CMN Clinical Trials Global Report 2026 *Sample*

This sample report is based on 149 publicly disclosed, manually curated clinical trials involving gene-editing technologies, which is a subset of the approximately 300 clinical trials identified by CMN to date. New trials are added on an ongoing basis and updated reports will be published every month. A small number of trials across editing modality, disease category, delivery approach, and geographic location are classified as unknown or involve combined or overlapping categories, reflecting either incomplete reporting or experimental complexity.

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Gene-editing modalities

As shown in Figures 1 and 2, the distribution of gene-editing modalities is dominated by CRISPR-Cas9-based approaches, which account for 51% of reported cases (n = 76). Base editing represents the second most frequently used modality (17%, n = 26). Other programmable technologies, including those based on TALENs, CRISPR-Cas12, and zinc finger nucleases, are represented albeit at lower frequencies with each contributing approximately 5-6% of the total (Figure 1). Less commonly used or newer editing strategies, including meganucleases, RNA exon editing, prime editing, and ADAR-based RNA editing, collectively represent approximately 8 % of the dataset.

Figure 1

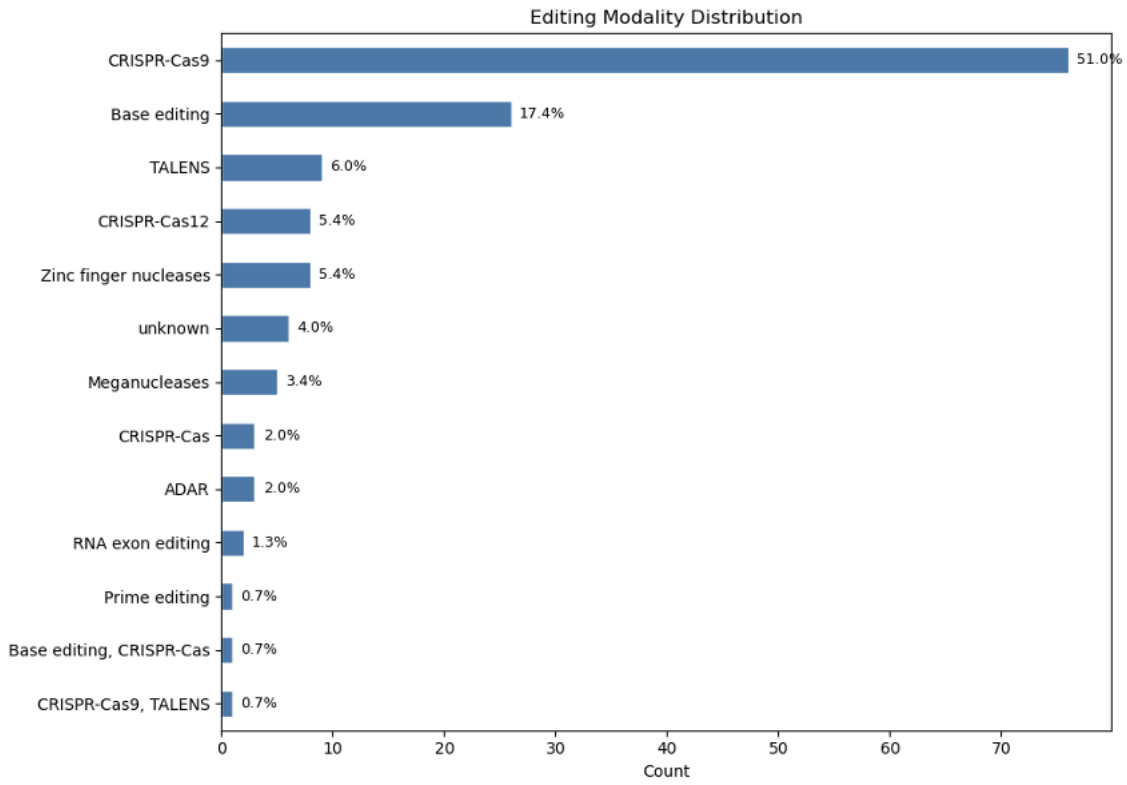

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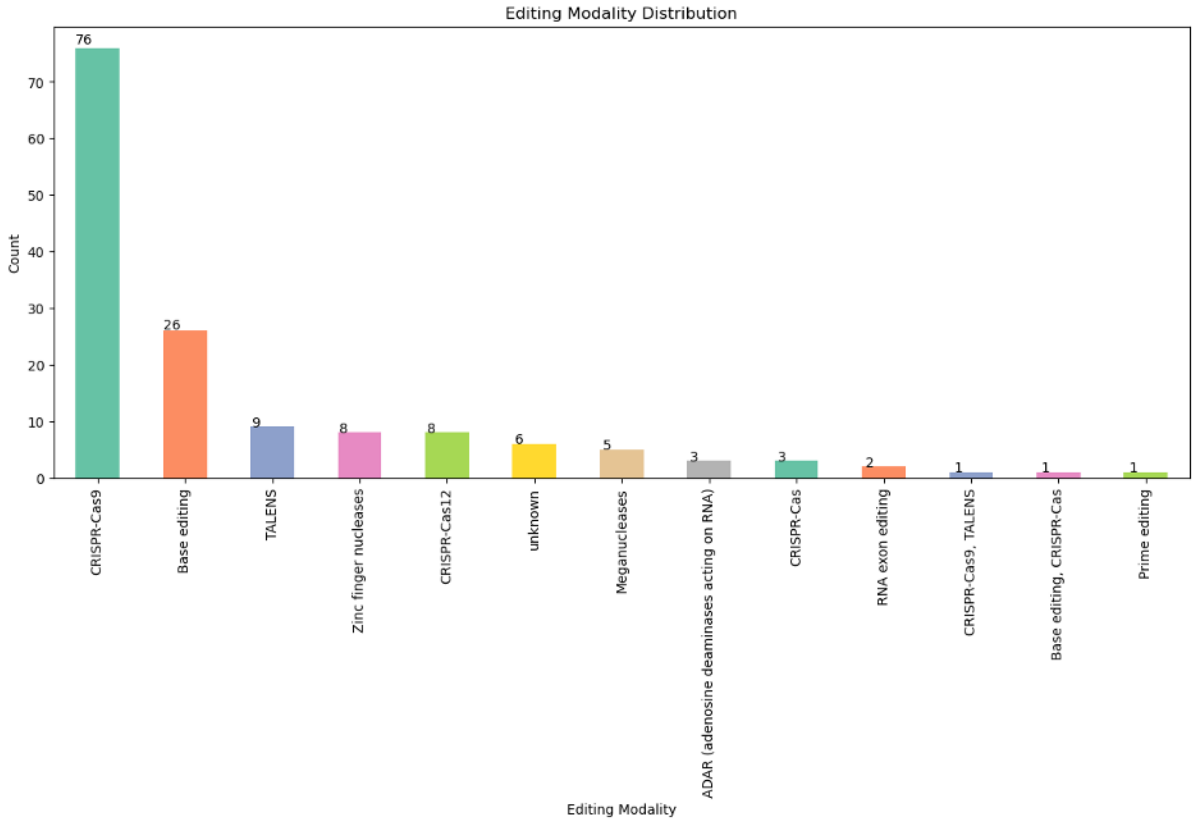
Figure 2



Disease categories

The 149 trials included in this report span a broad range of disease categories and editing strategies. *Ex vivo* editing is represented across multiple disease areas, with a large number of trials in haematological malignancies, diseases of the blood or blood-forming organs, and solid malignancies. *In vivo* editing is also applied across several disease categories, including genetic metabolic diseases, diseases of the visual system, infectious diseases, and disorders of the circulatory system, though at lower overall counts (Figure 3). Across disease categories, CRISPR-Cas9-based approaches are observed most frequently, while other editing modalities, including base editing, TALENs, zinc finger nucleases, and RNA-based approaches, are represented at lower frequencies (Figures 4).

Figure 3

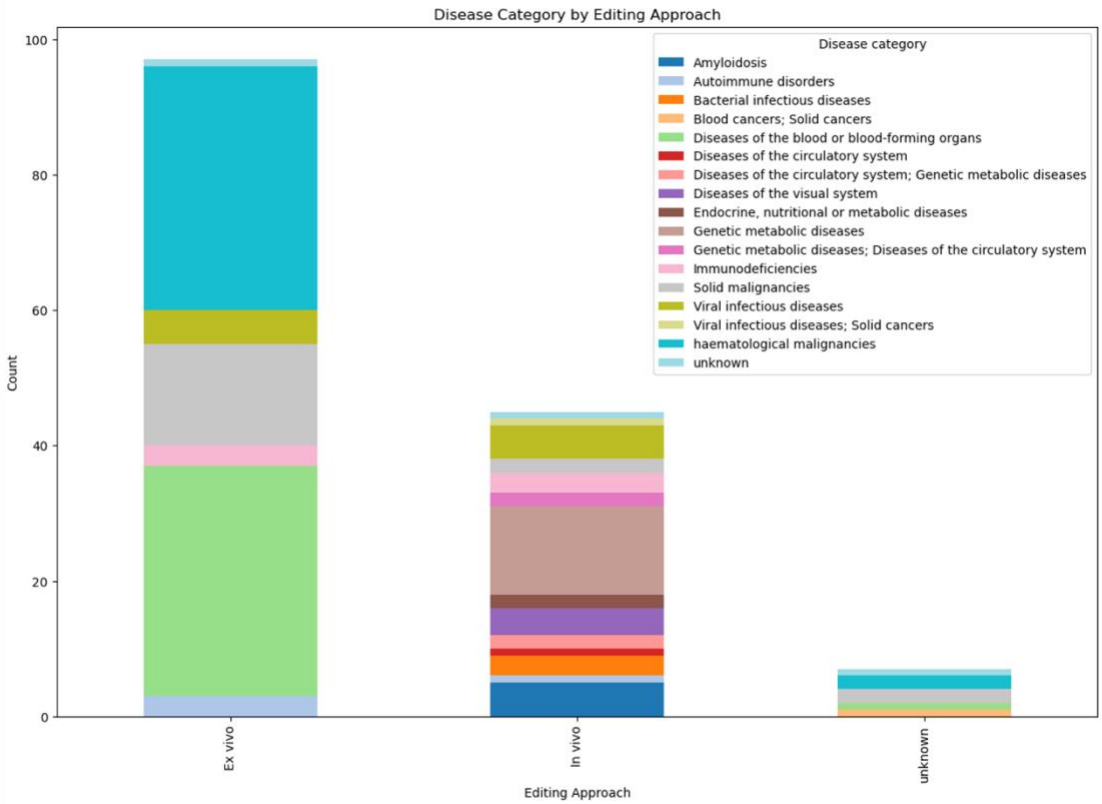
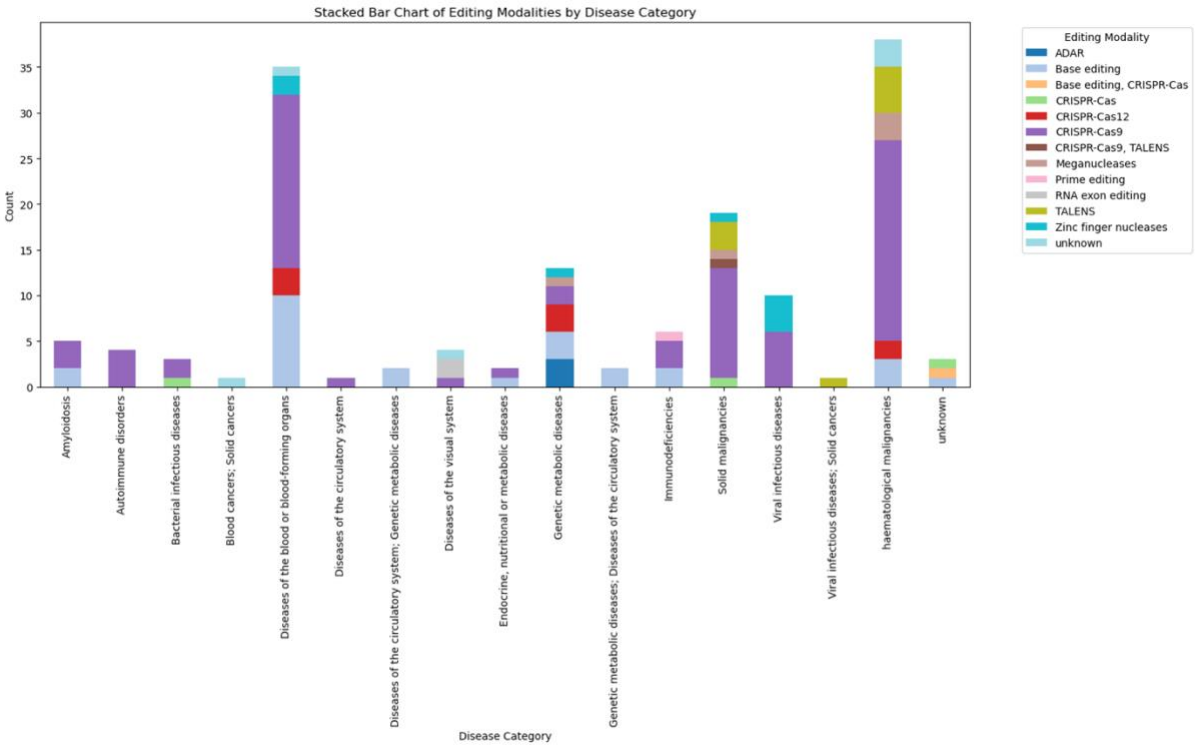


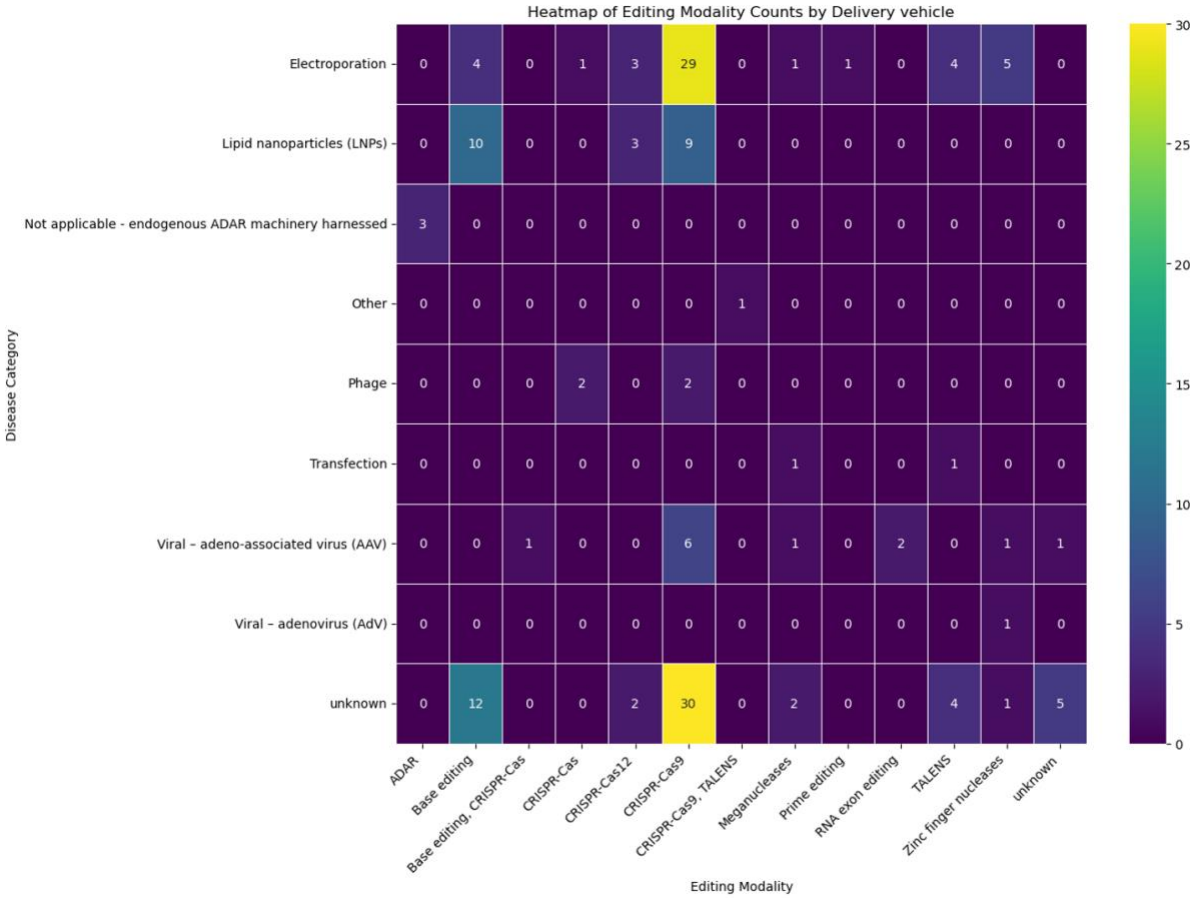
Figure 4



Delivery

With respect to delivery, viral and non-viral strategies are represented across trials, with delivery approach varying by editing modality and disease category (Figures 5).

Figure 5



Geographic distribution of trials

The geographic distribution of trials is summarised in Figures 6 and 7. When grouped by country, the highest numbers of trials are reported in the United States and China, followed by the United Kingdom, Australia, Canada, and several European countries (Figure 6). When grouped by UN region (Figure 7), trials are primarily concentrated in Northern America, Eastern Asia, and Europe, with trials also emerging across South America, Africa, and the Middle East.

Figure 6

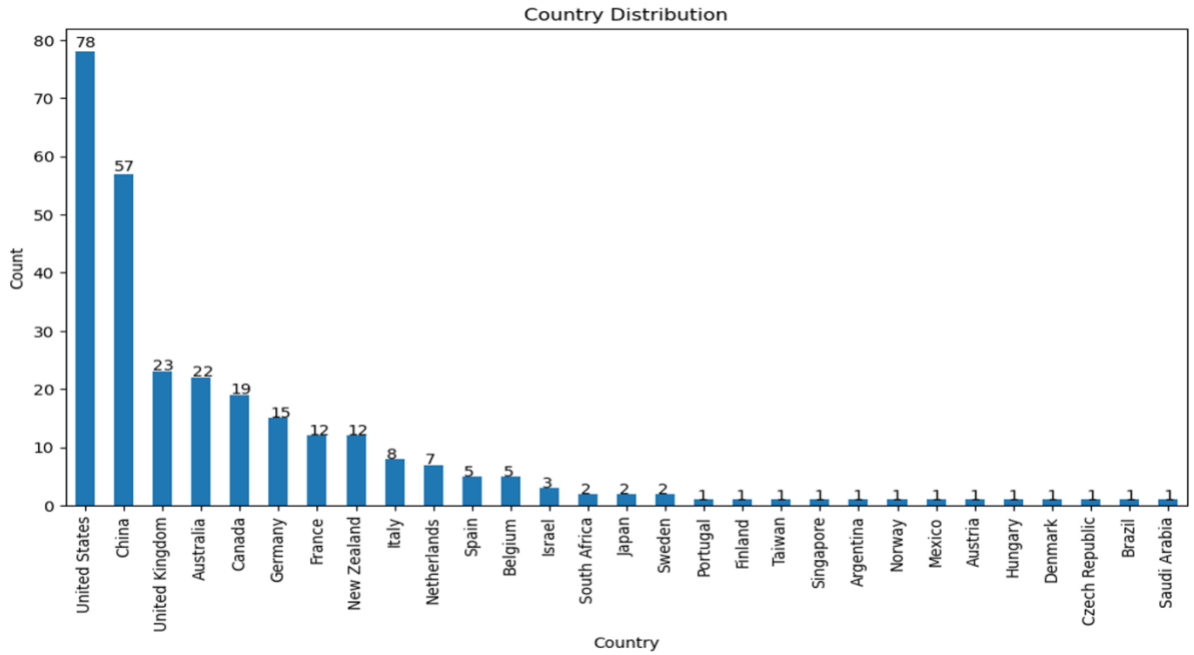
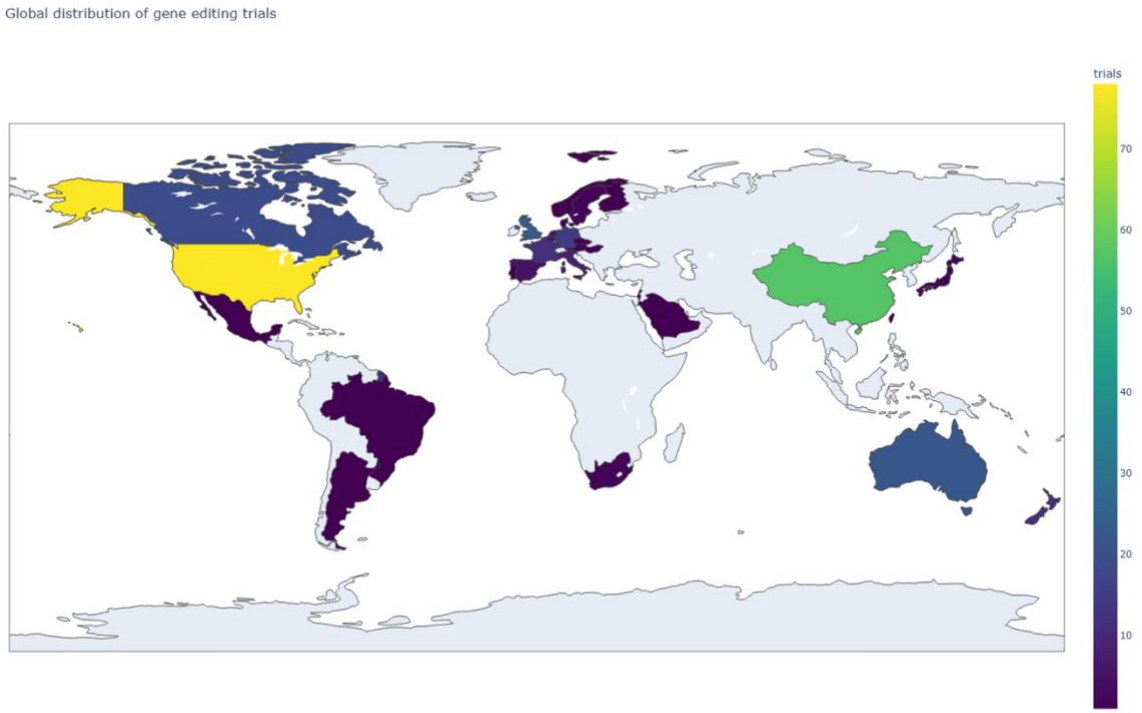


Figure 7



List of Abbreviations

- ADAR – Adenosine Deaminase Acting on RNA
- CRISPR – Clustered Regularly Interspaced Short Palindromic Repeats
- Cas – CRISPR-associated protein
- TALENs – Transcription Activator-Like Effector Nucleases

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