Supplementary Information
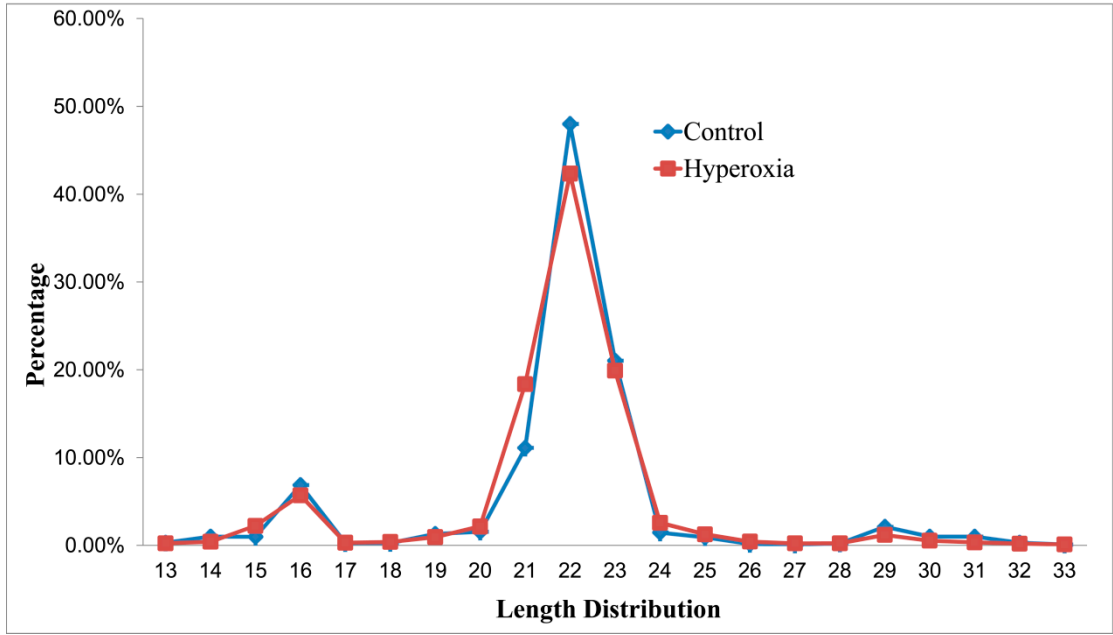

Figure S1. Length distribution and abundance of the sRNAs from hyperoxia model rats and normal control samples. sRNA reads with a length of 22 nt were the most abundant, which accounting for about 50% of total reads, then followed by 23 and 21 nt reads.
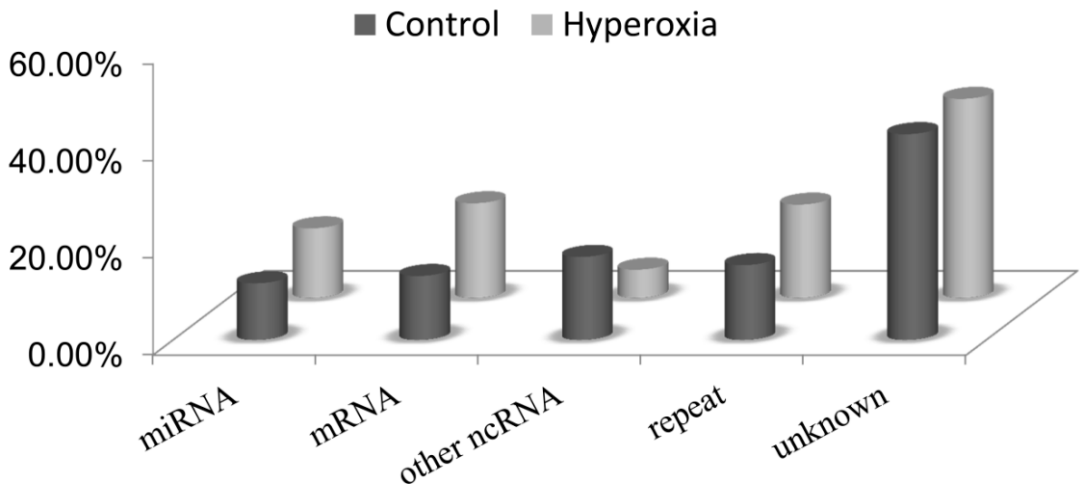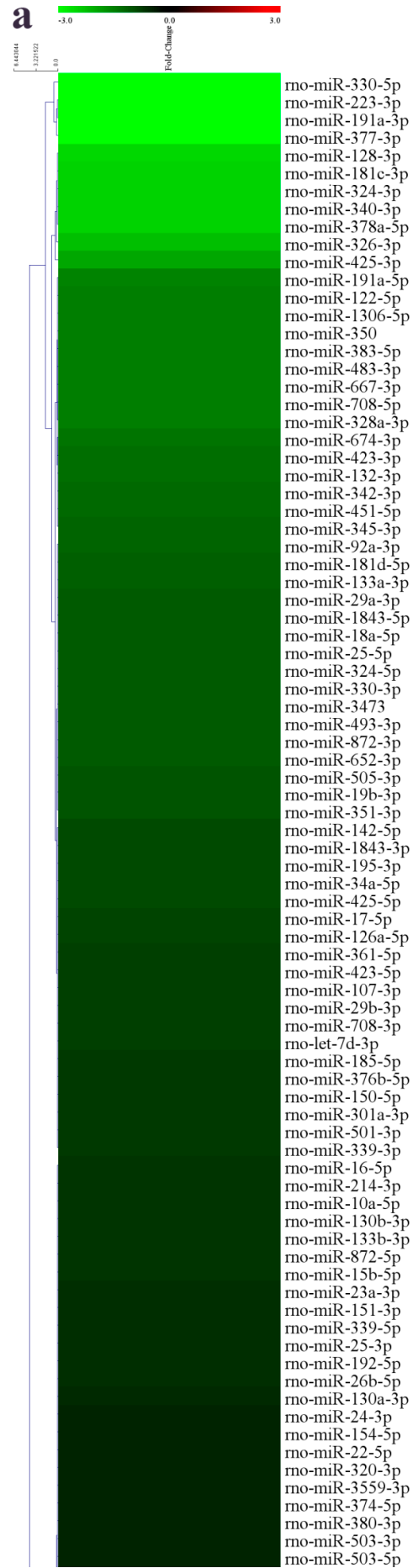

Figure S2. Distribution of different small RNA categories in hyperoxia and control libraries. Sequenced sRNAs were annotated and classified as: Other ncRNA, repeats, mRNA and miRNAs, *et al.*

rno-miR-330-5p
rno-miR-223-3p
rno-miR-191a-3p
rno-miR-377-3p
rno-miR-128-3p
rno-miR-181c-3p
rno-miR-324-3p
rno-miR-340-3p
rno-miR-378a-5p
rno-miR-326-3p
rno-miR-425-3p
rno-miR-191a-5p
rno-miR-122-5p
rno-miR-1306-5p
rno-miR-350
rno-miR-383-5p
rno-miR-483-3p
rno-miR-667-3p
rno-miR-708-5p
rno-miR-328a-3p
rno-miR-674-3p
rno-miR-423-3p
rno-miR-132-3p
rno-miR-342-3p
rno-miR-451-5p
rno-miR-345-3p
rno-miR-92a-3p
rno-miR-181d-5p
rno-miR-133a-3p
rno-miR-29a-3p
rno-miR-1843-5p
rno-miR-18a-5p
rno-miR-25-5p
rno-miR-324-5p
rno-miR-330-3p
rno-miR-3473
rno-miR-493-3p
rno-miR-872-3p
rno-miR-652-3p
rno-miR-505-3p
rno-miR-19b-3p
rno-miR-351-3p
rno-miR-142-5p
rno-miR-1843-3p
rno-miR-195-3p
rno-miR-34a-5p
rno-miR-425-5p
rno-miR-17-5p
rno-miR-126a-5p
rno-miR-361-5p
rno-miR-423-5p
rno-miR-107-3p
rno-miR-29b-3p
rno-miR-708-3p
rno-let-7d-3p
rno-miR-185-5p
rno-miR-376b-5p
rno-miR-150-5p
rno-miR-301a-3p
rno-miR-501-3p
rno-miR-339-3p
rno-miR-16-5p
rno-miR-214-3p
rno-miR-10a-5p
rno-miR-130b-3p
rno-miR-133b-3p
rno-miR-872-5p
rno-miR-15b-5p
rno-miR-23a-3p
rno-miR-151-3p
rno-miR-339-5p
rno-miR-25-3p
rno-miR-192-5p
rno-miR-26b-5p
rno-miR-130a-3p
rno-miR-24-3p
rno-miR-154-5p
rno-miR-22-5p
rno-miR-320-3p
rno-miR-3559-3p
rno-miR-374-5p
rno-miR-380-3p
rno-miR-503-3p
rno-miR-503-5p

b

rno-miR-7a-5p
rno-miR-215
rno-miR-322-3p
rno-miR-26a-5p
rno-miR-148b-3p
rno-miR-27a-3p
rno-miR-340-5p
rno-miR-27b-3p
rno-miR-106b-3p
rno-miR-210-3p
rno-miR-93-5p
rno-miR-410-3p
rno-miR-3559-5p
rno-miR-20a-5p
rno-miR-671
rno-miR-146b-5p
rno-miR-21-5p
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rno-miR-30b-5p
rno-miR-673-5p
rno-miR-98-5p
rno-miR-484
rno-miR-382-5p
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rno-miR-184
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rno-let-7i-5p
rno-miR-30c-5p
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rno-miR-200b-5p
rno-miR-365-3p
rno-miR-421-3p
rno-miR-485-3p
rno-miR-10b-5p
rno-miR-144-3p
rno-miR-542-5p
rno-miR-1839-5p
rno-miR-540-3p
rno-miR-15b-3p
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rno-miR-221-3p
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rno-miR-582-3p
rno-miR-874-3p
rno-miR-101a-3p
rno-miR-206-3p
rno-miR-125b-2-3p
rno-miR-1-3p
rno-miR-134-5p
rno-miR-27a-5p
rno-miR-378b
rno-miR-24-2-5p
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rno-miR-483-5p
rno-miR-126a-3p
rno-miR-30e-3p
rno-miR-30a-5p
rno-miR-136-3p
rno-miR-143-3p
rno-miR-30e-5p
rno-miR-28-5p
rno-let-7f-5p
rno-miR-181a-5p
rno-let-7a-1-3p
rno-let-7c-2-3p
rno-miR-31a-5p
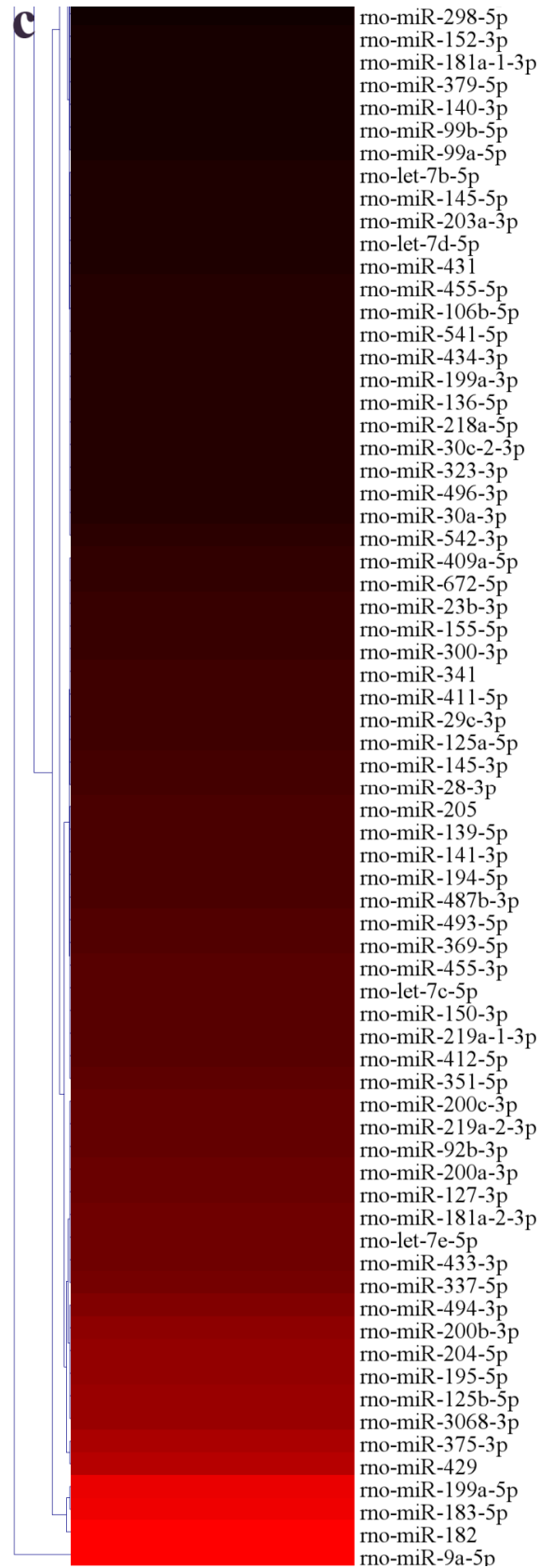rno-miR-434-5p
rno-miR-499-5p
rno-miR-100-5p

Figure S3. Hierarchical clustering analysis of miRNAs expression in hyperoxia model rats compared to the control. The data removed those low copy numbers of miRNAs (<5 copies). The each pattern means the fold change as Log 2 (treatment/control), from high (red) to low (green) (**a–c**).
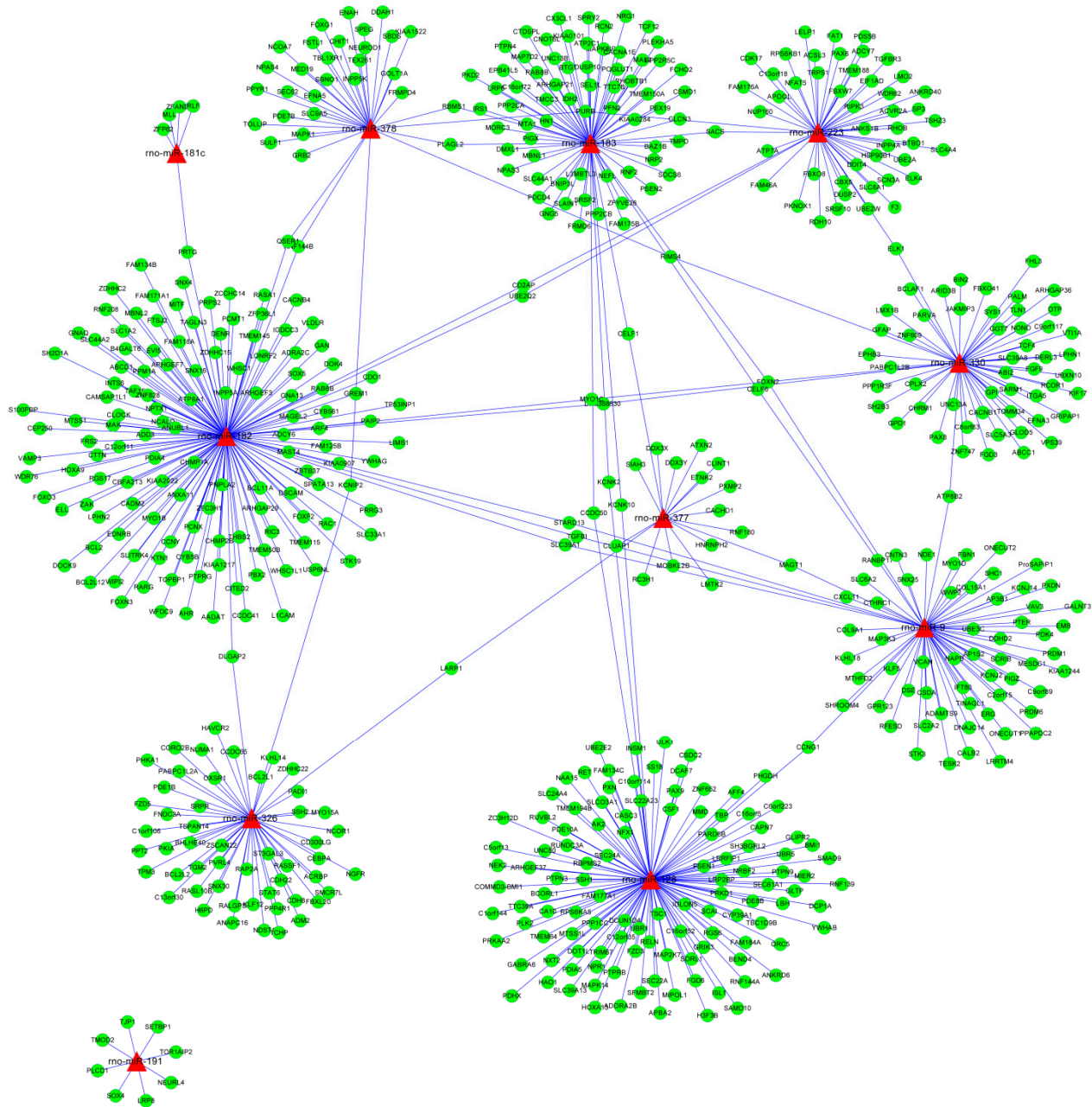
Figure S4. miRNA-mediated regulatory network in the hyperoxia model rats. The green nodes represent the miRNAs and the red nodes represent their targets.