Supplementary Materials

Table S3.

Days post infection	Genotype	Virus-Host Phenotype			
		Null	Chromosome- associated	Chromosome- associated / Telomere-integrated	Telomere-integrated only
1	63	36.0 ± 1.0	37.1 ± 5.9	25.7 ± 8.2	1.1 ± 0.6
1	72	28.3 ± 4.6	55.6 ± 2.5	15.0 ± 6.1	1.1 ± 0.6
4	63	53.7 ± 13.9	32.6 ± 14.2	8.0 ± 3.5	5.7 ± 4.0
4	72	23.9 ± 2.3	58.7 ± 6.7	15.5 ± 3.5	1.9 ± 0.0
7	63	52.8** ± 8.5	38.0 ± 1.5	7.9* ± 3.5	1.2* ± 1.2
7	72	16.1** ± 2.7	33.9 ± 3.6	39.8* ± 6.7	10.2 ‡* ± 1.2
14	63	37.8* ± 8.0	30.0 ± 6.1	14.4 ± 4.9	17.8** ± 5.1
14	72	10.6* ± 1.5	6.7 ± 3.6	20.6 ± 1.5	62.2** ± 5.9
21	63	51.9* ± 4.4	14.5 ± 1.5	18.4 ± 3.6	15.1* ± 2.7
21	72	16.2* ± 6.4	15.6 ± 4.5	23.5 ± 4.4	44.7 * ± 7.5

Supplementary Table 3. Viral-host cytogenomic interactions for oncogenic MDV in unvaccinated and challenged disease resistant versus susceptible birds. The mean percentages, in bold font, \pm standard deviation of mitotically-dividing cells with given virus-host phenotypes from 3 samples per bird 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 *challenged with oncogenic MDV (Md5) alone 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.