Figure S1  The distribution of single nucleotide variations (SNVs) in KR772.
Figure S2  Non-random distribution of EMS induced changes are seen in RB5002, VC1923, and VC1924. The X-axis represents the length of chromosomes. The Y-axis indicates each SNV ID. The data used to generate this figure was from the supplementary table of (FUBOTTE et al. 2010).
Figure S3  Distribution of homozygous and non-homozygous SNVs per 1Mbp window in each chromosome. The blue bars represent non-homozygous SNVs and the red bars represent homozygous SNVs. A SNV with allelic ratio between 40% and 89% are considered as non-homozygous. A SNV with allelic ratio 90% or above are considered as homozygous.
Figure S4  DAPI staining and DIC images for h888, h844, h137, and h448. The yellow line outlines the gonad. The h888 and h844 alleles show the more severe phenotype where the gonadal arms have yet to turn. The h137 and h448 alleles show milder phenotype where the gonadal arms have fully turned.
Table S1  All SNVs present in KR772 with more than 20% read support.

Table S1 is available for download at http://www.genetics.org/content/suppl/2012/01/20/genetics.111.137208.DC1 as an excel file.