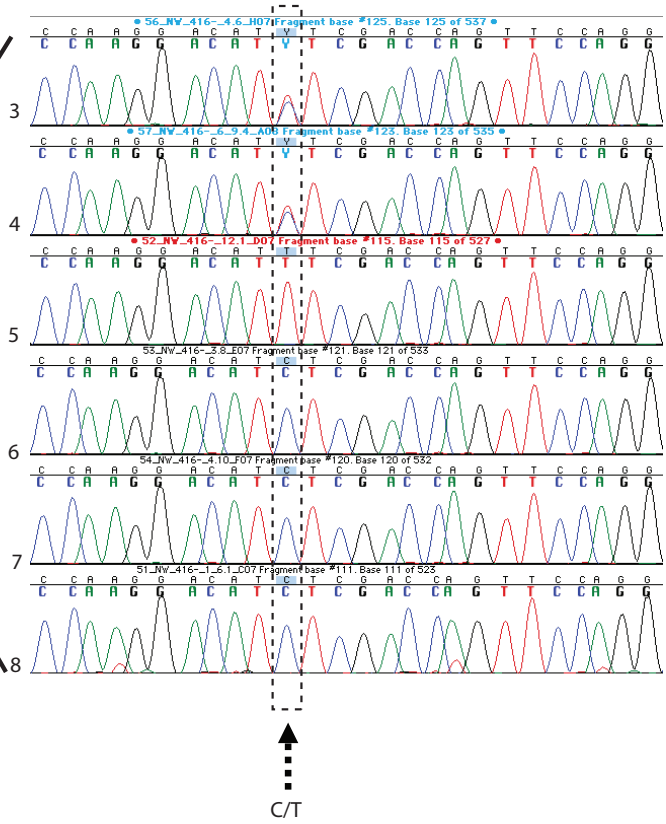
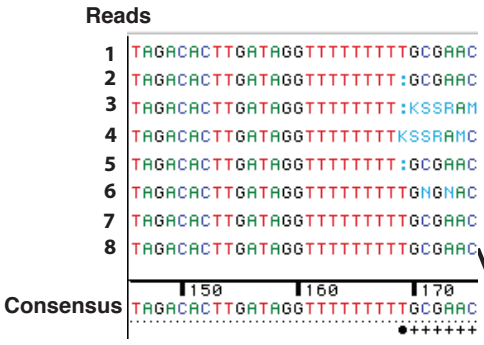
**SNP at p35**
PCR with primer pair bac416
sequenced with primer bac416r


**indel at p44**
PCR with primer pair bac502
sequenced with primer bac502f



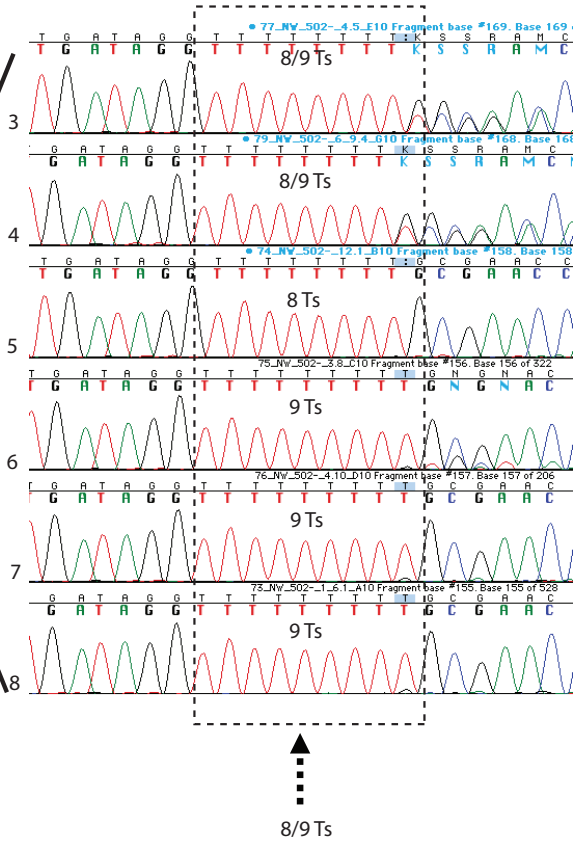



**Figure S2 Genotyping SNPs in reduction events.** Genotyping of the C/T SNP at position p35 is shown at the top. Sequences around the SNP region are shown for eight samples. Sample 1 was PCR amplified from pWalkman{nbs-Ilp} plasmid DNA showing a "C" at p35. Sample 2 was PCR amplified from genomic DNA of the starting line with *attP@nbs* showing a "T" at position p35. Samples 3 and 4 were amplified from genomic DNA of two NHEJ type lines (Figure 2). The sequencing data shown at the right displays a C/T double peak suggesting that both *nbs-Ilp* copies are present, which is consistent with NHEJ type events not being reduced. Samples 5-8 were derived from four lines that have been classified as "reduced" based on the PCR tests shown in Figures 1 and 2. Either a "C" or a "T" single peak was displayed in the sequencing data, consistent with the presence of a single *nbs-Ilp* copy. Genotyping of the T indel SNP at position p44 is shown at the bottom. The samples are the same as the ones used for genotyping p35. At this position, the *nbs-Ilp* region derived from the BAC clone (sample 1) has a string of nine "Ts", while the chromosomal copy has eight (sample 2). For samples 3 and 4 (NHEJ type), the deletion of a single "T" resulted in the appearance of a double peak for all bases downstream of the indel, due the presence of both *nbs-Ilp* copies. For reduced samples (samples 5-8), the indel is homozygous, again consistent with the presence of only one *nbs-Ilp* copy.