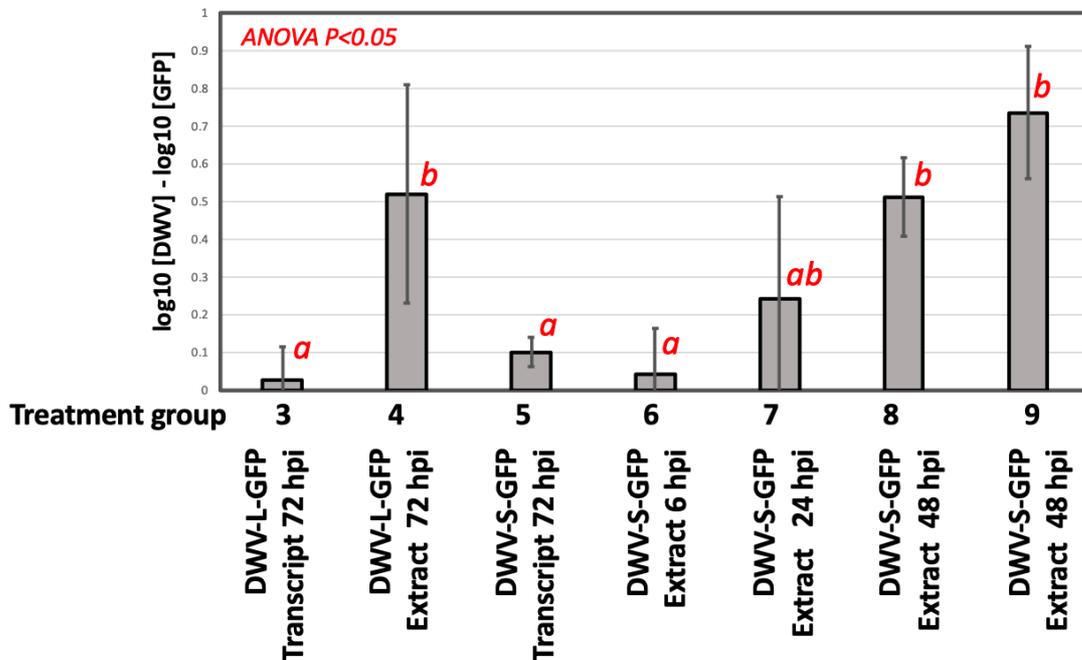


**A**

Difference between DWV and GFP RNA copy numbers in individual bee

**B**

Ttreatment group*		4	5	6	7	8	9
Ttreatment group *		DWV-L-GFP - Extract 72 hpi	DWV-S-GFP - Transcript 72 hpi	DWV-S-GFP - Extract 6 hpi	DWV-S-GFP - Extract 24 hpi	DWV-S-GFP - Extract 48 hpi	DWV-S-GFP - Extract 72 hpi
3	DWV-L-GFP - Transcript 72 hpi	0.03824	<b>0.282417</b>	<b>0.868186</b>	<b>0.267553</b>	0.000228	0.000342
4	DWV-L-GFP - Extract 72 hpi		0.033378	0.012333	<b>0.127334</b>	<b>1.0000</b>	<b>0.157573</b>
5	DWV-S-GFP - Transcript 72 hpi			<b>0.446633</b>	<b>0.383298</b>	<.0001	0.000125
6	DWV-S-GFP - Extract 6 hpi				<b>0.194915</b>	<.0001	<.0001
7	DWV-S-GFP - Extract 24 hpi					0.041487	0.0028
8	DWV-S-GFP - Extract 48 hpi						0.019779

\* Treatment group number as in Fig. 2

**Figure S3. Accumulation of the *egfp* deletant genomes in individual honey bee pupae. (A)** Average copy numbers for the differences between DWV and GFP loads ( $\text{Log}_{10}(\text{DWV}) - \text{Log}_{10}(\text{GFP})$ ) calculated for individual pupa in the treatment groups are shown as grey graphs, the error bars show  $\pm$  standard deviation (SD). Treatments are shown below the graphs. Inocula: PBS - phosphate buffered saline; "Transcript", *in vitro* RNA transcript; Extract, filtered extract from the pupae infected with the corresponding RNA transcript. Red letters above the bars indicate significantly groups (ANOVA,  $P < 0.05$ ). **(B)** Statistical significance of the  $\text{Log}_{10}(\text{DWV}) - \text{Log}_{10}(\text{GFP})$  differences between the treatment groups. P-values, ANOVA analysis. Non-significant ( $P > 0.05\%$ , ANOVA) are highlighted.