Figure (a) shows the distribution of gene sizes (bp) for different categories: all genes, CNV-hit genes, CNV-hit genes control, and epilepsy genes. The density distribution is plotted on a logarithmic scale.

Figure (b) illustrates the fold-enrichment of CNVs in public databases for deletion and duplication events. The enrichment is compared across different groups (controls, patients, Twins) and indicated by P-values: <0.05 and >0.05.