

**Table S1** Summary of the quality of RNA-seq

Sample	Raw_bases	Valid_bases	Q30	Mapped reads
Ctrl_1	7.41G	94.67%	94.51%	97.31%
Ctrl_2	8.00G	93.87%	94.49%	97.15%
Ctrl_3	7.64G	94.17%	94.47%	97.43%
Unl12h1	7.61G	94.86%	94.65%	97.21%
Unl12h2	8.20G	93.51%	94.64%	97.26%
Unl12h3	7.33G	94.76%	94.51%	97.34%
Unl1d1	7.94G	93.96%	94.58%	97.25%
Unl1d2	7.78G	94.36%	94.54%	97.29%
Unl1d3	7.47G	94.75%	94.41%	97.52%
Unl36h1	7.69G	94.26%	94.24%	97.34%
Unl36h2	7.46G	94.84%	94.30%	97.66%
Unl36h3	6.92G	95.15%	94.39%	97.64%
Unl3d1	7.97G	93.68%	94.55%	97.47%
Unl3d2	8.21G	93.94%	94.21%	97.62%
Unl3d3	7.55G	94.13%	94.54%	97.32%
Unl7d1	7.81G	94.46%	94.21%	97.52%
Unl7d2	8.72G	93.46%	94.41%	97.31%
Unl7d3	7.59G	95.33%	94.58%	97.25%

Raw\_bases: the number of raw bases; Valid\_base: the percentage of effective bases; Q30: the percentage of bases with a Qphred value greater than 30 in raw\_bases; Mapped reads: the percentage of sequencing sequences that can be located on the genome.