Figure S7. Proportion of true postzygotic single-nucleotide mutations (pSNMs) among all identified sites. The X axis denotes the expected minor allele fraction in pSNM sites. Our identification pipeline showed dramatically higher proportions of true pSNMs than the pooled sample model of GATK followed by its standard filters or our filters, because a large number of false positives were mis-identified in germline homozygous and heterozygous sites by GATK pooled sample model.