



Figure S2. Segregation of *we^{4J}* and nine microsatellite markers on mouse Chr 2 among a large backcross family of mice. To produce these 1035 N₂ generation mice, (C57BL/6J x AKR-*we^{4J}*)F₁ females were backcrossed to AKR-*we^{4J}* homozygous mutant males. The Chr 2 haplotype depicted by the vertical line (the knob at the top of which represents the centromere) was that transmitted by the F₁ dam. The number of backcross mice that inherited each haplotype is shown beneath it. The microsatellite markers typed are shown to the left, and genetic distances (in percent recombination ± 1 standard error) are shown to the right of the haplotypes. Blue-shaded boxes indicate C57BL/6J-derived alleles; red-shaded boxes represent AKR-derived alleles. The *we^{4J}* mutation is located between *D2Mit304* and *D2Mit78*, since it must lie below (telomeric to) the crossovers (depicted in blue) carried by the seven recombinants marked with an asterisk, and above (centromeric to) the crossovers (shown in red) carried by the four recombinants marked with a dagger. *D2Mit135* and *D2Nds3* were never meiotically separated from *we^{4J}* in this backcross panel. The deviation between wild type and mutant mice from this backcross is not significant ($\chi^2 = 1.05$; $P > 0.30$), suggesting that *we^{4J}* homozygotes are fully viable (at least to weaning age), compared with their heterozygous littermates.