees with miRBase at 3' end only	79	41%	76	42%	81	43%	81	43%	82	42%
Top isomiR disagrees with miRBase at both ends	11	6%	8	4%	7	4%	9	5%	8	4%