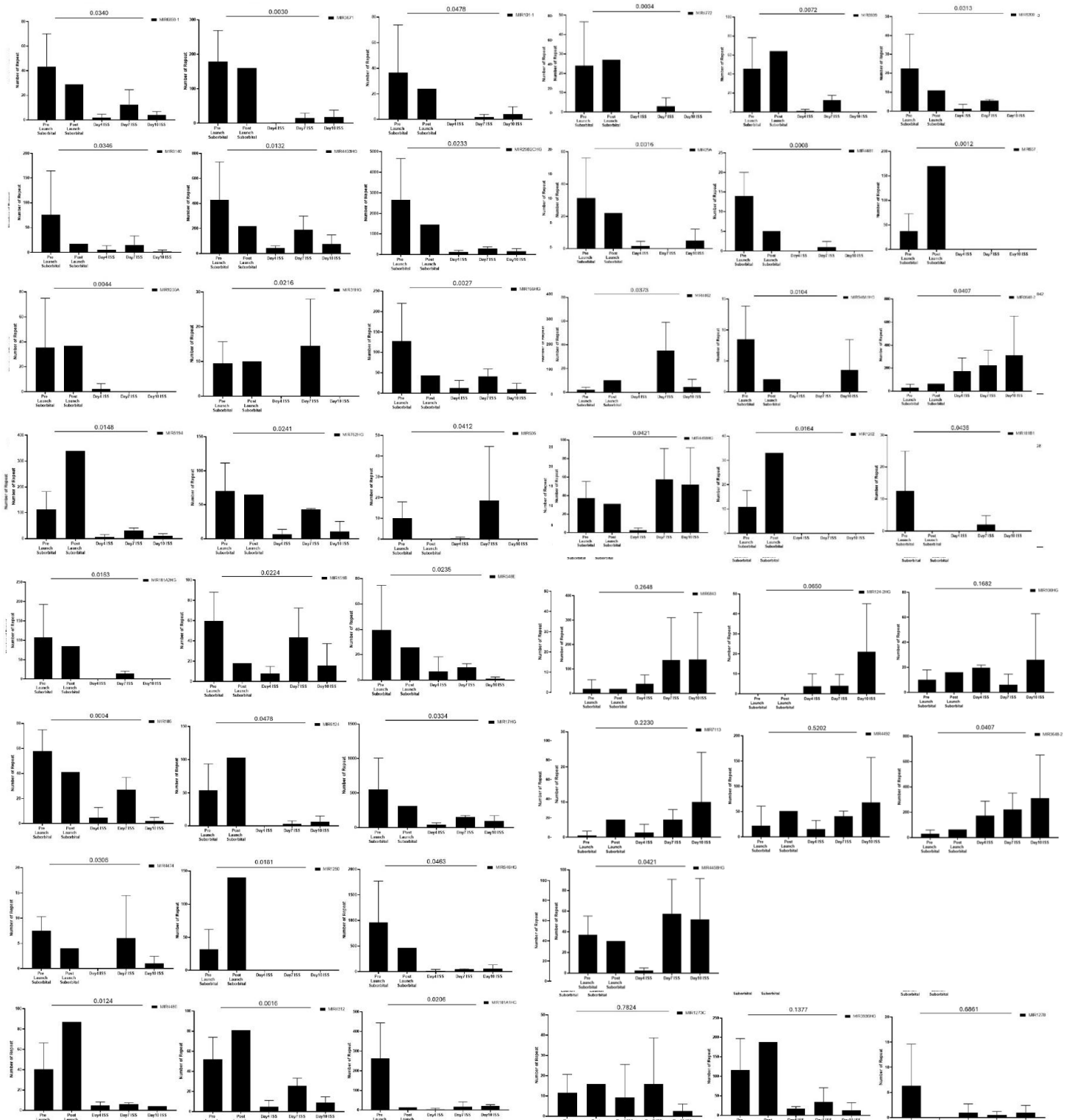
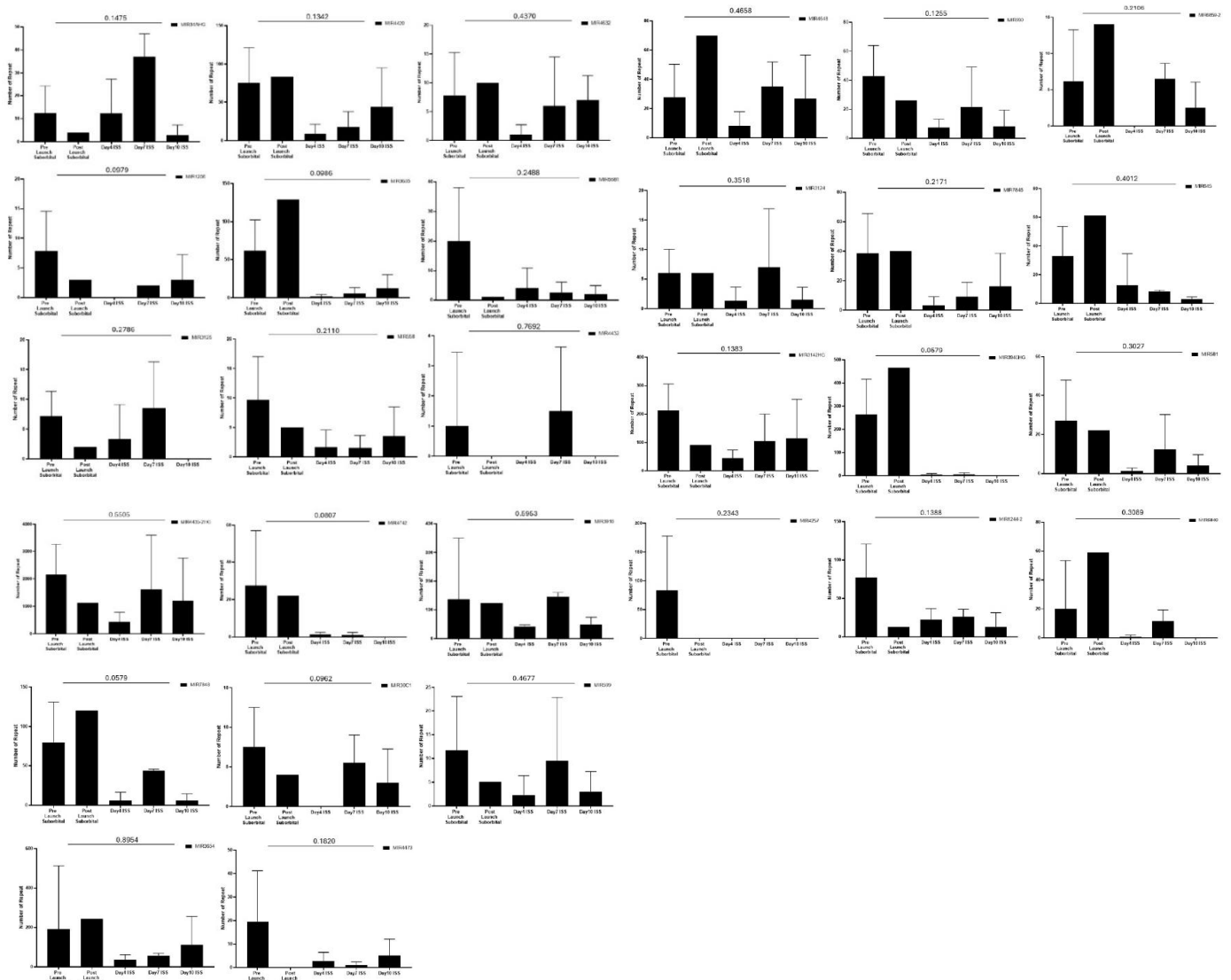
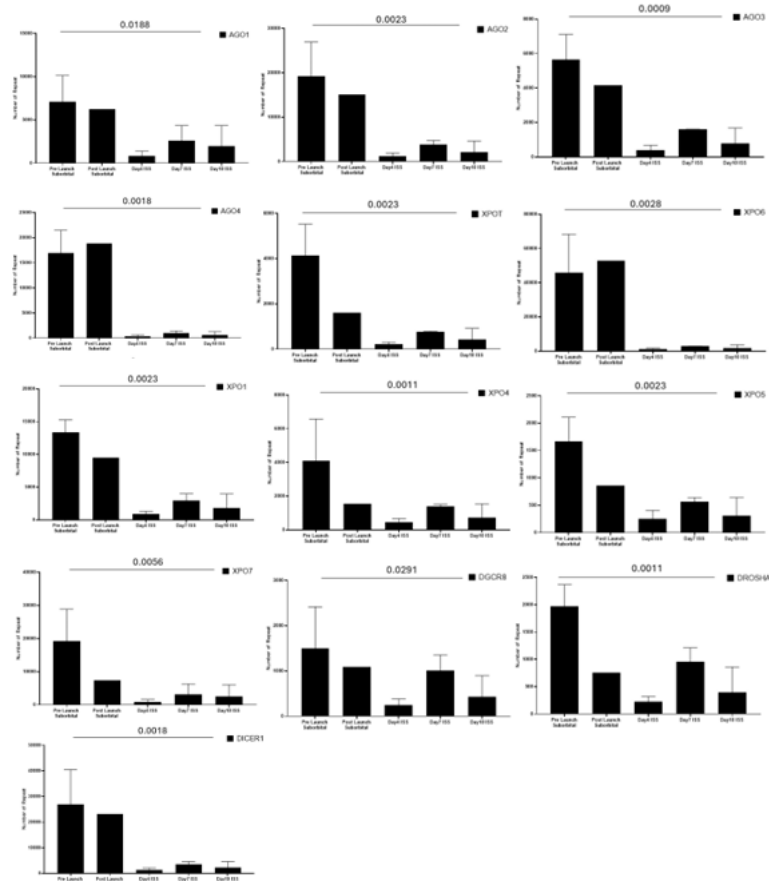


Supplementary Figure





Supplementary Figure 1. Differential expression patterns of miRNAs under microgravity-associated conditions. Bar graphs show miRNAs with variable expression patterns that did not reach statistical significance ($p > 0.05$) following microgravity exposure. Although below the predefined significance threshold, several miRNAs exhibited modest variation and temporal responses across post-flight time points, potentially reflecting subtle microgravity-induced regulatory effects, biological variability, or early adaptive responses to spaceflight. These miRNAs are presented to provide broader context for the transcriptomic changes observed alongside miRNAs exhibiting significant alterations at later time points. The clear separation between control and microgravity-exposed samples indicates coordinated remodeling of the miRNA transcriptomic landscape in association with spaceflight.



Supplementary Figure 2. Suppression of core miRNA biogenesis, RNA export, and RISC-associated genes under orbital microgravity conditions. Bar graph analysis of 13 genes involved in miRNA processing, nuclear-cytoplasmic RNA transport, and RNA-induced silencing complex formation across pre-launch suborbital, post-launch suborbital, and ISS orbital time points. The Argonaute family genes (AGO1, AGO2, AGO3, and AGO4), exportin-related genes (XPO1, XPO4, XPO5, XPO6, XPO7, and XPO7), and core miRNA biogenesis genes (DROSHA, DGCR8, and DICER1) showed significant expression changes across the experimental groups. Statistical significance was accepted at $p < 0.05$.

Supplementary Table S1. RNA quality and sequencing quality-control metrics for samples included in transcriptomic analysis

Sample ID	Sample source	A260/A280	A260/A230	Fluorometric conc. (ng/μL)	RIN	Pre-library QC	Library prep QC	Mreads, fragment	Mreads, R1+R2	Q30 (%)
P1	Uncultured PBMC/peripheral blood-derived RNA	2.07	1.47	34.0	7.7	Pass	Pass	63.1	126.2	85.7
P2	Uncultured PBMC/peripheral blood-derived RNA	1.98	1.01	18.95	6.7	Pass	Pass	58.1	116.2	85.1
P3	Uncultured PBMC/peripheral blood-derived RNA	2.08	0.57	13.25	6.0	Pass	Pass	57.4	114.8	85.7
A12	Uncultured PBMC/peripheral blood-derived RNA	1.34	0.39	1345	5.8	Pass	Pass	85.6	171.2	91.8
A15	Uncultured PBMC/peripheral blood-derived RNA	1.12	0.23	0.87	3.4	Pass	Pass	21.0	42.0	86.4
A16	Uncultured PBMC/peripheral blood-derived RNA	1.28	0.52	4.0	4.4	Pass	Pass	65.9	131.8	90.1
A7	Uncultured PBMC/peripheral blood-derived RNA	1.81	0.62	0.88	5.2	Pass	Pass	71.5	143.0	90.9
H10	Uncultured PBMC/peripheral blood-derived RNA	2.00	0.13	2.5	2.9	Pass	Pass	78.4	156.8	88.2
H11	Uncultured PBMC/peripheral blood-derived RNA	1.95	0.55	1.5	3.1	Pass	Pass	31.5	63.0	88.3
H2	Uncultured PBMC/peripheral blood-derived RNA	2.07	1.45	35.2	7.5	Pass	Pass	91.8	183.6	91.1
H3	Uncultured PBMC/peripheral blood-derived RNA	1.97	1.60	2.43	3.4	Pass	Pass	28.7	57.4	86.4
H4	Uncultured PBMC/peripheral blood-derived RNA	1.96	0.20	19.8	2.9	Pass	Pass	28.9	57.8	87.4
H5	Uncultured PBMC/peripheral blood-derived RNA	1.85	0.15	1.9	3.4	Pass	Pass	15.5	31.0	84.2
H6	Uncultured PBMC/peripheral blood-derived RNA	1.84	0.13	3.61	3.8	Pass	Pass	6.8	13.6	87.5
H7	Uncultured PBMC/peripheral blood-derived RNA	1.90	0.23	1.4	2.8	Pass	Pass	42.8	85.6	89.6
H8	Uncultured PBMC/peripheral blood-derived RNA	1.84	0.62	1.9	3.4	Pass	Pass	32.1	64.2	88.9
H9	Uncultured PBMC/peripheral blood-derived RNA	1.92	0.25	2.9	3.5	Pass	Pass	13.2	26.4	86.8
R12	Uncultured PBMC/peripheral blood-derived RNA	2.01	0.01	0.8	2.1	Pass	Pass	7.2	14.4	81.8
R13	Uncultured PBMC/peripheral blood-derived RNA	1.40	0.02	3.06	2.8	Pass	Pass	93.4	186.8	89.2
R14	Uncultured PBMC/peripheral blood-derived RNA	2.56	0.07	0.85	4.0	Pass	Pass	27.1	54.2	89.5
R8	Uncultured PBMC/peripheral blood-derived RNA	2.05	0.02	0.935	2.3	Pass	Pass	11.8	23.6	82.9