

**Identification of microRNAs involved in lipid biosynthesis and seed size in developing sea buckthorn seeds using high-throughput sequencing**

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## Supplementary legends

**Figure S1. Quality evaluation of the sRNA sequencing data by the FastQC software.**

**Table S1. Statistics of sequencing and mapping of reads on unigenes.** G, G/Y, Y/O and O/R indicate the developmental stage of the fruit as indicated by color green, green/yellow, yellow/orange and orange/red, respectively; Q20 and Q30 indicate the percentage of bases with Phred values > 20 and > 30, respectively; GC indicates the GC ratio of total base number.

**Table S2. Functional classifications of unigenes in developing seeds of sea buckthorn based on GO term, COG category and KEGG pathway.**

**Table S3. Unigenes involved in lipid metabolism based on KEGG pathway analysis.**

**Table S4. The information of known miRNAs in sea buckthorn seeds.**

**Table S5. List of known miRNAs identified in developing sea buckthorn seeds and their read counts in eight sRNA libraries.** SJ1-G, SJ1-G/Y, SJ1-Y/O and SJ1-O/R indicate the developmental stage of the line 'SJ1' fruit as indicated by color green, green/yellow, yellow/orange and orange/red, respectively; XE3-G, XE3-G/Y, XE3-Y/O and XE3-O/R indicate the developmental stage of the line 'XE3' fruit as indicated by color green, green/yellow, yellow/orange and orange/red, respectively.

**Table S6. The information of novel miRNAs in sea buckthorn seeds.**

**Table S7. List of novel miRNAs identified in developing sea buckthorn seeds and their read counts in eight sRNA libraries.** SJ1-G, SJ1-G/Y, SJ1-Y/O and SJ1-O/R indicate the developmental stage of the line 'SJ1' fruit as indicated by color green, green/yellow, yellow/orange and orange/red, respectively; XE3-G, XE3-G/Y, XE3-Y/O and XE3-O/R indicate the developmental stage of the line 'XE3' fruit as indicated by color green, green/yellow, yellow/orange and orange/red, respectively.

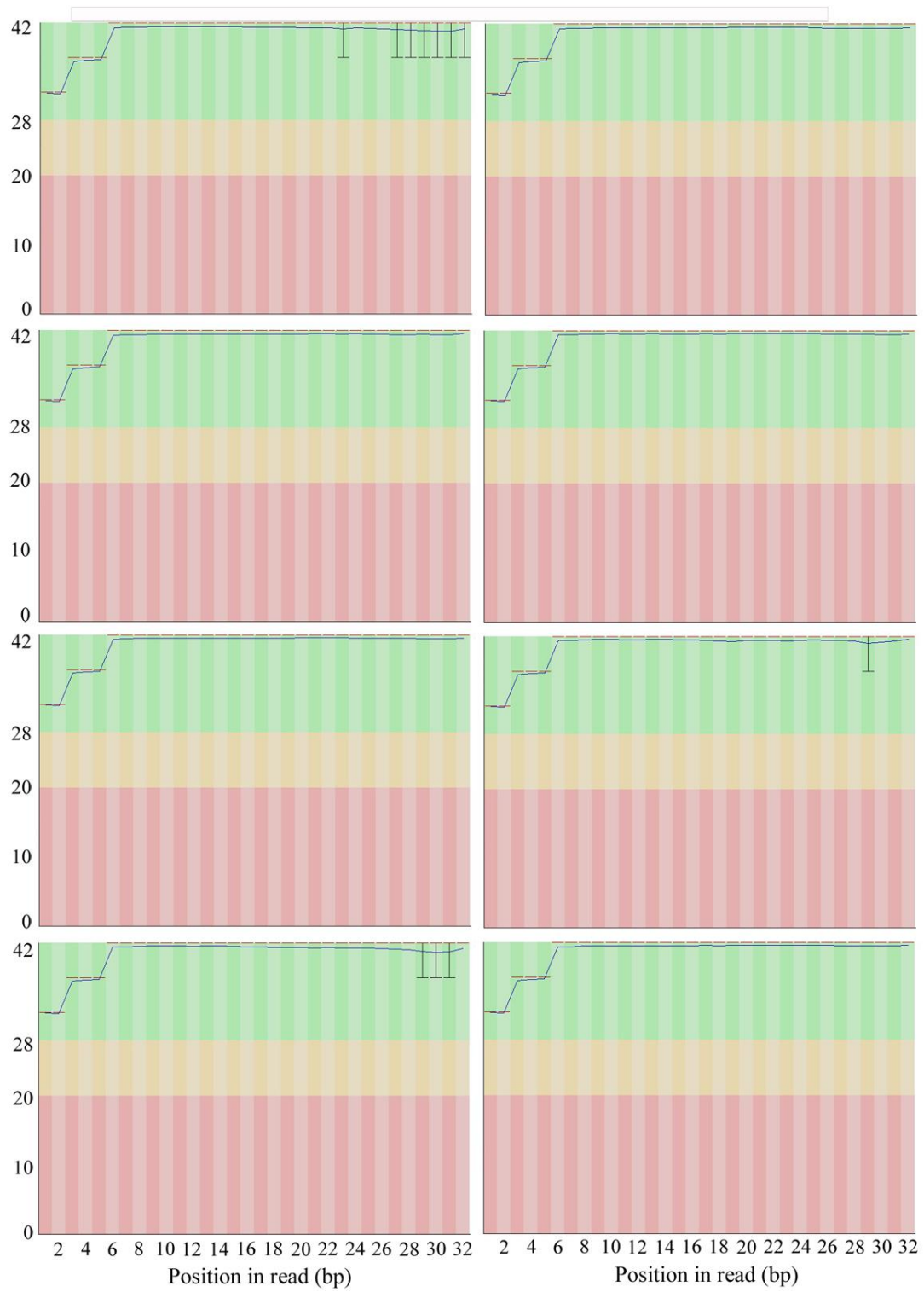
**Table S8. Differential expression miRNAs for each of 16 pairwise comparison groups.** SJ1-G, SJ1-G/Y, SJ1-Y/O and SJ1-O/R indicate the developmental stage of the line 'SJ1' fruit as indicated by color green, green/yellow, yellow/orange and orange/red, respectively; XE3-G, XE3-G/Y, XE3-Y/O and XE3-O/R indicate the developmental stage of the line 'XE3' fruit as indicated by color green, green/yellow, yellow/orange and orange/red, respectively. TPM indicate the read counts of identified miRNAs were normalized as transcripts per million.

**Table S9. Predicted targets for known and novel miRNAs and their functional annotations.**

**Table S10. Go analysis of targets of identified miRNAs in sea buckthorn seeds.**

**Table S11. Primers used for qRT-PCR of selected mature miRNAs.**

**Table S12. Primers used for qRT-PCR of predicted miRNAs target.**



**Figure S1. Quality evaluation of the sRNA sequencing data by the FastQC software.**