

## SUPPLEMENTARY DATA DESCRIPTION

The supplementary table holds the data from the 203 genotyped polymorphisms in the *Enhancer of split* gene complex [E(spl)-C]. The table is 210 columns by 2304 rows, tab-delimited and designed to be easily machine-readable. The “individual” column gives the names of each sample genotyped (f = female, m = male). The “blanks” column identifies control samples: 1 = DNA sample, 2 = blank control sample. The “plate” column identifies the 384-well plate (1–6) from which the sample is derived, and the “well.384” column gives the position of the sample in the plate. The “fly.type” column codes the different samples present on the plates: 1 = individual from one of the 16 *D. melanogaster* strains used for sequencing E(spl)-C, 2 = female from large nv2001 *D. melanogaster* population, 3 = blank, 33 = DNA sample that clusters with the blanks (presumably DNA isolation failures), 4 = male from large nv2001 *D. melanogaster* population, 5 = diploid *D. melanogaster* sampled from Benin, West Africa, 6 = diploid *D. melanogaster* sampled from Southern France, 7 = diploid *D. melanogaster* sampled from Madang, Papua New Guinea, 8 = *D. simulans* individual, 88 = *D. melanogaster* individual that clusters with *D. simulans* (presumably these are true *D. simulans* flies incorrectly scored as *D. melanogaster*). The “SBN” and “ABN” columns hold the sternopleural and abdominal bristle counts, respectively, for the flies from the large nv2001 population. The remaining 203 columns in the table hold the scored genotypes. The column names (e.g., es.C38733T) are constructed from a two-letter code specifying the locus (es = *Enhancer of split*), a period, followed by the major allele at the SNP, the position of the SNP in the alignment of 16 *D. melanogaster* alleles, and the minor allele at the SNP. Alleles ‘I’ and ‘D’ refer to the insertion and deletion allele, respectively, of an insertion/deletion polymorphism. The genotype calls are coded: NA = no genotype assigned, 0 = minor homozygote, 1 = heterozygote, 2 = major homozygote.