



**Figure S3** Allelic imbalance in SAM/ORE “hybrid” flies with both wild-type and *sd<sup>E3</sup>* genotypes. Only sequence tags represented by at least five reads of each allele in all samples are represented in this plot. (A) Genes showing evidence of allelic imbalance ( $q < 0.05$ ). (B) Genes showing evidence of genotype-dependent allelic imbalance ( $q < 0.05$ ). (C) Genes near polymorphic predicted SD binding site ( $p < 0.05$ ).