

Table S4. Sequencing analysis data for the enriched genes in the comparison naEVs vs blank control for total gene sequences.

id	chr	start	end	gene	logFC	logCPM	FWER
chr11_3125904_3131004	chr11	3125904	3131004	<i>Pisd-ps1</i>	9.172573713	7.397255473	4.64557E-05
chr11_3131850_3193463	chr11	3131850	3193463	<i>Sfil</i>	5.379296795	10.22434998	3.56108E-07
chr13_119487941_119610458	chr13	119487941	119610458	<i>Gm7120</i>	6.38645144	7.263377184	0.003043154
chr17_3076578_3084183	chr17	3076578	3084183	<i>Pisd-ps2</i>	7.60704978	6.515271948	0.004782967
chr2_177314520_177324307	chr2	177314520	177324307	<i>Gm14412</i>	8.346407844	5.312666059	0.038646267
chr4_146449023_146470292	chr4	146449023	146470292	<i>Gm13251</i>	9.078900696	5.716532392	0.021494435
chr4_147136278_147457019	chr4	147136278	147457019	<i>Gm26624</i>	5.087253628	8.424748607	0.000408962
chr4_94556546_94557078	chr4	94556546	94557078	<i>Gm10306</i>	-13.37921866	3.823907265	0.027535255
chr5_114917318_114923277	chr5	114917318	114923277	<i>Gm13822</i>	7.469887046	6.688467058	6.25324E-05
chr8_20267774_20424814	chr8	20267774	20424814	<i>2610005L07Rik</i>	6.972939883	6.896152288	0.000425689
chr8_20292477_20420781	chr8	20292477	20420781	<i>Gm26804</i>	7.025694476	6.50456744	0.004627101
chr9_3015654_3017210	chr9	3015654	3017210	<i>Gm10720</i>	5.84286223	7.897328595	0.01442196
chr9_3025417_3033289	chr9	3025417	3033289	<i>Gm10717</i>	6.495121466	10.88613073	0.011519888
chr9_3034599_3035805	chr9	3034599	3035805	<i>Gm17535</i>	8.148925239	7.805421127	1.10621E-05
chr9_3036877_3038316	chr9	3036877	3038316	<i>Gm10715</i>	7.711741567	7.297505812	0.000166673