

Table S7 Homozygosity of SNPs in genome

Overall SNPs ( $0.2 \leq$  frequency) were indentified using VarScan program and were classified into homo SNPs ( $0.9 \leq$  frequency) and floating SNPs ( $0.2 \leq$  frequency  $< 0.9$ ). The number of homo SNPs was slightly different from that of the homo SNPs in Table 2 and Table 3, due to the difference of data filtering. Homo SNP fraction and mean SNP frequency (homozygosity) were calculated from the VarScan data. \* indicates significant difference of mean homozygosity between Dark-fly and Oregon-R-S (Welch t-test, p-value = 2.2E-16).

fly line	Dark-fly	Oregon-R-S
overall SNPs ( $0.2 \leq$ freq)	522,391	499,507
homo SNPs ( $0.9 \leq$ freq)	463,633	445,666
floating SNPs ( $0.2 \leq$ freq $< 0.9$ )	58,758	53,841
homo SNP fraction (%)	88.8	89.2
homozygosity (mean $\pm$ SD) *	0.941 $\pm$ 0.176	0.944 $\pm$ 0.171