Figure S2 Sequence alignment for 74 alleles compared to the expected wild-type *Tyrosinase* sequence. The target site is indicated (red) along with deleted bases (-) and inserted or altered bases (lower case). Note that in some cases the exact breakpoint cannot be determined from the sequence data because bases on either side of the breakpoint are identical. For each allele, the number of founder mice observed carrying that allele is indicated along with the percentage of sequencing reads within the founder PCR product. For alleles observed in multiple founders, a range of percentages is given.