

Supplemental Table 2a. Transfer RNAs in the mitochondrial genome of *Citrullus lanatus*.

Gene	AA	Anticodon	Origin	Start	End
trnC	Cys	ACA	cp <sup>5</sup>	153988	154060
trnC	Cys	GCA	mt <sup>1</sup>	78204	78274
trnC	Cys	GCA	mt <sup>1</sup>	121267	121339
trnD	Asp	GTC	cp <sup>5</sup>	170502	170575
trnE	Glu	TTC	mt <sup>1</sup>	130201	130272
trnF	Phe	GAA	cp <sup>5</sup>	140379	140451
trnF	Phe	GAA	mt <sup>1</sup>	287216	287289
ψ trnfM	Met	- - - <sup>4</sup>	cp <sup>6</sup>	56341	56414
trnfM	Met	CAT	mt <sup>1</sup>	151918	151991
trnG	Gly	GCC	mt <sup>1</sup>	45547	45618
trnG	Gly	GCC	mt <sup>1</sup>	238845	238916
trnH	His	GTG	cp <sup>2</sup>	131226	131299
trnH	His	GTG	cp <sup>5</sup>	322701	322774
trnI	Ile	CAT <sup>3</sup>	mt <sup>1</sup>	155601	155681
trnK	Lys	TTT	mt <sup>1</sup>	227590	227662
trnM	Met	CAT	cp <sup>2</sup>	50761	50833
trnM	Met	CAT	cp <sup>5</sup>	5346	5418
trnN	Asn	GTT	cp <sup>2</sup>	76361	76432
trnP	Pro	TGG	cp <sup>5</sup>	224476	224550
trnP	Pro	TGG	mt <sup>1</sup>	286845	286919
trnQ	Gln	TTG	mt <sup>1</sup>	44457	44528
trnQ	Gln	TTG	mt <sup>1</sup>	239935	240006
trnS	Ser	GCT	mt <sup>1</sup>	287653	287740
trnS	Ser	TGA	mt <sup>1</sup>	358591	358677
ψ trnV	Val	- - - <sup>4</sup>	cp <sup>6</sup>	359637	359678
trnW	Trp	CCA	cp <sup>5</sup>	224257	224330
trnY	Tyr	GTA	mt <sup>1</sup>	75277	75359

<sup>1</sup>native mitochondrial tRNA

<sup>2</sup>intact chloroplast-like tRNA not embedded within larger region of chloroplast DNA

<sup>3</sup>C assumed to be post-transcriptionally modified to lysidine, which pairs with A, not G

<sup>4</sup>anticodon ambiguous or undetermined

<sup>5</sup>intact tRNA embedded within larger region of chloroplast DNA, possibly functional

<sup>6</sup>degenerate tRNA embedded within larger region of chloroplast DNA

Supplemental Table 2b. Transfer RNAs in the mitochondrial genome of *Cucurbita pepo*.

Gene	AA	Anticodon	Origin	Start	End
trnC	Cys	GCA	mt <sup>1</sup>	960030	960100
trnE	Glu	TTC	mt <sup>1</sup>	265505	265576
trnF	Phe	GAA	mt <sup>1</sup>	772934	773007
trnfM	Met	CAT	mt <sup>1</sup>	29561	29634
trnG	Gly	GCC	mt <sup>1</sup>	174750	174821
trnH	His	GTG	cp <sup>2</sup>	267364	267437
trnI	Ile	CAT <sup>3</sup>	mt <sup>1</sup>	873779	873859
trnK	Lys	TTT	mt <sup>1</sup>	837609	837681
trnM	Met	CAT	cp <sup>2</sup>	169697	169769
trnN	Asn	GTT	cp <sup>2</sup>	958219	958290
trnP	Pro	TGG	mt <sup>1</sup>	773199	773273
trnQ	Gln	TTG	mt <sup>1</sup>	517723	517794
trnY	Tyr	GTA	mt <sup>1</sup>	957149	957231
trnC	Cys	GCA	cp <sup>5</sup>	307922	307993
trnD	Asp	GTC	cp <sup>5</sup>	704568	704641
trnD	Asp	GTC	cp <sup>5</sup>	741975	742048
trnE	Glu	TTC	cp <sup>5</sup>	304824	304896
ψ trnE	Glu	--- <sup>4</sup>	cp <sup>6</sup>	741510	741570
trnF	Phe	GAA	cp <sup>5</sup>	11874	11946
ψ trnF	Phe	--- <sup>4</sup>	cp <sup>6</sup>	729196	729269
trnfM	Met	CAT	cp <sup>5</sup>	299903	299978
trnI	Ile	CAT	cp <sup>5</sup>	610481	610554
ψ trnL	Leu	CAA	cp <sup>6</sup>	12063	12130
trnL	Leu	CAA	cp <sup>5</sup>	766547	766627
trnM	Met	CAT	cp <sup>5</sup>	8036	8108
trnP	Pro	TGG	cp <sup>5</sup>	682940	683013
ψ trnP	Pro	TGG	cp <sup>6</sup>	966947	967017
trnQ	Gln	TTG	cp <sup>5</sup>	701050	701121
trnS	Ser	GGA	cp <sup>5</sup>	14267	14357
trnS	Ser	TGA	cp <sup>5</sup>	22546	22640
ψ trnS	Ser	GGA	cp <sup>6</sup>	292522	292621
ψ trnS	Ser	TGA	cp <sup>6</sup>	300640	300743
trnS	Ser	GCT	cp <sup>5</sup>	701979	702066
ψ trnV	Val	--- <sup>4</sup>	cp <sup>6</sup>	161629	161670
trnW	Trp	CCA	cp <sup>5</sup>	967163	967236
ψ trnY	Tyr	GTA	cp <sup>6</sup>	304956	305034
ψ trnY	Tyr	GTA	cp <sup>6</sup>	741640	741727

<sup>1</sup>native mitochondrial tRNA

<sup>2</sup>intact chloroplast-like tRNA not embedded within larger region of chloroplast DNA

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