

Table S1. Overview on resources, files and terms.

All references here are based on Homo sapiens.

Program for alignment	STAR	STAR	STAR	Bowtie2	Bowtie2	Bowtie2	BBMap
Fasta file	mt.trans.hu.miRtRNA.111.primary.fa	Homo_sapiens.GRCh38.111.dna.primary_assembly.fa	mte.trans.hu.GRCh38.111.primary.fa	m2_miRtRNA.fasta	Homo_sapiens.GRCh38.111.dna.primary_assembly.fa	r_star_pirbase_gold.fasta	m2_miRtRNA.fasta
Index folder	star2711x111HUmt	star2711x111HUpm	star2711x111HUmt	bt2_mt	bt2_111HU	bt2_pir	bb_mt
GTF file	mt.Homo_sapiens.miRtRNA.gtf	Homo_sapiens.GRCh38.111.mirbase.gtf	mte.Homo_sapiens.GRCh38.111.gtf	no gtf	mt.Homo_sapiens.miRtRNA.gtf (for QualiMap)	no gtf	no gtf
Program parameter	outFilterMismatchNmax 0, outFilterMultimapNmax 2, outSAMmultNmax 1, quantMode TranscriptomeSAM.	outFilterMismatchNmax 0, outFilterMultimapNmax 2, outSAMmultNmax 1, quantMode TranscriptomeSAM.	outFilterMismatchNmax 0, outFilterMultimapNmax 2, outSAMmultNmax 1, quantMode TranscriptomeSAM.	--end-to-end	--local	--local	no special features used (global)
Program to quantify	a) Salmon b) Samtools idxstats	a) Samtools idxstats	a) Salmon b) Samtools idxstats	a) Samtools idxstats	a) Samtools idxstats ** b) Qualimap count	a) Samtools idxstats	a) Samtools idxstats
Result acronyms	a) sts b) stm	a) pmm	a) ** b) mte **	a) btm	a) chr ** b) btq	a) pi	a) bbm
Result folder name	03star1out	03star2out	03star3out	04bt21out	04bt22out	04bt23out	05bbm1out
Quantification output file(s)	a) quant.sf b) mcounts.tsv	a) mcounts.tsv	a) mcounts.tsv	a) mcounts.tsv	a) mcounts.tsv ** b) qm.111HUmt.tsv	a) mcounts.tsv	a) mcounts.tsv
Reference features	2653 mirbase microRNAs, 260 tRNAs	1852 premature microRNAs	39 gene_biotype items with now 4114450 (v113) elements	2653 mirbase microRNAs, 260 tRNAs	39 gene_biotype items with now 4114450 (v113) elements	19222 pirbase small RNAs	2653 mirbase microRNAs, 260 tRNAs
Result id type	ENST - extra ENST names for micro/tRNAs (will be translated by R functions to a microRNA [mirbase] or tRNA name [tRNA database])	regular ENST name of premature microRNAs	regular ENST name of all features included in standard Homo_sapiens.GRCh38.111	mirbase name	chromosome and contig names respectively ENSG micro/tRNA name	pirbase name	mirbase name
Script function name	staroutA	staroutB	staroutC	bt2outA	bt2outB	bt2outC	bbmoutA
Support file for R import	namelist.txt	namelist.txt	namelist.txt	namelist.txt	namelist.txt	namelist.txt	namelist.txt

Note :

- 1) Not every aligner is used in all three script files.
- 2) ** : not used here.