**FIGURE S2.**— Genotypic analysis of the transmission of a centromere marker.  

(A) Genotyping of representative individuals from the pedigree described in Fig. 1A indicates inheritance of two alleles of the centromeric microsatellite marker Z11257 through the pedigree. (B) The *asm/+* P0 male 14-408 and the wild-type P0 female Tu 002 were each homozygous for a different allele of Z11257. Whereas all F1 females were heterozygous for z11257, a centromere-linked simple sequence repeat (SSR) marker on chromosome 18 ([https://wiki.zfin.org/display/prot/MGH-CVRC+Mapping+Resources](https://wiki.zfin.org/display/prot/MGH-CVRC+Mapping+Resources)), all 40 EP half-tetrad mutant offspring (with the exception of mut 30.2) and all 23 EP wild-type offspring, derived from designated (*) F1 females, carried only one allele of the centromere marker. One exceptional mutant (EP mut 30.2) could not have been derived from a sister chromatid pair; this mutant and its presumed wild-type counterpart were eliminated from further quantitative analyses. Genotypic analysis of EP half-tetrad *asm* mutant and WT offspring is shown, where EP mut 41.1 indicates a mutant parthenogenote derived from the #41 F1 *asm+/-* female. Thirty-six of the 39 *asm* mutant offspring inherited the larger SSR allele,
indicating linkage to the centromere of chromosome 18; the three mutants harboring the smaller SSR allele were subsequently shown to have resulted from four strand dco events. Groups of individuals with a particular genotype are designated with a different color. Color code: Parental individuals (yellow), F1 heterozygous parents (green), phenotypically mutant half-tetrad progeny (purple), and phenotypic wild-type half-tetrad siblings (orange).