Electronic Supplementary Material (ESI) for Integrative Biology.

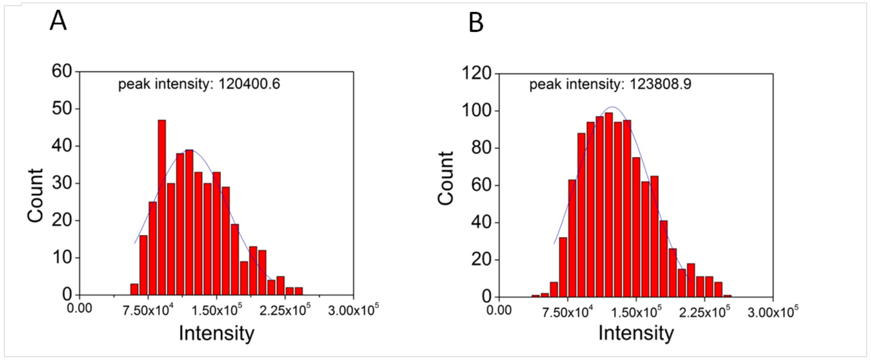

Fig. S1. Gaussian fitting of the intensity distribution of single RIG-I transcripts detected in (A) control cells, (B) IFN-β treated (6 hours) cells.

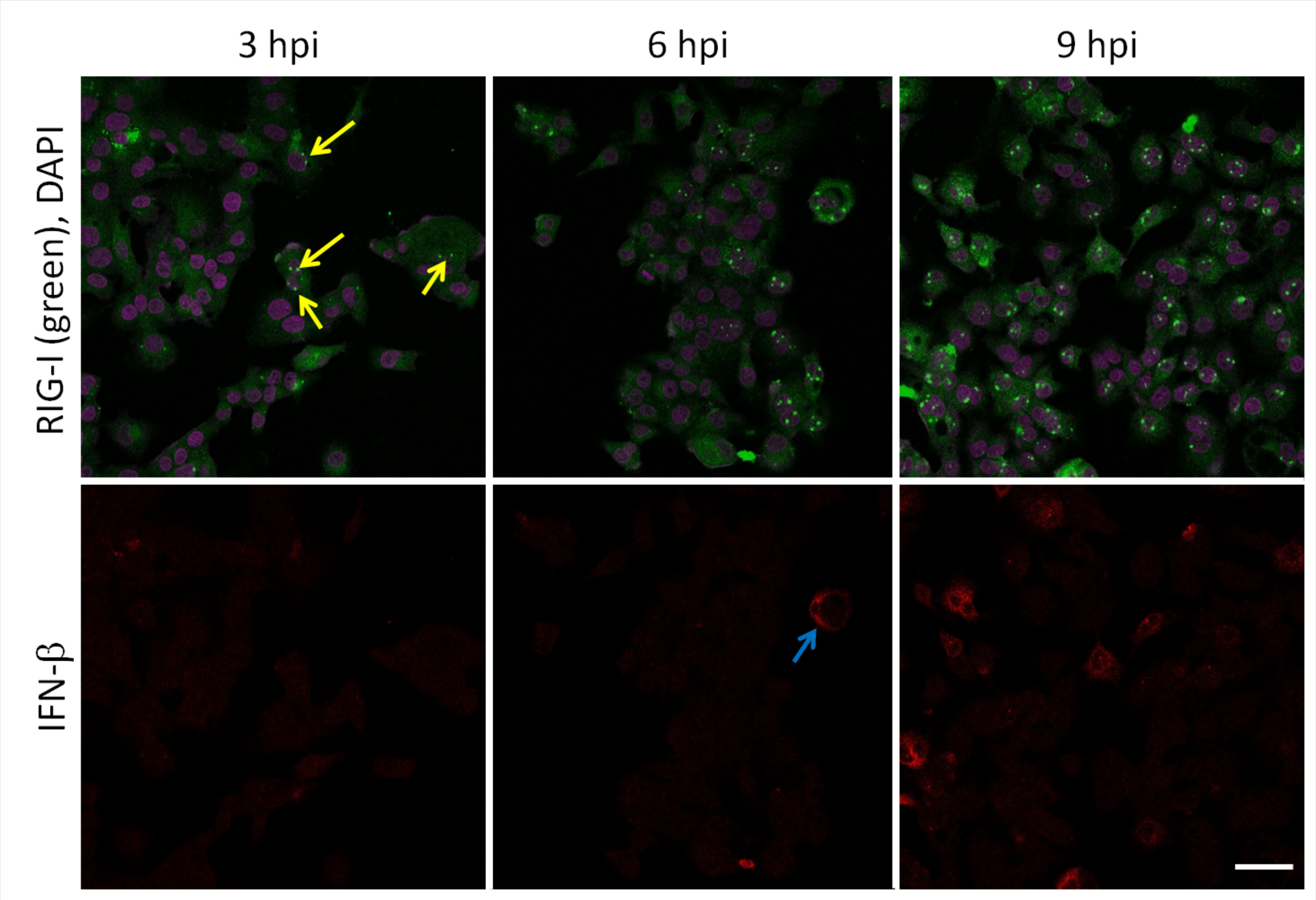

Fig. S2. Images of *RIG-I* and *IFNB1* mRNA in SeV infected (3, 6, and 9 hours) HepG2 cells obtained with a low magnification objective (40x). Yellow arrows show few RIG-I overexpressing cells with bright RIG-I transcription sites. Blue arrow shows an IFN-b overexpressing cell.

Table S1

Gene	Control	IFN-β st.	2 hpi	3 hpi	6 hpi	9 hpi
N gene	1	13	1511	3179	13252	101475
ADAR	4750	14675	4646	5216	4889	7644
APOBEC3A	4	16	11	9	7	14
C6orf150	4	15	9	5	10	17
DDIT4	677	904	960	773	699	1055
HPSE	25	99	21	21	33	101
IFNA1	1	14	2	1	2	7
IFNA4	7	14	6	3	9	19
IRF1	221	903	264	238	307	1256
IRF2	897	1739	723	712	704	1376
IRF3	132	268	109	135	195	212
IRF7	2	6	3	1	3	9
IRF9	753	9177	567	539	771	4195
MAP3K14	79	156	85	77	93	153
Mov10	512	1825	522	540	617	822
NLRC5	58	555	42	66	40	70
NLRX1	193	309	275	295	315	417
RNAseL	9	27	6	7	9	23
STAT1	641	14983	586	778	821	2317
TLR3	17	469	9	11	18	41
TRAIL	555	4837	386	369	528	1955

Table S1. Number of transcripts detected by Nanostring nCounter gene expression system in control, IFN-β treated (2 hours), and SeV infected (2, 3, 6, and 9 hours) HepG2 cells. Number of transcripts is normalized to housekeeping gene GAPDH.

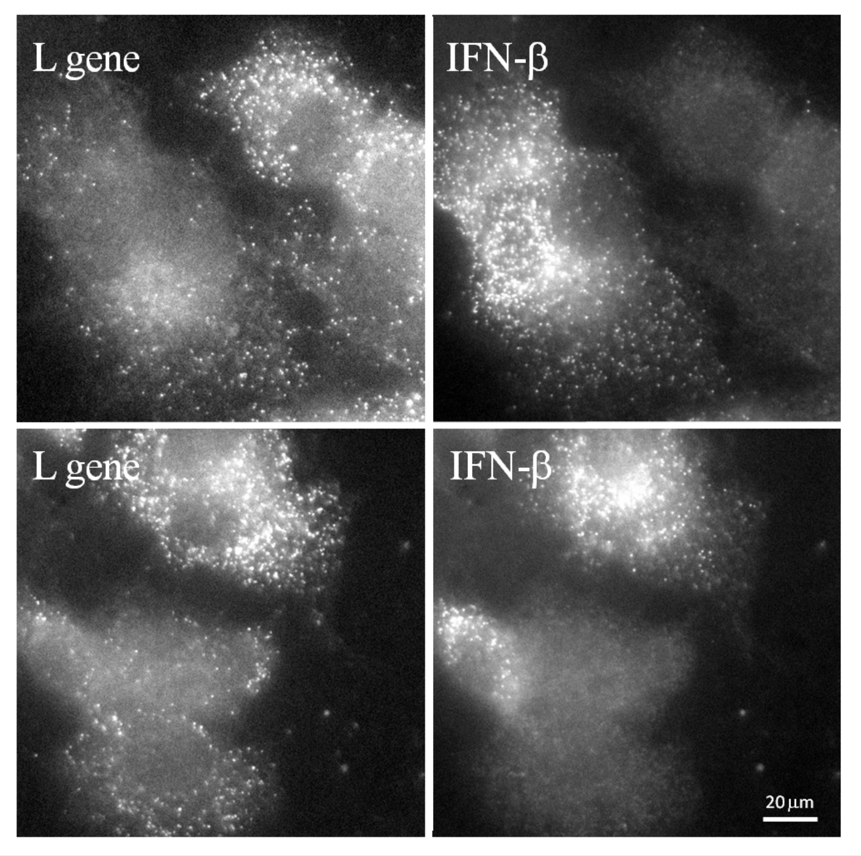

Fig. S3. Images of L gene and *IFNB1* mRNA in SeV infected (9 hours) HepG2 cells. Each row represents a different imaging area.

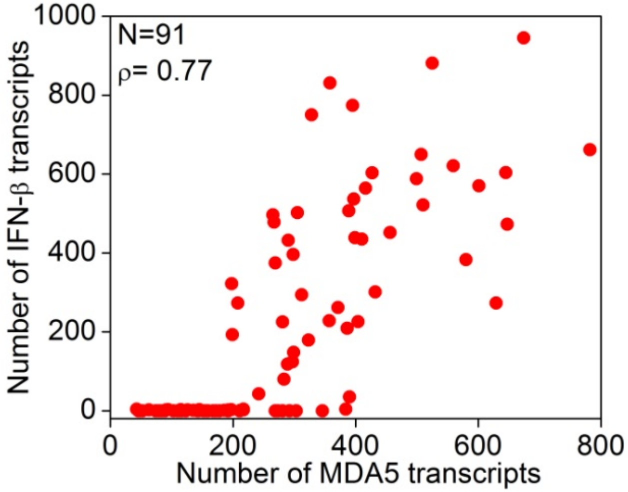

Fig. S4 Scatter plots of number of MDA5 against *IFNB1* transcripts in single HepG2 cells at 9 hours post SeV infection. N: Number of cells analyzed, r: Pearson's correlation coefficient.