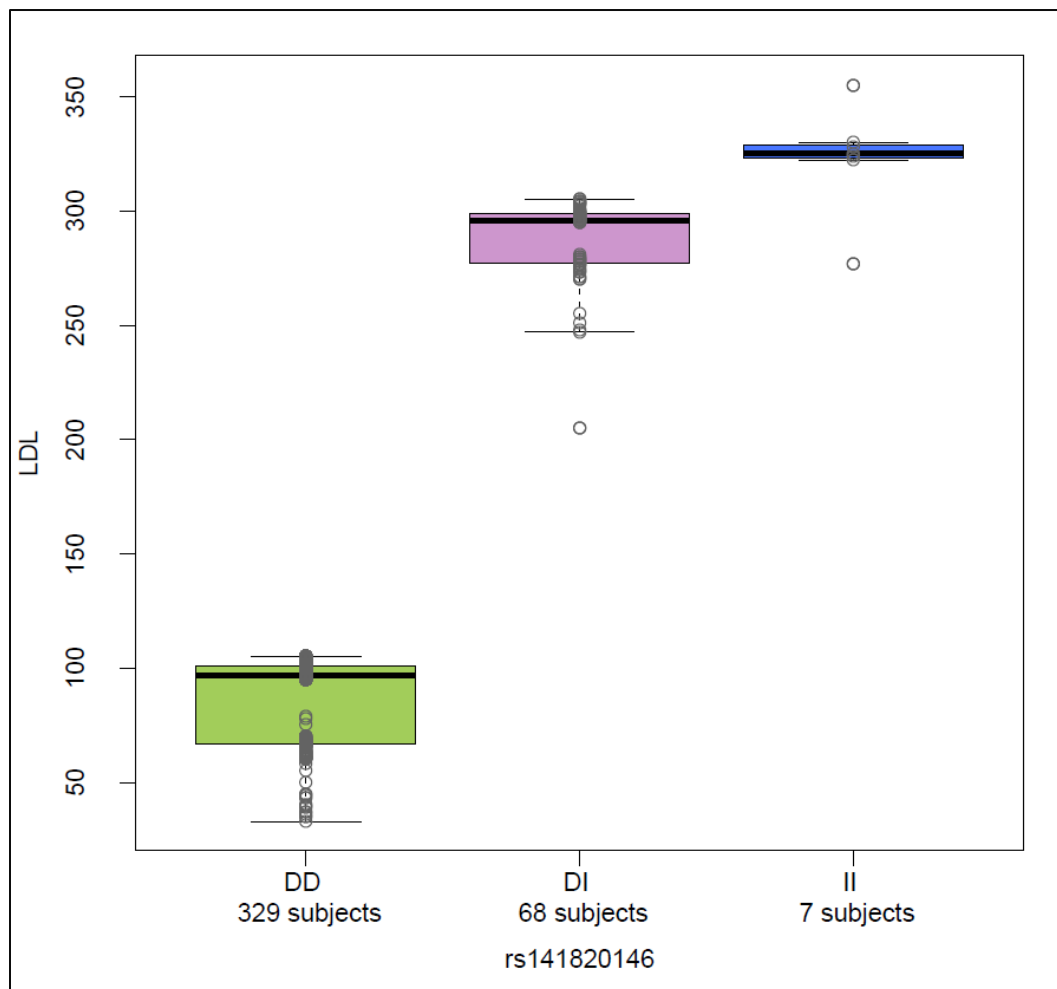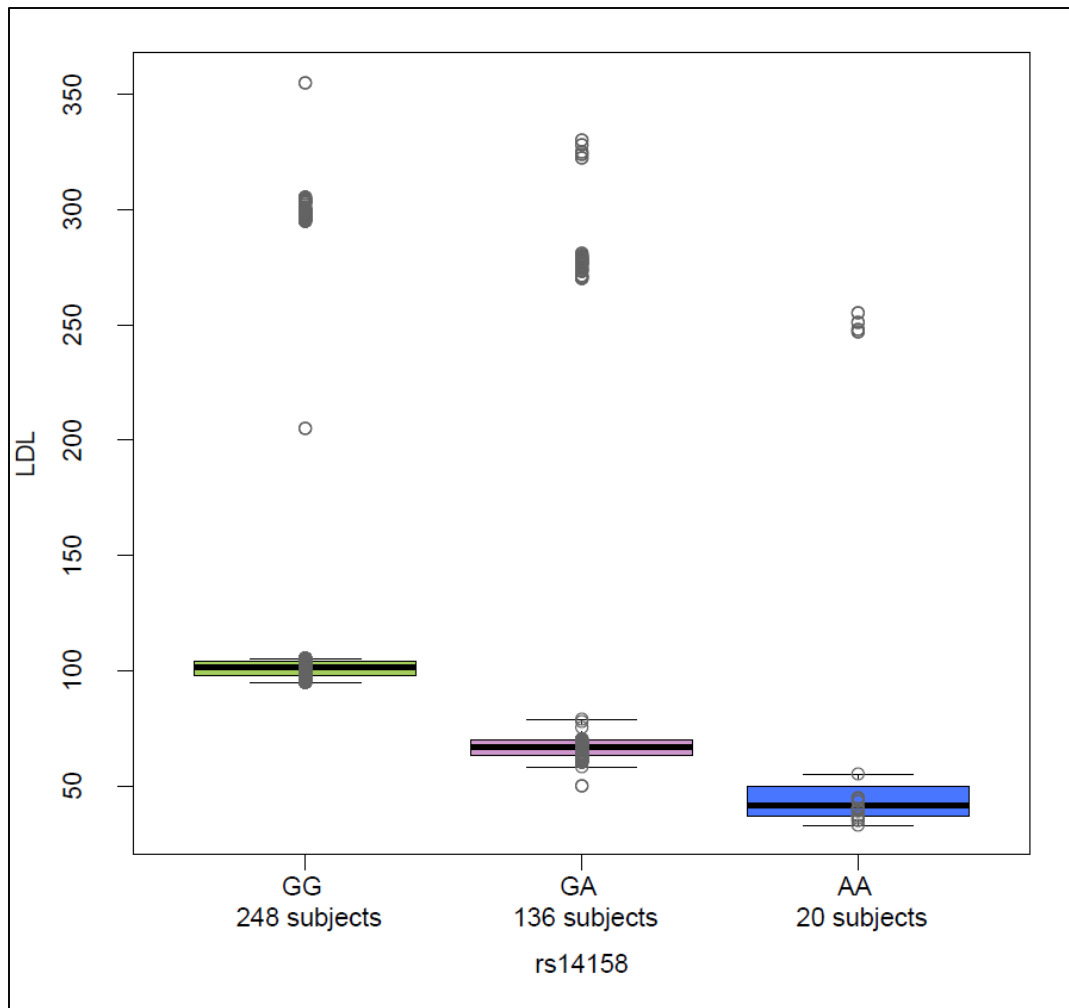```
Enter the line number of the desired variant to select as the
reference variant (columns are SNP, p-value, beta):
     1   rs141820146   1.498e-198   175.2
     2   rs142444132   1.498e-198   175.2
     3   rs17248769   1.498e-198   175.2
     4   rs17248776   1.498e-198   175.2
     5   rs17248783   1.498e-198   175.2
     6   rs2228671   1.498e-198   175.2
     7   rs73015033   1.498e-198   175.2
     8   rs73015034   1.498e-198   175.2
     9   rs74857287   1.498e-198   175.2
    10   rs117423069   2.333e-187   173.2
    11   rs17242395   2.333e-187   173.2
```
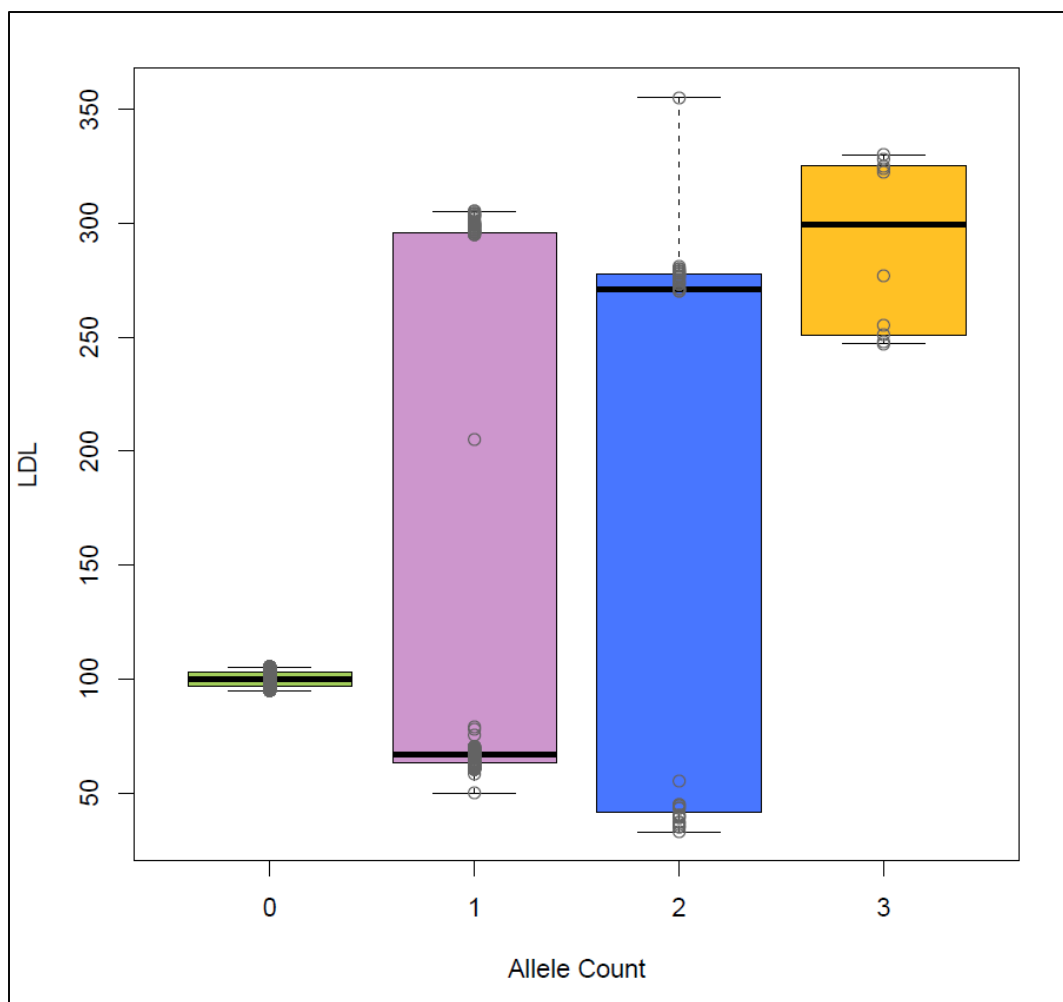
**Supplementary Figure 1.** Sample of output when choosing to manually select reference variant.



**Supplementary Figure 2.** Boxplot of LDL levels based on genotype of top variant from the first iteration of the Conditional Analysis Cakewalk on simulated data.

**Supplementary Figure 3.** Boxplot of LDL levels based on genotype of top variant from second iteration of Conditional Analysis Cakewalk on simulated data.

**Supplementary Figure 4.** Boxplot of LDL levels based on allele count of top variants from all iterations of the Conditional Analysis Cakewalk on simulated data.

```
SNPNAME         CHR:POS         PVALUE      BETA    LOCUSZOOM                       BOXPLOT
rs141820146     chr19:11209757  1.50E-198   175.2   LZ_LDL.chr19:11209757.pdf       LDL.test1.pdf
rs14158         chr19:11242044  1.90E-67    -32.9   LZ_LDL.chr19:11242044.pdf       LDL.test2.pdf


Statistics for final boxplot
Allele_count    Subject_count
      0              205
      1              150
      2               39
      3               10
```

Supplementary Figure 5. Contents of output file, TOP_SNPS.csv, containing data from each iteration of the Conditional Analysis Cakewalk on simulated data and statistics for the final boxplot.