

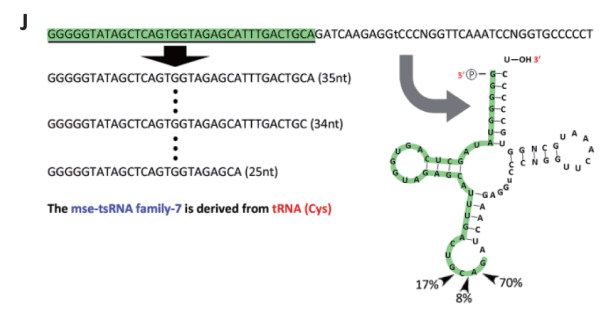
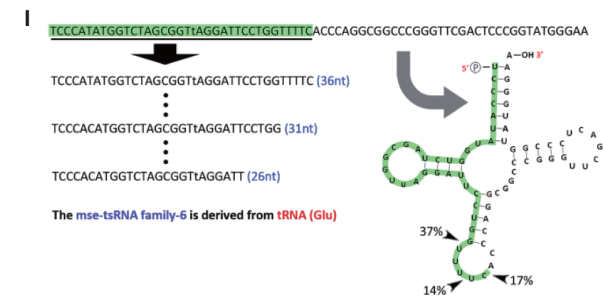
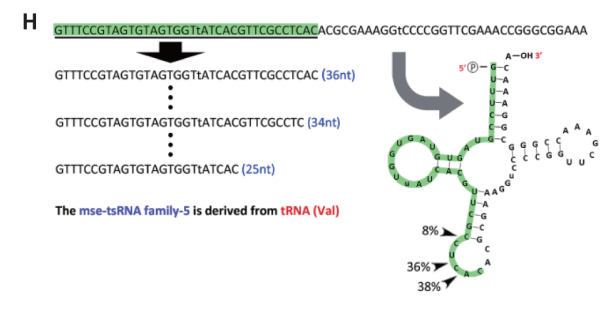
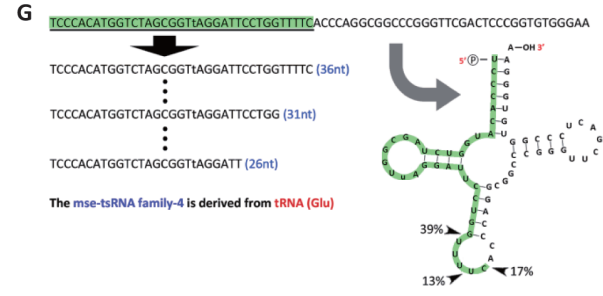
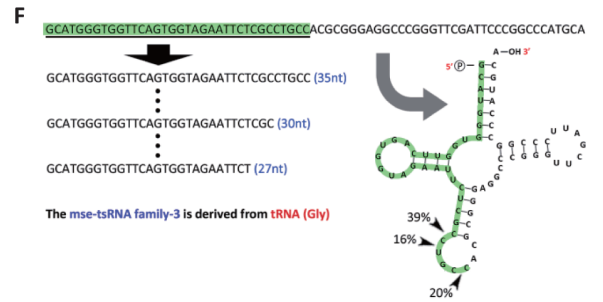
A	Sequence(5'-3') mse-tsRNA family-3	length(bp)	reads		
			sperm	testis	uterus
GCATGGGTGGTTCAGTGGTAGAATTCT	27	447	2	0	
GCATGGGTGGTTCAGTGGTAGAATTCTC	28	1926	1	0	
GCATGGGTGGTTCAGTGGTAGAATTCTCG	29	4829	0	0	
GCATGGGTGGTTCAGTGGTAGAATTCTCGC	30	31269	1	0	
GCATGGGTGGTTCAGTGGTAGAATTCTCGCC	31	13135	0	0	
GCATGGGTGGTTCAGTGGTAGAATTCTCGCCT	32	11204	1	0	
GCATGGGTGGTTCAGTGGTAGAATTCTCGCCTG	33	966	1	0	
GCATGGGTGGTTCAGTGGTAGAATTCTCGCCTGC	34	15821	7	0	
GCATGGGTGGTTCAGTGGTAGAATTCTCGCCTGCC	35	389	1	0	
		79986	14	0	

B	mse-tsRNA family-4	length(bp)	reads		
			sperm	testis	uterus
TCCCACATGGTCTAGCGGTTAGGATT	26	1166	14	35	
TCCCACATGGTCTAGCGGTTAGGATTC	27	186	102	11	
TCCCACATGGTCTAGCGGTTAGGATTC	28	344	94	7	
TCCCACATGGTCTAGCGGTTAGGATTCCT	29	215	278	3	
TCCCACATGGTCTAGCGGTTAGGATTCCTG	30	2821	1389	0	
TCCCACATGGTCTAGCGGTTAGGATTCCTGG	31	30068	358	0	
TCCCACATGGTCTAGCGGTTAGGATTCCTGGT	32	7447	54	0	
TCCCACATGGTCTAGCGGTTAGGATTCCTGGTT	33	6472	357	0	
TCCCACATGGTCTAGCGGTTAGGATTCCTGGTTT	34	10270	12	0	
TCCCACATGGTCTAGCGGTTAGGATTCCTGGTTTTC	35	5106	5	0	
TCCCACATGGTCTAGCGGTTAGGATTCCTGGTTTTC	36	13301	1	0	
		77396	2664	56	

C	mse-tsRNA family-5	length(bp)	reads		
			sperm	testis	uterus
GTTTCCGTAGTGTAGTGGTTATCAC	25	180	3	1	
GTTTCCGTAGTGTAGTGGTTATCACG	26	1647	3	2	
GTTTCCGTAGTGTAGTGGTTATCACG	27	585	13	6	
GTTTCCGTAGTGTAGTGGTTATCACGTT	28	484	4	2	
GTTTCCGTAGTGTAGTGGTTATCACGTTTC	29	361	9	2	
GTTTCCGTAGTGTAGTGGTTATCACGTTTCG	30	795	5	0	
GTTTCCGTAGTGTAGTGGTTATCACGTTTCGC	31	6075	9	0	
GTTTCCGTAGTGTAGTGGTTATCACGTTTCGCC	32	5866	28	0	
GTTTCCGTAGTGTAGTGGTTATCACGTTTCGCCT	33	26772	40	0	
GTTTCCGTAGTGTAGTGGTTATCACGTTTCGCCTC	34	28030	29	0	
GTTTCCGTAGTGTAGTGGTTATCACGTTTCGCCTCA	35	1499	1	0	
GTTTCCGTAGTGTAGTGGTTATCACGTTTCGCCTCAC	36	1635	0	0	
		73929	144	13	

D	mse-tsRNA family-6	length(bp)	reads		
			sperm	testis	uterus
TCCCATATGGTCTAGCGGTTAGGATT	26	676	17	9	
TCCCATATGGTCTAGCGGTTAGGATTC	27	92	114	6	
TCCCATATGGTCTAGCGGTTAGGATTC	28	190	109	5	
TCCCATATGGTCTAGCGGTTAGGATTCCT	29	111	441	0	
TCCCATATGGTCTAGCGGTTAGGATTCCTG	30	1144	1954	0	
TCCCATATGGTCTAGCGGTTAGGATTCCTGG	31	12381	666	0	
TCCCATATGGTCTAGCGGTTAGGATTCCTGGT	32	3099	69	0	
TCCCATATGGTCTAGCGGTTAGGATTCCTGGTT	33	2988	508	0	
TCCCATATGGTCTAGCGGTTAGGATTCCTGGTTT	34	4687	5	0	
TCCCATATGGTCTAGCGGTTAGGATTCCTGGTTTTC	35	2485	4	0	
TCCCATATGGTCTAGCGGTTAGGATTCCTGGTTTTC	36	5827	1	0	
		33680	3888	20	

E	mse-tsRNA family-7	length(bp)	reads		
			sperm	testis	uterus
GGGGGTATAGCTCAGTGGTAGAGCA	25	514	0	5	
GGGGGTATAGCTCAGTGGTAGAGCAT	26	37	0	2	
GGGGGTATAGCTCAGTGGTAGAGCATT	27	22	0	8	
GGGGGTATAGCTCAGTGGTAGAGCATTG	28	18	0	0	
GGGGGTATAGCTCAGTGGTAGAGCATTTG	29	113	0	0	
GGGGGTATAGCTCAGTGGTAGAGCATTTGA	30	385	11	1	
GGGGGTATAGCTCAGTGGTAGAGCATTTGAC	31	85	10	0	
GGGGGTATAGCTCAGTGGTAGAGCATTTGACT	32	5401	18	0	
GGGGGTATAGCTCAGTGGTAGAGCATTTGACTG	33	2557	18	0	
GGGGGTATAGCTCAGTGGTAGAGCATTTGACTGC	34	21985	30	0	
GGGGGTATAGCTCAGTGGTAGAGCATTTGACTGCA	35	109	9	0	
		31226	96	16	



Supplementary information, Figure S2 Alignments, statistics and tRNA origin of mse-tsRNA families 3-7 in mature sperm, testis and uterus. **(A-E)** Alignments and statistics of mse-tsRNA families 3-7 in mature sperm, testis and uterus. The top three enriched length for each family were highlighted. **(F-J)** Illustrations showing tRNA origin of mse-tsRNA families 3-7, all these mse-tsRNA families are derived from 5' halves of tRNA. The top three cleavage sites were marked by arrow heads. The preferred length distribution at 30-34 nt and cleavage sites suggested specific nuclease involved in the cleavage, possibly by recognizing the anticodon loops.