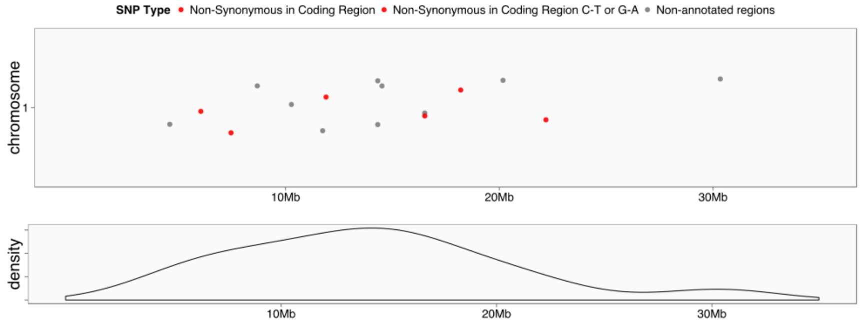
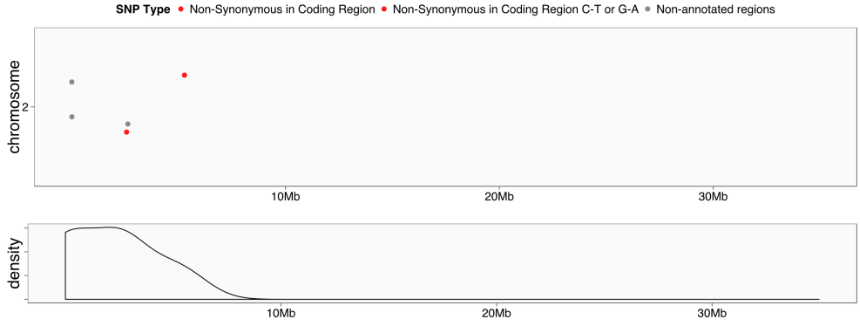
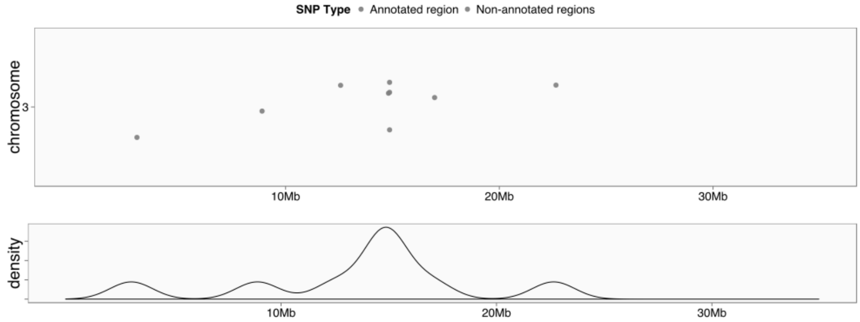
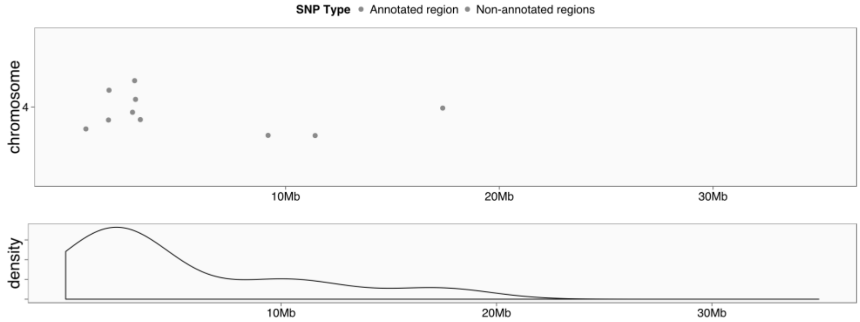
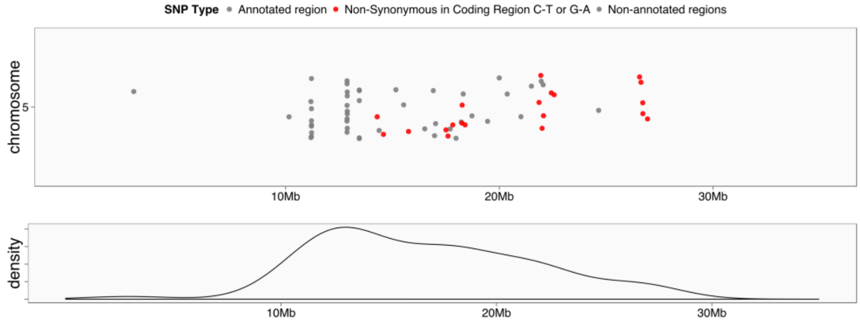

SNP Type
● Non-Synonymous in Coding Region
● Non-Synonymous in Coding Region C-T or G-A
● Non-annotated regions
chromosome
1
10Mb
20Mb
30Mb
density
10Mb
20Mb
30Mb


SNP Type
● Non-Synonymous in Coding Region
● Non-Synonymous in Coding Region C-T or G-A
● Non-annotated regions
chromosome
2
10Mb
20Mb
30Mb
density
10Mb
20Mb
30Mb


SNP Type
● Annotated region
● Non-annotated regions
chromosome
3
10Mb
20Mb
30Mb
density
10Mb
20Mb
30Mb


SNP Type
● Annotated region
● Non-annotated regions
chromosome
4
10Mb
20Mb
30Mb
density
10Mb
20Mb
30Mb


SNP Type
● Annotated region
● Non-Synonymous in Coding Region C-T or G-A
● Non-annotated regions
chromosome
5
10Mb
20Mb
30Mb
density
10Mb
20Mb
30Mb

Additional File 5: Genome-wide SNP density plots for *bak1-5 mob2.*

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.1250027.