

Supplementary File S8, Table S1

Comparison		Count number	Count number obtained
		from simulation	from mt_R find
Filename	stimulated-file-1	25165	25165
	stimulated-file-2	26740	26740
	stimulated-file-3	26328	26328
	stimulated-file-4	28058	28058
	Total count	106291	106291
Bio type	mt_rRNA	7182	7182
	mt_tRNA	71568	71568
	Non protein-coding	7252	7252
	Protein coding	20289	20289
	Total count	106291	106291

Table S2

Mitochondrial gene	Start position	End position	Strand
tRNA-Phe	577	647	Heavy
mtSSU rRNA	648	1601	Heavy
tRNA-Val	1602	1670	Heavy
mtLSU rRNA	1671	3229	Heavy
tRNA-Leu	3230	3304	Heavy
ND1	3307	4262	Heavy
tRNA-Ile	4263	4331	Heavy
tRNA-Gln	4329	4400	Light
tRNA-Met	4402	4469	Heavy
ND2	4470	5511	Heavy
tRNA-Trp	5512	5579	Heavy
tRNA-Ala	5587	5655	Light
tRNA-Asn	5657	5729	Light
tRNA-Cys	5761	5826	Light
tRNA-Tyr	5826	5891	Light
COI	5904	7445	Heavy
tRNA-Ser1	7446	7514	Light
tRNA-Asp	7518	7585	Heavy
COII	7586	8269	Heavy
tRNA-Lys	8295	8364	Heavy
ATP8	8366	8572	Heavy
ATP6	8527	9207	Heavy
COIII	9207	9990	Heavy
tRNA-Gly	9991	10058	Heavy
ND3	10059	10404	Heavy
tRNA-Arg	10405	10469	Heavy
ND4L	10470	10766	Heavy

ND4	10760	12137	Heavy
tRNA-His	12138	12206	Heavy
tRNA-Ser2	12207	12265	Heavy
tRNA-Leu2	12266	12336	Heavy
ND5	12337	14148	Heavy
ND6	14149	14673	Light
tRNA-Glu	14674	14742	Light
CytB	14747	15887	Heavy
tRNA-Thr	15888	15953	Heavy
tRNA-Pro	15956	16023	Light

Table S3

Gene	Acronym	Type	Criteria
tRNA	tRF-1	tRF-1	Mt-sRNAs mapping to 3' end of rRNA or protein-coding genes preceding a mitochondrial tRNA gene.
	tRF-2	tRNA-half-5'	1) The sequence is longer than or equal to a half of the total gene length, and the sequence spans the 5' half of a tRNA gene. 2) Sequence start position is ± 3 nt from the tRNA gene start position.
	tRF-4	tRNA-half-3'	1) The sequence is longer than or equal to a half of the total gene length, and the sequence spans the 3' half of a tRNA gene. 2) Sequence end position is ± 3 nt from the tRNA gene end position.
	tRF-5	tRF-5'	1) The sequence is shorter than a half of the total gene length. 2) Sequence start position is ± 3 nt from the tRNA gene start position.
	tRF-3	tRF-3'	1) The sequence is shorter than a half of the total gene length. 2) Sequence end position is ± 3 nt from the tRNA gene end position.
	tRF-6	i-tRF-5	1) The sequence is shorter than a half of the total gene length. 2) Sequence start position is within 5' half of tRNA, and it is not within a range ± 3 nt from the tRNA gene start position.
	tRF-7	i-tRF-3	1) The sequence is shorter than a half of the total gene length. 2) Sequence start position is within 3' half of tRNA, and its end

position is not within a range ± 3 nt from the tRNA gene end position.

protein coding/rRNA	5H	5prime-half	1) Sequence length is greater than or equal to half the length of total gene length and sequence spans the 5' half of gene boundary. 2) Sequence start position is ± 3 from the gene end position.
	3H	3prime-half	1) Sequence length is greater than or equal to half the length of total gene length and sequence spans the 3' half of gene boundary 2) Sequence end position is ± 3 from the gene start position.
	5p	5prime	Sequence end position is ± 3 from the gene end position.
	3p	3prime	Sequence start position is ± 3 from the gene start position.
	i-5p	i-5prime	Sequence end position is not in ± 3 from the gene start position and is within 5' half of gene length.
	i-3p	i-3prime	Sequence start position is within 3' half of gene and not ± 3 from the gene start position.

Table S4

Species	Abbreviation
<i>Homo sapiens</i>	hsa
<i>Danio rerio</i>	dre
<i>Mus musculus</i>	mmu
<i>Ratus norvegicus</i>	rno
<i>Xenopus</i> sp.	xen
<i>Gallus gallus</i>	gga

Table S5

Strand	Region	% distribution	Type	sub-distribution	Orientation	Substitutions	Length
H	28	15	itRF-5, itRF-3 and	15 %	sense	no	15-35
	genes		randomly fragments				
	tRNA	40	tRNA-half-3	7.5%	sense	no	half the length of mature tRNA
			tRF-1	7.5%	sense	no	16-21
			tRF-5	10 %	sense	yes	18-22
			tRF-3	7.5%	sense	no	15-20
			tRNA-half-5	7.5%	sense	yes	half the length of mature tRNA
	protein-	20	random	15	sense	no	15-22
	coding			5	anti-sense	no	22-25
	rRNA	20	random	15	sense	no	15-24
				5	anti-sense	no	18-23
L	random location	5	coding	5	sense	no	15-35

Table S6

Total no. of sequences	Length of sequence (range)	Strand	Distribution	Region	Orientation	Substitutions
16	75-150	H	1	non- coding	sense	no
			6	coding	sense	no
			4	coding	anti-sense	yes
		L	5	coding	sense	no

Figure S1

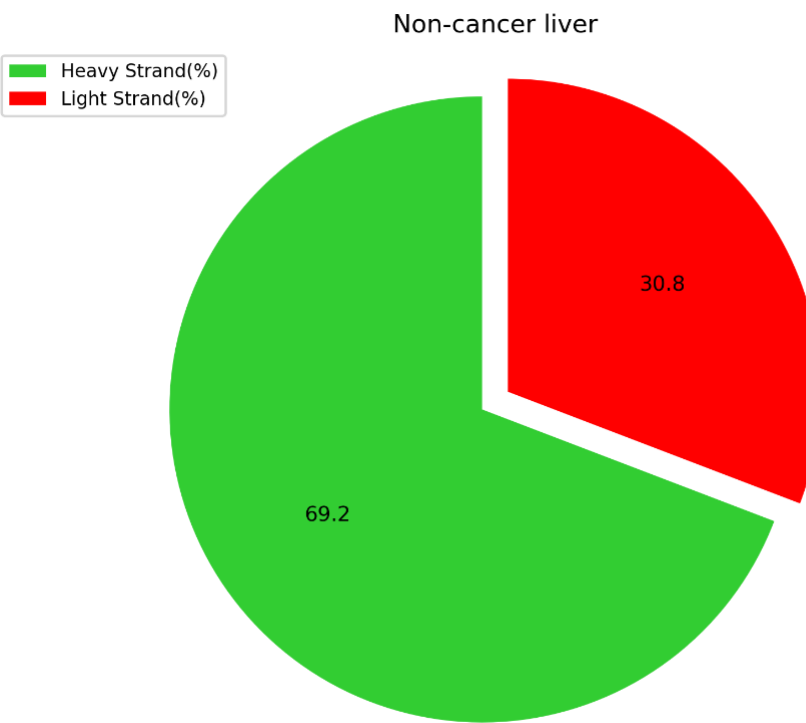
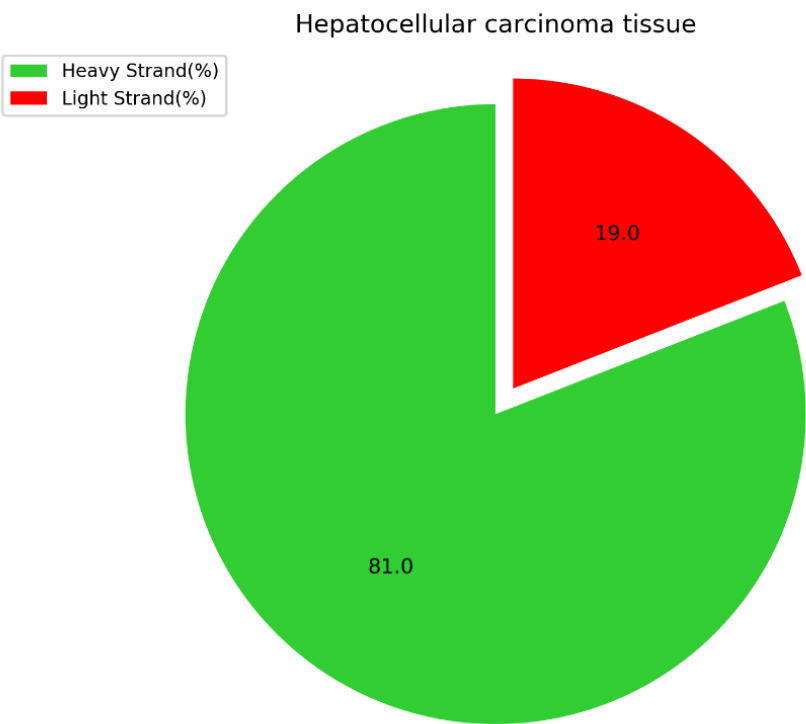


Figure S2

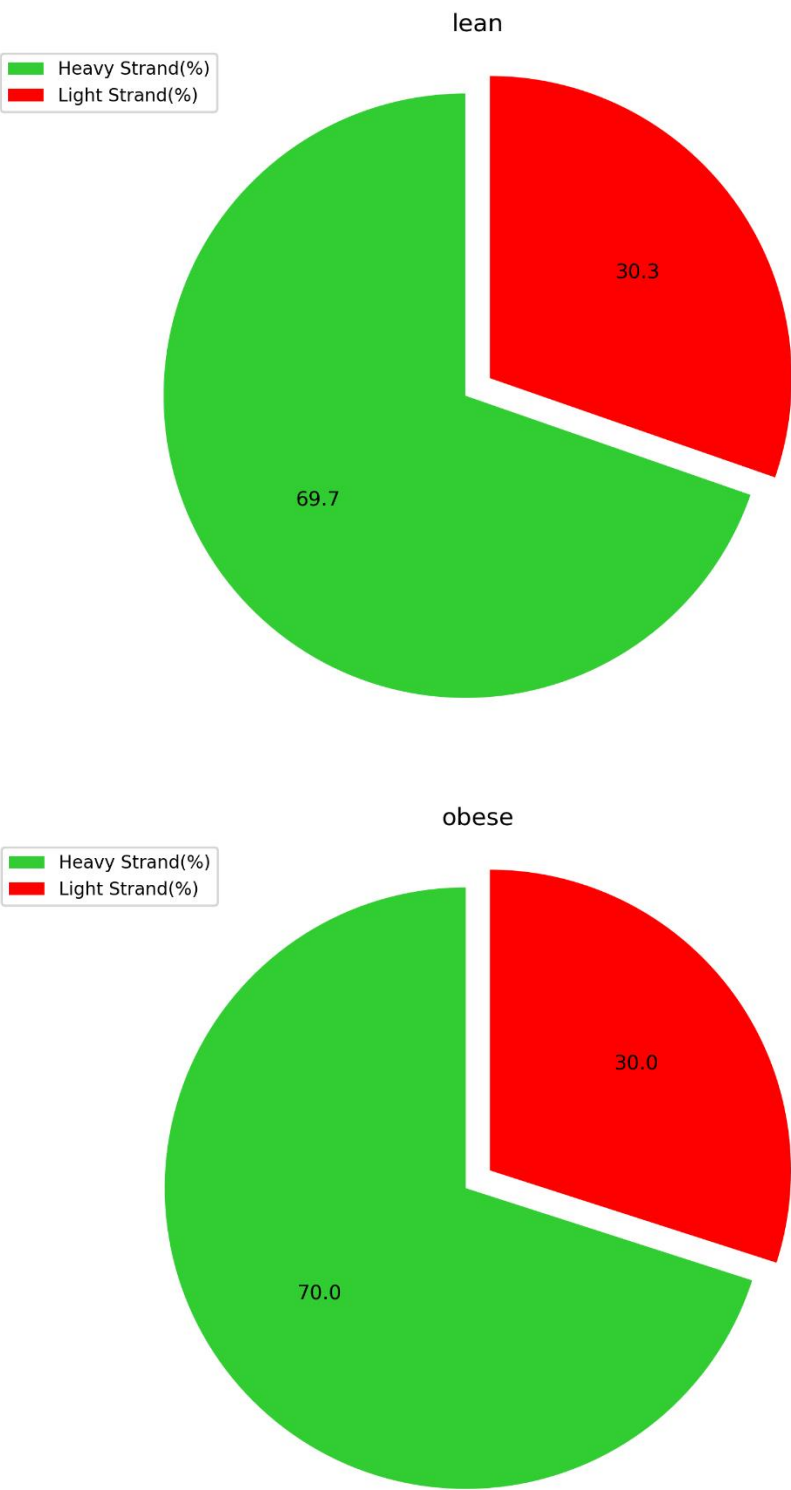


Figure S3

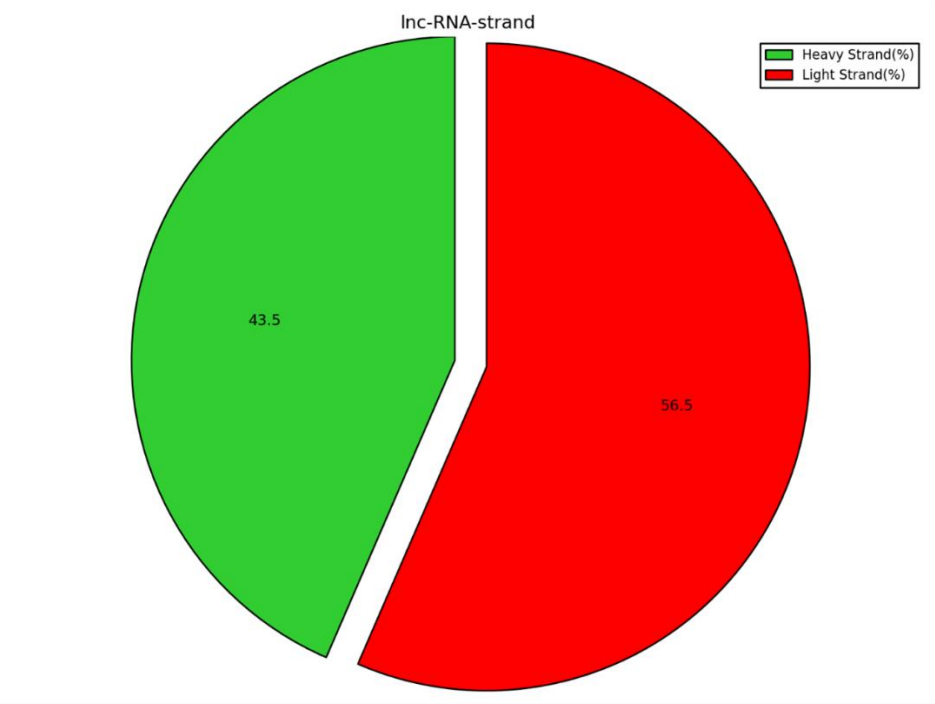


Figure S4A

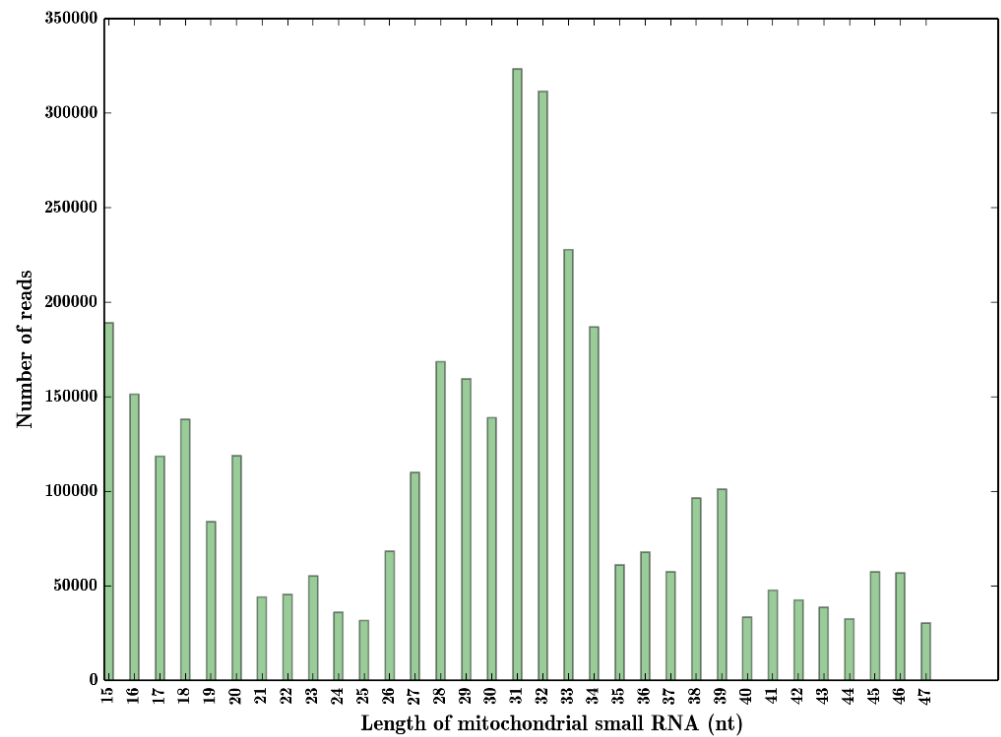


Figure S4B

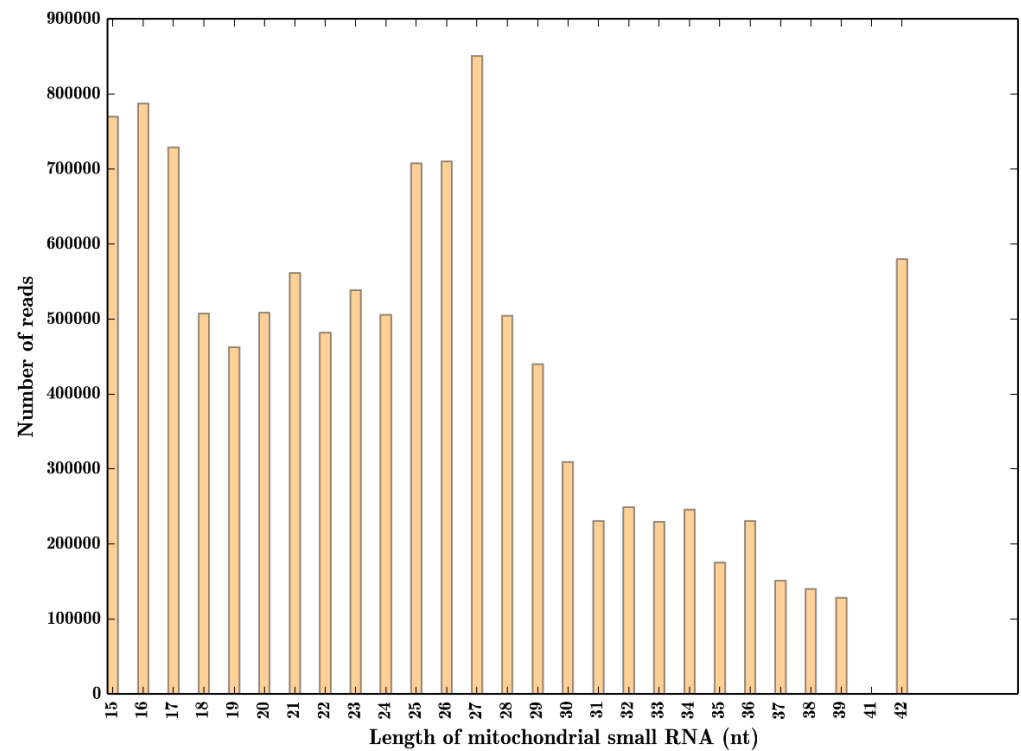


Figure S4C

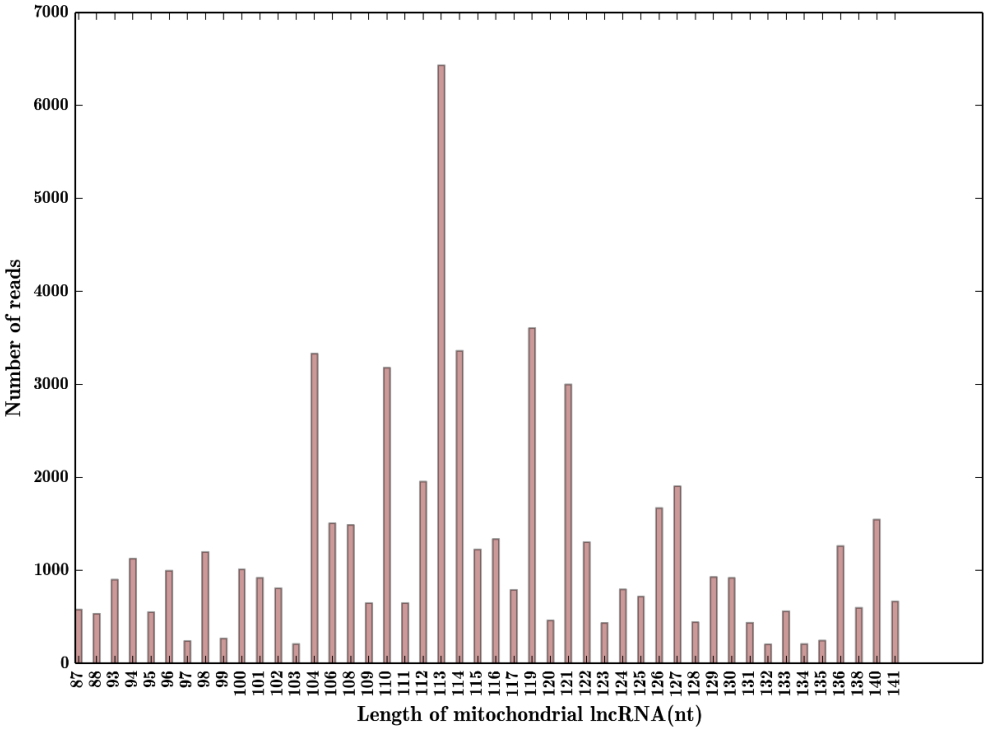


Figure S5A

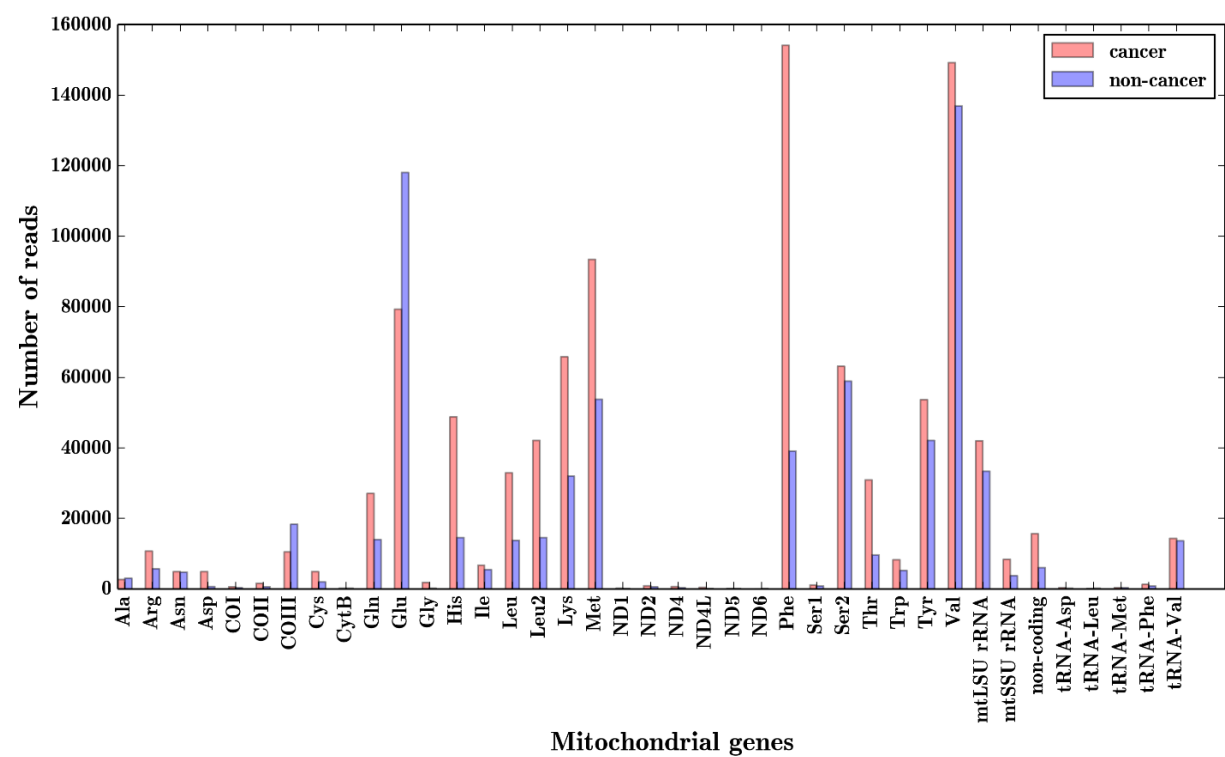


Figure S5B

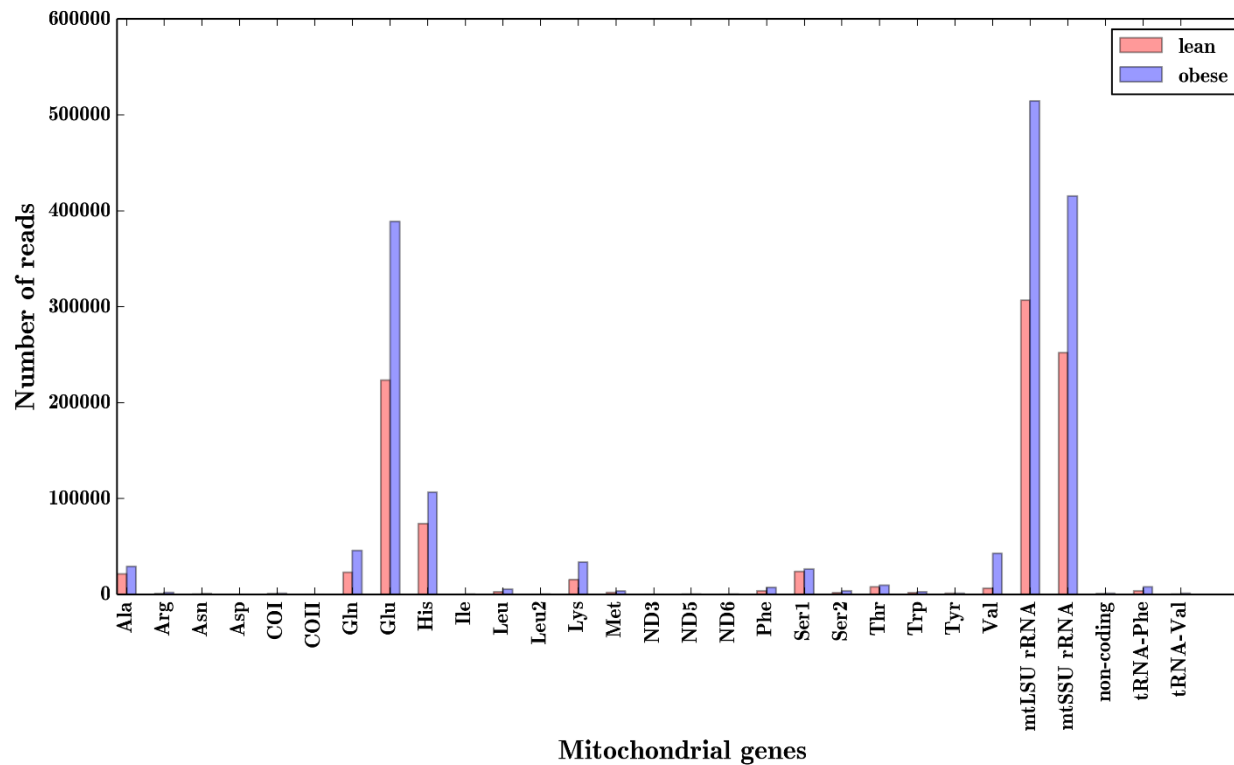


Figure S5C

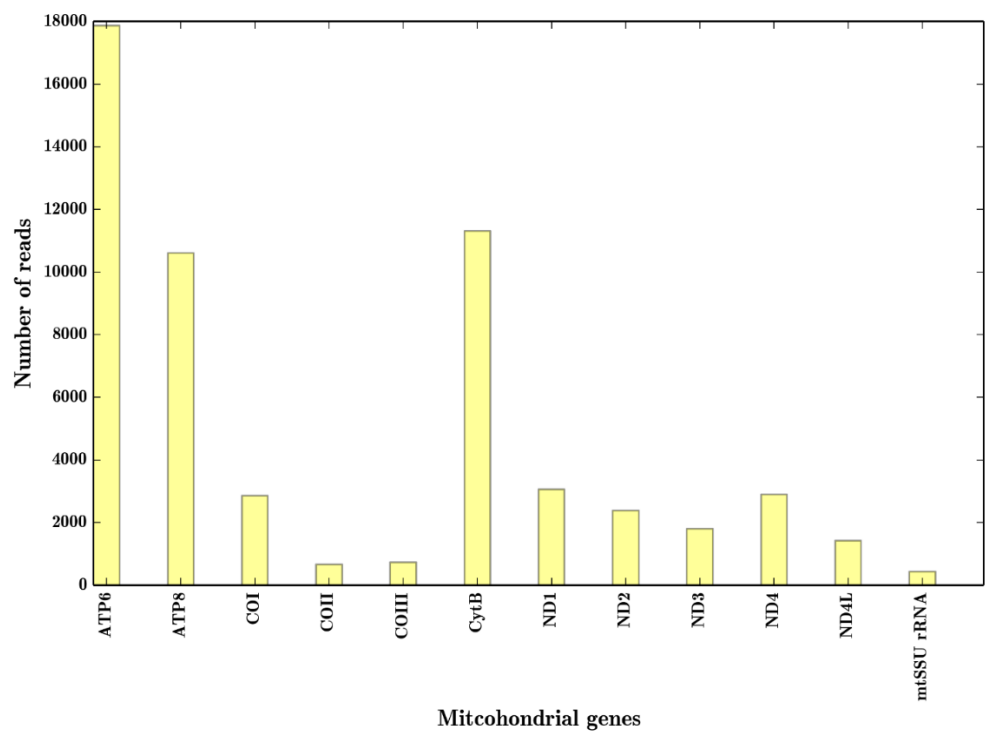


Figure S6

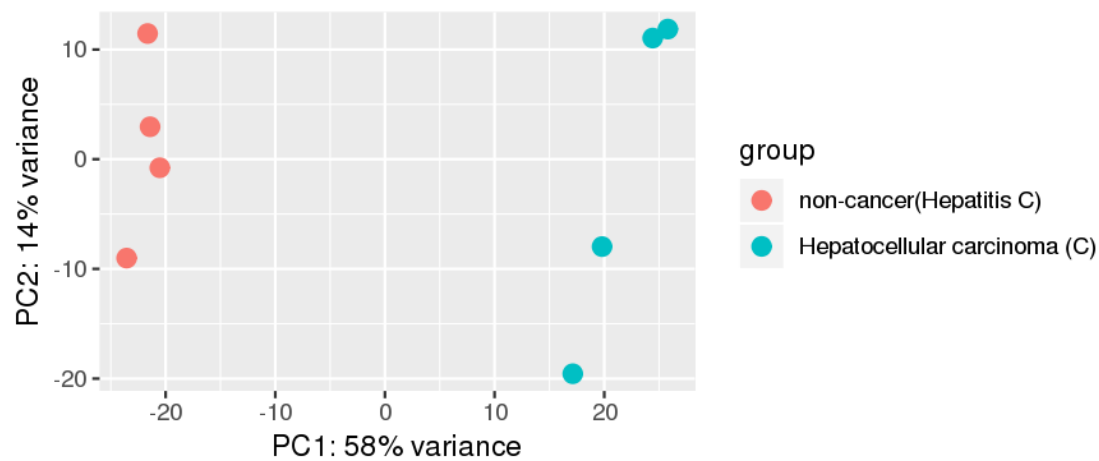


Figure S7

