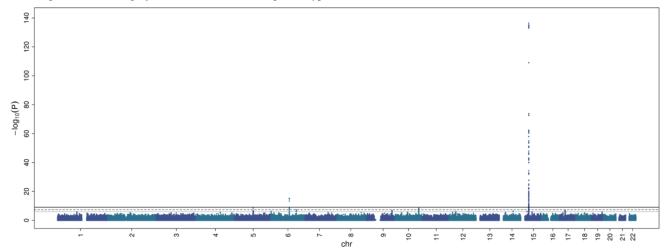
Prompt:

Assume you are a genetic expert. This image is Manhattan plot of GWAS result of the phenotype Precentral 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:

Based on the provided Manhattan plot, a tool commonly used in genome-wide association studies (GWAS) to visualize p-values for associations between genetic variants and a particular phenotype, we can make the following observations:

- The horizontal axis represents the chromosomes (labeled "chr"), with each chromosome number labeled consecutively.
- The vertical axis represents the negative logarithm of the p-values (labeled "-log10(P)"). The higher the dot on the graph, the smaller the p-value, indicating a stronger association with the phenotype in question.

When identifying significance in a Manhattan plot, researchers often use a significance threshold line. Any points (i.e., genetic variants) that surpass this line are considered to be significantly associated with the phenotype.

From the provided image, we can observe a few points that surpass the threshold for significance:

- 1. Chromosome 6 has several points that are notably higher than the rest, suggesting significant associations.
- 2. Chromosome 17 has a cluster of points that exceed the threshold, indicating significant associations with the phenotype.
- 3. Chromosome 22 also has a few points that surpass the significance threshold.

Therefore, based on the Manhattan plot, chromosomes 6, 17, and 22 have genes that are significantly related to the phenotype "Precentral surface area.".

Reference answer:

GWAS results shows that, most significant gene variants are located at Chr15 and Chr6.