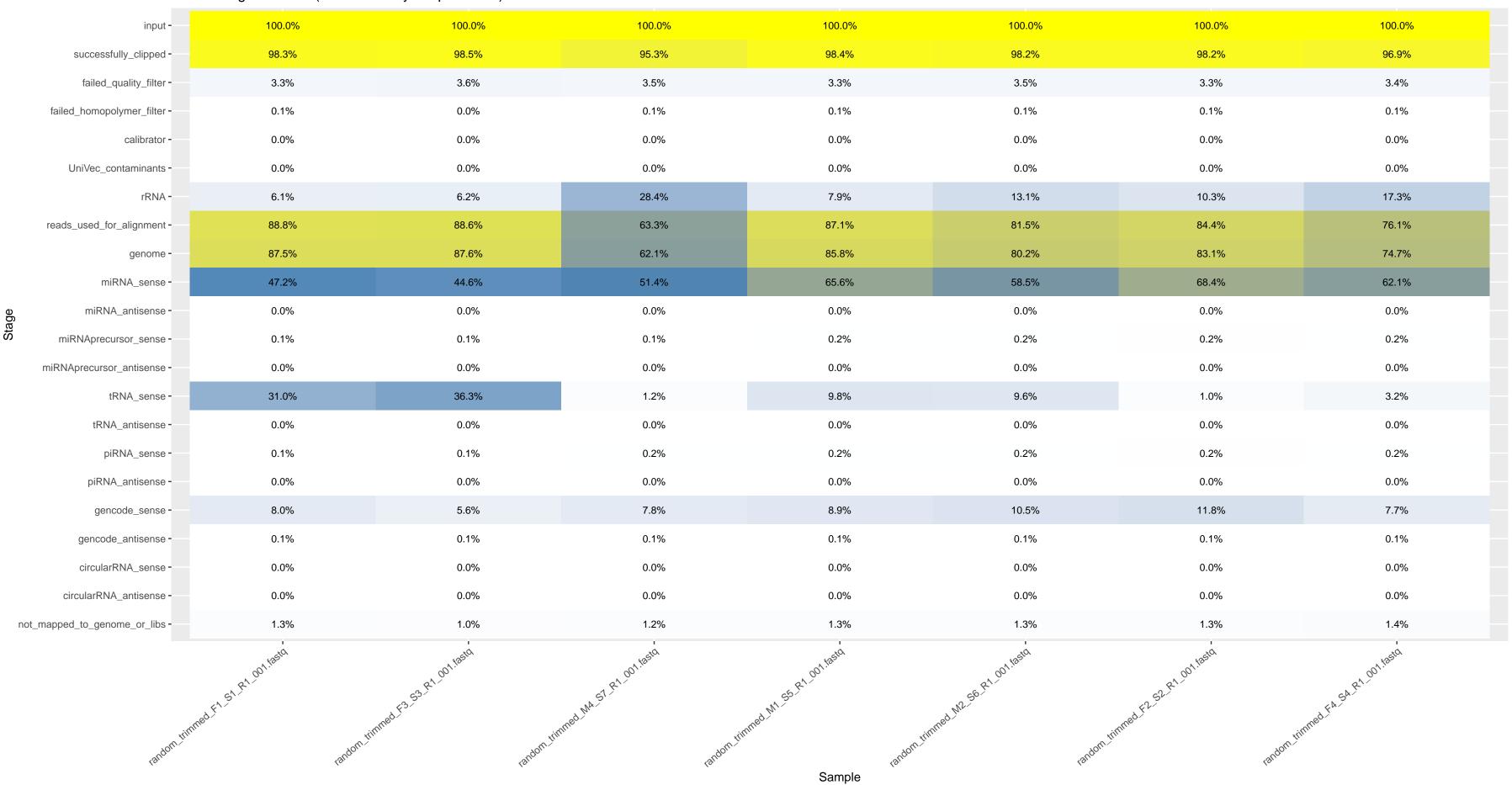


fraction aligned reads (normalised by # input reads)



ReadFraction

1.00

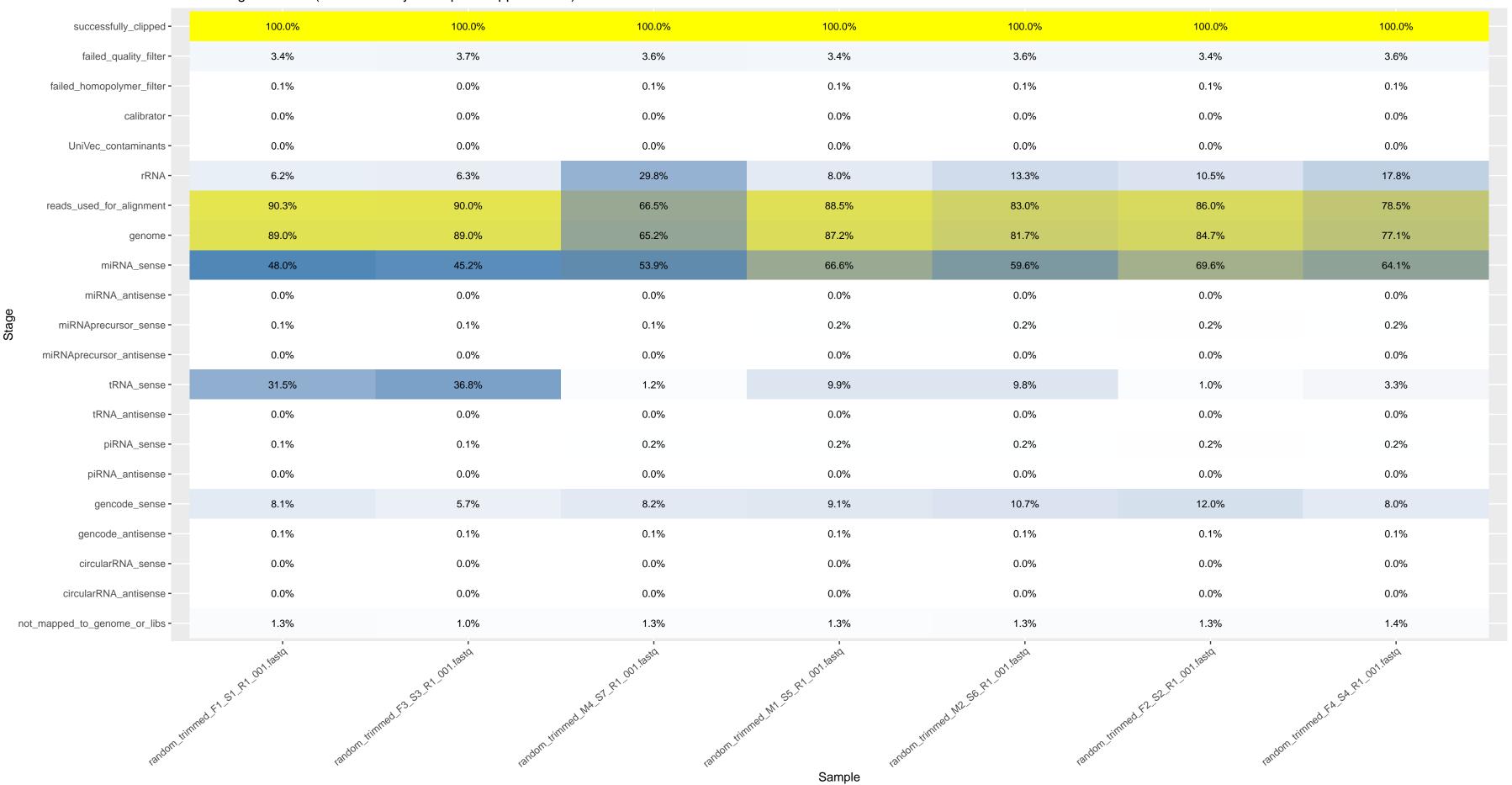
0.75

0.50

0.25

0.00

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



ReadFraction 1.00

0.75

0.50

0.25

0.00

fraction aligned reads (normalised by # non-contaminant reads) reads_used_for_alignment -100.0% 100.0% 100.0% 100.0% 100.0% 100.0% 100.0% 98.5% 98.9% 98.1% 98.5% 98.4% 98.4% genome -98.2% miRNA_sense -53.2% 50.3% 81.1% 75.2% 71.7% 81.0% 81.6% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% miRNA_antisense -0.2% 0.1% 0.2% 0.2% 0.2% 0.3% 0.2% miRNAprecursor_sense -0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% miRNAprecursor_antisense -1.8% 11.2% 1.2% 4.2% tRNA_sense -34.9% 40.9% 11.7% Stage 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% tRNA_antisense -0.1% 0.1% 0.3% 0.2% 0.2% 0.2% 0.2% piRNA_sense -0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% piRNA_antisense gencode_sense -9.0% 6.3% 12.3% 10.3% 12.9% 13.9% 10.1% 0.1% 0.1% 0.2% 0.1% 0.1% 0.1% 0.1% gencode_antisense -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% circularRNA_antisense -1.1% 1.9% 1.8% 1.5% 1.6% 1.5% 1.6% not_mapped_to_genome_or_libs -Sample

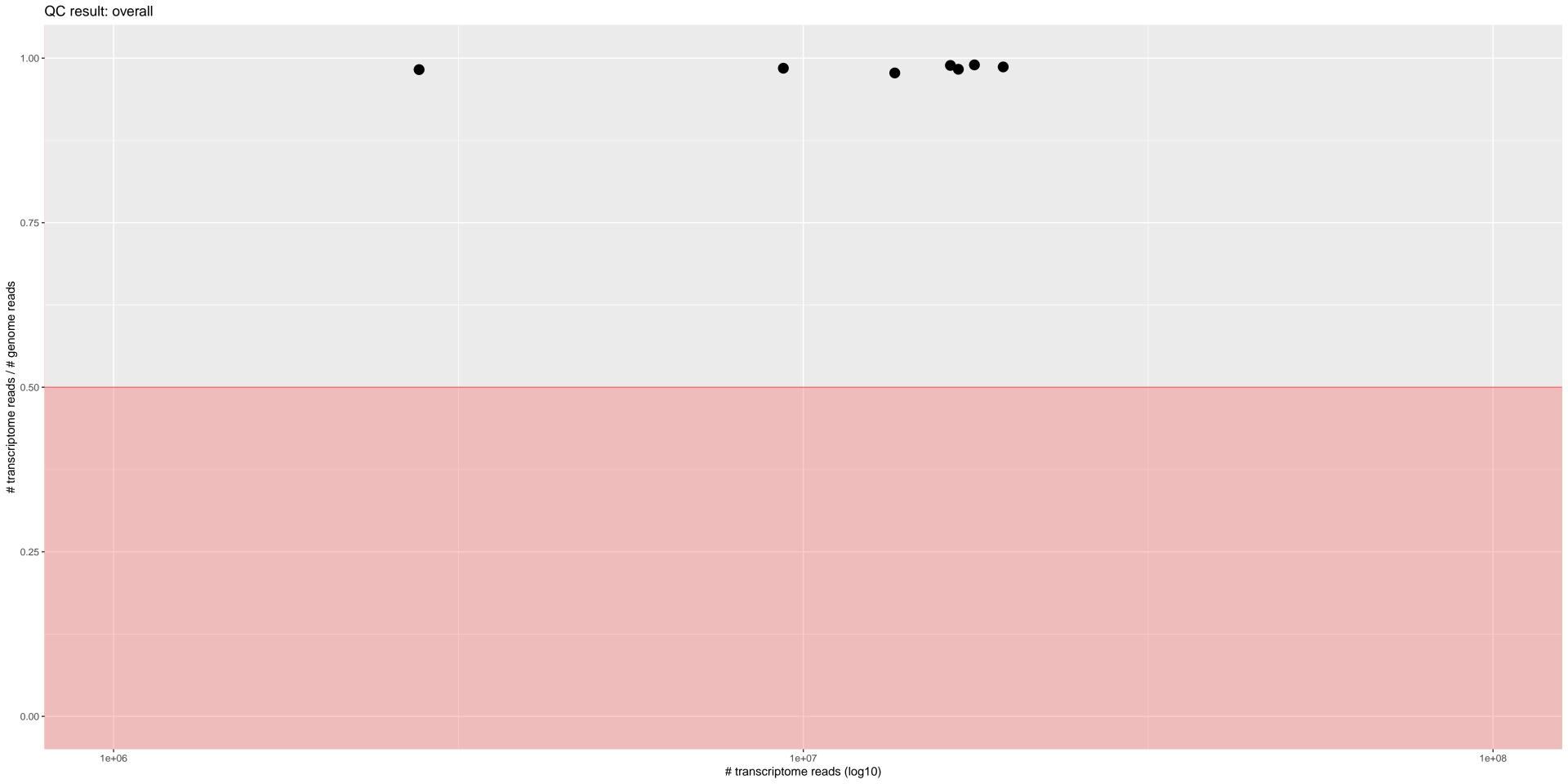
ReadFraction 1.00

0.75

0.50

0.25

0.00



random_trimmed_F4_S4_R1_001.fastq -	22848035	17068724	16779808	0.98	0.01
random_trimmed_F2_S2_R1_001.fastq -	3394690	2822304	2772970	0.98	0.022
random_trimmed_M2_S6_R1_001.fastq -	11842460	9500557	9354740	0.98	0.013
random_trimmed_M1_S5_R1_001.fastq -	23014568	19754120	19489721	0.99	0.007
random_trimmed_M4_S7_R1_001.fastq -	22342653	13883424	13570374	0.98	0.012
random_trimmed_F3_S3_R1_001.fastq -	20412449	17888332	17704591	0.99	0.009
random_trimmed_F1_S1_R1_001.fastq -	[18889418]	[16524189]	16340753	0.99	0.006
	InputReads	GenomeReads	_{TranscriptomeReads}	TranscriptomeGenomeRatio	_{TranscriptomeComplexity}

Biotypes: distributions, raw read-counts miRNA tRNA snoRNA retained_intron misc_RNA protein_coding -Mt_tRNA piRNA processed_transcript antisense lincRNA -Mt_rRNA nonsense_mediated_decay snRNA scaRNA sense_intronic -TEC ribozyme processed_pseudogene unprocessed_pseudogene non_coding biotype vaultRNA sense_overlapping transcribed_unprocessed_pseudogene transcribed_processed_pseudogene macro_IncRNA non_stop_decay sRNA unitary_pseudogene rRNA -3prime_overlapping_ncrna -IG_C_gene -IG_V_gene -TR_V_gene polymorphic_pseudogene exogenous_genomes pseudogene transcribed_unitary_pseudogene -TR_V_pseudogene -TR_C_gene -IG_V_pseudogene -IG_J_gene -IG_C_pseudogene -1e+06 1e+07 1e+01 1e+05 1e+02 1e+03 1e+04 1e+00 readCount

Biotypes: distributions, normalised

