

Table S2: Summary of the raw numbers from the analysis of the libraries described in this manuscript *

		Accession number / Genotype / Virus						
		wildtype VSV	<i>Dcr-2</i> VSV	<i>R2D2</i> VSV	<i>loqs</i> VSV	wildtype SINV	<i>R2D2</i> SINV	<i>loqs</i> SINV
<i>Drosophila</i>	Transposons	270,004	143,855	258,526	394,908	785,990	438,317	428,773
	rRNA	272,942	734,810	1,044,725	757,782	2,138,283	2,711,555	3,184,455
	miRNA	1,658,683	1,705,365	1,838,877	2,381,020	14,249,539	18,752,818	11,928,073
	repeat	3,215,314	2,596,031	4,013,364	5,452,095	11,696,828	7,127,218	8,768,479
	mRNA	259,933	78,834	150,161	215,182	895,951	656,939	387,897
	No features	598,262	346,507	499,296	813,823	2,302,877	2,029,849	1,617,725
	Total mapped	5,819,185	4,780,693	6,603,072	8,944,210	29,252,701	28,659,279	22,793,038
Virus	VSV	1,812	576	19,832	7,937	1	1	0
	SINV	0	0	1	5	3,463	20,143	5,612
	Unmapped	35,367,429	69,212,383	62,627,769	59,910,280	64,490,603	58,881,128	70,411,133
	Total	47,461,752	79,598,478	77,035,790	78,869,300	125,812,772	119,257,103	119,519,573

*Number of total reads in the library assigned per feature in the *Drosophila* genome or to VSV and SINV genomes. Reads >16 nt were considered.