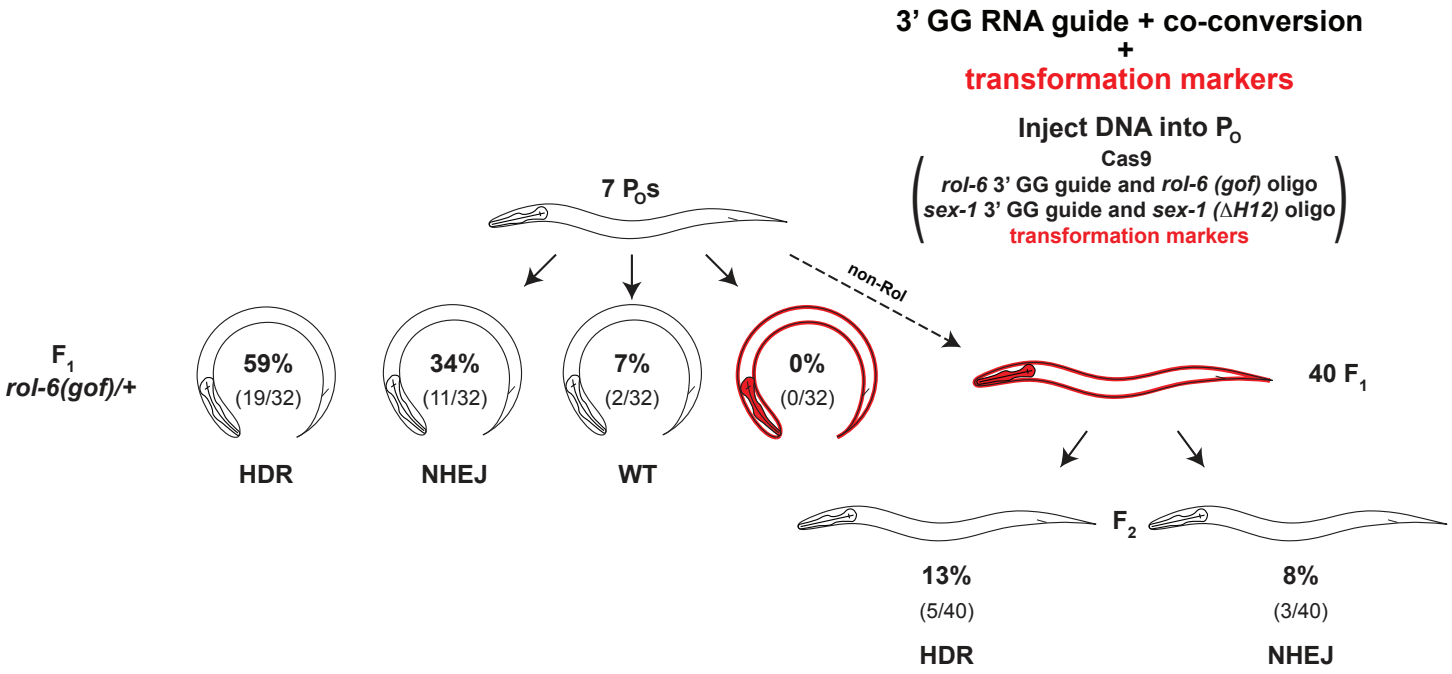

Figure S2 Comparison of the co-CRSPR / co-conversion scheme plus 3' GG guide RNA with the transformation marker scheme plus the 3' GG guide RNA. From 7 of the 61 P0 animals injected with Cas9, the *rol-6* and *sex-1* guides expressed from the R07E5.16 promoter, the *rol-6* and *sex-1* oligo repair templates, and the two DNA transformation markers *Pmyo-2::mCherry* and *Pmyo-3::mCherry,* we obtained Rol animals and red animals, with no overlap between the Rol and red animals. Of the Rol animals, 93% percent had a *sex-1* mutation: 59% from HDR repair and 34% from NHEJ repair. Of the red animals, 21% had a *sex-1* mutation: 13% from HDR repair and 8% from NHEJ repair. The reduced frequency of *sex-1* mutations among red animals (21% instead of 51%) in this experiment compared to that in Figure 2A is most likely due to the reduced concentration of *sex-1* guide RNA to make it equal that of the *rol-6* guide RNA. Thus, the easiest and most effective strategy to obtain mutations in loci of choice via HDR or NHEJ events is to combine our 3' GG guide RNA design with the co-CRISPR / co-conversion strategy.