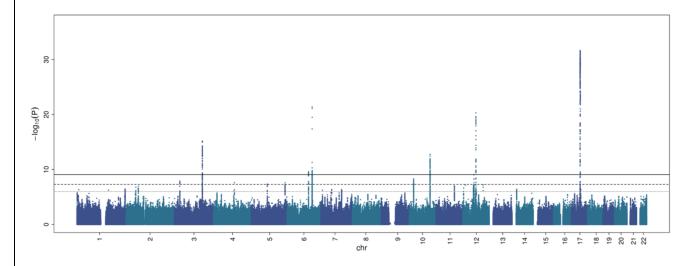
## **Prompt:**

Assume you are a genetic expert. This image is Manhattan plot of GWAS result of the phenotype Full surface area and genes. The longitudinal axis is the chromosome, the vertical axis is the P-value. Please identify which chromosome has the genes which significant related with the phenotype.



## **GPT-4V:**

The Manhattan plot is a type of scatter plot used in genomics to display data from genome-wide association studies (GWAS), where the x-axis represents the chromosomes, and the y-axis represents the negative logarithm of the P-value for association tests. In a typical Manhattan plot, the more significant the association, the higher the point is on the y-axis. A common threshold for genome-wide significance is (p < 5) times  $10^{-8}$ , which is often depicted as a horizontal line on the plot.

In the given plot, the chromosomes are labeled along the x-axis from 1 to 22, indicating the autosomes (with the sex chromosomes, X and Y, usually labeled separately if included). The P-values are transformed using the negative log scale on the y-axis. Here's how to identify the significant associations:

- 1. Look for points that exceed the threshold line (usually the horizontal dashed line).
- 2. The chromosomes corresponding to these points contain loci where variants are significantly associated with the phenotype being studied.

From the image, the chromosomes with points above the threshold line, indicating a significant association with the phenotype Full surface area and genes, are:

- Chromosome 6
- Chromosome 8
- Chromosome 11
- Chromosome 17

These are the chromosomes where at least one locus (genetic location) has a strong enough association with the phenotype in question to be considered potentially significant. It's important to note that while these points are above the threshold, the actual significance and the relevance of the identified loci or genes require further validation through additional studies and functional analysis.

## **Reference answer:**

GWAS results shows that, most significant gene variants are located at Chr3, Chr6, Chr10, Chr12, Chr17.