

Supplementary Materials

Table S4.

Days post infection	Genotype	Virus-Host Phenotype			
		Null	Chromosome-associated	Chromosome-associated / Telomere-integrated	Telomere-integrated only
1	6 ₃	60.6* ± 6.7	27.2* ± 2.3	7.2 ± 3.1	5.0** ± 1.7
1	7 ₂	29.4* ± 4.2	52.8* ± 5.5	17.8 ± 2.1	0.0** ± 0.0
4	6 ₃	53.7 ± 6.4	35.4** ± 2.3	9.2 ± 4.4	1.8** ± 0.0
4	7 ₂	28.3 ± 6.7	58.8** ± 3.8	13.0 ± 7.4	0.0** ± 0.0
7	6 ₃	43.7 ± 9.2	46.0 ± 5.9	9.2 ± 1.5	1.2 ± 1.2
7	7 ₂	42.3 ± 10.0	42.3 ± 13.8	13.7 ± 1.5	1.7 ± 1.7
14	6 ₃	38.5 ± 4.2	39.6* ± 3.6	14.8 ± 1.0	7.1 ± 4.2
14	7 ₂	50.6 ± 15.3	21.1* ± 2.1	20.0 ± 12.2	8.3 ± 4.4
21	6 ₃	32.5 ± 11.0	34.9 ± 8.1	27.2 ± 12.5	5.3 ± 3.5
21	7 ₂	45.8 ± 8.5	41.6 ± 5.3	10.8 ± 6.1	1.8 ± 1.7

Supplementary Table 4. Viral-host cytogenomic interactions for non-oncogenic Rispens vaccine and oncogenic MDV in vaccinated and challenged disease resistant versus susceptible birds. The mean percentages, in bold font, ± standard deviation of mitotically-dividing cells with given virus-host phenotypes from 3 samples per chicken genotype (6₃; MD-resistant, 7₂; MD-susceptible) between 24 hours and 21 days post-infection. The samples represent the replicating cell population in the spleens of individual birds *vaccinated with Rispens at day of hatch and challenged with oncogenic MDV (Md5) at 4 days post-hatch*. The values that were statistically-significant within a viral phenotype and within a timepoint as compared to the other genotype are indicated with a "*" ($p \leq 0.05$) or "**" ($p \leq 0.01$) symbol. The values that were found to be statistically-significant within a virus-host phenotype for a genotype across timepoints are indicated with a "†" ($p \leq 0.05$) or "‡" ($p \leq 0.01$) symbol.