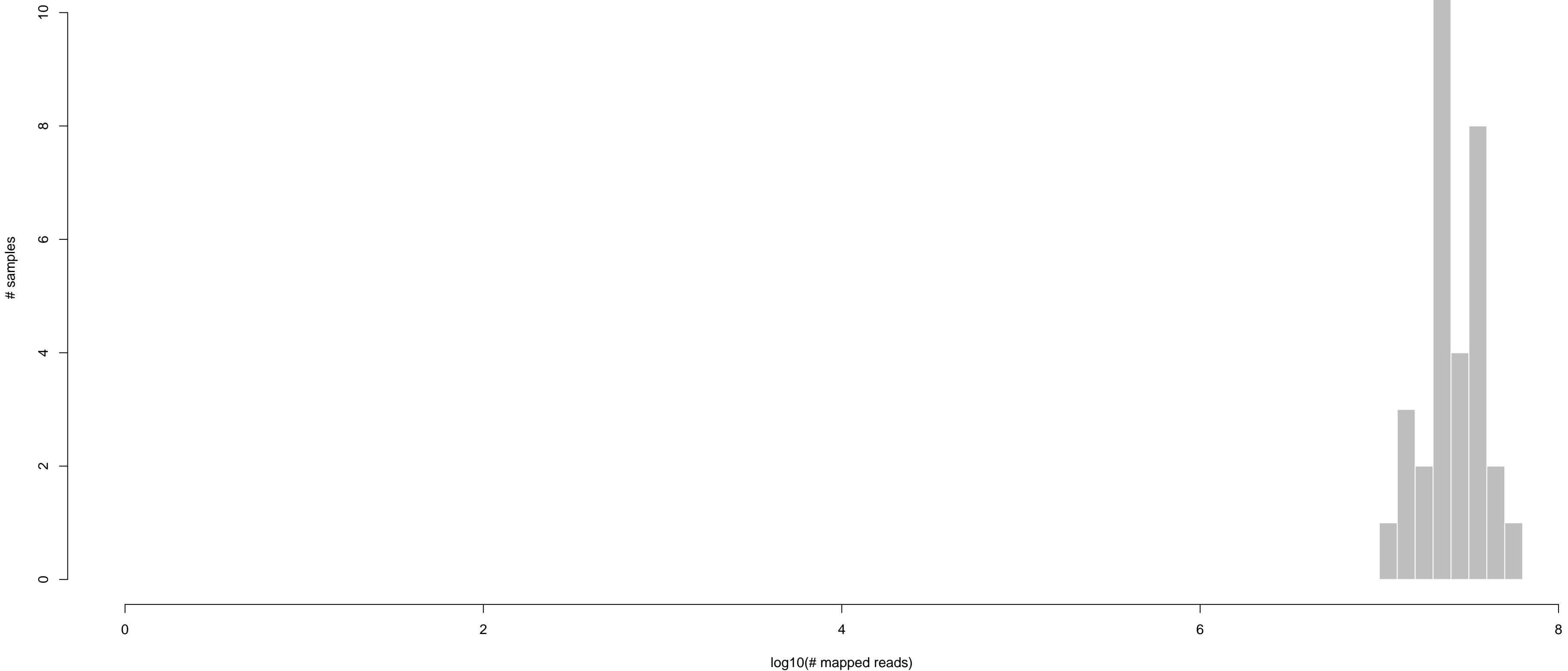


Library size (all mapped reads)



fraction aligned reads (normalised by # input reads)

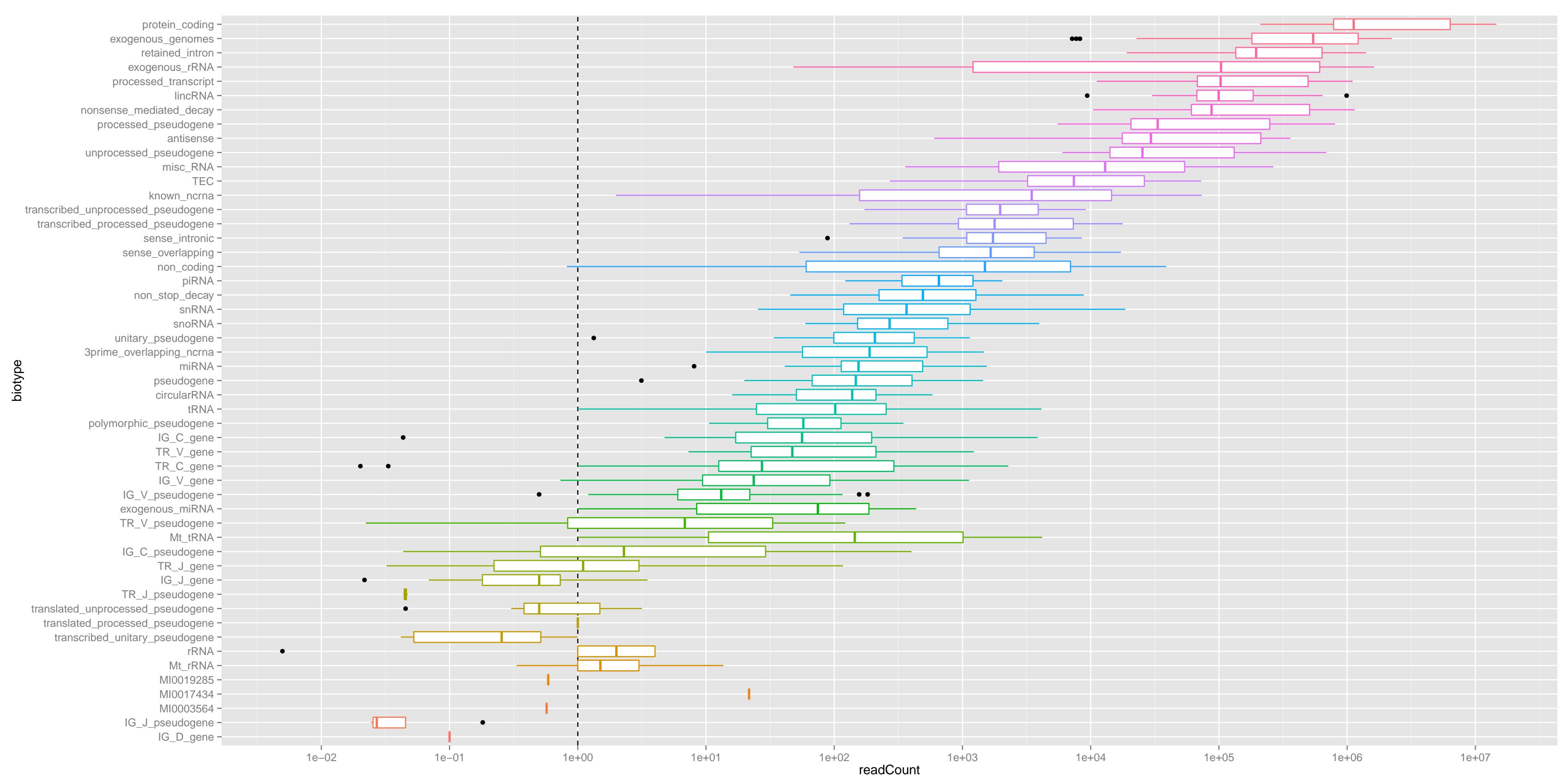
fraction aligned reads (normalised by # adapter-clipped reads)

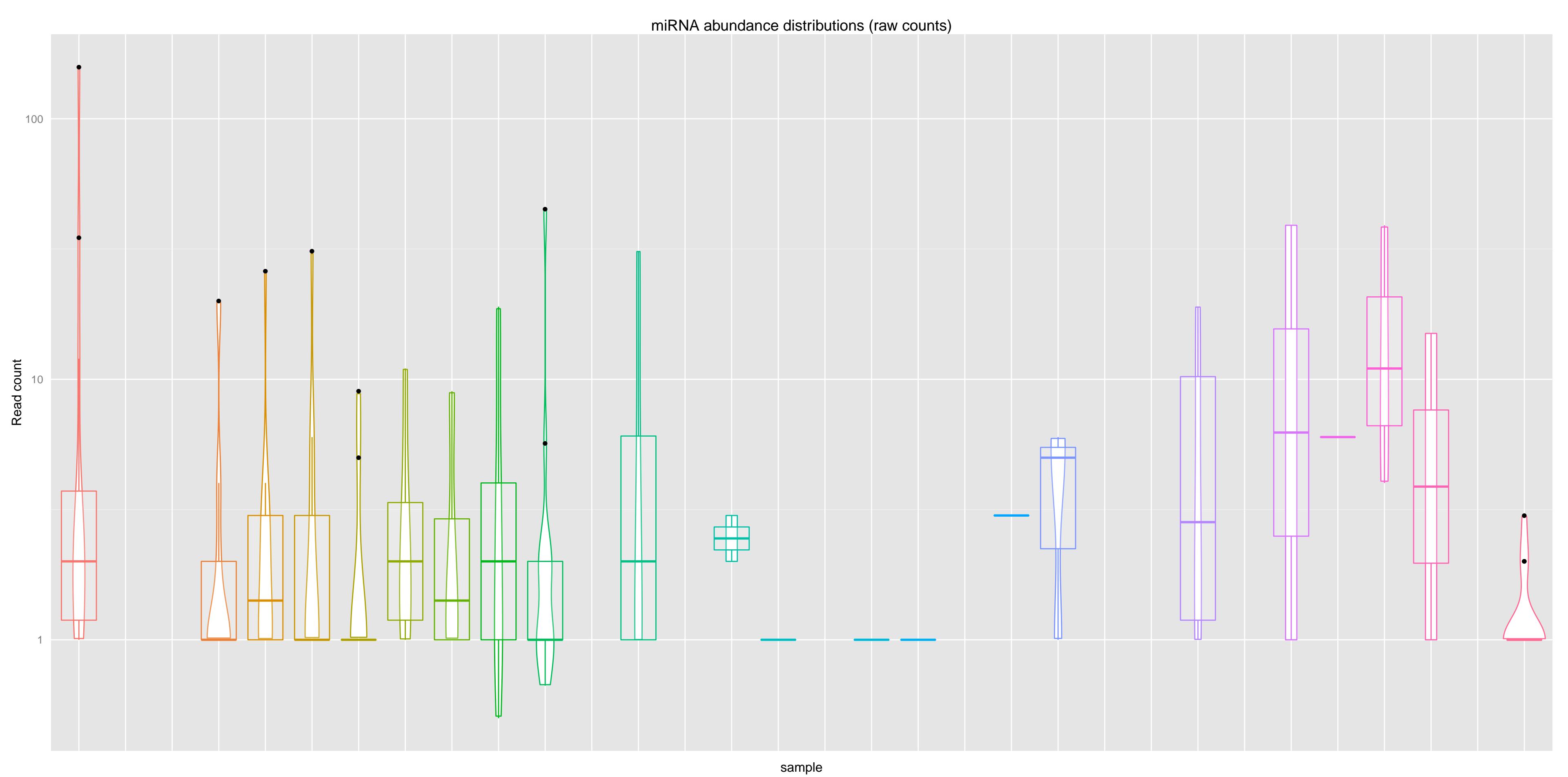
	ReadFraction																															
Stage	Sample_000-268_004_R1_all.fq	Sample_000-632_012_R1_all.fq	Sample_000-025_001_R1_all.fq	HSB123_AMY.fq	HSB123_CBC.fq	HSB123_MD.fq	Sample_000-465PF_006_R1_all.fq	SRR577579_1	Sample_000-484_007_R1_all.fq	Sample_000-297_002_R1_all.fq	Sample_000-330_005_R1_all.fq	Sample_BkSQ-117_001_R1_all.fq	Sample_BkSQ-139_003_R1_all.fq	Sample_BkSQ-49_004_R1_all.fq	Sample_BkSQ-157_004_R1_all.fq	Sample_BkSQ-3_005_R1_all.fq	Sample_BkSQ-5_007_R1_all.fq	Sample_BkSQ-6_012_R1_all.fq	Sample_BkSQ-105_008_R1_all.fq	Sample_BkSQ-153_007_R1_all.fq	Sample_BkSQ-2_004_R1_all.fq	Sample_BkSQ-26_002_R1_all.fq	Sample_BkSQ-70_006_R1_all.fq	Sample_BkSQ-89_007_R1_all.fq	Sample_BkSQ-10_001_R1_all.fq	Sample_BkSQ-124_002_R1_all.fq	Sample_BkSQ-29_003_R1_all.fq	Sample_BkSQ-65_005_R1_all.fq				
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%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%						
failed_quality_filter	6.4%	9.0%	7.3%	24.3%	24.2%	23.8%	5.4%	6.2%	4.3%	5.9%	7.3%	7.6%	5.1%	7.2%	6.2%	3.8%	2.1%	2.5%	2.0%	4.8%	2.6%	2.5%	2.6%	2.4%	5.7%	5.9%	4.7%	2.5%	5.6%	7.4%	5.3%	7.1%
failed_homopolymer_filter	0.9%	14.9%	2.7%	0.0%	0.0%	0.0%	0.9%	5.2%	0.0%	2.6%	2.4%	3.5%	0.1%	0.9%	0.5%	0.5%	0.0%	0.1%	0.1%	0.7%	0.1%	0.1%	0.0%	0.1%	1.2%	1.0%	0.6%	0.1%	0.8%	0.8%	0.8%	1.1%
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%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	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	0.8%	1.0%	0.1%	0.0%	0.0%	0.0%	1.2%	0.2%	0.0%	0.1%	0.0%	0.1%	0.0%	0.0%	0.0%	0.2%	0.0%	0.0%	0.0%	0.9%	0.0%	0.0%	0.2%	0.0%	0.9%	0.6%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
rRNA	15.6%	4.6%	10.8%	4.1%	4.5%	5.3%	10.3%	13.2%	20.8%	9.3%	10.3%	10.7%	81.2%	62.5%	63.2%	21.1%	8.7%	14.0%	14.2%	26.1%	9.6%	6.2%	12.5%	12.0%	48.0%	42.0%	23.1%	27.2%	33.5%	37.3%	37.9%	40.7%
reads_used_for_alignment	76.3%	70.5%	79.1%	71.5%	71.3%	71.0%	82.1%	75.3%	74.9%	82.0%	80.1%	78.1%	13.6%	29.4%	29.9%	74.5%	89.2%	83.4%	83.7%	67.5%	87.6%	91.1%	84.8%	85.3%	45.1%	50.2%	71.0%	70.3%	60.1%	54.6%	56.0%	51.0%
genome	73.8%	67.4%	77.7%	69.0%	68.7%	68.3%	77.6%	73.1%	73.7%	80.0%	78.2%	76.3%	4.6%	12.2%	9.9%	14.9%	27.6%	25.2%	24.7%	28.1%	34.6%	39.4%	36.1%	38.6%	14.5%	17.5%	24.0%	22.0%	17.7%	16.9%	14.3%	14.8%
miRNA_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%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
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%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	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%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	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_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%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	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	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	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_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%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	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	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	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_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%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	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	18.1%	2.8%	29.9%	30.4%	29.9%	31.2%	30.9%	28.9%	4.6%	38.2%	35.0%	35.3%	0.7%	2.6%	2.1%	1.3%	4.0%	4.0%	5.1%	7.0%	5.3%	7.8%	6.2%	7.9%	2.4%	3.3%	2.8%	4.3%	2.5%	2.9%	2.2%	2.4%
gencode_antisense	16.2%	2.7%	27.0%	29.0%	28.8%	30.6%	27.9%	28.2%	55.5%	34.8%	32.4%	32.2%	0.1%	0.4%	0.4%	0.3%	0.2%	0.3%	0.3%	0.8%	0.4%	0.5%	0.3%	0.4%	0.4%	0.8%	0.6%	0.3%	0.5%	0.3%	0.3%	0.3%
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%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	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%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	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	2.0%	3.1%	0.6%	1.6%	1.3%	1.4%	3.5%	1.5%	0.5%	0.8%	0.7%	0.8%	9.0%	17.1%	19.9%	59.6%	61.4%	58.0%	58.8%	39.2%	52.8%	51.4%	48.5%	46.4%	30.5%	32.6%	47.0%	48.1%	42.3%	37.6%	41.6%	36.2%
repetitiveElements	0.2%	1.0%	0.2%	0.1%	0.1%	0.1%	0.2%	0.3%	0.1%	0.2%	0.2%	0.2%	2.4%	5.6%	4.2%	3.5%	6.6%	12.1%	5.8%	8.1%	13.6%	12.5%	11.1%	13.5%	9.5%	10.5%	10.3%	6.1%	10.9%	7.0%	6.2%	6.1%
endogenous_gapped	0.3%	0.3%	0.3%	0.3%	0.5%	0.4%	0.6%	0.7%	0.4%	0.6%	0.4%	0.4%	4.3%	8.7%	8.0%	4.6%	17.8%	14.8%	17.7%	22.3%	22.5%	31.5%	28.4%	29.2%	7.2%	9.7%	8.6%	16.5%	8.7%	11.2%	7.2%	7.6%
ex																																

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

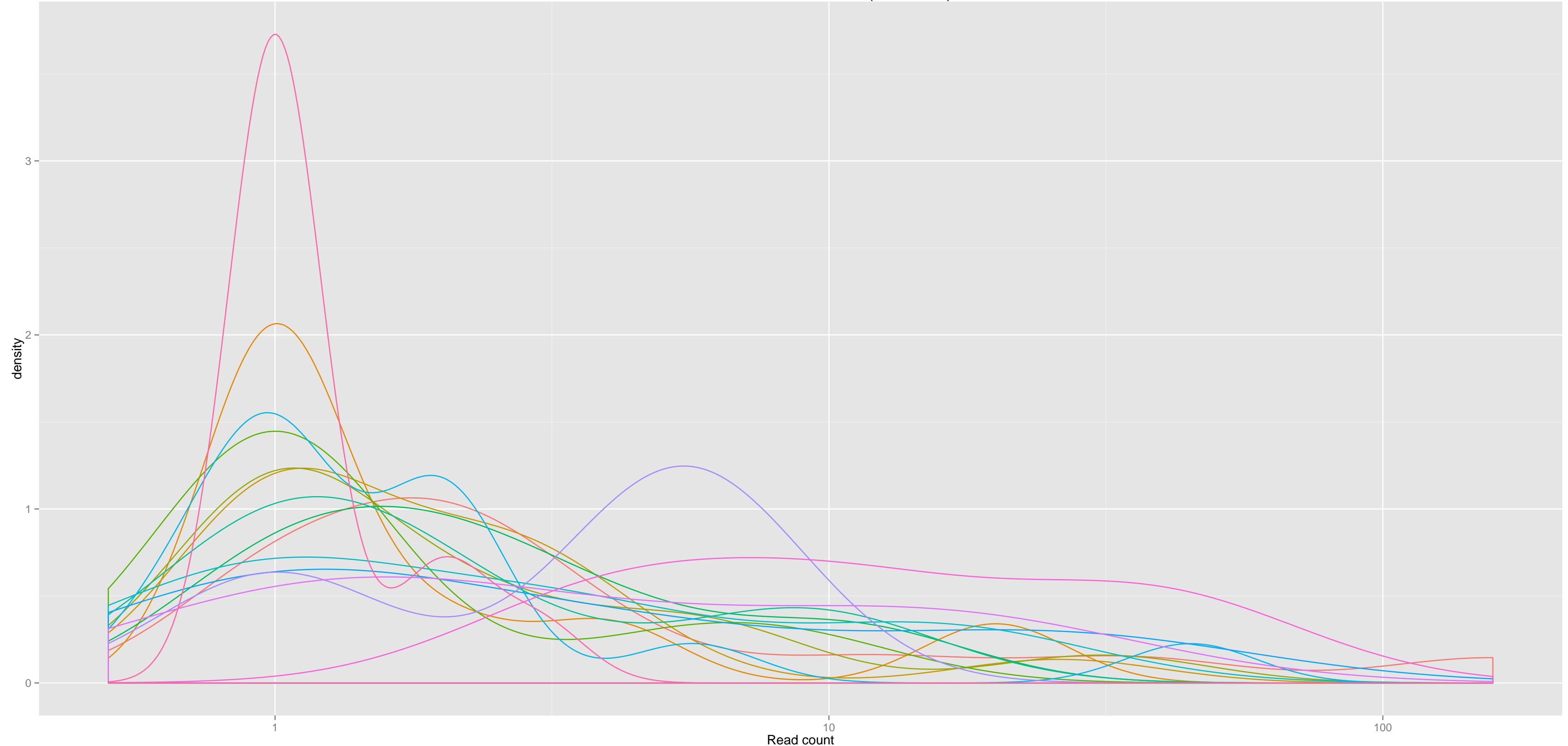
Heatmap showing ReadFraction values across various samples and stages. The heatmap uses a color scale from 0.00 (blue) to 1.00 (yellow). The y-axis lists stages and sample names. The x-axis lists samples. A color bar on the right is labeled 'ReadFraction'.

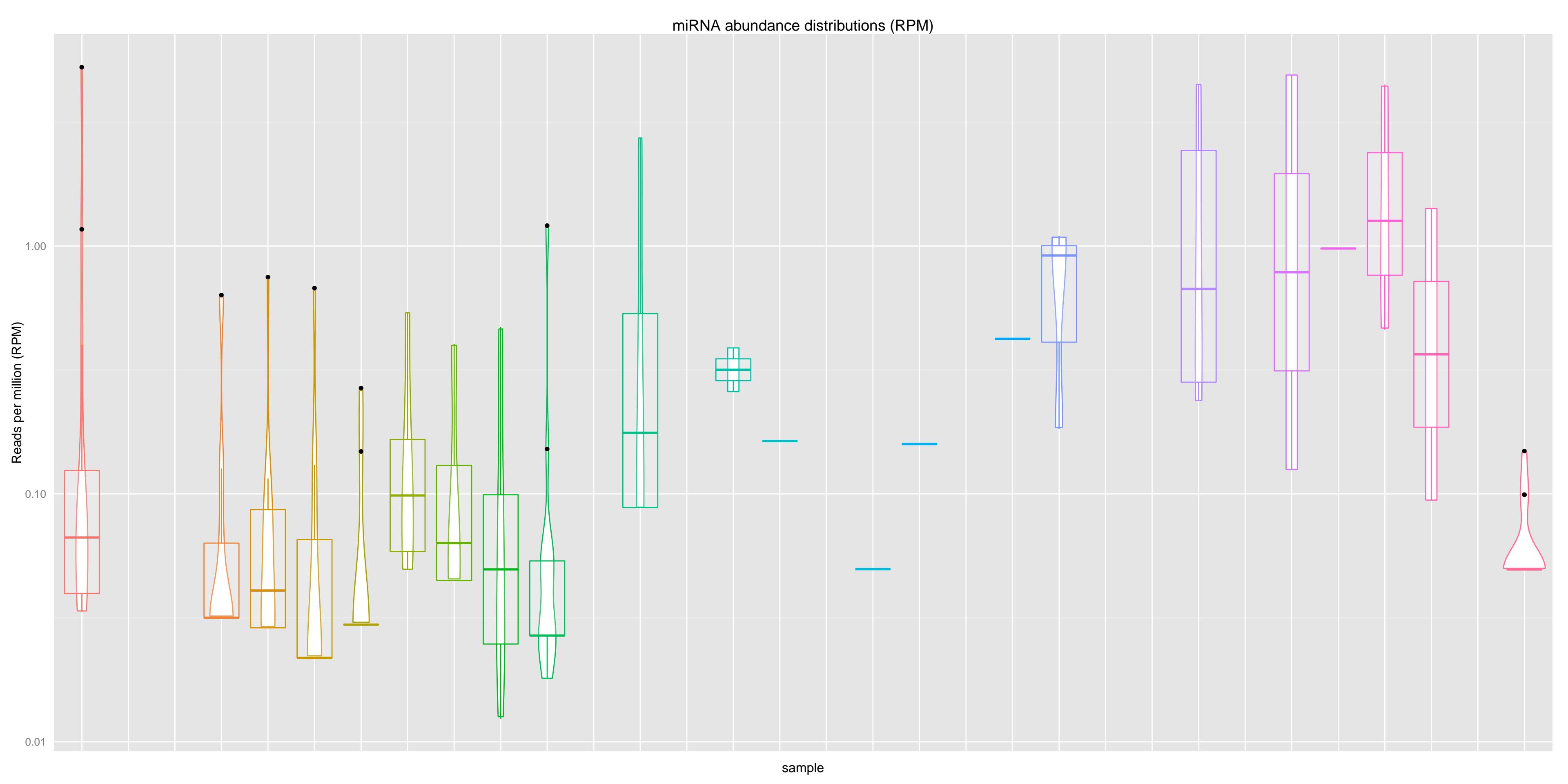
Stage	Sample	Value
reads_used_for_alignment	Sample_000-268_004_R1_all.fq	100.0%
genome	Sample_000-632_012_R1_all.fq	96.7%
miRNA_sense	HSB123.AMY.fq	0.0%
miRNA_antisense	HSB123.CBC.fq	0.0%
miRNAPrecursor_sense	HSB123.MD.fq	0.0%
miRNAPrecursor_antisense	SRR577579_1	0.0%
tRNA_sense	Sample_000-484_007_R1_all.fq	0.0%
tRNA_antisense	Sample_000-297_002_R1_all.fq	0.0%
piRNA_sense	Sample_000-554_009_R1_all.fq	0.0%
piRNA_antisense	Sample_000-465PF_006_R1_all.fq	0.0%
gencode_sense	Sample_BkSQ-117_001_R1_all.fq	23.7%
gencode_antisense	Sample_BkSQ-139_003_R1_all.fq	21.2%
circularRNA_sense	Sample_BkSQ-49_004_R1_all.fq	0.0%
circularRNA_antisense	Sample_BkSQ-157_004_R1_all.fq	0.0%
not_mapped_to_genome_or_libs	Sample_BkSQ-3_005_R1_all.fq	2.7%
repetitiveElements	Sample_BkSQ-5_007_R1_all.fq	4.4%
endogenous_gapped	Sample_BkSQ-6_012_R1_all.fq	0.3%
exogenous_miRNA	Sample_BkSQ-11_001_R1_all.fq	0.4%
exogenous_rRNA	Sample_BkSQ-26_002_R1_all.fq	0.0%
exogenous_genomes	Sample_BkSQ-49_007_R1_all.fq	0.0%



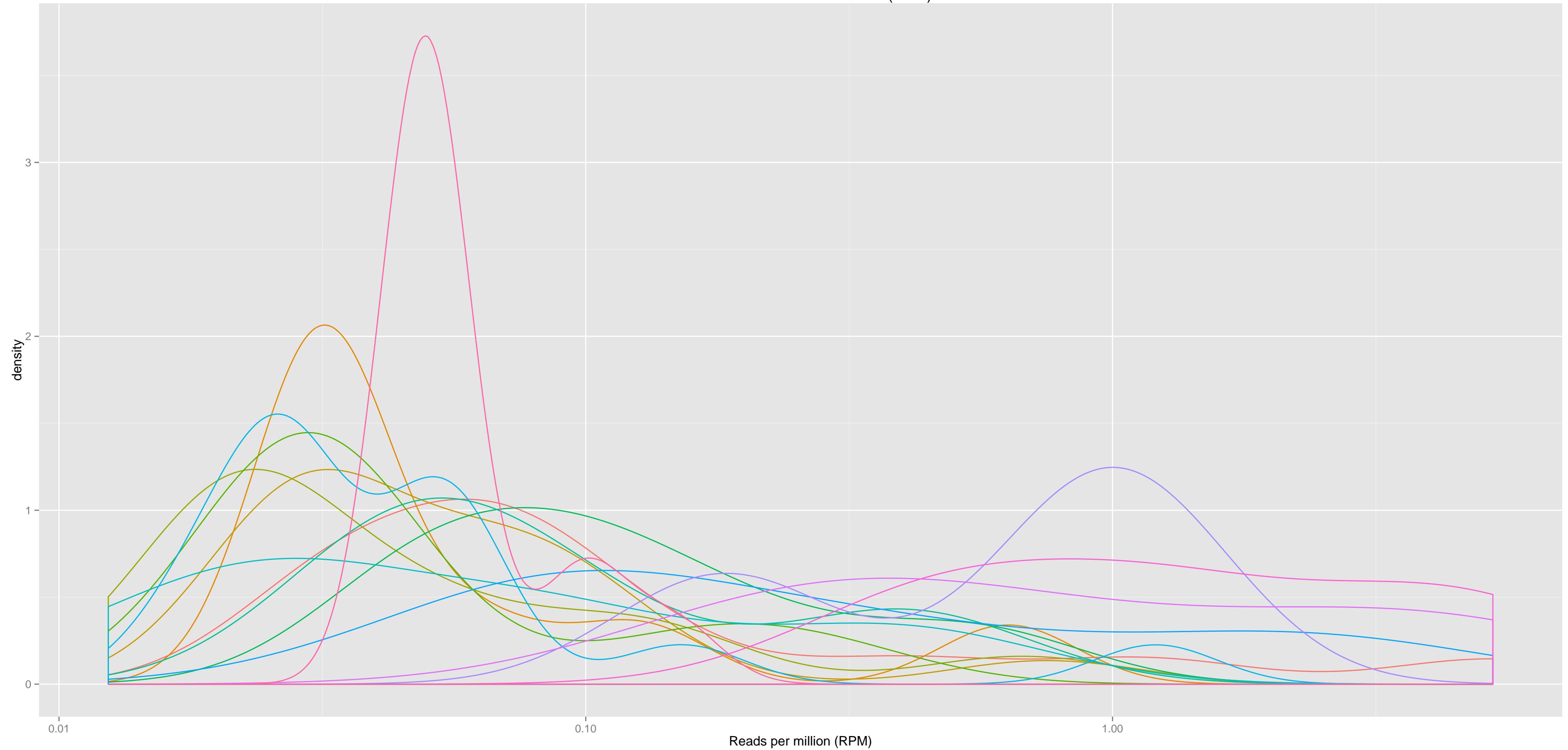


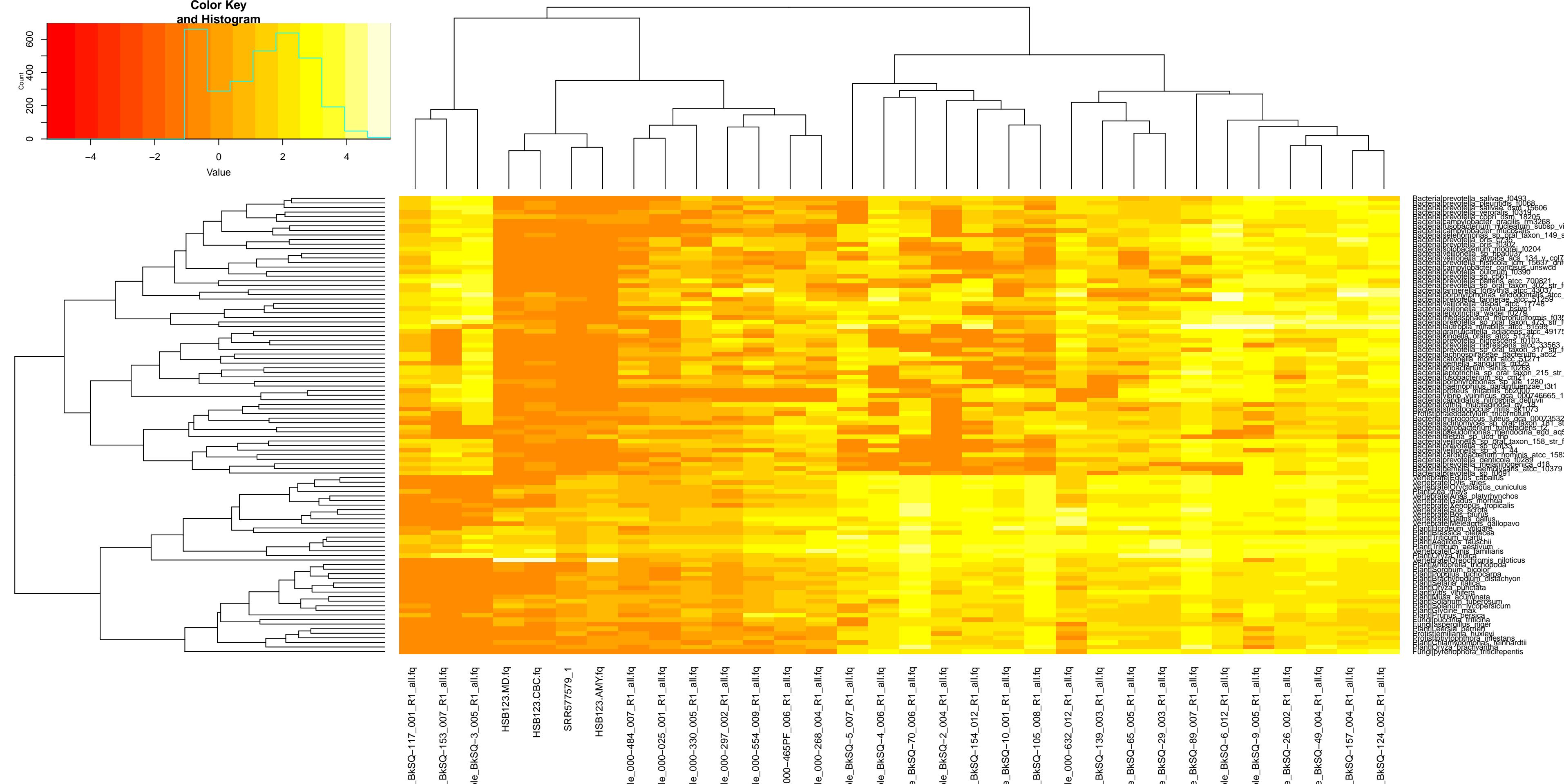
miRNA abundance distributions (raw counts)

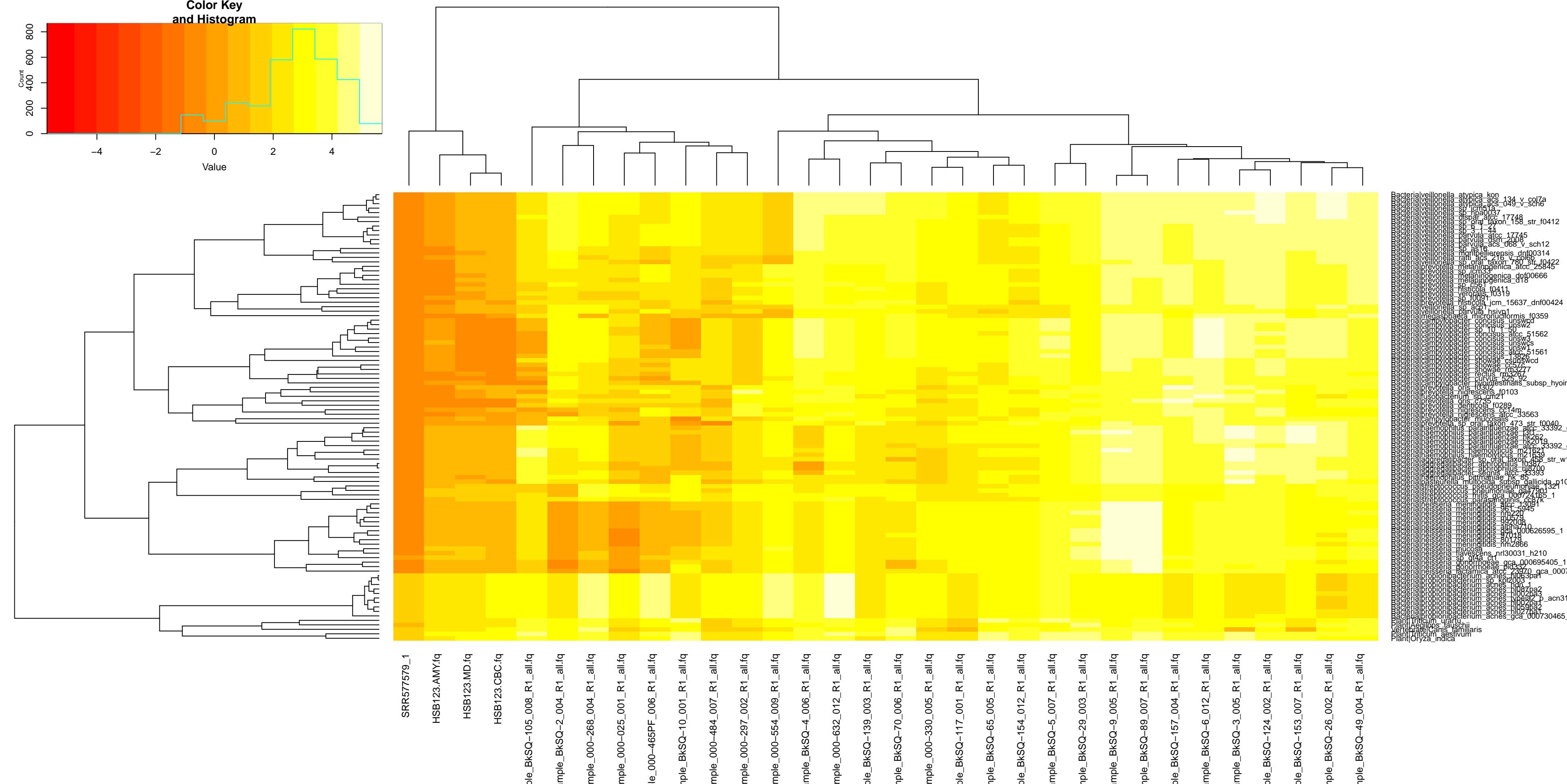


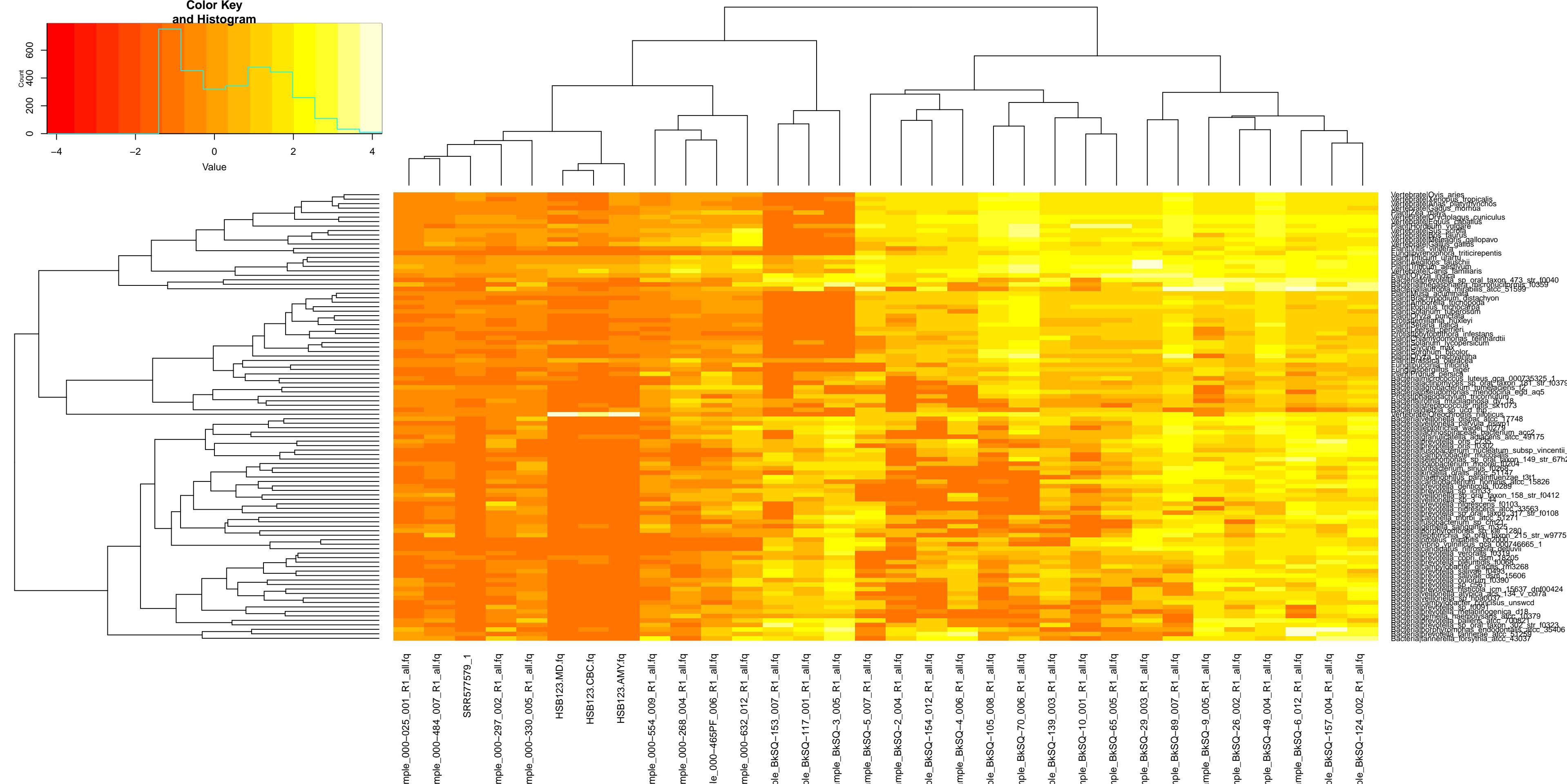


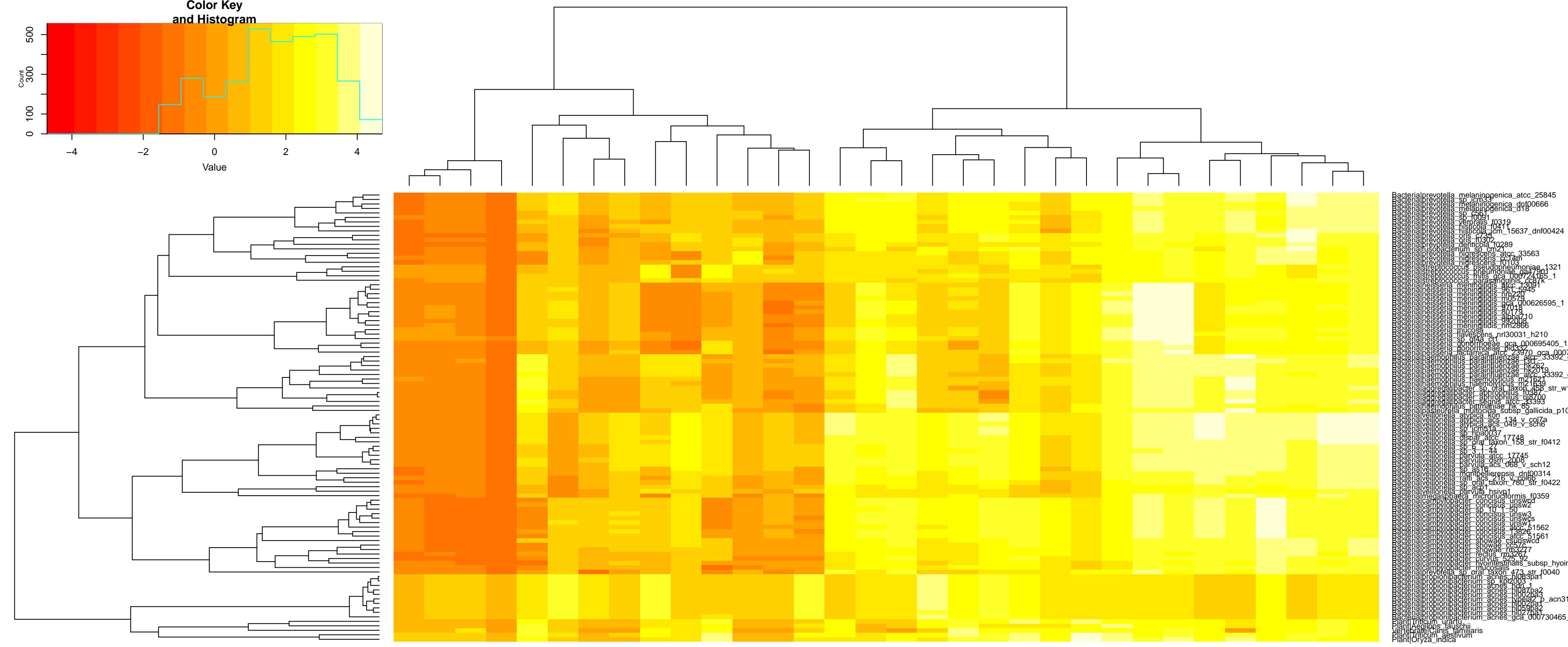
miRNA abundance distributions (RPM)











prevotella melaninogenica_atcc_25845
prevotella melaninogenica_dnf00666
prevotella melaninogenica_d18
prevotella sp_f0091
prevotella veroralis f0319
prevotella histicola f0411
prevotella pris c34
prevotella pris_f0302
prevotella dentifical 10289
prevotella dentifical_sp_mcm21
prevotella nigrifaciens atcc_33563
prevotella nigrifaciens cc4m
prevotella nigrifaciens f0103
streptococcus pseudopneumoniae 1321
streptococcus suis gca_0007724165_1
streptococcus suis gca_0007724165_1
streptococcus parasanguinis cc87k
neisseria meningitidis atcc_13051
neisseria meningitidis atcc_13051
neisseria meningitidis gca_0007724165_1
neisseria meningitidis gca_0007724165_1
neisseria meningitidis gca_0007724165_1
neisseria meningitidis gca_0007724165_1
neisseria meningitidis alpha710
neisseria meningitidis alpha710
neisseria meningitidis nm2866
neisseria flavescens nr10031_h210
neisseria sp_q49_c11
neisseria donovaniiae_gca_000695405_1
neisseria gonorrhoeae pid33
neisseria gonorrhoeae atcc35070_gca_0007724165_1
haemophilus parainfluenzae 13m
haemophilus parainfluenzae nk4629
haemophilus parainfluenzae nk4629
haemophilus parainfluenzae nk4629
haemophilus haemolyticus m21621
haemophilus haemolyticus m21621
addrepredatibacter sp oral taxon_158 str_w
addrepredatibacter abnormophilus n8700
addrepredatibacter sequeiae acc_p33393
haemophilus pertmaniae nk_85
veillonella atypica subspp gallicida_p10
veillonella atypica_acs_134_v_col7a
veillonella atypica_acs_049_v_sch6
veillonella atypica_acs_037
veillonella atypica_acs_17748
veillonella atypica_acs_17748
veillonella sp oral taxon_158_str_f0412
veillonella sp_b_1_44
veillonella barvula atcc_17745
veillonella barvula dsm_2008
veillonella stoma16
veillonella ratti16
veillonella sp oral taxon_780_str_f0422
veillonella sp_acp1
veillonella sp_hsp1
megaspilus micromonutriiformis_f0359
campylobacter concisus unswc
campylobacter concisus lpsw2
campylobacter sp_lpsw3
campylobacter concisus unsws3
campylobacter concisus unsws1
campylobacter concisus atcc_51562
campylobacter concisus atcc_51561
campylobacter showae csws61
campylobacter showae csw7c
campylobacter rectus rpm_267
campylobacter curvus 525_92
campylobacter hyoilectus subspp_hyoi
campylobacter mucosalis subsp_hyoi
prelimnibacterium ratovi 473_str_f0040
probionibacterium acnes_h0638pa1
probionibacterium sp_klp2003
probionibacterium acnes_h0638pa1
probionibacterium acnes_h0638pa2
probionibacterium acnes_h0638pa3
probionibacterium acnes_h0638pa4
probionibacterium acnes_h0638pa5
probionibacterium acnes_h0638pa6
lucoplas_tauschi
telomaias familiaris
vaginastrium
vaginastrium