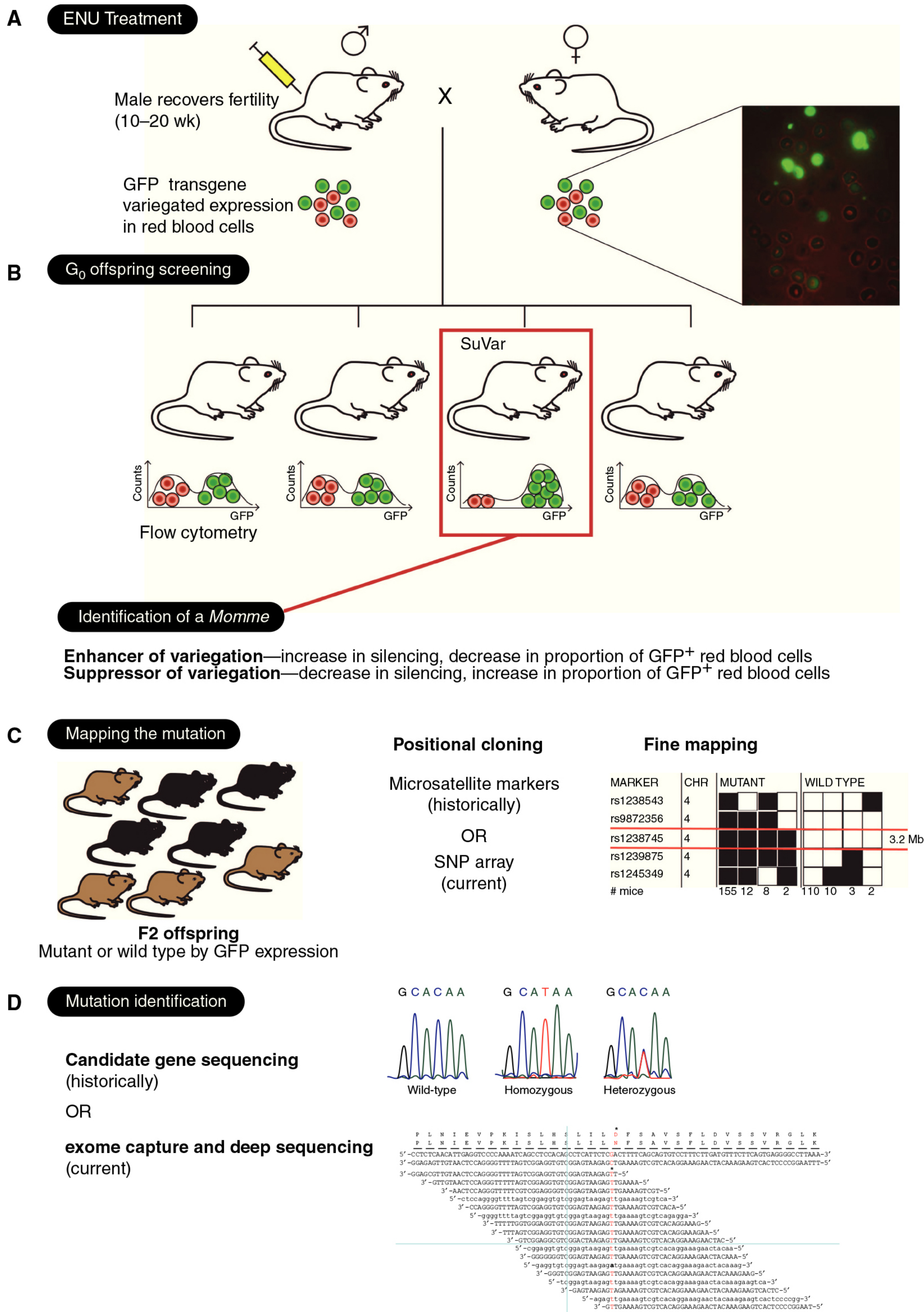

Figure 1. *Momme* screen for modifiers of epigenetic reprogramming. (*A*) GFP transgenic males are treated with ENU (now the G_0 generation), left to recover fertility, and then bred with GFP transgenic females to produce G_0 offspring. (*B*) A drop of blood is taken from all G_0 offspring at weaning and analyzed by flow cytometry to measure GFP expression in erythrocytes. Analysis is performed to look for variations in the extent of variegation of transgene expression. In this instance, an example of an individual with an enhancer of variegation phenotype is illustrated in the third mouse analyzed. (*C*) Animals with alterations in transgene variegation are backcrossed for two generations to allow mapping of the causative mutation. Mapping is performed with microsatellite markers or single-nucleotide polymorphism (SNP) arrays, and fine mapping followed up with large numbers of phenotypically mutant or wild-type animals, using additional SNPs or microsatellite markers. (*D*) The linked point mutation is then identified via exome capture (i.e., genomic DNA input selected using mouse exonic probes) followed by deep sequencing or by candidate gene sequencing.

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