



Additional File 4: Genome-wide SNP density plots for *bak1-5 mob1*.

All SNPs with allele frequencies >75% are plotted in grey, while candidate causative SNPs (defined as those causing non-synonymous changes in gene-coding regions) are plotted in red. These plots are also available at <http://dx.doi.org/10.6084/m9.figshare.1250028>.