

## SUPPLEMENTARY DATA

### SUPPLEMENTARY TABLE AND FIGURE LEGENDS

**Figure S1.** Quantitation of small RNA and miRNA in Optiprep fractions. **(A)** Bioanalyser gel showing RNA trace across the 17 fractions collected from Optiprep velocity gradient centrifugation. Extracted RNA from each fractions were analysed on the Bioanalyser Small RNA chips. **(B)** Line graph showing the concentration of small RNA and miRNA across all fractions ( $n_{F7-10} = 5$ ,  $n_{F1-6, F11-17} = 3$ ). RNA peak is observed at Optiprep Fraction 8. **(C)** Bioanalyser analysis of RNA isolated from Optiprep Fraction 8, 9 and UC exosomes on the small RNA Chips. Exosomes both contain small RNAs between 4 and 100 nucleotide (nt), with enriched small RNAs at 60 nt.

**Figure S2.** Matrix table displaying the correlation values of each samples. Distance mapping of small RNA expression using Euclidean distance metric of Optiprep fractions, ultracentrifugation exosomes (UCexo) samples and GT1-7 neuronal cells. Normalised expression counts are used to generate correlation coefficients by Spearman method.

**Figure S3.** Heatmaps of individual small RNA expression profiles, in respect to **(A)** miRNA, **(B)** piRNA, **(C)** tRNA, **(D)** rRNA, **(E)** snoRNA, **(F)** snRNA, that are analysed in this study. The majority of the heatmaps depict distinct expression profiles for exosome datasets across all RNA biotypes. The expression profiles for GT1-7 neuronal cells showing distinct profiles among other datasets. The degree of abundance level of different small RNA species is represented by a range of colour starting from blue to yellow to red.

**Figure S4.** Matrix table representing top small RNA identified in Optiprep fractions, ultracentrifugation exosomes and GT1-7 neuronal cells. '•' denotes the presence of respective miRNA, rRNA, snoRNA, snRNA, piRNA, and tRNA detected in the datasets. Abbreviations: 'miRNA' – microRNA; 'rRNA' – ribosomal RNA; 'tRNA' – transfer RNA; 'piRNA' – piwi-interacting RNA; 'snRNA' – small nuclear RNA; 'snoRNA' – small nucleolar RNA; 'UCexo' – exosomes from differential ultracentrifugation.

**Figure S5.** Percentage composition of the tRNA isoacceptor type showing abundancy of tRNA-Gly, tRNA-Lys and tRNA-Val. Stacked graph to further display the distribution of amino acid isoacceptor type across all replicates in each dataset.

**Figure S6.** Sequence coverage of tRNA-Gly fragments in exosomes. Nucleotide position of each fragments compared to the full-length tRNA-Gly to a resolution of 18 bps. The vertical axis indicates the number of reads.

**Supplementary Table S1.** Total number of sequencing reads among sample.

**Supplementary Table S2.** Percentage of each RNA biotype across all samples.

## SUPPLEMENTARY MATERIALS AND METHODS

### Small RNA profiling pipeline

The in-house pipeline aims to assess the profiles of small RNA expression. It is based around the commonly used open-source tools which includes BedIntersect from BEDtools and edgeR from Bioconductor. The pipeline is written in python and R language. Before running the pipeline, for this study, genome reference files were prepared and obtained from UCSC (mm10 and repeat elements references), Ensembl (snoRNA, snRNA and protein-coding mRNA references, miRBase (miRNA reference), piRNA Bank (piRNA reference) and Genomic tRNA database (tRNA reference). For small RNA analysis, the reference files were prepared in BED file format for the subsequent use in BEDtools. High quality aligned reads were parsed into the pipeline for profiling small RNA. The pipeline begins at the intersectBed from BEDtools. The aligned reads containing their respective genomic coordinates were intersected with the respective reference files consecutively, after removing the intersected reads.

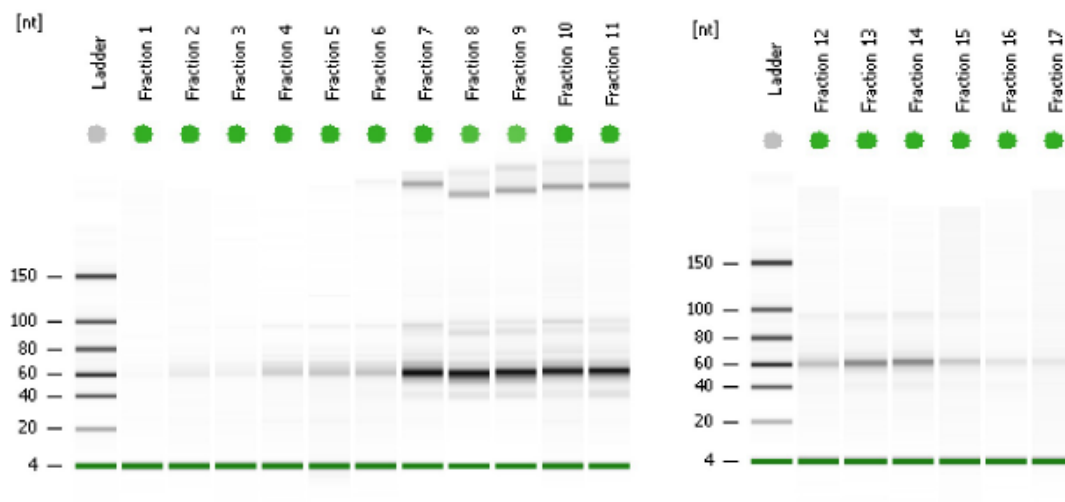
The following intersectBed command line is used in the pipeline:

**intersectBed -f 0.9 -abam ~/aligned-file.bam -b ~/reference.bed -wo > aligned-reference-file.txt**

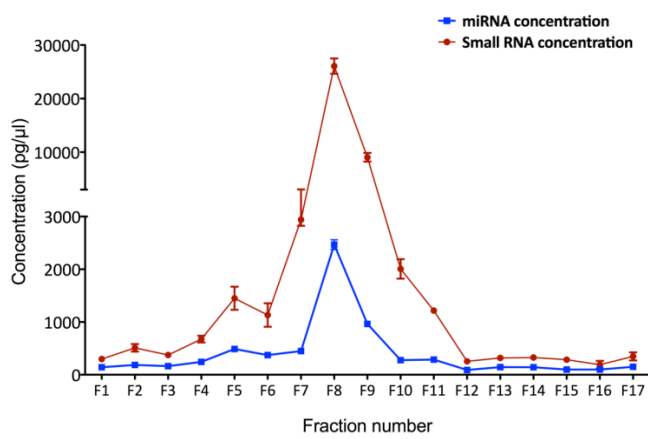
The `-f` option is used to restrict the reported overlaps between aligned reads and references by ensuring 90% of the reads were overlapped in the reference. This is to minimize false positive intersection. By default, bedtools intersect report an overlap between two files as long as there is at least one base pair of overlapping region.

After processing the aligned reads using BEDtools, raw counts of each respective biotype were generated in text files and were further parsed to edgeR for profiling purposes. At the profiling stage, the raw counts were normalised using trimmed mean of M-values. The calculated normalisation factor within edgeR were attained using the `calcNormFactors()` function. Subsequently, these normalisation factors were re-scaled by the mean of the normalised library sizes. After which, the normalised read counts were obtained by dividing raw read counts by re-scaled normalisation factors. The normalised expression values were displayed as counts per million (cpm) and can be further converted to log2 cpm. The normalised expression values were explored using MDS plot in edgeR. See edgeR manual for more details. Within the pipeline, the generated profiling results from edgeR were tabulated and further graphed using 'pheatmap' package and boxplot function in R.

**A**



**B**



**C**

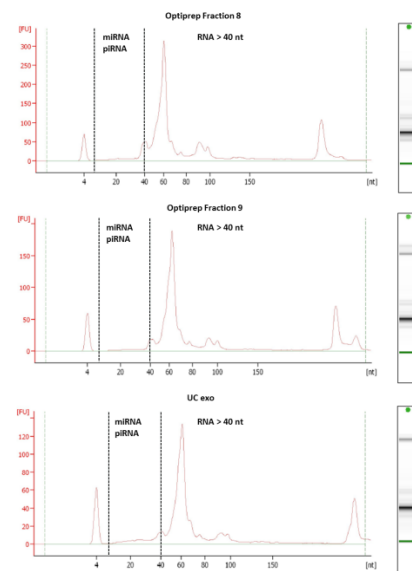


Figure S1

	F7_RP1	F7_RP2	F7_RP3	F7_RP4	F7_RP5	F8_RP1	F8_RP2	F8_RP3	F8_RP4	F8_RP5	F9_RP1	F9_RP2	F9_RP3	F9_RP4	F9_RP5	F10_RP1	F10_RP2	F10_RP3	F10_RP4	F10_RP5	UCexo_RP1	UCexo_RP2	UCexo_RP3	GTcell_RP1	GTcell_RP2	GTcell_RP3
F7_RP1	1.0000	0.9617	0.9619	0.9738	0.9072	0.9158	0.9172	0.9094	0.9149	0.9089	0.9228	0.9217	0.9046	0.9216	0.9103	0.9477	0.9491	0.9504	0.9440	0.9701	0.9300	0.9246	0.9223	0.0129	0.0368	0.0475
F7_RP2	0.9617	1.0000	0.9841	0.9596	0.8861	0.8979	0.9117	0.9056	0.8944	0.8867	0.9033	0.9202	0.9004	0.9017	0.8922	0.9317	0.9655	0.9613	0.9204	0.9697	0.9247	0.9213	0.9156	0.0051	0.0588	0.0541
F7_RP3	0.9619	0.9841	1.0000	0.9606	0.8891	0.9133	0.9239	0.9223	0.9087	0.9011	0.9149	0.9279	0.9163	0.9145	0.9048	0.9357	0.9694	0.9672	0.9249	0.9691	0.9268	0.9272	0.9183	0.0301	0.0296	0.0327
F7_RP4	0.9738	0.9596	0.9606	1.0000	0.8999	0.9152	0.9163	0.9098	0.9172	0.9091	0.9271	0.9200	0.9032	0.9222	0.9057	0.9568	0.9474	0.9443	0.9479	0.9679	0.9257	0.9230	0.9210	0.0249	0.0336	0.0379
F7_RP5	0.9072	0.8861	0.8891	0.8999	1.0000	0.8810	0.8890	0.8797	0.8804	0.8897	0.8805	0.8849	0.8851	0.8791	0.8825	0.8969	0.8849	0.8926	0.8853	0.8968	0.8875	0.8898	0.8825	0.0551	0.0823	0.1089
F8_RP1	0.9158	0.8979	0.9133	0.9152	0.8810	1.0000	0.9767	0.9755	0.9926	0.9661	0.9781	0.9593	0.9524	0.9793	0.9659	0.9039	0.9097	0.9149	0.8933	0.9125	0.9488	0.9635	0.9490	0.0702	0.0186	0.0067
F8_RP2	0.9172	0.9117	0.9239	0.9163	0.8890	0.9767	1.0000	0.9837	0.9731	0.9664	0.9640	0.9743	0.9639	0.9647	0.9644	0.9006	0.9256	0.9247	0.8929	0.9152	0.9578	0.9690	0.9599	0.0071	0.0426	0.0598
F8_RP3	0.9094	0.9056	0.9223	0.9098	0.8797	0.9755	0.9837	1.0000	0.9723	0.9611	0.9559	0.9672	0.9648	0.9599	0.9538	0.8913	0.9209	0.9234	0.8814	0.9081	0.9448	0.9626	0.9447	0.0165	0.0299	0.0556
F8_RP4	0.9149	0.8944	0.9087	0.9172	0.8804	0.9926	0.9731	0.9723	1.0000	0.9675	0.9787	0.9581	0.9483	0.9796	0.9665	0.9061	0.9059	0.9122	0.8948	0.9104	0.9457	0.9587	0.9455	0.0716	0.0234	0.0035
F8_RP5	0.9089	0.8867	0.9011	0.9091	0.8897	0.9661	0.9664	0.9611	0.9675	1.0000	0.9645	0.9546	0.9444	0.9605	0.9584	0.9040	0.9015	0.9039	0.8962	0.9049	0.9416	0.9472	0.9433	0.0537	0.0108	0.0110
F9_RP1	0.9228	0.9033	0.9149	0.9271	0.8805	0.9781	0.9640	0.9559	0.9787	0.9645	1.0000	0.9542	0.9391	0.9768	0.9572	0.9210	0.9127	0.9137	0.9121	0.9187	0.9425	0.9475	0.9422	0.0890	0.0419	0.0209
F9_RP2	0.9217	0.9202	0.9279	0.9200	0.8849	0.9593	0.9743	0.9672	0.9581	0.9546	0.9542	1.0000	0.9594	0.9562	0.9531	0.9057	0.9306	0.9396	0.8976	0.9222	0.9475	0.9547	0.9479	0.0027	0.0513	0.0535
F9_RP3	0.9046	0.9004	0.9163	0.9032	0.8851	0.9524	0.9639	0.9648	0.9483	0.9444	0.9391	0.9594	1.0000	0.9384	0.9367	0.8882	0.9168	0.9183	0.8848	0.9052	0.9328	0.9444	0.9323	0.0211	0.0653	0.0840
F9_RP4	0.9216	0.9017	0.9145	0.9222	0.8791	0.9793	0.9647	0.9599	0.9796	0.9605	0.9768	0.9562	0.9384	1.0000	0.9573	0.9174	0.9113	0.9144	0.9050	0.9197	0.9433	0.9504	0.9439	0.0813	0.0294	0.0091
F9_RP5	0.9103	0.8922	0.9048	0.9057	0.8825	0.9659	0.9644	0.9538	0.9665	0.9584	0.9572	0.9531	0.9367	0.9573	1.0000	0.8917	0.9057	0.9030	0.8842	0.9093	0.9392	0.9483	0.9401	0.0428	0.0031	0.0298
F10_RP1	0.9477	0.9317	0.9357	0.9568	0.8969	0.9039	0.9006	0.8913	0.9061	0.9040	0.9210	0.9057	0.8882	0.9174	0.8917	1.0000	0.9328	0.9342	0.9690	0.9523	0.9148	0.9084	0.9120	0.0575	0.0072	0.0044
F10_RP2	0.9491	0.9655	0.9694	0.9474	0.8849	0.9097	0.9256	0.9209	0.9059	0.9015	0.9127	0.9306	0.9168	0.9113	0.9057	0.9328	1.0000	0.9761	0.9193	0.9664	0.9260	0.9252	0.9187	0.0118	0.0483	0.0560
F10_RP3	0.9504	0.9613	0.9672	0.9443	0.8926	0.9149	0.9247	0.9234	0.9122	0.9039	0.9137	0.9296	0.9183	0.9144	0.9030	0.9342	0.9761	1.0000	0.9179	0.9693	0.9344	0.9270	0.9162	0.0092	0.0459	0.0555
F10_RP4	0.9440	0.9204	0.9249	0.9479	0.8853	0.8933	0.8929	0.8814	0.8948	0.8962	0.9121	0.8976	0.8848	0.9050	0.8842	0.9690	0.9193	0.9179	1.0000	0.9435	0.9088	0.8994	0.9074	0.0356	0.0165	0.0168
F10_RP5	0.9701	0.9697	0.9691	0.9679	0.8968	0.9125	0.9152	0.9081	0.9104	0.9049	0.9187	0.9222	0.9052	0.9197	0.9093	0.9523	0.9664	0.9693	0.9435	1.0000	0.9269	0.9204	0.9197	0.0366	0.0166	0.0214
UCexo_RP1	0.9300	0.9247	0.9268	0.9257	0.8875	0.9488	0.9578	0.9448	0.9457	0.9416	0.9425	0.9475	0.9328	0.9433	0.9392	0.9148	0.9260	0.9244	0.9088	0.9269	1.0000	0.9848	0.9844	0.0271	0.0301	0.0365
UCexo_RP2	0.9246	0.9213	0.9272	0.9230	0.8898	0.9635	0.9690	0.9626	0.9587	0.9472	0.9475	0.9547	0.9444	0.9504	0.9483	0.9084	0.9252	0.9270	0.8994	0.9204	0.9848	1.0000	0.9842	0.0211	0.0341	0.0511
UCexo_RP3	0.9223	0.9156	0.9183	0.9210	0.8825	0.9490	0.9599	0.9447	0.9455	0.9433	0.9422	0.9479	0.9323	0.9439	0.9401	0.9120	0.9187	0.9162	0.9074	0.9197	0.9844	0.9842	1.0000	0.0310	0.0227	0.0303
GTcell_RP1	0.0129	0.0051	0.0301	0.0249	0.0551	0.0702	0.0071	0.0165	0.0537	0.0716	0.0537	0.0890	0.0027	0.0211	0.0813	0.0428	0.0575	0.0118	0.0092	0.0366	0.0271	0.0211	0.0310	1.0000	0.8964	0.8780
GTcell_RP2	0.0368	0.0588	0.0296	0.0336	0.0823	0.0186	0.0426	0.0299	0.0234	0.0108	0.0419	0.0513	0.0653	0.0294	0.0031	0.0072	0.0483	0.0459	0.0165	0.0166	0.0301	0.0341	0.0227	0.8964	1.0000	0.8556
GTcell_RP3	0.0475	0.0541	0.0327	0.0379	0.1089	0.0067	0.0598	0.0556	0.0035	0.0110	0.0209	0.0535	0.0840	0.0091	0.0298	0.0044	0.0560	0.0555	0.0168	0.0214	0.0365	0.0511	0.0303	0.8780	0.8556	1.0000

Figure S2

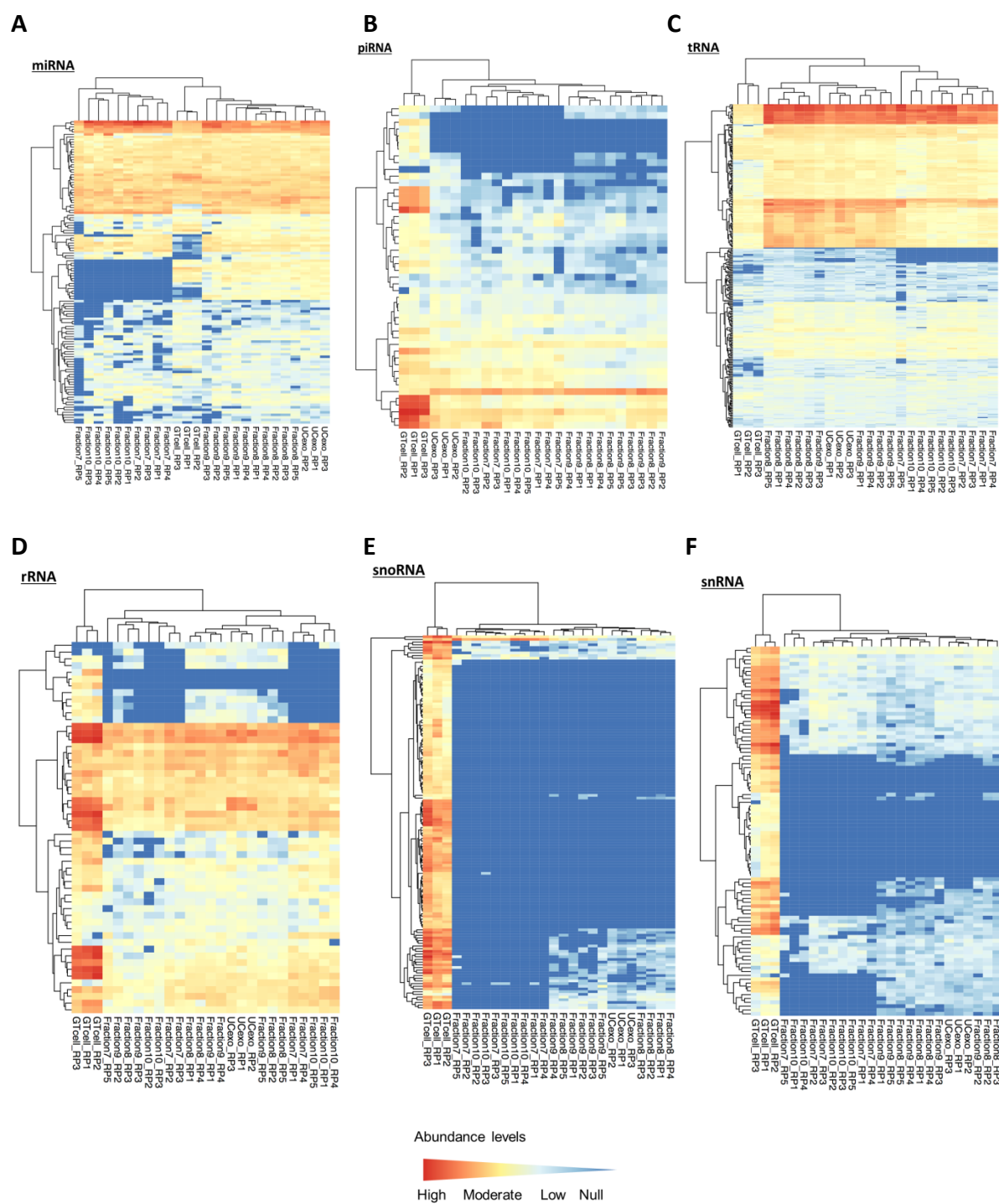


Figure S3

miRNA	F7	F8	F9	F10	UC	GT	rRNA	F7	F8	F9	F10	UC	GT	snoRNA	F7	F8	F9	F10	UC	GT
mmu-let-7a-5p	•			•			n-R5s193						•	Gm26224		•				•
mmu-let-7b-5p	•	•	•	•	•	•	n-R5-8s1	•	•	•	•	•	•	Snord37						•
mmu-let-7c-5p	•	•	•	•	•	•	n-R5s124	•	•	•	•	•	•	Snord45b						•
mmu-let-7d-5p	•	•	•	•	•	•	n-R5s100	•	•	•	•	•	•	Gm22574						•
mmu-let-7e-5p	•	•	•	•	•	•	Gm25018	•	•	•	•	•	•	Snord32a						•
mmu-let-7f-5p	•	•	•	•	•	•	n-R5s113	•	•	•	•	•	•	Gm25789						•
mmu-let-7g-5p		•	•	•	•	•	n-R5s110						•	Gm25894						•
mmu-miR-103-3p		•	•	•	•	•	n-R5s10					•		Snord45c		•				
mmu-miR-125a-5p	•	•	•	•	•		Gm23284	•	•	•	•	•	•	Snord49a						•
mmu-miR-125b-5p	•	•	•	•	•		Gm22109						•	Gm24489						•
mmu-miR-16-5p						•	n-R5s121	•	•	•	•	•	•	Gm24494						•
mmu-miR-191-5p	•	•	•	•			n-R5s149	•	•	•	•	•	•	Rnu3a	•	•	•	•	•	•
mmu-miR-195a-5p						•	n-R5s143	•	•	•	•	•	•	Gm26109		•				
mmu-miR-218-5p				•	•		Gm23647	•	•	•	•	•	•	Gm25506						•
mmu-miR-23a-3p		•	•			•	n-R5s105						•	Snord19		•				
mmu-miR-296-5p	•	•					n-R5s134		•					Gm22489						•
mmu-miR-30b-5p					•	•	n-R5s125	•	•	•	•	•		Snord100						•
mmu-miR-30d-5p		•					Gm25212	•						Snord99		•				
mmu-miR-320-3p	•	•	•	•	•	•	n-R5s104	•		•	•	•	•	Snord2						•
mmu-miR-342-3p	•	•	•			•	n-R5s108	•	•	•	•	•	•	Scarna10		•			•	
mmu-miR-378a-3p	•	•	•	•			n-R5s133	•	•	•	•	•	•	Snord93		•				
mmu-miR-484	•	•	•	•	•		Rn5s	•	•	•	•			Gm24949	•	•	•	•		
mmu-miR-672-5p	•	•	•	•	•		n-R5s102	•	•	•	•	•	•							
mmu-miR-93-5p					•		n-R5s130	•	•	•	•	•	•							
snRNA	F7	F8	F9	F10	UC	GT	piRNA	F7	F8	F9	F10	UC	GT	tRNA	F7	F8	F9	F10	UC	GT
Gm24950		•					mmu_piR_000159						•	tRNA1003-GlyTCC	•	•	•	•	•	•
Gm26331					•		mmu_piR_000362	•		•	•	•		tRNA1006-GlyTCC	•	•	•		•	•
Gm23444		•					mmu_piR_000366	•	•	•				tRNA1009-GlyTCC	•	•	•	•	•	•
Gm22042						•	mmu_piR_000536	•	•	•	•	•		tRNA1012-GlyTCC	•	•	•	•	•	•
Gm23510						•	mmu_piR_000585	•		•	•	•	•	tRNA708-GlyTCC	•	•	•	•	•	•
Gm23971		•					mmu_piR_000616		•	•	•	•	•	tRNA866-AspGTC						•
Gm24260		•			•		mmu_piR_000619						•	tRNA1824-GlyTCC	•	•	•	•	•	•
Gm23849		•					mmu_piR_000620	•	•	•	•	•		tRNA2023-LysCTT	•	•			•	
Rnu1b6		•			•	•	mmu_piR_000622	•	•	•	•	•	•	tRNA103-LysCTT	•		•	•	•	
Gm25189		•			•	•	mmu_piR_000644		•			•		tRNA991-AspGTC						•
Gm26110					•	•	mmu_piR_000935	•	•	•	•	•		tRNA112-GlyCCC						•
Rnu2-10		•			•		mmu_piR_001570						•	tRNA81-LysCTT	•			•		
Rnu11		•					mmu_piR_002435	•			•	•		tRNA83-LysCTT	•	•	•	•	•	
Gm26444					•	•	mmu_piR_002643	•	•	•	•	•	•	tRNA999-LysCTT	•		•		•	
Rnu1b2						•	mmu_piR_003758		•					tRNA109-ValTAC		•	•	•	•	•
Gm25939		•					mmu_piR_003770						•	tRNA110-ValTAC		•	•	•	•	•
Gm23143					•		mmu_piR_004567	•	•	•	•	•		tRNA292-LysCTT	•	•	•	•		•
Gm24871		•			•		mmu_piR_005109						•	tRNA746-GlyTCC	•	•	•	•	•	•
Gm22614						•	mmu_piR_005355	•	•	•	•	•	•	tRNA748-LysCTT	•	•	•	•	•	•
Gm23804						•	mmu_piR_008475					•		tRNA317-GlyCCC						•
Rnu1b1					•	•	mmu_piR_017405	•	•	•	•			tRNA863-LeuTAG	•	•		•		•
Gm25099		•			•		mmu_piR_020492	•	•	•	•	•	•	tRNA562-GlyGCC						•
Gm24830					•	•	mmu_piR_022097	•	•	•	•	•	•	tRNA460-ValTAC		•	•	•	•	•
Gm25313		•	•	•	•	•	mmu_piR_038322	•	•	•	•	•	•							
Rnu5g	•	•	•	•	•	•	mmu_piR_039114						•							
Rnu1a1		•			•	•	mmu_piR_039147						•							
Gm22317						•														
Gm25679					•	•														
Gm26232					•	•														

Figure S4

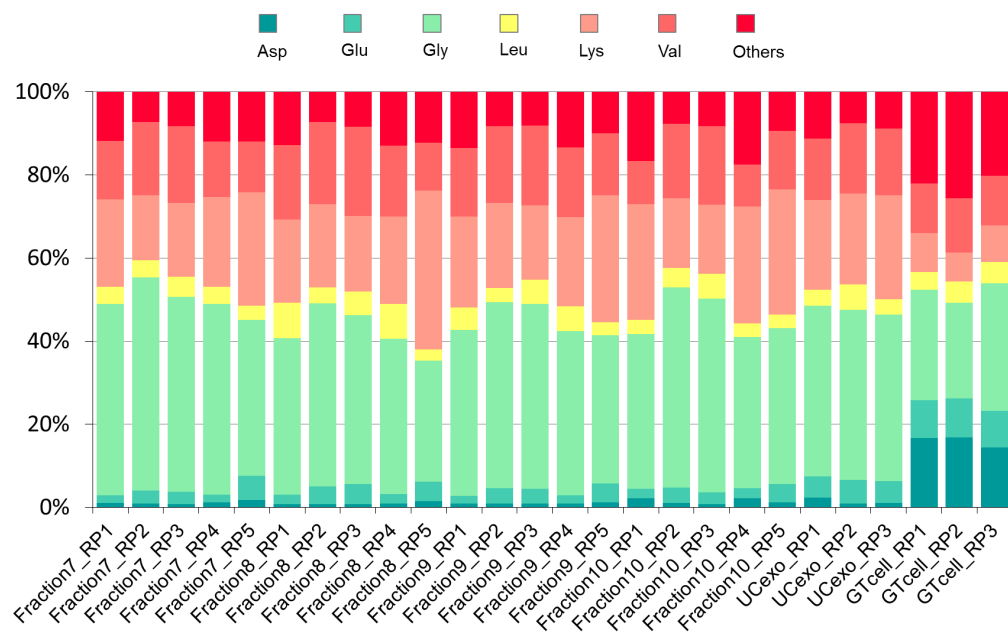


Figure S5

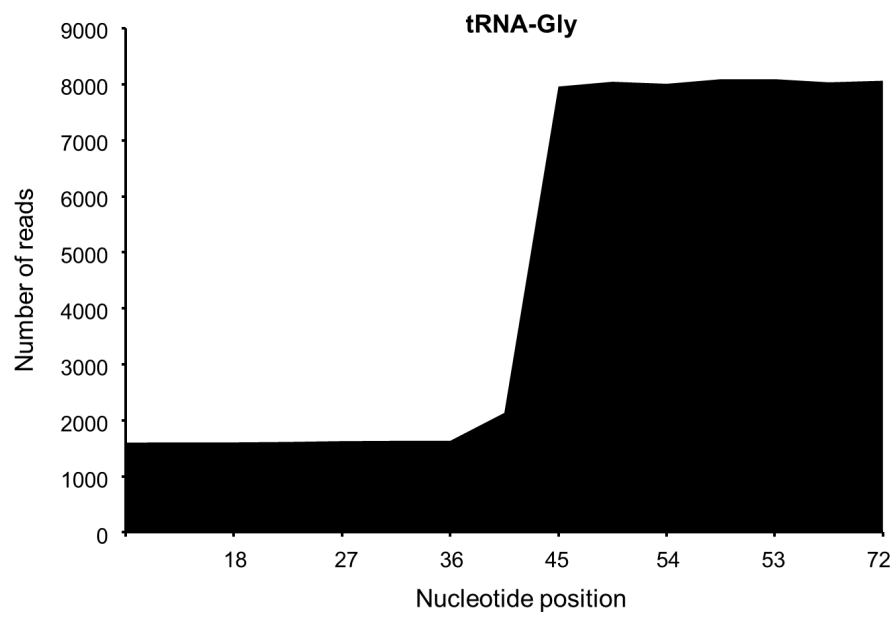


Figure S6



**Supplementary Table S1.** Total number of sequencing reads among samples.

Samples	Reads mapped to genome	miRNA reads	piRNA reads	snRNA reads	snoRNA reads	Protein coding reads	rRNA reads	tRNA reads
<b>Optiprep velocity gradient ultracentrifugation (<i>n</i> = 5)</b>								
Fraction7_RP1	382011	1564	1258	246	287	4418	941	57358
Fraction7_RP2	785860	3342	3680	917	397	7629	1414	254858
Fraction7_RP3	542195	2921	2588	526	233	4351	769	190835
Fraction7_RP4	363080	1475	1228	239	225	2756	989	49269
Fraction7_RP5	50707	483	357	80	79	207	222	10535
Fraction8_RP1	1284511	7770	5152	1261	677	11775	4503	663947
Fraction8_RP2	1032928	6973	5520	1205	441	11572	2176	500674
Fraction8_RP3	884638	4540	3595	878	362	9361	1557	522460
Fraction8_RP4	1000468	6271	4776	927	508	3929	3712	490624
Fraction8_RP5	277266	4310	2232	361	96	1492	1350	98884
Fraction9_RP1	494620	3235	2279	410	254	4579	1732	166780
Fraction9_RP2	529854	2586	2249	546	238	6439	878	161000
Fraction9_RP3	263940	1064	1025	280	123	2389	374	101773
Fraction9_RP4	445116	3017	1978	396	233	2159	1535	159156
Fraction9_RP5	259521	3306	1889	345	209	1710	1098	118162
Fraction10_RP1	422015	1477	1004	166	321	3515	780	20947
Fraction10_RP2	486256	1348	1353	454	240	5956	581	116566
Fraction10_RP3	471190	1237	1339	396	226	4173	428	140984
Fraction10_RP4	329447	1126	774	156	219	2826	608	15876
Fraction10_RP5	353162	3298	2356	460	401	911	1389	129025
<b>Differential ultracentrifugation (<i>n</i> = 3)</b>								
UCexo_RP1	1215157	3700	13249	1781	387	7515	6817	322116
UCexo_RP2	958247	3889	4790	1031	335	8568	2359	513370
UCexo_RP3	799567	5087	7460	937	260	5393	3322	265014
<b>GT1-7 neuronal cell (<i>n</i> = 3)</b>								
GTcell_RP1	970055	7506	20428	30530	13669	4616	3160	9423
GTcell_RP2	999998	7656	19159	37397	8524	6950	3190	7503
GTcell_RP3	814473	4502	12951	22930	20611	3868	3059	11056

**Supplementary Table S2.** Percentage of each RNA biotype across all samples.

Samples	miRNA reads	piRNA reads	snRNA reads	snoRNA reads	Protein coding reads	rRNA reads	tRNA reads	Others
<b>Optiprep velocity gradient ultracentrifugation (<i>n</i> = 5)</b>								
Fraction7_RP1	1.05	0.84	0.17	0.19	2.97	0.63	38.52	55.63
Fraction7_RP2	0.64	0.70	0.18	0.08	1.46	0.27	48.71	47.96
Fraction7_RP3	0.80	0.70	0.14	0.06	1.18	0.21	51.94	44.96
Fraction7_RP4	1.07	0.89	0.17	0.16	2.00	0.72	35.71	59.28
Fraction7_RP5	1.61	1.19	0.27	0.26	0.69	0.74	35.17	60.06
Fraction8_RP1	0.73	0.49	0.12	0.06	1.11	0.43	62.68	34.38
Fraction8_RP2	0.83	0.66	0.14	0.05	1.37	0.26	59.41	37.28
Fraction8_RP3	0.58	0.46	0.11	0.05	1.20	0.20	66.99	30.41
Fraction8_RP4	0.78	0.59	0.11	0.06	0.49	0.46	60.84	36.66
Fraction8_RP5	2.11	1.09	0.18	0.05	0.73	0.66	48.38	46.80
Fraction9_RP1	1.04	0.73	0.13	0.08	1.47	0.55	53.37	42.63
Fraction9_RP2	0.73	0.64	0.15	0.07	1.82	0.25	45.51	50.83
Fraction9_RP3	0.56	0.54	0.15	0.07	1.27	0.20	53.99	43.23
Fraction9_RP4	1.03	0.68	0.14	0.08	0.74	0.53	54.53	42.28
Fraction9_RP5	1.57	0.90	0.16	0.10	0.81	0.52	56.01	39.94
Fraction10_RP1	1.51	1.02	0.17	0.33	3.58	0.79	21.35	71.25
Fraction10_RP2	0.46	0.46	0.15	0.08	2.03	0.20	39.77	56.84
Fraction10_RP3	0.41	0.45	0.13	0.08	1.40	0.14	47.22	50.17
Fraction10_RP4	1.50	1.03	0.21	0.29	3.77	0.81	21.15	71.24
Fraction10_RP5	1.27	0.91	0.18	0.15	0.35	0.54	49.81	46.79
<b>Differential ultracentrifugation (<i>n</i> = 3)</b>								
UCexo_RP1	0.48	1.71	0.23	0.05	0.97	0.88	41.57	54.12
UCexo_RP2	0.48	0.59	0.13	0.04	1.05	0.29	63.03	34.40
UCexo_RP3	0.89	1.30	0.16	0.05	0.94	0.58	46.22	49.86
<b>GT1-7 neuronal cell (<i>n</i> = 3)</b>								
GTcell_RP1	1.38	3.77	5.63	2.52	0.85	0.58	1.74	83.53
GTcell_RP2	1.23	3.07	5.98	1.36	1.11	0.51	1.20	85.54
GTcell_RP3	0.76	2.19	3.88	3.49	0.66	0.52	1.87	86.62

Others: repeat elements