

Table S2.

Days post infection	Virus type	Virus-Host Phenotype			
		Null	Chromosome-associated	Chromosome-associated / Telomere-integrated	Telomere-integrated only
1	Md5	17.6 ± 1.2	50.6 ± 4.6	27.5 ± 4.0	4.4 ± 2.3
1	Rispens	28.6 ± 3.5	42.9 ± 2.7	27.3 ± 5.6	1.3 ± 0.6
1	HVT	19.5 ± 6.8	44.1 ± 8.7	36.4 ± 4.0	0.0 ± 0.0
4	Md5	27.0 ± 3.8	42.8 ± 4.5	20.1 ± 7.6	10.1 ± 4.6
4	Rispens	12.1 ± 7.8	51.6 ± 10.0	36.3 ± 6.0	0.0 ± 0.0
4	HVT	16.3 ± 2.1	75.6 ± 8.0	8.1 ± 2.1	0.0 ± 0.0
7	Md5	26.2 ± 9.3	11.4 ± 2.9	37.6 ± 15.2	24.8* ± 10.8
7	Rispens	24.8 ± 9.1	33.6 ± 7.8	40.9 ± 15.7	0.7 ± 0.6
7	HVT	21.4 ± 11.8	35.0 ± 6.7	42.9 ± 15.9	0.7 ± 0.6
14	Md5	11.9 ± 3.1	5.9** ± 3.1	36.4 ± 5.5	45.6** ± 8.9
14	Rispens	8.4 ± 1.2	53.2 ± 6.0	37.9 ± 9.0	0.5 ± 0.6
14	HVT	10.2 ± 1.2	53.2 ± 6.6	36.6 ± 10.4	0.0 ± 0.0
21	Md5	1.2†** ± 0.6	3.6** ± 1.7	39.4 ± 22.0	55.8* ± 18.5
21	Rispens	24.3 ± 3.5	60.4 ± 5.0	15.3 ± 4.0	0.0 ± 0.0
21	HVT	35.2 ± 4.0	50.9 ± 5.2	12.0 ± 5.0	1.9 ± 1.7

Supplementary Table 2. Viral-host cytogenomic interactions for oncogenic and non-oncogenic MDV strains in disease-susceptible, genotype 7₂, chickens. The mean percentages, in bold font, ± standard deviation of mitotically-dividing cells with given virus-host phenotypes from 3 samples per treatment type (Md5; oncogenic MDV, non-oncogenic MD vaccines; Rispens, HVT) between 24 hours and 21 days post-infection. The samples represent the replicating cell population in the spleens of individual genotype 7₂ (MD-susceptible) birds. The values that were statistically-significant within a viral phenotype and within a timepoint as compared to the other treatment types (MDV

strains) 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 treatment type (MDV strain) across timepoints are indicated with a "†" ($p \leq 0.05$) or "‡" ($p \leq 0.01$) symbol.