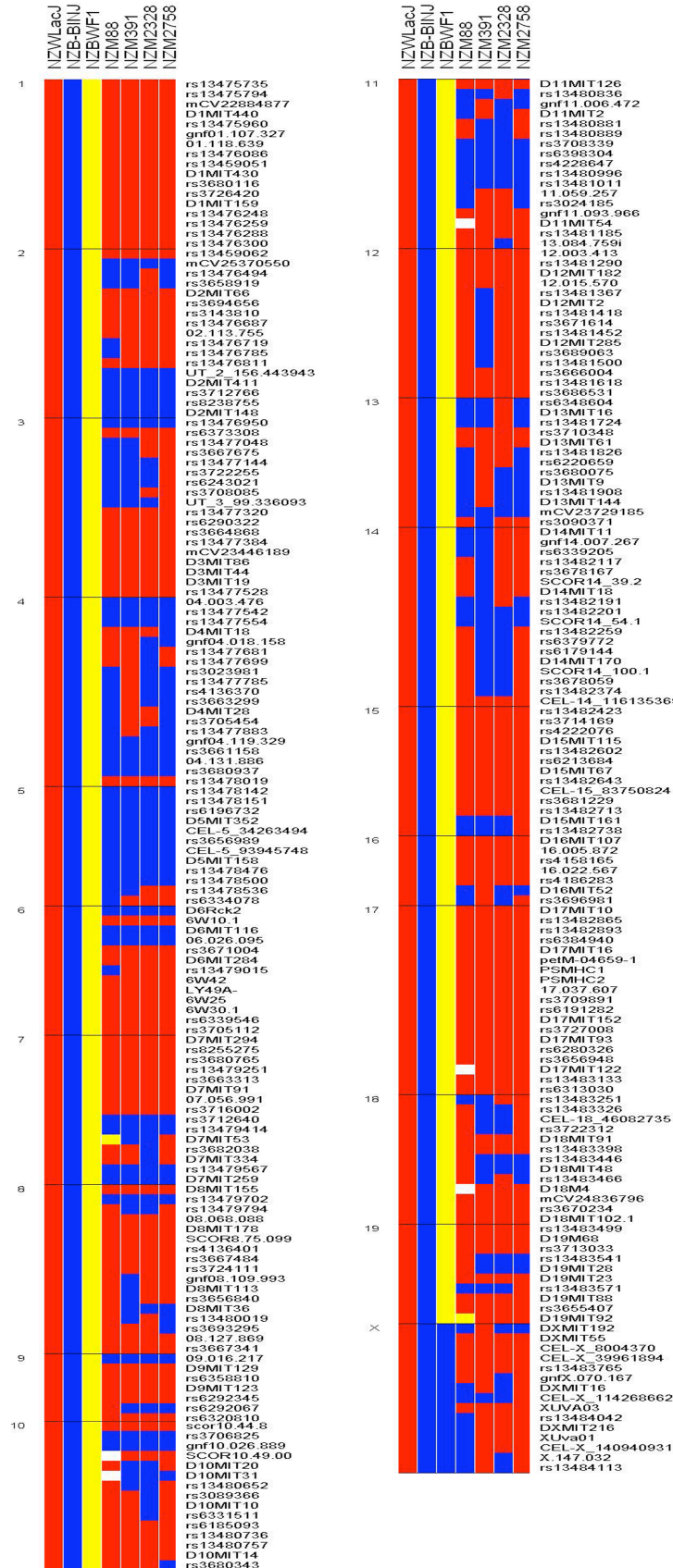
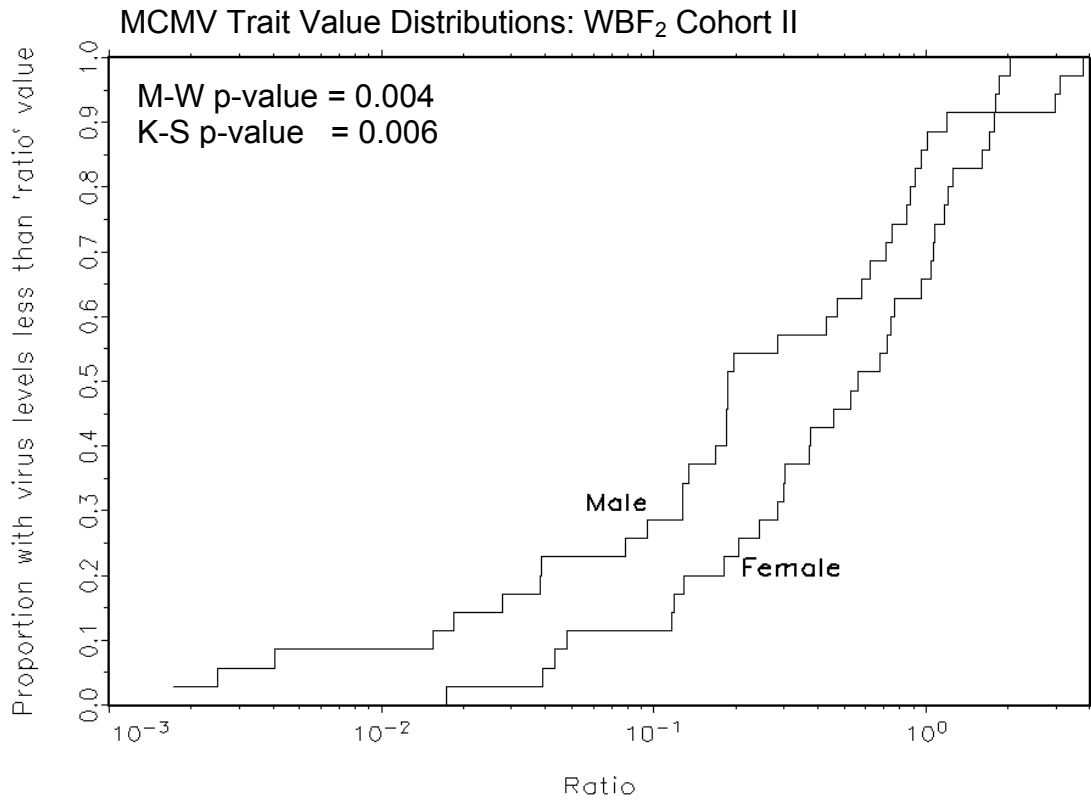


Supplementary Figure 1.



Supplementary Figure 1. Genome-wide allelic distribution map of the NZM strains. Genomic DNA from NZW, NZB, WBF₁ and the NZM strains were genotyped with a dense panel of 86 SSLP markers and 196 SNPs. Shown are the NZW (red), NZB (blue), and WBF₁ (yellow) alleles at each genotyped marker (White – genotype not determined). Note that all NZM strains contain NZW alleles on chromosome 17.

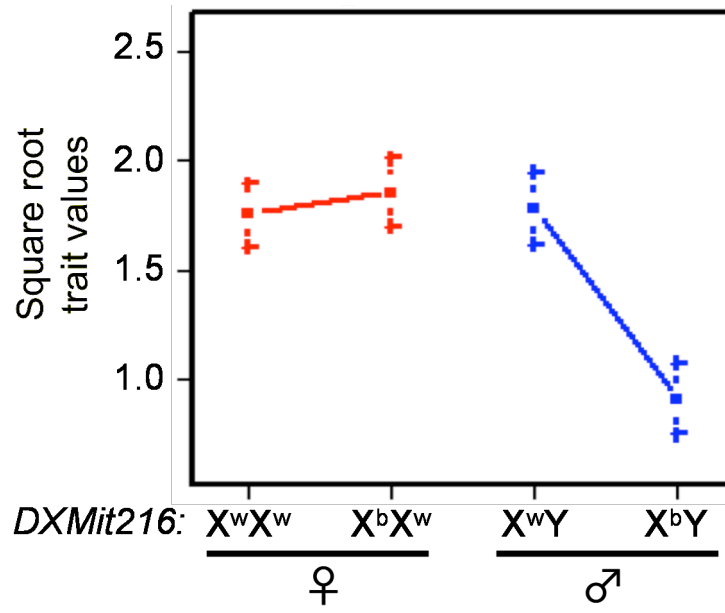
Supplementary Figure 2.



Supplementary Figure 2. Gender Stratification of WBF₂ Cohort II Animals -

The proportion of WBF₂ cohort II offspring with less than a given MCMV trait value was plotted. Statistical comparisons for gender-related differences in early MCMV control were performed using the Mann-Whitney, and Kolmogorov-Smirnov. P-values for WBF₂ cohort II are shown.

Supplementary Figure 3.



Supplementary Figure 3. Impact of *DXMit216* on MCMV Trait Values - A
DXMit216 effect plot generated in R/qtl whereby the square root trait values for WBF₂ males and females are stratified by their genotype.

Supplementary Figure 4. Comparison of MCMV Trait Values in New Zealand F₁ Offspring and NZW.NZB-DXMit216 Congenic Mice – (a) WBF₁ and BWF₁ mice and NZW controls were i.p. infected with 1 x 10⁵ PFU of MCMV (3.5 dpi). QPCR determined spleen (open circles) and liver (closed circles) MCMV levels for individual mice are shown on Log₁₀ scale. Bars shown represent the arithmetic mean of the Log₁₀ transformed (CMV/ β -actin) copy # ratios. **(b)** B6, NZW, NZB and NZW.NZB-DXMit216 mice were infected i.p. with 1 x 10⁵ PFU of MCMV. QPCR determined spleen (open circles) and liver (closed circles) MCMV levels were are shown on a Log₁₀ scale. Bars shown represent the arithmetic mean of the Log₁₀ transformed (CMV/b-actin) copy # ratios.