

fraction aligned reads (normalised by # input reads)

fraction aligned reads (normalised by # input reads)												
input -	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%
successfully_clipped -	65.6%	89.1%	91.8%	90.0%	96.0%	96.4%	90.8%	86.8%	86.3%	90.5%	89.2%	70.4%
failed_quality_filter -	0.5%	0.5%	0.4%	0.5%	0.4%	0.6%	0.4%	0.5%	0.4%	0.6%	0.5%	0.4%
failed_homopolymer_filter -	6.9%	3.5%	4.2%	3.2%	6.2%	5.4%	3.8%	5.5%	3.3%	4.9%	5.6%	2.4%
calibrator -	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
UniVec_contaminants -	0.4%	0.3%	0.2%	0.2%	0.2%	0.3%	0.2%	0.4%	0.4%	0.2%	0.4%	0.3%
rRNA -	3.5%	4.6%	4.7%	5.5%	5.4%	6.2%	6.5%	5.2%	5.8%	5.5%	4.5%	3.9%
reads_used_for_alignment -	54.2%	80.2%	82.4%	80.6%	83.8%	83.8%	79.9%	75.2%	76.4%	79.3%	78.2%	63.4%
genome -	17.8%	51.8%	37.5%	38.9%	39.5%	36.5%	30.6%	32.8%	35.9%	35.8%	23.3%	23.0%
miRNA_sense -	8.6%	31.3%	22.8%	19.6%	16.5%	18.5%	13.0%	16.0%	14.8%	18.8%	11.7%	10.7%
miRNA_antisense -	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
miRNAprecursor_sense -	0.0%	0.1%	0.1%	0.2%	0.0%	0.1%	0.0%	0.0%	0.0%	0.1%	0.1%	0.1%
miRNAprecursor_antisense -	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
tRNA_sense -	1.8%	12.0%	6.3%	8.5%	9.1%	7.4%	6.6%	5.4%	8.6%	7.0%	2.3%	3.6%
tRNA_antisense -	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
piRNA_sense -	0.2%	0.5%	0.4%	0.8%	0.3%	0.6%	0.8%	0.3%	1.4%	0.5%	0.2%	0.7%
piRNA_antisense -	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
gencode_sense -	4.4%	5.7%	4.5%	6.2%	9.5%	6.5%	5.8%	6.9%	7.7%	5.8%	4.0%	3.9%
gencode_antisense -	0.2%	0.2%	0.3%	0.3%	0.4%	0.4%	0.5%	0.4%	0.4%	0.2%	0.4%	0.4%
circularRNA_sense -	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
circularRNA_antisense -	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
not_mapped_to_genome_or_libs -	36.5%	28.4%	44.9%	41.7%	44.4%	47.3%	49.3%	42.4%	40.6%	43.5%	54.9%	40.4%
repetitiveElements -	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
endogenous_gapped -	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
exogenous_miRNA -	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
exogenous_rRNA -	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
exogenous_genomes -	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	11.fastq -	11.fastq -	11.fastq -	11.fastq -	(1.fastq -	11.fastq -	11.fastq -	11.fastq -	11.fastq -	1.fastq -	11.fastq -	11.fastq -
	80°	\rangle \sigma_1 \rangle \rang	S . R_	S .	δ Γ	80 F	8. F	S. T.	\rightarrow \frac{\rightarrow}{\rightarrow} \frac{\rightarrow}	∞ F	ω Γ	\range \frac{\range 0}{\range 1}
	mple01_	mple07_	mple08_	mple11_	mple02_	mple03_	mple05_	mple04_	mple06_	mple09_	mple10_	mple12_
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ReadFraction
1.00
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fraction aligned reads (normalised by # adapter-clipped reads)

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		successfully_clipped -	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%
Color   Colo		failed_quality_filter -	0.7%	0.5%	0.4%	0.6%	0.4%	0.7%	0.5%	0.6%	0.5%	0.6%	0.6%	0.5%
Uniform, comminiment   Co.75   Co.55   Co.55   Co.55   Co.75		failed_homopolymer_filter -	10.6%	3.9%	4.6%	3.5%	6.5%	5.6%	4.2%	6.4%	3.8%	5.4%	6.3%	3.5%
## 1704   \$38, \$28, \$28, \$19, \$19, \$19, \$27, \$29, \$29, \$29, \$29, \$29, \$29, \$29, \$29		calibrator -	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
		UniVec_contaminants -	0.7%	0.3%	0.2%	0.3%	0.2%	0.3%	0.2%	0.5%	0.4%	0.2%	0.5%	0.4%
## 17/15   56.1%   43.9%   43.2%   41.1%   37.9%   53.7%   37.2%   41.5%   39.6%   26.1%   32.7%   ## 17/15   41.2%   41.1%   42.9%   11.1%   11.2%		rRNA -	5.3%	5.2%	5.1%	6.1%	5.7%	6.5%	7.1%	6.0%	6.7%	6.1%	5.0%	5.5%
### ### ### ### ### ### ### ### ### ##		reads_used_for_alignment -	82.7%	90.0%	89.8%	89.5%	87.3%	86.9%	88.0%	86.6%	88.5%	87.7%	87.6%	90.0%
MRIVA_Initionio		genome -	27.1%	58.1%	40.9%	43.2%	41.1%	37.9%	33.7%	37.8%	41.5%	39.6%	26.1%	32.7%
### PAPER PROPRIESTING - 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.		miRNA_sense -	13.2%	35.1%	24.9%	21.8%	17.1%	19.2%	14.3%	18.5%	17.1%	20.8%	13.1%	15.2%
### Ministrates - 10.0%		miRNA_antisense -	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Final Service   2.7%   13.5%   6.8%   9.4%   9.4%   9.6%   7.7%   7.3%   6.2%   9.9%   7.7%   2.5%   5.1%     Final Service   0.0%		miRNAprecursor_sense -	0.0%	0.1%	0.1%	0.2%	0.0%	0.1%	0.0%	0.0%	0.0%	0.1%	0.1%	0.1%
## BRNA_anitisense - 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.		miRNAprecursor_antisense -	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
piRNA_seriae	ıge	tRNA_sense -	2.7%	13.5%	6.9%	9.4%	9.5%	7.7%	7.3%	6.2%	9.9%	7.7%	2.5%	5.1%
PIRNA antisense - 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.	Sta	tRNA_antisense -	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
genoode_senser- 6.7% 6.4% 4.9% 6.9% 9.9% 6.7% 6.4% 8.0% 8.9% 6.4% 4.5% 5.5%  genoode_antisenser- 0.3% 0.2% 0.3% 0.3% 0.4% 0.4% 0.4% 0.5% 0.4% 0.4% 0.5% 0.4% 0.4% 0.6%  circularRNA_senser- 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0%		piRNA_sense -	0.4%	0.5%	0.4%	0.9%	0.4%	0.7%	0.9%	0.3%	1.6%	0.6%	0.2%	1.0%
gencode_antisense- 0.3% 0.2% 0.3% 0.3% 0.4% 0.4% 0.5% 0.4% 0.4% 0.3% 0.4% 0.6% 0.6% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0		piRNA_antisense -	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
diroularRNA_sense         0.0% <td></td> <td>gencode_sense -</td> <td>6.7%</td> <td>6.4%</td> <td>4.9%</td> <td>6.9%</td> <td>9.9%</td> <td>6.7%</td> <td>6.4%</td> <td>8.0%</td> <td>8.9%</td> <td>6.4%</td> <td>4.5%</td> <td>5.5%</td>		gencode_sense -	6.7%	6.4%	4.9%	6.9%	9.9%	6.7%	6.4%	8.0%	8.9%	6.4%	4.5%	5.5%
CircularRNA antisense - 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.		gencode_antisense -	0.3%	0.2%	0.3%	0.3%	0.4%	0.4%	0.5%	0.4%	0.4%	0.3%	0.4%	0.6%
not_mapped_to_genome_or_libs- repetitiveElements- 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0%		circularRNA_sense -	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
repetitiveElements - 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.		circularRNA_antisense -	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
endogenous_gapped - 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.	not_	_mapped_to_genome_or_libs -	55.6%	31.9%	48.9%	46.3%	46.2%	49.1%	54.3%	48.8%	47.0%	48.1%	61.5%	57.3%
exogenous_miRNA- 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0		repetitiveElements -	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
exogenous_genomes - 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.		endogenous_gapped -	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
sample 004_S1_R1.fastiq - sample 002_S1_R1.fastiq - sample 002_S1_R1.f		exogenous_miRNA -	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
sample01_S1_R1.fastq-sample06_S1_R1.fastq-sample06_S1_R1.fastq-sample06_S1_R1.fastq-sample06_S1_R1.fastq-sample06_S1_R1.fastq-sample10_S1_R1.fastq-sample10_S1_R1.fastq-sample10_S1_R1.fastq-sample10_S1_R1.fastq-sample10_S1_R1.fastq-sample10_S1_R1.fastq-sample12_		exogenous_rRNA -	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
sample001_S1_R1.fas sample002_S1_R1.fas sample006_S1_R1.fas sample006_S1_R1.fas sample006_S1_R1.fas sample010_S1_R1.fas sample010_S1_R1.fas sample110_S1_R1.fas sample110_S1_R1.fas		exogenous_genomes -	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
sample 0.5 S1 sa			sstg -	astq -	astg -	astq -	astg-	- std	astg -	- sstd	- astd -	- std	- std	sstq -
sample 0.5 S1 sa			R1.fe	요 한	7. 1. 1.	7. 1. 1.	R1.fe	R1.fe	R1.fs	7.1. 3.	٦. ئ <del>ة</del>	R1.fe	R1.fs	R1.fe
sample 02_ sample 06_ sample 10_ sample 10_ sample 11_ sample 12_ sample 12_ sample 12_	l		1_10		<u></u>	<u></u>	1_10	_	<u>.</u>	<u></u>	<u></u> _l	-12	20	7_
Sample Sample			27_5	77	38_ {	<u> </u>	22_{	33_6	)5(	4C 5,1	90	60		12_6
E E E E E E E E E E E E E E E E E E E			ple(	ple(	)eld	ble	ple(	ple(	ple(	ple(	ple(	ple(	ple,	ple,
Sample			šam	šam	šam	šam	заш	sam	sam	заш	sam	ЗаШ	Заш	хаш
			U)	U)	U)	U)	U)	Sam	ple	v)	U)	07	U)	U)

ReadFraction 1.00

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fraction aligned reads (normalised by # non-contaminant reads)

	maction diighed reads (normalised by in non-contaminant reads)												
reads_used_for_	alignment -	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%
	genome -	32.8%	64.6%	45.5%	48.3%	47.1%	43.5%	38.3%	43.6%	46.9%	45.2%	29.8%	36.3%
miRI	NA_sense -	15.9%	39.0%	27.7%	24.4%	19.6%	22.1%	16.2%	21.3%	19.3%	23.7%	15.0%	16.9%
miRNA_	_antisense -	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
miRNAprecurs	sor_sense -	0.0%	0.1%	0.1%	0.2%	0.0%	0.1%	0.1%	0.0%	0.0%	0.2%	0.1%	0.1%
miRNAprecursor_	_antisense -	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
tRI	NA_sense -	3.3%	15.0%	7.7%	10.5%	10.9%	8.8%	8.3%	7.2%	11.2%	8.8%	2.9%	5.6%
tRNA_	_antisense -	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
piRI	NA_sense -	0.4%	0.6%	0.5%	1.0%	0.4%	0.8%	1.1%	0.4%	1.8%	0.6%	0.2%	1.2%
φ piRNA_	_antisense -	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Stage piRNA_	ode_sense -	8.1%	7.1%	5.4%	7.7%	11.3%	7.7%	7.3%	9.2%	10.1%	7.3%	5.2%	6.1%
gencode_	_antisense -	0.4%	0.2%	0.4%	0.3%	0.4%	0.5%	0.6%	0.5%	0.5%	0.3%	0.5%	0.6%
circularRI	NA_sense -	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
circularRNA_	_antisense -	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
not_mapped_to_genon	ne_or_libs -	67.2%	35.4%	54.5%	51.7%	52.9%	56.5%	61.7%	56.4%	53.1%	54.8%	70.2%	63.7%
repetitive	eElements -	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
endogenou	s_gapped -	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
exogenou	us_miRNA -	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
exogeno	ous_rRNA -	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
exogenous_	_genomes -	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
		ample01_S1_R1.fastq -	ample07_S1_R1.fastq -	ample08_S1_R1.fastq -	ample11_S1_R1.fastq -	ample02_S1_R1.fastq	ample03_S1_R1.fastq -	ample05_S1_R1.fastq -	ample04_S1_R1.fastq -	ample06_S1_R1.fastq -	ample09_S1_R1.fastq -	ample10_S1_R1.fastq -	ample12_S1_R1.fastq -
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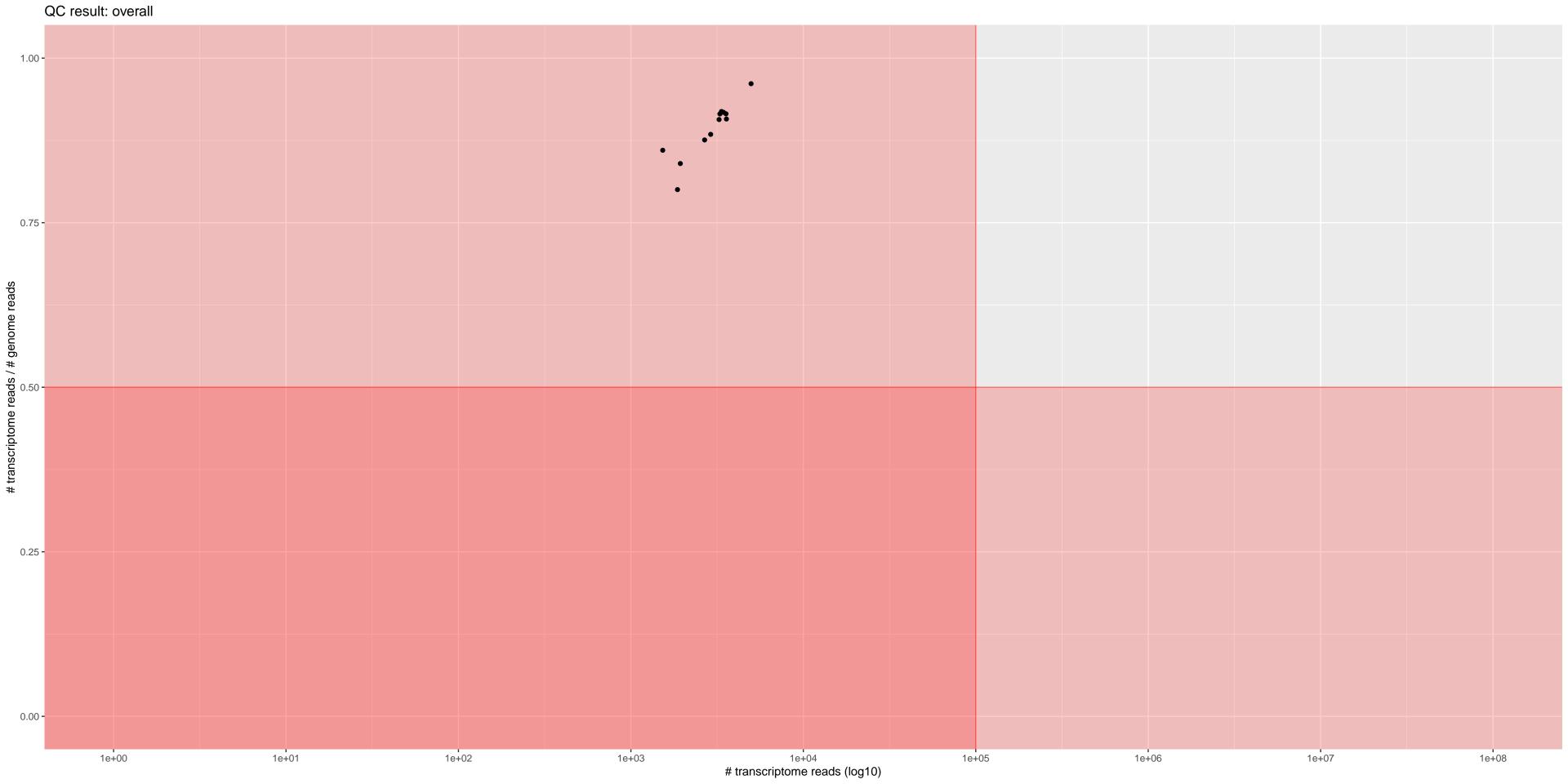
ReadFraction 1.00

0.75

0.50

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0.00



sample12_S1_R1.fastq -	10000	2304	1935	0.84	0.226
sample10_S1_R1.fastq -	10000	2328	1863	0.8	0.221
sample09_S1_R1.fastq -	10000	3581	3247	0.91	0.215
sample06_S1_R1.fastq -	10000	3586	3282	0.92	0.178
sample04_S1_R1.fastq -	10000	3282	2902	0.88	0.222
sample05_S1_R1.fastq -	10000	3057	<b>2677</b>	0.88	0.205
sample03_S1_R1.fastq -	10000	3649	3353	0.92	0.211
sample02_S1_R1.fastq -	10000	3946	3581	0.91	0.195
sample11_S1_R1.fastq -	10000	3890	3561	0.92	0.168
sample08_S1_R1.fastq -	10000	3753	3444	0.92	0.175
sample07_S1_R1.fastq -	10000	5177	4976	0.96	0.156
sample01_S1_R1.fastq -	10000	1779	1530	0.86	0.2
	InputReads -	Genome Reads -	Transcriptome Reads -	anscriptomeGenomeRatio -	TranscriptomeComplexity -

