

**Table S3: Percentage of reads in each feature class for the libraries described in this manuscript \***

|                    | wildtype | <i>Dcr-2</i> | <i>R2D2</i> | <i>loqs</i> | wildtype | <i>R2D2</i> | <i>loqs</i> |
|--------------------|----------|--------------|-------------|-------------|----------|-------------|-------------|
|                    | VSV      | VSV          | VSV         | VSV         | SINV     | SINV        | SINV        |
| <b>Transposon</b>  | 4.640    | 3.009        | 3.915       | 4.415       | 2.687    | 1.529       | 1.881       |
| <b>rRNA</b>        | 4.690    | 15.370       | 15.822      | 8.472       | 7.310    | 9.461       | 13.971      |
| <b>miRNA</b>       | 28.504   | 35.672       | 27.849      | 26.621      | 48.712   | 65.434      | 52.332      |
| <b>repeats</b>     | 55.254   | 54.302       | 60.780      | 60.957      | 39.985   | 24.869      | 38.470      |
| <b>mRNA</b>        | 4.467    | 1.649        | 2.274       | 2.406       | 3.063    | 2.292       | 1.702       |
| <b>No features</b> | 10.281   | 7.248        | 7.562       | 9.099       | 7.872    | 7.083       | 7.097       |
| <b>VSV</b>         | 0.031    | 0.012        | 0.300       | 0.089       | 0.000    | 0.000       | 0.000       |
| <b>SINV</b>        | 0.000    | 0.000        | 0.000       | 0.000       | 0.012    | 0.070       | 0.025       |

\* Percentage of reads in each feature calculated relative to the total of mapped reads.

Mapped reads >16 nt were considered. Unmapped reads are not included.